



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 08:59 PM UTC

PDB ID : 5MMI / pdb_00005mmi
EMDB ID : EMD-3531
Title : Structure of the large subunit of the chloroplast ribosome
Authors : Bieri, P.; Leibundgut, M.; Saurer, M.; Boehringer, D.; Ban, N.
Deposited on : 2016-12-10
Resolution : 3.20 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:

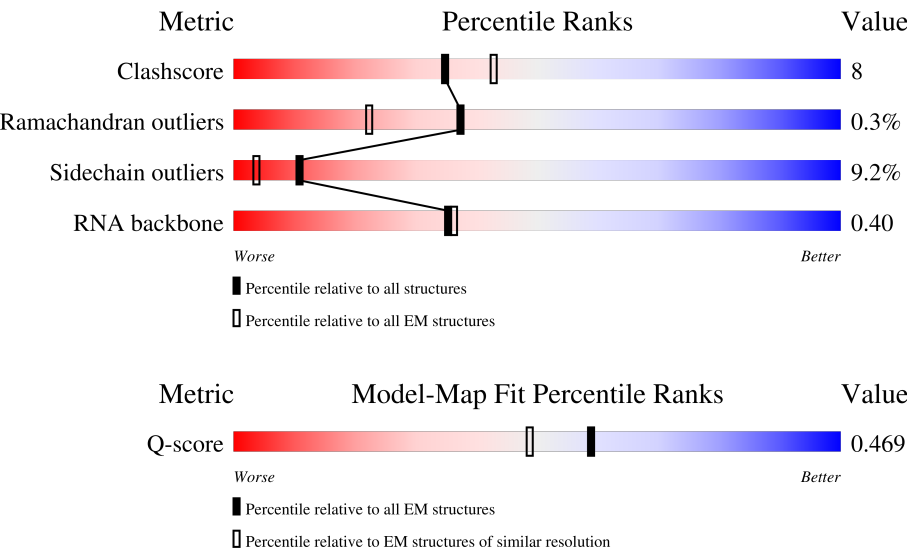
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.20 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.



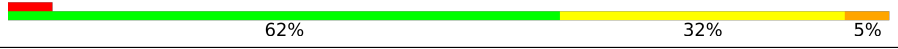
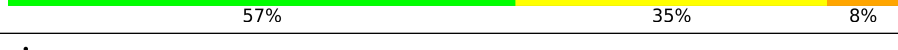
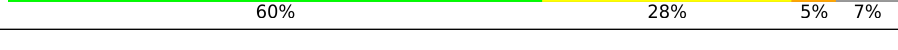
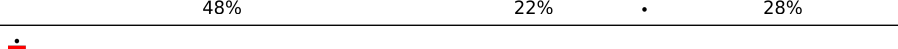
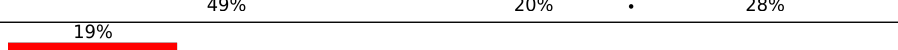
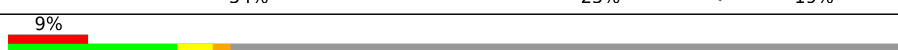
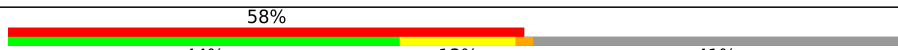
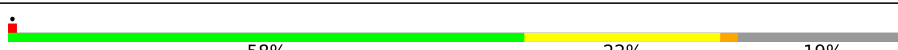
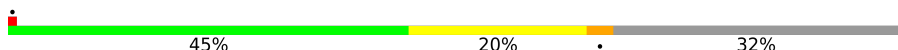
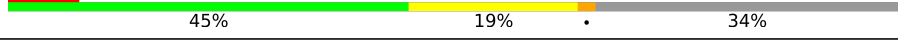
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	130	
2	1	57	
3	2	66	

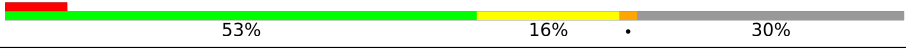
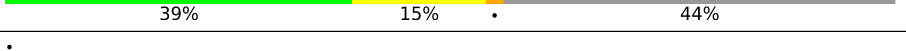
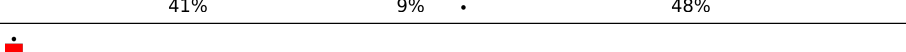
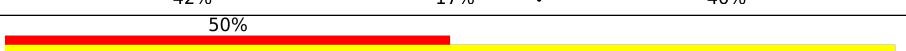
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Mol	Chain	Length	Quality of chain
4	3	152	
5	4	159	
6	5	37	
7	6	142	
8	7	116	
9	A	2810	
10	B	121	
11	C	272	
12	D	305	
13	E	293	
14	F	258	
15	G	220	
16	H	196	
17	I	232	
18	J	224	
19	K	250	
20	L	121	
21	M	271	
22	N	135	
23	O	126	
24	P	166	
25	Q	233	
26	R	128	
27	S	256	
28	T	199	

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Mol	Chain	Length	Quality of chain
29	U	198	
30	V	192	
31	W	106	
32	X	194	
33	Y	148	
34	Z	168	
35	z	2	

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 95397 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 L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	44	Total	C	N	O	S	0	0
			359	226	61	70	2		

- Molecule 2 is a protein called 50S ribosomal protein L32, chloroplastic.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	48	Total	C	N	O	0	0
			396	261	75	60		

- Molecule 3 is a protein called 50S ribosomal protein L33, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	60	Total	C	N	O	S	0	0
			489	304	98	83	4		

- Molecule 4 is a protein called 50S ribosomal protein L34, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	60	Total	C	N	O	S	0	0
			467	282	107	75	3		

- Molecule 5 is a protein called 50S ribosomal protein L35, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	72	Total	C	N	O	S	0	0
			588	370	124	93	1		

- Molecule 6 is a protein called 50S ribosomal protein L36, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	37	Total	C	N	O	S	0	0
			305	186	70	45	4		

- Molecule 7 is a protein called plastid ribosomal protein cL37, PSRP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	49	Total	C	N	O	S	0	0
			422	268	92	57	5		

- Molecule 8 is a protein called 50S ribosomal protein 6, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	46	Total	C	N	O	S	0	0
			368	237	71	59	1		

- Molecule 9 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	2798	Total	C	N	O	P	0	0
			60083	26804	11116	19365	2798		

- Molecule 10 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	121	Total	C	N	O	P	0	0
			2584	1154	466	843	121		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	253	Total	C	N	O	S	0	0
			1952	1209	401	336	6		

- Molecule 12 is a protein called plastid ribosomal protein uL3c.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D	221	Total	C	N	O	S	0	0
			1686	1066	308	301	11		

- Molecule 13 is a protein called plastid ribosomal protein uL4c.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E	212	Total	C	N	O	S	0	0
			1676	1061	312	300	3		

- Molecule 14 is a protein called plastid ribosomal protein uL5c.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	193	Total	C	N	O	S	0	0
			1454	923	255	268	8		

- Molecule 15 is a protein called plastid ribosomal protein uL6c.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	G	178	Total	C	N	O	S	0	0
			1391	878	256	253	4		

- Molecule 16 is a protein called plastid ribosomal protein bL9c.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	H	48	Total	C	N	O	0	0
			382	251	69	62		

- Molecule 17 is a protein called plastid ribosomal protein uL10c.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	137	Total	C	N	O	S	0	0
			1106	711	186	203	6		

- Molecule 18 is a protein called 50S ribosomal protein L11, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	133	Total	C	N	O	S	0	0
			977	624	161	186	6		

- Molecule 19 is a protein called 50S ribosomal protein L13, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	203	Total	C	N	O	S	0	0
			1648	1047	307	289	5		

- Molecule 20 is a protein called 50S ribosomal protein L14, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	121	Total	C	N	O	S	0	0
			942	588	179	170	5		

- Molecule 21 is a protein called plastid ribosomal protein uL15c.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	M	185	Total	C	N	O	S	0	0
			1410	879	280	245	6		

- Molecule 22 is a protein called 50S ribosomal protein L16, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	N	135	Total	C	N	O	S	0	0
			1075	677	218	174	6		

- Molecule 23 is a protein called plastid ribosomal protein bL17c.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	O	116	Total	C	N	O	S	0	0
			944	592	193	155	4		

- Molecule 24 is a protein called plastid ribosomal protein uL18c.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	P	122	Total	C	N	O	S	0	0
			962	598	186	173	5		

- Molecule 25 is a protein called 50S ribosomal protein L19, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Q	118	Total	C	N	O	S	0	0
			953	611	186	155	1		

- Molecule 26 is a protein called 50S ribosomal protein L20, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	R	119	Total	C	N	O	S	0	0
			1029	652	213	162	2		

- Molecule 27 is a protein called 50S ribosomal protein L21, chloroplastic.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	S	170	Total	C	N	O	0	0
			1310	844	227	239		

- Molecule 28 is a protein called 50S ribosomal protein L22, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	T	172	Total	C	N	O	S	0	0
			1395	892	257	237	9		

- Molecule 29 is a protein called 50S ribosomal protein L23, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	U	96	Total	C	N	O	S	0	0
			776	503	135	136	2		

- Molecule 30 is a protein called plastid ribosomal protein uL24c.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	V	134	Total	C	N	O	S	0	0
			1078	677	203	195	3		

- Molecule 31 is a RNA chain called 4.5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	W	106	Total	C	N	O	P	0	0
			2277	1017	423	731	106		

- Molecule 32 is a protein called plastid ribosomal protein bL27c.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	X	109	Total	C	N	O	0	0
			888	560	175	153		

- Molecule 33 is a protein called plastid ribosomal protein bL28c.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Y	77	Total	C	N	O	S	0	0
			634	402	128	103	1		

- Molecule 34 is a protein called plastid ribosomal protein uL29c.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Z	101	Total	C	N	O	S	0	0
			846	529	167	147	3		

- Molecule 35 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	z	2	Total	C	N	O	P	0	0
			42	19	8	13	2		

- Molecule 36 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
36	2	1	Total	Zn	0
			1	1	
36	5	1	Total	Zn	0
			1	1	

- Molecule 37 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
37	4	1	Total	Mg	0
			1	1	
37	6	1	Total	Mg	0
			1	1	
37	7	1	Total	Mg	0
			1	1	
37	A	453	Total	Mg	0
			453	453	
37	B	15	Total	Mg	0
			15	15	
37	C	1	Total	Mg	0
			1	1	
37	D	2	Total	Mg	0
			2	2	
37	E	1	Total	Mg	0
			1	1	
37	H	1	Total	Mg	0
			1	1	
37	M	2	Total	Mg	0
			2	2	
37	N	1	Total	Mg	0
			1	1	
37	P	1	Total	Mg	0
			1	1	
37	R	1	Total	Mg	0
			1	1	
37	T	1	Total	Mg	0
			1	1	
37	U	1	Total	Mg	0
			1	1	

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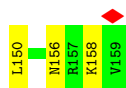
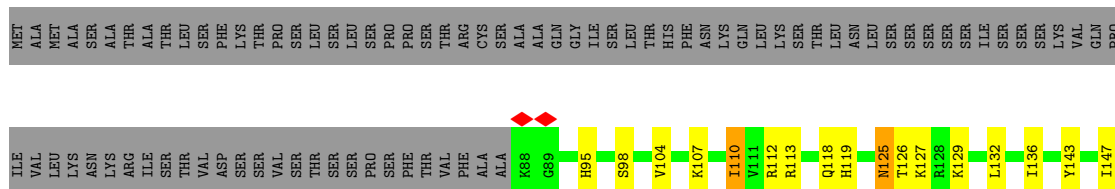
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Mol	Chain	Residues	Atoms		AltConf
37	V	2	Total 2	Mg 2	0
37	W	14	Total 14	Mg 14	0
37	X	1	Total 1	Mg 1	0
37	Y	1	Total 1	Mg 1	0



