



wwPDB EM Validation Summary Report ⓘ

Apr 15, 2026 – 11:36 AM UTC

PDB ID : 9Y49 / pdb_00009y49
EMDB ID : EMD-72475
Title : Structure of tuco-tuco ribosome with P/E tRNA and eEF2 (rotated)
Authors : Gutierrez-Vargas, C.; De, S.; Maji, S.; Liu, Z.; Nieb, M.; Seluanov, A.; Gorbunova, V.; Frank, J.
Deposited on : 2025-09-02
Resolution : 3.40 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:

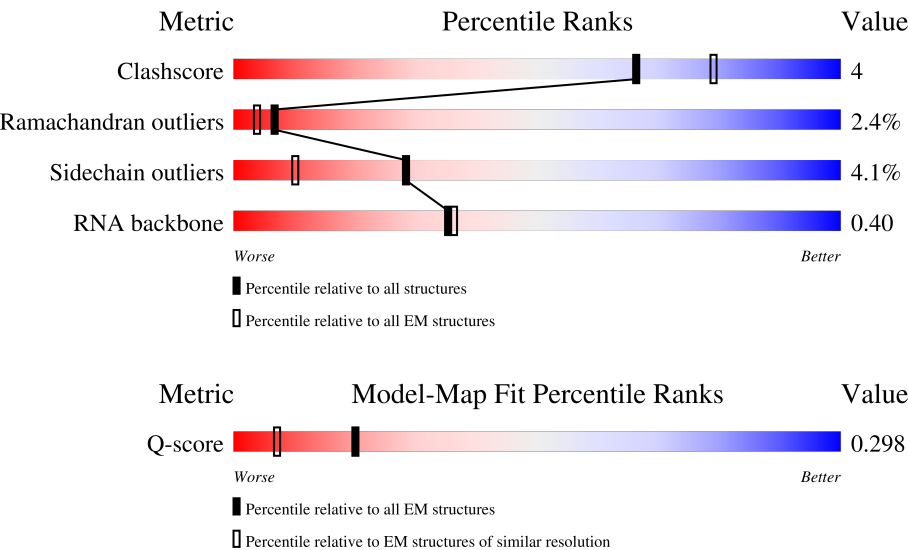
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 3.40 Å.

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






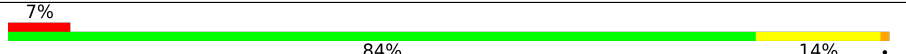
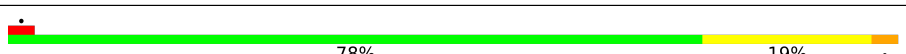
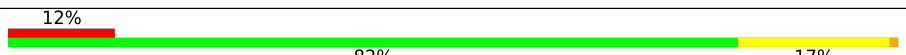
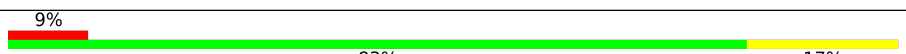
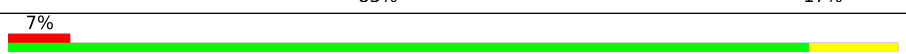
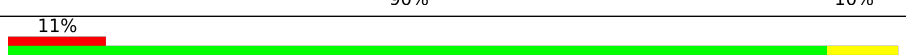
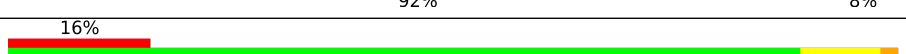
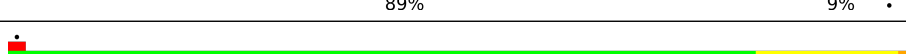

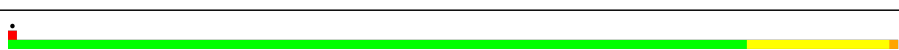
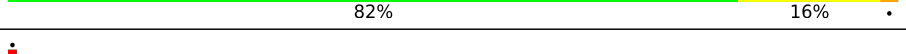





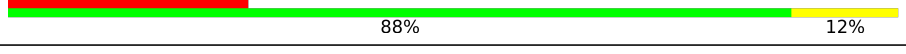

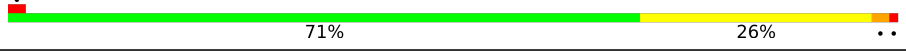



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

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

Mol	Chain	Length	Quality of chain
1	tR	77	
2	Ct	847	
3	AO	136	

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Mol	Chain	Length	Quality of chain
4	AX	139	
5	AN	149	
6	AL	157	
7	AB	212	
8	AA	208	
9	AV	82	
10	AY	126	
11	Aa	102	
12	Ab	84	
13	Ae	57	
14	AJ	178	
15	AE	262	
16	AC	220	
17	AG	237	
18	AH	189	
19	AW	129	
20	AI	206	
21	B2	1786	
22	CW	124	
23	Ag	313	
24	AU	104	
25	AK	98	
26	AM	122	
27	AS	137	
28	Ad	53	





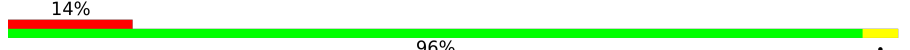
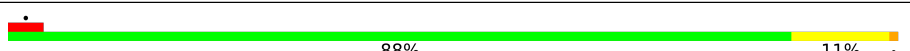
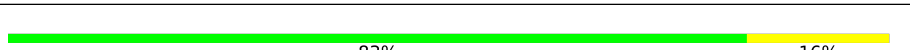

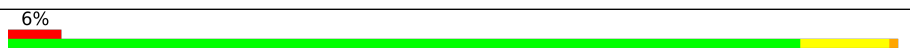

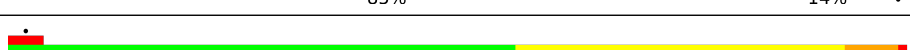
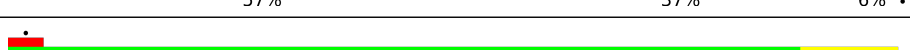

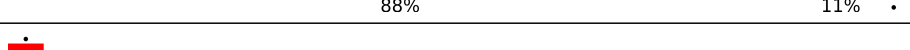
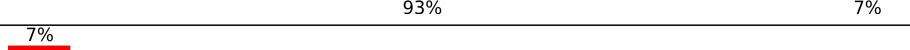
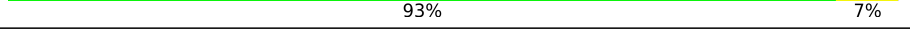
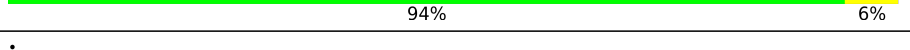


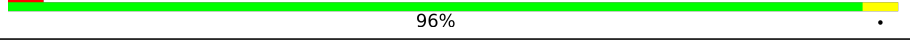
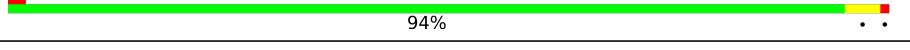
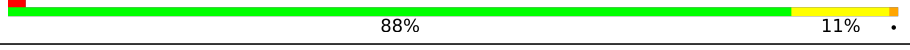
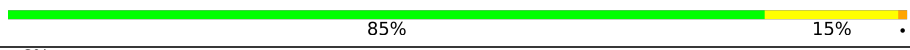


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Mol	Chain	Length	Quality of chain
29	AR	126	
30	AP	124	
31	AT	141	
32	AZ	75	
33	Ac	64	
34	AD	227	
35	Af	71	
36	AF	188	
37	AQ	141	
38	Cz	207	
39	CO	199	
40	CL	208	
41	CV	132	
42	CM	139	
43	Ca	147	
44	CN	203	
45	CI	207	
46	CD	289	
47	CQ	188	
48	CA	255	
49	CS	175	
50	CT	159	
51	CP	152	
52	CU	110	
53	CX	121	





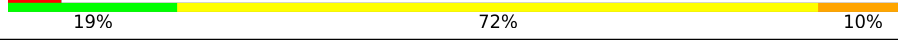
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Mol	Chain	Length	Quality of chain
54	CY	133	
55	CZ	135	
56	Cr	137	
57	Ch	123	
58	Cb	73	
59	CB	395	
60	CF	229	
61	Cc	100	
62	Cd	113	
63	Ce	130	
64	Cf	109	
65	Cg	114	
66	Ci	103	
67	Cj	89	
68	Ck	68	
69	Cl	49	
70	CC	365	
71	Cm	50	
72	Cn	24	
73	Cp	89	
74	Co	104	
75	CJ	168	
76	CH	191	
77	CE	254	
78	CG	246	

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Mol	Chain	Length	Quality of chain
79	A5	1722	
80	A7	121	
81	A8	157	
82	A6	2069	
83	CR	189	

2 Entry composition

There are 83 unique types of molecules in this entry. The entry contains 392048 atoms, of which 166649 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called tRNA (77-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
1	tR	77	Total	C	H	N	O	P	0	0
			2477	732	833	298	537	77		

- Molecule 2 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	Ct	847	Total	C	H	N	O	S	0	0
			13315	4202	6696	1137	1236	44		

- Molecule 3 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	AO	136	Total	C	H	N	O	S	0	0
			2040	618	1028	198	190	6		

- Molecule 4 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	AX	139	Total	C	H	N	O	S	0	0
			2235	685	1150	216	181	3		

- Molecule 5 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	AN	149	Total	C	H	N	O	S	0	0
			2491	770	1289	228	203	1		

- Molecule 6 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	AL	157	Total	C	H	N	O	S	0	0
			2647	822	1359	240	220	6		

- Molecule 7 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	AB	212	Total	C	H	N	O	S	0	0
			3532	1099	1805	309	305	14		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
8	AA	208	Total	C	H	N	O	S	0	0
			3284	1045	1642	289	300	8		

- Molecule 9 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	AV	82	Total	C	H	N	O	S	0	0
			1250	384	625	116	120	5		

- Molecule 10 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	AY	126	Total	C	H	N	O	S	0	0
			2111	646	1088	200	172	5		

- Molecule 11 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	Aa	102	Total	C	H	N	O	S	0	0
			1695	512	874	171	133	5		

- Molecule 12 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	Ab	84	Total	C	H	N	O	S	0	0
			1339	413	680	122	116	8		

- Molecule 13 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	Ae	57	Total	C	H	N	O	S	0	0
			946	281	494	99	71	1		

- Molecule 14 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	AJ	178	Total	C	H	N	O	S	0	0
			3063	942	1583	296	240	2		

- Molecule 15 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	AE	262	Total	C	H	N	O	S	0	0
			4265	1327	2186	386	357	9		

- Molecule 16 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	AC	220	Total	C	H	N	O	S	0	0
			3496	1105	1787	292	302	10		

- Molecule 17 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	AG	237	Total	C	H	N	O	S	0	0
			4008	1200	2085	387	329	7		

- Molecule 18 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	AH	189	Total	C	H	N	O	S	0	0
			3134	969	1613	280	271	1		

- Molecule 19 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	AW	129	Total	C	H	N	O	S	0	0
			2113	659	1079	193	176	6		

- Molecule 20 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	AI	206	Total	C	H	N	O	S	0	0
			3456	1058	1770	332	291	5		

- Molecule 21 is a RNA chain called 18S rRNA (1786-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
21	B2	1786	Total	C	H	N	O	P	0	0
			56628	16798	18952	6720	12373	1785		

- Molecule 22 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	CW	124	Total	C	H	N	O	S	0	0
			2085	634	1070	207	170	4		

- Molecule 23 is a protein called Guanine nucleotide-binding protein subunit beta-2-like 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	Ag	313	Total	C	H	N	O	S	0	0
			4824	1535	2388	424	465	12		

- Molecule 24 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	AU	104	Total	C	H	N	O	S	0	0
			1708	514	886	156	148	4		

- Molecule 25 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	AK	98	Total	C	H	N	O	S	0	0
			1680	539	853	148	134	6		

- Molecule 26 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	AM	122	Total	C	H	N	O	S	0	0
			1903	588	962	167	178	8		

- Molecule 27 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	AS	137	Total	C	H	N	O	S	0	0
			2326	714	1187	231	193	1		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
28	Ad	53	Total	C	H	N	O	S	0	0
			887	278	442	90	72	5		

- Molecule 29 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	AR	126	Total	C	H	N	O	S	0	0
			2089	639	1070	188	187	5		

- Molecule 30 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	AP	124	Total	C	H	N	O	S	0	0
			2135	660	1098	194	176	7		

- Molecule 31 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	AT	141	Total	C	H	N	O	S	0	0
			2236	690	1135	212	196	3		

- Molecule 32 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	AZ	75	Total	C	H	N	O	S	0	0
			1250	382	652	111	104	1		

- Molecule 33 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	Ac	64	Total	C	H	N	O	S	0	0
			1042	308	536	102	94	2		

- Molecule 34 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	AD	227	Total	C	H	N	O	S	0	0
			3620	1125	1855	317	315	8		

- Molecule 35 is a protein called 40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	Af	71	Total	C	H	N	O	S	0	0
			1179	367	598	109	98	7		

- Molecule 36 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	AF	188	Total	C	H	N	O	S	0	0
			3038	934	1545	283	269	7		

- Molecule 37 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	AQ	141	Total	C	H	N	O	S	0	0
			2317	715	1193	212	194	3		

- Molecule 38 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	Cz	207	Total	C	H	N	O	S	0	0
			3434	1068	1769	298	291	8		

- Molecule 39 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	CO	199	Total	C	H	N	O	S	0	0
			3410	1053	1776	319	257	5		

- Molecule 40 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	CL	208	Total	C	H	N	O	S	0	0
			3471	1052	1789	348	278	4		

- Molecule 41 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	CV	132	Total	C	H	N	O	S	0	0
			2022	620	1039	185	173	5		

- Molecule 42 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	CM	139	Total	C	H	N	O	S	0	0
			2348	730	1209	218	183	8		

- Molecule 43 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	Ca	147	Total	C	H	N	O	S	0	0
			2372	736	1210	237	186	3		

- Molecule 44 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	CN	203	Total	C	H	N	O	S	0	0
			3448	1072	1747	359	266	4		

- Molecule 45 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	CI	207	Total	C	H	N	O	S	0	0
			3383	1061	1711	320	277	14		

- Molecule 46 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	CD	289	Total	C	H	N	O	S	0	0
			4723	1483	2370	429	427	14		

- Molecule 47 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	CQ	188	Total	C	H	N	O	S	0	0
			3161	949	1640	315	251	6		

- Molecule 48 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	CA	255	Total	C	H	N	O	S	0	0
			4009	1225	2052	399	327	6		

- Molecule 49 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	CS	175	Total	C	H	N	O	S	0	0
			2938	925	1485	283	235	10		

- Molecule 50 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	CT	159	Total	C	H	N	O	S	0	0
			2661	823	1363	252	217	6		

- Molecule 51 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	CP	152	Total	C	H	N	O	S	0	0
			2493	771	1260	240	213	9		

- Molecule 52 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	CU	110	Total	C	H	N	O	S	0	0
			1804	571	904	155	172	2		

- Molecule 53 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	CX	121	Total	C	H	N	O	S	0	0
			2072	636	1078	187	170	1		

- Molecule 54 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	CY	133	Total	C	H	N	O	S	0	0
			2300	695	1193	225	185	2		

- Molecule 55 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	CZ	135	Total	C	H	N	O	S	0	0
			2289	714	1182	208	182	3		

- Molecule 56 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	Cr	137	Total	C	H	N	O	S	0	0
			2288	682	1184	231	185	6		

- Molecule 57 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	Ch	123	Total	C	H	N	O	S	0	0
			2182	646	1159	206	169	2		

- Molecule 58 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	Cb	73	Total	C	H	N	O	S	0	0
			1225	367	630	128	97	3		

- Molecule 59 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
59	CB	395	Total	C	H	N	O	S	0	0
			6505	2030	3316	600	545	14		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
60	CF	229	Total	C	H	N	O	S	0	0
			3956	1226	2046	370	305	9		

- Molecule 61 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms						AltConf	Trace
61	Cc	100	Total	C	H	N	O	S	0	0
			1588	492	812	136	141	7		

- Molecule 62 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms						AltConf	Trace
62	Cd	113	Total	C	H	N	O	S	0	0
			1910	586	979	181	162	2		

- Molecule 63 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
63	Ce	130	Total	C	H	N	O	S	0	0
			2235	676	1165	221	168	5		

- Molecule 64 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms						AltConf	Trace
64	Cf	109	Total	C	H	N	O	S	0	0
			1786	555	910	174	144	3		

- Molecule 65 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms						AltConf	Trace
65	Cg	114	Total	C	H	N	O	S	0	0
			1905	566	999	187	147	6		

- Molecule 66 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms						AltConf	Trace
66	Ci	103	Total	C	H	N	O	S	0	0
			1765	526	925	178	130	6		

- Molecule 67 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms						AltConf	Trace
67	Cj	89	Total	C	H	N	O	S	0	0
			1490	446	764	161	114	5		

- Molecule 68 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms						AltConf	Trace
68	Ck	68	Total	C	H	N	O	S	0	0
			1183	360	624	101	97	1		

- Molecule 69 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms						AltConf	Trace
69	Cl	49	Total	C	H	N	O	S	0	0
			907	275	472	97	62	1		

- Molecule 70 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms						AltConf	Trace
70	CC	365	Total	C	H	N	O	S	0	0
			5982	1829	3074	580	486	13		

- Molecule 71 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms						AltConf	Trace
71	Cm	50	Total	C	H	N	O	S	0	0
			857	254	446	87	64	6		

- Molecule 72 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms						AltConf	Trace
72	Cn	24	Total	C	H	N	O	S	0	0
			504	139	274	62	26	3		

- Molecule 73 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms						AltConf	Trace
73	Cp	89	Total	C	H	N	O	S	0	0
			1440	437	747	133	116	7		

- Molecule 74 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms						AltConf	Trace
74	Co	104	Total	C	H	N	O	S	0	0
			1772	533	921	174	138	6		

- Molecule 75 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms						AltConf	Trace
75	CJ	168	Total	C	H	N	O	S	0	0
			2731	853	1382	251	239	6		

- Molecule 76 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms						AltConf	Trace
76	CH	191	Total	C	H	N	O	S	0	0
			3129	960	1603	285	275	6		

- Molecule 77 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms						AltConf	Trace
77	CE	254	Total	C	H	N	O	S	0	0
			4290	1317	2240	389	340	4		

- Molecule 78 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms						AltConf	Trace
78	CG	246	Total	C	H	N	O	S	0	0
			4096	1256	2123	379	334	4		

- Molecule 79 is a RNA chain called LSU-alpha rRNA (1722-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
79	A5	1715	Total	C	H	N	O	P	0	0
			54360	16069	18197	6597	11783	1714		

- Molecule 80 is a RNA chain called 5S rRNA (121-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
80	A7	121	Total	C	H	N	O	P	0	0
			3884	1150	1306	458	850	120		

- Molecule 81 is a RNA chain called 5.8S rRNA (157-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
81	A8	157	Total	C	H	N	O	P	0	0
			5027	1489	1693	587	1102	156		

- Molecule 82 is a RNA chain called LSU-beta rRNA (2069-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
82	A6	2069	Total	C	H	N	O	P	0	0
			65289	19344	21793	7815	14268	2069		

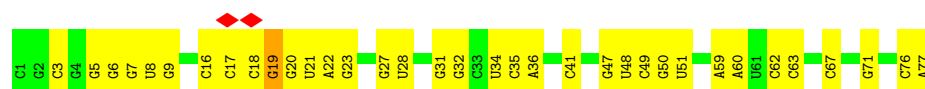
- Molecule 83 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	CR	189	Total	C	N	O	S	0	0
			1580	979	338	253	10		

