



wwPDB EM Validation Summary Report ⓘ

Mar 17, 2026 – 03:00 PM UTC

PDB ID : 7PH9 / pdb_00007ph9
EMDB ID : EMD-13410
Title : 70S ribosome with P-site tRNA in chloramphenicol-treated Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-08-16
Resolution : 8.70 Å (reported)
Based on initial models : 7OOD, 4V7C, 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:

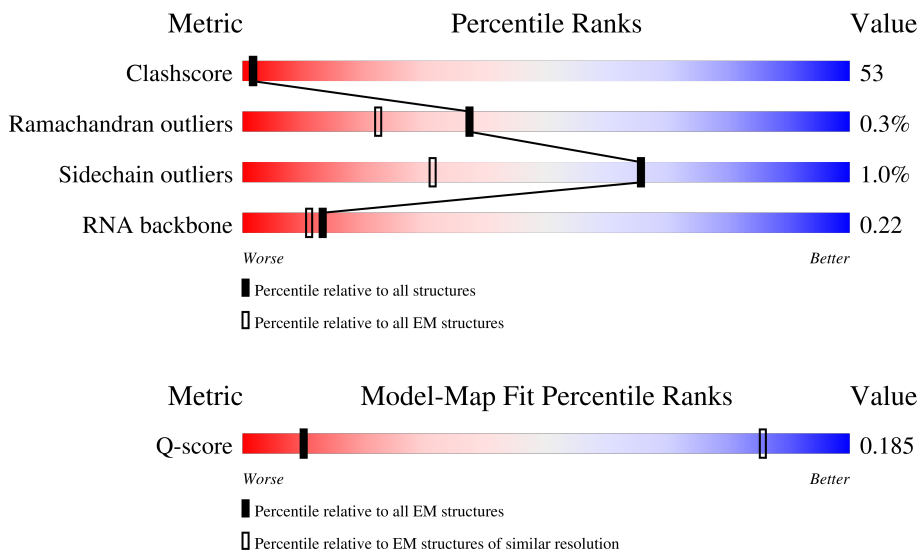
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 8.70 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	282 (8.20 - 9.20)

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	



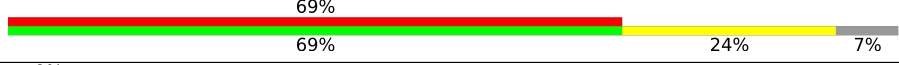
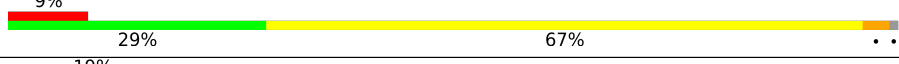
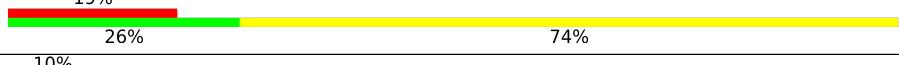
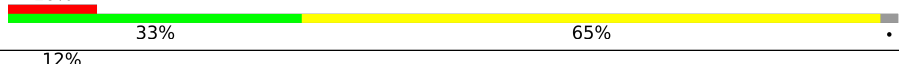
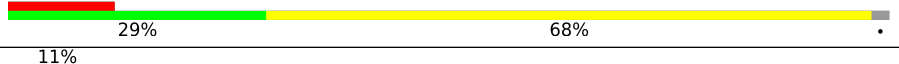
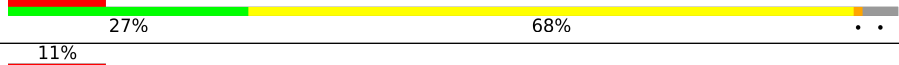
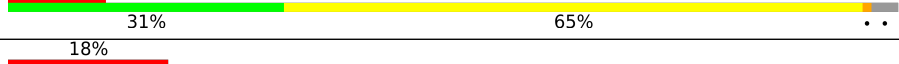
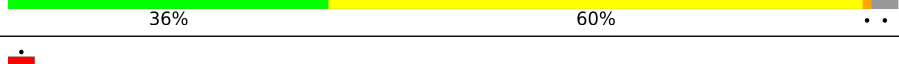

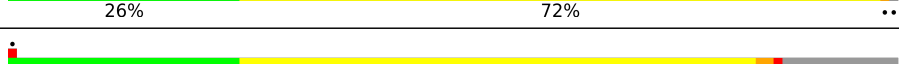

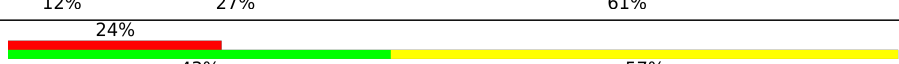
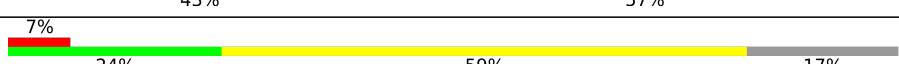
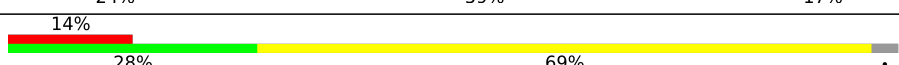
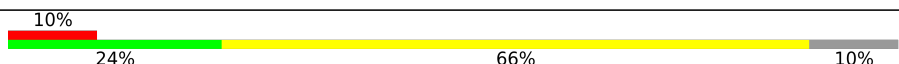

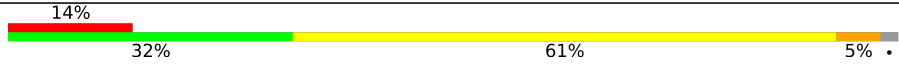




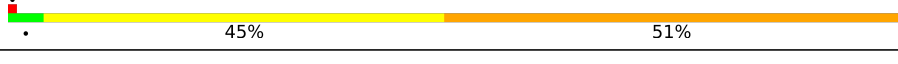

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Mol	Chain	Length	Quality of chain
4	A	294	21% 29% 53% 18%
5	B	273	19% 30% 49% 21%
6	C	205	26% 35% 64%
7	D	219	12% 24% 46% 30%
8	E	215	27% 32% 45% 22%
9	F	155	21% 41% 57%
10	G	142	16% 27% 70%
11	H	132	19% 35% 62%
12	I	108	24% 32% 60% 6%
13	J	121	26% 40% 55% 6%
14	K	139	15% 32% 63%
15	L	124	20% 34% 61% 5%
16	M	61	15% 28% 70%
17	N	86	8% 34% 63%
18	O	94	6% 44% 40% 15%
19	P	85	19% 22% 75%
20	Q	104	9% 17% 41% 38%
21	R	87	21% 30% 67%
22	S	87	26% 62% 11%
23	T	60	7% 48% 40% 12%
24	a	287	8% 32% 67%
25	b	287	14% 26% 54% 20%
26	c	212	12% 34% 64%
27	d	180	15% 38% 56%
28	e	184	25% 30% 66%

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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
			Total	C	N	O	S		
1	0	47	380	236	81	61	2	0	0

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

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

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

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

- Molecule 4 is a protein called 30S ribosomal protein S2.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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	0	0
			1396	899	247	250		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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



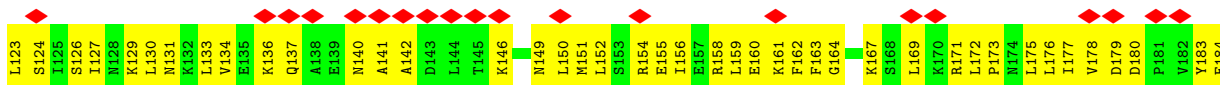
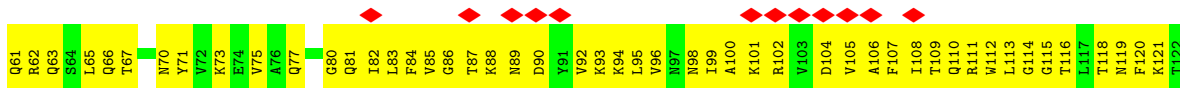
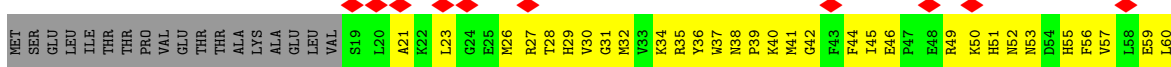
- Molecule 2: 50S ribosomal protein L35

