wwPDB EM Validation Summary Report (i)

Jul 3, 2024 – 11:47 pm BST

PDB ID	:	6ZSB
EMDB ID	:	EMD-11392
Title	:	Human mitochondrial ribosome in complex with mRNA and P-site tRNA
Authors	:	Aibara, S.; Singh, V.; Modelska, A.; Amunts, A.
Deposited on	:	2020-07-15
Resolution	:	4.50 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 (i) 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 (1)) were used in the production of this report:

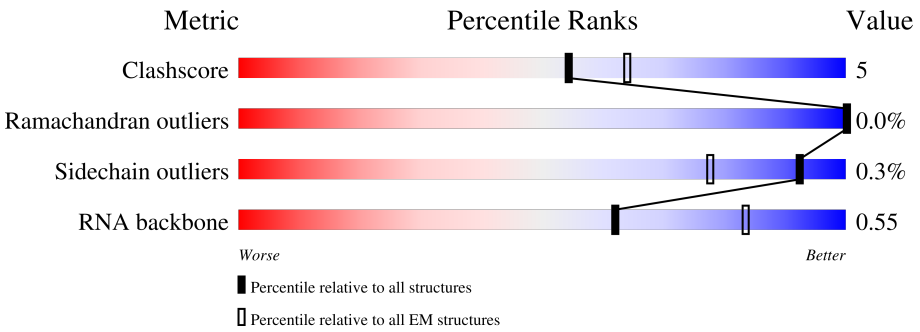
EMDB validation analysis	:	0.0.1.dev92
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 4.50 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 <=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	49% 8% 43%
2	1	65	68% 14% 18%
3	2	92	43% 7% 50%
4	3	188	39% 12% 49%
5	4	103	33% • 63%
6	5	423	80% 13% 7%
7	6	380	79% 14% 7%

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Mol	Chain	Length	Quality of chain
8	7	338	75% 11% 14%
9	8	206	6% 61% 6% 33%
10	9	137	81% 9% 9%
11	XA	1561	61% 30% 5%
12	A0	218	17% 79% 13% 8%
13	A1	323	12% 74% 11% 15%
14	A2	118	15% 80% 19%
15	A3	199	26% 9% 65%
16	A4	689	34% 70% 10% 20%
17	AA	954	64% 27% 5%
18	AB	296	63% 10% 26%
19	AC	167	6% 71% 8% 21%
20	AD	430	7% 73% 7% 20%
21	AE	125	6% 81% 17%
22	AF	242	6% 71% 12% 17%
23	AG	396	5% 67% 9% 23%
24	AH	201	9% 58% 9% 33%
25	AI	194	61% 9% 30%
26	AJ	138	7% 62% 17% 22%
27	AK	128	5% 62% 17% 21%
28	AL	257	55% 9% 36%
29	AM	137	7% 74% 11% 15%
30	AN	130	72% 10% 18%
31	AO	258	9% 62% 9% 28%
32	AP	142	58% 9% 33%

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Mol	Chain	Length	Quality of chain
33	AQ	87	7% 89% 9%
34	AR	360	9% 58% 11% 31%
35	AS	190	12% 66% 30%
36	AT	173	78% 16% 6%
37	AU	205	69% 15% 16%
38	AV	414	26% 72% 12% 16%
39	AW	187	5% 46% 6% 48%
40	AX	398	12% 75% 12% 13%
41	AY	395	5% 24% 71%
42	AZ	106	71% 10% 19%
43	XB	72	50% 26% 6% 18%
44	XD	305	66% 10% 23%
45	XE	348	79% 8% 13%
46	XF	311	67% 13% 20%
47	XH	267	33% 64%
48	XI	261	25% 73% 8% 19%
49	XJ	192	12% 76% 12% 11%
50	XK	178	87% 12%
51	XL	145	70% 10% 21%
52	XM	296	81% 16%
53	XN	251	78% 10% 12%
54	XO	175	70% 17% 13%
55	XP	180	74% 6% 21%
56	XQ	292	6% 71% 11% 18%
57	XR	149	76% 18% 6%

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Mol	Chain	Length	Quality of chain
58	XS	205	70% 8% 22%
59	XT	206	68% 12% 19%
60	XU	153	78% 14% 8%
61	XV	216	79% 13% 6%
62	XW	148	66% 8% 25%
63	XX	256	84% 11% 5%
64	XY	250	57% 14% 29%
65	XZ	161	67% 7% 25%
66	a	142	68% 32%
67	b	215	69% 31%
68	c	332	83% 17%
69	d	306	6% 70% 29%
70	e	279	15% 76% 22%
71	f	212	6% 67% 33%
72	g	166	78% 20%
73	h	158	68% 32%
74	i	128	76% 24%
75	j	123	70% 30%
76	k	112	5% 85% 15%
77	l	138	7% 58% 42%
78	m	128	47% 53%
79	o	102	92% 8%
80	p	206	62% 38%
81	q	222	14% 73% 26%
82	r	196	78% 22%

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Mol	Chain	Length	Quality of chain
83	r1	4	100%
84	r3	75	5%, 100%
85	s	439	84%, 16%
86	t1	198	19%, 23%, 77%
86	t2	198	14%, 15%, 85%
86	t3	198	15%, 15%, 85%
86	t4	198	15%, 15%, 85%
86	t5	198	15%, 15%, 85%
86	t6	198	14%, 14%, 86%
87	A	8	12%, 38%, 38%, 12%

2 Entry composition (i)

There are 91 unique types of molecules in this entry. The entry contains 312076 atoms, of which 143042 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	1783	545	903	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	703	217	362	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	6404	2070	3200	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	139	2377	747	1202	208	218	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 mitochondrial rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
11	XA	1499	47993	14284	16160	5756	10294	1499	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	552	8955	2866	4485	756	820	28	0	0

- Molecule 17 is a RNA chain called 12S mitochondrial rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
17	AA	924	29592	8800	9964	3540	6364	924	0	0

- Molecule 18 is a protein called 28S ribosomal protein S2, mitochondrial.

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

- Molecule 19 is a protein called 28S ribosomal protein S24, mitochondrial.

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

- Molecule 20 is a protein called 28S ribosomal protein S5, mitochondrial.

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

- Molecule 21 is a protein called 28S ribosomal protein S6, mitochondrial.

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

- Molecule 22 is a protein called 28S ribosomal protein S7, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
22	AF	201	3383	1069	1715	305	283	11	0	0

- Molecule 23 is a protein called 28S ribosomal protein S9, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
23	AG	304	4996	1593	2491	444	454	14	0	0

- Molecule 24 is a protein called 28S ribosomal protein S10, mitochondrial.

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

- Molecule 25 is a protein called 28S ribosomal protein S11, mitochondrial.

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

- Molecule 26 is a protein called 28S ribosomal protein S12, mitochondrial.

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

- Molecule 27 is a protein called 28S ribosomal protein S14, mitochondrial.

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

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

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

- Molecule 29 is a protein called 28S ribosomal protein S16, mitochondrial.

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

- Molecule 30 is a protein called 28S ribosomal protein S17, mitochondrial.

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

- Molecule 31 is a protein called 28S ribosomal protein S18b, mitochondrial.

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

- Molecule 32 is a protein called 28S ribosomal protein S18c, mitochondrial.

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

- Molecule 33 is a protein called 28S ribosomal protein S21, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
33	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 34 is a protein called 28S ribosomal protein S22, mitochondrial.

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

- Molecule 35 is a protein called 28S ribosomal protein S23, mitochondrial.

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

- Molecule 36 is a protein called 28S ribosomal protein S25, mitochondrial.

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

- Molecule 37 is a protein called 28S ribosomal protein S26, mitochondrial.

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

- Molecule 38 is a protein called 28S ribosomal protein S27, mitochondrial.

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

- Molecule 39 is a protein called 28S ribosomal protein S28, mitochondrial.

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

- Molecule 40 is a protein called 28S ribosomal protein S29, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
40	AX	348	5619	1802	2805	491	510	11	0	0

- Molecule 41 is a protein called 28S ribosomal protein S31, mitochondrial.

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

- Molecule 42 is a protein called 28S ribosomal protein S33, mitochondrial.

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

- Molecule 43 is a RNA chain called mitochondrial tRNAVal.

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

- Molecule 44 is a protein called 39S ribosomal protein L2, mitochondrial.

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

- Molecule 45 is a protein called 39S ribosomal protein L3, mitochondrial.

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

- Molecule 46 is a protein called 39S ribosomal protein L4, mitochondrial.

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

- Molecule 47 is a protein called 39S ribosomal protein L9, mitochondrial.

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

- Molecule 48 is a protein called 39S ribosomal protein L10, mitochondrial.

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

- Molecule 49 is a protein called 39S ribosomal protein L11, mitochondrial.

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

- Molecule 50 is a protein called 39S ribosomal protein L13, mitochondrial.

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

- Molecule 51 is a protein called 39S ribosomal protein L14, mitochondrial.

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

- Molecule 52 is a protein called 39S ribosomal protein L15, mitochondrial.

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

- Molecule 53 is a protein called 39S ribosomal protein L16, mitochondrial.

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

- Molecule 54 is a protein called 39S ribosomal protein L17, mitochondrial.

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

- Molecule 55 is a protein called 39S ribosomal protein L18, mitochondrial.

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

- Molecule 56 is a protein called 39S ribosomal protein L19, mitochondrial.

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

- Molecule 57 is a protein called 39S ribosomal protein L20, mitochondrial.

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

- Molecule 58 is a protein called 39S ribosomal protein L21, mitochondrial.

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

- Molecule 59 is a protein called 39S ribosomal protein L22, mitochondrial.

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

- Molecule 60 is a protein called 39S ribosomal protein L23, mitochondrial.

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

- Molecule 61 is a protein called 39S ribosomal protein L24, mitochondrial.

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

- Molecule 62 is a protein called 39S ribosomal protein L27, mitochondrial.

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

- Molecule 63 is a protein called 39S ribosomal protein L28, mitochondrial.

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

- Molecule 64 is a protein called 39S ribosomal protein L47, mitochondrial.

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

- Molecule 65 is a protein called 39S ribosomal protein L30, mitochondrial.

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

- Molecule 66 is a protein called 39S ribosomal protein L42, mitochondrial.

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

- Molecule 67 is a protein called 39S ribosomal protein L43, mitochondrial.

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

- Molecule 68 is a protein called 39S ribosomal protein L44, mitochondrial.

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

- Molecule 69 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
69	d	216	3501	1125	1743	305	315	13	0	0

- Molecule 70 is a protein called 39S ribosomal protein L46, mitochondrial.

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

- Molecule 71 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
71	f	143	2314	737	1165	187	221	4	0	0

- Molecule 72 is a protein called 39S ribosomal protein L49, mitochondrial.

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

- Molecule 73 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
73	h	108	1748	560	866	154	165	3	0	0

- Molecule 74 is a protein called 39S ribosomal protein L51, mitochondrial.

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

- Molecule 75 is a protein called 39S ribosomal protein L52, mitochondrial.

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

- Molecule 76 is a protein called 39S ribosomal protein L53, mitochondrial.

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

- Molecule 77 is a protein called 39S ribosomal protein L54, mitochondrial.

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

- Molecule 78 is a protein called 39S ribosomal protein L55, mitochondrial.

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

- Molecule 79 is a protein called Ribosomal protein 63, mitochondrial.

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

- Molecule 80 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

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

- Molecule 81 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		
81	q	164	2737	858	1358	267	249	5	0	0

- Molecule 82 is a protein called 39S ribosomal protein S18a, mitochondrial.

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

- Molecule 83 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
83	r1	4	72	36	8	24	4	0	0

- Molecule 84 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
84	r3	75	1459	711	222	451	75	0	0

- Molecule 85 is a protein called 39S ribosomal protein S30, mitochondrial.

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

- Molecule 86 is a protein called 39S ribosomal protein L12, mitochondrial.

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

- Molecule 87 is a protein called Quinupristin.

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

- Molecule 88 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
88	0	1	1	1	0

Continued on next page...

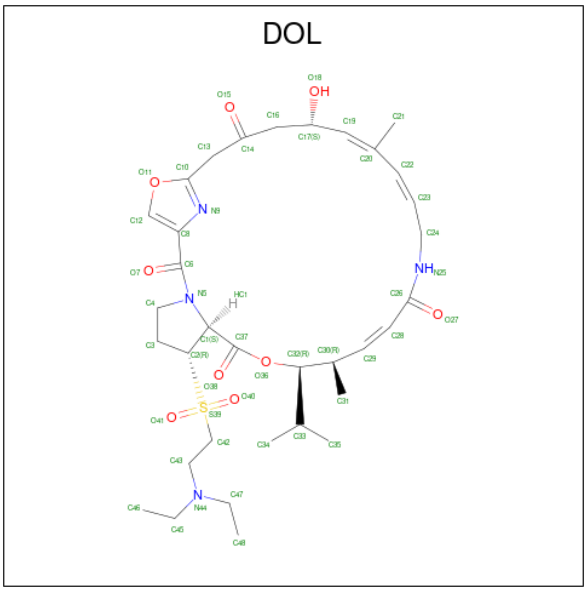
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
88	4	1	1	1	0
88	AB	1	1	1	0
88	AO	1	1	1	0
88	AP	1	1	1	0
88	AT	1	1	1	0
88	r	1	1	1	0

- Molecule 89 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

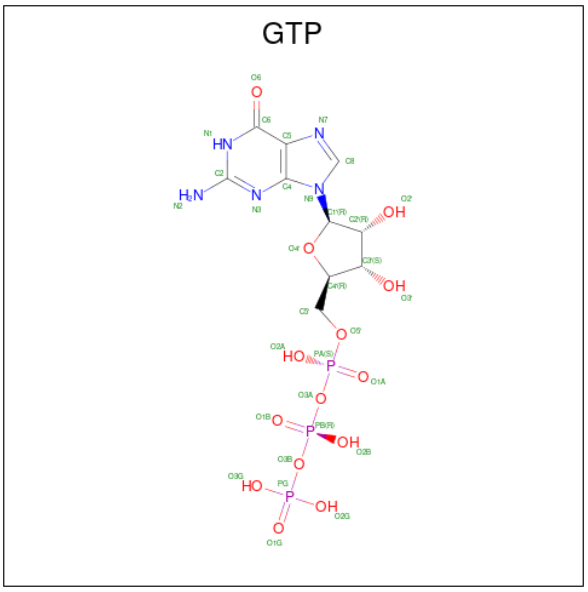
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
89	9	1	1	1	0
89	XA	142	142	142	0
89	A2	1	1	1	0
89	AA	45	45	45	0
89	XD	1	1	1	0
89	XE	1	1	1	0
89	XM	2	2	2	0
89	XW	1	1	1	0
89	g	1	1	1	0

- Molecule 90 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: $C_{34}H_{50}N_4O_9S$).



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

- Molecule 91 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



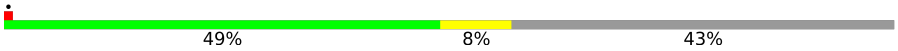
Mol	Chain	Residues	Atoms						AltConf
			Total	C	H	N	O	P	
91	AX	1	42	10	10	5	14	3	0

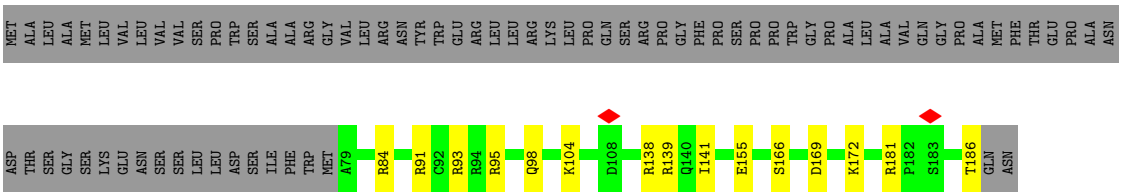
3 Residue-property plots (i)

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

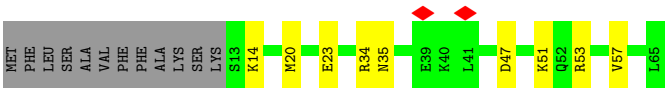
Chain 0:





- Molecule 2: 39S ribosomal protein L33, mitochondrial

Chain 1:

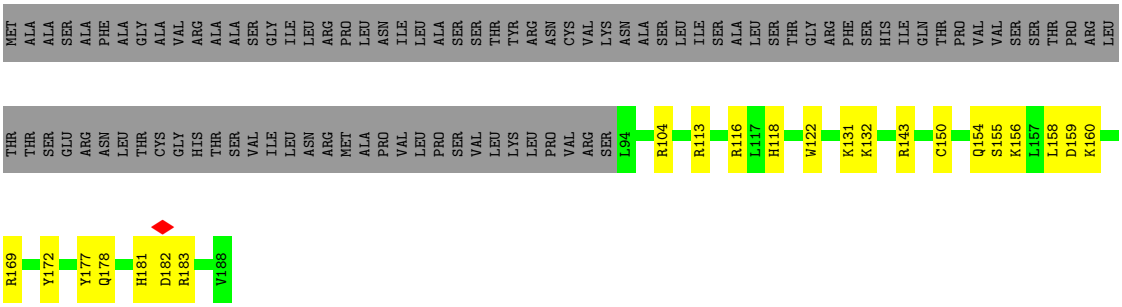


- Molecule 3: 39S ribosomal protein L34, mitochondrial

Chain 2:

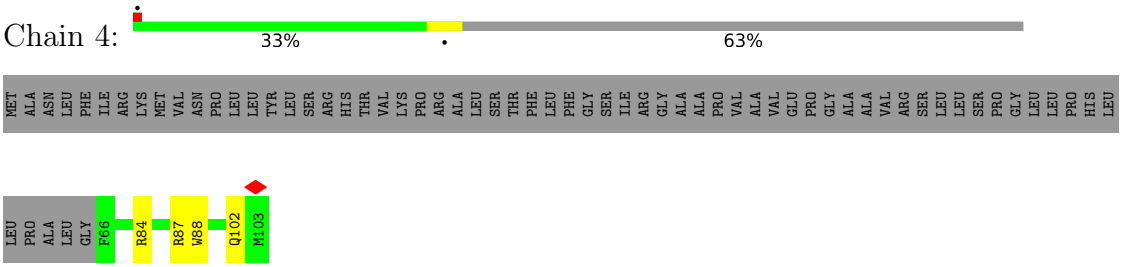
- Molecule 4: 39S ribosomal protein L35, mitochondrial

Chain 3:



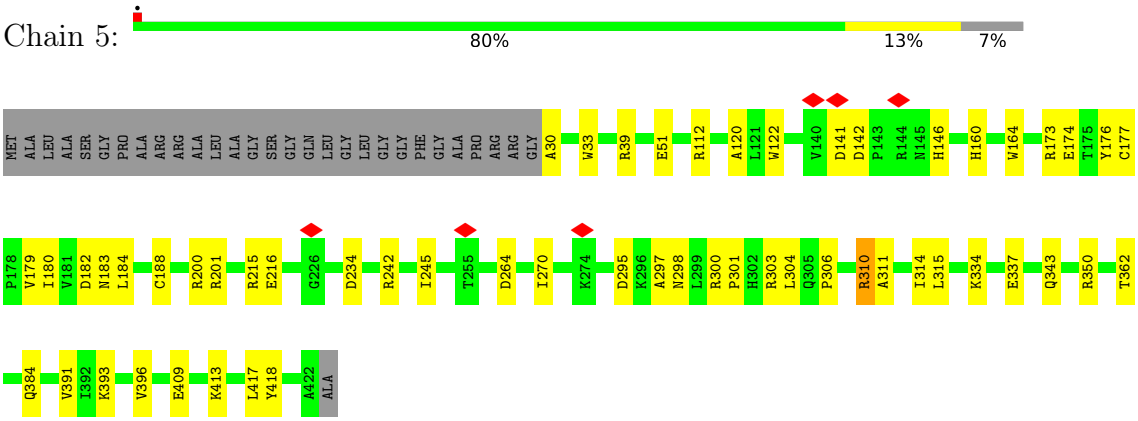
• Molecule 5: 39S ribosomal protein L36, mitochondrial

Chain 4:



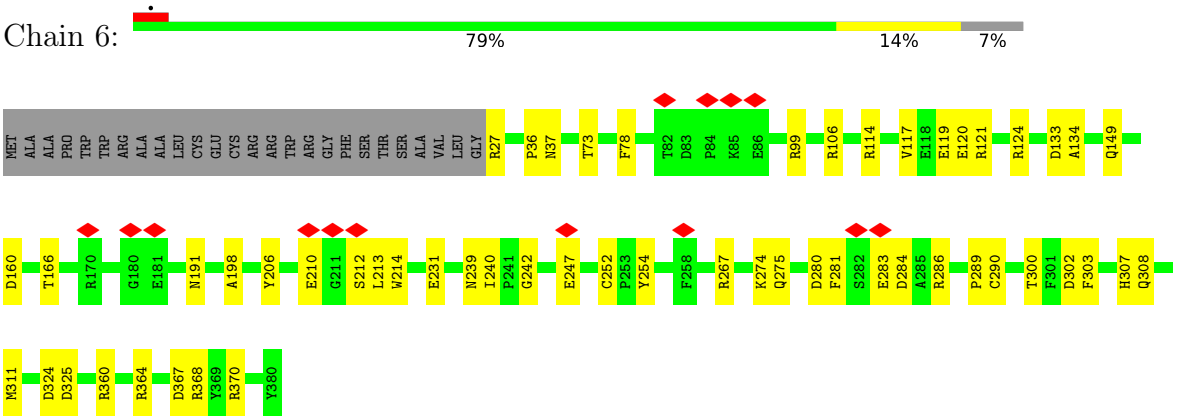
• Molecule 6: 39S ribosomal protein L37, mitochondrial

Chain 5:



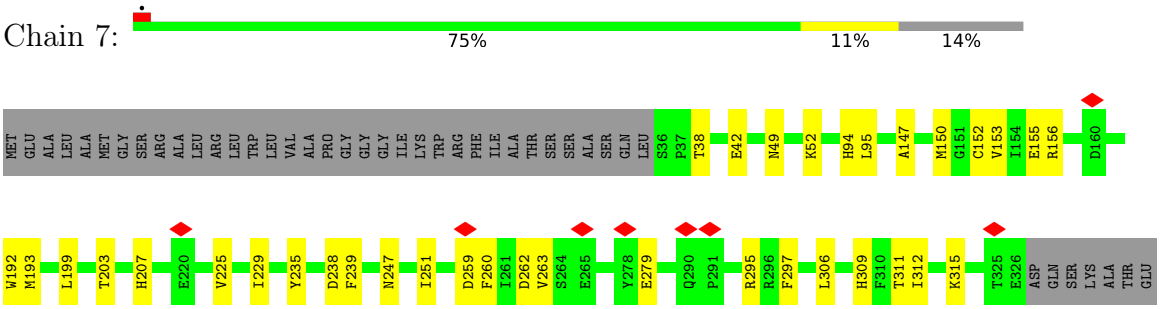
• Molecule 7: 39S ribosomal protein L38, mitochondrial

