wwPDB EM Validation Summary Report

Dec 15, 2022 – 05:05 pm GMT

PDB ID	:	6XU7
EMDB ID	:	EMD-10623
Title	:	Drosophila melanogaster Testis polysome ribosome
Authors	:	Hopes, T.; Agapiou, M.; Norris, K.; McCarthy, C.G.P.; OConnell, M.J.; Fontana, J.; Aspden, J.L.
Deposited on	:	2020-01-17
Resolution	:	4.90 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

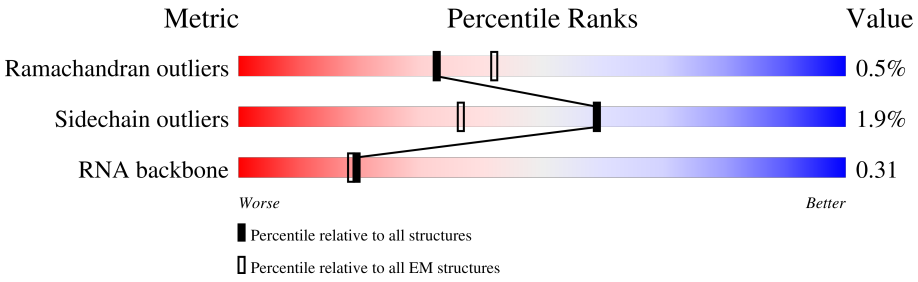
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

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 4.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=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	AA	218	10% 99%
2	CA	253	94% 5%
3	AB	220	8% 98%
4	CB	414	95% 5%
5	AC	227	5% 99%
6	CC	392	95% 5%
7	Ag	318	19% 98%
8	AU	102	13% 98%

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Mol	Chain	Length	Quality of chain
9	AO	134	13% 97%
10	AX	143	97%
11	AM	119	61% 98%
12	AS	137	96%
13	Ad	52	92% 8%
14	AN	150	99%
15	AL	155	24% 99%
16	AR	120	11% 100%
17	AP	124	19% 98%
18	AV	82	7% 99%
19	AY	126	7% 100%
20	AZ	74	15% 95% 5%
21	Aa	107	10% 95%
22	Ab	84	15% 99%
23	AD	227	14% 99%
24	Ae	58	16% 95%
25	Af	80	44% 99%
26	AJ	181	97%
27	Ca	149	92% 7%
28	CN	203	90% 10%
29	CI	217	97%
30	CD	290	97%
31	CQ	187	95%
32	CR	203	10% 95% 5%
33	CS	173	91% 9%

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Mol	Chain	Length	Quality of chain
34	CT	158	95%
35	CP	185	13% 93% 7%
36	CX	120	98%
37	CY	131	99%
38	CZ	134	98%
39	Cr	134	85% 13%
40	Ch	123	99%
41	Cb	75	91% 8%
42	Cc	100	98%
43	Cd	111	95% 5%
44	Ce	132	90% 9%
45	Cf	157	94%
46	Ci	113	6% 93% 7%
47	Ck	70	97%
48	Cl	50	90% 8%
49	Cm	52	100%
50	Cn	25	96%
51	Cp	91	97%
52	Co	104	96%
53	CJ	182	5% 98%
54	CH	190	99%
55	CE	228	8% 93% 7%
56	CG	241	10% 95% 5%
57	A9	30	60% 33% 7%
58	A7	120	58% 38%

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Mol	Chain	Length	Quality of chain
59	A8	123	28% 50% 23%
60	Cz	217	95% 97%
61	B2	1995	6% 56% 36% 5%
62	A5	3974	35% 39% 19% 7%
63	Ac	62	10% 98%
64	AW	129	98%
65	CW	58	95% 5%
66	Cg	104	93% 6%
67	CU	96	98%
68	AK	90	11% 96%
69	AT	143	79% 11% 8%
70	AF	189	10% 96%
71	CF	226	95%
72	AE	261	99%
73	AG	231	12% 99%
74	AH	194	13% 96%
75	AI	207	7% 98%
76	AQ	148	7% 98%
77	CO	205	94% 5%
78	CL	210	7% 91% 8%
79	CV	134	98%
80	CM	159	9% 98%
81	B	75	60% 35% 5%
82	v	12	50% 50%
83	Cj	87	66% 33%

2 Entry composition (i)

There are 83 unique types of molecules in this entry. The entry contains 219005 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	AA	218	1737	1113	298	321	5	0	0

- Molecule 2 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	CA	253	1935	1206	395	326	8	0	0

- Molecule 3 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	AB	220	1798	1138	328	324	8	0	0

- Molecule 4 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	CB	414	3287	2083	621	565	18	0	0

- Molecule 5 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	AC	227	1746	1126	302	311	7	0	0

- Molecule 6 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	CC	392	3109	1959	622	522	6	0	0

- Molecule 7 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Ag	318	Total	C	N	O	S	0	0
			2511	1577	444	480	10		

- Molecule 8 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AU	102	Total	C	N	O	S	0	0
			815	505	161	145	4		

- Molecule 9 is a protein called 40S ribosomal protein S14a.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AO	134	Total	C	N	O	S	0	0
			1003	616	196	187	4		

- Molecule 10 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AX	143	Total	C	N	O	S	0	0
			1131	712	226	191	2		

- Molecule 11 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AM	119	Total	C	N	O	S	0	0
			924	582	165	171	6		

- Molecule 12 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AS	137	Total	C	N	O	S	0	0
			1128	707	220	198	3		

- Molecule 13 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Ad	52	Total	C	N	O	S	0	0
			433	269	87	72	5		

- Molecule 14 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	150	Total	C	N	O	S	0	0
			1202	767	229	203	3		

- Molecule 15 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AL	155	Total	C	N	O	S	0	0
			1274	803	254	211	6		

- Molecule 16 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AR	120	Total	C	N	O	S	0	0
			981	618	183	176	4		

- Molecule 17 is a protein called GEO07301p1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AP	124	Total	C	N	O	S	0	0
			1016	652	189	169	6		

- Molecule 18 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AV	82	Total	C	N	O	S	0	0
			617	373	114	125	5		

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AV	2	GLN	GLU	conflict	UNP O76927
AV	8	PHE	ASN	conflict	UNP O76927
AV	25	GLY	HIS	conflict	UNP O76927
AV	32	ILE	VAL	conflict	UNP O76927
AV	34	MET	LEU	conflict	UNP O76927
AV	35	ASN	SER	conflict	UNP O76927
AV	36	VAL	ILE	conflict	UNP O76927
AV	58	ALA	GLU	conflict	UNP O76927
AV	68	SER	CYS	conflict	UNP O76927
AV	70	LEU	VAL	conflict	UNP O76927
AV	75	ALA	LYS	conflict	UNP O76927
AV	79	VAL	ILE	conflict	UNP O76927

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Chain	Residue	Modelled	Actual	Comment	Reference
AV	80	SER	THR	conflict	UNP O76927

- Molecule 19 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AY	126	Total	C	N	O	S	0	0
			1016	644	196	171	5		

- Molecule 20 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	AZ	74	Total	C	N	O	0	0
			608	390	112	106		

- Molecule 21 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Aa	107	Total	C	N	O	S	0	0
			867	539	182	140	6		

- Molecule 22 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Ab	84	Total	C	N	O	S	0	0
			653	412	123	110	8		

- Molecule 23 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AD	227	Total	C	N	O	S	0	0
			1782	1127	319	326	10		

- Molecule 24 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	Ae	58	Total	C	N	O	0	0
			469	289	105	75		

- Molecule 25 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Af	80	Total	C	N	O	S	0	0
			659	417	128	109	5		

- Molecule 26 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AJ	181	Total	C	N	O	S	0	0
			1503	957	298	247	1		

- Molecule 27 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Ca	149	Total	C	N	O	S	0	0
			1204	769	242	189	4		

- Molecule 28 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	CN	203	Total	C	N	O	S	0	0
			1710	1072	362	271	5		

- Molecule 29 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	CI	217	Total	C	N	O	S	0	0
			1785	1125	343	304	13		

- Molecule 30 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	CD	290	Total	C	N	O	S	0	0
			2334	1471	434	423	6		

- Molecule 31 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	CQ	187	Total	C	N	O	S	0	0
			1518	957	306	251	4		

- Molecule 32 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	CR	203	Total	C	N	O	S	0	0
			1683	1047	350	277	9		

- Molecule 33 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	CS	173	Total	C	N	O	S	0	0
			1454	935	275	240	4		

- Molecule 34 is a protein called RE62581p.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	CT	158	Total	C	N	O	S	0	0
			1297	829	253	212	3		

- Molecule 35 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	CP	185	Total	C	N	O	S	0	0
			1505	928	305	263	9		

- Molecule 36 is a protein called IP17216p.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	CX	120	Total	C	N	O	S	0	0
			984	625	192	165	2		

- Molecule 37 is a protein called GEO07453p1.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	CY	131	Total	C	N	O	S	0	0
			1078	676	224	176	2		

- Molecule 38 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	CZ	134	Total	C	N	O	S	0	0
			1115	723	209	180	3		

- Molecule 39 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	Cr	134	Total 1051	C 670	N 205	O 176	0	0

- Molecule 40 is a protein called FI02809p.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Ch	123	Total 1015	C 646	N 202	O 164	S 3	0	0

- Molecule 41 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Cb	75	Total 619	C 378	N 133	O 107	S 1	0	0

- Molecule 42 is a protein called RE25263p.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Cc	100	Total 770	C 486	N 132	O 147	S 5	0	0

- Molecule 43 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Cd	111	Total 924	C 573	N 180	O 169	S 2	0	0

- Molecule 44 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Ce	132	Total 1110	C 698	N 230	O 177	S 5	0	0

- Molecule 45 is a protein called GEO07455p1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Cf	157	Total 1244	C 781	N 255	O 203	S 5	0	0

- Molecule 46 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Ci	113	Total	C	N	O	S	0	0
			934	585	193	153	3		

- Molecule 47 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Ck	70	Total	C	N	O	S	0	0
			576	366	108	100	2		

- Molecule 48 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	Cl	50	Total	C	N	O	0	0
			437	276	98	63		

- Molecule 49 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Cm	52	Total	C	N	O	S	0	0
			429	267	89	67	6		

- Molecule 50 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Cn	25	Total	C	N	O	S	0	0
			236	143	63	27	3		

- Molecule 51 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Cp	91	Total	C	N	O	S	0	0
			710	441	140	122	7		

- Molecule 52 is a protein called TA01007p.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Co	104	Total	C	N	O	S	0	0
			874	548	180	138	8		

- Molecule 53 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	CJ	182	Total	C	N	O	S	0	0
			1468	926	278	258	6		

- Molecule 54 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	CH	190	Total	C	N	O	S	0	0
			1499	947	265	278	9		

- Molecule 55 is a protein called Ribosomal protein L6, isoform A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	CE	228	Total	C	N	O	S	0	0
			1845	1185	351	305	4		

- Molecule 56 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	CG	241	Total	C	N	O	S	0	0
			1936	1237	368	327	4		

- Molecule 57 is a RNA chain called 2S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	A9	30	Total	C	N	O	P	0	0
			639	286	111	213	29		

- Molecule 58 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	A7	120	Total	C	N	O	P	0	0
			2554	1141	456	838	119		

- Molecule 59 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	A8	123	Total	C	N	O	P	0	0
			2621	1173	474	852	122		

- Molecule 60 is a protein called 60S ribosomal protein L10a-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Cz	217	Total	C	N	O	S	0	0
			1702	1084	303	305	10		

- Molecule 61 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	B2	1936	Total	C	N	O	P	0	0
			39355	17526	6780	13114	1935		

- Molecule 62 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	A5	3707	Total	C	N	O	P	0	0
			77175	34473	13566	25431	3705		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A5	1301	A	U	conflict	GB NR_133562.1
A5	1319	A	U	conflict	GB NR_133562.1
A5	1320	U	G	conflict	GB NR_133562.1
A5	1321	G	U	conflict	GB NR_133562.1
A5	1322	U	G	conflict	GB NR_133562.1
A5	1686	A	-	insertion	GB NR_133562.1
A5	1710	G	-	insertion	GB NR_133562.1
A5	2158A	C	-	insertion	GB NR_133562.1
A5	2279	C	G	conflict	GB NR_133562.1
A5	3569	C	-	insertion	GB NR_133562.1

- Molecule 63 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Ac	62	Total	C	N	O	S	0	0
			498	307	100	89	2		

- Molecule 64 is a protein called 40S ribosomal protein S15Aa.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AW	129	Total	C	N	O	S	0	0
			1028	656	189	176	7		

- Molecule 65 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	CW	58	Total	C	N	O	S	0	0
			483	314	89	76	4		

- Molecule 66 is a protein called RH48056p.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Cg	104	Total	C	N	O	S	0	0
			852	530	177	139	6		

- Molecule 67 is a protein called Ribosomal protein L22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	CU	96	Total	C	N	O	S	0	0
			811	531	137	139	4		

- Molecule 68 is a protein called 40S ribosomal protein S10b.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	AK	90	Total	C	N	O	S	0	0
			760	500	130	127	3		

- Molecule 69 is a protein called 40S ribosomal protein S19a.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	AT	132	Total	C	N	O	S	0	0
			1041	659	200	179	3		

- Molecule 70 is a protein called 40S ribosomal protein S5a.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	AF	189	Total	C	N	O	S	0	0
			1490	929	284	268	9		

- Molecule 71 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	CF	226	Total	C	N	O	S	0	0
			1895	1216	368	308	3		

- Molecule 72 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	AE	261	Total	C	N	O	S	0	0
			2054	1314	380	353	7		

- Molecule 73 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	AG	231	Total	C	N	O	S	0	0
			1866	1172	372	315	7		

- Molecule 74 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	AH	194	Total	C	N	O	S	0	0
			1566	1006	278	281	1		

- Molecule 75 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	AI	207	Total	C	N	O	S	0	0
			1665	1037	329	296	3		

- Molecule 76 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	AQ	148	Total	C	N	O	S	0	0
			1183	753	223	204	3		

- Molecule 77 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	CO	205	Total	C	N	O	S	0	0
			1668	1063	331	268	6		

- Molecule 78 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	CL	210	Total	C	N	O	S	0	0
			1695	1066	342	284	3		

- Molecule 79 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	CV	134	Total	C	N	O	S	0	0
			998	629	190	173	6		

- Molecule 80 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	CM	159	Total	C	N	O	S	0	0
			1302	826	256	218	2		

- Molecule 81 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	B	75	Total	C	N	O	P	0	0
			1605	717	296	518	74		

- Molecule 82 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	v	12	Total	C	N	O	P	0	0
			255	113	43	87	12		

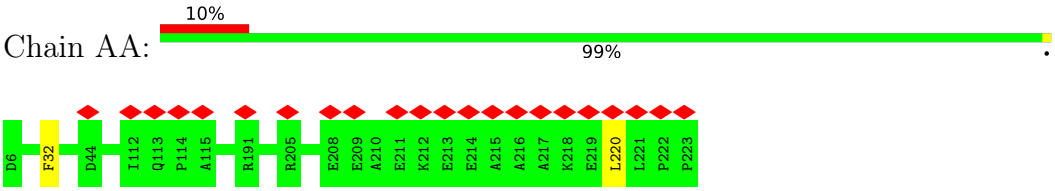
- Molecule 83 is a protein called Probable 60S ribosomal protein L37-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Cj	87	Total	C	N	O	S	0	0
			696	422	154	115	5		

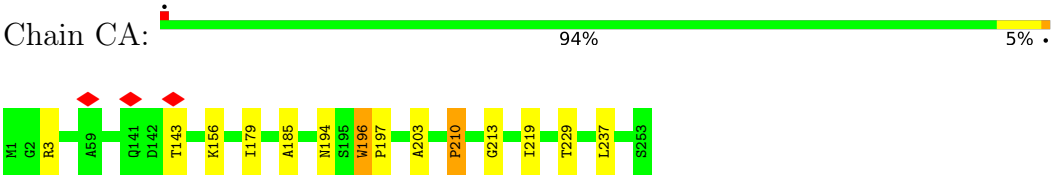
3 Residue-property plots (i)

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.