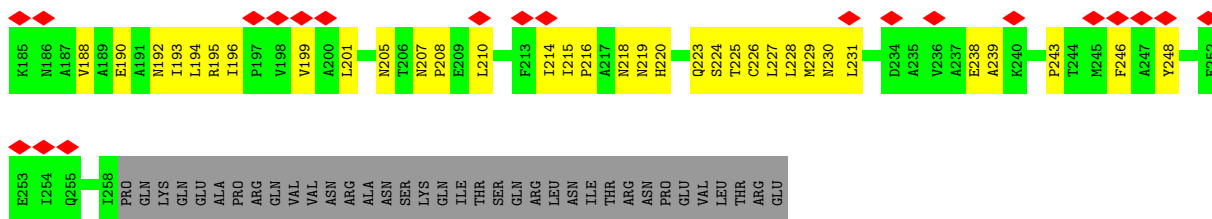


- Molecule 3: 50S ribosomal protein L36

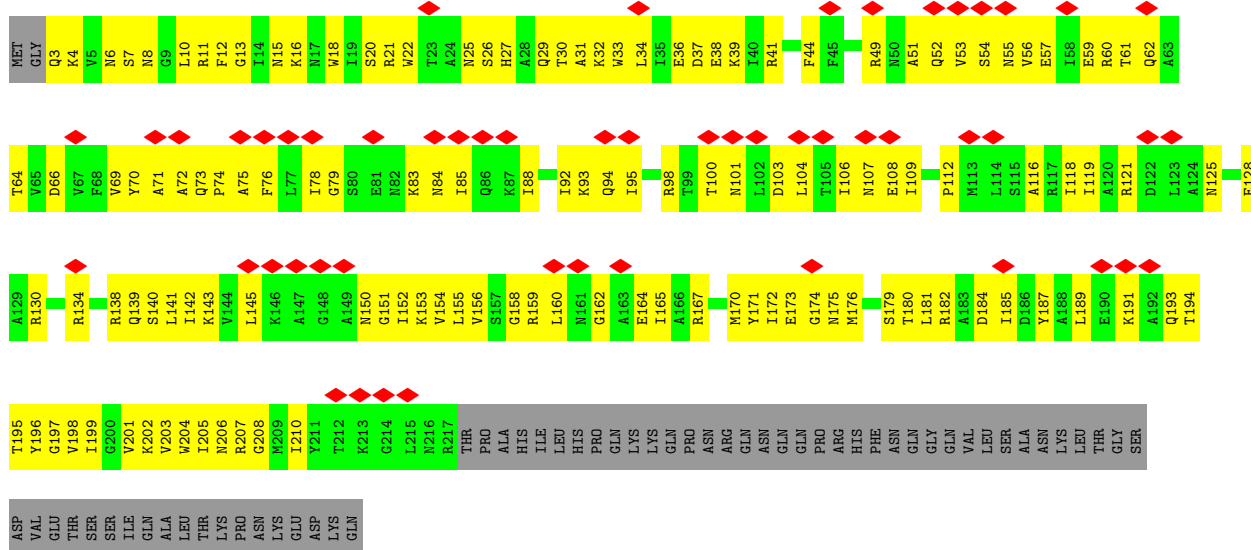


- Molecule 4: 30S ribosomal protein S2

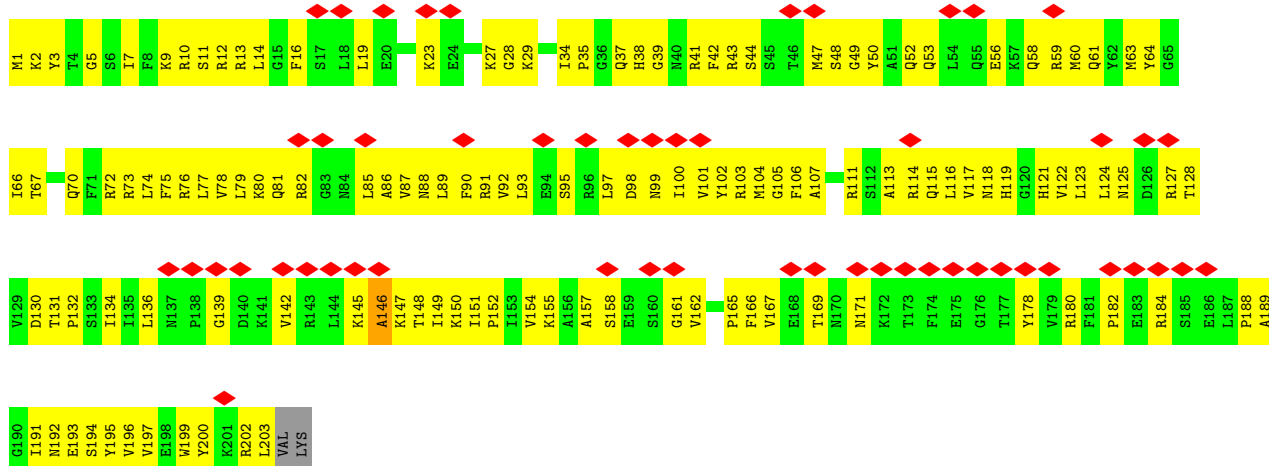




• Molecule 5: 30S ribosomal protein S3

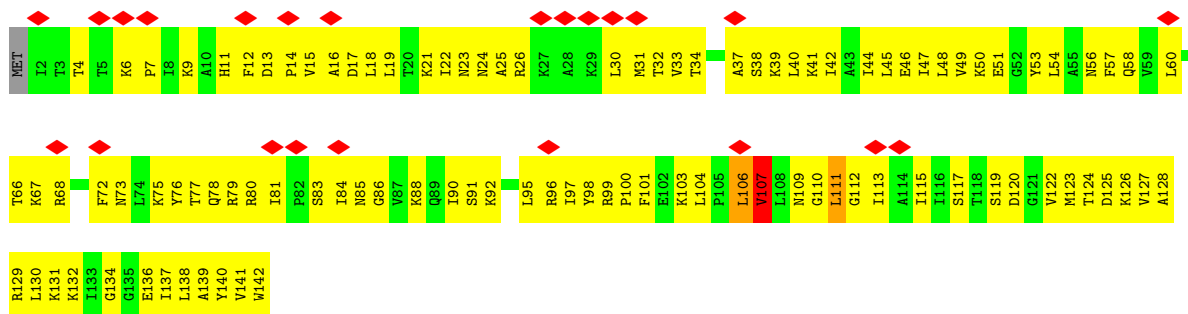


• Molecule 6: 30S ribosomal protein S4

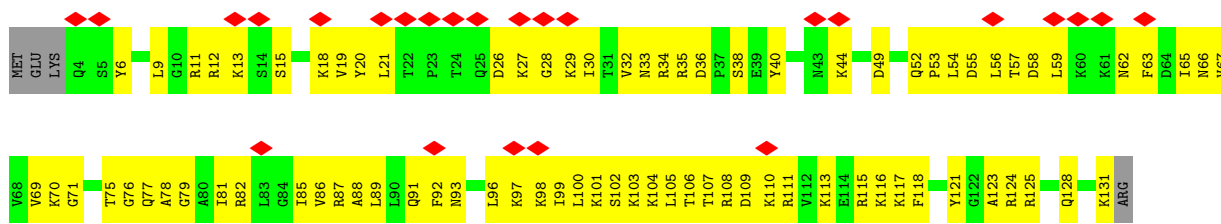


• Molecule 7: 30S ribosomal protein S5

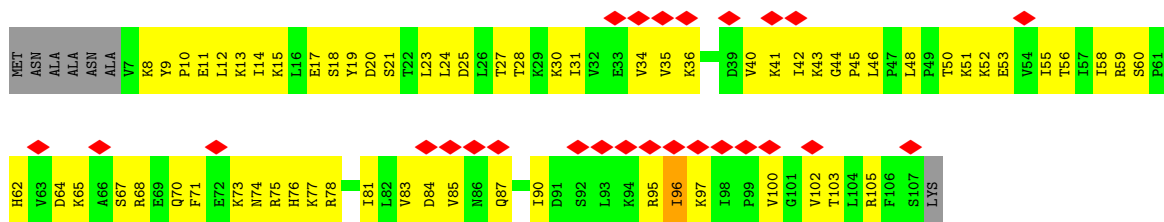
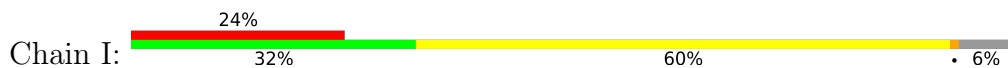




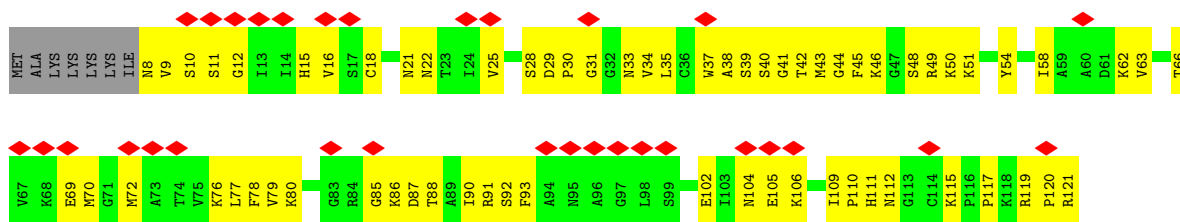
• Molecule 11: 30S ribosomal protein S9



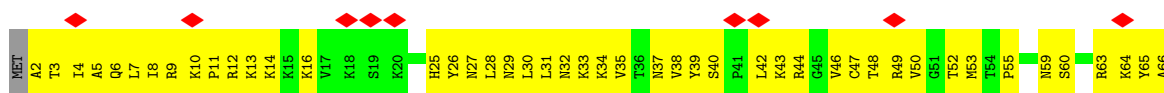
• Molecule 12: 30S ribosomal protein S10

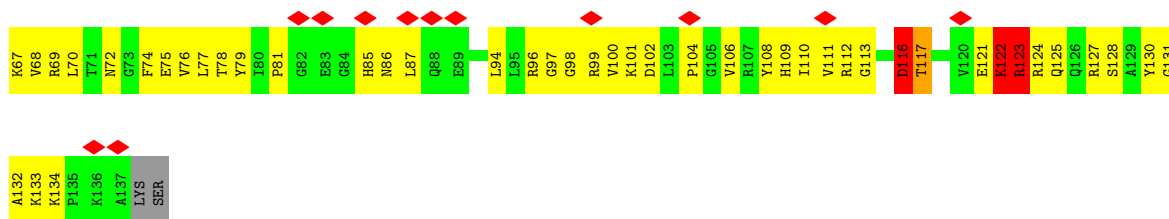


• Molecule 13: 30S ribosomal protein S11

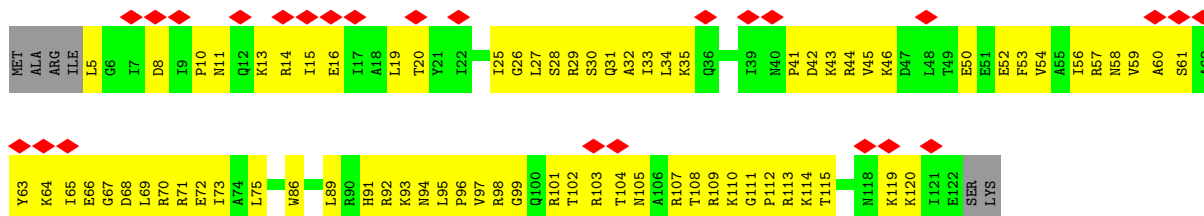


• Molecule 14: 30S ribosomal protein S12

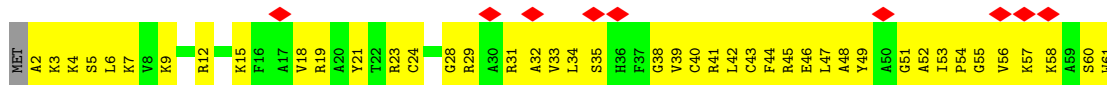




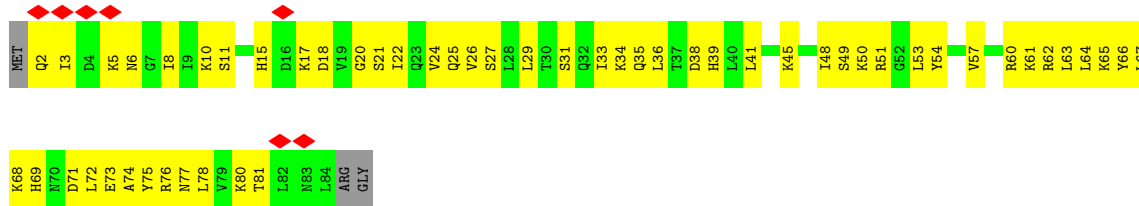
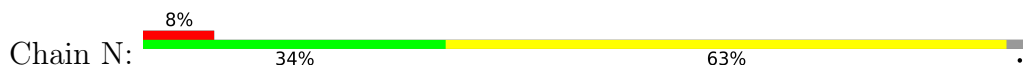
• Molecule 15: 30S ribosomal protein S13



• Molecule 16: 30S ribosomal protein S14 type Z



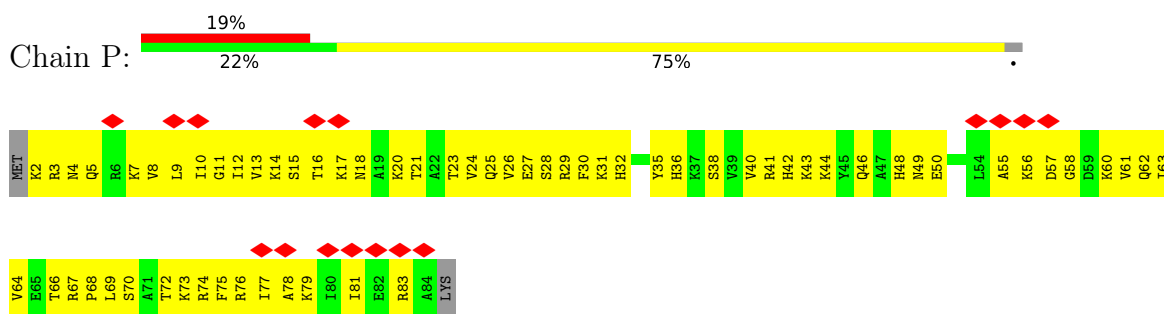
• Molecule 17: 30S ribosomal protein S15



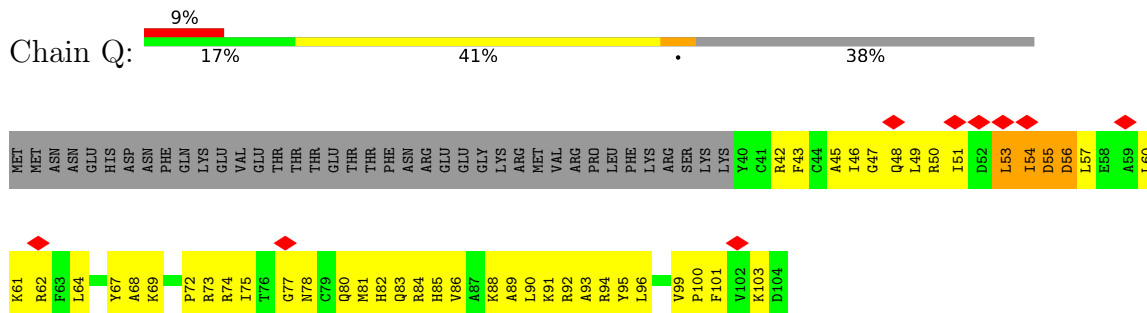
• Molecule 18: 30S ribosomal protein S16



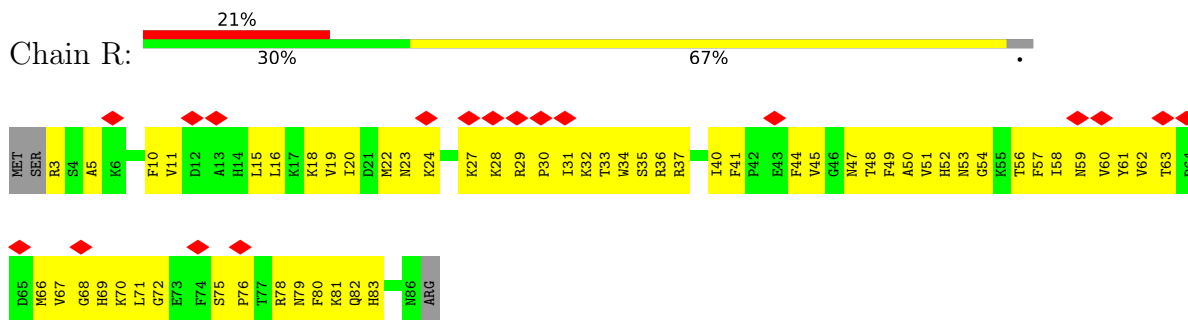
• Molecule 19: 30S ribosomal protein S17



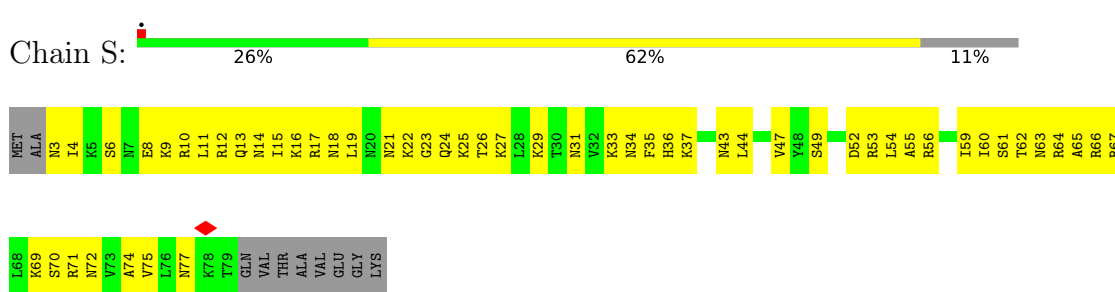
• Molecule 20: 30S ribosomal protein S18



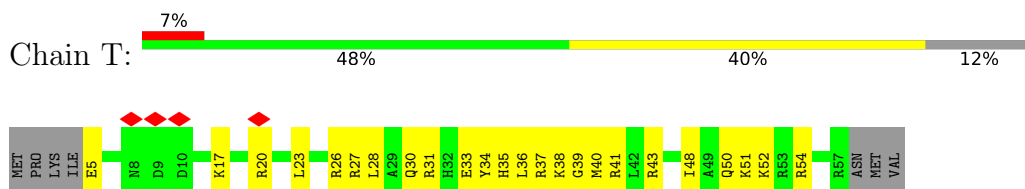
• Molecule 21: 30S ribosomal protein S19



