



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 01:27 PM UTC

PDB ID : 7PI9 / pdb_00007pi9
EMDB ID : EMD-13433
Title : 70S ribosome with EF-Tu-tRNA and P-site tRNA in spectinomycin-treated
Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-08-19
Resolution : 6.30 Å (reported)
Based on initial models : 4V7C, 7OOD, 4V5L, 7OOC

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

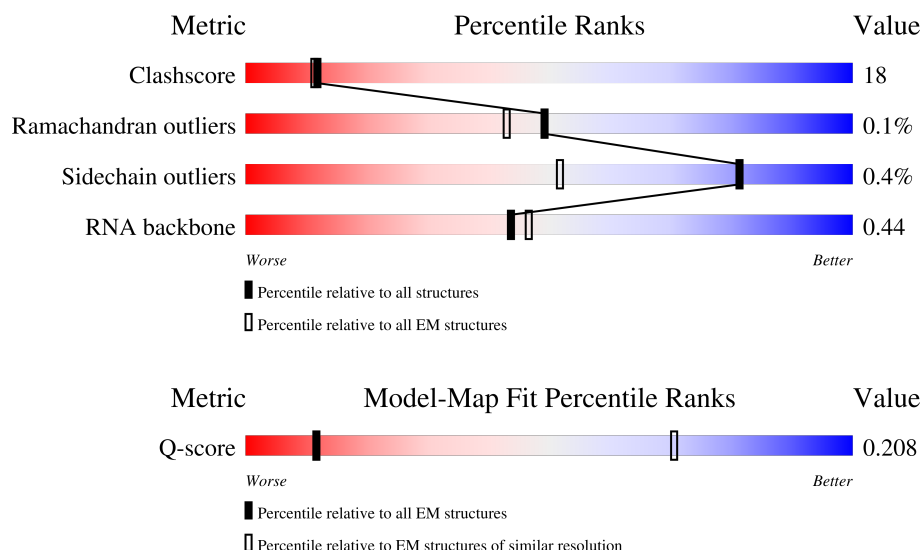
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.30 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	550 (5.80 - 6.80)

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	48	
2	1	59	
3	2	37	

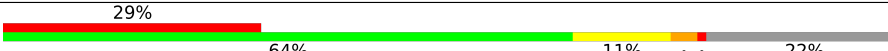
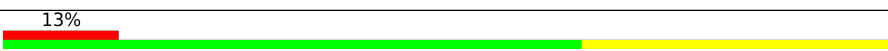
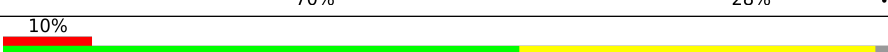
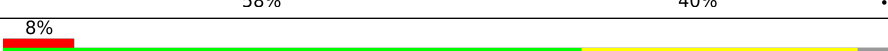
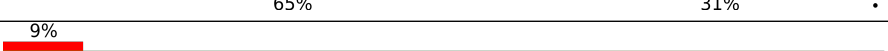
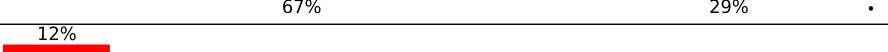
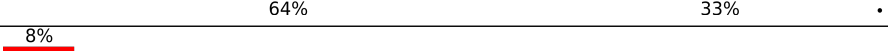
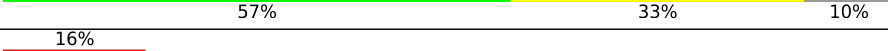
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Mol	Chain	Length	Quality of chain
4	9	394	
5	A	294	
6	B	273	
7	C	205	
8	D	219	
9	E	215	
10	F	155	
11	G	142	
12	H	132	
13	I	108	
14	J	121	
15	K	139	
16	L	124	
17	M	61	
18	N	86	
19	O	94	
20	P	85	
21	Q	104	
22	R	87	
23	S	87	
24	T	60	
25	a	287	
26	b	287	
27	c	212	
28	d	180	

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Mol	Chain	Length	Quality of chain
29	e	184	
30	f	149	
31	g	161	
32	h	137	
33	i	146	
34	j	122	
35	k	151	
36	l	139	
37	m	124	
38	n	116	
39	o	119	
40	p	127	
41	q	100	
42	r	159	
43	s	237	
44	t	111	
45	u	104	
46	v	65	
47	w	111	
48	x	97	
49	y	57	
50	z	53	
51	3	2907	
52	4	108	
53	5	1520	

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Mol	Chain	Length	Quality of chain
54	6	76	21% 33% 46% 20%
54	7	76	25% 53% 22%

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 149163 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 L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	47	Total	C	N	O	S	0	0
			380	236	81	61	2		

- Molecule 2 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	59	Total	C	N	O	S	0	0
			477	300	99	77	1		

- Molecule 3 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	37	Total	C	N	O	S	0	0
			304	189	65	46	4		

- Molecule 4 is a protein called Elongation factor Tu.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	9	393	Total	C	N	O	S	0	0
			3021	1892	533	583	13		

- Molecule 5 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	240	Total	C	N	O	S	0	0
			1921	1226	334	352	9		

- Molecule 6 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	215	Total	C	N	O	S	0	0
			1698	1073	313	307	5		

- Molecule 7 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	203	Total	C	N	O	S	0	0
			1660	1051	314	290	5		

- Molecule 8 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	153	Total	C	N	O	S	0	0
			1173	742	226	202	3		

- Molecule 9 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E	167	Total	C	N	O	S	0	0
			1362	857	240	263	2		

- Molecule 10 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	154	Total	C	N	O	S	0	0
			1246	785	239	216	6		

- Molecule 11 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	G	141	Total	C	N	O	S	0	0
			1110	723	193	192	2		

- Molecule 12 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	H	128	Total	C	N	O	S	0	0
			1028	655	191	181	1		

- Molecule 13 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	I	101	Total	C	N	O	S	0	0
			809	523	142	143	1		

- Molecule 14 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	J	114	Total	C	N	O	S	0	0
			829	514	153	156	6		

- Molecule 15 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	K	136	Total	C	N	O	S	0	0
			1076	680	213	181	2		

- Molecule 16 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	118	Total	C	N	O		0	0
			951	594	191	166			

- Molecule 17 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	60	Total	C	N	O	S	0	0
			474	302	96	72	4		

- Molecule 18 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	83	Total	C	N	O		0	0
			673	428	125	120			

- Molecule 19 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	O	80	Total	C	N	O	S	0	0
			646	414	119	111	2		

- Molecule 20 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	83	Total	C	N	O		0	0
			675	425	135	115			

- Molecule 21 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Q	65	Total	C	N	O	S	0	0
			535	342	103	86	4		

- Molecule 22 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R	84	Total	C	N	O	S	0	0
			682	435	127	118	2		

- Molecule 23 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	77	Total	C	N	O		0	0
			629	383	135	111			

- Molecule 24 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	53	Total	C	N	O	S	0	0
			471	295	103	72	1		

- Molecule 25 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	a	285	Total	C	N	O	S	0	0
			2225	1385	437	397	6		

- Molecule 26 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	b	229	Total	C	N	O	S	0	0
			1762	1119	318	318	7		

- Molecule 27 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	c	210	Total	C	N	O	S	0	0
			1644	1047	297	297	3		

- Molecule 28 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d	175	Total	C	N	O	S	0	0
			1388	893	245	246	4		

- Molecule 29 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	e	176	Total	C	N	O	S	0	0
			1396	899	247	250			

- Molecule 30 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	f	145	Total	C	N	O	S	0	0
			1182	763	206	210	3		

- Molecule 31 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	g	126	Total	C	N	O	S	0	0
			960	612	167	178	3		

- Molecule 32 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	h	128	Total	C	N	O	S	0	0
			959	616	160	177	6		

- Molecule 33 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	i	144	Total	C	N	O	S	0	0
			1164	737	213	209	5		

- Molecule 34 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	j	122	Total	C	N	O	S	0	0
			944	595	178	167	4		

- Molecule 35 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	k	148	Total	C	N	O	0	0
			1153	731	226	196		

- Molecule 36 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	l	136	Total	C	N	O	S	0	0
			1079	694	196	182	7		

- Molecule 37 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	m	119	Total	C	N	O	S	0	0
			958	609	175	171	3		

- Molecule 38 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	n	112	Total	C	N	O	S	0	0
			889	557	175	155	2		

- Molecule 39 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	o	115	Total	C	N	O	S	0	0
			938	592	180	165	1		

- Molecule 40 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	p	114	Total	C	N	O	S	0	0
			947	603	188	154	2		

- Molecule 41 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	q	99	Total	C	N	O	S	0	0
			811	525	148	134	4		

- Molecule 42 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r	139	Total	C	N	O	S	0	0
			1068	663	207	191	7		

- Molecule 43 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	92	Total	C	N	O	S	0	0
			720	475	122	122	1		

- Molecule 44 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t	111	Total	C	N	O	S	0	0
			872	550	166	153	3		

- Molecule 45 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	u	86	Total	C	N	O	S	0	0
			657	409	130	117	1		

- Molecule 46 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	v	63	Total	C	N	O	S	0	0
			513	317	108	87	1		

- Molecule 47 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	w	100	Total	C	N	O	S	0	0
			818	517	153	148			

- Molecule 48 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	x	44	Total	C	N	O	S	0	0
			344	221	55	64	4		

- Molecule 49 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	y	56	Total	C	N	O	S	0	0
			452	274	98	75	5		

- Molecule 50 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	z	50	Total	C	N	O	S	0	0
			408	255	81	68	4		

- Molecule 51 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

- Molecule 52 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

- Molecule 53 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	5	1493	Total	C	N	O	P	0	0
			31943	14279	5792	10382	1490		

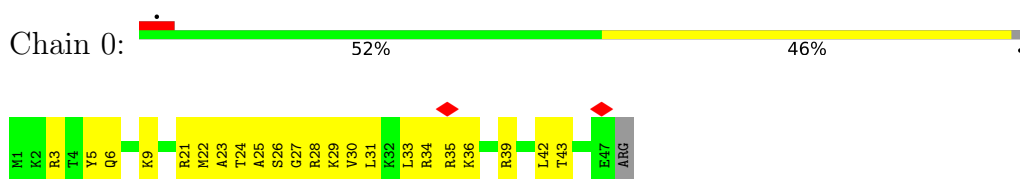
- Molecule 54 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	6	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		
54	7	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

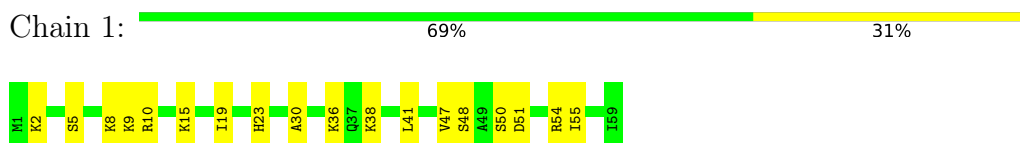
3 Residue-property plots [i](#)

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.

