



wwPDB EM Validation Summary Report ⓘ

Jul 3, 2025 – 08:41 AM EDT

PDB ID : 8UXB / pdb_00008uxb
EMDB ID : EMD-42721
Title : E. coli 70S ribosome with unmodified P/E-tRNA^{Pro}(GGG) bound to slippery
P-site CCC-C codon
Authors : Kimbrough, E.M.; Dunham, C.M.; Nguyen, H.A.
Deposited on : 2023-11-09
Resolution : 2.90 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev118
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0rc1
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) : 2.44

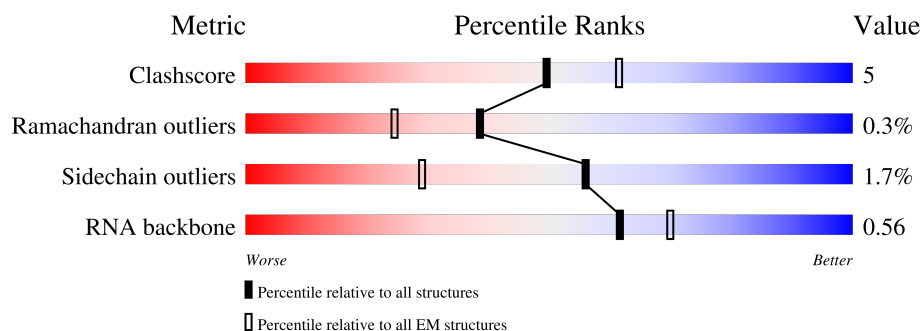
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
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	1	2904	<div> <div>9%</div> <div>68%</div> <div>25%</div> <div>6%</div> </div>
2	2	1540	<div> <div>13%</div> <div>69%</div> <div>26%</div> <div>5%</div> </div>
3	3	120	<div> <div>7%</div> <div>74%</div> <div>21%</div> <div>5%</div> </div>
4	4	18	<div> <div>22%</div> <div>17%</div> <div>33%</div> <div>50%</div> </div>
5	5	77	<div> <div>6%</div> <div>60%</div> <div>35%</div> <div>5%</div> </div>
6	B	273	<div> <div>83%</div> <div>15%</div> </div>
7	C	209	<div> <div>11%</div> <div>88%</div> <div>12%</div> </div>



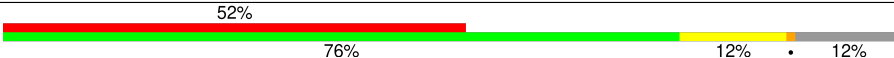

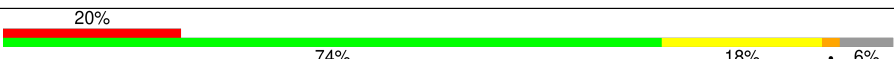
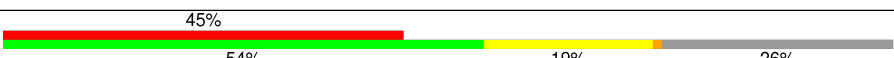

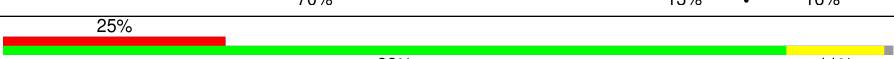










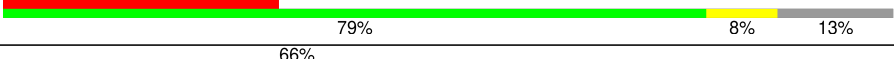


Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
8	D	201	
9	E	179	
10	F	177	
11	G	149	
12	J	142	
13	K	123	
14	L	144	
15	M	136	
16	N	127	
17	O	117	
18	P	115	
19	Q	118	
20	R	103	
21	S	110	
22	T	100	
23	U	104	
24	V	94	
25	W	84	
26	X	78	
27	Y	63	
28	Z	59	
29	b	57	
30	c	55	
31	d	46	
32	e	65	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
33	f	38	
34	g	241	
35	h	233	
36	i	206	
37	j	167	
38	k	135	
39	l	179	
40	m	130	
41	n	130	
42	o	103	
43	p	129	
44	q	124	
45	r	118	
46	s	102	
47	t	89	
48	u	82	
49	v	84	
50	w	75	
51	x	92	
52	y	87	
53	z	71	

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 145220 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 ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2900	Total	C	N	O	P	0	0
			62262	27774	11460	20128	2900		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 1109114233
1	887	A	U	conflict	GB 1109114233
1	1847	G	A	conflict	GB 1109114233

- Molecule 2 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1539	Total	C	N	O	P	0	0
			33015	14725	6052	10699	1539		

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	120	Total	C	N	O	P	0	0
			2572	1145	471	836	120		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3	120	A	U	conflict	GB 1370526515

- Molecule 4 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	9	Total	C	N	O	P	0	0
			188	84	31	64	9		

- Molecule 5 is a RNA chain called tRNA[^]ProL (GGG).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	77	Total	C	N	O	P	0	0
			1648	733	297	541	77		

- Molecule 6 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 7 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 8 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 9 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 10 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 11 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	G	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 13 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	K	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 14 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 15 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 16 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	N	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
17	O	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 18 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	P	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 19 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	Q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 20 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 21 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 22 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	T	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 23 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	U	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 24 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	V	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 25 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 26 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	X	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 27 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 28 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 29 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 30 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	c	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 31 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 32 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 33 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 34 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 35 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 36 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	i	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 37 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	j	157	Total	C	N	O	S	0	0
			1141	709	218	208	6		

- Molecule 38 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	k	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 39 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	l	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 40 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	m	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 41 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	n	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 42 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	o	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 43 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	p	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 44 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	q	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 45 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 46 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	s	101	Total	C	N	O	S	0	0
			799	498	165	133	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
s	36	ALA	-	insertion	UNP C3SR07

- Molecule 47 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	t	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 48 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	u	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 49 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	v	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 50 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	w	65	Total	C	N	O	0	0
			504	317	96	91		

- Molecule 51 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	x	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 52 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	y	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 53 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	z	65	Total	C	N	O	S	0	0
			495	307	100	87	1		

- Molecule 54 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
54	1	203	Total	Mg	0
			203	203	
54	2	76	Total	Mg	0
			76	76	
54	3	1	Total	Mg	0
			1	1	
54	5	1	Total	Mg	0
			1	1	
54	B	2	Total	Mg	0
			2	2	
54	D	1	Total	Mg	0
			1	1	
54	Q	1	Total	Mg	0
			1	1	
54	b	1	Total	Mg	0
			1	1	
54	e	1	Total	Mg	0
			1	1	

- Molecule 55 is water.

Mol	Chain	Residues	Atoms		AltConf
55	1	935	Total	O	0
			935	935	
55	2	356	Total	O	0
			356	356	
55	3	14	Total	O	0
			14	14	
55	4	1	Total	O	0
			1	1	
55	5	10	Total	O	0
			10	10	
55	B	7	Total	O	0
			7	7	
55	C	5	Total	O	0
			5	5	
55	D	5	Total	O	0
			5	5	

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
55	E	3	Total 3	O 3	0
55	F	4	Total 4	O 4	0
55	G	1	Total 1	O 1	0
55	J	3	Total 3	O 3	0
55	K	2	Total 2	O 2	0
55	L	4	Total 4	O 4	0
55	M	4	Total 4	O 4	0
55	O	3	Total 3	O 3	0
55	P	5	Total 5	O 5	0
55	Q	3	Total 3	O 3	0
55	R	3	Total 3	O 3	0
55	S	2	Total 2	O 2	0
55	V	2	Total 2	O 2	0
55	W	2	Total 2	O 2	0
55	X	1	Total 1	O 1	0
55	Y	2	Total 2	O 2	0
55	b	1	Total 1	O 1	0
55	c	1	Total 1	O 1	0
55	d	3	Total 3	O 3	0
55	f	1	Total 1	O 1	0
55	g	9	Total 9	O 9	0

Continued on next page...

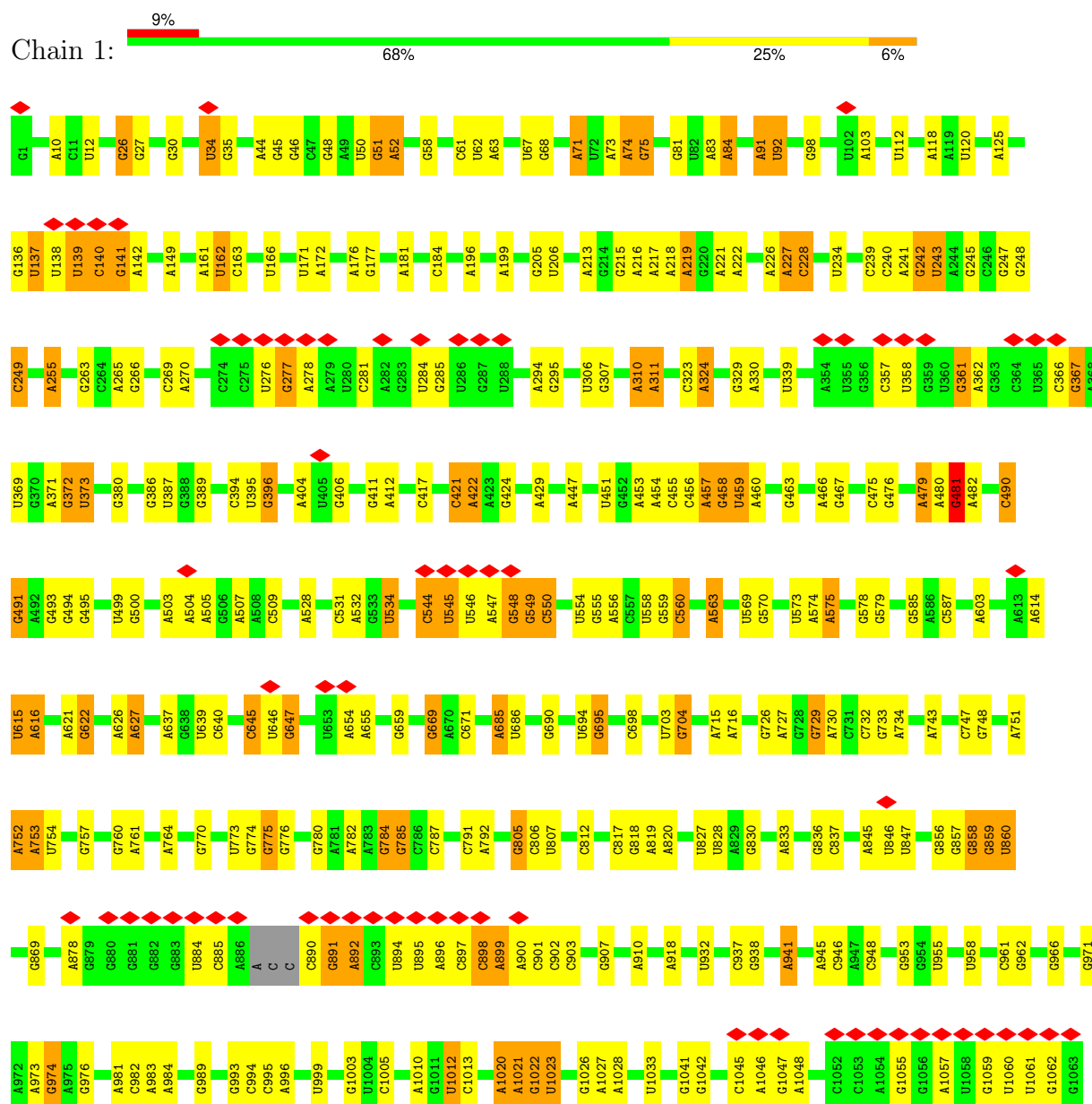
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
55	h	7	Total 7	O 7	0
55	i	8	Total 8	O 8	0
55	j	1	Total 1	O 1	0
55	k	2	Total 2	O 2	0
55	l	10	Total 10	O 10	0
55	m	1	Total 1	O 1	0
55	o	1	Total 1	O 1	0
55	p	1	Total 1	O 1	0
55	q	2	Total 2	O 2	0
55	r	7	Total 7	O 7	0
55	s	2	Total 2	O 2	0
55	t	1	Total 1	O 1	0
55	u	3	Total 3	O 3	0
55	v	4	Total 4	O 4	0
55	x	4	Total 4	O 4	0
55	z	3	Total 3	O 3	0

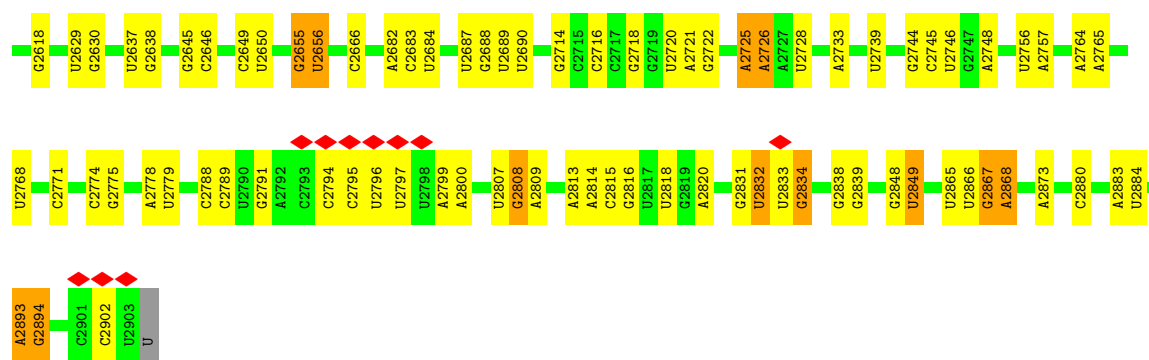
3 Residue-property plots

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.