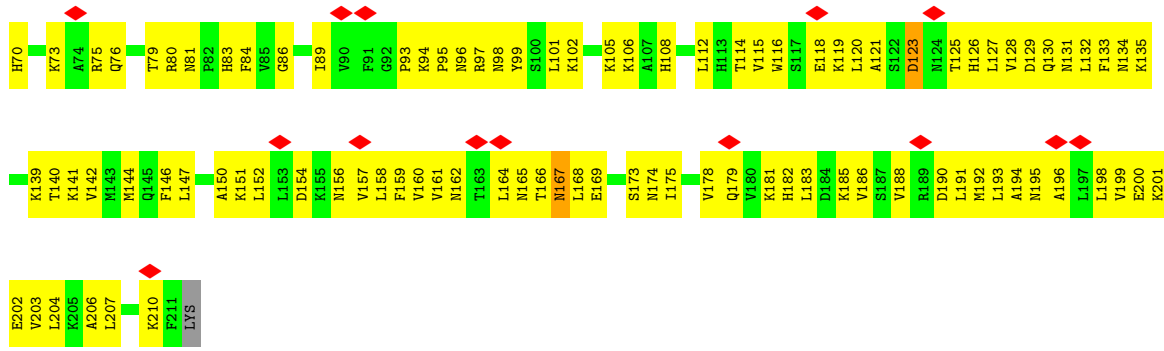
• Molecule 22: 30S ribosomal protein S20



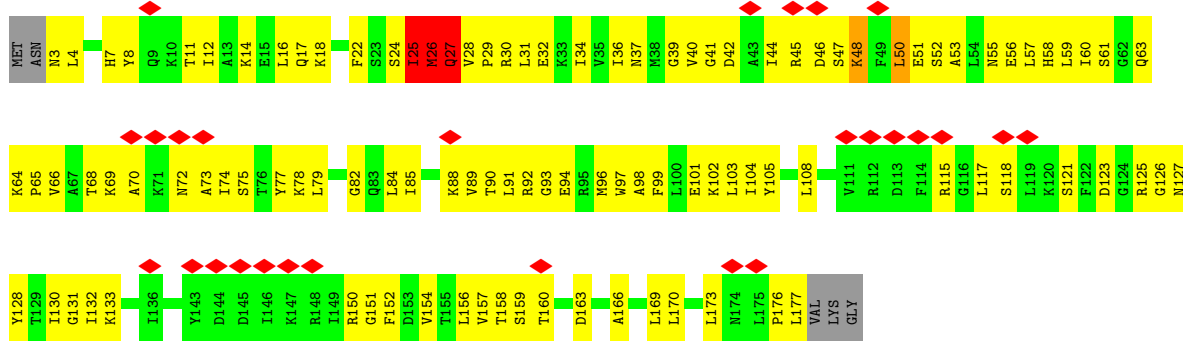
• Molecule 23: 30S ribosomal protein S21



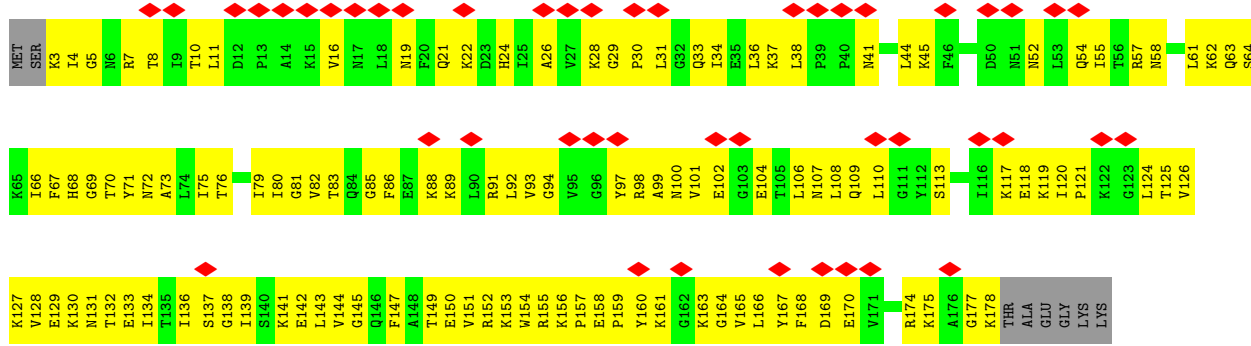
• Molecule 24: 50S ribosomal protein L2



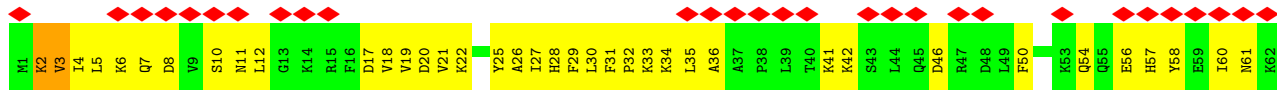
• Molecule 27: 50S ribosomal protein L5

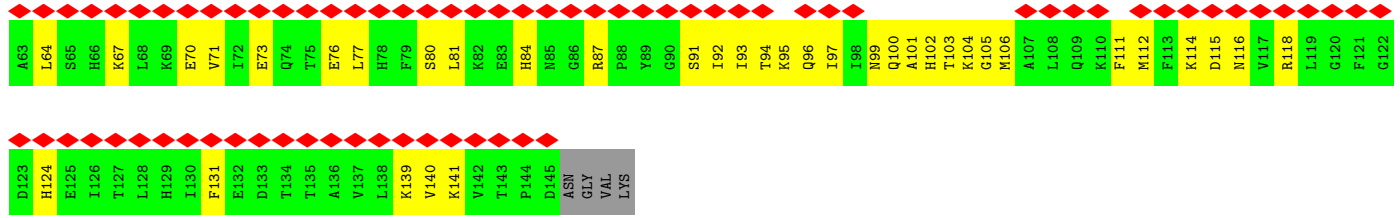


• Molecule 28: 50S ribosomal protein L6

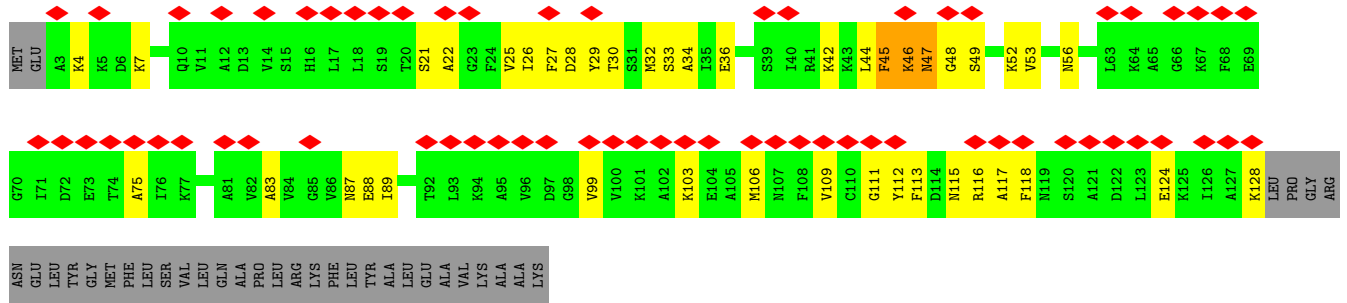


• Molecule 29: 50S ribosomal protein L9

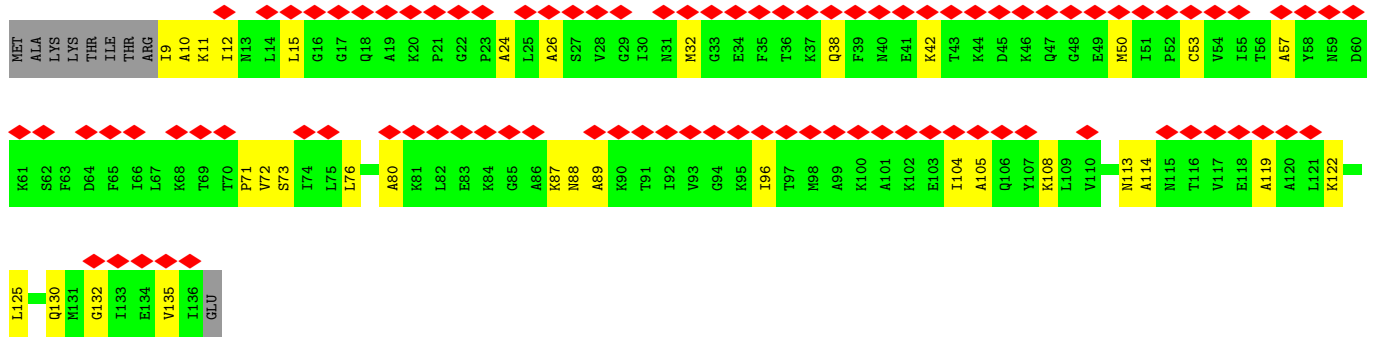




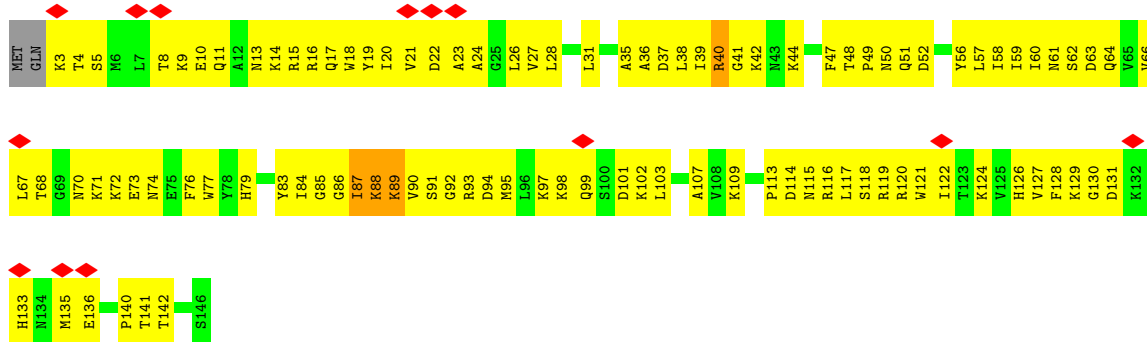
• Molecule 30: 50S ribosomal protein L10

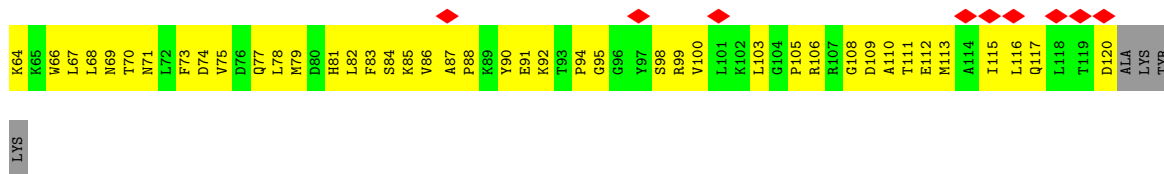


• Molecule 31: 50S ribosomal protein L11

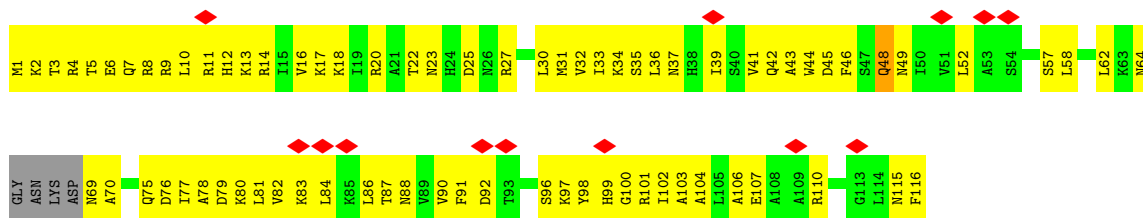


• Molecule 32: 50S ribosomal protein L13

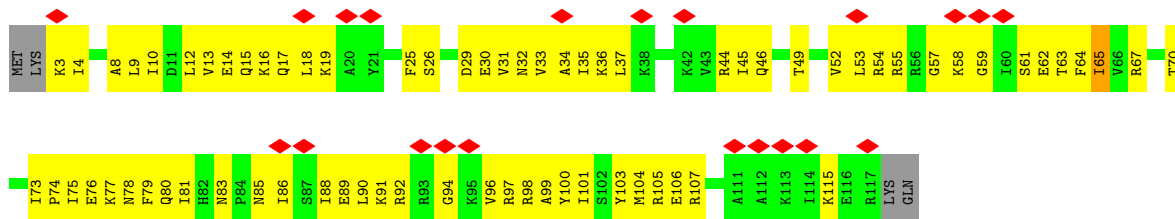




• Molecule 37: 50S ribosomal protein L18



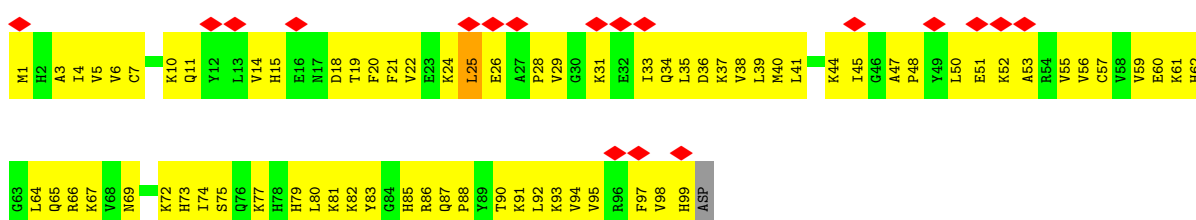
• Molecule 38: 50S ribosomal protein L19

