



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 04:08 PM UTC

PDB ID : 7ZP8 / pdb_00007zp8
EMDB ID : EMD-14850
Title : 70S E. coli ribosome with a stalled flamin domain 5 nascent chain
Authors : Mitropoulou, A.; Plessa, E.; Wlodarski, T.; Ahn, M.; Chan, S.H.S.; Becker, T.A.; Beckmann, R.; Cabrita, L.D.; Christodoulou, J.
Deposited on : 2022-04-26
Resolution : 2.20 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

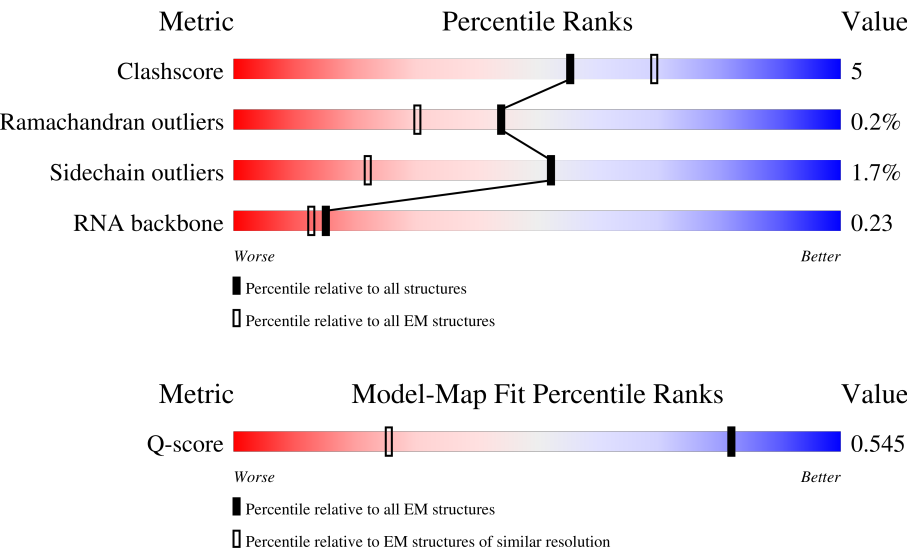
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	3184 (1.71 - 2.70)

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	0	78	85%14%
2	1	63	19% 67%30%
3	2	59	7% 80%17%

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Mol	Chain	Length	Quality of chain
4	3	57	
5	4	55	
6	6	46	
7	7	65	
8	8	50	
9	a	120	
10	b	2904	
11	c	273	
12	d	209	
13	e	201	
14	f	179	
15	g	177	
16	h	149	
17	j	142	
18	k	123	
19	l	144	
20	m	136	
21	n	127	
22	o	117	
23	p	115	
24	q	118	
25	r	103	
26	s	110	
27	t	100	
28	u	104	

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Mol	Chain	Length	Quality of chain
29	w	94	13% 88% 12%
30	y	85	8% 78% 19%
31	v	77	10% 39% 47% 13%
32	z	148	18% 10% 9% 78%

2 Entry composition

There are 32 unique types of molecules in this entry. The entry contains 90951 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 2 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	61	Total	C	N	O	S	0	0
			495	305	97	92	1		

- Molecule 3 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	57	Total	C	N	O	S	0	0
			439	276	86	75	2		

- Molecule 4 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	55	Total	C	N	O	S	0	0
			434	263	92	78	1		

- Molecule 5 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	4	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 6 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 7 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 8 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	8	38	Total	C	N	O	S	0	0
			301	185	65	47	4		

- Molecule 9 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	a	118	Total	C	N	O	P	0	0
			2529	1126	464	821	118		

- Molecule 10 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	b	2901	Total	C	N	O	P	0	0
			62281	27784	11464	20132	2901		

- Molecule 11 is a protein called 50S ribosomal protein L2.

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

- Molecule 12 is a protein called 50S ribosomal protein L3.

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

- Molecule 13 is a protein called 50S ribosomal protein L4.

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

- Molecule 14 is a protein called 50S ribosomal protein L5.

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

- Molecule 15 is a protein called 50S ribosomal protein L6.

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

- Molecule 16 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	h	39	Total	C	N	O	S	0	0
			287	184	51	51	1		

- Molecule 17 is a protein called 50S ribosomal protein L13.

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

- Molecule 18 is a protein called 50S ribosomal protein L14.

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

- Molecule 19 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	l	143	Total	C	N	O	S	0	0
			1043	649	206	186	2		

- Molecule 20 is a protein called 50S ribosomal protein L16.

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

- Molecule 21 is a protein called 50S ribosomal protein L17.

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

- Molecule 22 is a protein called 50S ribosomal protein L18.

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

- Molecule 23 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	p	113	Total	C	N	O	S	0	0
			908	570	177	160	1		

- Molecule 24 is a protein called 50S ribosomal protein L20.

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

- Molecule 25 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	r	102	Total	C	N	O	S	0	0
			810	513	152	143	2		

- Molecule 26 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	s	109	Total	C	N	O	S	0	0
			845	526	162	154	3		

- Molecule 27 is a protein called 50S ribosomal protein L23.

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

- Molecule 28 is a protein called 50S ribosomal protein L24.

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

- Molecule 29 is a protein called 50S ribosomal protein L25.

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

- Molecule 30 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	y	82	Total	C	N	O	S	0	0
			619	383	127	108	1		

- Molecule 31 is a RNA chain called Pro-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	v	76	Total	C	N	O	P	0	0
			1626	724	292	534	76		

- Molecule 32 is a protein called Gelation factor.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	z	33	Total	C	N	O	0	0
			277	186	44	47		

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
z	20	MET	-	initiating methionine	UNP P13466
z	21	HIS	-	expression tag	UNP P13466
z	22	HIS	-	expression tag	UNP P13466
z	23	HIS	-	expression tag	UNP P13466
z	24	HIS	-	expression tag	UNP P13466
z	25	HIS	-	expression tag	UNP P13466
z	26	HIS	-	expression tag	UNP P13466
z	27	ALA	-	expression tag	UNP P13466
z	28	SER	-	expression tag	UNP P13466
z	149	GLU	-	expression tag	UNP P13466
z	150	LEU	-	expression tag	UNP P13466
z	151	PHE	-	expression tag	UNP P13466
z	152	SER	-	expression tag	UNP P13466

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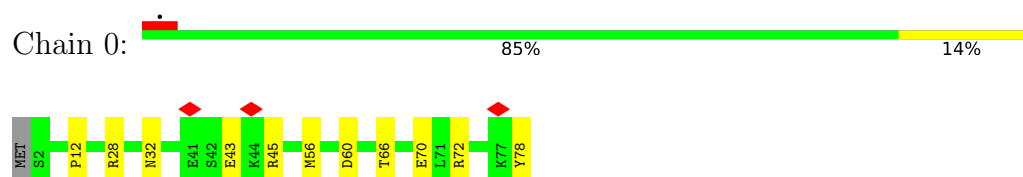
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Chain	Residue	Modelled	Actual	Comment	Reference
z	153	THR	-	expression tag	UNP P13466
z	154	PRO	-	expression tag	UNP P13466
z	155	VAL	-	expression tag	UNP P13466
z	156	TRP	-	expression tag	UNP P13466
z	157	ILE	-	expression tag	UNP P13466
z	158	TRP	-	expression tag	UNP P13466
z	159	TRP	-	expression tag	UNP P13466
z	160	TRP	-	expression tag	UNP P13466
z	161	PRO	-	expression tag	UNP P13466
z	162	ARG	-	expression tag	UNP P13466
z	163	ILE	-	expression tag	UNP P13466
z	164	ARG	-	expression tag	UNP P13466
z	165	GLY	-	expression tag	UNP P13466
z	166	PRO	-	expression tag	UNP P13466
z	167	PRO	-	expression tag	UNP P13466

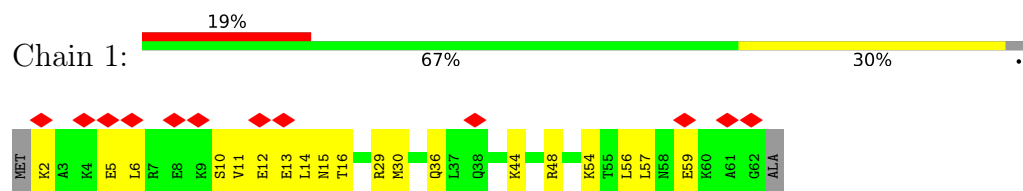
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

