



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 05:10 AM UTC

PDB ID : 7PI8 / pdb_00007pi8
EMDB ID : EMD-13432
Title : 70S ribosome with P-site tRNA in spectinomycin-treated *Mycoplasma pneumoniae* cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-08-19
Resolution : 8.90 Å (reported)
Based on initial models : 7OOC, 4V7C, 7OOD

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:

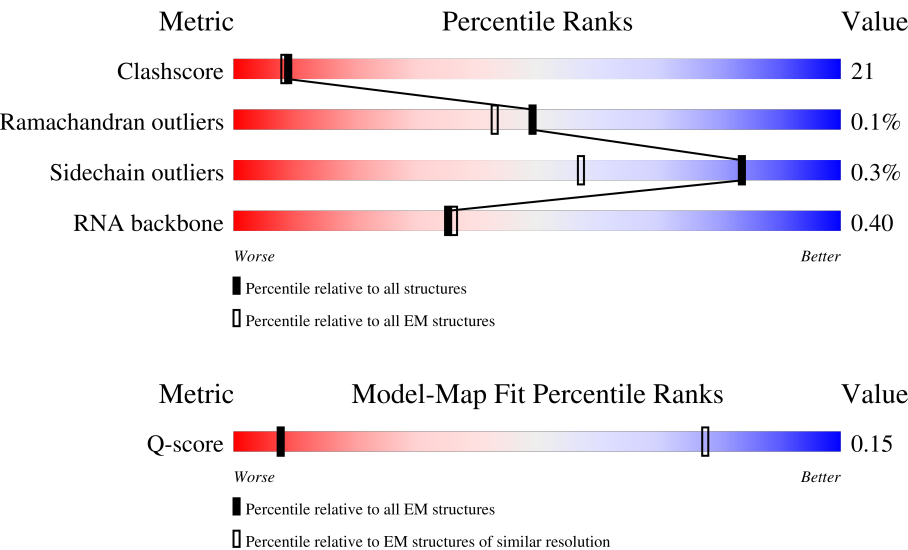
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 8.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	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	258 (8.40 - 9.40)

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	19% 73% 25% .
2	1	59	27% 64% 36%
3	2	37	8% 43% 57%

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Mol	Chain	Length	Quality of chain
4	A	294	
5	B	273	
6	C	205	
7	D	219	
8	E	215	
9	F	155	
10	G	142	
11	H	132	
12	I	108	
13	J	121	
14	K	139	
15	L	124	
16	M	61	
17	N	86	
18	O	94	
19	P	85	
20	Q	104	
21	R	87	
22	S	87	
23	T	60	
24	a	287	
25	b	287	
26	c	212	
27	d	180	
28	e	184	

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Mol	Chain	Length	Quality of chain
29	f	149	
30	g	161	
31	h	137	
32	i	146	
33	j	122	
34	k	151	
35	l	139	
36	m	124	
37	n	116	
38	o	119	
39	p	127	
40	q	100	
41	r	159	
42	s	237	
43	t	111	
44	u	104	
45	v	65	
46	w	111	
47	x	97	
48	y	57	
49	z	53	
50	3	2907	
51	4	108	
52	5	1520	
53	7	76	

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 144524 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 30S ribosomal protein S2.

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

- Molecule 5 is a protein called 30S ribosomal protein S3.

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

- Molecule 6 is a protein called 30S ribosomal protein S4.

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

- Molecule 7 is a protein called 30S ribosomal protein S5.

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

- Molecule 8 is a protein called 30S ribosomal protein S6.

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

- Molecule 9 is a protein called 30S ribosomal protein S7.

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

- Molecule 10 is a protein called 30S ribosomal protein S8.

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

- Molecule 11 is a protein called 30S ribosomal protein S9.

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

- Molecule 12 is a protein called 30S ribosomal protein S10.

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

- Molecule 13 is a protein called 30S ribosomal protein S11.

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

- Molecule 14 is a protein called 30S ribosomal protein S12.

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

- Molecule 15 is a protein called 30S ribosomal protein S13.

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

- Molecule 16 is a protein called 30S ribosomal protein S14 type Z.

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

- Molecule 17 is a protein called 30S ribosomal protein S15.

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

- Molecule 18 is a protein called 30S ribosomal protein S16.

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

- Molecule 19 is a protein called 30S ribosomal protein S17.

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

- Molecule 20 is a protein called 30S ribosomal protein S18.

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

- Molecule 21 is a protein called 30S ribosomal protein S19.

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

- Molecule 22 is a protein called 30S ribosomal protein S20.

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

- Molecule 23 is a protein called 30S ribosomal protein S21.

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

- Molecule 24 is a protein called 50S ribosomal protein L2.

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

- Molecule 25 is a protein called 50S ribosomal protein L3.

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

- Molecule 26 is a protein called 50S ribosomal protein L4.

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

- Molecule 27 is a protein called 50S ribosomal protein L5.

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

- Molecule 28 is a protein called 50S ribosomal protein L6.

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

- Molecule 29 is a protein called 50S ribosomal protein L9.

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

- Molecule 30 is a protein called 50S ribosomal protein L10.

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

- Molecule 31 is a protein called 50S ribosomal protein L11.

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

- Molecule 32 is a protein called 50S ribosomal protein L13.

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

- Molecule 33 is a protein called 50S ribosomal protein L14.

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

- Molecule 34 is a protein called 50S ribosomal protein L15.

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

- Molecule 35 is a protein called 50S ribosomal protein L16.

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

- Molecule 36 is a protein called 50S ribosomal protein L17.

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

- Molecule 37 is a protein called 50S ribosomal protein L18.

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

- Molecule 38 is a protein called 50S ribosomal protein L19.

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

- Molecule 39 is a protein called 50S ribosomal protein L20.

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

- Molecule 40 is a protein called 50S ribosomal protein L21.

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

- Molecule 41 is a protein called 50S ribosomal protein L22.

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

- Molecule 42 is a protein called 50S ribosomal protein L23.

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

- Molecule 43 is a protein called 50S ribosomal protein L24.

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

- Molecule 44 is a protein called 50S ribosomal protein L27.

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

- Molecule 45 is a protein called 50S ribosomal protein L28.

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

- Molecule 46 is a protein called 50S ribosomal protein L29.

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

- Molecule 47 is a protein called 50S ribosomal protein L31.

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

- Molecule 48 is a protein called 50S ribosomal protein L32.

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

- Molecule 49 is a protein called 50S ribosomal protein L33 1.

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

- Molecule 50 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

- Molecule 51 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

- Molecule 52 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	5	1493	Total	C	N	O	P	0	0
			31943	14279	5792	10382	1490		

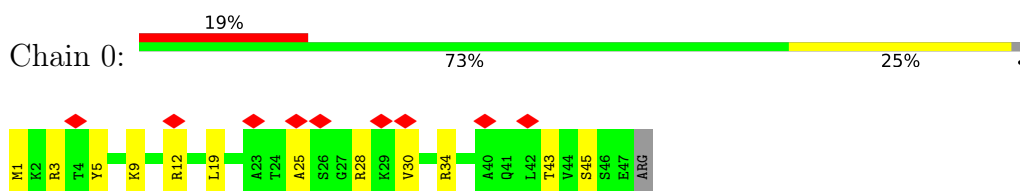
- Molecule 53 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	7	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

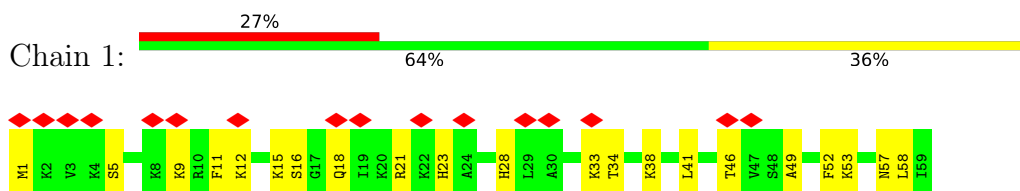
3 Residue-property plots [i](#)

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.