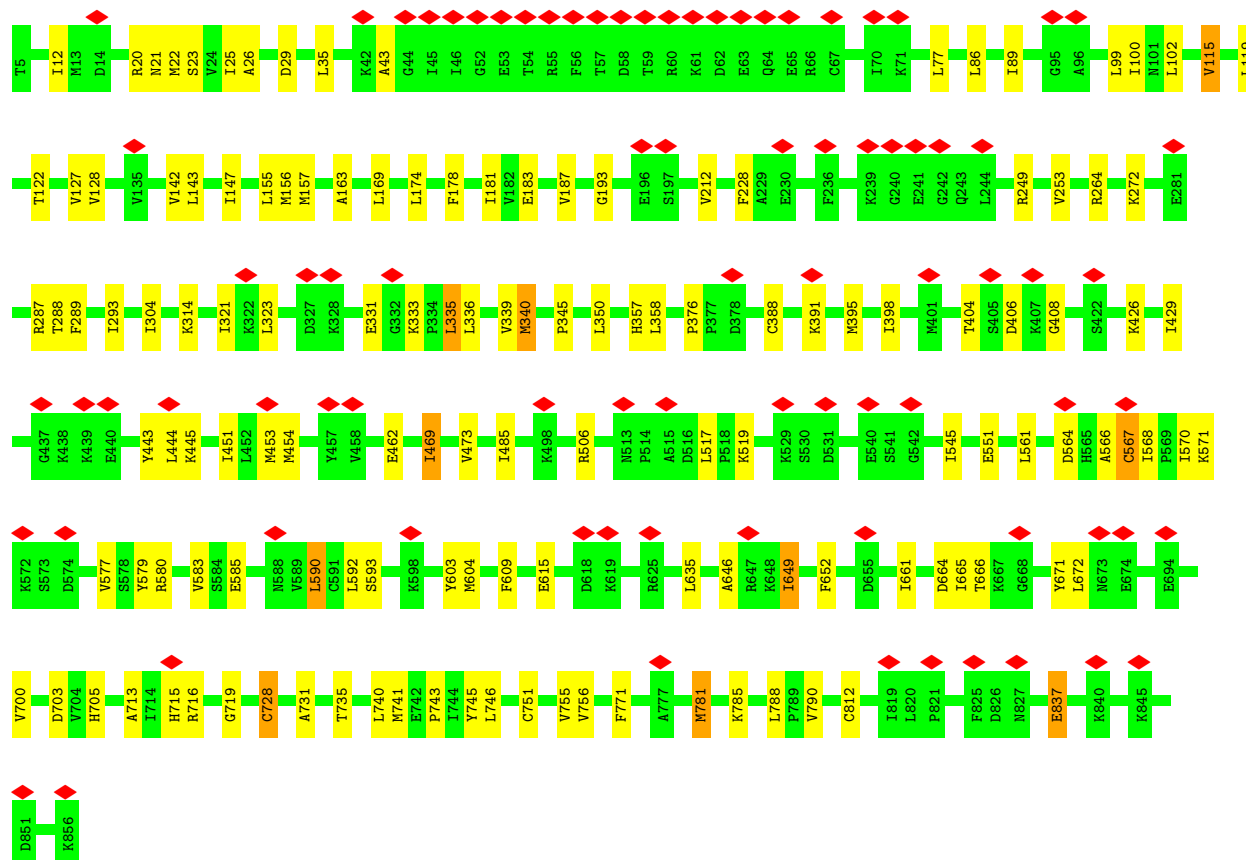
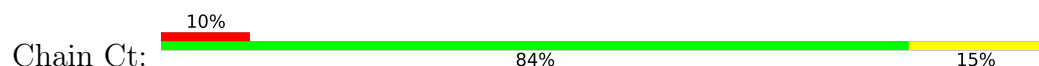
3 Residue-property plots

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

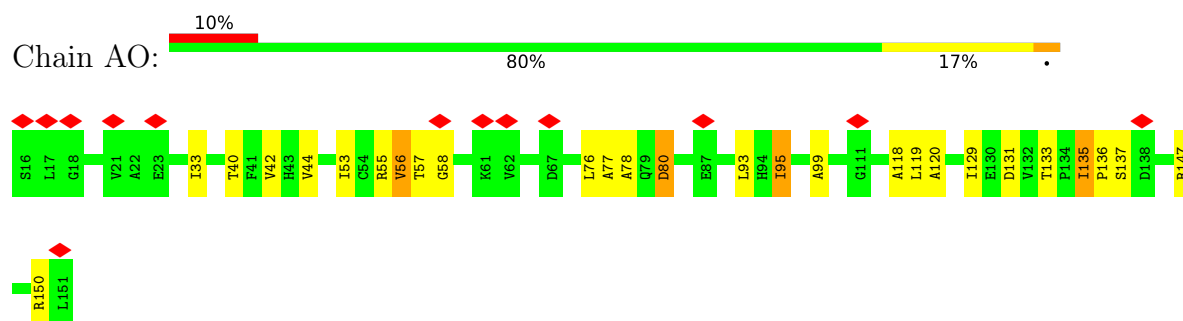
- Molecule 1: tRNA (77-MER)



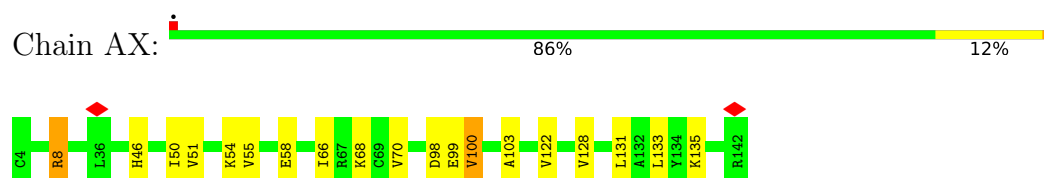
- Molecule 2: Elongation factor 2



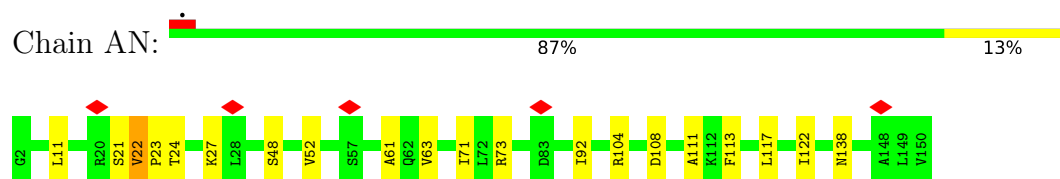
- Molecule 3: 40S ribosomal protein S14



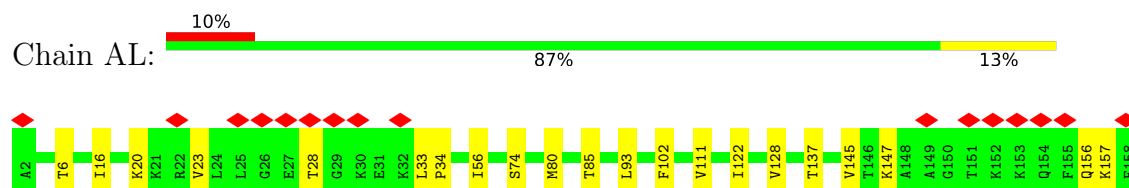
- Molecule 4: 40S ribosomal protein S23



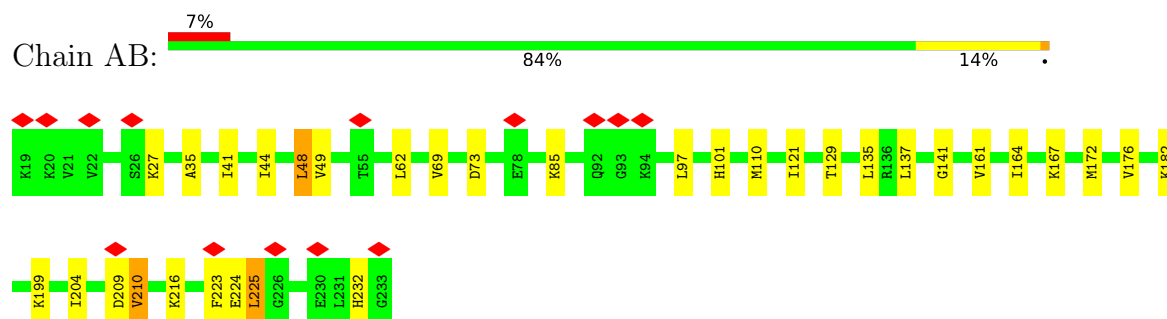
- Molecule 5: 40S ribosomal protein S13



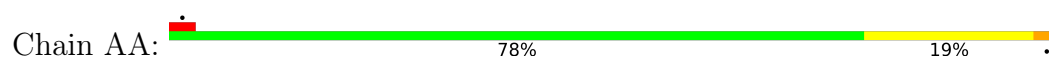
- Molecule 6: 40S ribosomal protein S11

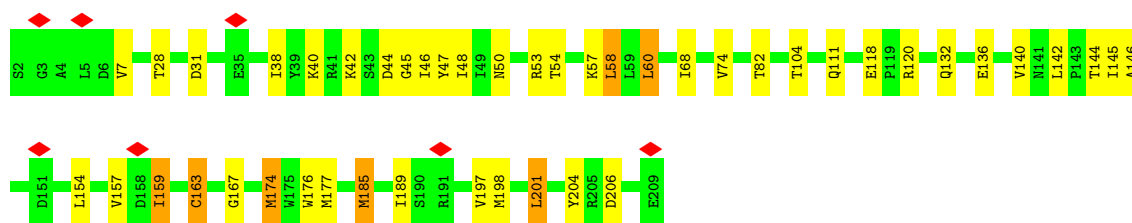


- Molecule 7: 40S ribosomal protein S3a

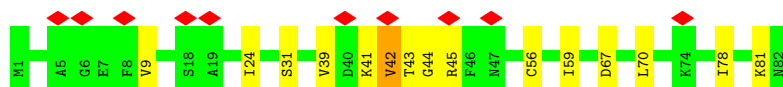
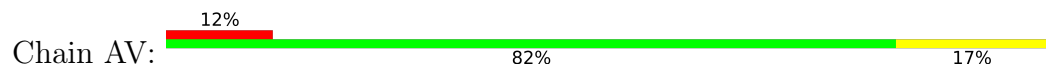


- Molecule 8: 40S ribosomal protein SA

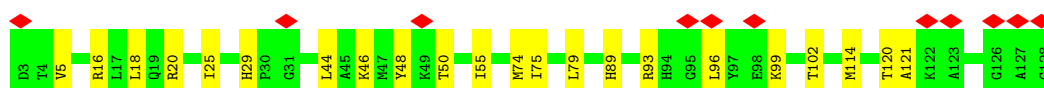
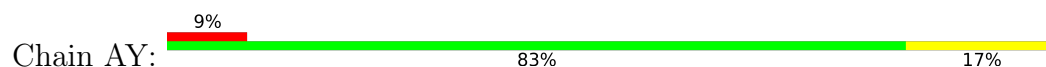




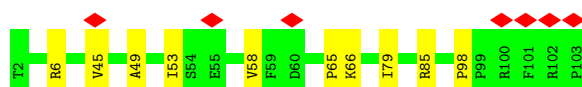
• Molecule 9: 40S ribosomal protein S21



• Molecule 10: 40S ribosomal protein S24



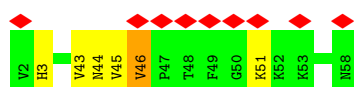
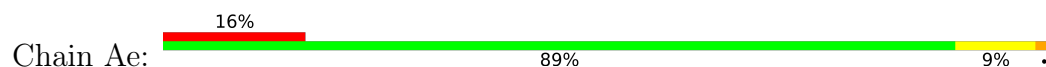
• Molecule 11: 40S ribosomal protein S26



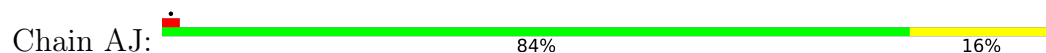
• Molecule 12: 40S ribosomal protein S27



• Molecule 13: 40S ribosomal protein S30

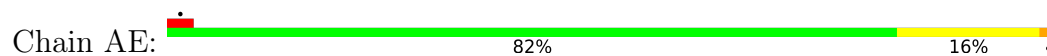


• Molecule 14: 40S ribosomal protein S9

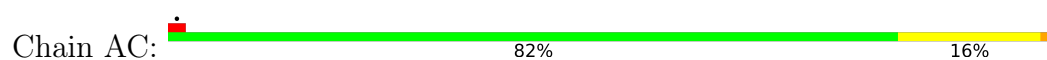




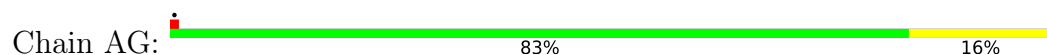
- Molecule 15: 40S ribosomal protein S4, X isoform



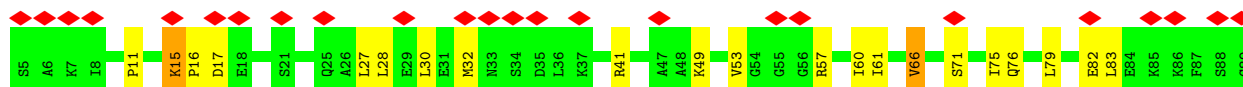
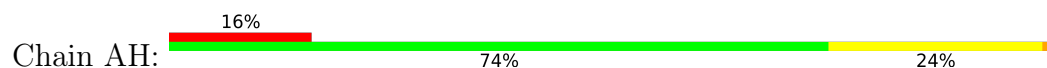
- Molecule 16: 40S ribosomal protein S2



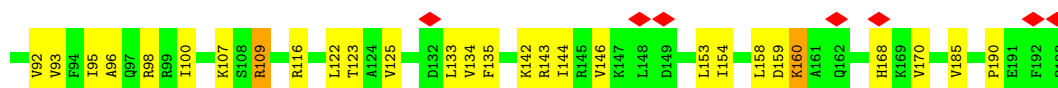
- Molecule 17: 40S ribosomal protein S6




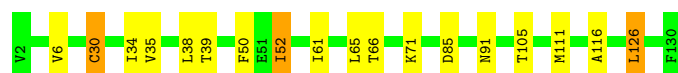
- Molecule 18: 40S ribosomal protein S7



- Molecule 19: 40S ribosomal protein S15a

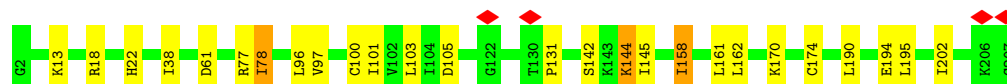


Chain AW:  86% 12%




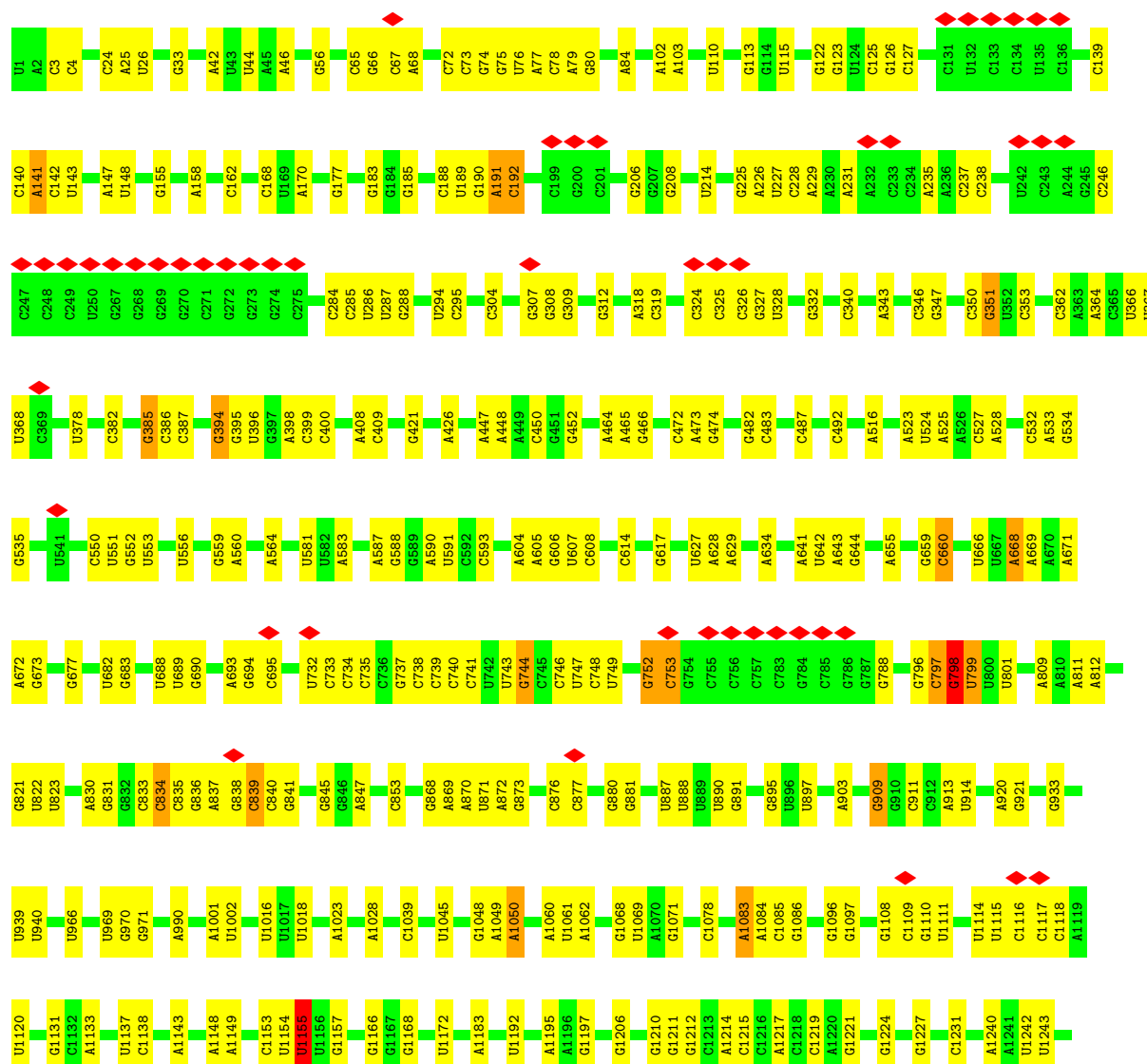
- Molecule 20: 40S ribosomal protein S8

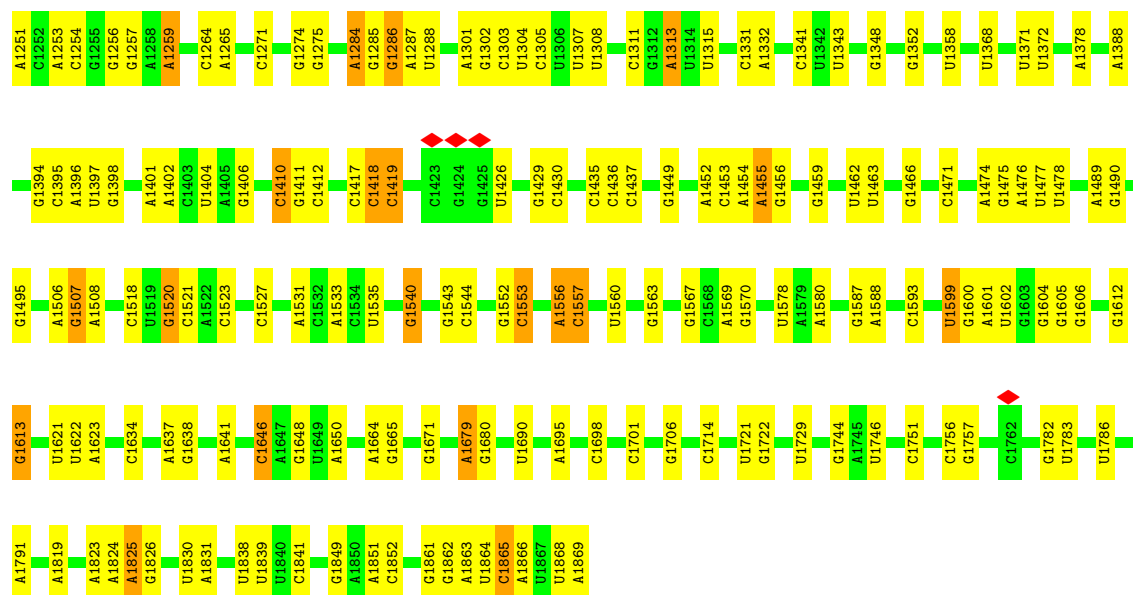
Chain AI:  87% 11%



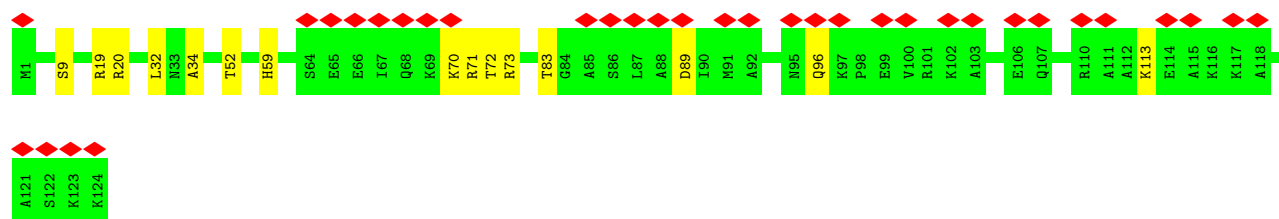
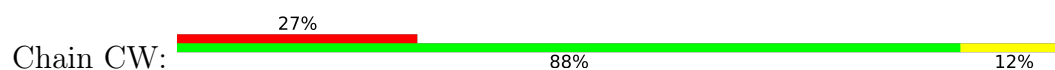
- Molecule 21: 18S rRNA (1786-MER)