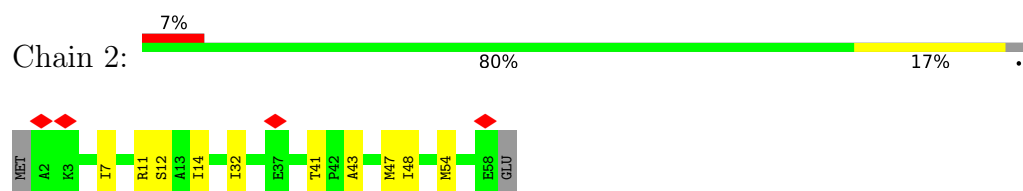
- Molecule 1: 50S ribosomal protein L28



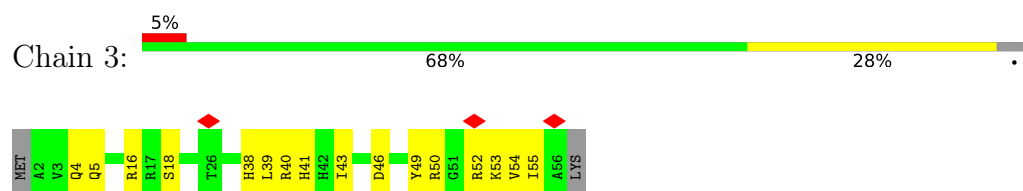
- Molecule 2: 50S ribosomal protein L29



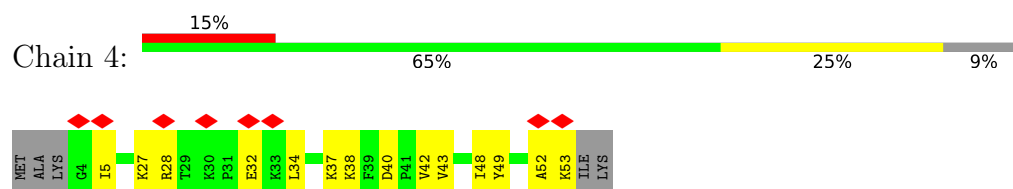
- Molecule 3: 50S ribosomal protein L30



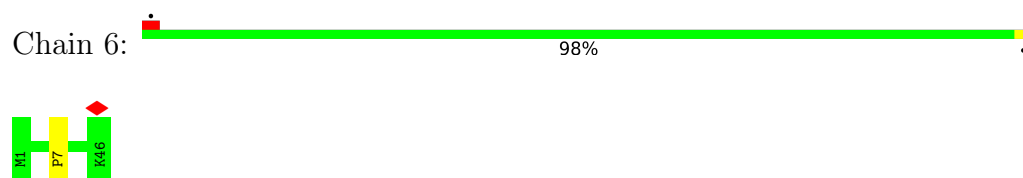
- Molecule 4: 50S ribosomal protein L32



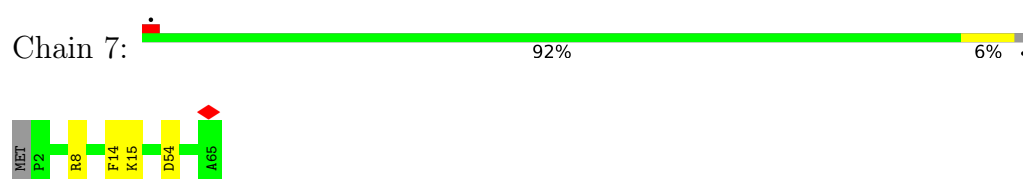
- Molecule 5: 50S ribosomal protein L33



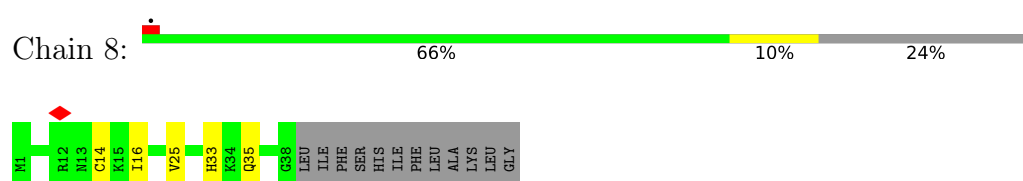
- Molecule 6: 50S ribosomal protein L34



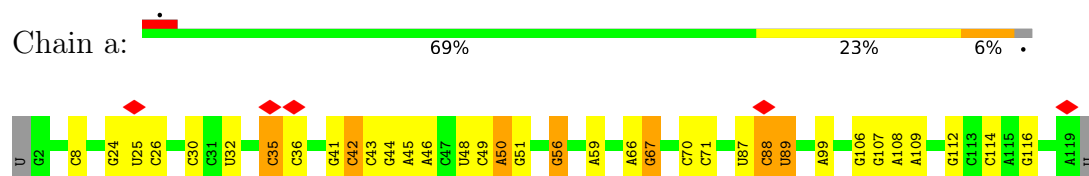
- Molecule 7: 50S ribosomal protein L35



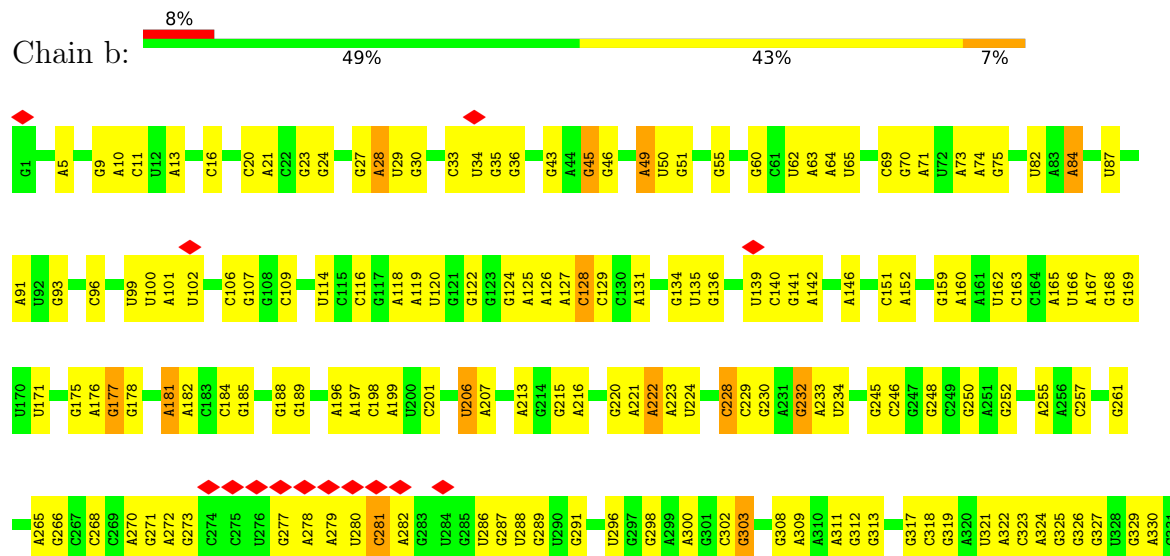
- Molecule 8: 50S ribosomal protein L36

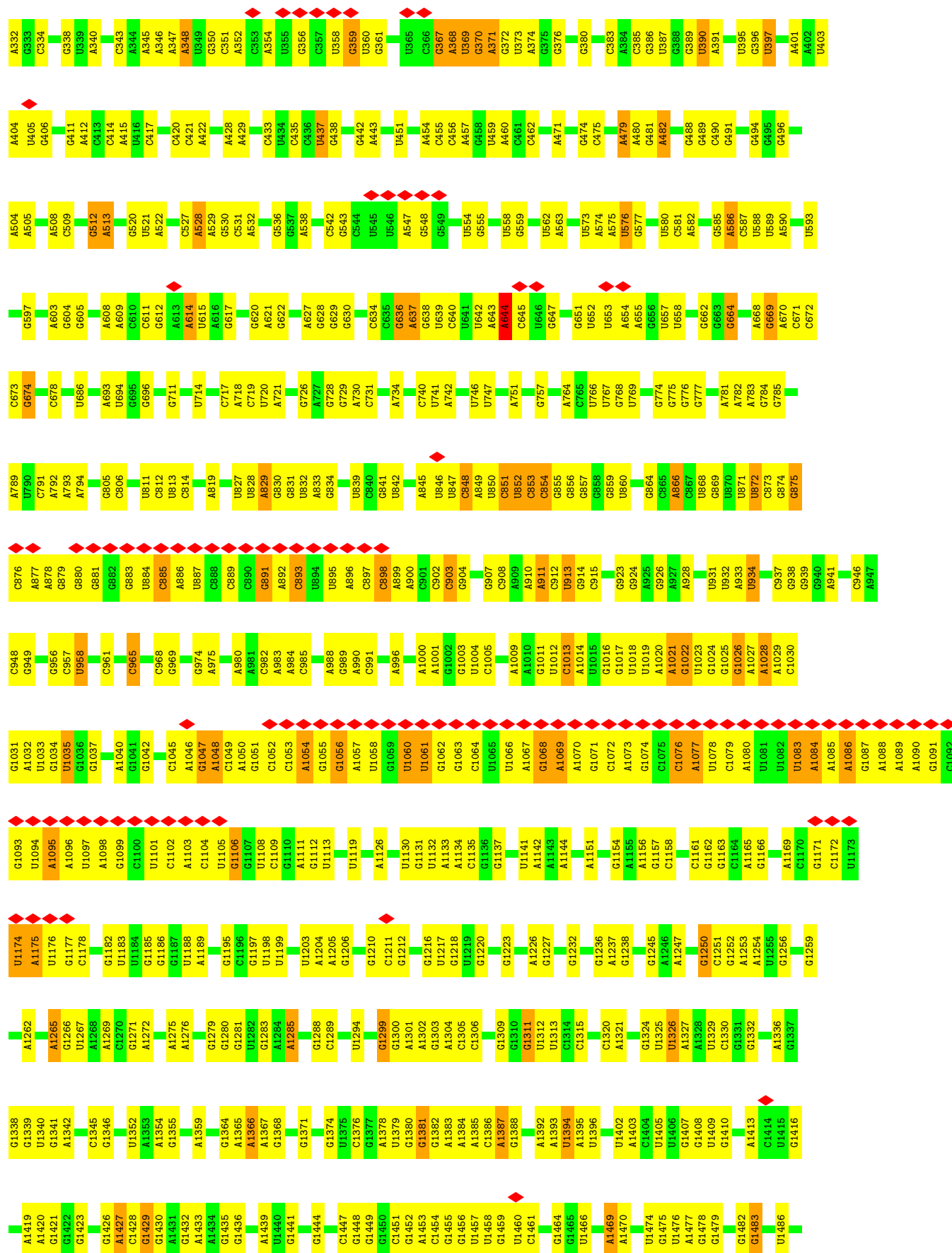


- Molecule 9: 5S rRNA

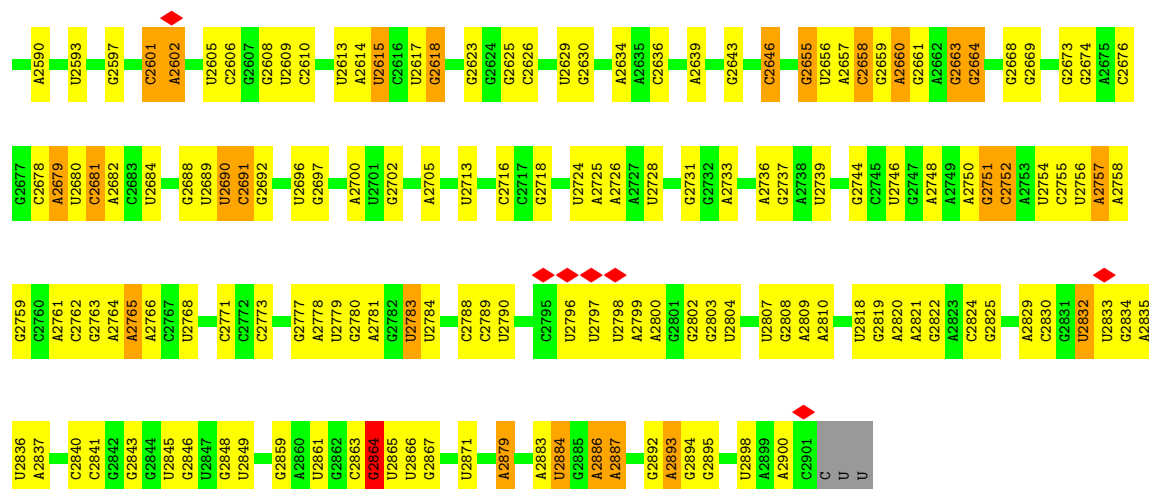


- Molecule 10: 23S rRNA

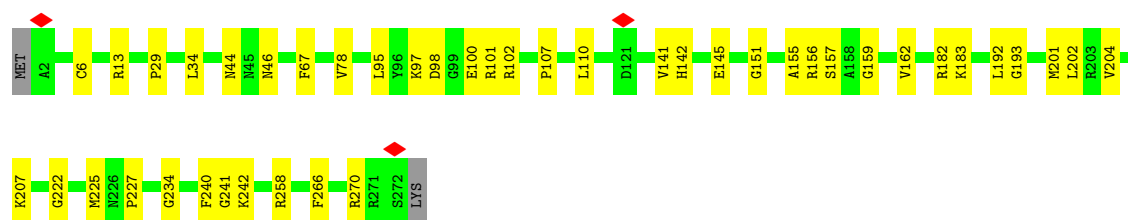
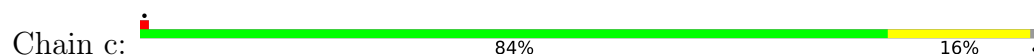