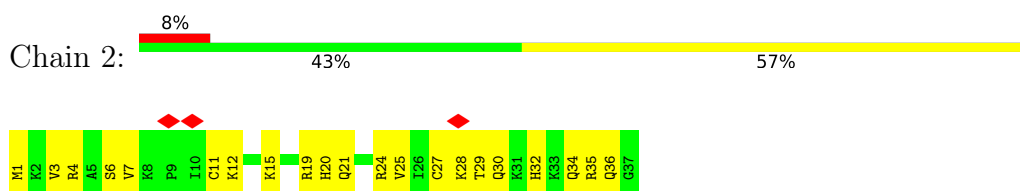
- Molecule 1: 50S ribosomal protein L34



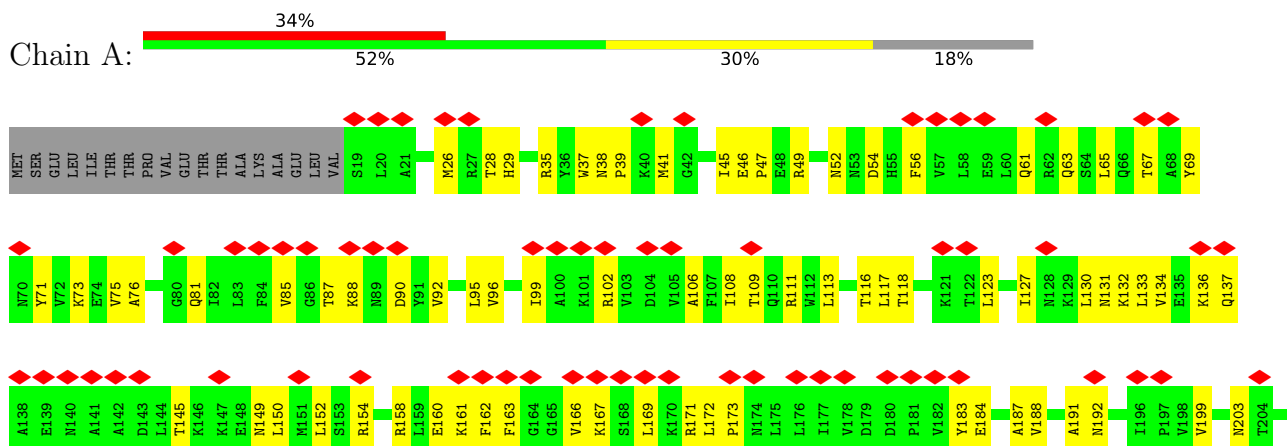
- Molecule 2: 50S ribosomal protein L35



- Molecule 3: 50S ribosomal protein L36

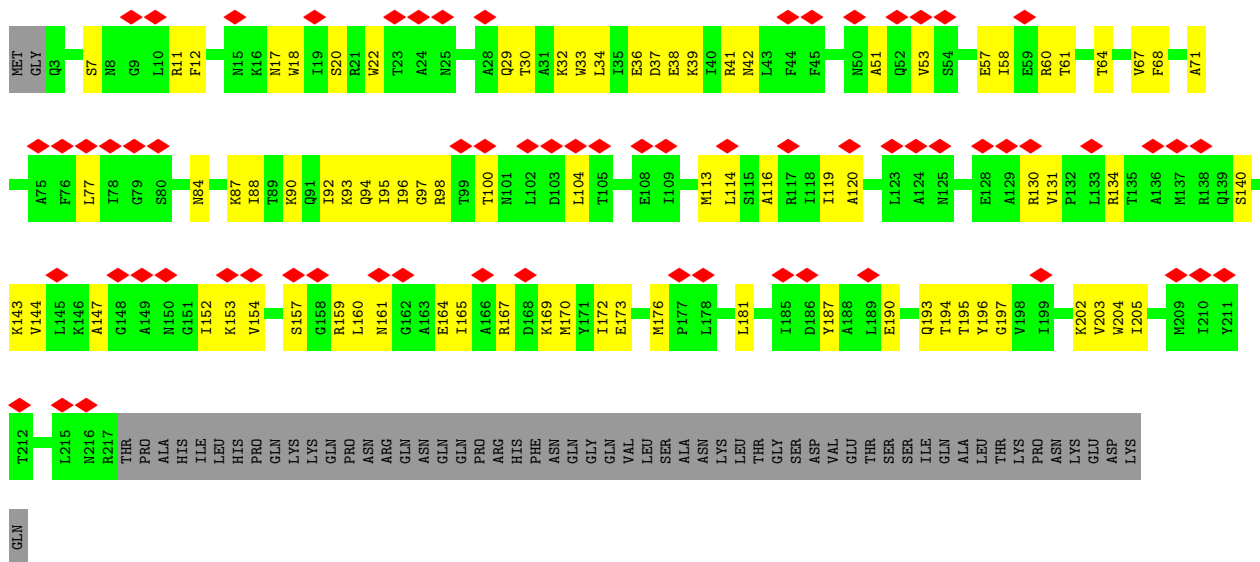


- Molecule 4: 30S ribosomal protein S2

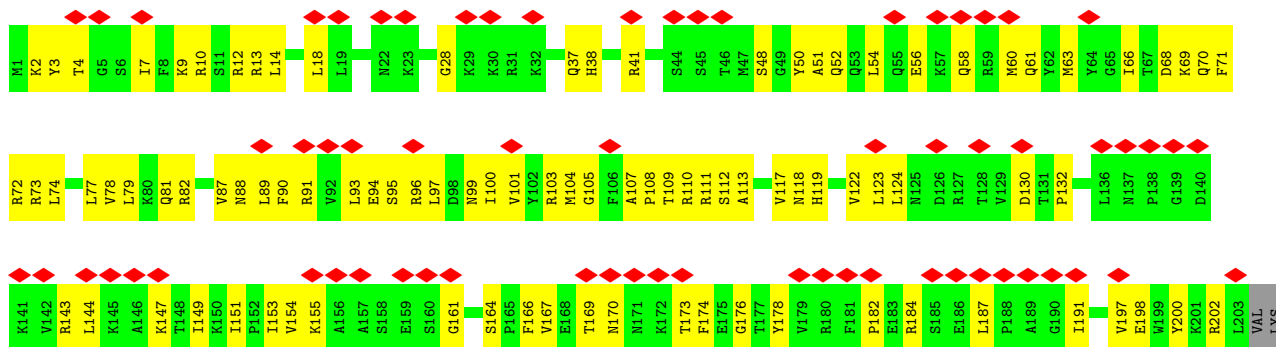




• Molecule 5: 30S ribosomal protein S3

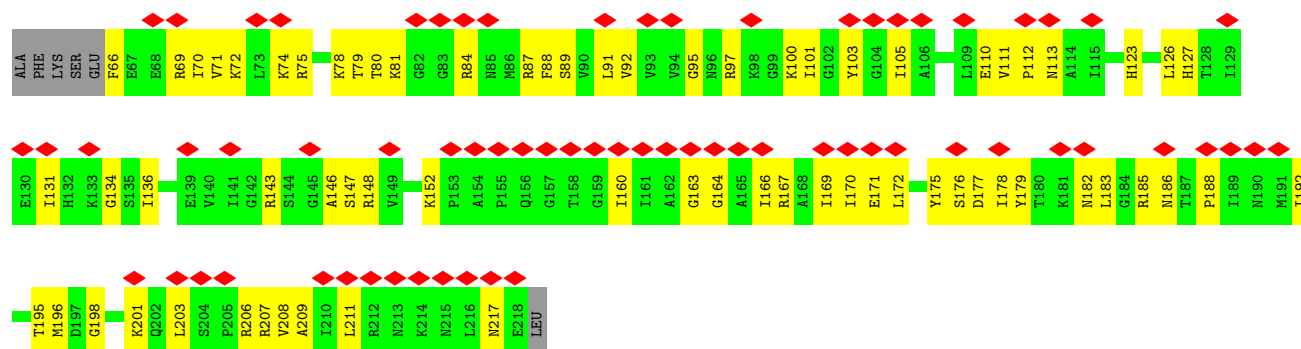


• Molecule 6: 30S ribosomal protein S4

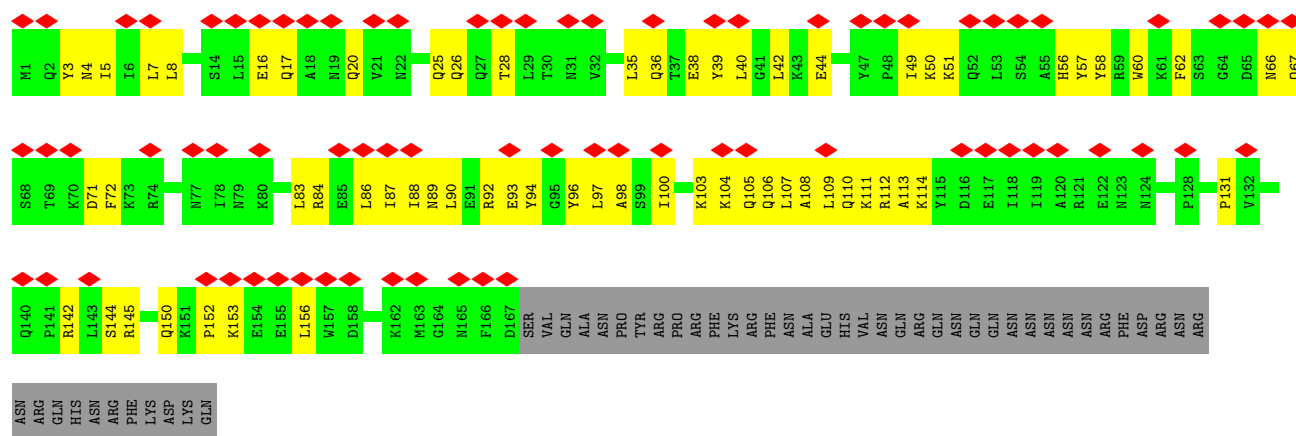


• Molecule 7: 30S ribosomal protein S5

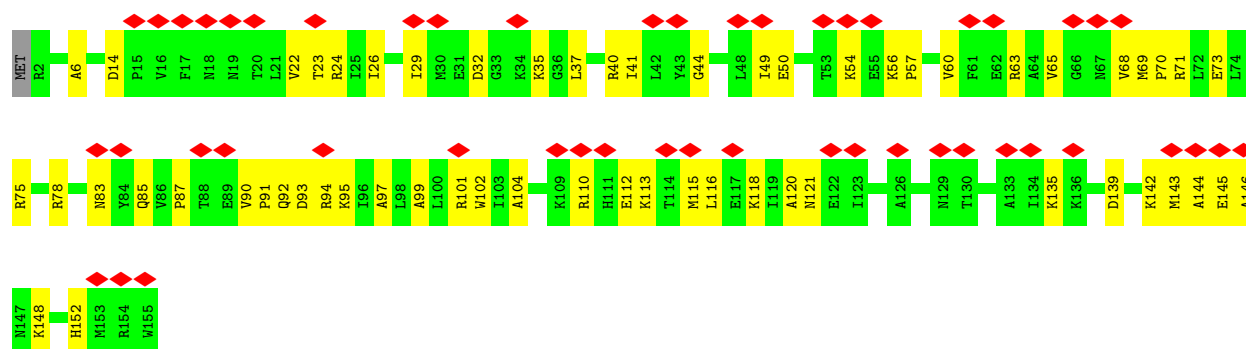




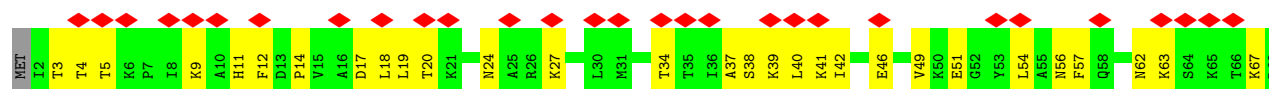
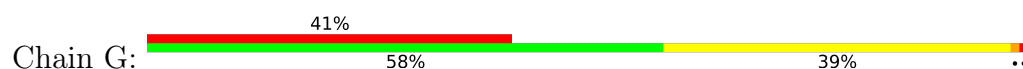
• Molecule 8: 30S ribosomal protein S6

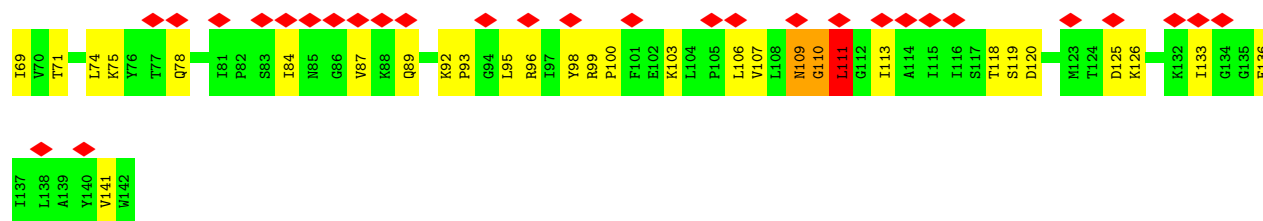


• Molecule 9: 30S ribosomal protein S7

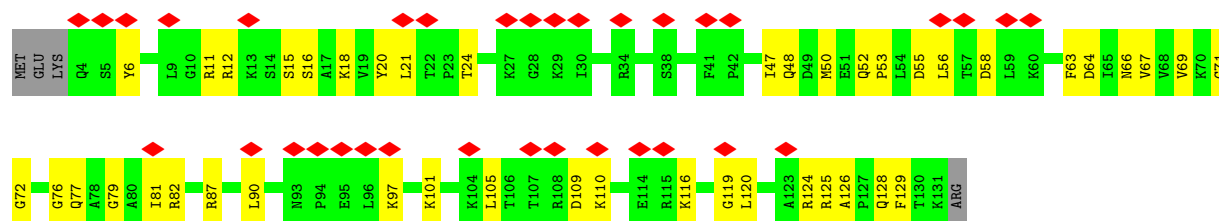


• Molecule 10: 30S ribosomal protein S8

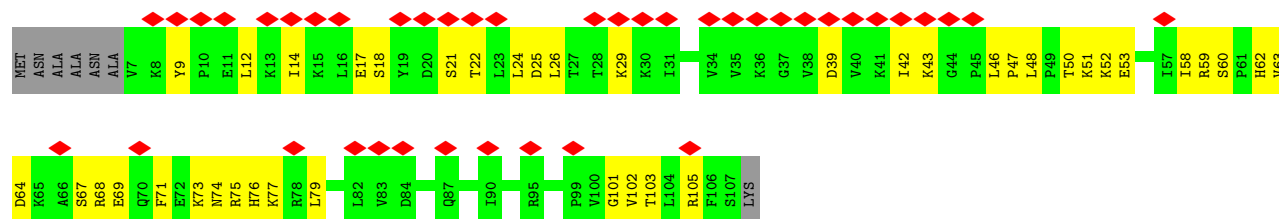




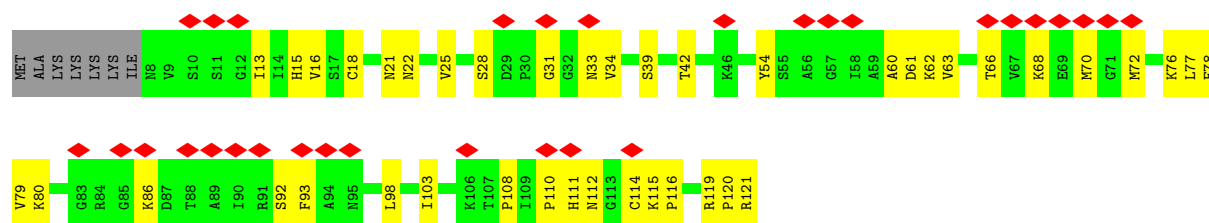
• Molecule 11: 30S ribosomal protein S9



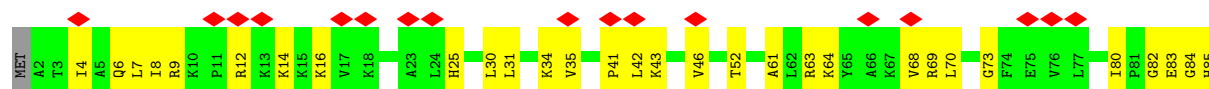
• Molecule 12: 30S ribosomal protein S10

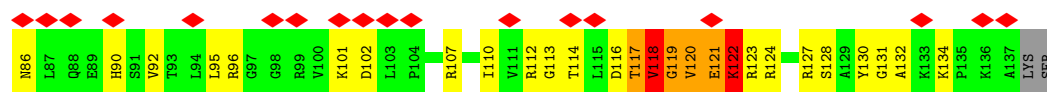


• Molecule 13: 30S ribosomal protein S11

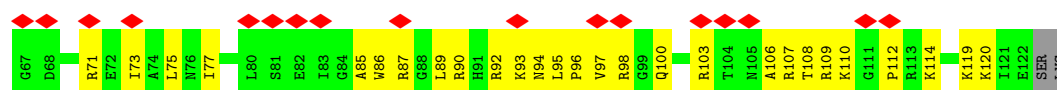
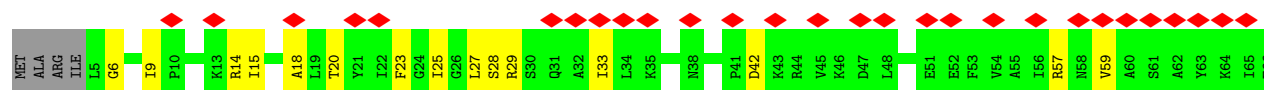


• Molecule 14: 30S ribosomal protein S12

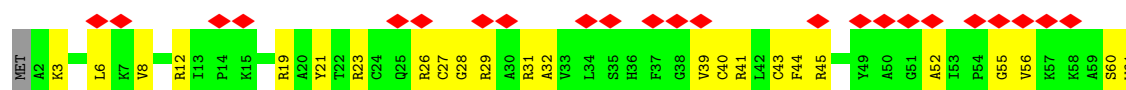
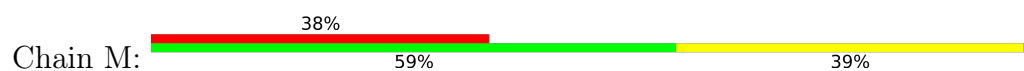




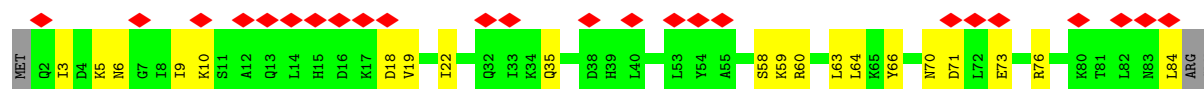
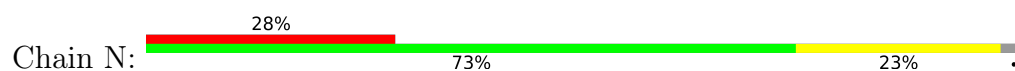
• Molecule 15: 30S ribosomal protein S13



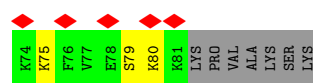
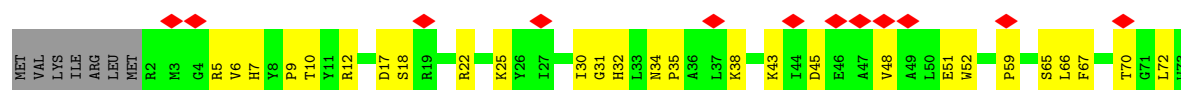
• Molecule 16: 30S ribosomal protein S14 type Z



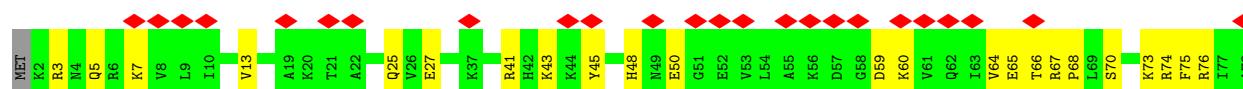
• Molecule 17: 30S ribosomal protein S15

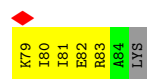


• Molecule 18: 30S ribosomal protein S16

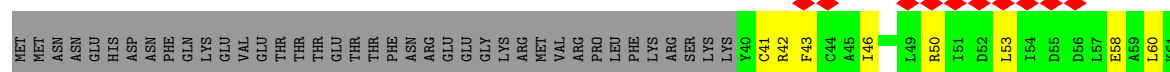
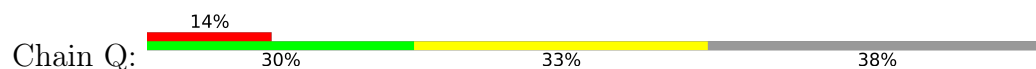


• Molecule 19: 30S ribosomal protein S17

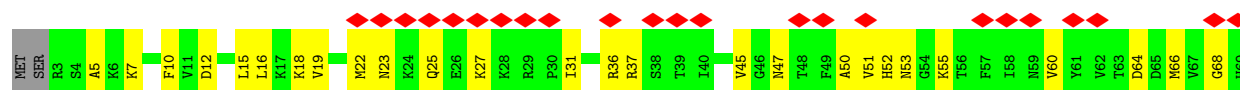




- Molecule 20: 30S ribosomal protein S18



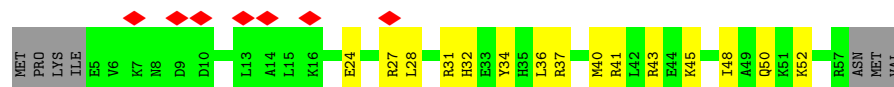
- Molecule 21: 30S ribosomal protein S19



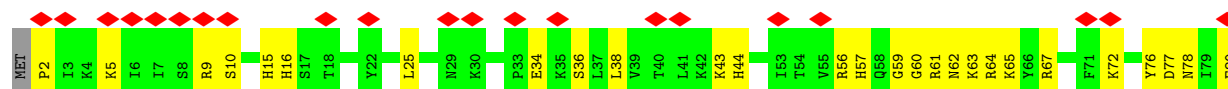
- Molecule 22: 30S ribosomal protein S20