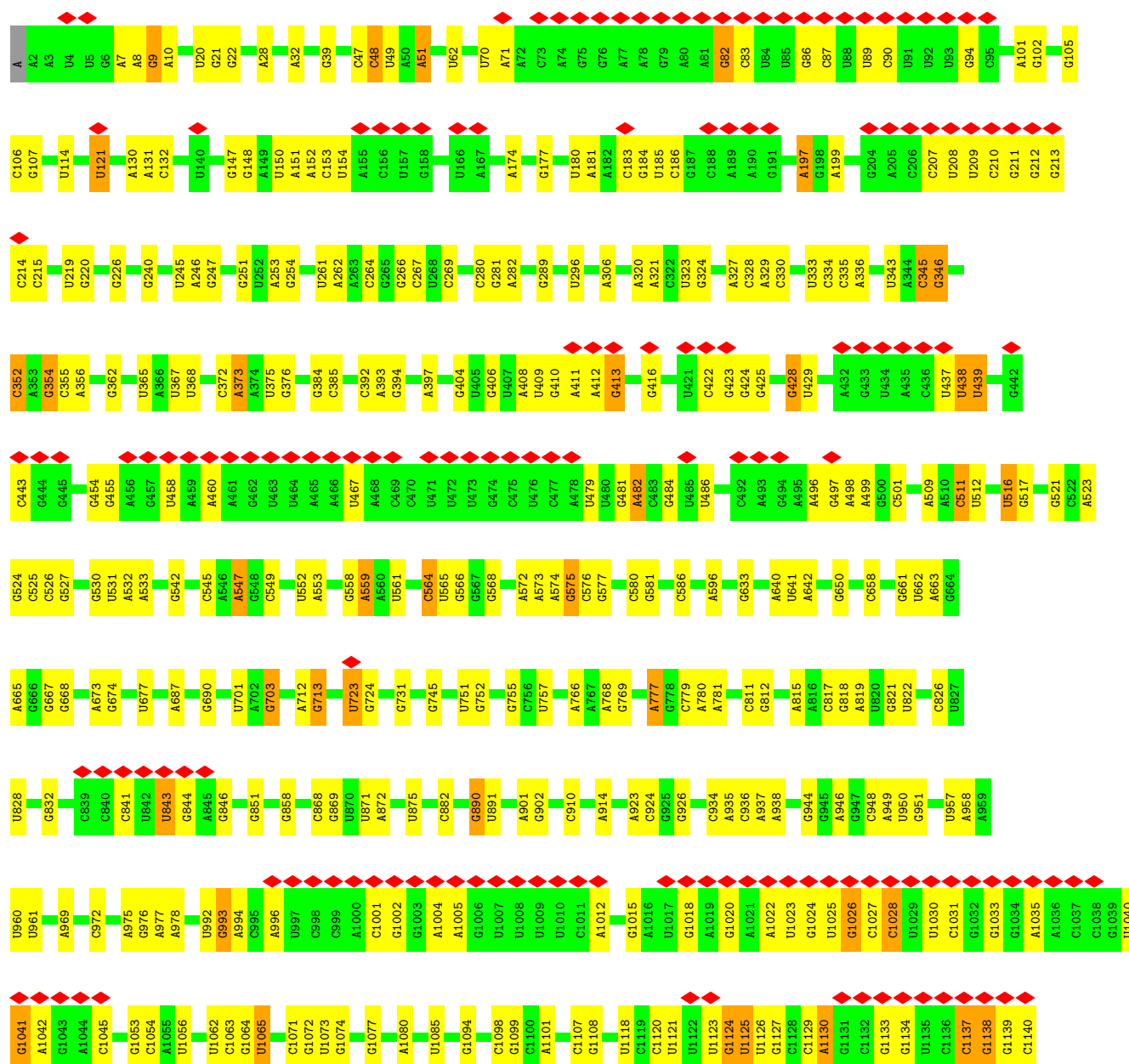
• Molecule 1: 23S ribosomal RNA

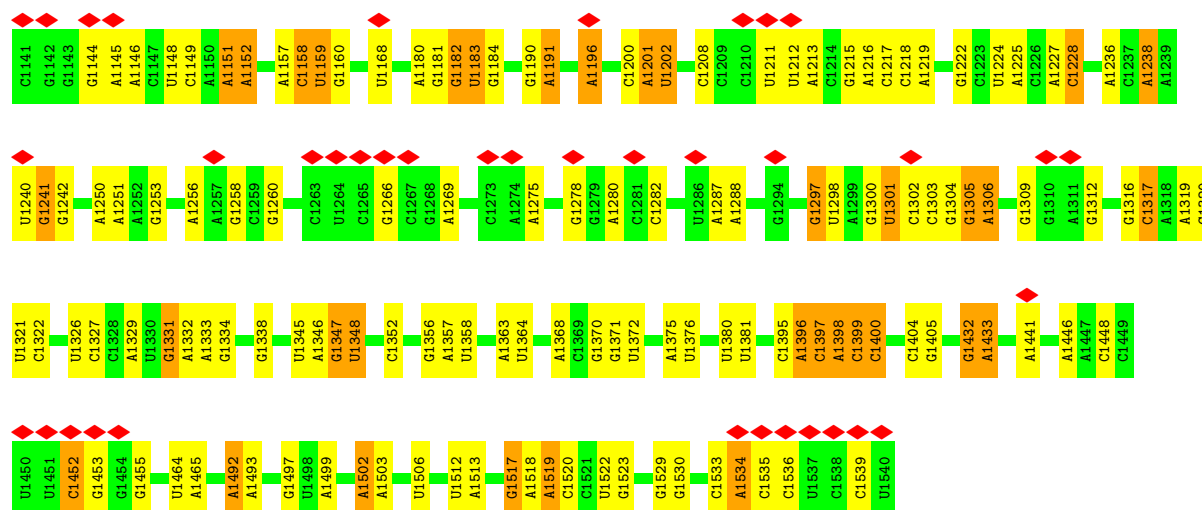


A2503	U2504	G2505	U2506	C2512	A2513	A2516	C2517	A2518	U2519	C2520	G2526	U2529	G2535	A2547	C2551	U2552	G2553	U2554	C2559	A2566	G2567	A2572	C2573	G2574	C2575	G2576	C2579	U2580	G2581	C2582	U2585	U2586	A2587	G2588	A2589	A2590	A2602	G2603	U2604	U2605	C2606	U2609	C2610	U2613											
G2383	U2384	C2385	G2391	A2392	U2393	C2394	C2395	A2396	U2402	C2403	U2404	G2405	A2406	A2407	G2410	U2423	C2424	A2425	G2428	G2429	A2430	A2435	U2441	G2446	G2447	A2448	U2449	C2452	U2453	C2467	A2468	C2475	A2476	U2477	A2478	C2486	U2489	G2490	C2496	A2497	C2498	C2499	G2502												
C2258	A2266	A2267	G2279	G2280	A2281	C2282	C2283	G2286	A2287	A2288	U2291	U2292	G2293	G2294	C2295	U2296	G2304	U2305	C2306	G2307	G2308	A2309	U2312	C2313	A2314	U2320	G2325	C2326	A2327	A2328	U2329	A2333	U2334	G2345	A2346	C2347	U2348	G2349	C2350	C2354	G2361	C2364	G2365	A2369											
G2152	C2153	A2154	U2155	G2156	C2157	A2158	G2159	C2160	C2161	G2162	A2163	C2164	C2165	U2166	U2167	G2168	A2169	A2170	A2171	U2172	A2173	C2174	C2175	A2176	C2177	C2178	A2184	U2185	G2186	U2187	U2188	U2189	G2190	A2191	U2192	G2193	U2194	U2195	A2198	A2199	G2204	A2211	U2212	U2213	A2225	C2226	U2233	G2238	G2239	G2250	G2251				
A2062	G2069	C2072	C2096	A2097	U2098	U2099	G2100	C2104	U2105	U2106	G2107	A2108	U2109	G2110	U2111	G2112	U2113	A2114	G2115	G2116	A2117	U2118	A2119	G2120	G2121	U2122	G2123	G2124	G2125	A2126	G2127	G2128	C2129	U2130	U2131	U2132	G2133	A2134	A2135	G2136	U2137	G2138	U2139	G2140	G2141	A2142	C2143	G2144	C2145	C2146	A2147	G2148	U2149	C2150	U2151
U1940	C1941	C1942	U1943	A1953	G1954	U1955	A1960	C1961	C1967	A1970	U1971	G1972	G1980	U1981	U1982	U1991	G1992	U1993	C1996	C1997	U2011	G2012	A2013	A2019	A2020	C2021	U2022	C2023	G2024	C2025	G2029	A2030	A2031	G2032	A2033	U2034	G2035	C2043	C2050	A2051	A2052	C2055	G2056	A2060	G2061										
G1799	C1800	A1801	A1808	A1809	C1816	G1826	A1829	C1833	C1837	G1846	G1847	A1848	A1853	U1856	G1857	A1858	U1859	U1864	G1869	C1870	A1871	A1872	G1873	A1900	A1901	G1906	G1907	A1913	C1914	U1917	C1920	C1925	U1926	A1927	G1930	U1931	A1936	A1937	A1938	U1939															
G1674	C1675	A1677	G1681	G1682	U1693	C1694	G1695	U1712	A1713	U1714	G1715	U1716	U1720	G1721	U1725	C1726	C1727	G1728	U1729	G1731	C1732	G1733	G1734	A1735	U1736	G1737	G1738	G1743	A1754	A1757	U1758	C1764	A1773	G1776	A1780	U1781	U1782	A1783	A1784	C1790	A1791	G1797	U1798												
A1509	A1515	G1521	A1522	U1523	G1524	A1528	C1531	A1532	C1533	U1534	A1535	C1536	G1537	G1538	U1542	G1543	G1555	C1558	U1559	U1560	C1564	C1565	A1569	U1578	A1579	C1582	A1583	U1584	C1585	C1607	C1611	G1619	C1625	A1626	C1646	U1647	U1648	G1667	A1668	A1669	C1670														
G1371	A1378	U1379	G1380	A1383	C1386	A1387	A1392	U1396	U1397	C1398	C1399	U1412	A1413	U1414	U1415	G1416	C1417	A1418	A1419	A1420	G1421	C1428	C1437	C1454	G1455	G1456	U1459	U1460	C1461	G1475	G1482	A1490	G1491	G1492	C1493	A1494	A1495	C1499	G1500	A1504	A1505	U1506	C1507	A1508											
A1254	U1255	G1256	U1263	G1271	A1272	U1273	A1274	A1275	U1282	G1283	G1288	C1295	G1296	G1297	C1298	G1299	A1301	C1306	C1315	C1319	G1320	A1321	C1322	C1323	G1324	U1325	A1328	U1329	C1330	G1333	G1341	C1345	C1351	U1352	C1357	G1358	C1363	G1364	A1365	G1368	G1369	C1370													
A1133	A1134	C1135	U1141	A1142	G1149	C1150	C1153	G1154	A1155	C1170	G1171	C1172	U1173	U1174	A1175	U1176	G1177	C1178	G1179	U1180	U1181	G1182	U1183	U1188	U1203	A1204	A1205	G1206	U1209	G1210	C1211	G1212	A1213	A1214	G1223	U1224	G1225	A1226	G1236	A1237	G1238	A1244	G1248	U1249	G1250	C1251	G1252	A1253							
C1064	U1065	U1066	A1067	G1068	A1069	A1070	G1071	C1072	A1073	G1074	C1075	C1076	A1077	U1078	C1079	A1080	U1081	U1082	U1083	A1084	A1085	A1086	G1087	A1088	A1089	A1090	G1091	C1092	G1093	U1094	A1095	A1096	U1097	A1098	G1099	C1100	U1101	C1102	A1103	C1104	U1105	G1106	G1107	U1108	C1109	G1110	A1111	G1112							

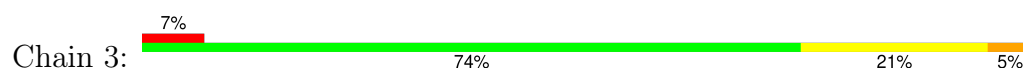


• Molecule 2: 16S ribosomal RNA

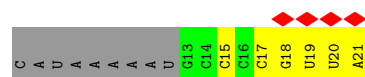




• Molecule 3: 5S ribosomal RNA



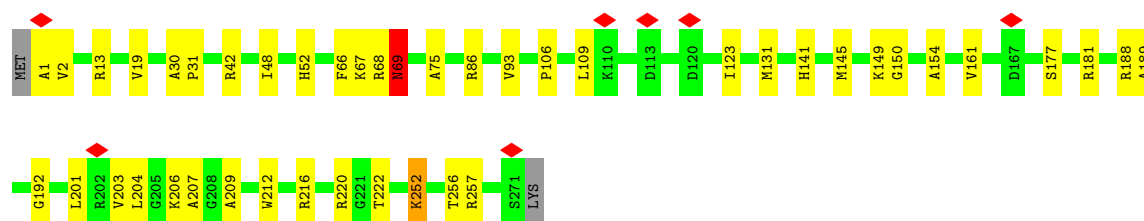
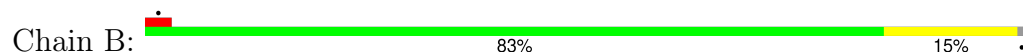
• Molecule 4: mRNA



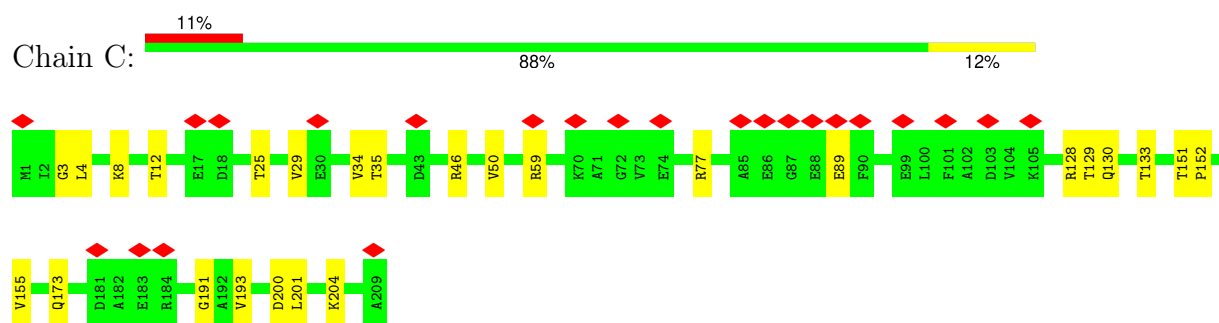
• Molecule 5: tRNA^{ProL} (GGG)