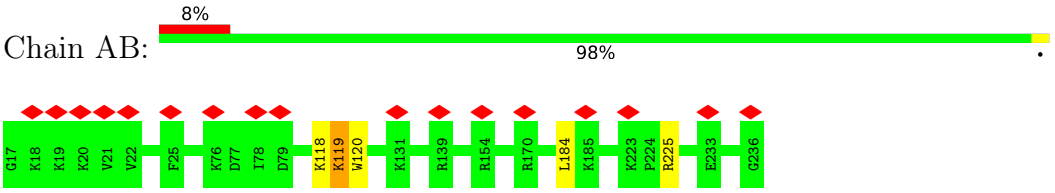
• Molecule 1: 40S ribosomal protein SA



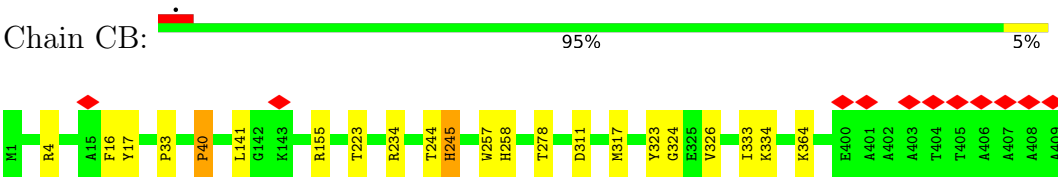
• Molecule 2: 60S ribosomal protein L8



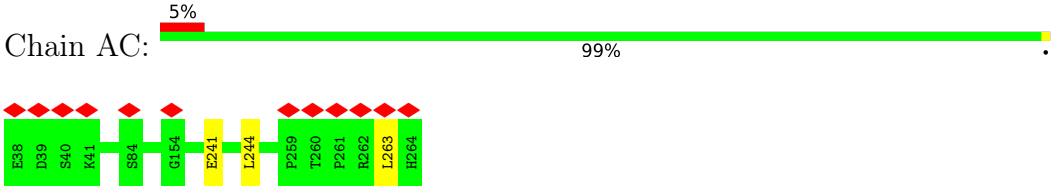
• Molecule 3: 40S ribosomal protein S3a



• Molecule 4: 60S ribosomal protein L3

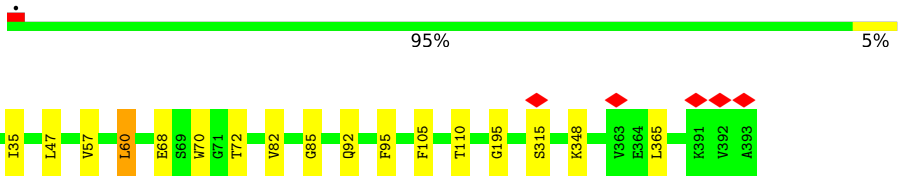


• Molecule 5: 40S ribosomal protein S2



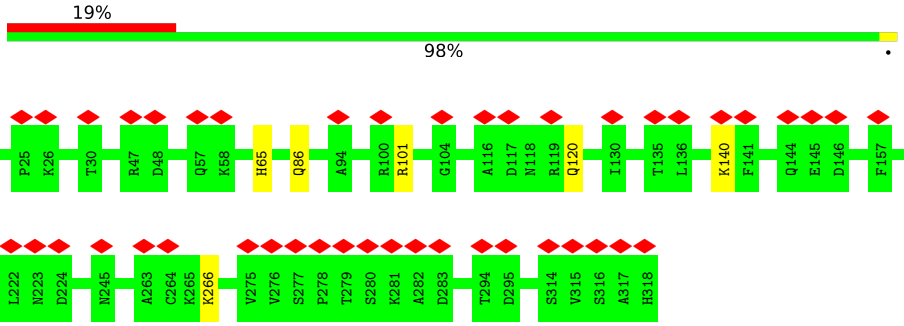
• Molecule 6: 60S ribosomal protein L4

Chain CC:



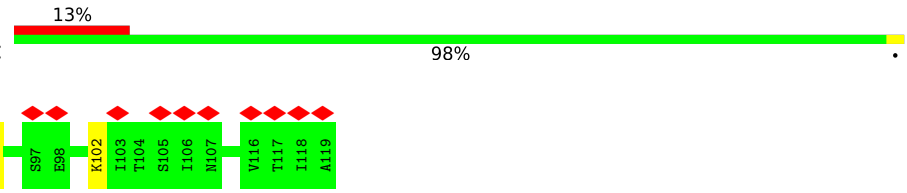
• Molecule 7: Guanine nucleotide-binding protein subunit beta-like protein

Chain Ag:



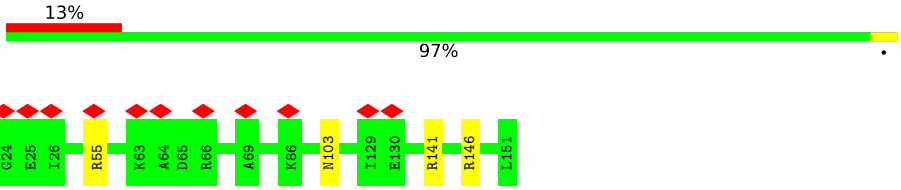
• Molecule 8: 40S ribosomal protein S20

Chain AU:



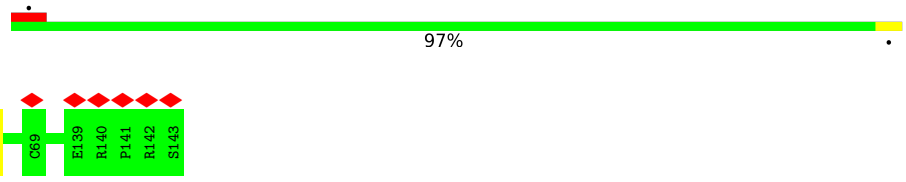
• Molecule 9: 40S ribosomal protein S14a

Chain AO:



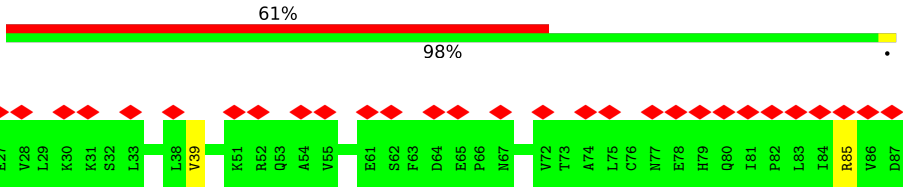
• Molecule 10: 40S ribosomal protein S23

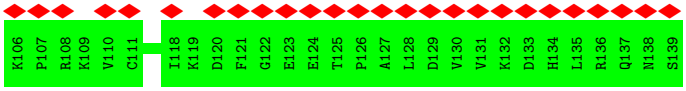
Chain AX:



• Molecule 11: 40S ribosomal protein S12

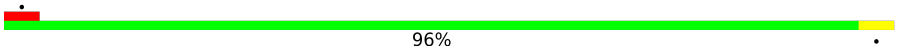
Chain AM:

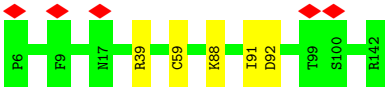




• Molecule 12: 40S ribosomal protein S18

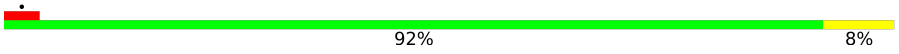
Chain AS:

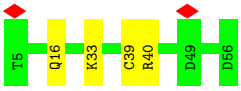




• Molecule 13: 40S ribosomal protein S29

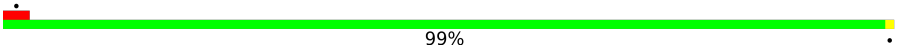
Chain Ad:

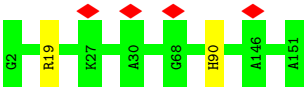




• Molecule 14: 40S ribosomal protein S13

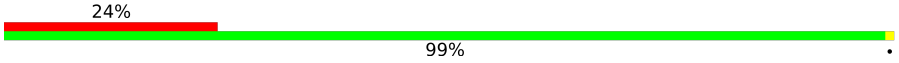
Chain AN:

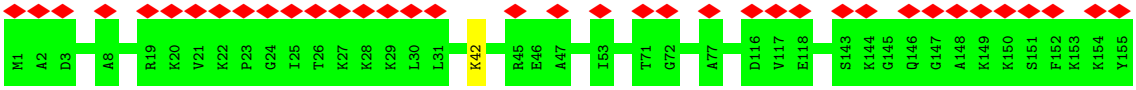




• Molecule 15: 40S ribosomal protein S11

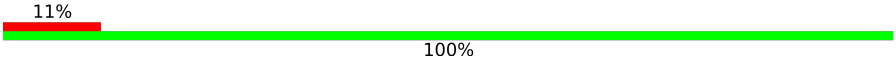
Chain AL:

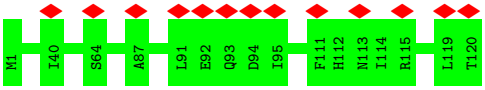




• Molecule 16: 40S ribosomal protein S17

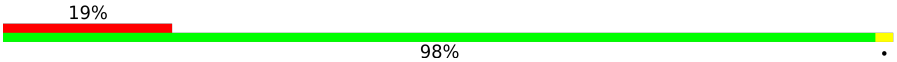
Chain AR:

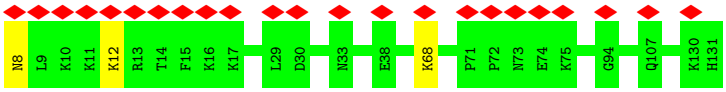




• Molecule 17: GEO07301p1

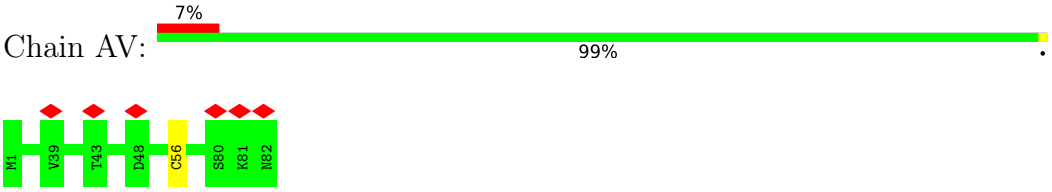
Chain AP:





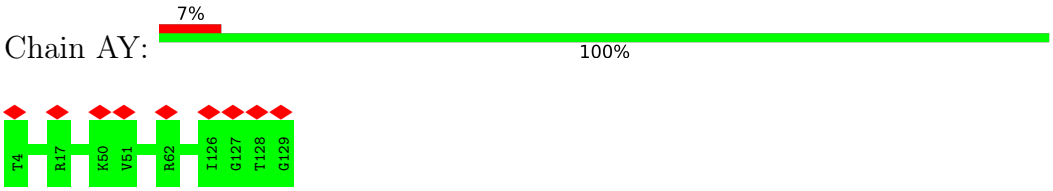
• Molecule 18: 40S ribosomal protein S21

Chain AV:



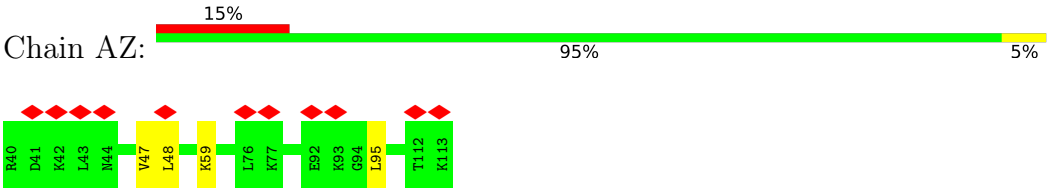
• Molecule 19: 40S ribosomal protein S24

Chain AY:



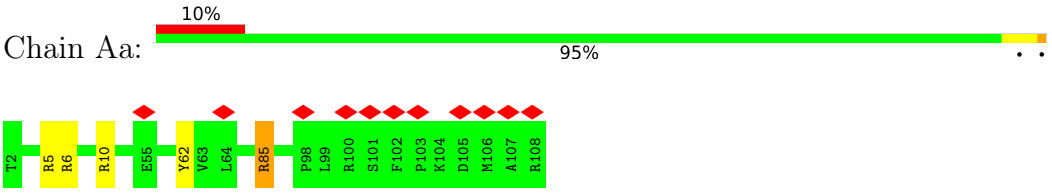
• Molecule 20: 40S ribosomal protein S25

Chain AZ:



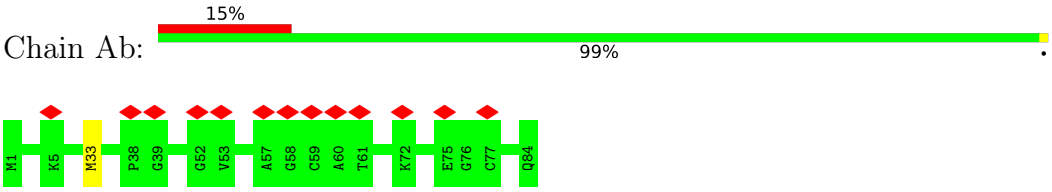
• Molecule 21: 40S ribosomal protein S26

Chain Aa:



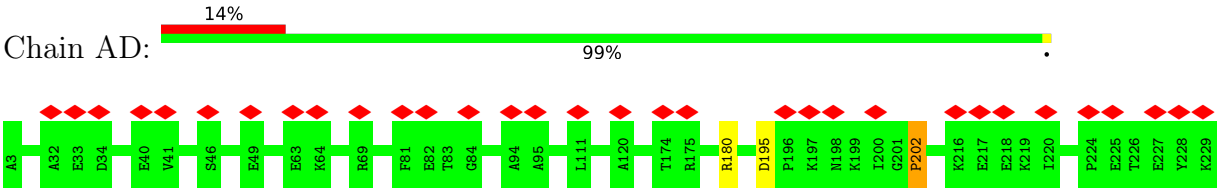
• Molecule 22: 40S ribosomal protein S27

Chain Ab:



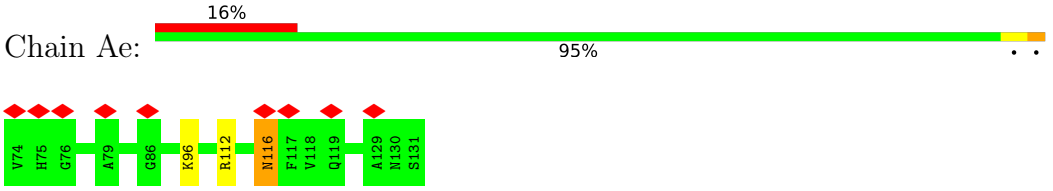
• Molecule 23: 40S ribosomal protein S3

Chain AD:



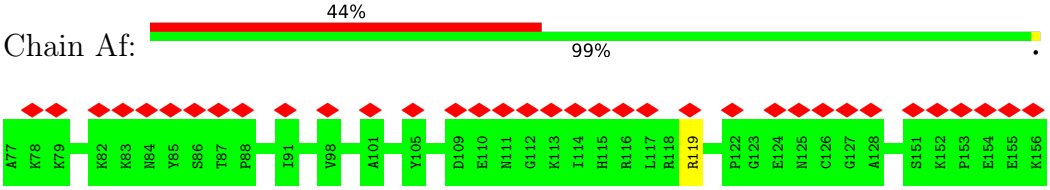
• Molecule 24: 40S ribosomal protein S30

Chain Ae:



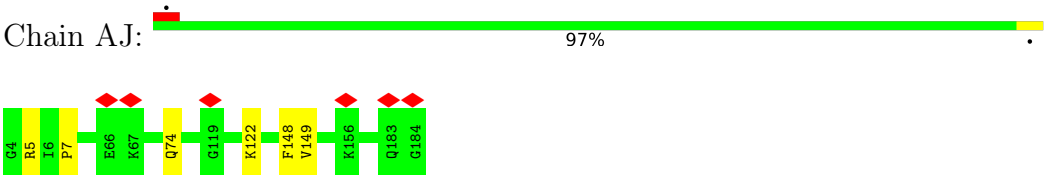
• Molecule 25: Ubiquitin-40S ribosomal protein S27a

Chain Af:



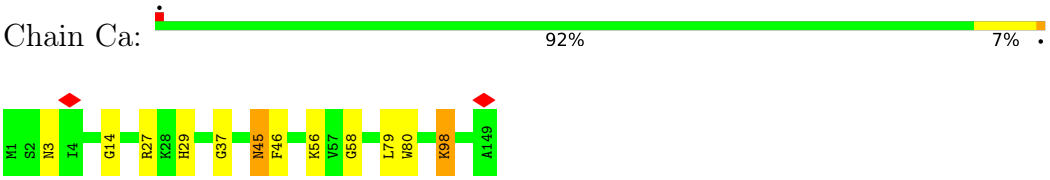
• Molecule 26: 40S ribosomal protein S9

Chain AJ:



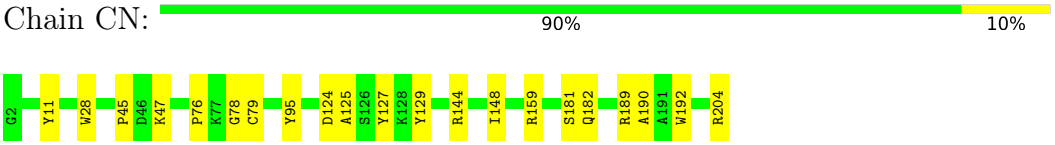
• Molecule 27: 60S ribosomal protein L27a

Chain Ca:



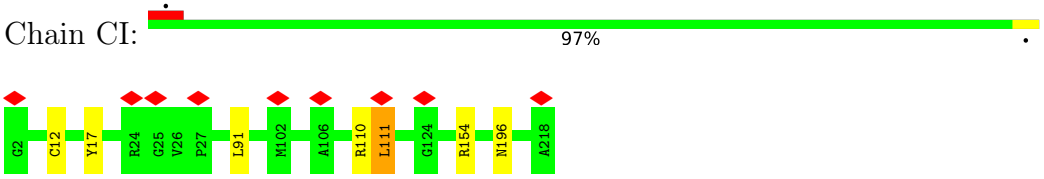
• Molecule 28: 60S ribosomal protein L15