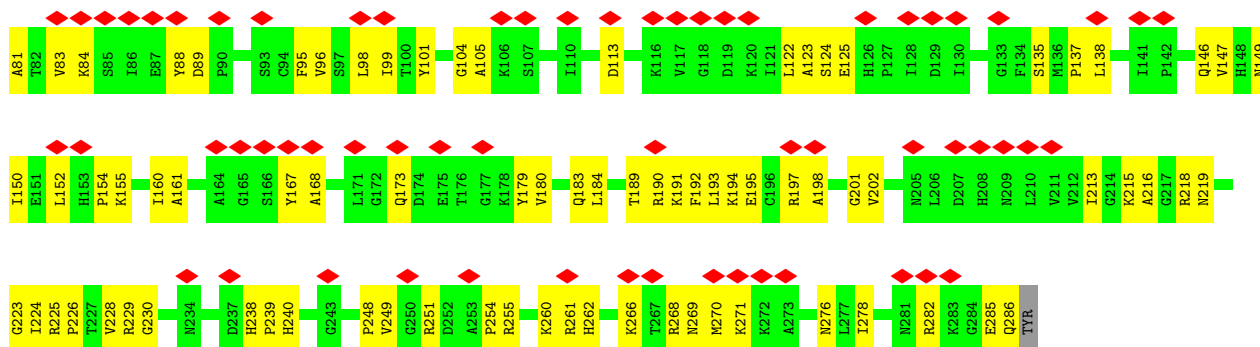


- Molecule 23: 30S ribosomal protein S21

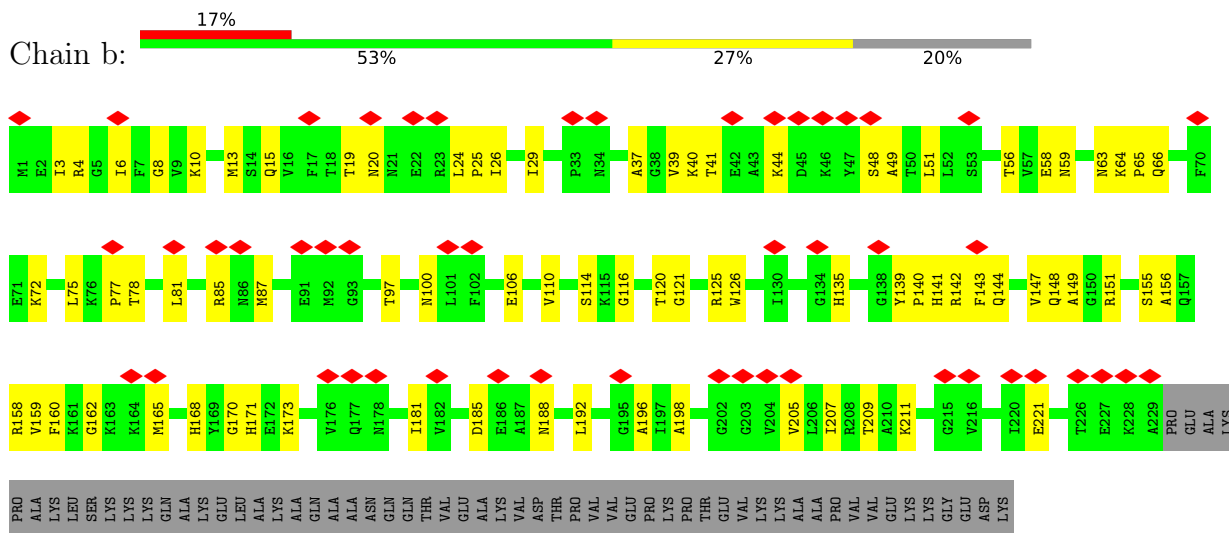


- Molecule 24: 50S ribosomal protein L2

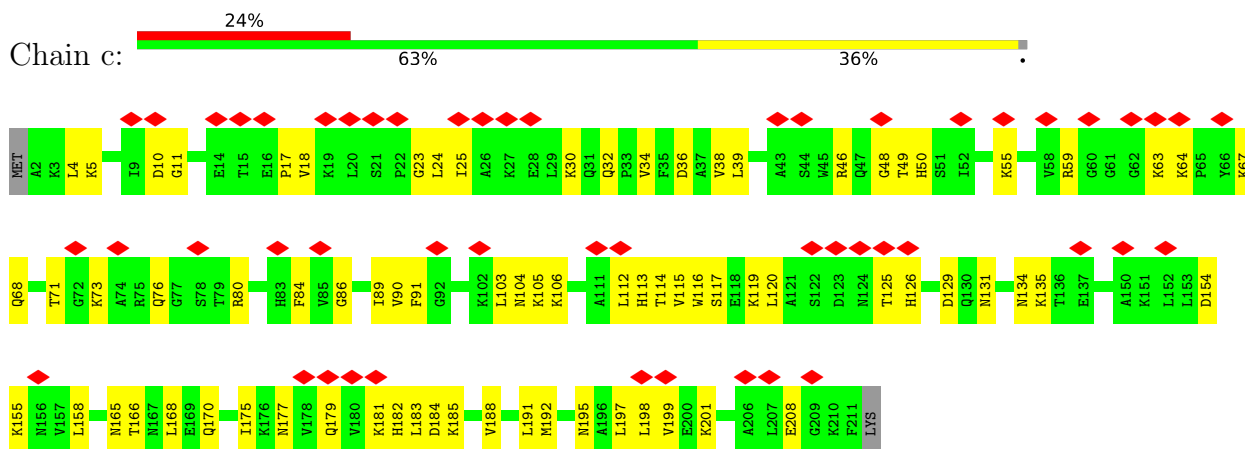




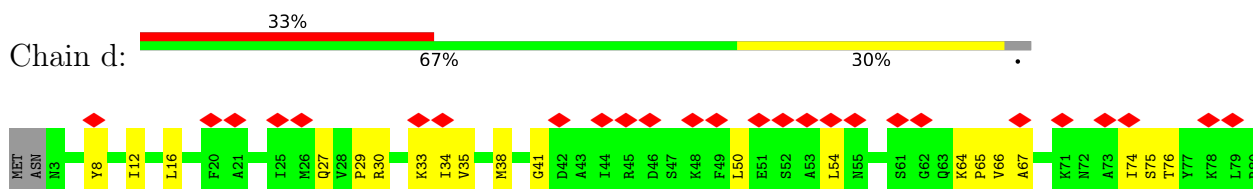
• Molecule 25: 50S ribosomal protein L3

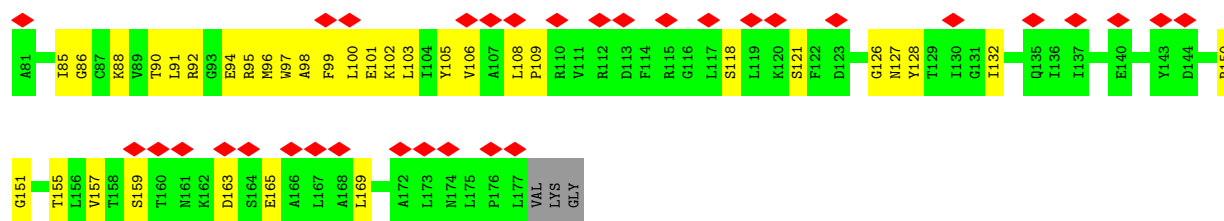


• Molecule 26: 50S ribosomal protein L4

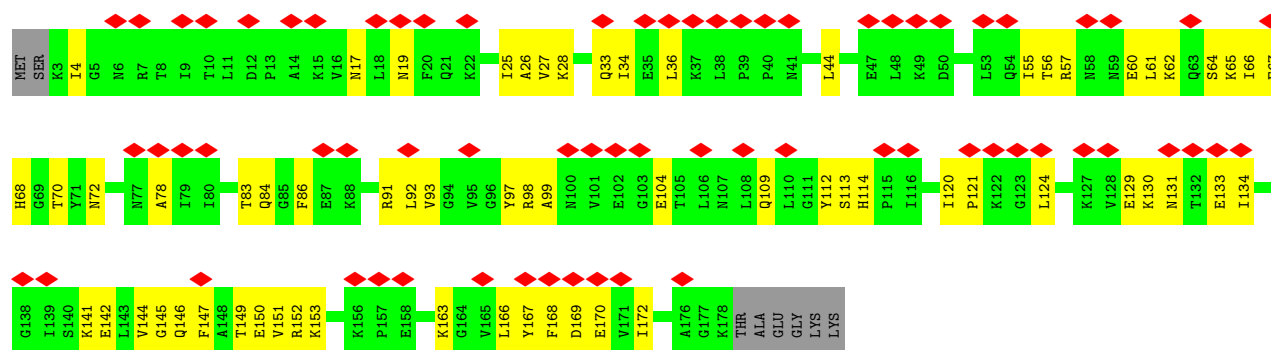
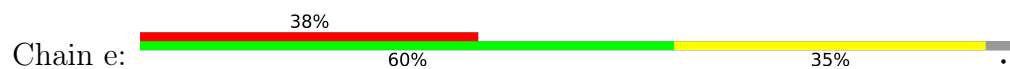


• Molecule 27: 50S ribosomal protein L5

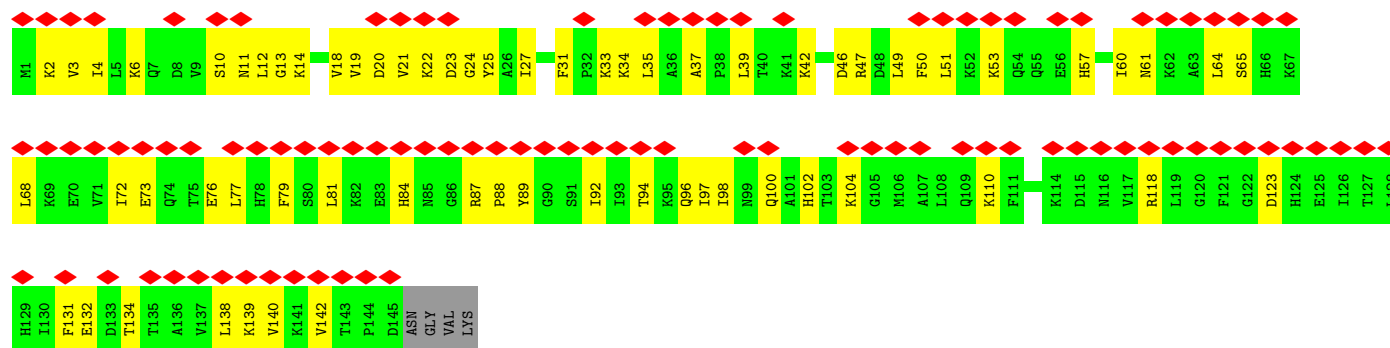




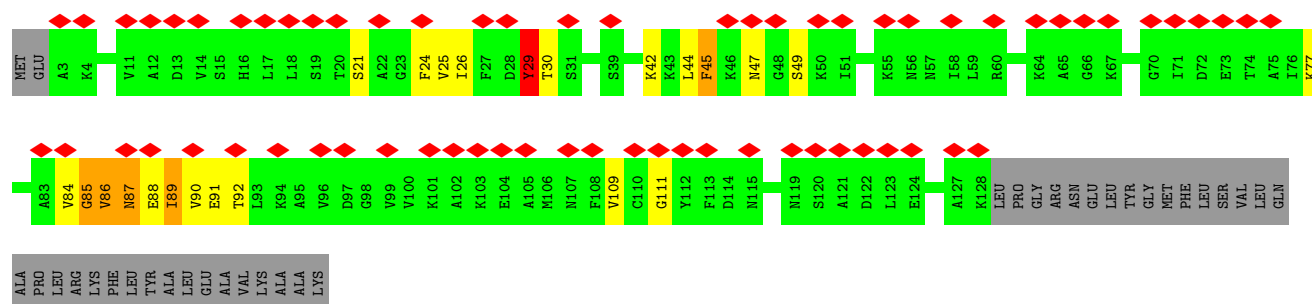
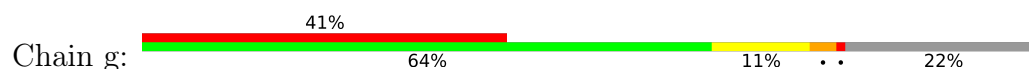
• Molecule 28: 50S ribosomal protein L6



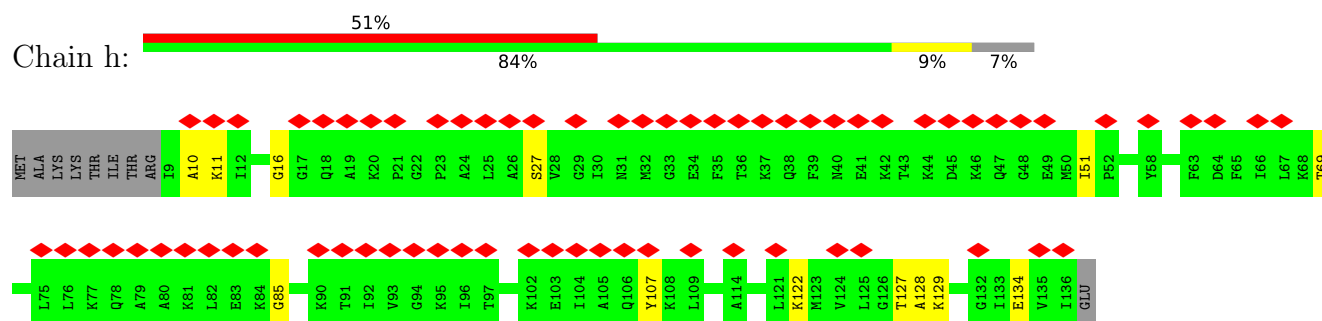
• Molecule 29: 50S ribosomal protein L9



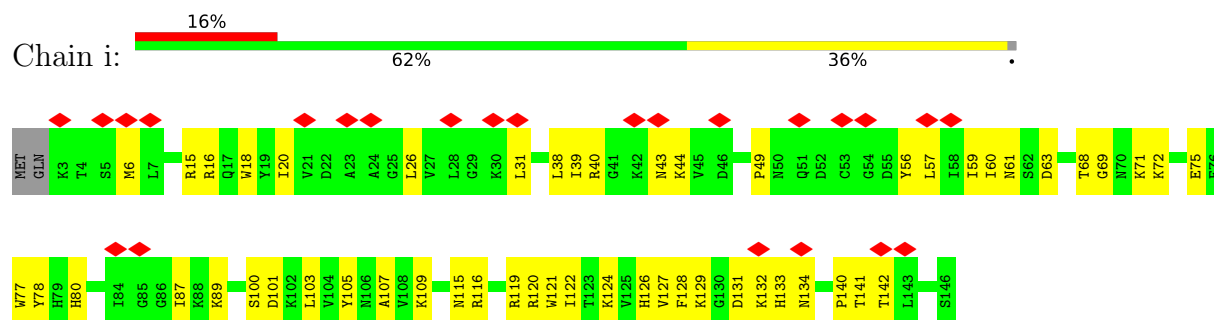
• Molecule 30: 50S ribosomal protein L10



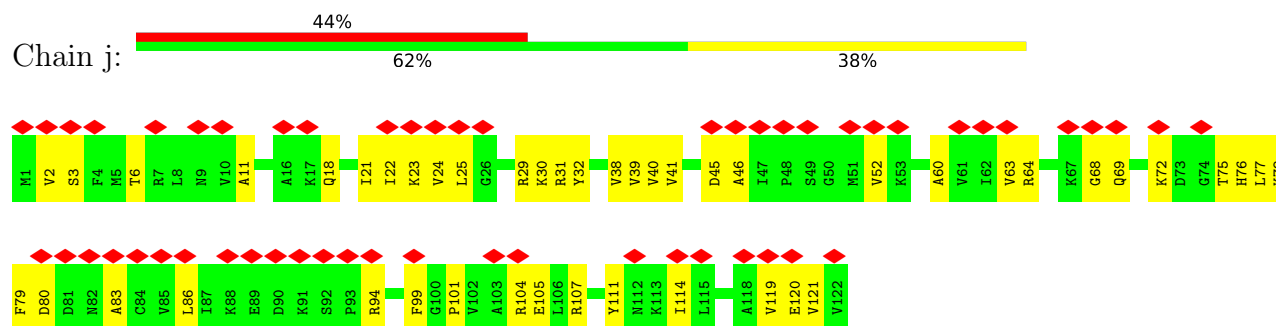
- Molecule 31: 50S ribosomal protein L11



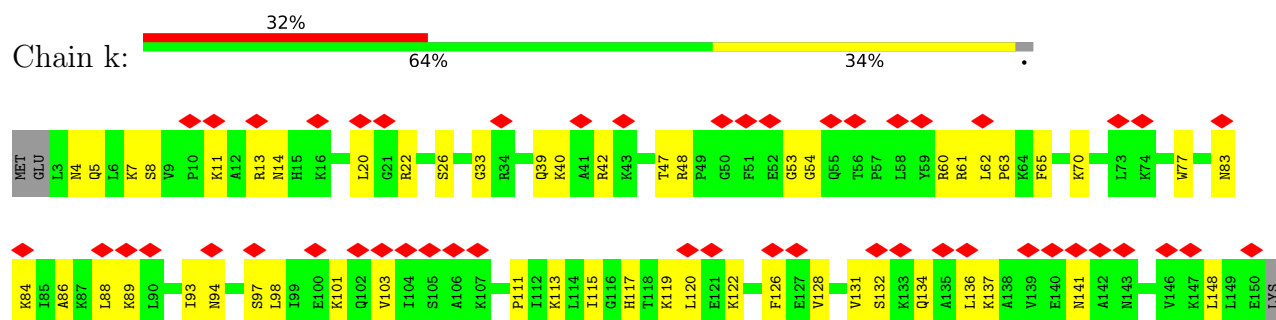
- Molecule 32: 50S ribosomal protein L13



- Molecule 33: 50S ribosomal protein L14

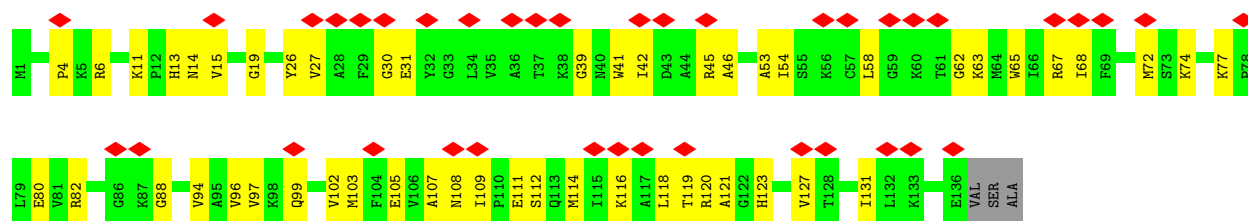


- Molecule 34: 50S ribosomal protein L15

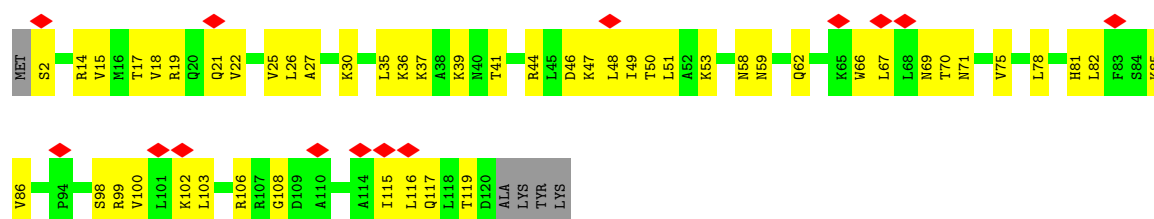


- Molecule 35: 50S ribosomal protein L16

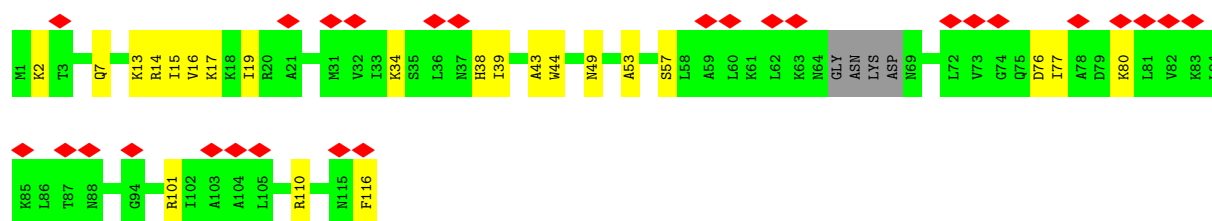
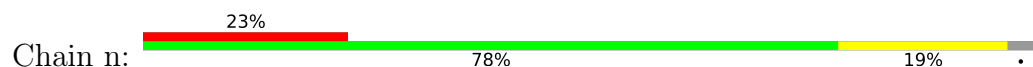




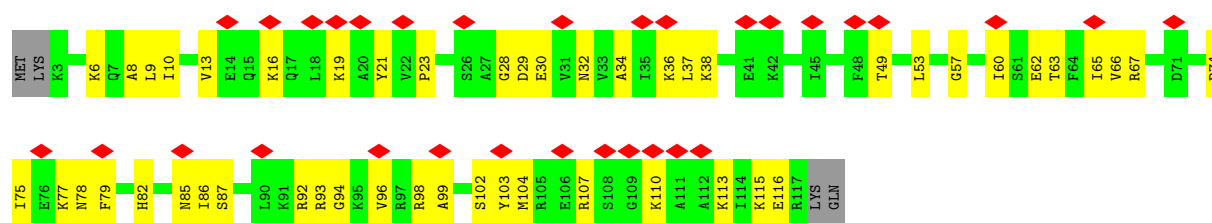
• Molecule 36: 50S ribosomal protein L17