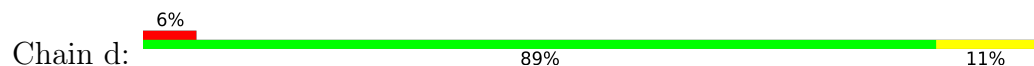
G2502	A2503	C2427	A2428	A2386	A2266	A2173	U2113	G2032	G1945	U1856	A1755	G1673	C1575	A1490
U2504	G2505	G2428	G2429	C2338	A2268	C2174	A2114	U2034	U1946	G1857	G1756	G1674	U1576	G1491
G2506	U2507	A2430	U2431	A2340	A2274	C2175	G2115	G2035	A1952	A1858	A1759	C1675	U1577	C1492
G2508	C2509	G2432	A2433	G2346	A2278	C2176	G2116	A2036	G1954	G1862	A1762	G1681	G1581	A1494
A2513	U2514	A2434	A2435	C2347	A2282	C2177	A2117	G2038	U1955	G1863	G1763	G1682	C1582	A1495
U2515	A2516	G2350	G2351	G2347	C2283	C2179	U2118	U2039	U1956	U1864	G1764	G1684	U1583	A1496
G2517	G2518	G2352	A2352	G2347	C2286	U2180	A2119	G2040	C1957	G1869	A1773	A1690	C1586	U1497
U2519	C2520	G2353	A2353	G2347	A2287	U2181	G2121	A2041	C1958	A1871	G1776	U1588	U1589	A1509
G2526	U2527	G2354	G2355	G2347	A2288	U2182	G2122	A2042	C1961	A1872	U1779	U1693	C1507	U1506
C2527	G2528	G2356	G2357	G2347	A2289	U2183	G2123	A2043	U1962	A1873	U1782	A1593	A1508	A1508
U2529	G2530	G2358	G2359	G2347	A2290	U2184	G2124	C2055	G1963	G1874	U1783	A1594	A1509	G1510
G2533	A2534	G2361	G2362	G2347	U2291	U2185	G2125	G2056	G1964	G1875	A1784	C1595	G1516	G1516
A2536	G2537	G2363	G2364	G2347	U2292	U2186	G2126	A2059	G1965	A1876	A1785	G1702	C1600	G1517
G2546	G2547	G2365	G2366	G2347	U2293	U2187	G2127	A2060	G1966	G1887	A1792	G1703	U1602	G1518
G2547	G2548	G2367	G2368	G2347	U2294	U2188	G2128	A2061	G1967	G1888	G1793	G1704	A1603	G1519
G2550	G2551	G2369	G2370	G2347	U2295	U2189	G2129	A2062	C1974	G1889	C1792	G1705	U1603	G1523
U2554	U2555	G2371	G2372	G2347	U2296	U2190	U2130	A2063	G1975	A1890	A1794	G1706	A1606	G1524
C2556	G2557	G2373	G2374	G2347	U2297	U2191	U2131	U2068	G1980	G1895	C1800	A1714	C1607	G1529
A2560	U2561	G2375	G2376	G2347	U2298	U2192	G2132	G2069	G1981	C1896	C1801	U1715	A1608	G1530
U2562	U2563	G2377	G2378	G2347	U2299	U2193	G2133	U2074	G1982	C1897	A1802	U1716	A1609	G1531
A2564	U2565	G2379	G2380	G2347	U2300	U2194	G2134	U2075	G1993	C1906	A1803	A1717	C1612	A1532
G2566	G2567	G2381	G2382	G2347	U2301	U2195	G2135	U2076	U1994	A1913	A1804	G1721	C1613	C1533
U2568	U2569	G2383	G2384	G2347	U2302	U2196	G2136	U2077	C1996	C1914	A1805	C1728	G1622	U1534
G2572	C2573	G2385	G2386	G2347	U2303	U2197	G2137	A2078	C1997	A1915	C1816	U1729	A1626	G1536
U2574	C2575	G2387	G2388	G2347	U2304	U2198	G2138	U2079	C1998	A1916	U1817	G1730	G1627	G1537
C2579	U2580	G2389	G2390	G2347	U2305	U2199	G2139	U2080	C1999	U1917	U1818	U1731	A1630	U1539
G2581	G2582	G2391	G2392	G2347	U2306	U2200	G2140	U2081	G2002	G1921	U1819	G1732	A1634	A1544
C2583	U2584	G2393	G2394	G2347	U2307	U2201	G2141	U2082	C2008	G1922	U1820	U1733	A1635	C1547
U2586	U2587	G2395	G2396	G2347	U2308	U2202	G2142	U2083	A2009	C1923	A1821	G1734	G1642	A1552
		G2397	G2398	G2347	U2309	U2203	G2143	U2084	G2010	U1924	C1822	U1735	G1643	A1553
		G2400	G2401	G2347	U2310	U2204	G2144	U2085	U2011	U1925	U1823	U1736	G1643	G1555
		G2402	G2403	G2347	U2311	U2205	G2145	U2086	A2012	A1928	G1824	G1737	U1647	C1558
		G2404	G2405	G2347	U2312	U2206	G2146	U2087	G2013	G1929	A1825	G1738	U1648	U1559
		G2406	G2407	G2347	U2313	U2207	G2147	U2088	A2014	G1930	U1826	G1739	U1649	G1560
		A2408	A2409	G2347	U2314	U2208	G2148	U2089	C2020	U1931	C1833	A1744	A1664	U1563
		G2410	G2411	G2347	U2315	U2209	G2149	U2090	A2021	G1935	C1836	A1745	A1665	C1564
		G2412	G2413	G2347	U2151	U2210	G2150	G2100	C2022	A1937	A1848	A1749	G1666	C1565
		G2414	G2415	G2347	G2152	U2211	G2151	A2101	U2022	A1938	G1849	G1750	A1566	A1567
		G2416	G2417	G2347	G2153	U2212	G2152	A2102	C2023	U1940	A1853	G1751	A1667	G1568
		U2419	U2420	G2347	G2154	U2213	G2153	G2103	G2024			G1752	A1669	A1569
		G2421	G2422	G2347	G2155	U2214	G2154	C2104				A1754		A1570
		U2423	U2424	G2347	G2156	U2215	G2155	U2105						A1571
		G2425	G2426	G2347	G2157	U2216	G2156	U2106						
				G2347	G2158	U2217	G2157	G2107						
				G2347	G2159	U2218	G2158	A2108						
				G2347	G2160	U2219	G2159	U2109						
				G2347	G2161	U2220	G2160	U2110						
				G2347	G2162	U2221	G2161	U2111						
				G2347	G2163	U2222	G2163	G2112						
				G2347	G2164	U2223	G2164							
				G2347	G2165	U2224	G2165							
				G2347	G2166	U2225	G2166							
				G2347	G2167	U2226	G2167							
				G2347	G2168	U2227	G2168							
				G2347	G2169	U2228	G2169							
				G2347	G2170	U2229	G2170							
				G2347	G2171	U2230	G2171							
				G2347	G2172	U2231	G2172							



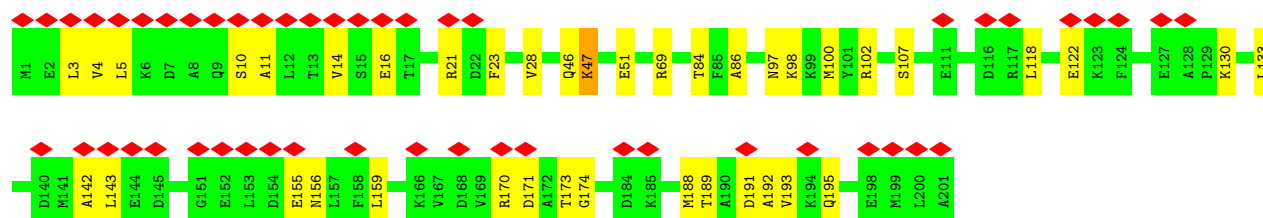
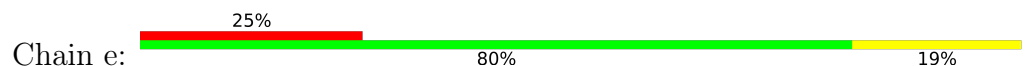
• Molecule 11: 50S ribosomal protein L2



• Molecule 12: 50S ribosomal protein L3

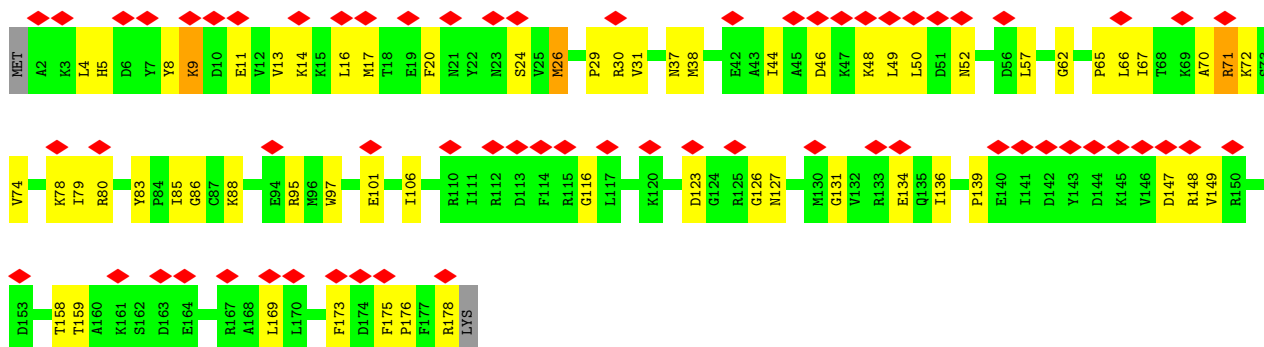


• Molecule 13: 50S ribosomal protein L4

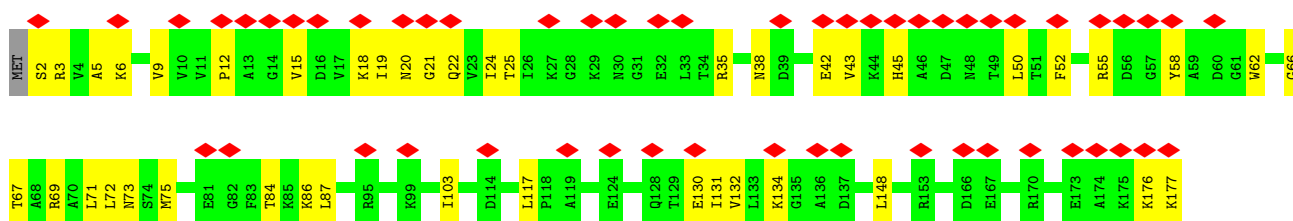
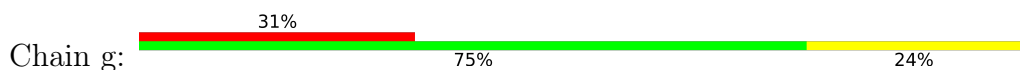