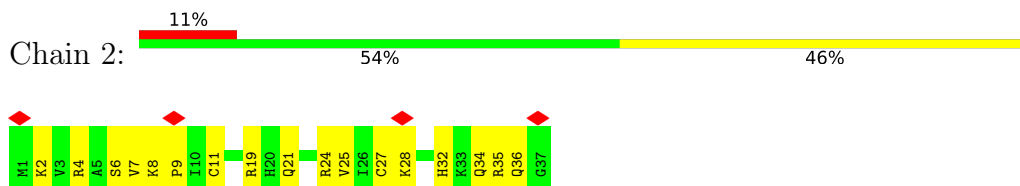
- Molecule 1: 50S ribosomal protein L34



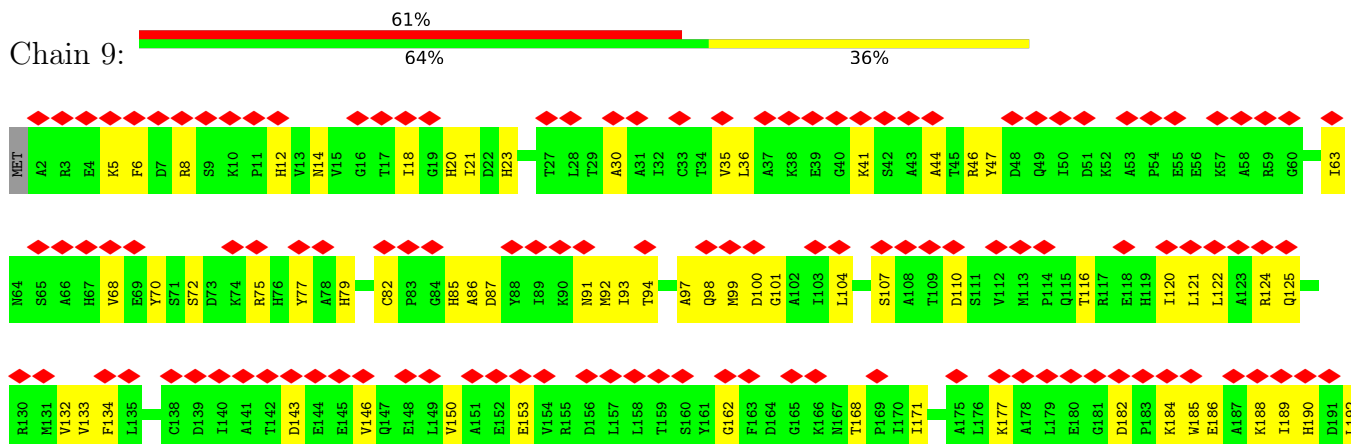
- Molecule 2: 50S ribosomal protein L35

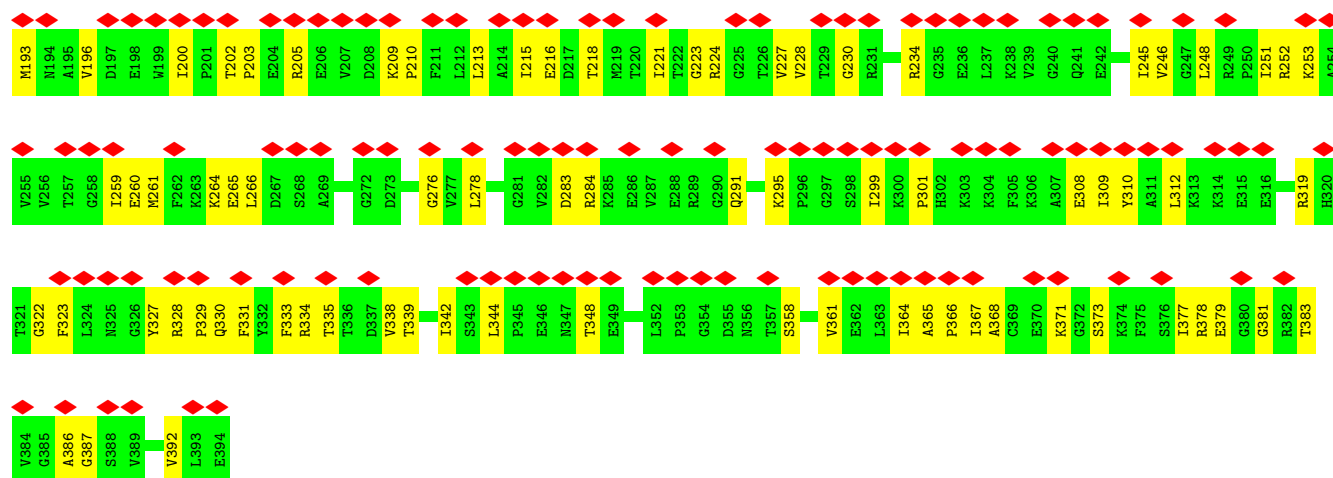


- Molecule 3: 50S ribosomal protein L36

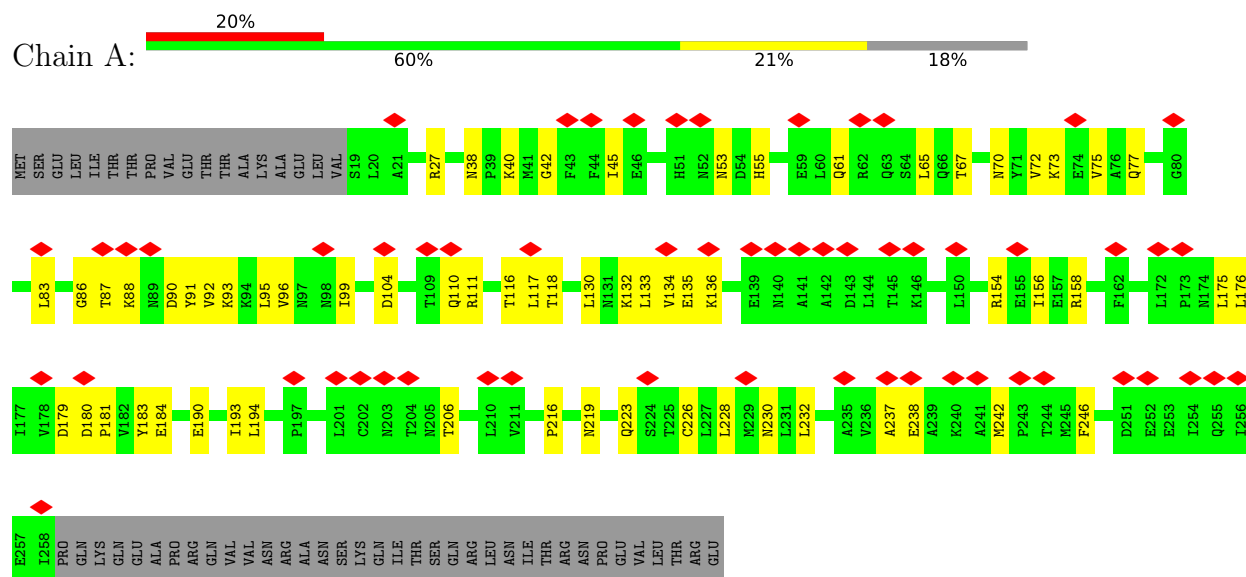


- Molecule 4: Elongation factor Tu

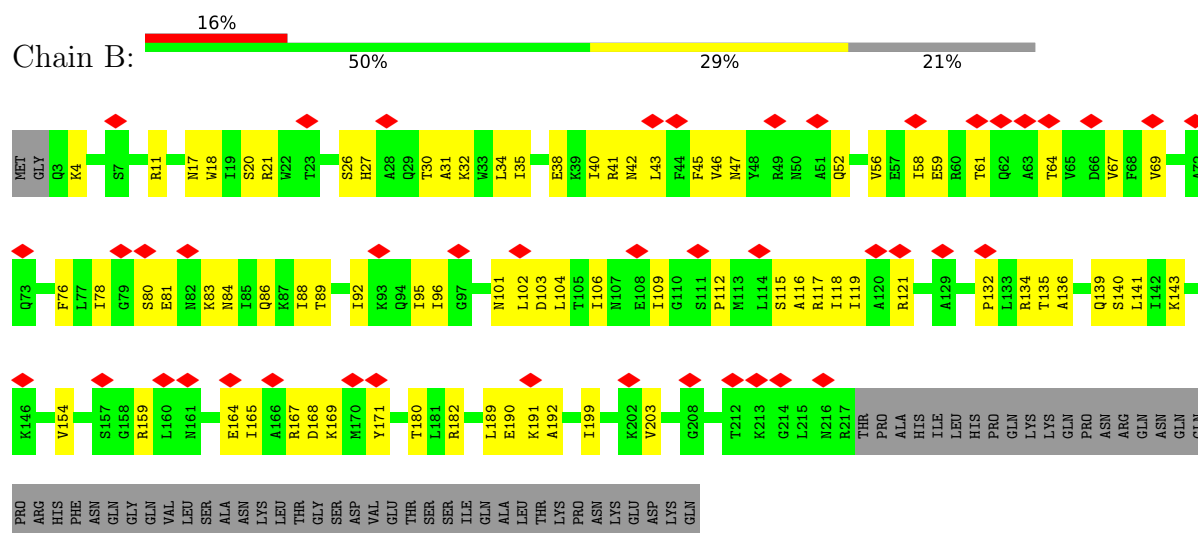




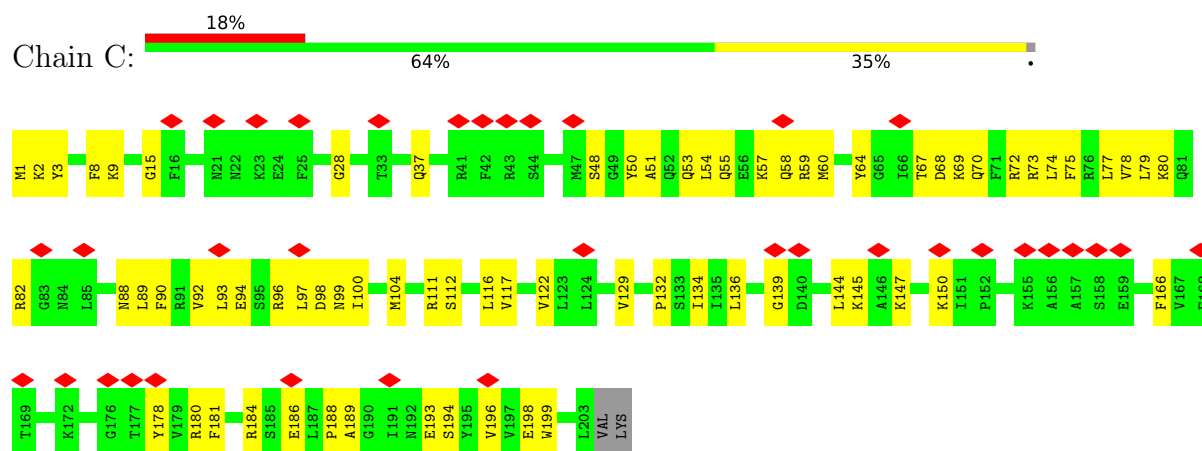
• Molecule 5: 30S ribosomal protein S2



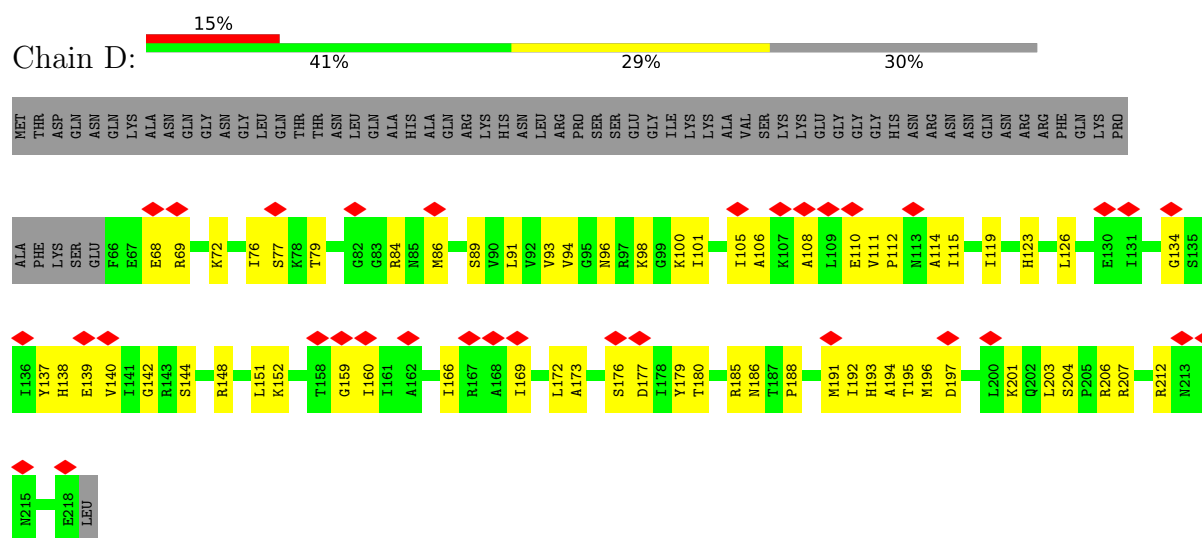
• Molecule 6: 30S ribosomal protein S3



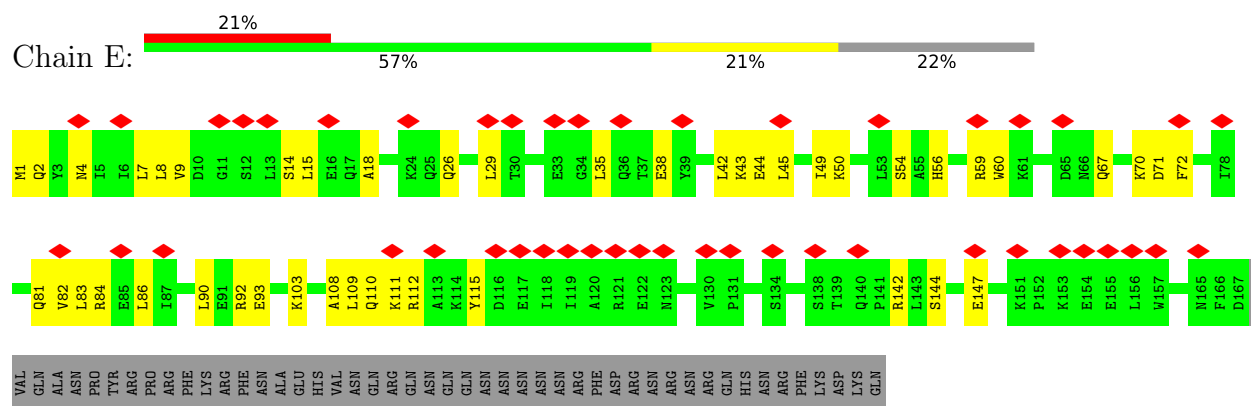
- Molecule 7: 30S ribosomal protein S4



- Molecule 8: 30S ribosomal protein S5

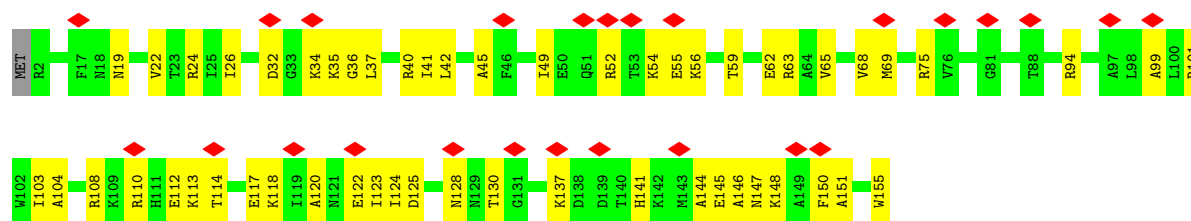


- Molecule 9: 30S ribosomal protein S6

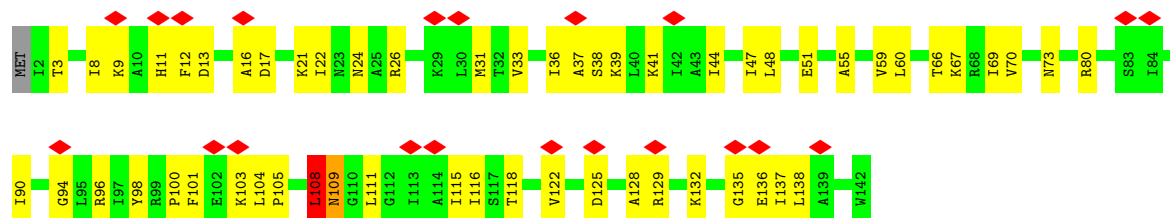


- Molecule 10: 30S ribosomal protein S7

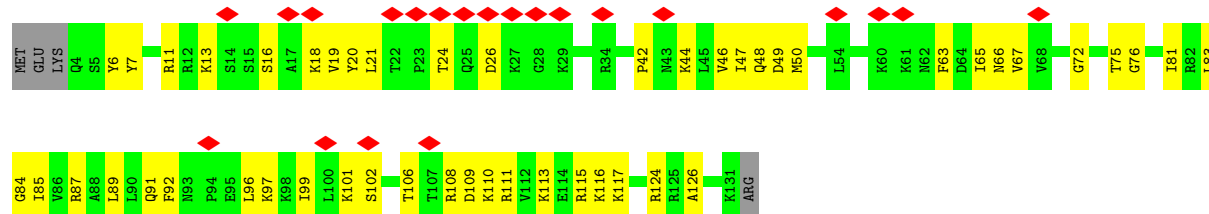




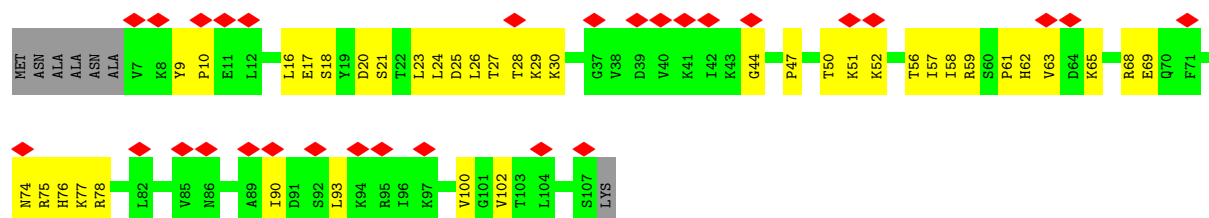
• Molecule 11: 30S ribosomal protein S8



• Molecule 12: 30S ribosomal protein S9

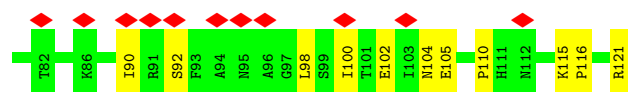


• Molecule 13: 30S ribosomal protein S10

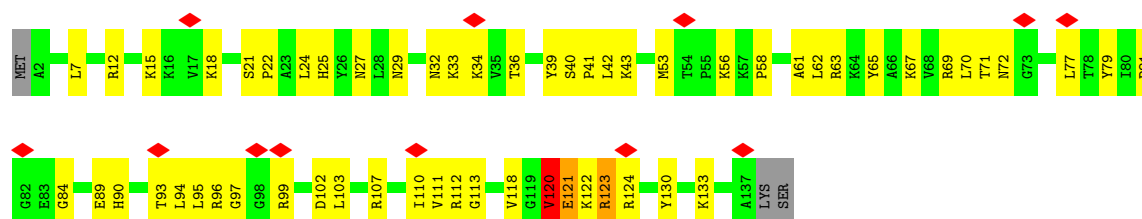


• Molecule 14: 30S ribosomal protein S11

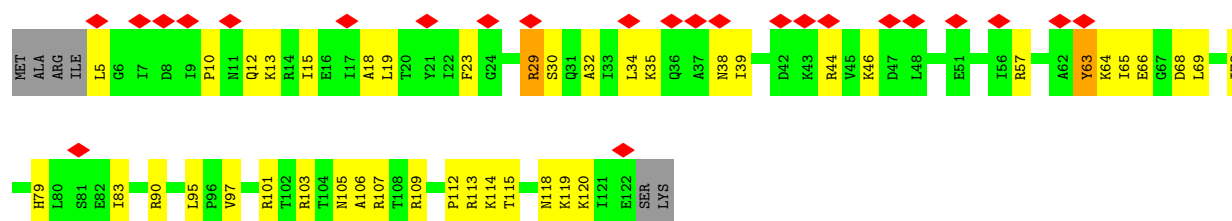




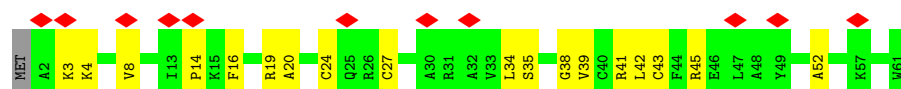
- Molecule 15: 30S ribosomal protein S12



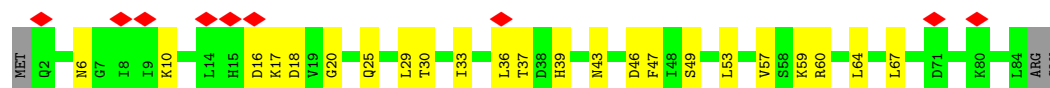
- Molecule 16: 30S ribosomal protein S13



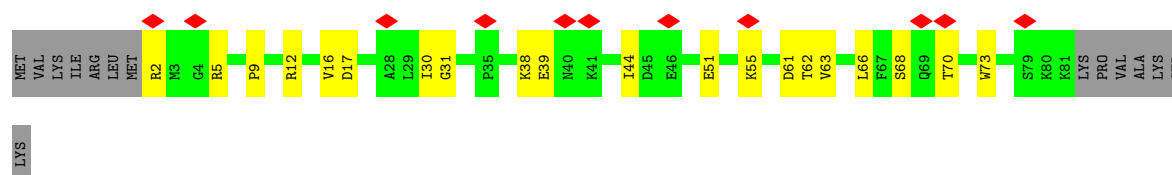
- Molecule 17: 30S ribosomal protein S14 type Z