• Molecule 37: 50S ribosomal protein L18

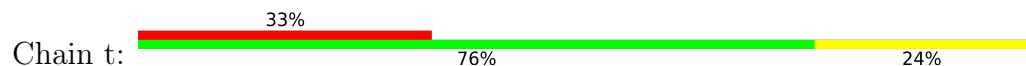


• Molecule 38: 50S ribosomal protein L19

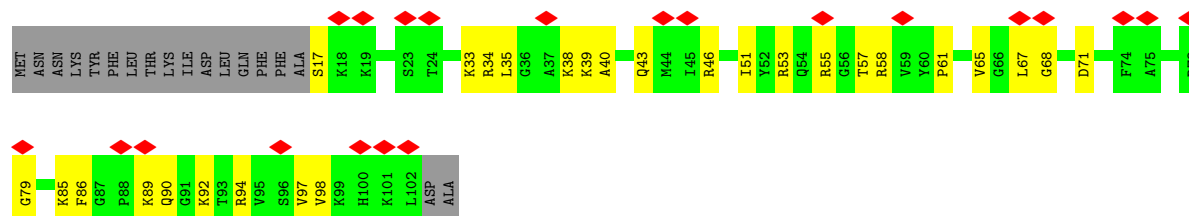


• Molecule 39: 50S ribosomal protein L20





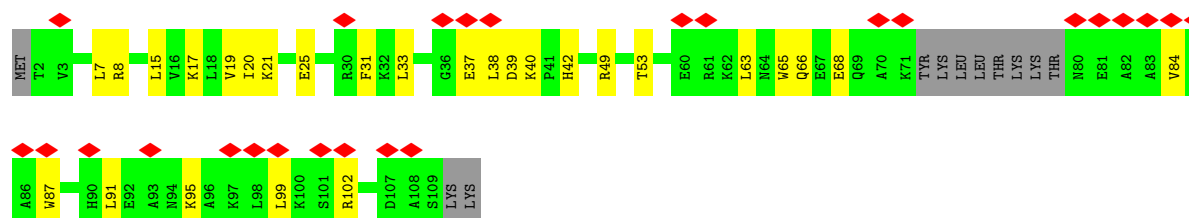
- Molecule 44: 50S ribosomal protein L27



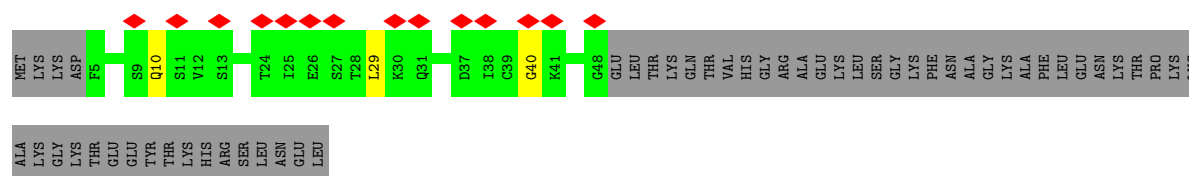
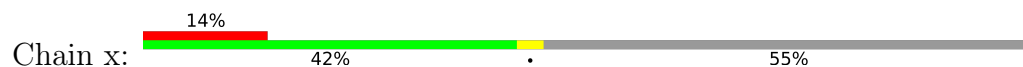
- Molecule 45: 50S ribosomal protein L28



- Molecule 46: 50S ribosomal protein L29

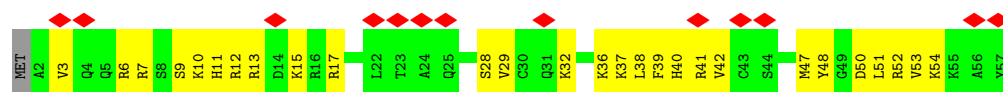


- Molecule 47: 50S ribosomal protein L31

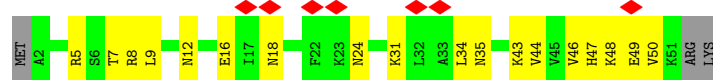


- Molecule 48: 50S ribosomal protein L32

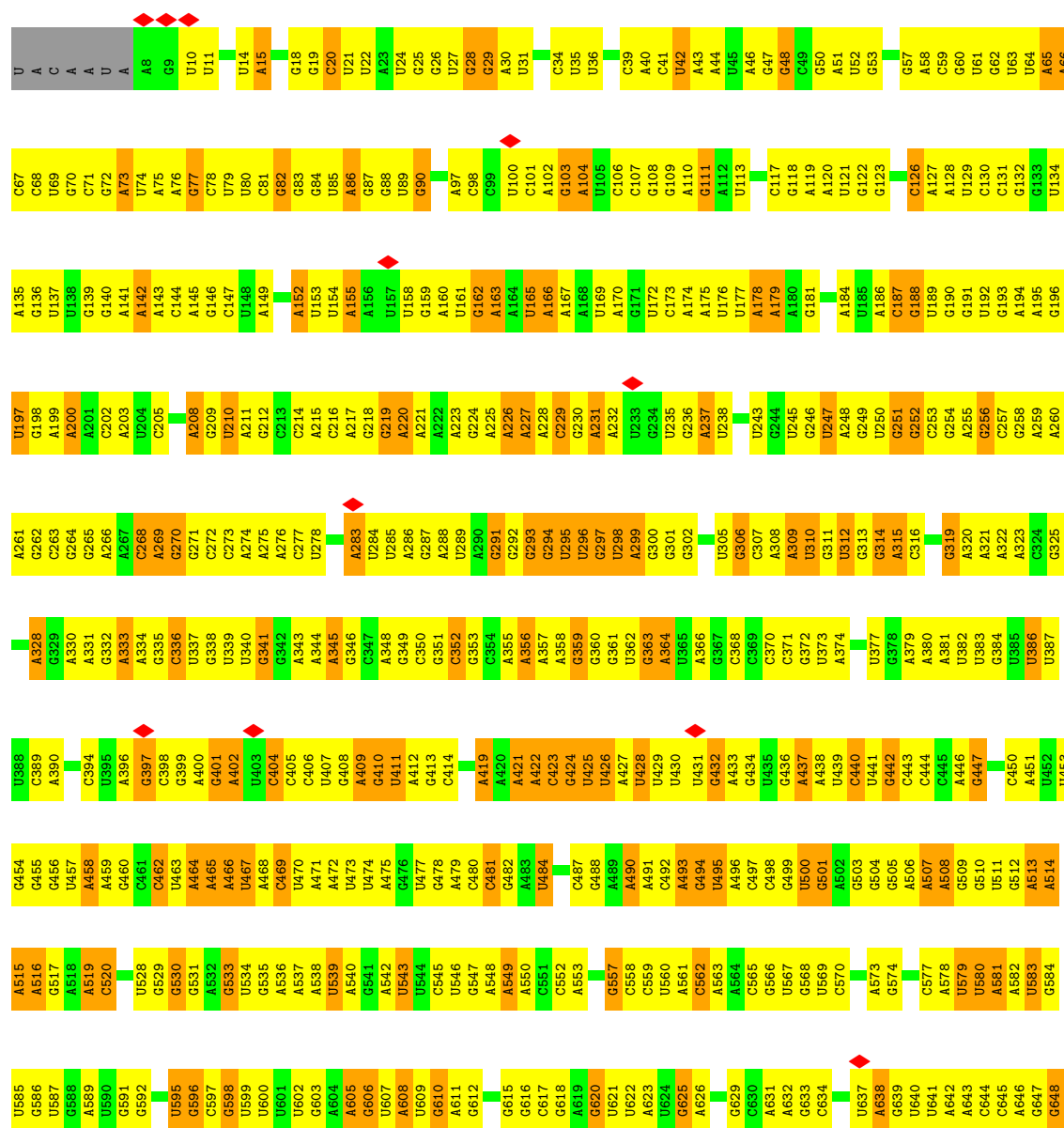




• Molecule 49: 50S ribosomal protein L33 1

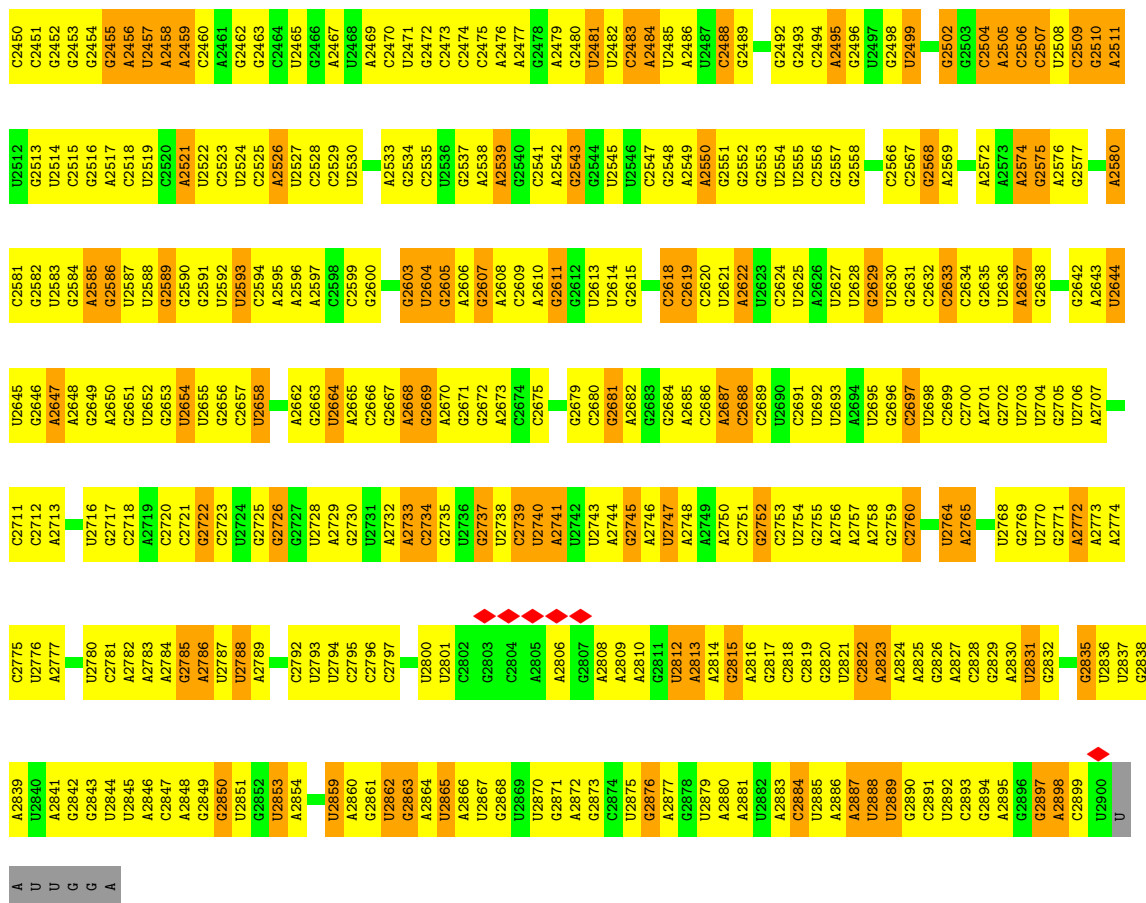


• Molecule 50: 23S ribosomal RNA



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G1289	G1290	C1291	U1292	U1293	U1294	U1295	G1296	U1297	A1298	G1301	U1304	U1305	G1306	U1307	U1308	A1309	U1310	G1311	A1312	G1313</																																							

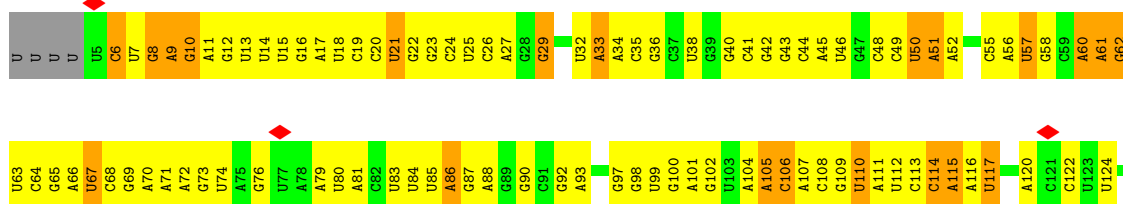
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G2259	U2260	G2261	C2262	G2263	C2266	G2267	G2268	C2269	U2270	C2271	U2272	U2273	G2274	U2275	A2276	G2277	G2278	G2279	U2280	A2281	A2282	G2283	G2284	G2285	A2286	G2287	G2288	U2289	A2290	U2291	A2292	C2293	A2294	A2295	A2296	G2297	G2298	U2299	C2302	U2303	U2304	C2305	A2306	G2307	U2308	A2309	C2310	C2311	G2312	U2313	U2314	U2315	G2316	C2317	C2318	A2319	U2320	C2321	
U2192	U2193	C2194	U2195	U2196	U2197	G2198	U2202	U2203	U2204	U2205	A2206	G2210	G2211	U2212	U2213	A2214	G2215	U2216	G2217	U2218	U2219	A2220	G2221	C2222	G2223	A2224	G2225	U2226	U2227	U2228	C2229	A2230	A2231	G2232	A2233	G2234	A2235	G2238	U2239	U2240	A2241	G2242	G2243	U2244	G2245	G2246	G2247	G2248	A2249	G2250	U2253	G2254	A2255	G2258					
G2132	A2133	G2134	C2135	A2136	A2137	U2138	G2139	G2140	G2141	U2142	G2143	C2144	A2145	A2146	G2147	U2148	U2149	C2150	G2151	C2152	U2153	A2154	G2155	G2156	A2157	C2158	U2159	U2160	G2161	U2162	U2163	G2164	A2165	U2166	G2167	G2168	A2169	A2170	A2171	G2172	G2173	G2174	G2175	G2176	G2177	A2178	U2179	U2180	A2181	C2182	U2183	A2184	C2185	G2186	U2187	U2188	U2189	G2190	G2191
C2070	C2071	C2072	C2073	C2074	U2075	G2076	A2077	U2078	C2079	C2080	U2081	U2082	U2083	A2084	U2085	U2086	G2087	U2088	A2089	G2090	U2093	A2094	A2095	U2096	A2097	U2098	U2099	G2100	A2101	U2102	C2103	A2104	G2105	G2106	C2108	A2109	U2110	U2111	A2112	U2113	C2114	U2115	U2116	G2117	U2118	A2119	G2120	A2121	G2122	A2123	A2124	U2125	A2126	G2127	G2128	G2131			
U2009	A2010	G2011	A2012	C2013	U2014	C2015	G2016	U2017	U2018	G2019	C2080	A2021	A2022	U2023	C2024	G2025	A2026	G2027	G2028	U2029	C2030	C2031	G2032	U2035	G2036	A2037	U2038	A2039	U2040	C2041	A2042	C2043	C2044	G2045	G2046	U2047	U2048	A2049	G2050	G2051	C2052	G2053	C2054	A2055	A2056	C2057	G2058	G2059	G2060	A2061	C2062	G2063	G2064	U2065	A2066	A2067	G2068	A2069	
G1870	U1871	A1872	A1873	U1874	C1875	G1876	A1879	G1880	C1881	G1882	A1883	U1884	G1885	A1886	U1887	U1888	U1889	A1890	A1891	A1892	C1893	U1894	G1895	A1896	U1897	G1898	C1901	G1902	A1903	G1904	U1905	G1906	A1907	U1908	A1919	A1920	C1921	A1926	U1930	C1931	C1932	U1933	A1934	U1935	G1936	G1937	U1938	A1939	G1940	C1941	G1942	A1943	U1944	A1945					
U1945	U1947	U1950	A1951	C1952	U1953	C1954	G1955	U1956	G1957	U1958	A1959	A1960	A1961	U1962	U1963	G1964	C1965	G1966	U1967	C1968	G1971	C1972	U1973	U1974	G1975	A1976	C1977	U1978	G1979	G1980	U1981	G1982	U1983	A1984	A1985	C1986	C1987	A1988	U1989	C1990	U1991	G1992	U1993	U1994	G1995	A1996	C1997	U1998	U1999	U2000	C2003	G2004	G2005	G2006	U2007	A2008			
G1672	G1676	G1677	U1678	U1679	U1680	G1681	U1684	G1685	A1686	G1687	U1688	A1689	G1690	U1691	G1692	U1693	G1694	A1695	C1696	C1697	A1698	G1699	A1700	G1701	A1702	A1703	G1704	U1705	G1706	U1707	G1708	G1709	A1710	A1711	U1712	U1713	U1714	A1715	U1716	G1717	C1718	U1719	A1723	A1724	G1725	U1726	U1727	G1728	G1729	C1730	G1731	A1732	A1735	G1736					
U1610	C1611	U1612	A1613	G1614	G1615	U1616	U1617	U1618	A1619	A1620	U1621	C1622	G1625	C1626	U1627	G1628	U1629	A1630	U1631	C1632	C1633	A1634	G1635	U1636	A1637	G1638	C1639	G1640	A1641	G1642	A1643	U1644	G1645	G1646	A1647	A1648	C1649	C1651	A1652	C1653	A1656	U1658	C1659	A1660	A1661	G1662	G1663	G1664	G1665	A1666	G1667	G1668	A1669	U1670	C1671				
U1548	U1549	G1550	U1551	C1552	G1553	A1554	G1555	U1556	G1557	U1558	A1559	U1560	C1561	A1562	C1563	A1564	G1565	U1566	A1567	C1568	A1569	U1570	G1571	U1572	A1573	G1574	C1575	G1576	A1577	U1578	G1579	G1583	U1584	A1585	U1586	U1587	A1588	A1589	U1590	C1591	A1592	U1593	G1594	C1595	U1596	U1597	A1601	G1602	A1603	A1604	A1605	G1606	G1607	C1608	U1609				