Chain CN:



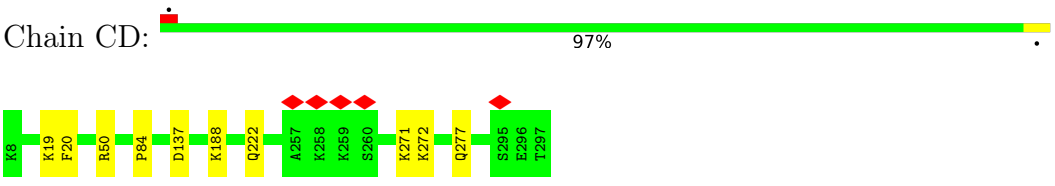
• Molecule 29: 60S ribosomal protein L10

Chain CI:



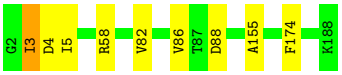
• Molecule 30: 60S ribosomal protein L5

Chain CD:



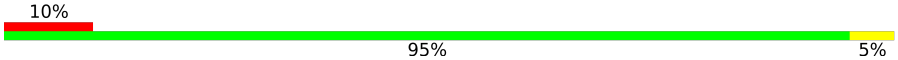
• Molecule 31: 60S ribosomal protein L18

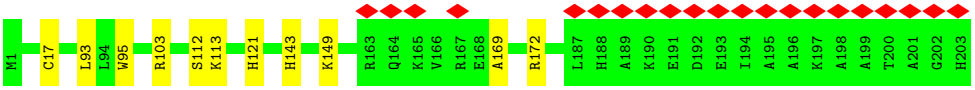
Chain CQ:



• Molecule 32: 60S ribosomal protein L19

Chain CR:



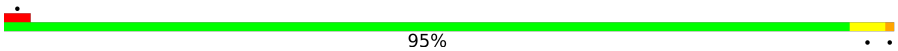


• Molecule 33: 60S ribosomal protein L18a

Chain CS:

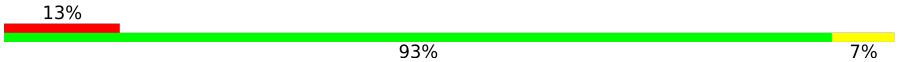
• Molecule 34: RE62581p

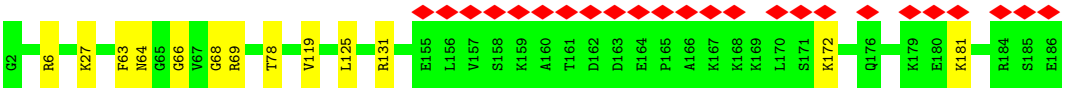
Chain CT:



• Molecule 35: 60S ribosomal protein L17

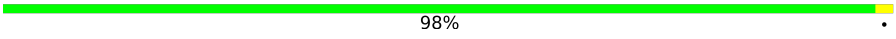
Chain CP:





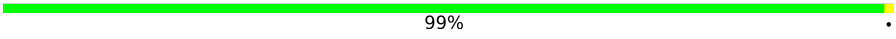
• Molecule 36: IP17216p

Chain CX:



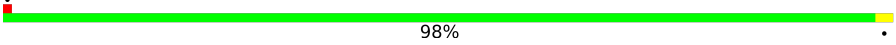
• Molecule 37: GEO07453p1

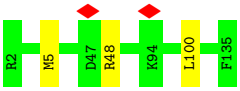
Chain CY:



• Molecule 38: 60S ribosomal protein L27

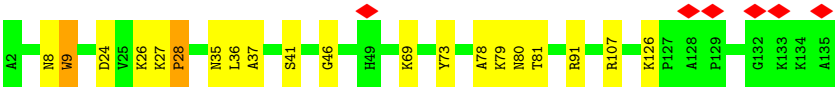
Chain CZ:





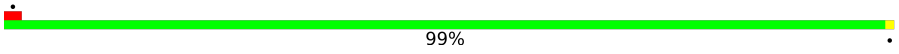
• Molecule 39: 60S ribosomal protein L28

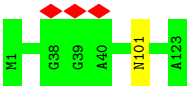
Chain Cr:



• Molecule 40: FI02809p

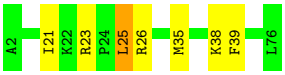
Chain Ch:





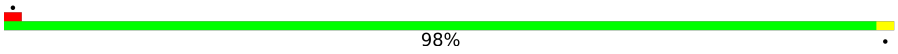
• Molecule 41: 60S ribosomal protein L29

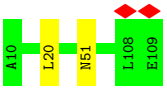
Chain Cb:



• Molecule 42: RE25263p

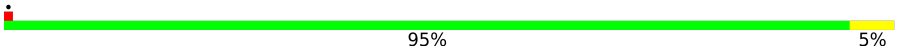
Chain Cc:

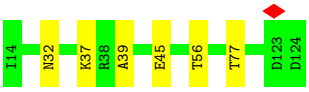




• Molecule 43: 60S ribosomal protein L31

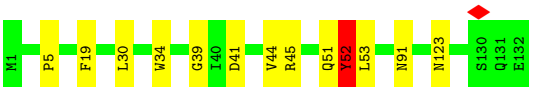
Chain Cd:





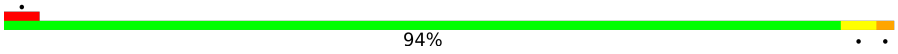
• Molecule 44: 60S ribosomal protein L32

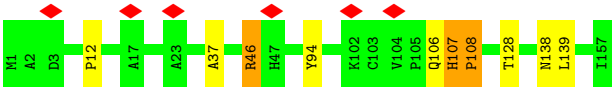
Chain Ce:



• Molecule 45: GEO07455p1

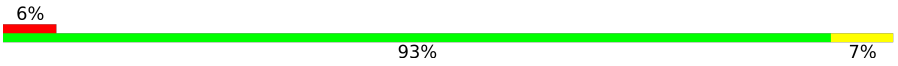
Chain Cf:

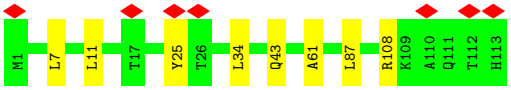




• Molecule 46: 60S ribosomal protein L36

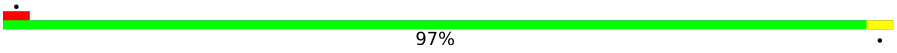
Chain Ci:

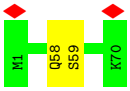




• Molecule 47: 60S ribosomal protein L38

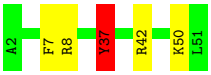
Chain Ck:





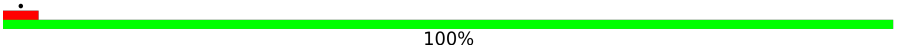
• Molecule 48: 60S ribosomal protein L39

Chain Cl:



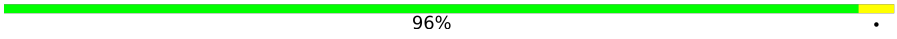
• Molecule 49: Ubiquitin-60S ribosomal protein L40

Chain Cm:



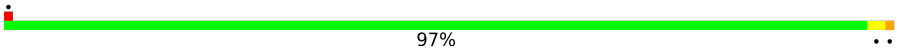
• Molecule 50: 60S ribosomal protein L41

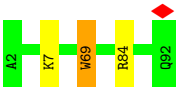
Chain Cn:



• Molecule 51: 60S ribosomal protein L37a

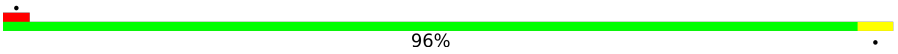
Chain Cp:

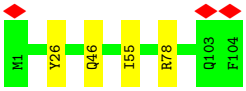




• Molecule 52: TA01007p

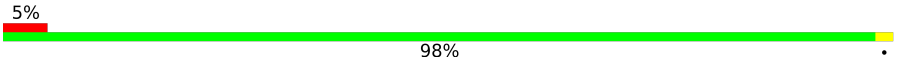
Chain Co:

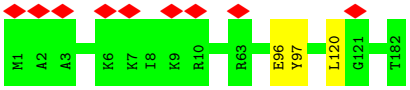




• Molecule 53: 60S ribosomal protein L11

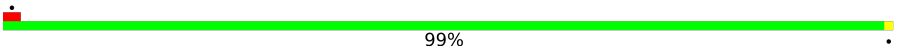
Chain CJ:

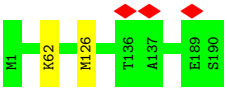




• Molecule 54: 60S ribosomal protein L9

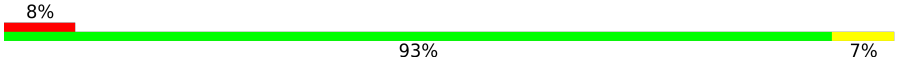
Chain CH:

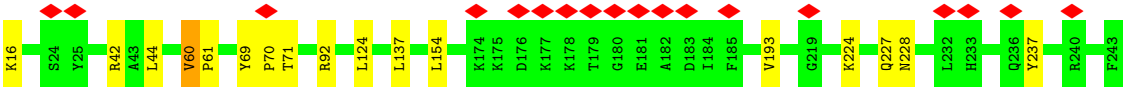




• Molecule 55: Ribosomal protein L6, isoform A

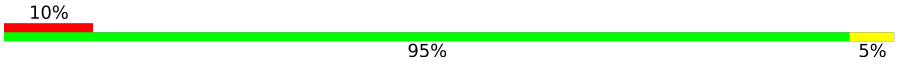
Chain CE:

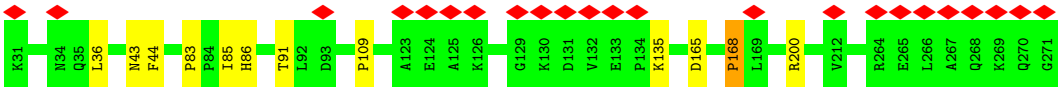




• Molecule 56: 60S ribosomal protein L7a

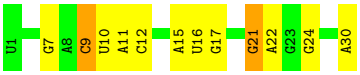
Chain CG:





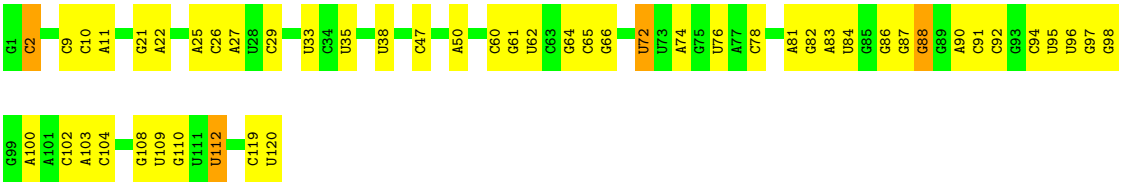
• Molecule 57: 2S ribosomal RNA

Chain A9:



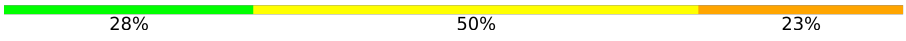
• Molecule 58: 5S ribosomal RNA

Chain A7:



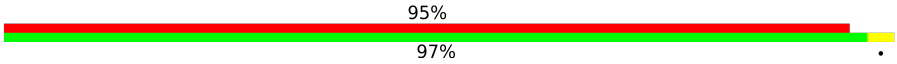
• Molecule 59: 5.8S ribosomal RNA

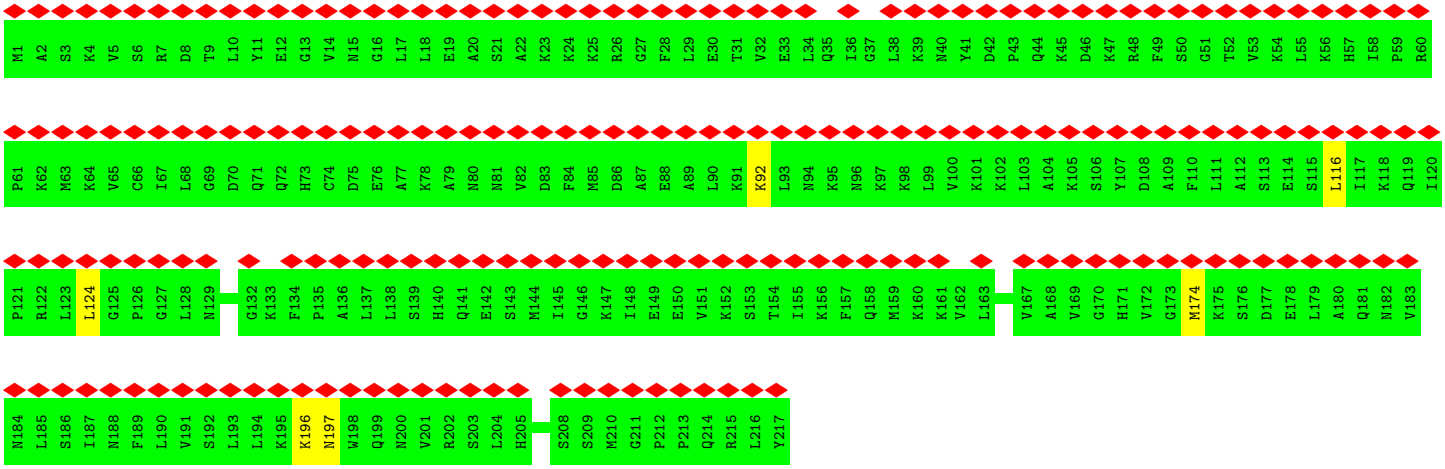
Chain A8:



• Molecule 60: 60S ribosomal protein L10a-2

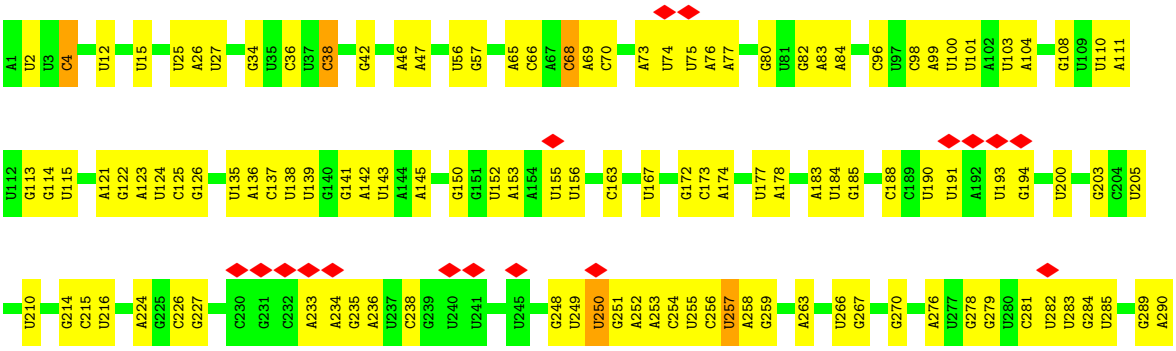
Chain Cz:

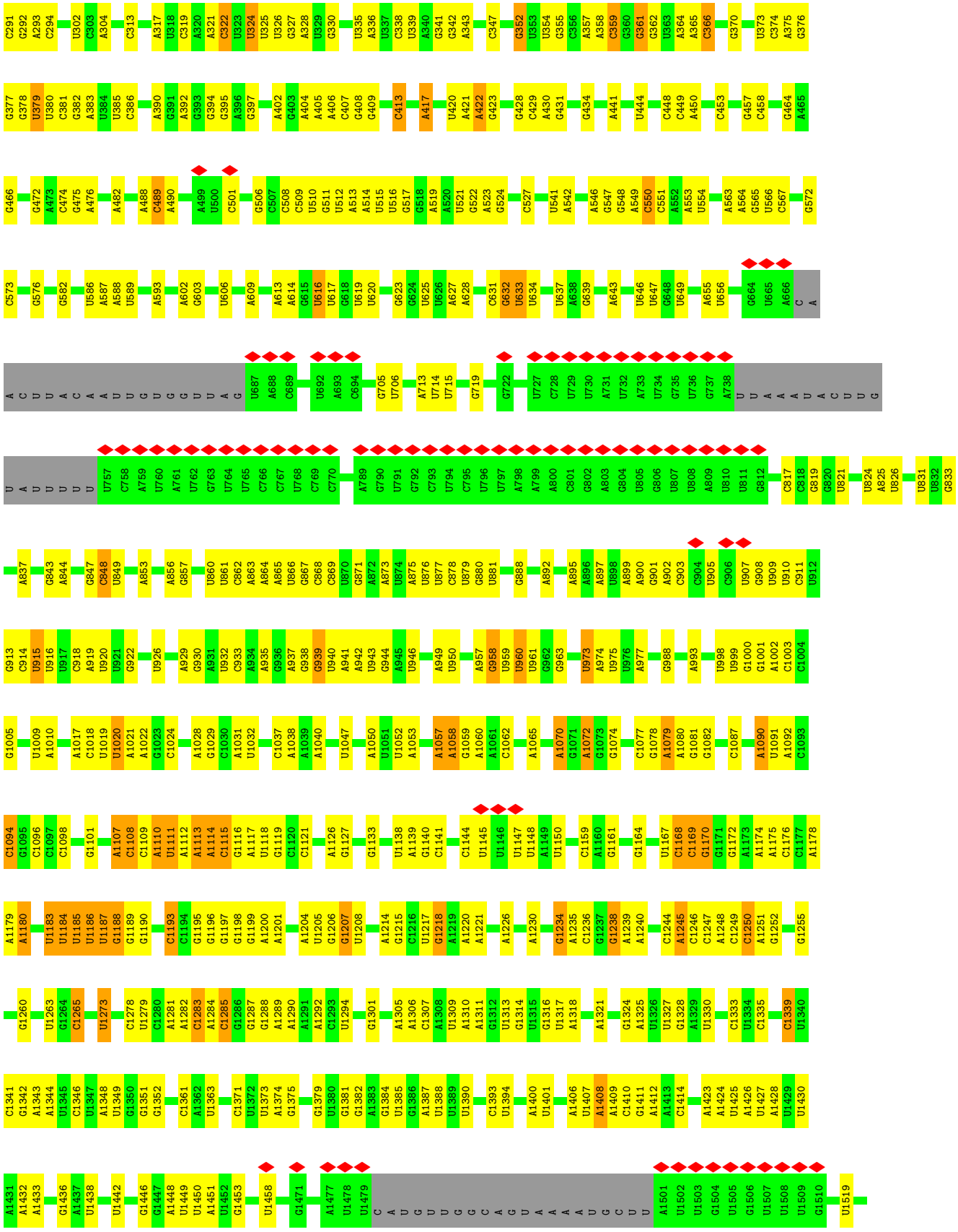


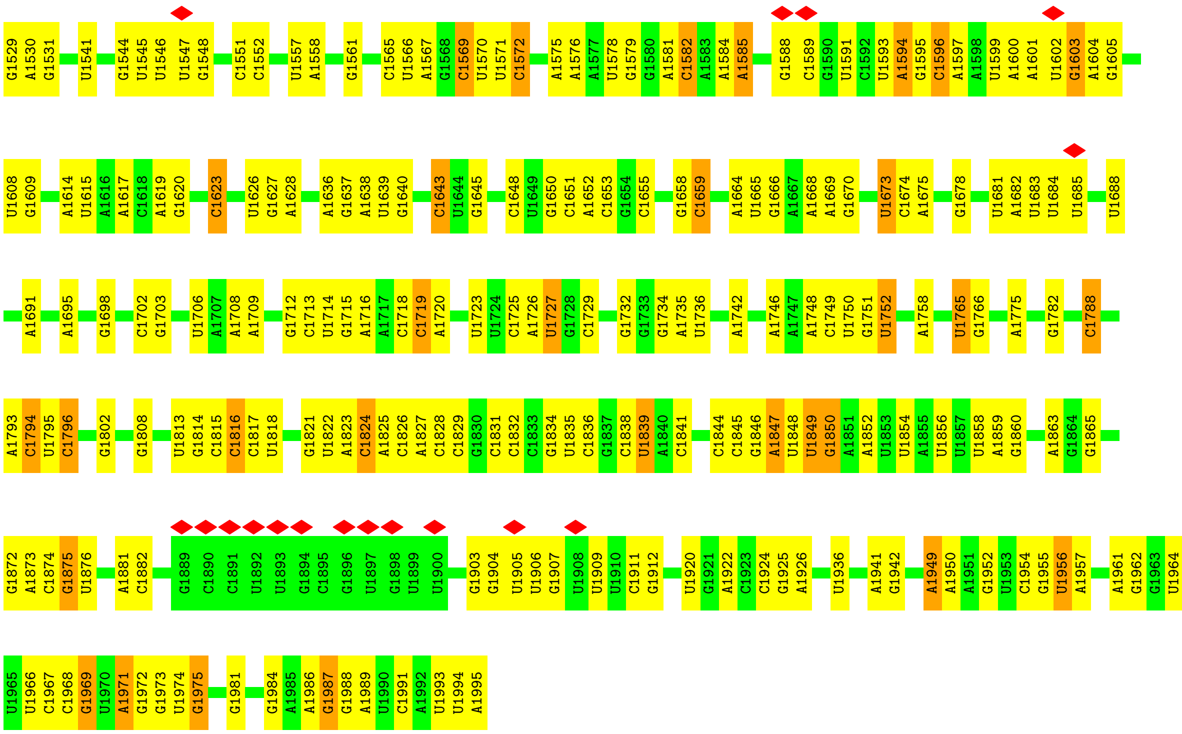


• Molecule 61: 18S ribosomal RNA

Chain B2:

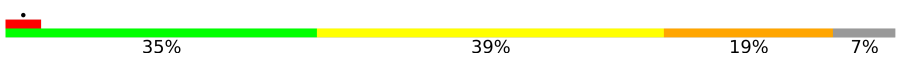


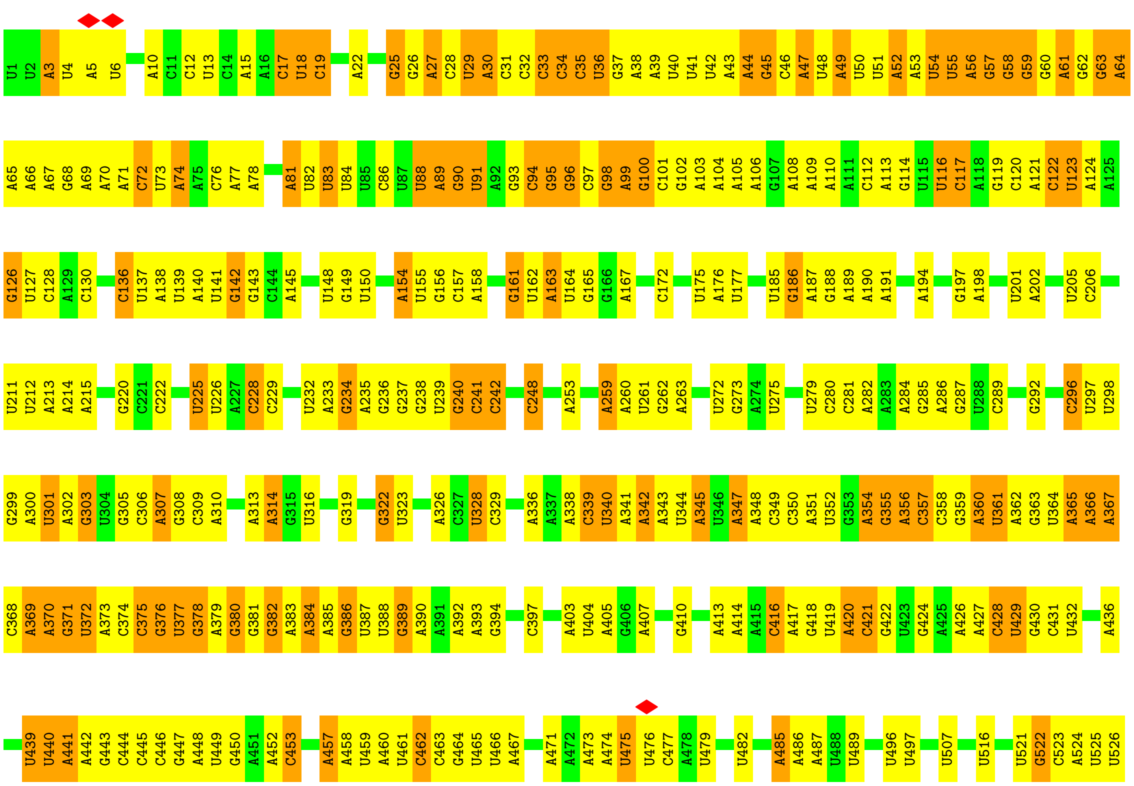


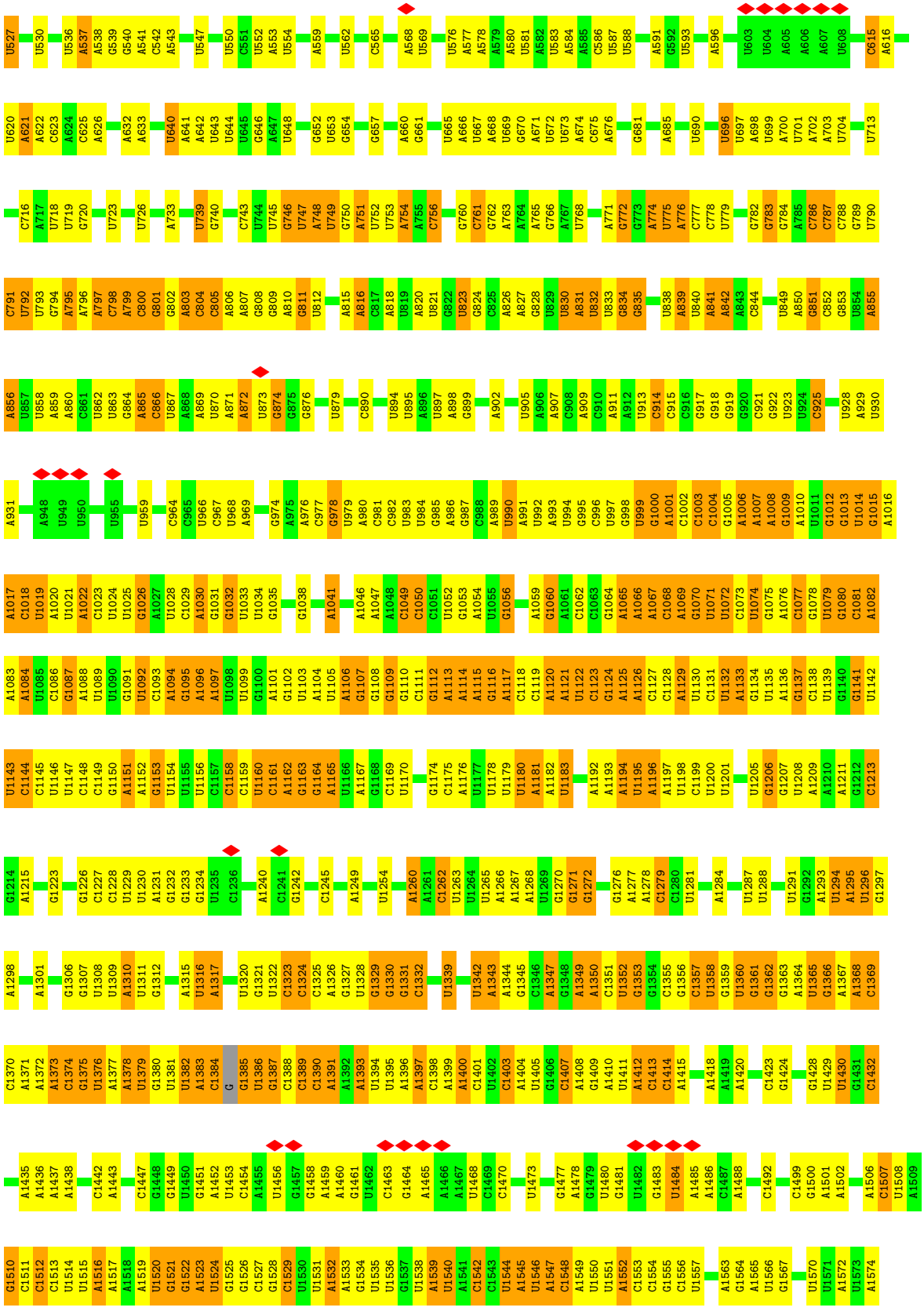


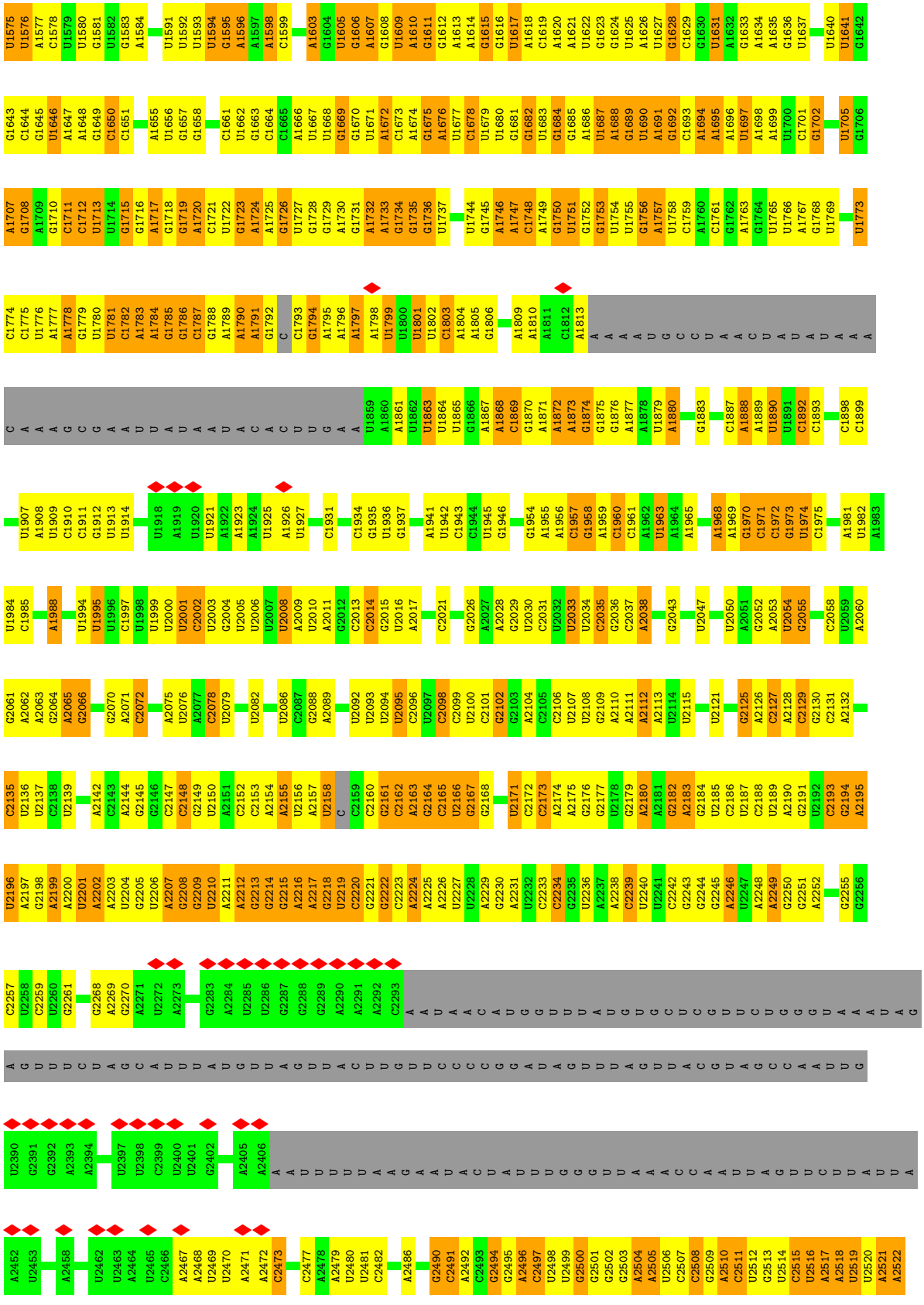
- Molecule 62: 28S ribosomal RNA

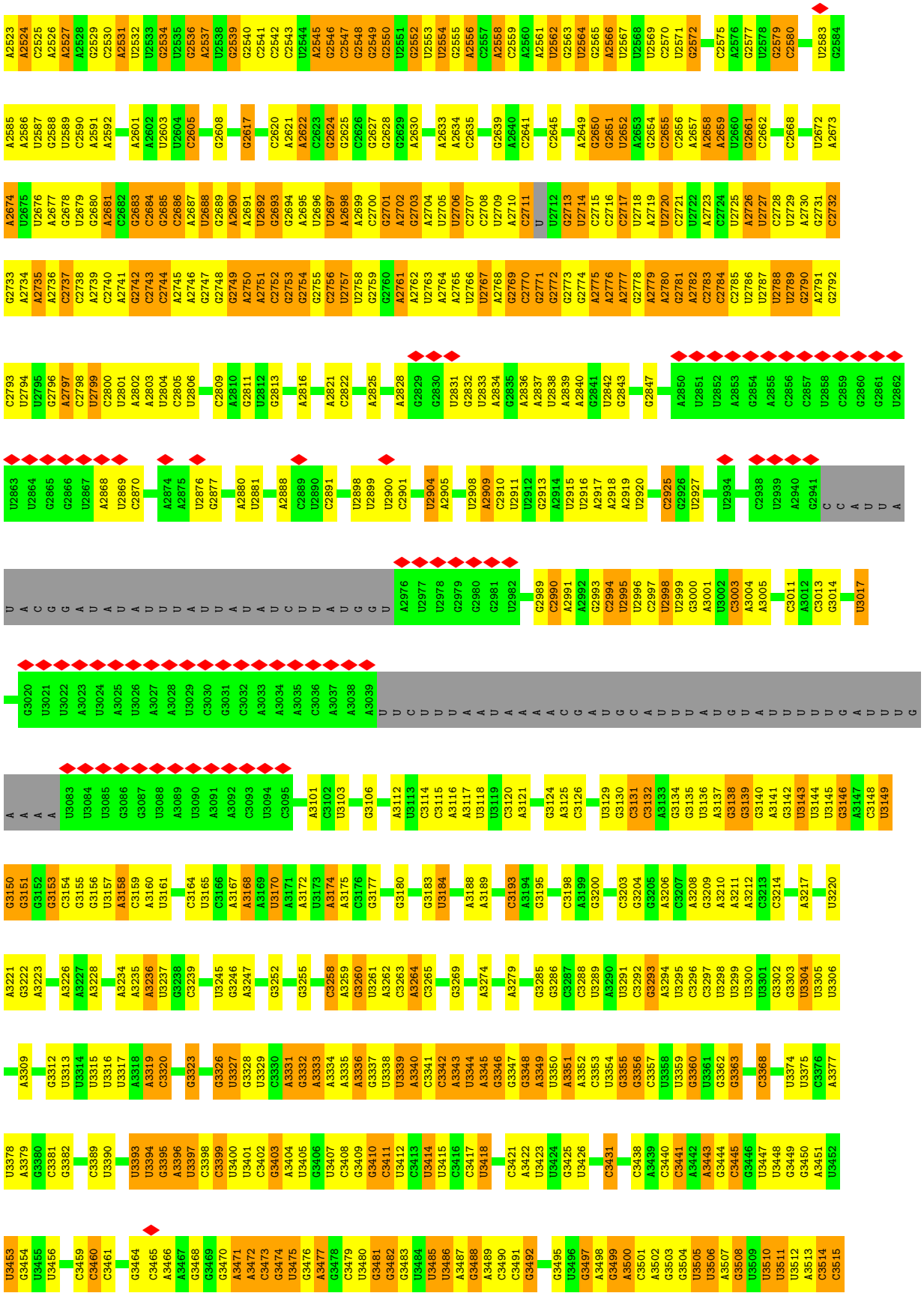
Chain A5:

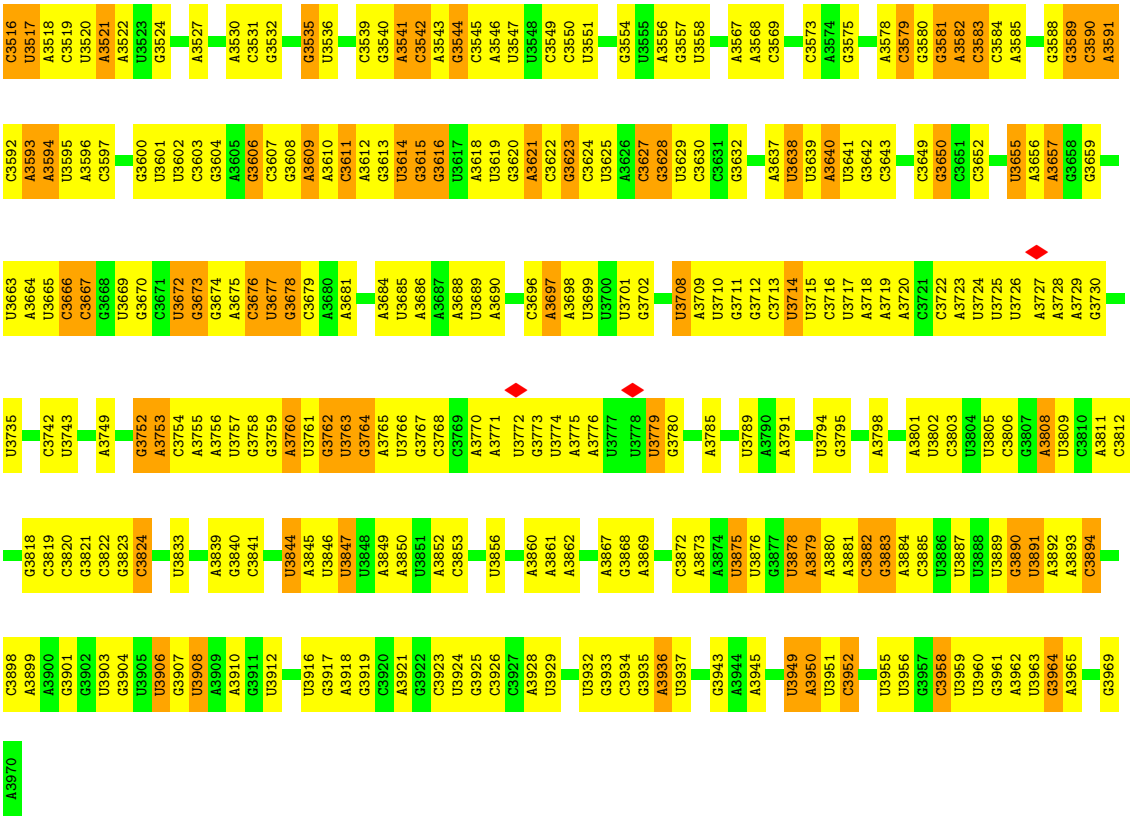






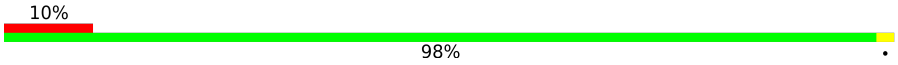


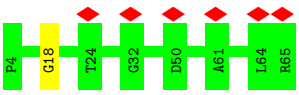




• Molecule 63: 40S ribosomal protein S28

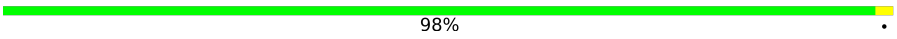
Chain Ac:

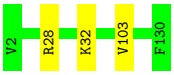




• Molecule 64: 40S ribosomal protein S15Aa

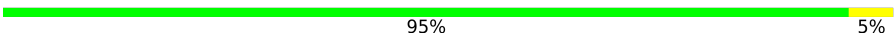
Chain AW:

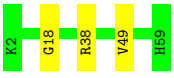




• Molecule 65: 60S ribosomal protein L24

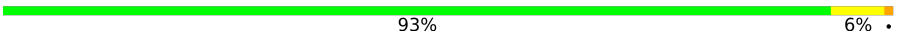
Chain CW:

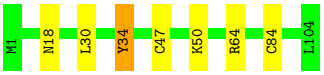




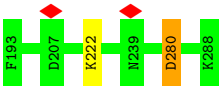
• Molecule 66: RH48056p

Chain Cg:

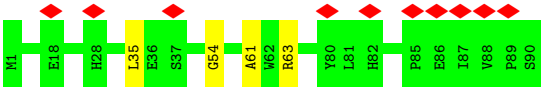




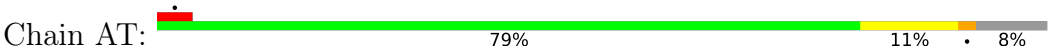
• Molecule 67: Ribosomal protein L22-like protein

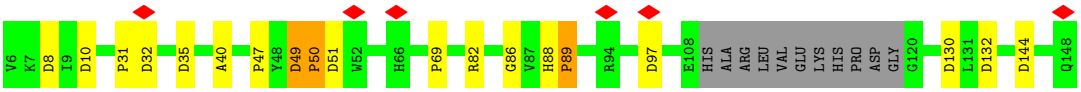


• Molecule 68: 40S ribosomal protein S10b

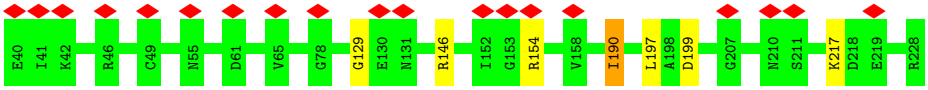


• Molecule 69: 40S ribosomal protein S19a



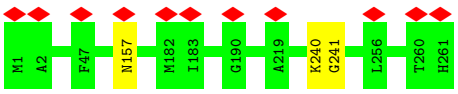


• Molecule 70: 40S ribosomal protein S5a



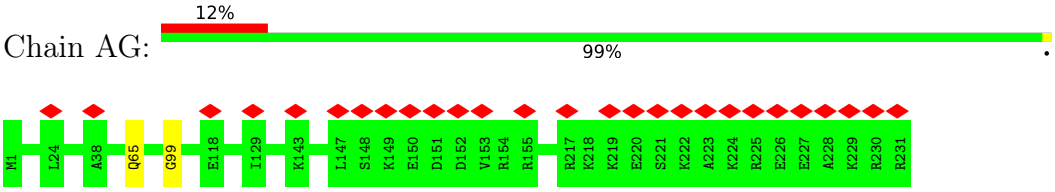
• Molecule 71: 60S ribosomal protein L7

• Molecule 72: 40S ribosomal protein S4



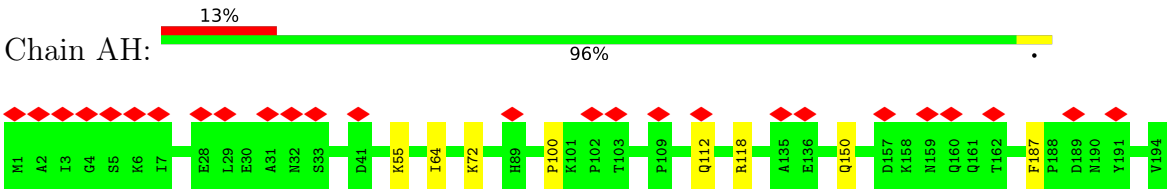
• Molecule 73: 40S ribosomal protein S6

Chain AG:



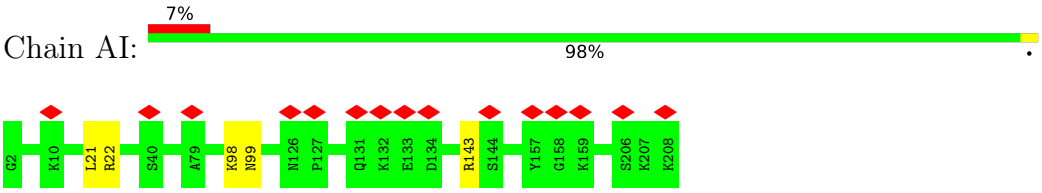
• Molecule 74: 40S ribosomal protein S7

Chain AH:



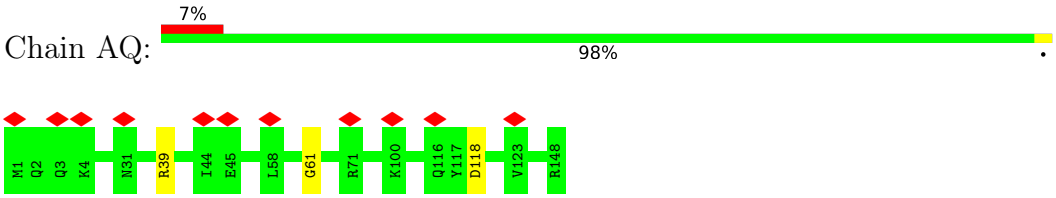
• Molecule 75: 40S ribosomal protein S8

Chain AI:



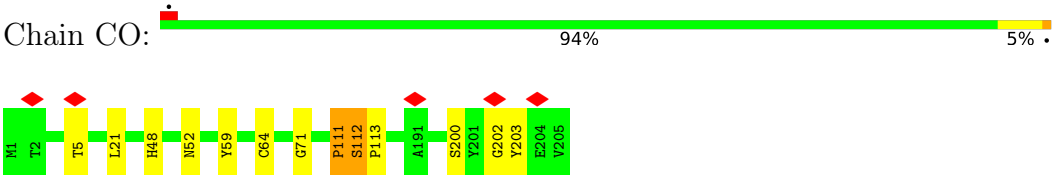
• Molecule 76: 40S ribosomal protein S16

Chain AQ:



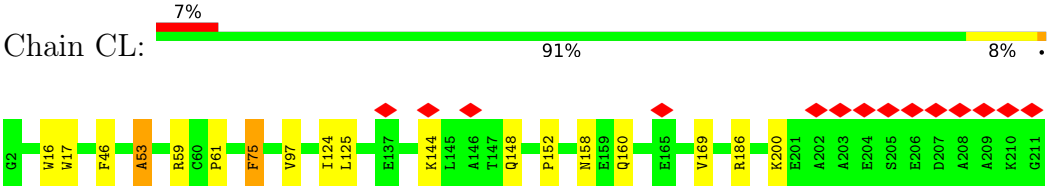
• Molecule 77: 60S ribosomal protein L13a

Chain CO:



• Molecule 78: 60S ribosomal protein L13

Chain CL:

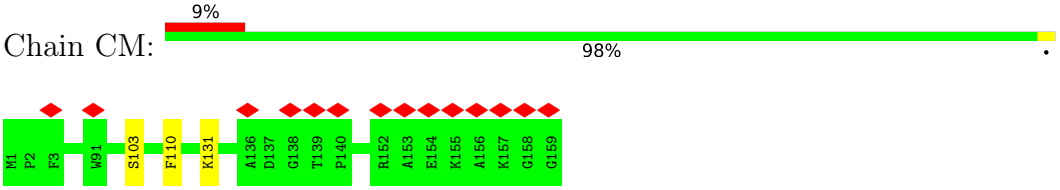


• Molecule 79: 60S ribosomal protein L23

Chain CV:

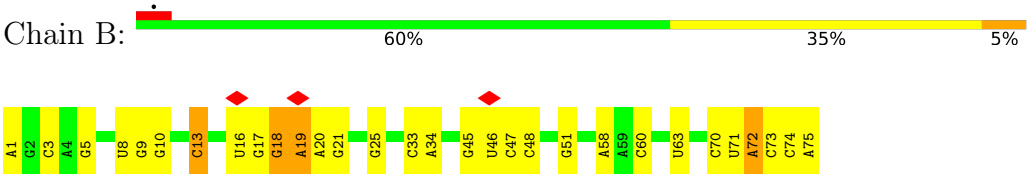
• Molecule 80: 60S ribosomal protein L14

Chain CM:



• Molecule 81: P-tRNA

Chain B:

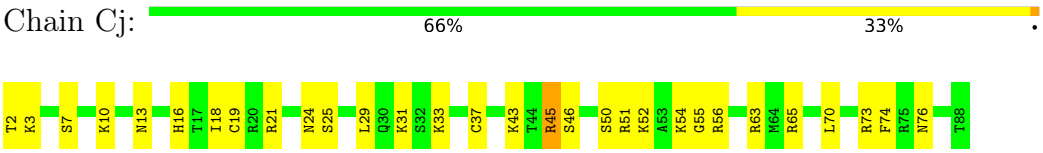


• Molecule 82: mRNA

Chain v:

• Molecule 83: Probable 60S ribosomal protein L37-B

Chain Cj:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	10392	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	80	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.643	Depositor
Minimum map value	-0.491	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.020	Depositor
Recommended contour level	0.035	Depositor
Map size (Å)	426.00003, 426.00003, 426.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.065, 1.065, 1.065	Depositor