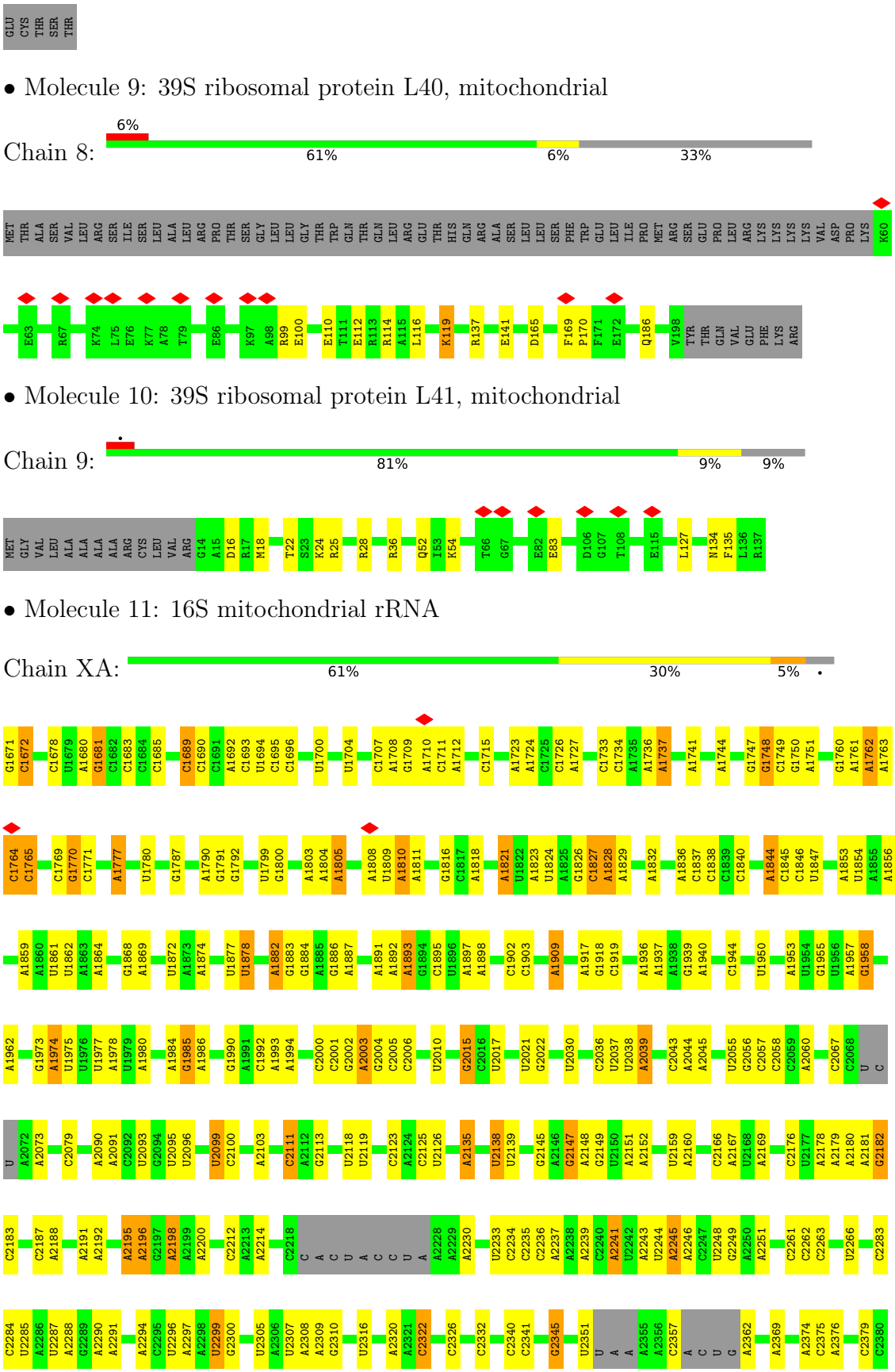
Chain 6:

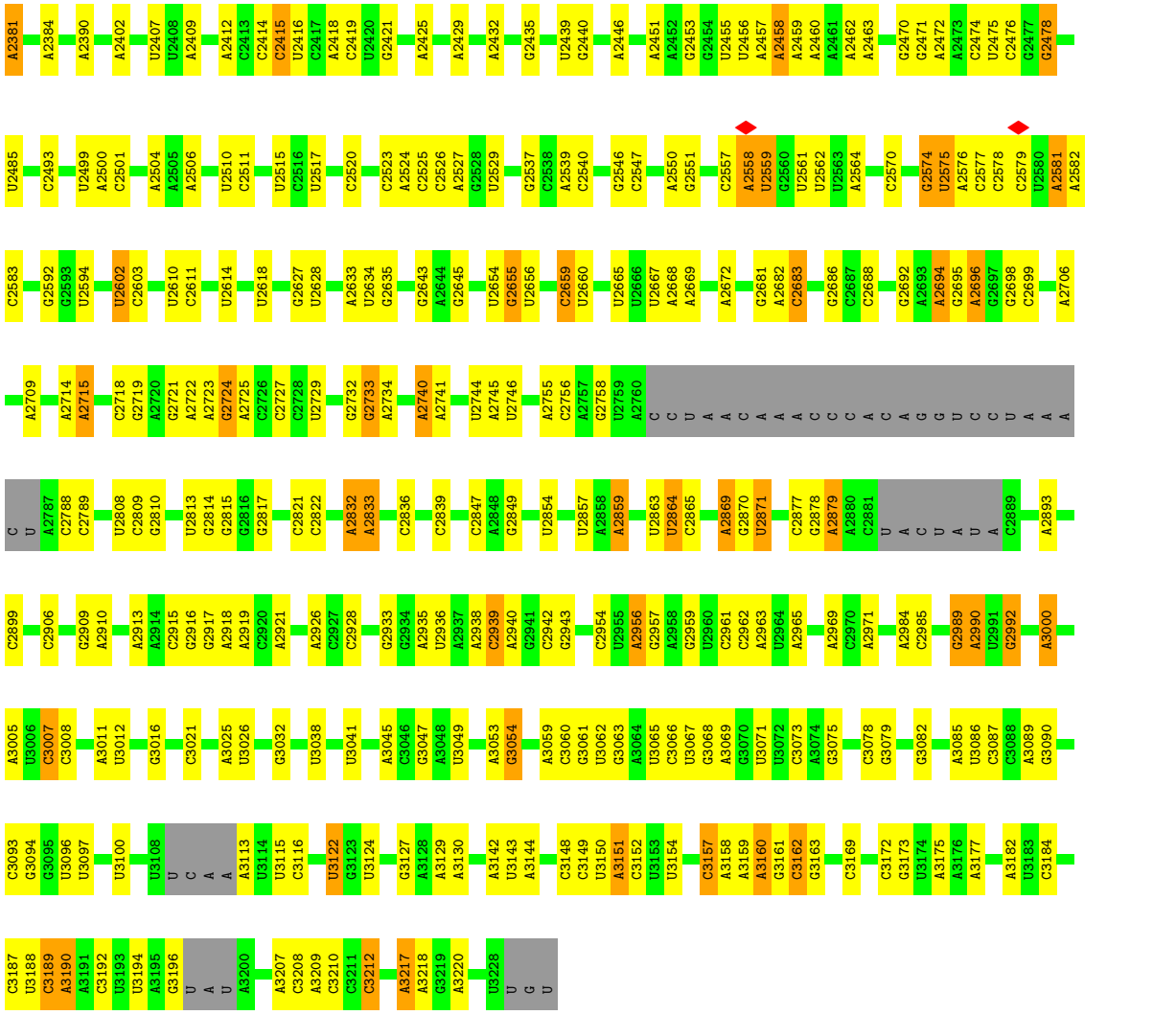


• Molecule 8: 39S ribosomal protein L39, mitochondrial

Chain 7:

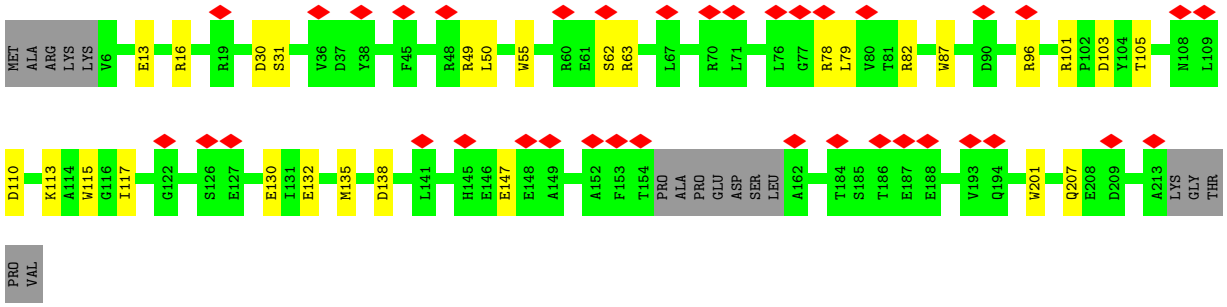



GLU CYS THR SER THR
• Molecule 9: 39S ribosomal protein L40, mitochondrial
Chain 8:
6%
61%
6%
33%
• Molecule 10: 39S ribosomal protein L41, mitochondrial
Chain 9:
81%
9%
9%
• Molecule 11: 16S mitochondrial rRNA
Chain XA:
61%
30%
5%



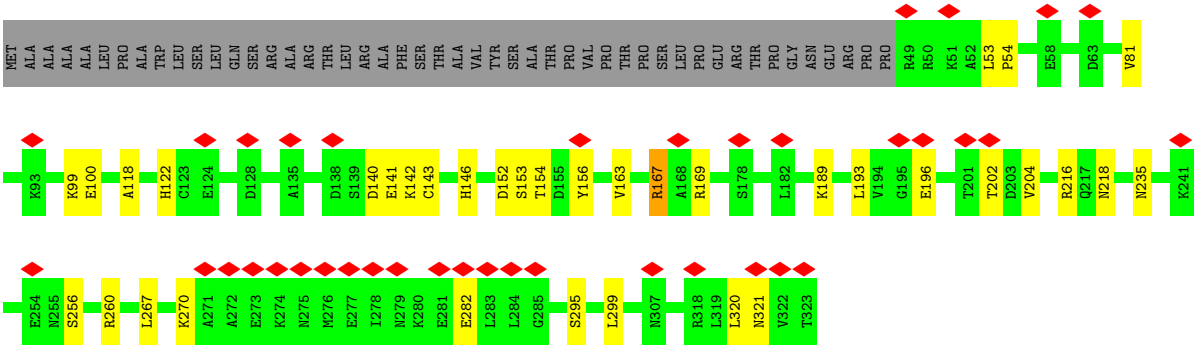
• Molecule 12: 28S ribosomal protein S34, mitochondrial

Chain A0:



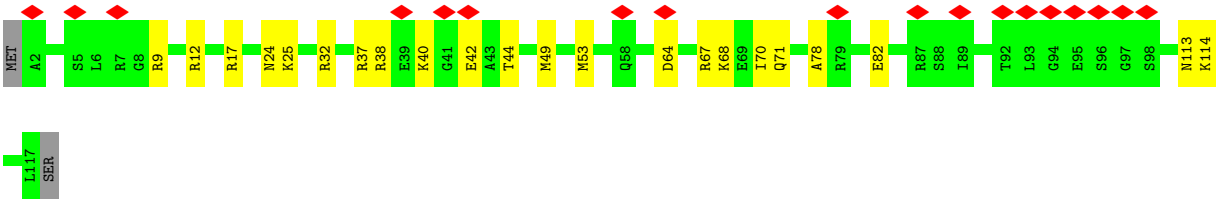
• Molecule 13: 28S ribosomal protein S35, mitochondrial

Chain A1:



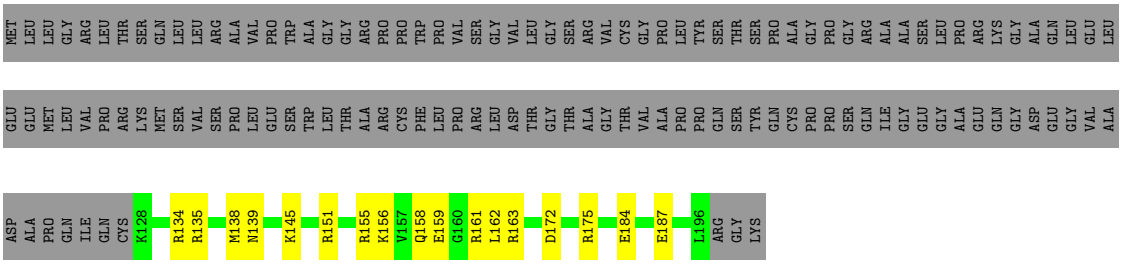
• Molecule 14: Coiled-coil-helix-coiled-coil-helix domain-containing protein 1

Chain A2:



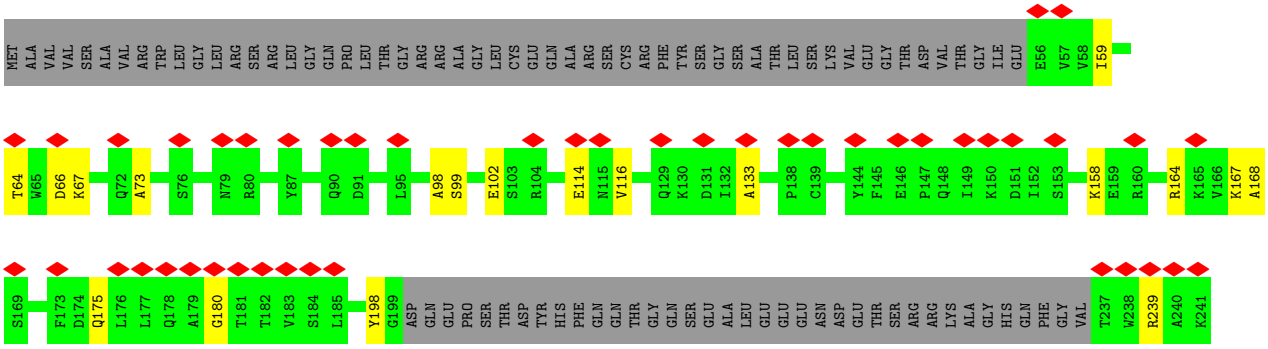
• Molecule 15: Aurora kinase A-interacting protein

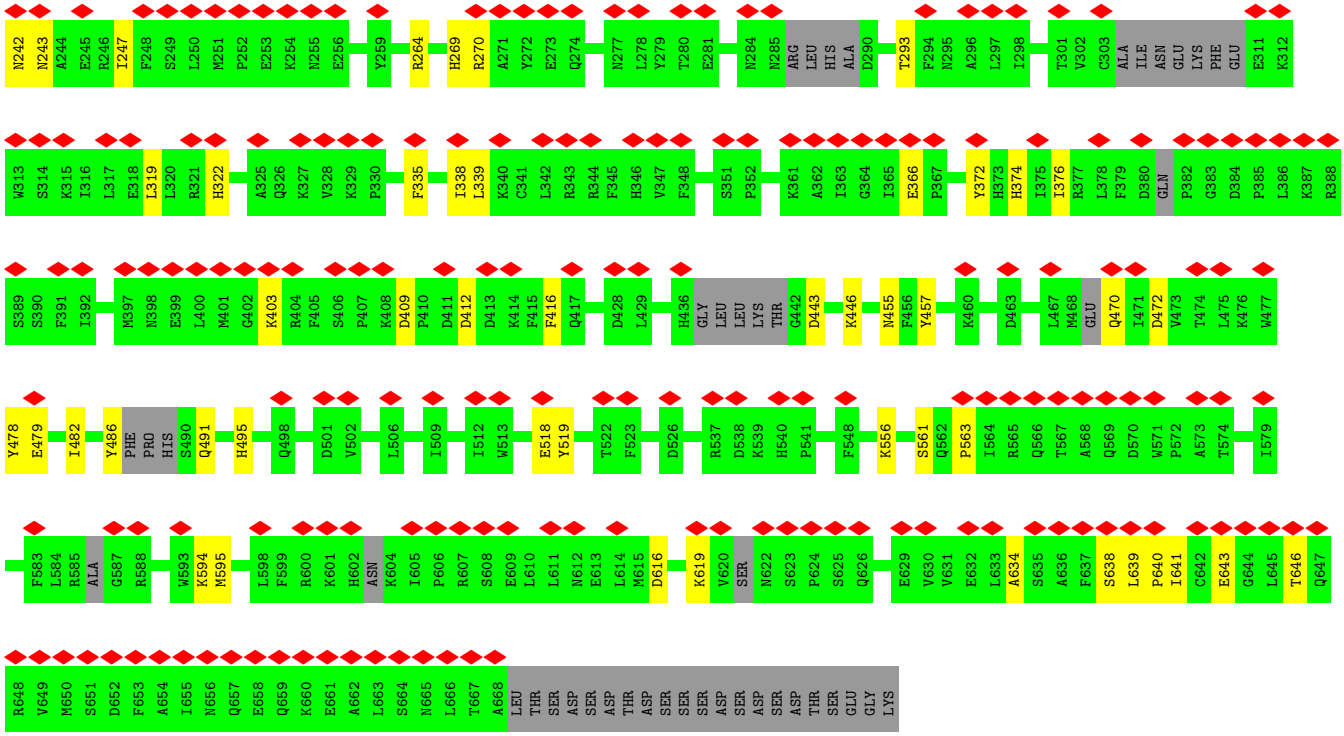
Chain A3:



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

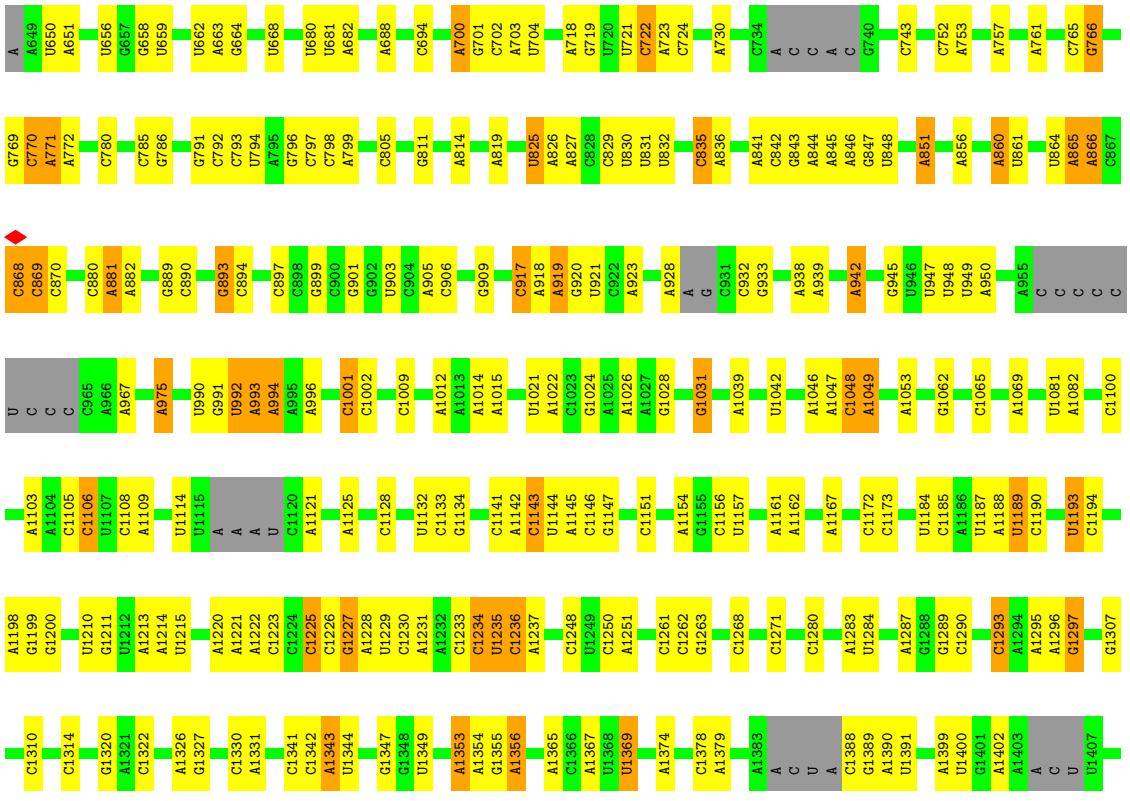
Chain A4:

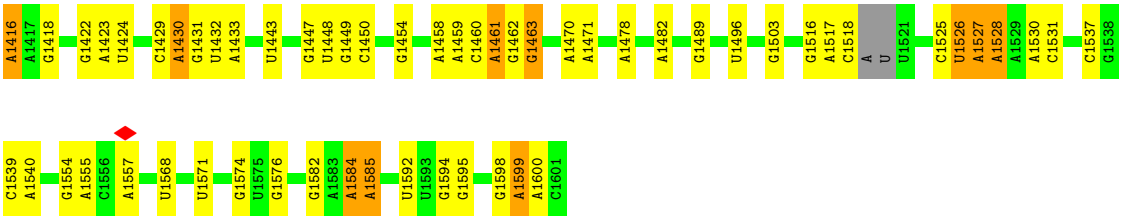




- Molecule 17: 12S mitochondrial rRNA

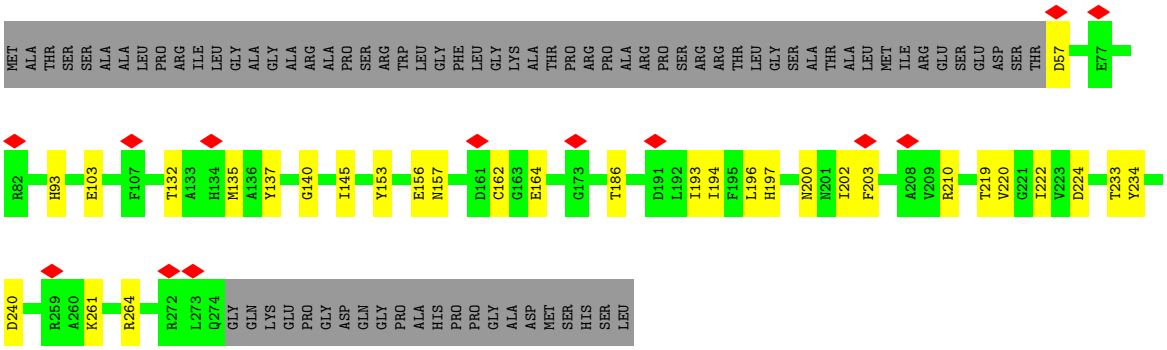
Chain AA: 64% 27% 5% •





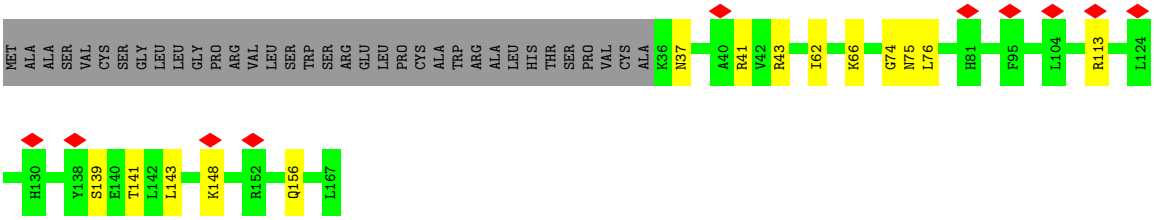
- Molecule 18: 28S ribosomal protein S2, mitochondrial

Chain AB:



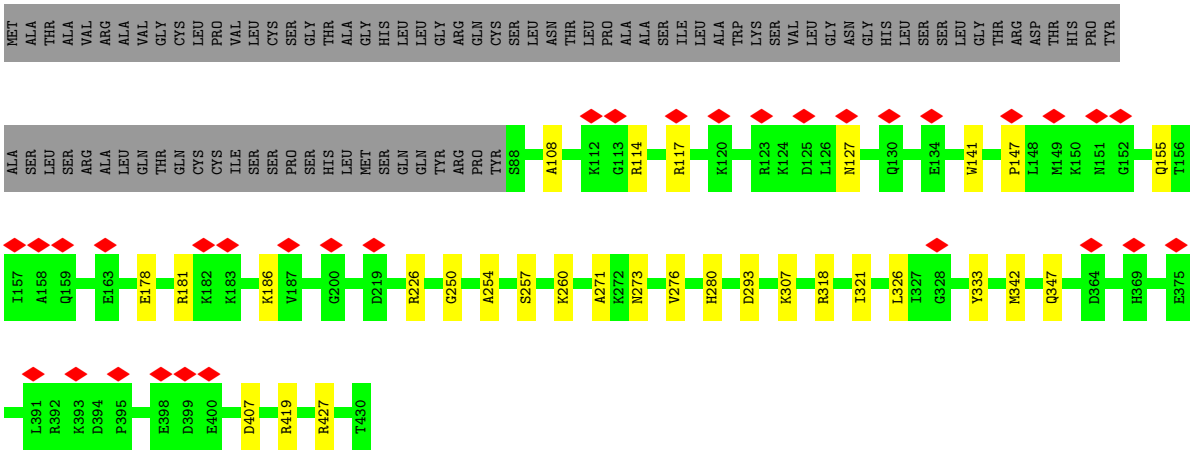
- Molecule 19: 28S ribosomal protein S24, mitochondrial

Chain AC:



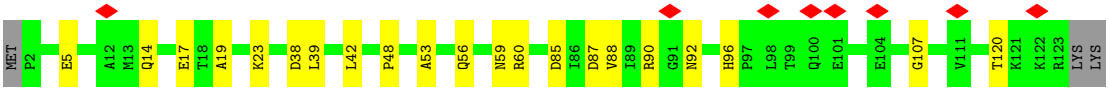
- Molecule 20: 28S ribosomal protein S5, mitochondrial