Chain B2:  72% 26%

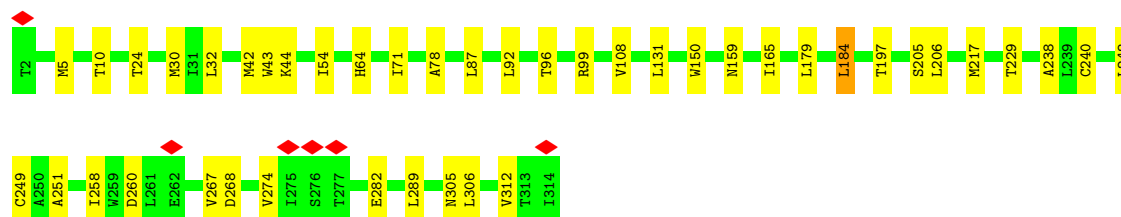




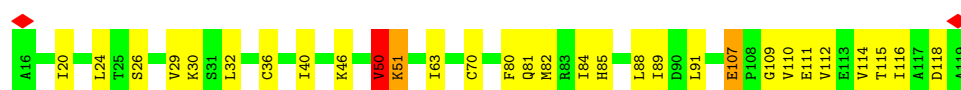
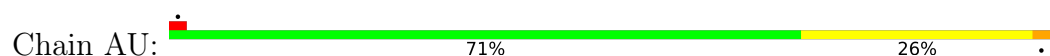
• Molecule 22: 60S ribosomal protein L24



• Molecule 23: Guanine nucleotide-binding protein subunit beta-2-like 1



• Molecule 24: 40S ribosomal protein S20




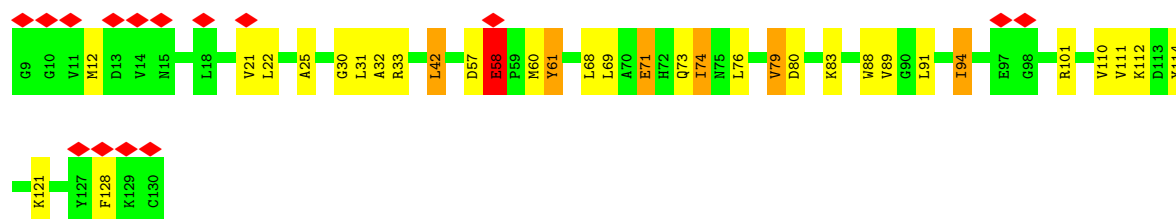
• Molecule 25: 40S ribosomal protein S10

Chain AK:  69% 29% .




- Molecule 26: 40S ribosomal protein S12

Chain AM:  12% 73% 21% 5% .



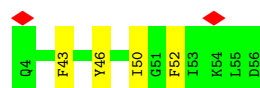
- Molecule 27: 40S ribosomal protein S18

Chain AS:  84% 15% ..




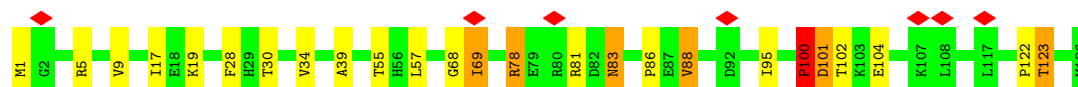
- Molecule 28: 40S ribosomal protein S29

Chain Ad:  92% 8%




- Molecule 29: 40S ribosomal protein S17

Chain AR:  6% 80% 14% 5% .



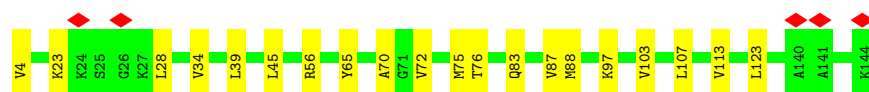
- Molecule 30: 40S ribosomal protein S15

Chain AP:  11% 86% 9% ..

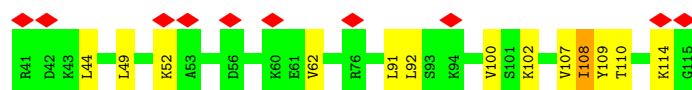
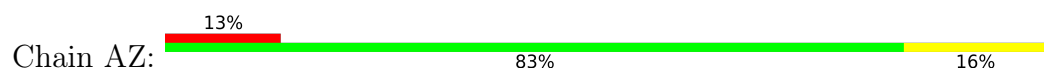


- Molecule 31: 40S ribosomal protein S19

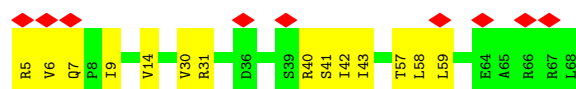
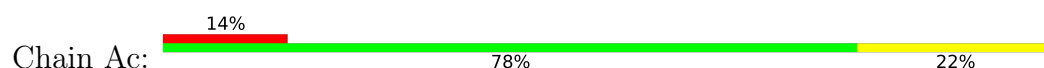
Chain AT:  86% 14%



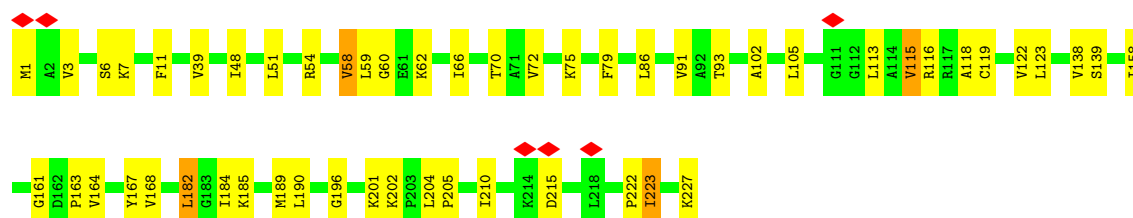
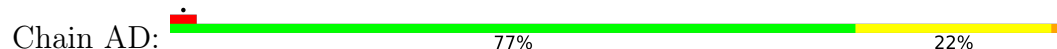
- Molecule 32: 40S ribosomal protein S25



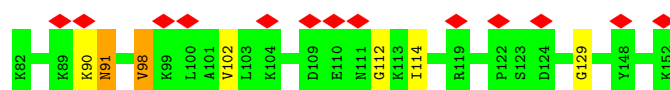
- Molecule 33: 40S ribosomal protein S28



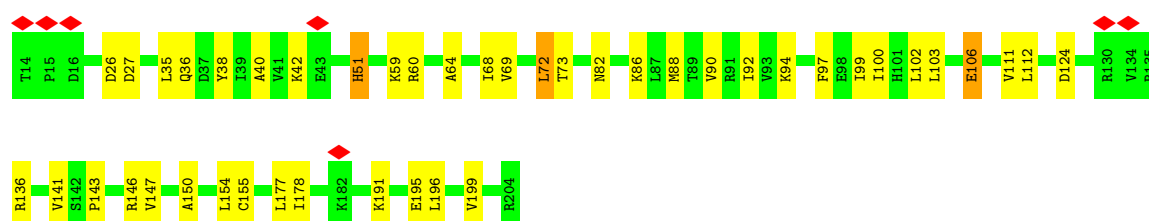
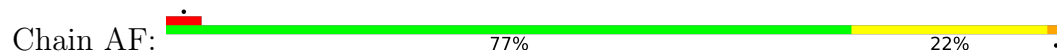
- Molecule 34: 40S ribosomal protein S3




- Molecule 35: 40S ribosomal protein S27a

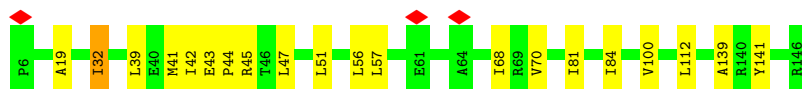


- Molecule 36: 40S ribosomal protein S5




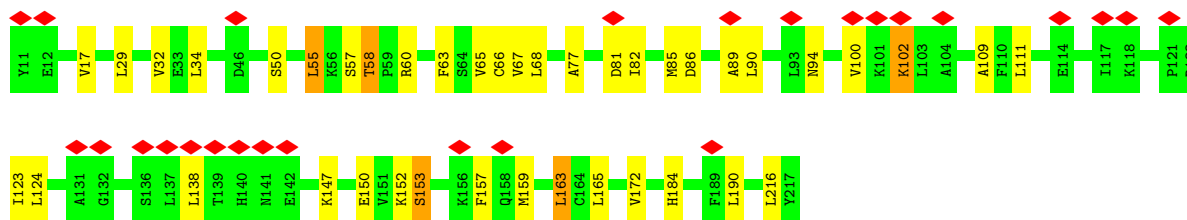
- Molecule 37: 40S ribosomal protein S16

Chain AQ:  86% 13%




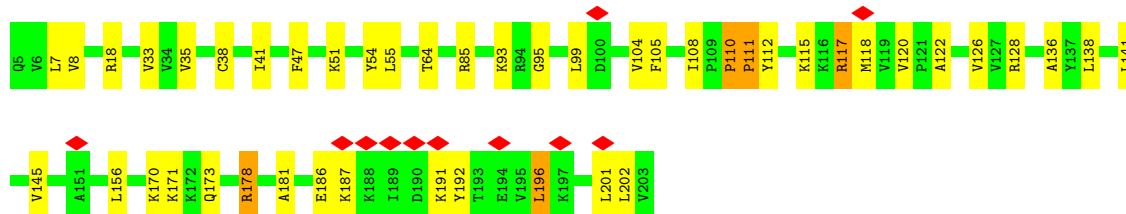
- Molecule 38: 60S ribosomal protein L10a

Chain Cz:  13% 80% 17%



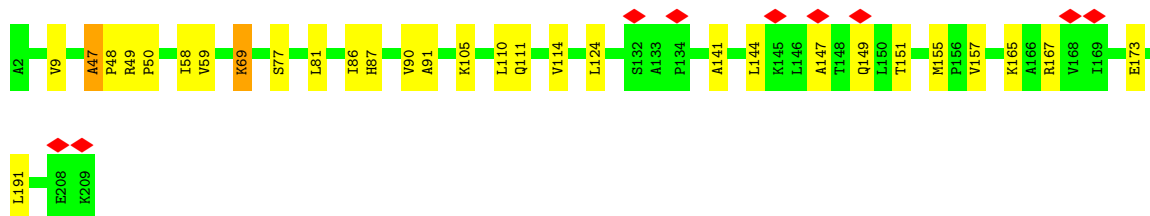
- Molecule 39: 60S ribosomal protein L13a

Chain CO:  6% 77% 21%

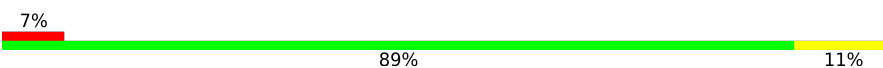


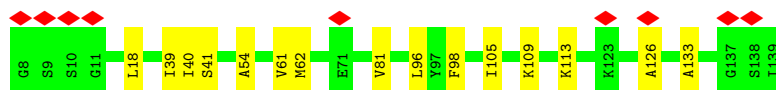
- Molecule 40: 60S ribosomal protein L13

Chain CL:  86% 13%




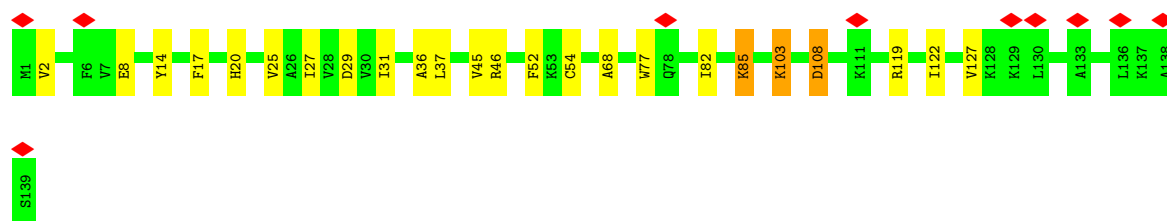
- Molecule 41: 60S ribosomal protein L23

Chain CV:  7% 89% 11%

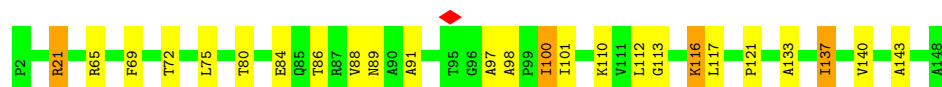
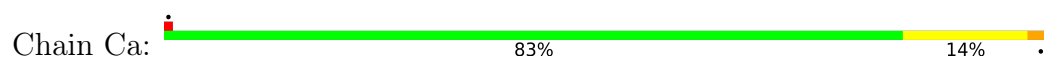


- Molecule 42: 60S ribosomal protein L14

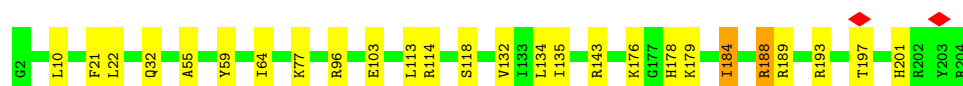
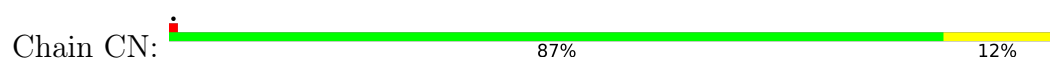
Chain CM:  7% 83% 15%



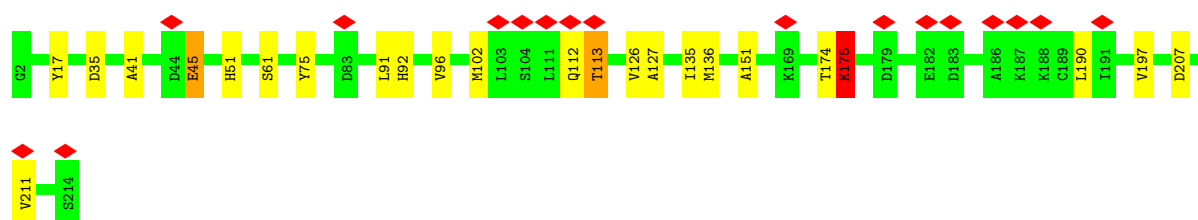
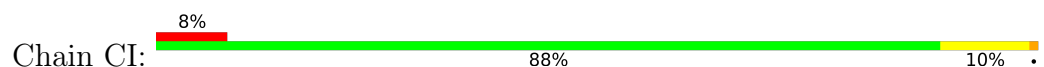
- Molecule 43: 60S ribosomal protein L27a



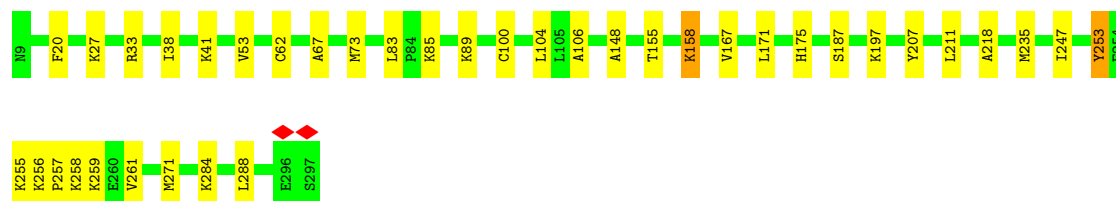
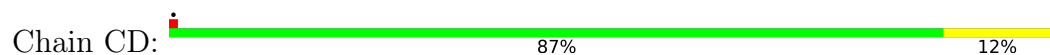
- Molecule 44: 60S ribosomal protein L15



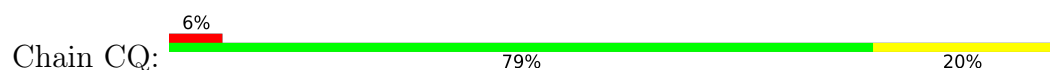
- Molecule 45: 60S ribosomal protein L10-like

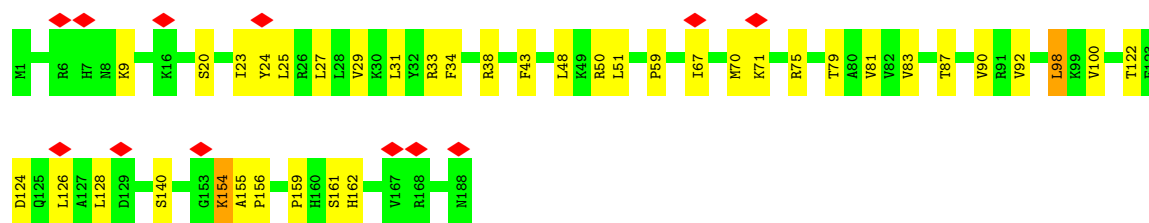


- Molecule 46: 60S ribosomal protein L5

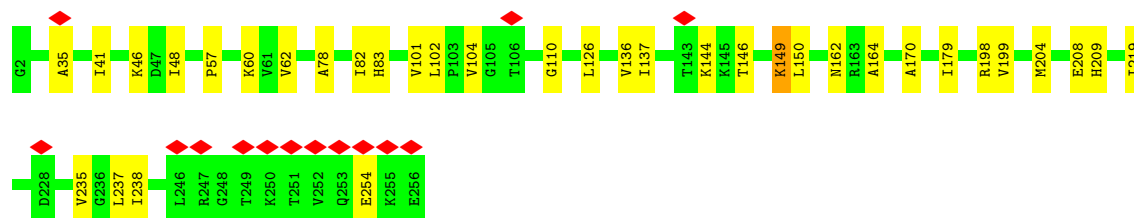
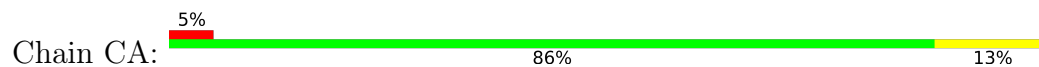