5 Model quality

5.1 Standard geometry

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	AA	0.33	0/1777	0.62	1/2422 (0.0%)
2	CA	0.78	2/1970 (0.1%)	0.81	0/2635
3	AB	0.31	0/1825	0.64	0/2448
4	CB	0.69	0/3356	0.84	4/4494 (0.1%)
5	AC	0.34	0/1785	0.66	2/2415 (0.1%)
6	CC	0.70	4/3163 (0.1%)	0.83	7/4253 (0.2%)
7	Ag	0.30	0/2574	0.58	0/3506
8	AU	0.31	0/825	0.57	0/1111
9	AO	0.35	0/1016	0.71	0/1364
10	AX	0.42	0/1152	0.66	0/1540
11	AM	0.29	0/937	0.65	1/1260 (0.1%)
12	AS	0.31	0/1146	0.71	3/1535 (0.2%)
13	Ad	0.37	0/443	0.71	0/589
14	AN	0.38	0/1225	0.63	0/1641
15	AL	0.40	0/1296	0.60	0/1725
16	AR	0.31	0/993	0.63	0/1333
17	AP	0.31	0/1036	0.65	0/1383
18	AV	0.34	0/622	0.61	0/835
19	AY	0.31	0/1032	0.62	0/1373
20	AZ	0.31	0/616	0.67	2/826 (0.2%)
21	Aa	0.43	0/883	0.68	0/1184
22	Ab	0.30	0/668	0.61	0/898
23	AD	0.34	0/1808	0.66	0/2427
24	Ae	0.33	0/475	0.68	1/625 (0.2%)
25	Af	0.32	0/672	0.62	0/887
26	AJ	0.33	0/1526	0.65	1/2037 (0.0%)
27	Ca	0.73	1/1235 (0.1%)	0.87	2/1640 (0.1%)
28	CN	0.89	3/1750 (0.2%)	0.91	1/2335 (0.0%)
29	CI	0.41	0/1827	0.63	2/2447 (0.1%)
30	CD	0.38	0/2379	0.62	2/3196 (0.1%)
31	CQ	0.65	1/1544 (0.1%)	0.76	0/2069
32	CR	0.48	1/1703 (0.1%)	0.62	0/2255
33	CS	0.54	0/1491	0.75	1/1998 (0.1%)
34	CT	0.61	0/1326	0.87	6/1773 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
35	CP	0.76	0/1529	0.80	2/2042 (0.1%)
36	CX	0.44	0/1001	0.67	1/1348 (0.1%)
37	CY	0.50	0/1094	0.63	0/1456
38	CZ	0.39	1/1141 (0.1%)	0.60	2/1517 (0.1%)
39	Cr	0.55	1/1069 (0.1%)	0.94	2/1432 (0.1%)
40	Ch	0.40	0/1024	0.64	0/1353
41	Cb	0.49	0/628	0.89	2/832 (0.2%)
42	Cc	0.38	0/779	0.65	1/1048 (0.1%)
43	Cd	0.69	0/939	0.76	0/1262
44	Ce	0.94	2/1132 (0.2%)	0.98	3/1508 (0.2%)
45	Cf	0.66	0/1270	0.86	2/1696 (0.1%)
46	Ci	0.38	0/944	0.73	0/1250
47	Ck	0.37	0/583	0.66	1/774 (0.1%)
48	Cl	0.74	0/445	0.95	1/589 (0.2%)
49	Cm	0.37	0/435	0.60	0/575
50	Cn	0.55	0/237	0.80	0/300
51	Cp	0.70	1/719 (0.1%)	0.74	0/954
52	Co	0.53	0/887	0.69	0/1162
53	CJ	0.32	0/1494	0.67	1/2001 (0.0%)
54	CH	0.39	0/1519	0.66	1/2042 (0.0%)
55	CE	0.38	0/1883	0.75	3/2514 (0.1%)
56	CG	0.38	0/1968	0.66	1/2637 (0.0%)
57	A9	1.05	0/714	1.39	7/1112 (0.6%)
58	A7	1.05	9/2854 (0.3%)	1.38	41/4447 (0.9%)
59	A8	1.58	29/2932 (1.0%)	2.00	170/4568 (3.7%)
60	Cz	0.31	0/1727	0.70	2/2308 (0.1%)
61	B2	1.30	34/43887 (0.1%)	1.20	319/68161 (0.5%)
62	A5	1.62	1753/86239 (2.0%)	1.90	4119/134149 (3.1%)
63	Ac	0.29	0/502	0.61	0/670
64	AW	0.37	0/1046	0.59	1/1402 (0.1%)
65	CW	0.60	0/495	0.72	0/658
66	Cg	0.60	0/863	0.84	3/1152 (0.3%)
67	CU	0.33	0/828	0.62	1/1110 (0.1%)
68	AK	0.35	0/786	0.64	2/1064 (0.2%)
69	AT	0.35	0/1060	0.87	15/1421 (1.1%)
70	AF	1.95	2/1510 (0.1%)	0.75	5/2026 (0.2%)
71	CF	0.71	0/1931	0.81	2/2587 (0.1%)
72	AE	0.30	0/2096	0.58	0/2819
73	AG	0.28	0/1891	0.54	0/2519
74	AH	0.32	0/1593	0.68	1/2145 (0.0%)
75	AI	0.35	0/1689	0.67	1/2250 (0.0%)
76	AQ	0.33	0/1202	0.70	1/1608 (0.1%)
77	CO	0.69	0/1700	0.80	1/2277 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
78	CL	0.60	2/1726 (0.1%)	0.86	1/2308 (0.0%)
79	CV	0.61	0/1014	0.71	0/1362
80	CM	0.39	0/1326	0.67	0/1780
81	B	0.56	0/1796	1.21	11/2800 (0.4%)
82	v	0.52	0/283	1.10	0/439
83	Cj	0.57	0/707	0.68	0/932
All	All	1.20	1846/235193 (0.8%)	1.41	4762/344825 (1.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	CA	0	9
3	AB	0	2
4	CB	0	9
5	AC	0	1
6	CC	0	6
8	AU	0	1
10	AX	0	2
12	AS	0	1
13	Ad	0	2
21	Aa	0	3
23	AD	0	2
24	Ae	0	2
26	AJ	0	2
27	Ca	0	8
28	CN	0	11
29	CI	0	2
30	CD	0	4
31	CQ	0	5
32	CR	0	5
33	CS	0	10
34	CT	0	5
35	CP	0	6
39	Cr	0	11
41	Cb	0	5
43	Cd	0	4
44	Ce	0	7
45	Cf	0	4
46	Ci	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
47	Ck	0	1
48	Cl	0	3
50	Cn	0	1
51	Cp	0	1
52	Co	0	3
53	CJ	0	1
55	CE	0	7
56	CG	0	7
63	Ac	0	1
65	CW	0	2
66	Cg	0	2
69	AT	0	3
70	AF	0	1
71	CF	0	3
72	AE	0	2
73	AG	0	1
74	AH	0	3
75	AI	0	1
77	CO	0	8
78	CL	0	9
80	CM	0	1
All	All	0	194

The worst 5 of 1846 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
61	B2	1727	U	C2-N3	115.56	2.18	1.37
61	B2	1727	U	N1-C2	91.04	2.20	1.38
61	B2	1727	U	N3-C4	90.77	2.20	1.38
61	B2	1727	U	N1-C6	84.49	2.13	1.38
61	B2	1727	U	C4-C5	80.97	2.16	1.43

The worst 5 of 4762 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
62	A5	1366	G	N1-C6-O6	18.38	130.93	119.90
59	A8	34	C	C6-N1-C2	-17.41	113.34	120.30
62	A5	1526	G	C6-C5-N7	-17.19	120.09	130.40
62	A5	3143	U	N3-C2-O2	-16.65	110.55	122.20
62	A5	3408	C	C6-N1-C2	-16.63	113.65	120.30

There are no chirality outliers.

5 of 194 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	CA	179	ILE	Peptide
2	CA	185	ALA	Peptide
2	CA	196	TRP	Peptide
2	CA	197	PRO	Peptide
2	CA	3	ARG	Peptide

5.2 Too-close contacts (i)

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

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	AA	216/218 (99%)	188 (87%)	27 (12%)	1 (0%)	29 68
2	CA	251/253 (99%)	197 (78%)	52 (21%)	2 (1%)	19 60
3	AB	218/220 (99%)	186 (85%)	29 (13%)	3 (1%)	11 46
4	CB	412/414 (100%)	327 (79%)	84 (20%)	1 (0%)	47 81
5	AC	225/227 (99%)	200 (89%)	25 (11%)	0	100 100
6	CC	390/392 (100%)	308 (79%)	82 (21%)	0	100 100
7	Ag	316/318 (99%)	276 (87%)	40 (13%)	0	100 100
8	AU	100/102 (98%)	93 (93%)	7 (7%)	0	100 100
9	AO	132/134 (98%)	112 (85%)	19 (14%)	1 (1%)	19 60
10	AX	141/143 (99%)	112 (79%)	29 (21%)	0	100 100
11	AM	117/119 (98%)	100 (86%)	17 (14%)	0	100 100
12	AS	135/137 (98%)	120 (89%)	15 (11%)	0	100 100
13	Ad	50/52 (96%)	38 (76%)	12 (24%)	0	100 100
14	AN	148/150 (99%)	137 (93%)	11 (7%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	AL	153/155 (99%)	127 (83%)	26 (17%)	0	100	100
16	AR	118/120 (98%)	107 (91%)	11 (9%)	0	100	100
17	AP	122/124 (98%)	108 (88%)	14 (12%)	0	100	100
18	AV	80/82 (98%)	67 (84%)	13 (16%)	0	100	100
19	AY	124/126 (98%)	106 (86%)	18 (14%)	0	100	100
20	AZ	72/74 (97%)	59 (82%)	13 (18%)	0	100	100
21	Aa	105/107 (98%)	85 (81%)	20 (19%)	0	100	100
22	Ab	82/84 (98%)	66 (80%)	16 (20%)	0	100	100
23	AD	225/227 (99%)	191 (85%)	33 (15%)	1 (0%)	34	72
24	Ae	56/58 (97%)	39 (70%)	17 (30%)	0	100	100
25	Af	78/80 (98%)	64 (82%)	14 (18%)	0	100	100
26	AJ	179/181 (99%)	156 (87%)	22 (12%)	1 (1%)	25	65
27	Ca	147/149 (99%)	112 (76%)	34 (23%)	1 (1%)	22	62
28	CN	201/203 (99%)	153 (76%)	46 (23%)	2 (1%)	15	54
29	CI	215/217 (99%)	184 (86%)	31 (14%)	0	100	100
30	CD	288/290 (99%)	247 (86%)	40 (14%)	1 (0%)	41	76
31	CQ	185/187 (99%)	152 (82%)	32 (17%)	1 (0%)	29	68
32	CR	201/203 (99%)	182 (90%)	19 (10%)	0	100	100
33	CS	171/173 (99%)	127 (74%)	41 (24%)	3 (2%)	8	41
34	CT	156/158 (99%)	118 (76%)	37 (24%)	1 (1%)	25	65
35	CP	183/185 (99%)	153 (84%)	30 (16%)	0	100	100
36	CX	118/120 (98%)	94 (80%)	23 (20%)	1 (1%)	19	60
37	CY	129/131 (98%)	111 (86%)	18 (14%)	0	100	100
38	CZ	132/134 (98%)	112 (85%)	20 (15%)	0	100	100
39	Cr	132/134 (98%)	92 (70%)	37 (28%)	3 (2%)	6	36
40	Ch	121/123 (98%)	107 (88%)	14 (12%)	0	100	100
41	Cb	73/75 (97%)	56 (77%)	17 (23%)	0	100	100
42	Cc	98/100 (98%)	94 (96%)	4 (4%)	0	100	100
43	Cd	109/111 (98%)	89 (82%)	20 (18%)	0	100	100
44	Ce	130/132 (98%)	99 (76%)	31 (24%)	0	100	100
45	Cf	155/157 (99%)	119 (77%)	34 (22%)	2 (1%)	12	48

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	Ci	111/113 (98%)	82 (74%)	29 (26%)	0	100	100
47	Ck	68/70 (97%)	63 (93%)	5 (7%)	0	100	100
48	Cl	48/50 (96%)	33 (69%)	14 (29%)	1 (2%)	7	38
49	Cm	50/52 (96%)	41 (82%)	9 (18%)	0	100	100
50	Cn	23/25 (92%)	21 (91%)	2 (9%)	0	100	100
51	Cp	89/91 (98%)	72 (81%)	17 (19%)	0	100	100
52	Co	102/104 (98%)	79 (78%)	23 (22%)	0	100	100
53	CJ	180/182 (99%)	147 (82%)	32 (18%)	1 (1%)	25	65
54	CH	188/190 (99%)	165 (88%)	23 (12%)	0	100	100
55	CE	226/228 (99%)	178 (79%)	46 (20%)	2 (1%)	17	56
56	CG	239/241 (99%)	205 (86%)	31 (13%)	3 (1%)	12	48
60	Cz	215/217 (99%)	192 (89%)	23 (11%)	0	100	100
63	Ac	60/62 (97%)	53 (88%)	7 (12%)	0	100	100
64	AW	127/129 (98%)	109 (86%)	18 (14%)	0	100	100
65	CW	56/58 (97%)	45 (80%)	11 (20%)	0	100	100
66	Cg	102/104 (98%)	88 (86%)	14 (14%)	0	100	100
67	CU	94/96 (98%)	76 (81%)	18 (19%)	0	100	100
68	AK	88/90 (98%)	68 (77%)	19 (22%)	1 (1%)	14	52
69	AT	128/143 (90%)	104 (81%)	20 (16%)	4 (3%)	4	30
70	AF	187/189 (99%)	158 (84%)	28 (15%)	1 (0%)	29	68
71	CF	224/226 (99%)	188 (84%)	32 (14%)	4 (2%)	8	41
72	AE	259/261 (99%)	225 (87%)	34 (13%)	0	100	100
73	AG	229/231 (99%)	211 (92%)	18 (8%)	0	100	100
74	AH	192/194 (99%)	161 (84%)	31 (16%)	0	100	100
75	AI	205/207 (99%)	162 (79%)	40 (20%)	3 (2%)	10	46
76	AQ	146/148 (99%)	117 (80%)	28 (19%)	1 (1%)	22	62
77	CO	203/205 (99%)	161 (79%)	38 (19%)	4 (2%)	7	39
78	CL	208/210 (99%)	151 (73%)	54 (26%)	3 (1%)	11	46
79	CV	132/134 (98%)	115 (87%)	17 (13%)	0	100	100
80	CM	157/159 (99%)	131 (83%)	26 (17%)	0	100	100
83	Cj	85/87 (98%)	57 (67%)	25 (29%)	3 (4%)	3	28

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	11610/11775 (99%)	9628 (83%)	1926 (17%)	56 (0%)	32 68

5 of 56 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AB	120	TRP
69	AT	40	ALA
71	CF	237	PHE
77	CO	113	PRO
30	CD	20	PHE

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	AA	190/190 (100%)	190 (100%)	0	100 100
2	CA	195/195 (100%)	192 (98%)	3 (2%)	65 80
3	AB	199/199 (100%)	198 (100%)	1 (0%)	88 93
4	CB	349/349 (100%)	339 (97%)	10 (3%)	42 64
5	AC	188/188 (100%)	188 (100%)	0	100 100
6	CC	323/323 (100%)	317 (98%)	6 (2%)	57 75
7	Ag	280/280 (100%)	273 (98%)	7 (2%)	47 68
8	AU	95/95 (100%)	94 (99%)	1 (1%)	73 85
9	AO	103/103 (100%)	100 (97%)	3 (3%)	42 64
10	AX	116/116 (100%)	114 (98%)	2 (2%)	60 78
11	AM	104/104 (100%)	103 (99%)	1 (1%)	76 86
12	AS	123/123 (100%)	122 (99%)	1 (1%)	81 89
13	Ad	45/45 (100%)	43 (96%)	2 (4%)	28 53
14	AN	130/130 (100%)	128 (98%)	2 (2%)	65 80
15	AL	138/138 (100%)	137 (99%)	1 (1%)	84 90
16	AR	108/108 (100%)	108 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
17	AP	111/111 (100%)	108 (97%)	3 (3%)	44 65
18	AV	67/67 (100%)	66 (98%)	1 (2%)	65 80
19	AY	105/106 (99%)	105 (100%)	0	100 100
20	AZ	67/67 (100%)	65 (97%)	2 (3%)	41 63
21	Aa	94/94 (100%)	91 (97%)	3 (3%)	39 61
22	Ab	72/72 (100%)	71 (99%)	1 (1%)	67 81
23	AD	192/192 (100%)	191 (100%)	1 (0%)	88 93
24	Ae	47/47 (100%)	46 (98%)	1 (2%)	53 72
25	Af	70/70 (100%)	69 (99%)	1 (1%)	67 81
26	AJ	161/161 (100%)	159 (99%)	2 (1%)	71 84
27	Ca	122/122 (100%)	120 (98%)	2 (2%)	62 79
28	CN	174/174 (100%)	169 (97%)	5 (3%)	42 64
29	CI	187/187 (100%)	183 (98%)	4 (2%)	53 72
30	CD	241/241 (100%)	238 (99%)	3 (1%)	71 84
31	CQ	164/164 (100%)	161 (98%)	3 (2%)	59 77
32	CR	176/176 (100%)	171 (97%)	5 (3%)	43 65
33	CS	156/156 (100%)	153 (98%)	3 (2%)	57 75
34	CT	137/137 (100%)	137 (100%)	0	100 100
35	CP	160/160 (100%)	155 (97%)	5 (3%)	40 62
36	CX	106/106 (100%)	105 (99%)	1 (1%)	78 88
37	CY	116/116 (100%)	115 (99%)	1 (1%)	78 88
38	CZ	121/121 (100%)	121 (100%)	0	100 100
39	Cr	112/112 (100%)	107 (96%)	5 (4%)	27 53
40	Ch	112/112 (100%)	111 (99%)	1 (1%)	78 88
41	Cb	67/67 (100%)	66 (98%)	1 (2%)	65 80
42	Cc	84/84 (100%)	83 (99%)	1 (1%)	71 84
43	Cd	103/103 (100%)	101 (98%)	2 (2%)	57 75
44	Ce	120/120 (100%)	117 (98%)	3 (2%)	47 68
45	Cf	123/123 (100%)	118 (96%)	5 (4%)	30 55
46	Ci	100/100 (100%)	96 (96%)	4 (4%)	31 56
47	Ck	65/65 (100%)	65 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
48	Cl	45/45 (100%)	43 (96%)	2 (4%)	28 53
49	Cm	48/48 (100%)	48 (100%)	0	100 100
50	Cn	23/23 (100%)	23 (100%)	0	100 100
51	Cp	74/74 (100%)	72 (97%)	2 (3%)	44 65
52	Co	94/94 (100%)	93 (99%)	1 (1%)	73 85
53	CJ	155/155 (100%)	155 (100%)	0	100 100
54	CH	169/169 (100%)	168 (99%)	1 (1%)	86 92
55	CE	197/197 (100%)	191 (97%)	6 (3%)	41 63
56	CG	210/210 (100%)	208 (99%)	2 (1%)	76 86
60	Cz	190/190 (100%)	186 (98%)	4 (2%)	53 72
63	Ac	54/54 (100%)	54 (100%)	0	100 100
64	AW	113/113 (100%)	111 (98%)	2 (2%)	59 77
65	CW	52/52 (100%)	51 (98%)	1 (2%)	57 75
66	Cg	96/96 (100%)	93 (97%)	3 (3%)	40 62
67	CU	90/90 (100%)	88 (98%)	2 (2%)	52 71
68	AK	81/81 (100%)	80 (99%)	1 (1%)	71 84
69	AT	107/116 (92%)	107 (100%)	0	100 100
70	AF	160/160 (100%)	156 (98%)	4 (2%)	47 68
71	CF	200/200 (100%)	197 (98%)	3 (2%)	65 80
72	AE	220/220 (100%)	219 (100%)	1 (0%)	88 93
73	AG	200/200 (100%)	199 (100%)	1 (0%)	88 93
74	AH	175/175 (100%)	171 (98%)	4 (2%)	50 70
75	AI	175/175 (100%)	175 (100%)	0	100 100
76	AQ	122/122 (100%)	121 (99%)	1 (1%)	81 89
77	CO	175/175 (100%)	173 (99%)	2 (1%)	73 85
78	CL	173/173 (100%)	167 (96%)	6 (4%)	36 60
79	CV	101/101 (100%)	98 (97%)	3 (3%)	41 63
80	CM	138/138 (100%)	136 (99%)	2 (1%)	67 81
83	Cj	71/71 (100%)	43 (61%)	28 (39%)	0 0
All	All	10126/10136 (100%)	9935 (98%)	191 (2%)	59 75

