



wwPDB EM Validation Summary Report ⓘ

Jan 30, 2025 – 12:48 PM JST

PDB ID : 8HKZ
EMDB ID : EMD-34864
Title : Cryo-EM Structures and Translocation Mechanism of Crenarchaeota Ribosome
Authors : Wang, Y.H.; Zhou, J.
Deposited on : 2022-11-28
Resolution : 4.78 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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

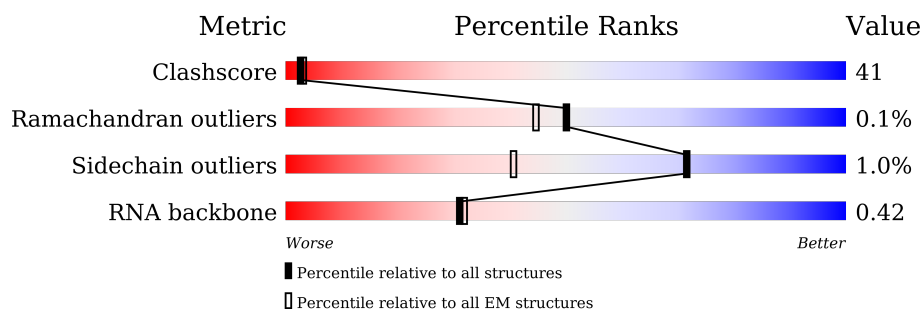
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.78 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	A23S	3022	
2	A16S	1503	
3	A5S	122	
4	AL1P	216	
5	AL2P	234	
6	AL3P	339	
7	AL4P	251	

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Mol	Chain	Length	Quality of chain
8	AL5P	168	40% 99% .
9	AL6P	181	36% 99% .
10	ALX0	76	30% 96% .
11	L10E	164	32% 99% .
12	L13P	140	29% 100%
13	L141	86	31% 99% .
13	L142	86	53% 100%
14	L14P	134	61% 99% .
15	L15E	169	37% 99% .
16	L18E	112	7% 100%
17	L18P	193	34% 100%
18	L19E	144	17% 99% .
19	L22P	150	37% 99% .
20	L23P	81	33% 100%
21	L24E	54	31% 100%
22	L24P	122	18% 99% .
23	L29P	63	21% 98% .
24	L30E	94	16% 100%
25	L30P	155	26% 99% .
26	L31E	75	35% 99% .
27	L32E	123	50% 100%
28	L34E	77	39% 96% ...
29	L37A	65	25% 100%
30	L37E	54	20% 100%
31	L39E	49	31% 100%

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Mol	Chain	Length	Quality of chain
32	L40E	55	87% 100%
33	L44E	92	35% 99%
34	L7A1	123	42% 99%
34	L7A2	123	36% 100%
34	SL7A	123	89% 100%
35	L15P	144	15% 65% 35%
36	L21E	97	25% 99%
37	L45A	101	42% 95% 5%
38	L46A	70	70% 100%
39	L47A	80	94% 99%
40	AS2P	196	51% 100%
41	AS4E	240	37% 99%
42	AS4P	166	29% 99%
43	AS5P	204	30% 100%
44	AS6E	105	64% 98%
45	AS8E	126	55% 100%
46	AS8P	130	15% 98%
47	S11P	128	48% 100%
48	S12P	143	66% 99%
49	S15P	149	23% 97%
50	S17P	111	48% 99%
51	S24E	96	34% 98%
52	S27E	59	24% 100%
53	S3AE	189	44% 98%
54	AS3P	201	50% 100%

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Mol	Chain	Length	Quality of chain
55	AS7P	193	<div>54%</div> <div>98%</div> <div>.</div>
56	S10P	100	<div>56%</div> <div>100%</div>
57	S13P	147	<div>44%</div> <div>98%</div> <div>.</div>
58	S14P	52	<div>58%</div> <div>100%</div>
59	S17E	62	<div>61%</div> <div>100%</div>
60	S19E	150	<div>45%</div> <div>99%</div> <div>.</div>
61	S19P	115	<div>33%</div> <div>96%</div> <div>.</div>
62	AS9P	136	<div>46%</div> <div>99%</div> <div>.</div>
63	S28E	63	<div>67%</div> <div>100%</div>
64	S27A	54	<div>19%</div> <div>94%</div> <div>6%</div>
65	APTP	6	<div>100%</div> <div>100%</div>
66	AETN	76	<div>80%</div> <div>57%</div> <div>37%</div> <div>7%</div>
66	APTN	76	<div>.</div> <div>70%</div> <div>26%</div> <div>.</div>
67	AMRN	9	<div>56%</div> <div>89%</div> <div>11%</div>

2 Entry composition

There are 68 unique types of molecules in this entry. The entry contains 167743 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 RNA chain called 23S rRNA (2996-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A23S	2996	Total	C	N	O	P	0	0
			64360	28674	11914	20776	2996		

- Molecule 2 is a RNA chain called 16S rRNA (1493-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A16S	1493	Total	C	N	O	P	0	0
			32063	14279	5930	10361	1493		

- Molecule 3 is a RNA chain called 5S rRNA (122-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A5S	122	Total	C	N	O	P	0	0
			2609	1163	476	849	121		

- Molecule 4 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AL1P	216	Total	C	N	O	S	0	0
			1715	1096	303	312	4		

- Molecule 5 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AL2P	234	Total	C	N	O	S	0	0
			1754	1101	344	307	2		

- Molecule 6 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AL3P	339	Total	C	N	O	S	0	0
			2695	1730	484	477	4		

- Molecule 7 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AL4P	251	Total	C	N	O	S	0	0
			1926	1223	356	345	2		

- Molecule 8 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AL5P	168	Total	C	N	O	S	0	0
			1343	854	253	232	4		

- Molecule 9 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AL6P	181	Total	C	N	O	S	0	0
			1431	920	246	264	1		

- Molecule 10 is a protein called 50S ribosomal protein L18Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	ALX0	76	Total	C	N	O	S	0	0
			629	403	110	115	1		

- Molecule 11 is a protein called 50S ribosomal protein L10e.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L10E	164	Total	C	N	O	S	0	0
			1310	837	239	227	7		

- Molecule 12 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L13P	140	Total	C	N	O	S	0	0
			1109	707	208	190	4		

- Molecule 13 is a protein called 50S ribosomal protein L14e.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L141	86	Total	C	N	O	S	0	0
			669	417	123	127	2		
13	L142	86	Total	C	N	O	S	0	0
			669	417	123	127	2		

- Molecule 14 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L14P	134	Total	C	N	O	S	0	0
			1034	655	194	181	4		

- Molecule 15 is a protein called 50S ribosomal protein L15e.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L15E	169	Total	C	N	O	S	0	0
			1423	899	283	236	5		

- Molecule 16 is a protein called 50S ribosomal protein L18e.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L18E	112	Total	C	N	O	S	0	0
			895	576	163	153	3		

- Molecule 17 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L18P	193	Total	C	N	O	S	0	0
			1539	990	274	274	1		

- Molecule 18 is a protein called 50S ribosomal protein L19e.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	L19E	144	Total	C	N	O	0	0
			1206	753	247	206		

- Molecule 19 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L22P	150	Total	C	N	O	S	0	0
			1223	782	225	213	3		

- Molecule 20 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L23P	81	Total	C	N	O	S	0	0
			650	419	109	121	1		

- Molecule 21 is a protein called 50S ribosomal protein L24e.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	L24E	54	Total	C	N	O	S	0	0
			441	282	80	73	6		

- Molecule 22 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	L24P	122	Total	C	N	O	S	0	0
			989	620	189	176	4		

- Molecule 23 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	L29P	63	Total	C	N	O	S	0	0
			513	319	95	96	3		

- Molecule 24 is a protein called 50S ribosomal protein L30e.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	L30E	94	Total	C	N	O	S	0	0
			729	474	116	136	3		

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	L30P	155	Total	C	N	O	S	0	0
			1254	804	222	223	5		

- Molecule 26 is a protein called 50S ribosomal protein L31e.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	L31E	75	Total	C	N	O	S	0	0
			625	398	126	97	4		

- Molecule 27 is a protein called 50S ribosomal protein L32e.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	L32E	123	Total	C	N	O	S	0	0
			1010	650	193	166	1		

- Molecule 28 is a protein called 50S ribosomal protein L34e.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	L34E	77	Total	C	N	O	S	0	0
			629	395	119	110	5		

- Molecule 29 is a protein called 50S ribosomal protein L37Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	L37A	65	Total	C	N	O	S	0	0
			527	335	99	87	6		

- Molecule 30 is a protein called 50S ribosomal protein L37e.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	L37E	54	Total	C	N	O	S	0	0
			436	267	94	69	6		

- Molecule 31 is a protein called 50S ribosomal protein L39e.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	L39E	49	Total	C	N	O	0	0
			414	265	88	61		

- Molecule 32 is a protein called 50S ribosomal protein L40E.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	L40E	55	Total	C	N	O	S	0	0
			439	273	89	72	5		

- Molecule 33 is a protein called 50S ribosomal protein L44e.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	L44E	92	Total	C	N	O	S	0	0
			753	474	144	129	6		

- Molecule 34 is a protein called 50S ribosomal protein L7Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	L7A1	123	Total	C	N	O	S	0	0
			935	593	155	184	3		
34	L7A2	123	Total	C	N	O	S	0	0
			935	593	155	184	3		
34	SL7A	123	Total	C	N	O	S	0	0
			935	593	155	184	3		

- Molecule 35 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	L15P	94	Total	C	N	O	S	0	0
			752	487	131	133	1		

- Molecule 36 is a protein called 50S ribosomal protein L21e.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	L21E	97	Total	C	N	O	S	0	0
			785	502	152	129	2		

- Molecule 37 is a protein called DUF2280 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	L45A	101	Total	C	N	O	S	0	0
			816	515	141	156	4		

- Molecule 38 is a protein called Conserved protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	L46A	70	Total	C	N	O	S	0	0
			586	382	101	102	1		

- Molecule 39 is a protein called 50S ribosomal protein L47A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	L47A	80	Total	C	N	O	S	0	0
			648	405	113	128	2		

- Molecule 40 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	AS2P	196	Total	C	N	O	S	0	0
			1587	1022	277	286	2		

- Molecule 41 is a protein called 30S ribosomal protein S4e.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AS4E	240	Total	C	N	O	S	0	0
			1925	1238	335	348	4		

- Molecule 42 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	AS4P	166	Total	C	N	O	S	0	0
			1370	874	252	241	3		

- Molecule 43 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AS5P	204	Total	C	N	O	S	0	0
			1600	1028	277	287	8		

- Molecule 44 is a protein called 30S ribosomal protein S6e.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	AS6E	105	Total	C	N	O	S	0	0
			805	506	149	147	3		

- Molecule 45 is a protein called 30S ribosomal protein S8e.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	AS8E	126	Total	C	N	O	S	0	0
			993	619	187	187			

- Molecule 46 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AS8P	130	Total	C	N	O	S	0	0
			1028	661	181	182	4		

- Molecule 47 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S11P	128	Total	C	N	O	S	0	0
			960	595	190	173	2		

- Molecule 48 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	S12P	143	Total	C	N	O	S	0	0
			1103	701	209	189	4		

- Molecule 49 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S15P	149	Total	C	N	O	S	0	0
			1225	778	228	214	5		

- Molecule 50 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	S17P	111	Total	C	N	O	S	0	0
			885	557	165	160	3		

- Molecule 51 is a protein called 30S ribosomal protein S24e.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	S24E	96	Total	C	N	O	S	0	0
			759	479	133	147			

- Molecule 52 is a protein called 30S ribosomal protein S27e.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	S27E	59	Total	C	N	O	S	0	0
			458	294	83	76	5		

- Molecule 53 is a protein called 30S ribosomal protein S3Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	S3AE	189	Total	C	N	O	S	0	0
			1545	1004	264	276	1		

- Molecule 54 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AS3P	201	Total	C	N	O	S	0	0
			1576	1020	274	278	4		

- Molecule 55 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	AS7P	193	Total	C	N	O	S	0	0
			1537	969	285	279	4		

- Molecule 56 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	S10P	100	Total	C	N	O	S	0	0
			824	522	154	142	6		

- Molecule 57 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	S13P	147	Total	C	N	O	S	0	0
			1204	753	230	217	4		

- Molecule 58 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	S14P	52	Total	C	N	O	S	0	0
			432	273	85	69	5		

- Molecule 59 is a protein called 30S ribosomal protein S17e.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	S17E	62	Total	C	N	O	S	0	0
			517	326	92	99			

- Molecule 60 is a protein called 30S ribosomal protein S19e.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	S19E	150	Total	C	N	O	S	0	0
			1239	801	223	213	2		

- Molecule 61 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	S19P	115	Total	C	N	O	S	0	0
			968	620	181	162	5		

- Molecule 62 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AS9P	136	Total	C	N	O	S	0	0
			1096	692	200	197	7		

- Molecule 63 is a protein called 30S ribosomal protein S28e.

Mol	Chain	Residues	Atoms				AltConf	Trace
63	S28E	63	Total	C	N	O	0	0
			498	308	99	91		

- Molecule 64 is a protein called 30S ribosomal protein S27ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	S27A	54	Total	C	N	O	S	0	0
			435	274	79	76	6		

- Molecule 65 is a protein called PHE-PHE-PHE-PHE-PHE-PHE.

Mol	Chain	Residues	Atoms				AltConf	Trace
65	APTP	6	Total	C	N	O	0	0
			67	54	6	7		

- Molecule 66 is a RNA chain called tRNA (76-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
66	APTN	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		
66	AETN	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

- Molecule 67 is a RNA chain called mRNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*U)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
67	AMRN	9	Total	C	N	O	P	0	0
			180	81	18	72	9		

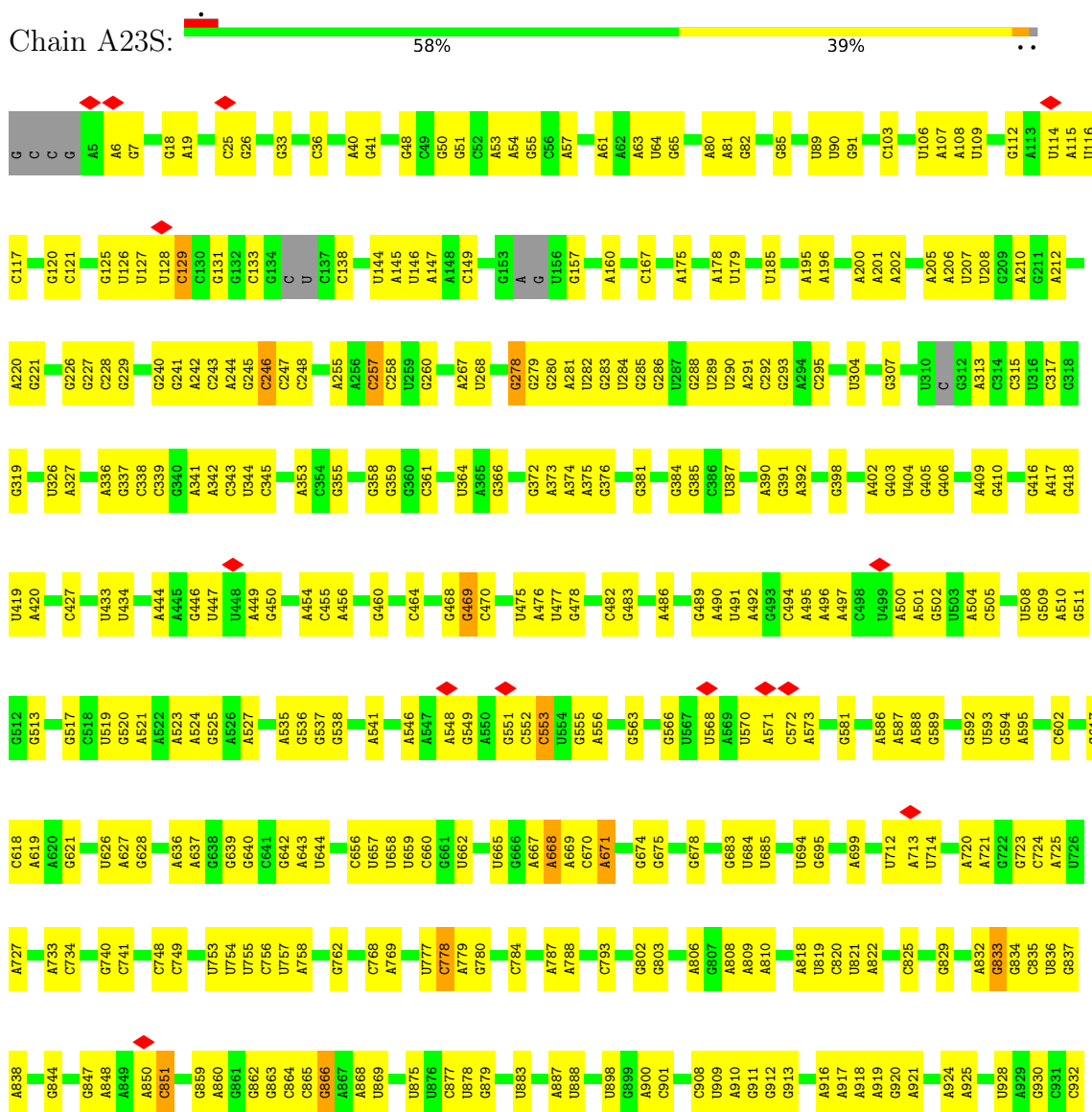
- Molecule 68 is UNKNOWN LIGAND (three-letter code: UNL) (formula:) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms				AltConf
68	AS2P	34	Total	C	N	O	0
			171	102	34	35	
68	AS5P	18	Total	C	N	O	0
			90	54	18	18	
68	AS8P	5	Total	C	N	O	0
			25	15	5	5	