Chain AD:



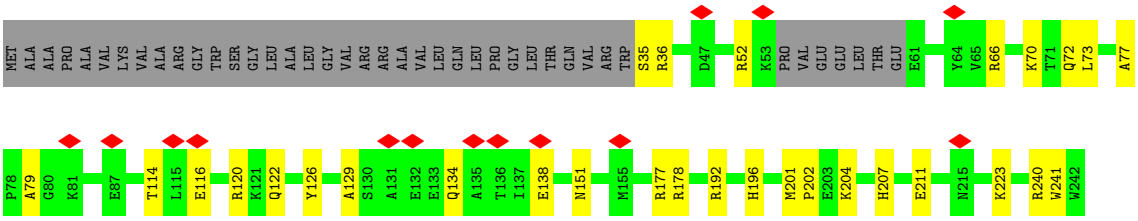
• Molecule 21: 28S ribosomal protein S6, mitochondrial

Chain AE:



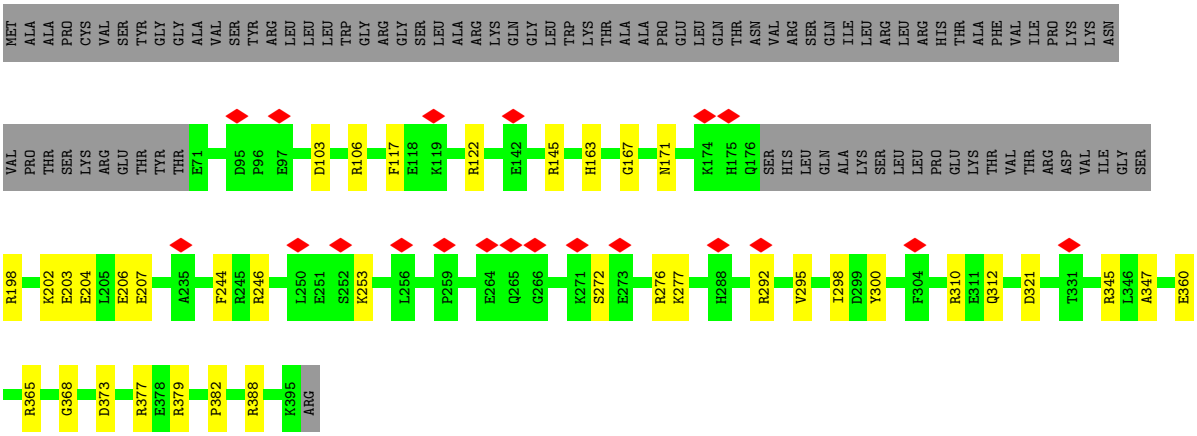
• Molecule 22: 28S ribosomal protein S7, mitochondrial

Chain AF:



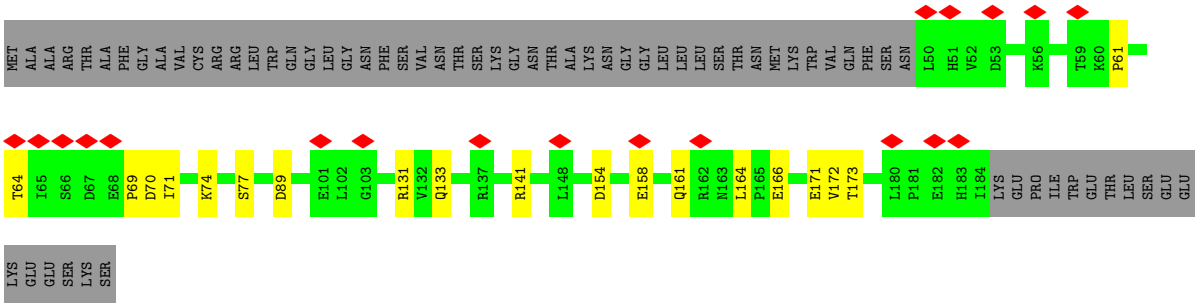
• Molecule 23: 28S ribosomal protein S9, mitochondrial

Chain AG:



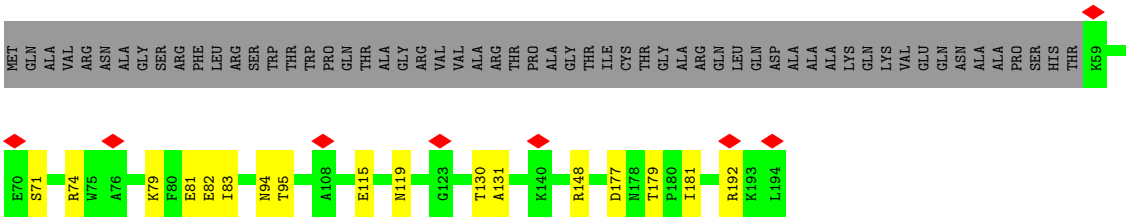
• Molecule 24: 28S ribosomal protein S10, mitochondrial

Chain AH:



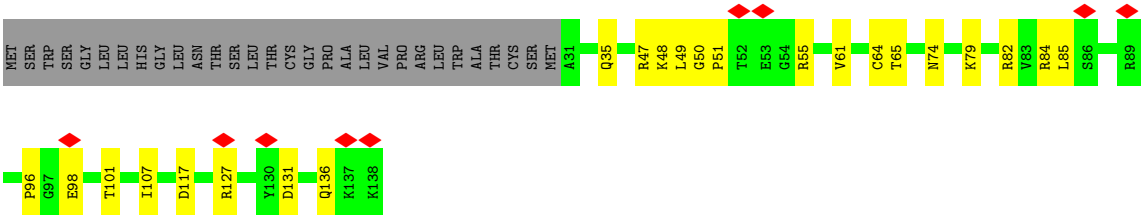
• Molecule 25: 28S ribosomal protein S11, mitochondrial

Chain AI:



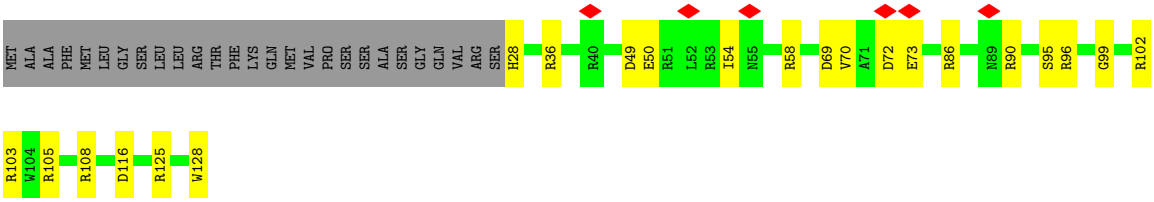
- Molecule 26: 28S ribosomal protein S12, mitochondrial

Chain AJ:



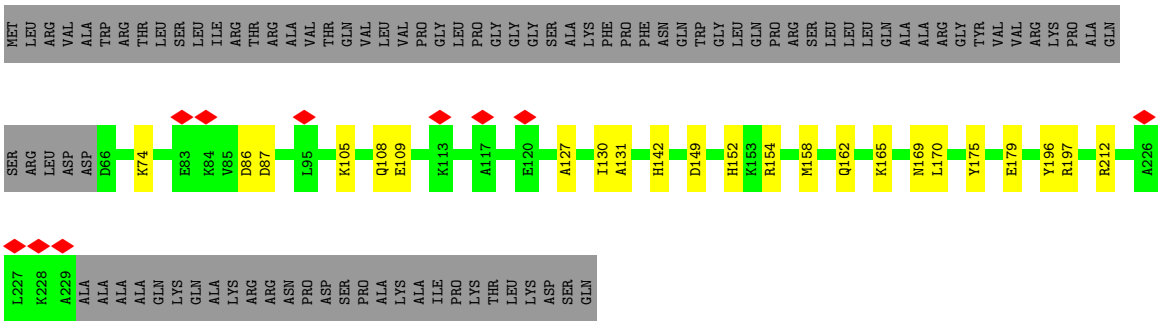
- Molecule 27: 28S ribosomal protein S14, mitochondrial

Chain AK:



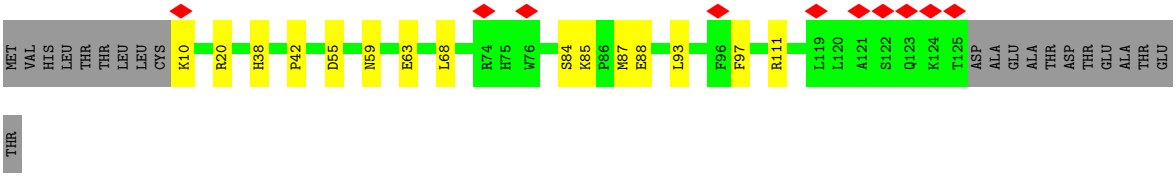
- Molecule 28: 28S ribosomal protein S15, mitochondrial

Chain AL:



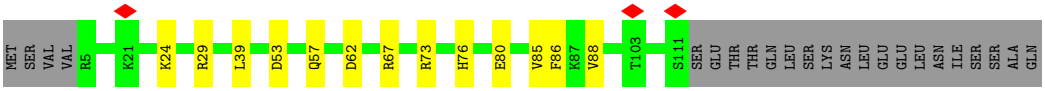
- Molecule 29: 28S ribosomal protein S16, mitochondrial

Chain AM:



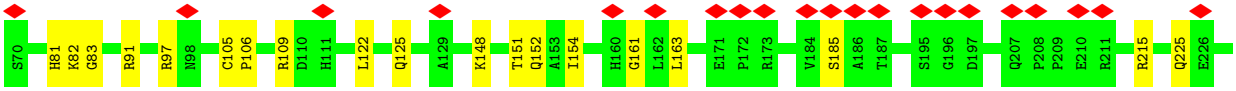
• Molecule 30: 28S ribosomal protein S17, mitochondrial

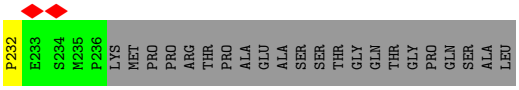
Chain AN:



• Molecule 31: 28S ribosomal protein S18b, mitochondrial

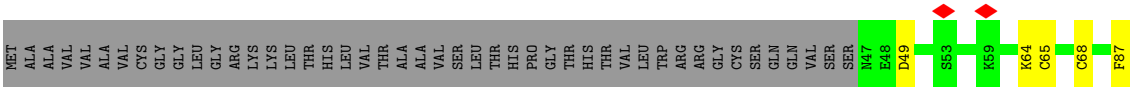
Chain AO:





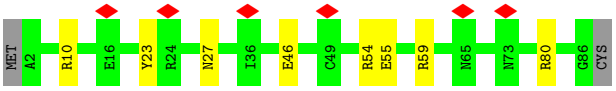
• Molecule 32: 28S ribosomal protein S18c, mitochondrial

Chain AP:



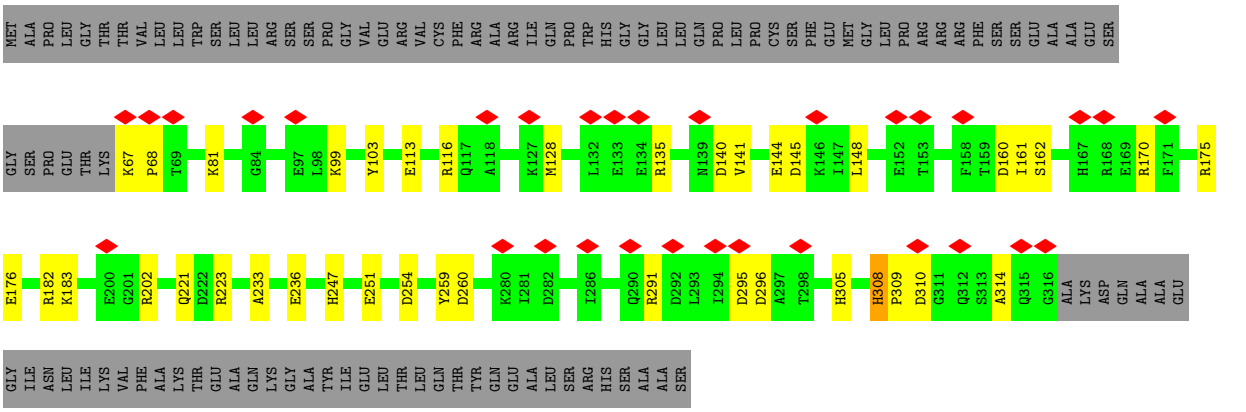
• Molecule 33: 28S ribosomal protein S21, mitochondrial

Chain AQ:



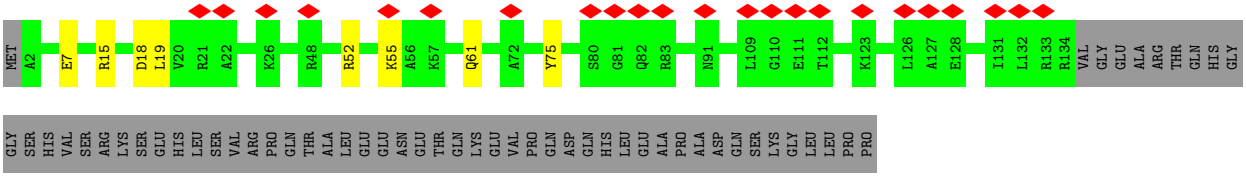
• Molecule 34: 28S ribosomal protein S22, mitochondrial

Chain AR:



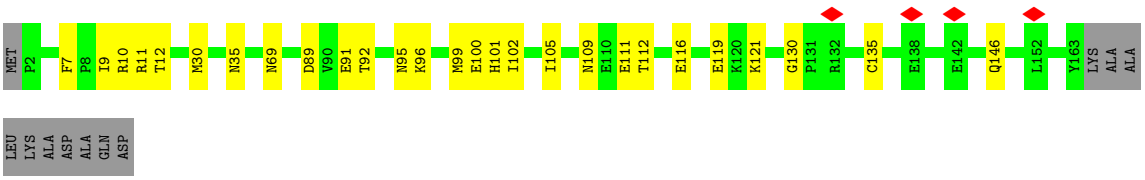
- Molecule 35: 28S ribosomal protein S23, mitochondrial

Chain AS: 12% 66% 30%



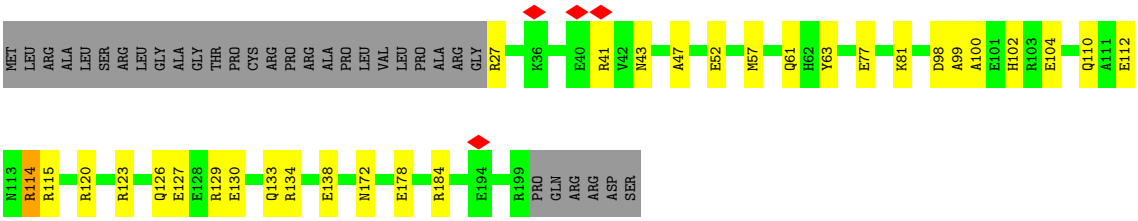
- Molecule 36: 28S ribosomal protein S25, mitochondrial

Chain AT: 78% 16% 6%



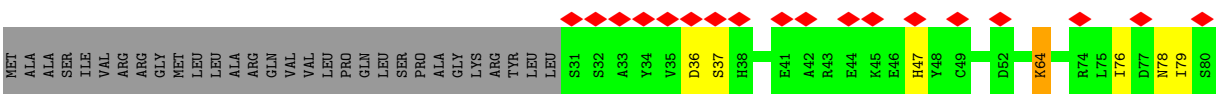
- Molecule 37: 28S ribosomal protein S26, mitochondrial

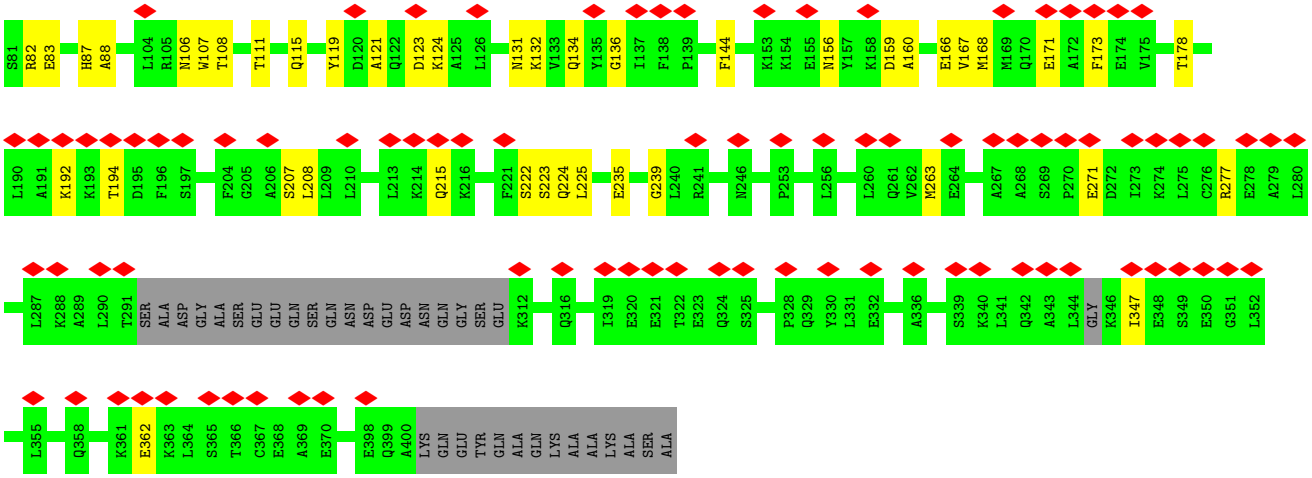
Chain AU: 69% 15% 16%



- Molecule 38: 28S ribosomal protein S27, mitochondrial

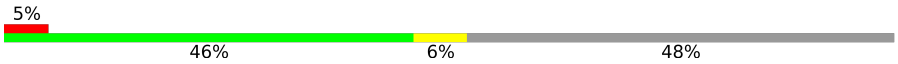
Chain AV: 26% 72% 12% 16%

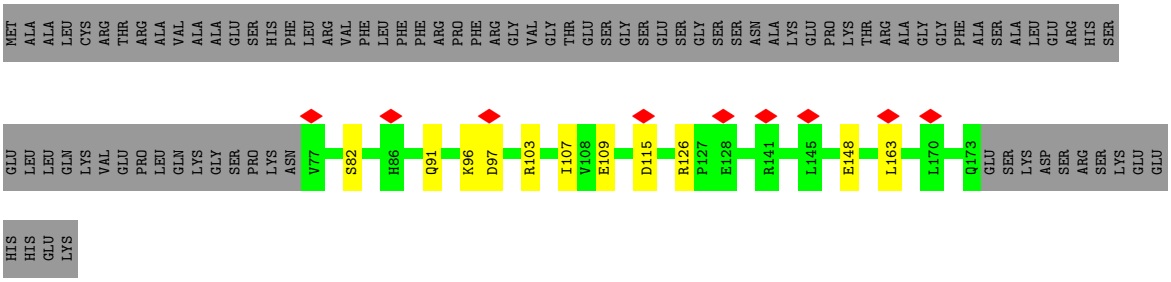




- Molecule 39: 28S ribosomal protein S28, mitochondrial

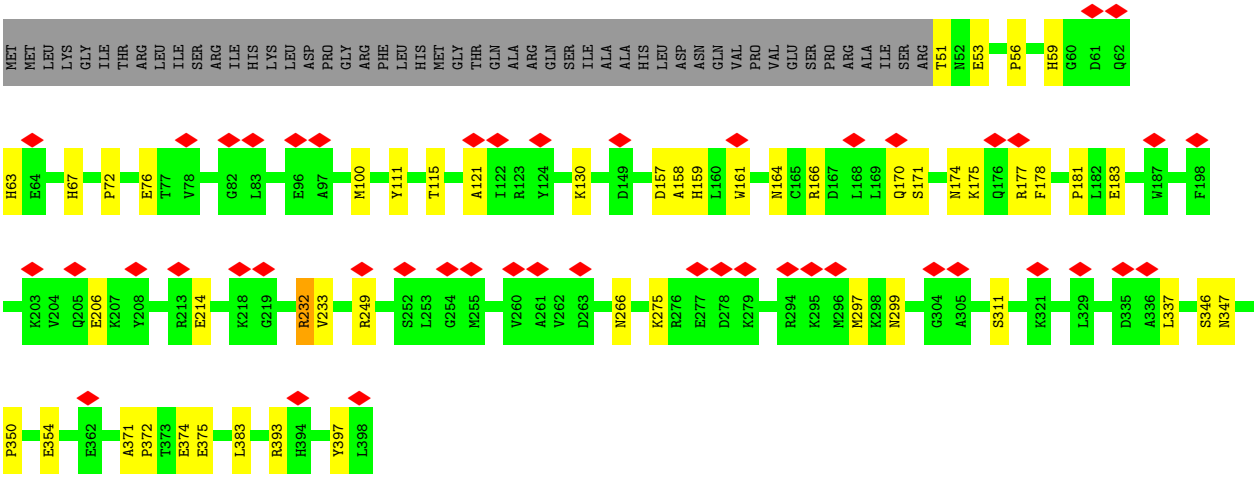
Chain AW:





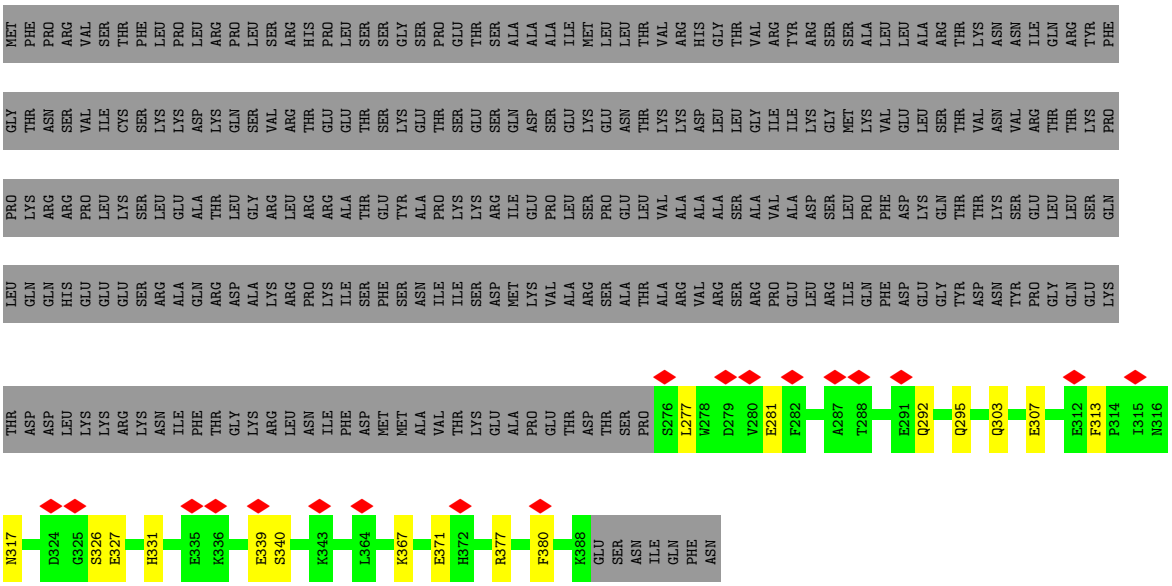
- Molecule 40: 28S ribosomal protein S29, mitochondrial

Chain AX:



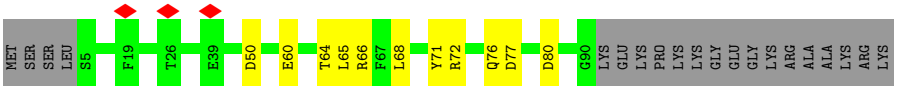
- Molecule 41: 28S ribosomal protein S31, mitochondrial

Chain AY:



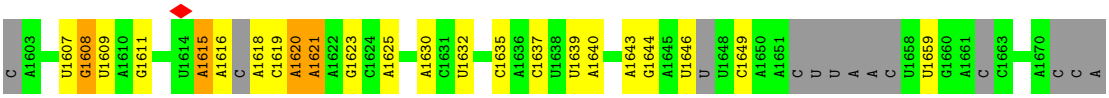
- Molecule 42: 28S ribosomal protein S33, mitochondrial