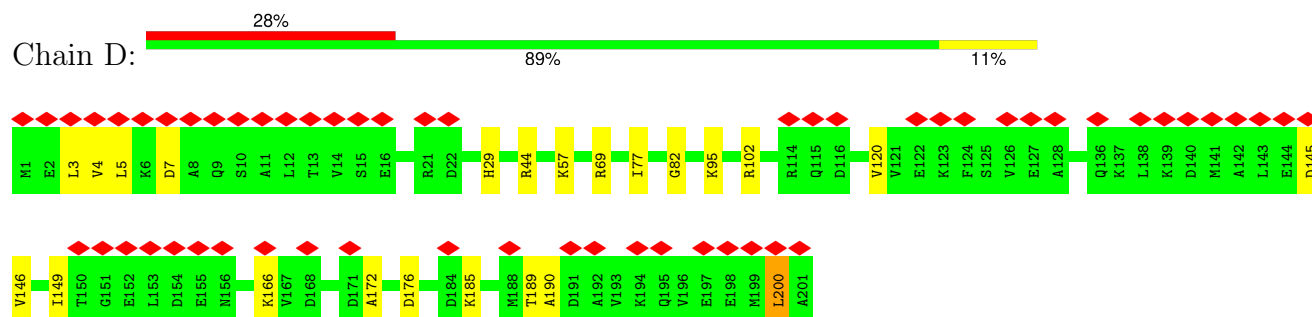
• Molecule 6: 50S ribosomal protein L2



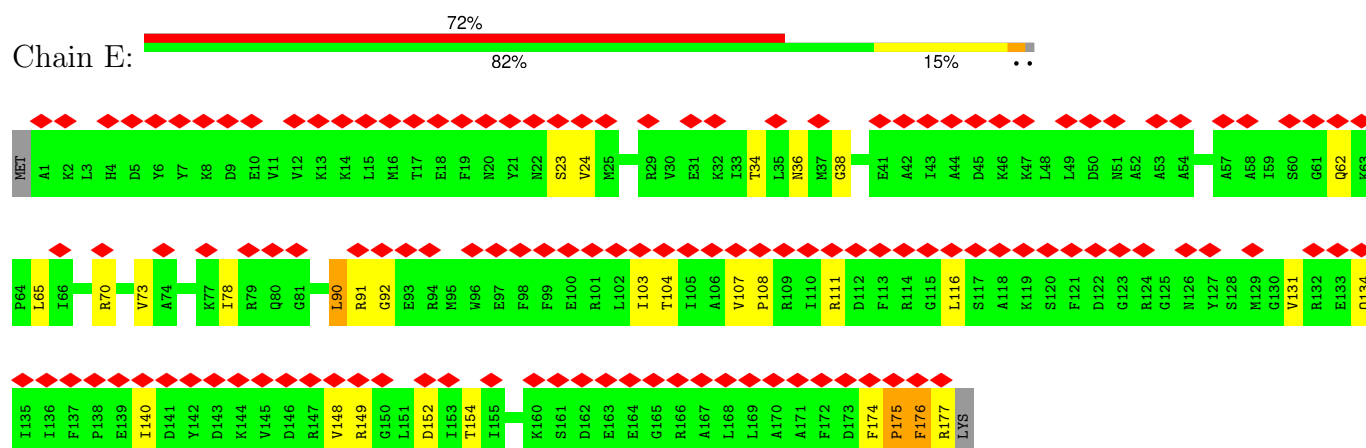
• Molecule 7: 50S ribosomal protein L3



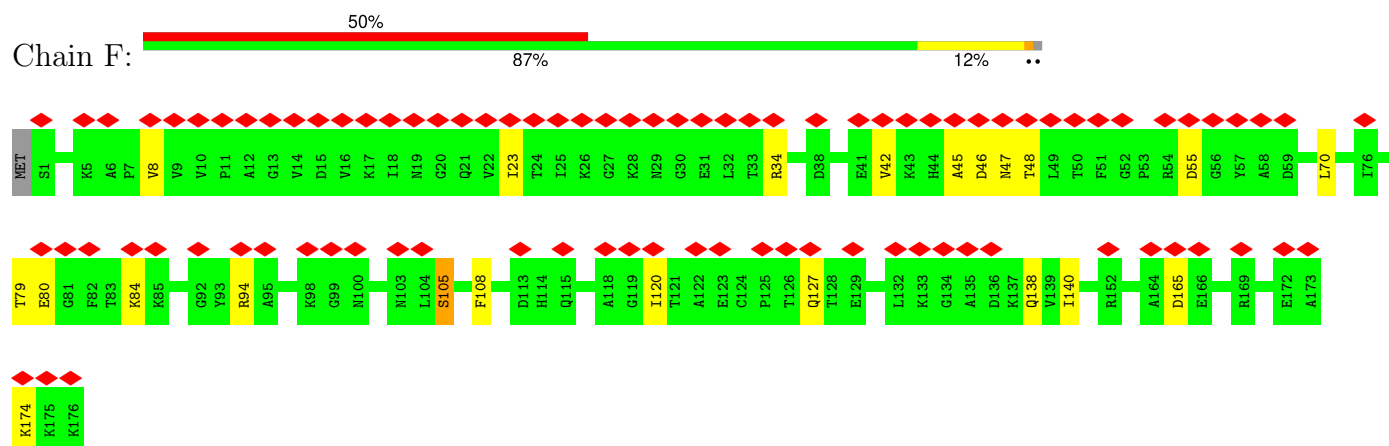
- Molecule 8: 50S ribosomal protein L4



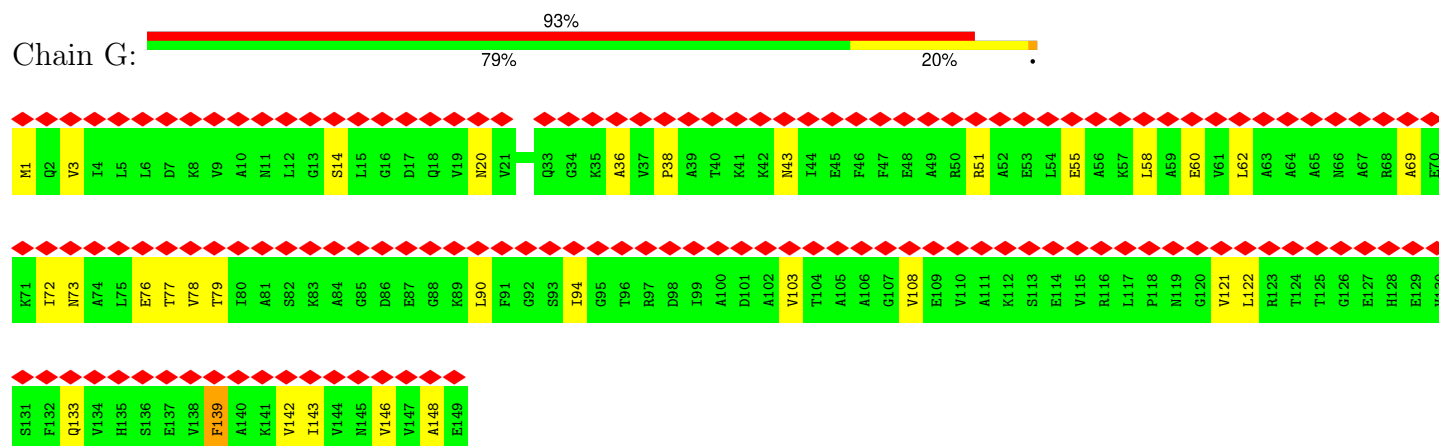
- Molecule 9: 50S ribosomal protein L5



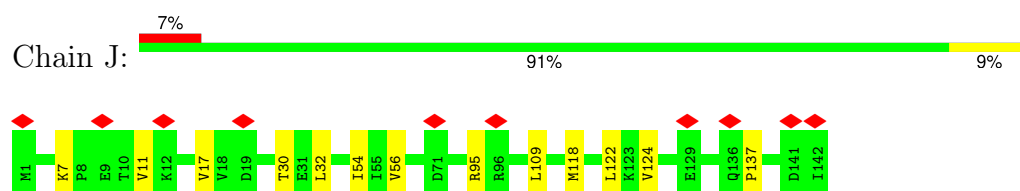
- Molecule 10: 50S ribosomal protein L6



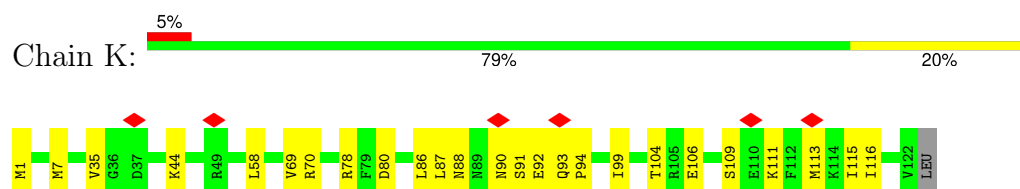
- Molecule 11: 50S ribosomal protein L9



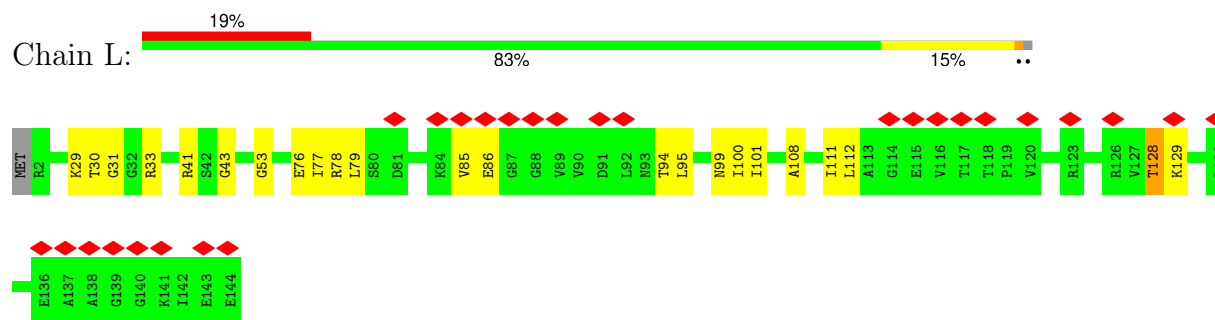
- Molecule 12: 50S ribosomal protein L13



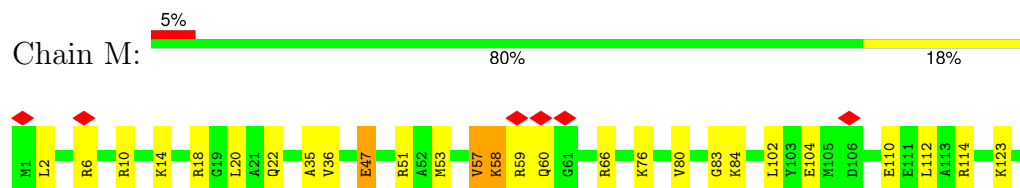
- Molecule 13: 50S ribosomal protein L14



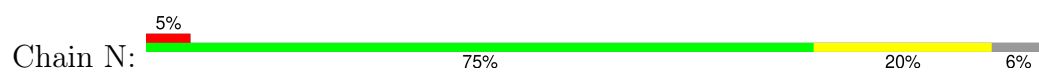
- Molecule 14: 50S ribosomal protein L15



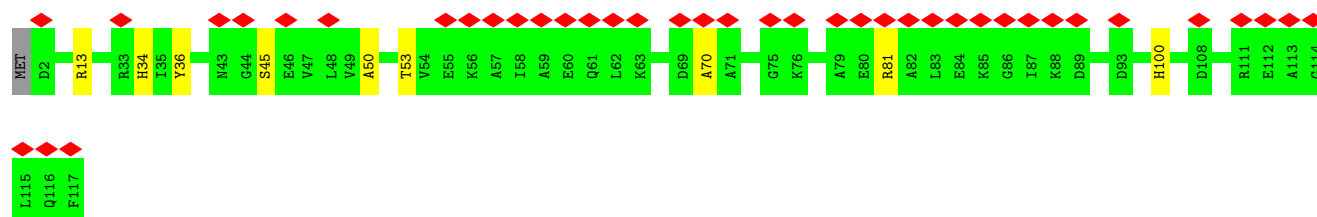
- Molecule 15: 50S ribosomal protein L16



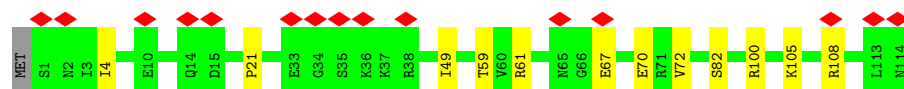
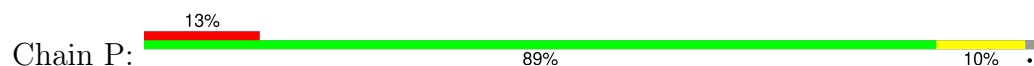
- Molecule 16: 50S ribosomal protein L17



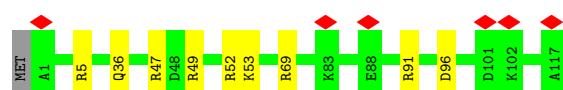
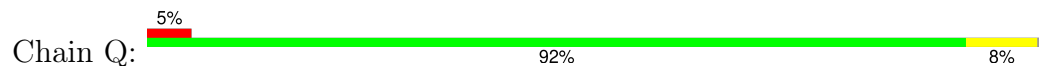
- Molecule 17: 50S ribosomal protein L18



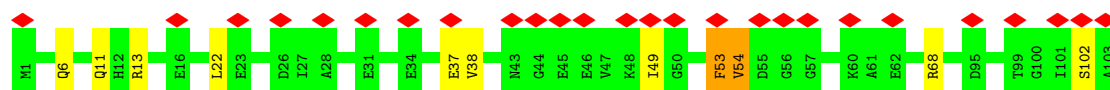
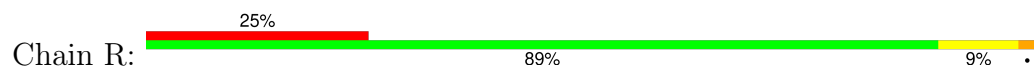
- Molecule 18: 50S ribosomal protein L19



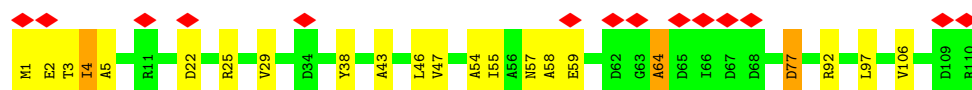
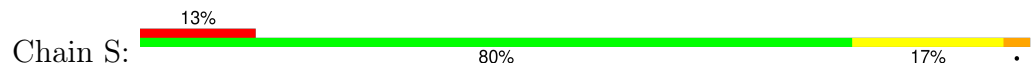
- Molecule 19: 50S ribosomal protein L20



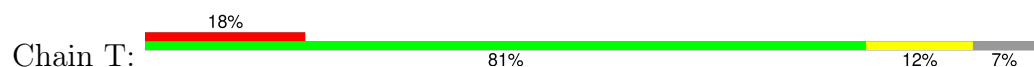
- Molecule 20: 50S ribosomal protein L21

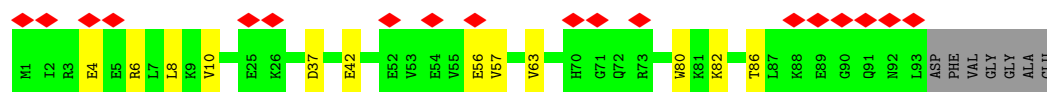


- Molecule 21: 50S ribosomal protein L22

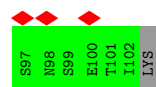
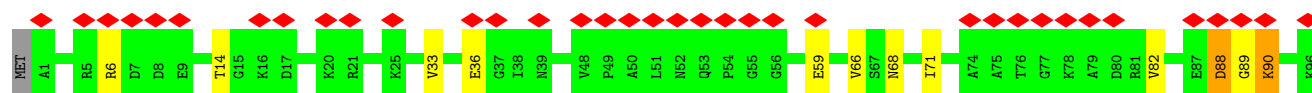
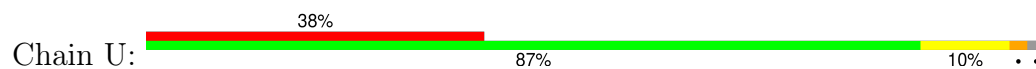


- Molecule 22: 50S ribosomal protein L23

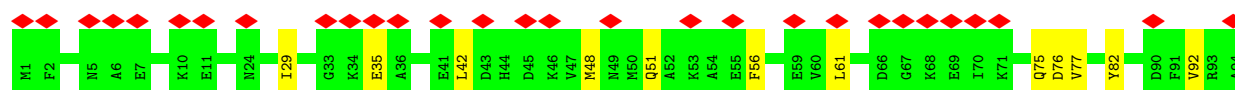
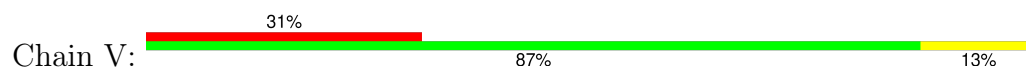




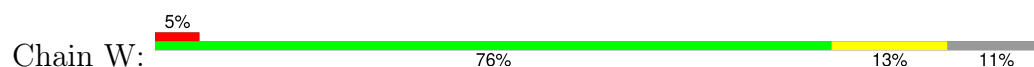
- Molecule 23: 50S ribosomal protein L24



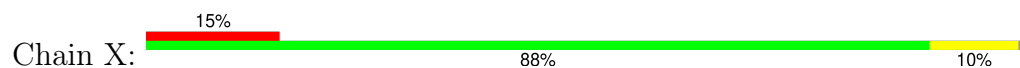
- Molecule 24: 50S ribosomal protein L25



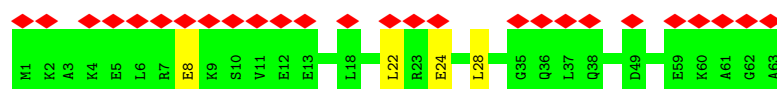
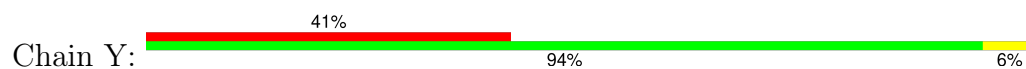
- Molecule 25: 50S ribosomal protein L27



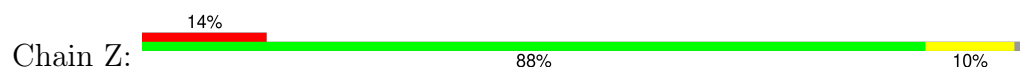
- Molecule 26: 50S ribosomal protein L28

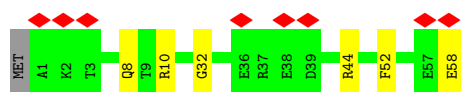


- Molecule 27: 50S ribosomal protein L29

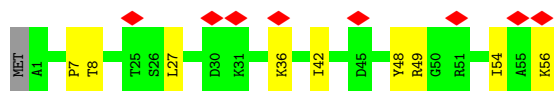
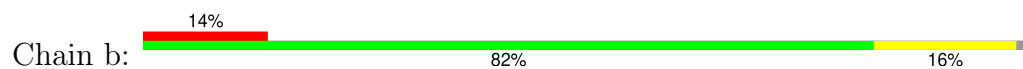


- Molecule 28: 50S ribosomal protein L30

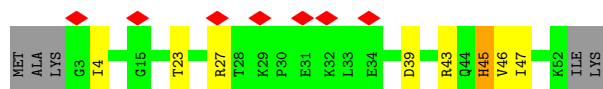
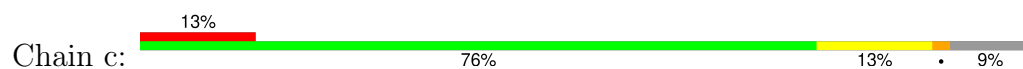




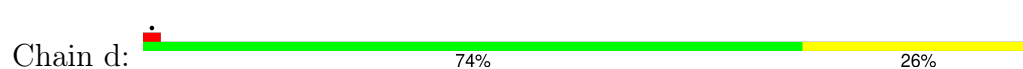
- Molecule 29: 50S ribosomal protein L32



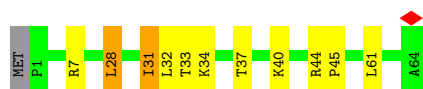
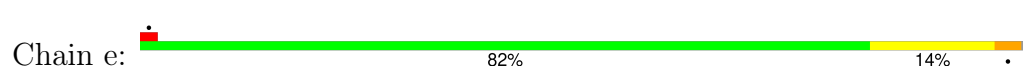
- Molecule 30: 50S ribosomal protein L33