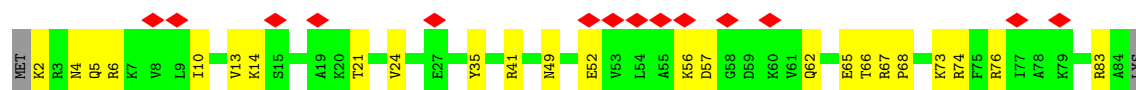
- Molecule 18: 30S ribosomal protein S15



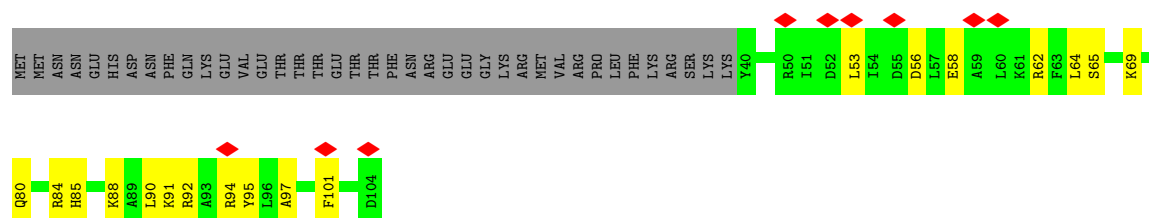
- Molecule 19: 30S ribosomal protein S16



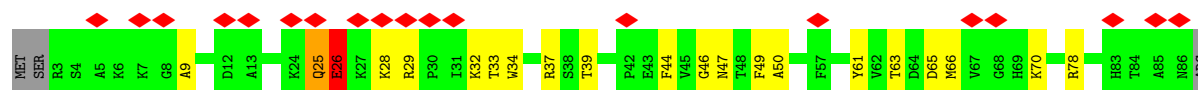
- Molecule 20: 30S ribosomal protein S17



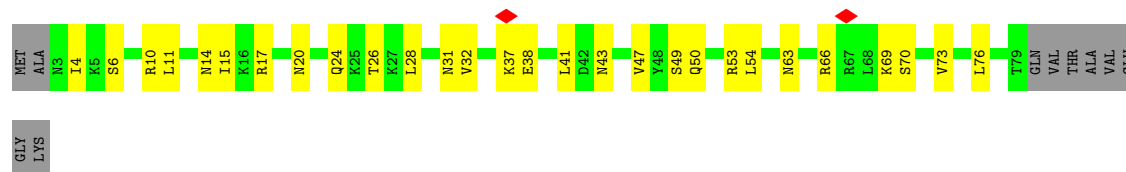
- Molecule 21: 30S ribosomal protein S18



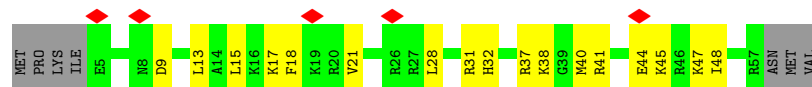
- Molecule 22: 30S ribosomal protein S19



- Molecule 23: 30S ribosomal protein S20

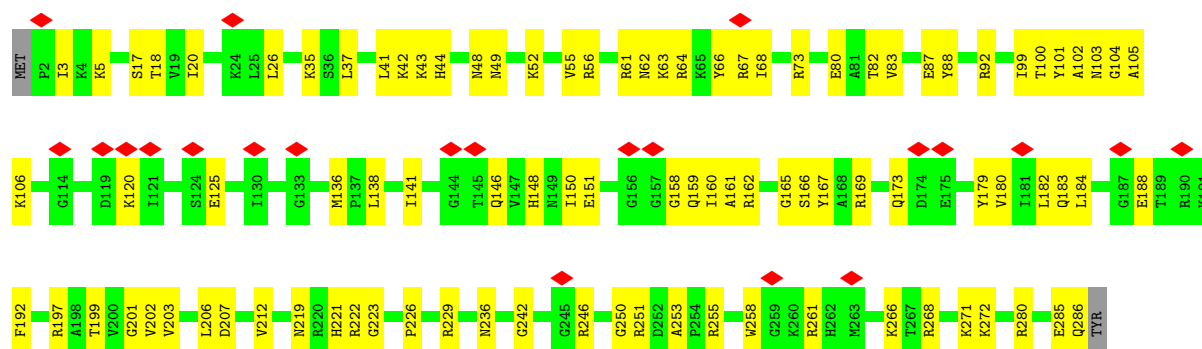


- Molecule 24: 30S ribosomal protein S21

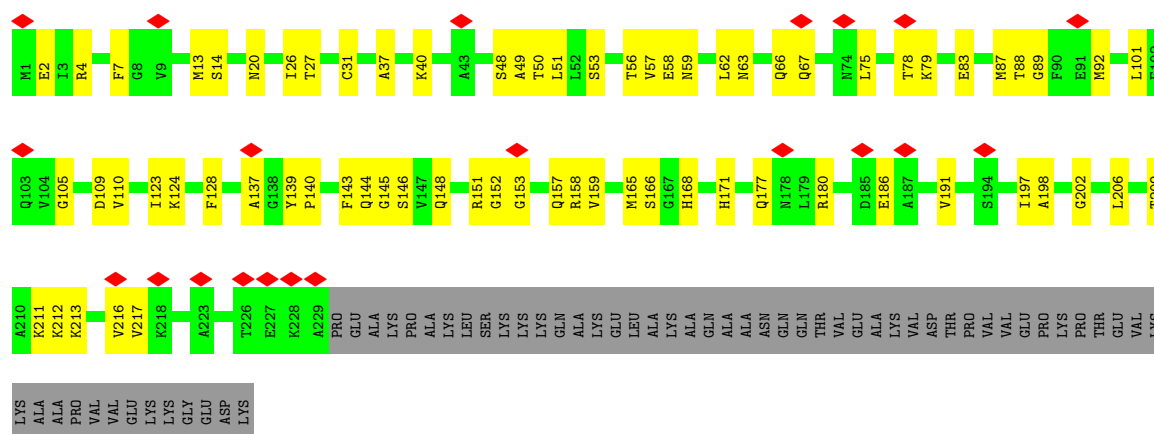


- Molecule 25: 50S ribosomal protein L2

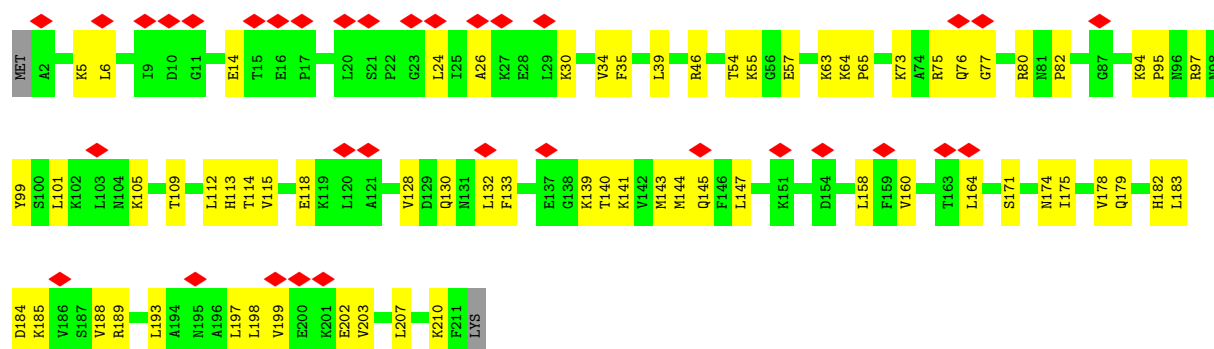




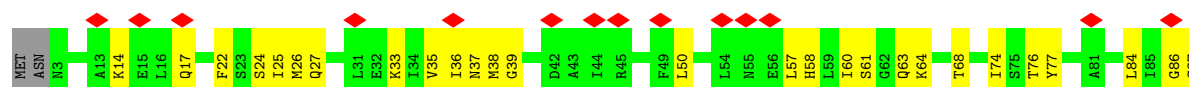
• Molecule 26: 50S ribosomal protein L3

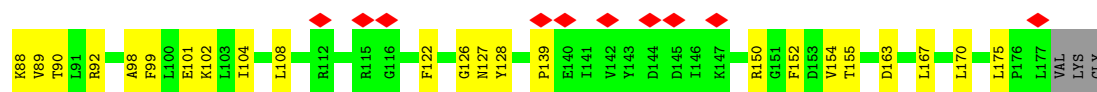


• Molecule 27: 50S ribosomal protein L4

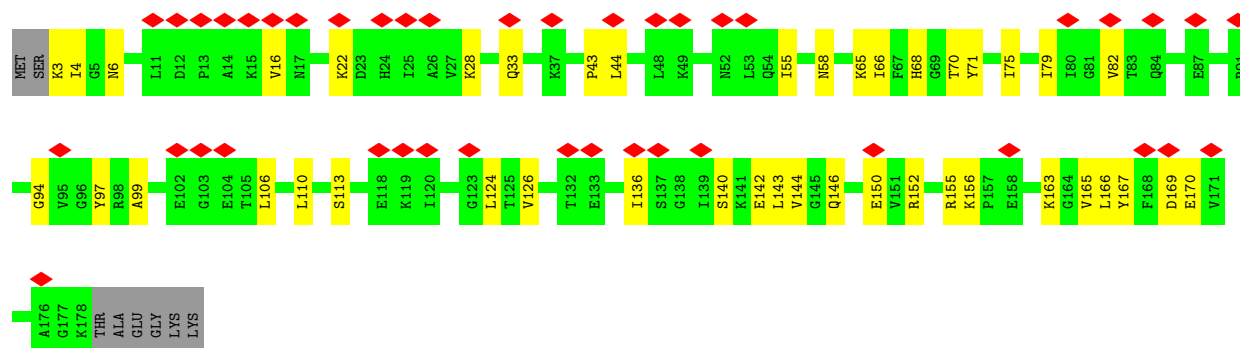
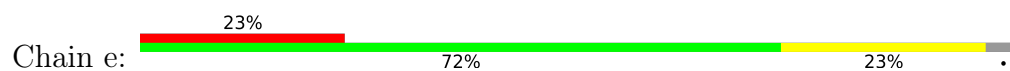


• Molecule 28: 50S ribosomal protein L5

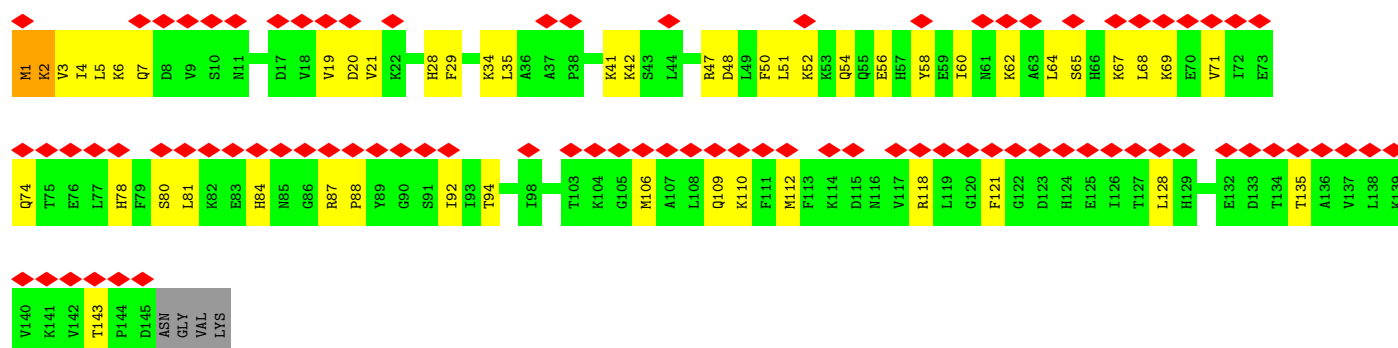




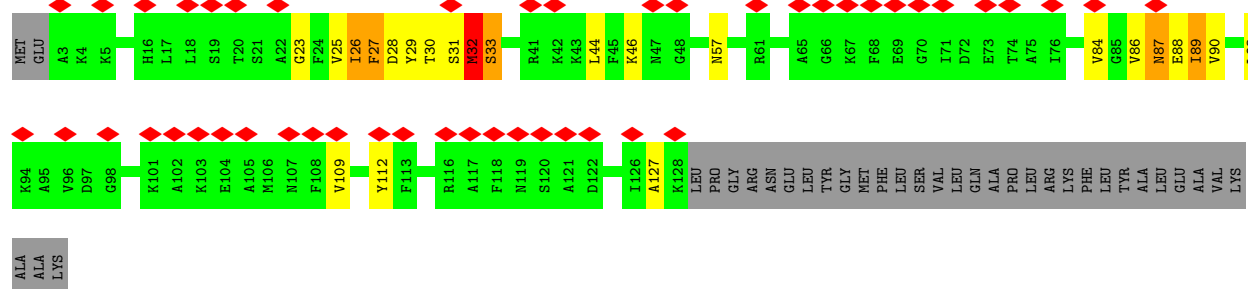
• Molecule 29: 50S ribosomal protein L6



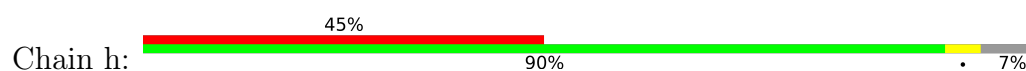
• Molecule 30: 50S ribosomal protein L9

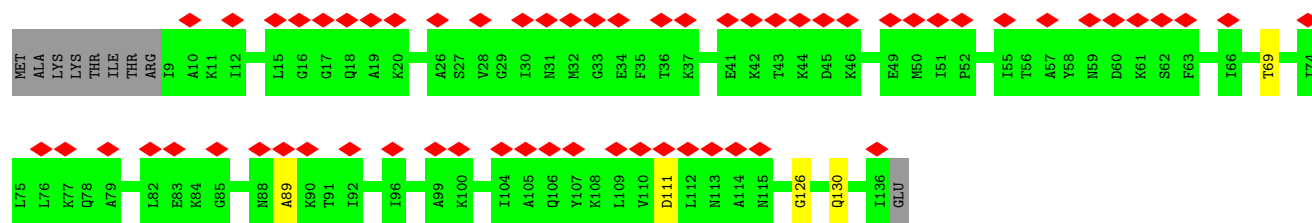


• Molecule 31: 50S ribosomal protein L10

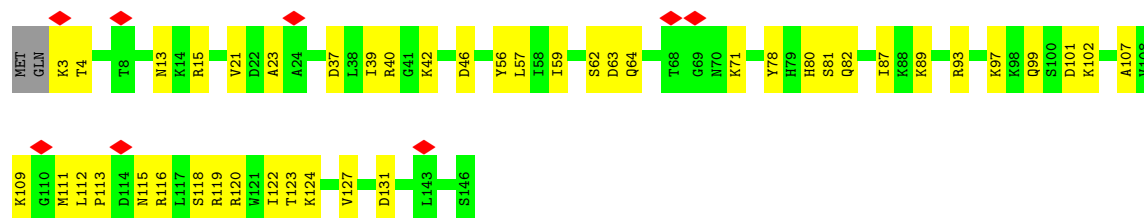


• Molecule 32: 50S ribosomal protein L11

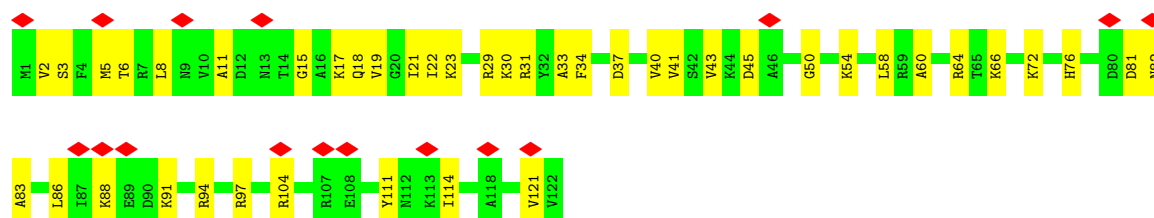




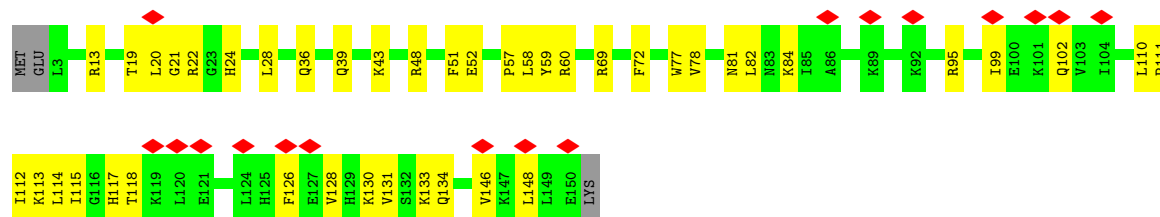
• Molecule 33: 50S ribosomal protein L13