Chain AZ:



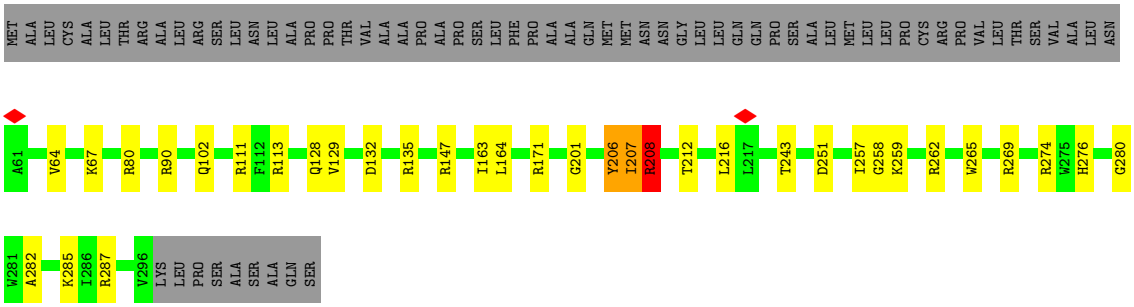
- Molecule 43: mitochondrial tRNAVal

Chain XB:



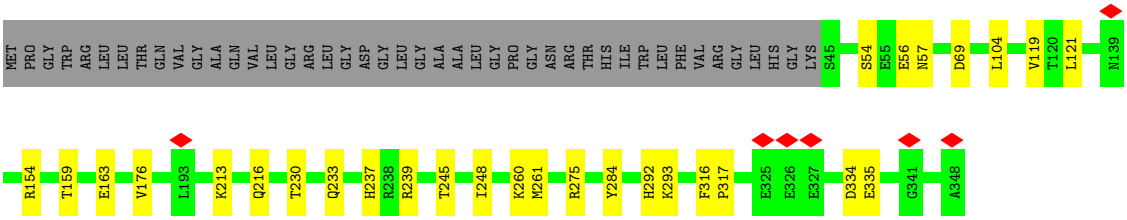
- Molecule 44: 39S ribosomal protein L2, mitochondrial

Chain XD:



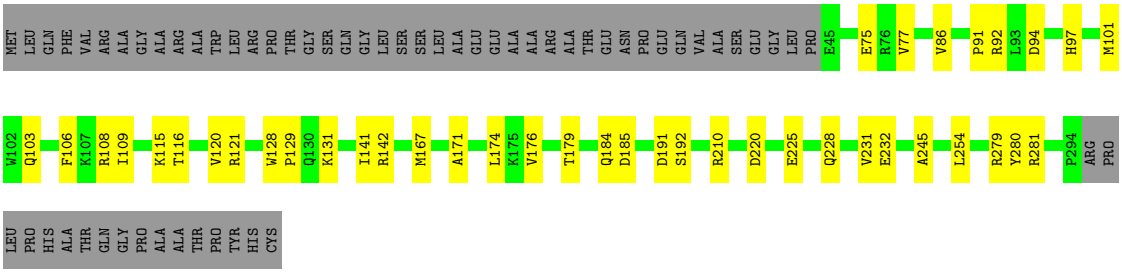
- Molecule 45: 39S ribosomal protein L3, mitochondrial

Chain XE:



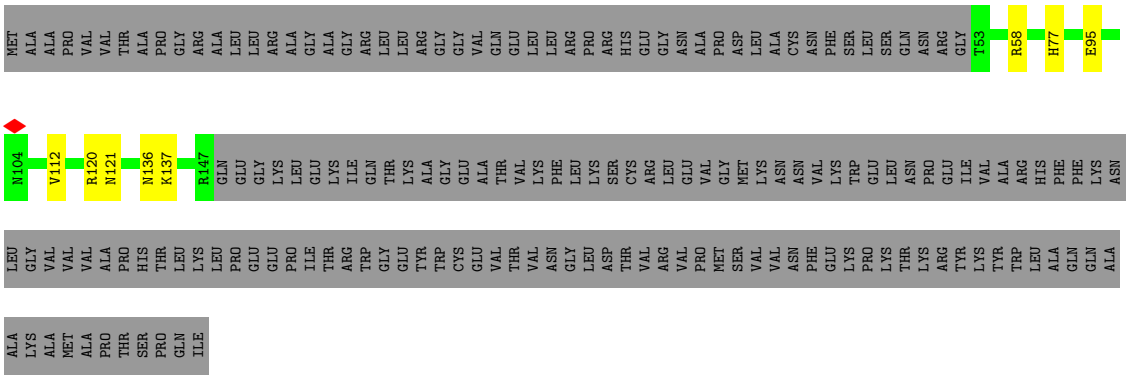
• Molecule 46: 39S ribosomal protein L4, mitochondrial

Chain XF:



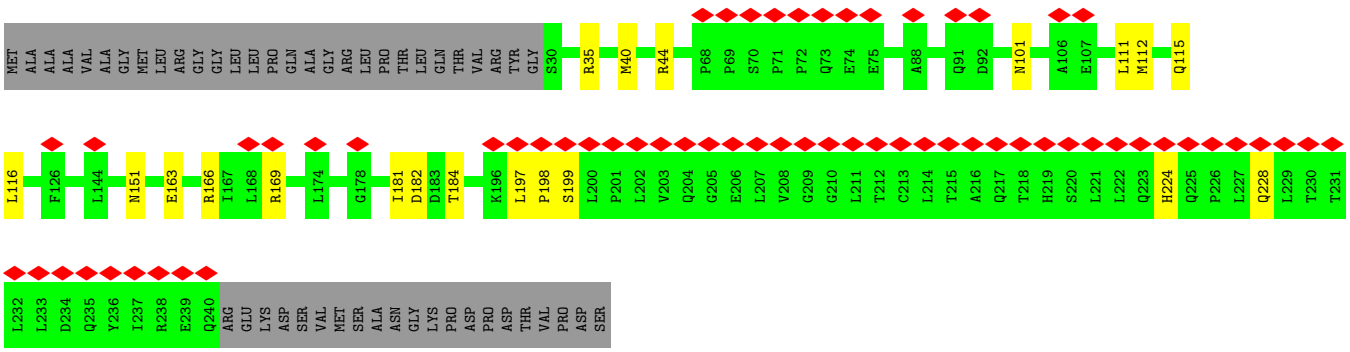
• Molecule 47: 39S ribosomal protein L9, mitochondrial

Chain XH:



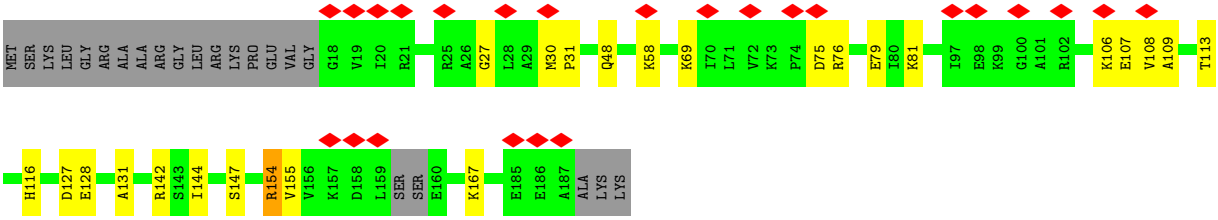
• Molecule 48: 39S ribosomal protein L10, mitochondrial

Chain XI:



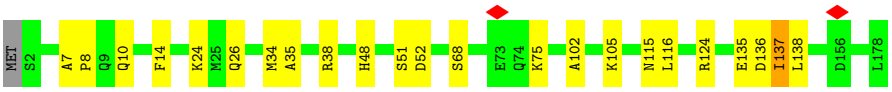
• Molecule 49: 39S ribosomal protein L11, mitochondrial

Chain XJ:



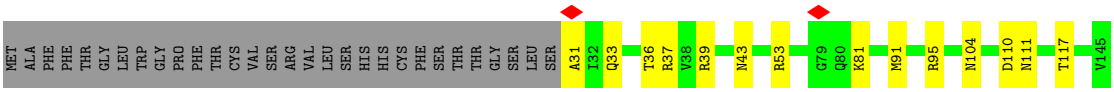
• Molecule 50: 39S ribosomal protein L13, mitochondrial

Chain XK:



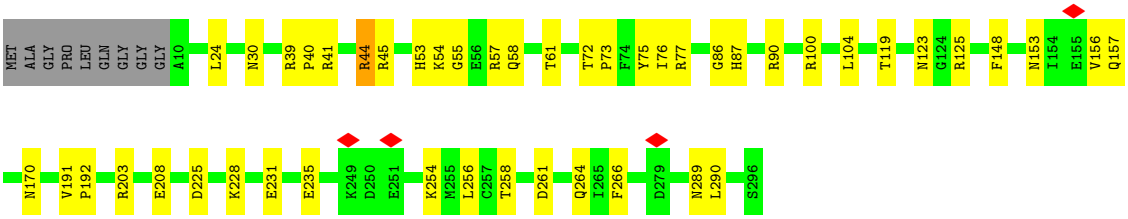
• Molecule 51: 39S ribosomal protein L14, mitochondrial

Chain XL:



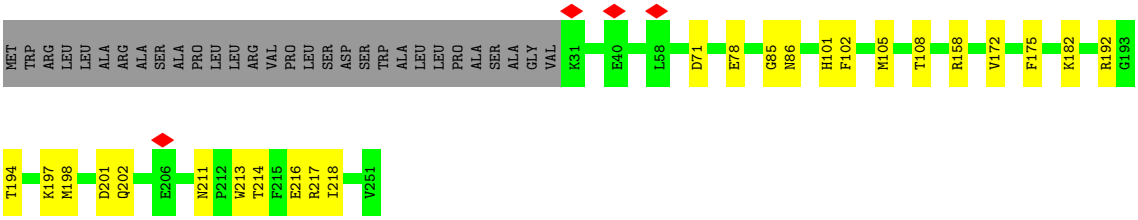
• Molecule 52: 39S ribosomal protein L15, mitochondrial

Chain XM:



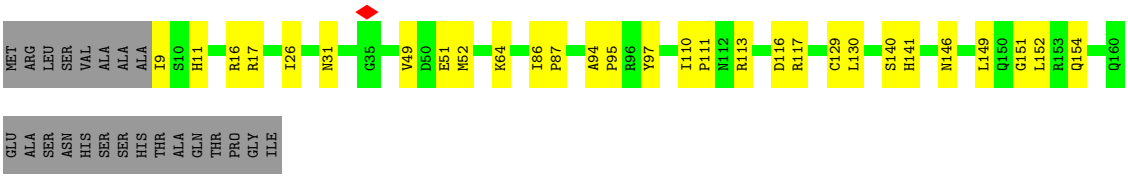
• Molecule 53: 39S ribosomal protein L16, mitochondrial

Chain XN:



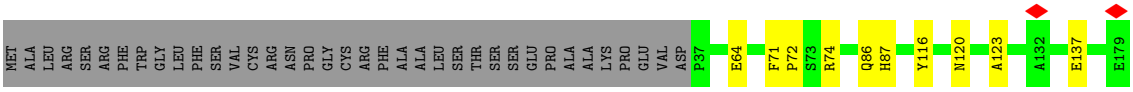
• Molecule 54: 39S ribosomal protein L17, mitochondrial

Chain XO:



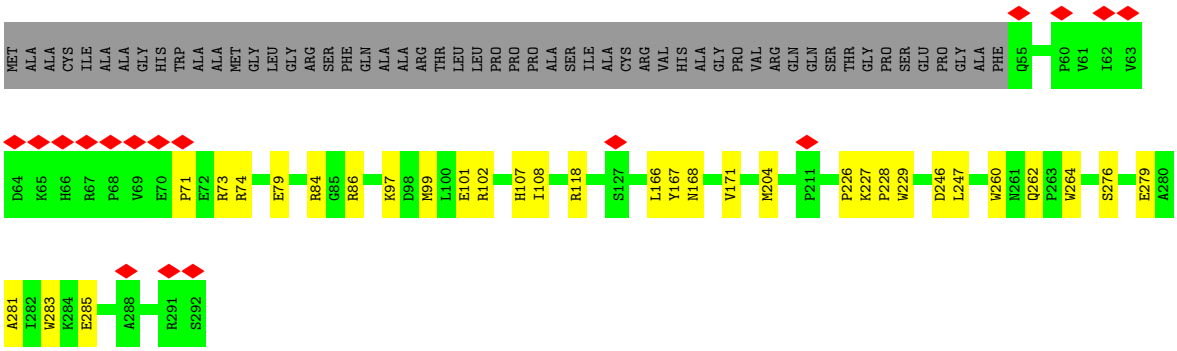
- Molecule 55: 39S ribosomal protein L18, mitochondrial

Chain XP:



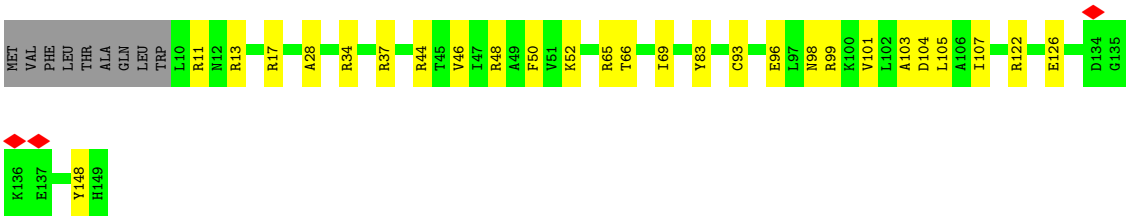
- Molecule 56: 39S ribosomal protein L19, mitochondrial

Chain XQ:



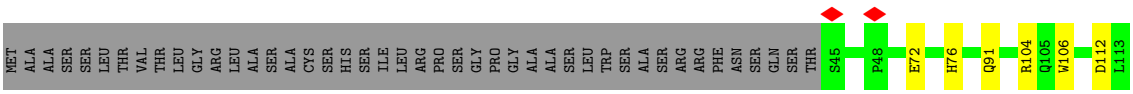
- Molecule 57: 39S ribosomal protein L20, mitochondrial

Chain XR:



- Molecule 58: 39S ribosomal protein L21, mitochondrial

Chain XS:



• Molecule 59: 39S ribosomal protein L22, mitochondrial

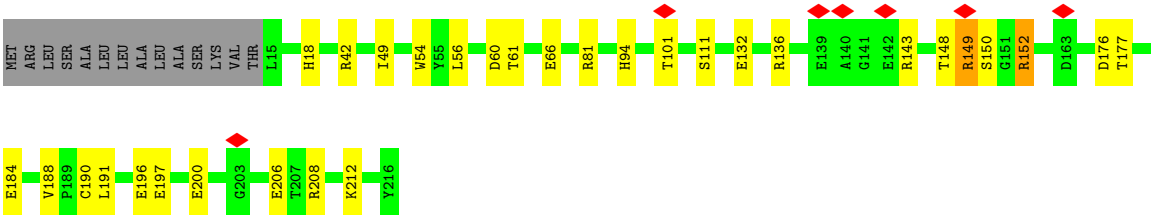
Chain XT:

• Molecule 60: 39S ribosomal protein L23, mitochondrial

Chain XU:

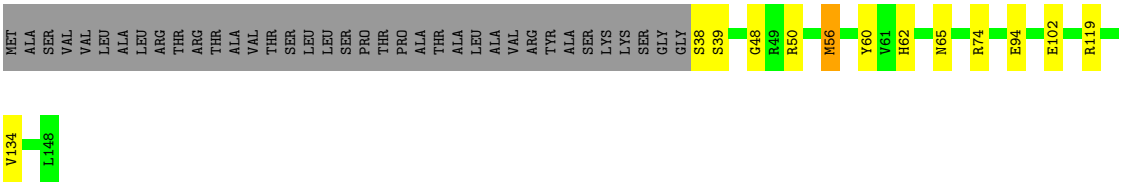
• Molecule 61: 39S ribosomal protein L24, mitochondrial

Chain XV:



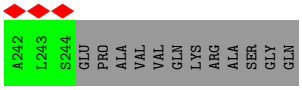
• Molecule 62: 39S ribosomal protein L27, mitochondrial

Chain XW:



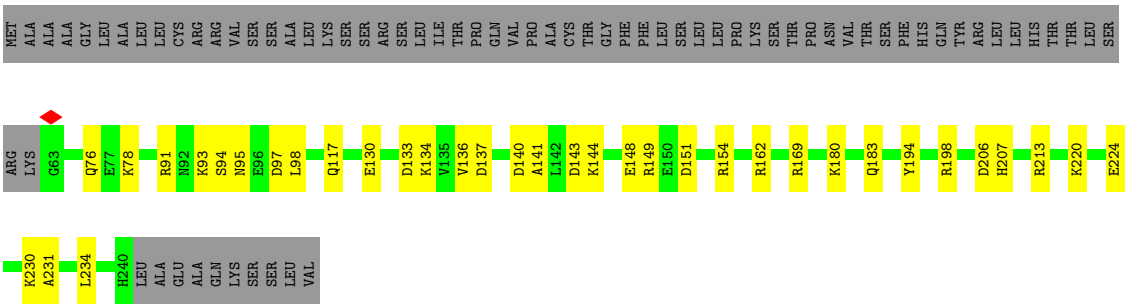
• Molecule 63: 39S ribosomal protein L28, mitochondrial

Chain XX:



• Molecule 64: 39S ribosomal protein L47, mitochondrial

Chain XY:

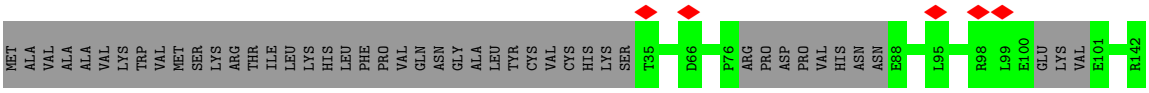


• Molecule 65: 39S ribosomal protein L30, mitochondrial

Chain XZ:

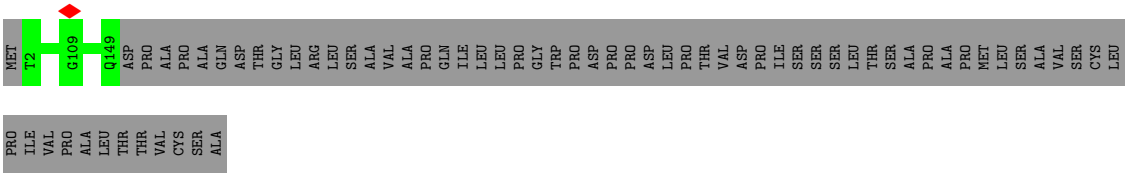
• Molecule 66: 39S ribosomal protein L42, mitochondrial

Chain a:



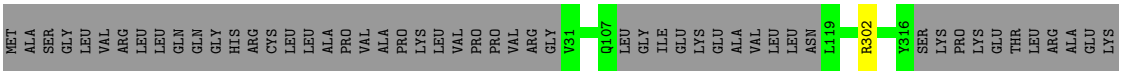
• Molecule 67: 39S ribosomal protein L43, mitochondrial

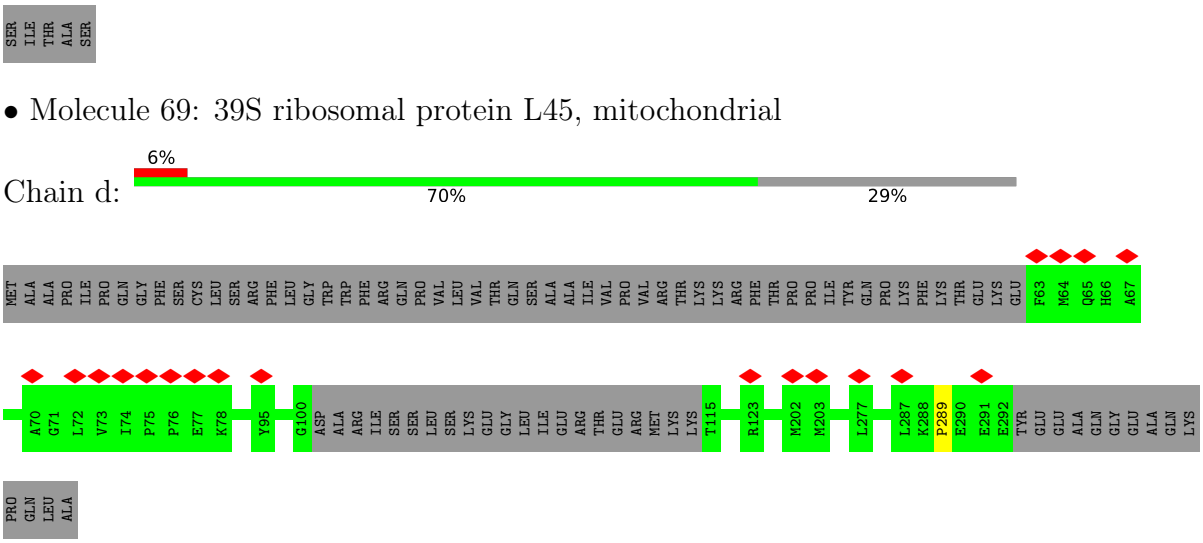
Chain b:

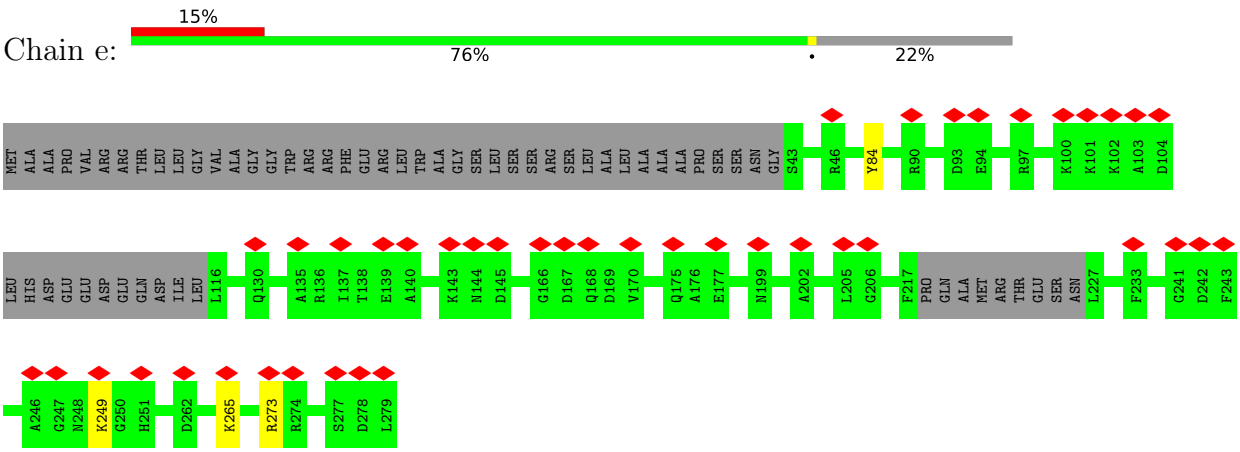


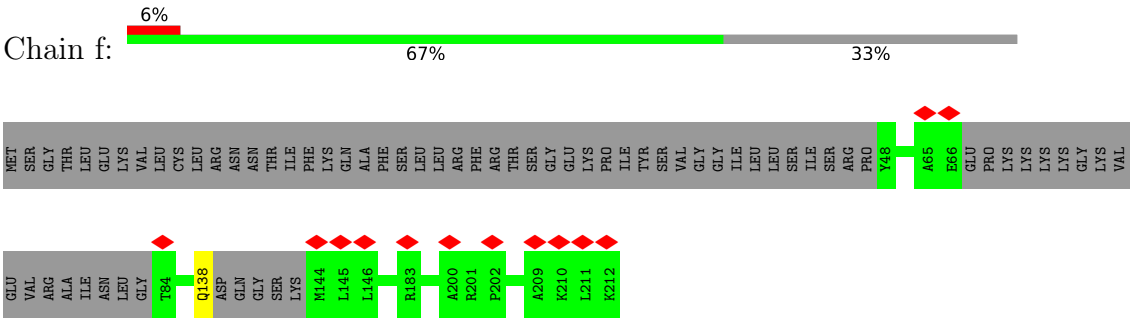
• Molecule 68: 39S ribosomal protein L44, mitochondrial