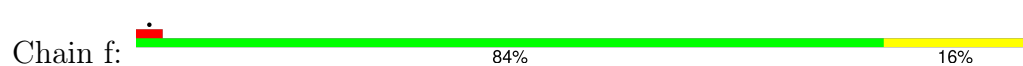
- Molecule 31: 50S ribosomal protein L34



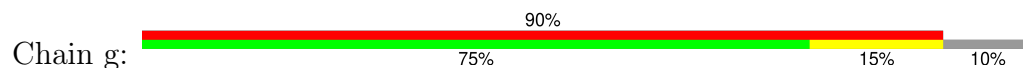
- Molecule 32: 50S ribosomal protein L35

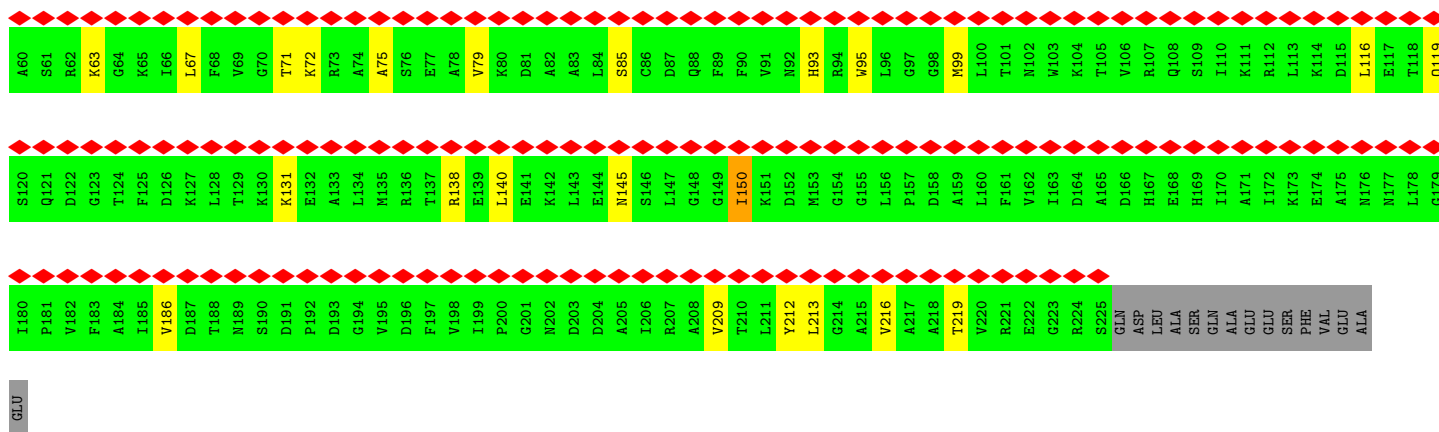


- Molecule 33: 50S ribosomal protein L36

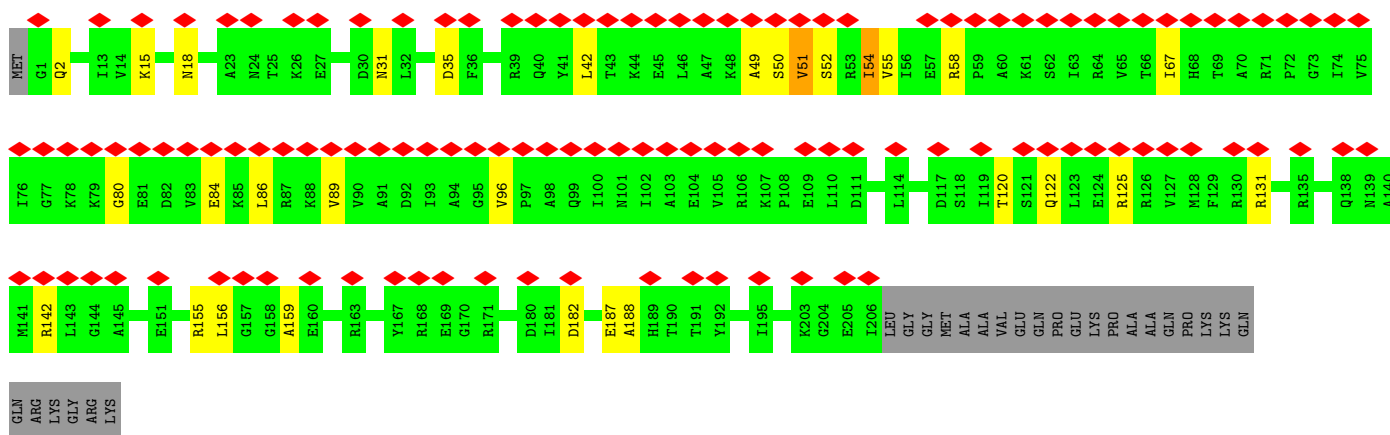
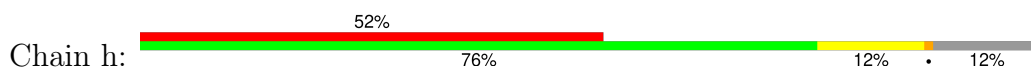


- Molecule 34: 30S ribosomal protein S2

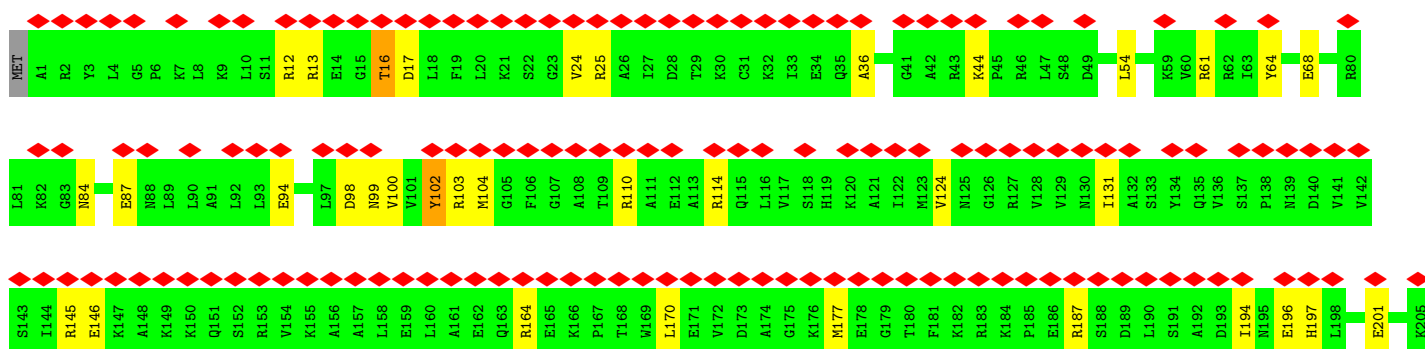
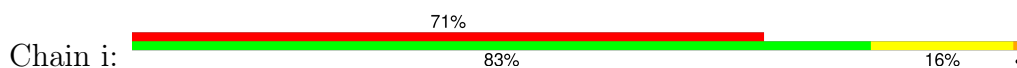




• Molecule 35: 30S ribosomal protein S3

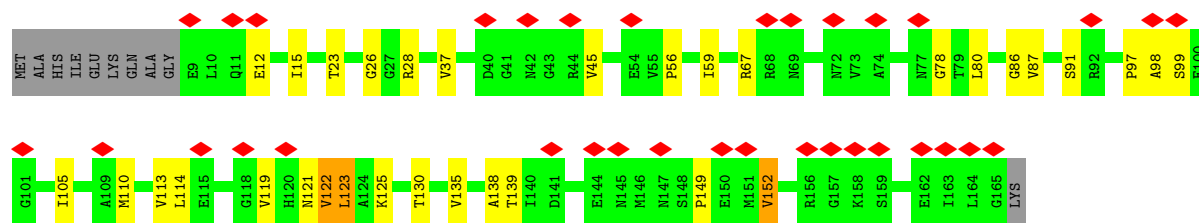


• Molecule 36: 30S ribosomal protein S4

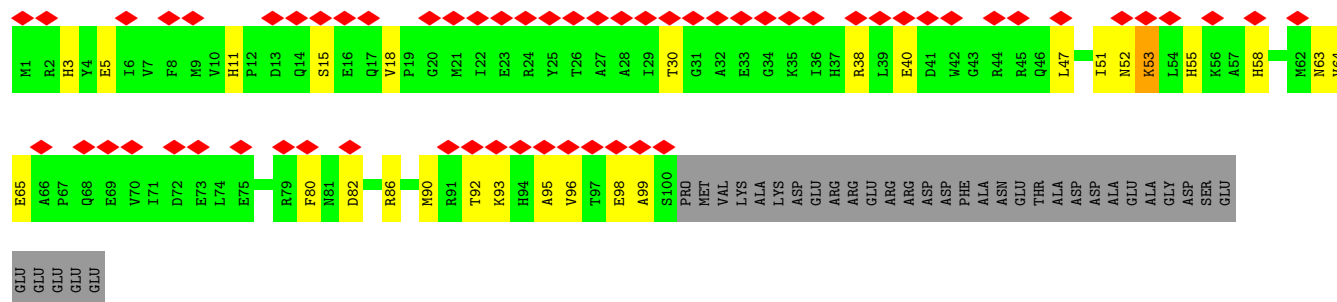


• Molecule 37: 30S ribosomal protein S5

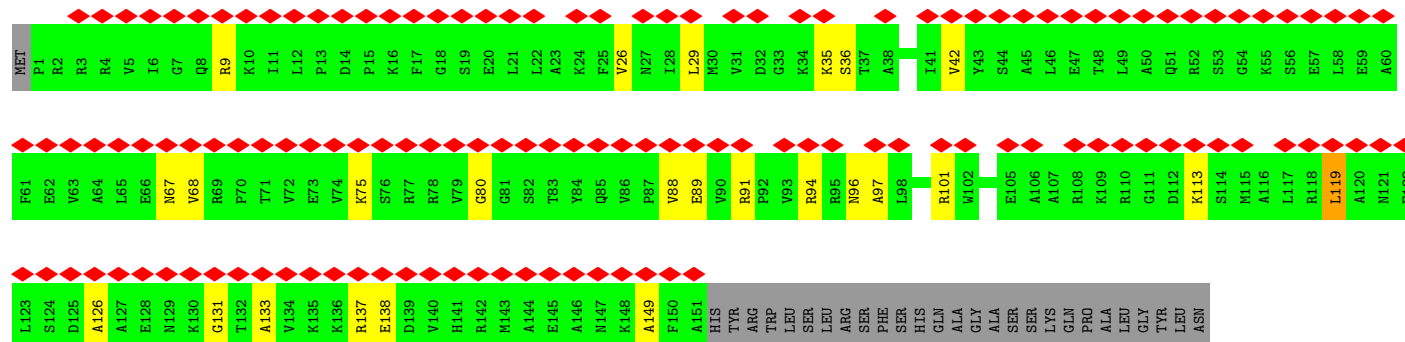
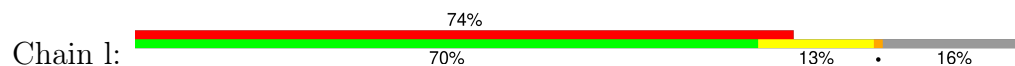




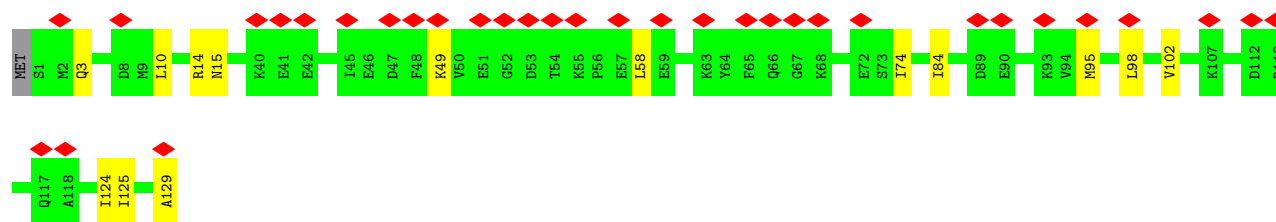
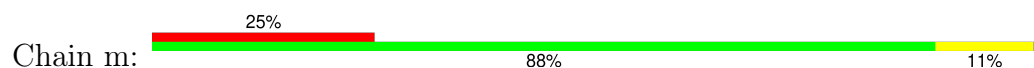
• Molecule 38: 30S ribosomal protein S6



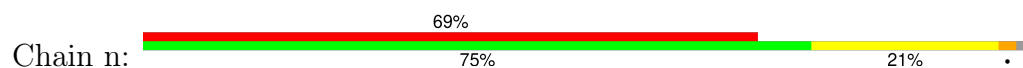
• Molecule 39: 30S ribosomal protein S7

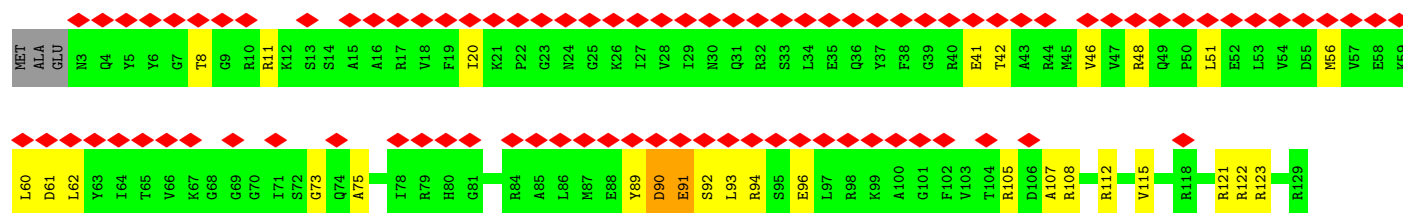


• Molecule 40: 30S ribosomal protein S8



• Molecule 41: 30S ribosomal protein S9

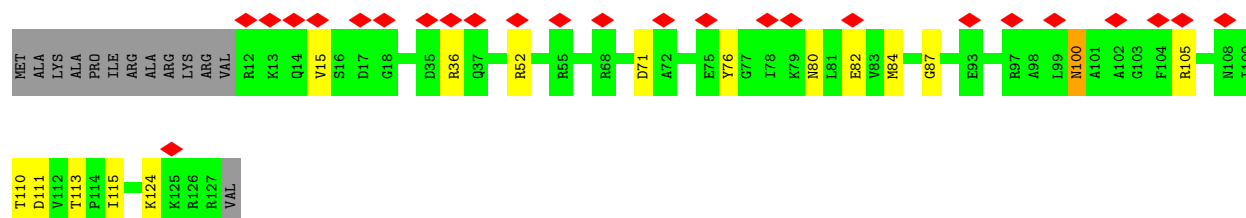
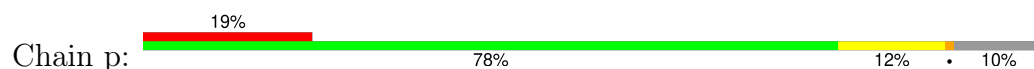




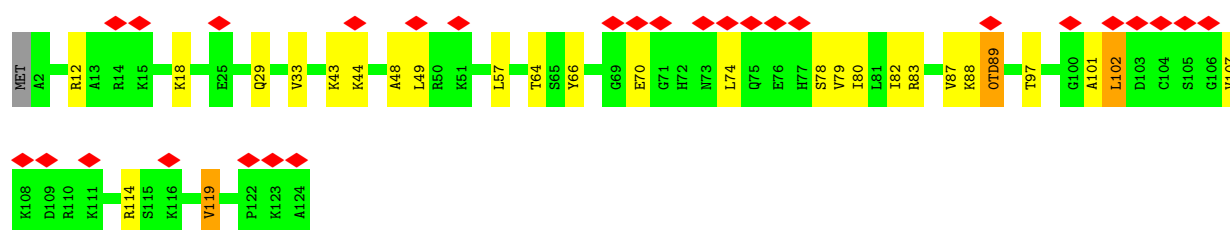
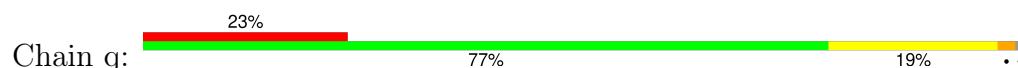
• Molecule 42: 30S ribosomal protein S10