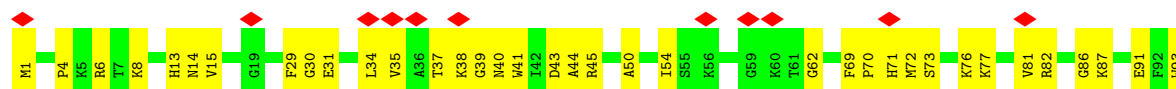
• Molecule 34: 50S ribosomal protein L14



• Molecule 35: 50S ribosomal protein L15

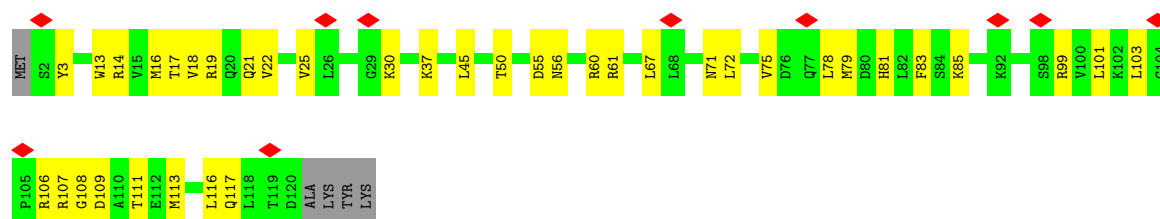


• Molecule 36: 50S ribosomal protein L16

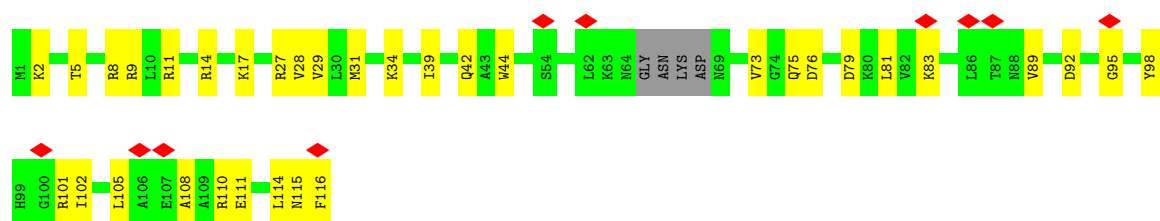




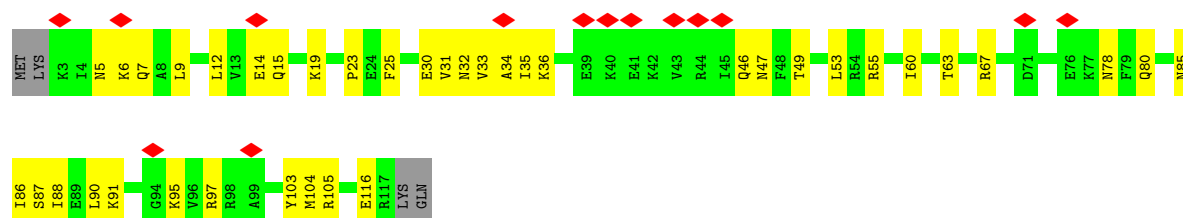
- Molecule 37: 50S ribosomal protein L17



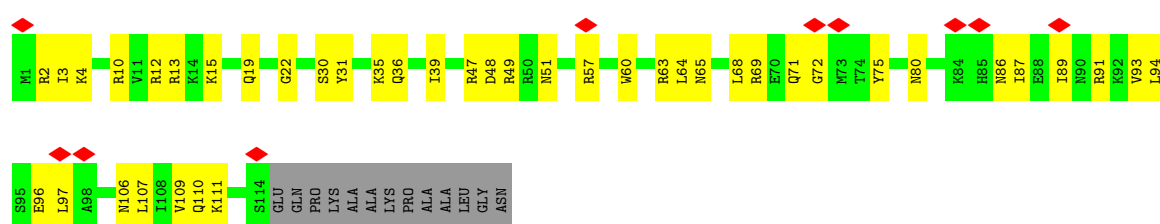
- Molecule 38: 50S ribosomal protein L18



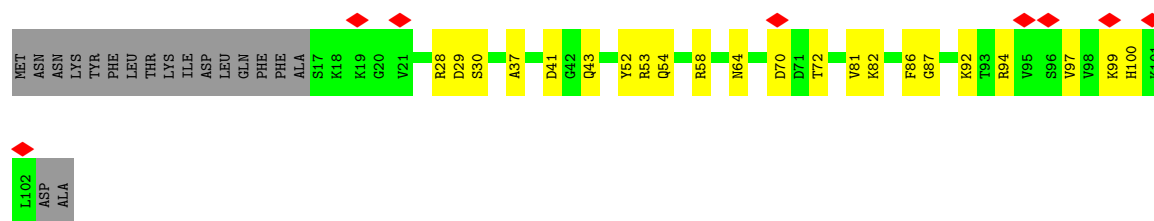
- Molecule 39: 50S ribosomal protein L19



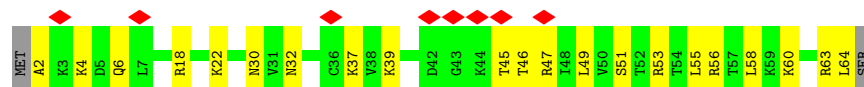
- Molecule 40: 50S ribosomal protein L20



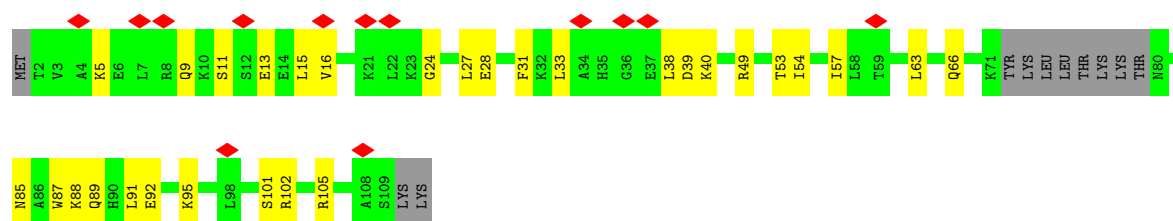
- Molecule 41: 50S ribosomal protein L21



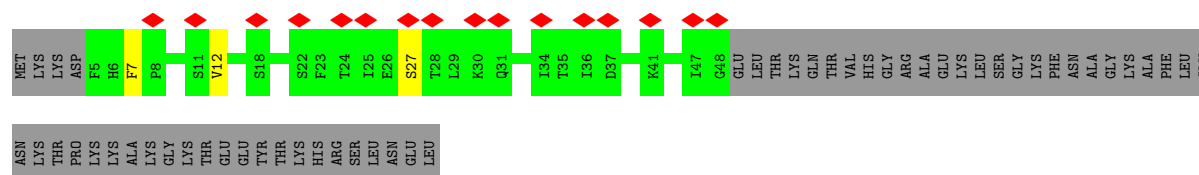
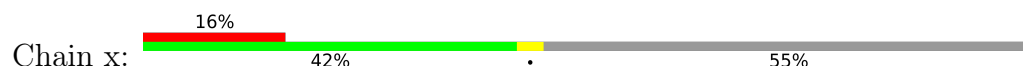
- Molecule 46: 50S ribosomal protein L28



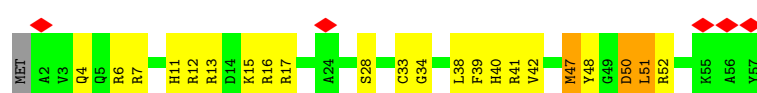
- Molecule 47: 50S ribosomal protein L29



- Molecule 48: 50S ribosomal protein L31

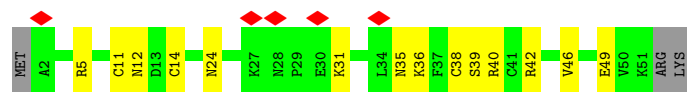


- Molecule 49: 50S ribosomal protein L32



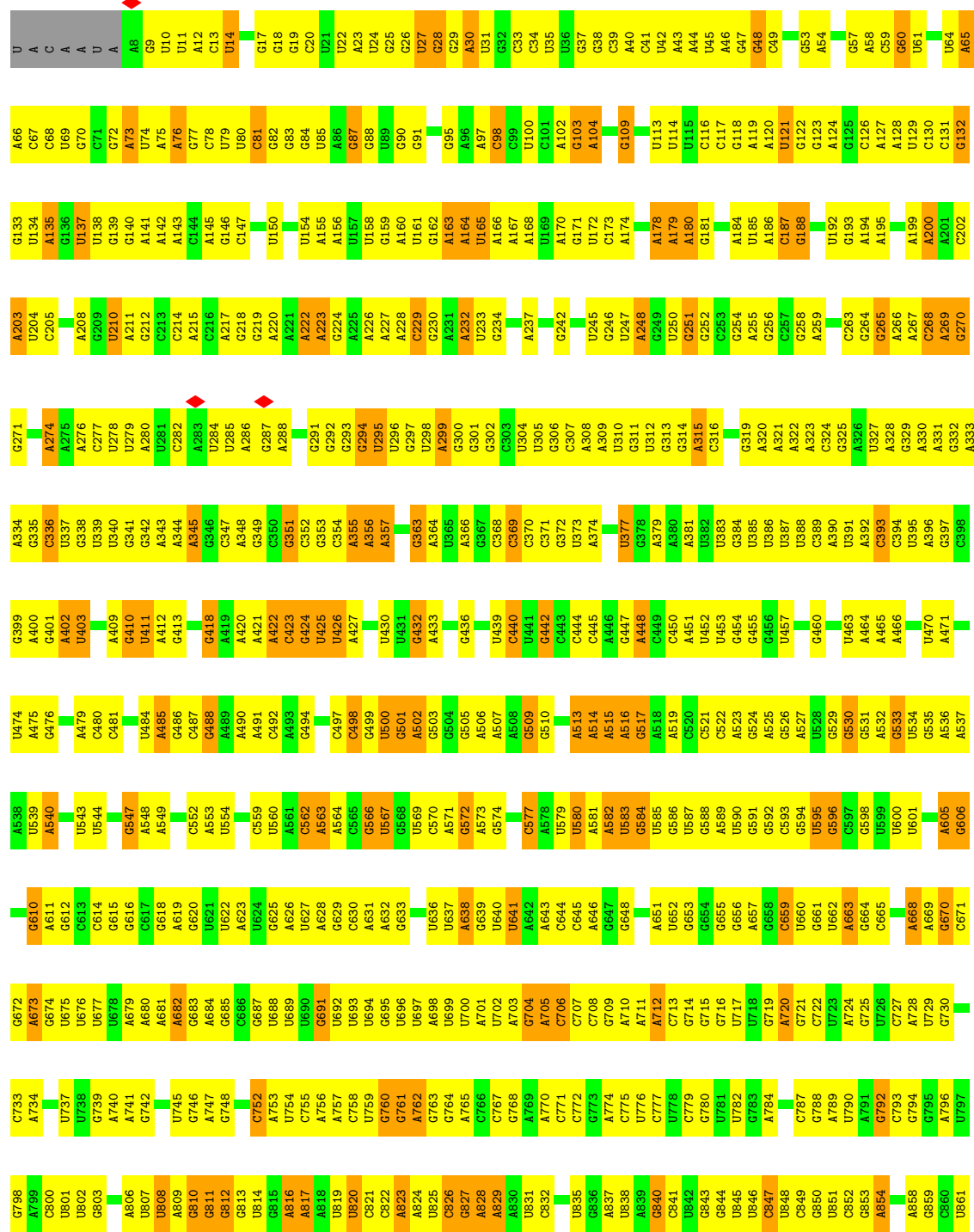
- Molecule 50: 50S ribosomal protein L33 1





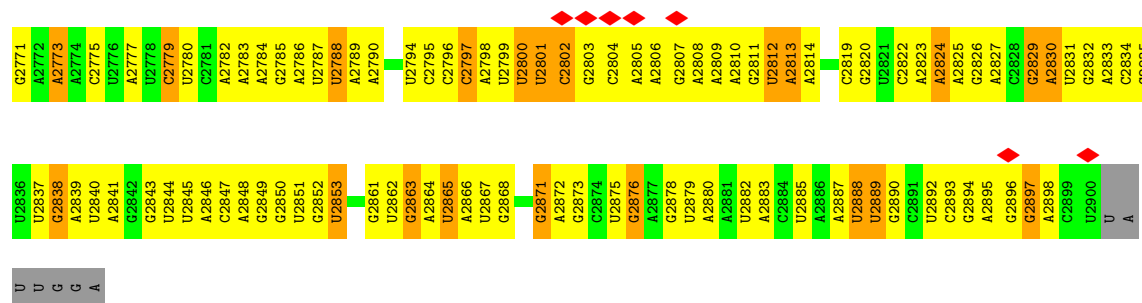
• Molecule 51: 23S ribosomal RNA

Chain 3: 28% 55% 16%



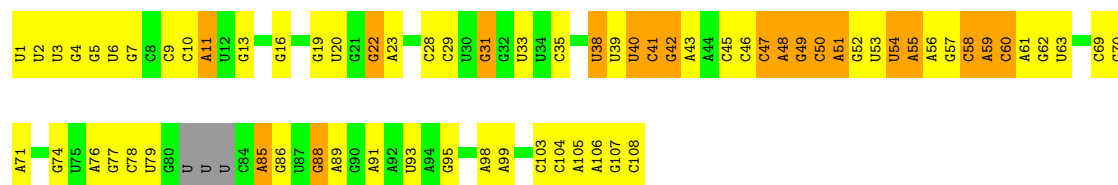
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G1738	G1663	A1596	U1529	U1464	A1396	A1266	G1198	A1132	G1069	U1004	U864
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C1742	G1668	U1599	U1533	U1468	A1401	C1270	A1202	A1138	A1072	A1008	G867
C1743	A1600	C1599	A1534	C1469	G1402	A1271	A1202	C1139	A1073	A1009	C968
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U1748	U1673	U1539	G1408	C1475	G1408	U1286	U1209	U1144	U1079	A1016	A876
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G2225	U2226	U2227	U2228	U2229	U2230	U2231	U2232	U2233	U2234	U2235	U2238	U2239	U2240	U2241	U2242	A2241	U2243	U2244	U2245	U2246	U2247	U2248	U2249	U2250	U2251	U2252	U2253	U2254	U2255	U2256	U2257	U2258	U2259	U2260	U2262	U2263	U2264	U2265	U2266	U2269	U2272	U2273	U2274	U2275	U2276	U2277	U2281	U2282	U2283	U2286	U2287	U2288	U2289	U2290	U2291	U2292	U2293	U2294	U2295	U2296								
G2161	U2162	U2163	U2164	U2165	U2166	U2167	U2168	U2169	U2170	U2171	U2172	U2173	U2174	U2175	U2176	U2177	U2178	U2179	U2180	U2181	U2182	U2183	U2184	U2185	U2186	U2187	U2188	U2189	U2190	U2191	U2192	U2193	U2194	U2195	U2196	U2197	U2198	U2199	U2200	U2201	U2202	U2203	U2206	U2207	U2208	U2209	U2210	U2211	U2212	U2216	U2217	U2218	U2219	U2220	U2221	U2222	U2223	U2224										
U2096	U2097	U2098	U2099	U2100	U2101	U2102	U2103	U2104	U2105	U2106	U2107	U2108	U2109	U2110	U2111	U2112	U2113	U2114	U2115	U2116	U2117	U2118	U2119	U2121	U2122	U2123	U2124	U2125	U2126	U2127	U2130	U2131	U2132	U2133	U2134	U2135	U2138	U2139	U2140	U2141	U2142	U2143	U2144	U2145	U2146	U2147	U2148	U2149	U2150	U2151	U2152	U2153	U2154	U2155	U2156	U2157	U2160											
A1945	U1946	U1947	C1948	U1949	U1950	U1951	U1952	U1953	U1954	U1955	U1956	U1957	U1958	U1959	U1960	U1961	U1962	U1963	U1964	U1965	U1966	U1969	U1970	U1971	U1972	U1973	U1974	U1975	U1976	U1977	U1978	U1979	U1989	U1990	U1991	U1994	U1995	U1996	U1997	U1998	U1999	U2000	U2001	U2002	U2003	U2007	U2008	U2009	U2010	U2011	U2012	U2013	U2014	U2015	U2016	U2017	U2018	U2019	U2020									
A2020	A2021	U2022	U2023	U2024	U2025	U2026	U2027	U2028	U2029	U2030	U2031	U2032	U2033	U2034	U2035	U2036	U2037	U2038	U2039	U2040	U2041	U2047	U2048	U2049	U2050	U2054	U2055	U2056	U2057	U2058	U2059	U2062	U2063	U2064	U2065	U2066	U2067	U2068	U2069	U2070	U2071	U2072	U2073	U2074	U2075	U2076	U2077	U2081	U2082	U2083	U2091	U2092	U2093	U2094	U2095													
U1801	C1802	U1803	A1804	U1805	U1806	C1807	U1808	U1809	U1810	U1811	U1812	U1813	U1814	U1815	U1816	U1817	U1818	U1819	U1820	U1821	U1822	U1823	U1824	U1825	U1826	U1827	U1828	U1829	U1830	U1831	U1832	U1833	U1834	U1835	U1836	U1837	U1838	U1839	U1841	U1842	U1843	U1844	U1845	U1846	U1847	U1848	U1849	U1850	U1851	U1852	U1853	U1854	U1861	U1862	U1863	U1865	U1866	U1867	U1868	U1869								
G1870	A1871	A1872	U1873	U1874	U1875	U1876	U1877	U1878	U1879	U1880	U1881	U1882	U1883	U1884	U1885	U1886	U1887	U1888	U1889	U1890	U1891	U1892	U1893	U1894	U1895	U1896	U1897	U1898	U1899	U1900	U1901	U1902	U1903	U1906	U1907	U1908	U1909	U1910	U1911	U1912	U1913	U1914	U1915	U1916	U1917	U1918	U1919	U1920	U1921	U1922	U1923	U1924	U1925	U1926	U1927	U1930	U1931	U1932	U1933	U1934	U1935	U1936	U1937	U1938	U1939	U1942	U1943	U1944