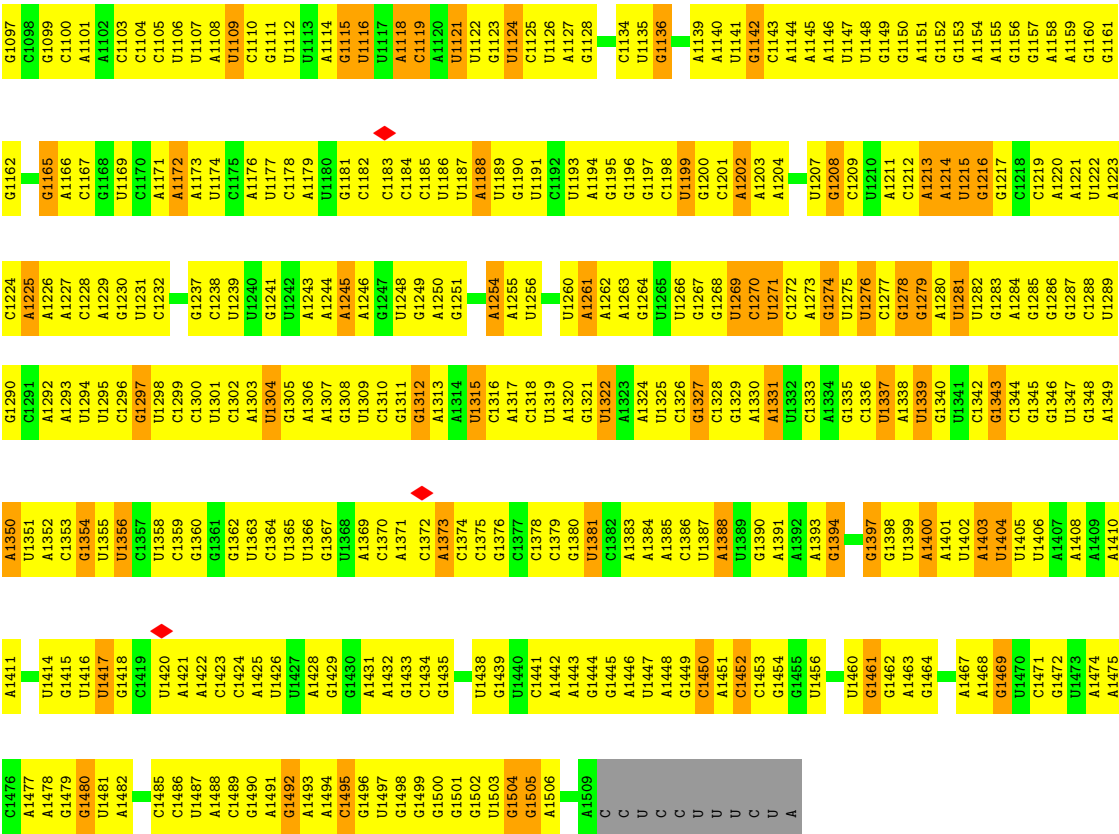
• Molecule 51: 5S ribosomal RNA



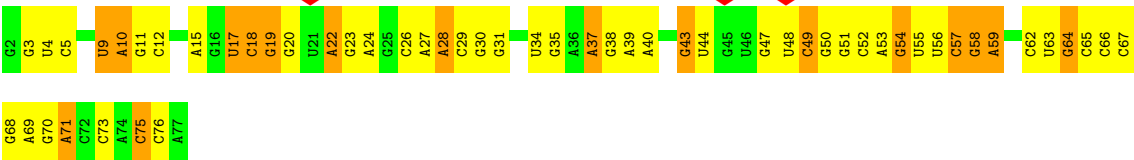
• Molecule 52: 16S ribosomal RNA



G1034	A128	A197	G262	C329	C591	A452	C517	C578	A645	A712	A779	C843	A907	A973	G1034
A1035	U129	A198	C263	C330	A392	C453	A518	G579	A646	A713	U780	U844	A908	C974	A1035
C1036	G130	A199	A330	C331	A393	U454	G519	G579	U647	C714	A781	C845	A909	C975	C1036
A1037	G131	G200	U265	A332	U394	U455	U456	A581	C648	A715	G782	G846	A910	U976	A1037
G1038	G132	G201	A266	A333	G395	U456	U456	G582	U649	C716	G783	G847	G911	U977	G1038
U1040	G133	A202	G133	U333	G396	U456	U456	G583	A650	C717	A784	U848	G912	A978	U1040
G1041	G134	C203	A270	C335	C397	A460	A460	C584	G651	A718	U785	A849	A913	C979	G1041
U1042	A135	C204	G271	U336	G398	A461	A461	G585	A652	G719	U786	G850	A914	C980	U1042
G1043	U205	G272	G271	C337	G399	A462	A462	U652	A653	U720	A787	U851	A915	U981	G1043
U1044	G206	A137	C273	C338	G400	U463	U463	G590	U654	G721	U788	G852	U916	A982	U1044
C1045	A138	C207	A274	U339	A401	A464	A464	A591	U655	G722	A789	G853	U917	G983	C1045
A1046	G139	A208	U275	A340	G402	A465	A465	A592	U656	C723	U790	A854	A918	A984	A1046
U1047	U140	A209	U276	A341	G403	U466	U466	A593	G657	G724	A791	G855	C919	C985	U1047
G1048	A141	A210	G277	G404	A404	G467	G467	A594	U658	A725	C792	G856	G920	U986	G1048
U1049	U143	G211	A278	G343	C405	G468	G468	G595	U659	G727	C793	A858	G921	U987	U1049
A1051	U144	G212	G280	G344	G406	C469	C469	U596	A660	G728	A796	A859	G922	C988	U1051
G1052	G145	U213	G280	A407	A407	U470	U470	C597	G661	C729	G797	C860	G923	A989	U1052
U1053	A146	U214	G285	G346	U408	A471	A471	U598	G662	G730	U798	G862	A930	C990	U1053
G1055	A147	G215	C286	C348	G409	G472	G472	G599	A664	A731	U799	A863	C931	U992	U1055
U1056	U217	U217	C286	A349	G412	G474	G474	G602	U665	A732	A800	U864	A932	C993	U1056
A1057	A218	U218	U288	G350	G413	U475	U475	U603	U666	C733	G803	U865	A933	C994	A1057
C1058	A219	U219	U289	C351	U414	U476	U476	A605	U667	A734	A804	A866	G934	U996	C1058
G1059	G290	U220	G290	A352	C415	G477	G477	A607	U668	C735	C805	G868	U935	C997	G1059
U1060	U221	U221	C291	A352	U416	A479	A479	A607	G670	U737	G808	U869	G936	G998	U1060
G1061	A156	U222	U292	A355	U417	C480	C480	G608	G671	A738	C808	A870	U938	C999	G1061
C1062	A157	G227	G293	G356	U418	U481	U481	G609	A672	G739	G809	U871	G939	A1000	C1062
U1063	U158	U228	A294	G357	U419	U482	U482	C610	A673	C740	A810	C872	A940	C999	U1063
G1064	A160	G295	G295	G358	A420	U483	U483	A611	U674	C741	G811	U873	G941	A1001	G1064
U1065	G161	G230	U299	A359	U422	A484	A484	G612	U675	A743	A812	C874	G942	A1002	U1065
G1066	C163	U231	A300	U361	U423	C485	C485	C616	U676	A744	A813	G875	C943	G1003	G1066
U1067	C164	G232	A301	U362	U424	U488	U488	U617	C677	U745	C814	C876	A944	A1006	U1067
G1068	U165	G233	A302	U363	G425	U489	U489	U618	U678	A746	G815	C877	U945	U1007	G1068
U1069	C235	C235	A303	U364	U426	U489	U489	A619	U679	C747	A816	C878	G946	C999	U1069
G1070	C236	U237	U304	U365	A427	U489	U489	C620	G680	U748	A817	G880	U947	A1009	G1070
A1071	G169	A239	A305	A367	U428	U489	U489	C621	U681	G749	A818	U881	U948	A1010	A1071
G1072	A170	U238	G306	A367	A429	U489	U489	C622	U682	A750	G819	G882	G949	A1011	G1072
U1073	C307	U240	C308	C368	G430	U493	U493	C623	U683	C751	A820	U883	C950	A1012	U1073
G1074	U241	C241	A309	A369	U431	U495	U495	G624	U684	G752	A821	U884	U951	C1013	G1074
U1075	A242	A242	C310	A370	U432	U496	U496	U625	U685	C753	A822	G884	U952	A1014	U1075
G1076	G243	G243	A311	U371	C433	U497	U497	U626	G687	U754	A823	U885	A953	U1015	G1076
U1077	A246	A246	A312	G372	U434	U498	U498	G627	G688	U755	A824	U886	A954	A1016	U1077
G1080	G314	G314	U313	A373	U435	U500	U500	U627	U688	A756	A825	C887	U955	A1017	G1080
U1081	G315	G315	G314	G374	U436	G501	G501	A628	A692	G762	G826	U888	U956	U1018	U1081
U1082	G316	U248	G315	C375	U437	C502	C502	U629	A693	A763	C827	U889	U957	G1019	U1082
G1085	A317	U249	G316	A377	U438	G503	G503	G630	U694	A764	U828	C891	C958	G	G1085
U1086	C318	G250	A317	A378	U439	A504	A504	G631	U694	C765	A829	G892	A959	A	U1086
C1087	G251	U251	C318	A379	U440	C505	C505	C632	U698	A766	U830	G893	C960	G	C1087
C1088	U252	G252	U319	A380	U441	U506	U506	A633	U698	U767	U831	C894	C961	U	C1088
G1089	G253	G253	G320	G380	U442	U507	U507	U634	U702	G768	C832	A894	G961	U	G1089
C1091	G254	G254	A321	U383	G443	A508	A508	U635	A703	A769	G833	A895	A964	U	C1091
A1092	G255	G255	G322	G384	G444	C509	C509	G636	U704	G770	G834	G896	A966	A	A1092
U1093	G256	G256	A323	A385	U445	U510	U510	A637	A705	A773	G835	A897	A967	G	U1093
C1094	A325	A325	C324	A386	A446	A511	A511	A638	U706	G774	G836	A898	C967	C	C1094
G1095	U257	U257	G324	A387	G447	A512	A512	A639	G707	A775	G837	A899	C968	U	G1095
A1096	A258	A258	A326	A388	U448	U513	U513	C640	U708	G776	A838	A900	A969	U	A1096
	U195	U195	G327	A389	A449	U514	U514	U643	A709	A777	A903	U905	A970	A	
	G196	G196	G328	G390	U450	G515	G515	U644	A711	A778	C940	C906	A971	G	
													A972		



● Molecule 53: tRNA-Phe



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	485	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	1.837	Depositor
Minimum map value	-0.665	Depositor
Average map value	0.026	Depositor
Map value standard deviation	0.131	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 [i](#)

5.1 Standard geometry [i](#)

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	0.13	0/383	0.39	0/504
2	1	0.14	0/484	0.43	0/637
3	2	0.18	0/306	0.49	0/401
4	A	0.15	0/1954	0.40	0/2642
5	B	0.16	0/1721	0.41	0/2323
6	C	0.17	0/1691	0.44	0/2267
7	D	0.15	0/1188	0.43	0/1593
8	E	0.17	0/1384	0.42	0/1867
9	F	0.15	0/1266	0.42	0/1700
10	G	0.24	0/1126	0.58	3/1517 (0.2%)
11	H	0.15	0/1044	0.42	0/1395
12	I	0.15	0/820	0.42	0/1103
13	J	0.15	0/844	0.39	0/1136
14	K	0.27	0/1094	0.53	1/1468 (0.1%)
15	L	0.16	0/962	0.45	0/1289
16	M	0.15	0/483	0.38	0/643
17	N	0.13	0/679	0.39	0/907
18	O	0.14	0/659	0.42	0/885
19	P	0.14	0/684	0.44	0/913
20	Q	0.20	0/545	0.52	0/730
21	R	0.15	0/698	0.42	0/936
22	S	0.15	0/631	0.39	0/838
23	T	0.16	0/475	0.48	0/621
24	a	0.15	0/2267	0.41	0/3044
25	b	0.14	0/1795	0.41	0/2412
26	c	0.13	0/1671	0.41	0/2246
27	d	0.20	0/1409	0.47	0/1894
28	e	0.15	0/1420	0.41	0/1912
29	f	0.16	0/1205	0.46	0/1616
30	g	0.40	0/969	0.78	3/1295 (0.2%)
31	h	0.14	0/968	0.43	0/1298
32	i	0.13	0/1186	0.37	0/1592
33	j	0.14	0/953	0.40	0/1275
34	k	0.15	0/1170	0.40	0/1559

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	l	0.16	0/1104	0.43	0/1481
36	m	0.15	0/973	0.41	0/1309
37	n	0.14	0/897	0.41	0/1198
38	o	0.16	0/948	0.47	0/1262
39	p	0.14	0/961	0.39	0/1278
40	q	0.17	0/828	0.41	0/1111
41	r	0.16	0/1077	0.41	0/1441
42	s	0.14	0/732	0.42	1/988 (0.1%)
43	t	0.15	0/879	0.41	0/1165
44	u	0.17	0/665	0.48	0/884
45	v	0.17	0/519	0.41	0/695
46	w	0.14	0/826	0.37	0/1104
47	x	0.13	0/353	0.38	0/474
48	y	0.30	0/457	0.54	0/601
49	z	0.15	0/412	0.45	0/547
50	3	0.10	0/69073	0.26	0/107710
51	4	0.11	0/2505	0.27	0/3902
52	5	0.10	0/35768	0.25	0/55764
53	7	0.10	0/1808	0.26	0/2817
All	All	0.13	0/156919	0.32	8/234189 (0.0%)

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	G	110	GLY	N-CA-C	-8.54	104.91	115.08
30	g	91	GLU	N-CA-C	-8.21	102.36	112.38
42	s	3	VAL	N-CA-C	-5.72	107.71	113.20
10	G	111	LEU	CA-C-N	-5.27	114.02	121.13
10	G	111	LEU	C-N-CA	-5.27	114.02	121.13

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	11	0
2	1	477	0	530	19	0
3	2	304	0	350	19	0
4	A	1921	0	1973	59	0
5	B	1698	0	1768	70	0
6	C	1660	0	1719	83	0
7	D	1173	0	1267	51	0
8	E	1362	0	1377	70	0
9	F	1246	0	1308	47	0
10	G	1110	0	1226	52	0
11	H	1028	0	1094	41	0
12	I	809	0	894	36	0
13	J	829	0	855	36	0
14	K	1076	0	1170	53	0
15	L	951	0	1014	34	0
16	M	474	0	509	25	0
17	N	673	0	730	14	0
18	O	646	0	677	22	0
19	P	675	0	728	22	0
20	Q	535	0	562	41	0
21	R	682	0	691	29	0
22	S	629	0	681	29	0
23	T	471	0	522	16	0
24	a	2225	0	2301	98	0
25	b	1762	0	1808	69	0
26	c	1644	0	1731	54	0
27	d	1388	0	1469	46	0
28	e	1396	0	1481	44	0
29	f	1182	0	1228	71	0
30	g	960	0	1014	17	0
31	h	959	0	1039	11	0
32	i	1164	0	1192	42	0
33	j	944	0	1019	37	0
34	k	1153	0	1256	43	0
35	l	1079	0	1134	42	0
36	m	958	0	1011	40	0
37	n	889	0	952	17	0
38	o	938	0	1008	48	0
39	p	947	0	1028	34	0
40	q	811	0	858	34	0
41	r	1068	0	1150	43	0
42	s	720	0	803	27	0
43	t	872	0	972	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	u	657	0	695	25	0
45	v	513	0	560	25	0
46	w	818	0	870	22	0
47	x	344	0	333	3	0
48	y	452	0	472	28	0
49	z	408	0	440	13	0
50	3	61664	0	30954	2116	0
51	4	2239	0	1137	70	0
52	5	31943	0	16058	1168	0
53	7	1618	0	821	41	0
All	All	144524	0	98868	4665	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 21.