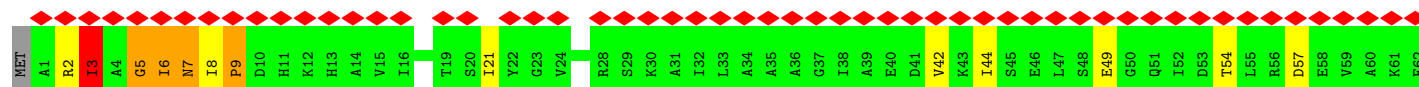
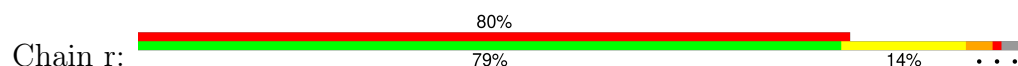
• Molecule 43: 30S ribosomal protein S11

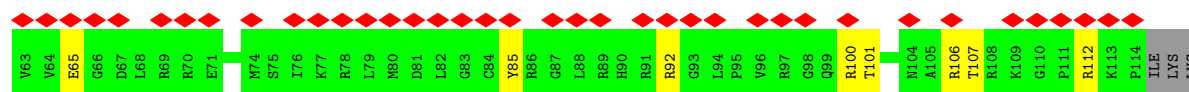


• Molecule 44: 30S ribosomal protein S12

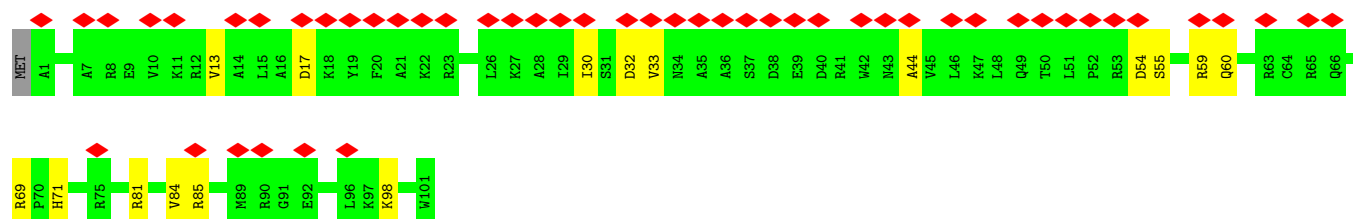
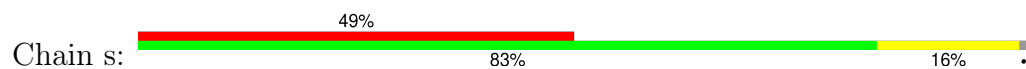


• Molecule 45: 30S ribosomal protein S13

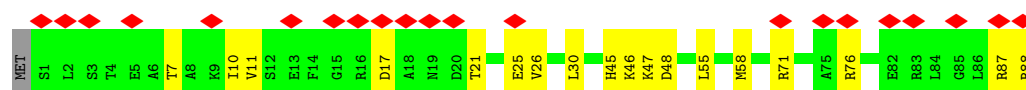
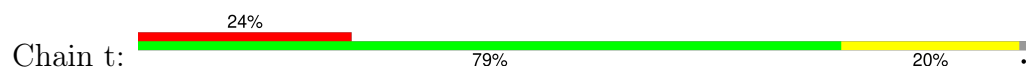




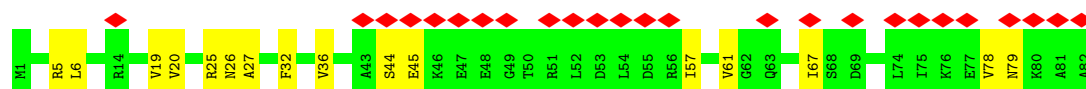
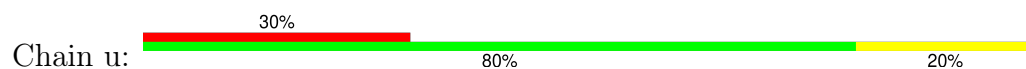
- Molecule 46: 30S ribosomal protein S14



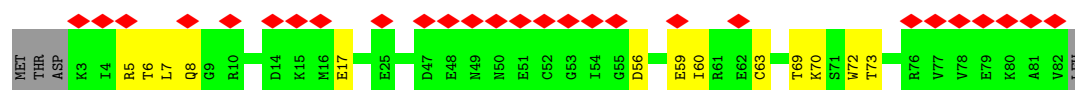
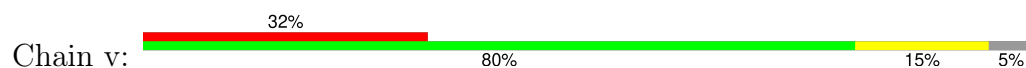
- Molecule 47: 30S ribosomal protein S15



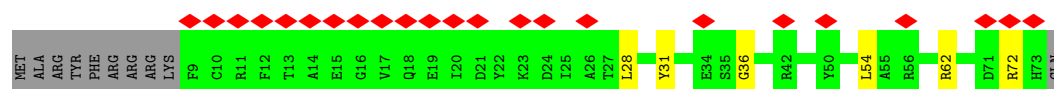
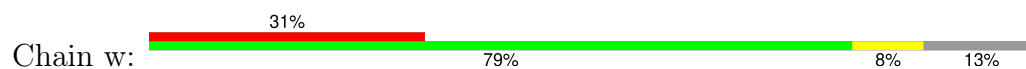
- Molecule 48: 30S ribosomal protein S16



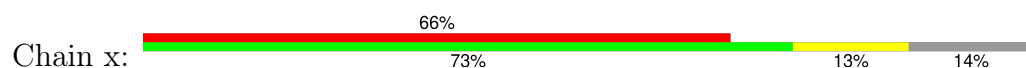
- Molecule 49: 30S ribosomal protein S17

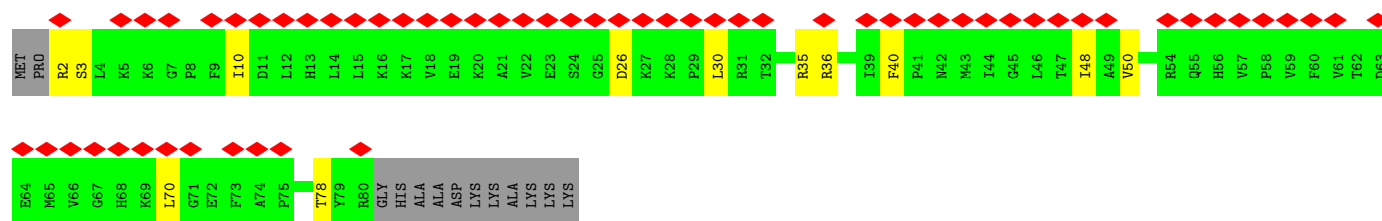


- Molecule 50: 30S ribosomal protein S18

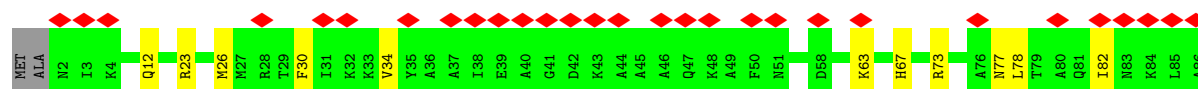
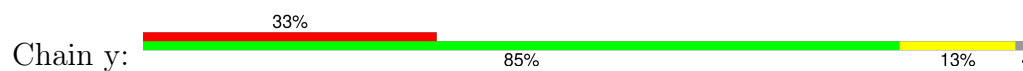


- Molecule 51: 30S ribosomal protein S19

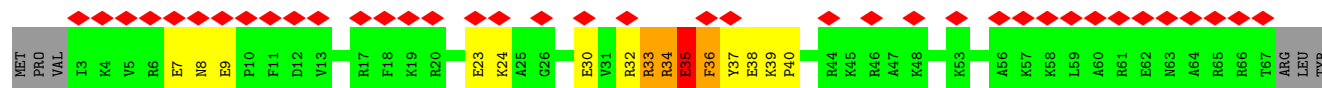




- Molecule 52: 30S ribosomal protein S20



- Molecule 53: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	361087	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	61.23	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.053	Depositor
Minimum map value	-0.004	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.0198	Depositor
Map size (Å)	427.64, 427.64, 427.64	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0691, 1.0691, 1.0691	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 0TD, MG

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	1	0.17	0/69734	0.30	7/108788 (0.0%)
2	2	0.15	0/36966	0.28	2/57666 (0.0%)
3	3	0.15	0/2876	0.29	0/4483
4	4	0.39	0/208	0.69	0/321
5	5	0.16	0/1841	0.35	0/2870
6	B	0.29	0/2121	0.46	1/2852 (0.0%)
7	C	0.20	0/1586	0.39	0/2134
8	D	0.35	0/1571	0.44	1/2113 (0.0%)
9	E	0.30	0/1434	0.47	0/1926
10	F	0.29	0/1343	0.50	1/1816 (0.1%)
11	G	0.22	0/1122	0.48	0/1515
12	J	0.20	0/1152	0.34	0/1551
13	K	0.20	0/947	0.43	0/1268
14	L	0.21	0/1054	0.45	0/1403
15	M	0.37	1/1093 (0.1%)	0.49	1/1460 (0.1%)
16	N	0.21	0/973	0.45	0/1301
17	O	0.17	0/902	0.39	0/1209
18	P	0.20	0/929	0.34	0/1242
19	Q	0.21	0/960	0.39	0/1278
20	R	0.29	0/829	0.44	0/1107
21	S	0.21	0/864	0.40	0/1156
22	T	0.18	0/744	0.34	0/994
23	U	0.48	0/787	0.73	5/1051 (0.5%)
24	V	0.29	0/766	0.36	0/1025
25	W	0.19	0/582	0.37	0/769
26	X	0.20	0/635	0.31	0/848
27	Y	0.17	0/510	0.39	0/677
28	Z	0.20	0/453	0.35	0/605
29	b	0.19	0/450	0.38	0/599
30	c	0.16	0/416	0.32	0/554
31	d	0.23	0/380	0.45	0/498
32	e	0.47	0/513	0.50	0/676

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	f	0.20	0/303	0.40	0/397
34	g	0.19	0/1735	0.44	0/2338
35	h	0.20	0/1651	0.49	4/2225 (0.2%)
36	i	0.28	0/1665	0.44	1/2227 (0.0%)
37	j	0.18	0/1154	0.45	0/1554
38	k	0.22	0/835	0.45	0/1128
39	l	0.22	0/1195	0.41	0/1602
40	m	0.17	0/989	0.35	0/1326
41	n	0.17	0/1034	0.45	0/1375
42	o	0.18	0/796	0.45	0/1077
43	p	0.33	0/885	0.48	1/1195 (0.1%)
44	q	0.24	0/960	0.53	0/1286
45	r	0.23	0/892	0.52	1/1193 (0.1%)
46	s	0.17	0/811	0.41	0/1081
47	t	0.17	0/722	0.35	0/964
48	u	0.17	0/659	0.38	0/884
49	v	0.28	0/657	0.47	0/881
50	w	0.16	0/511	0.37	0/689
51	x	0.13	0/652	0.29	0/877
52	y	0.14	0/671	0.36	0/888
53	z	0.44	1/500 (0.2%)	0.80	2/668 (0.3%)
All	All	0.19	2/156018 (0.0%)	0.34	27/233610 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
53	z	33	ARG	CA-C	-6.84	1.43	1.52
15	M	58	LYS	CA-C	-5.24	1.46	1.52

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	U	88	ASP	N-CA-C	-8.62	98.35	110.50
35	h	50	SER	N-CA-C	8.56	123.51	111.52
23	U	6	ARG	N-CA-C	8.23	119.88	111.07
8	D	82	GLY	N-CA-C	8.04	122.83	112.54
15	M	57	VAL	N-CA-C	-6.88	96.57	106.55

There are no chirality outliers.

There are no planarity outliers.

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	1	62262	0	31314	453	0
2	2	33015	0	16617	254	0
3	3	2572	0	1302	20	0
4	4	188	0	98	4	0
5	5	1648	0	834	9	0
6	B	2082	0	2157	34	0
7	C	1565	0	1616	18	0
8	D	1552	0	1619	17	0
9	E	1410	0	1447	31	0
10	F	1323	0	1374	16	0
11	G	1111	0	1148	20	0
12	J	1129	0	1162	8	0
13	K	938	0	1012	21	0
14	L	1045	0	1117	19	0
15	M	1074	0	1157	24	0
16	N	960	0	1000	17	0
17	O	892	0	923	8	0
18	P	917	0	965	8	0
19	Q	947	0	1022	8	0
20	R	816	0	839	9	0
21	S	857	0	922	15	0
22	T	738	0	807	8	0
23	U	779	0	834	6	0
24	V	753	0	780	7	0
25	W	575	0	592	6	0
26	X	625	0	655	6	0
27	Y	509	0	543	4	0
28	Z	449	0	491	3	0
29	b	444	0	461	9	0
30	c	409	0	440	5	0
31	d	377	0	418	10	0
32	e	504	0	574	10	0
33	f	302	0	343	6	0
34	g	1704	0	1732	23	0
35	h	1624	0	1699	17	0
36	i	1643	0	1710	27	0
37	j	1141	0	1170	24	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	k	817	0	808	19	0
39	l	1181	0	1240	22	0
40	m	979	0	1034	12	0
41	n	1022	0	1070	24	0
42	o	786	0	828	23	0
43	p	869	0	878	12	0
44	q	957	0	1017	19	0
45	r	883	0	944	17	0
46	s	799	0	841	8	0
47	t	714	0	737	14	0
48	u	649	0	666	10	0
49	v	648	0	691	13	0
50	w	504	0	502	3	0
51	x	637	0	665	11	0
52	y	665	0	714	8	0
53	z	495	0	486	17	0
54	1	203	0	0	0	0
54	2	76	0	0	0	0
54	3	1	0	0	0	0
54	5	1	0	0	0	0
54	B	2	0	0	0	0
54	D	1	0	0	0	0
54	Q	1	0	0	0	0
54	b	1	0	0	0	0
54	e	1	0	0	0	0
55	1	935	0	0	69	0
55	2	356	0	0	29	0
55	3	14	0	0	5	0
55	4	1	0	0	0	0
55	5	10	0	0	0	0
55	B	7	0	0	2	0
55	C	5	0	0	2	0
55	D	5	0	0	2	0
55	E	3	0	0	2	0
55	F	4	0	0	0	0
55	G	1	0	0	3	0
55	J	3	0	0	0	0
55	K	2	0	0	3	0
55	L	4	0	0	0	0
55	M	4	0	0	4	0
55	O	3	0	0	1	0
55	P	5	0	0	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	Q	3	0	0	0	0
55	R	3	0	0	0	0
55	S	2	0	0	2	0
55	V	2	0	0	0	0
55	W	2	0	0	1	0
55	X	1	0	0	1	0
55	Y	2	0	0	0	0
55	b	1	0	0	0	0
55	c	1	0	0	2	0
55	d	3	0	0	1	0
55	f	1	0	0	0	0
55	g	9	0	0	3	0
55	h	7	0	0	6	0
55	i	8	0	0	3	0
55	j	1	0	0	0	0
55	k	2	0	0	2	0
55	l	10	0	0	8	0
55	m	1	0	0	0	0
55	o	1	0	0	1	0
55	p	1	0	0	0	0
55	q	2	0	0	0	0
55	r	7	0	0	7	0
55	s	2	0	0	4	0
55	t	1	0	0	1	0
55	u	3	0	0	2	0
55	v	4	0	0	3	0
55	x	4	0	0	2	0
55	z	3	0	0	4	0
All	All	145220	0	96015	1260	0

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

The worst 5 of 1260 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)
1:1:2142:A:H3'	55:1:3339:HOH:O	1.28	1.24
1:1:2168:G:H5'	55:1:3875:HOH:O	1.36	1.24
1:1:2136:G:H1'	55:1:3846:HOH:O	1.45	1.15
2:2:723:U:H1'	55:2:1751:HOH:O	1.46	1.15
46:s:85:ARG:HD2	55:s:201:HOH:O	1.50	1.12