• Molecule 14: 50S ribosomal protein L5

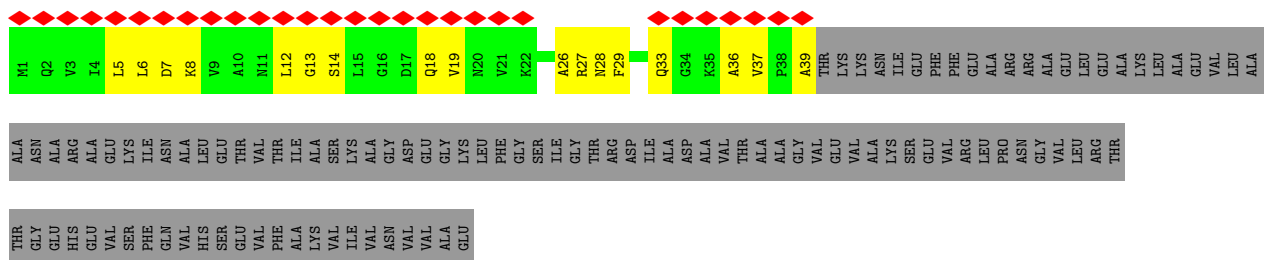




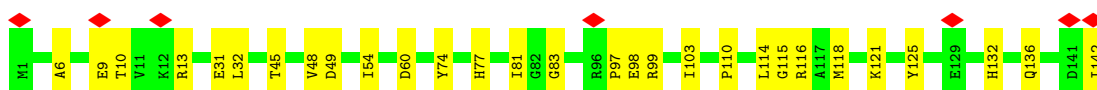
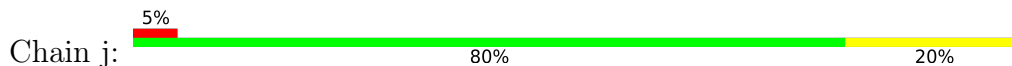
• Molecule 15: 50S ribosomal protein L6



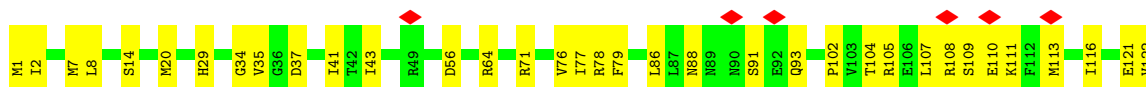
• Molecule 16: 50S ribosomal protein L9



• Molecule 17: 50S ribosomal protein L13



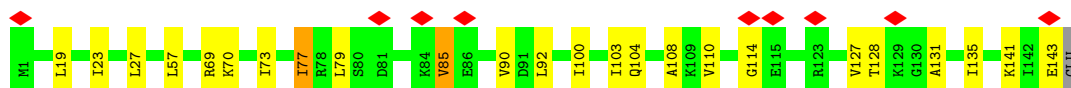
• Molecule 18: 50S ribosomal protein L14



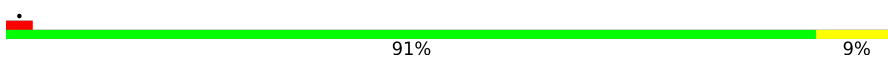
LEU

- Molecule 19: 50S ribosomal protein L15

Chain l: 



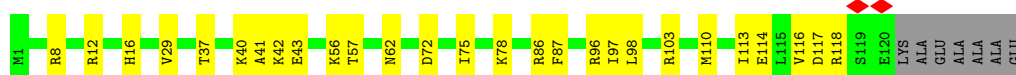
- Molecule 20: 50S ribosomal protein L16

Chain m: 



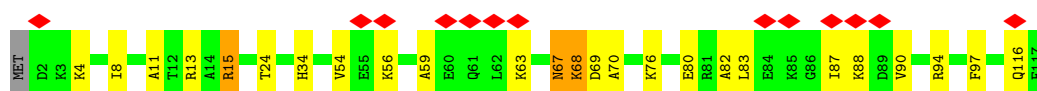
- Molecule 21: 50S ribosomal protein L17

Chain n: 



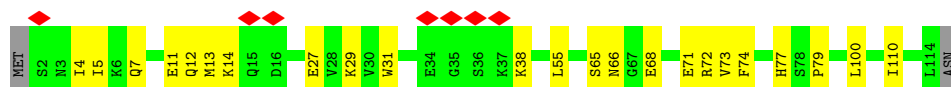
- Molecule 22: 50S ribosomal protein L18

Chain o: 



- Molecule 23: 50S ribosomal protein L19

Chain p: 

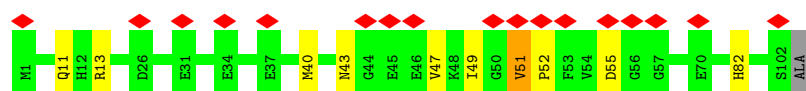
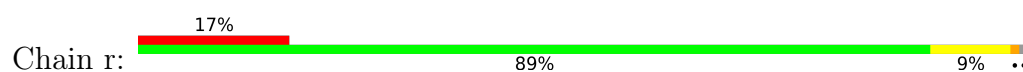


- Molecule 24: 50S ribosomal protein L20

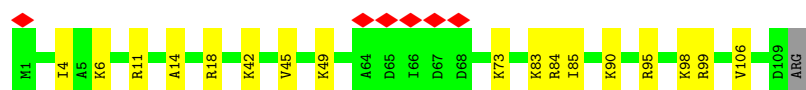
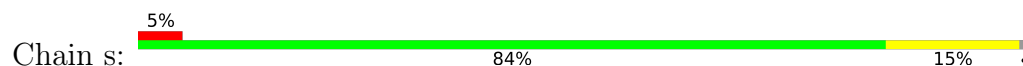
Chain q: 



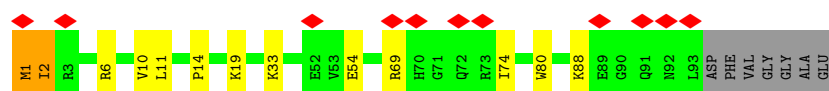
- Molecule 25: 50S ribosomal protein L21



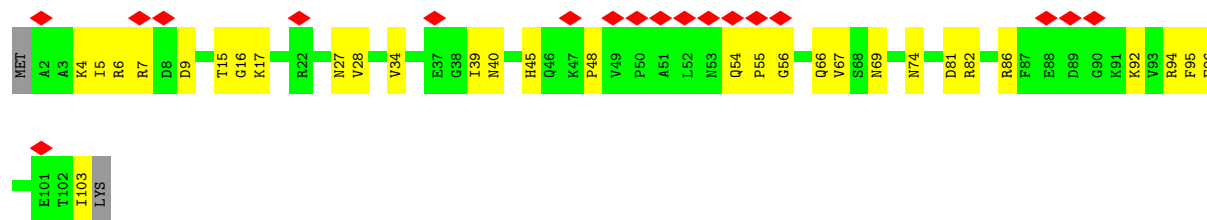
- Molecule 26: 50S ribosomal protein L22



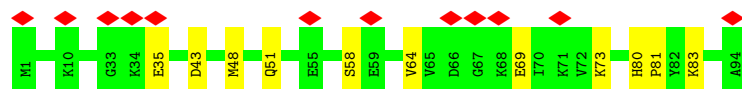
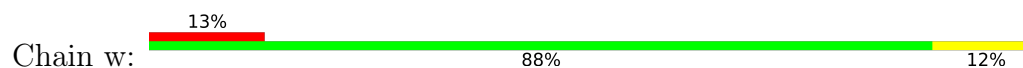
- Molecule 27: 50S ribosomal protein L23



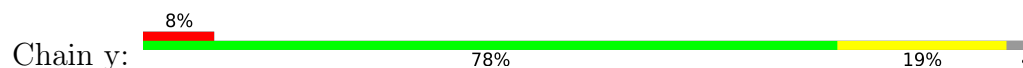
- Molecule 28: 50S ribosomal protein L24



- Molecule 29: 50S ribosomal protein L25

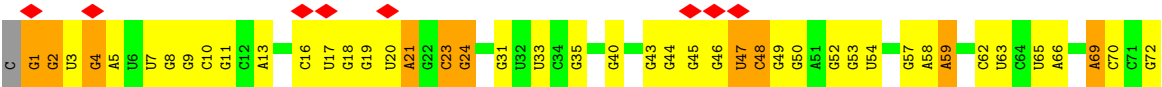


- Molecule 30: 50S ribosomal protein L27

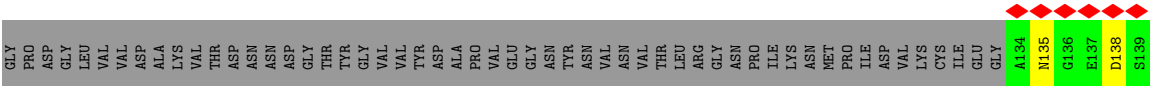
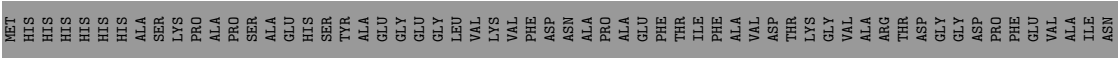


- Molecule 31: Pro-tRNA





• Molecule 32: Gelation factor



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	614463	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	14.45	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.099	Depositor
Minimum map value	-0.013	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.02965	Depositor
Map size ($\text{\AA}$)	411.648, 411.648, 411.648	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.072, 1.072, 1.072	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	0	0.39	0/635	0.52	0/848
2	1	0.31	0/496	0.46	0/660
3	2	0.35	0/443	0.40	0/593
4	3	0.46	0/440	0.72	0/588
5	4	0.47	0/416	0.65	0/554
6	6	0.38	0/380	0.48	0/498
7	7	0.46	0/513	0.57	0/676
8	8	0.39	0/302	0.48	0/397
9	a	0.38	0/2828	0.36	0/4410
10	b	0.51	0/69757	0.72	19/108827 (0.0%)
11	c	0.37	0/2121	0.48	0/2852
12	d	0.40	0/1586	0.48	0/2134
13	e	0.33	0/1571	0.43	1/2113 (0.0%)
14	f	0.40	0/1434	0.62	0/1926
15	g	0.35	0/1343	0.51	0/1816
16	h	0.28	0/290	0.62	0/392
17	j	0.42	0/1152	0.47	1/1551 (0.1%)
18	k	0.40	0/947	0.47	0/1268
19	l	0.63	0/1052	0.82	1/1401 (0.1%)
20	m	0.36	0/1093	0.50	0/1460
21	n	0.40	0/973	0.52	0/1301
22	o	0.42	0/902	0.60	0/1209
23	p	0.38	0/920	0.43	0/1231
24	q	0.41	0/960	0.47	0/1278
25	r	0.53	0/823	0.65	0/1100
26	s	0.37	0/852	0.41	0/1142
27	t	0.39	0/744	0.53	0/994
28	u	0.39	0/787	0.57	0/1051
29	w	0.33	0/766	0.43	0/1025
30	y	0.39	0/627	0.55	0/829
31	v	0.52	0/1817	0.75	1/2832 (0.0%)
32	z	0.99	0/291	1.13	1/400 (0.2%)
All	All	0.48	0/99261	0.68	24/149356 (0.0%)

There are no bond length outliers.