- Molecule 47: 60S ribosomal protein L18

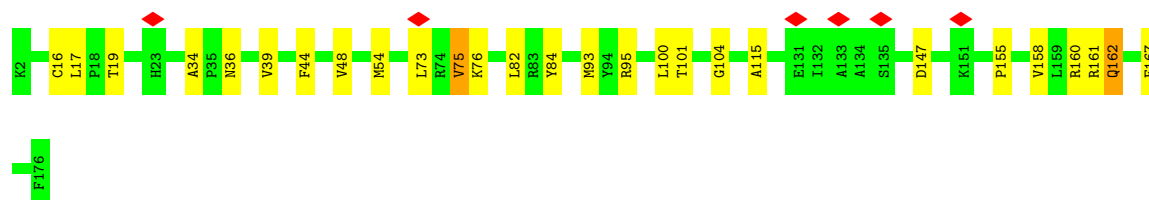
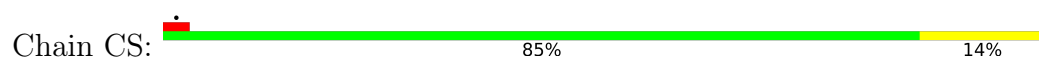




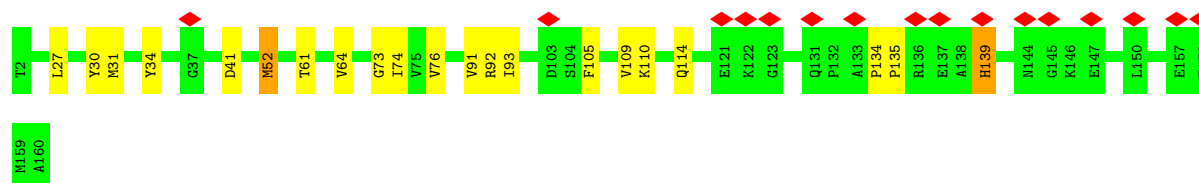
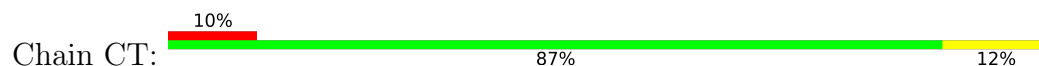
- Molecule 48: 60S ribosomal protein L8



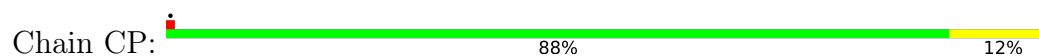
- Molecule 49: 60S ribosomal protein L18a



- Molecule 50: 60S ribosomal protein L21

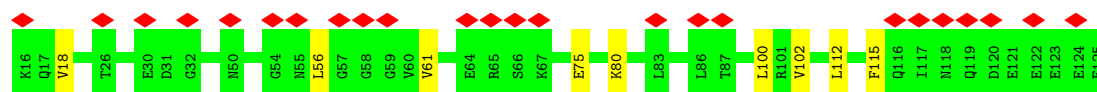


- Molecule 51: 60S ribosomal protein L17

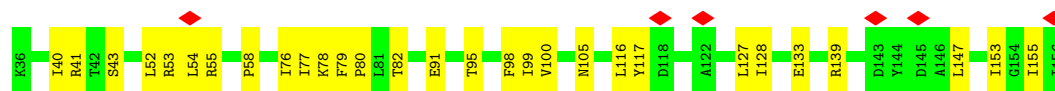
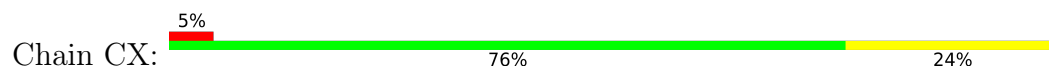


- Molecule 52: 60S ribosomal protein L22

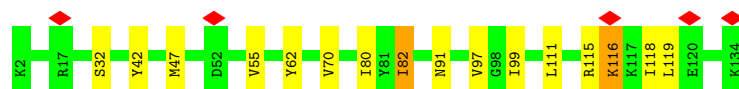




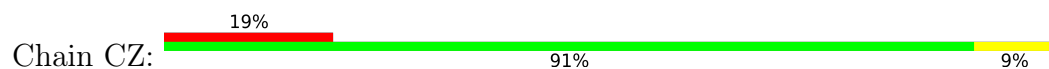
- Molecule 53: 60S ribosomal protein L23a



- Molecule 54: 60S ribosomal protein L26



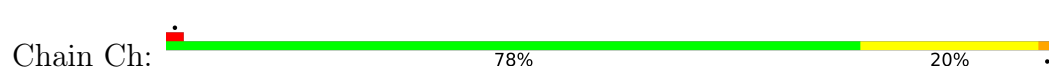
- Molecule 55: 60S ribosomal protein L27



- Molecule 56: 60S ribosomal protein L28

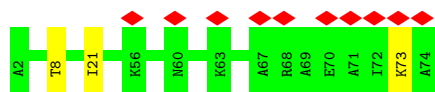


- Molecule 57: 60S ribosomal protein L35



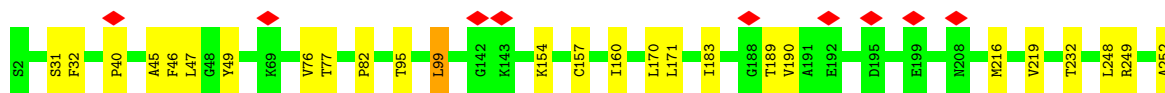
- Molecule 58: 60S ribosomal protein L29





- Molecule 59: 60S ribosomal protein L3

Chain CB: 88% 11%



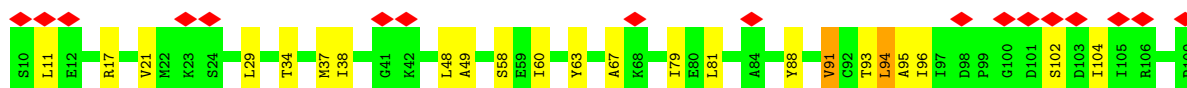
- Molecule 60: 60S ribosomal protein L7

Chain CF: 83% 16%



- Molecule 61: 60S ribosomal protein L30

Chain Cc: 17% 77% 21%



- Molecule 62: 60S ribosomal protein L31

Chain Cd: 6% 89% 10%



- Molecule 63: 60S ribosomal protein L32

Chain Ce: 85% 14%

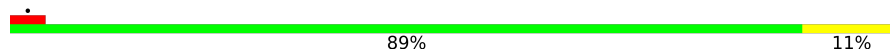


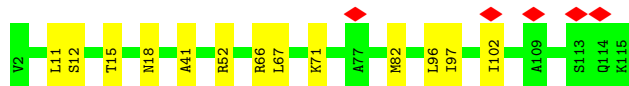
- Molecule 64: 60S ribosomal protein L35a

Chain Cf:  57% 37% 6%




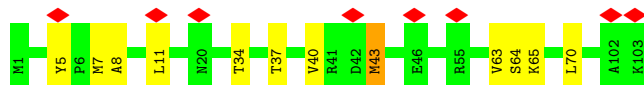
- Molecule 65: 60S ribosomal protein L34

Chain Cg:  89% 11%



- Molecule 66: 60S ribosomal protein L36

Chain Ci:  8% 88% 11%



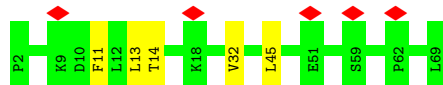
- Molecule 67: 60S ribosomal protein L37

Chain Cj:  93% 7%



- Molecule 68: 60S ribosomal protein L38

Chain Ck:  7% 93% 7%



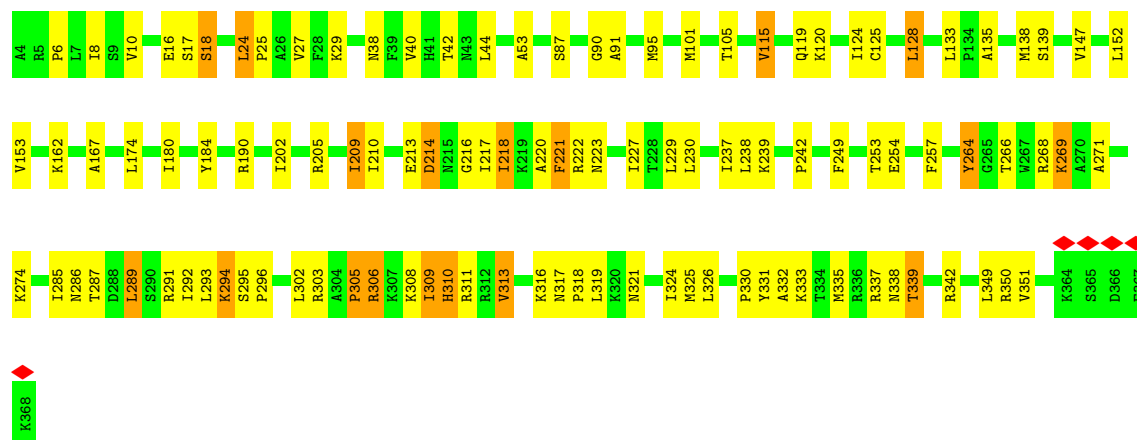
- Molecule 69: 60S ribosomal protein L39

Chain Cl:  94% 6%

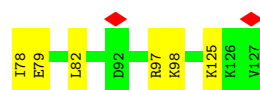
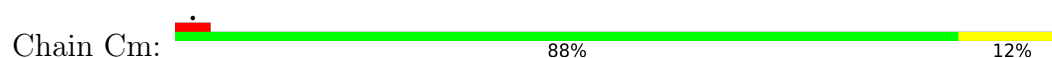


- Molecule 70: 60S ribosomal protein L4

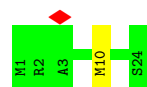
Chain CC:  70% 25% 5%



- Molecule 71: 60S ribosomal protein L40



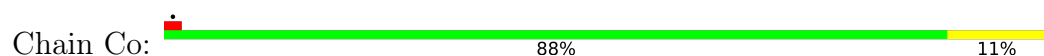
- Molecule 72: 60S ribosomal protein L41



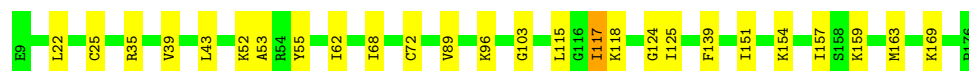
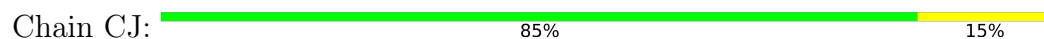
- Molecule 73: 60S ribosomal protein L37a



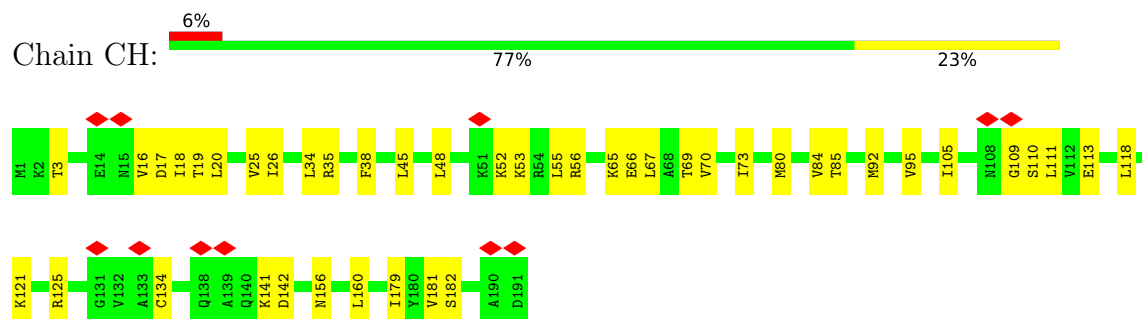
- Molecule 74: 60S ribosomal protein L36a



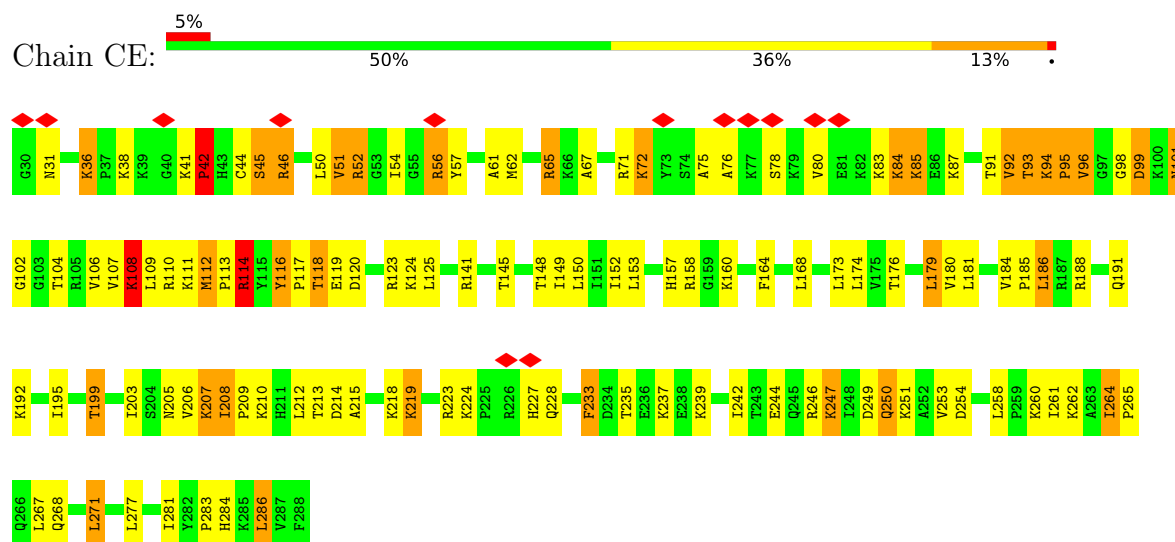
- Molecule 75: 60S ribosomal protein L11



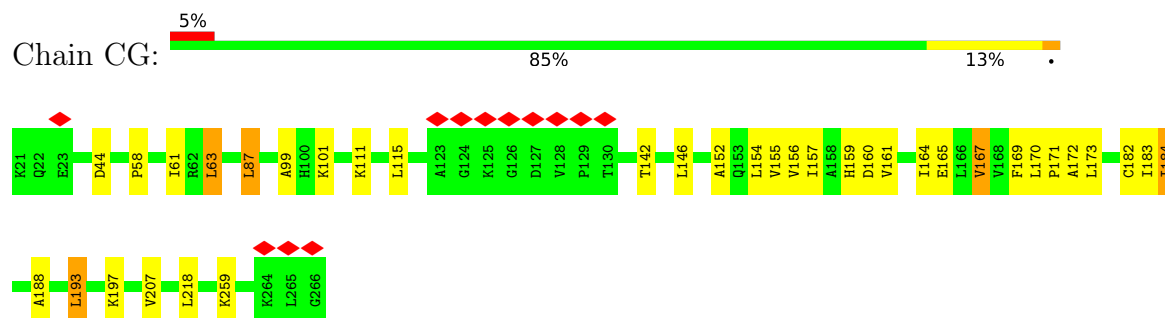
- Molecule 76: 60S ribosomal protein L9



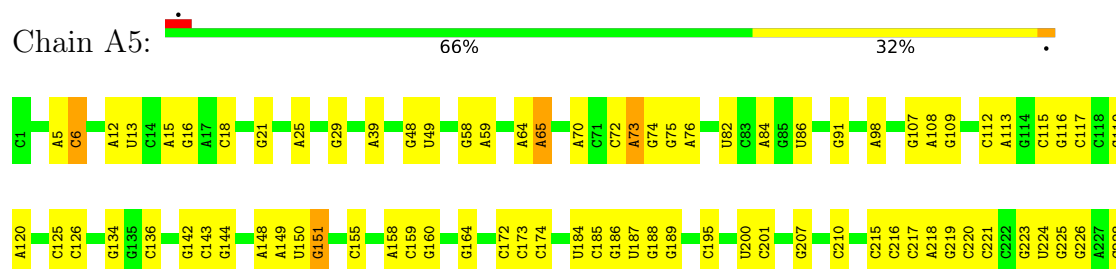
- Molecule 77: 60S ribosomal protein L6

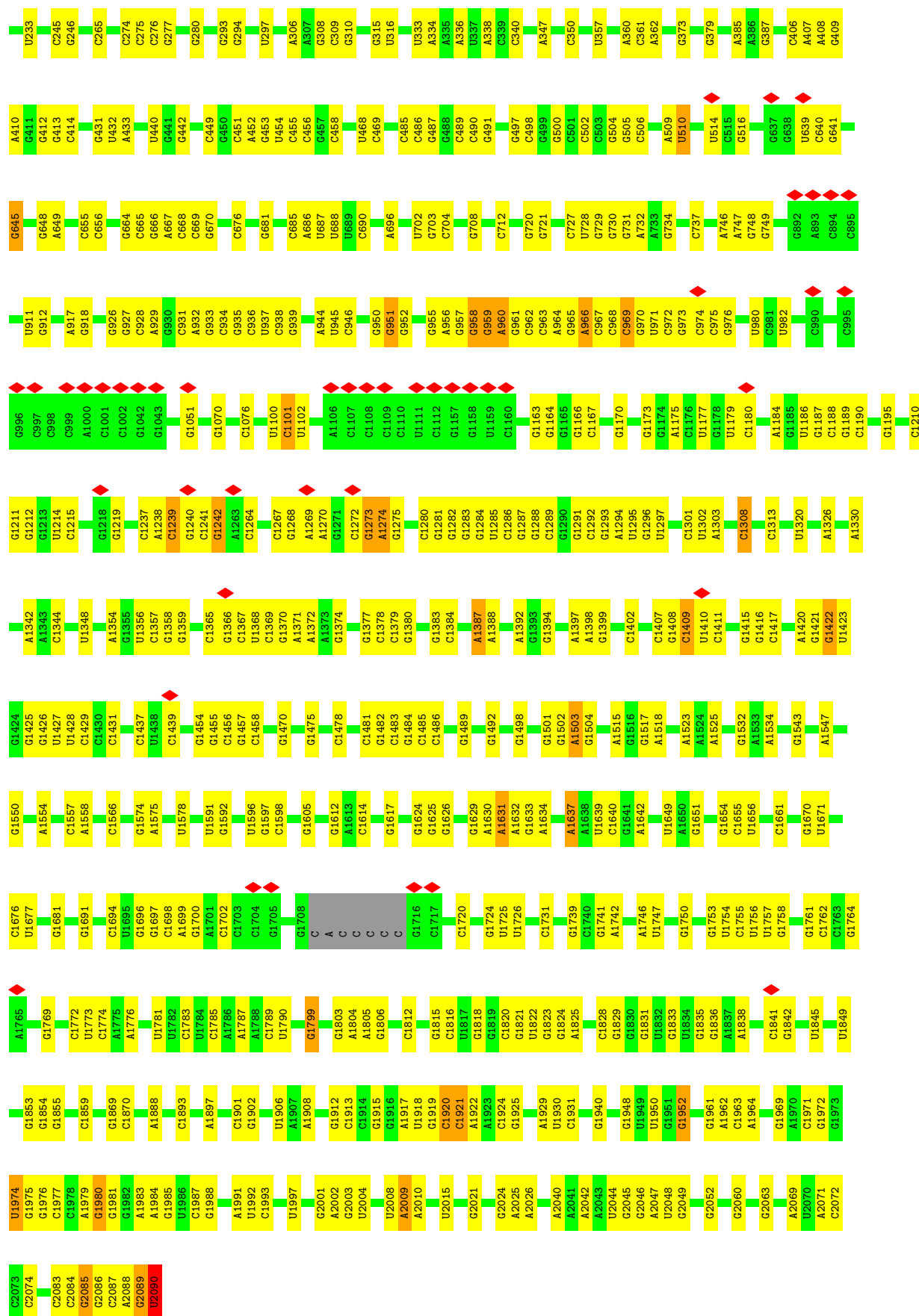


- Molecule 78: 60S ribosomal protein L7a




- Molecule 79: LSU-alpha rRNA (1722-MER)