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	
6	B	269/273 (98%)	252 (94%)	17 (6%)	0	100	100
7	C	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
8	D	199/201 (99%)	187 (94%)	12 (6%)	0	100	100
9	E	175/179 (98%)	166 (95%)	9 (5%)	0	100	100
10	F	174/177 (98%)	168 (97%)	6 (3%)	0	100	100
11	G	147/149 (99%)	133 (90%)	14 (10%)	0	100	100
12	J	140/142 (99%)	134 (96%)	6 (4%)	0	100	100
13	K	120/123 (98%)	107 (89%)	13 (11%)	0	100	100
14	L	141/144 (98%)	121 (86%)	19 (14%)	1 (1%)	19	49
15	M	134/136 (98%)	129 (96%)	4 (3%)	1 (1%)	19	49
16	N	118/127 (93%)	108 (92%)	10 (8%)	0	100	100
17	O	114/117 (97%)	110 (96%)	4 (4%)	0	100	100
18	P	112/115 (97%)	108 (96%)	4 (4%)	0	100	100
19	Q	115/118 (98%)	112 (97%)	3 (3%)	0	100	100
20	R	101/103 (98%)	92 (91%)	8 (8%)	1 (1%)	13	40
21	S	108/110 (98%)	100 (93%)	7 (6%)	1 (1%)	14	43
22	T	91/100 (91%)	86 (94%)	5 (6%)	0	100	100
23	U	100/104 (96%)	89 (89%)	10 (10%)	1 (1%)	13	40
24	V	92/94 (98%)	92 (100%)	0	0	100	100
25	W	73/84 (87%)	73 (100%)	0	0	100	100
26	X	75/78 (96%)	71 (95%)	4 (5%)	0	100	100
27	Y	61/63 (97%)	58 (95%)	3 (5%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	Z	56/59 (95%)	56 (100%)	0	0	100	100
29	b	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
30	c	48/55 (87%)	45 (94%)	3 (6%)	0	100	100
31	d	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
32	e	62/65 (95%)	58 (94%)	4 (6%)	0	100	100
33	f	36/38 (95%)	30 (83%)	6 (17%)	0	100	100
34	g	216/241 (90%)	195 (90%)	21 (10%)	0	100	100
35	h	204/233 (88%)	201 (98%)	3 (2%)	0	100	100
36	i	203/206 (98%)	180 (89%)	23 (11%)	0	100	100
37	j	155/167 (93%)	140 (90%)	14 (9%)	1 (1%)	22	52
38	k	98/135 (73%)	83 (85%)	13 (13%)	2 (2%)	6	23
39	l	149/179 (83%)	139 (93%)	10 (7%)	0	100	100
40	m	127/130 (98%)	117 (92%)	10 (8%)	0	100	100
41	n	125/130 (96%)	105 (84%)	18 (14%)	2 (2%)	8	28
42	o	96/103 (93%)	82 (85%)	14 (15%)	0	100	100
43	p	114/129 (88%)	104 (91%)	10 (9%)	0	100	100
44	q	120/124 (97%)	109 (91%)	11 (9%)	0	100	100
45	r	112/118 (95%)	99 (88%)	9 (8%)	4 (4%)	3	12
46	s	99/102 (97%)	89 (90%)	10 (10%)	0	100	100
47	t	86/89 (97%)	78 (91%)	7 (8%)	1 (1%)	11	35
48	u	80/82 (98%)	71 (89%)	9 (11%)	0	100	100
49	v	78/84 (93%)	70 (90%)	8 (10%)	0	100	100
50	w	63/75 (84%)	57 (90%)	6 (10%)	0	100	100
51	x	77/92 (84%)	74 (96%)	3 (4%)	0	100	100
52	y	83/87 (95%)	80 (96%)	3 (4%)	0	100	100
53	z	63/71 (89%)	46 (73%)	14 (22%)	3 (5%)	2	7
All	All	5514/5843 (94%)	5097 (92%)	399 (7%)	18 (0%)	38	66

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	M	59	ARG
23	U	89	GLY

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
45	r	3	ILE
45	r	5	GLY
45	r	9	PRO

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	
6	B	216/218 (99%)	213 (99%)	3 (1%)	62	86
7	C	164/164 (100%)	163 (99%)	1 (1%)	84	95
8	D	165/165 (100%)	164 (99%)	1 (1%)	84	95
9	E	148/150 (99%)	143 (97%)	5 (3%)	32	67
10	F	137/138 (99%)	136 (99%)	1 (1%)	81	94
11	G	114/114 (100%)	109 (96%)	5 (4%)	24	57
12	J	116/116 (100%)	116 (100%)	0	100	100
13	K	103/104 (99%)	102 (99%)	1 (1%)	73	91
14	L	102/103 (99%)	102 (100%)	0	100	100
15	M	109/109 (100%)	108 (99%)	1 (1%)	75	92
16	N	100/103 (97%)	100 (100%)	0	100	100
17	O	86/87 (99%)	86 (100%)	0	100	100
18	P	99/100 (99%)	98 (99%)	1 (1%)	73	91
19	Q	89/90 (99%)	89 (100%)	0	100	100
20	R	84/84 (100%)	80 (95%)	4 (5%)	21	54
21	S	93/93 (100%)	90 (97%)	3 (3%)	34	69
22	T	80/84 (95%)	78 (98%)	2 (2%)	42	75
23	U	83/85 (98%)	82 (99%)	1 (1%)	67	89
24	V	78/78 (100%)	77 (99%)	1 (1%)	65	88
25	W	57/62 (92%)	56 (98%)	1 (2%)	54	82
26	X	67/68 (98%)	67 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	Y	55/55 (100%)	55 (100%)	0	100	100
28	Z	48/49 (98%)	48 (100%)	0	100	100
29	b	47/48 (98%)	47 (100%)	0	100	100
30	c	45/49 (92%)	43 (96%)	2 (4%)	24	57
31	d	38/38 (100%)	37 (97%)	1 (3%)	41	74
32	e	51/52 (98%)	49 (96%)	2 (4%)	27	62
33	f	34/34 (100%)	33 (97%)	1 (3%)	37	72
34	g	180/199 (90%)	176 (98%)	4 (2%)	47	78
35	h	170/190 (90%)	165 (97%)	5 (3%)	37	72
36	i	172/173 (99%)	168 (98%)	4 (2%)	45	77
37	j	114/126 (90%)	111 (97%)	3 (3%)	41	74
38	k	87/116 (75%)	85 (98%)	2 (2%)	45	77
39	l	124/147 (84%)	123 (99%)	1 (1%)	79	93
40	m	104/105 (99%)	104 (100%)	0	100	100
41	n	105/107 (98%)	104 (99%)	1 (1%)	73	91
42	o	86/90 (96%)	85 (99%)	1 (1%)	67	89
43	p	89/99 (90%)	87 (98%)	2 (2%)	47	78
44	q	102/103 (99%)	95 (93%)	7 (7%)	13	37
45	r	92/96 (96%)	88 (96%)	4 (4%)	25	57
46	s	79/84 (94%)	76 (96%)	3 (4%)	28	63
47	t	76/77 (99%)	76 (100%)	0	100	100
48	u	65/65 (100%)	65 (100%)	0	100	100
49	v	74/78 (95%)	74 (100%)	0	100	100
50	w	48/65 (74%)	47 (98%)	1 (2%)	48	78
51	x	70/79 (89%)	69 (99%)	1 (1%)	62	86
52	y	65/66 (98%)	64 (98%)	1 (2%)	60	85
53	z	44/61 (72%)	42 (96%)	2 (4%)	23	56
All	All	4554/4766 (96%)	4475 (98%)	79 (2%)	56	83

5 of 79 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
42	o	101	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	s	17	ASP
43	p	100	ASN
44	q	102	LEU
51	x	3	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
30	c	45	HIS
34	g	57	ASN
49	v	49	ASN
31	d	26	ASN
33	f	35	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2898/2904 (99%)	482 (16%)	50 (1%)
2	2	1538/1540 (99%)	224 (14%)	19 (1%)
3	3	119/120 (99%)	13 (10%)	2 (1%)
4	4	8/18 (44%)	4 (50%)	1 (12%)
5	5	76/77 (98%)	22 (28%)	2 (2%)
All	All	4639/4659 (99%)	745 (16%)	74 (1%)

5 of 745 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	A
1	1	12	U
1	1	26	G
1	1	34	U
1	1	35	G

5 of 74 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	1125	U
4	4	17	C
2	2	1182	G
2	2	1305	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	1130	U

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	$\# Z > 2$
44	0TD	q	89	44	8,9,10	1.44	0	6,11,13	2.65	3 (50%)

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
44	0TD	q	89	44	-	5/7/12/14	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	q	89	0TD	OD2-CG-CB	3.91	121.61	113.15
44	q	89	0TD	CSB-SB-CB	3.74	109.08	102.36
44	q	89	0TD	OD1-CG-CB	-2.62	116.96	122.44

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
44	q	89	0TD	CA-CB-SB-CSB
44	q	89	0TD	CA-CB-CG-OD1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
44	q	89	0TD	SB-CB-CG-OD1
44	q	89	0TD	CA-CB-CG-OD2
44	q	89	0TD	CG-CB-SB-CSB

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
44	q	89	0TD	5	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 287 ligands modelled in this entry, 287 are monoatomic - 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.

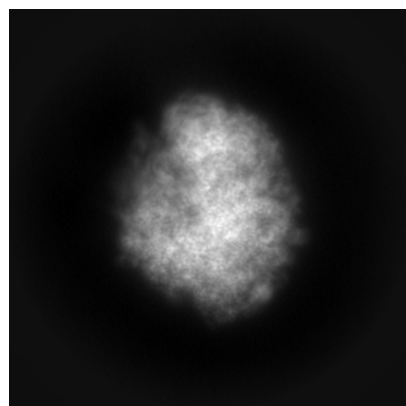
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42721. These allow visual inspection of the internal detail of the map and identification of artifacts.

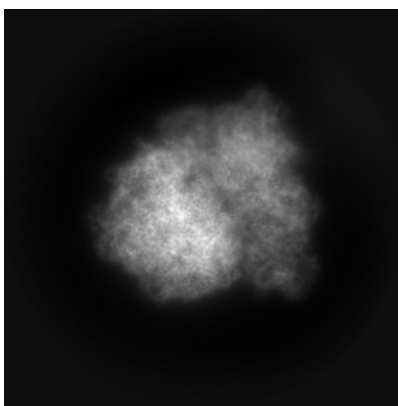
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

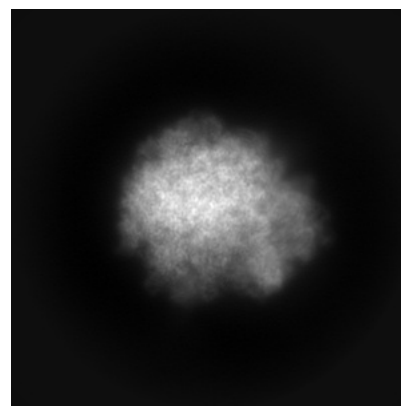
6.1.1 Primary map



X

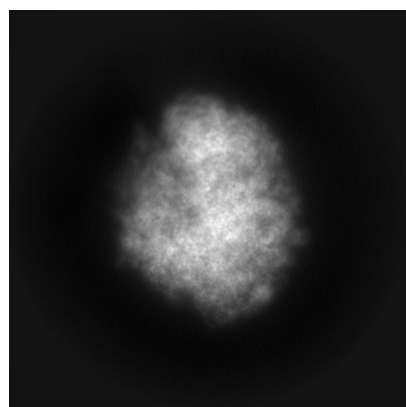


Y

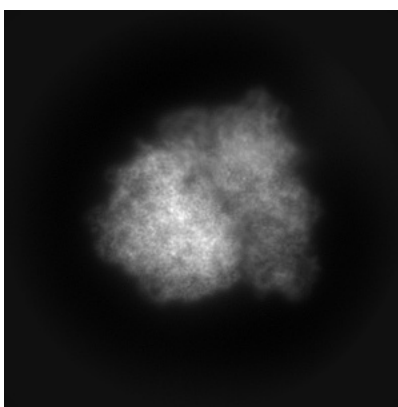


Z

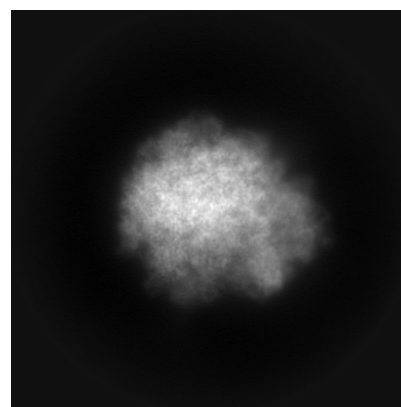
6.1.2 Raw map



X



Y

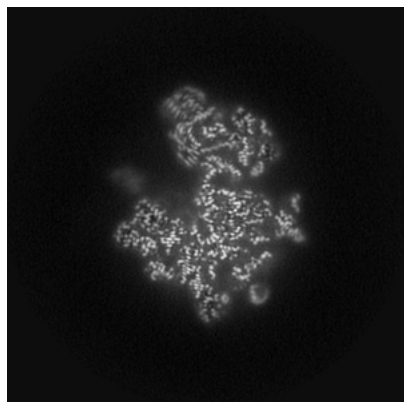


Z

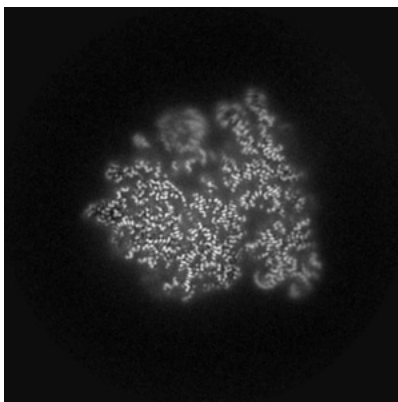
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

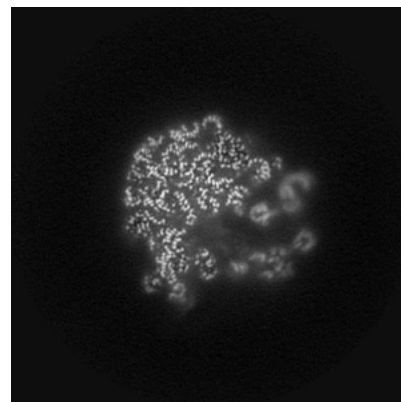
6.2.1 Primary map



X Index: 200

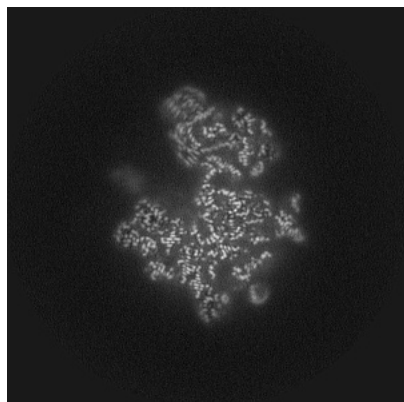


Y Index: 200

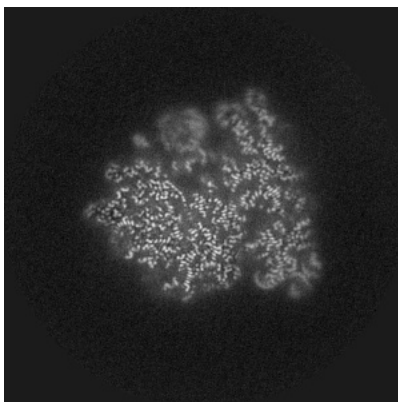


Z Index: 200

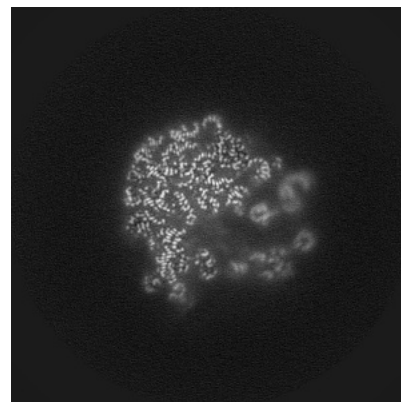
6.2.2 Raw map



X Index: 200



Y Index: 200

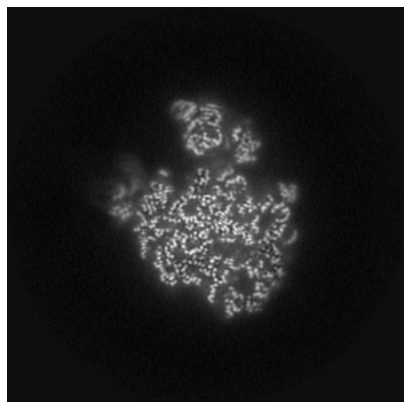


Z Index: 200

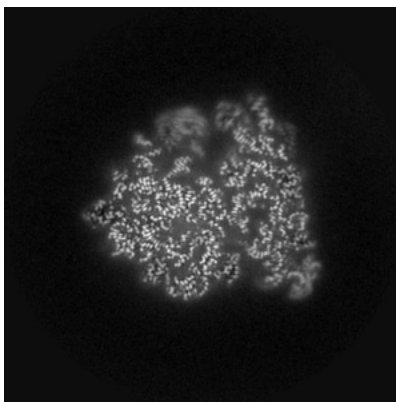
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