The worst 5 of 4665 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)
29:f:4:ILE:CD1	29:f:37:ALA:HB3	1.51	1.40
52:5:407:A:N6	52:5:409:G:H21	1.26	1.34
52:5:407:A:H62	52:5:409:G:N2	1.27	1.30
29:f:4:ILE:HD11	29:f:37:ALA:CB	1.59	1.29
29:f:4:ILE:HD12	29:f:37:ALA:N	1.50	1.26

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	45/48 (94%)	45 (100%)	0	0	100	100
2	1	57/59 (97%)	50 (88%)	7 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	2	35/37 (95%)	31 (89%)	4 (11%)	0	100	100
4	A	238/294 (81%)	228 (96%)	10 (4%)	0	100	100
5	B	213/273 (78%)	201 (94%)	12 (6%)	0	100	100
6	C	201/205 (98%)	192 (96%)	9 (4%)	0	100	100
7	D	151/219 (69%)	144 (95%)	7 (5%)	0	100	100
8	E	165/215 (77%)	148 (90%)	17 (10%)	0	100	100
9	F	152/155 (98%)	140 (92%)	12 (8%)	0	100	100
10	G	139/142 (98%)	128 (92%)	10 (7%)	1 (1%)	18	56
11	H	126/132 (96%)	117 (93%)	9 (7%)	0	100	100
12	I	99/108 (92%)	89 (90%)	10 (10%)	0	100	100
13	J	112/121 (93%)	105 (94%)	7 (6%)	0	100	100
14	K	134/139 (96%)	116 (87%)	16 (12%)	2 (2%)	8	40
15	L	116/124 (94%)	101 (87%)	15 (13%)	0	100	100
16	M	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
17	N	81/86 (94%)	77 (95%)	4 (5%)	0	100	100
18	O	78/94 (83%)	73 (94%)	5 (6%)	0	100	100
19	P	81/85 (95%)	79 (98%)	2 (2%)	0	100	100
20	Q	63/104 (61%)	53 (84%)	10 (16%)	0	100	100
21	R	82/87 (94%)	73 (89%)	9 (11%)	0	100	100
22	S	75/87 (86%)	75 (100%)	0	0	100	100
23	T	51/60 (85%)	47 (92%)	4 (8%)	0	100	100
24	a	283/287 (99%)	262 (93%)	21 (7%)	0	100	100
25	b	227/287 (79%)	211 (93%)	16 (7%)	0	100	100
26	c	208/212 (98%)	201 (97%)	7 (3%)	0	100	100
27	d	173/180 (96%)	163 (94%)	10 (6%)	0	100	100
28	e	174/184 (95%)	167 (96%)	6 (3%)	1 (1%)	21	59
29	f	143/149 (96%)	128 (90%)	15 (10%)	0	100	100
30	g	124/161 (77%)	112 (90%)	11 (9%)	1 (1%)	16	54
31	h	126/137 (92%)	112 (89%)	14 (11%)	0	100	100
32	i	142/146 (97%)	134 (94%)	8 (6%)	0	100	100
33	j	120/122 (98%)	116 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	k	146/151 (97%)	134 (92%)	12 (8%)	0	100	100
35	l	134/139 (96%)	126 (94%)	8 (6%)	0	100	100
36	m	117/124 (94%)	108 (92%)	9 (8%)	0	100	100
37	n	108/116 (93%)	99 (92%)	9 (8%)	0	100	100
38	o	113/119 (95%)	101 (89%)	12 (11%)	0	100	100
39	p	112/127 (88%)	107 (96%)	5 (4%)	0	100	100
40	q	97/100 (97%)	86 (89%)	11 (11%)	0	100	100
41	r	137/159 (86%)	132 (96%)	5 (4%)	0	100	100
42	s	90/237 (38%)	85 (94%)	5 (6%)	0	100	100
43	t	109/111 (98%)	98 (90%)	11 (10%)	0	100	100
44	u	84/104 (81%)	77 (92%)	7 (8%)	0	100	100
45	v	61/65 (94%)	58 (95%)	3 (5%)	0	100	100
46	w	96/111 (86%)	93 (97%)	3 (3%)	0	100	100
47	x	42/97 (43%)	40 (95%)	2 (5%)	0	100	100
48	y	54/57 (95%)	48 (89%)	5 (9%)	1 (2%)	6	32
49	z	48/53 (91%)	43 (90%)	5 (10%)	0	100	100
All	All	5820/6670 (87%)	5408 (93%)	406 (7%)	6 (0%)	49	83

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	K	122	LYS
28	e	169	ASP
10	G	109	ASN
30	g	85	GLY
48	y	53	VAL

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	A	212/262 (81%)	212 (100%)	0	100	100
5	B	180/232 (78%)	180 (100%)	0	100	100
6	C	181/183 (99%)	181 (100%)	0	100	100
7	D	123/178 (69%)	123 (100%)	0	100	100
8	E	150/196 (76%)	150 (100%)	0	100	100
9	F	131/132 (99%)	131 (100%)	0	100	100
10	G	123/124 (99%)	121 (98%)	2 (2%)	55	70
11	H	111/115 (96%)	111 (100%)	0	100	100
12	I	95/99 (96%)	95 (100%)	0	100	100
13	J	91/97 (94%)	91 (100%)	0	100	100
14	K	117/120 (98%)	112 (96%)	5 (4%)	26	47
15	L	100/105 (95%)	100 (100%)	0	100	100
16	M	47/48 (98%)	47 (100%)	0	100	100
17	N	76/78 (97%)	76 (100%)	0	100	100
18	O	69/82 (84%)	69 (100%)	0	100	100
19	P	73/75 (97%)	73 (100%)	0	100	100
20	Q	56/94 (60%)	56 (100%)	0	100	100
21	R	74/77 (96%)	74 (100%)	0	100	100
22	S	70/77 (91%)	70 (100%)	0	100	100
23	T	49/56 (88%)	49 (100%)	0	100	100
24	a	241/243 (99%)	241 (100%)	0	100	100
25	b	186/233 (80%)	186 (100%)	0	100	100
26	c	182/184 (99%)	182 (100%)	0	100	100
27	d	150/154 (97%)	150 (100%)	0	100	100
28	e	153/159 (96%)	153 (100%)	0	100	100
29	f	131/134 (98%)	131 (100%)	0	100	100
30	g	101/129 (78%)	94 (93%)	7 (7%)	14	36
31	h	102/110 (93%)	102 (100%)	0	100	100
32	i	126/128 (98%)	126 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	j	103/103 (100%)	103 (100%)	0	100	100
34	k	123/126 (98%)	123 (100%)	0	100	100
35	l	113/115 (98%)	113 (100%)	0	100	100
36	m	105/109 (96%)	105 (100%)	0	100	100
37	n	96/99 (97%)	96 (100%)	0	100	100
38	o	101/105 (96%)	101 (100%)	0	100	100
39	p	100/108 (93%)	100 (100%)	0	100	100
40	q	90/91 (99%)	90 (100%)	0	100	100
41	r	116/132 (88%)	116 (100%)	0	100	100
42	s	82/208 (39%)	82 (100%)	0	100	100
43	t	96/96 (100%)	96 (100%)	0	100	100
44	u	69/85 (81%)	69 (100%)	0	100	100
45	v	58/60 (97%)	58 (100%)	0	100	100
46	w	87/98 (89%)	87 (100%)	0	100	100
47	x	41/86 (48%)	41 (100%)	0	100	100
48	y	48/49 (98%)	47 (98%)	1 (2%)	47	65
49	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5101/5751 (89%)	5086 (100%)	15 (0%)	84	86

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	g	29	TYR
30	g	89	ILE
30	g	44	LEU
48	y	51	LEU
30	g	87	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 80 such sidechains are listed below:

Mol	Chain	Res	Type
29	f	28	HIS
39	p	80	ASN
29	f	84	HIS
35	l	108	ASN

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Mol	Chain	Res	Type
41	r	112	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	3	2875/2907 (98%)	898 (31%)	40 (1%)
51	4	103/108 (95%)	34 (33%)	4 (3%)
52	5	1490/1520 (98%)	382 (25%)	7 (0%)
53	7	75/76 (98%)	30 (40%)	0
All	All	4543/4611 (98%)	1344 (29%)	51 (1%)

5 of 1344 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	3	14	U
50	3	15	A
50	3	20	C
50	3	28	G
50	3	29	G

5 of 51 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	3	2116	U
50	3	2668	A
52	5	1115	G
50	3	2118	U
50	3	2504	C

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

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.

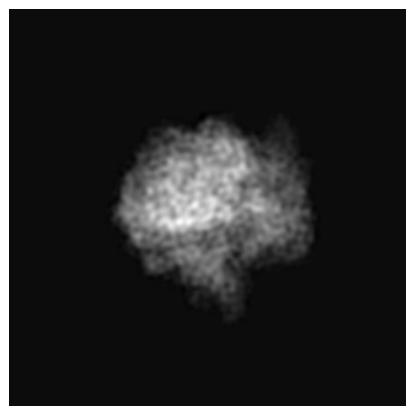
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13432. These allow visual inspection of the internal detail of the map and identification of artifacts.

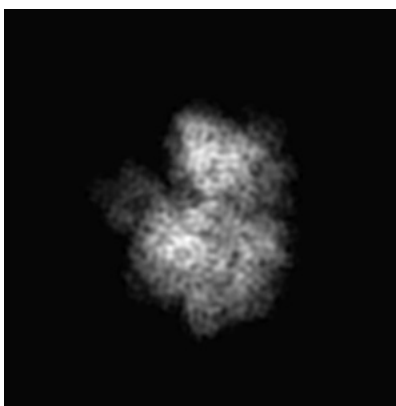
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

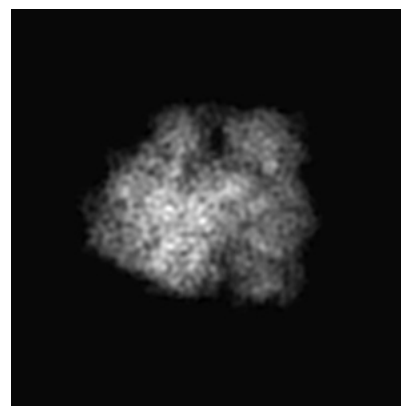
6.1.1 Primary map



X

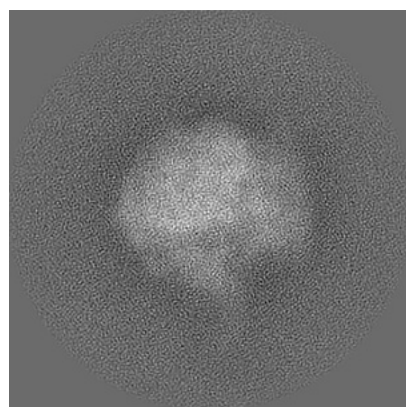


Y

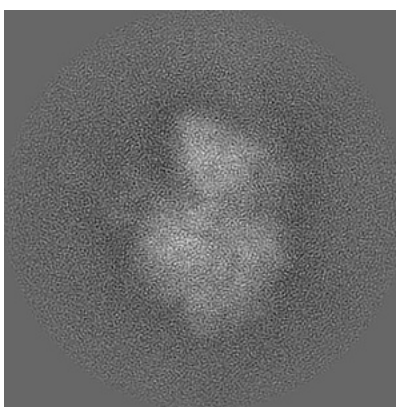


Z

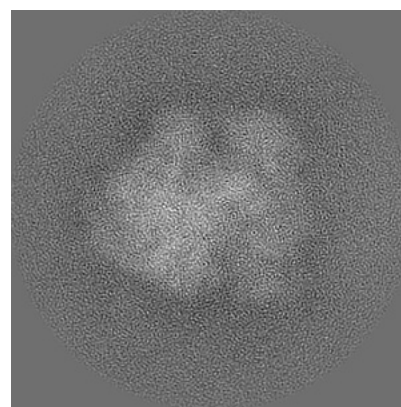
6.1.2 Raw map



X



Y

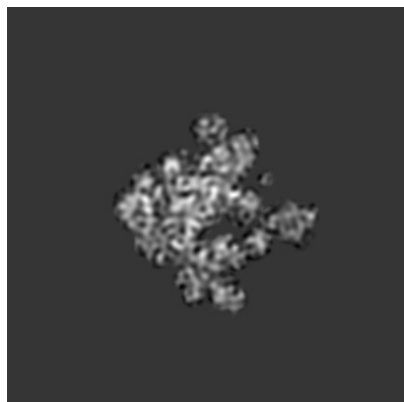


Z

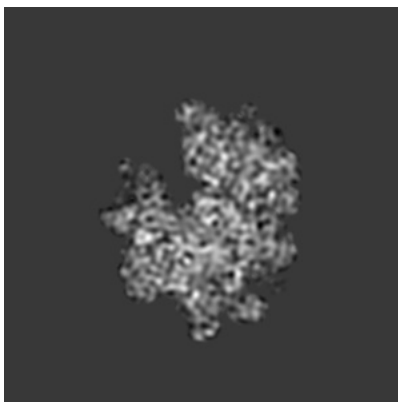
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

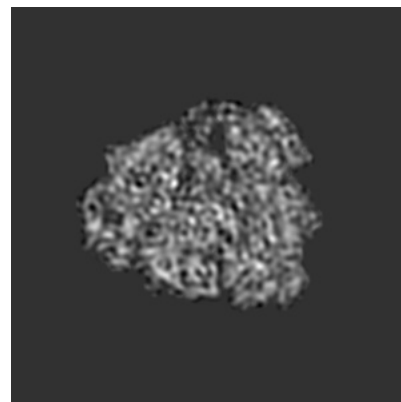
6.2.1 Primary map



X Index: 128

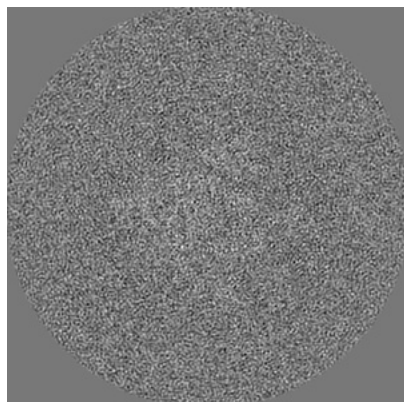


Y Index: 128

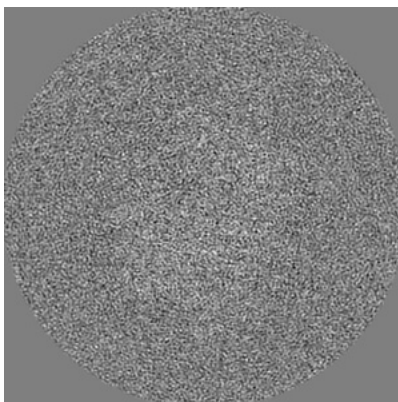


Z Index: 128

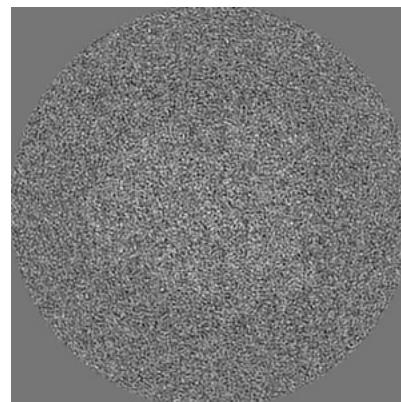
6.2.2 Raw map



X Index: 128



Y Index: 128

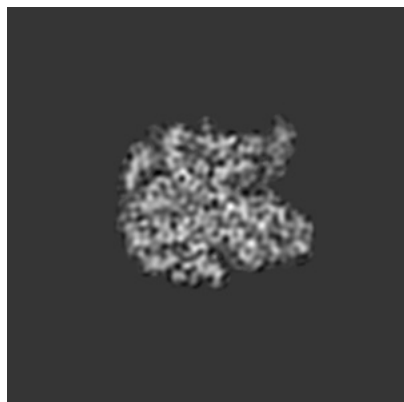


Z Index: 128

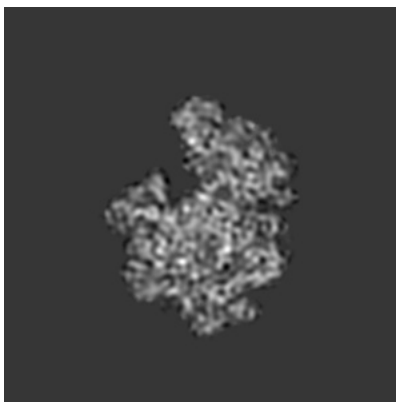
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

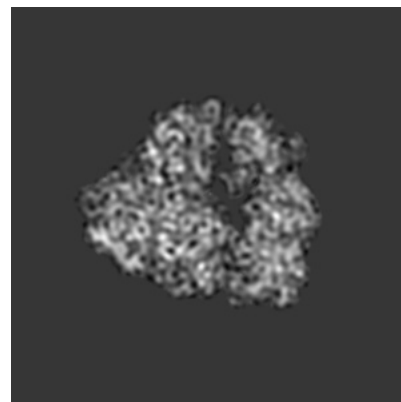
6.3.1 Primary map



X Index: 104

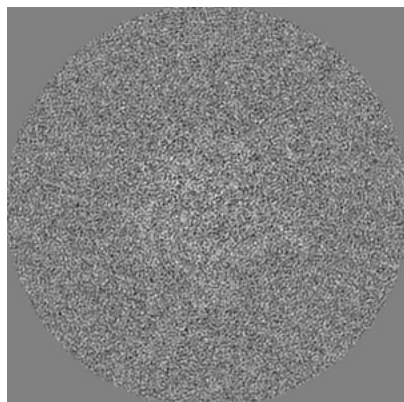


Y Index: 121

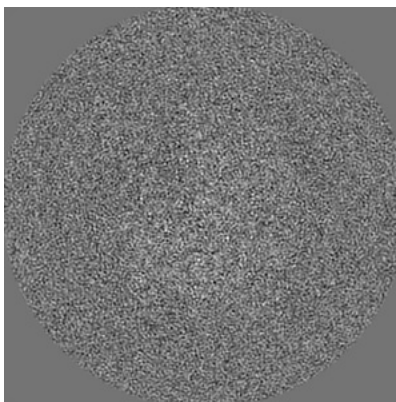


Z Index: 120

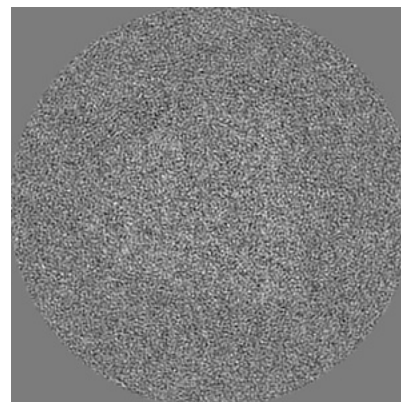
6.3.2 Raw map



X Index: 122



Y Index: 127

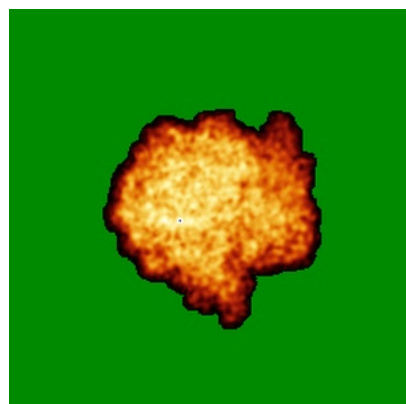


Z Index: 127

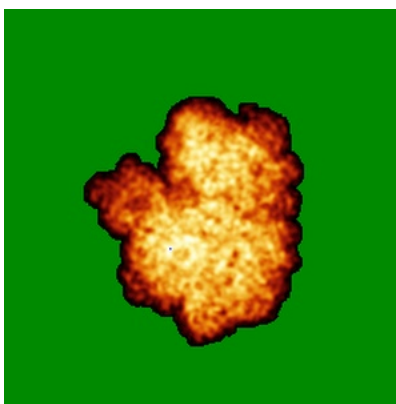
The images above show the largest variance slices of the map in three orthogonal directions.