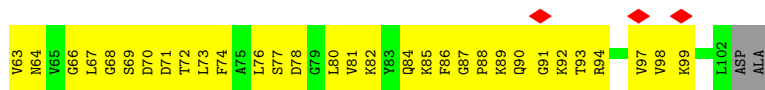


• Molecule 39: 50S ribosomal protein L20

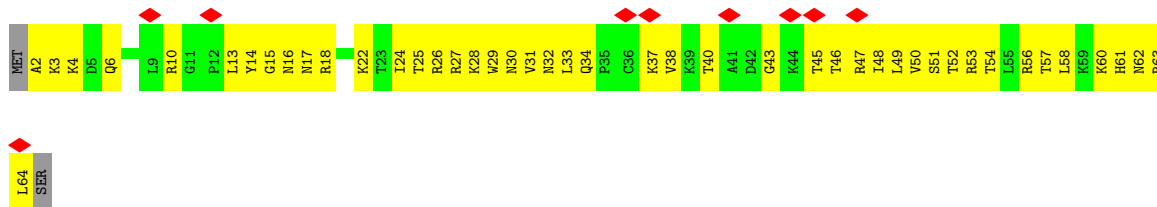


• Molecule 40: 50S ribosomal protein L21

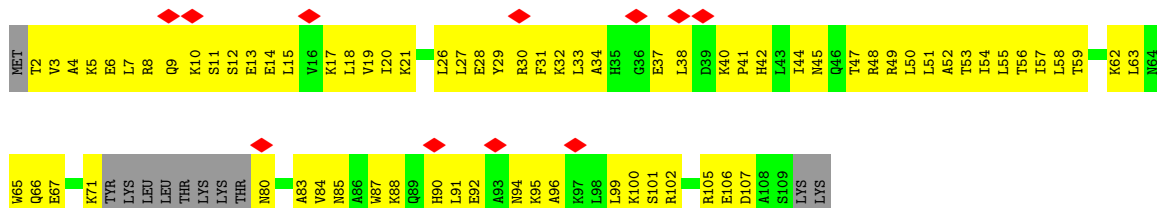




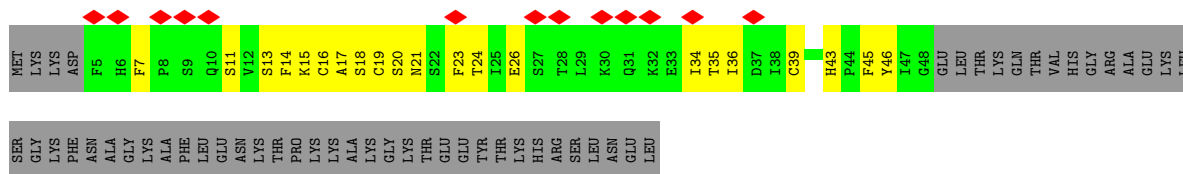
• Molecule 45: 50S ribosomal protein L28



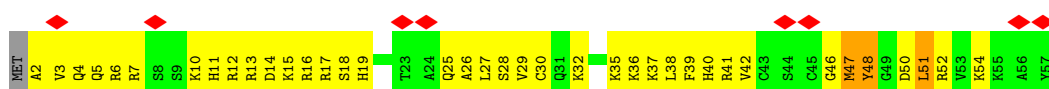
• Molecule 46: 50S ribosomal protein L29



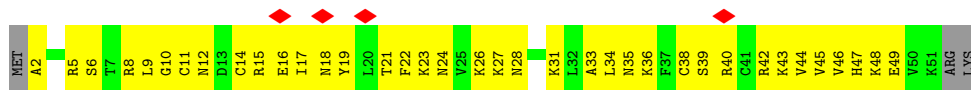
• Molecule 47: 50S ribosomal protein L31



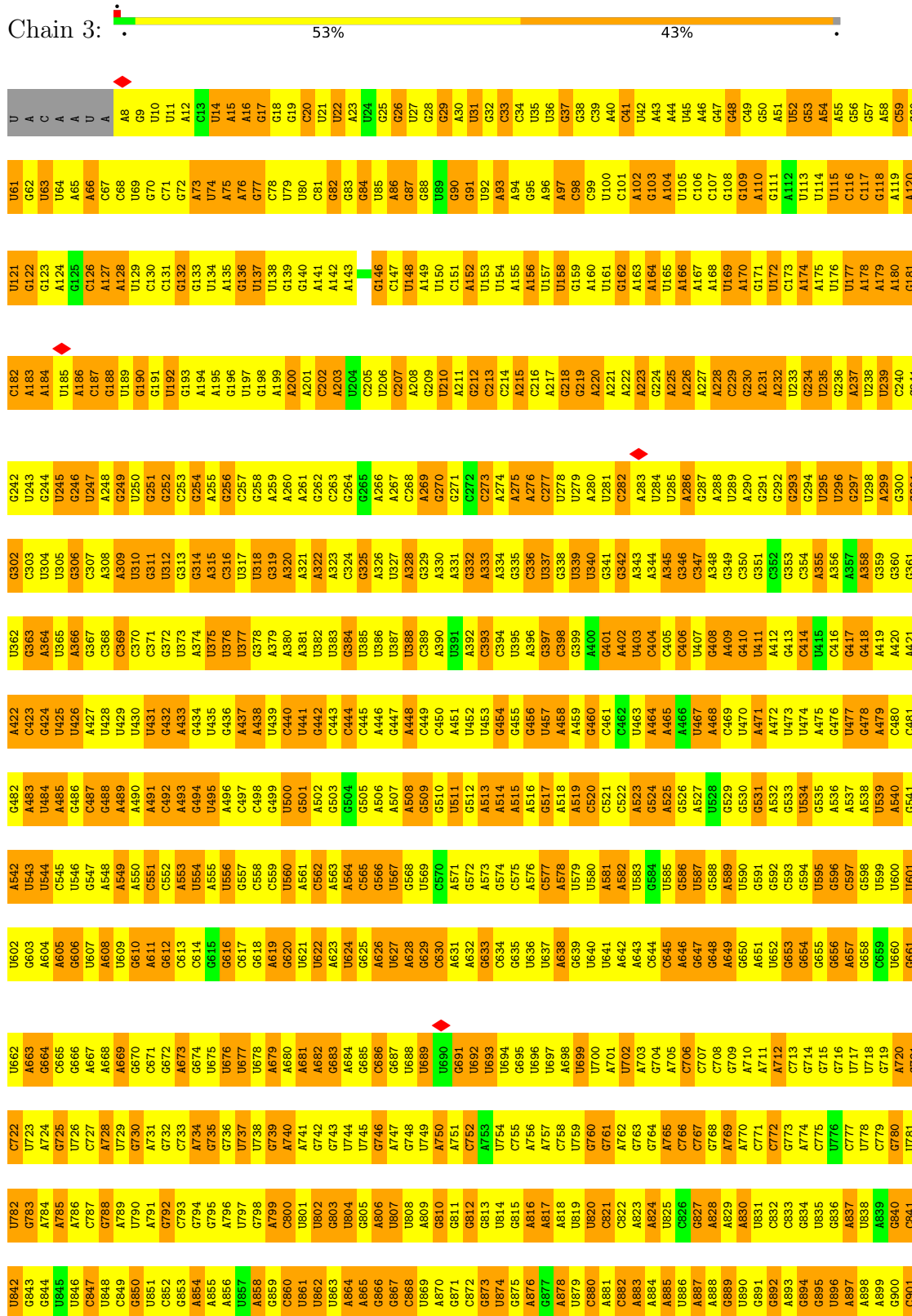
• Molecule 48: 50S ribosomal protein L32



• Molecule 49: 50S ribosomal protein L33 1



• Molecule 50: 23S ribosomal RNA



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C2402	C2403	C2404	C2405	C2406	C2407	C2408	C2409	C2410	C2411	C2412	C2413	C2414	C2415	C2416	C2417	C2418	C2419	C2420	C2421	C2422	C2423	C2424	C2425	C2426	C2427	C2428	C2429	C2430	C2431	C2432	C2433	C2434	C2435	C2436	C2437	C2438	C2439	C2440	C2441	C2442	C2443	C2444	C2445	C2446	C2447	C2448	C2449	C2450	C2451	C2452	C2453	C2454	C2455	C2456	C2457	C2458	C2459	C2460	C2461																				
U2342	U2343	U2344	U2345	U2346	U2347	U2348	U2349	U2350	U2351	U2352	U2353	U2354	U2355	U2356	U2357	U2358	U2359	U2360	U2361	U2362	U2363	U2364	U2365	U2366	U2367	U2368	U2369	U2370	U2371	U2372	U2373	U2374	U2375	U2376	U2377	U2378	U2379	U2380	U2381	U2382	U2383	U2384	U2385	U2386	U2387	U2388	U2389	U2390	U2391	U2392	U2393	U2394	U2395	U2396	U2397	U2398	U2399	U2400	U2401																				
A2382	A2383	A2384	A2385	A2386	A2387	A2388	A2389	A2390	A2391	A2392	A2393	A2394	A2395	A2396	A2397	A2398	A2399	A2400	A2401	A2402	A2403	A2404	A2405	A2406	A2407	A2408	A2409	A2410	A2411	A2412	A2413	A2414	A2415	A2416	A2417	A2418	A2419	A2420	A2421	A2422	A2423	A2424	A2425	A2426	A2427	A2428	A2429	A2430	A2431	A2432	A2433	A2434	A2435	A2436	A2437	A2438	A2439	A2440	A2441	A2442	A2443	A2444	A2445	A2446	A2447	A2448	A2449	A2450	A2451	A2452	A2453	A2454	A2455	A2456	A2457	A2458	A2459	A2460	A2461
C2222	C2223	C2224	C2225	C2226	C2227	C2228	C2229	C2230	C2231	C2232	C2233	C2234	C2235	C2236	C2237	C2238	C2239	C2240	C2241	C2242	C2243	C2244	C2245	C2246	C2247	C2248	C2249	C2250	C2251	C2252	C2253	C2254	C2255	C2256	C2257	C2258	C2259	C2260	C2261	C2262	C2263	C2264	C2265	C2266	C2267	C2268	C2269	C2270	C2271	C2272	C2273	C2274	C2275	C2276	C2277	C2278	C2279	C2280	C2281	C2282																			
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	U2204	U2205	U2206	U2207	U2208	U2209	U2210	U2211	U2212	U2213	U2214	U2215	U2216	U2217	U2218	U2219	U2220	U2221																				
C2042	C2043	C2044	C2045	C2046	C2047	C2048	C2049	C2050	C2051	C2052	C2053	C2054	C2055	C2056	C2057	C2058	C2059	C2060	C2061	C2062	C2063	C2064	C2065	C2066	C2067	C2068	C2069	C2070	C2071	C2072	C2073	C2074	C2075	C2076	C2077	C2078	C2079	C2080	C2081	C2082	C2083	C2084	C2085	C2086	C2087	C2088	C2089	C2090	C2091	C2092	C2093	C2094	C2095	C2096	C2097	C2098	C2099	C2100	C2101																				
U2102	U2103	U2104	U2105	U2106	U2107	U2108	U2109	U2110	U2111	U2112	U2113	U2114	U2115	U2116	U2117	U2118	U2119	U2120	U2121	U2122	U2123	U2124	U2125	U2126	U2127	U2128	U2129	U2130	U2131	U2132	U2133	U2134	U2135	U2136	U2137	U2138	U2139	U2140	U2141	U2142	U2143	U2144	U2145	U2146	U2147	U2148	U2149	U2150	U2151	U2152	U2153	U2154	U2155	U2156	U2157	U2158	U2159	U2160	U2161																				
G1982	G1983	G1984	G1985	G1986	G1987	G1988	G1989	G1990	G1991	G1992	G1993	G1994	G1995	G1996	G1997	G1998	G1999	G2000	G2001	G2002	G2003	G2004	G2005	G2006	G2007	G2008	G2009	G2010	G2011	G2012	G2013	G2014	G2015	G2016	G2017	G2018	G2019	G2020	G2021	G2022	G2023	G2024	G2025	G2026	G2027	G2028	G2029	G2030	G2031	G2032	G2033	G2034	G2035	G2036	G2037	G2038	G2039	G2040	G2041																				
A1862	A1863	A1864	A1865	A1866	A1867	A1868	A1869	A1870	A1871	A1872	A1873	A1874	A1875	A1876	A1877	A1878	A1879	A1880	A1881	A1882	A1883	A1884	A1885	A1886	A1887	A1888	A1889	A1890	A1891	A1892	A1893	A1894	A1895	A1896	A1897	A1898	A1899	A1900	A1901	A1902	A1903	A1904	A1905	A1906	A1907	A1908	A1909	A1910	A1911	A1912	A1913	A1914	A1915	A1916	A1917	A1918	A1919	A1920	A1921																				
U1922	U1923	U1924	U1925	U1926	U1927	U1928	U1929	U1930	U1931	U1932	U1933	U1934	U1935	U1936	U1937	U1938	U1939	U1940	U1941	U1942	U1943	U1944	U1945	U1946	U1947	U1948	U1949	U1950	U1951	U1952	U1953	U1954	U1955	U1956	U1957	U1958	U1959	U1960	U1961	U1962	U1963	U1964	U1965	U1966	U1967	U1968	U1969	U1970	U1971	U1972	U1973	U1974	U1975	U1976	U1977	U1978	U1979	U1980	U1981																				

C2822	C2823	A2824	A2825	A2826	A2827	C2828	G2829	A2830	C2831	G2832	A2833	C2834	G2835	G2836	G2837	G2838	A2839	U2840	A2841	G2842	G2843	U2844	U2845	A2846	C2847	A2848	G2849	G2850	U2851	G2852	U2853	A2854	G2855	G2856	C2857	A2858	U2859	A2860	G2861	U2862	G2863	A2864	U2865	A2866	U2867	G2868	U2869	U2870	G2871	A2872	G2873	C2874	U2875	U2876	G2877	G2878	U2879	A2880	A2881
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U2883	A2883	C2884	U2885	A2886	A2887	U2888	U2889	G2890	C2891	U2892	C2893	G2894	A2895	G2896	G2897	A2898	C2899	U2900	U	A	U	U	U	U	G	G	A
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• Molecule 51: 5S ribosomal RNA