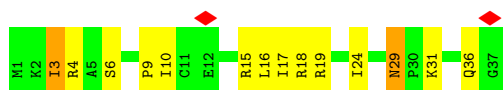
- Molecule 5: 50S ribosomal protein L35, chloroplastic

Chain 4: 33% 11% 55%



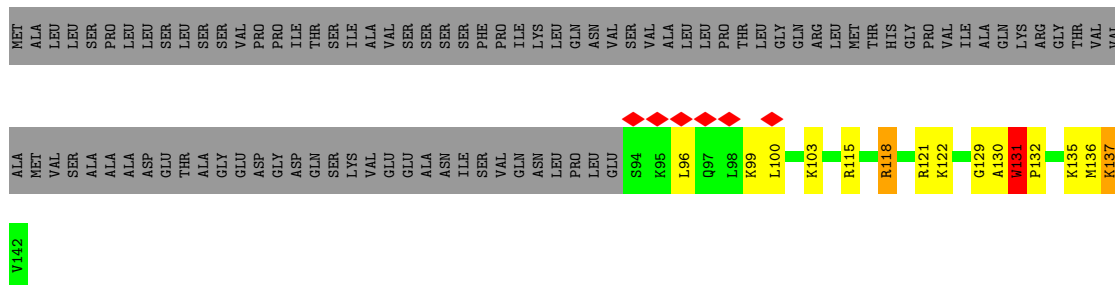
- Molecule 6: 50S ribosomal protein L36, chloroplastic

Chain 5: 5% 62% 32% 5%



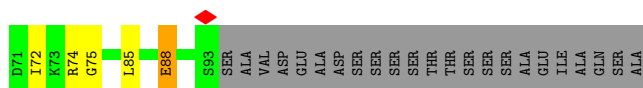
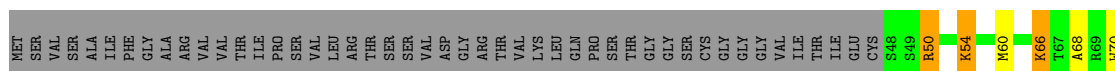
- Molecule 7: plastid ribosomal protein cL37, PSRP5

Chain 6: 23% 8% 65%



- Molecule 8: 50S ribosomal protein 6, chloroplastic

Chain 7: 30% 6% 60%



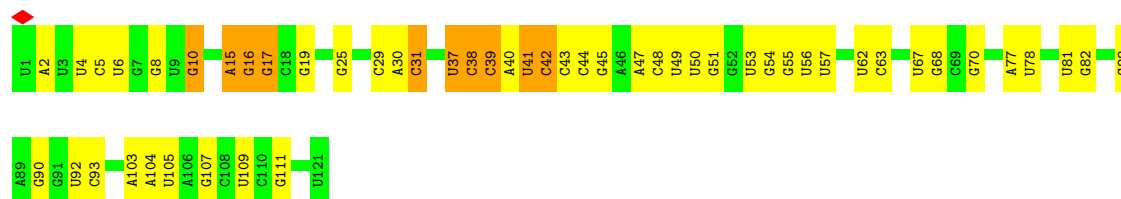
- Molecule 9: 23S ribosomal RNA



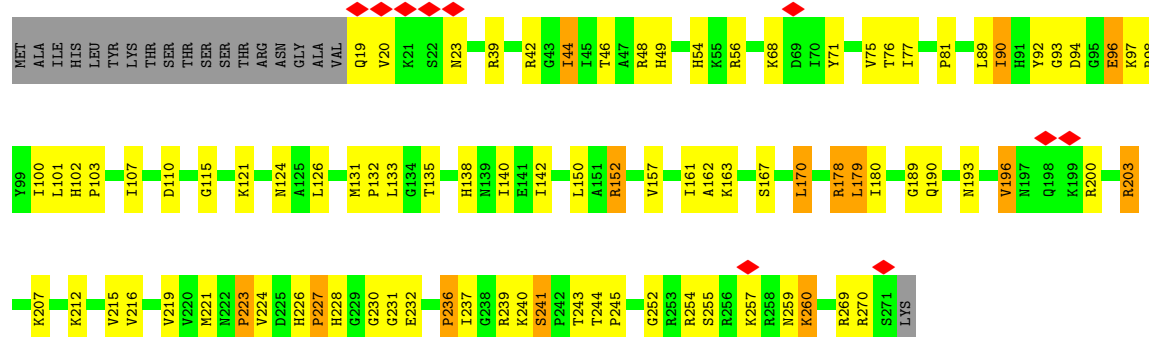
U2602	C2483	G2400	U2309	G2218	C2156	C2087	A1984	A1864	C1762	G1631	G1530	G1450
C2603	A2486	C2401	U2310	U2219	U2157	U2088	A1985	G1865	U1766	U1632	A1531	G1454
A2619	G2487	C2402	G2315	G2220	U2158	U2089	G1986	G1866	G1766	A1633	G1532	A1455
G2690	U2403	A2223	G2316	A2223	C2159	G2094	A1992	G1869	A1769	C1635	A1534	A1456
U2621	G2406	C2227	G2320	C2227	C2160	U2093	U2005	U1870	A1772	U1638	A1536	G1458
G2625	U2407	C2226	G2321	C2226	G2161	G2101	G2006	C1877	G1774	C1642	G1543	A1465
U2626	G2408	U2229	A2322	U2229	G2162	G2102	U2007	G1880	G1778	G1643	A1544	A1472
C2627	A2409	A2230	C2323	A2230	G2163	A2104	G2011	G1882	G1783	A1644	G1545	A1473
C2628	U2410	G2231	G2324	G2231	G2164	U2105	A2015	G1883	A1784	A1645	C1547	A1474
C2629	C2411	G2232	G2325	G2232	G2165	U2106	G2016	C1884	U1785	U1672	A1548	U1475
U2630	A2414	A2237	U2329	A2237	G2166	G2107	A2017	G1885	C1791	A1673	A1549	G1477
U2646	C2415	A2238	U2330	A2238	G2167	G2108	G2018	C1886	G1800	G1678	U1550	G1477
U2649	G2416	A2242	G2331	A2242	C2168	U2112	A2027	G1887	C1807	G1679	C1554	A1480
U2653	U2417	U2245	G2332	U2245	C2169	G2113	A2028	G1888	C1808	C1682	G1557	G1483
U2658	U2418	U2246	C2333	U2246	G2170	G2114	A2029	G1889	C1809	G1683	U1558	G1484
U2659	G2419	C2249	G2334	C2249	G2171	C2115	U2030	G1890	A1801	C1684	A1559	U1486
C2518	A2423	G2252	U2341	G2252	G2172	U2116	C2034	G1913	C1810	C1689	C1560	C1487
G2519	G2427	U2253	G2342	U2253	G2173	U2117	G2037	A1914	A1811	A1690	G1563	A1488
G2520	A2428	G2254	G2343	G2254	G2174	U2118	U2038	G1917	A1812	U1693	G1566	G1491
U2521	A2429	A2255	A2344	A2255	C2175	U2119	C2039	G1920	A1813	C1694	C1567	A1492
G2522	G2430	G2256	A2345	G2256	A2176	U2120	U2040	G1921	U1817	U1702	U1568	C1493
A2661	U2523	A2257	A2346	A2257	U2177	C2121	G2041	A1913	C1807	G1703	C1572	G1494
C2524	G2431	C2258	A2347	C2258	C2178	U2122	G2042	U1929	C1817	A1704	C1573	C1501
G2525	G2432	A2259	C2349	A2259	A2179	U2123	A2045	A1930	U1818	G1710	C1574	G1501
G2526	U2436	G2260	C2350	G2260	G2180	G2124	C2046	U1931	U1826	C1711	A1582	A1502
C2535	A2442	U2261	A2352	U2261	U2181	C2125	G2047	U1932	G1827	G1715	A1583	C1503
G2546	A2443	G2262	G2353	G2262	G2182	U2126	U2048	A1933	U1828	A1716	U1588	C1504
U2547	G2444	U2266	G2354	U2266	G2183	C2127	G2049	A1934	G1832	U1715	U1589	C1505
A2548	G2445	G2267	U2360	G2267	G2184	U2128	A2053	C1934	U1833	A1717	A1594	U1506
G2549	U2446	G2268	U2361	G2268	A2185	C2129	C2054	U1935	G1834	G1733	A1600	U1507
U2701	U2448	G2269	G2362	G2269	U2186	C2130	U2055	U1940	G1835	A1734	A1603	U1508
G2553	A2449	G2270	A2363	G2270	U2187	U2131	A2056	G1943	U1836	G1739	A1604	U1509
C2556	U2452	C2271	G2364	C2271	C2188	U2132	C2057	G1944	C1840	C1746	A1605	U1511
U2569	U2458	A2284	C2367	A2284	C2189	G2133	U2065	A1951	U1844	C1750	A1612	C1513
G2570	C2459	A2285	A2368	A2285	A2190	U2134	G2066	A1952	G1845	A	G1615	U1518
U2571	U2460	A2290	G2370	A2290	C2191	G2135	C2069	U1953	A1849	C	A1616	A1519
U2572	A2461	A2291	C2374	A2291	U2192	U2136	A2070	U1969	G1850	A	U1620	A1520
G2583	G2462	G2296	A2375	G2296	G2195	C2137	A2073	C1975	A	G1756	C1621	G1522
G2584	G2464	C2297	C2376	C2297	A2196	A2140	G2074	C1976	A	G1760	G1629	G1523
A2589	A2465	C2298	G2377	C2298	A2197	G2142	G2075	C1977	A	G1761	G1630	G1525
C2590	A2467	U2300	C2378	U2300	A2198	G2143	C2077	C1978	A			G1527
G2591	G2468	G2301	G2381	G2301	G2199	U2144	A2081					
C2720	C2469	C2302	G2382	C2302	A2200	G2145	U2082					
C2721	A2470	A2303	G2383	A2303	G2201	A2146	G2083					
C2722	G2473	A2304	A2396	A2304	C2202	A2145	G2086					
A2594	C2473	A2305	G2396	A2305	U2203	A2146						
G2595	C2481	G2307	U2397	G2307	U2204	A2148						
C2723	C2482	U2308		U2308	G2205	A2149						
G2725					A2206	G2150						
G2726					A2207	G2151						
					U2208	C2152						
					U2209	C2153						
					C2210	C2154						
					U2211	C2155						
					A2212							
					A2213							
					U2217							