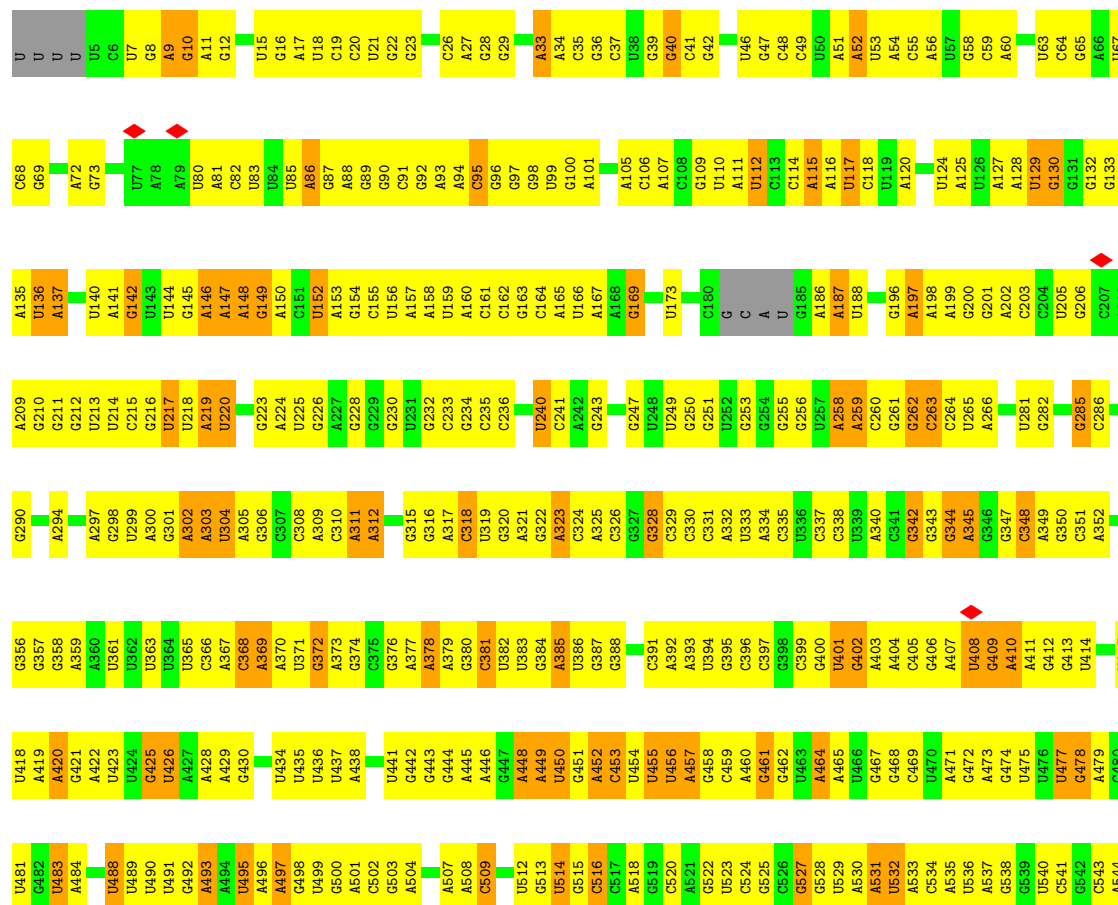
• Molecule 52: 5S ribosomal RNA

Chain 4: 33% 46% 18%



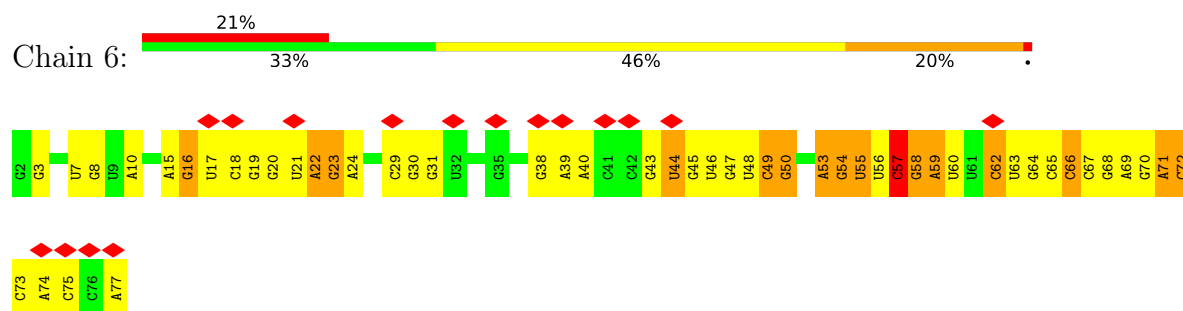
• Molecule 53: 16S ribosomal RNA

Chain 5: 28% 57% 13%

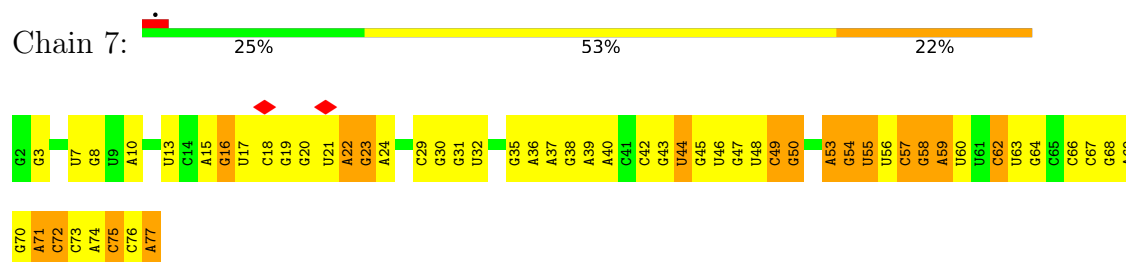




● Molecule 54: tRNA-Phe



● Molecule 54: tRNA-Phe



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	2239	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 ($e^-/\text{\AA}^2$)	3.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.410	Depositor
Minimum map value	-1.114	Depositor
Average map value	0.026	Depositor
Map value standard deviation	0.144	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	435.328, 435.328, 435.328	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.7005, 1.7005, 1.7005	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	0.14	0/383	0.43	0/504
2	1	0.14	0/484	0.43	0/637
3	2	0.16	0/306	0.41	0/401
4	9	0.15	0/3071	0.42	0/4147
5	A	0.14	0/1954	0.39	0/2642
6	B	0.15	0/1721	0.44	0/2323
7	C	0.14	0/1691	0.42	0/2267
8	D	0.14	0/1188	0.42	0/1593
9	E	0.14	0/1384	0.40	0/1867
10	F	0.14	0/1266	0.44	0/1700
11	G	0.21	0/1126	0.49	1/1517 (0.1%)
12	H	0.15	0/1044	0.41	0/1395
13	I	0.15	0/820	0.49	0/1103
14	J	0.16	0/844	0.39	0/1136
15	K	0.26	0/1094	0.55	0/1468
16	L	2.18	8/962 (0.8%)	0.83	3/1289 (0.2%)
17	M	0.14	0/483	0.44	0/643
18	N	0.12	0/679	0.39	0/907
19	O	0.15	0/659	0.48	0/885
20	P	0.15	0/684	0.43	0/913
21	Q	0.14	0/545	0.41	0/730
22	R	0.21	0/698	0.61	1/936 (0.1%)
23	S	0.13	0/631	0.41	0/838
24	T	0.12	0/475	0.41	0/621
25	a	0.15	0/2267	0.43	0/3044
26	b	0.14	0/1795	0.44	0/2412
27	c	0.14	0/1671	0.44	0/2246
28	d	0.14	0/1409	0.43	0/1894
29	e	0.14	0/1420	0.39	0/1912
30	f	0.16	0/1205	0.42	0/1616
31	g	0.40	0/969	0.75	1/1295 (0.1%)
32	h	0.17	0/968	0.45	0/1298
33	i	0.13	0/1186	0.38	0/1592
34	j	0.14	0/953	0.43	0/1275

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	k	0.12	0/1170	0.37	0/1559
36	l	0.15	0/1104	0.44	0/1481
37	m	0.15	0/973	0.44	0/1309
38	n	0.15	0/897	0.44	0/1198
39	o	0.13	0/948	0.41	0/1262
40	p	0.14	0/961	0.45	0/1278
41	q	0.15	0/828	0.43	0/1111
42	r	0.15	0/1077	0.44	0/1441
43	s	0.15	0/732	0.44	0/988
44	t	0.13	0/879	0.38	0/1165
45	u	0.14	0/665	0.42	0/884
46	v	0.13	0/519	0.37	0/695
47	w	0.13	0/826	0.35	0/1104
48	x	0.15	0/353	0.41	0/474
49	y	0.32	0/457	0.67	1/601 (0.2%)
50	z	0.14	0/412	0.43	0/547
51	3	0.22	6/69073 (0.0%)	0.25	0/107710
52	4	0.09	0/2505	0.23	0/3902
53	5	0.09	0/35768	0.23	0/55764
54	6	0.45	2/1808 (0.1%)	0.48	2/2817 (0.1%)
54	7	0.45	2/1808 (0.1%)	0.48	2/2817 (0.1%)
All	All	0.25	18/161798 (0.0%)	0.32	11/241153 (0.0%)

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	L	63	TYR	CD1-CE1	31.84	2.34	1.38
16	L	63	TYR	CD2-CE2	29.37	2.26	1.38
16	L	29	ARG	CD-NE	28.09	1.85	1.46
51	3	1130	A	N3-C4	24.29	1.83	1.34
51	3	1130	A	C6-N1	23.29	1.82	1.35

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	L	29	ARG	CD-NE-CZ	20.98	153.77	124.40
54	6	57	C	P-O5'-C5'	15.38	143.97	120.90
54	7	57	C	P-O5'-C5'	15.36	143.94	120.90
16	L	29	ARG	NE-CZ-NH2	12.53	130.48	119.20
22	R	26	GLU	N-CA-C	-7.37	95.11	110.80

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	380	0	429	22	0
2	1	477	0	530	15	0
3	2	304	0	350	17	0
4	9	3021	0	3050	89	0
5	A	1921	0	1973	41	0
6	B	1698	0	1768	55	0
7	C	1660	0	1719	63	0
8	D	1173	0	1267	47	0
9	E	1362	0	1377	35	0
10	F	1246	0	1308	46	0
11	G	1110	0	1226	47	0
12	H	1028	0	1094	42	0
13	I	809	0	894	27	0
14	J	829	0	855	27	0
15	K	1076	0	1170	53	0
16	L	951	0	1014	67	0
17	M	474	0	509	15	0
18	N	673	0	730	18	0
19	O	646	0	677	17	0
20	P	675	0	728	26	0
21	Q	535	0	562	14	0
22	R	682	0	691	16	0
23	S	629	0	681	19	0
24	T	471	0	522	11	0
25	a	2225	0	2301	79	0
26	b	1762	0	1808	65	0
27	c	1644	0	1731	51	0
28	d	1388	0	1469	41	0
29	e	1396	0	1481	35	0
30	f	1182	0	1228	43	0
31	g	960	0	1014	9	0
32	h	959	0	1039	4	0
33	i	1164	0	1192	37	0
34	j	944	0	1019	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	k	1153	0	1256	39	0
36	l	1079	0	1134	41	0
37	m	958	0	1011	26	0
38	n	889	0	952	32	0
39	o	938	0	1008	26	0
40	p	947	0	1028	45	0
41	q	811	0	858	27	0
42	r	1068	0	1150	35	0
43	s	720	0	803	19	0
44	t	872	0	972	26	0
45	u	657	0	695	14	0
46	v	513	0	560	20	0
47	w	818	0	870	22	0
48	x	344	0	333	2	0
49	y	452	0	472	25	0
50	z	408	0	440	10	0
51	3	61664	0	30954	1811	0
52	4	2239	0	1137	51	0
53	5	31943	0	16058	985	0
54	6	1618	0	821	72	0
54	7	1618	0	821	47	0
All	All	149163	0	102739	4132	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 18.

The worst 5 of 4132 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)
16:L:63:TYR:CD2	16:L:63:TYR:CG	1.79	1.69
51:3:1130:A:C5	51:3:1130:A:C6	1.82	1.63
16:L:63:TYR:CG	16:L:63:TYR:CD1	1.76	1.62
16:L:63:TYR:CE1	16:L:63:TYR:CZ	1.90	1.60
16:L:63:TYR:CZ	16:L:63:TYR:CE2	1.89	1.58

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	
1	0	45/48 (94%)	44 (98%)	1 (2%)	0	100	100
2	1	57/59 (97%)	55 (96%)	2 (4%)	0	100	100
3	2	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
4	9	391/394 (99%)	366 (94%)	25 (6%)	0	100	100
5	A	238/294 (81%)	223 (94%)	15 (6%)	0	100	100
6	B	213/273 (78%)	202 (95%)	11 (5%)	0	100	100
7	C	201/205 (98%)	193 (96%)	8 (4%)	0	100	100
8	D	151/219 (69%)	146 (97%)	5 (3%)	0	100	100
9	E	165/215 (77%)	149 (90%)	16 (10%)	0	100	100
10	F	152/155 (98%)	147 (97%)	5 (3%)	0	100	100
11	G	139/142 (98%)	128 (92%)	10 (7%)	1 (1%)	18	56
12	H	126/132 (96%)	115 (91%)	11 (9%)	0	100	100
13	I	99/108 (92%)	84 (85%)	15 (15%)	0	100	100
14	J	112/121 (93%)	109 (97%)	3 (3%)	0	100	100
15	K	134/139 (96%)	114 (85%)	19 (14%)	1 (1%)	18	56
16	L	116/124 (94%)	106 (91%)	10 (9%)	0	100	100
17	M	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
18	N	81/86 (94%)	79 (98%)	2 (2%)	0	100	100
19	O	78/94 (83%)	72 (92%)	6 (8%)	0	100	100
20	P	81/85 (95%)	78 (96%)	3 (4%)	0	100	100
21	Q	63/104 (61%)	57 (90%)	6 (10%)	0	100	100
22	R	82/87 (94%)	72 (88%)	10 (12%)	0	100	100
23	S	75/87 (86%)	73 (97%)	2 (3%)	0	100	100
24	T	51/60 (85%)	48 (94%)	3 (6%)	0	100	100
25	a	283/287 (99%)	264 (93%)	19 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	b	227/287 (79%)	214 (94%)	13 (6%)	0	100	100
27	c	208/212 (98%)	197 (95%)	11 (5%)	0	100	100
28	d	173/180 (96%)	161 (93%)	12 (7%)	0	100	100
29	e	174/184 (95%)	165 (95%)	9 (5%)	0	100	100
30	f	143/149 (96%)	131 (92%)	12 (8%)	0	100	100
31	g	124/161 (77%)	109 (88%)	11 (9%)	4 (3%)	3	21
32	h	126/137 (92%)	117 (93%)	9 (7%)	0	100	100
33	i	142/146 (97%)	132 (93%)	10 (7%)	0	100	100
34	j	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
35	k	146/151 (97%)	137 (94%)	9 (6%)	0	100	100
36	l	134/139 (96%)	125 (93%)	9 (7%)	0	100	100
37	m	117/124 (94%)	108 (92%)	9 (8%)	0	100	100
38	n	108/116 (93%)	101 (94%)	7 (6%)	0	100	100
39	o	113/119 (95%)	107 (95%)	6 (5%)	0	100	100
40	p	112/127 (88%)	109 (97%)	3 (3%)	0	100	100
41	q	97/100 (97%)	83 (86%)	14 (14%)	0	100	100
42	r	137/159 (86%)	130 (95%)	7 (5%)	0	100	100
43	s	90/237 (38%)	82 (91%)	8 (9%)	0	100	100
44	t	109/111 (98%)	104 (95%)	5 (5%)	0	100	100
45	u	84/104 (81%)	81 (96%)	3 (4%)	0	100	100
46	v	61/65 (94%)	58 (95%)	3 (5%)	0	100	100
47	w	96/111 (86%)	91 (95%)	5 (5%)	0	100	100
48	x	42/97 (43%)	39 (93%)	3 (7%)	0	100	100
49	y	54/57 (95%)	50 (93%)	4 (7%)	0	100	100
50	z	48/53 (91%)	45 (94%)	3 (6%)	0	100	100
All	All	6211/7064 (88%)	5803 (93%)	402 (6%)	6 (0%)	49	83