5 of 191 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
55	CE	16	LYS
72	AE	157	ASN
55	CE	193	VAL
66	Cg	34	TYR
77	CO	48	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
69	AT	88	HIS
69	AT	128	GLN
83	Cj	30	GLN
79	CV	135	ASN
22	Ab	49	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
57	A9	29/30 (96%)	10 (34%)	1 (3%)
58	A7	119/120 (99%)	30 (25%)	1 (0%)
59	A8	122/123 (99%)	58 (47%)	2 (1%)
61	B2	1792/1995 (89%)	726 (40%)	26 (1%)
62	A5	3566/3974 (89%)	1650 (46%)	86 (2%)
81	B	74/75 (98%)	27 (36%)	1 (1%)
82	v	11/12 (91%)	6 (54%)	0
All	All	5713/6329 (90%)	2507 (43%)	117 (2%)

5 of 2507 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
57	A9	7	G
57	A9	9	C
57	A9	10	U
57	A9	11	A
57	A9	15	A

5 of 117 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
62	A5	1161	C
62	A5	3808	A

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Mol	Chain	Res	Type
62	A5	1594	U
62	A5	3765	A
62	A5	3516	C

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

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
61	B2	2
62	A5	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B2	1236:C	O3'	1237:G	P	6.91
1	A5	2896:U	O3'	2897:G	P	5.92
1	B2	1817:C	O3'	1818:U	P	4.83
1	A5	2819:A	O3'	2820:G	P	3.80

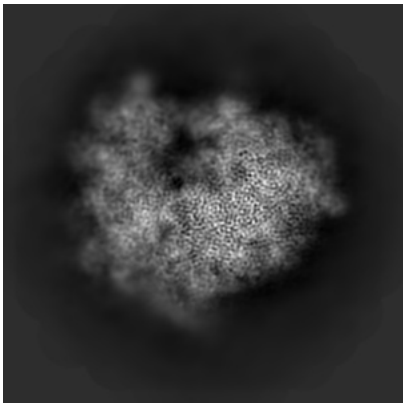
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-10623. These allow visual inspection of the internal detail of the map and identification of artifacts.

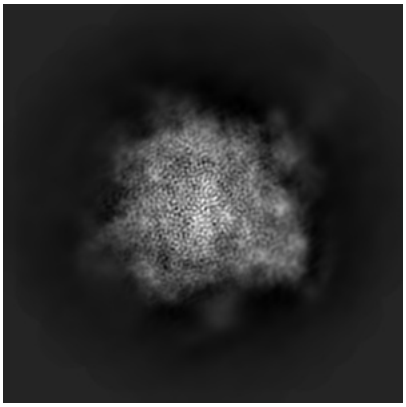
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

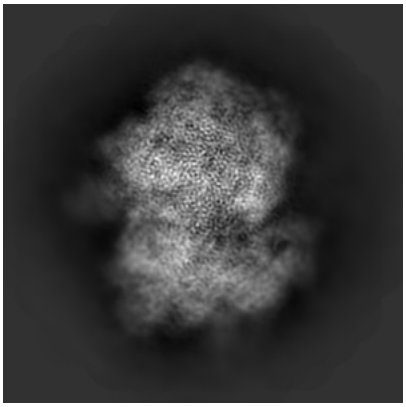
6.1.1 Primary map



X



Y

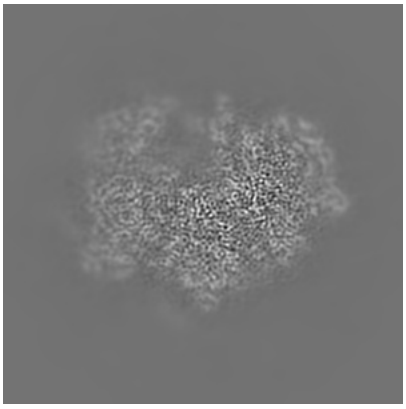


Z

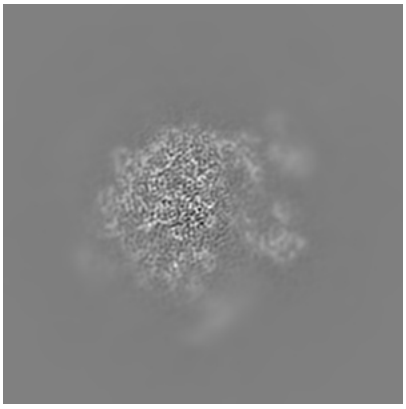
The images above show the map projected in three orthogonal directions.

6.2 Central slices

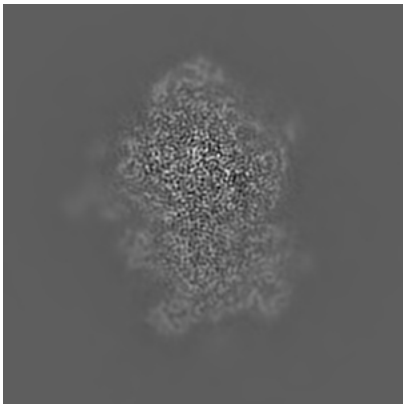
6.2.1 Primary map



X Index: 200



Y Index: 200

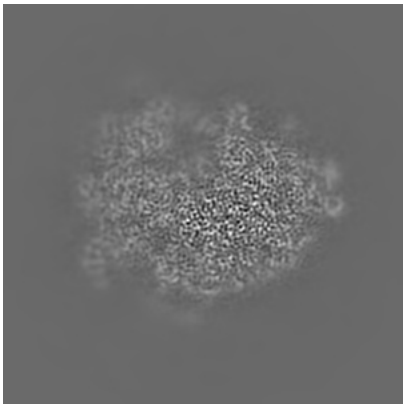


Z Index: 200

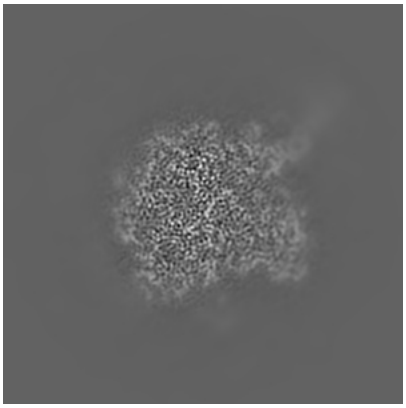
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

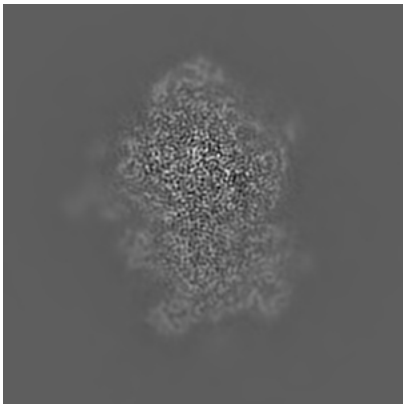
6.3.1 Primary map



X Index: 185



Y Index: 230

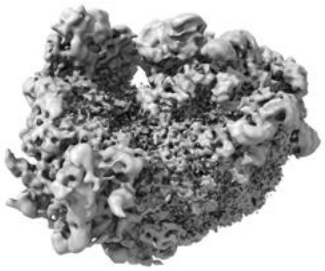


Z Index: 200

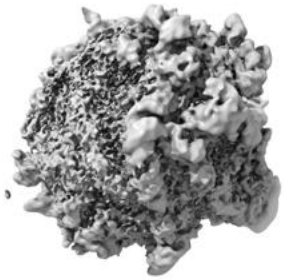
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

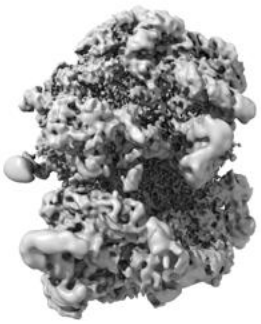
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.035. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

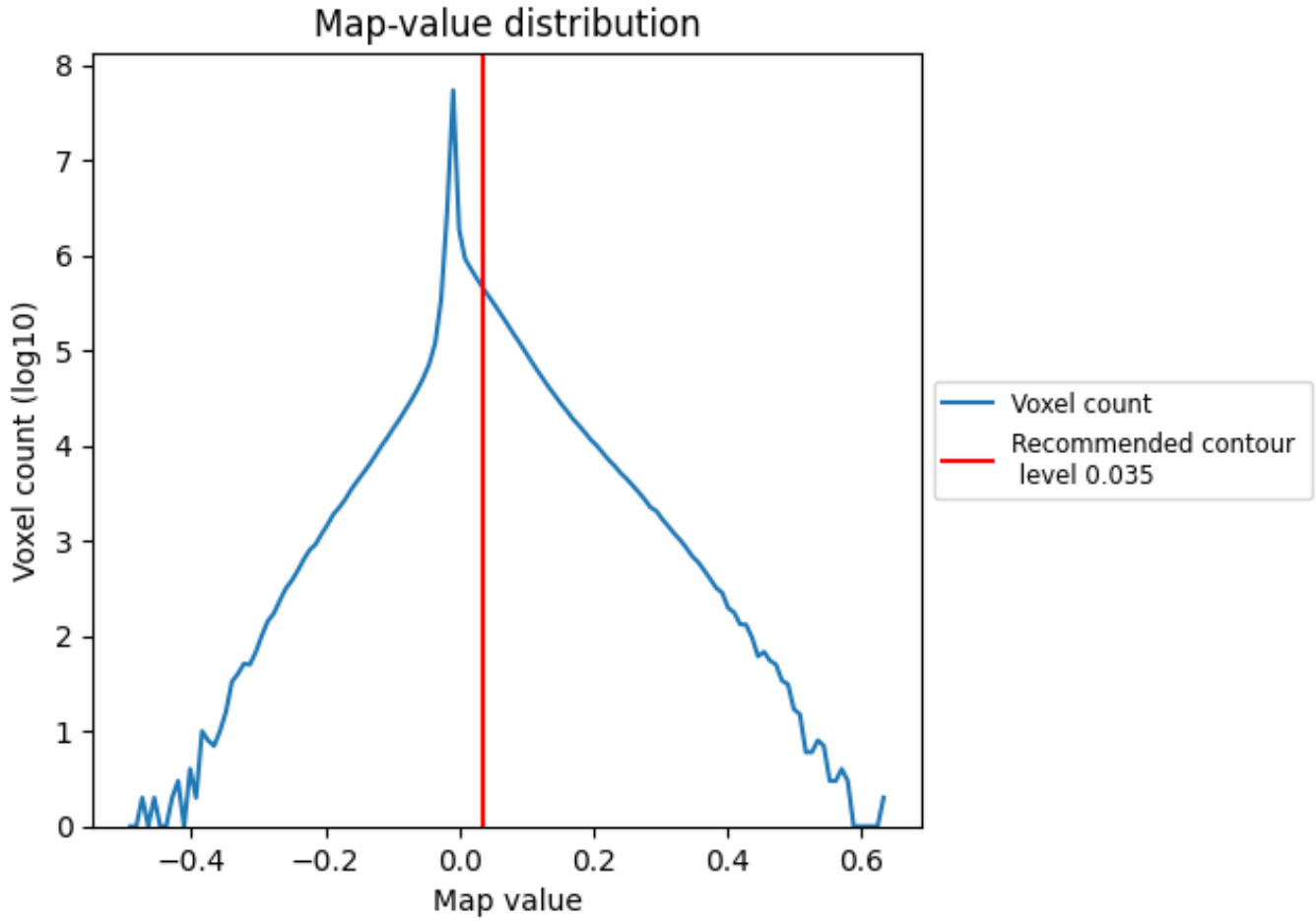
6.5 Mask visualisation (i)

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

7 Map analysis

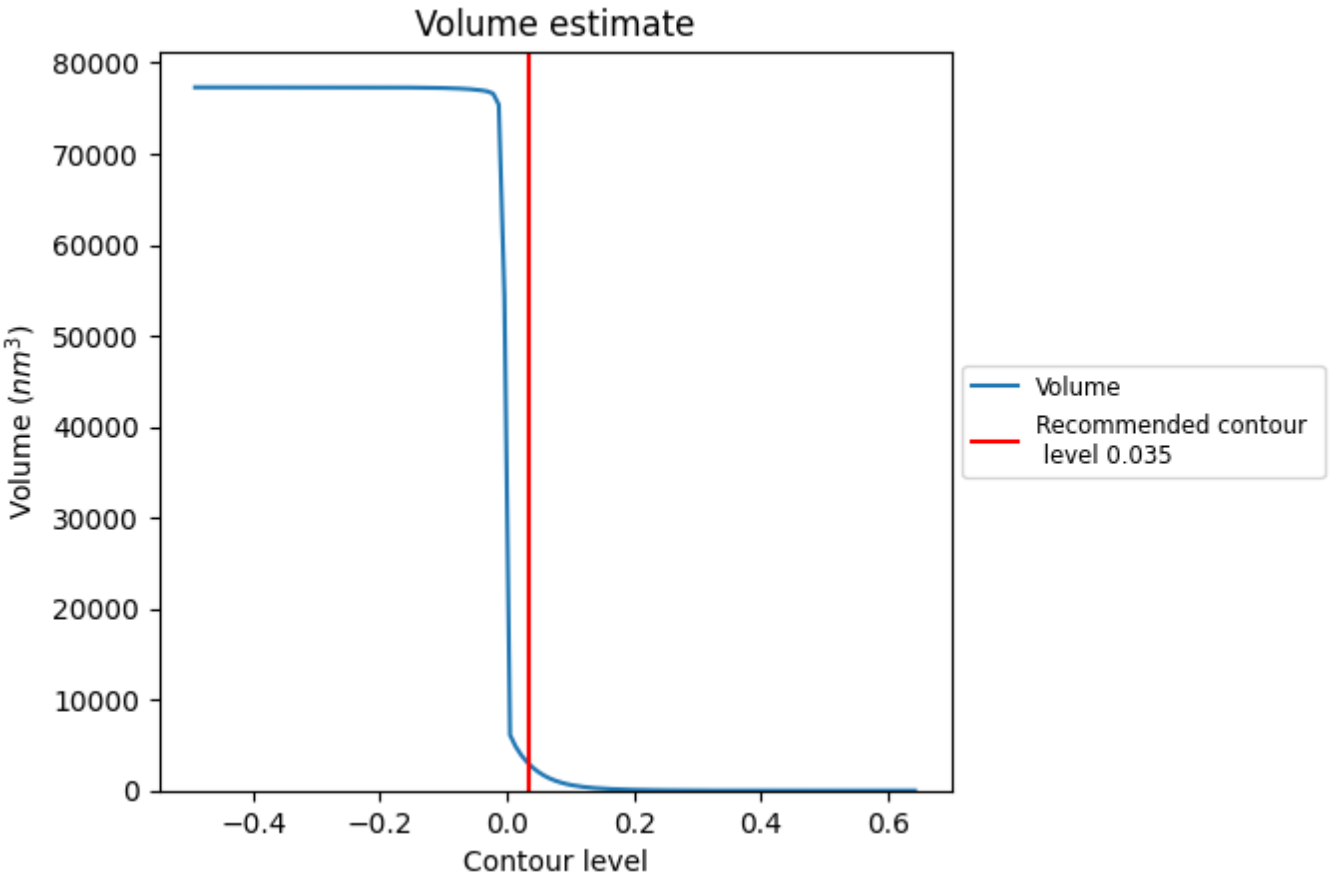
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