U1	U2	U3	G4	G5	U6	G7	C8	C9	C10	A11	U12	G13	U14	C15	G16	G19	U20	G21	G22	A23	U24	G25	U26	G27	U28	G29	U30	G31	U32	U33	U34	G35	G36	G37	U38	U39	U40	C41	G42	A43	G44	C45	A46	A47	A48	C49	C50	C51	G52	U53	U54	A55	A56	G57	C58	A59	C60	A61
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G62	U63	G64	G65	A66	G67	C68	C69	G70	A71	C10	A72	U73	G74	U75	A76	G77	C78	U79	G80	U	U	U	G85	A86	U87	G88	C89	G90	U91	G92	U93	U94	G95	G96	A97	U98	A99	G100	C101	A102	C103	G104	A105	A106	C108
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• Molecule 52: 16S ribosomal RNA



U	U	U	U	U5	C6	U7	G8	A9	G10	A11	G12	U13	U14	U15	G16	C78	U79	G80	U	U	G85	A86	U87	G88	C89	G90	U91	G92	U93	U94	G95	G96	A97	U98	A99	G100	C101	A102	C103	G104	A105	A106	C108
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A61	G62	U63	C64	A65	G66	U67	C68	G69	A70	A71	A72	G73	U74	U75	G76	U77	A78	U79	U80	A81	C82	U83	U84	U85	A86	G87	A88	G89	U90	C91	U92	A93	A94	C95	G96	G97	U98	U99	G100	A101	G102	U103	A104	A105	C106	U107	G108	C109	U110	A111	U112	C113	C114	A115	A116	U117	C118	U119	A120
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C121	C122	U123	U124	A125	U126	A127	A128	U129	G130	G131	A132	G133	G134	A135	U136	A137	A138	C139	U140	U144	G145	U146	A147	A148	G149	A150	C151	U152	U153	G154	C155	U156	U157	A158	U159	A160	C161	G162	G163	C164	A165	U166	A167	A168	G169	A170	A171	C172	U173	U174	U175	G176	U177	U178	U179	C180	G	C
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A	U	G185	A186	A187	U188	C189	A190	A191	A192	G193	U194	G195	G196	A197	A198	A199	G200	G201	A202	C203	C204	U205	G206	A207	A208	A209	G210	G211	G212	U213	U214	C215	G216	U217	U218	A219	U220	U221	U222	G223	A224	U225	G226	A227	G228	G229	G230	U231	G232	C233	G234	C235	C236	A237	U238	A239	U240	G301	C241	A242
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G243	C244	U245	A246	G247	U248	U249	G250	A251	U252	G253	G254	U255	G256	U257	A258	A259	C260	G261	C262	G263	C264	U265	A266	C267	C268	A269	A270	G271	G272	C273	A274	A275	U276	U277	G278	C279	G280	U281	G282	U283	A284	U285	G286	U287	A288	U289	G290	C291	U292	G293	A294	C295	A296	A297	U298	U299	A300	U362	A302
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A303	U304	A305	C306	A307	C308	A309	C310	A311	G312	U313	G314	U315	G316	A317	A318	U319	G320	A321	G322	A323	C324	A325	C326	G327	G328	C329	C330	C331	A332	U333	A334	C335	U336	C337	G338	C339	A340	C341	G342	A343	G344	A345	G346	G347	C348	A349	G350	C351	A352	G353	U354	A355	A356	G357	U358	G359	A360	U362
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U363	U364	U365	U366	A367	A368	A369	A370	U371	G372	A373	G374	C375	G376	A377	A378	G379	A380	C381	U382	U383	A384	A385	U386	G387	G388	A389	G390	C391	A392	A393	U394	G395	C396	C397	G398	C399	G400	U401	G402	A403	A404	C405	G406	A407	U408	A409	A410	A411	G412	U413	U414	C415	U416	U417	A418	U419	A420	G421	A422
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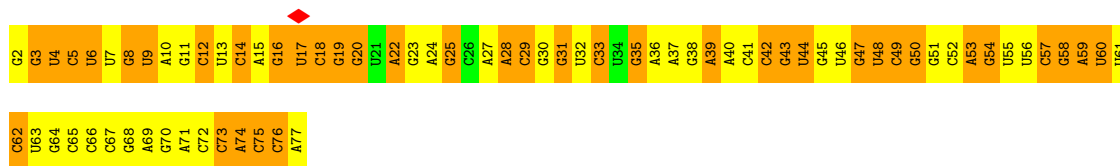
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C485	C486	A487	U488	U489	U490	U491	G492	C493	A494	U495	U496	A497	U498	U499	G500	A501	C502	G503	U504	G505	C506	G507	A508	C509	U510	A511	U512	G513	U514	G515	U516	C517	U518	G519	C520	A521	G522	U523	C524	G525	C526	G527	U528	U529	A530	A531	U532	A533	C534	G535	U536	C537	U538	U539	G540	U541	G542	U543	C544	A544
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A545	G546	C547	G548	U549	U550	A551	U552	C553	A554	U555	U556	A557	U558	U559	U560	A561	C562	U563	G564	G565	C566	C567	G568	C569	U570	A571	A572	G573	C574	U575	A576	G577	C578	G579	C580	A581	G582	G583	C584	G585	G586	C587	U588	U589	A590	A591	U592	A593	C594	G595	U596	C597	U598	U599	G600	U601	G602	G603	C604	A544
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A1509	C	G1449	A1388	G1327	G1267	U1207	U1147	C1087	C967	C986	G846	U785	A725	G665	A605
C	U	C1450	U1389	C1328	G1268	G1208	U1148	C1088	G968	A907	G847	U786	A726	U666	A606
U	C	A1451	G1390	G1329	G1269	C1209	G1149	C1089	G969	A908	U848	A787	G727	U667	G608
C	U	C1452	A1391	A1330	C1270	U1210	U1150	G1090	A970	A909	U849	G728	G728	U668	G609
C	C	G1453	A1392	C1331	G1271	A1211	A1151	C1091	A971	C910	U850	C729	C729	U669	C610
U	U	G1454	A1393	U1332	C1272	C1212	G1152	A1092	A972	G911	U851	U790	G730	G670	C611
U	U	G1455	G1394	C1333	A1273	A1213	G1153	A1093	A973	G912	A791	A731	A731	G671	A611
U	U	U1456	C1395	A1384	G1274	A1214	A1154	C1094	C974	A913	A852	C732	A732	A672	G612
U	U	G1457	G1396	U1385	U1275	U1215	A1155	A1095	C975	A914	A853	C733	A733	A673	G613
C	U	A1458	G1397	U1337	G1276	U1216	A1156	A1096	U976	U916	G854	C734	A734	U674	U614
U	U	U1459	G1398	C1338	C1277	G1217	G1157	G1097	U977	C794	G855	C735	A735	U675	G615
A	A	G1460	A1399	U1339	G1278	C1218	A1158	C1098	A978	U978	U856	U736	C736	U676	C616
		G1461	A1400	G1340	G1279	C1219	A1159	G1099	C979	U798	U857	U737	U737	G677	U617
		G1462	A1401	U1341	A1280	A1220	G1160	C1100	C980	A799	A858	U738	A738	A678	U618
		A1463	A1402	C1342	U1281	A1221	G1161	A1101	U981	G921	A859	A739	A739	A679	A619
		G1464	A1403	G1343	U1282	U1222	G1162	A1102	U982	G922	C860	G739	G739	U679	G620
		U1465	U1404	C1344	G1283	A1223	G1163	C1103	A983	G923	C861	U801	C741	U681	C621
		U1466	A1405	G1345	A1284	C1224	U1164	C1104	A984	G924	C862	C802	C742	U682	C622
		A1467	U1406	G1346	G1285	A1225	G1165	C1105	A985	C925	U864	C803	C743	G683	G623
		A1468	A1407	U1347	G1286	A1226	A1166	U1106	U986	C926	U865	C804	U744	A684	U624
		G1469	G1408	G1348	G1287	A1227	C1167	U1107	U987	C927	U866	A806	U745	G685	U625
		U1470	A1409	A1349	C1288	C1228	U1168	A1108	G988	G928	A867	C807	U746	G686	G626
		C1471	A1410	A1350	U1289	A1229	G1169	U1109	A989	C929	C868	C808	C747	G687	U627
		G1472	A1411	U1351	G1290	U1230	C1170	C1110	C990	A930	U868	G809	U748	G688	A628
		U1473	C1412	A1352	U1291	U1231	A1171	U1051	C991	C931	U870	U810	C749	U689	U629
		A1474	G1413	C1353	A1292	C1232	A1172	G1052	U992	U932	A871	A811	A750	G690	G630
		U1475	U1414	G1354	A1293	G1233	U1173	U1053	C993	A933	C872	A812	C751	C631	C631
		G1476	G1415	U1355	U1294	C1234	U1174	C1054	C994	G934	C873	A813	G752	A691	A691
		A1477	U1416	U1356	G1295	A1235	C1175	G1055	C995	U935	U874	C814	C753	A692	A692
		G1478	U1417	C1357	G1296	U1236	U1176	U1056	U996	U936	C875	C815	C754	A693	U633
		G1479	G1418	U1237	G1297	A1237	U1177	C1057	G997	G937	U876	A816	U755	U694	U634
		G1480	U1420	C1358	U1298	C1238	C1178	A1058	G998	U938	C877	U817	A756	G695	G635
		U1481	A1421	G1360	C1299	C1239	U1179	G1059	C999	U939	U878	A818	C757	C696	G636
		A1482	C1422	G1361	C1300	U1240	U1180	A1120	A1000	G940	U879	A819	G758	U697	A637
		C1483	A1423	U1362	U1301	G1241	G1181	U1121	A1001	A941	G880	A820	C759	U698	A638
		C1484	C1424	U1363	C1302	U1242	C1182	U1122	A1002	U942	C881	U821	U760	A699	A639
		C1485	A1425	C1364	A1303	A1243	C1183	G1063	G1003	C943	U882	A822	U761	G700	C640
		C1486	U1426	U1365	U1304	A1244	C1184	U1064	U1004	A944	U883	C823	G762	A701	U641
		U1487	U1427	U1366	G1305	A1245	C1185	G1065	U1005	U945	G884	U824	A763	U702	A642
		A1488	A1428	G1367	A1306	A1246	U1186	U1066	A1006	G946	U885	A825	A764	A703	U643
		G1489	G1429	A1368	G1307	G1247	U1187	C1067	U1007	U947	A886	G826	G765	U704	U644
		A1490	A1430	G1370	A1308	U1248	U1188	G1068	G1008	U948	C887	C827	G766	A705	A645
		G1491	A1431	A1371	U1309	G1249	U1189	U1069	G1009	G949	A888	U828	U767	G707	A646
		G1492	A1432	C1372	G1310	A1250	G1190	A1070	A1010	C950	U889	G829	G768	A708	U647
		A1493	G1433	C1373	G1311	G1251	U1191	A1071	U951	U830	U890	U830	U769	A709	U648
		C1494	A1434	C1374	C1312	C1252	C1192	G1072	A1012	U952	C891	G831	G770	G710	A650
		G1495	G1435	U1375	A1313	A1253	U1193	A1073	C1013	A953	G892	G832	G771	G711	G651
		U1496	C1436	G1376	G1314	A1254	A1194	U1074	A1014	A954	C893	G833	G772	A712	A652
		A1497	A1437	C1377	C1315	A1255	G1195	G1075	U1015	U955	A894	G834	G773	A713	G653
		G1498	U1438	C1378	C1316	A1256	G1196	U1076	A1016	U956	A895	C835	A774	C714	U654
		G1499	G1439	C1379	A1317	C1257	G1197	U1077	A1017	C957	G896	C836	G775	A715	G655
		U1500	A1440	U1380	G1318	C1258	U1198	G1078	U1018	G958	A897	G837	G776	A716	G656
		G1501	C1441	G1381	U1319	U1259	U1199	G1079	G1019	A959	A898	A838	A777	C717	U657
		U1502	A1442	A1320	G1320	G1260	G1200	G1080	G	C960	U899	U839	A778	A718	G658
		U1503	A1443	C1382	U1321	A1261	C1201	U1081	A	G961	G900	C840	A779	A719	U659
		G1504	G1444	A1383	G1322	A1262	A1202	U1082	G	C962	A901	C841	U780	U720	A660
		G1505	G1445	A1384	A1323	A1263	A1203	A1083	G	U963	A902	C842	A781	G721	G661
		U1506	A1446	C1385	A1324	G1264	C1204	A1084	U	A964	A903	C843	G782	G722	G662
		U1507	U1447	C1386	U1325	U1265	C1205	G1085	U	C965	C904	U844	G783	G723	G663
		C1508	A1448	U1387	C1326	U1266	G1206	U1086	A	A966	U905	C845	A784	G724	A664