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

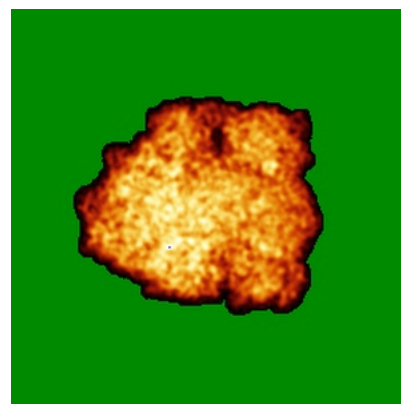
6.4.1 Primary map



X

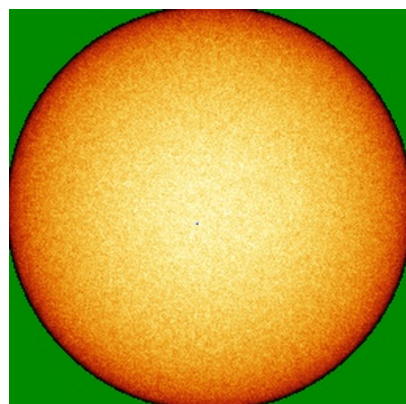


Y

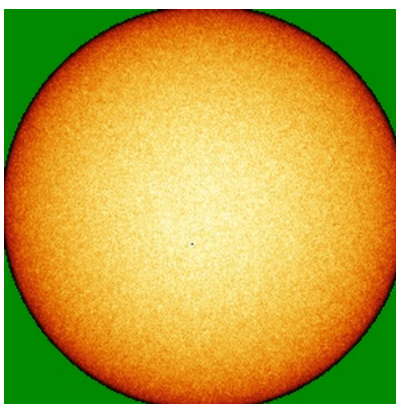


Z

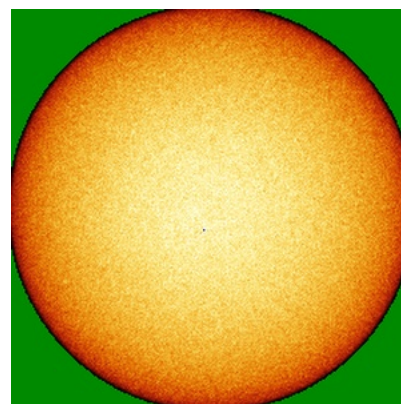
6.4.2 Raw map



X



Y



Z

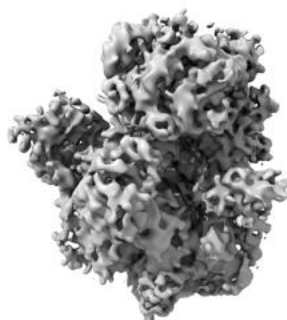
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

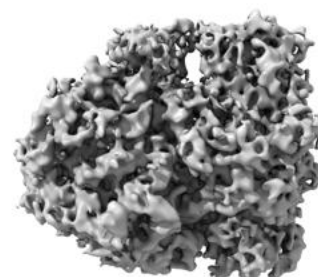
6.5.1 Primary map



X



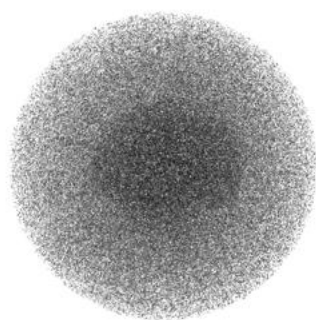
Y



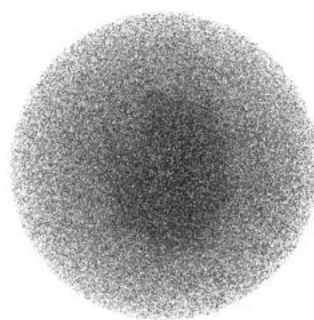
Z

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.

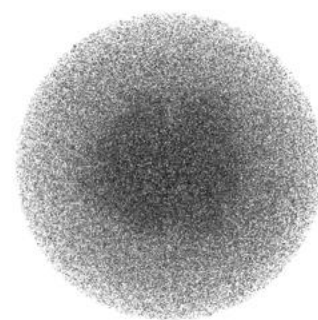
6.5.2 Raw map



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.

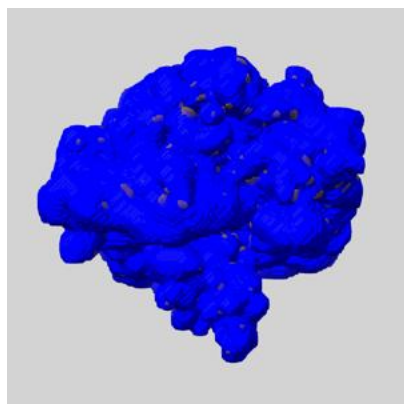
6.6 Mask visualisation [i](#)

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

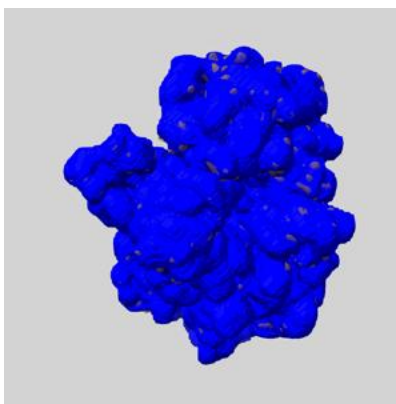
A mask typically either:

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

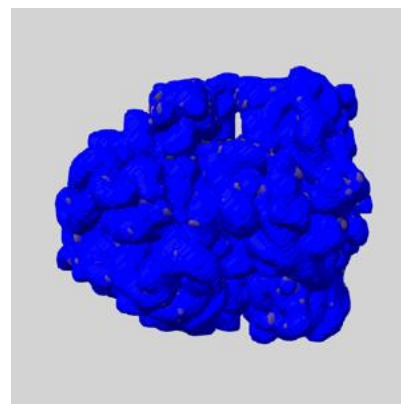
6.6.1 emd_13432_msk_1.map [i](#)



X



Y

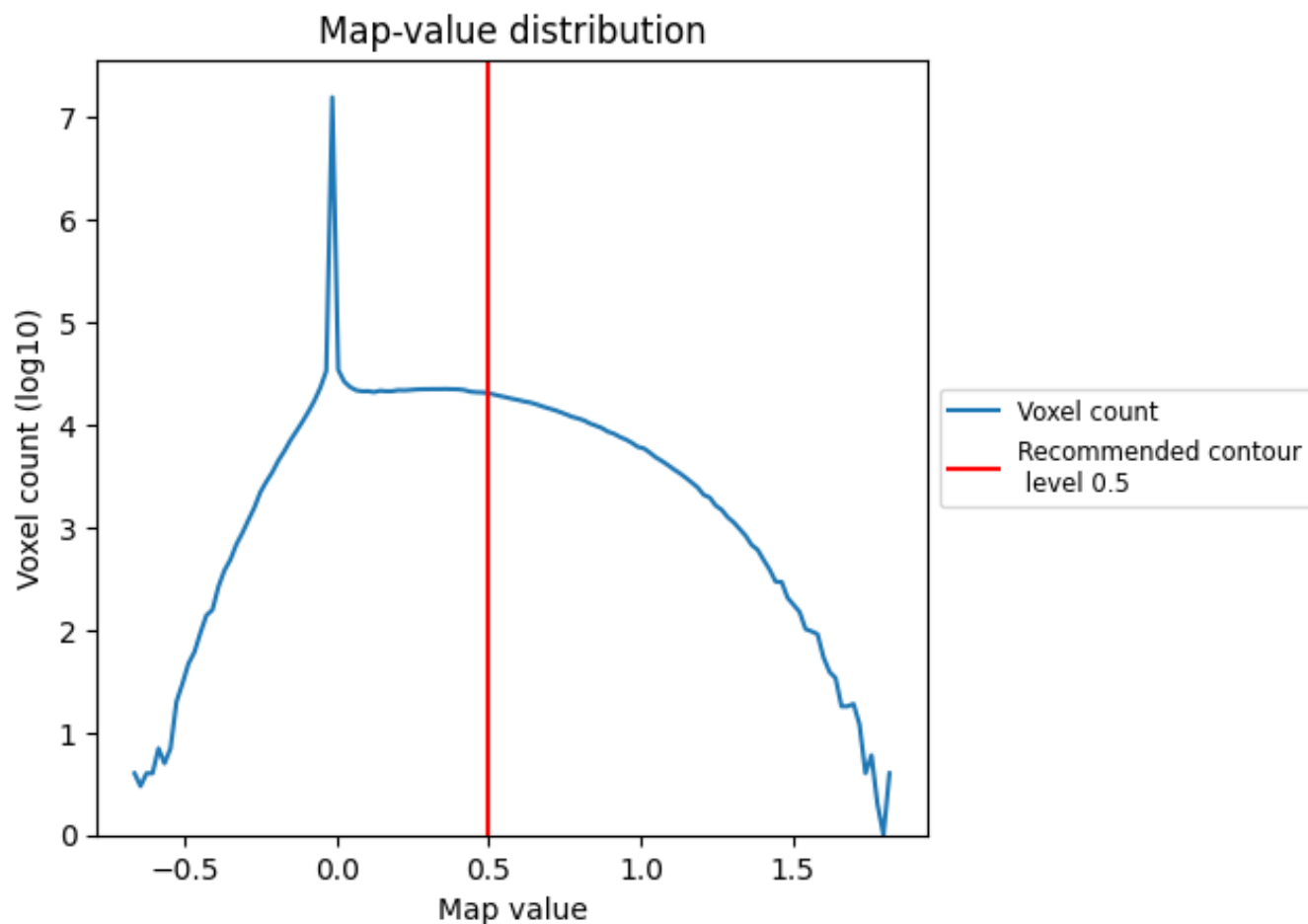


Z

7 Map analysis [i](#)

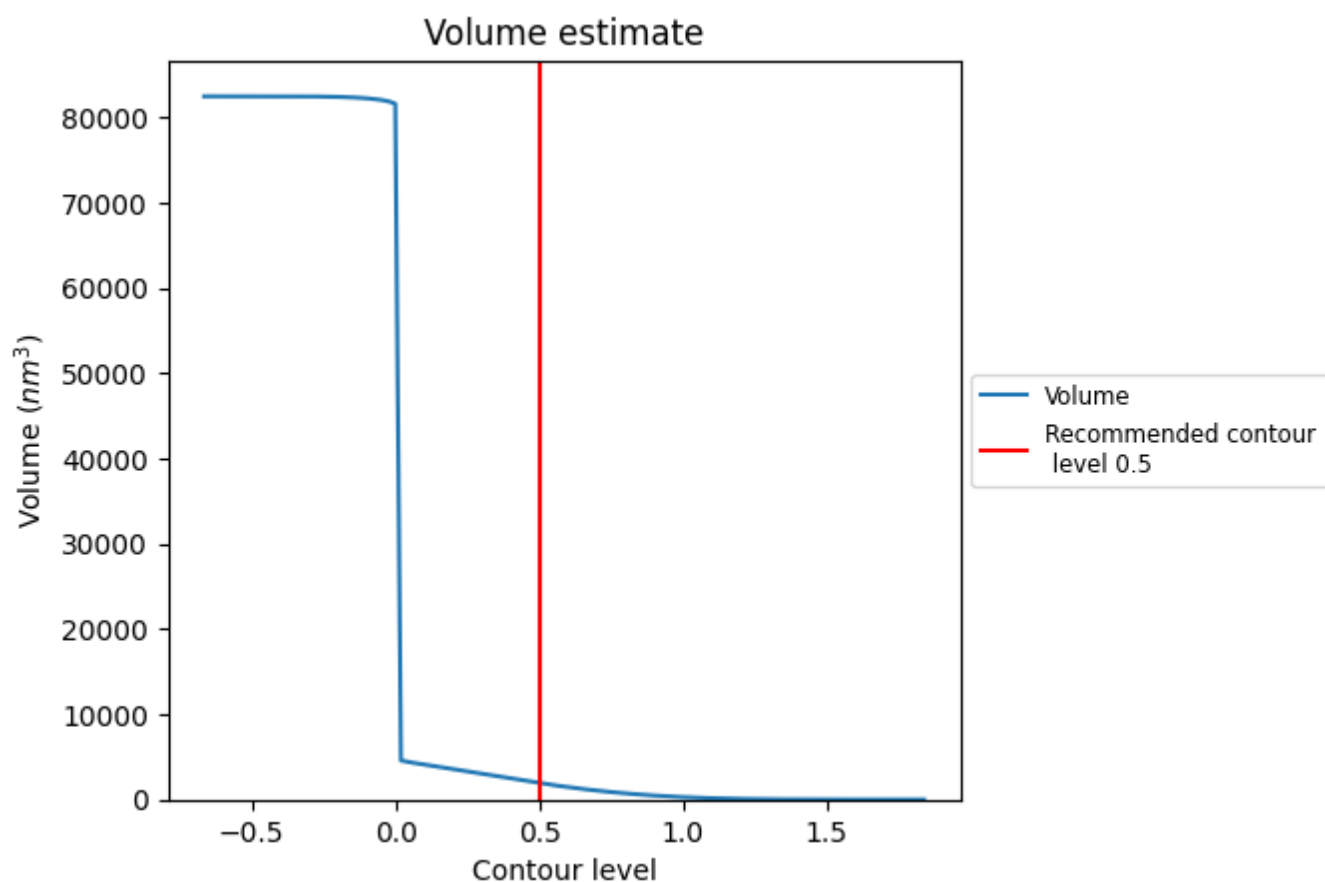
This section contains the results of statistical analysis of the map.

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.