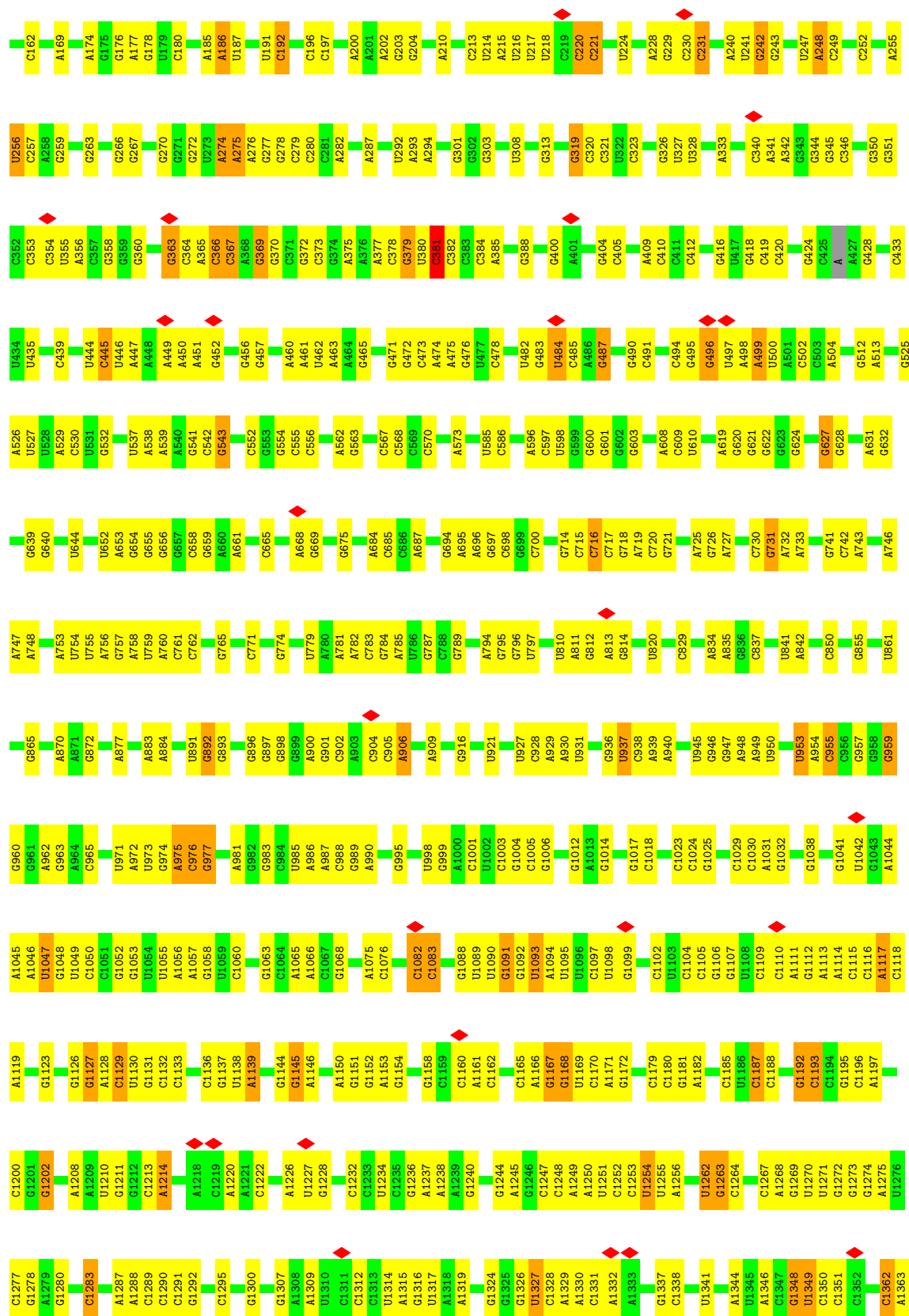
3 Residue-property plots

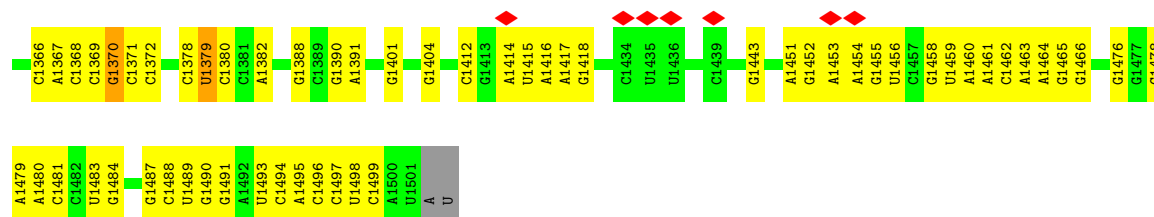
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 23S rRNA (2996-MER)



G2039	U2040	A2041	A2042	C2043	U2044	C2045	U2046	G2047	A2048	C2049	C2050	C2051	U2052	C2053	U2054	A2056	A2057	G2058	C2059	U2060	A2061	C2062	A2065	A2066	A2067	C2074	U2080	A2081	A2082	G2083	U2084	U2085	C2092	G2093	C2094	A2095	A2098	A2099	U2100	G2101	C2105	A2106	A2107	C2108	G2109	C2110	G2111	U2120	G2121	C2125							
G1951	A1952	A1953	A1954	G1955	G1956	G1957	U1958	G1959	U1960	G1961	C1964	U1965	A1973	C1976	U1977	U1978	G1979	G1980	C1981	C1982	U1985	U1991	U1992	G1993	U	U	A1997	G2004	G2005	U2006	U2007	C2008	G2013	G2014	G2015	C2016	G2017	A1928	A1929	U1930	A1931	C1932	A1933	U1934	A1935	G2026	C2027	G2028	A2029	A2030	G2031	G2032	U1945	G2035	G2036	G2037	G2038
U1850	C1851	A1855	G1856	A1857	G1861	G1864	C1865	C1866	U1867	A1868	G1873	C1877	C	U	G1782	G1783	G1784	U1785	G1786	A1789	A1790	C1791	U1992	C1793	A1796	G1800	U1801	C1802	U1803	G1804	G1809	U1810	A1811	G1817	G1818	G1822	A1825	A1826	C1827	U1828	C1829	G1830	G1831	C1832	U1836	A1846	A1847										
G1674	U1675	G1676	A1679	U1680	G1681	G1682	C1684	C1685	U1686	C1689	G1690	U1691	U1692	A1693	G1694	G1695	A1696	G1699	U1700	U1701	C1704	A1708	U1709	C1710	U1713	A1714	G1715	C1720	A1721	U1722	G1723	A1724	U1725	A1726	U1727	G1728	G1729	G1730	C1734	G1740	G1741	A1742	U1743	C1744	G1748	G1749	A1750	G1751									
C1584	C1585	U1586	G1587	U1588	C1589	U1594	G1598	G1601	G1602	G1611	A1612	C1613	A1614	A1615	C1616	G1617	G1618	U1619	C1625	C1626	A1627	C1630	U1633	C1634	A1635	A1636	U1641	G1644	A1645	G1646	A1647	G1648	C1649	A1654	C1655	G1656	A1660	G1661	A1662	A1663	G1664	A1665	G1666	G1667	A1671												
A1508	A1509	U1510	A1511	G1512	U1513	U1514	A1515	C1520	A1523	A1524	G1525	G1526	G1527	A1528	A1529	A1530	A1531	G1532	U1536	U1537	A1538	C1540	A1541	U1542	U1543	C1544	C1545	G1549	C1555	G1558	U1559	A1560	G1561	U1562	U1563	G1564	C1565	G1566	U1567	U1568	A1569	A1570	A1574	A1575	G1576	C1577	C1578	U1579	G1580	A1581							
C1416	G1417	A1418	A1419	G1422	G1423	G1424	U1426	G1427	C1433	C1434	C1435	G1444	A1445	A1446	G1447	C1450	A1451	A1452	G1453	U1457	U1458	C1459	C1460	G1461	G1462	A1465	A1466	C1467	G1468	U1469	C1474	A1475	G1476	G1479	U1484	U1485	A1486	G1487	C1488	C1489	G1490	G	U	C1493	C1494	U1500	A1501	G1502									
G1306	C1312	U1315	A1316	C1317	U1318	A	G1320	A1321	G1322	G1330	A1333	G1334	G1338	G1346	A1347	U1348	G1350	G1351	G1352	U1353	U1354	A1354	G1355	A1356	U1364	C1365	G1366	U1367	G1368	A1369	G1370	G1379	A1380	C1381	U1392	G1393	C1394	A1395	G1396	U1397	U1398	C1399	G1406	U1410	A1414	G1415											
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C1141	A1144	U1148	C1149	G1153	C1154	U1155	A1156	A1157	G1158	C1162	A1163	A1164	C1165	G1166	A1167	A1168	C1173	G1174	U1175	C1176	U1177	C1178	C1179	A1180	G1181	U1185	A1186	G1187	A1188	C1189	A1190	G1191	C1192	G1193	A1196	A1197	G1198	G1199	U1200	G1201	G1202	A1125	G1126	C1128	A1136	A1137	G1138	U1045	A1046	A1047	C1048						
U1049	C1050	C1051	C1055	G1060	C1066	G1067	A1068	A1069	G1070	A1071	A1072	G1082	G1083	G1084	U1085	U1089	C1090	G1094	U1095	G1098	G1099	G1102	G1103	G1104	U1105	C1108	A1109	A1110	A1111	G1112	G1113	G1114	A1117	A1118	C1119	A1120	A1121	C1122	A1125	G1126	C1128	A1136	A1137	G1138	U1045	A1046	A1047	C1048									
A936	G941	U947	C948	A957	C963	C964	U965	A966	G967	C968	G969	C970	A981	A982	G983	G984	A986	G993	G994	G995	G996	A1000	G1001	U1002	G1003	A1004	G1005	A1006	G1007	A1008	G1011	G1012	G1013	G1022	C1023	G	A	A	G1028	A1127	C1029	C1030	C1044	U1045	A1046	A1047	C1048										





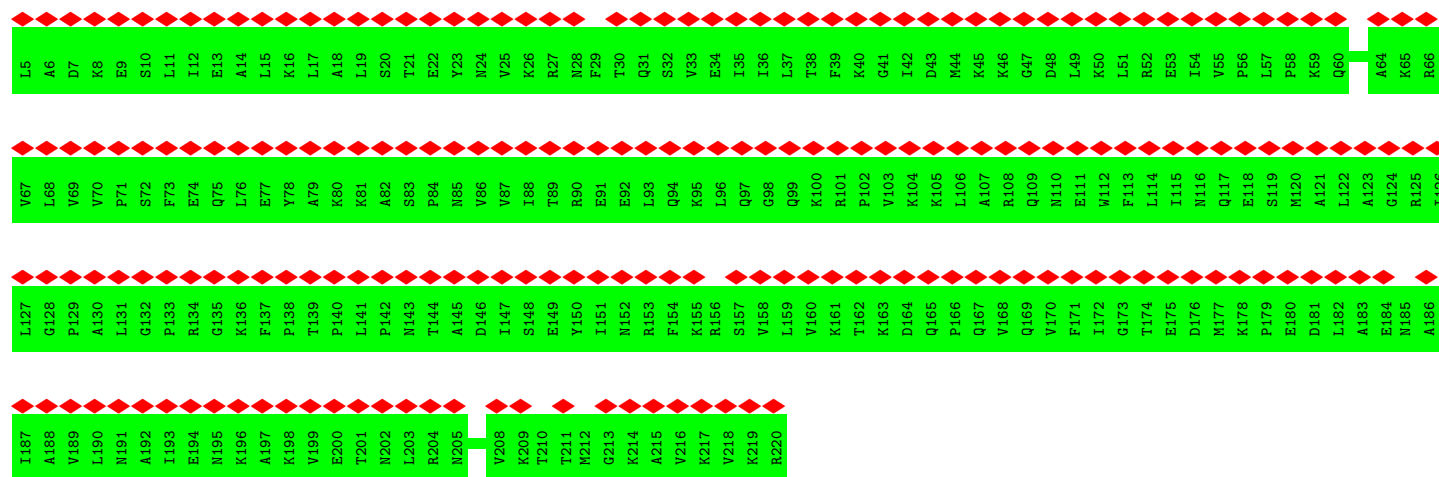
• Molecule 3: 5S rRNA (122-MER)

Chain A5S: 12% 61% 27%



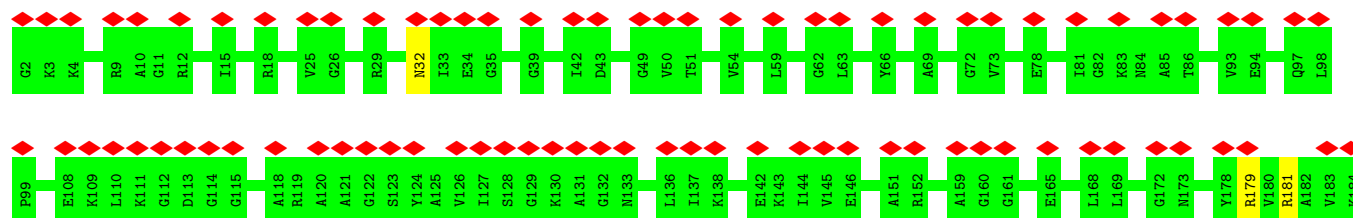
• Molecule 4: 50S ribosomal protein L1

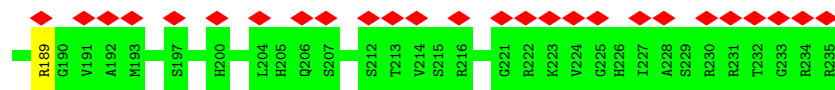
Chain AL1P: 95% 100%



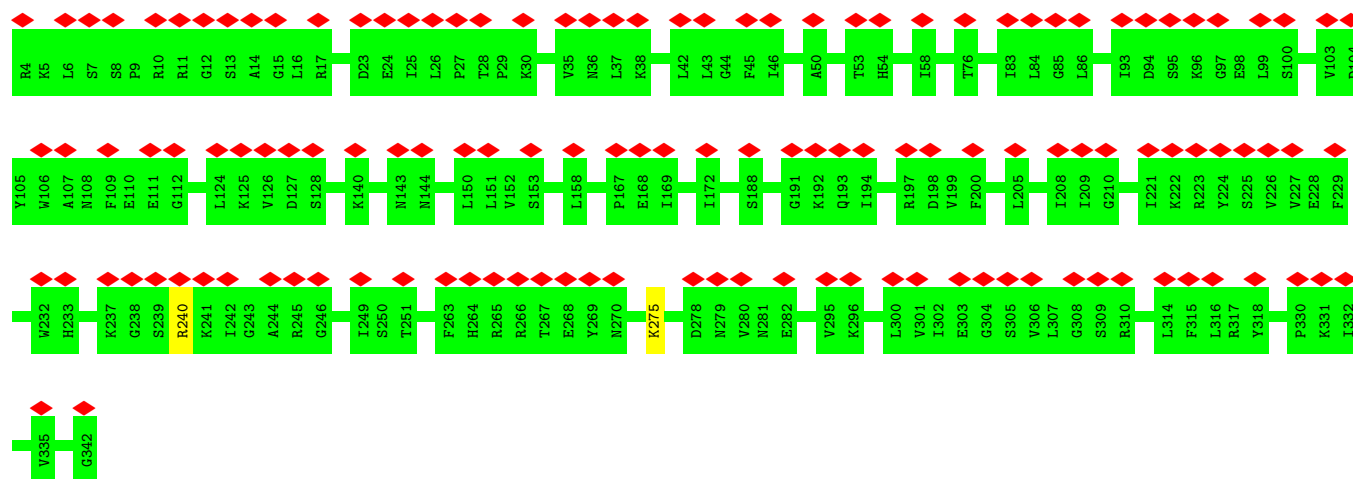
• Molecule 5: 50S ribosomal protein L2

Chain AL2P: 46% 98%

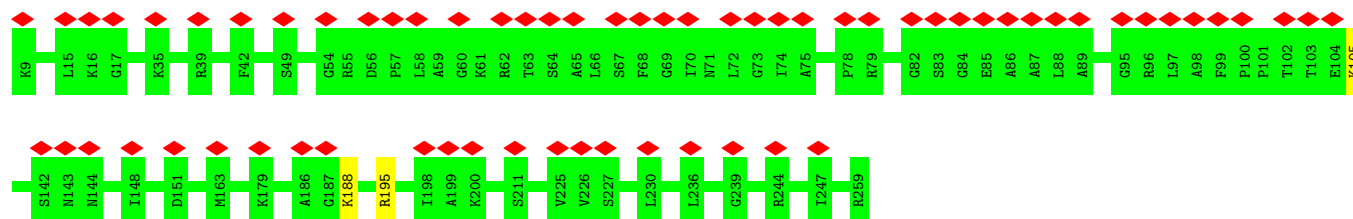




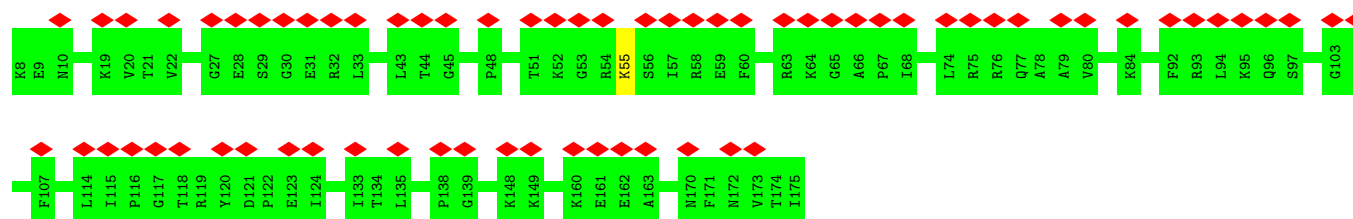
• Molecule 6: 50S ribosomal protein L3



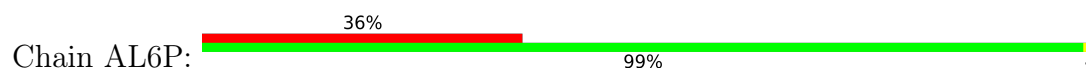
• Molecule 7: 50S ribosomal protein L4

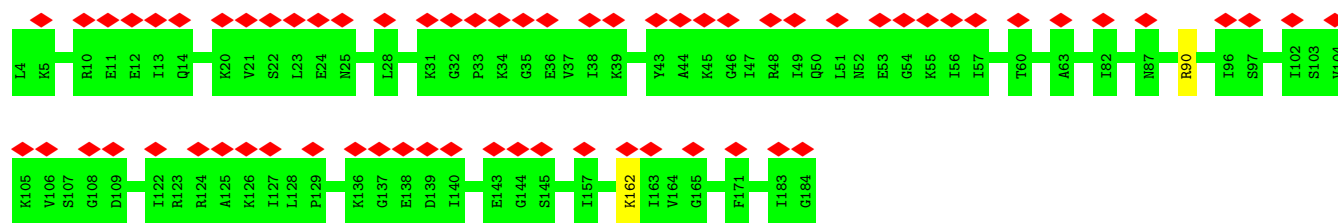


• Molecule 8: 50S ribosomal protein L5



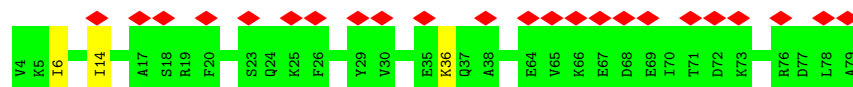
• Molecule 9: 50S ribosomal protein L6





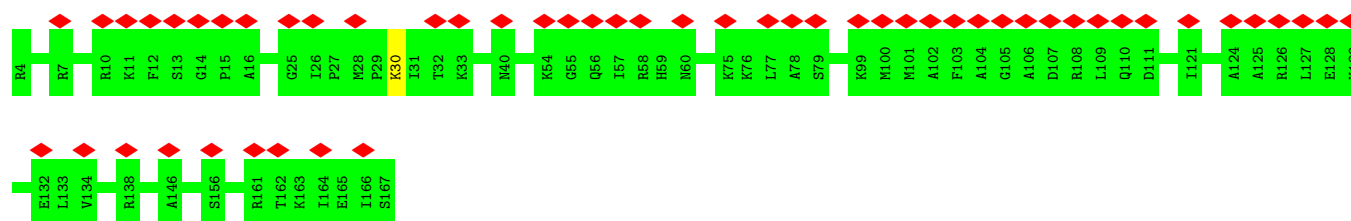
- Molecule 10: 50S ribosomal protein L18Ae