● Molecule 53: tRNA-Phe

Chain 7:  45% 51%

4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	2218	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 K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.451	Depositor
Minimum map value	-0.444	Depositor
Average map value	0.024	Depositor
Map value standard deviation	0.116	Depositor
Recommended contour level	0.45	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	0.29	0/383	0.63	0/504
2	1	0.24	0/484	0.65	0/637
3	2	0.28	0/306	0.81	2/401 (0.5%)
4	A	0.28	0/1954	0.61	0/2642
5	B	0.28	0/1721	0.62	0/2323
6	C	0.22	0/1691	0.60	0/2267
7	D	0.30	0/1188	0.67	0/1593
8	E	0.26	0/1384	0.64	0/1867
9	F	0.26	0/1266	0.62	3/1700 (0.2%)
10	G	0.32	0/1126	0.67	1/1517 (0.1%)
11	H	0.25	0/1044	0.66	3/1395 (0.2%)
12	I	0.25	0/820	0.72	1/1103 (0.1%)
13	J	0.23	0/844	0.56	0/1136
14	K	0.36	0/1094	0.78	2/1468 (0.1%)
15	L	0.23	0/962	0.59	0/1289
16	M	0.26	0/483	0.58	0/643
17	N	0.26	0/679	0.59	0/907
18	O	0.28	0/659	0.66	1/885 (0.1%)
19	P	0.29	0/684	0.66	0/913
20	Q	0.34	0/545	0.69	0/730
21	R	0.28	0/698	0.71	0/936
22	S	0.23	0/631	0.54	0/838
23	T	0.23	0/475	0.61	0/621
24	a	0.27	0/2267	0.62	1/3044 (0.0%)
25	b	0.29	0/1795	0.64	2/2412 (0.1%)
26	c	0.28	0/1671	0.64	0/2246
27	d	0.30	0/1409	0.71	4/1894 (0.2%)
28	e	0.31	0/1420	0.66	1/1912 (0.1%)
29	f	0.27	0/1205	0.64	0/1616
30	g	0.48	0/969	0.92	1/1295 (0.1%)
31	h	0.24	0/968	0.63	0/1298
32	i	0.28	0/1186	0.65	1/1592 (0.1%)
33	j	0.24	0/953	0.61	1/1275 (0.1%)
34	k	0.27	0/1170	0.65	0/1559

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	l	0.27	0/1104	0.61	0/1481
36	m	0.32	0/973	0.65	0/1309
37	n	0.26	0/897	0.62	1/1198 (0.1%)
38	o	0.27	0/948	0.63	0/1262
39	p	0.28	0/961	0.59	0/1278
40	q	0.32	0/828	0.75	1/1111 (0.1%)
41	r	0.30	0/1077	0.69	0/1441
42	s	0.28	0/732	0.62	0/988
43	t	0.25	0/879	0.62	0/1165
44	u	0.27	0/665	0.69	0/884
45	v	0.27	0/519	0.77	0/695
46	w	0.24	0/826	0.63	1/1104 (0.1%)
47	x	0.23	0/353	0.63	0/474
48	y	0.37	0/457	0.81	0/601
49	z	0.26	0/412	0.67	0/547
50	3	0.25	0/69073	0.44	0/107710
51	4	0.26	0/2505	0.49	0/3902
52	5	0.25	0/35768	0.43	0/55764
53	7	0.22	0/1808	0.44	0/2817
All	All	0.26	0/156919	0.51	27/234189 (0.0%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	i	86	GLY	N-CA-C	-10.95	101.73	115.31
40	q	25	LEU	N-CA-C	-8.10	103.30	113.02
9	F	16	VAL	N-CA-C	-7.88	106.22	113.71
14	K	116	ASP	N-CA-C	-7.53	103.06	111.71
27	d	27	GLN	N-CA-C	-6.83	104.05	112.38

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	63	0
2	1	477	0	530	60	0
3	2	304	0	350	41	0
4	A	1921	0	1973	171	0
5	B	1698	0	1768	143	0
6	C	1660	0	1719	142	0
7	D	1173	0	1267	106	0
8	E	1362	0	1377	115	0
9	F	1246	0	1308	109	0
10	G	1110	0	1226	112	0
11	H	1028	0	1094	94	0
12	I	809	0	894	90	0
13	J	829	0	855	76	0
14	K	1076	0	1170	115	0
15	L	951	0	1014	89	0
16	M	474	0	509	67	0
17	N	673	0	730	56	0
18	O	646	0	677	44	0
19	P	675	0	728	80	0
20	Q	535	0	562	63	0
21	R	682	0	691	66	0
22	S	629	0	681	67	0
23	T	471	0	522	31	0
24	a	2225	0	2301	234	0
25	b	1762	0	1808	180	0
26	c	1644	0	1731	175	0
27	d	1388	0	1469	113	0
28	e	1396	0	1481	134	0
29	f	1182	0	1228	110	0
30	g	960	0	1014	26	0
31	h	959	0	1039	28	0
32	i	1164	0	1192	109	0
33	j	944	0	1019	95	0
34	k	1153	0	1256	136	0
35	l	1079	0	1134	124	0
36	m	958	0	1011	98	0
37	n	889	0	952	101	0
38	o	938	0	1008	86	0
39	p	947	0	1028	109	0
40	q	811	0	858	86	0
41	r	1068	0	1150	109	0
42	s	720	0	803	76	0
43	t	872	0	972	77	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	u	657	0	695	79	0
45	v	513	0	560	67	0
46	w	818	0	870	71	0
47	x	344	0	333	19	0
48	y	452	0	472	54	0
49	z	408	0	440	47	0
50	3	61664	0	30953	5546	0
51	4	2239	0	1137	217	0
52	5	31943	0	16056	2826	0
53	7	1618	0	821	141	0
All	All	144524	0	98865	11957	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 53.

The worst 5 of 11957 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)
50:3:2360:A:N7	50:3:2373:G:N2	1.69	1.35
50:3:1785:U:C2	50:3:1792:A:N6	1.96	1.34
50:3:2126:A:C2	50:3:2176:G:N2	1.99	1.29
50:3:2175:U:N3	50:3:2179:A:C8	1.97	1.29
50:3:47:G:N2	50:3:184:A:H61	1.28	1.28

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%)	39 (87%)	6 (13%)	0	100	100
2	1	57/59 (97%)	48 (84%)	9 (16%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	2	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
4	A	238/294 (81%)	204 (86%)	34 (14%)	0	100	100
5	B	213/273 (78%)	183 (86%)	29 (14%)	1 (0%)	24	63
6	C	201/205 (98%)	177 (88%)	23 (11%)	1 (0%)	24	63
7	D	151/219 (69%)	132 (87%)	19 (13%)	0	100	100
8	E	165/215 (77%)	126 (76%)	37 (22%)	2 (1%)	10	44
9	F	152/155 (98%)	132 (87%)	20 (13%)	0	100	100
10	G	139/142 (98%)	110 (79%)	28 (20%)	1 (1%)	18	56
11	H	126/132 (96%)	109 (86%)	17 (14%)	0	100	100
12	I	99/108 (92%)	82 (83%)	17 (17%)	0	100	100
13	J	112/121 (93%)	99 (88%)	13 (12%)	0	100	100
14	K	134/139 (96%)	110 (82%)	23 (17%)	1 (1%)	18	56
15	L	116/124 (94%)	99 (85%)	17 (15%)	0	100	100
16	M	58/61 (95%)	47 (81%)	11 (19%)	0	100	100
17	N	81/86 (94%)	74 (91%)	7 (9%)	0	100	100
18	O	78/94 (83%)	73 (94%)	5 (6%)	0	100	100
19	P	81/85 (95%)	67 (83%)	14 (17%)	0	100	100
20	Q	63/104 (61%)	52 (82%)	9 (14%)	2 (3%)	3	21
21	R	82/87 (94%)	74 (90%)	8 (10%)	0	100	100
22	S	75/87 (86%)	72 (96%)	3 (4%)	0	100	100
23	T	51/60 (85%)	43 (84%)	8 (16%)	0	100	100
24	a	283/287 (99%)	242 (86%)	41 (14%)	0	100	100
25	b	227/287 (79%)	195 (86%)	32 (14%)	0	100	100
26	c	208/212 (98%)	180 (86%)	27 (13%)	1 (0%)	24	63
27	d	173/180 (96%)	144 (83%)	29 (17%)	0	100	100
28	e	174/184 (95%)	155 (89%)	18 (10%)	1 (1%)	21	59
29	f	143/149 (96%)	121 (85%)	21 (15%)	1 (1%)	18	56
30	g	124/161 (77%)	103 (83%)	19 (15%)	2 (2%)	7	38
31	h	126/137 (92%)	108 (86%)	18 (14%)	0	100	100
32	i	142/146 (97%)	124 (87%)	18 (13%)	0	100	100
33	j	120/122 (98%)	111 (92%)	9 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	k	146/151 (97%)	123 (84%)	23 (16%)	0	100	100
35	l	134/139 (96%)	117 (87%)	17 (13%)	0	100	100
36	m	117/124 (94%)	103 (88%)	14 (12%)	0	100	100
37	n	108/116 (93%)	91 (84%)	17 (16%)	0	100	100
38	o	113/119 (95%)	96 (85%)	17 (15%)	0	100	100
39	p	112/127 (88%)	95 (85%)	17 (15%)	0	100	100
40	q	97/100 (97%)	82 (84%)	14 (14%)	1 (1%)	12	49
41	r	137/159 (86%)	122 (89%)	14 (10%)	1 (1%)	18	56
42	s	90/237 (38%)	77 (86%)	13 (14%)	0	100	100
43	t	109/111 (98%)	94 (86%)	15 (14%)	0	100	100
44	u	84/104 (81%)	78 (93%)	6 (7%)	0	100	100
45	v	61/65 (94%)	55 (90%)	6 (10%)	0	100	100
46	w	96/111 (86%)	87 (91%)	9 (9%)	0	100	100
47	x	42/97 (43%)	33 (79%)	9 (21%)	0	100	100
48	y	54/57 (95%)	44 (82%)	10 (18%)	0	100	100
49	z	48/53 (91%)	42 (88%)	6 (12%)	0	100	100
All	All	5820/6670 (87%)	5007 (86%)	798 (14%)	15 (0%)	37	72

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	B	62	GLN
14	K	122	LYS
20	Q	55	ASP
26	c	123	ASP
6	C	146	ALA

5.3.2 Protein sidechains [i](#)

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%)	34 (97%)	1 (3%)	37	58
4	A	212/262 (81%)	212 (100%)	0	100	100
5	B	180/232 (78%)	179 (99%)	1 (1%)	78	83
6	C	181/183 (99%)	181 (100%)	0	100	100
7	D	123/178 (69%)	122 (99%)	1 (1%)	73	80
8	E	150/196 (76%)	148 (99%)	2 (1%)	61	74
9	F	131/132 (99%)	131 (100%)	0	100	100
10	G	123/124 (99%)	120 (98%)	3 (2%)	43	64
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%)	113 (97%)	4 (3%)	32	54
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%)	53 (95%)	3 (5%)	20	41
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%)	185 (100%)	1 (0%)	81	83
26	c	182/184 (99%)	179 (98%)	3 (2%)	55	70
27	d	150/154 (97%)	145 (97%)	5 (3%)	33	55
28	e	153/159 (96%)	153 (100%)	0	100	100
29	f	131/134 (98%)	130 (99%)	1 (1%)	73	80
30	g	101/129 (78%)	92 (91%)	9 (9%)	9	28
31	h	102/110 (93%)	102 (100%)	0	100	100
32	i	126/128 (98%)	122 (97%)	4 (3%)	34	56

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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%)	104 (99%)	1 (1%)	68	78
37	n	96/99 (97%)	96 (100%)	0	100	100
38	o	101/105 (96%)	100 (99%)	1 (1%)	68	78
39	p	100/108 (93%)	100 (100%)	0	100	100
40	q	90/91 (99%)	88 (98%)	2 (2%)	45	64
41	r	116/132 (88%)	112 (97%)	4 (3%)	32	54
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%)	45 (94%)	3 (6%)	16	37
49	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5101/5751 (89%)	5052 (99%)	49 (1%)	65	78

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	g	44	LEU
32	i	87	ILE
30	g	45	PHE
30	g	88	GLU
32	i	89	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 164 such sidechains are listed below:

Mol	Chain	Res	Type
29	f	85	ASN
41	r	38	ASN
32	i	64	GLN
35	l	71	HIS

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Mol	Chain	Res	Type
44	u	64	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	3	2875/2907 (98%)	1322 (45%)	52 (1%)
51	4	103/108 (95%)	48 (46%)	4 (3%)
52	5	1490/1520 (98%)	634 (42%)	18 (1%)
53	7	75/76 (98%)	40 (53%)	2 (2%)
All	All	4543/4611 (98%)	2044 (44%)	76 (1%)

5 of 2044 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	3	9	G
50	3	12	A
50	3	14	U
50	3	15	A
50	3	16	A

5 of 76 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	5	219	A
52	5	1170	C
52	5	348	C
52	5	975	C
53	7	47	G

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.

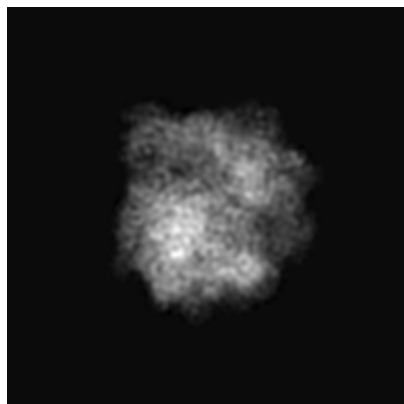
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13410. These allow visual inspection of the internal detail of the map and identification of artifacts.