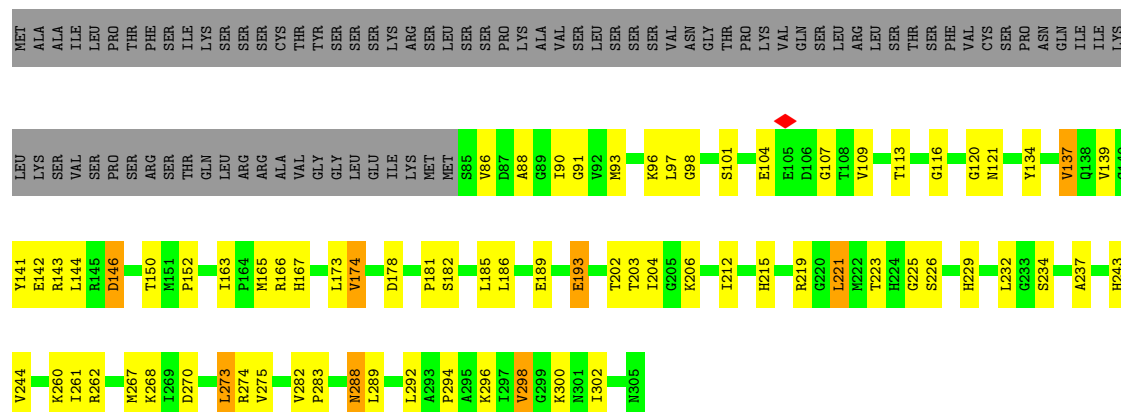
• Molecule 10: 5S ribosomal RNA



• Molecule 11: 50S ribosomal protein L2, chloroplastic



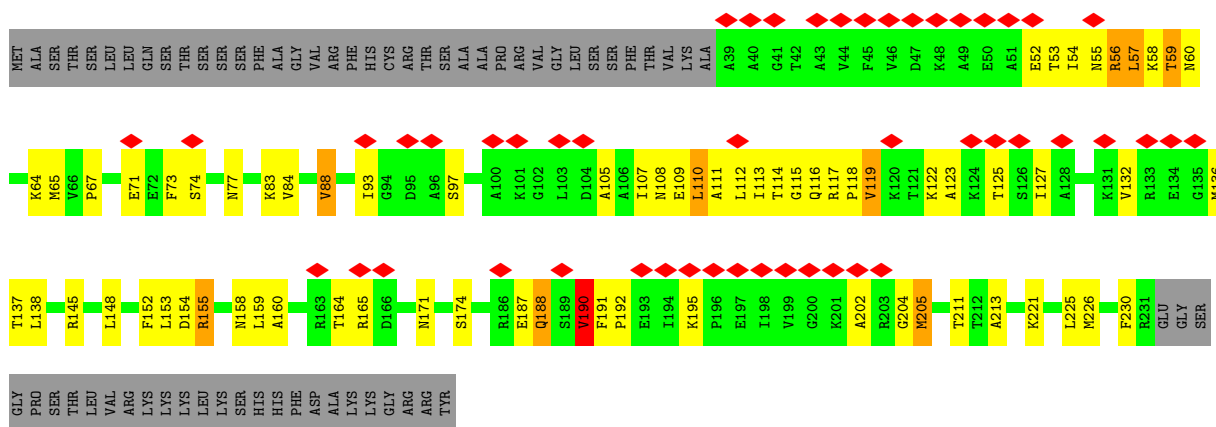
• Molecule 12: plastid ribosomal protein uL3c



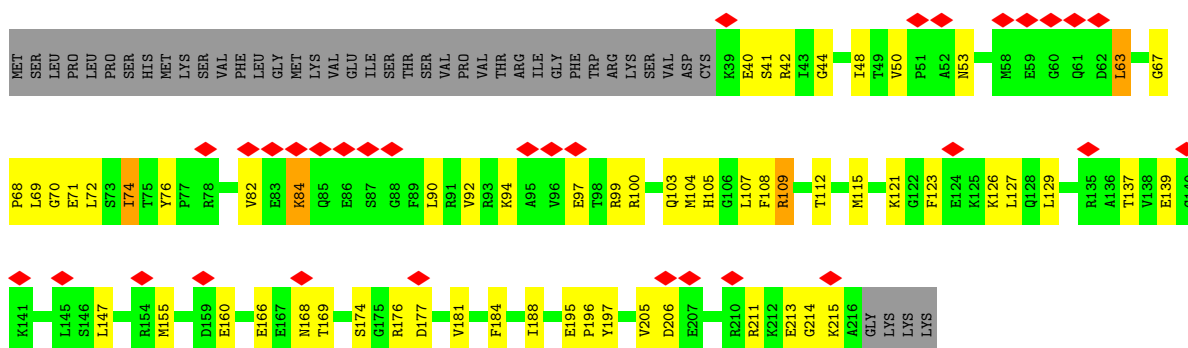
• Molecule 13: plastid ribosomal protein uL4c



- Molecule 14: plastid ribosomal protein uL5c



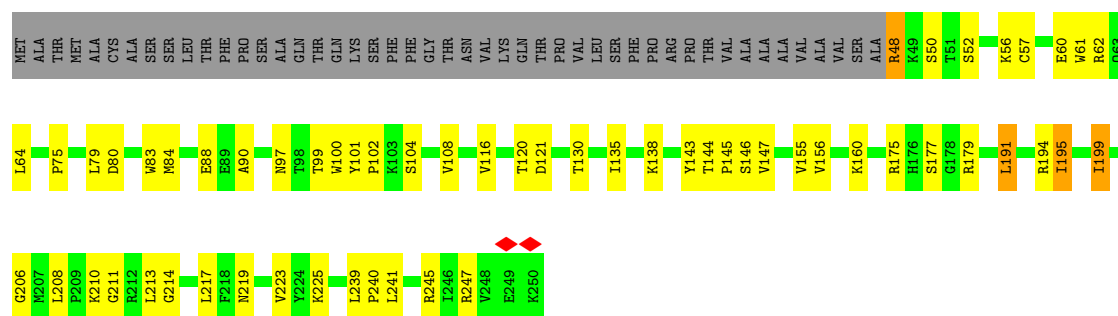
- Molecule 15: plastid ribosomal protein uL6c



- Molecule 16: plastid ribosomal protein bL9c

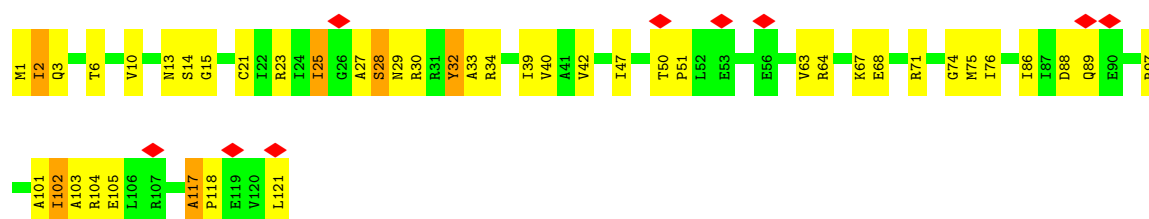


Chain K: 



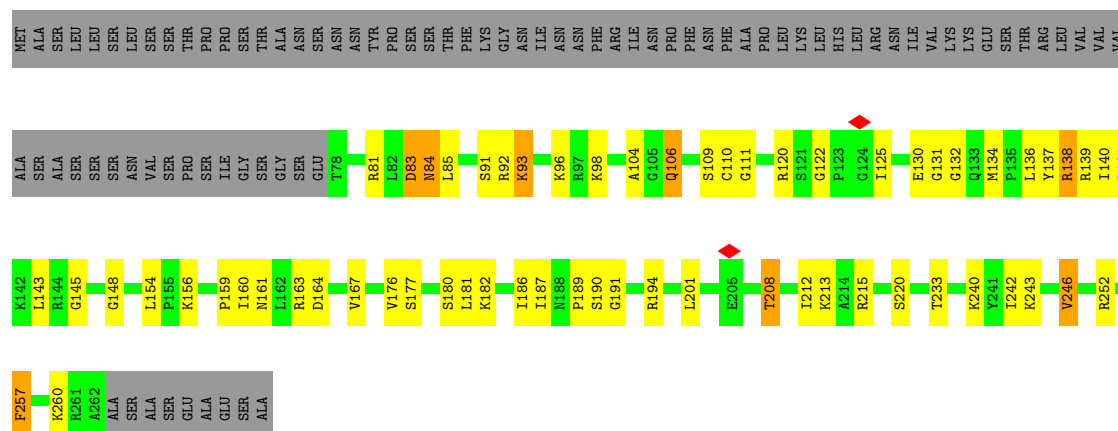
- Molecule 20: 50S ribosomal protein L14, chloroplastic

Chain L: 



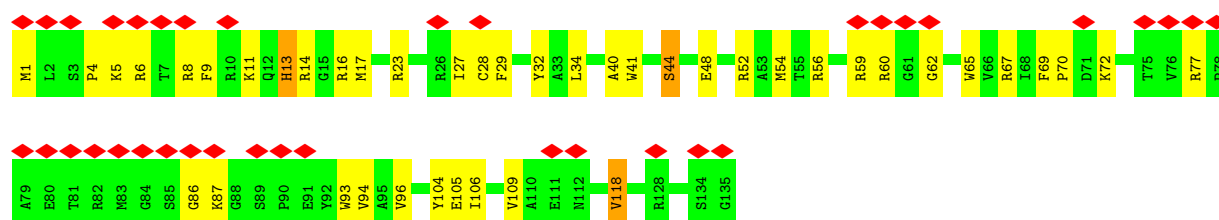
- Molecule 21: plastid ribosomal protein uL15c

Chain M: 



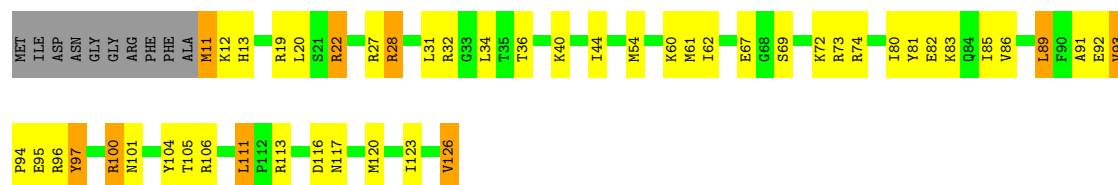
- Molecule 22: 50S ribosomal protein L16, chloroplastic

Chain N: 



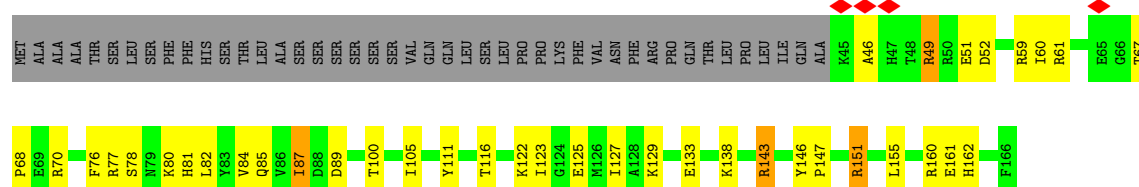
- Molecule 23: plastid ribosomal protein bL17c

Chain O: 



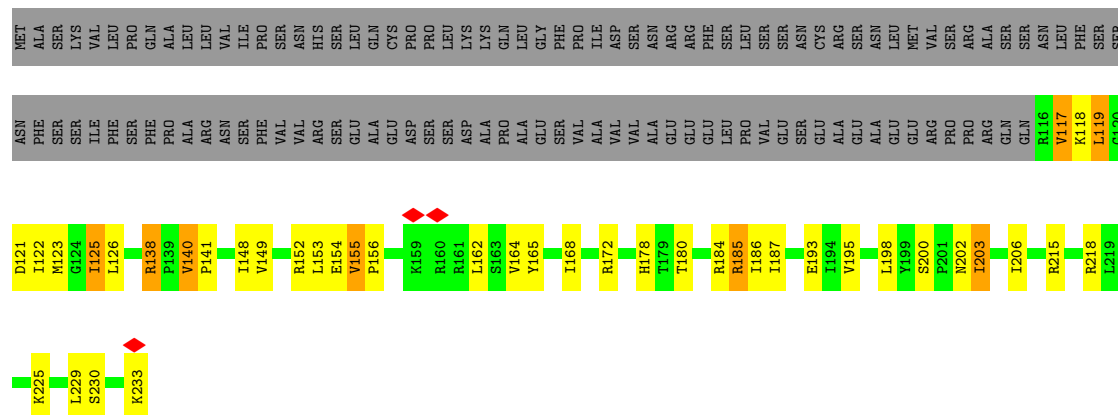
- Molecule 24: plastid ribosomal protein uL18c