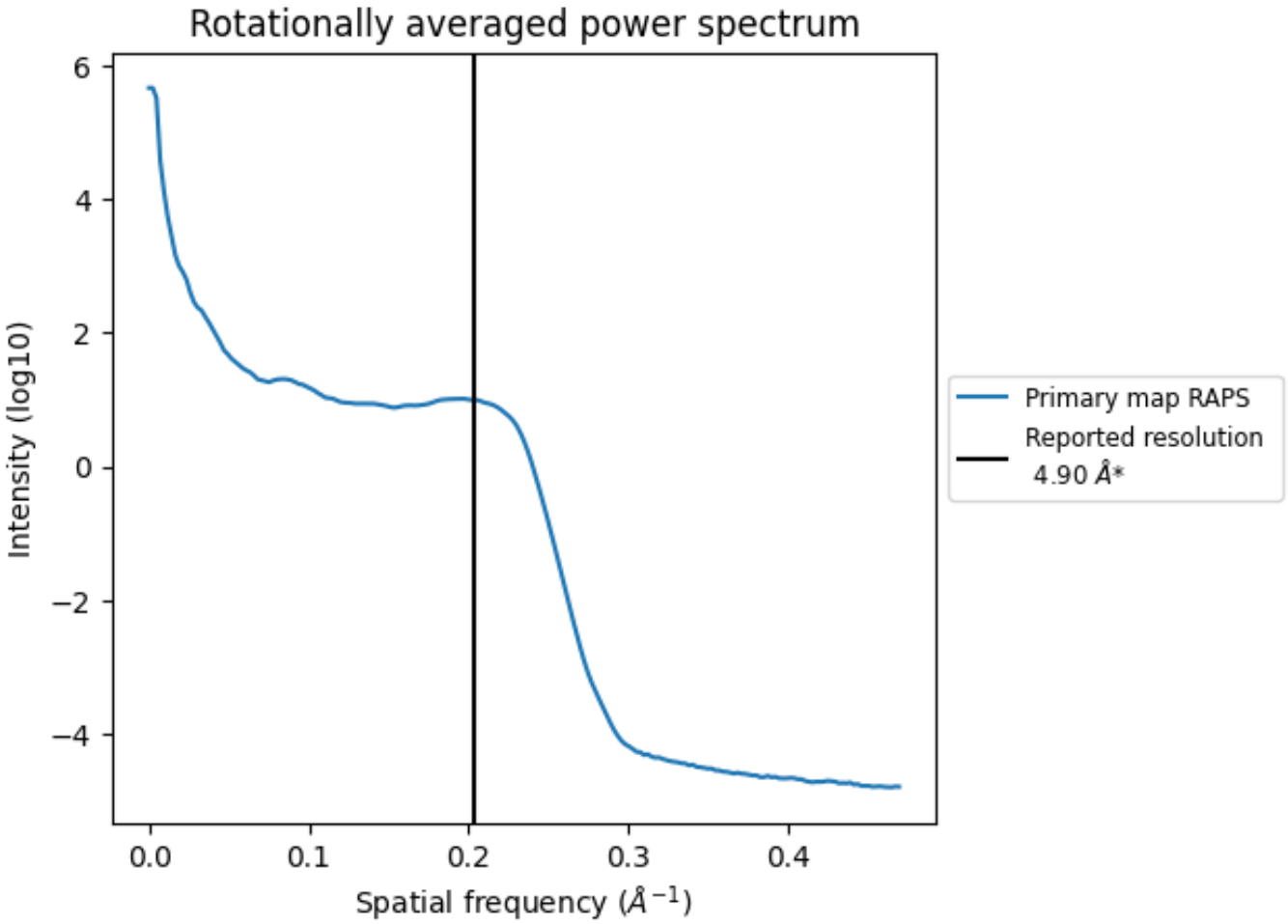
7.2 Volume estimate (i)



The volume at the recommended contour level is 2920 nm^3; this corresponds to an approximate mass of 2638 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)

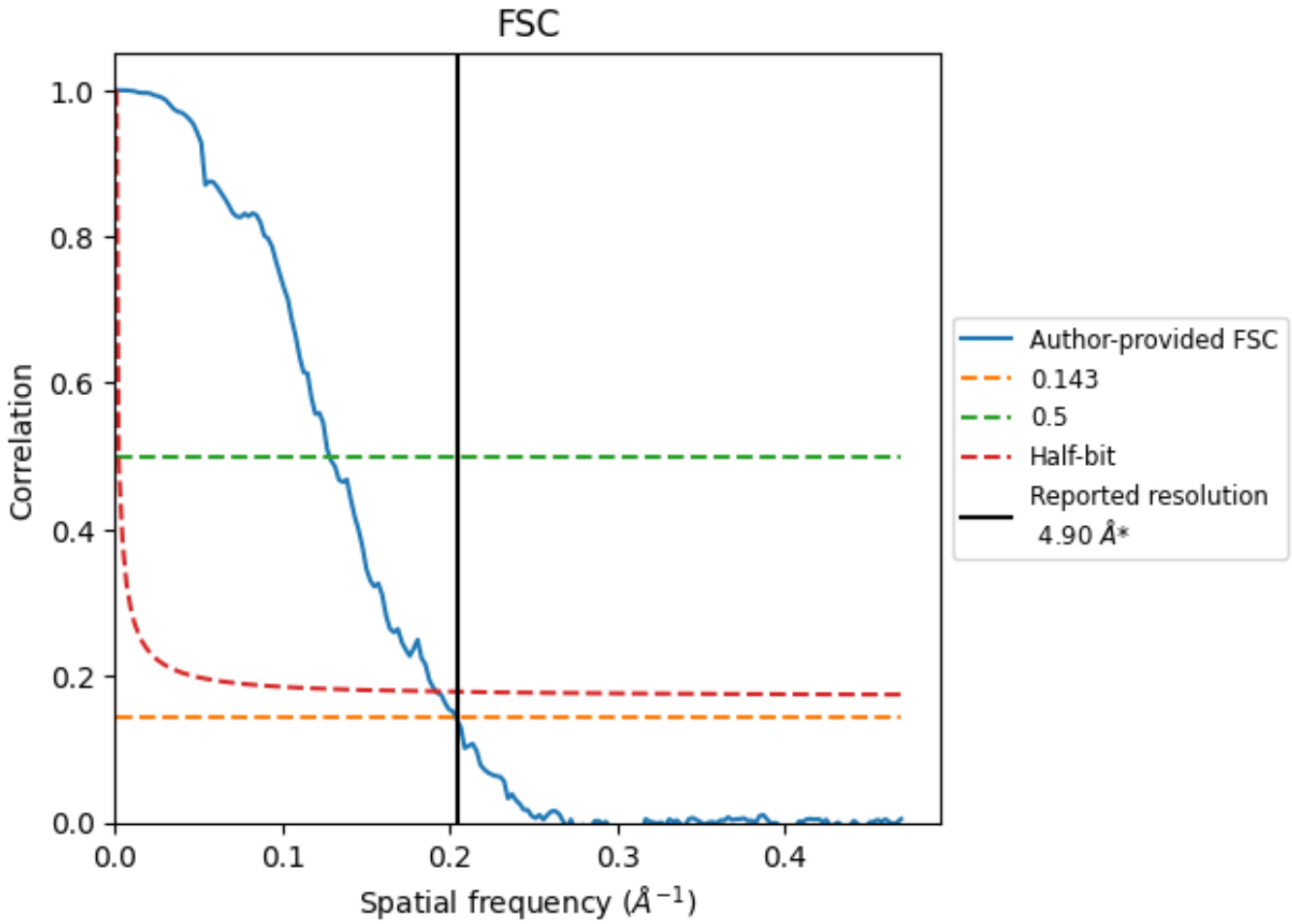


*Reported resolution corresponds to spatial frequency of 0.204 $Å^{-1}$

8 Fourier-Shell correlation

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

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.204 Å^{-1}

8.2 Resolution estimates (i)

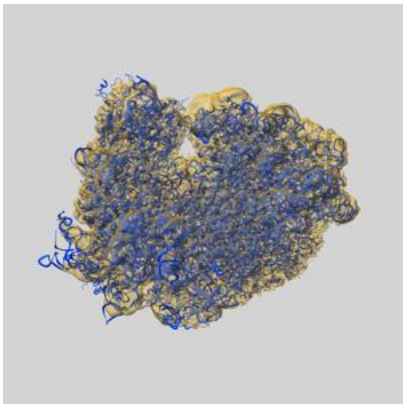
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.90	-	-
Author-provided FSC curve	4.91	7.80	5.21
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

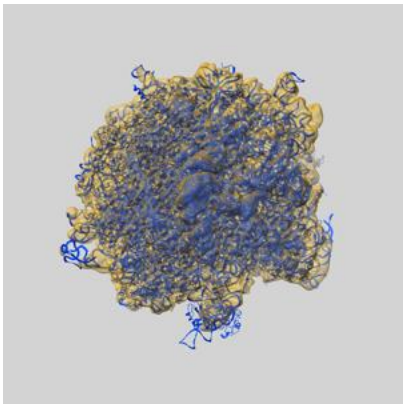
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-10623 and PDB model 6XU7. Per-residue inclusion information can be found in section 3 on page 19.

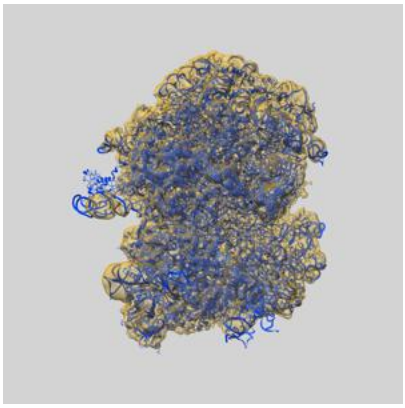
9.1 Map-model overlay



X



Y



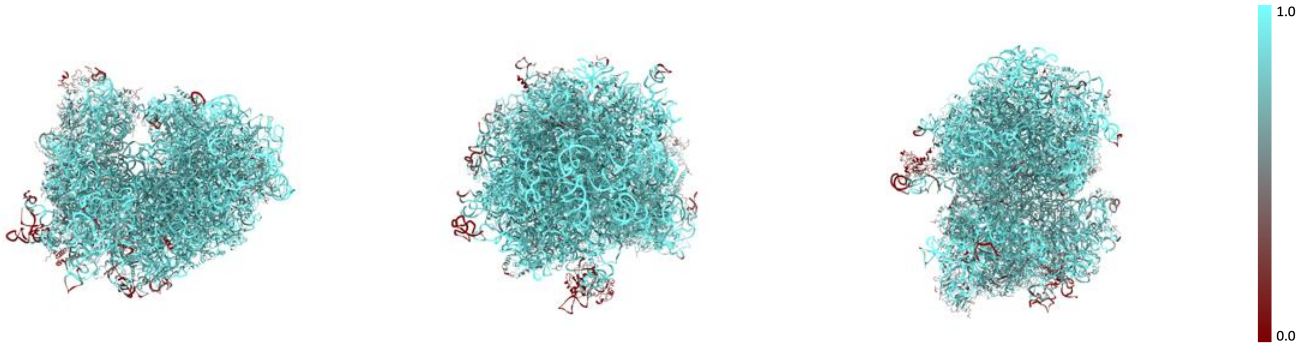
Z

The images above show the 3D surface view of the map at the recommended contour level 0.035 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)

This section was not generated.

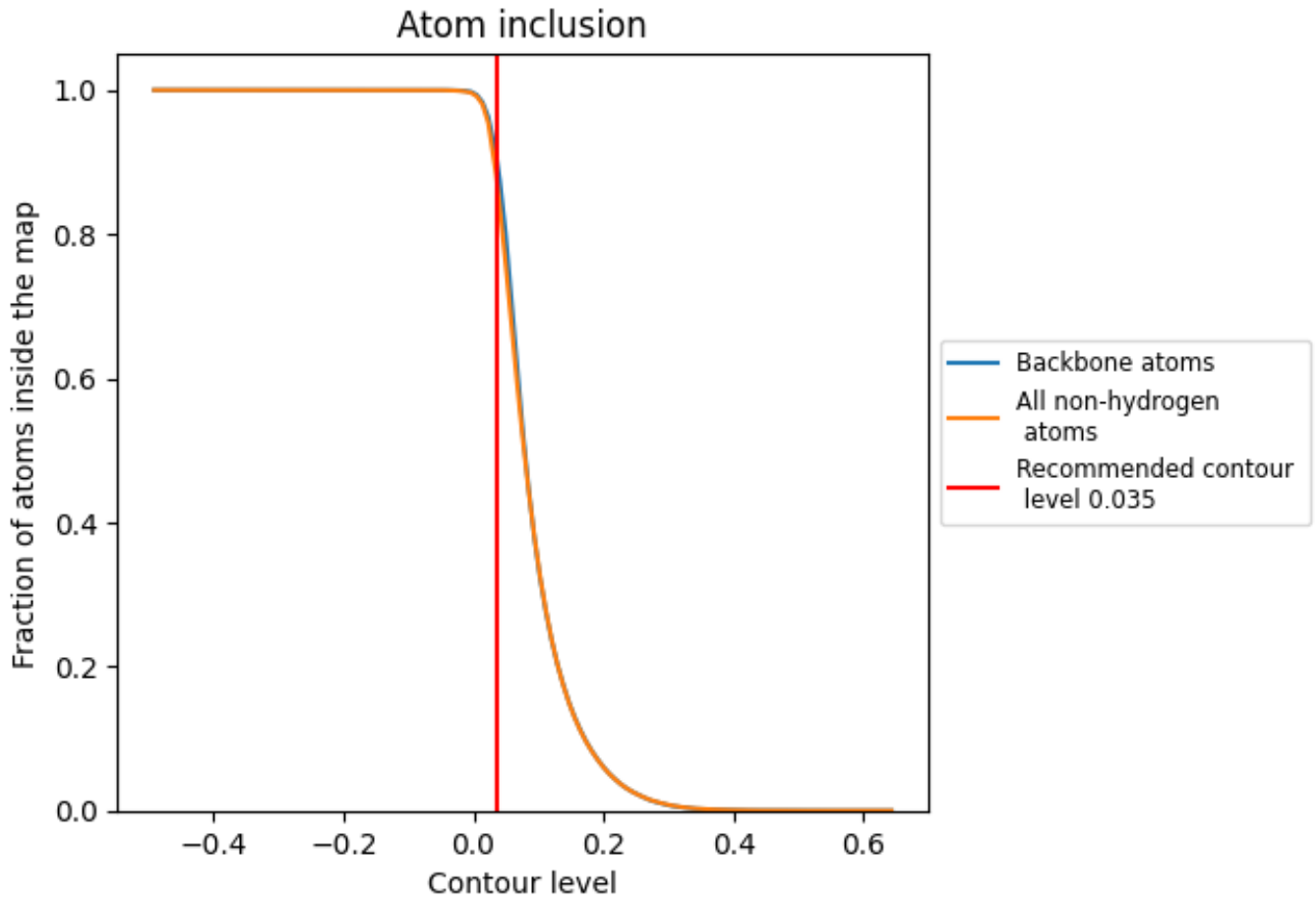
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.035).

9.4 Atom inclusion (i)



At the recommended contour level, 91% of all backbone atoms, 88% 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 (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion
All	0.8817
A5	0.9388
A7	0.9894
A8	0.9721
A9	0.9937
AA	0.7251
AB	0.7433
AC	0.7883
AD	0.6776
AE	0.7875
AF	0.7635
AG	0.7643
AH	0.6971
AI	0.7826
AJ	0.8010
AK	0.7473
AL	0.7055
AM	0.3326
AN	0.8460
AO	0.7318
AP	0.6865
AQ	0.7637
AR	0.7051
AS	0.7846
AT	0.8008
AU	0.7190
AV	0.7745
AW	0.8308
AX	0.8324
AY	0.8000
AZ	0.7264
Aa	0.8039
Ab	0.7402
Ac	0.7140
Ad	0.8333

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Chain	Atom inclusion
Ae	0.7022
Af	0.5086
Ag	0.7054
B	0.8548
B2	0.9250
CA	0.8975
CB	0.8973
CC	0.9161
CD	0.8994
CE	0.8215
CF	0.9144
CG	0.7963
CH	0.8878
CI	0.8416
CJ	0.8378
CL	0.8481
CM	0.8287
CN	0.9359
CO	0.9085
CP	0.8192
CQ	0.9350
CR	0.8132
CS	0.9055
CT	0.8936
CU	0.8667
CV	0.9168
CW	0.9316
CX	0.9053
CY	0.9489
CZ	0.8871
Ca	0.9275
Cb	0.9282
Cc	0.8355
Cd	0.9236
Ce	0.9315
Cf	0.8969
Cg	0.8781
Ch	0.9157
Ci	0.8246
Cj	0.8844
Ck	0.8615
Cl	0.9303

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Chain	Atom inclusion
Cm	0.8530
Cn	0.9442
Co	0.8878
Cp	0.9050
Cr	0.8506
Cz	0.0410
v	0.8745