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	K	120	VAL
11	G	108	LEU
31	g	28	ASP

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Mol	Chain	Res	Type
31	g	87	ASN
31	g	32	MET

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	40/41 (98%)	40 (100%)	0	100	100
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	35 (100%)	0	100	100
4	9	324/325 (100%)	324 (100%)	0	100	100
5	A	212/262 (81%)	212 (100%)	0	100	100
6	B	180/232 (78%)	180 (100%)	0	100	100
7	C	181/183 (99%)	181 (100%)	0	100	100
8	D	123/178 (69%)	123 (100%)	0	100	100
9	E	150/196 (76%)	150 (100%)	0	100	100
10	F	131/132 (99%)	131 (100%)	0	100	100
11	G	123/124 (99%)	122 (99%)	1 (1%)	73	80
12	H	111/115 (96%)	111 (100%)	0	100	100
13	I	95/99 (96%)	95 (100%)	0	100	100
14	J	91/97 (94%)	91 (100%)	0	100	100
15	K	117/120 (98%)	114 (97%)	3 (3%)	40	61
16	L	100/105 (95%)	100 (100%)	0	100	100
17	M	47/48 (98%)	47 (100%)	0	100	100
18	N	76/78 (97%)	76 (100%)	0	100	100
19	O	69/82 (84%)	69 (100%)	0	100	100
20	P	73/75 (97%)	73 (100%)	0	100	100
21	Q	56/94 (60%)	56 (100%)	0	100	100
22	R	74/77 (96%)	72 (97%)	2 (3%)	39	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	S	70/77 (91%)	70 (100%)	0	100	100
24	T	49/56 (88%)	49 (100%)	0	100	100
25	a	241/243 (99%)	241 (100%)	0	100	100
26	b	186/233 (80%)	186 (100%)	0	100	100
27	c	182/184 (99%)	182 (100%)	0	100	100
28	d	150/154 (97%)	150 (100%)	0	100	100
29	e	153/159 (96%)	153 (100%)	0	100	100
30	f	131/134 (98%)	129 (98%)	2 (2%)	57	72
31	g	101/129 (78%)	92 (91%)	9 (9%)	9	28
32	h	102/110 (93%)	102 (100%)	0	100	100
33	i	126/128 (98%)	126 (100%)	0	100	100
34	j	103/103 (100%)	103 (100%)	0	100	100
35	k	123/126 (98%)	123 (100%)	0	100	100
36	l	113/115 (98%)	113 (100%)	0	100	100
37	m	105/109 (96%)	104 (99%)	1 (1%)	68	78
38	n	96/99 (97%)	96 (100%)	0	100	100
39	o	101/105 (96%)	101 (100%)	0	100	100
40	p	100/108 (93%)	100 (100%)	0	100	100
41	q	90/91 (99%)	90 (100%)	0	100	100
42	r	116/132 (88%)	116 (100%)	0	100	100
43	s	82/208 (39%)	82 (100%)	0	100	100
44	t	96/96 (100%)	96 (100%)	0	100	100
45	u	69/85 (81%)	69 (100%)	0	100	100
46	v	58/60 (97%)	58 (100%)	0	100	100
47	w	87/98 (89%)	87 (100%)	0	100	100
48	x	41/86 (48%)	41 (100%)	0	100	100
49	y	48/49 (98%)	44 (92%)	4 (8%)	10	30
50	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5425/6076 (89%)	5403 (100%)	22 (0%)	81	84

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
31	g	84	VAL
37	m	117	GLN
31	g	90	VAL
49	y	47	MET
30	f	1	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 76 such sidechains are listed below:

Mol	Chain	Res	Type
33	i	138	GLN
42	r	121	GLN
34	j	76	HIS
38	n	49	ASN
47	w	94	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	3	2875/2907 (98%)	779 (27%)	32 (1%)
52	4	103/108 (95%)	29 (28%)	4 (3%)
53	5	1490/1520 (98%)	341 (22%)	7 (0%)
54	6	75/76 (98%)	28 (37%)	5 (6%)
54	7	75/76 (98%)	28 (37%)	5 (6%)
All	All	4618/4687 (98%)	1205 (26%)	53 (1%)

5 of 1205 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
51	3	14	U
51	3	27	U
51	3	28	G
51	3	29	G
51	3	30	A

5 of 53 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
51	3	2604	U
52	4	59	A
54	7	18	C
51	3	2668	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
52	4	10	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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.

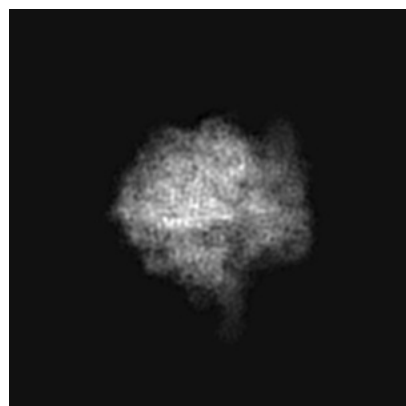
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13433. These allow visual inspection of the internal detail of the map and identification of artifacts.

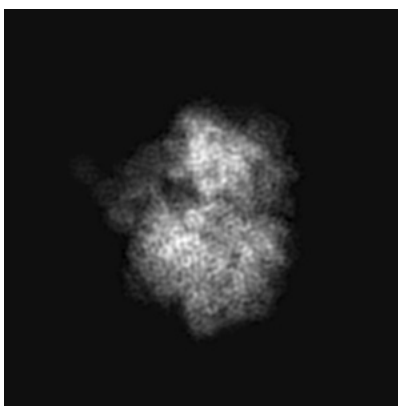
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

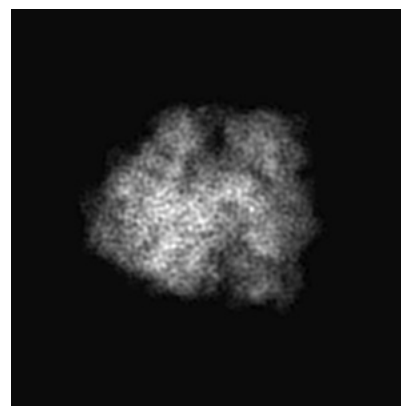
6.1.1 Primary map



X

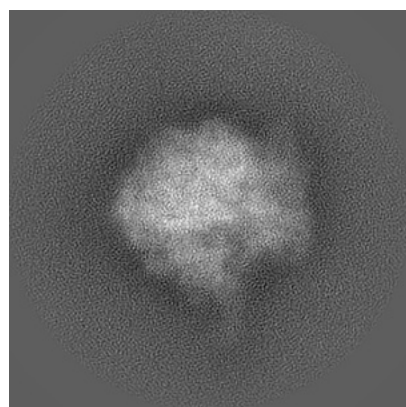


Y

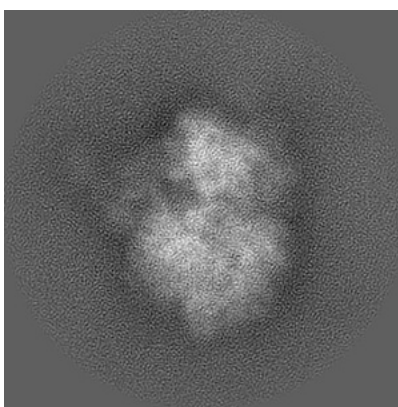


Z

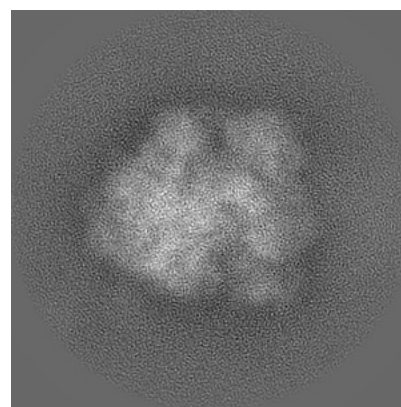
6.1.2 Raw map



X



Y

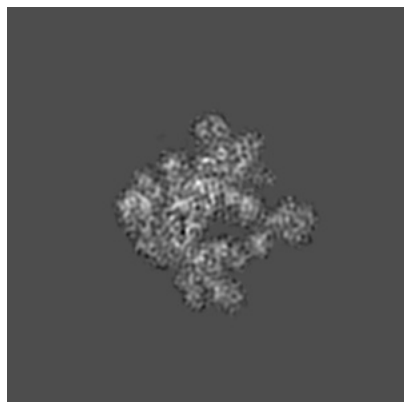


Z

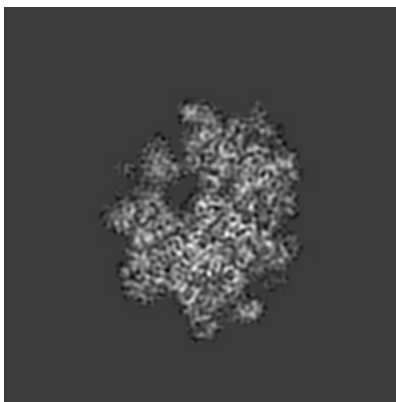
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

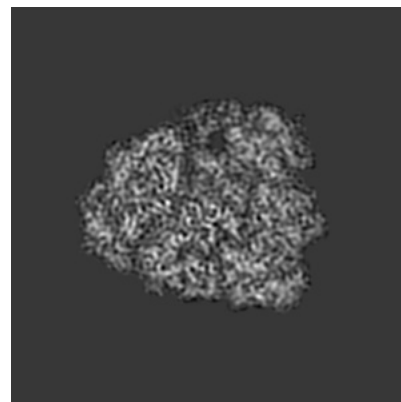
6.2.1 Primary map



X Index: 128

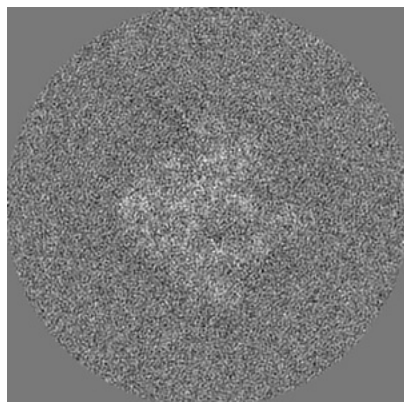


Y Index: 128

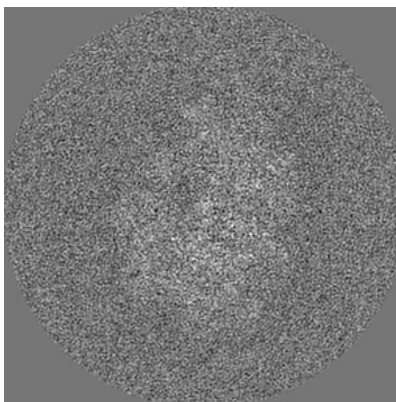


Z Index: 128

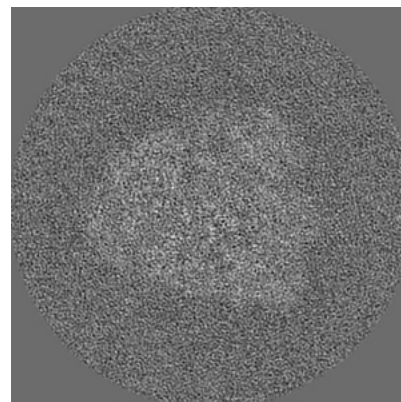
6.2.2 Raw map



X Index: 128



Y Index: 128

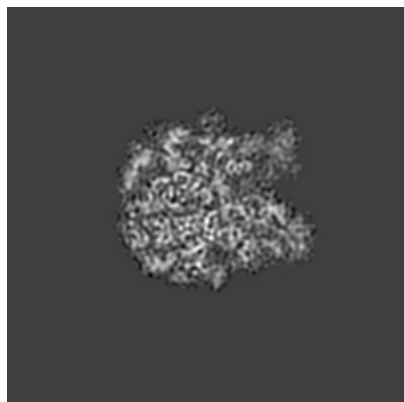


Z Index: 128

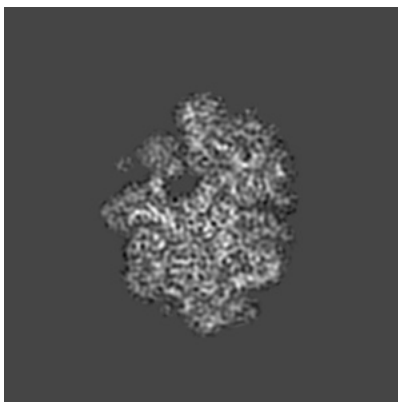
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

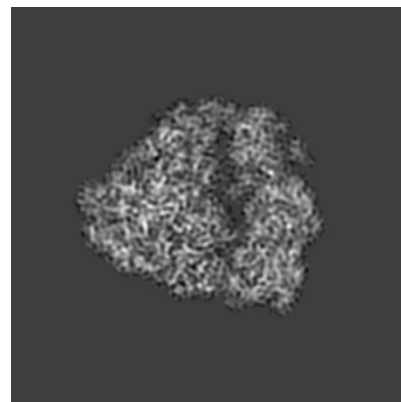
6.3.1 Primary map



X Index: 103

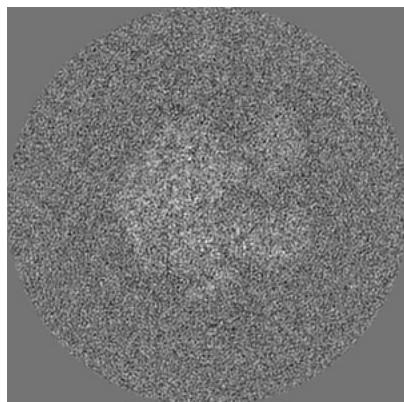


Y Index: 120

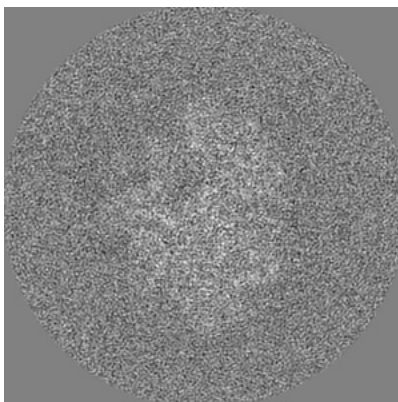


Z Index: 122

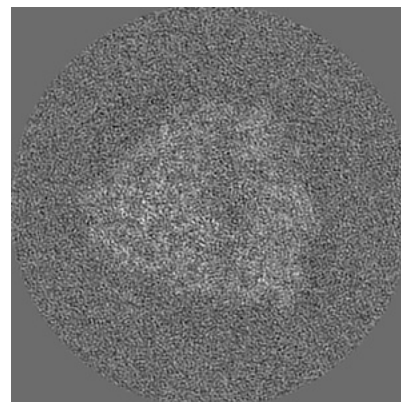
6.3.2 Raw map



X Index: 114



Y Index: 120

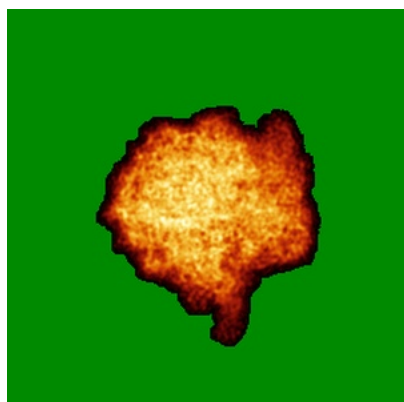


Z Index: 122

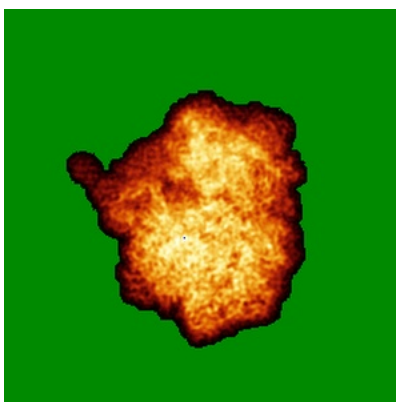
The images above show the largest variance slices of the map in three orthogonal directions.