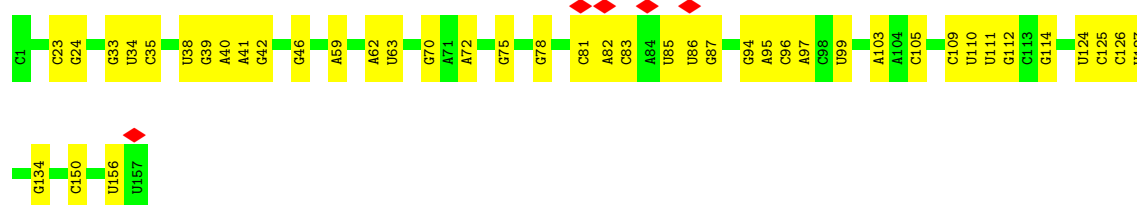
- Molecule 80: 5S rRNA (121-MER)

Chain A7:  77% 22%




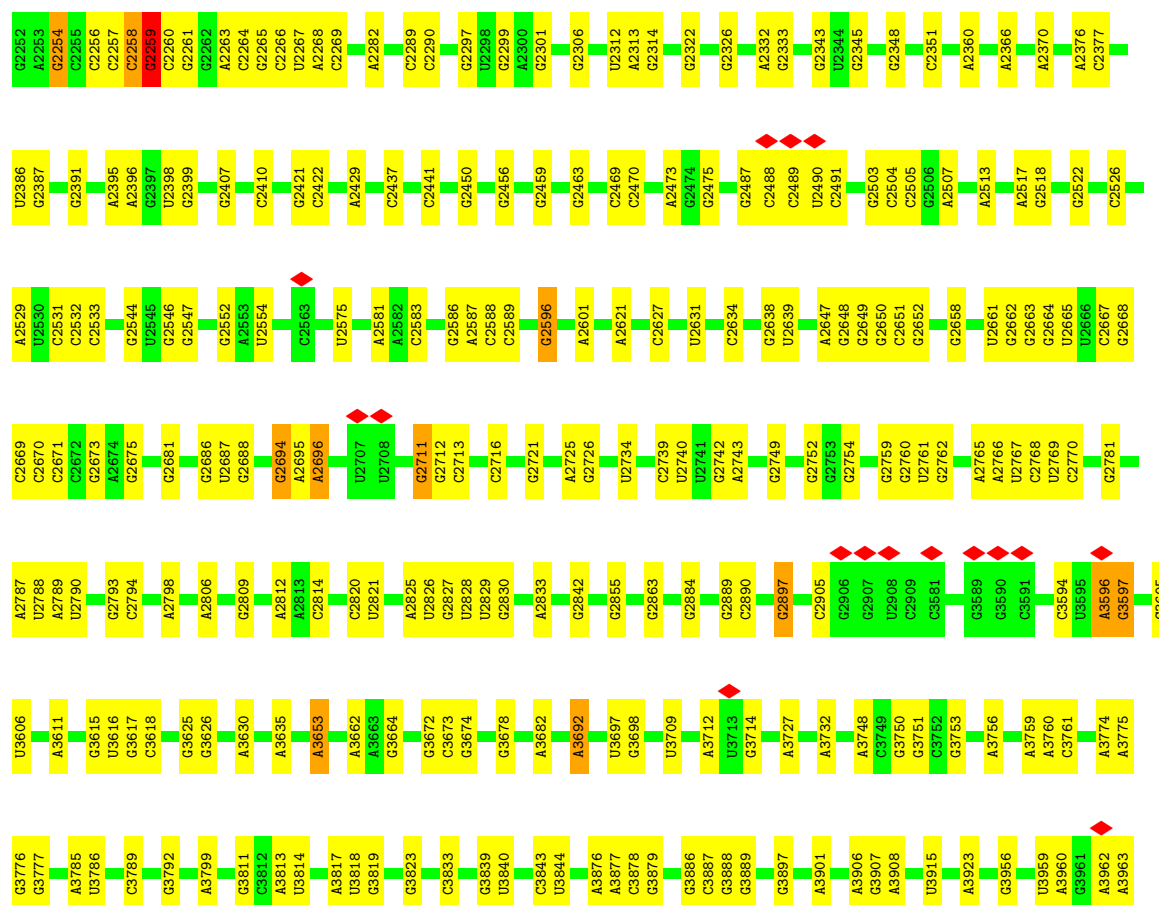
- Molecule 81: 5.8S rRNA (157-MER)

Chain A8:  73% 27%



- Molecule 82: LSU-beta rRNA (2069-MER)

Chain A6:  75% 24%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	295008	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.044	Depositor
Minimum map value	-0.015	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.006	Depositor
Map size (Å)	417.99997, 417.99997, 417.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: DDE

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	tR	0.15	0/1836	0.35	0/2859
2	Ct	0.32	1/6726 (0.0%)	0.64	8/9082 (0.1%)
3	AO	0.25	0/1025	0.58	0/1376
4	AX	0.26	0/1103	0.66	0/1474
5	AN	0.32	0/1226	0.66	0/1649
6	AL	0.30	0/1311	0.63	0/1751
7	AB	0.32	0/1753	0.69	1/2342 (0.0%)
8	AA	0.31	0/1679	0.74	1/2283 (0.0%)
9	AV	0.36	0/631	0.83	0/844
10	AY	0.24	0/1040	0.62	0/1382
11	Aa	0.22	0/836	0.50	0/1121
12	Ab	0.23	0/673	0.59	0/902
13	Ae	0.29	0/458	0.72	0/604
14	AJ	0.28	0/1504	0.63	0/2007
15	AE	0.34	1/2121 (0.0%)	0.62	2/2854 (0.1%)
16	AC	0.28	0/1745	0.62	0/2356
17	AG	0.25	0/1946	0.60	1/2590 (0.0%)
18	AH	0.27	0/1544	0.66	0/2068
19	AW	0.39	1/1051 (0.1%)	0.75	0/1406
20	AI	0.29	0/1715	0.67	2/2287 (0.1%)
21	B2	0.16	0/42094	0.40	9/65553 (0.0%)
22	CW	0.32	0/1030	0.65	0/1364
23	Ag	0.20	0/2493	0.48	0/3394
24	AU	0.37	0/832	0.84	1/1117 (0.1%)
25	AK	0.38	0/851	0.84	2/1147 (0.2%)
26	AM	0.31	0/951	0.70	1/1278 (0.1%)
27	AS	0.27	0/1157	0.66	1/1548 (0.1%)
28	Ad	0.27	0/455	0.59	0/603
29	AR	0.40	0/1031	0.83	2/1383 (0.1%)
30	AP	0.32	0/1055	0.79	3/1406 (0.2%)
31	AT	0.21	0/1119	0.54	0/1499
32	AZ	0.30	0/604	0.52	0/810

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Ac	0.25	0/508	0.55	0/680
34	AD	0.32	0/1793	0.72	2/2414 (0.1%)
35	Af	0.28	0/593	0.67	0/786
36	AF	0.31	0/1514	0.71	2/2034 (0.1%)
37	AQ	0.30	0/1142	0.62	0/1528
38	Cz	0.30	0/1693	0.66	0/2270
39	CO	0.33	0/1666	0.73	2/2228 (0.1%)
40	CL	0.31	0/1713	0.71	1/2293 (0.0%)
41	CV	0.26	0/997	0.67	0/1338
42	CM	0.29	0/1161	0.69	0/1552
43	Ca	0.28	0/1191	0.62	0/1591
44	CN	0.36	0/1746	0.69	0/2338
45	CI	0.30	0/1711	0.71	1/2285 (0.0%)
46	CD	0.26	0/2398	0.65	2/3210 (0.1%)
47	CQ	0.36	1/1545 (0.1%)	0.80	2/2062 (0.1%)
48	CA	0.31	0/1995	0.69	2/2674 (0.1%)
49	CS	0.30	0/1493	0.68	2/2003 (0.1%)
50	CT	0.32	0/1326	0.73	1/1770 (0.1%)
51	CP	0.28	0/1259	0.65	0/1689
52	CU	0.26	0/914	0.62	0/1226
53	CX	0.33	0/1011	0.71	0/1356
54	CY	0.30	0/1124	0.64	0/1494
55	CZ	0.22	0/1130	0.50	0/1507
56	Cr	0.65	0/1120	1.31	8/1497 (0.5%)
57	Ch	0.40	0/1031	0.76	0/1361
58	Cb	0.27	0/605	0.64	0/798
59	CB	0.28	0/3257	0.64	2/4359 (0.0%)
60	CF	0.32	0/1945	0.68	0/2589
61	Cc	0.30	0/787	0.68	0/1057
62	Cd	0.34	0/946	0.71	1/1272 (0.1%)
63	Ce	0.42	0/1088	0.73	0/1451
64	Cf	0.61	0/895	1.10	4/1198 (0.3%)
65	Cg	0.26	0/916	0.63	0/1220
66	Ci	0.31	0/851	0.75	0/1125
67	Cj	0.25	0/741	0.57	0/980
68	Ck	0.26	0/565	0.58	0/750
69	Cl	0.26	0/445	0.59	0/588
70	CC	0.52	0/2962	0.96	3/3977 (0.1%)
71	Cm	0.26	0/417	0.58	0/553
72	Cn	0.31	0/231	0.75	0/294
73	Cp	0.23	0/703	0.62	0/934
74	Co	0.37	0/864	0.77	1/1140 (0.1%)
75	CJ	0.26	0/1372	0.60	0/1836

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	CH	0.26	0/1545	0.58	0/2077
77	CE	0.60	0/2088	1.20	5/2792 (0.2%)
78	CG	0.28	0/2006	0.65	0/2697
79	A5	0.40	5/40404 (0.0%)	0.46	13/62957 (0.0%)
80	A7	0.16	0/2880	0.37	0/4489
81	A8	0.17	0/3723	0.41	0/5800
82	A6	0.40	1/48600 (0.0%)	0.40	4/75715 (0.0%)
83	CR	0.46	0/1596	1.06	7/2109 (0.3%)
All	All	0.33	10/241801 (0.0%)	0.55	99/354282 (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
3	AO	0	1
4	AX	0	2
8	AA	0	2
15	AE	0	1
16	AC	0	1
18	AH	0	3
22	CW	0	1
23	Ag	0	1
24	AU	0	2
25	AK	0	2
27	AS	0	1
29	AR	0	3
30	AP	0	3
34	AD	0	1
37	AQ	0	1
39	CO	0	3
42	CM	0	1
43	Ca	0	1
44	CN	0	1
47	CQ	0	1
48	CA	0	1
53	CX	0	1
56	Cr	0	9
64	Cf	0	2
67	Cj	0	1
70	CC	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
73	Cp	0	1
75	CJ	0	1
76	CH	0	2
77	CE	0	12
All	All	0	65

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	A6	2259	G	O5'-C5'	79.44	3.02	1.43
79	A5	2090	U	O4'-C1'	37.83	2.17	1.41
79	A5	2090	U	C4'-O4'	36.26	2.17	1.45
79	A5	2090	U	C2'-C1'	28.51	2.10	1.53
79	A5	2090	U	C3'-C2'	27.69	2.08	1.53

The worst 5 of 99 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
79	A5	1702	C	O5'-C5'-C4'	-18.76	82.66	110.80
21	B2	246	C	O5'-C5'-C4'	-18.66	82.82	110.80
82	A6	2259	G	P-O5'-C5'	12.48	158.33	120.90
82	A6	2259	G	O5'-C5'-C4'	10.25	131.00	110.50
2	Ct	837	GLU	CA-CB-CG	9.83	133.75	114.10

There are no chirality outliers.

5 of 65 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	AA	185	MET	Peptide
8	AA	31	ASP	Peptide
3	AO	137	SER	Peptide
4	AX	8	ARG	Sidechain
4	AX	98	ASP	Peptide

5.2 Too-close contacts

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	tR	1644	833	837	1	0
2	Ct	6619	6696	6701	64	0
3	AO	1012	1028	1028	17	0
4	AX	1085	1150	1151	12	0
5	AN	1202	1289	1289	11	0
6	AL	1288	1359	1362	13	0
7	AB	1727	1805	1810	18	0
8	AA	1642	1642	1646	30	0
9	AV	625	625	628	12	0
10	AY	1023	1088	1090	14	0
11	Aa	821	874	872	5	0
12	Ab	659	680	683	3	0
13	Ae	452	494	498	1	0
14	AJ	1480	1583	1592	13	0
15	AE	2079	2186	2186	29	0
16	AC	1709	1787	1793	24	0
17	AG	1923	2085	2089	18	0
18	AH	1521	1613	1616	22	0
19	AW	1034	1079	1080	10	0
20	AI	1686	1770	1772	13	0
21	B2	37676	18952	18977	60	0
22	CW	1015	1070	1079	4	0
23	Ag	2436	2388	2393	26	0
24	AU	822	886	887	18	0
25	AK	827	853	854	14	0
26	AM	941	962	963	20	0
27	AS	1139	1187	1191	11	0
28	Ad	445	442	442	4	0
29	AR	1019	1070	1075	17	0
30	AP	1037	1098	1098	5	0
31	AT	1101	1135	1135	13	0
32	AZ	598	652	656	11	0
33	Ac	506	536	536	10	0
34	AD	1765	1855	1865	34	0
35	Af	581	598	599	2	0
36	AF	1493	1545	1547	25	0
37	AQ	1124	1193	1193	10	0
38	Cz	1665	1769	1770	25	0
39	CO	1634	1776	1779	25	0
40	CL	1682	1789	1792	17	0
41	CV	983	1039	1042	14	0
42	CM	1139	1209	1209	18	0
43	Ca	1162	1210	1213	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	CN	1701	1747	1749	19	0
45	CI	1672	1711	1713	16	0
46	CD	2353	2370	2372	18	0
47	CQ	1521	1640	1640	29	0
48	CA	1957	2052	2055	19	0
49	CS	1453	1485	1490	14	0
50	CT	1298	1363	1366	12	0
51	CP	1233	1260	1263	12	0
52	CU	900	904	905	4	0
53	CX	994	1078	1079	14	0
54	CY	1107	1193	1193	9	0
55	CZ	1107	1182	1182	6	0
56	Cr	1104	1184	1189	53	0
57	Ch	1023	1159	1160	23	0
58	Cb	595	630	630	0	0
59	CB	3189	3316	3327	29	0
60	CF	1910	2046	2048	18	0
61	Cc	776	812	812	18	0
62	Cd	931	979	980	6	0
63	Ce	1070	1165	1165	11	0
64	Cf	876	910	912	25	0
65	Cg	906	999	999	9	0
66	Ci	840	925	929	5	0
67	Cj	726	764	764	2	0
68	Ck	559	624	624	2	0
69	Cl	435	472	472	2	0
70	CC	2908	3074	3082	74	0
71	Cm	411	446	445	3	0
72	Cn	230	274	276	3	0
73	Cp	693	747	747	3	0
74	Co	851	921	922	7	0
75	CJ	1349	1382	1383	11	0
76	CH	1526	1603	1605	21	0
77	CE	2050	2240	2244	90	0
78	CG	1973	2123	2128	23	0
79	A5	36163	18197	18215	86	0
80	A7	2578	1306	1306	3	0
81	A8	3334	1693	1693	3	0
82	A6	43496	21793	21810	107	0
83	CR	1580	0	1746	254	0
All	All	225399	166649	168638	1524	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 4.