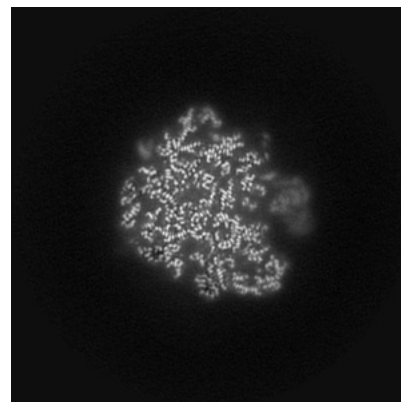
6.3.1 Primary map



X Index: 169

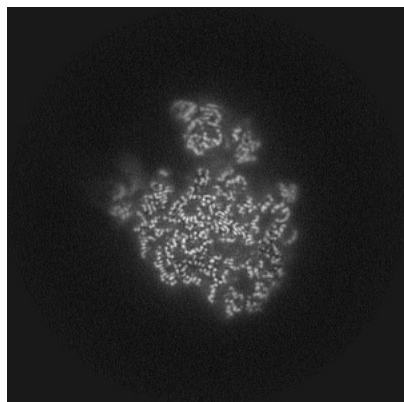


Y Index: 205

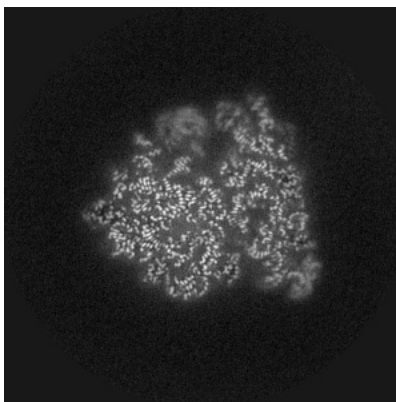


Z Index: 169

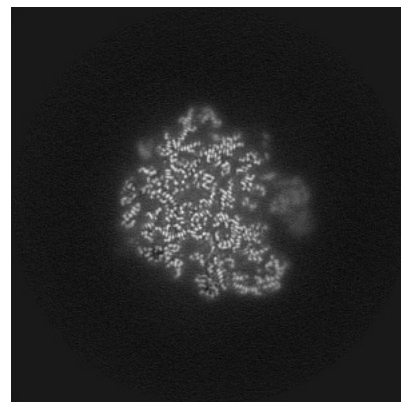
6.3.2 Raw map



X Index: 169



Y Index: 205

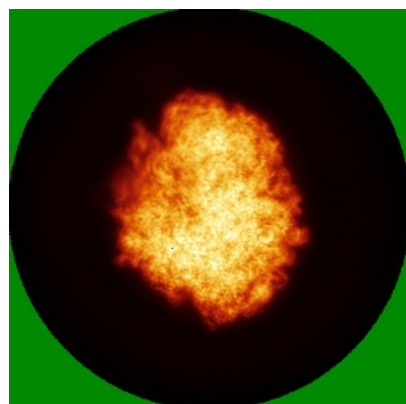


Z Index: 169

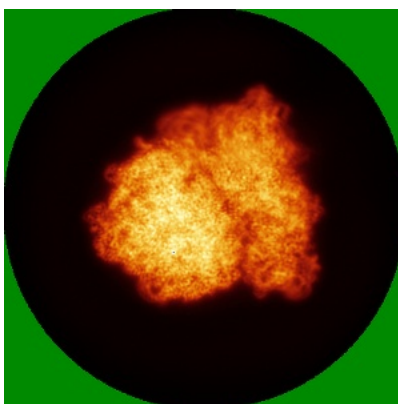
The images above show the largest variance slices of the map in three orthogonal directions.

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

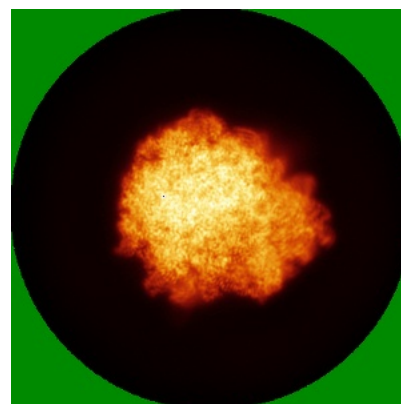
6.4.1 Primary map



X

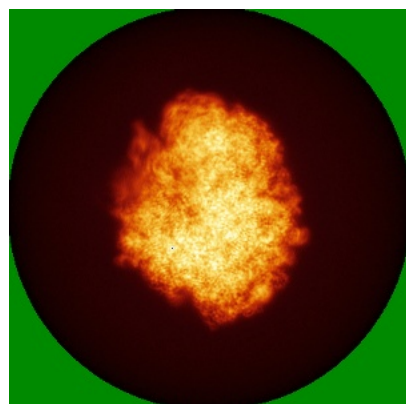


Y

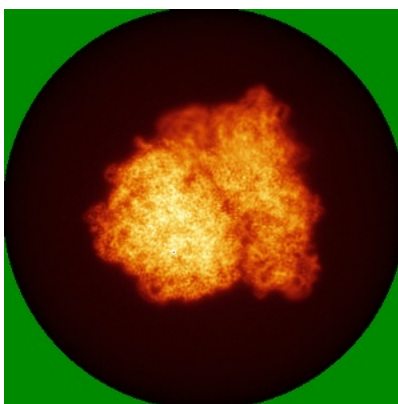


Z

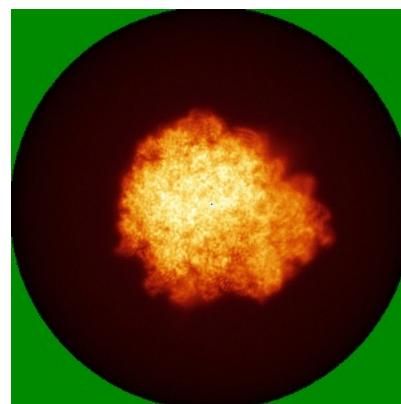
6.4.2 Raw map



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



X



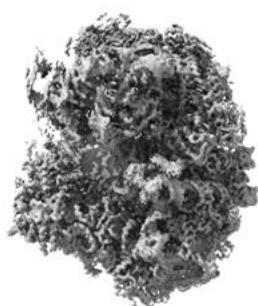
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0198. 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



X



Y



Z

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.

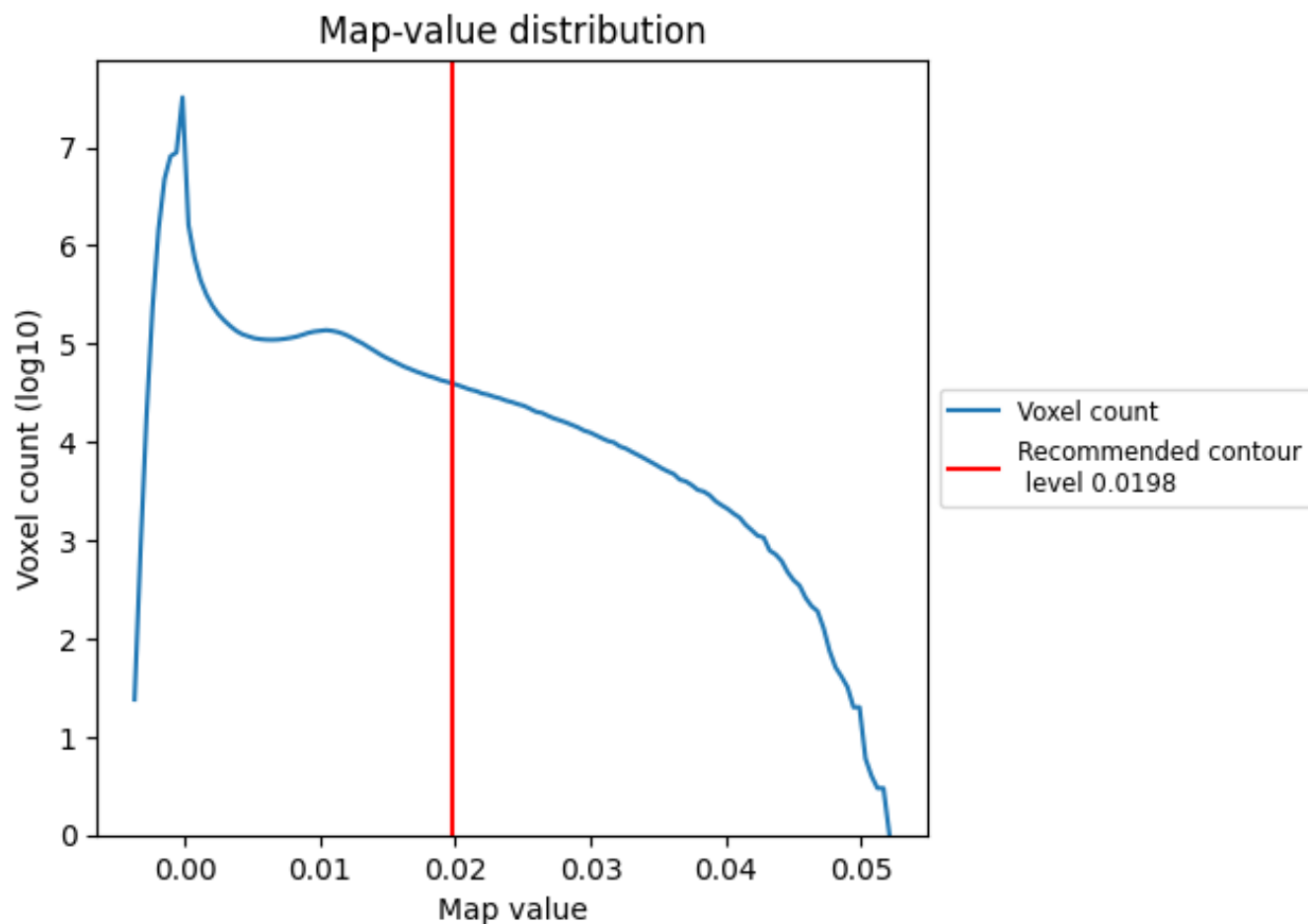
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

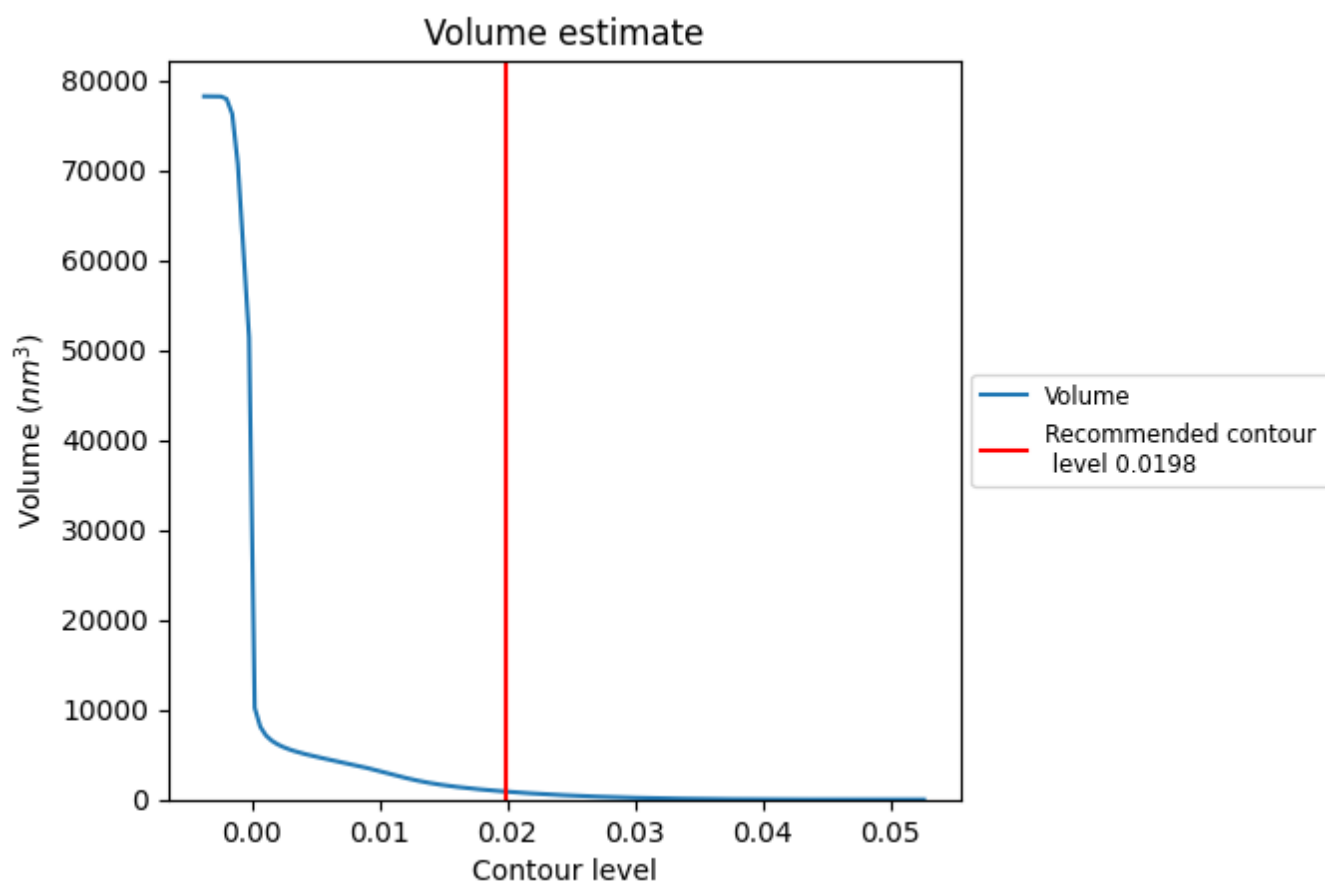
This section contains the results of statistical analysis of the map.

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.