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	b	2864	G	C2'-C3'-O3'	8.66	126.69	113.70
10	b	390	U	C2'-C3'-O3'	8.34	122.01	109.50
10	b	1595	C	C2'-C3'-O3'	7.92	125.58	113.70
10	b	2832	U	C4'-C3'-O3'	7.74	121.01	109.40
10	b	1626	A	C2'-C3'-O3'	7.08	124.33	113.70

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	0	625	0	652	7	0
2	1	495	0	526	15	0
3	2	439	0	482	6	0
4	3	434	0	445	12	0
5	4	409	0	440	8	0
6	6	377	0	418	1	0
7	7	504	0	572	3	0
8	8	301	0	341	3	0
9	a	2529	0	1281	15	0
10	b	62281	0	31323	387	0
11	c	2082	0	2154	27	0
12	d	1565	0	1616	21	0
13	e	1552	0	1619	24	0
14	f	1410	0	1444	44	0
15	g	1323	0	1371	26	0
16	h	287	0	307	12	0
17	j	1129	0	1162	21	0
18	k	938	0	1012	25	0
19	l	1043	0	1123	10	0
20	m	1074	0	1157	9	0
21	n	960	0	1000	19	0
22	o	892	0	923	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	p	908	0	956	21	0
24	q	947	0	1019	15	0
25	r	810	0	834	5	0
26	s	845	0	909	15	0
27	t	738	0	807	9	0
28	u	779	0	831	22	0
29	w	753	0	780	7	0
30	y	619	0	642	14	0
31	v	1626	0	821	11	0
32	z	277	0	250	3	0
All	All	90951	0	59217	755	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 755 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)
10:b:892:A:C8	10:b:893:C:C6	1.96	1.54
10:b:892:A:H8	10:b:893:C:C6	1.26	1.52
10:b:892:A:C8	10:b:893:C:C5	2.13	1.34
10:b:370:G:OP2	10:b:370:G:C8	1.81	1.30
10:b:1871:A:H5''	10:b:1872:A:C2	1.74	1.22

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
2	1	59/63 (94%)	56 (95%)	3 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	2	55/59 (93%)	53 (96%)	2 (4%)	0	100	100
4	3	53/57 (93%)	49 (92%)	4 (8%)	0	100	100
5	4	48/55 (87%)	45 (94%)	3 (6%)	0	100	100
6	6	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
7	7	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
8	8	36/50 (72%)	35 (97%)	1 (3%)	0	100	100
11	c	269/273 (98%)	258 (96%)	11 (4%)	0	100	100
12	d	207/209 (99%)	197 (95%)	10 (5%)	0	100	100
13	e	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
14	f	175/179 (98%)	164 (94%)	10 (6%)	1 (1%)	21	23
15	g	174/177 (98%)	159 (91%)	15 (9%)	0	100	100
16	h	37/149 (25%)	32 (86%)	5 (14%)	0	100	100
17	j	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
18	k	120/123 (98%)	116 (97%)	4 (3%)	0	100	100
19	l	141/144 (98%)	132 (94%)	9 (6%)	0	100	100
20	m	134/136 (98%)	133 (99%)	1 (1%)	0	100	100
21	n	118/127 (93%)	111 (94%)	7 (6%)	0	100	100
22	o	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
23	p	111/115 (96%)	110 (99%)	1 (1%)	0	100	100
24	q	115/118 (98%)	115 (100%)	0	0	100	100
25	r	100/103 (97%)	93 (93%)	5 (5%)	2 (2%)	6	4
26	s	107/110 (97%)	100 (94%)	7 (6%)	0	100	100
27	t	91/100 (91%)	87 (96%)	4 (4%)	0	100	100
28	u	100/104 (96%)	83 (83%)	17 (17%)	0	100	100
29	w	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
30	y	80/85 (94%)	76 (95%)	3 (4%)	1 (1%)	9	8
32	z	31/148 (21%)	23 (74%)	6 (19%)	2 (6%)	1	0
All	All	3087/3427 (90%)	2937 (95%)	144 (5%)	6 (0%)	44	51

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
25	r	52	PRO

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Mol	Chain	Res	Type
32	z	148	VAL
25	r	51	VAL
30	y	44	LYS
14	f	71	ARG

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	
1	0	67/68 (98%)	67 (100%)	0	100	100
2	1	54/55 (98%)	54 (100%)	0	100	100
3	2	47/49 (96%)	47 (100%)	0	100	100
4	3	46/48 (96%)	44 (96%)	2 (4%)	26	35
5	4	45/49 (92%)	44 (98%)	1 (2%)	45	61
6	6	38/38 (100%)	38 (100%)	0	100	100
7	7	51/52 (98%)	51 (100%)	0	100	100
8	8	34/44 (77%)	34 (100%)	0	100	100
11	c	216/218 (99%)	216 (100%)	0	100	100
12	d	164/164 (100%)	164 (100%)	0	100	100
13	e	165/165 (100%)	165 (100%)	0	100	100
14	f	148/150 (99%)	144 (97%)	4 (3%)	39	53
15	g	137/138 (99%)	136 (99%)	1 (1%)	76	87
16	h	30/114 (26%)	30 (100%)	0	100	100
17	j	116/116 (100%)	116 (100%)	0	100	100
18	k	103/104 (99%)	103 (100%)	0	100	100
19	l	102/103 (99%)	94 (92%)	8 (8%)	11	13
20	m	109/109 (100%)	109 (100%)	0	100	100
21	n	100/103 (97%)	100 (100%)	0	100	100
22	o	86/87 (99%)	82 (95%)	4 (5%)	23	31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	p	98/100 (98%)	98 (100%)	0	100	100
24	q	89/90 (99%)	89 (100%)	0	100	100
25	r	84/84 (100%)	79 (94%)	5 (6%)	17	21
26	s	92/93 (99%)	92 (100%)	0	100	100
27	t	80/84 (95%)	78 (98%)	2 (2%)	42	56
28	u	83/85 (98%)	82 (99%)	1 (1%)	63	78
29	w	78/78 (100%)	78 (100%)	0	100	100
30	y	61/63 (97%)	61 (100%)	0	100	100
32	z	29/121 (24%)	14 (48%)	15 (52%)	0	0
All	All	2552/2772 (92%)	2509 (98%)	43 (2%)	52	69

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	z	135	ASN
32	z	149	GLU
32	z	138	ASP
32	z	145	THR
32	z	152	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 44 such sidechains are listed below:

Mol	Chain	Res	Type
22	o	98	GLN
24	q	81	ASN
22	o	116	GLN
23	p	66	ASN
26	s	7	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	b	2900/2904 (99%)	1200 (41%)	0
31	v	75/77 (97%)	41 (54%)	0
9	a	117/120 (97%)	21 (17%)	0
All	All	3092/3101 (99%)	1262 (40%)	0

5 of 1262 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	a	25	U
9	a	26	C
9	a	30	C
9	a	32	U
9	a	35	C

There are no RNA pucker outliers to report.

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

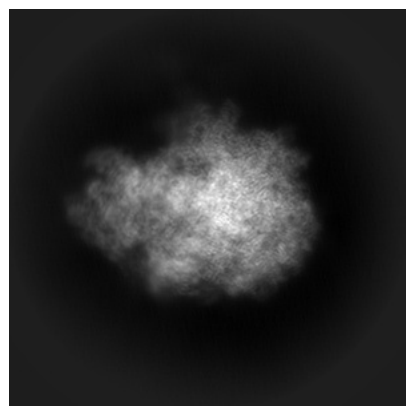
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14850. These allow visual inspection of the internal detail of the map and identification of artifacts.

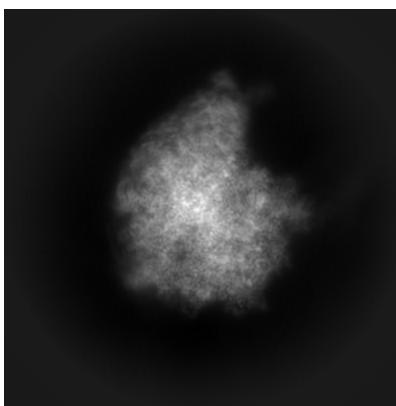
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

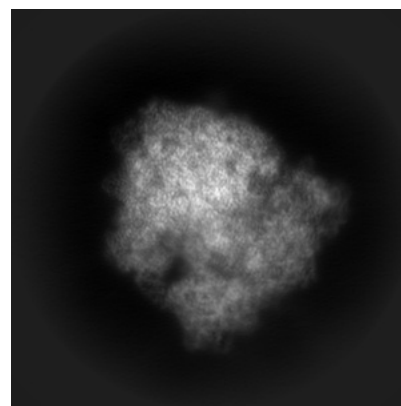
6.1.1 Primary map



X

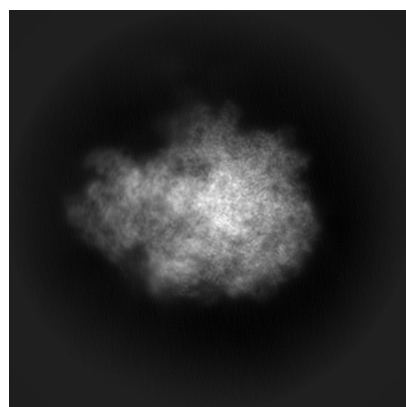


Y

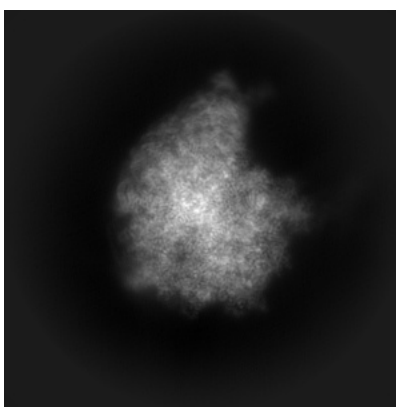


Z

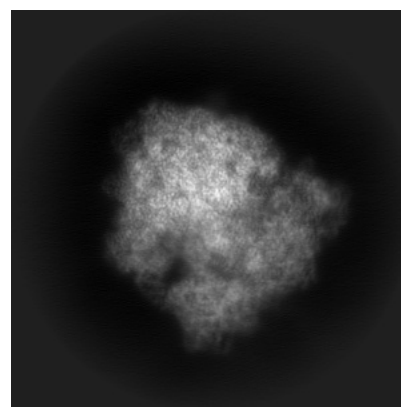
6.1.2 Raw map



X



Y

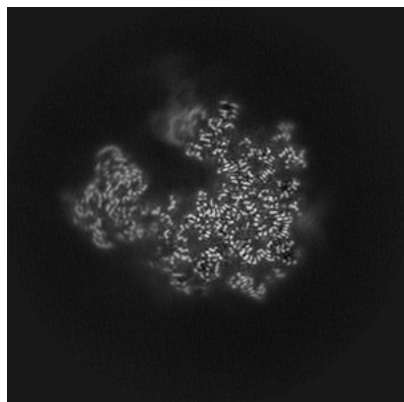


Z

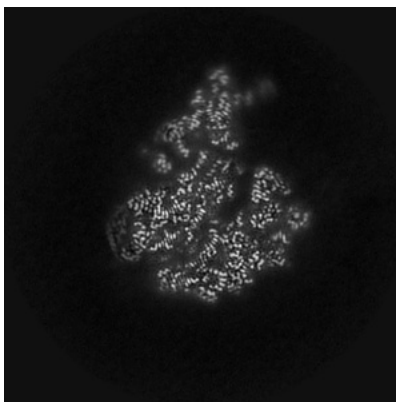
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