The worst 5 of 1524 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)
79:A5:2090:U:C4'	79:A5:2090:U:C3'	2.02	1.34
79:A5:2090:U:C3'	79:A5:2090:U:C2'	2.08	1.30
79:A5:2090:U:C2'	79:A5:2090:U:C1'	2.10	1.28
83:CR:78:ILE:HA	83:CR:81:ARG:HD2	1.40	1.02
83:CR:24:LEU:HD12	83:CR:32:ILE:HG21	1.43	1.00

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	
2	Ct	842/847 (99%)	730 (87%)	98 (12%)	14 (2%)	7	28
3	AO	134/136 (98%)	109 (81%)	23 (17%)	2 (2%)	8	30
4	AX	137/139 (99%)	119 (87%)	16 (12%)	2 (2%)	8	30
5	AN	147/149 (99%)	127 (86%)	18 (12%)	2 (1%)	9	31
6	AL	155/157 (99%)	126 (81%)	28 (18%)	1 (1%)	21	50
7	AB	208/212 (98%)	181 (87%)	23 (11%)	4 (2%)	6	26
8	AA	206/208 (99%)	162 (79%)	40 (19%)	4 (2%)	6	26
9	AV	80/82 (98%)	61 (76%)	16 (20%)	3 (4%)	2	15
10	AY	124/126 (98%)	104 (84%)	18 (14%)	2 (2%)	7	29
11	Aa	100/102 (98%)	79 (79%)	19 (19%)	2 (2%)	6	25
12	Ab	82/84 (98%)	64 (78%)	16 (20%)	2 (2%)	4	22
13	Ae	55/57 (96%)	43 (78%)	8 (14%)	4 (7%)	1	5
14	AJ	176/178 (99%)	161 (92%)	11 (6%)	4 (2%)	5	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	AE	260/262 (99%)	220 (85%)	33 (13%)	7 (3%)	4	20
16	AC	218/220 (99%)	195 (89%)	21 (10%)	2 (1%)	14	42
17	AG	235/237 (99%)	209 (89%)	21 (9%)	5 (2%)	5	24
18	AH	187/189 (99%)	151 (81%)	24 (13%)	12 (6%)	1	7
19	AW	127/129 (98%)	108 (85%)	19 (15%)	0	100	100
20	AI	204/206 (99%)	165 (81%)	34 (17%)	5 (2%)	4	21
22	CW	122/124 (98%)	105 (86%)	14 (12%)	3 (2%)	4	21
23	Ag	311/313 (99%)	268 (86%)	39 (12%)	4 (1%)	9	33
24	AU	102/104 (98%)	84 (82%)	11 (11%)	7 (7%)	1	6
25	AK	96/98 (98%)	61 (64%)	24 (25%)	11 (12%)	0	2
26	AM	120/122 (98%)	87 (72%)	28 (23%)	5 (4%)	2	14
27	AS	135/137 (98%)	114 (84%)	19 (14%)	2 (2%)	8	30
28	Ad	51/53 (96%)	43 (84%)	8 (16%)	0	100	100
29	AR	124/126 (98%)	103 (83%)	15 (12%)	6 (5%)	2	11
30	AP	122/124 (98%)	98 (80%)	18 (15%)	6 (5%)	1	11
31	AT	139/141 (99%)	131 (94%)	7 (5%)	1 (1%)	18	47
32	AZ	73/75 (97%)	58 (80%)	14 (19%)	1 (1%)	9	31
33	Ac	62/64 (97%)	51 (82%)	11 (18%)	0	100	100
34	AD	225/227 (99%)	190 (84%)	28 (12%)	7 (3%)	3	18
35	Af	69/71 (97%)	44 (64%)	20 (29%)	5 (7%)	1	5
36	AF	184/188 (98%)	162 (88%)	20 (11%)	2 (1%)	11	38
37	AQ	139/141 (99%)	114 (82%)	21 (15%)	4 (3%)	3	19
38	Cz	205/207 (99%)	165 (80%)	35 (17%)	5 (2%)	4	22
39	CO	197/199 (99%)	183 (93%)	12 (6%)	2 (1%)	12	40
40	CL	206/208 (99%)	171 (83%)	30 (15%)	5 (2%)	4	22
41	CV	130/132 (98%)	118 (91%)	12 (9%)	0	100	100
42	CM	137/139 (99%)	118 (86%)	17 (12%)	2 (2%)	8	30
43	Ca	145/147 (99%)	117 (81%)	24 (17%)	4 (3%)	4	19
44	CN	201/203 (99%)	175 (87%)	24 (12%)	2 (1%)	12	40
45	CI	203/207 (98%)	171 (84%)	30 (15%)	2 (1%)	12	40
46	CD	287/289 (99%)	244 (85%)	37 (13%)	6 (2%)	5	24

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
47	CQ	186/188 (99%)	158 (85%)	26 (14%)	2 (1%)	11	38
48	CA	253/255 (99%)	215 (85%)	37 (15%)	1 (0%)	30	59
49	CS	173/175 (99%)	142 (82%)	27 (16%)	4 (2%)	5	23
50	CT	157/159 (99%)	138 (88%)	16 (10%)	3 (2%)	6	26
51	CP	150/152 (99%)	133 (89%)	15 (10%)	2 (1%)	9	33
52	CU	108/110 (98%)	96 (89%)	12 (11%)	0	100	100
53	CX	119/121 (98%)	101 (85%)	15 (13%)	3 (2%)	4	21
54	CY	131/133 (98%)	120 (92%)	11 (8%)	0	100	100
55	CZ	133/135 (98%)	116 (87%)	16 (12%)	1 (1%)	16	44
56	Cr	135/137 (98%)	92 (68%)	28 (21%)	15 (11%)	0	2
57	Ch	121/123 (98%)	104 (86%)	14 (12%)	3 (2%)	4	21
58	Cb	71/73 (97%)	62 (87%)	8 (11%)	1 (1%)	9	31
59	CB	393/395 (100%)	349 (89%)	37 (9%)	7 (2%)	6	26
60	CF	227/229 (99%)	200 (88%)	22 (10%)	5 (2%)	5	24
61	Cc	98/100 (98%)	89 (91%)	8 (8%)	1 (1%)	12	40
62	Cd	111/113 (98%)	92 (83%)	17 (15%)	2 (2%)	6	26
63	Ce	128/130 (98%)	108 (84%)	16 (12%)	4 (3%)	3	18
64	Cf	107/109 (98%)	85 (79%)	18 (17%)	4 (4%)	2	16
65	Cg	112/114 (98%)	95 (85%)	17 (15%)	0	100	100
66	Ci	101/103 (98%)	88 (87%)	9 (9%)	4 (4%)	2	15
67	Cj	87/89 (98%)	76 (87%)	10 (12%)	1 (1%)	11	38
68	Ck	66/68 (97%)	61 (92%)	4 (6%)	1 (2%)	8	30
69	Cl	47/49 (96%)	42 (89%)	4 (8%)	1 (2%)	5	24
70	CC	363/365 (100%)	276 (76%)	62 (17%)	25 (7%)	1	6
71	Cm	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
72	Cn	22/24 (92%)	22 (100%)	0	0	100	100
73	Cp	87/89 (98%)	75 (86%)	11 (13%)	1 (1%)	11	38
74	Co	102/104 (98%)	79 (78%)	19 (19%)	4 (4%)	2	15
75	CJ	166/168 (99%)	150 (90%)	15 (9%)	1 (1%)	21	50
76	CH	189/191 (99%)	167 (88%)	21 (11%)	1 (0%)	24	54
77	CE	250/254 (98%)	156 (62%)	67 (27%)	27 (11%)	0	2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
78	CG	244/246 (99%)	198 (81%)	41 (17%)	5 (2%)	6	25
83	CR	187/189 (99%)	164 (88%)	19 (10%)	4 (2%)	5	24
All	All	12334/12499 (99%)	10384 (84%)	1648 (13%)	302 (2%)	7	22

5 of 302 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	Ct	333	LYS
2	Ct	345	PRO
2	Ct	443	TYR
2	Ct	716	ARG
3	AO	56	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	Ct	722/722 (100%)	698 (97%)	24 (3%)	33	57
3	AO	105/106 (99%)	100 (95%)	5 (5%)	23	50
4	AX	112/112 (100%)	109 (97%)	3 (3%)	39	60
5	AN	130/130 (100%)	127 (98%)	3 (2%)	44	63
6	AL	141/141 (100%)	134 (95%)	7 (5%)	22	49
7	AB	194/194 (100%)	189 (97%)	5 (3%)	40	61
8	AA	174/174 (100%)	168 (97%)	6 (3%)	32	57
9	AV	66/66 (100%)	64 (97%)	2 (3%)	36	59
10	AY	108/108 (100%)	100 (93%)	8 (7%)	13	38
11	Aa	89/89 (100%)	87 (98%)	2 (2%)	45	63
12	Ab	76/76 (100%)	76 (100%)	0	100	100
13	Ae	46/46 (100%)	45 (98%)	1 (2%)	45	63
14	AJ	157/157 (100%)	153 (98%)	4 (2%)	42	62
15	AE	225/225 (100%)	219 (97%)	6 (3%)	39	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
16	AC	186/186 (100%)	178 (96%)	8 (4%)	26	51	
17	AG	207/207 (100%)	194 (94%)	13 (6%)	16	42	
18	AH	169/169 (100%)	164 (97%)	5 (3%)	36	59	
19	AW	112/112 (100%)	108 (96%)	4 (4%)	31	56	
20	AI	178/178 (100%)	172 (97%)	6 (3%)	32	57	
22	CW	103/103 (100%)	97 (94%)	6 (6%)	18	45	
23	Ag	272/272 (100%)	266 (98%)	6 (2%)	45	63	
24	AU	94/94 (100%)	91 (97%)	3 (3%)	34	58	
25	AK	89/89 (100%)	88 (99%)	1 (1%)	65	74	
26	AM	102/102 (100%)	90 (88%)	12 (12%)	5	20	
27	AS	119/119 (100%)	114 (96%)	5 (4%)	26	52	
28	Ad	47/47 (100%)	47 (100%)	0	100	100	
29	AR	114/114 (100%)	107 (94%)	7 (6%)	17	43	
30	AP	114/114 (100%)	106 (93%)	8 (7%)	14	40	
31	AT	112/112 (100%)	110 (98%)	2 (2%)	51	67	
32	AZ	66/66 (100%)	64 (97%)	2 (3%)	36	59	
33	Ac	57/57 (100%)	56 (98%)	1 (2%)	51	67	
34	AD	190/190 (100%)	183 (96%)	7 (4%)	30	55	
35	Af	64/64 (100%)	63 (98%)	1 (2%)	55	68	
36	AF	160/160 (100%)	150 (94%)	10 (6%)	16	42	
37	AQ	117/117 (100%)	116 (99%)	1 (1%)	70	76	
38	Cz	185/186 (100%)	177 (96%)	8 (4%)	26	51	
39	CO	171/171 (100%)	159 (93%)	12 (7%)	14	40	
40	CL	174/174 (100%)	169 (97%)	5 (3%)	37	60	
41	CV	102/102 (100%)	100 (98%)	2 (2%)	48	65	
42	CM	118/118 (100%)	112 (95%)	6 (5%)	21	48	
43	Ca	120/120 (100%)	116 (97%)	4 (3%)	33	57	
44	CN	171/171 (100%)	164 (96%)	7 (4%)	27	52	
45	CI	177/177 (100%)	174 (98%)	3 (2%)	53	67	
46	CD	243/243 (100%)	234 (96%)	9 (4%)	30	55	
47	CQ	165/165 (100%)	161 (98%)	4 (2%)	43	62	

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	CA	197/197 (100%)	193 (98%)	4 (2%)	48	65
49	CS	156/156 (100%)	148 (95%)	8 (5%)	21	48
50	CT	139/139 (100%)	136 (98%)	3 (2%)	45	63
51	CP	133/133 (100%)	131 (98%)	2 (2%)	57	69
52	CU	99/100 (99%)	97 (98%)	2 (2%)	48	65
53	CX	109/109 (100%)	101 (93%)	8 (7%)	13	39
54	CY	123/123 (100%)	117 (95%)	6 (5%)	22	49
55	CZ	117/117 (100%)	113 (97%)	4 (3%)	32	57
56	Cr	121/121 (100%)	106 (88%)	15 (12%)	4	18
57	Ch	110/110 (100%)	105 (96%)	5 (4%)	24	51
58	Cb	61/61 (100%)	59 (97%)	2 (3%)	33	57
59	CB	344/344 (100%)	333 (97%)	11 (3%)	34	58
60	CF	198/198 (100%)	190 (96%)	8 (4%)	28	53
61	Cc	85/85 (100%)	82 (96%)	3 (4%)	32	56
62	Cd	102/102 (100%)	101 (99%)	1 (1%)	68	75
63	Ce	116/116 (100%)	113 (97%)	3 (3%)	40	61
64	Cf	88/88 (100%)	77 (88%)	11 (12%)	4	18
65	Cg	98/98 (100%)	95 (97%)	3 (3%)	35	59
66	Ci	87/87 (100%)	84 (97%)	3 (3%)	32	57
67	Cj	74/74 (100%)	72 (97%)	2 (3%)	39	60
68	Ck	63/63 (100%)	63 (100%)	0	100	100
69	Cl	46/46 (100%)	46 (100%)	0	100	100
70	CC	304/304 (100%)	286 (94%)	18 (6%)	18	44
71	Cm	46/46 (100%)	42 (91%)	4 (9%)	9	32
72	Cn	23/23 (100%)	23 (100%)	0	100	100
73	Cp	73/73 (100%)	73 (100%)	0	100	100
74	Co	92/92 (100%)	90 (98%)	2 (2%)	45	63
75	CJ	142/142 (100%)	135 (95%)	7 (5%)	22	49
76	CH	170/170 (100%)	161 (95%)	9 (5%)	20	47
77	CE	225/225 (100%)	195 (87%)	30 (13%)	4	15
78	CG	209/209 (100%)	199 (95%)	10 (5%)	23	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
83	CR	168/168 (100%)	158 (94%)	10 (6%)	17	43
All	All	10761/10764 (100%)	10323 (96%)	438 (4%)	28	52

5 of 438 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	CD	27	LYS
56	Cr	41	ASN
77	CE	145	THR
46	CD	258	LYS
51	CP	95	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such sidechains are listed below:

Mol	Chain	Res	Type
46	CD	202	GLN
52	CU	27	HIS
83	CR	178	GLN
47	CQ	160	HIS
49	CS	162	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	tR	76/77 (98%)	34 (44%)	0
21	B2	1747/1786 (97%)	431 (24%)	52 (2%)
79	A5	1657/1722 (96%)	527 (31%)	84 (5%)
80	A7	120/121 (99%)	25 (20%)	1 (0%)
81	A8	156/157 (99%)	39 (25%)	6 (3%)
82	A6	2003/2069 (96%)	450 (22%)	61 (3%)
All	All	5759/5932 (97%)	1506 (26%)	204 (3%)

5 of 1506 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	tR	3	C
1	tR	5	G
1	tR	6	G
1	tR	7	G
1	tR	8	U

5 of 204 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
79	A5	1398	A
82	A6	2256	C
82	A6	4937	C
79	A5	1455	G
79	A5	1921	C

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

1 non-standard protein/DNA/RNA residue is 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
2	DDE	Ct	715	2	18,20,21	1.12	2 (11%)	17,28,30	0.92	1 (5%)

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
2	DDE	Ct	715	2	-	6/20/21/23	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	Ct	715	DDE	CD2-CG	2.58	1.41	1.36
2	Ct	715	DDE	CBW-CBI	2.12	1.57	1.53

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Ct	715	DDE	CAU-CBW-CBI	-2.37	106.58	111.22

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	Ct	715	DDE	CA-CB-CG-ND1
2	Ct	715	DDE	NAD-CBI-CBW-NCB
2	Ct	715	DDE	OAG-CBI-CBW-CAU
2	Ct	715	DDE	CAT-CAU-CBW-NCB
2	Ct	715	DDE	CAT-CAU-CBW-CBI

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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
21	B2	9
79	A5	9
82	A6	4
7	AB	1
45	CI	1
77	CE	1
2	Ct	1
36	AF	1

The worst 5 of 27 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B2	757:C	O3'	783:C	P	20.08
1	A5	1112:C	O3'	1157:G	P	20.00
1	A5	1439:C	O3'	1447:C	P	19.55
1	A6	3987:C	O3'	4011:G	P	18.44
1	B2	250:U	O3'	267:G	P	18.43

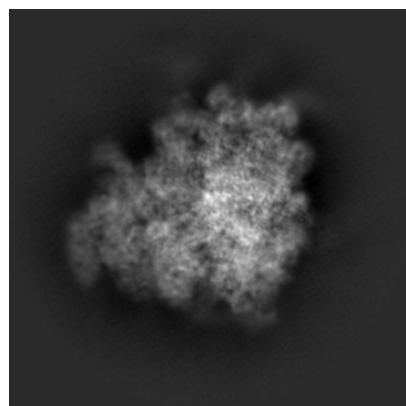
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72475. These allow visual inspection of the internal detail of the map and identification of artifacts.

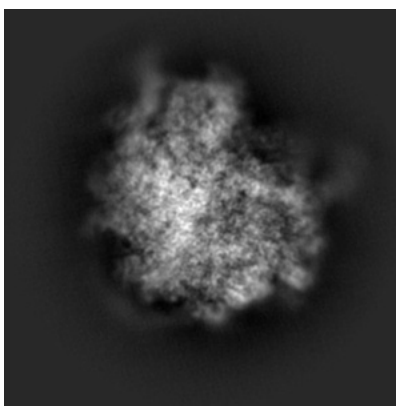
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

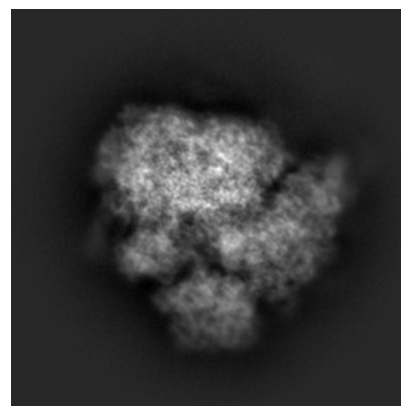
6.1.1 Primary map



X

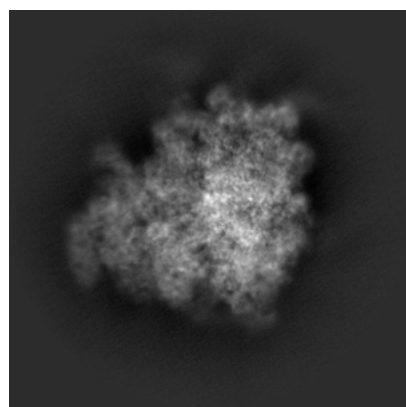


Y

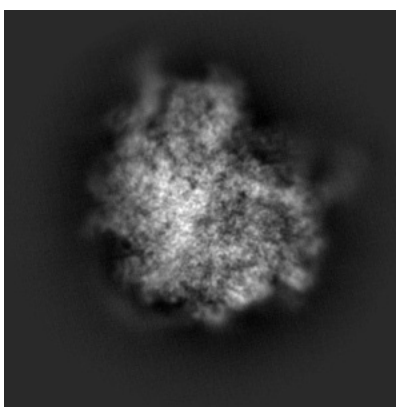


Z

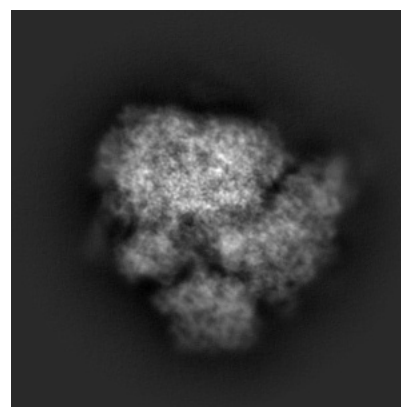
6.1.2 Raw map



X



Y

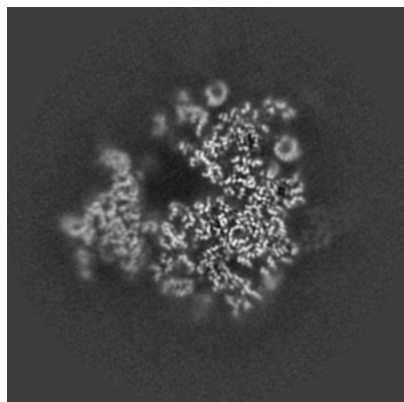


Z

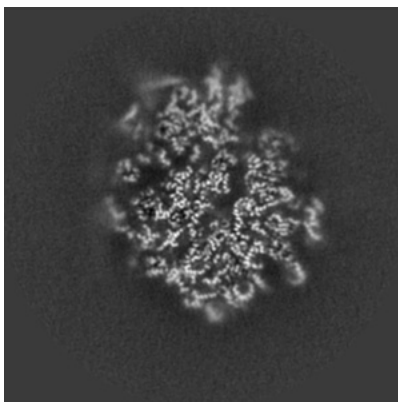
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