Chain P: 



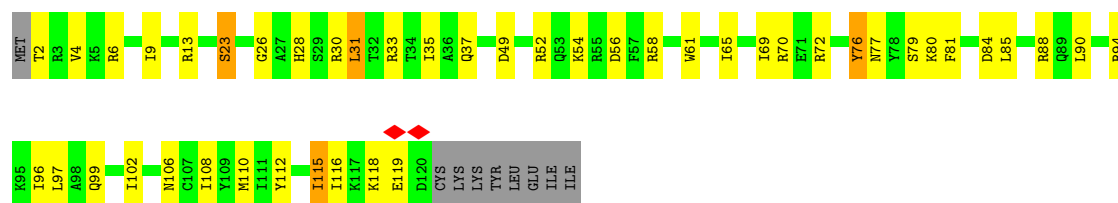
- Molecule 25: 50S ribosomal protein L19, chloroplastic

Chain Q: 

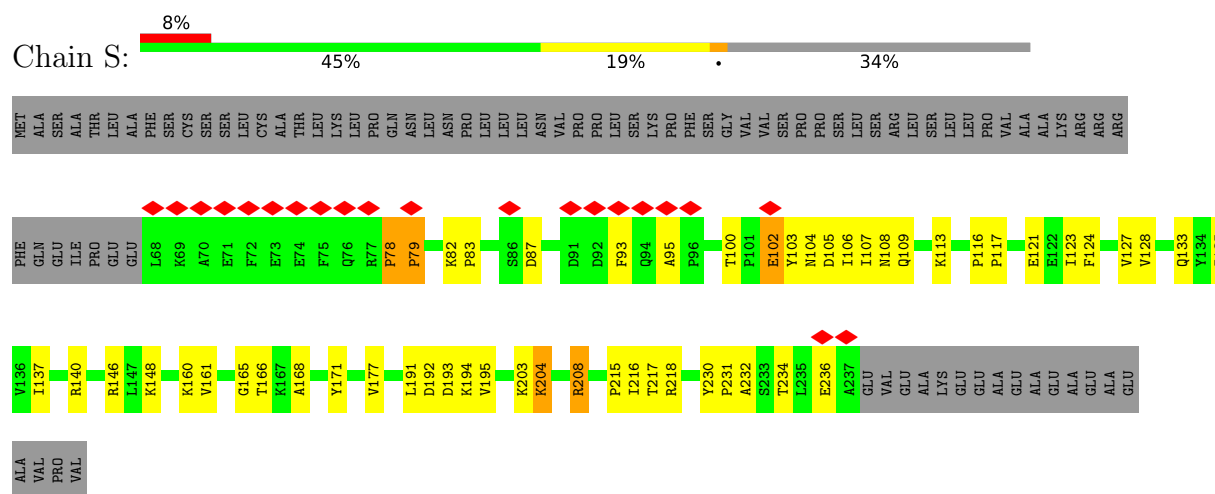


- Molecule 26: 50S ribosomal protein L20, chloroplastic

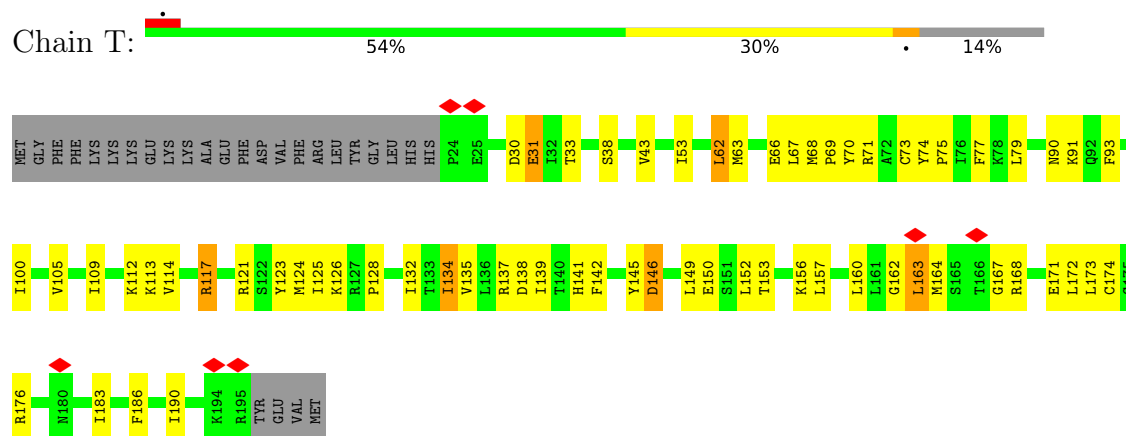
Chain R: 



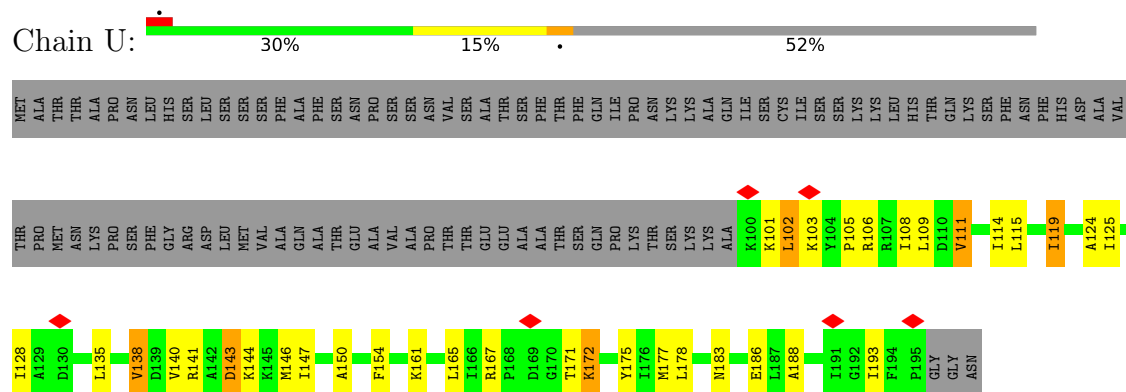
- Molecule 27: 50S ribosomal protein L21, chloroplastic



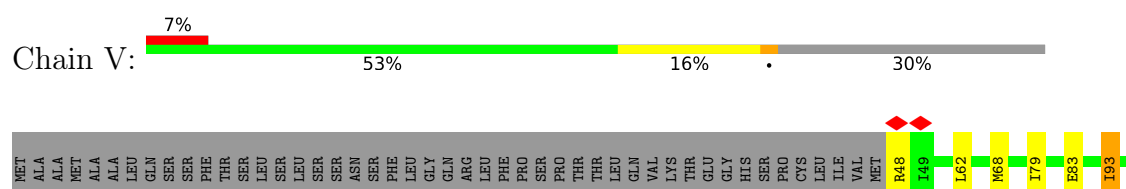
- Molecule 28: 50S ribosomal protein L22, chloroplastic

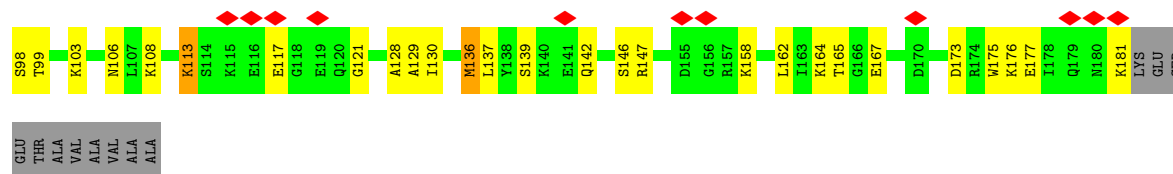


- Molecule 29: 50S ribosomal protein L23, chloroplastic

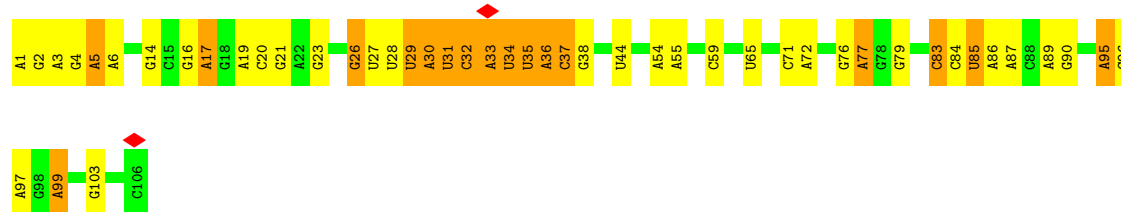


- Molecule 30: plastid ribosomal protein uL24c

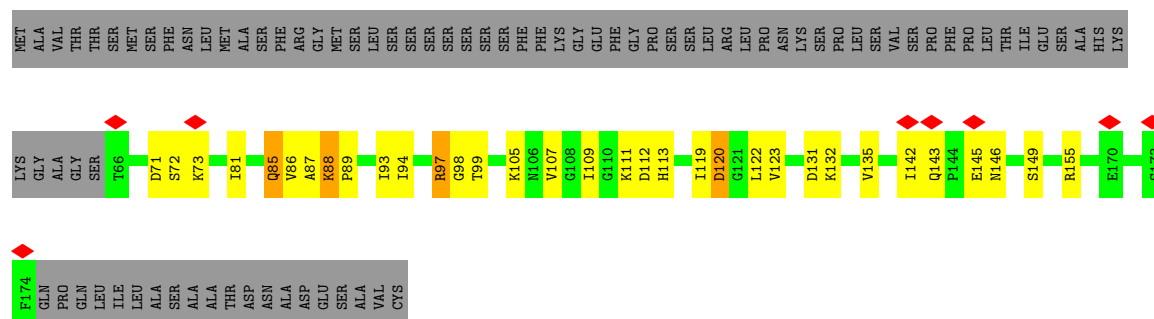




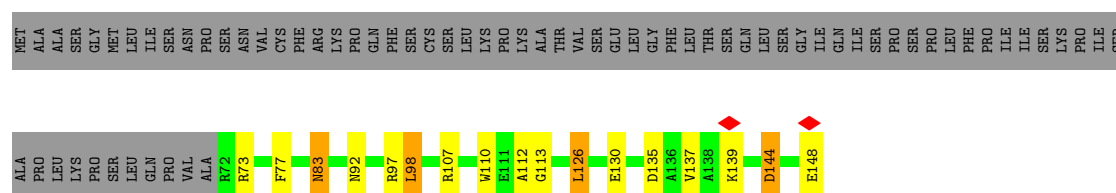
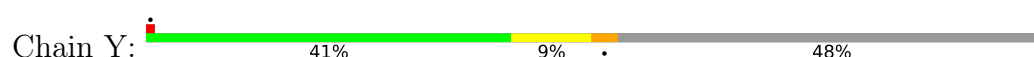
- Molecule 31: 4.5S ribosomal RNA



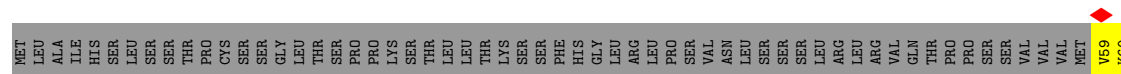
- Molecule 32: plastid ribosomal protein bL27c