Chain ALX0: 30% 96%



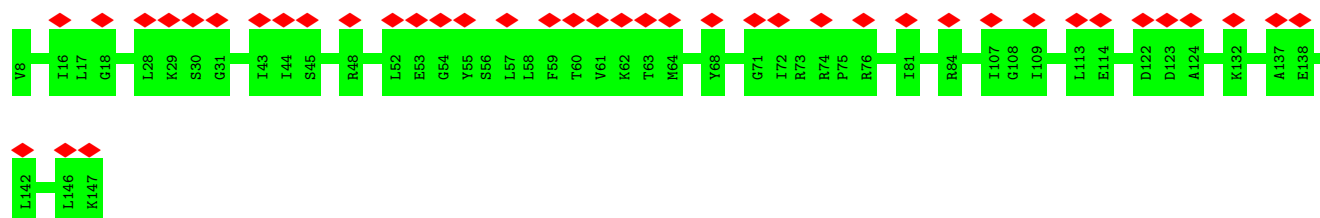
- Molecule 11: 50S ribosomal protein L10e

Chain L10E: 32% 99%



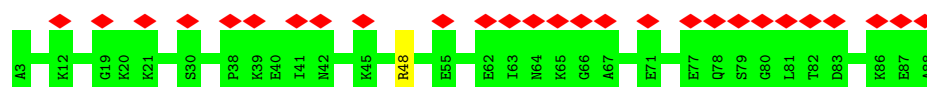
- Molecule 12: 50S ribosomal protein L13

Chain L13P: 29% 100%



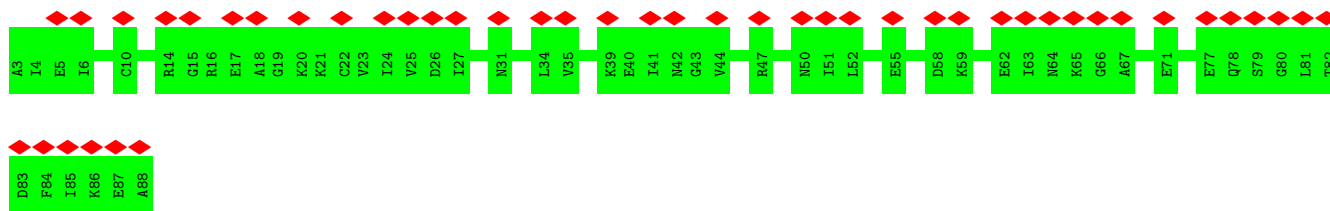
- Molecule 13: 50S ribosomal protein L14e

Chain L141: 31% 99%

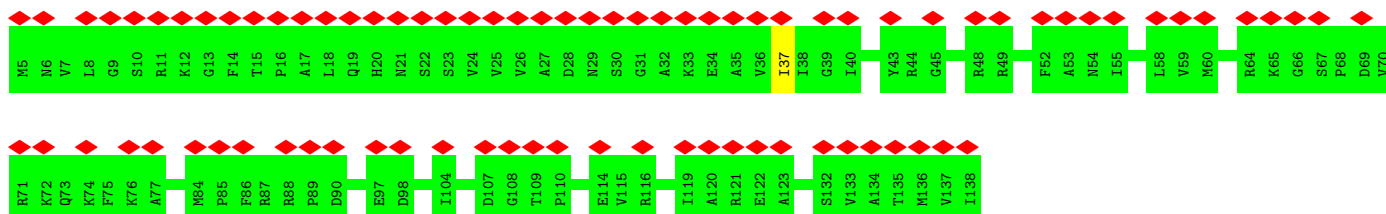


- Molecule 13: 50S ribosomal protein L14e

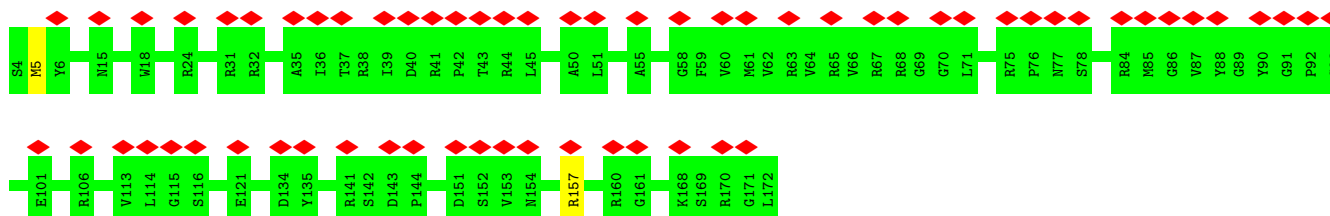
Chain L142: 53% 100%



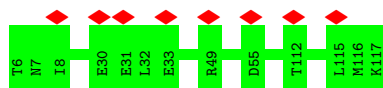
• Molecule 14: 50S ribosomal protein L14



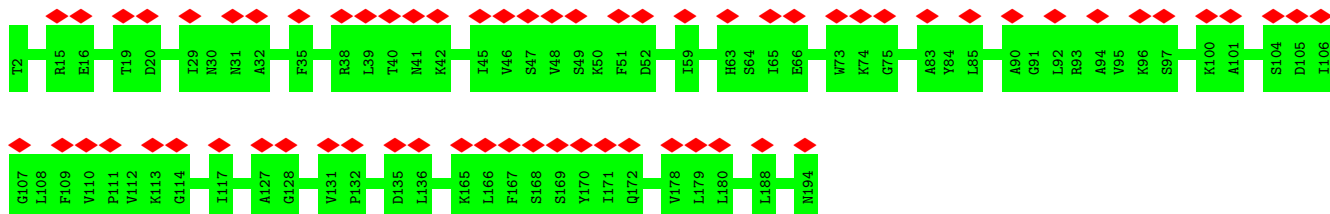
• Molecule 15: 50S ribosomal protein L15e



• Molecule 16: 50S ribosomal protein L18e

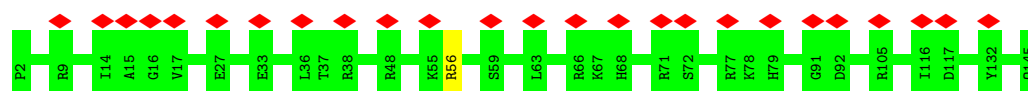


• Molecule 17: 50S ribosomal protein L18

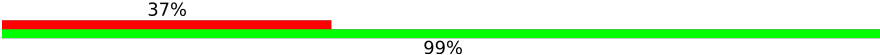


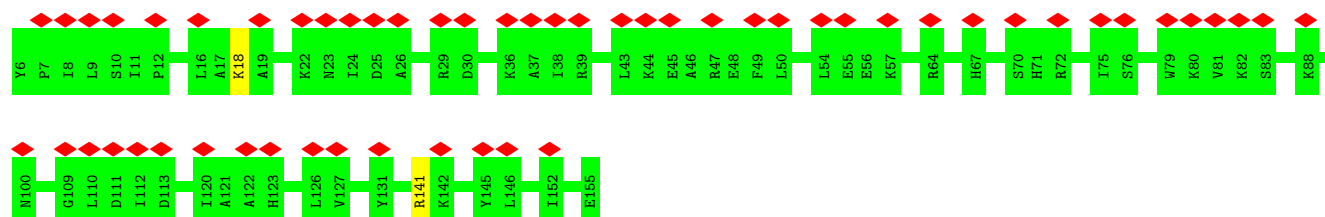
• Molecule 18: 50S ribosomal protein L19e

Chain L19E:  17% 99%



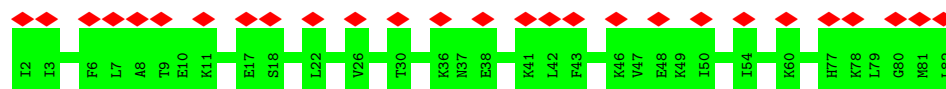
- Molecule 19: 50S ribosomal protein L22

Chain L22P:  37% 99%



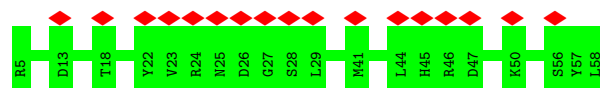
- Molecule 20: 50S ribosomal protein L23

Chain L23P:  33% 100%



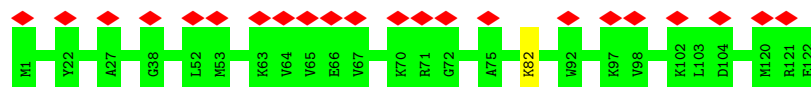
- Molecule 21: 50S ribosomal protein L24e

Chain L24E:  31% 100%



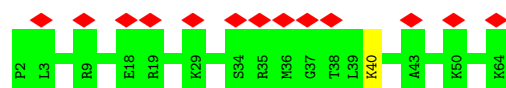
- Molecule 22: 50S ribosomal protein L24

Chain L24P:  18% 99%



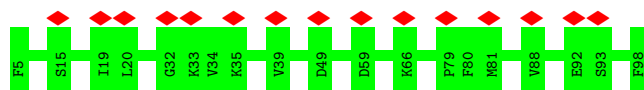
- Molecule 23: 50S ribosomal protein L29

Chain L29P:  21% 98%

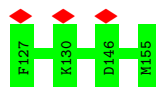
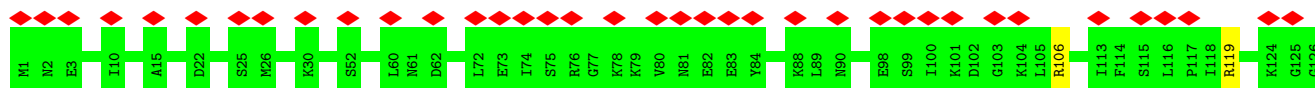


- Molecule 24: 50S ribosomal protein L30e

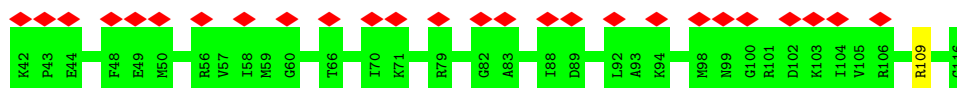
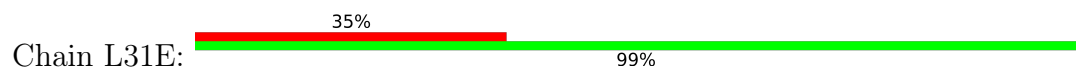
Chain L30E:  16% 100%



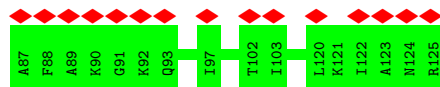
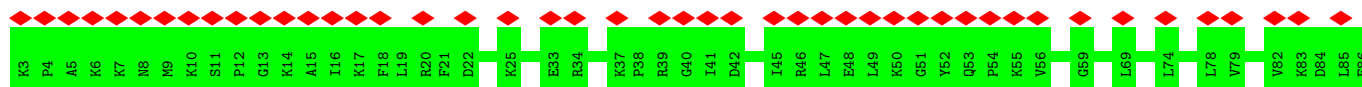
- Molecule 25: 50S ribosomal protein L30



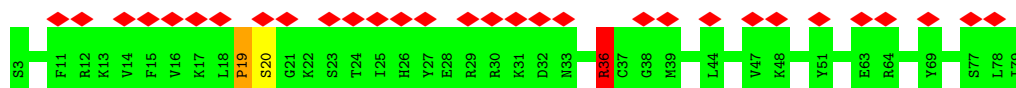
- Molecule 26: 50S ribosomal protein L31e



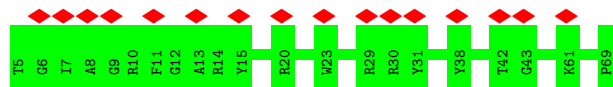
- Molecule 27: 50S ribosomal protein L32e



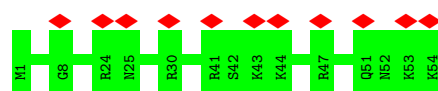
- Molecule 28: 50S ribosomal protein L34e



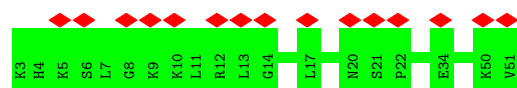
- Molecule 29: 50S ribosomal protein L37Ae



- Molecule 30: 50S ribosomal protein L37e



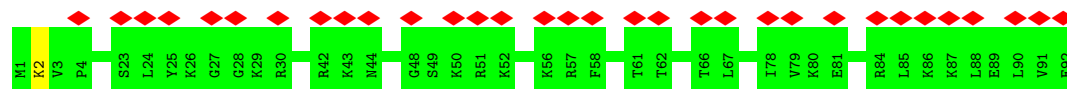
- Molecule 31: 50S ribosomal protein L39e



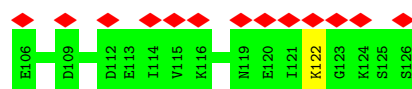
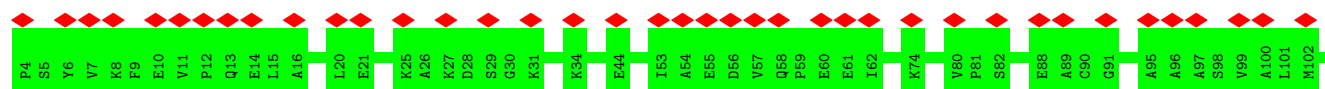
- Molecule 32: 50S ribosomal protein L40E



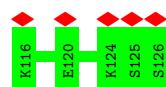
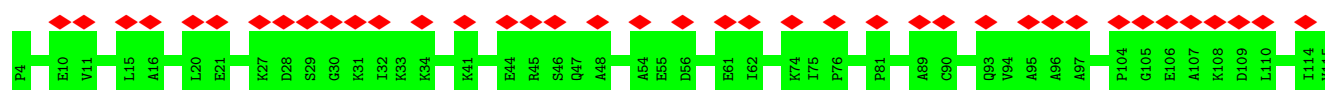
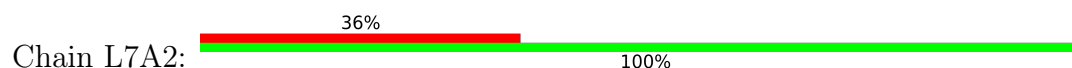
- Molecule 33: 50S ribosomal protein L44e



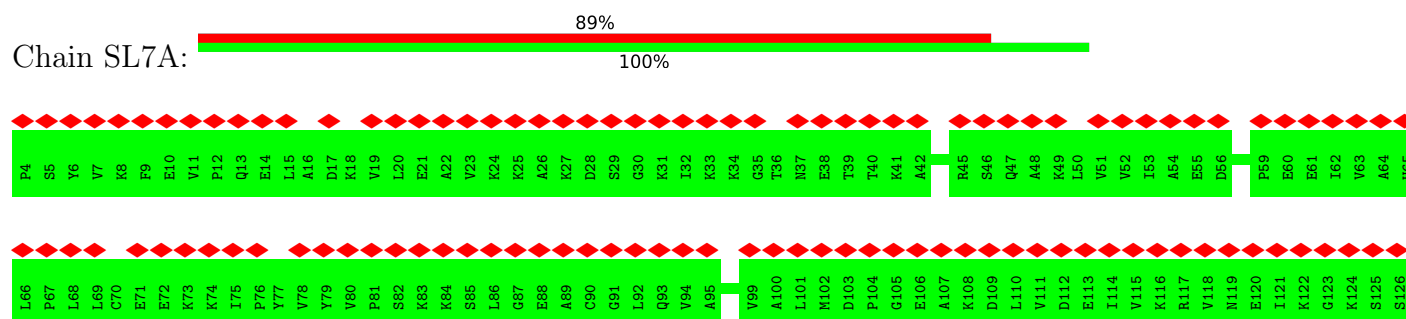
- Molecule 34: 50S ribosomal protein L7Ae



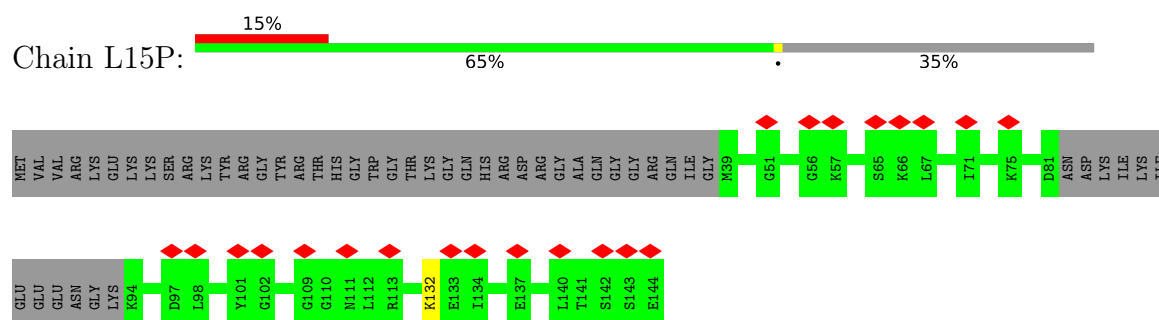
- Molecule 34: 50S ribosomal protein L7Ae



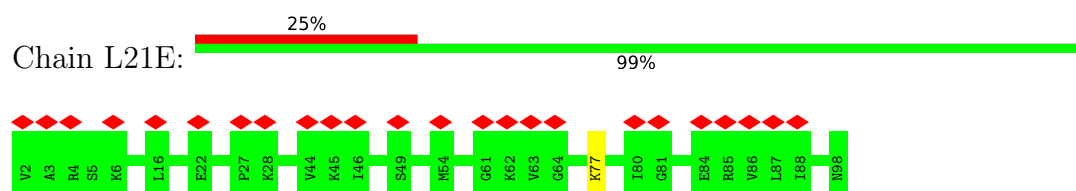
- Molecule 34: 50S ribosomal protein L7Ae