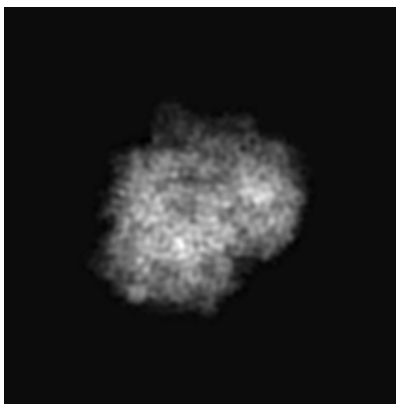
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

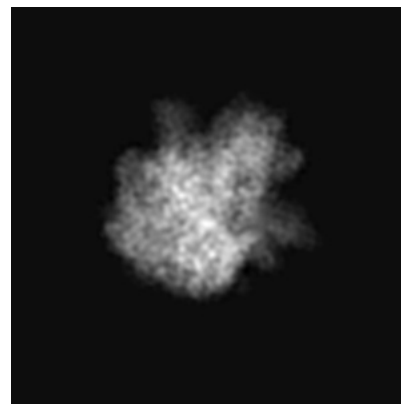
6.1.1 Primary map



X

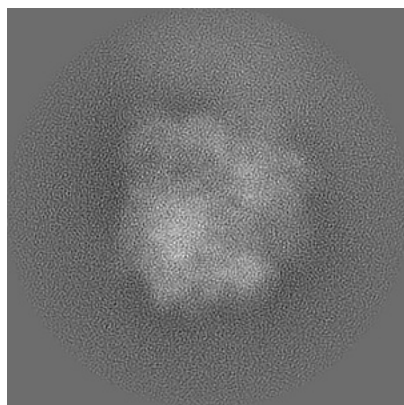


Y

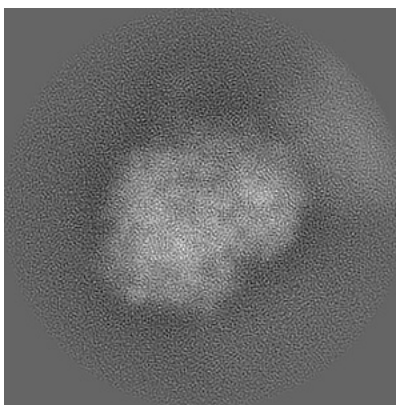


Z

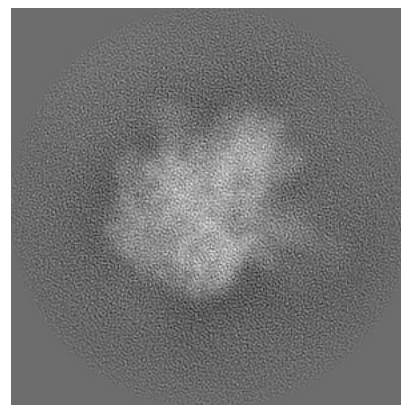
6.1.2 Raw map



X



Y

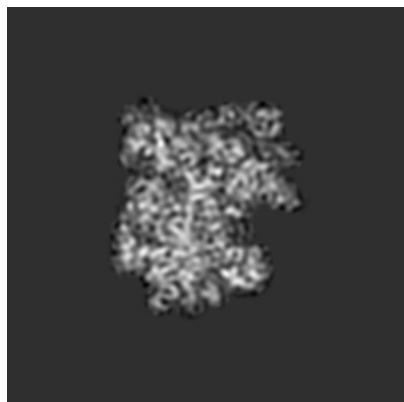


Z

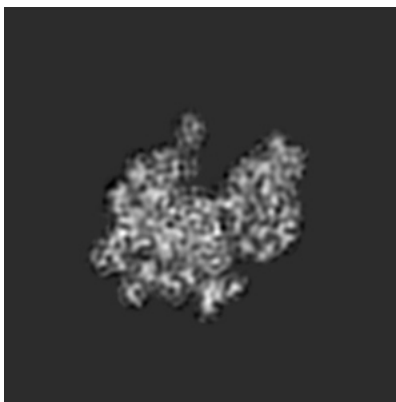
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 128

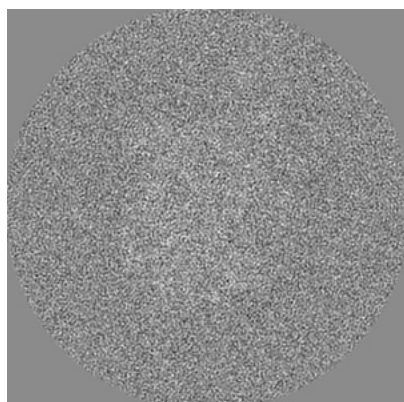


Y Index: 128

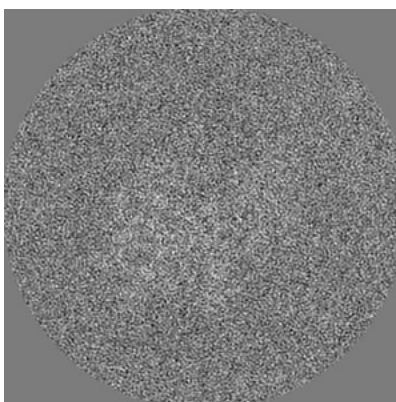


Z Index: 128

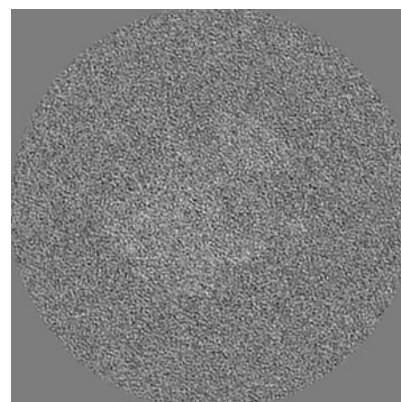
6.2.2 Raw map



X Index: 128



Y Index: 128

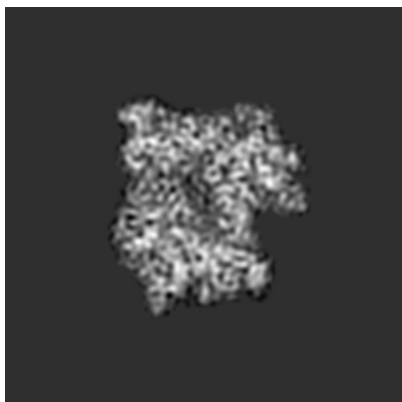


Z Index: 128

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

6.3 Largest variance slices [i](#)

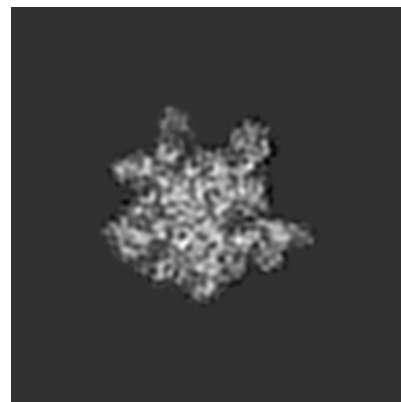
6.3.1 Primary map



X Index: 135

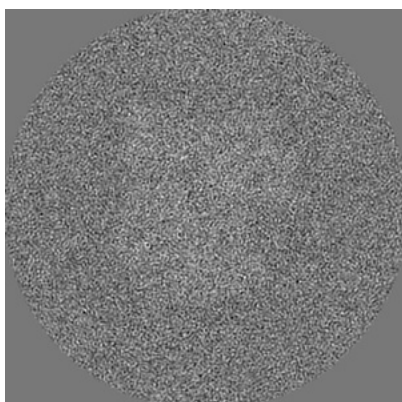


Y Index: 116

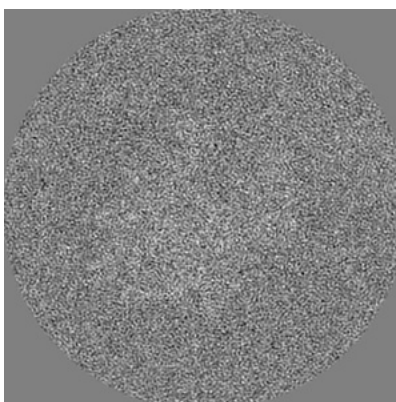


Z Index: 97

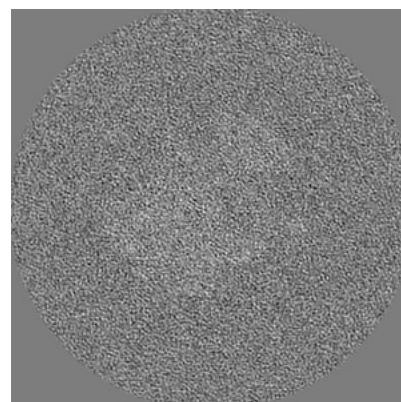
6.3.2 Raw map



X Index: 133



Y Index: 120

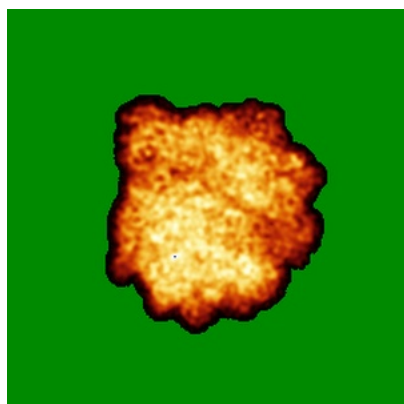


Z Index: 128

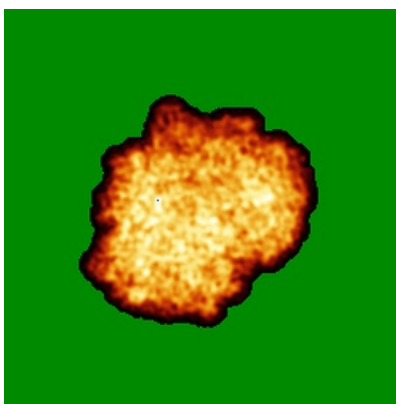
The images above show the largest variance slices of the map in three orthogonal directions.

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

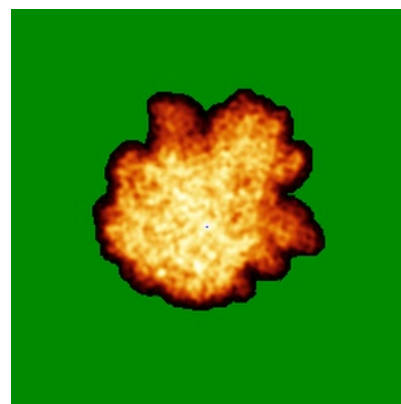
6.4.1 Primary map



X

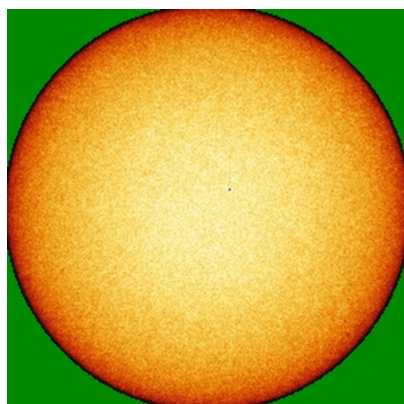


Y

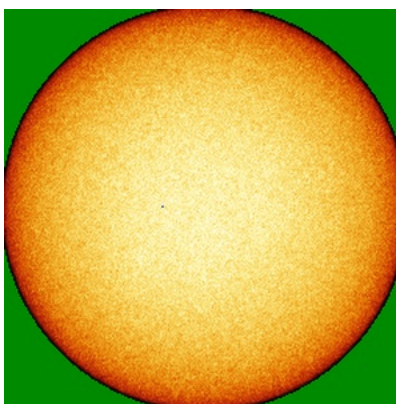


Z

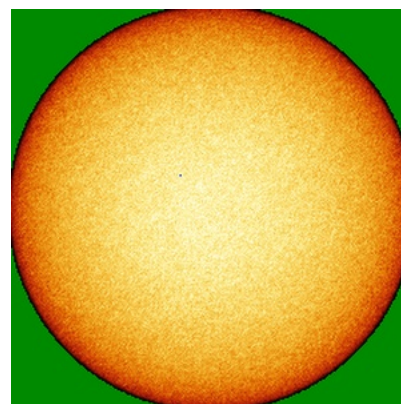
6.4.2 Raw map



X



Y

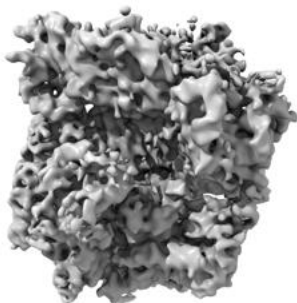


Z

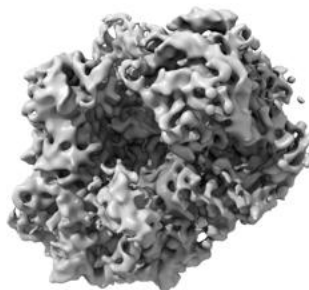
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

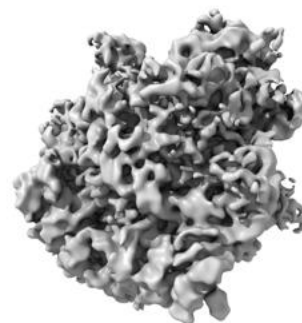
6.5.1 Primary map



X



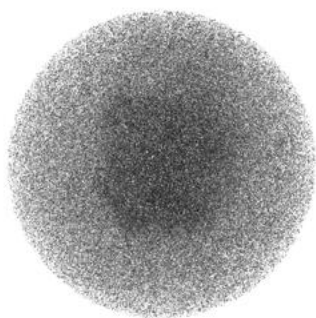
Y



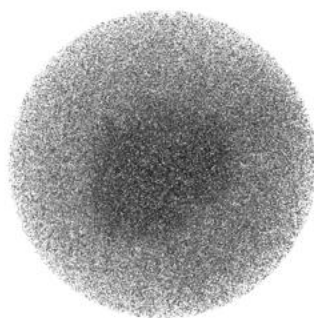
Z

The images above show the 3D surface view of the map at the recommended contour level 0.45. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

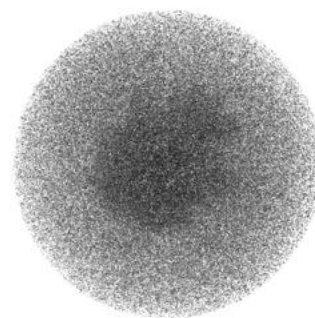
6.5.2 Raw map



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.