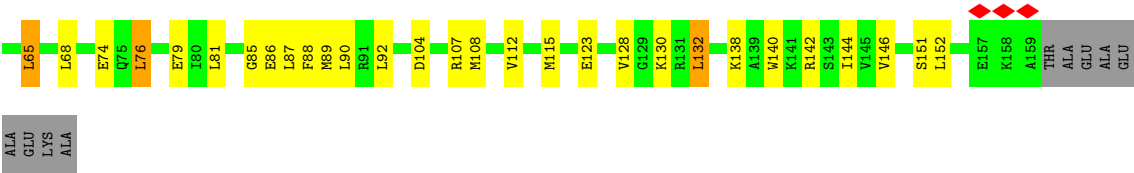


- Molecule 33: plastid ribosomal protein bL28c



- Molecule 34: plastid ribosomal protein uL29c





● Molecule 35: E-site tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	154332	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.616	Depositor
Minimum map value	-0.270	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.08	Depositor
Map size (Å)	444.8, 444.8, 444.8	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.39, 1.39, 1.39	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.63	0/369	0.97	2/499 (0.4%)
2	1	0.73	0/405	1.01	2/537 (0.4%)
3	2	0.60	0/497	1.04	5/664 (0.8%)
4	3	0.81	0/470	1.12	4/619 (0.6%)
5	4	0.71	0/594	1.11	0/784
6	5	0.52	0/307	0.92	0/403
7	6	0.62	0/425	1.47	5/551 (0.9%)
8	7	0.66	0/382	0.89	2/520 (0.4%)
9	A	0.40	0/67297	0.47	0/104984
10	B	0.24	0/2890	0.39	0/4503
11	C	0.65	0/1986	1.12	9/2666 (0.3%)
12	D	0.71	0/1713	1.08	3/2291 (0.1%)
13	E	0.69	0/1707	1.12	8/2298 (0.3%)
14	F	0.57	0/1475	1.04	10/1990 (0.5%)
15	G	0.50	0/1412	1.00	3/1898 (0.2%)
16	H	0.57	0/386	0.98	1/514 (0.2%)
17	I	0.77	0/1129	0.90	1/1521 (0.1%)
18	J	0.85	1/992 (0.1%)	0.99	3/1343 (0.2%)
19	K	0.67	1/1688 (0.1%)	0.96	2/2279 (0.1%)
20	L	0.64	0/951	1.13	4/1282 (0.3%)
21	M	0.65	0/1430	1.08	1/1896 (0.1%)
22	N	0.68	2/1097 (0.2%)	1.03	2/1471 (0.1%)
23	O	0.73	0/959	1.11	7/1280 (0.5%)
24	P	0.47	0/978	0.88	1/1311 (0.1%)
25	Q	0.70	0/967	1.14	8/1299 (0.6%)
26	R	0.79	0/1046	1.04	1/1395 (0.1%)
27	S	0.65	0/1339	1.13	4/1826 (0.2%)
28	T	0.65	0/1420	0.96	1/1900 (0.1%)
29	U	0.64	0/787	1.02	0/1056
30	V	0.55	0/1093	1.03	1/1457 (0.1%)
31	W	0.36	0/2551	0.48	0/3977
32	X	0.57	0/905	0.97	3/1204 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Y	0.64	0/644	0.93	0/856
34	Z	0.48	0/854	0.84	0/1131
35	z	0.55	0/46	1.01	0/69
All	All	0.49	4/103191 (0.0%)	0.67	93/154274 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
21	M	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	N	13	HIS	ND1-CE1	-8.30	1.24	1.32
22	N	13	HIS	CG-ND1	7.11	1.46	1.38
18	J	93	PRO	CA-C	5.46	1.57	1.52
19	K	108	VAL	CA-CB	5.11	1.60	1.54

The worst 5 of 93 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	6	131	TRP	CA-C-N	-16.13	103.76	120.38
7	6	131	TRP	C-N-CA	-16.13	103.76	120.38
11	C	231	GLY	N-CA-C	-8.92	98.84	113.02
20	L	117	ALA	CA-C-N	8.32	128.01	119.19
20	L	117	ALA	C-N-CA	8.32	128.01	119.19

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	M	104	ALA	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	359	0	330	25	0
2	1	396	0	437	15	0
3	2	489	0	507	10	0
4	3	467	0	526	15	0
5	4	588	0	658	12	0
6	5	305	0	344	9	0
7	6	422	0	508	16	0
8	7	368	0	386	6	0
9	A	60083	0	30260	544	0
10	B	2584	0	1305	38	0
11	C	1952	0	2038	56	0
12	D	1686	0	1772	51	0
13	E	1676	0	1737	39	0
14	F	1454	0	1488	52	0
15	G	1391	0	1458	38	0
16	H	382	0	437	5	0
17	I	1106	0	1122	41	0
18	J	977	0	1027	29	0
19	K	1648	0	1684	43	0
20	L	942	0	996	27	0
21	M	1410	0	1495	46	0
22	N	1075	0	1134	29	0
23	O	944	0	1004	34	0
24	P	962	0	984	28	0
25	Q	953	0	1050	27	0
26	R	1029	0	1092	34	0
27	S	1310	0	1315	38	0
28	T	1395	0	1482	44	0
29	U	776	0	837	25	0
30	V	1078	0	1144	24	0
31	W	2277	0	1146	28	0
32	X	888	0	923	15	0
33	Y	634	0	684	12	0
34	Z	846	0	918	20	0
35	z	42	0	23	1	0
36	2	1	0	0	0	0
36	5	1	0	0	0	0
37	4	1	0	0	0	0
37	6	1	0	0	0	0
37	7	1	0	0	0	0
37	A	453	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	B	15	0	0	0	0
37	C	1	0	0	0	0
37	D	2	0	0	0	0
37	E	1	0	0	0	0
37	H	1	0	0	0	0
37	M	2	0	0	0	0
37	N	1	0	0	0	0
37	P	1	0	0	0	0
37	R	1	0	0	0	0
37	T	1	0	0	0	0
37	U	1	0	0	0	0
37	V	2	0	0	0	0
37	W	14	0	0	0	0
37	X	1	0	0	0	0
37	Y	1	0	0	0	0
All	All	95397	0	64251	1245	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 8.

The worst 5 of 1245 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)
9:A:652:C:N4	9:A:657:U:O4	1.86	1.08
9:A:2077:C:H42	9:A:2464:G:H1	1.10	0.98
20:L:15:GLY:HA3	20:L:50:THR:HG21	1.51	0.90
9:A:817:C:OP2	21:M:120:ARG:NH1	2.06	0.89
9:A:540:A:H62	9:A:2055:U:H3	1.18	0.88

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	42/130 (32%)	39 (93%)	3 (7%)	0	100	100
2	1	46/57 (81%)	44 (96%)	2 (4%)	0	100	100
3	2	58/66 (88%)	53 (91%)	5 (9%)	0	100	100
4	3	58/152 (38%)	54 (93%)	4 (7%)	0	100	100
5	4	70/159 (44%)	66 (94%)	4 (6%)	0	100	100
6	5	35/37 (95%)	35 (100%)	0	0	100	100
7	6	47/142 (33%)	46 (98%)	0	1 (2%)	5	31
8	7	44/116 (38%)	40 (91%)	3 (7%)	1 (2%)	5	29
11	C	251/272 (92%)	238 (95%)	12 (5%)	1 (0%)	30	62
12	D	219/305 (72%)	205 (94%)	13 (6%)	1 (0%)	24	59
13	E	210/293 (72%)	193 (92%)	17 (8%)	0	100	100
14	F	191/258 (74%)	178 (93%)	13 (7%)	0	100	100
15	G	176/220 (80%)	167 (95%)	9 (5%)	0	100	100
16	H	46/196 (24%)	43 (94%)	3 (6%)	0	100	100
17	I	135/232 (58%)	132 (98%)	3 (2%)	0	100	100
18	J	131/224 (58%)	126 (96%)	5 (4%)	0	100	100
19	K	201/250 (80%)	194 (96%)	7 (4%)	0	100	100
20	L	119/121 (98%)	115 (97%)	4 (3%)	0	100	100
21	M	183/271 (68%)	169 (92%)	12 (7%)	2 (1%)	11	43
22	N	133/135 (98%)	122 (92%)	11 (8%)	0	100	100
23	O	114/126 (90%)	110 (96%)	4 (4%)	0	100	100
24	P	120/166 (72%)	114 (95%)	6 (5%)	0	100	100
25	Q	116/233 (50%)	114 (98%)	2 (2%)	0	100	100
26	R	117/128 (91%)	110 (94%)	7 (6%)	0	100	100
27	S	168/256 (66%)	157 (94%)	9 (5%)	2 (1%)	10	42
28	T	170/199 (85%)	161 (95%)	8 (5%)	1 (1%)	21	56
29	U	94/198 (48%)	89 (95%)	5 (5%)	0	100	100
30	V	132/192 (69%)	121 (92%)	10 (8%)	1 (1%)	16	50
32	X	107/194 (55%)	95 (89%)	12 (11%)	0	100	100
33	Y	75/148 (51%)	74 (99%)	1 (1%)	0	100	100
34	Z	99/168 (59%)	95 (96%)	3 (3%)	1 (1%)	12	45
All	All	3707/5644 (66%)	3499 (94%)	197 (5%)	11 (0%)	37	68

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	C	232	GLU
21	M	131	GLY
27	S	78	PRO
34	Z	151	SER
7	6	131	TRP

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	39/117 (33%)	36 (92%)	3 (8%)	12	41
2	1	41/50 (82%)	36 (88%)	5 (12%)	5	22
3	2	56/60 (93%)	49 (88%)	7 (12%)	4	21
4	3	50/125 (40%)	42 (84%)	8 (16%)	2	13
5	4	62/140 (44%)	56 (90%)	6 (10%)	8	32
6	5	34/34 (100%)	29 (85%)	5 (15%)	3	16
7	6	46/124 (37%)	43 (94%)	3 (6%)	15	47
8	7	40/96 (42%)	35 (88%)	5 (12%)	4	21
11	C	201/217 (93%)	179 (89%)	22 (11%)	6	26
12	D	182/259 (70%)	165 (91%)	17 (9%)	8	33
13	E	179/255 (70%)	160 (89%)	19 (11%)	6	27
14	F	152/214 (71%)	137 (90%)	15 (10%)	7	31
15	G	151/190 (80%)	140 (93%)	11 (7%)	13	43
16	H	42/170 (25%)	35 (83%)	7 (17%)	2	11
17	I	119/204 (58%)	112 (94%)	7 (6%)	18	50
18	J	106/189 (56%)	102 (96%)	4 (4%)	29	62
19	K	176/213 (83%)	166 (94%)	10 (6%)	18	51
20	L	101/101 (100%)	92 (91%)	9 (9%)	9	34
21	M	141/215 (66%)	125 (89%)	16 (11%)	5	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	N	108/108 (100%)	97 (90%)	11 (10%)	7	29
23	O	96/103 (93%)	84 (88%)	12 (12%)	4	21
24	P	100/139 (72%)	92 (92%)	8 (8%)	11	40
25	Q	104/207 (50%)	93 (89%)	11 (11%)	6	27
26	R	106/115 (92%)	97 (92%)	9 (8%)	10	37
27	S	137/223 (61%)	131 (96%)	6 (4%)	25	59
28	T	152/176 (86%)	138 (91%)	14 (9%)	8	33
29	U	85/171 (50%)	76 (89%)	9 (11%)	6	27
30	V	121/169 (72%)	114 (94%)	7 (6%)	18	51
32	X	92/163 (56%)	78 (85%)	14 (15%)	3	14
33	Y	67/130 (52%)	61 (91%)	6 (9%)	9	34
34	Z	93/153 (61%)	85 (91%)	8 (9%)	10	36
All	All	3179/4830 (66%)	2885 (91%)	294 (9%)	11	33

5 of 294 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
27	S	102	GLU
34	Z	59	VAL
28	T	53	ILE
30	V	93	ILE
13	E	245	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 54 such sidechains are listed below:

Mol	Chain	Res	Type
22	N	13	HIS
24	P	85	GLN
29	U	127	ASN
23	O	18	HIS
23	O	84	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B	120/121 (99%)	19 (15%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
31	W	105/106 (99%)	38 (36%)	0
35	z	1/2 (50%)	1 (100%)	0
9	A	2794/2810 (99%)	642 (22%)	8 (0%)
All	All	3020/3039 (99%)	700 (23%)	8 (0%)

5 of 700 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	A	9	A
9	A	10	G
9	A	12	A
9	A	13	A
9	A	14	A

5 of 8 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	A	2753	C
9	A	2518	C
9	A	1520	A
9	A	795	U
9	A	2447	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 503 ligands modelled in this entry, 503 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

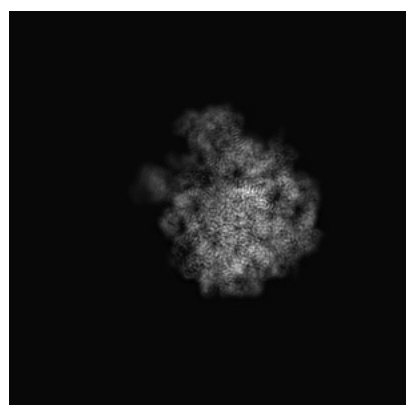
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3531. These allow visual inspection of the internal detail of the map and identification of artifacts.