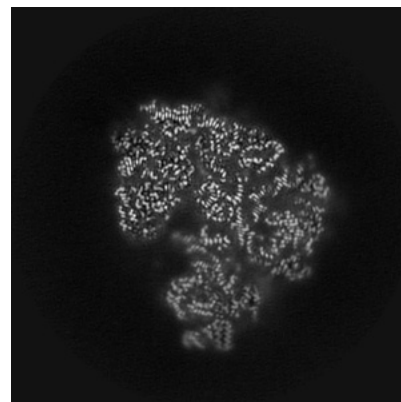
6.2.1 Primary map



X Index: 192

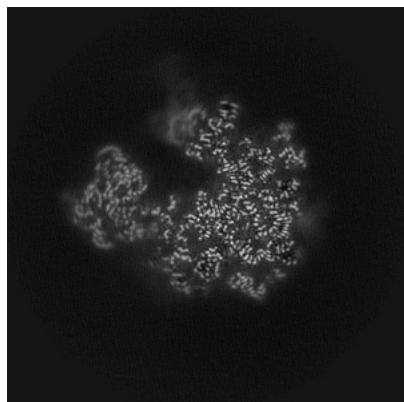


Y Index: 192

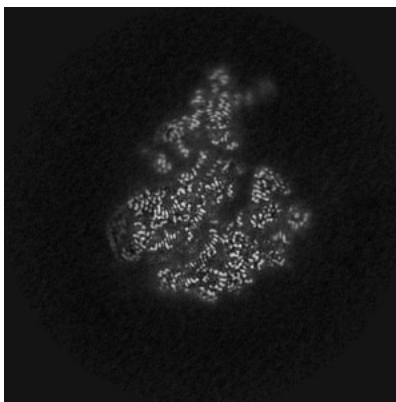


Z Index: 192

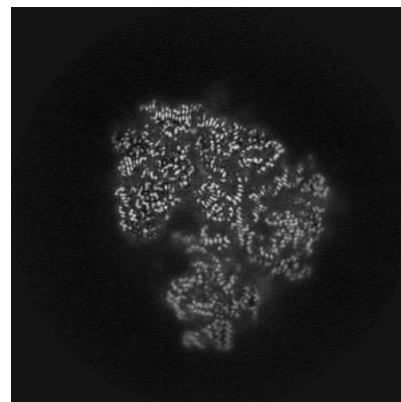
6.2.2 Raw map



X Index: 192



Y Index: 192

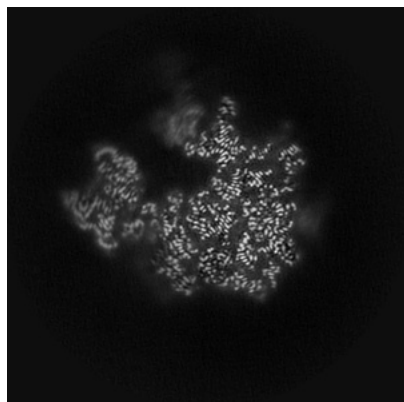


Z Index: 192

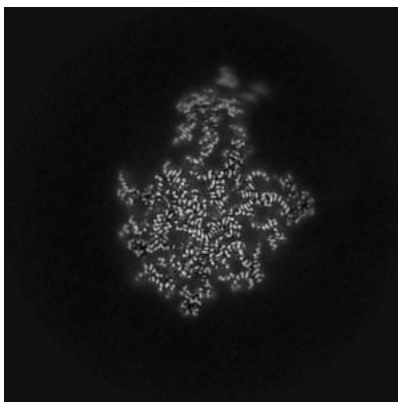
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

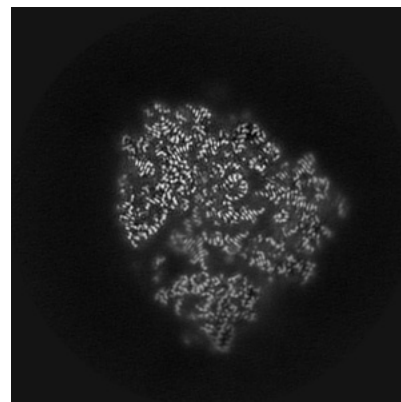
6.3.1 Primary map



X Index: 197

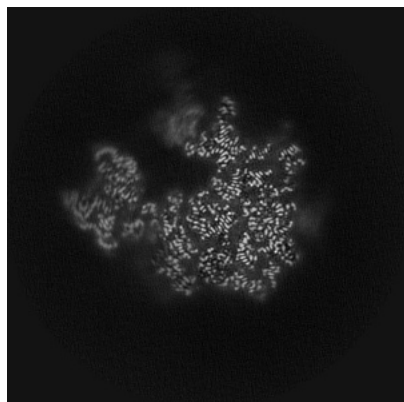


Y Index: 211

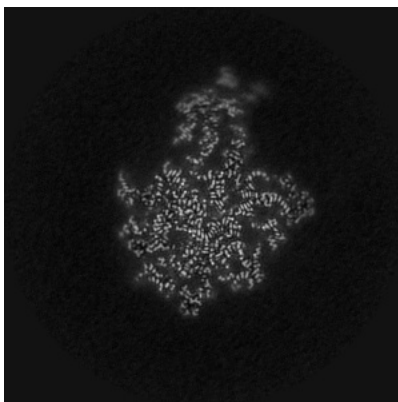


Z Index: 198

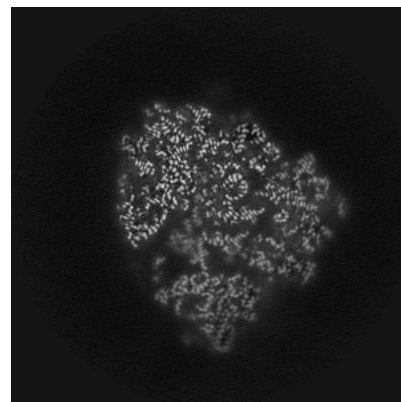
6.3.2 Raw map



X Index: 197



Y Index: 211

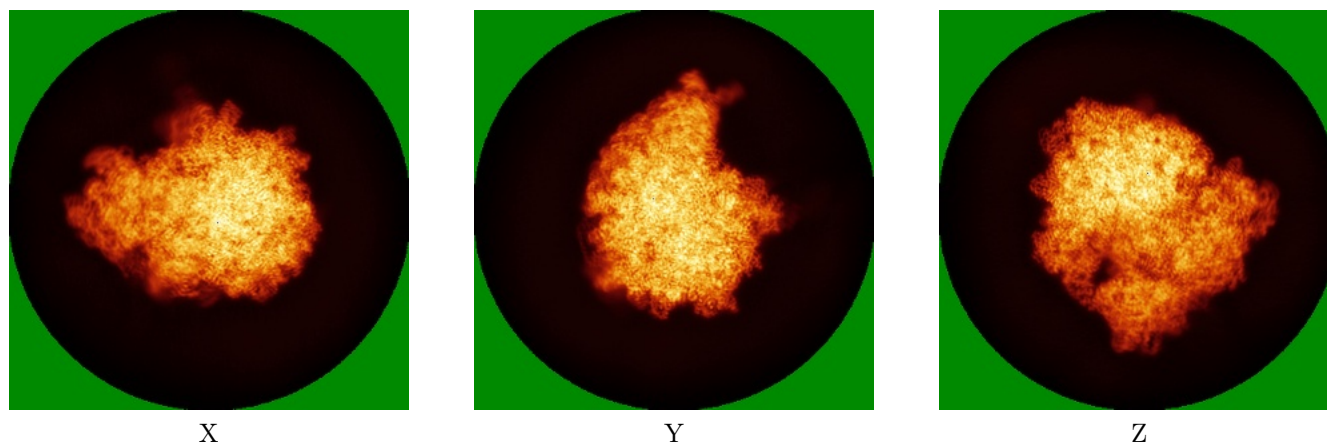


Z Index: 198

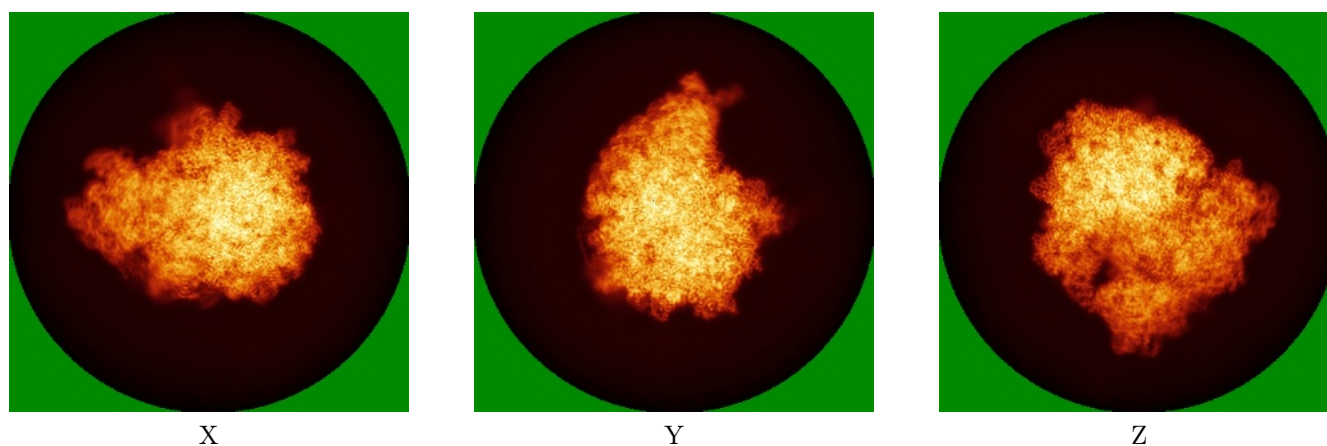
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