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

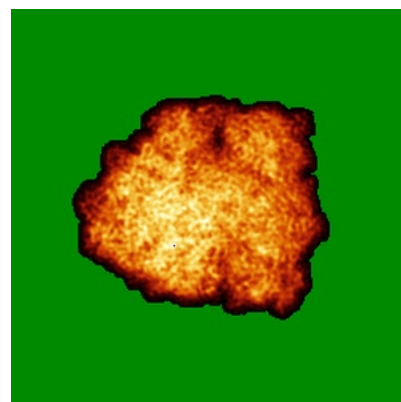
6.4.1 Primary map



X

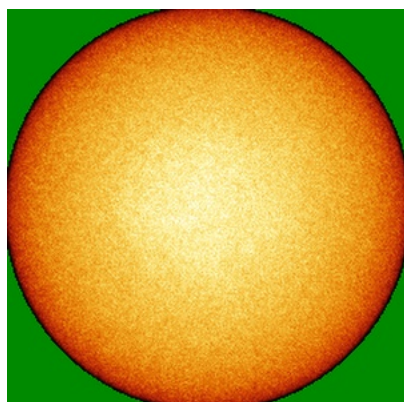


Y

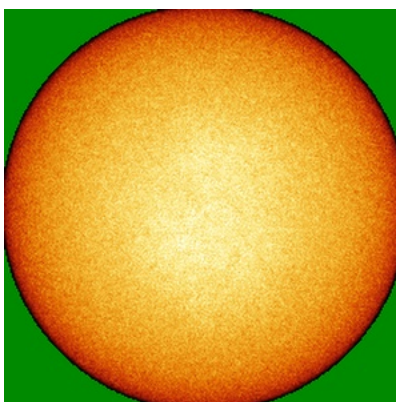


Z

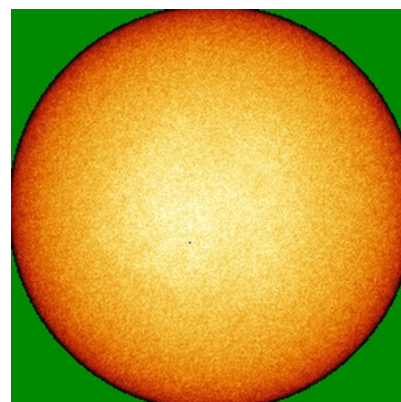
6.4.2 Raw map



X



Y



Z

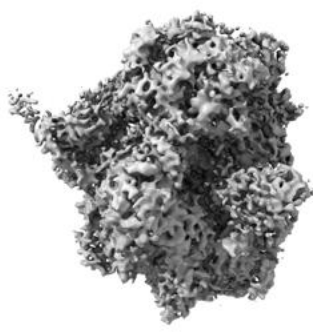
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

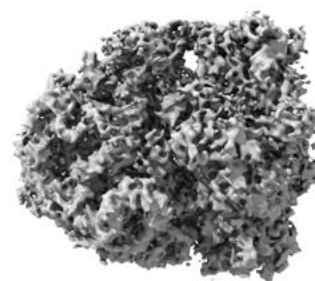
6.5.1 Primary map



X



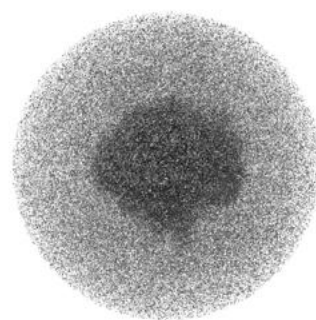
Y



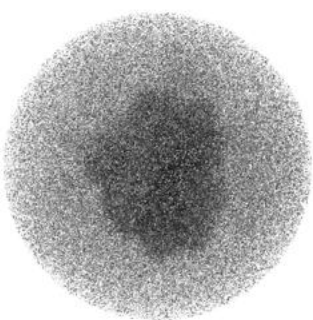
Z

The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

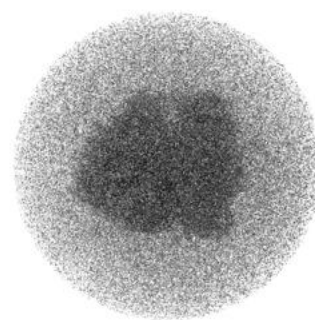
6.5.2 Raw map



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.

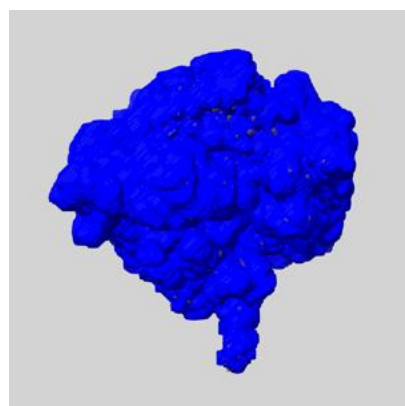
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

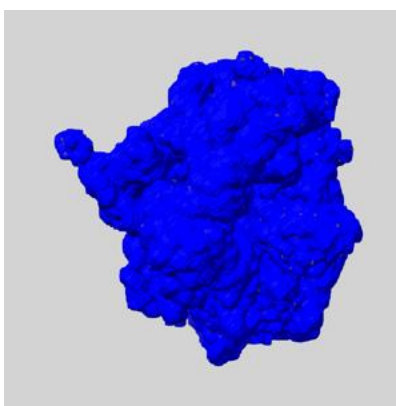
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

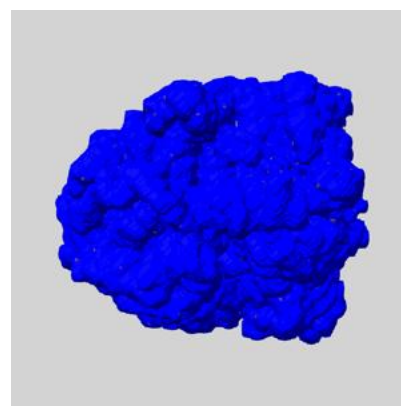
6.6.1 emd_13433_msk_1.map [i](#)



X



Y

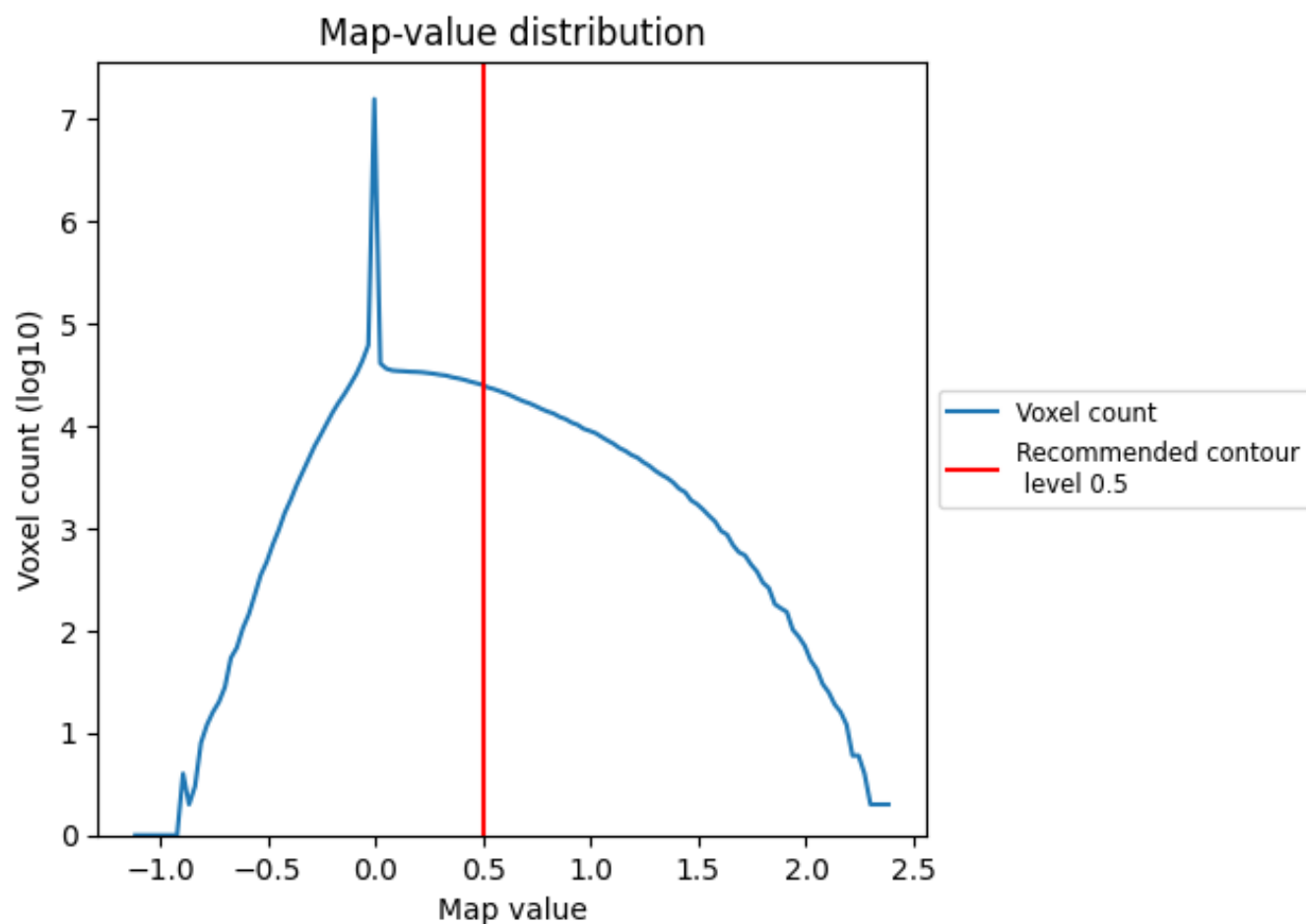


Z

7 Map analysis [i](#)

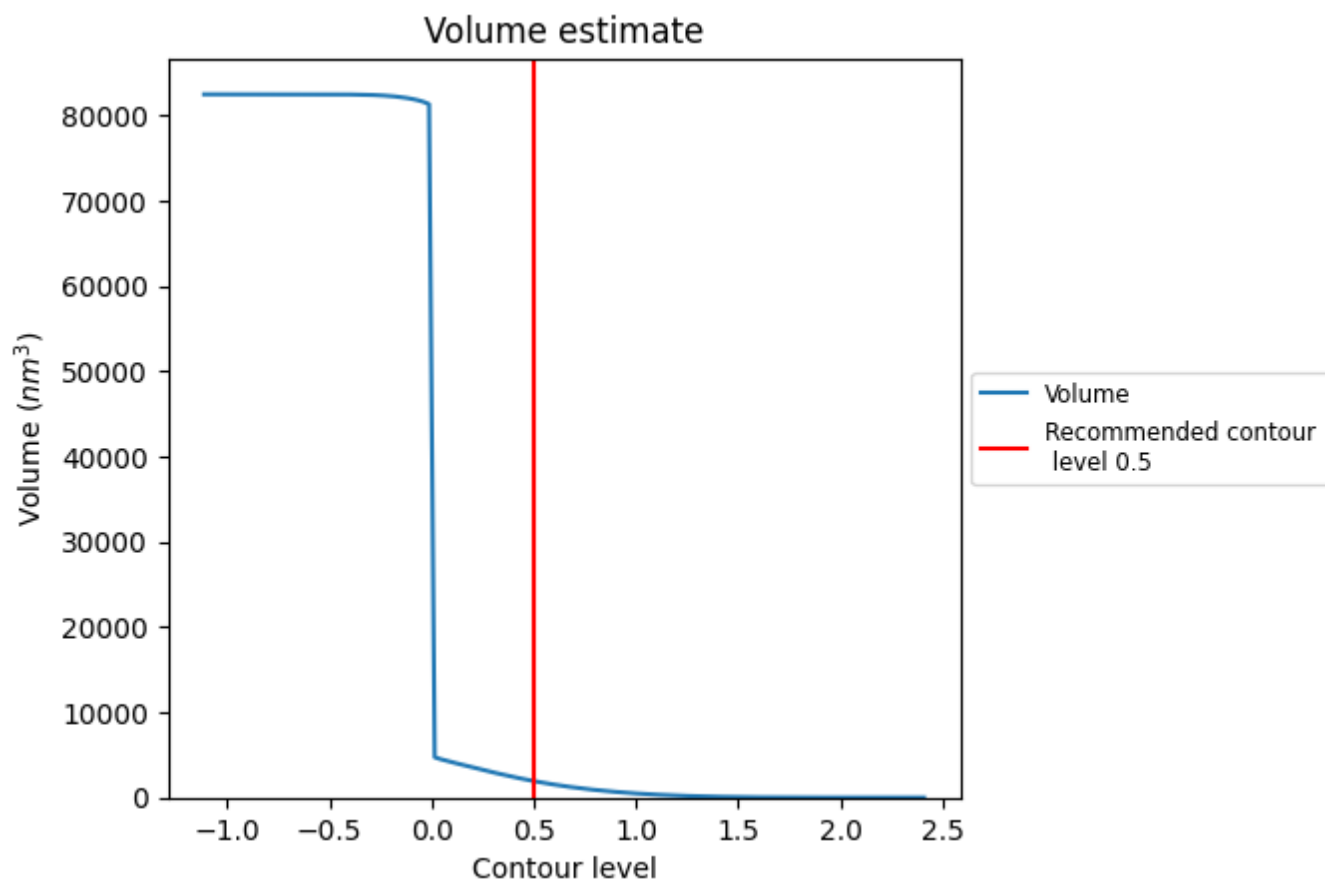
This section contains the results of statistical analysis of the map.

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.

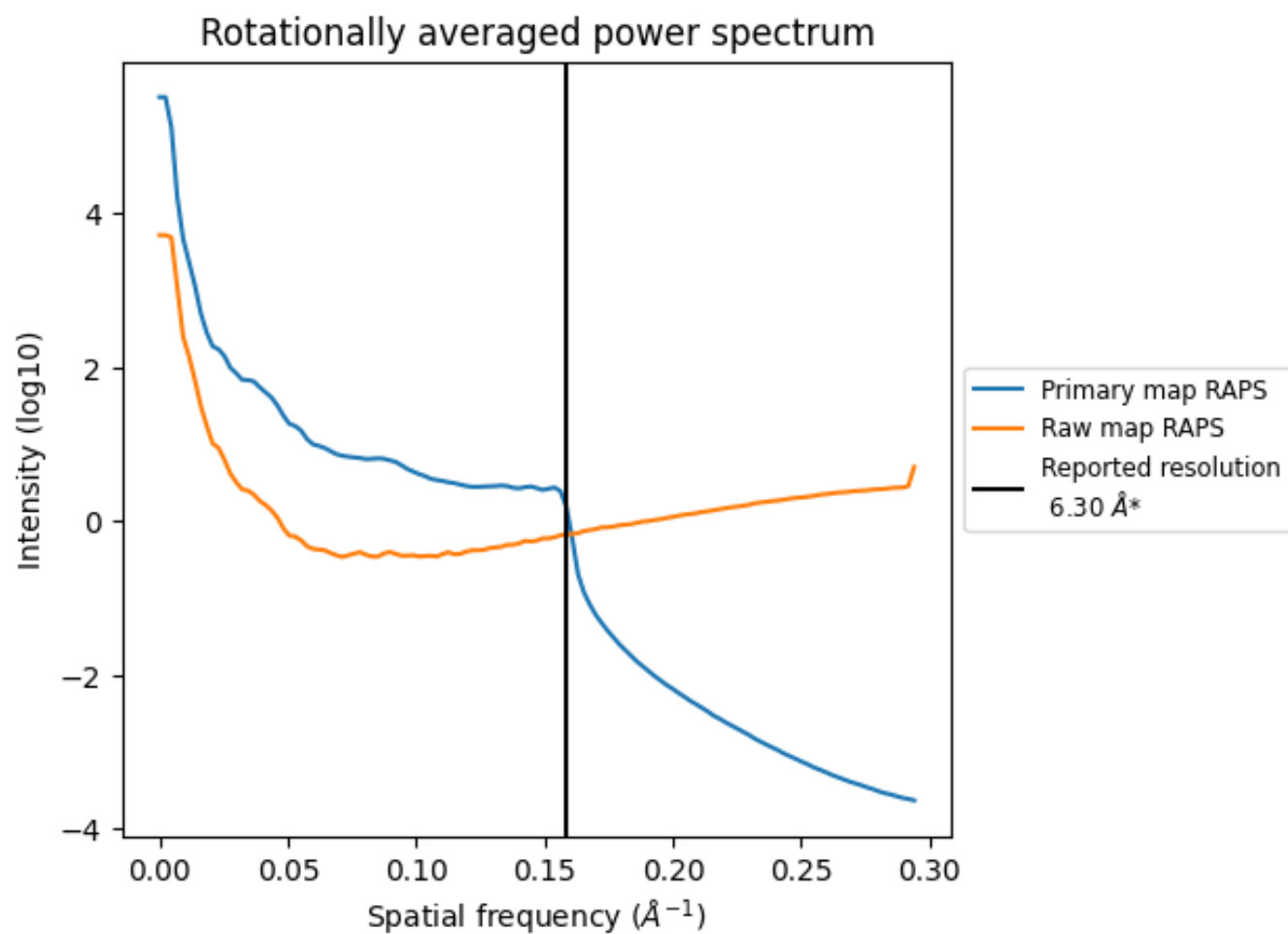
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1935 nm³; this corresponds to an approximate mass of 1748 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 ⓘ