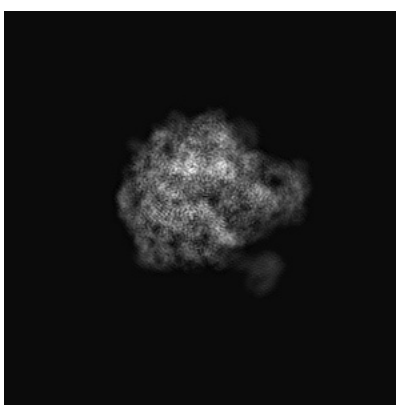
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

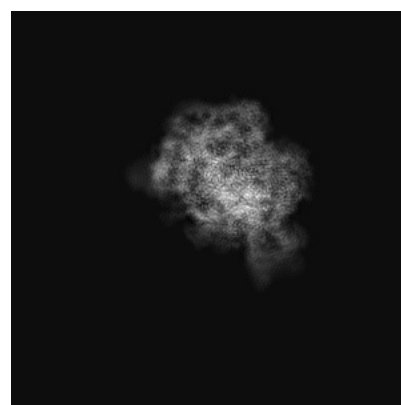
6.1.1 Primary map



X



Y

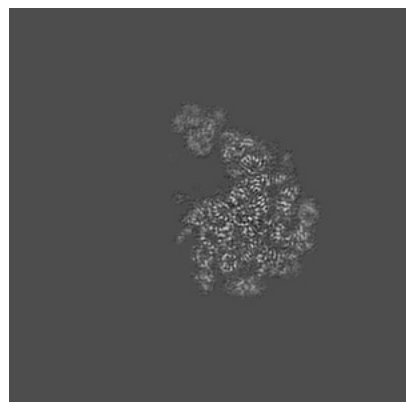


Z

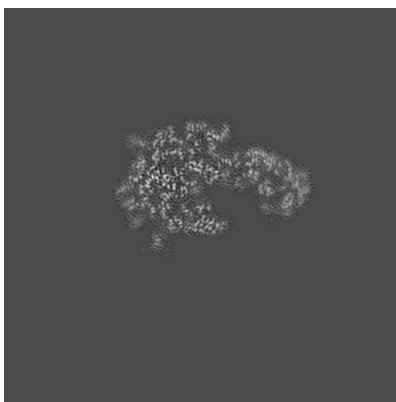
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 160



Y Index: 160

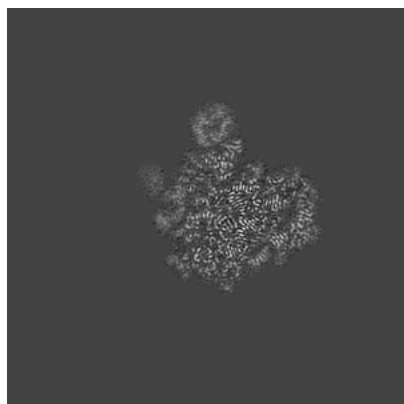


Z Index: 160

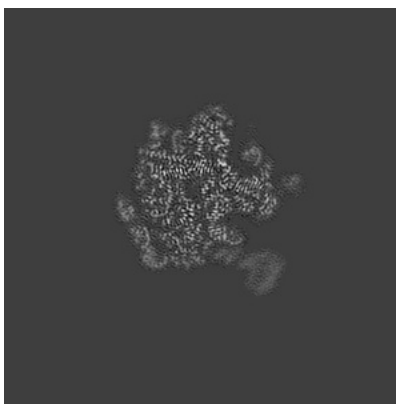
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

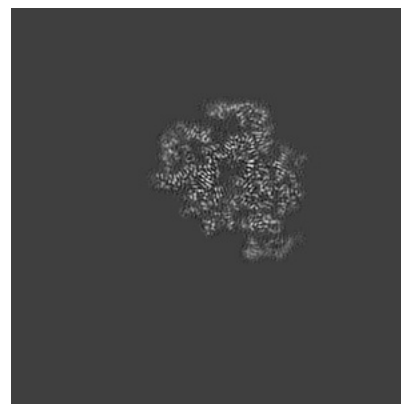
6.3.1 Primary map



X Index: 190



Y Index: 187

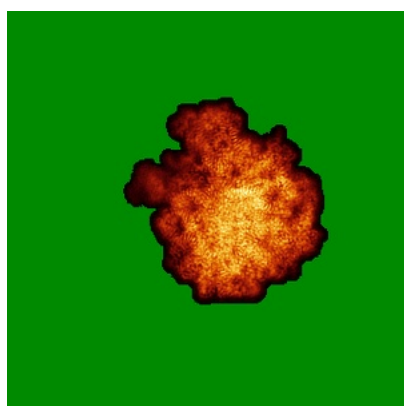


Z Index: 149

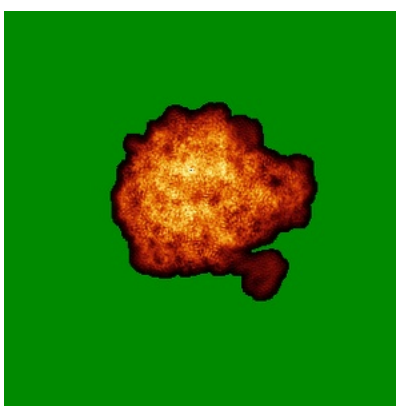
The images above show the largest variance slices of the map in three orthogonal directions.

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

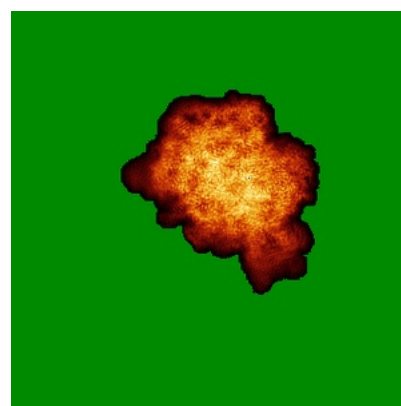
6.4.1 Primary map



X



Y

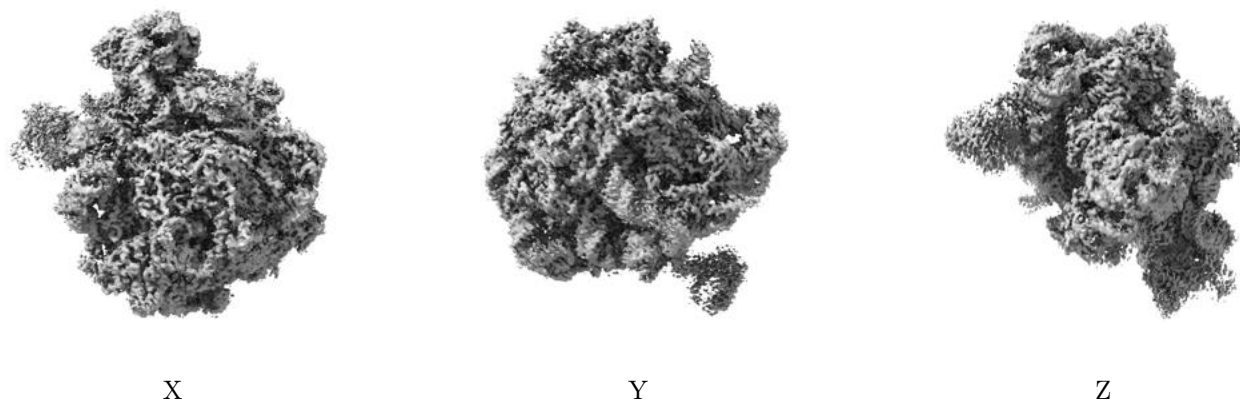


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.08. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

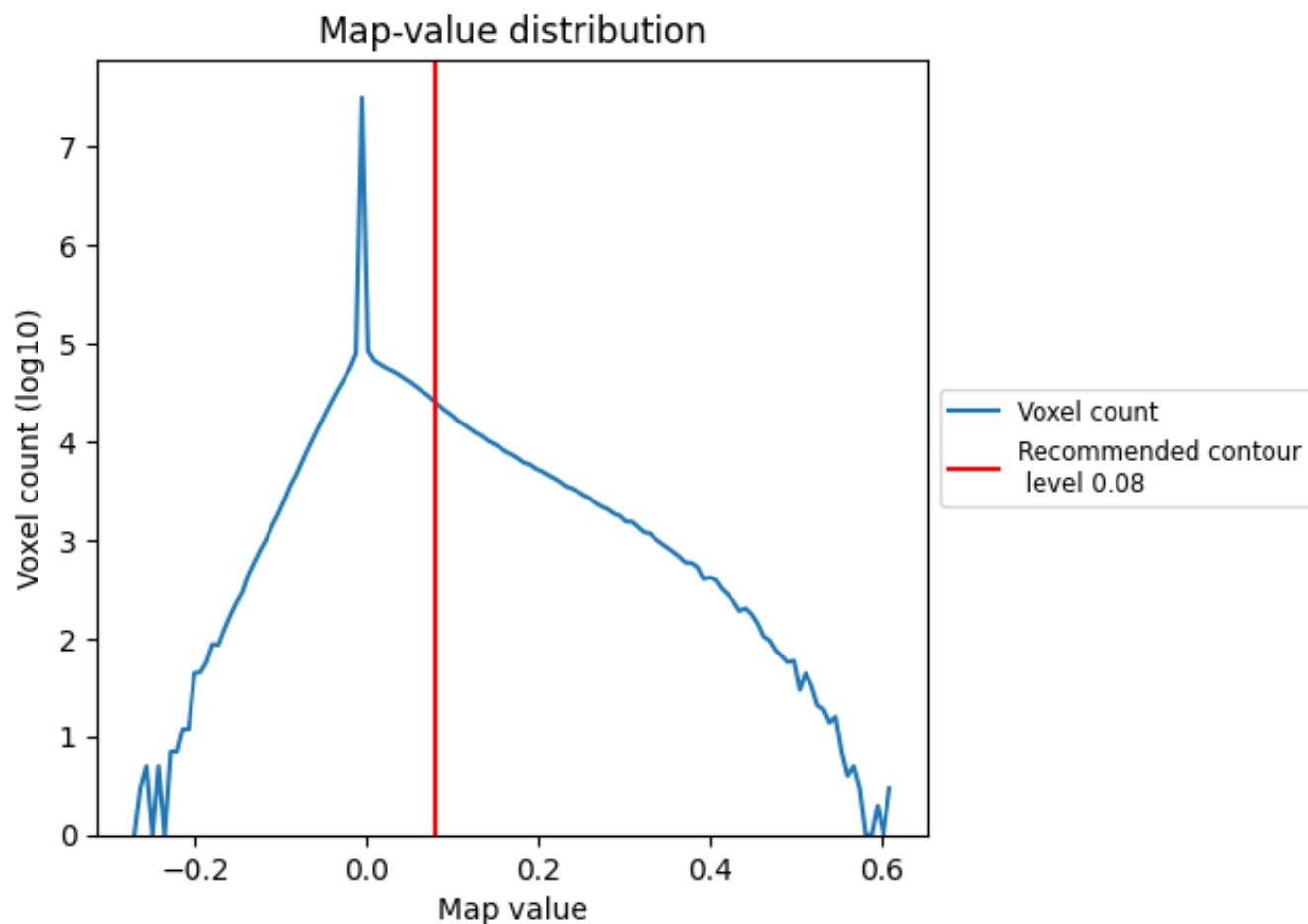
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