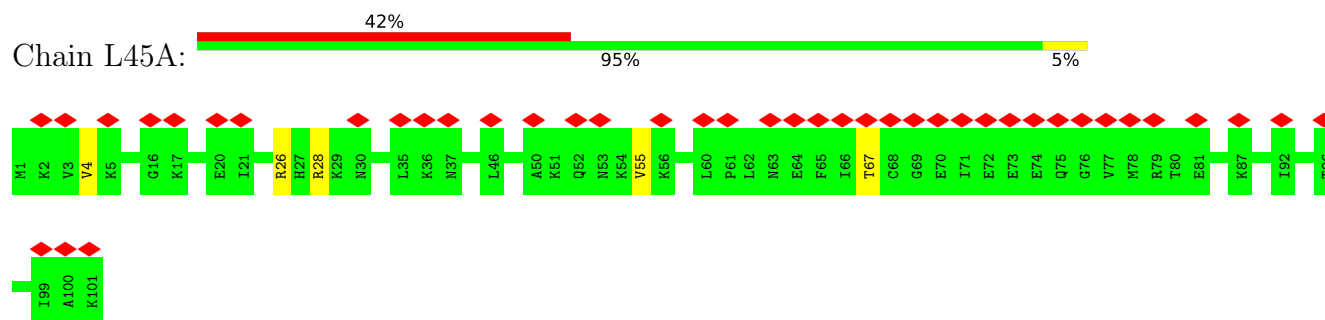
- Molecule 35: Large ribosomal subunit protein uL15



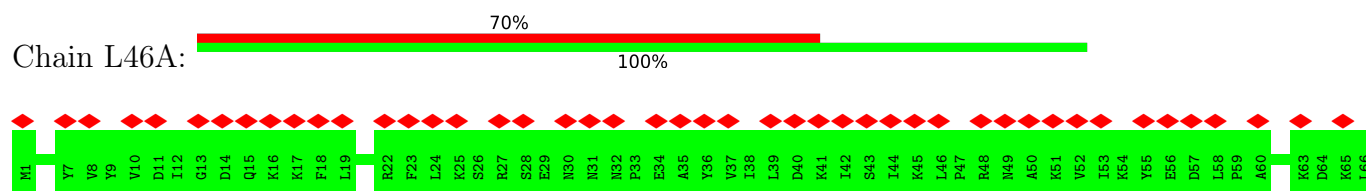
- Molecule 36: 50S ribosomal protein L21e

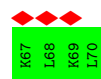


- Molecule 37: DUF2280 domain-containing protein

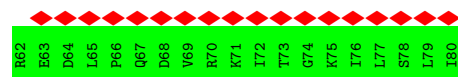
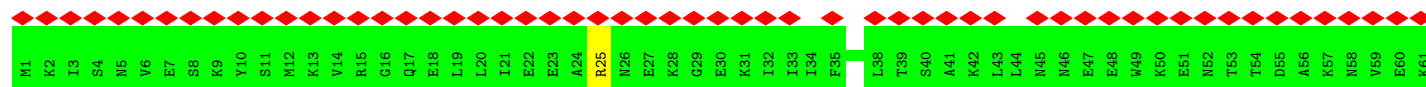


- Molecule 38: Conserved protein

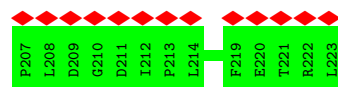
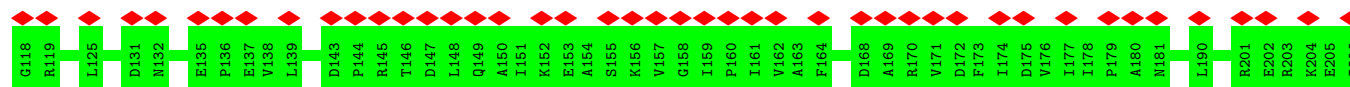
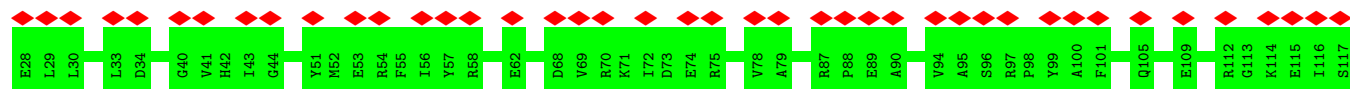




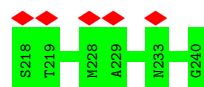
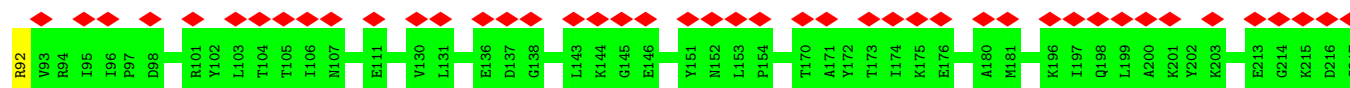
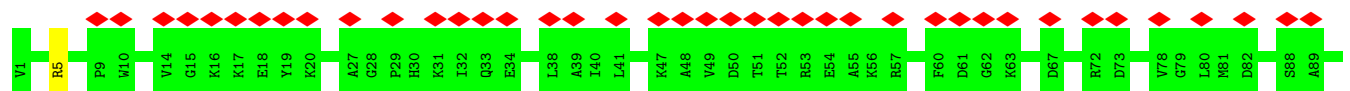
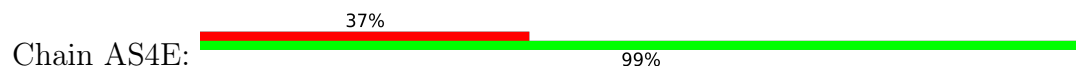
- Molecule 39: 50S ribosomal protein L47A



- Molecule 40: 30S ribosomal protein S2

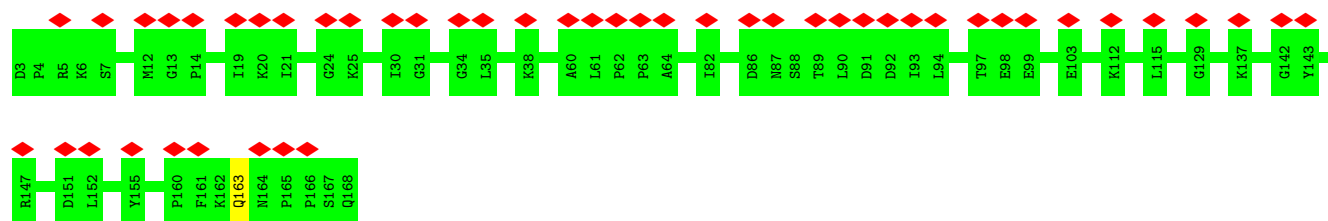


- Molecule 41: 30S ribosomal protein S4e

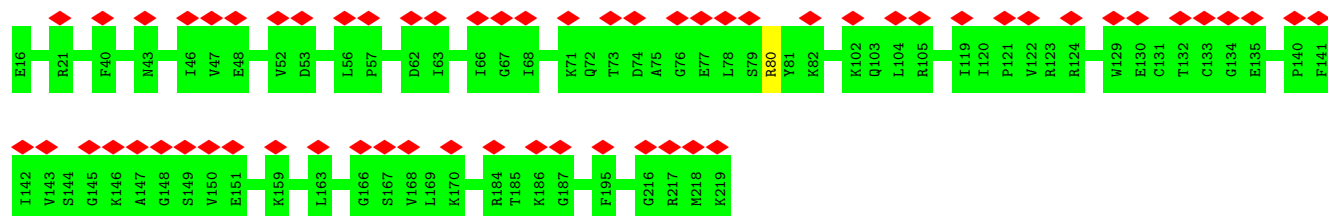


- Molecule 42: 30S ribosomal protein S4

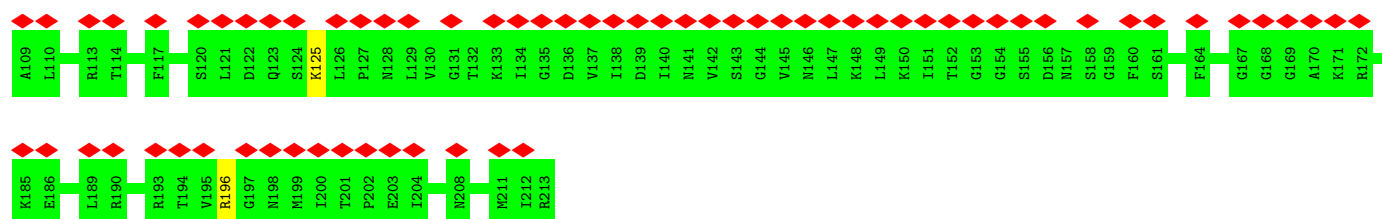




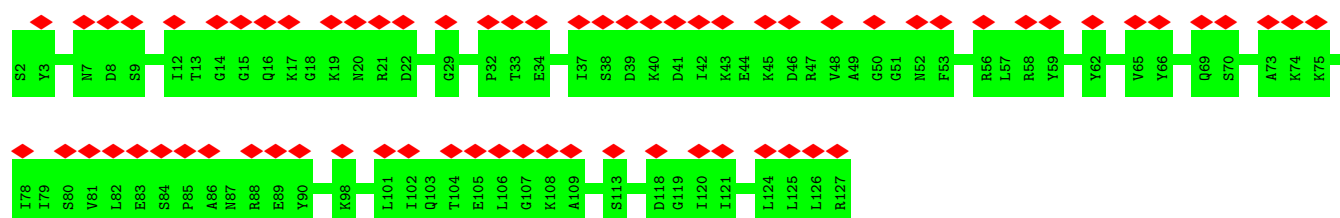
- Molecule 43: 30S ribosomal protein S5



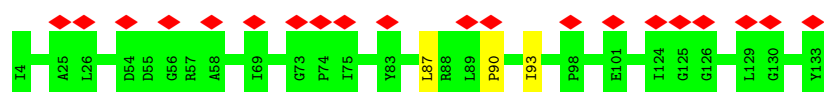
- Molecule 44: 30S ribosomal protein S6



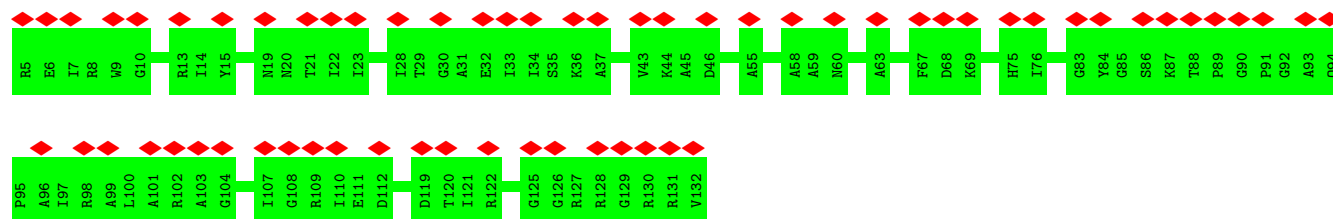
- Molecule 45: 30S ribosomal protein S8e



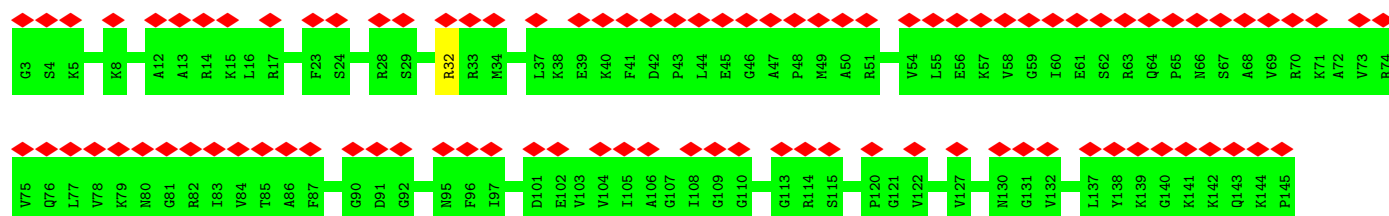
- Molecule 46: 30S ribosomal protein S8



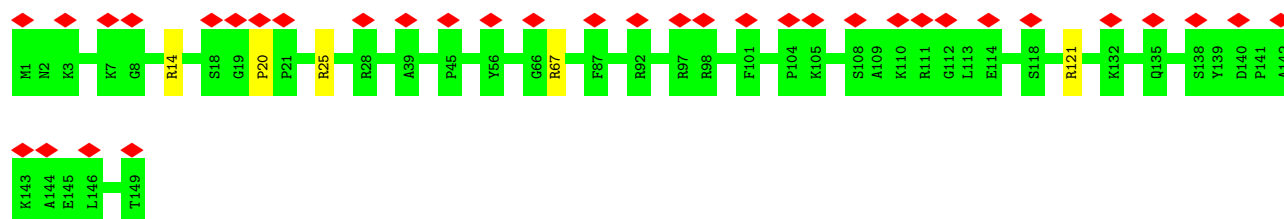
- Molecule 47: 30S ribosomal protein S11



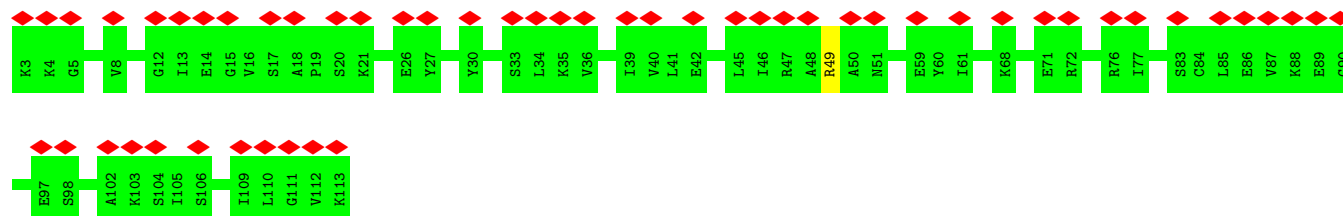
• Molecule 48: 30S ribosomal protein S12



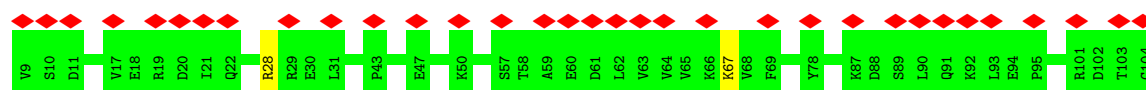
• Molecule 49: 30S ribosomal protein S15



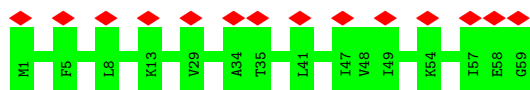
• Molecule 50: 30S ribosomal protein S17



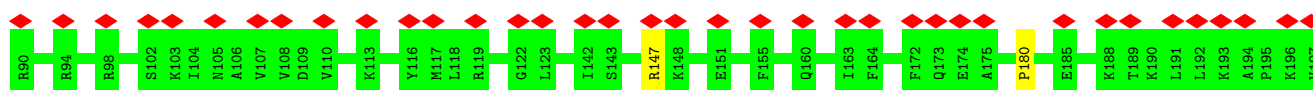
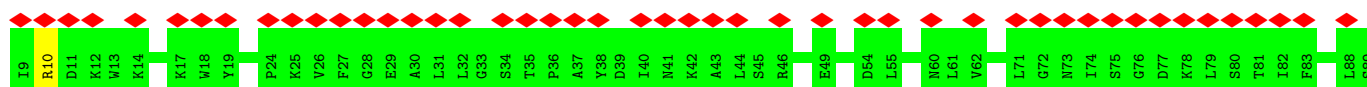
• Molecule 51: 30S ribosomal protein S24e



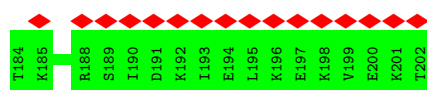
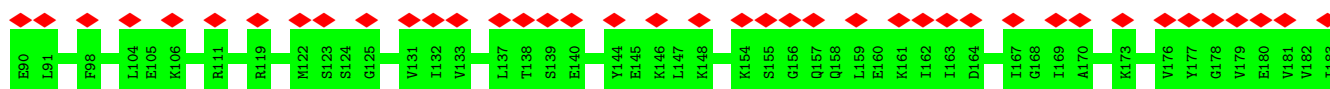
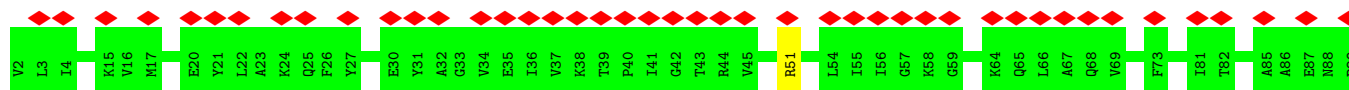
- Molecule 52: 30S ribosomal protein S27e



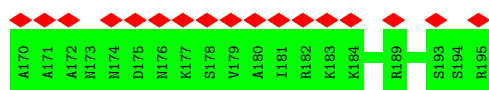
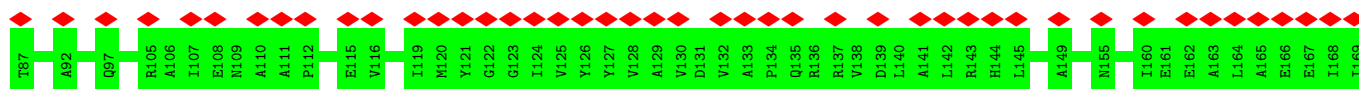
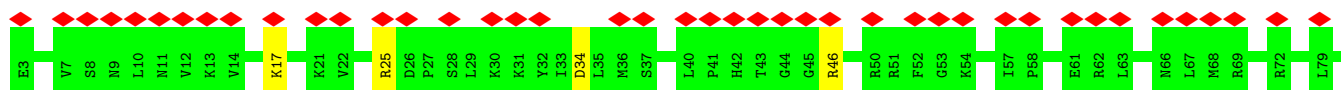
- Molecule 53: 30S ribosomal protein S3Ae