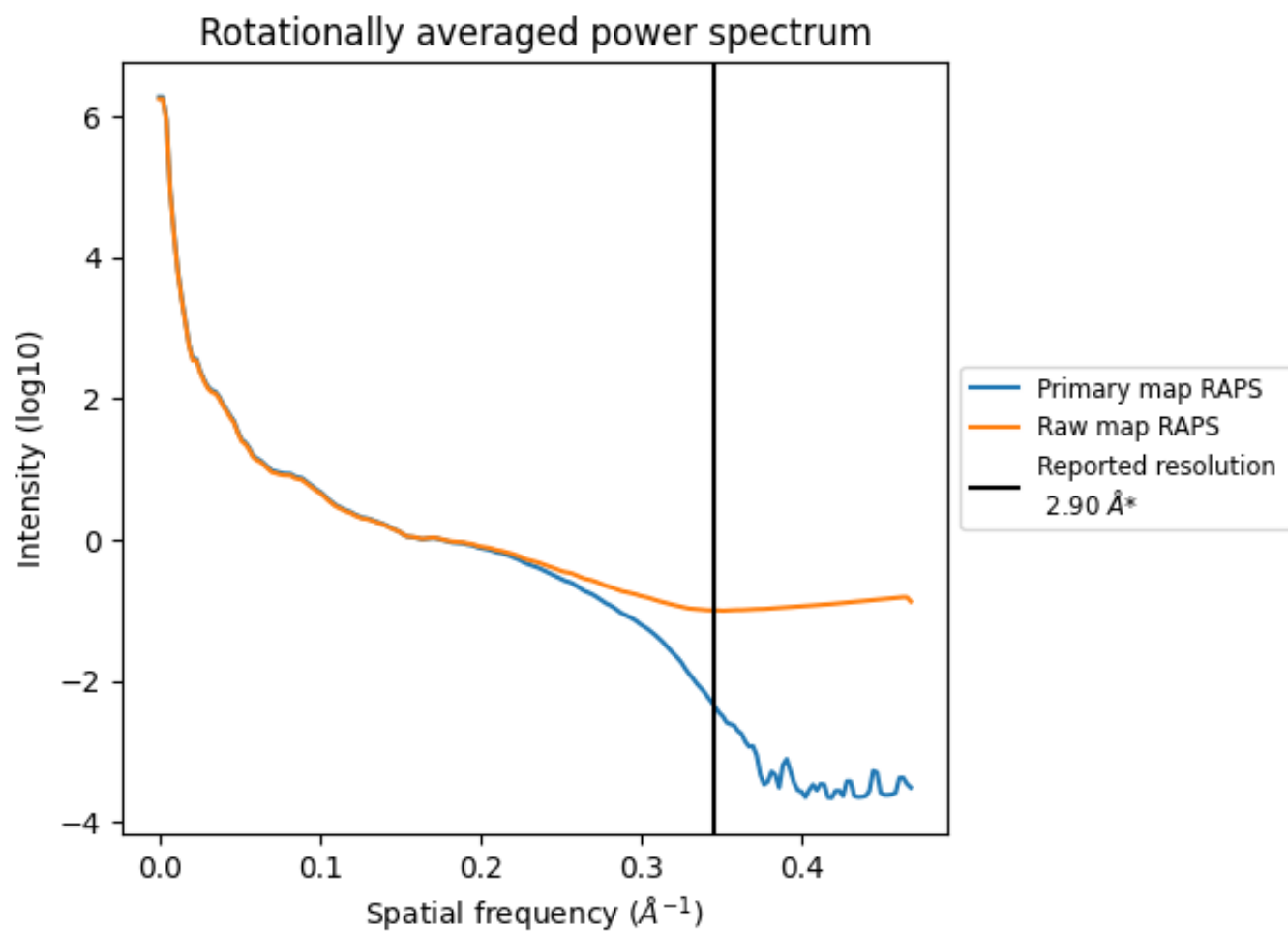
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 895 nm³; this corresponds to an approximate mass of 809 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 ⓘ

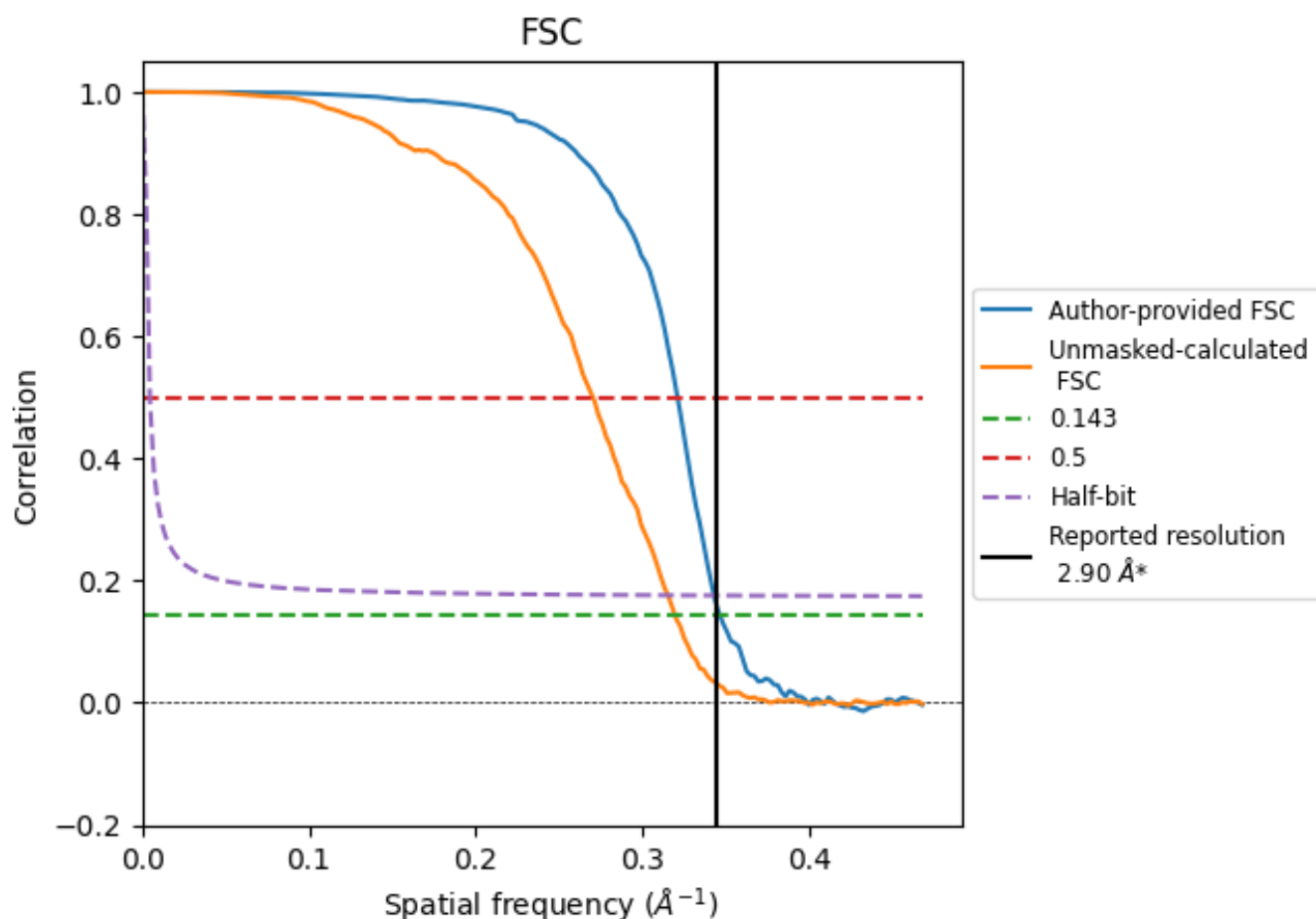


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

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 0.345 \AA^{-1}

8.2 Resolution estimates [i](#)

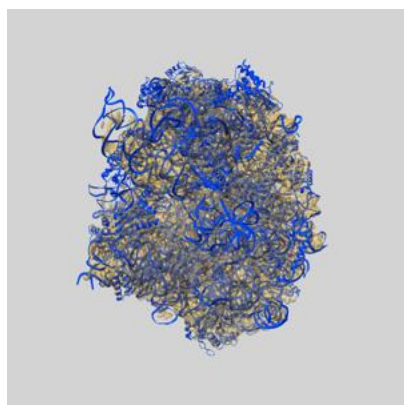
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.89	3.12	2.92
Unmasked-calculated*	3.13	3.70	3.17

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

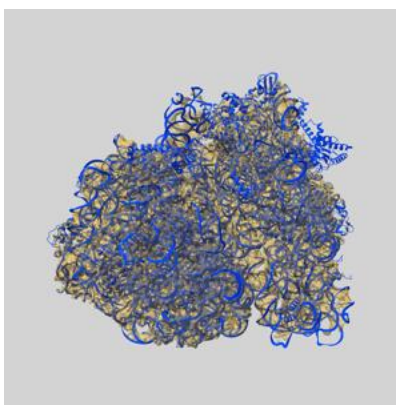
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-42721 and PDB model 8UXB. Per-residue inclusion information can be found in section [3](#) on page [16](#).

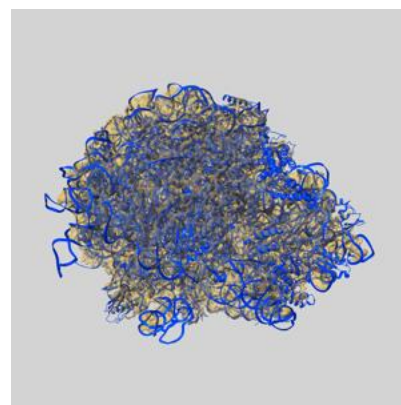
9.1 Map-model overlay [i](#)



X



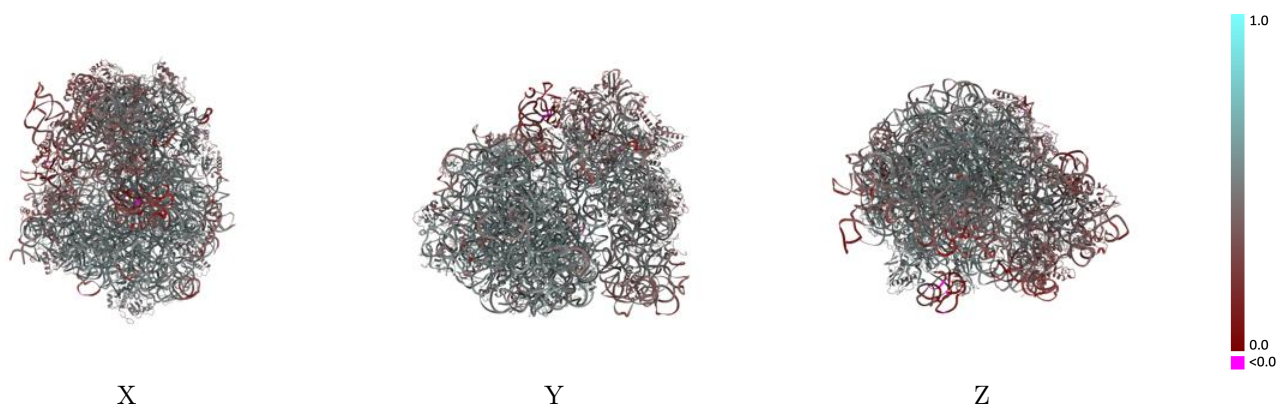
Y



Z

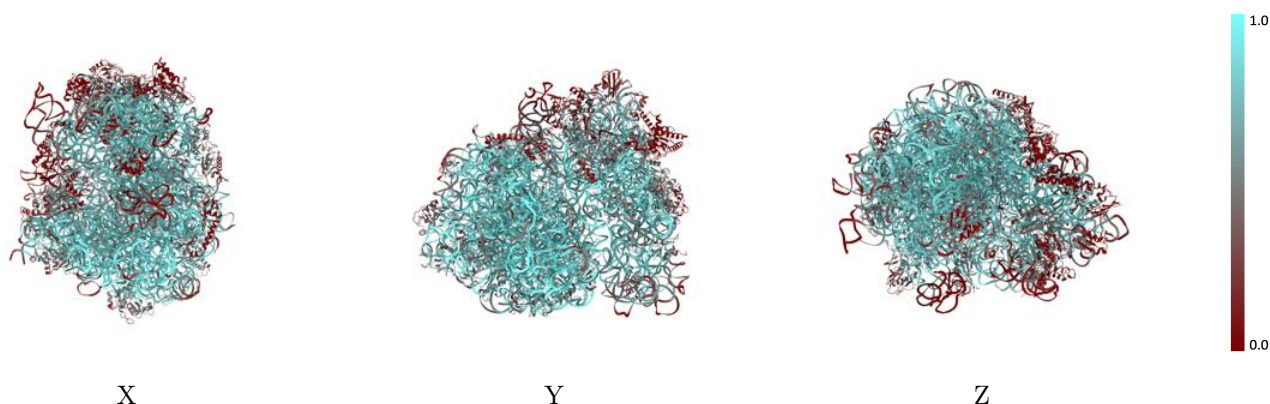
The images above show the 3D surface view of the map at the recommended contour level 0.0198 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



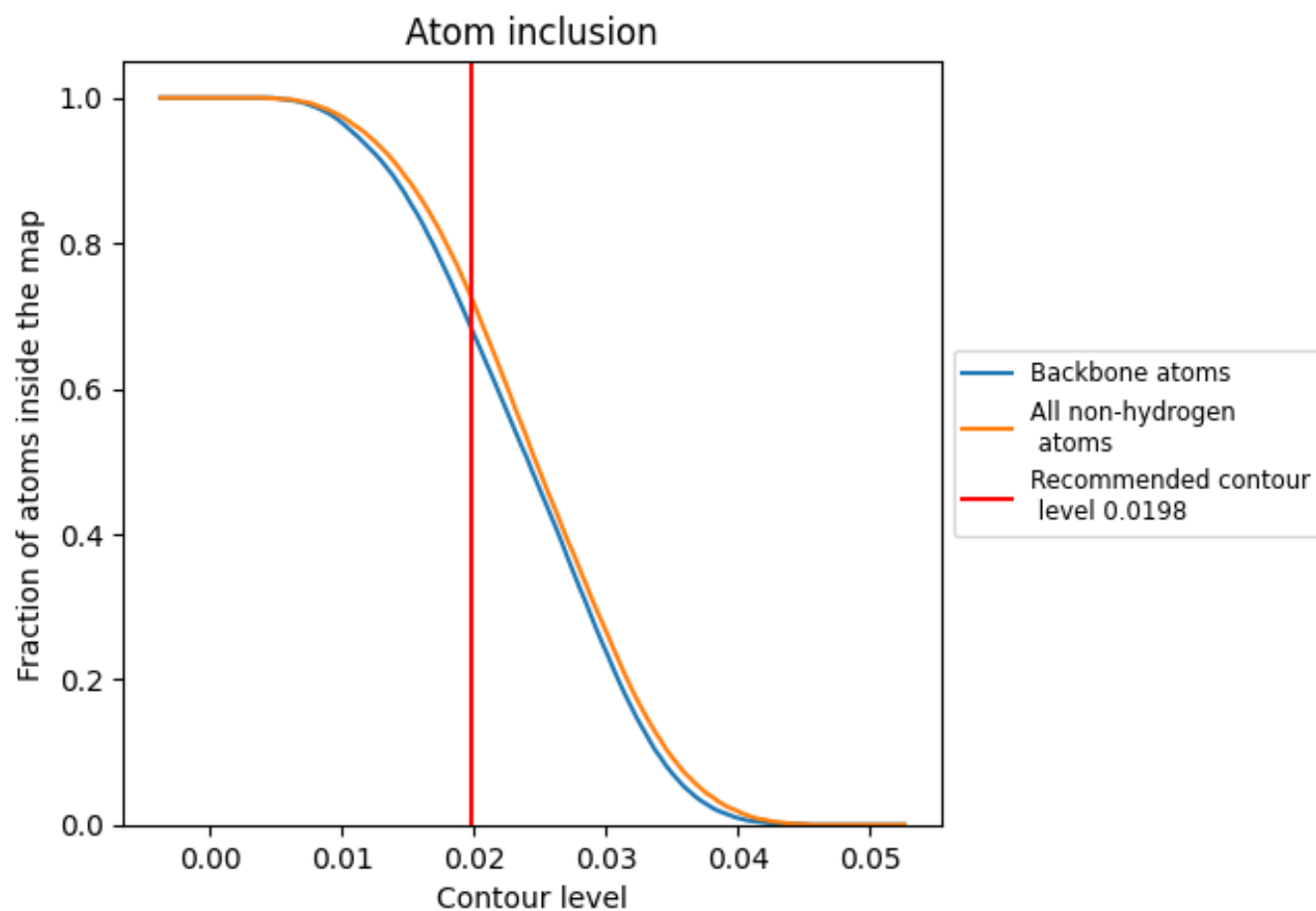
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0198).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 72% 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 (0.0198) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7250	 0.4680
1	 0.8650	 0.4980
2	 0.7730	 0.4420
3	 0.7780	 0.4760
4	 0.6220	 0.4620
5	 0.7790	 0.3930
B	 0.7790	 0.5390
C	 0.6850	 0.5340
D	 0.5660	 0.4970
E	 0.2540	 0.3400
F	 0.3620	 0.4640
G	 0.0500	 0.3370
J	 0.6960	 0.5170
K	 0.7040	 0.5160
L	 0.6460	 0.5060
M	 0.7050	 0.5220
N	 0.7290	 0.5250
O	 0.4540	 0.4560
P	 0.6060	 0.5040
Q	 0.7580	 0.5260
R	 0.5670	 0.5040
S	 0.6850	 0.5110
T	 0.5720	 0.4880
U	 0.4380	 0.4920
V	 0.5140	 0.4940
W	 0.7210	 0.5320
X	 0.7120	 0.5040
Y	 0.4610	 0.4200
Z	 0.6250	 0.5200
b	 0.7060	 0.5090
c	 0.6230	 0.4980
d	 0.8730	 0.5120
e	 0.8210	 0.5460
f	 0.7400	 0.5080
g	 0.0010	 0.3740



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
h	 0.3480	 0.4090
i	 0.2520	 0.3540
j	 0.5760	 0.4570
k	 0.3190	 0.3790
l	 0.1330	 0.3040
m	 0.5200	 0.4890
n	 0.2410	 0.3470
o	 0.2500	 0.3740
p	 0.5690	 0.4620
q	 0.5950	 0.4720
r	 0.1840	 0.3140
s	 0.3750	 0.3640
t	 0.5510	 0.4480
u	 0.5090	 0.4450
v	 0.4890	 0.4530
w	 0.4660	 0.4350
x	 0.1920	 0.2980
y	 0.4650	 0.3560
z	 0.3420	 0.3170