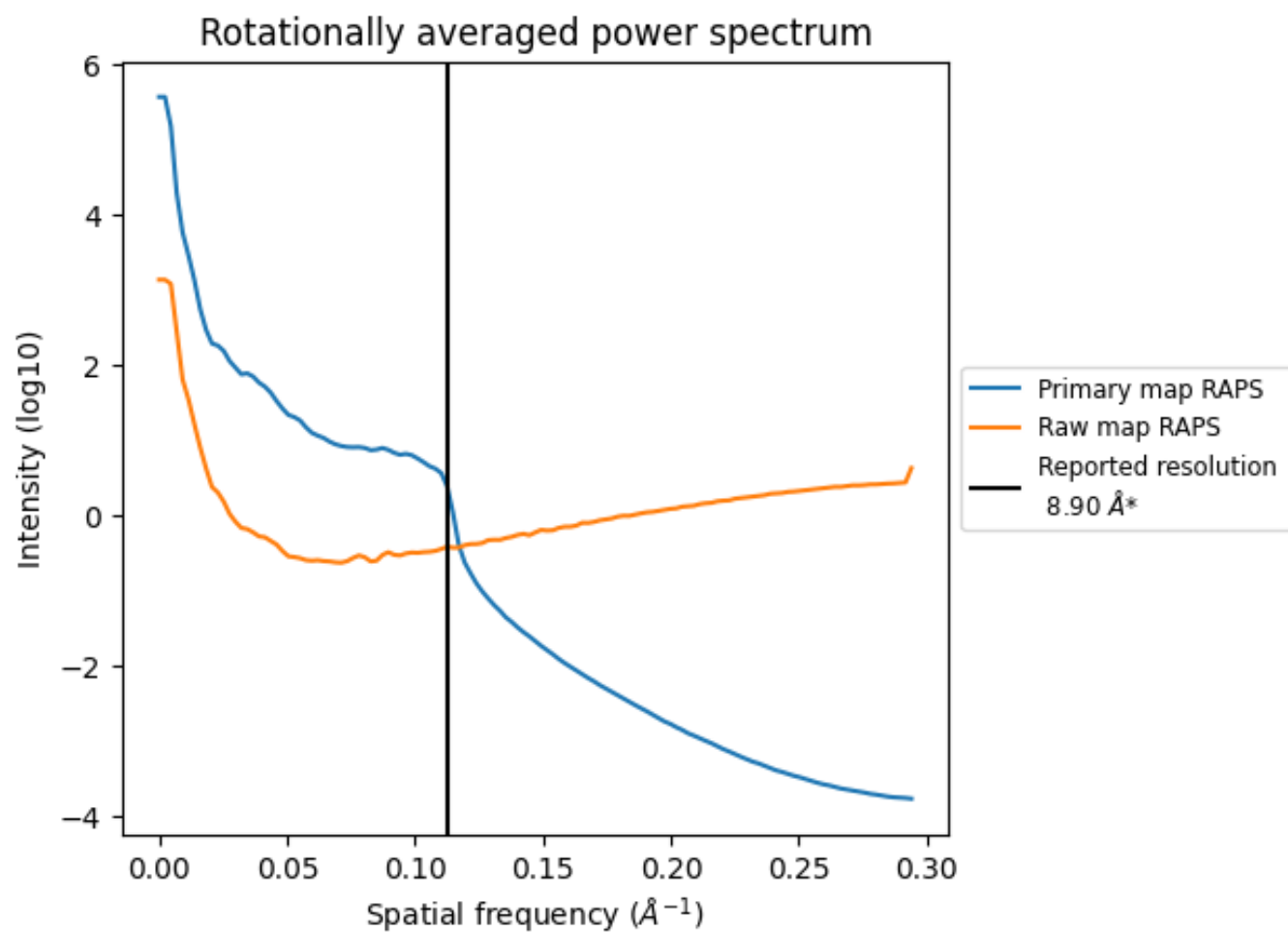
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1938 nm^3 ; this corresponds to an approximate mass of 1751 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 ⓘ

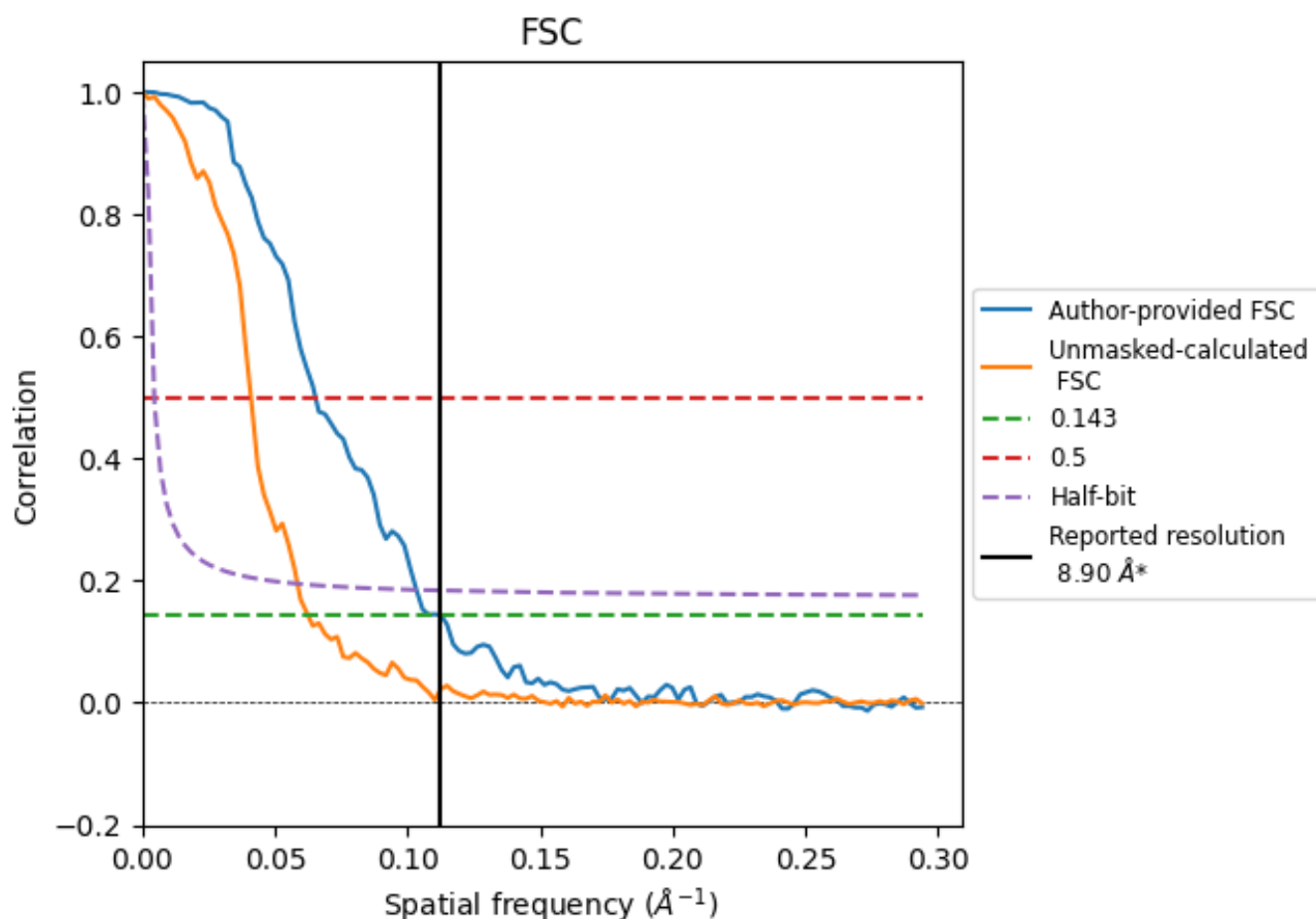


*Reported resolution corresponds to spatial frequency of 0.112 Å⁻¹

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 0.112 Å⁻¹

8.2 Resolution estimates [i](#)

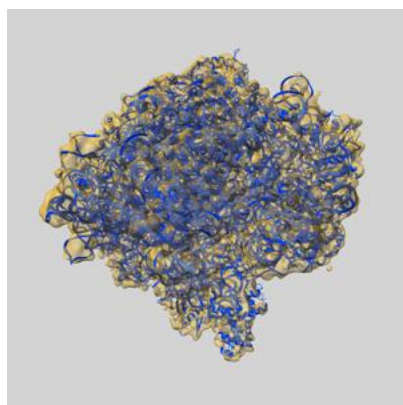
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	8.90	-	-
Author-provided FSC curve	8.88	15.31	9.68
Unmasked-calculated*	16.00	24.39	17.06

*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 16.00 differs from the reported value 8.9 by more than 10 %

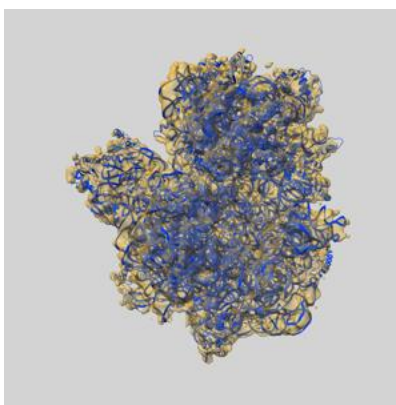
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13432 and PDB model 7PI8. Per-residue inclusion information can be found in section 3 on page 13.

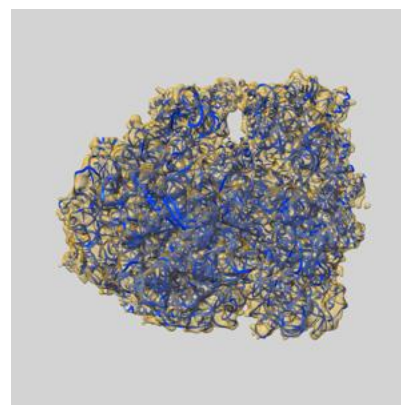
9.1 Map-model overlay [i](#)



X



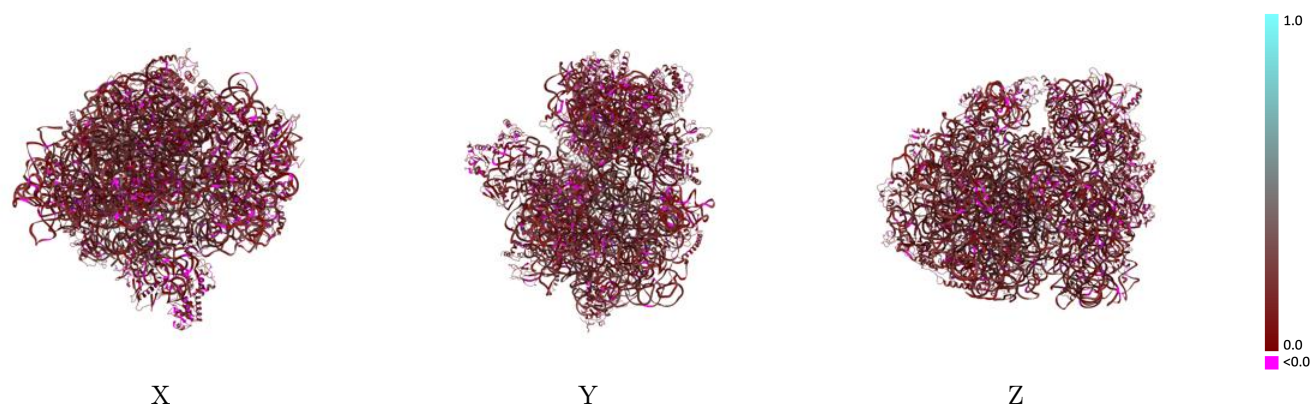
Y



Z

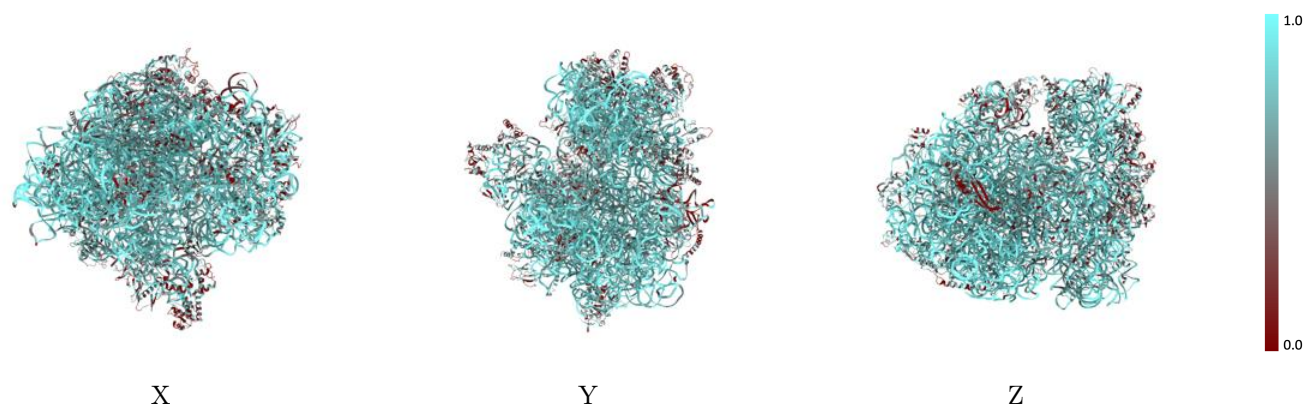
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



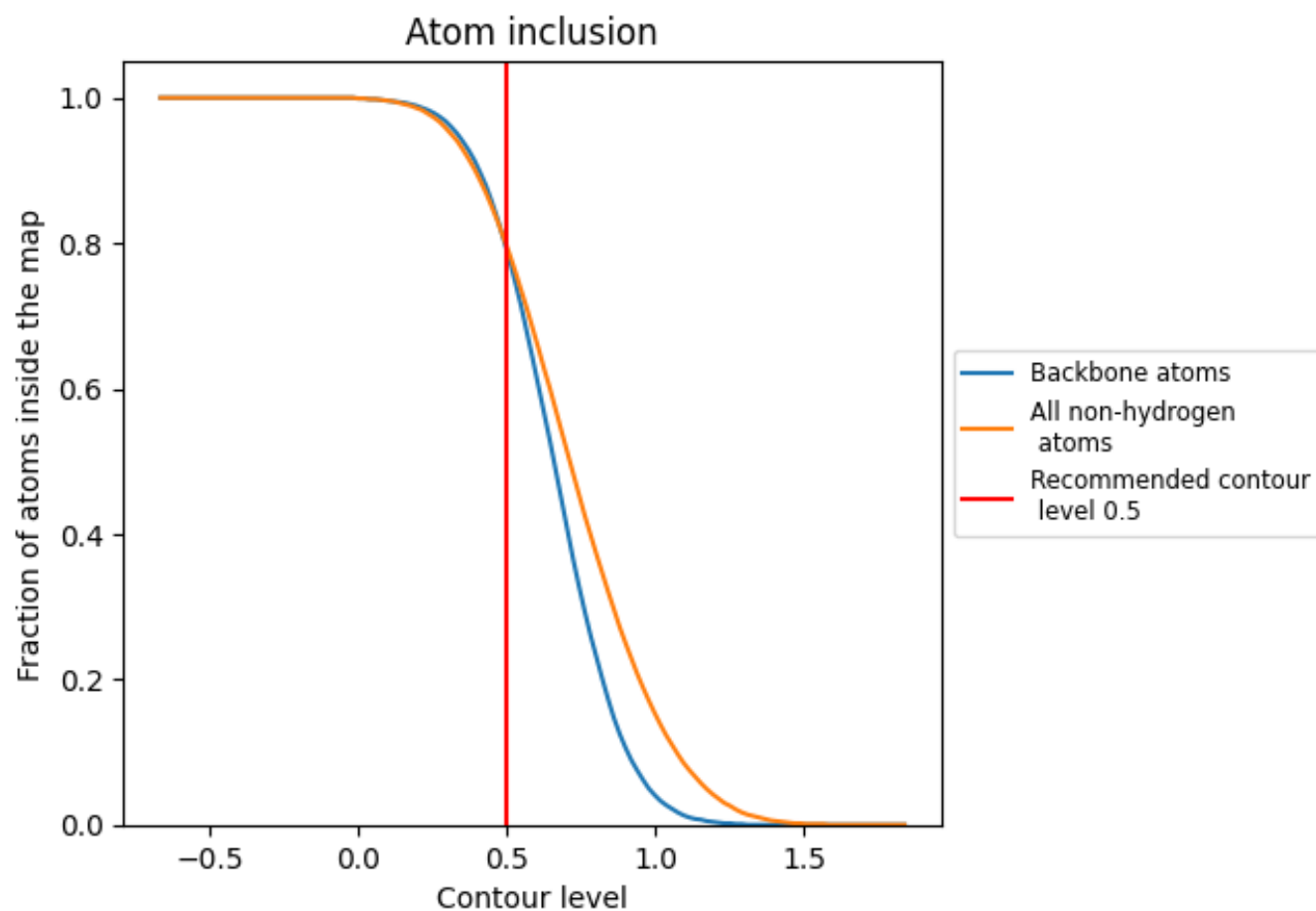
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 79% of all backbone atoms, 80% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7950	 0.1500
0	 0.6140	 0.1030
1	 0.5970	 0.1160
2	 0.7400	 0.1230
3	 0.9030	 0.1620
4	 0.8980	 0.1550
5	 0.8980	 0.1500
7	 0.8510	 0.1750
A	 0.4800	 0.1510
B	 0.5460	 0.1540
C	 0.5730	 0.1200
D	 0.4600	 0.1120
E	 0.4420	 0.1470
F	 0.5640	 0.1390
G	 0.4870	 0.1140
H	 0.5960	 0.1280
I	 0.5070	 0.1250
J	 0.6000	 0.1240
K	 0.5920	 0.1240
L	 0.5240	 0.1270
M	 0.5520	 0.0890
N	 0.6130	 0.1570
O	 0.6790	 0.1380
P	 0.6120	 0.1440
Q	 0.5950	 0.1240
R	 0.5820	 0.1150
S	 0.7150	 0.1530
T	 0.6850	 0.1820
a	 0.5900	 0.1220
b	 0.6560	 0.1310
c	 0.6240	 0.1460
d	 0.5430	 0.1410
e	 0.5280	 0.1410
f	 0.2950	 0.1220
g	 0.4300	 0.1190



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Chain	Atom inclusion	Q-score
h	 0.3930	 0.1040
i	 0.6990	 0.1540
j	 0.4620	 0.1420
k	 0.5500	 0.1210
l	 0.6080	 0.1300
m	 0.6910	 0.1310
n	 0.6150	 0.1440
o	 0.5930	 0.1490
p	 0.6900	 0.1330
q	 0.6080	 0.1500
r	 0.6850	 0.1510
s	 0.6640	 0.1540
t	 0.5730	 0.1410
u	 0.6440	 0.1160
v	 0.6280	 0.1310
w	 0.6010	 0.1720
x	 0.5420	 0.1530
y	 0.6430	 0.0860
z	 0.7410	 0.1430