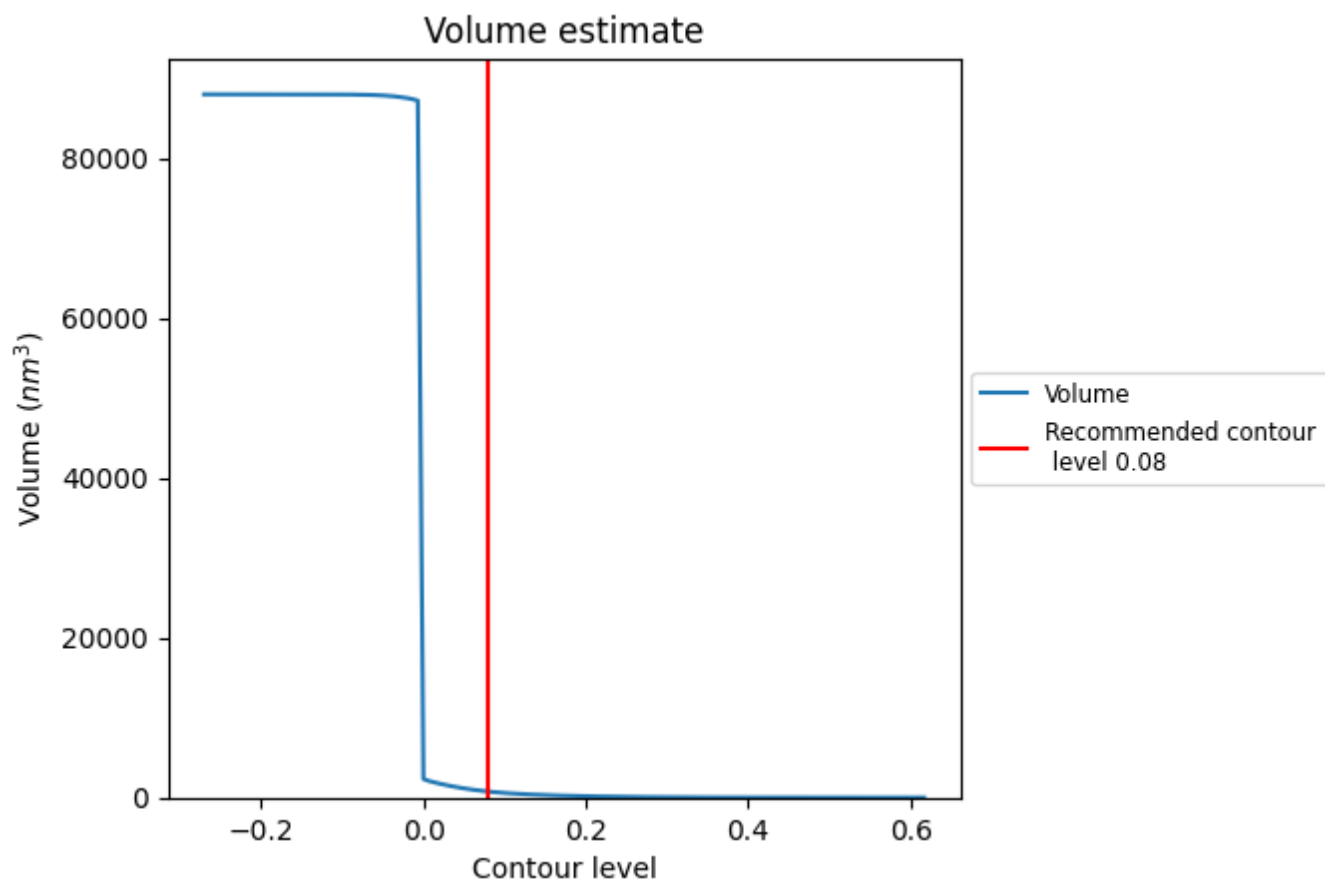
This section contains the results of statistical analysis of the map.

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.

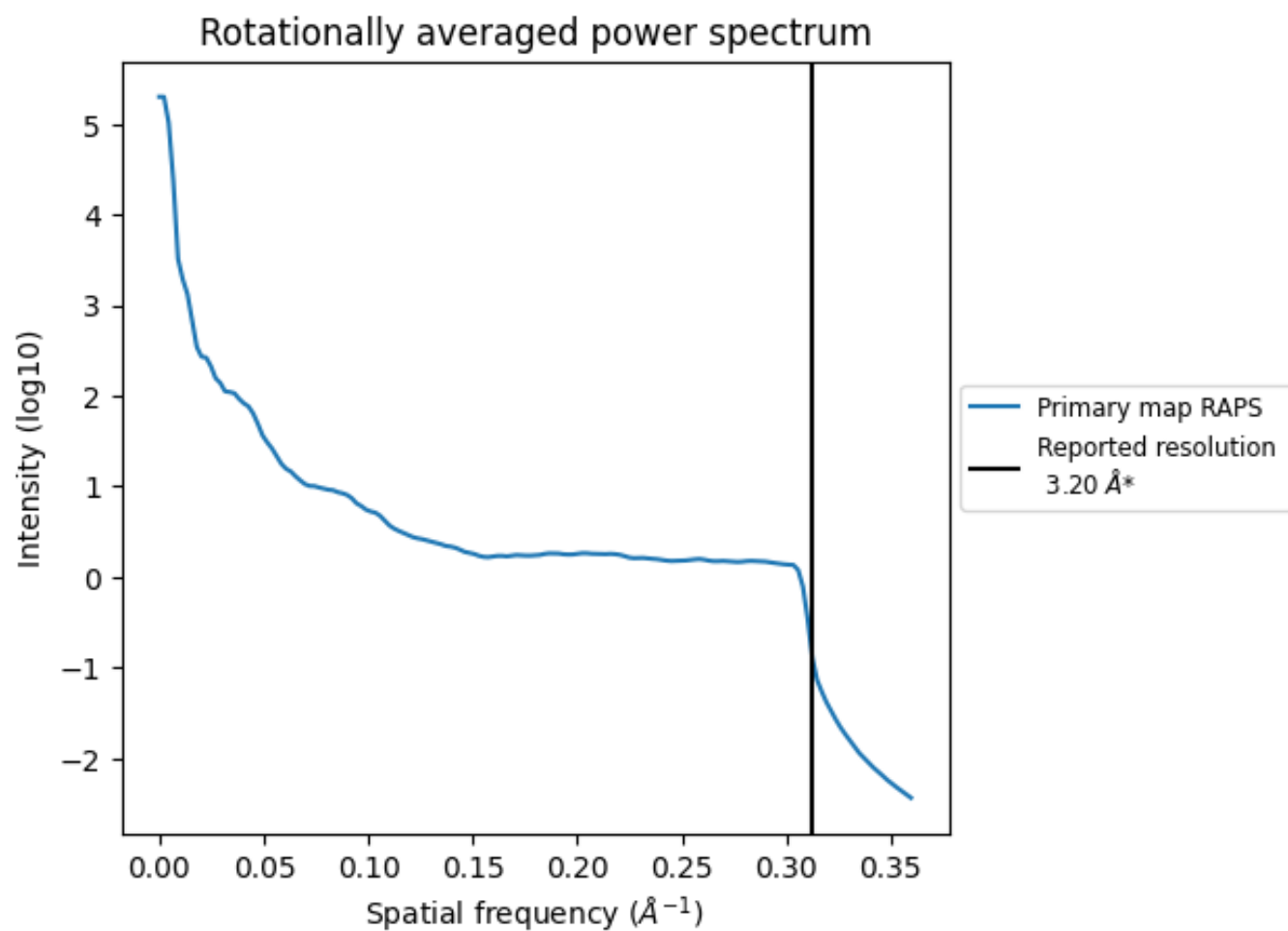
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 750 nm^3 ; this corresponds to an approximate mass of 678 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