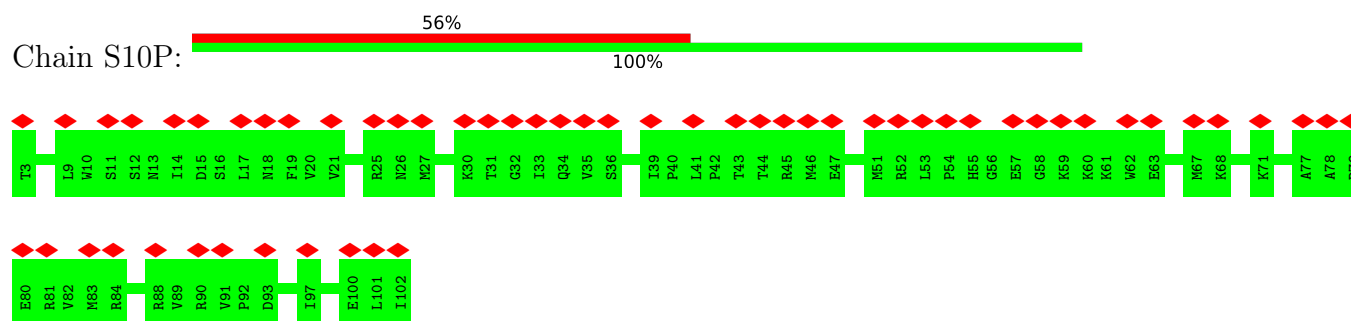
- Molecule 54: 30S ribosomal protein S3



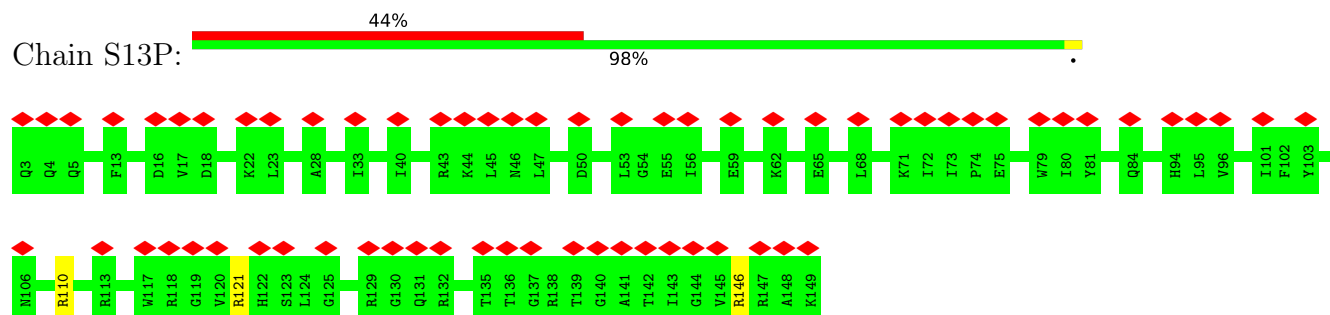
- Molecule 55: 30S ribosomal protein S7



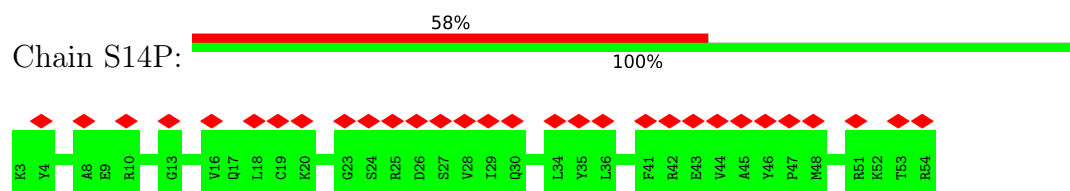
- Molecule 56: 30S ribosomal protein S10



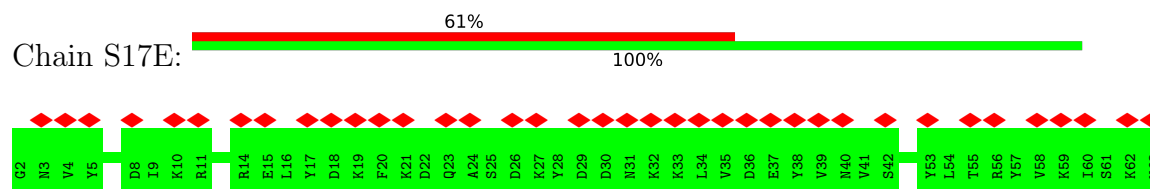
- Molecule 57: 30S ribosomal protein S13



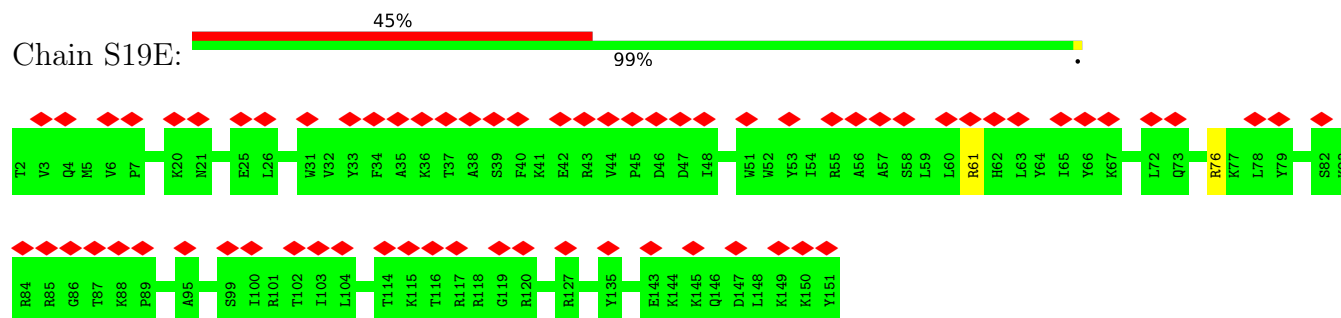
- Molecule 58: 30S ribosomal protein S14 type Z



- Molecule 59: 30S ribosomal protein S17e

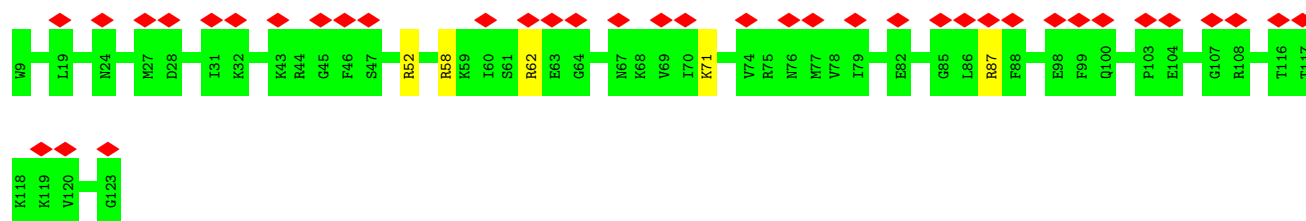


- Molecule 60: 30S ribosomal protein S19e



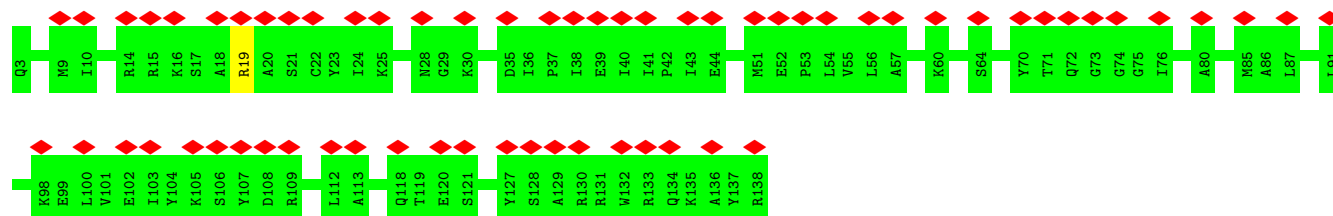
- Molecule 61: 30S ribosomal protein S19





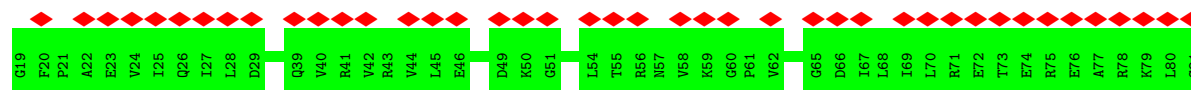
- Molecule 62: 30S ribosomal protein S9

Chain AS9P: 46% 99%



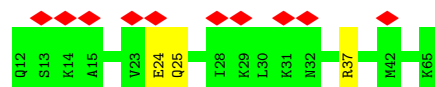
- Molecule 63: 30S ribosomal protein S28e

Chain S28E: 67% 100%



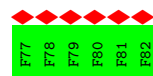
- Molecule 64: 30S ribosomal protein S27ae

Chain S27A: 19% 94% 6%



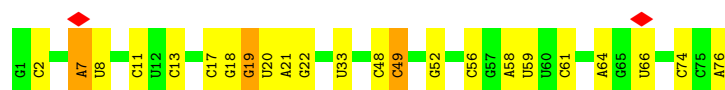
- Molecule 65: PHE-PHE-PHE-PHE-PHE-PHE

Chain APTP: 100% 100%

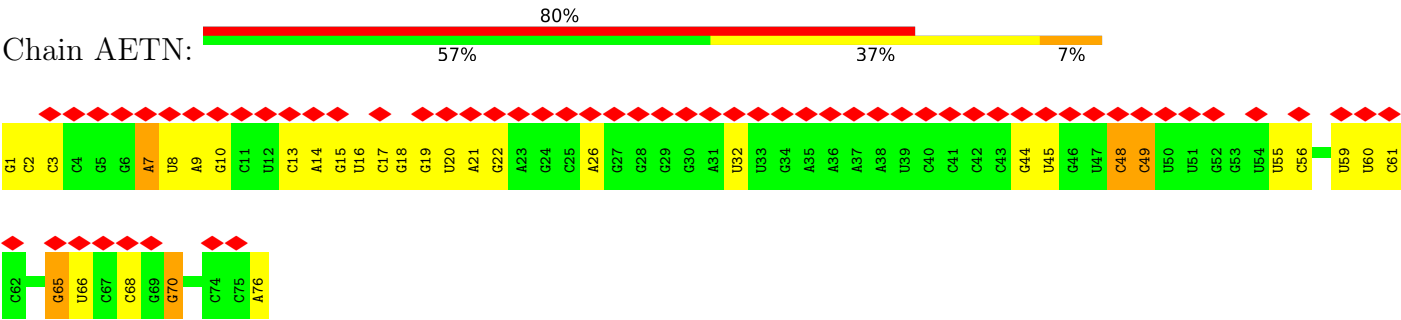


- Molecule 66: tRNA (76-MER)

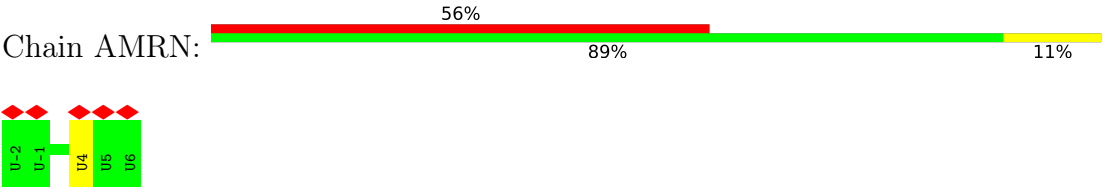
Chain APTN: 70% 26%



- Molecule 66: tRNA (76-MER)



- Molecule 67: mRNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*UP*U)-3')



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	3842	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	26.7	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.115	Depositor
Minimum map value	-0.446	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.089	Depositor
Recommended contour level	0.33	Depositor
Map size (Å)	413.06, 413.06, 413.06	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.087, 1.087, 1.087	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	A23S	0.52	43/72052 (0.1%)	1.06	380/112414 (0.3%)
2	A16S	0.60	43/35889 (0.1%)	1.24	382/56002 (0.7%)
3	A5S	0.38	0/2917	0.77	0/4549
4	AL1P	0.25	0/1739	0.52	0/2338
5	AL2P	0.29	0/1787	0.55	0/2409
6	AL3P	0.29	0/2758	0.55	0/3727
7	AL4P	0.27	0/1956	0.55	0/2635
8	AL5P	0.28	0/1364	0.56	0/1827
9	AL6P	0.29	0/1450	0.54	0/1949
10	ALX0	0.31	0/638	0.63	0/851
11	L10E	0.29	0/1334	0.55	0/1787
12	L13P	0.27	0/1123	0.56	0/1502
13	L141	0.27	0/673	0.51	0/900
13	L142	0.27	0/673	0.54	0/900
14	L14P	0.29	0/1054	0.56	0/1425
15	L15E	0.30	0/1458	0.61	0/1956
16	L18E	0.28	0/907	0.53	0/1214
17	L18P	0.28	0/1570	0.50	0/2115
18	L19E	0.28	0/1223	0.57	0/1622
19	L22P	0.28	0/1246	0.51	0/1671
20	L23P	0.28	0/655	0.50	0/874
21	L24E	0.29	0/451	0.53	0/599
22	L24P	0.28	0/1000	0.60	0/1329
23	L29P	0.25	0/513	0.60	0/678
24	L30E	0.30	0/738	0.51	0/985
25	L30P	0.29	0/1278	0.56	0/1713
26	L31E	0.28	0/632	0.67	0/837
27	L32E	0.28	0/1027	0.57	0/1366
28	L34E	0.55	1/642 (0.2%)	0.93	7/854 (0.8%)
29	L37A	0.32	0/542	0.57	0/726
30	L37E	0.30	0/445	0.60	0/585
31	L39E	0.28	0/422	0.63	0/562

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	L40E	0.25	0/443	0.69	0/587
33	L44E	0.28	0/763	0.55	0/1008
34	L7A1	0.27	0/946	0.45	0/1272
34	L7A2	0.26	0/946	0.45	0/1272
34	SL7A	0.26	0/946	0.48	0/1272
35	L15P	0.26	0/766	0.51	0/1023
36	L21E	0.28	0/800	0.55	0/1067
37	L45A	0.28	0/824	0.52	0/1094
38	L46A	0.27	0/595	0.49	0/793
39	L47A	0.24	0/652	0.56	0/870
40	AS2P	0.27	0/1621	0.54	0/2202
41	AS4E	0.27	0/1956	0.58	0/2635
42	AS4P	0.26	0/1399	0.57	0/1883
43	AS5P	0.29	0/1631	0.53	0/2200
44	AS6E	0.27	0/815	0.60	0/1093
45	AS8E	0.27	0/1005	0.57	0/1342
46	AS8P	0.31	0/1046	0.58	0/1410
47	S11P	0.27	0/976	0.60	0/1315
48	S12P	0.28	0/1120	0.58	0/1495
49	S15P	0.28	0/1250	0.56	0/1677
50	S17P	0.28	0/899	0.55	0/1203
51	S24E	0.27	0/769	0.49	0/1034
52	S27E	0.28	0/465	0.50	0/618
53	S3AE	0.27	0/1573	0.53	0/2115
54	AS3P	0.28	0/1599	0.52	0/2147
55	AS7P	0.27	0/1561	0.56	0/2105
56	S10P	0.27	0/840	0.55	0/1132
57	S13P	0.26	0/1221	0.59	0/1634
58	S14P	0.31	0/441	0.66	0/583
59	S17E	0.25	0/523	0.47	0/696
60	S19E	0.26	0/1267	0.56	0/1705
61	S19P	0.27	0/985	0.56	0/1310
62	AS9P	0.28	0/1115	0.58	0/1496
63	S28E	0.25	0/500	0.65	0/669
64	S27A	0.36	0/444	0.66	0/590
65	APTP	0.37	0/72	0.47	0/93
66	AETN	0.49	1/1809 (0.1%)	1.30	29/2819 (1.0%)
66	APTN	0.48	1/1809 (0.1%)	1.35	22/2819 (0.8%)
67	AMRN	0.24	0/197	0.83	0/302
All	All	0.47	89/180745 (0.0%)	0.97	820/267481 (0.3%)

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	A16S	0	1
28	L34E	0	1
42	AS4P	0	1
46	AS8P	0	3
49	S15P	0	1
55	AS7P	0	1
64	S27A	0	1
All	All	0	9

The worst 5 of 89 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A16S	381	C	C2-O2	-16.42	1.09	1.24
2	A16S	381	C	N1-C6	-14.93	1.28	1.37
28	L34E	19	PRO	C-N	10.21	1.57	1.34
2	A16S	379	G	N1-C2	9.11	1.45	1.37
2	A16S	381	C	C4-C5	-9.04	1.35	1.43

The worst 5 of 820 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A16S	381	C	N1-C2-O2	-58.89	83.57	118.90
1	A23S	1626	C	C6-N1-C2	-47.77	101.19	120.30
1	A23S	1626	C	C5-C6-N1	34.41	138.21	121.00
2	A16S	381	C	N3-C2-O2	33.62	145.44	121.90
1	A23S	2433	C	N3-C4-N4	-31.08	96.24	118.00

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A16S	381	C	Sidechain
42	AS4P	163	GLN	Peptide
46	AS8P	87	LEU	Peptide
46	AS8P	90	PRO	Peptide
28	L34E	36	ARG	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	A23S	64360	0	0	0	0
2	A16S	32063	0	0	0	0
3	A5S	2609	0	1324	102	0
4	AL1P	1715	0	0	0	0
5	AL2P	1754	0	0	0	0
6	AL3P	2695	0	0	0	0
7	AL4P	1926	0	0	0	0
8	AL5P	1343	0	0	0	0
9	AL6P	1431	0	0	0	0
10	ALX0	629	0	0	0	0
11	L10E	1310	0	0	0	0
12	L13P	1109	0	0	0	0
13	L141	669	0	0	0	0
13	L142	669	0	0	0	0
14	L14P	1034	0	0	0	0
15	L15E	1423	0	0	0	0
16	L18E	895	0	0	0	0
17	L18P	1539	0	0	0	0
18	L19E	1206	0	0	0	0
19	L22P	1223	0	0	0	0
20	L23P	650	0	0	0	0
21	L24E	441	0	0	0	0
22	L24P	989	0	0	0	0
23	L29P	513	0	0	0	0
24	L30E	729	0	0	0	0
25	L30P	1254	0	0	0	0
26	L31E	625	0	0	0	0
27	L32E	1010	0	0	0	0
28	L34E	629	0	0	0	0
29	L37A	527	0	0	0	0
30	L37E	436	0	0	0	0
31	L39E	414	0	0	0	0
32	L40E	439	0	0	0	0
33	L44E	753	0	0	0	0
34	L7A1	935	0	0	0	0
34	L7A2	935	0	0	0	0
34	SL7A	935	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	L15P	752	0	0	0	0
36	L21E	785	0	0	0	0
37	L45A	816	0	0	0	0
38	L46A	586	0	0	0	0
39	L47A	648	0	0	0	0
40	AS2P	1587	0	0	0	0
41	AS4E	1925	0	0	0	0
42	AS4P	1370	0	0	0	0
43	AS5P	1600	0	0	0	0
44	AS6E	805	0	0	0	0
45	AS8E	993	0	0	0	0
46	AS8P	1028	0	0	0	0
47	S11P	960	0	0	0	0
48	S12P	1103	0	0	0	0
49	S15P	1225	0	0	0	0
50	S17P	885	0	0	0	0
51	S24E	759	0	0	0	0
52	S27E	458	0	0	0	0
53	S3AE	1545	0	0	0	0
54	AS3P	1576	0	0	0	0
55	AS7P	1537	0	0	0	0
56	S10P	824	0	0	0	0
57	S13P	1204	0	0	0	0
58	S14P	432	0	0	0	0
59	S17E	517	0	0	0	0
60	S19E	1239	0	0	0	0
61	S19P	968	0	0	0	0
62	AS9P	1096	0	0	0	0
63	S28E	498	0	0	0	0
64	S27A	435	0	0	0	0
65	APTP	67	0	0	0	0
66	AETN	1619	0	0	0	0
66	APTN	1619	0	0	0	0
67	AMRN	180	0	0	0	0
68	AS2P	171	0	0	0	0
68	AS5P	90	0	0	0	0
68	AS8P	25	0	0	0	0
All	All	167743	0	1324	102	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 41.