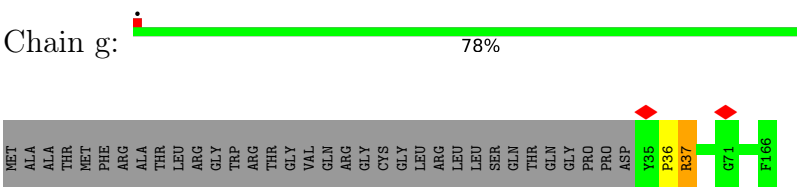
Chain c:





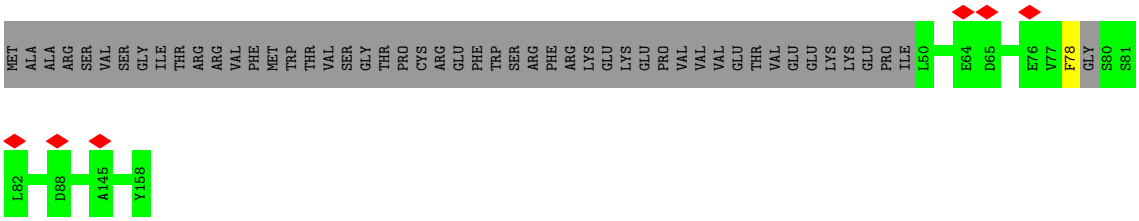






• Molecule 73: 39S ribosomal protein L50, mitochondrial

Chain h: 68% 32%

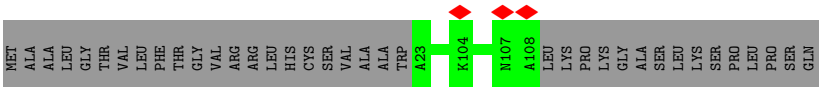


• Molecule 74: 39S ribosomal protein L51, mitochondrial

Chain i: 76% 24%

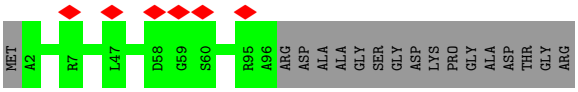
• Molecule 75: 39S ribosomal protein L52, mitochondrial

Chain j: 70% 30%



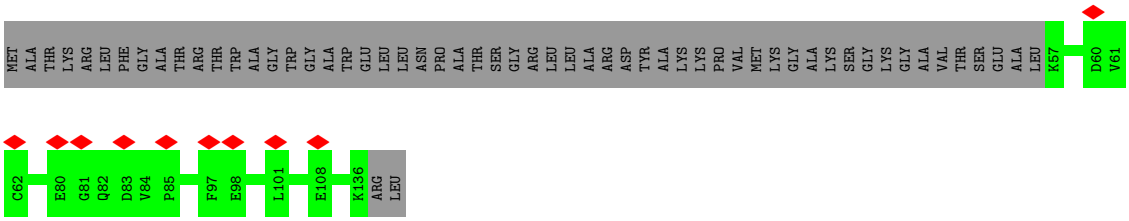
• Molecule 76: 39S ribosomal protein L53, mitochondrial

Chain k: 5% 85% 15%



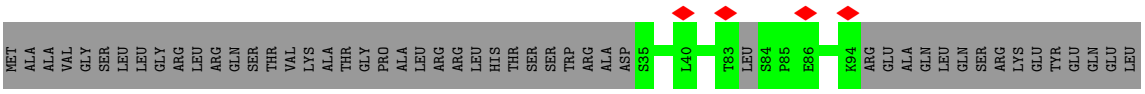
• Molecule 77: 39S ribosomal protein L54, mitochondrial

Chain l: 7% 58% 42%



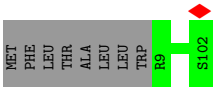
• Molecule 78: 39S ribosomal protein L55, mitochondrial

Chain m: 47% 53%



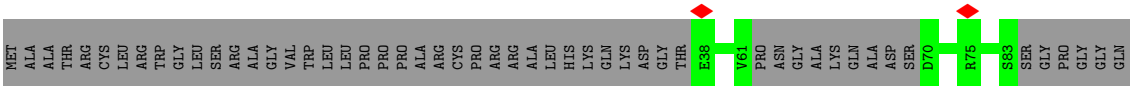
• Molecule 79: Ribosomal protein 63, mitochondrial

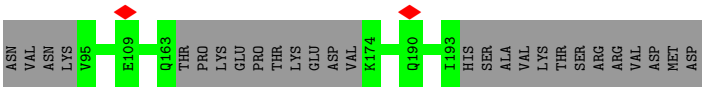
Chain o:



• Molecule 80: Peptidyl-tRNA hydrolase ICT1, mitochondrial

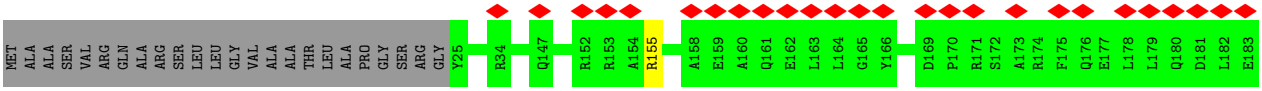
Chain p:

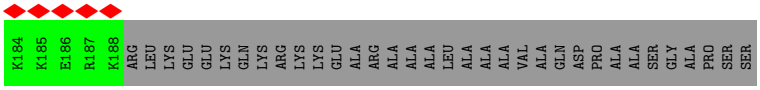




• Molecule 81: Growth arrest and DNA damage-inducible proteins-interacting protein 1

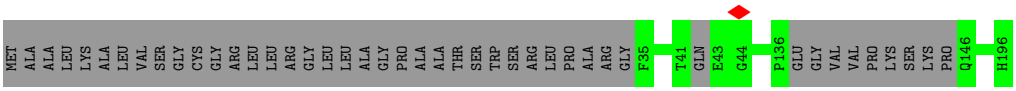
Chain q:





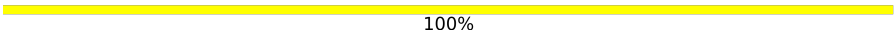
• Molecule 82: 39S ribosomal protein S18a, mitochondrial

Chain r:



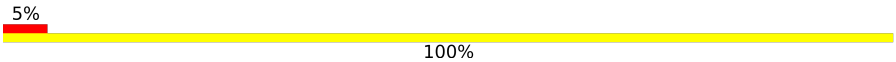
• Molecule 83: mRNA

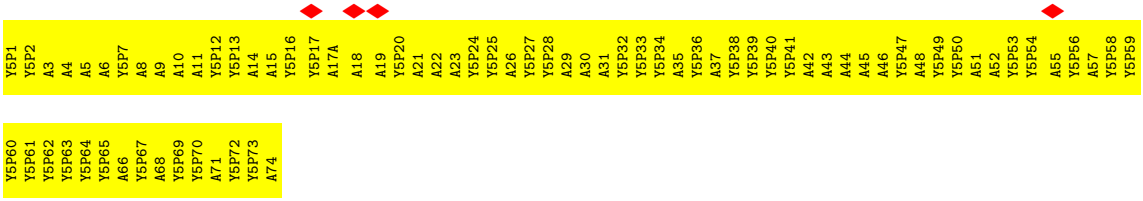
Chain r1:



• Molecule 84: P-site tRNA

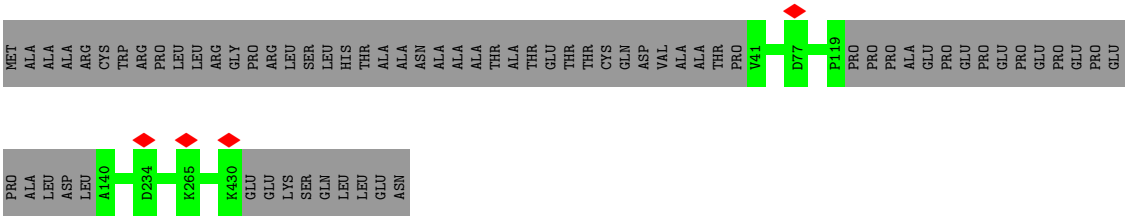
Chain r3:





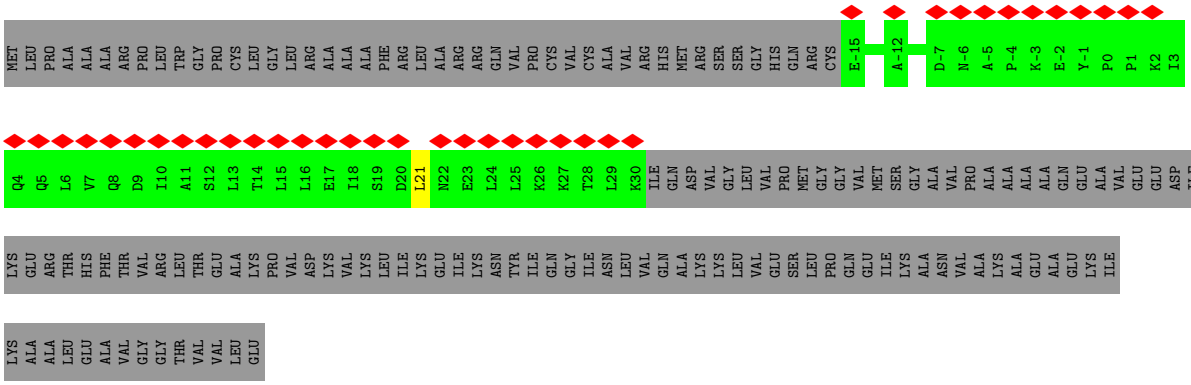
• Molecule 85: 39S ribosomal protein S30, mitochondrial

Chain s:



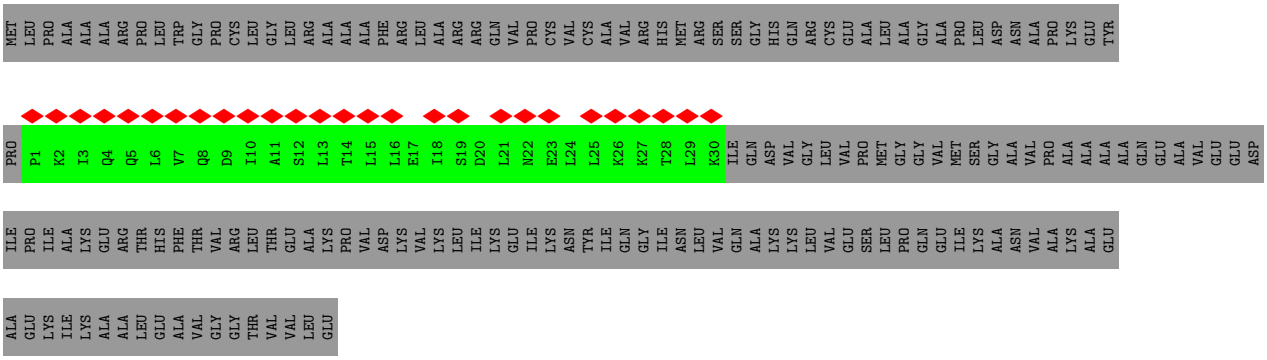
• Molecule 86: 39S ribosomal protein L12, mitochondrial

Chain t1:



• Molecule 86: 39S ribosomal protein L12, mitochondrial

Chain t2:



• Molecule 86: 39S ribosomal protein L12, mitochondrial

Chain t3: 15% 15% 85%

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

PRO P1 K2 I3 Q4 Q5 L6 V7 Q8 D9 I10 A11 S12 L13 T14 L15 L16 E17 I18 S19 D20 L21 N22 E23 L24 L25 K26 K27 T28 L29 K30 ILE GLN ASP VAL GLY LEU VAL PRO MET GLY GLY VAL MET SER GLY ALA VAL PRO ALA ALA ALA ALA GLN GLU ALA VAL GLU GLU ASP

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

ALA GLU LYS ILE LYS ALA ALA LEU GLU ALA VAL GLY GLY THR VAL VAL LEU GLU

- Molecule 86: 39S ribosomal protein L12, mitochondrial

Chain t4: 15% 15% 85%

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

PRO P1 K2 I3 Q4 Q5 L6 V7 Q8 D9 I10 A11 S12 L13 T14 L15 L16 E17 I18 S19 D20 L21 N22 E23 L24 L25 K26 K27 T28 L29 LYS ILE GLN ASP VAL GLY LEU VAL PRO MET GLY GLY VAL MET SER GLY ALA VAL PRO ALA ALA ALA ALA GLN GLU ALA VAL GLU GLU ASP

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

ALA GLU LYS ILE LYS ALA ALA LEU GLU ALA VAL GLY GLY THR VAL VAL LEU GLU

- Molecule 86: 39S ribosomal protein L12, mitochondrial

Chain t5: 15% 15% 85%

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

PRO P1 K2 I3 Q4 Q5 L6 V7 Q8 D9 I10 A11 S12 L13 T14 L15 L16 E17 I18 S19 D20 L21 N22 E23 L24 L25 K26 K27 T28 L29 LYS ILE GLN ASP VAL GLY LEU VAL PRO MET GLY GLY VAL MET SER GLY ALA VAL PRO ALA ALA ALA ALA GLN GLU ALA VAL GLU GLU ASP

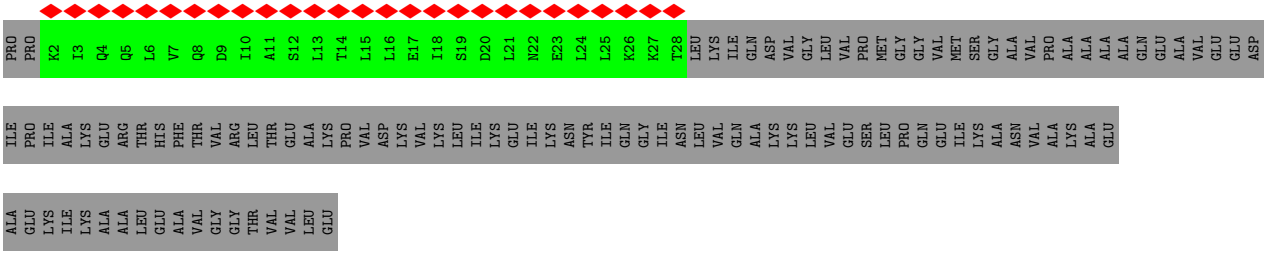
ILE PRO ILE ALA LYS GLU ARG THR HIS PHE THR VAL ARG LEU THR GLU ALA LYS PRO VAL ASP LYS VAL LYS LEU ILE LYS GLU ILE LYS ASN TYR ILE GLN GLY ILE ASN LEU VAL GLN ALA LYS LYS LEU VAL GLU SER LEU PRO GLN GLU ILE LYS ALA ASN VAL ALA LYS ALA GLU

ALA GLU LYS ILE LYS ALA ALA LEU GLU ALA VAL GLY GLY THR VAL VAL LEU GLU

- Molecule 86: 39S ribosomal protein L12, mitochondrial

Chain t6: 14% 14% 86%

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



- Molecule 87: Quinupristin

Chain A:

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	6692	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	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	0.239	Depositor
Minimum map value	-0.167	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: DBB, 004, P5P, MHV, MHT, MG, GTP, MHU, ZN, Y5P, MHW, DOL

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	0.27	0/895	0.44	0/1201
2	1	0.26	0/444	0.45	0/591
3	2	0.32	0/382	0.42	0/507
4	3	0.32	0/852	0.46	0/1136
5	4	0.27	0/349	0.44	0/461
6	5	0.26	0/3298	0.43	0/4492
7	6	0.27	0/3042	0.42	0/4140
8	7	0.25	0/2420	0.41	0/3270
9	8	1.81	1/1199 (0.1%)	0.46	2/1612 (0.1%)
10	9	0.28	0/1024	0.43	0/1379
11	XA	0.35	0/35615	0.79	0/55429
12	A0	0.23	0/1727	0.42	0/2338
13	A1	0.24	0/2276	0.40	0/3079
14	A2	0.25	0/939	0.43	0/1256
15	A3	0.28	0/621	0.44	0/820
16	A4	0.25	0/4559	0.41	0/6149
17	AA	0.23	0/21952	0.76	1/34164 (0.0%)
18	AB	0.25	0/1819	0.41	0/2462
19	AC	0.25	0/1112	0.41	0/1505
20	AD	0.25	0/2768	0.43	0/3707
21	AE	0.25	0/989	0.44	0/1335
22	AF	0.24	0/1708	0.39	0/2291
23	AG	0.25	0/2559	0.41	0/3429
24	AH	0.25	0/1128	0.43	0/1529
25	AI	0.25	0/1031	0.42	0/1390
26	AJ	0.25	0/854	0.46	0/1148
27	AK	0.23	0/879	0.41	0/1182
28	AL	0.25	0/1406	0.40	0/1878
29	AM	0.25	0/941	0.41	0/1265
30	AN	0.25	0/864	0.44	0/1169
31	AO	0.24	0/1580	0.40	0/2150
32	AP	0.25	0/782	0.38	0/1050

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	AQ	0.24	0/746	0.43	0/993
34	AR	0.30	1/2103 (0.0%)	0.52	3/2842 (0.1%)
35	AS	0.25	0/1127	0.39	0/1518
36	AT	0.25	0/1361	0.42	0/1829
37	AU	0.24	0/1482	0.41	0/1987
38	AV	0.24	0/2925	0.40	0/3948
39	AW	0.25	0/778	0.45	0/1048
40	AX	0.25	0/2886	0.43	0/3909
41	AY	0.25	0/985	0.37	0/1329
42	AZ	0.25	0/748	0.39	0/1000
43	XB	0.20	0/1400	0.73	0/2168
44	XD	0.28	0/1879	0.46	0/2527
45	XE	0.29	0/2465	0.44	0/3344
46	XF	0.32	0/2071	0.49	0/2817
47	XH	0.26	0/798	0.44	0/1073
48	XI	0.26	0/1727	0.44	0/2340
49	XJ	0.24	0/1309	0.40	0/1764
50	XK	0.29	0/1495	0.42	0/2029
51	XL	0.27	0/904	0.44	0/1218
52	XM	0.31	0/2359	0.45	0/3185
53	XN	0.28	0/1825	0.45	0/2458
54	XO	0.26	0/1269	0.44	0/1708
55	XP	0.26	0/1190	0.42	0/1611
56	XQ	0.26	0/2026	0.44	0/2734
57	XR	0.33	0/1174	0.45	0/1572
58	XS	0.29	0/1311	0.47	0/1778
59	XT	0.31	0/1402	0.44	0/1886
60	XU	0.28	0/1200	0.43	0/1623
61	XV	0.26	0/1693	0.45	0/2297
62	XW	0.29	0/893	0.45	0/1204
63	XX	0.29	1/2090 (0.0%)	0.43	0/2825
64	XY	0.27	0/1571	0.43	0/2106
65	XZ	0.29	0/1003	0.44	0/1354
66	a	0.27	0/838	0.45	0/1138
67	b	0.29	0/1202	0.47	0/1626
68	c	0.26	0/2264	0.41	0/3059
69	d	0.25	0/1807	0.42	0/2450
70	e	1.42	6/1797 (0.3%)	0.43	0/2422
71	f	0.26	0/1169	0.42	0/1576
72	g	0.44	2/1134 (0.2%)	0.45	0/1547
73	h	0.25	0/905	0.43	0/1233
74	i	0.32	0/849	0.48	0/1135
75	j	0.27	0/703	0.41	0/947

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
76	k	0.24	0/743	0.45	0/1003
77	l	0.24	0/692	0.38	0/939
78	m	0.23	0/508	0.44	0/682
79	o	0.28	0/818	0.46	0/1097
80	p	0.23	0/1071	0.42	0/1433
81	q	0.26	0/1413	0.42	0/1906
82	r	0.26	0/1282	0.41	0/1734
85	s	0.26	0/3114	0.44	0/4225
86	t1	0.26	0/366	0.39	0/497
86	t2	0.22	0/238	0.38	0/319
86	t3	0.22	0/238	0.37	0/319
86	t4	0.22	0/229	0.37	0/308
86	t5	0.23	0/229	0.37	0/308
86	t6	0.24	0/213	0.40	0/286
87	A	0.55	0/13	0.66	0/15
All	All	0.35	11/176044 (0.0%)	0.58	6/249742 (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
44	XD	0	1
48	XI	0	1
50	XK	0	1
70	e	0	1
71	f	0	1
72	g	0	1
73	h	0	1
87	A	2	3
All	All	2	10

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	8	99	ARG	CG-CD	61.84	3.06	1.51
70	e	84	TYR	CD2-CE2	31.66	1.86	1.39
70	e	84	TYR	CD1-CE1	31.19	1.86	1.39
70	e	84	TYR	CE2-CZ	21.63	1.66	1.38
70	e	84	TYR	CE1-CZ	21.08	1.66	1.38

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
34	AR	309	PRO	O-C-N	11.63	141.32	122.70
34	AR	309	PRO	CA-C-N	-8.78	97.89	117.20
9	8	99	ARG	CG-CD-NE	5.94	124.27	111.80
34	AR	309	PRO	C-N-CA	-5.91	106.92	121.70
9	8	99	ARG	CB-CG-CD	5.59	126.12	111.60

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
87	A	2	THR	CB
87	A	4	PRO	CA

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
44	XD	206	TYR	Peptide
48	XI	197	LEU	Peptide
50	XK	137	ILE	Peptide
70	e	265	LYS	Peptide
71	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	903	903	13	0
2	1	439	480	480	7	0
3	2	376	406	406	7	0
4	3	831	883	883	16	0
5	4	341	362	361	3	0
6	5	3204	3200	3200	35	0
7	6	2947	2839	2841	37	0
8	7	2365	2373	2372	23	0
9	8	1175	1202	1202	8	0
10	9	996	987	987	12	0
11	XA	31833	16160	16167	297	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	A0	1684	1685	1685	17	0
13	A1	2230	2261	2261	26	0
14	A2	925	964	964	14	0
15	A3	610	682	682	16	0
16	A4	4470	4485	4486	43	0
17	AA	19628	9964	9971	163	0
18	AB	1776	1769	1769	21	0
19	AC	1082	1088	1088	12	0
20	AD	2716	2785	2785	21	0
21	AE	972	1001	1001	14	0
22	AF	1668	1715	1716	24	0
23	AG	2505	2491	2490	29	0
24	AH	1105	1136	1136	15	0
25	AI	1011	1052	1052	11	0
26	AJ	838	887	887	20	0
27	AK	861	885	885	17	0
28	AL	1382	1472	1472	16	0
29	AM	920	951	951	13	0
30	AN	846	908	908	10	0
31	AO	1528	1490	1490	18	0
32	AP	765	796	796	9	0
33	AQ	734	749	749	6	0
34	AR	2060	2074	2074	30	0
35	AS	1100	1103	1103	7	0
36	AT	1330	1343	1343	16	0
37	AU	1461	1471	1471	23	0
38	AV	2867	2862	2862	29	0
39	AW	766	785	785	7	0
40	AX	2814	2805	2804	28	0
41	AY	956	912	911	13	0
42	AZ	731	734	734	8	0
43	XB	1255	635	640	12	0
44	XD	1842	1896	1896	25	0
45	XE	2396	2402	2402	21	0
46	XF	2013	2045	2044	32	0
47	XH	784	832	832	5	0
48	XI	1691	1783	1783	12	0
49	XJ	1291	1367	1364	16	0
50	XK	1451	1448	1448	16	0
51	XL	889	941	941	10	0
52	XM	2305	2378	2378	32	0
53	XN	1778	1808	1808	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
54	XO	1245	1283	1283	20	0
55	XP	1164	1162	1162	9	0
56	XQ	1978	2022	2022	21	0
57	XR	1153	1214	1214	23	0
58	XS	1284	1354	1354	14	0
59	XT	1368	1410	1410	18	0
60	XU	1171	1164	1164	15	0
61	XV	1648	1656	1654	26	0
62	XW	871	898	898	9	0
63	XX	2035	2054	2054	19	0
64	XY	1534	1575	1575	29	0
65	XZ	978	1030	1030	9	0
66	a	813	777	777	0	0
67	b	1178	1180	1180	0	0
68	c	2217	2220	2220	0	0
69	d	1758	1743	1742	0	0
70	e	1762	1767	1767	0	0
71	f	1149	1165	1165	0	0
72	g	1097	1086	1084	0	0
73	h	882	866	867	0	0
74	i	827	857	857	0	0
75	j	689	678	678	0	0
76	k	732	745	745	0	0
77	l	673	654	653	0	0
78	m	500	525	525	0	0
79	o	797	804	804	0	0
80	p	1058	1083	1083	0	0
81	q	1379	1358	1359	0	0
82	r	1247	1267	1267	0	0
83	r1	72	0	49	0	0
84	r3	1459	0	829	0	0
85	s	3036	3022	3022	0	0
86	t1	354	379	374	0	0
86	t2	238	268	270	0	0
86	t3	238	268	270	0	0
86	t4	229	255	257	0	0
86	t5	229	255	257	0	0
86	t6	214	236	236	0	0
87	A	73	67	64	4	0
88	0	1	0	0	0	0
88	4	1	0	0	0	0
88	AB	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
88	AO	1	0	0	0	0
88	AP	1	0	0	0	0
88	AT	1	0	0	0	0
88	r	1	0	0	0	0
89	9	1	0	0	0	0
89	A2	1	0	0	0	0
89	AA	45	0	0	0	0
89	XA	142	0	0	0	0
89	XD	1	0	0	0	0
89	XE	1	0	0	0	0
89	XM	2	0	0	0	0
89	XW	1	0	0	0	0
89	g	1	0	0	0	0
90	XA	48	50	50	4	0
91	AX	32	10	12	1	0
All	All	169034	143042	143932	1266	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 1266 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)
63:XX:144:TYR:O	63:XX:148:THR:HG23	1.56	1.05
4:3:104:ARG:NH1	4:3:160:LYS:O	2.03	0.90
11:XA:2517:U:OP1	44:XD:287:ARG:NH2	2.04	0.90
23:AG:276:ARG:NH1	23:AG:373:ASP:OD2	2.04	0.90
45:XE:216:GLN:NE2	45:XE:261:MET:SD	2.45	0.90