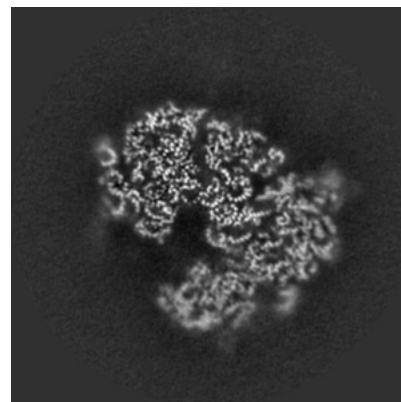
6.2.1 Primary map



X Index: 200

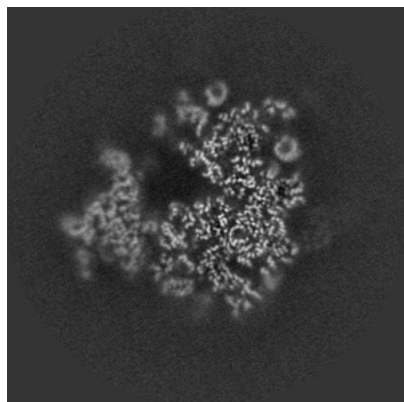


Y Index: 200

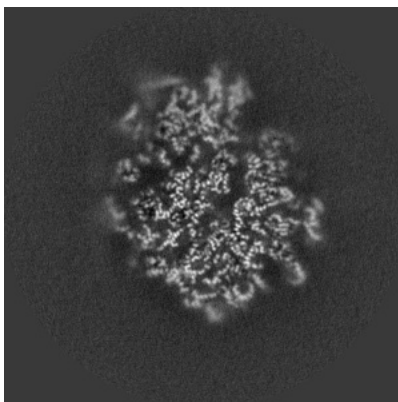


Z Index: 200

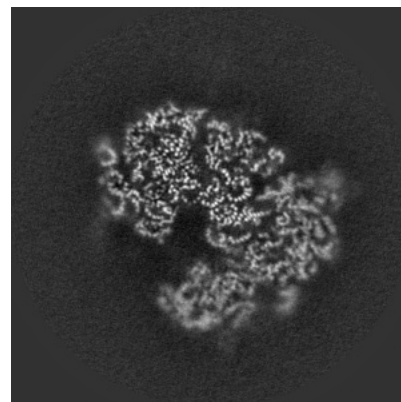
6.2.2 Raw map



X Index: 200



Y Index: 200

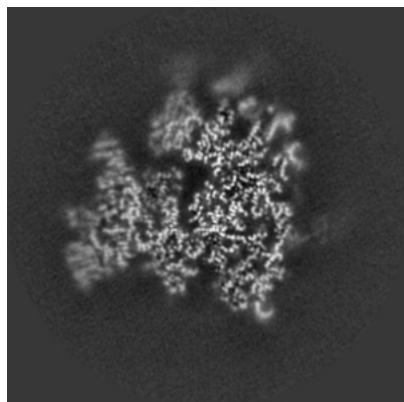


Z Index: 200

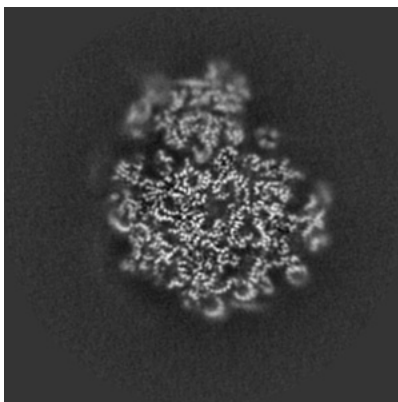
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

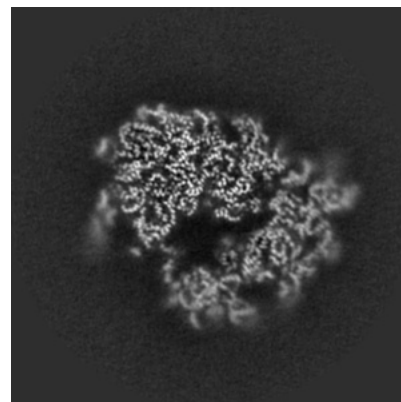
6.3.1 Primary map



X Index: 217

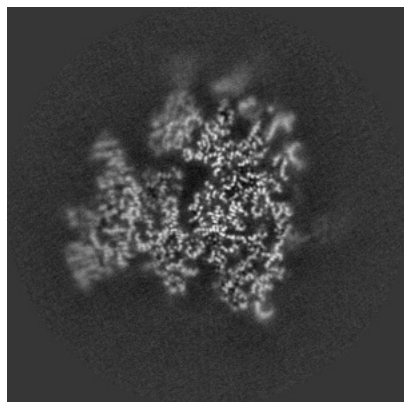


Y Index: 207

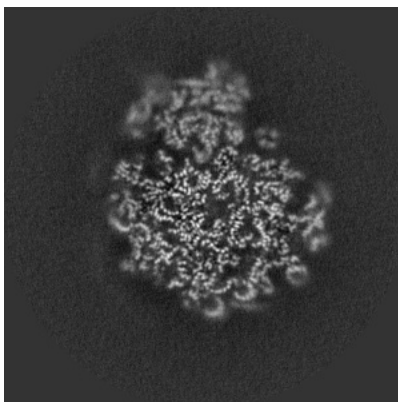


Z Index: 210

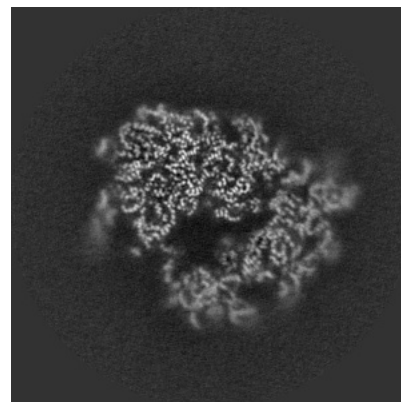
6.3.2 Raw map



X Index: 217



Y Index: 207

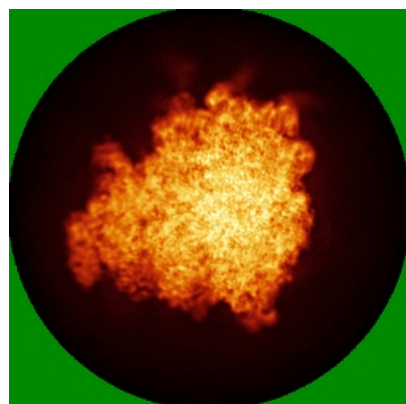


Z Index: 210

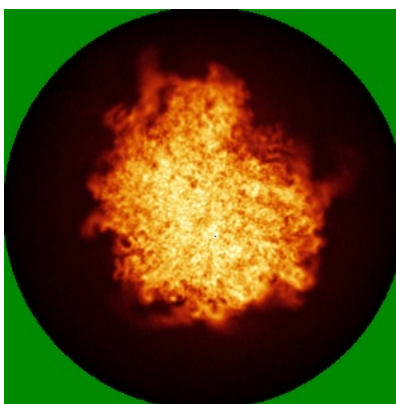
The images above show the largest variance slices of the map in three orthogonal directions.

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

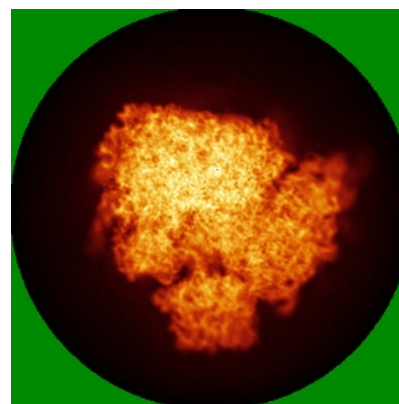
6.4.1 Primary map



X

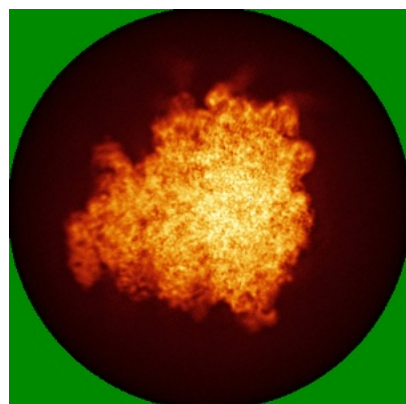


Y

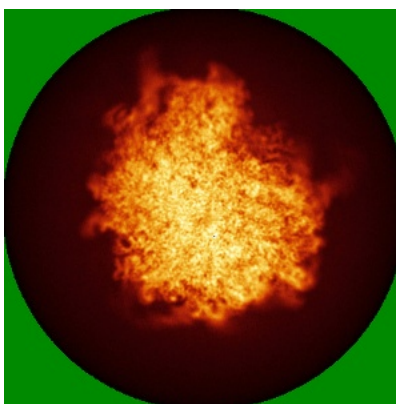


Z

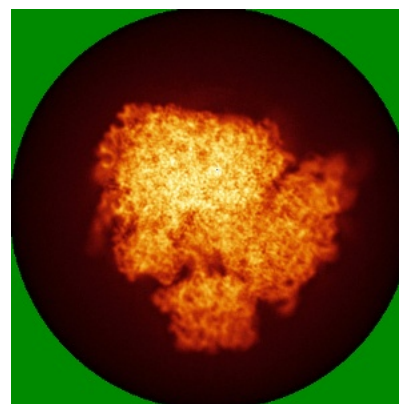
6.4.2 Raw map



X



Y

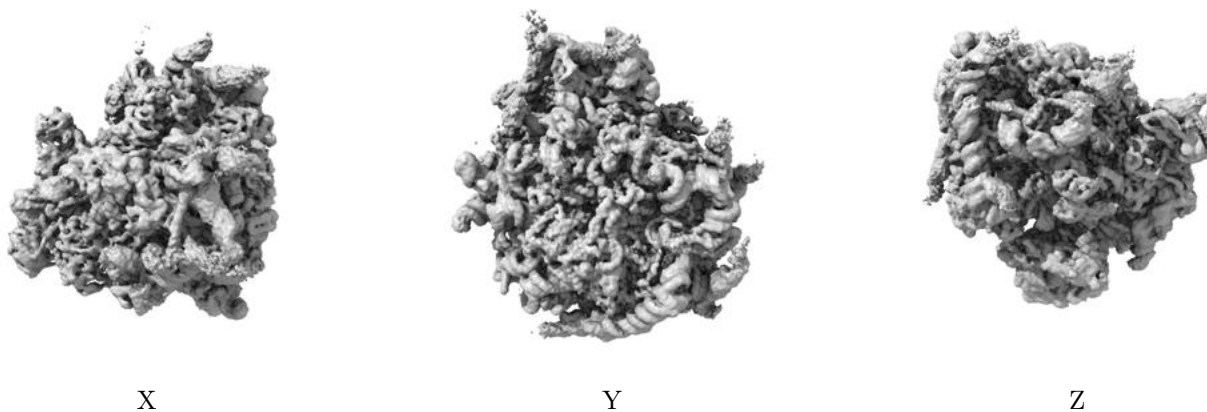


Z

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

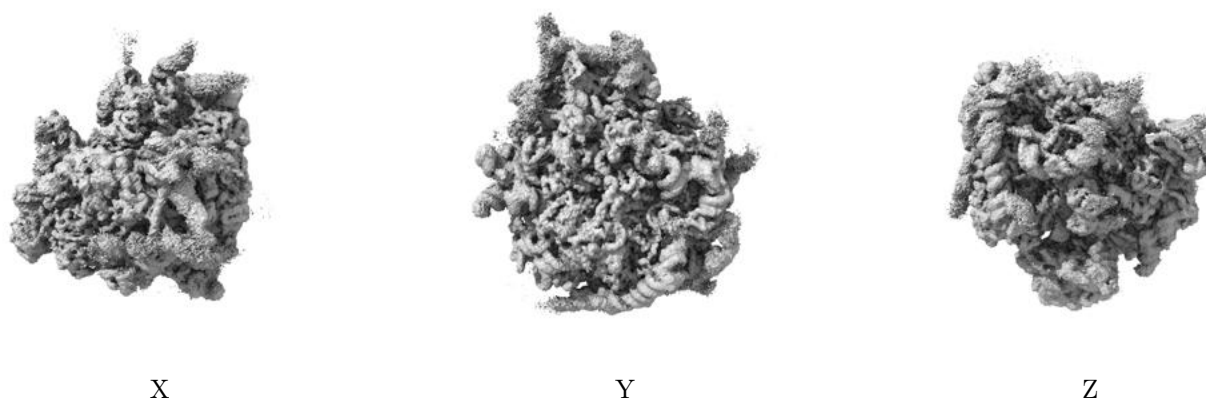
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.006. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

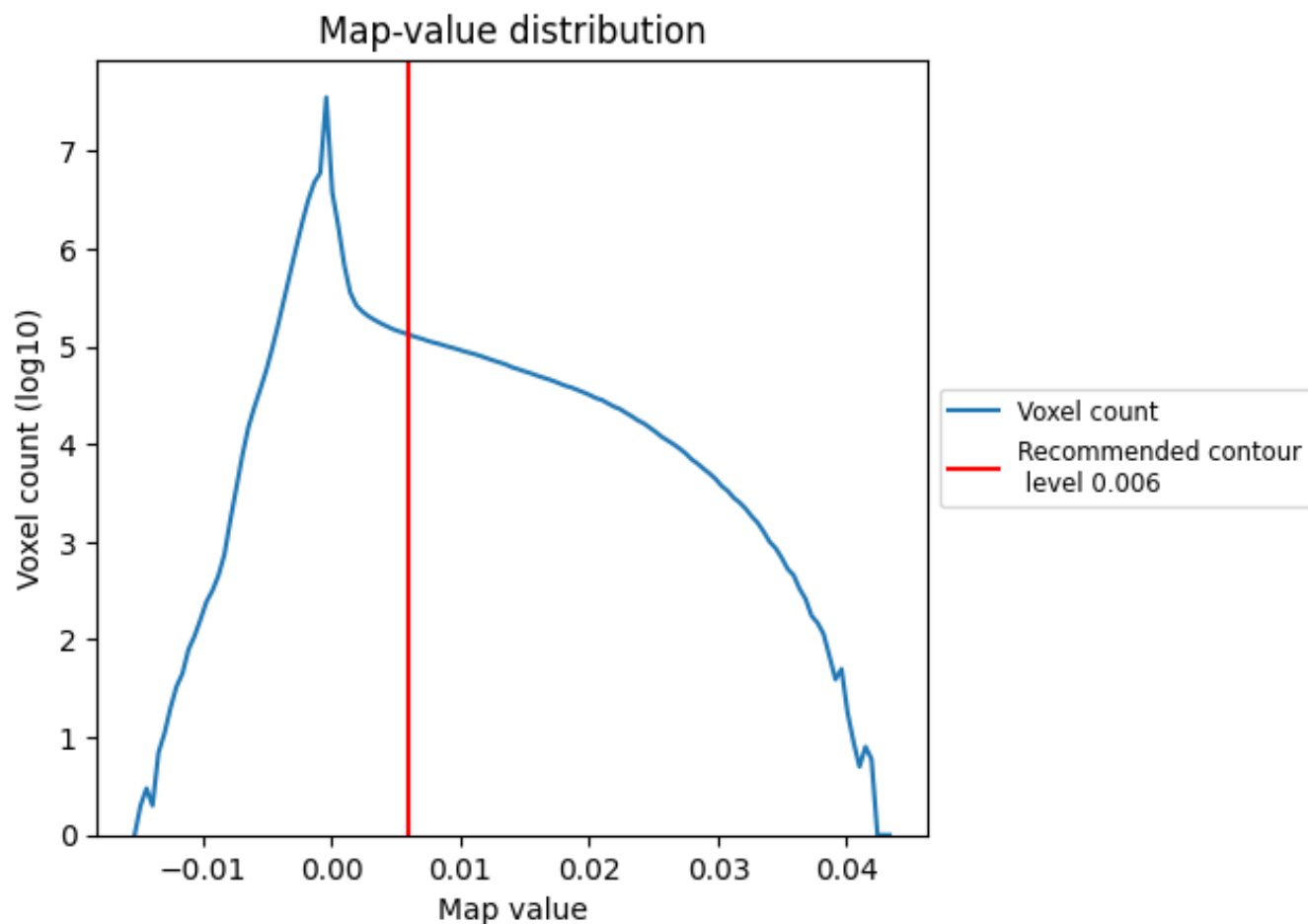
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

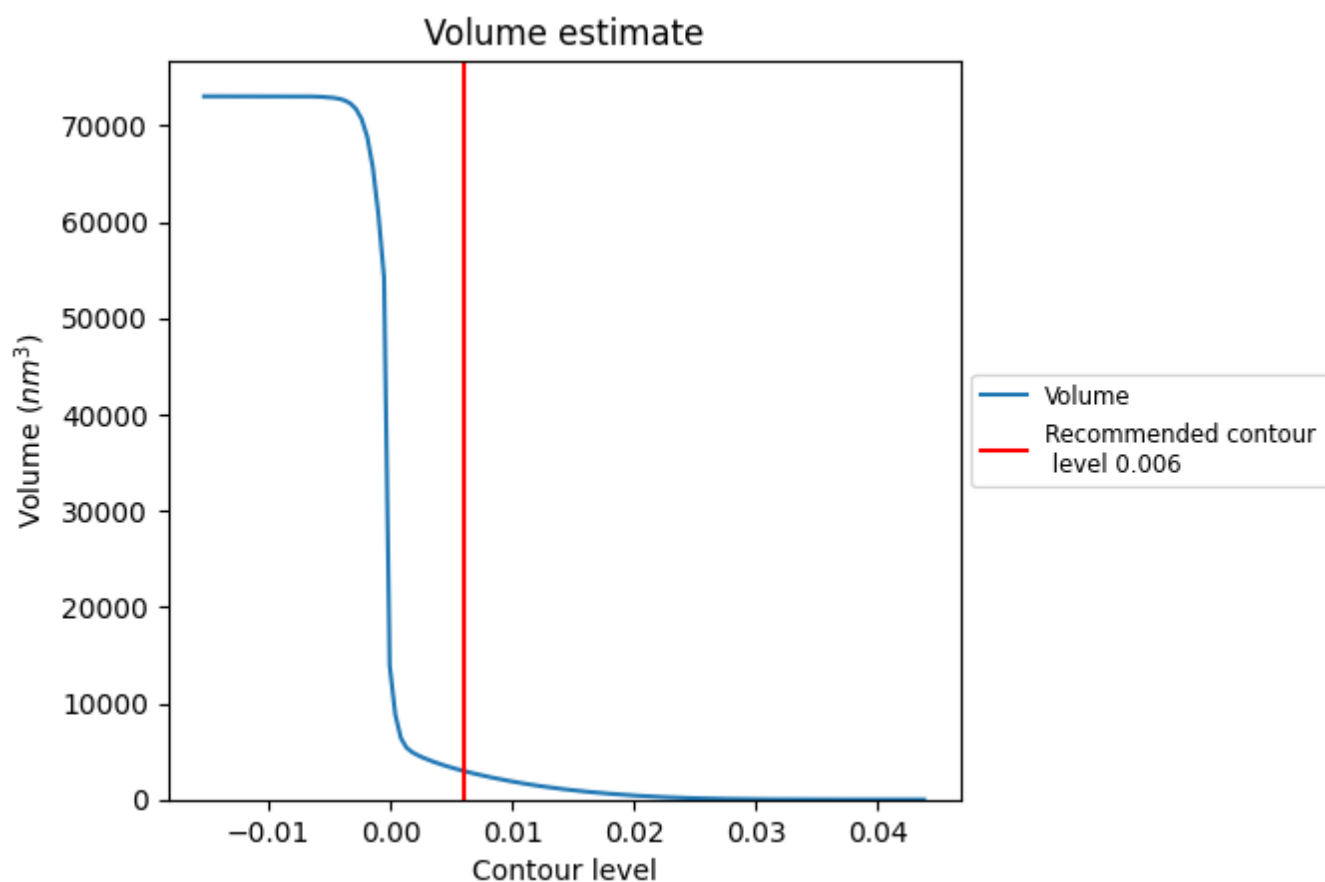
This section contains the results of statistical analysis of the map.

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.