The worst 5 of 102 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)
3:A5S:75:G:N1	3:A5S:107:C:O2	2.13	0.81
3:A5S:10:G:N1	3:A5S:115:U:O2	2.15	0.75
3:A5S:35:G:C6	3:A5S:45:G:H1'	2.23	0.73
3:A5S:2:G:H1	3:A5S:122:G:H2'	1.53	0.73
3:A5S:121:G:H2'	3:A5S:122:G:C8	2.28	0.69

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	
4	AL1P	214/216 (99%)	194 (91%)	20 (9%)	0	100	100
5	AL2P	232/234 (99%)	219 (94%)	13 (6%)	0	100	100
6	AL3P	337/339 (99%)	295 (88%)	42 (12%)	0	100	100
7	AL4P	249/251 (99%)	229 (92%)	20 (8%)	0	100	100
8	AL5P	166/168 (99%)	145 (87%)	21 (13%)	0	100	100
9	AL6P	179/181 (99%)	156 (87%)	23 (13%)	0	100	100
10	ALX0	74/76 (97%)	63 (85%)	11 (15%)	0	100	100
11	L10E	162/164 (99%)	148 (91%)	14 (9%)	0	100	100
12	L13P	138/140 (99%)	122 (88%)	16 (12%)	0	100	100
13	L141	84/86 (98%)	74 (88%)	10 (12%)	0	100	100
13	L142	84/86 (98%)	69 (82%)	15 (18%)	0	100	100
14	L14P	132/134 (98%)	118 (89%)	14 (11%)	0	100	100
15	L15E	167/169 (99%)	156 (93%)	11 (7%)	0	100	100
16	L18E	110/112 (98%)	105 (96%)	5 (4%)	0	100	100
17	L18P	191/193 (99%)	178 (93%)	13 (7%)	0	100	100
18	L19E	142/144 (99%)	132 (93%)	10 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	L22P	148/150 (99%)	136 (92%)	12 (8%)	0	100	100
20	L23P	79/81 (98%)	70 (89%)	9 (11%)	0	100	100
21	L24E	52/54 (96%)	49 (94%)	3 (6%)	0	100	100
22	L24P	120/122 (98%)	112 (93%)	8 (7%)	0	100	100
23	L29P	61/63 (97%)	52 (85%)	9 (15%)	0	100	100
24	L30E	92/94 (98%)	83 (90%)	9 (10%)	0	100	100
25	L30P	153/155 (99%)	128 (84%)	25 (16%)	0	100	100
26	L31E	73/75 (97%)	66 (90%)	7 (10%)	0	100	100
27	L32E	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
28	L34E	75/77 (97%)	57 (76%)	17 (23%)	1 (1%)	10	42
29	L37A	63/65 (97%)	50 (79%)	13 (21%)	0	100	100
30	L37E	52/54 (96%)	47 (90%)	5 (10%)	0	100	100
31	L39E	47/49 (96%)	37 (79%)	10 (21%)	0	100	100
32	L40E	53/55 (96%)	43 (81%)	10 (19%)	0	100	100
33	L44E	90/92 (98%)	85 (94%)	5 (6%)	0	100	100
34	L7A1	121/123 (98%)	116 (96%)	5 (4%)	0	100	100
34	L7A2	121/123 (98%)	115 (95%)	6 (5%)	0	100	100
34	SL7A	121/123 (98%)	107 (88%)	14 (12%)	0	100	100
35	L15P	90/144 (62%)	81 (90%)	9 (10%)	0	100	100
36	L21E	95/97 (98%)	89 (94%)	6 (6%)	0	100	100
37	L45A	99/101 (98%)	77 (78%)	19 (19%)	3 (3%)	3	22
38	L46A	68/70 (97%)	62 (91%)	6 (9%)	0	100	100
39	L47A	78/80 (98%)	67 (86%)	11 (14%)	0	100	100
40	AS2P	194/196 (99%)	178 (92%)	16 (8%)	0	100	100
41	AS4E	238/240 (99%)	199 (84%)	39 (16%)	0	100	100
42	AS4P	164/166 (99%)	138 (84%)	26 (16%)	0	100	100
43	AS5P	202/204 (99%)	177 (88%)	25 (12%)	0	100	100
44	AS6E	103/105 (98%)	79 (77%)	24 (23%)	0	100	100
45	AS8E	124/126 (98%)	114 (92%)	10 (8%)	0	100	100
46	AS8P	128/130 (98%)	107 (84%)	21 (16%)	0	100	100
47	S11P	126/128 (98%)	108 (86%)	18 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	S12P	141/143 (99%)	116 (82%)	25 (18%)	0	100	100
49	S15P	147/149 (99%)	129 (88%)	18 (12%)	0	100	100
50	S17P	109/111 (98%)	96 (88%)	13 (12%)	0	100	100
51	S24E	94/96 (98%)	84 (89%)	10 (11%)	0	100	100
52	S27E	57/59 (97%)	47 (82%)	10 (18%)	0	100	100
53	S3AE	187/189 (99%)	164 (88%)	22 (12%)	1 (0%)	25	64
54	AS3P	199/201 (99%)	183 (92%)	16 (8%)	0	100	100
55	AS7P	191/193 (99%)	165 (86%)	26 (14%)	0	100	100
56	S10P	98/100 (98%)	90 (92%)	8 (8%)	0	100	100
57	S13P	145/147 (99%)	124 (86%)	21 (14%)	0	100	100
58	S14P	50/52 (96%)	40 (80%)	10 (20%)	0	100	100
59	S17E	60/62 (97%)	55 (92%)	5 (8%)	0	100	100
60	S19E	148/150 (99%)	125 (84%)	23 (16%)	0	100	100
61	S19P	113/115 (98%)	98 (87%)	15 (13%)	0	100	100
62	AS9P	134/136 (98%)	121 (90%)	13 (10%)	0	100	100
63	S28E	61/63 (97%)	52 (85%)	9 (15%)	0	100	100
64	S27A	52/54 (96%)	39 (75%)	12 (23%)	1 (2%)	6	32
65	APTP	4/6 (67%)	2 (50%)	2 (50%)	0	100	100
All	All	8002/8184 (98%)	7073 (88%)	923 (12%)	6 (0%)	50	83

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
28	L34E	19	PRO
37	L45A	55	VAL
37	L45A	4	VAL
37	L45A	67	THR
64	S27A	25	GLN

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	
4	AL1P	189/190 (100%)	189 (100%)	0	100	100
5	AL2P	181/181 (100%)	177 (98%)	4 (2%)	47	66
6	AL3P	297/297 (100%)	295 (99%)	2 (1%)	81	87
7	AL4P	212/212 (100%)	209 (99%)	3 (1%)	62	76
8	AL5P	144/144 (100%)	143 (99%)	1 (1%)	81	87
9	AL6P	157/157 (100%)	155 (99%)	2 (1%)	65	77
10	ALX0	68/68 (100%)	65 (96%)	3 (4%)	24	46
11	L10E	137/137 (100%)	136 (99%)	1 (1%)	81	87
12	L13P	121/121 (100%)	121 (100%)	0	100	100
13	L141	74/74 (100%)	73 (99%)	1 (1%)	62	76
13	L142	74/74 (100%)	74 (100%)	0	100	100
14	L14P	110/110 (100%)	109 (99%)	1 (1%)	75	83
15	L15E	146/146 (100%)	144 (99%)	2 (1%)	62	76
16	L18E	98/98 (100%)	98 (100%)	0	100	100
17	L18P	162/162 (100%)	162 (100%)	0	100	100
18	L19E	126/126 (100%)	125 (99%)	1 (1%)	79	85
19	L22P	131/131 (100%)	129 (98%)	2 (2%)	60	75
20	L23P	74/74 (100%)	74 (100%)	0	100	100
21	L24E	50/50 (100%)	50 (100%)	0	100	100
22	L24P	108/108 (100%)	107 (99%)	1 (1%)	75	83
23	L29P	59/59 (100%)	58 (98%)	1 (2%)	56	73
24	L30E	83/83 (100%)	83 (100%)	0	100	100
25	L30P	136/136 (100%)	134 (98%)	2 (2%)	60	75
26	L31E	66/66 (100%)	65 (98%)	1 (2%)	60	75
27	L32E	106/106 (100%)	106 (100%)	0	100	100
28	L34E	70/70 (100%)	69 (99%)	1 (1%)	62	76
29	L37A	53/53 (100%)	53 (100%)	0	100	100
30	L37E	45/45 (100%)	45 (100%)	0	100	100
31	L39E	44/44 (100%)	44 (100%)	0	100	100
32	L40E	50/50 (100%)	50 (100%)	0	100	100
33	L44E	84/84 (100%)	83 (99%)	1 (1%)	67	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	L7A1	104/104 (100%)	103 (99%)	1 (1%)	73	82
34	L7A2	104/104 (100%)	104 (100%)	0	100	100
34	SL7A	104/104 (100%)	104 (100%)	0	100	100
35	L15P	78/118 (66%)	77 (99%)	1 (1%)	65	77
36	L21E	85/85 (100%)	84 (99%)	1 (1%)	67	79
37	L45A	91/91 (100%)	89 (98%)	2 (2%)	47	66
38	L46A	66/66 (100%)	66 (100%)	0	100	100
39	L47A	74/74 (100%)	73 (99%)	1 (1%)	62	76
40	AS2P	174/174 (100%)	174 (100%)	0	100	100
41	AS4E	210/210 (100%)	208 (99%)	2 (1%)	73	82
42	AS4P	149/149 (100%)	149 (100%)	0	100	100
43	AS5P	174/174 (100%)	173 (99%)	1 (1%)	84	88
44	AS6E	88/88 (100%)	86 (98%)	2 (2%)	45	64
45	AS8E	106/106 (100%)	106 (100%)	0	100	100
46	AS8P	111/111 (100%)	111 (100%)	0	100	100
47	S11P	94/94 (100%)	94 (100%)	0	100	100
48	S12P	116/116 (100%)	115 (99%)	1 (1%)	75	83
49	S15P	133/133 (100%)	129 (97%)	4 (3%)	36	56
50	S17P	97/97 (100%)	96 (99%)	1 (1%)	73	82
51	S24E	84/84 (100%)	82 (98%)	2 (2%)	44	63
52	S27E	51/51 (100%)	51 (100%)	0	100	100
53	S3AE	170/170 (100%)	168 (99%)	2 (1%)	67	79
54	AS3P	165/165 (100%)	164 (99%)	1 (1%)	84	88
55	AS7P	166/166 (100%)	163 (98%)	3 (2%)	54	71
56	S10P	92/92 (100%)	92 (100%)	0	100	100
57	S13P	129/129 (100%)	126 (98%)	3 (2%)	45	64
58	S14P	45/45 (100%)	45 (100%)	0	100	100
59	S17E	57/57 (100%)	57 (100%)	0	100	100
60	S19E	134/134 (100%)	132 (98%)	2 (2%)	60	75
61	S19P	106/106 (100%)	101 (95%)	5 (5%)	22	44
62	AS9P	113/113 (100%)	112 (99%)	1 (1%)	75	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
63	S28E	54/54 (100%)	54 (100%)	0	100	100
64	S27A	47/47 (100%)	46 (98%)	1 (2%)	48	67
65	APTP	6/6 (100%)	6 (100%)	0	100	100
All	All	7032/7073 (99%)	6965 (99%)	67 (1%)	71	82

5 of 67 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
57	S13P	146	ARG
60	S19E	76	ARG
62	AS9P	19	ARG
23	L29P	40	LYS
22	L24P	82	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A23S	2986/3022 (98%)	1168 (39%)	55 (1%)
2	A16S	1491/1503 (99%)	618 (41%)	58 (3%)
3	A5S	121/122 (99%)	39 (32%)	1 (0%)
66	AETN	75/76 (98%)	31 (41%)	2 (2%)
66	APTN	75/76 (98%)	21 (28%)	1 (1%)
67	AMRN	8/9 (88%)	1 (12%)	0
All	All	4756/4808 (98%)	1878 (39%)	117 (2%)

5 of 1878 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A23S	6	A
1	A23S	7	G
1	A23S	18	G
1	A23S	19	A
1	A23S	25	C

5 of 117 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	A16S	63	A
2	A16S	1453	A
2	A16S	293	A
2	A16S	1451	A
2	A16S	1165	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 57 ligands modelled in this entry, 57 are unknown - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

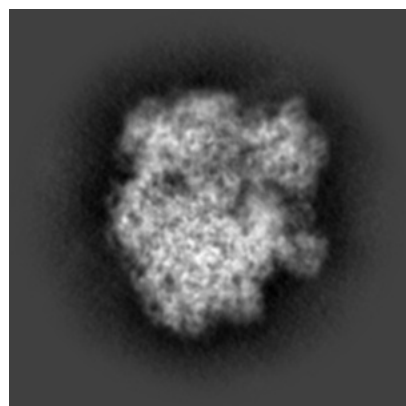
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34864. These allow visual inspection of the internal detail of the map and identification of artifacts.

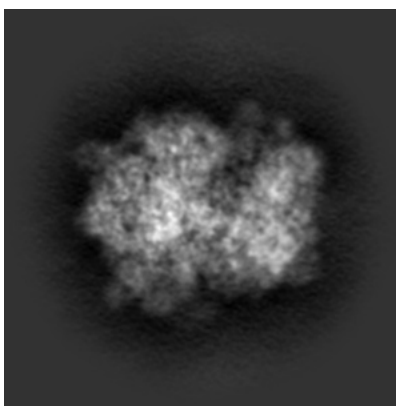
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

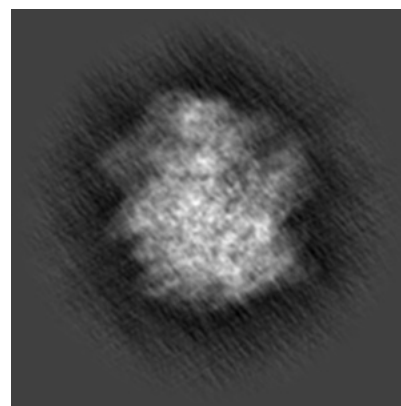
6.1.1 Primary map



X

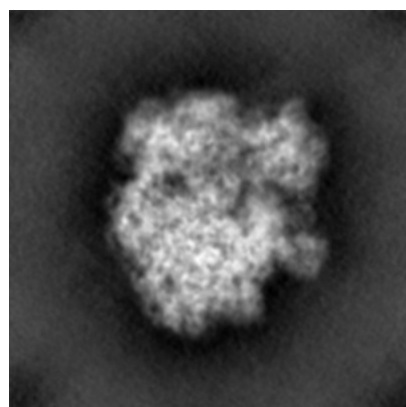


Y

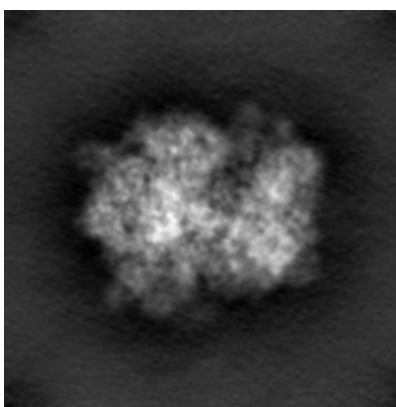


Z

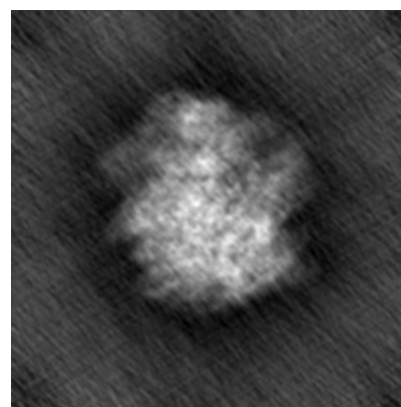
6.1.2 Raw map



X



Y

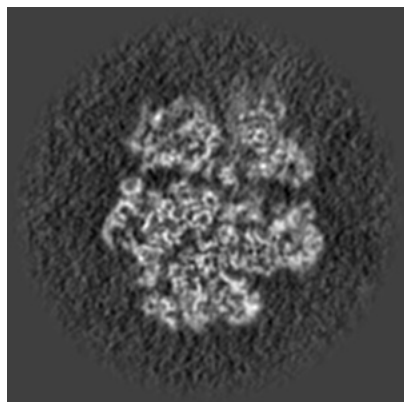


Z

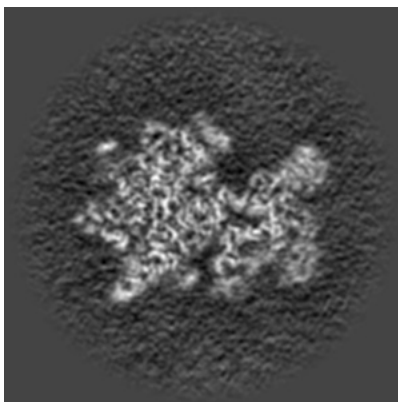
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