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%)	50 (98%)	1 (2%)	0	100	100
3	2	44/92 (48%)	43 (98%)	1 (2%)	0	100	100
4	3	93/188 (50%)	93 (100%)	0	0	100	100
5	4	36/103 (35%)	35 (97%)	1 (3%)	0	100	100
6	5	389/423 (92%)	365 (94%)	24 (6%)	0	100	100
7	6	352/380 (93%)	325 (92%)	27 (8%)	0	100	100
8	7	285/338 (84%)	265 (93%)	20 (7%)	0	100	100
9	8	137/206 (66%)	131 (96%)	6 (4%)	0	100	100
10	9	122/137 (89%)	115 (94%)	7 (6%)	0	100	100
12	A0	197/218 (90%)	189 (96%)	8 (4%)	0	100	100
13	A1	273/323 (84%)	258 (94%)	15 (6%)	0	100	100
14	A2	114/118 (97%)	110 (96%)	4 (4%)	0	100	100
15	A3	67/199 (34%)	66 (98%)	1 (2%)	0	100	100
16	A4	526/689 (76%)	493 (94%)	33 (6%)	0	100	100
18	AB	216/296 (73%)	211 (98%)	5 (2%)	0	100	100
19	AC	130/167 (78%)	128 (98%)	2 (2%)	0	100	100
20	AD	341/430 (79%)	325 (95%)	16 (5%)	0	100	100
21	AE	120/125 (96%)	116 (97%)	4 (3%)	0	100	100
22	AF	197/242 (81%)	195 (99%)	2 (1%)	0	100	100
23	AG	300/396 (76%)	288 (96%)	12 (4%)	0	100	100
24	AH	133/201 (66%)	124 (93%)	9 (7%)	0	100	100
25	AI	134/194 (69%)	126 (94%)	8 (6%)	0	100	100
26	AJ	106/138 (77%)	98 (92%)	8 (8%)	0	100	100
27	AK	99/128 (77%)	97 (98%)	2 (2%)	0	100	100
28	AL	162/257 (63%)	156 (96%)	6 (4%)	0	100	100
29	AM	114/137 (83%)	113 (99%)	1 (1%)	0	100	100
30	AN	105/130 (81%)	103 (98%)	2 (2%)	0	100	100
31	AO	183/258 (71%)	179 (98%)	4 (2%)	0	100	100
32	AP	93/142 (66%)	86 (92%)	7 (8%)	0	100	100
33	AQ	83/87 (95%)	78 (94%)	5 (6%)	0	100	100
34	AR	248/360 (69%)	239 (96%)	9 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	AS	131/190 (69%)	123 (94%)	8 (6%)	0	100	100
36	AT	160/173 (92%)	150 (94%)	10 (6%)	0	100	100
37	AU	171/205 (83%)	168 (98%)	3 (2%)	0	100	100
38	AV	341/414 (82%)	318 (93%)	23 (7%)	0	100	100
39	AW	95/187 (51%)	90 (95%)	5 (5%)	0	100	100
40	AX	346/398 (87%)	328 (95%)	18 (5%)	0	100	100
41	AY	111/395 (28%)	106 (96%)	5 (4%)	0	100	100
42	AZ	84/106 (79%)	81 (96%)	3 (4%)	0	100	100
44	XD	234/305 (77%)	217 (93%)	15 (6%)	2 (1%)	17	56
45	XE	302/348 (87%)	291 (96%)	11 (4%)	0	100	100
46	XF	248/311 (80%)	237 (96%)	11 (4%)	0	100	100
47	XH	93/267 (35%)	89 (96%)	4 (4%)	0	100	100
48	XI	209/261 (80%)	193 (92%)	16 (8%)	0	100	100
49	XJ	168/192 (88%)	156 (93%)	12 (7%)	0	100	100
50	XK	175/178 (98%)	167 (95%)	8 (5%)	0	100	100
51	XL	113/145 (78%)	108 (96%)	5 (4%)	0	100	100
52	XM	285/296 (96%)	273 (96%)	12 (4%)	0	100	100
53	XN	219/251 (87%)	208 (95%)	11 (5%)	0	100	100
54	XO	150/175 (86%)	142 (95%)	8 (5%)	0	100	100
55	XP	141/180 (78%)	131 (93%)	10 (7%)	0	100	100
56	XQ	236/292 (81%)	222 (94%)	14 (6%)	0	100	100
57	XR	138/149 (93%)	131 (95%)	7 (5%)	0	100	100
58	XS	158/205 (77%)	151 (96%)	7 (4%)	0	100	100
59	XT	164/206 (80%)	159 (97%)	5 (3%)	0	100	100
60	XU	137/153 (90%)	130 (95%)	7 (5%)	0	100	100
61	XV	200/216 (93%)	191 (96%)	9 (4%)	0	100	100
62	XW	109/148 (74%)	105 (96%)	4 (4%)	0	100	100
63	XX	241/256 (94%)	230 (95%)	10 (4%)	1 (0%)	34	72
64	XY	176/250 (70%)	168 (96%)	8 (4%)	0	100	100
65	XZ	118/161 (73%)	112 (95%)	6 (5%)	0	100	100
66	a	93/142 (66%)	86 (92%)	7 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
67	b	146/215 (68%)	132 (90%)	14 (10%)	0	100	100
68	c	271/332 (82%)	257 (95%)	14 (5%)	0	100	100
69	d	212/306 (69%)	200 (94%)	11 (5%)	1 (0%)	29	68
70	e	211/279 (76%)	203 (96%)	8 (4%)	0	100	100
71	f	139/212 (66%)	133 (96%)	6 (4%)	0	100	100
72	g	130/166 (78%)	124 (95%)	6 (5%)	0	100	100
73	h	106/158 (67%)	99 (93%)	7 (7%)	0	100	100
74	i	95/128 (74%)	93 (98%)	2 (2%)	0	100	100
75	j	84/123 (68%)	83 (99%)	1 (1%)	0	100	100
76	k	93/112 (83%)	88 (95%)	5 (5%)	0	100	100
77	l	78/138 (56%)	73 (94%)	5 (6%)	0	100	100
78	m	58/128 (45%)	52 (90%)	6 (10%)	0	100	100
79	o	92/102 (90%)	89 (97%)	3 (3%)	0	100	100
80	p	119/206 (58%)	113 (95%)	6 (5%)	0	100	100
81	q	162/222 (73%)	155 (96%)	7 (4%)	0	100	100
82	r	144/196 (74%)	139 (96%)	5 (4%)	0	100	100
85	s	366/439 (83%)	346 (94%)	20 (6%)	0	100	100
86	t1	45/198 (23%)	39 (87%)	6 (13%)	0	100	100
86	t2	28/198 (14%)	28 (100%)	0	0	100	100
86	t3	28/198 (14%)	27 (96%)	1 (4%)	0	100	100
86	t4	27/198 (14%)	26 (96%)	1 (4%)	0	100	100
86	t5	27/198 (14%)	26 (96%)	1 (4%)	0	100	100
86	t6	25/198 (13%)	25 (100%)	0	0	100	100
87	A	2/8 (25%)	0	1 (50%)	1 (50%)	0	0
All	All	13790/19168 (72%)	13114 (95%)	671 (5%)	5 (0%)	100	100

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
63	XX	150	LYS
87	A	4	PRO
44	XD	208	ARG
44	XD	207	ILE
69	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%)	352 (100%)	1 (0%)	92	95
7	6	313/332 (94%)	312 (100%)	1 (0%)	92	95
8	7	267/303 (88%)	267 (100%)	0	100	100
9	8	128/190 (67%)	127 (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%)	252 (100%)	1 (0%)	91	94
14	A2	99/101 (98%)	97 (98%)	2 (2%)	55	73
15	A3	63/166 (38%)	63 (100%)	0	100	100
16	A4	494/609 (81%)	490 (99%)	4 (1%)	81	89
18	AB	192/249 (77%)	192 (100%)	0	100	100
19	AC	115/143 (80%)	115 (100%)	0	100	100
20	AD	283/357 (79%)	282 (100%)	1 (0%)	91	94
21	AE	104/107 (97%)	104 (100%)	0	100	100
22	AF	178/209 (85%)	178 (100%)	0	100	100
23	AG	264/342 (77%)	264 (100%)	0	100	100
24	AH	125/180 (69%)	125 (100%)	0	100	100
25	AI	104/147 (71%)	104 (100%)	0	100	100
26	AJ	93/118 (79%)	93 (100%)	0	100	100
27	AK	91/113 (80%)	91 (100%)	0	100	100
28	AL	152/226 (67%)	152 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	AM	95/113 (84%)	95 (100%)	0	100	100
30	AN	93/115 (81%)	93 (100%)	0	100	100
31	AO	166/230 (72%)	166 (100%)	0	100	100
32	AP	86/123 (70%)	86 (100%)	0	100	100
33	AQ	77/79 (98%)	77 (100%)	0	100	100
34	AR	229/318 (72%)	227 (99%)	2 (1%)	78	87
35	AS	115/164 (70%)	115 (100%)	0	100	100
36	AT	150/157 (96%)	148 (99%)	2 (1%)	69	82
37	AU	149/174 (86%)	148 (99%)	1 (1%)	84	90
38	AV	315/364 (86%)	314 (100%)	1 (0%)	92	95
39	AW	84/158 (53%)	84 (100%)	0	100	100
40	AX	307/351 (88%)	305 (99%)	2 (1%)	84	90
41	AY	104/357 (29%)	104 (100%)	0	100	100
42	AZ	79/95 (83%)	79 (100%)	0	100	100
44	XD	190/245 (78%)	189 (100%)	1 (0%)	88	93
45	XE	259/290 (89%)	259 (100%)	0	100	100
46	XF	217/262 (83%)	217 (100%)	0	100	100
47	XH	86/228 (38%)	86 (100%)	0	100	100
48	XI	194/232 (84%)	194 (100%)	0	100	100
49	XJ	133/150 (89%)	131 (98%)	2 (2%)	65	80
50	XK	155/156 (99%)	155 (100%)	0	100	100
51	XL	98/124 (79%)	98 (100%)	0	100	100
52	XM	245/249 (98%)	244 (100%)	1 (0%)	91	94
53	XN	188/211 (89%)	188 (100%)	0	100	100
54	XO	133/150 (89%)	133 (100%)	0	100	100
55	XP	125/155 (81%)	125 (100%)	0	100	100
56	XQ	220/256 (86%)	220 (100%)	0	100	100
57	XR	118/126 (94%)	117 (99%)	1 (1%)	81	89
58	XS	145/180 (81%)	145 (100%)	0	100	100
59	XT	146/176 (83%)	144 (99%)	2 (1%)	67	81
60	XU	126/135 (93%)	126 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
61	XV	179/191 (94%)	177 (99%)	2 (1%)	73	85
62	XW	91/119 (76%)	89 (98%)	2 (2%)	52	71
63	XX	219/229 (96%)	218 (100%)	1 (0%)	88	93
64	XY	161/223 (72%)	161 (100%)	0	100	100
65	XZ	111/147 (76%)	110 (99%)	1 (1%)	78	87
66	a	93/133 (70%)	93 (100%)	0	100	100
67	b	130/186 (70%)	130 (100%)	0	100	100
68	c	241/288 (84%)	240 (100%)	1 (0%)	91	94
69	d	196/274 (72%)	196 (100%)	0	100	100
70	e	188/236 (80%)	186 (99%)	2 (1%)	73	85
71	f	128/188 (68%)	128 (100%)	0	100	100
72	g	122/148 (82%)	122 (100%)	0	100	100
73	h	103/148 (70%)	103 (100%)	0	100	100
74	i	86/110 (78%)	86 (100%)	0	100	100
75	j	68/97 (70%)	68 (100%)	0	100	100
76	k	80/90 (89%)	80 (100%)	0	100	100
77	l	74/116 (64%)	74 (100%)	0	100	100
78	m	54/113 (48%)	54 (100%)	0	100	100
79	o	80/87 (92%)	80 (100%)	0	100	100
80	p	117/181 (65%)	117 (100%)	0	100	100
81	q	141/178 (79%)	140 (99%)	1 (1%)	84	90
82	r	138/169 (82%)	138 (100%)	0	100	100
85	s	326/381 (86%)	326 (100%)	0	100	100
86	t1	41/158 (26%)	40 (98%)	1 (2%)	49	69
86	t2	29/158 (18%)	29 (100%)	0	100	100
86	t3	29/158 (18%)	29 (100%)	0	100	100
86	t4	28/158 (18%)	28 (100%)	0	100	100
86	t5	28/158 (18%)	28 (100%)	0	100	100
86	t6	26/158 (16%)	26 (100%)	0	100	100
87	A	2/2 (100%)	2 (100%)	0	100	100
All	All	12399/16509 (75%)	12361 (100%)	38 (0%)	92	95

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
61	XV	152	ARG
70	e	273	ARG
62	XW	56	MET
65	XZ	152	LYS
86	t1	21[A]	LEU

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

Mol	Chain	Res	Type
33	AQ	27	ASN
85	s	207	HIS
40	AX	347	ASN
67	b	129	GLN
40	AX	54	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	XA	1490/1561 (95%)	266 (17%)	6 (0%)
17	AA	916/954 (96%)	158 (17%)	3 (0%)
43	XB	54/72 (75%)	10 (18%)	0
83	r1	0/4	-	-
84	r3	0/75	-	-
All	All	2460/2666 (92%)	434 (17%)	9 (0%)

5 of 434 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	XA	1672	C
11	XA	1681	G
11	XA	1685	C
11	XA	1689	C
11	XA	1692	A

5 of 9 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
17	AA	1048	C
17	AA	1234	C

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Mol	Chain	Res	Type
11	XA	2602	U
11	XA	2961	C
11	XA	2962	C

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

84 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	$\#\|Z\| > 2$
84	P5P	r3	10	84	16,23,24	0.95	1 (6%)	14,33,36	1.98	3 (21%)
87	DBB	A	3	87	4,5,6	0.56	0	1,5,7	0.66	0
84	Y5P	r3	32	84	14,19,20	3.14	3 (21%)	18,26,29	0.56	0
84	Y5P	r3	61	84	14,19,20	3.13	3 (21%)	18,26,29	0.56	0
84	P5P	r3	37	84	16,23,24	0.96	1 (6%)	14,33,36	1.98	3 (21%)
84	Y5P	r3	53	84	14,19,20	3.15	3 (21%)	18,26,29	0.58	0
84	Y5P	r3	60	84	14,19,20	3.13	3 (21%)	18,26,29	0.59	0
84	P5P	r3	23	84	16,23,24	0.95	1 (6%)	14,33,36	2.00	3 (21%)
84	P5P	r3	42	84	16,23,24	0.96	1 (6%)	14,33,36	1.99	3 (21%)
83	Y5P	r1	46	83	14,19,20	3.13	3 (21%)	18,26,29	0.62	0
84	Y5P	r3	67	84	14,19,20	3.13	3 (21%)	18,26,29	0.58	0
87	MHV	A	6	87	7,9,10	0.35	0	7,11,13	1.73	2 (28%)
84	P5P	r3	15	84	16,23,24	0.97	1 (6%)	14,33,36	1.96	3 (21%)
84	Y5P	r3	59	84	14,19,20	3.14	3 (21%)	18,26,29	0.57	0
84	P5P	r3	3	84	16,23,24	0.95	1 (6%)	14,33,36	1.99	3 (21%)
84	Y5P	r3	54	84	14,19,20	3.14	3 (21%)	18,26,29	0.59	0
84	P5P	r3	11	84	16,23,24	0.95	1 (6%)	14,33,36	1.98	3 (21%)
84	P5P	r3	14	84	16,23,24	0.95	1 (6%)	14,33,36	2.02	3 (21%)
84	Y5P	r3	16	84	14,19,20	3.13	3 (21%)	18,26,29	0.60	0
84	Y5P	r3	36	84	14,19,20	3.11	3 (21%)	18,26,29	0.59	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
84	P5P	r3	55	84	16,23,24	0.95	1 (6%)	14,33,36	1.96	3 (21%)
84	P5P	r3	29	84	16,23,24	0.95	1 (6%)	14,33,36	2.00	3 (21%)
87	004	A	7	87	9,10,11	1.08	1 (11%)	9,12,14	1.80	3 (33%)
84	P5P	r3	8	84	16,23,24	0.95	1 (6%)	14,33,36	1.99	3 (21%)
87	MHU	A	5	87	14,15,16	0.44	0	18,19,21	1.23	3 (16%)
84	P5P	r3	52	84	16,23,24	0.95	1 (6%)	14,33,36	1.99	3 (21%)
84	P5P	r3	68	84	16,23,24	0.95	1 (6%)	14,33,36	1.99	3 (21%)
84	P5P	r3	31	84	16,23,24	0.94	1 (6%)	14,33,36	1.97	3 (21%)
84	Y5P	r3	38	84	14,19,20	3.13	3 (21%)	18,26,29	0.57	0
84	Y5P	r3	39	84	14,19,20	3.13	3 (21%)	18,26,29	0.59	0
84	Y5P	r3	28	84	14,19,20	3.13	3 (21%)	18,26,29	0.59	0
84	P5P	r3	21	84	16,23,24	0.95	1 (6%)	14,33,36	1.96	3 (21%)
84	P5P	r3	57	84	16,23,24	0.94	1 (6%)	14,33,36	1.93	3 (21%)
84	Y5P	r3	7	84	14,19,20	3.11	3 (21%)	18,26,29	0.62	0
84	Y5P	r3	47	84	14,19,20	3.14	3 (21%)	18,26,29	0.60	0
84	Y5P	r3	62	84	14,19,20	3.14	3 (21%)	18,26,29	0.59	0
84	P5P	r3	74	84	16,23,24	0.97	1 (6%)	14,33,36	2.03	3 (21%)
84	Y5P	r3	12	84	14,19,20	3.12	3 (21%)	18,26,29	0.56	0
84	P5P	r3	46	84	16,23,24	0.96	1 (6%)	14,33,36	1.99	3 (21%)
84	Y5P	r3	58	84	14,19,20	3.13	4 (28%)	18,26,29	0.66	0
84	Y5P	r3	25	84	14,19,20	3.14	3 (21%)	18,26,29	0.60	0
84	Y5P	r3	40	84	14,19,20	3.13	3 (21%)	18,26,29	0.59	0
84	Y5P	r3	41	84	14,19,20	3.13	3 (21%)	18,26,29	0.56	0
87	MHW	A	1	87	9,9,10	0.82	0	10,11,13	3.06	3 (30%)
84	Y5P	r3	34	84	14,19,20	3.13	3 (21%)	18,26,29	0.58	0
84	P5P	r3	6	84	16,23,24	0.95	1 (6%)	14,33,36	2.01	3 (21%)
84	P5P	r3	45	84	16,23,24	0.95	1 (6%)	14,33,36	1.95	3 (21%)
84	Y5P	r3	1	84	18,20,20	2.78	3 (16%)	25,29,29	0.67	0
84	Y5P	r3	65	84	14,19,20	3.13	3 (21%)	18,26,29	0.63	0
84	P5P	r3	17(A)	84	16,23,24	0.93	1 (6%)	14,33,36	2.01	3 (21%)
83	Y5P	r1	47	83	14,19,20	3.12	3 (21%)	18,26,29	0.56	0
84	Y5P	r3	73	84	14,19,20	3.11	3 (21%)	18,26,29	0.54	0
84	Y5P	r3	64	84	14,19,20	3.13	3 (21%)	18,26,29	0.58	0
84	Y5P	r3	56	84	14,19,20	3.13	3 (21%)	18,26,29	0.64	0
84	P5P	r3	71	84	16,23,24	0.95	1 (6%)	14,33,36	1.98	3 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
84	P5P	r3	43	84	16,23,24	0.94	1 (6%)	14,33,36	1.97	3 (21%)
84	P5P	r3	66	84	16,23,24	0.94	1 (6%)	14,33,36	2.01	3 (21%)
84	P5P	r3	30	84	16,23,24	0.95	1 (6%)	14,33,36	1.99	3 (21%)
84	Y5P	r3	72	84	14,19,20	3.10	3 (21%)	18,26,29	0.65	0
84	Y5P	r3	33	84	14,19,20	3.13	3 (21%)	18,26,29	0.58	0
84	Y5P	r3	69	84	14,19,20	3.13	3 (21%)	18,26,29	0.53	0
84	P5P	r3	5	84	16,23,24	0.95	1 (6%)	14,33,36	2.01	3 (21%)
84	P5P	r3	26	84	16,23,24	0.95	1 (6%)	14,33,36	2.00	3 (21%)
84	Y5P	r3	63	84	14,19,20	3.14	3 (21%)	18,26,29	0.57	0
83	Y5P	r1	48	83	14,19,20	3.13	3 (21%)	18,26,29	0.57	0
84	P5P	r3	4	84	16,23,24	0.96	1 (6%)	14,33,36	2.00	3 (21%)
84	Y5P	r3	17	84	14,19,20	3.16	3 (21%)	18,26,29	0.56	0
84	Y5P	r3	50	84	14,19,20	3.15	3 (21%)	18,26,29	0.58	0
84	Y5P	r3	24	84	14,19,20	3.13	3 (21%)	18,26,29	0.61	0
84	P5P	r3	18	84	16,23,24	0.95	1 (6%)	14,33,36	2.01	3 (21%)
84	P5P	r3	9	84	16,23,24	0.98	1 (6%)	14,33,36	1.98	3 (21%)
84	P5P	r3	51	84	16,23,24	0.96	1 (6%)	14,33,36	1.99	3 (21%)
84	P5P	r3	19	84	16,23,24	0.96	1 (6%)	14,33,36	2.01	3 (21%)
84	Y5P	r3	27	84	14,19,20	3.14	3 (21%)	18,26,29	0.55	0
84	Y5P	r3	70	84	14,19,20	3.13	3 (21%)	18,26,29	0.59	0
84	Y5P	r3	2	84	14,19,20	3.13	3 (21%)	18,26,29	0.57	0
84	Y5P	r3	13	84	14,19,20	3.13	4 (28%)	18,26,29	0.64	0
84	Y5P	r3	20	84	14,19,20	3.13	3 (21%)	18,26,29	0.58	0
84	Y5P	r3	49	84	14,19,20	3.14	3 (21%)	18,26,29	0.56	0
84	P5P	r3	44	84	16,23,24	0.96	1 (6%)	14,33,36	1.97	3 (21%)
84	P5P	r3	35	84	16,23,24	0.95	1 (6%)	14,33,36	1.99	3 (21%)
84	P5P	r3	22	84	16,23,24	0.95	1 (6%)	14,33,36	1.98	3 (21%)
83	Y5P	r1	49	83	14,19,20	3.14	3 (21%)	18,26,29	0.57	0
84	P5P	r3	48	84	16,23,24	0.95	1 (6%)	14,33,36	1.99	3 (21%)