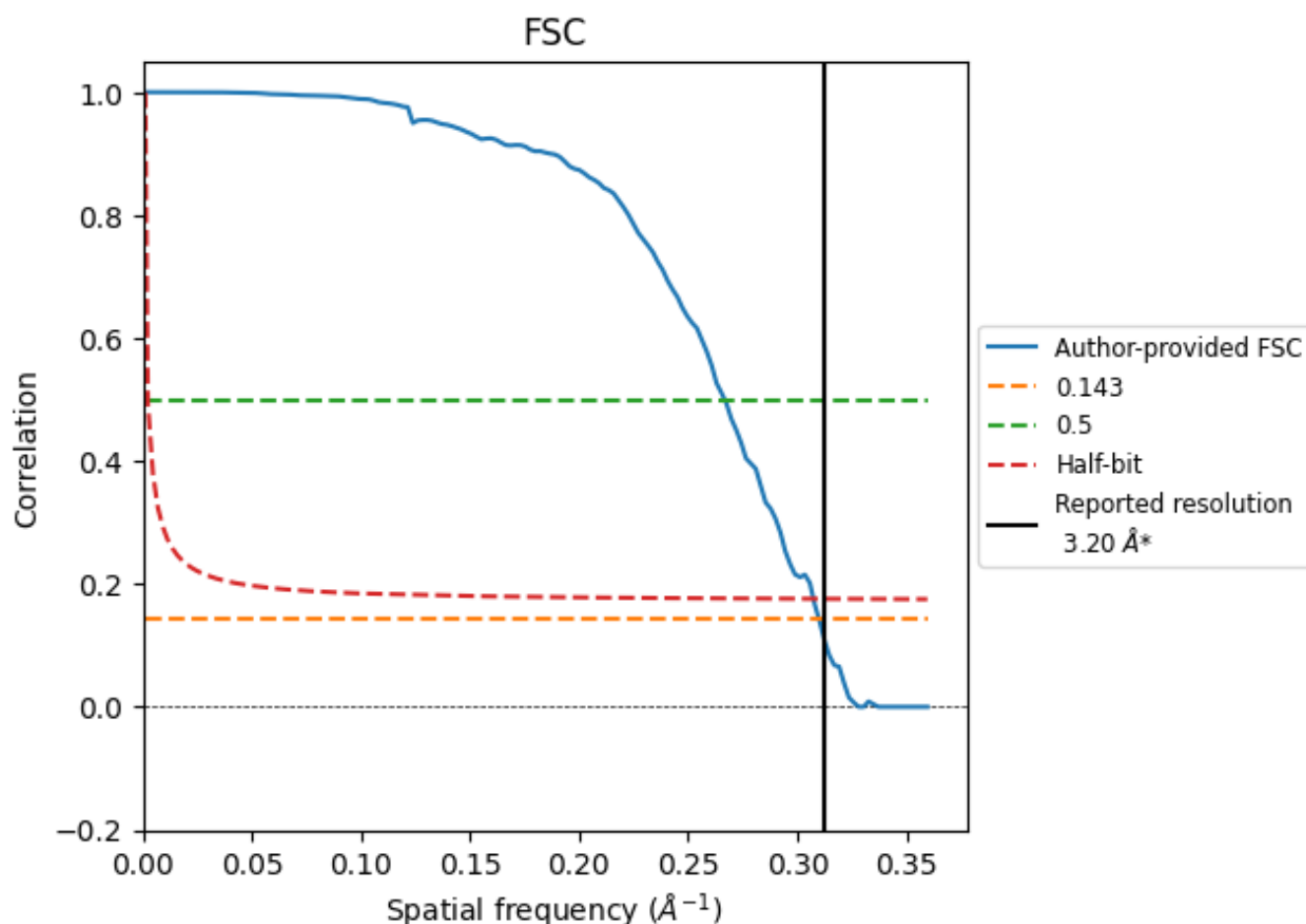


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

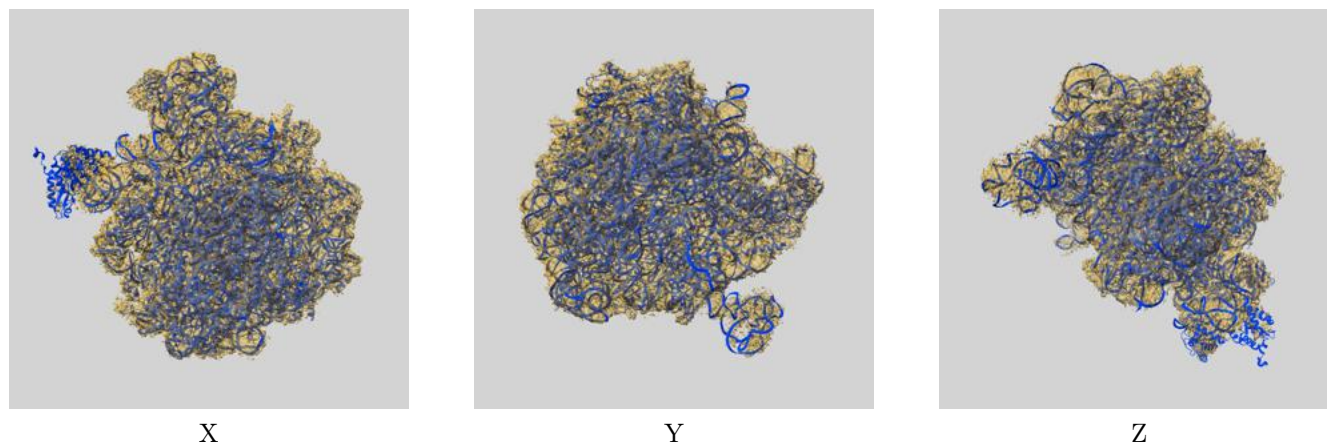
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.23	3.75	3.25
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

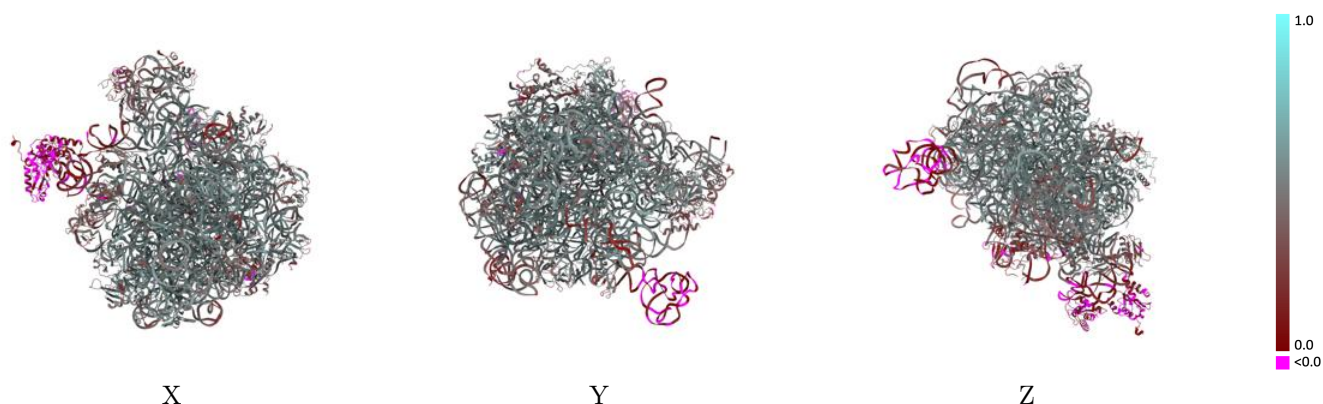
This section contains information regarding the fit between EMDB map EMD-3531 and PDB model 5MMI. Per-residue inclusion information can be found in section [3](#) on page [12](#).

9.1 Map-model overlay [i](#)



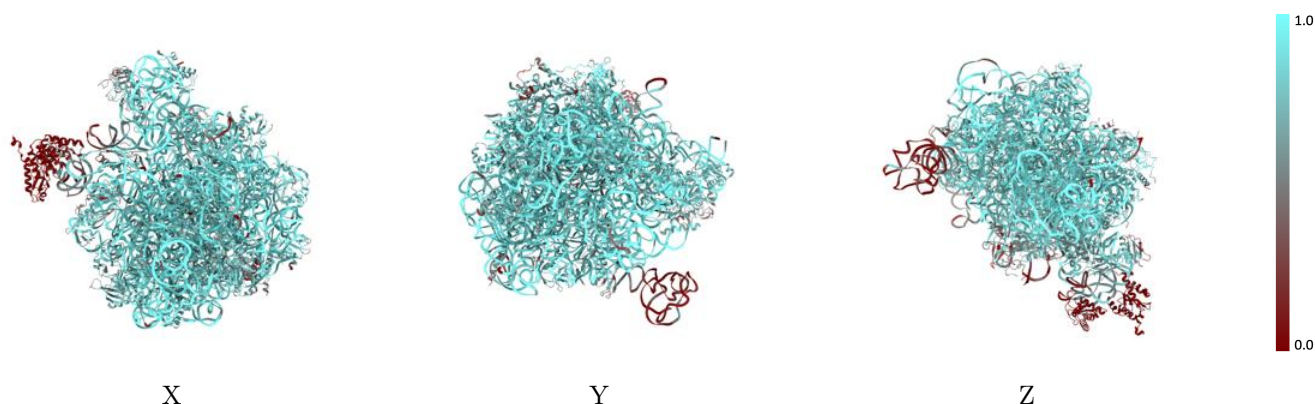
The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



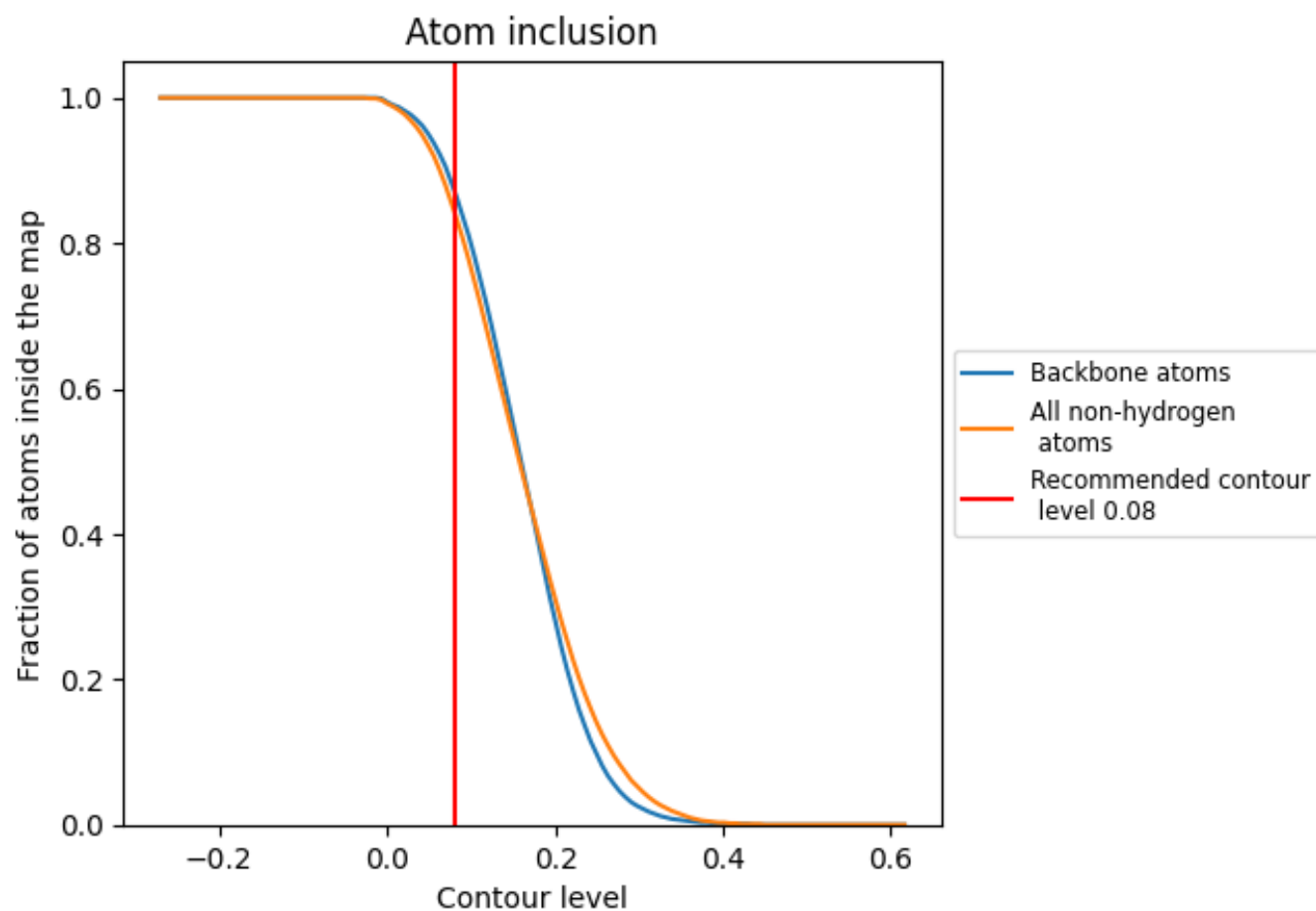
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.08).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 84% 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 (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8430	 0.4690
0	 0.4420	 0.2120
1	 0.8360	 0.5280
2	 0.7610	 0.4720
3	 0.8600	 0.5580
4	 0.8310	 0.5360
5	 0.7550	 0.4690
6	 0.7270	 0.4260
7	 0.8270	 0.4900
A	 0.8990	 0.4880
B	 0.9400	 0.4510
C	 0.7870	 0.4900
D	 0.8460	 0.5130
E	 0.8080	 0.4880
F	 0.5710	 0.3020
G	 0.6580	 0.3450
H	 0.4830	 0.3860
I	 0.0380	 0.0170
J	 0.0700	 0.0320
K	 0.8320	 0.4980
L	 0.7310	 0.4880
M	 0.8290	 0.4810
N	 0.5410	 0.4030
O	 0.8500	 0.5190
P	 0.8050	 0.4350
Q	 0.7780	 0.4790
R	 0.8710	 0.5220
S	 0.7600	 0.4590
T	 0.7690	 0.4630
U	 0.7460	 0.4570
V	 0.7460	 0.4450
W	 0.9460	 0.5100
X	 0.8170	 0.4850
Y	 0.8070	 0.5030
Z	 0.7470	 0.4290
z	 0.4050	 0.4000