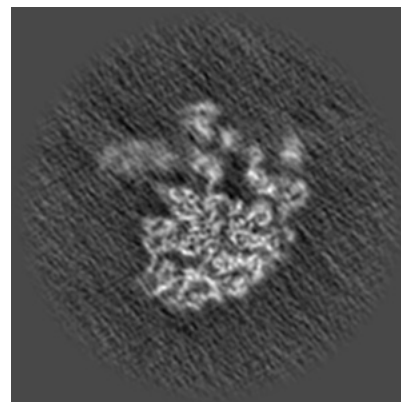
6.2.1 Primary map



X Index: 190

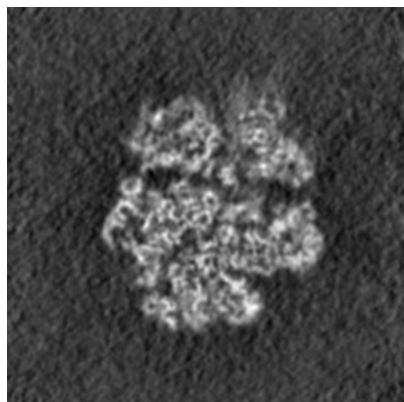


Y Index: 190

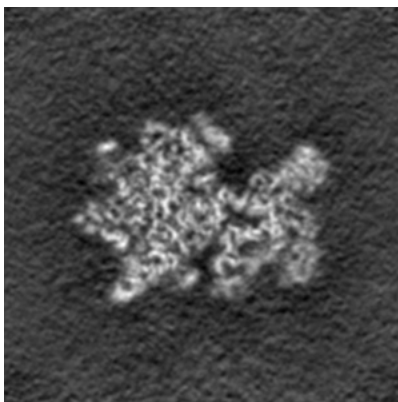


Z Index: 190

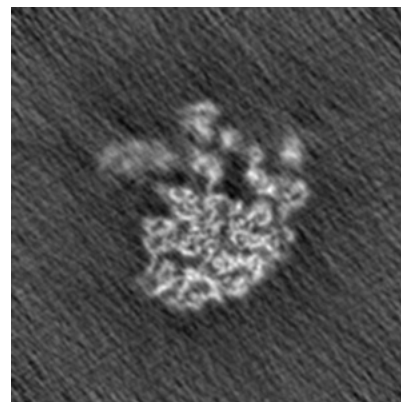
6.2.2 Raw map



X Index: 190



Y Index: 190

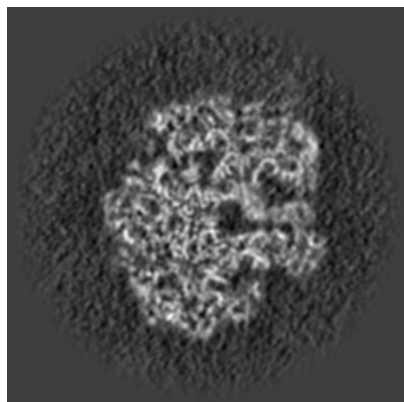


Z Index: 190

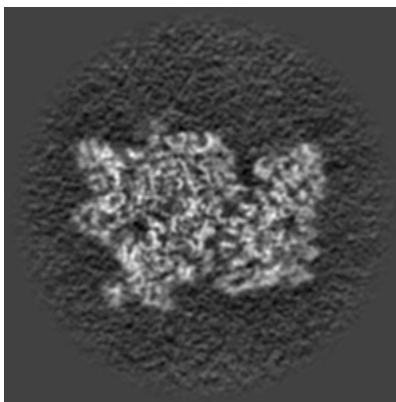
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

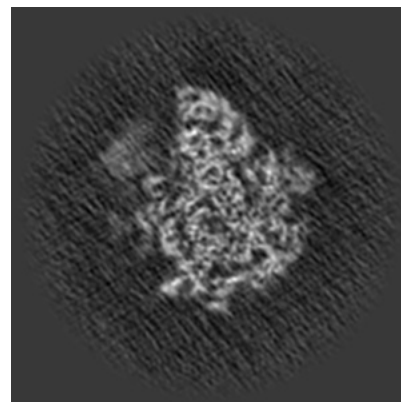
6.3.1 Primary map



X Index: 177

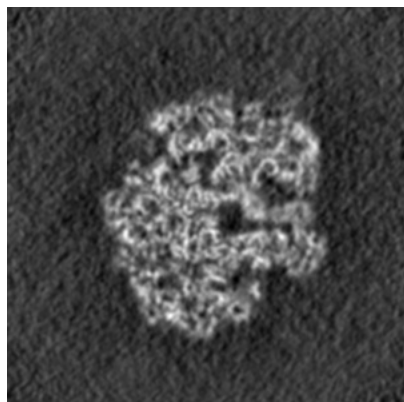


Y Index: 178

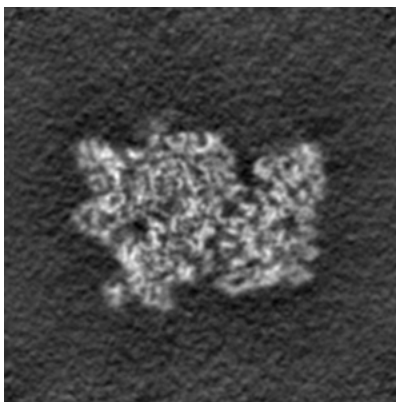


Z Index: 159

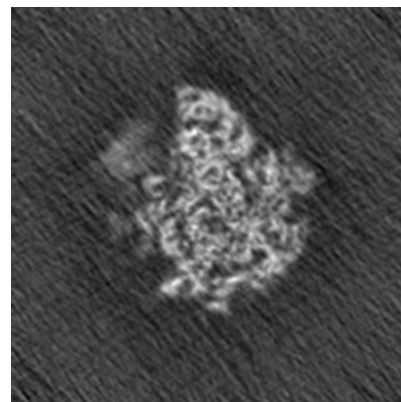
6.3.2 Raw map



X Index: 176



Y Index: 178

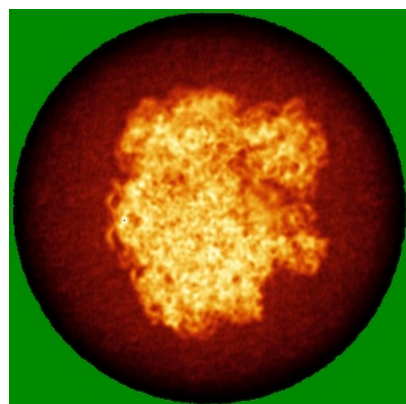


Z Index: 159

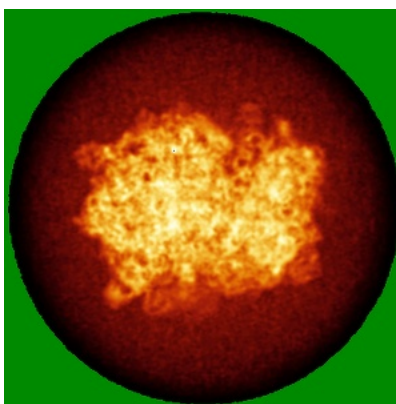
The images above show the largest variance slices of the map in three orthogonal directions.

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

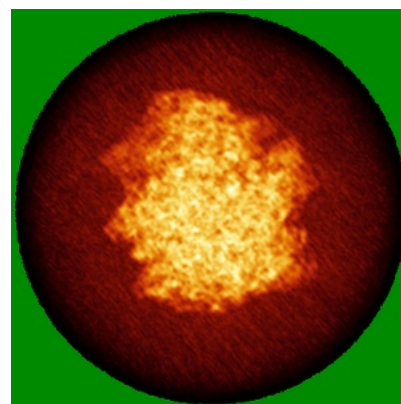
6.4.1 Primary map



X

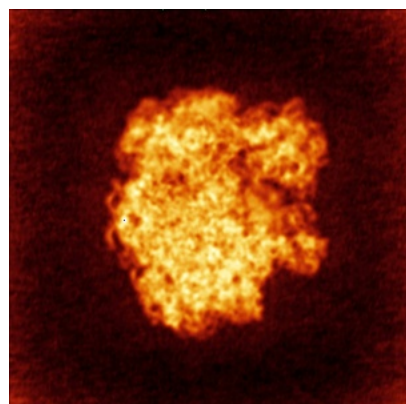


Y

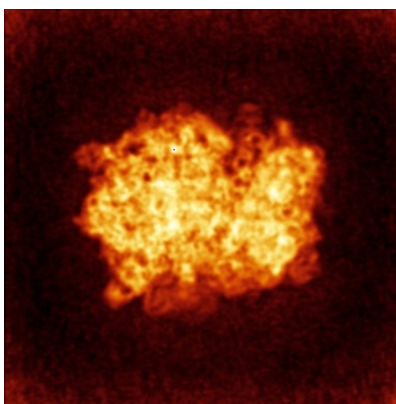


Z

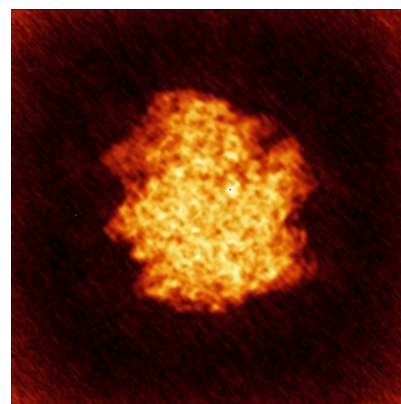
6.4.2 Raw map



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.

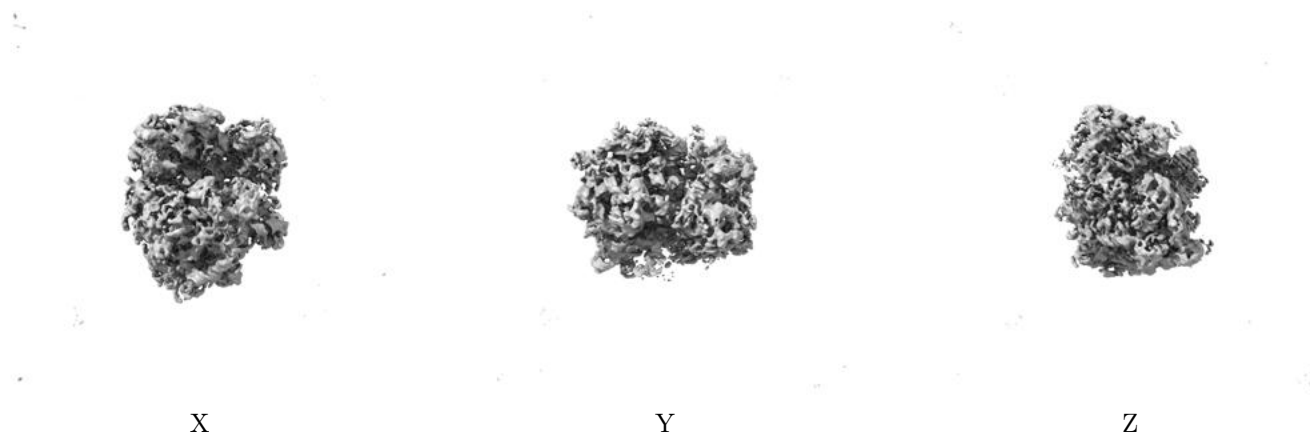
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.33. 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.

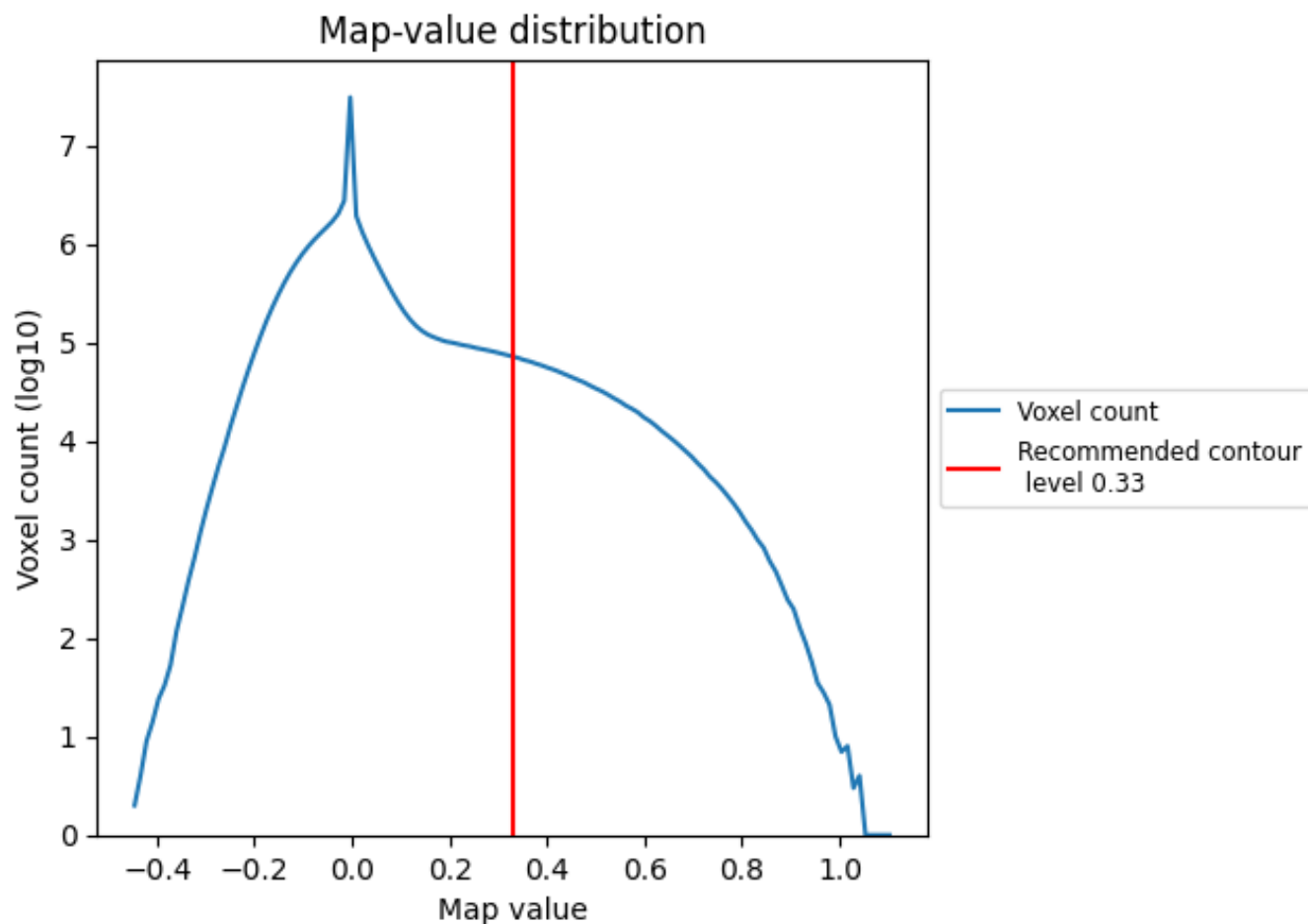
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

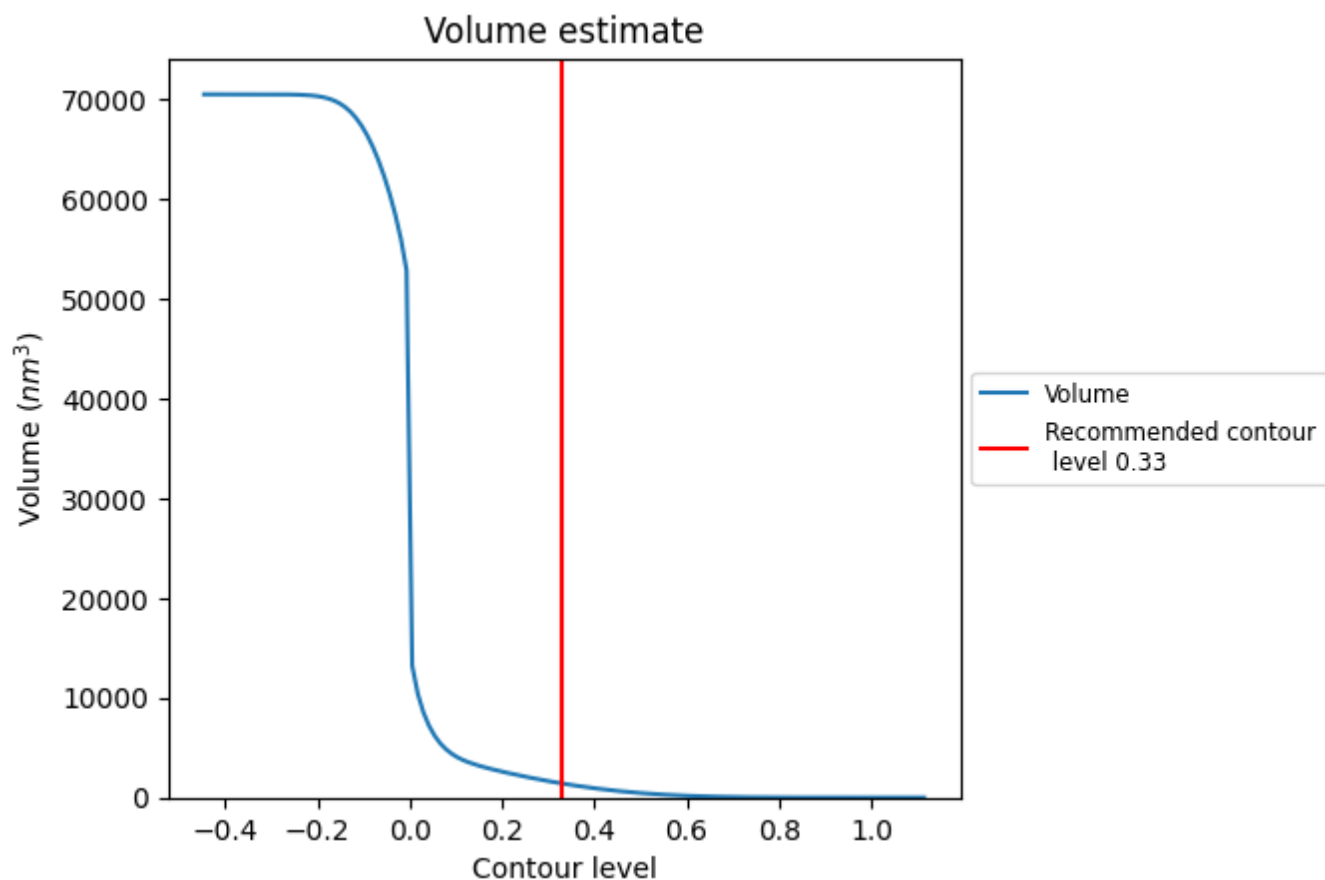
This section contains the results of statistical analysis of the map.

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.