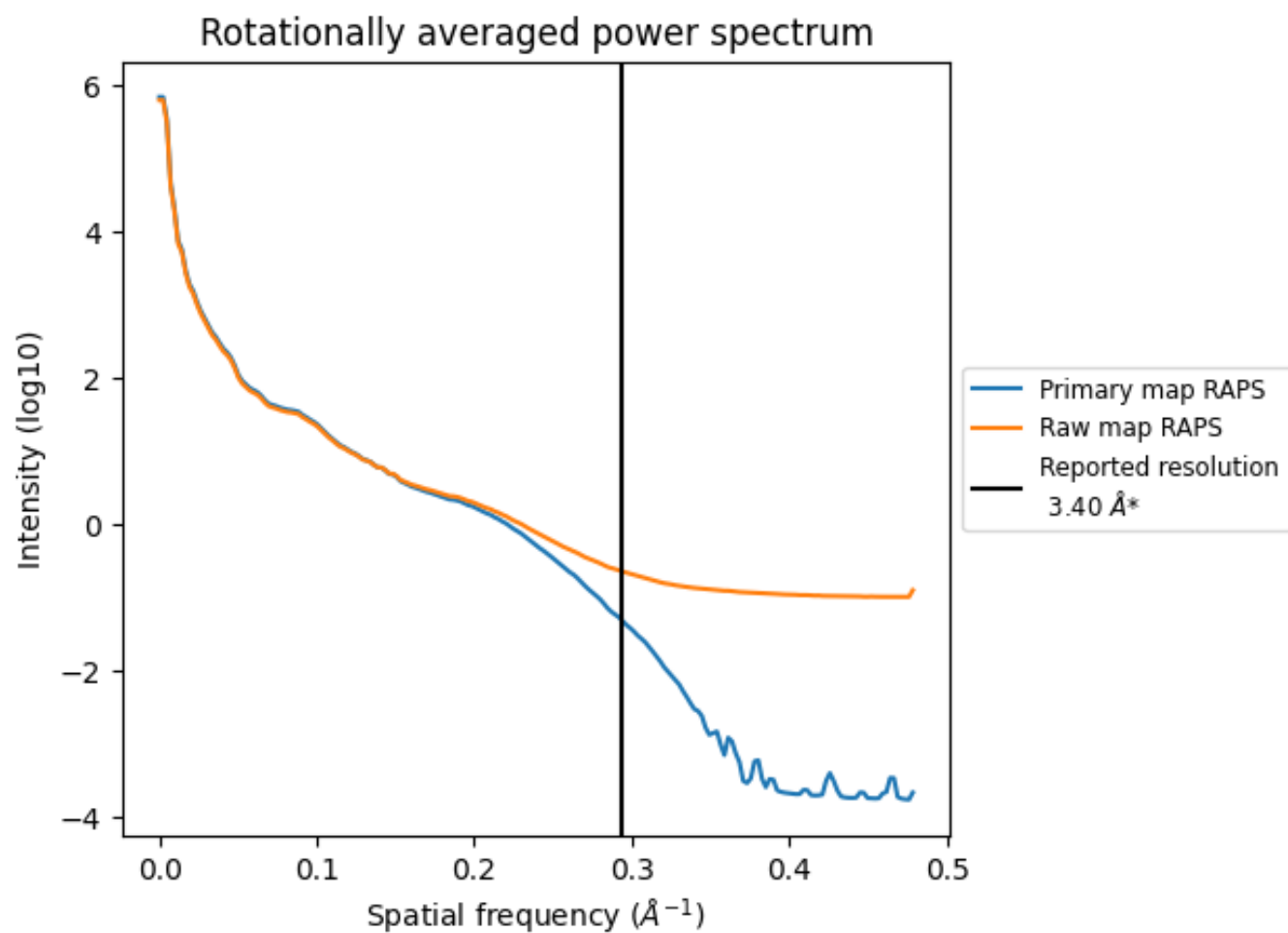
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2972 nm³; this corresponds to an approximate mass of 2685 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

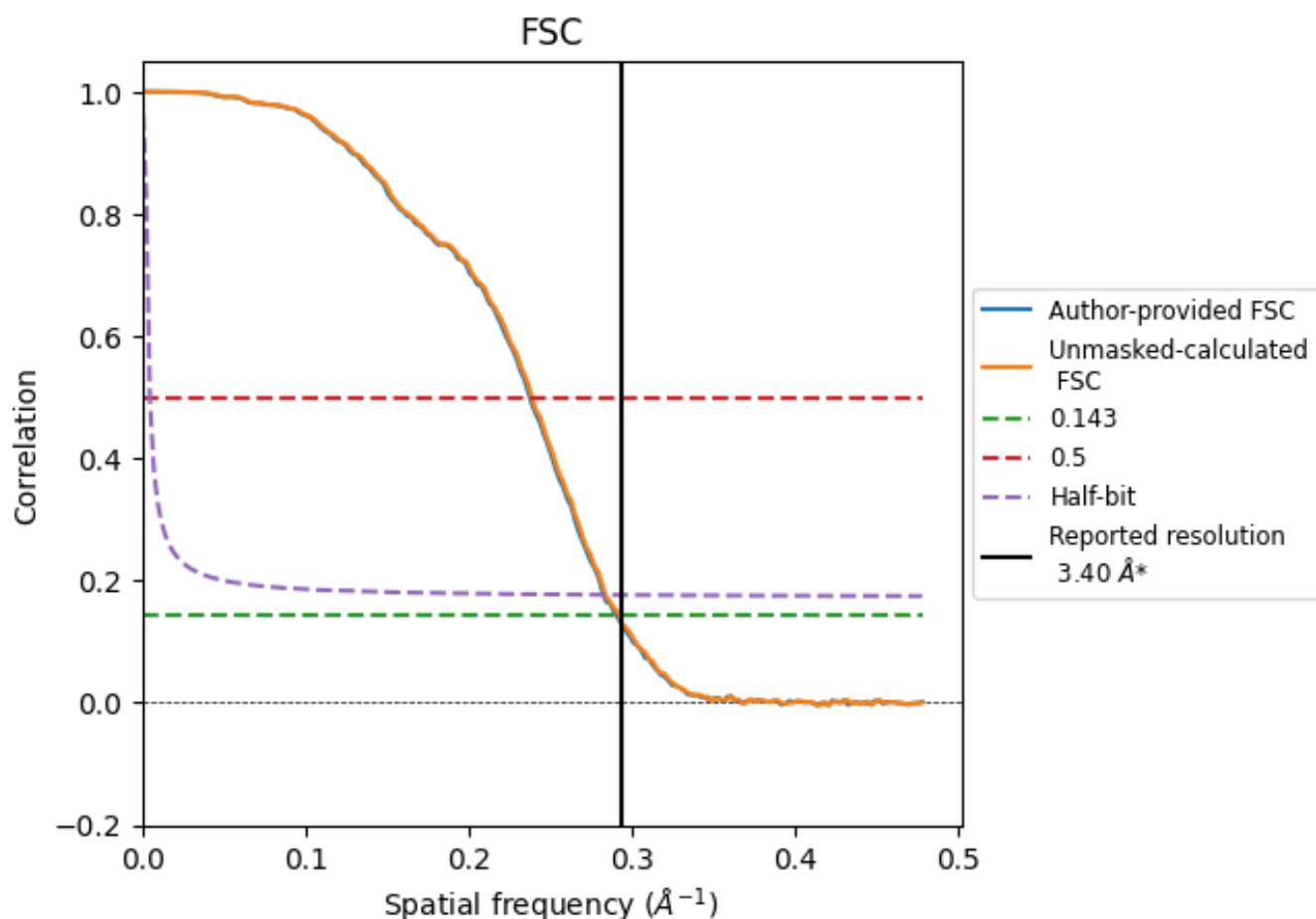


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

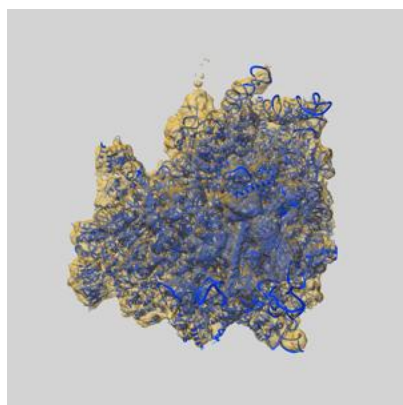
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.44	4.20	3.53
Unmasked-calculated*	3.42	4.18	3.52

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

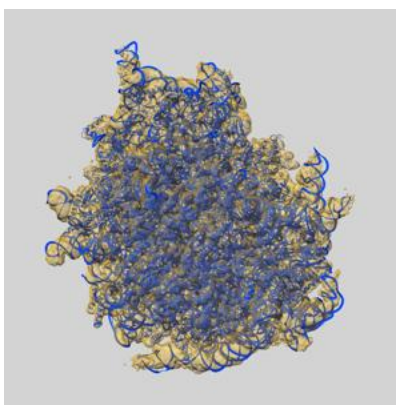
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-72475 and PDB model 9Y49. Per-residue inclusion information can be found in [section 3](#) on [page 19](#).

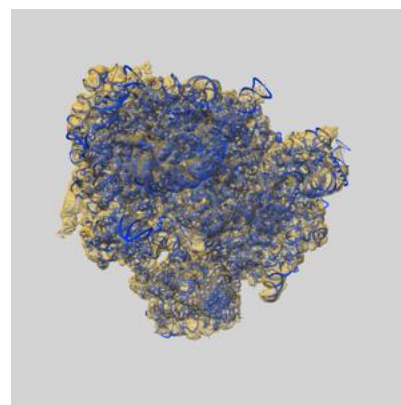
9.1 Map-model overlay [i](#)



X



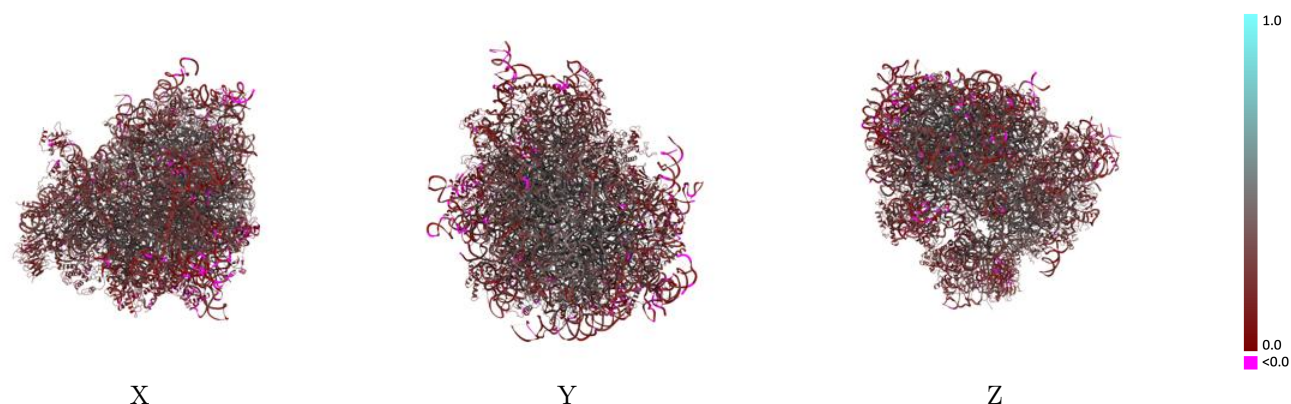
Y



Z

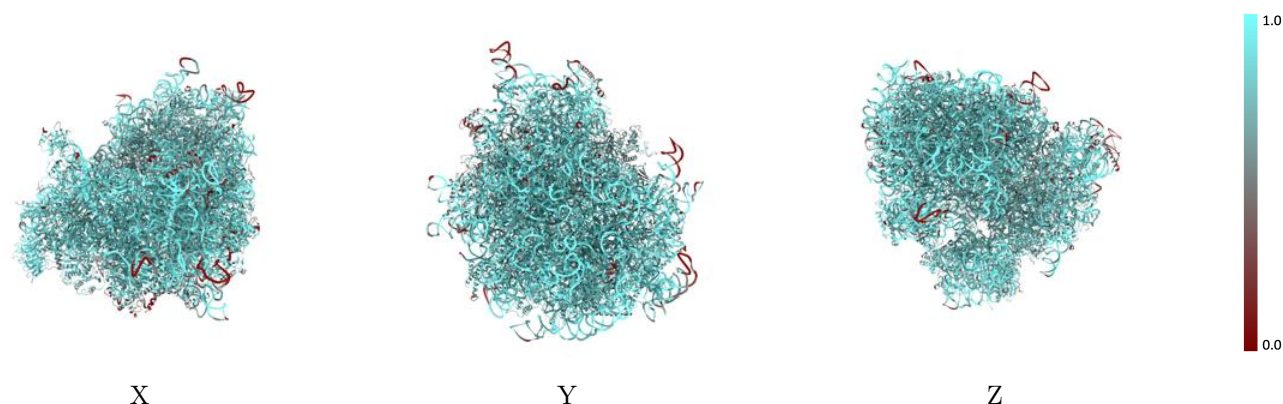
The images above show the 3D surface view of the map at the recommended contour level 0.006 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



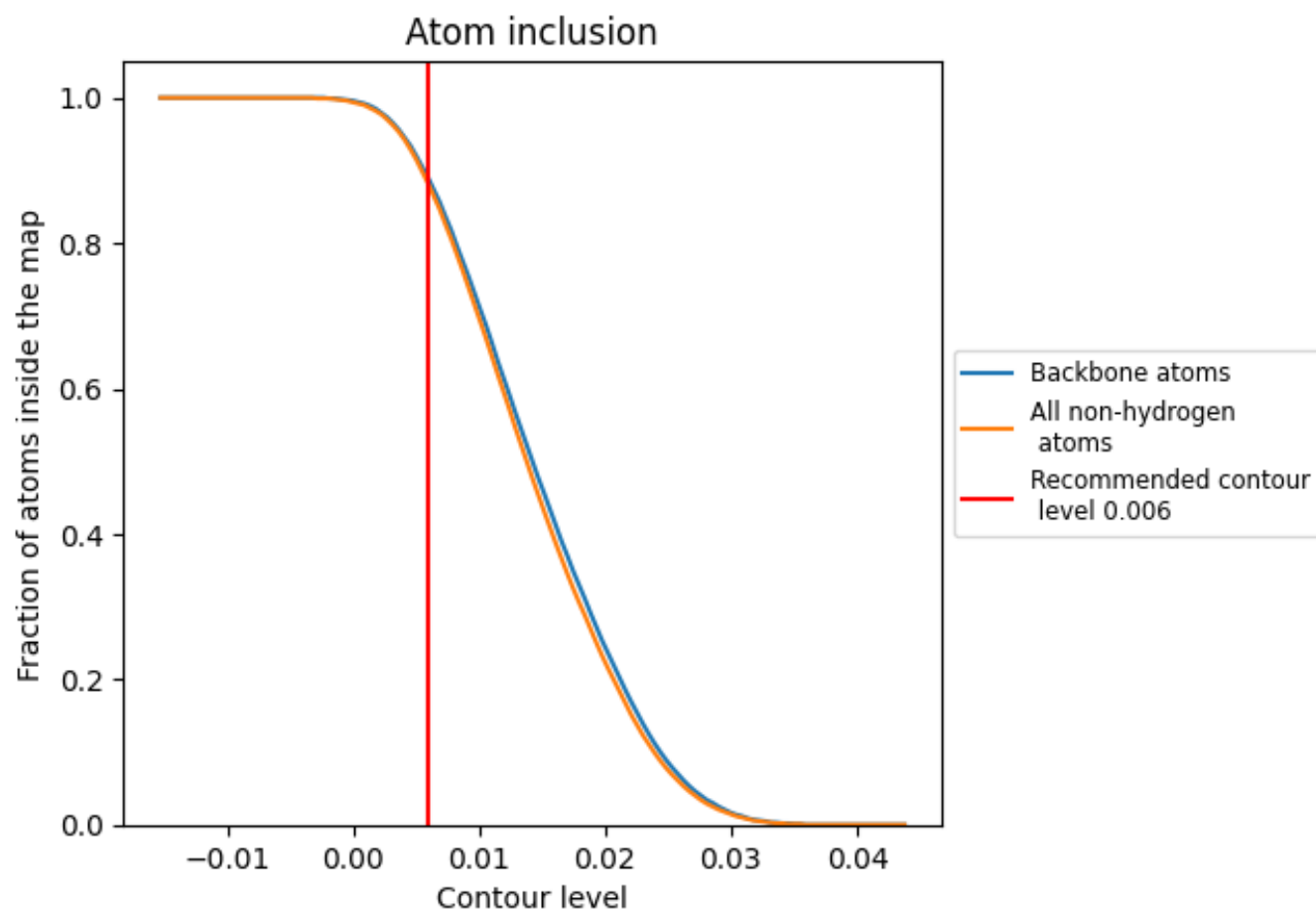
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.006).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 89% of all backbone atoms, 88% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.006) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8800	 0.2980
A5	 0.9360	 0.3060
A6	 0.9440	 0.3430
A7	 0.9510	 0.2870
A8	 0.9510	 0.3380
AA	 0.8300	 0.2880
AB	 0.8230	 0.2030
AC	 0.8150	 0.3080
AD	 0.8320	 0.2790
AE	 0.8490	 0.2770
AF	 0.8530	 0.2080
AG	 0.8770	 0.2110
AH	 0.6980	 0.2020
AI	 0.8450	 0.2510
AJ	 0.8800	 0.2660
AK	 0.8880	 0.1970
AL	 0.7550	 0.3160
AM	 0.7870	 0.1510
AN	 0.7800	 0.2780
AO	 0.8110	 0.2190
AP	 0.7650	 0.1830
AQ	 0.8670	 0.2100
AR	 0.7980	 0.2520
AS	 0.8440	 0.1880
AT	 0.8810	 0.1910
AU	 0.8750	 0.2500
AV	 0.7610	 0.2290
AW	 0.8280	 0.3250
AX	 0.8350	 0.3620
AY	 0.8480	 0.2020
AZ	 0.7860	 0.1630
Aa	 0.8270	 0.2880
Ab	 0.7420	 0.2300
Ac	 0.7280	 0.2250
Ad	 0.9090	 0.2480

















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Chain	Atom inclusion	Q-score
Ae	 0.7760	 0.2530
Af	 0.7100	 0.1480
Ag	 0.8900	 0.2150
B2	 0.9450	 0.3000
CA	 0.8280	 0.3510
CB	 0.8250	 0.2970
CC	 0.8810	 0.3870
CD	 0.9050	 0.2790
CE	 0.8340	 0.2500
CF	 0.8820	 0.3650
CG	 0.8090	 0.2910
CH	 0.8070	 0.2560
CI	 0.8110	 0.3120
CJ	 0.8690	 0.2970
CL	 0.8540	 0.3170
CM	 0.8510	 0.2260
CN	 0.8820	 0.3630
CO	 0.8050	 0.2970
CP	 0.8870	 0.3730
CQ	 0.7940	 0.2930
CR	 0.8430	 0.3470
CS	 0.8550	 0.2580
CT	 0.7900	 0.2760
CU	 0.6860	 0.1350
CV	 0.7960	 0.3590
CW	 0.6650	 0.2500
CX	 0.8210	 0.2610
CY	 0.8770	 0.2890
CZ	 0.7340	 0.1130
Ca	 0.8880	 0.3650
Cb	 0.7890	 0.2810
Cc	 0.7190	 0.1710
Cd	 0.8350	 0.3040
Ce	 0.8640	 0.3980
Cf	 0.8880	 0.3960
Cg	 0.8390	 0.2680
Ch	 0.8610	 0.2700
Ci	 0.7800	 0.2090
Cj	 0.8750	 0.3600
Ck	 0.7600	 0.2030
Cl	 0.9130	 0.3590
Cm	 0.8560	 0.3290

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Chain	Atom inclusion	Q-score
Cn	 0.7990	 0.3220
Co	 0.8380	 0.3180
Cp	 0.8230	 0.3310
Cr	 0.8040	 0.3060
Ct	 0.6630	 0.2910
Cz	 0.7690	 0.1080
tR	 0.9510	 0.3030