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
84	P5P	r3	10	84	-	0/3/25/26	0/3/3/3
87	DBB	A	3	87	-	0/3/4/6	-
84	Y5P	r3	32	84	-	1/7/33/34	0/2/2/2
84	Y5P	r3	61	84	-	3/7/33/34	0/2/2/2
84	P5P	r3	37	84	-	0/3/25/26	0/3/3/3
84	Y5P	r3	53	84	-	3/7/33/34	0/2/2/2
84	Y5P	r3	60	84	-	1/7/33/34	0/2/2/2
84	P5P	r3	23	84	-	0/3/25/26	0/3/3/3
84	P5P	r3	42	84	-	0/3/25/26	0/3/3/3
83	Y5P	r1	46	83	-	5/7/33/34	0/2/2/2
84	Y5P	r3	67	84	-	1/7/33/34	0/2/2/2
87	MHV	A	6	87	-	0/1/12/14	0/1/1/1
84	P5P	r3	15	84	-	0/3/25/26	0/3/3/3
84	Y5P	r3	59	84	-	4/7/33/34	0/2/2/2
84	P5P	r3	3	84	-	3/3/25/26	0/3/3/3
84	Y5P	r3	54	84	-	1/7/33/34	0/2/2/2
84	P5P	r3	11	84	-	0/3/25/26	0/3/3/3
84	P5P	r3	14	84	-	1/3/25/26	0/3/3/3
84	Y5P	r3	16	84	-	2/7/33/34	0/2/2/2
84	Y5P	r3	36	84	-	1/7/33/34	0/2/2/2
84	P5P	r3	55	84	-	2/3/25/26	0/3/3/3
84	P5P	r3	29	84	-	0/3/25/26	0/3/3/3
87	004	A	7	87	-	1/4/6/8	0/1/1/1
84	P5P	r3	8	84	-	0/3/25/26	0/3/3/3
87	MHU	A	5	87	-	5/9/12/14	0/1/1/1
84	P5P	r3	52	84	-	0/3/25/26	0/3/3/3
84	P5P	r3	68	84	-	0/3/25/26	0/3/3/3
84	P5P	r3	31	84	-	2/3/25/26	0/3/3/3
84	Y5P	r3	38	84	-	1/7/33/34	0/2/2/2
84	Y5P	r3	39	84	-	1/7/33/34	0/2/2/2
84	Y5P	r3	28	84	-	1/7/33/34	0/2/2/2
84	P5P	r3	21	84	-	3/3/25/26	0/3/3/3
84	P5P	r3	57	84	-	1/3/25/26	0/3/3/3
84	Y5P	r3	7	84	-	3/7/33/34	0/2/2/2
84	Y5P	r3	47	84	-	2/7/33/34	0/2/2/2
84	Y5P	r3	62	84	-	1/7/33/34	0/2/2/2
84	P5P	r3	74	84	-	0/3/25/26	0/3/3/3
84	Y5P	r3	12	84	-	1/7/33/34	0/2/2/2
84	P5P	r3	46	84	-	1/3/25/26	0/3/3/3
84	Y5P	r3	58	84	-	1/7/33/34	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
84	Y5P	r3	25	84	-	3/7/33/34	0/2/2/2
84	Y5P	r3	40	84	-	3/7/33/34	0/2/2/2
84	Y5P	r3	41	84	-	1/7/33/34	0/2/2/2
87	MHW	A	1	87	-	0/2/2/4	0/1/1/1
84	Y5P	r3	34	84	-	3/7/33/34	0/2/2/2
84	P5P	r3	6	84	-	0/3/25/26	0/3/3/3
84	P5P	r3	45	84	-	0/3/25/26	0/3/3/3
84	Y5P	r3	1	84	-	1/10/34/34	0/2/2/2
84	Y5P	r3	65	84	-	1/7/33/34	0/2/2/2
84	P5P	r3	17(A)	84	-	3/3/25/26	0/3/3/3
83	Y5P	r1	47	83	-	5/7/33/34	0/2/2/2
84	Y5P	r3	73	84	-	1/7/33/34	0/2/2/2
84	Y5P	r3	64	84	-	1/7/33/34	0/2/2/2
84	Y5P	r3	56	84	-	4/7/33/34	0/2/2/2
84	P5P	r3	71	84	-	0/3/25/26	0/3/3/3
84	P5P	r3	43	84	-	1/3/25/26	0/3/3/3
84	P5P	r3	66	84	-	2/3/25/26	0/3/3/3
84	P5P	r3	30	84	-	0/3/25/26	0/3/3/3
84	Y5P	r3	72	84	-	2/7/33/34	0/2/2/2
84	Y5P	r3	33	84	-	1/7/33/34	0/2/2/2
84	Y5P	r3	69	84	-	3/7/33/34	0/2/2/2
84	P5P	r3	5	84	-	2/3/25/26	0/3/3/3
84	P5P	r3	26	84	-	2/3/25/26	0/3/3/3
84	Y5P	r3	63	84	-	3/7/33/34	0/2/2/2
83	Y5P	r1	48	83	-	1/7/33/34	0/2/2/2
84	P5P	r3	4	84	-	3/3/25/26	0/3/3/3
84	Y5P	r3	17	84	-	3/7/33/34	0/2/2/2
84	Y5P	r3	50	84	-	4/7/33/34	0/2/2/2
84	Y5P	r3	24	84	-	1/7/33/34	0/2/2/2
84	P5P	r3	18	84	-	2/3/25/26	0/3/3/3
84	P5P	r3	9	84	-	0/3/25/26	0/3/3/3
84	P5P	r3	51	84	-	2/3/25/26	0/3/3/3
84	P5P	r3	19	84	-	2/3/25/26	0/3/3/3
84	Y5P	r3	27	84	-	1/7/33/34	0/2/2/2
84	Y5P	r3	70	84	-	1/7/33/34	0/2/2/2
84	Y5P	r3	2	84	-	3/7/33/34	0/2/2/2
84	Y5P	r3	13	84	-	5/7/33/34	0/2/2/2
84	Y5P	r3	20	84	-	1/7/33/34	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
84	Y5P	r3	49	84	-	3/7/33/34	0/2/2/2
84	P5P	r3	44	84	-	0/3/25/26	0/3/3/3
84	P5P	r3	35	84	-	0/3/25/26	0/3/3/3
84	P5P	r3	22	84	-	0/3/25/26	0/3/3/3
83	Y5P	r1	49	83	-	3/7/33/34	0/2/2/2
84	P5P	r3	48	84	-	1/3/25/26	0/3/3/3

The worst 5 of 168 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	r3	17	Y5P	C6-C5	10.59	1.52	1.33
84	r3	27	Y5P	C6-C5	10.59	1.52	1.33
84	r3	32	Y5P	C6-C5	10.56	1.52	1.33
84	r3	59	Y5P	C6-C5	10.55	1.52	1.33
84	r3	1	Y5P	C6-C5	10.54	1.52	1.33

The worst 5 of 119 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
87	A	1	MHW	O-C-CA	-8.04	116.60	124.22
84	r3	42	P5P	N1-C2-N3	-6.00	119.97	127.65
84	r3	11	P5P	N1-C2-N3	-5.97	120.01	127.65
84	r3	48	P5P	N1-C2-N3	-5.97	120.01	127.65
84	r3	66	P5P	N1-C2-N3	-5.97	120.01	127.65

There are no chirality outliers.

5 of 130 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
83	r1	46	Y5P	C4'-C5'-O5'-P
83	r1	46	Y5P	C3'-C4'-C5'-O5'
83	r1	47	Y5P	C3'-C4'-C5'-O5'
83	r1	48	Y5P	O4'-C1'-N1-C2
84	r3	3	P5P	O4'-C4'-C5'-O5'

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	A	7	004	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	A	5	MHU	1	0
87	A	1	MHW	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

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	$\#\|Z\| > 2$
91	GTP	AX	500	-	26,34,34	1.13	2 (7%)	32,54,54	1.53	6 (18%)
90	DOL	XA	5143	-	43,50,50	3.48	15 (34%)	51,70,70	2.66	10 (19%)

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
91	GTP	AX	500	-	-	8/18/38/38	0/3/3/3
90	DOL	XA	5143	-	-	16/58/77/77	0/2/3/3

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
90	XA	5143	DOL	C28-C29	9.91	1.55	1.32
90	XA	5143	DOL	C22-C23	9.51	1.56	1.32
90	XA	5143	DOL	C19-C20	7.30	1.57	1.34
90	XA	5143	DOL	C6-N5	6.38	1.49	1.34
90	XA	5143	DOL	C26-N25	6.38	1.48	1.34

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
90	XA	5143	DOL	O40-S39-O41	-14.97	101.12	118.19
90	XA	5143	DOL	C24-N25-C26	-5.00	113.94	122.03
90	XA	5143	DOL	C23-C22-C20	-4.38	119.27	125.89
91	AX	500	GTP	PA-O3A-PB	-3.92	119.36	132.83
90	XA	5143	DOL	C4-N5-C1	-3.44	108.23	112.45

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
90	XA	5143	DOL	C3-C2-S39-C42
90	XA	5143	DOL	C1-C2-S39-O41
90	XA	5143	DOL	C1-C2-S39-O40
90	XA	5143	DOL	C43-C42-S39-C2
90	XA	5143	DOL	C43-C42-S39-O41

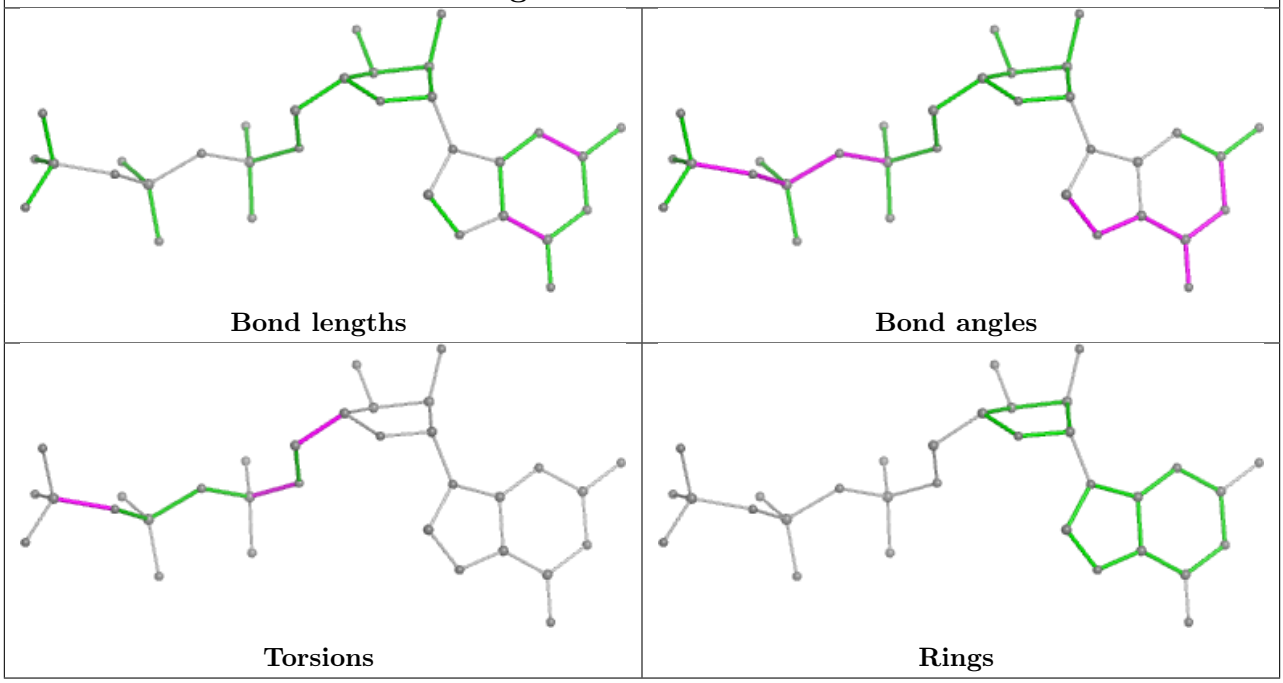
There are no ring outliers.

2 monomers are involved in 5 short contacts:

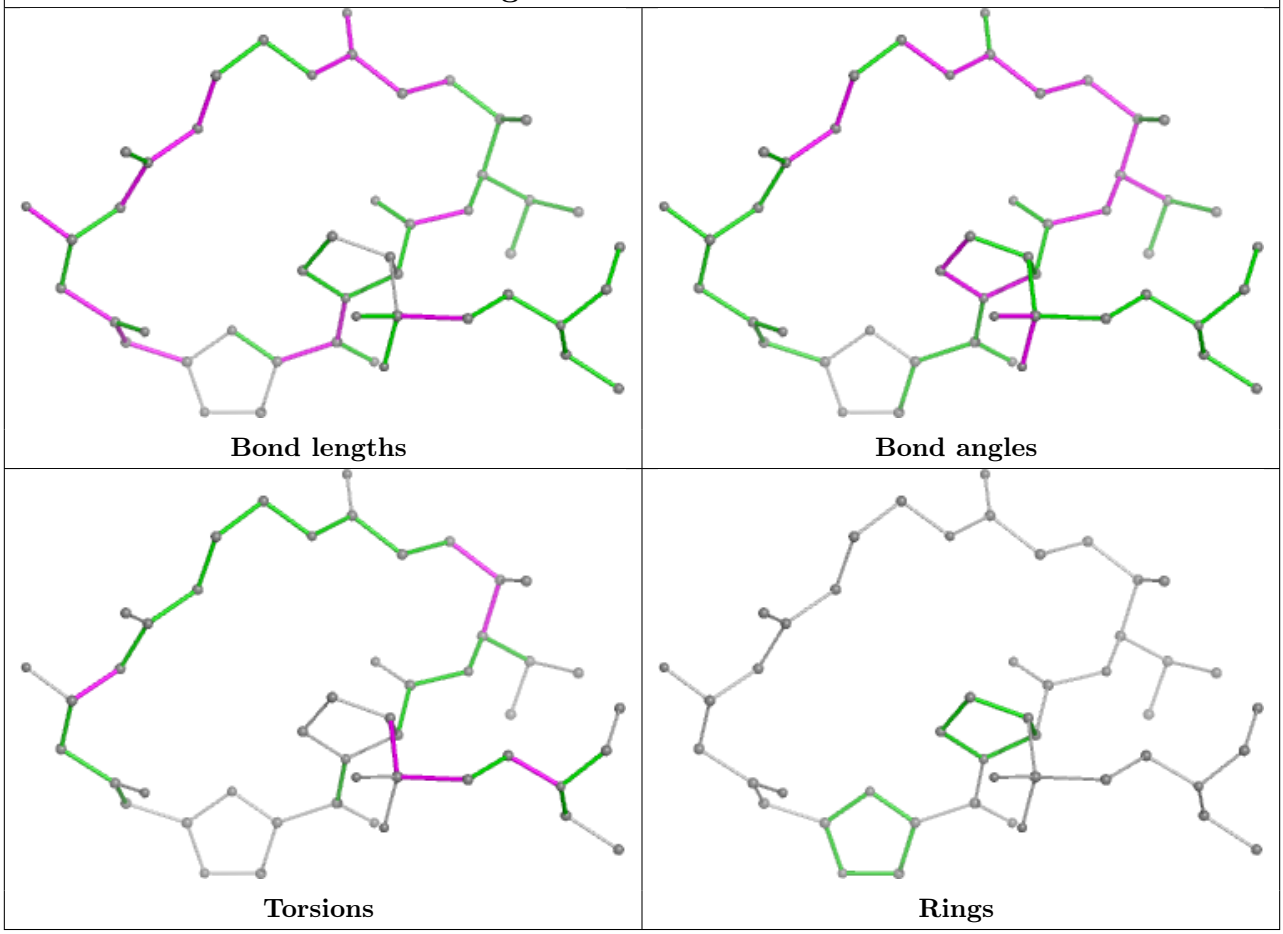
Mol	Chain	Res	Type	Clashes	Symm-Clashes
91	AX	500	GTP	1	0
90	XA	5143	DOL	4	0

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 then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand GTP AX 500



Ligand DOL XA 5143



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
16	A4	2
8	7	2
82	r	1
38	AV	1
6	5	1
72	g	1

The worst 5 of 8 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A4	537:ARG	C	538:ASP	N	6.17
1	7	285:ASN	C	286:LEU	N	6.12
1	r	134:ARG	C	135:LEU	N	5.70
1	AV	269:SER	C	270:PRO	N	4.50
1	7	185:LEU	C	186:ASP	N	3.18

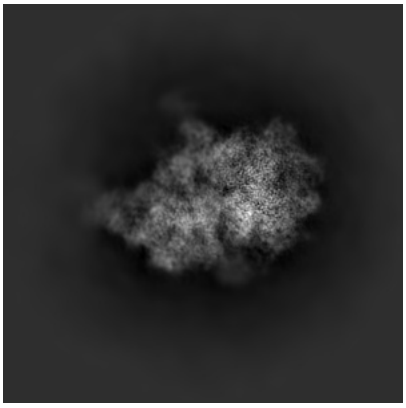
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-11392. These allow visual inspection of the internal detail of the map and identification of artifacts.

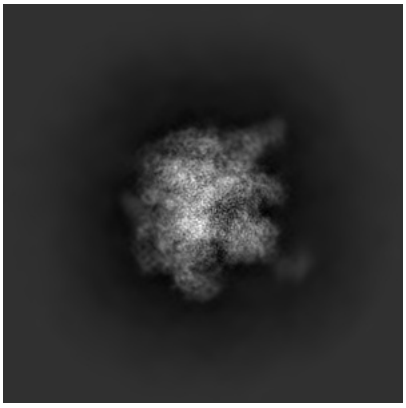
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

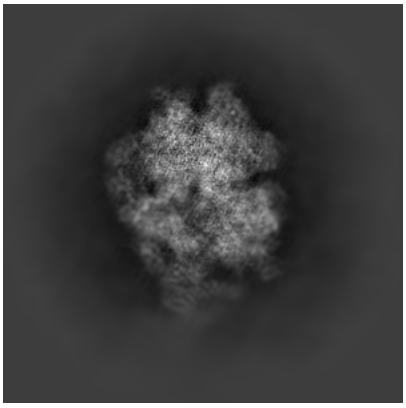
6.1.1 Primary map



X



Y

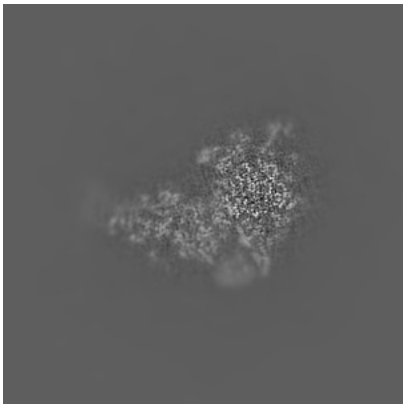


Z

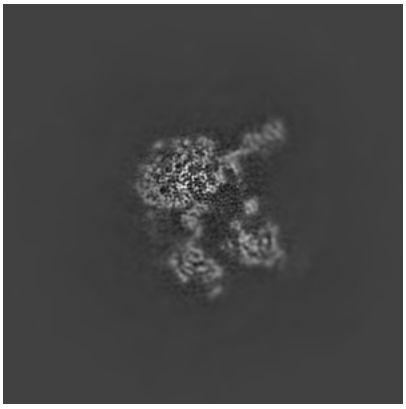
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

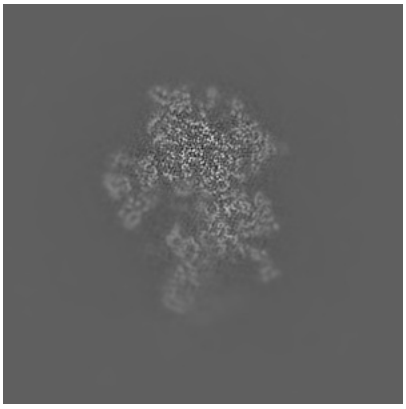
6.2.1 Primary map



X Index: 260



Y Index: 260

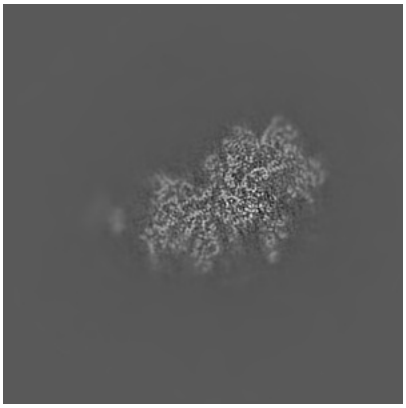


Z Index: 260

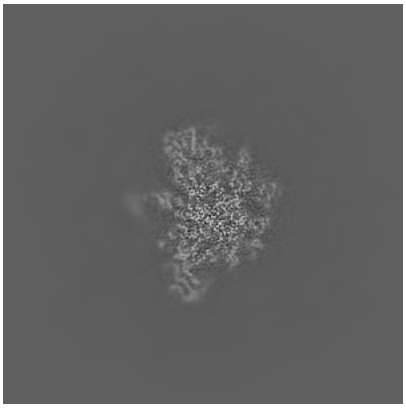
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

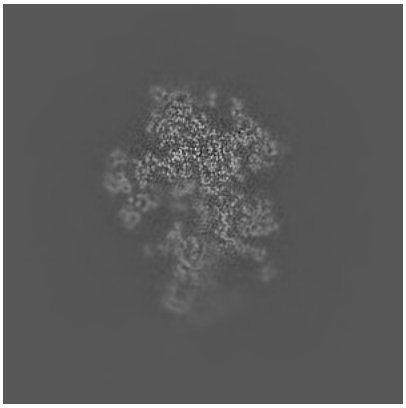
6.3.1 Primary map



X Index: 282



Y Index: 320

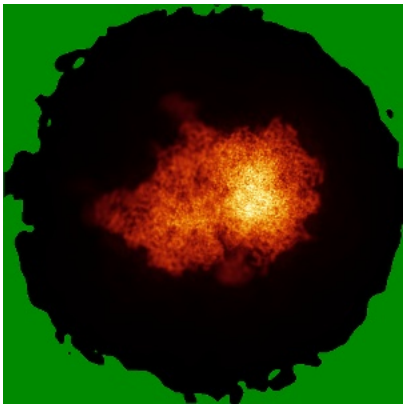


Z Index: 257

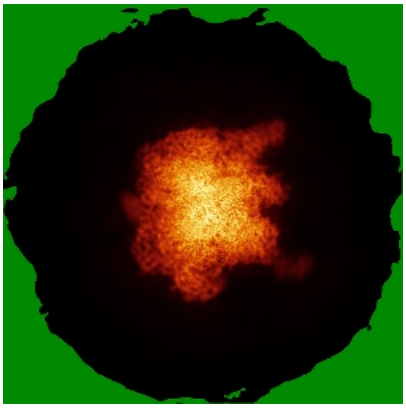
The images above show the largest variance slices of the map in three orthogonal directions.

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

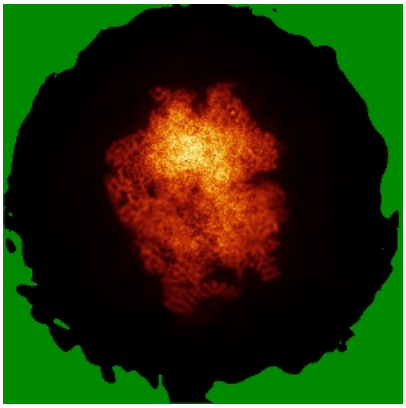
6.4.1 Primary map



X



Y

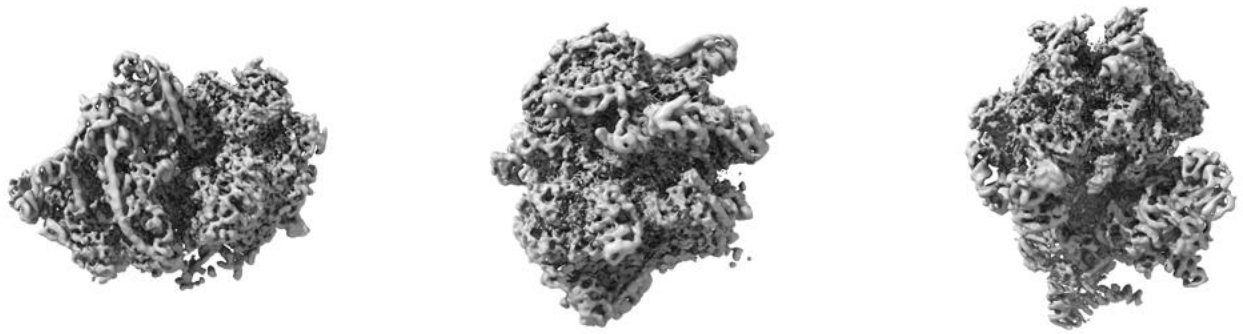


Z

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



X Y Z

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.