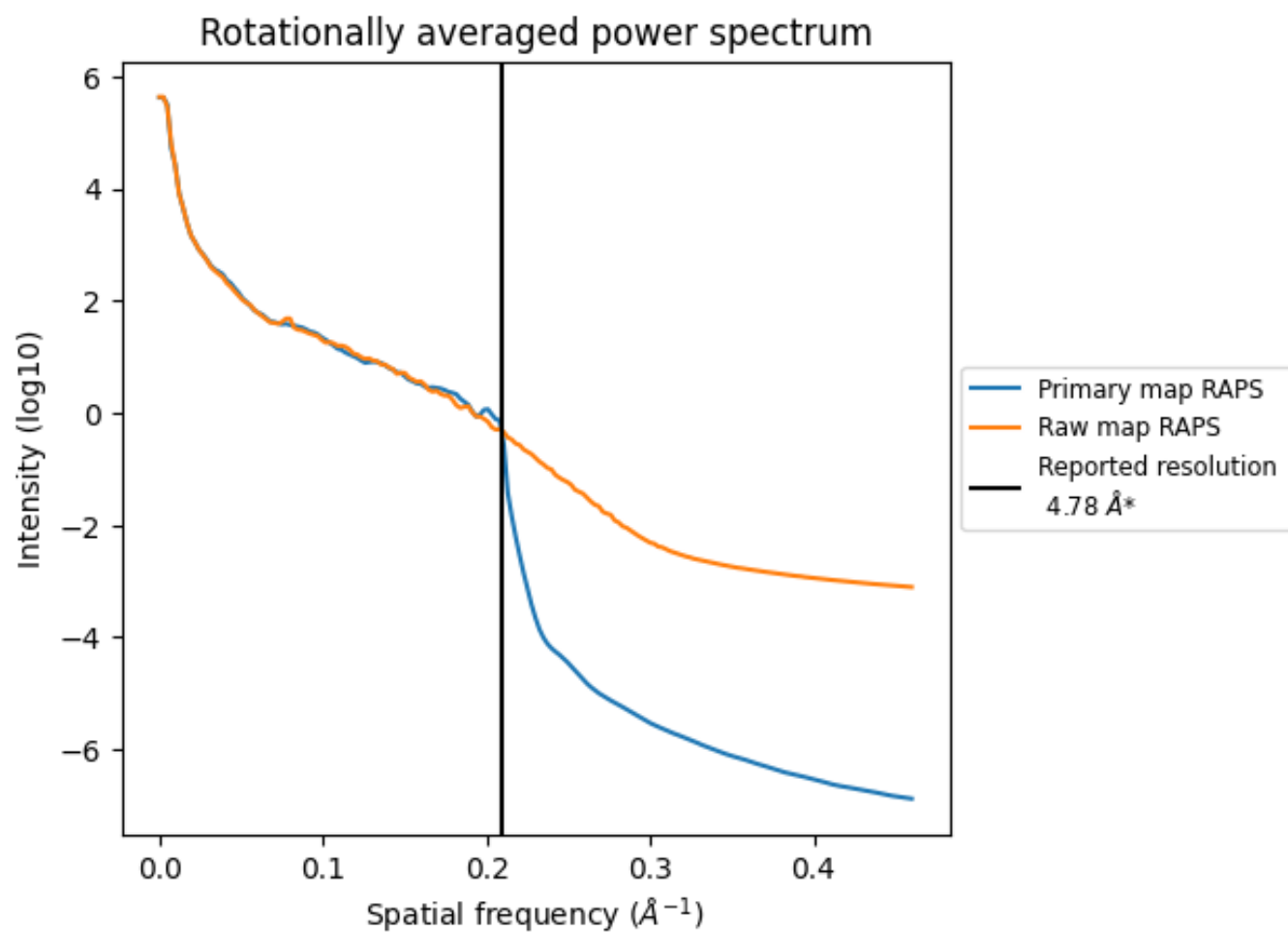
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1414 nm³; this corresponds to an approximate mass of 1277 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 ⓘ

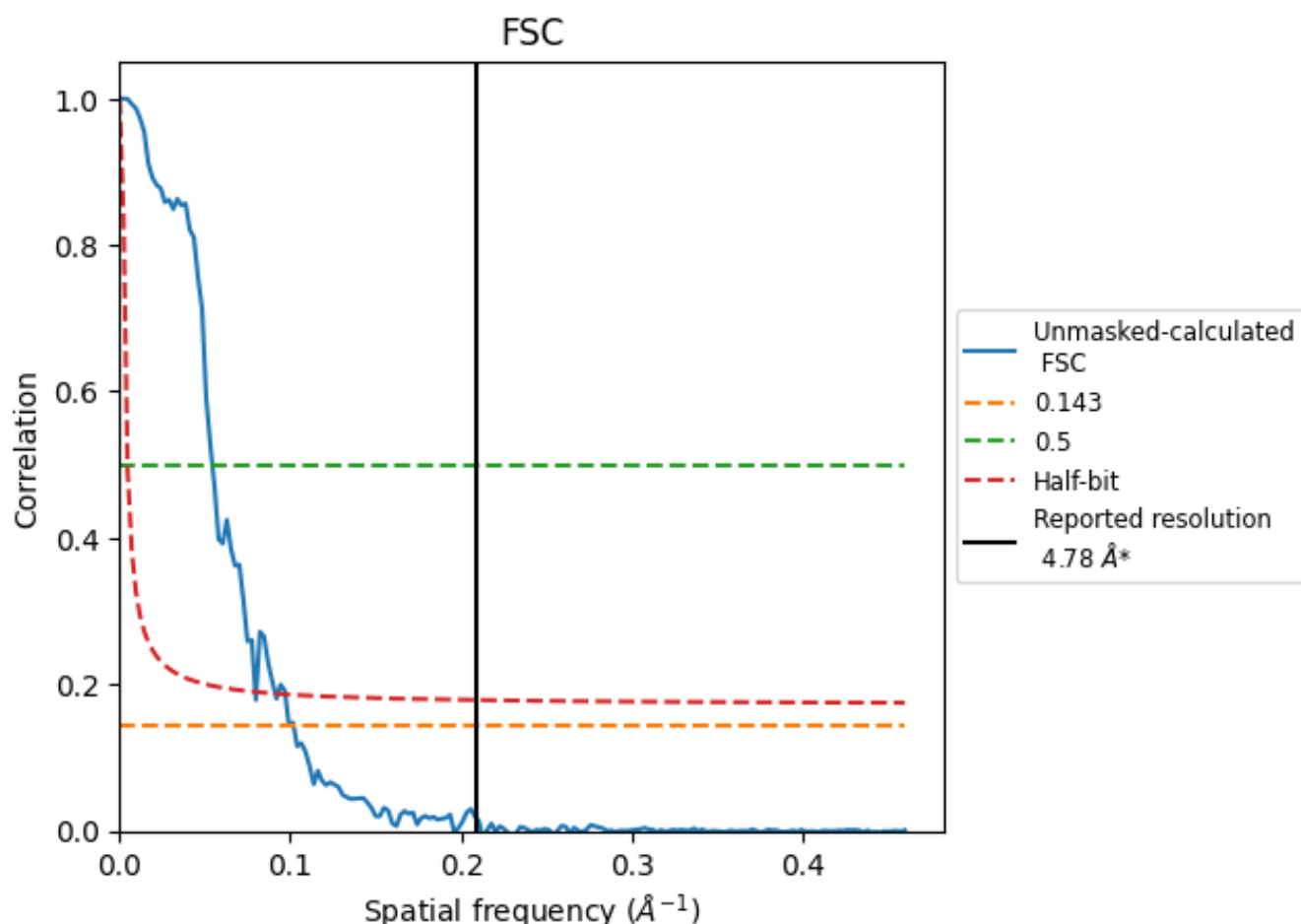


*Reported resolution corresponds to spatial frequency of 0.209 Å⁻¹

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 0.209 Å⁻¹

8.2 Resolution estimates [i](#)

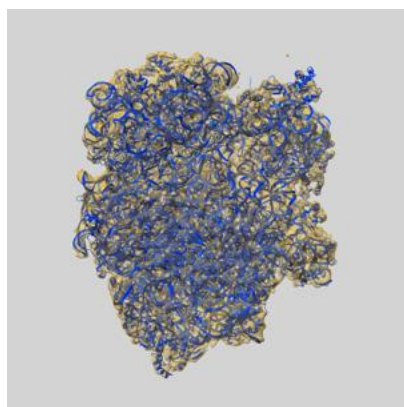
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.78	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	9.80	18.38	12.56

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 9.80 differs from the reported value 4.78 by more than 10 %

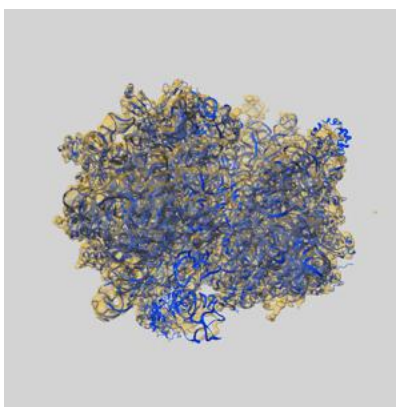
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-34864 and PDB model 8HKZ. Per-residue inclusion information can be found in section 3 on page 16.

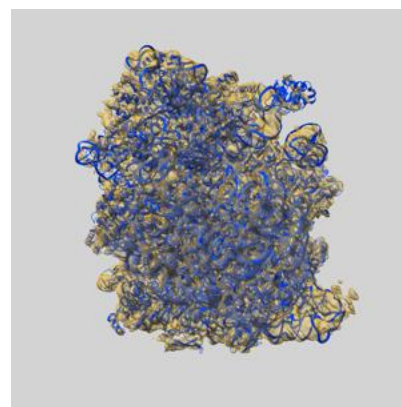
9.1 Map-model overlay [i](#)



X



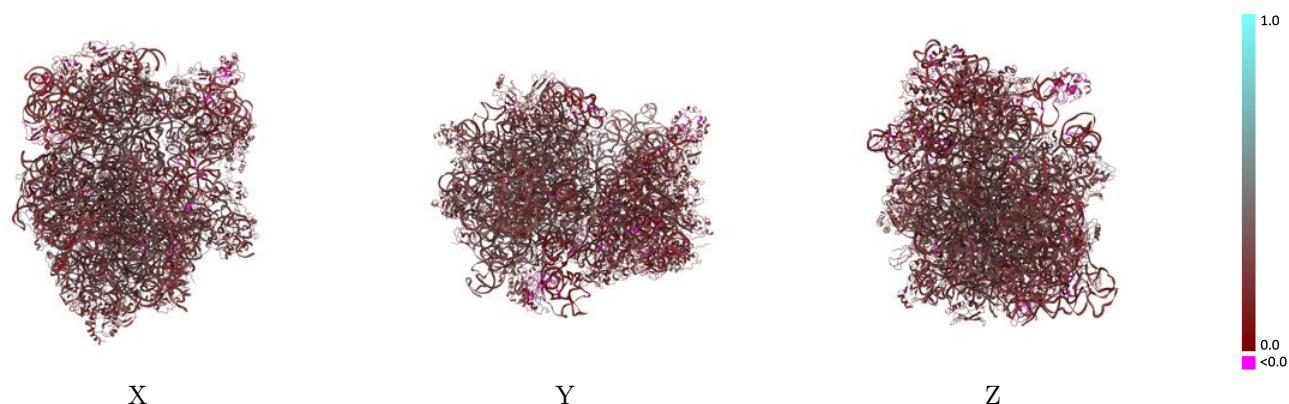
Y



Z

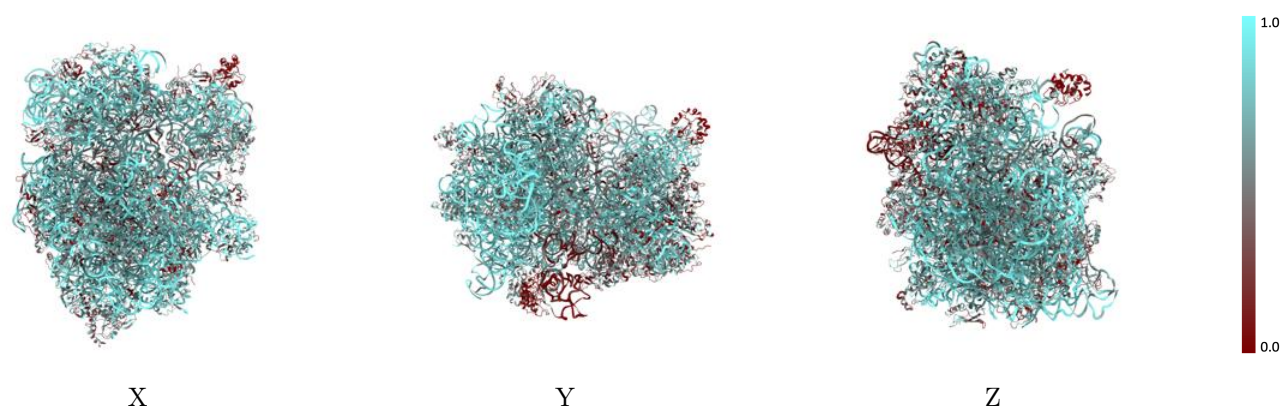
The images above show the 3D surface view of the map at the recommended contour level 0.33 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



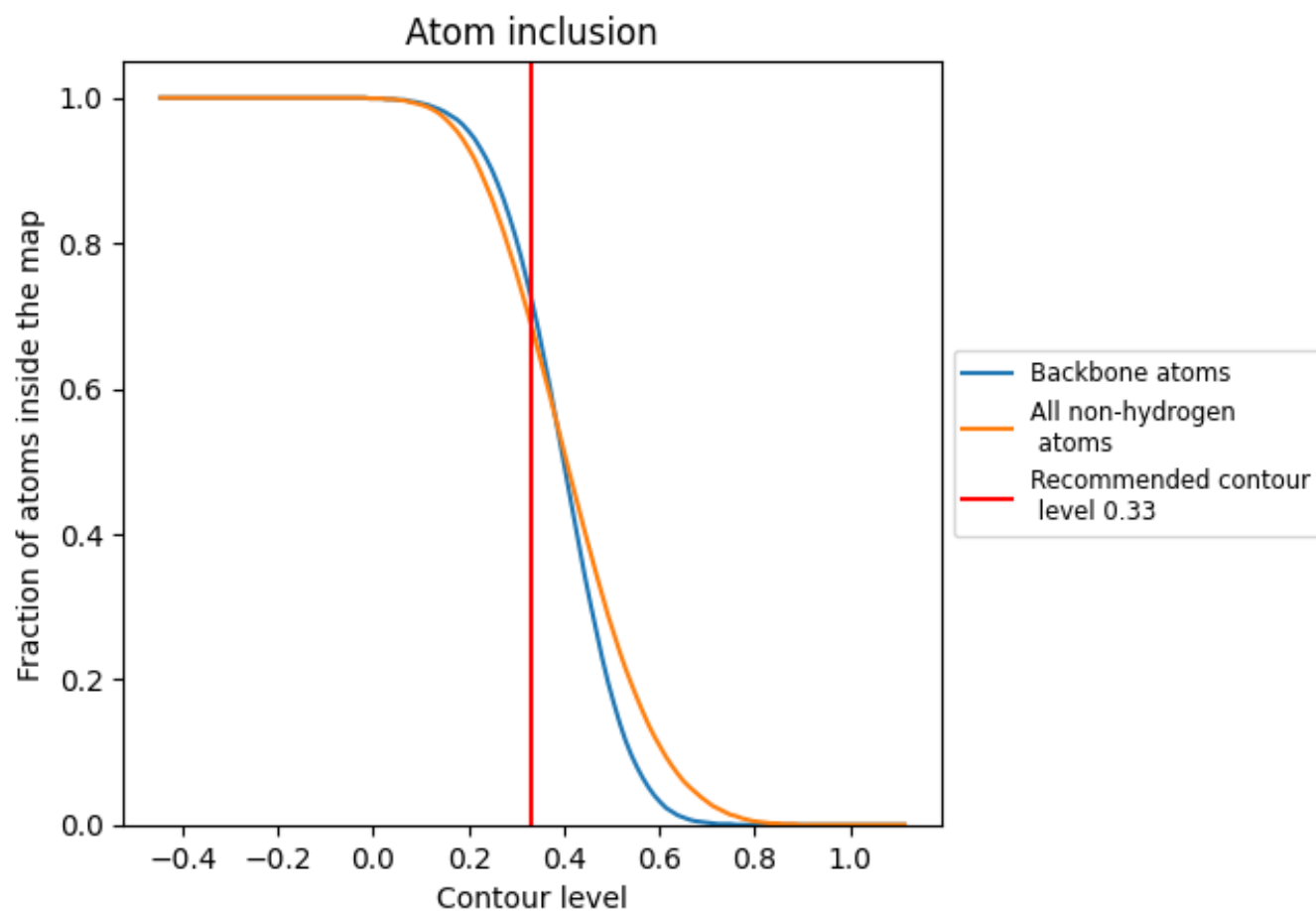
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.33).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 73% of all backbone atoms, 69% 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 (0.33) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6920	 0.2530
A16S	 0.8400	 0.2480
A23S	 0.8460	 0.2750
A5S	 0.9210	 0.2650
AETN	 0.1950	 0.1260
AL1P	 0.0500	 0.1750
AL2P	 0.4320	 0.2770
AL3P	 0.4840	 0.2520
AL4P	 0.5370	 0.2670
AL5P	 0.4760	 0.2210
AL6P	 0.4830	 0.2380
ALX0	 0.5380	 0.2160
AMRN	 0.4500	 0.2680
APTn	 0.7740	 0.2250
APTP	 0.0600	 0.1570
AS2P	 0.4410	 0.2550
AS3P	 0.3870	 0.2480
AS4E	 0.5020	 0.2210
AS4P	 0.5550	 0.2290
AS5P	 0.5270	 0.2660
AS6E	 0.3010	 0.2060
AS7P	 0.3840	 0.2200
AS8E	 0.3920	 0.2130
AS8P	 0.6280	 0.2650
AS9P	 0.4410	 0.2020
L10E	 0.5330	 0.2710
L13P	 0.5420	 0.2370
L141	 0.5420	 0.2400
L142	 0.3710	 0.2140
L14P	 0.3420	 0.2620
L15E	 0.4980	 0.2580
L15P	 0.6040	 0.2570
L18E	 0.6840	 0.2760
L18P	 0.5350	 0.2460
L19E	 0.6280	 0.2720



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Chain	Atom inclusion	Q-score
L21E	0.5180	0.2670
L22P	0.4960	0.2550
L23P	0.4910	0.2510
L24E	0.4940	0.2380
L24P	0.6090	0.2350
L29P	0.5570	0.2400
L30E	0.6150	0.2580
L30P	0.5680	0.2300
L31E	0.5170	0.2420
L32E	0.4130	0.2520
L34E	0.5240	0.2360
L37A	0.5520	0.2520
L37E	0.6090	0.2570
L39E	0.5850	0.2320
L40E	0.1550	0.2000
L44E	0.5590	0.2610
L45A	0.4680	0.2480
L46A	0.3110	0.2480
L47A	0.0660	0.2120
L7A1	0.4520	0.2520
L7A2	0.4680	0.2240
S10P	0.3470	0.2120
S11P	0.4090	0.2440
S12P	0.3030	0.2440
S13P	0.4350	0.2120
S14P	0.4010	0.2190
S15P	0.5910	0.2480
S17E	0.3500	0.1850
S17P	0.4620	0.2450
S19E	0.4350	0.1830
S19P	0.5430	0.2130
S24E	0.5360	0.2110
S27A	0.6890	0.1270
S27E	0.6200	0.2340
S28E	0.2590	0.2090
S3AE	0.4680	0.2300
SL7A	0.1180	0.1550