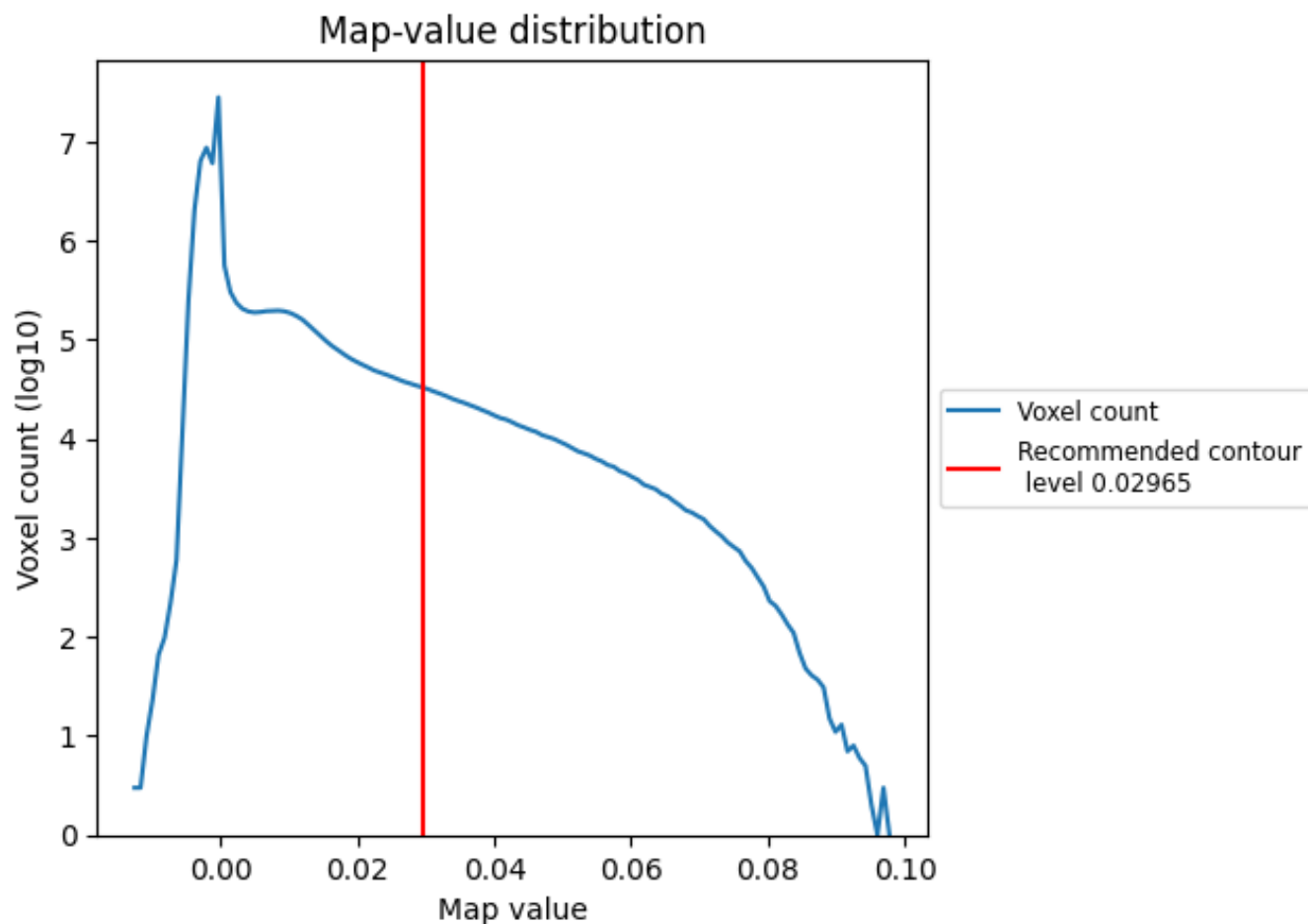
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

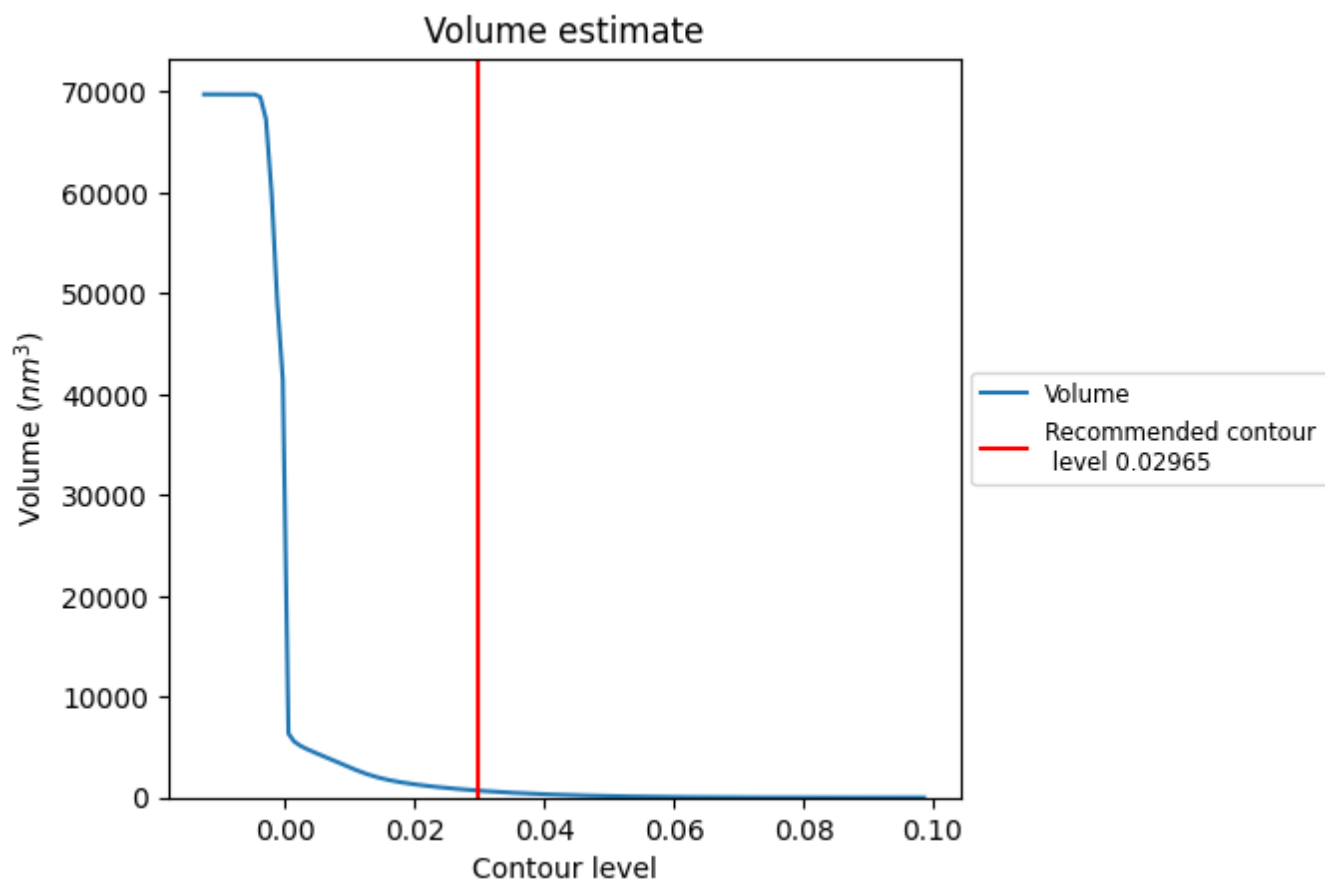
This section contains the results of statistical analysis of the map.

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.

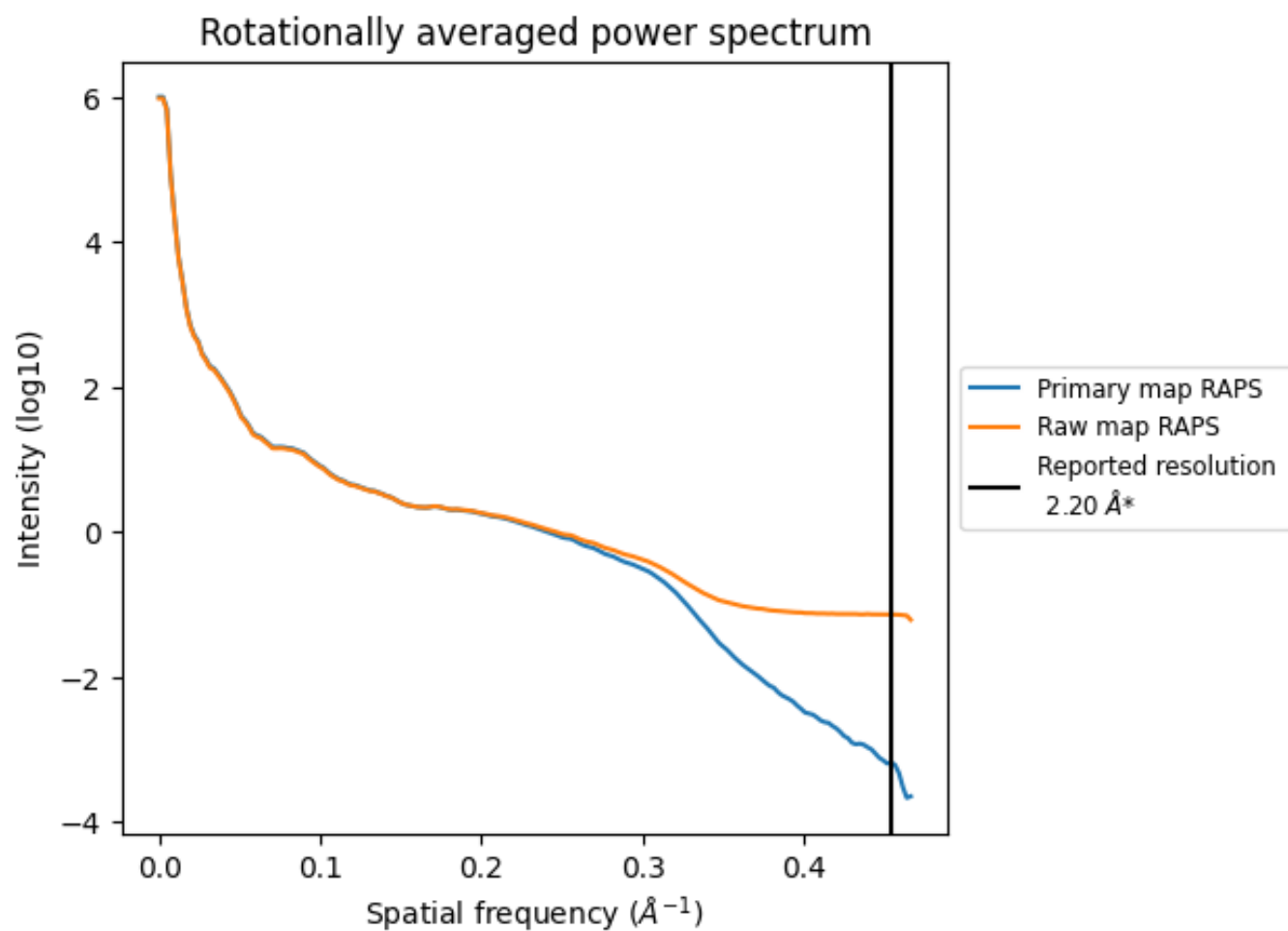
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 698 nm^3 ; this corresponds to an approximate mass of 631 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 ⓘ