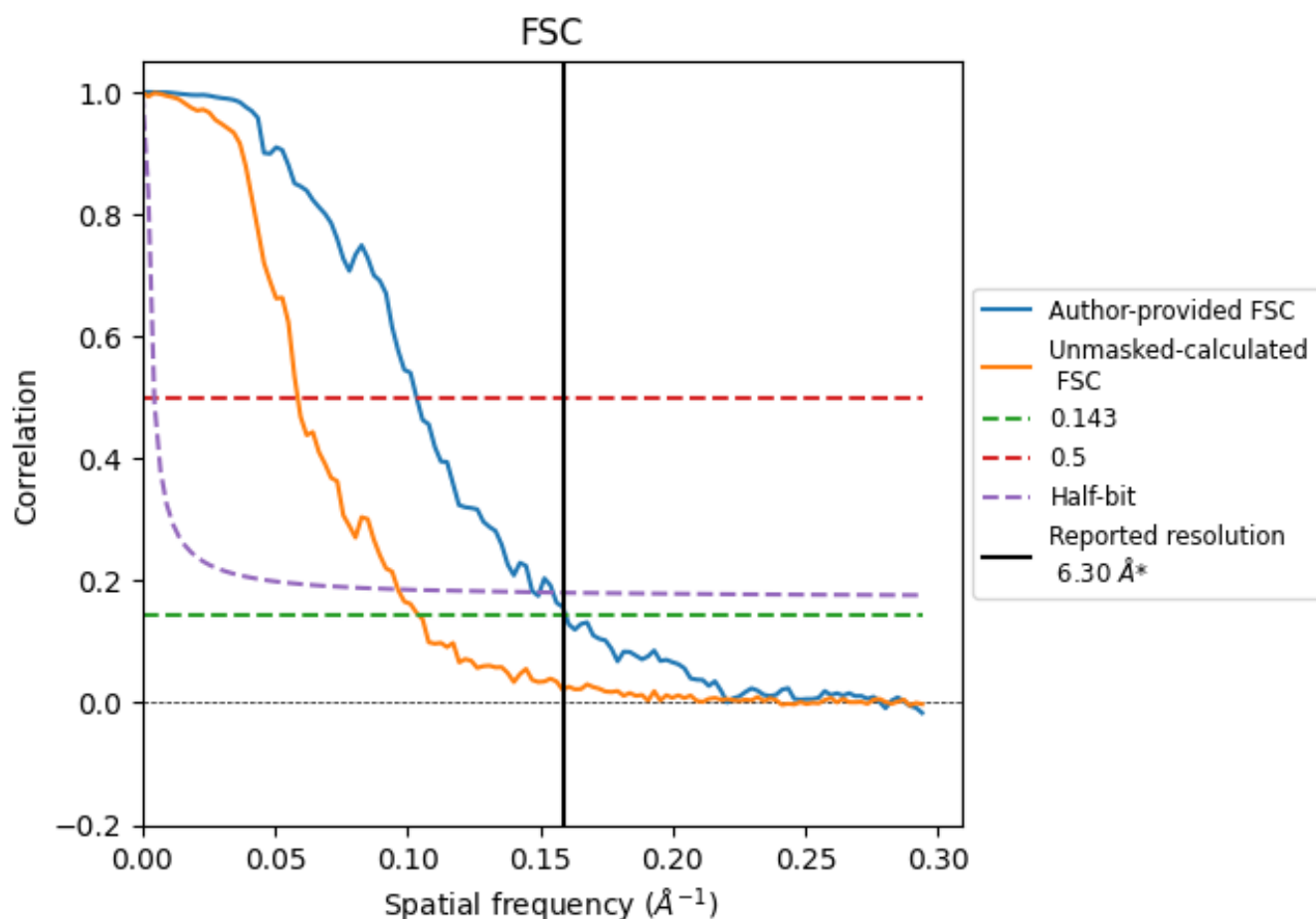


*Reported resolution corresponds to spatial frequency of 0.159 $\text{\AA}^{-1}$

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 0.159 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

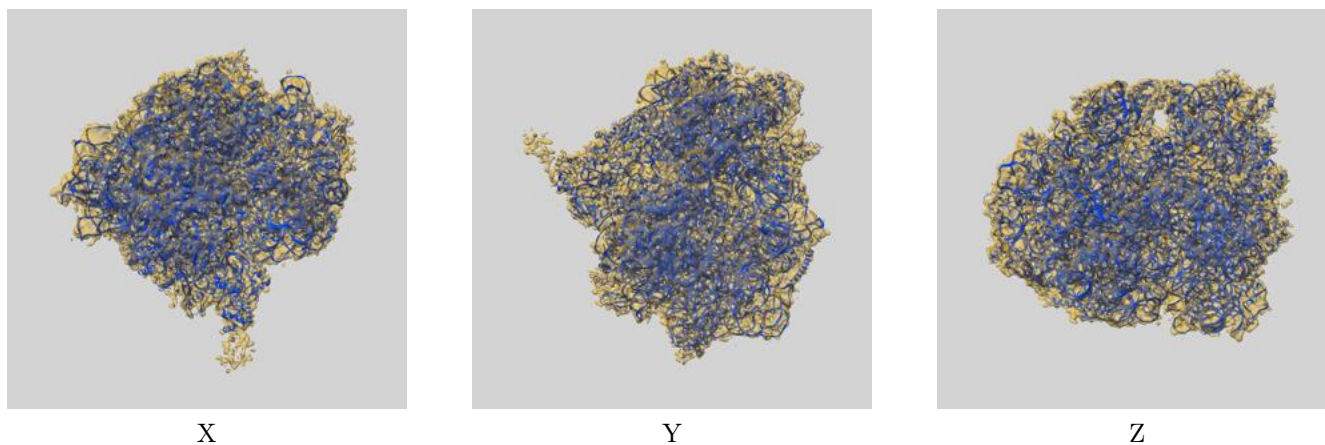
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.30	-	-
Author-provided FSC curve	6.27	9.67	6.77
Unmasked-calculated*	9.59	17.06	10.37

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 9.59 differs from the reported value 6.3 by more than 10 %

9 Map-model fit [i](#)

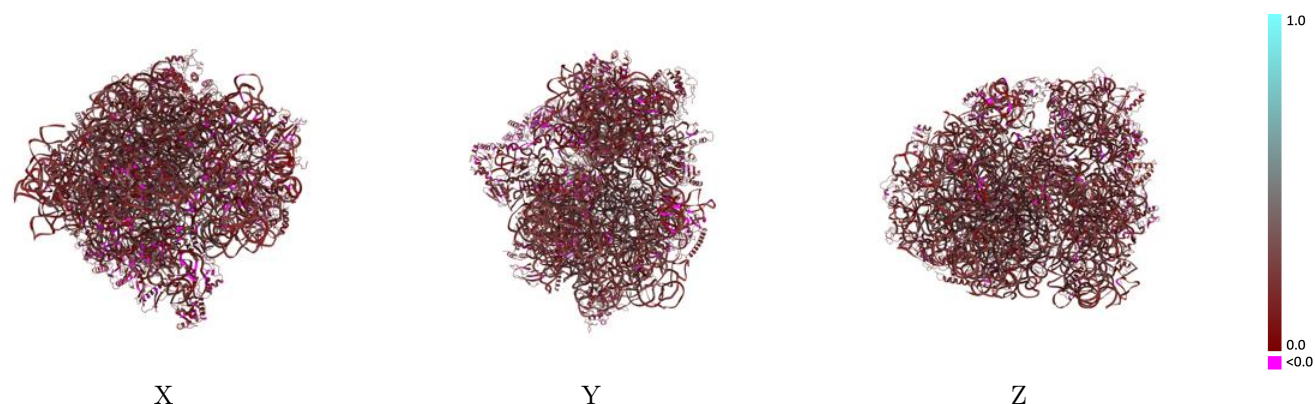
This section contains information regarding the fit between EMDB map EMD-13433 and PDB model 7PI9. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)



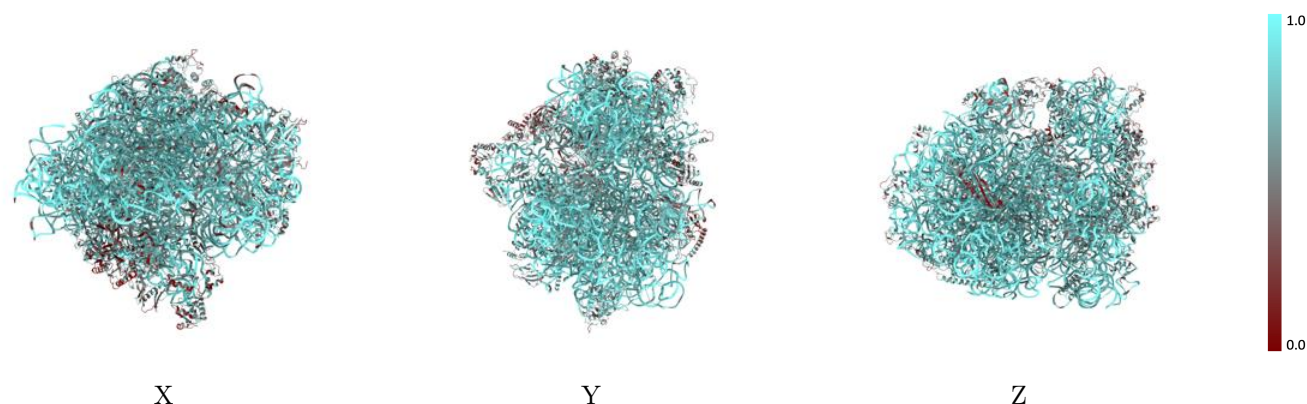
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



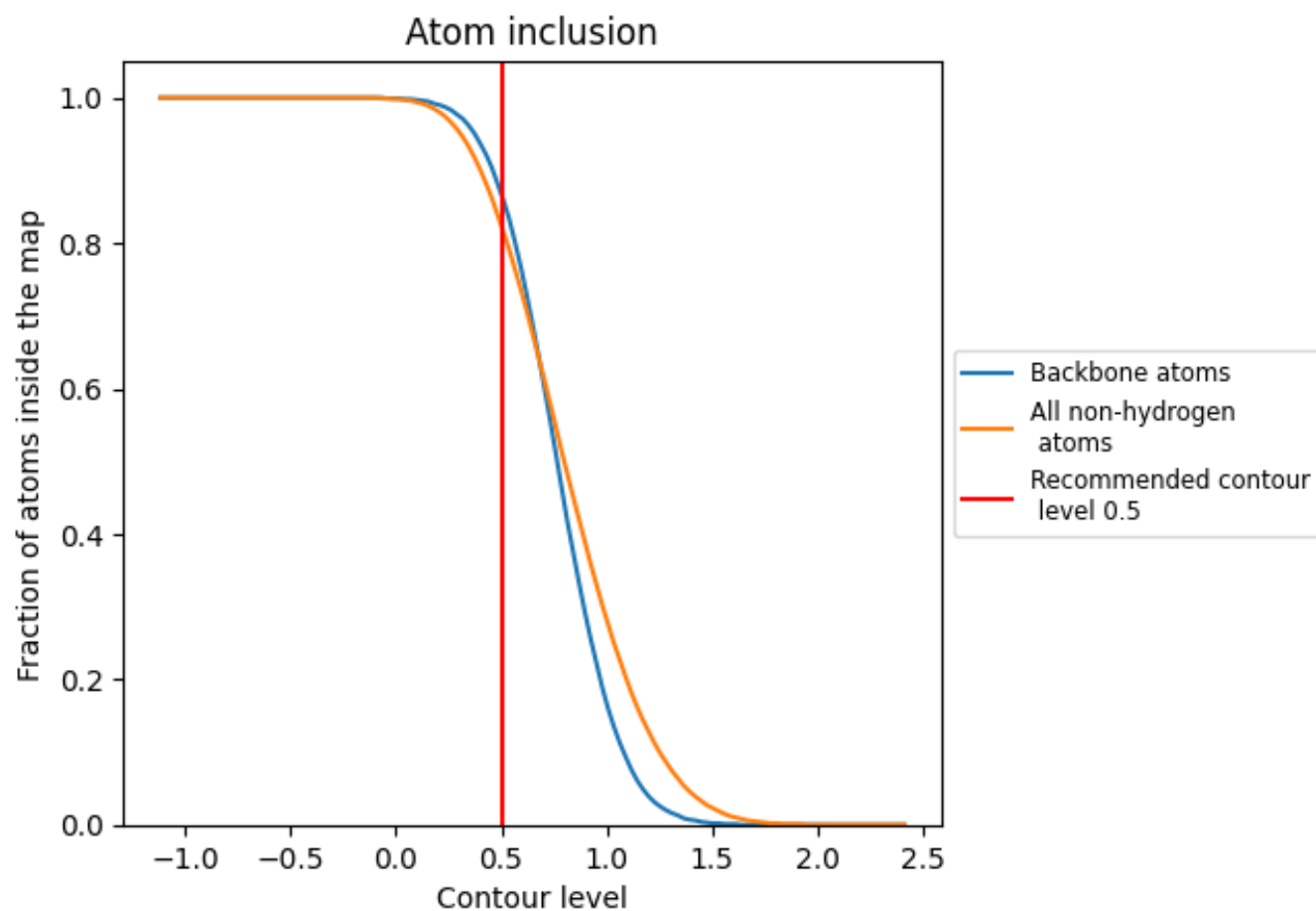
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 82% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8240	 0.2080
0	 0.7430	 0.1890
1	 0.7790	 0.2090
2	 0.7230	 0.2040
3	 0.9270	 0.2200
4	 0.9300	 0.2240
5	 0.9270	 0.2140
6	 0.5980	 0.0730
7	 0.8510	 0.1790
9	 0.3290	 0.1580
A	 0.5830	 0.1990
B	 0.6140	 0.1880
C	 0.6450	 0.1760
D	 0.6100	 0.1960
E	 0.5580	 0.2050
F	 0.6340	 0.1920
G	 0.6460	 0.1960
H	 0.6640	 0.1920
I	 0.5580	 0.1630
J	 0.6250	 0.1930
K	 0.6890	 0.1950
L	 0.6260	 0.1870
M	 0.6900	 0.1760
N	 0.6510	 0.2100
O	 0.7010	 0.1840
P	 0.6420	 0.2130
Q	 0.6720	 0.2110
R	 0.6390	 0.1570
S	 0.7230	 0.1790
T	 0.6740	 0.2060
a	 0.7280	 0.2080
b	 0.6880	 0.2020
c	 0.6670	 0.2000
d	 0.6470	 0.1920
e	 0.5760	 0.2020



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Chain	Atom inclusion	Q-score
f	 0.3440	 0.1760
g	 0.4950	 0.1680
h	 0.4340	 0.1800
i	 0.7390	 0.2140
j	 0.6590	 0.2150
k	 0.7080	 0.2230
l	 0.7280	 0.2160
m	 0.7210	 0.1910
n	 0.7090	 0.1950
o	 0.6640	 0.2180
p	 0.7060	 0.1790
q	 0.6810	 0.2150
r	 0.7420	 0.1890
s	 0.7380	 0.2160
t	 0.5900	 0.2030
u	 0.7470	 0.2150
v	 0.7150	 0.2090
w	 0.6800	 0.2080
x	 0.5390	 0.1930
y	 0.7510	 0.2000
z	 0.7050	 0.2020