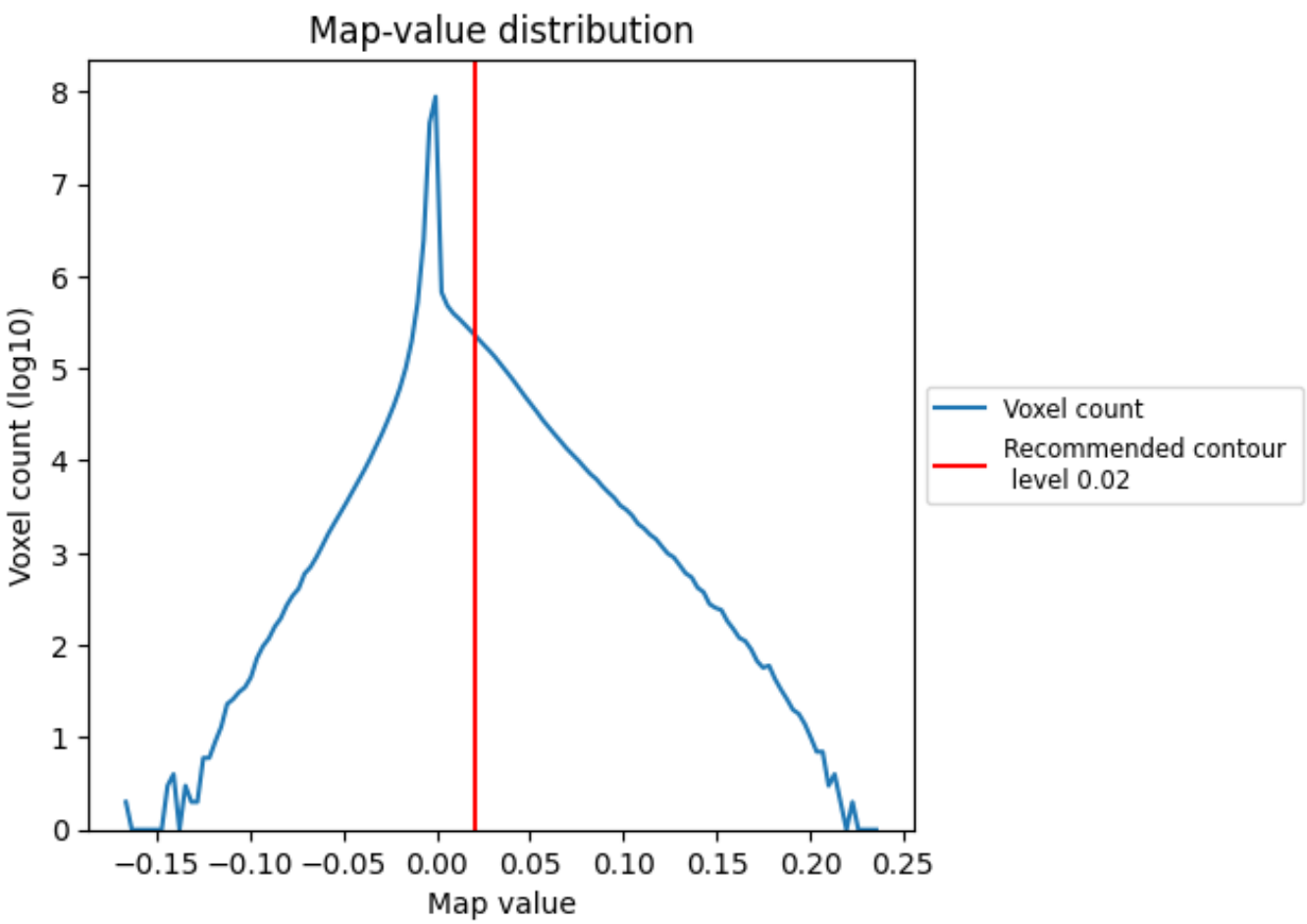
6.6 Mask visualisation (i)

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

7 Map analysis (i)

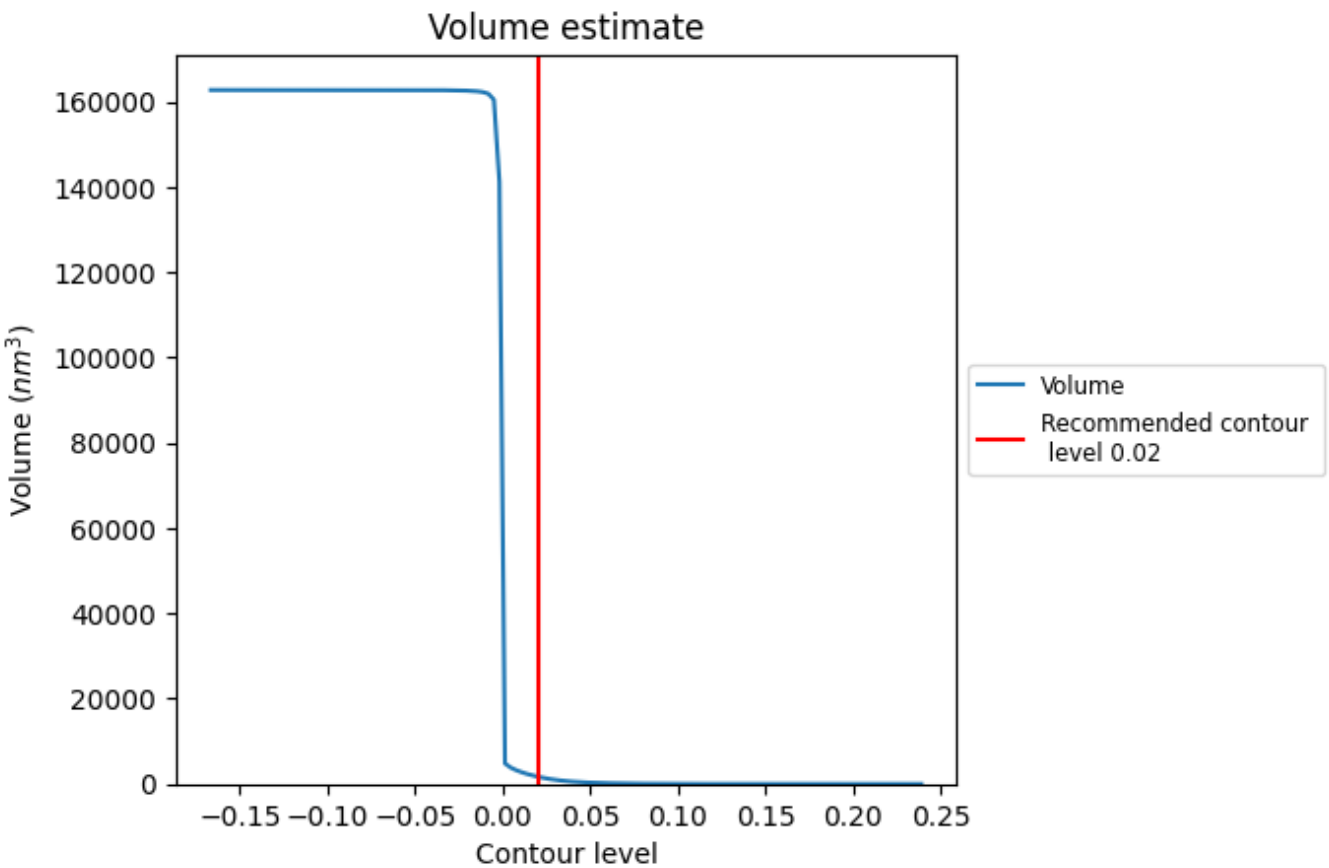
This section contains the results of statistical analysis of the map.

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.

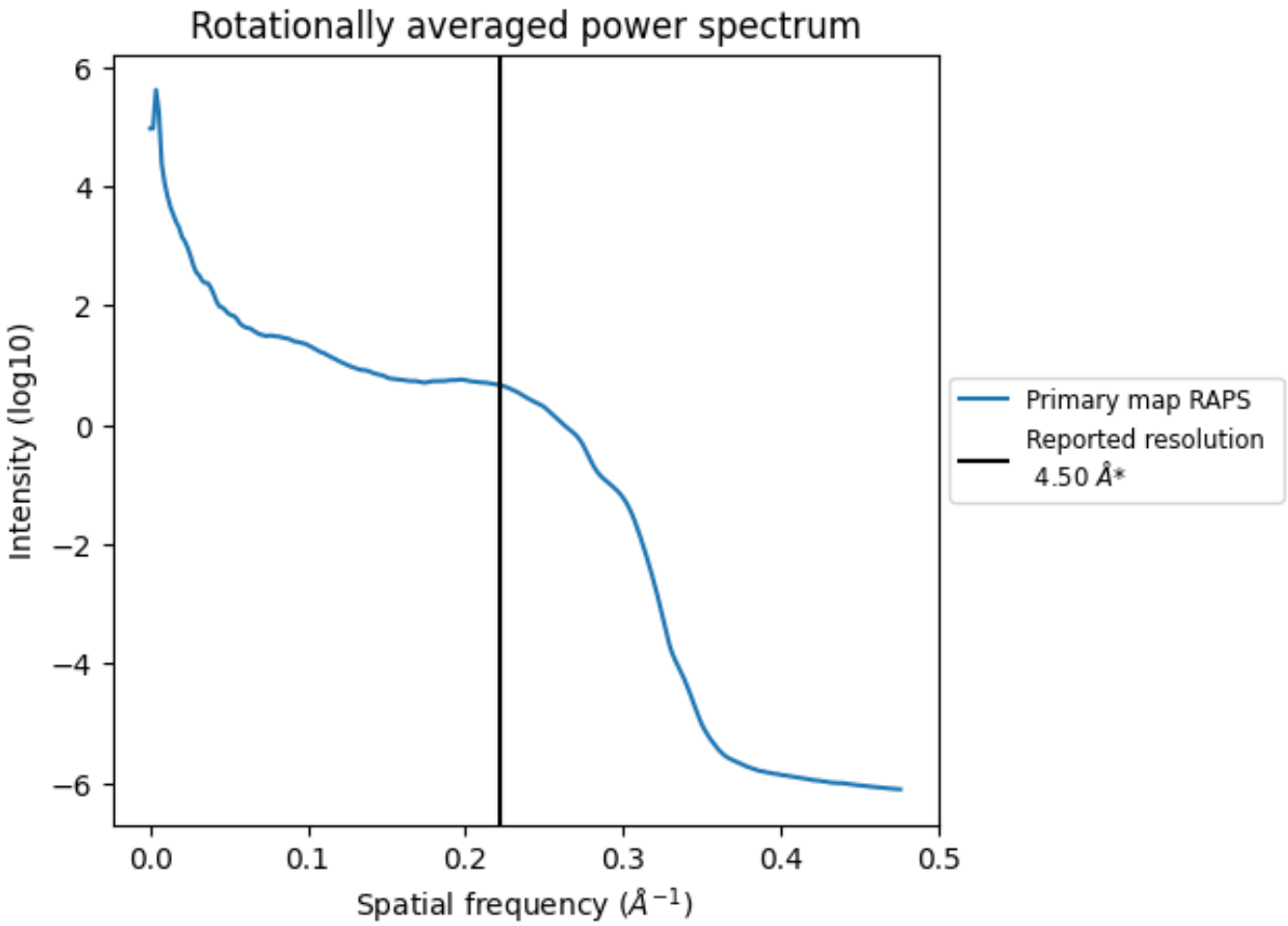
7.2 Volume estimate (i)



The volume at the recommended contour level is 1693 nm^3; this corresponds to an approximate mass of 1529 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 0.222 Å^{-1}

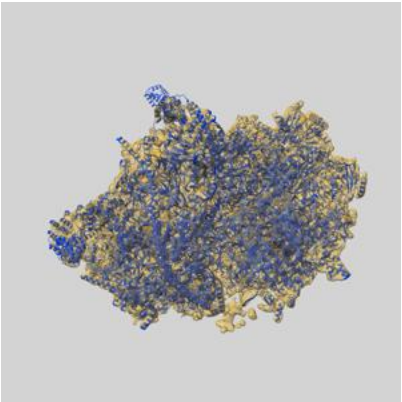
8 Fourier-Shell correlation (i)

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

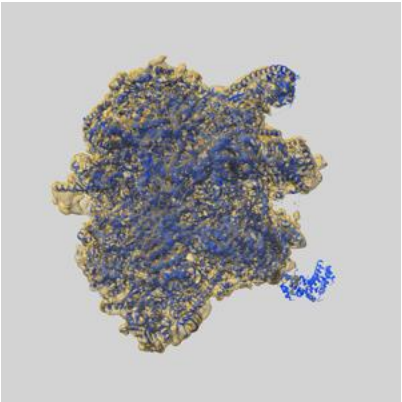
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-11392 and PDB model 6ZSB. Per-residue inclusion information can be found in section 3 on page 22.

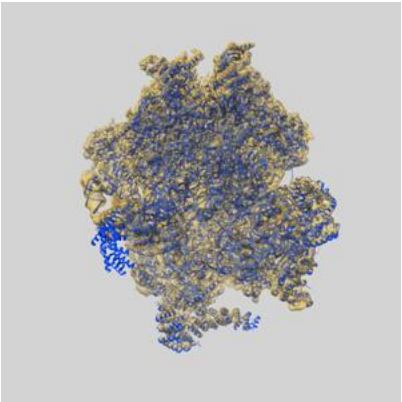
9.1 Map-model overlay (i)



X



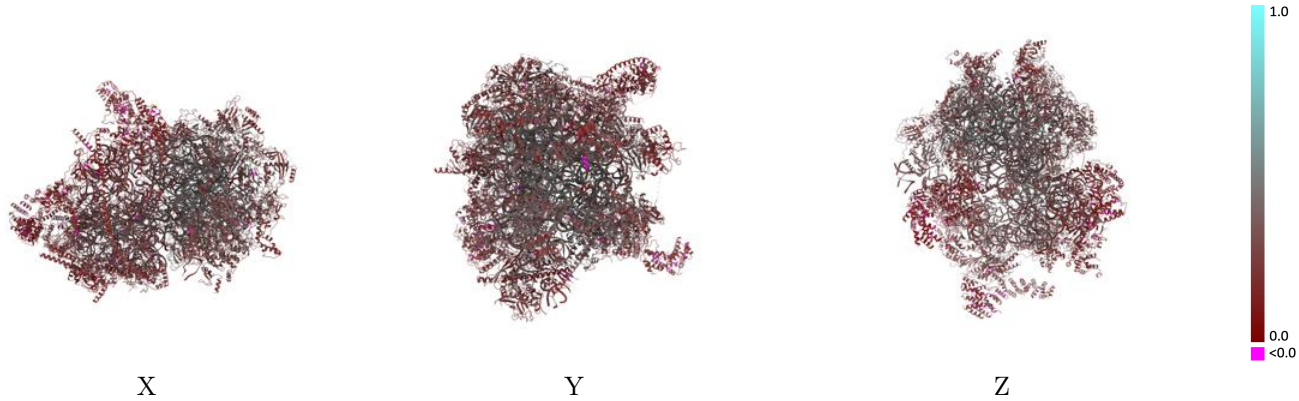
Y



Z

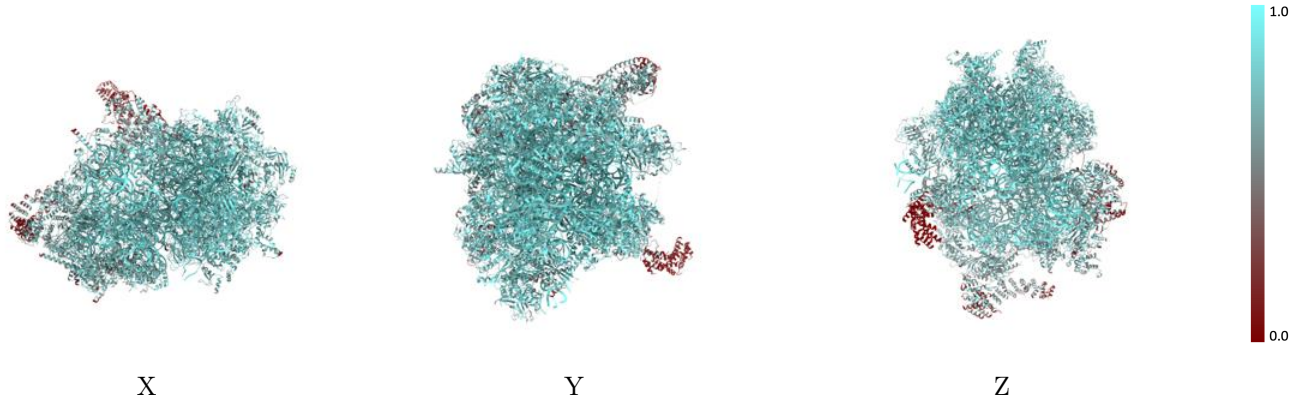
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



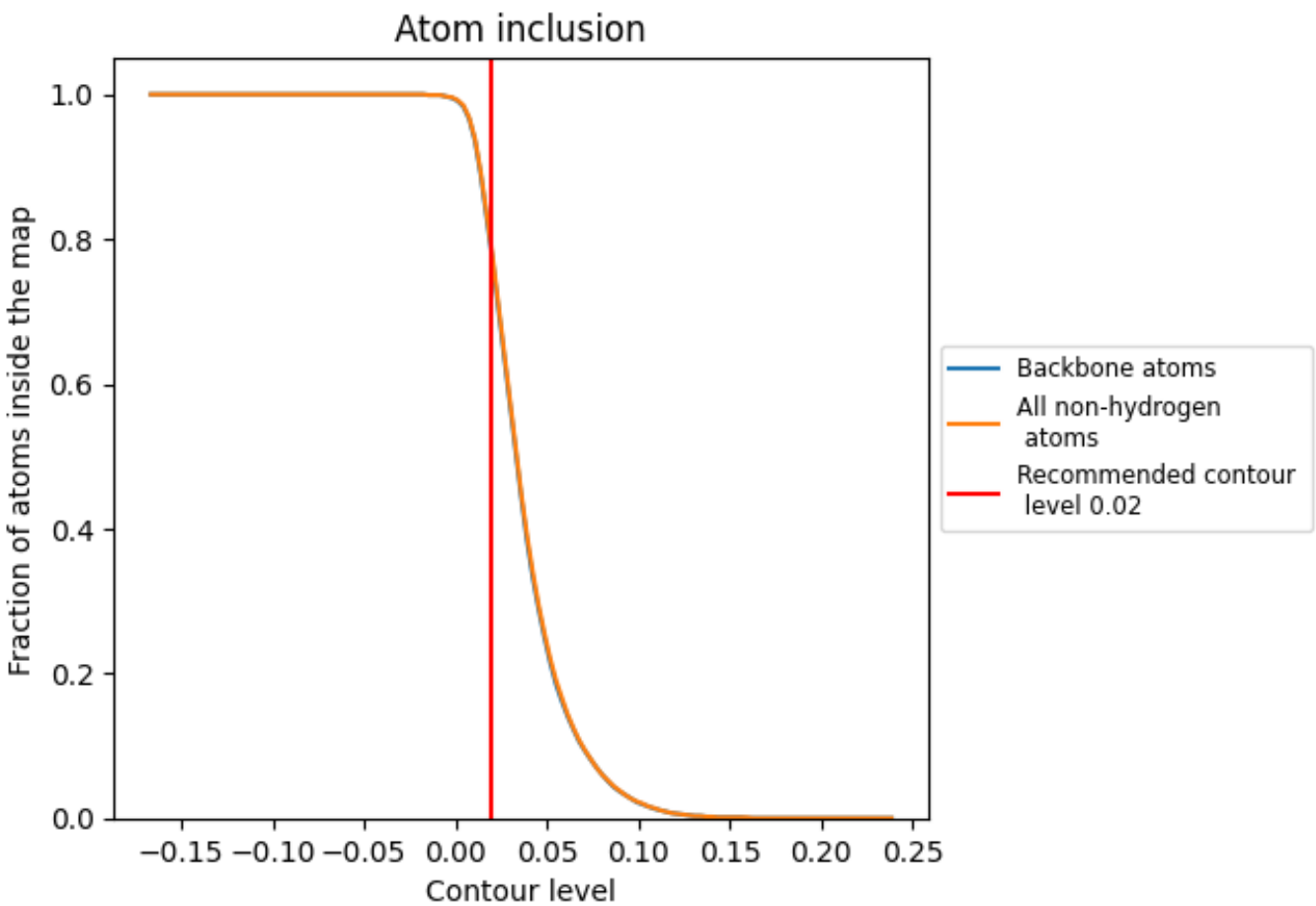
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 78% of all backbone atoms, 78% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

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	0.7840	0.3100
0	0.8200	0.3430
1	0.7980	0.3280
2	0.8720	0.4530
3	0.8530	0.4210
4	0.8590	0.3650
5	0.7840	0.3060
6	0.7620	0.2900
7	0.7460	0.2780
8	0.6490	0.1910
9	0.7870	0.3350
A	0.8220	0.3910
A0	0.6010	0.1780
A1	0.6160	0.2050
A2	0.6660	0.2640
A3	0.8350	0.3590
A4	0.4540	0.1600
AA	0.9310	0.3270
AB	0.7120	0.2560
AC	0.7040	0.2780
AD	0.7010	0.2810
AE	0.7180	0.3060
AF	0.6950	0.2510
AG	0.6810	0.2350
AH	0.6710	0.2560
AI	0.7190	0.2900
AJ	0.7510	0.3030
AK	0.7160	0.2460
AL	0.7440	0.2700
AM	0.6620	0.1890
AN	0.7650	0.2980
AO	0.6760	0.2350
AP	0.7410	0.2930
AQ	0.7680	0.3060
AR	0.6240	0.1820

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Chain	Atom inclusion	Q-score
AS	0.6320	0.2340
AT	0.7350	0.2680
AU	0.6940	0.2140
AV	0.5240	0.1670
AW	0.6800	0.2480
AX	0.6320	0.1800
AY	0.6090	0.2000
AZ	0.6560	0.2050
XA	0.9360	0.4010
XB	0.9520	0.2910
XD	0.8430	0.3800
XE	0.8240	0.3740
XF	0.8520	0.3880
XH	0.7380	0.3080
XI	0.5470	0.2060
XJ	0.6300	0.1820
XK	0.8390	0.3820
XL	0.8380	0.3760
XM	0.8380	0.3820
XN	0.8120	0.3680
XO	0.8120	0.3450
XP	0.7950	0.3140
XQ	0.7370	0.3180
XR	0.8300	0.3830
XS	0.8220	0.3870
XT	0.8590	0.4030
XU	0.8210	0.3640
XV	0.7800	0.2970
XW	0.8660	0.4180
XX	0.7870	0.3210
XY	0.8380	0.3420
XZ	0.8510	0.3950
a	0.7980	0.3590
b	0.8590	0.3880
c	0.7920	0.3170
d	0.6960	0.2630
e	0.6410	0.1700
f	0.6630	0.2160
g	0.8230	0.3520
h	0.7600	0.2910
i	0.8590	0.4120
j	0.7960	0.3400

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Chain	Atom inclusion	Q-score
k	0.6980	0.2030
l	0.6700	0.2020
m	0.7500	0.2220
o	0.8680	0.3940
p	0.7740	0.2760
q	0.6460	0.2420
r	0.8280	0.3240
r1	0.7640	0.3090
r3	0.8600	0.2650
s	0.8050	0.3260
t1	0.1590	0.1780
t2	0.0920	0.1670
t3	0.0000	0.1750
t4	0.0000	0.1220
t5	0.0000	0.1440
t6	0.0000	0.0900