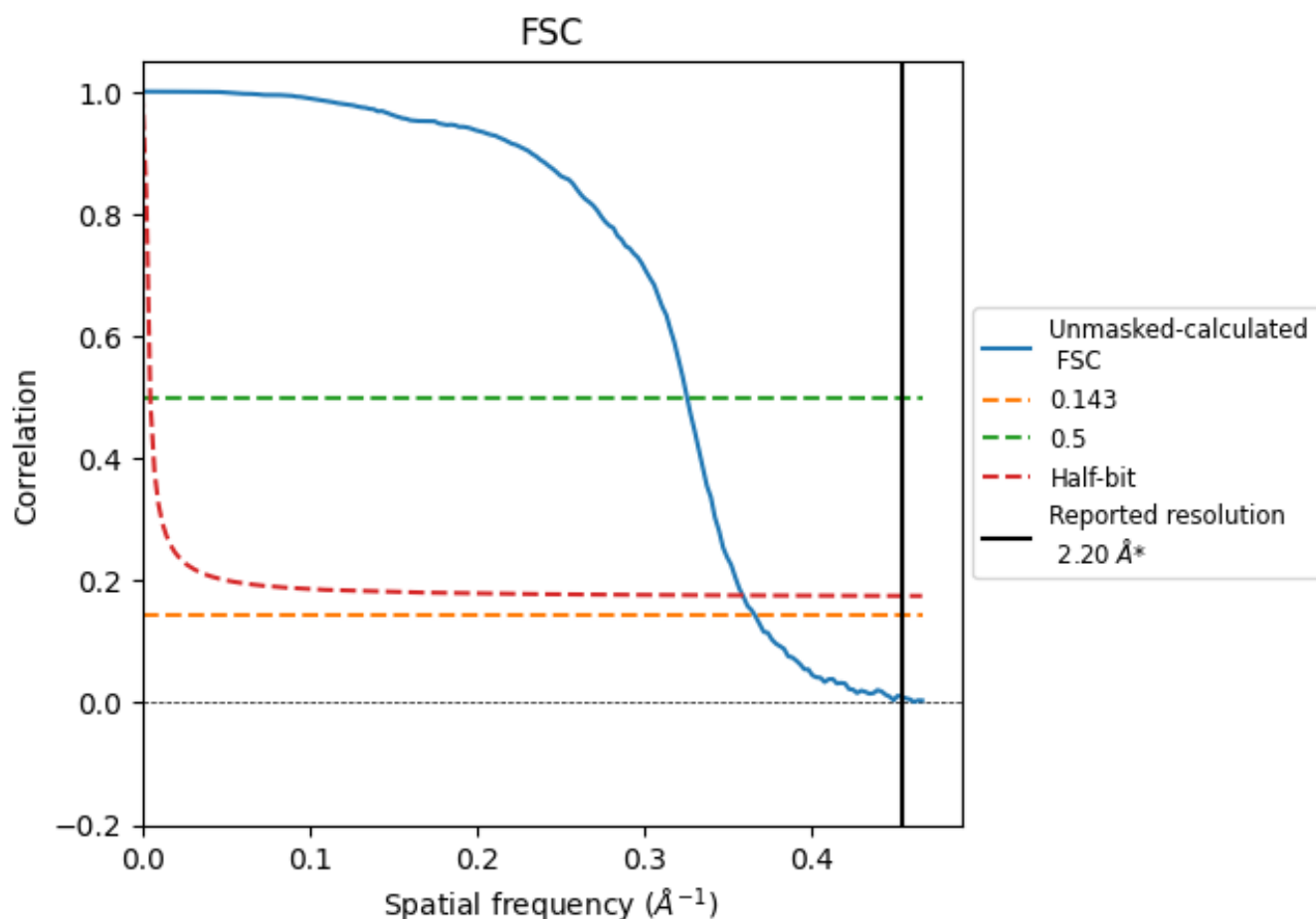


*Reported resolution corresponds to spatial frequency of 0.455 $\text{\AA}^{-1}$

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 0.455 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.73	3.07	2.78

*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 2.73 differs from the reported value 2.2 by more than 10 %

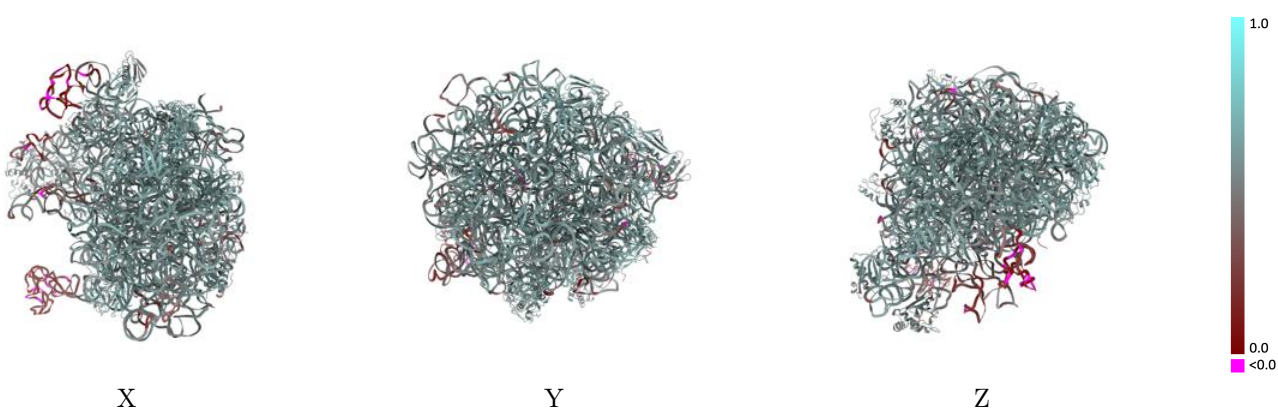
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14850 and PDB model 7ZP8. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)

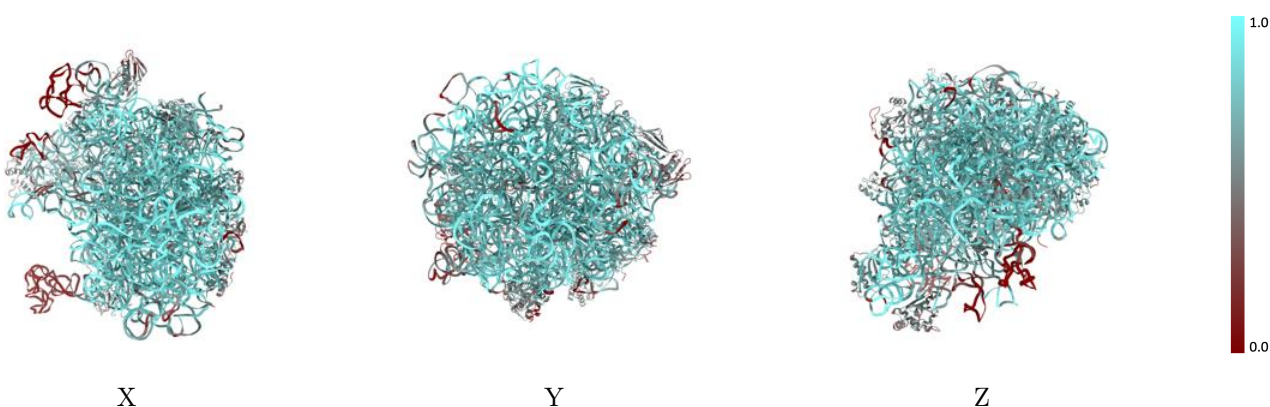
This section was not generated.

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



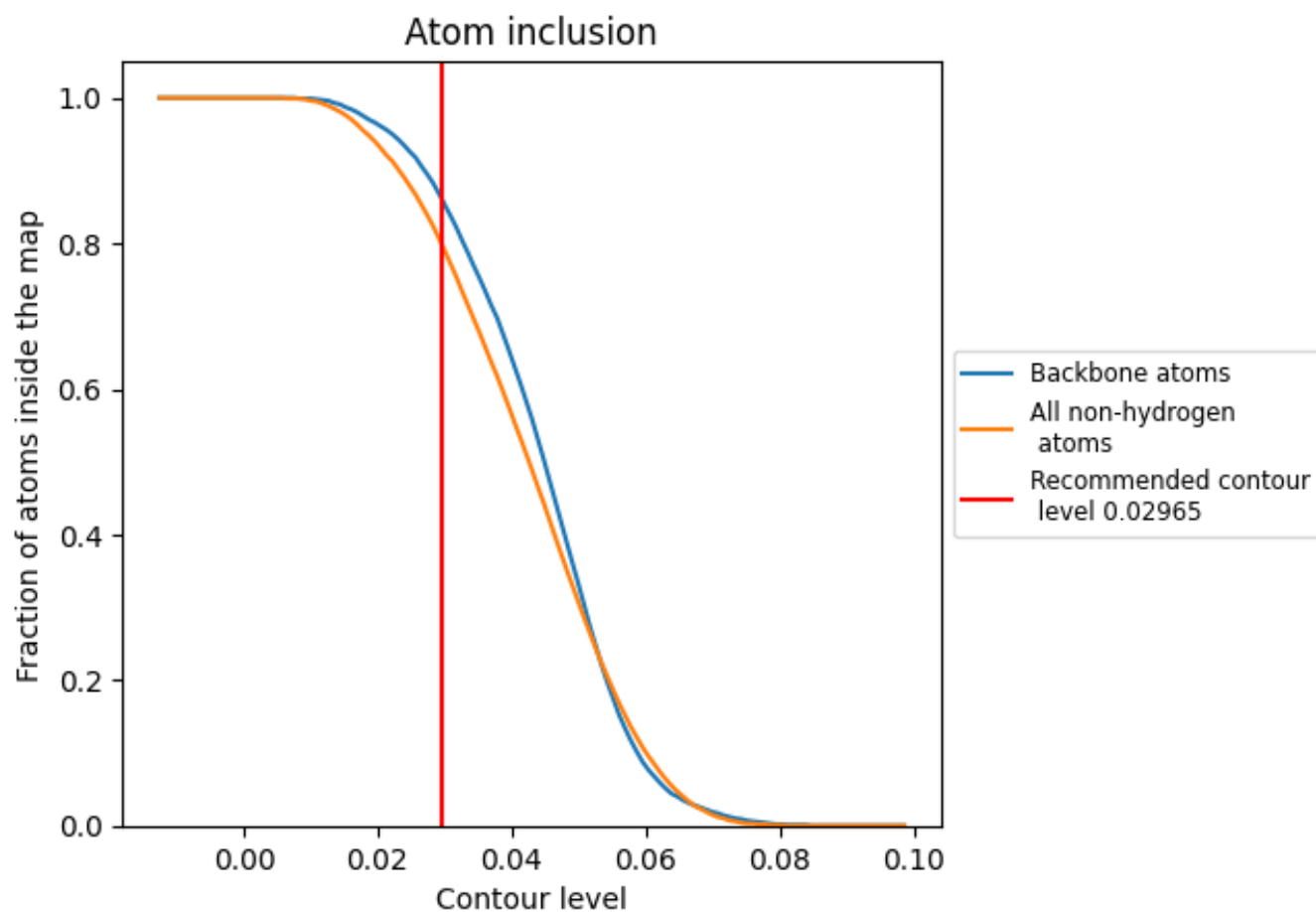
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02965).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 80% 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 (0.02965) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7970	 0.5450
0	 0.8050	 0.6060
1	 0.5900	 0.5440
2	 0.7490	 0.5970
3	 0.7490	 0.5780
4	 0.6230	 0.5630
6	 0.9150	 0.6310
7	 0.8660	 0.6240
8	 0.7770	 0.6060
a	 0.8650	 0.5650
b	 0.8380	 0.5330
c	 0.8400	 0.6180
d	 0.7650	 0.6110
e	 0.6060	 0.5800
f	 0.4740	 0.5080
g	 0.4990	 0.5400
h	 0.1970	 0.4970
j	 0.7710	 0.5980
k	 0.7360	 0.6060
l	 0.7310	 0.5870
m	 0.7730	 0.6040
n	 0.8080	 0.6130
o	 0.6360	 0.5540
p	 0.7530	 0.6060
q	 0.8090	 0.6100
r	 0.6570	 0.5740
s	 0.7590	 0.6060
t	 0.6510	 0.5780
u	 0.5500	 0.5500
v	 0.6440	 0.4040
w	 0.6580	 0.5880
y	 0.7550	 0.5950
z	 0.1780	 0.3270