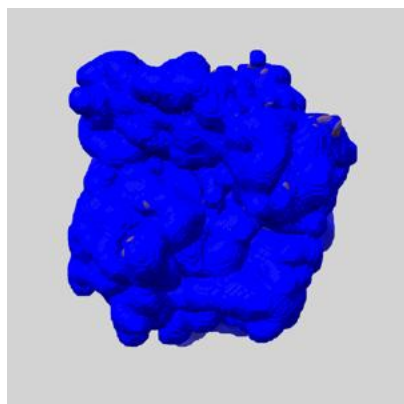
6.6 Mask visualisation [i](#)

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

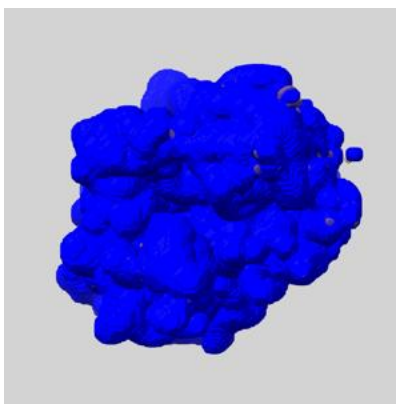
A mask typically either:

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

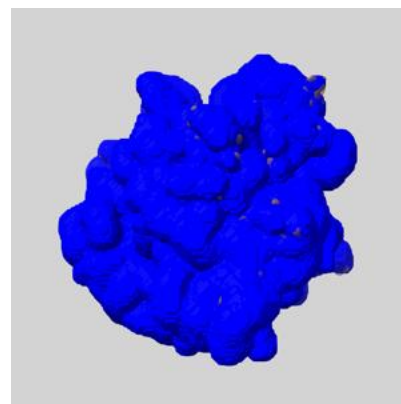
6.6.1 emd_13410_msk_1.map [i](#)



X



Y

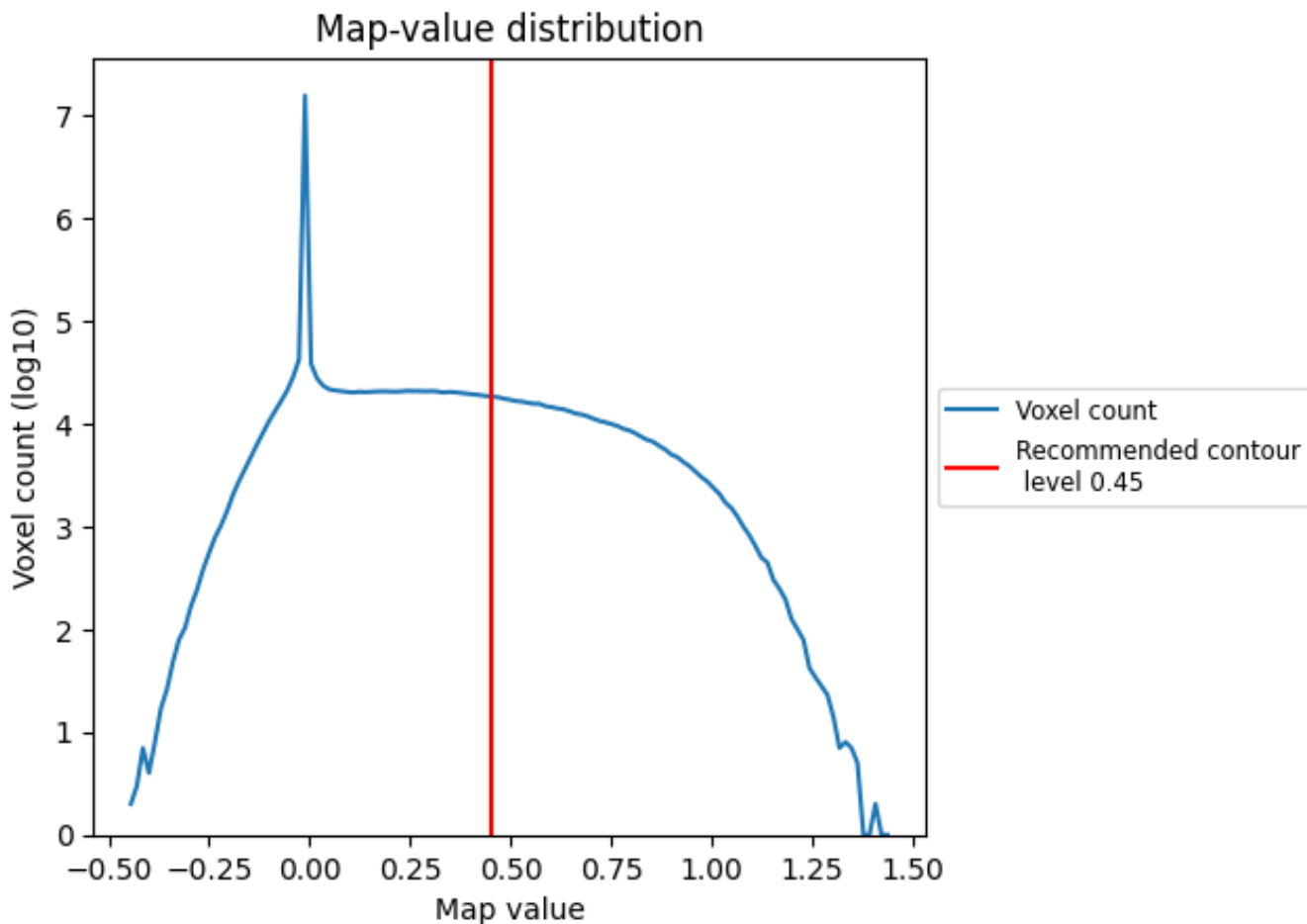


Z

7 Map analysis [i](#)

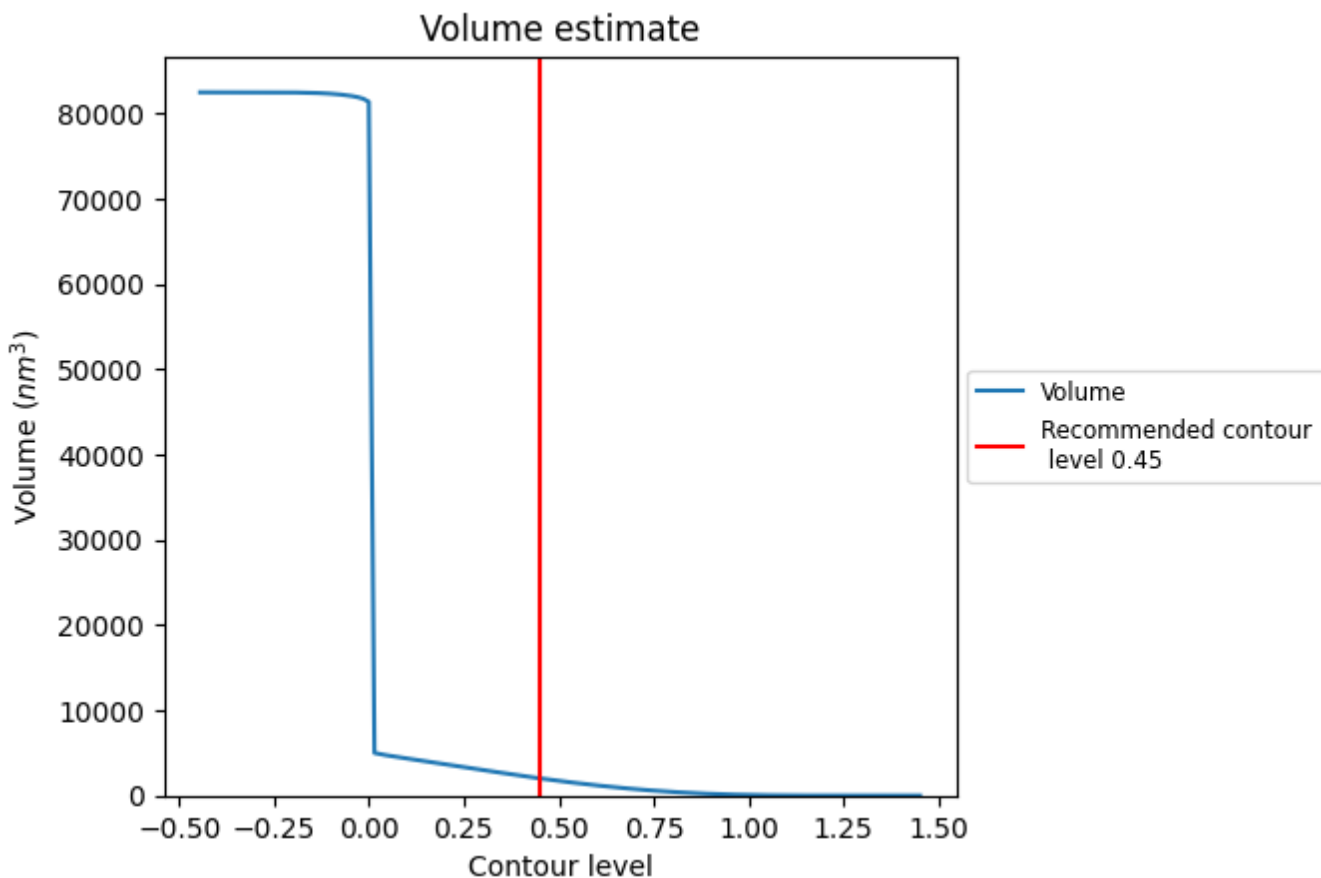
This section contains the results of statistical analysis of the map.

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.

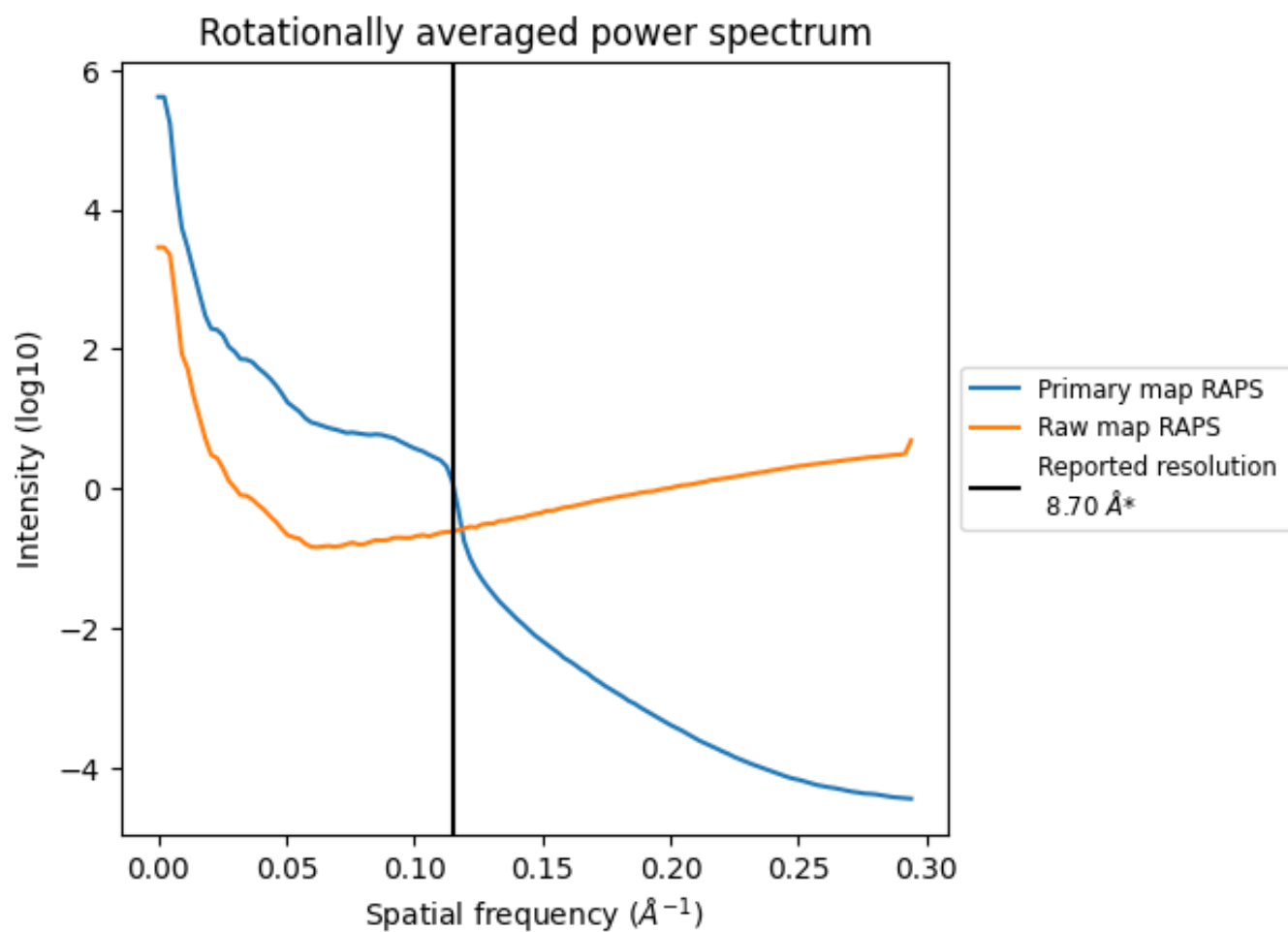
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2019 nm³; this corresponds to an approximate mass of 1824 kDa.

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

7.3 Rotationally averaged power spectrum i

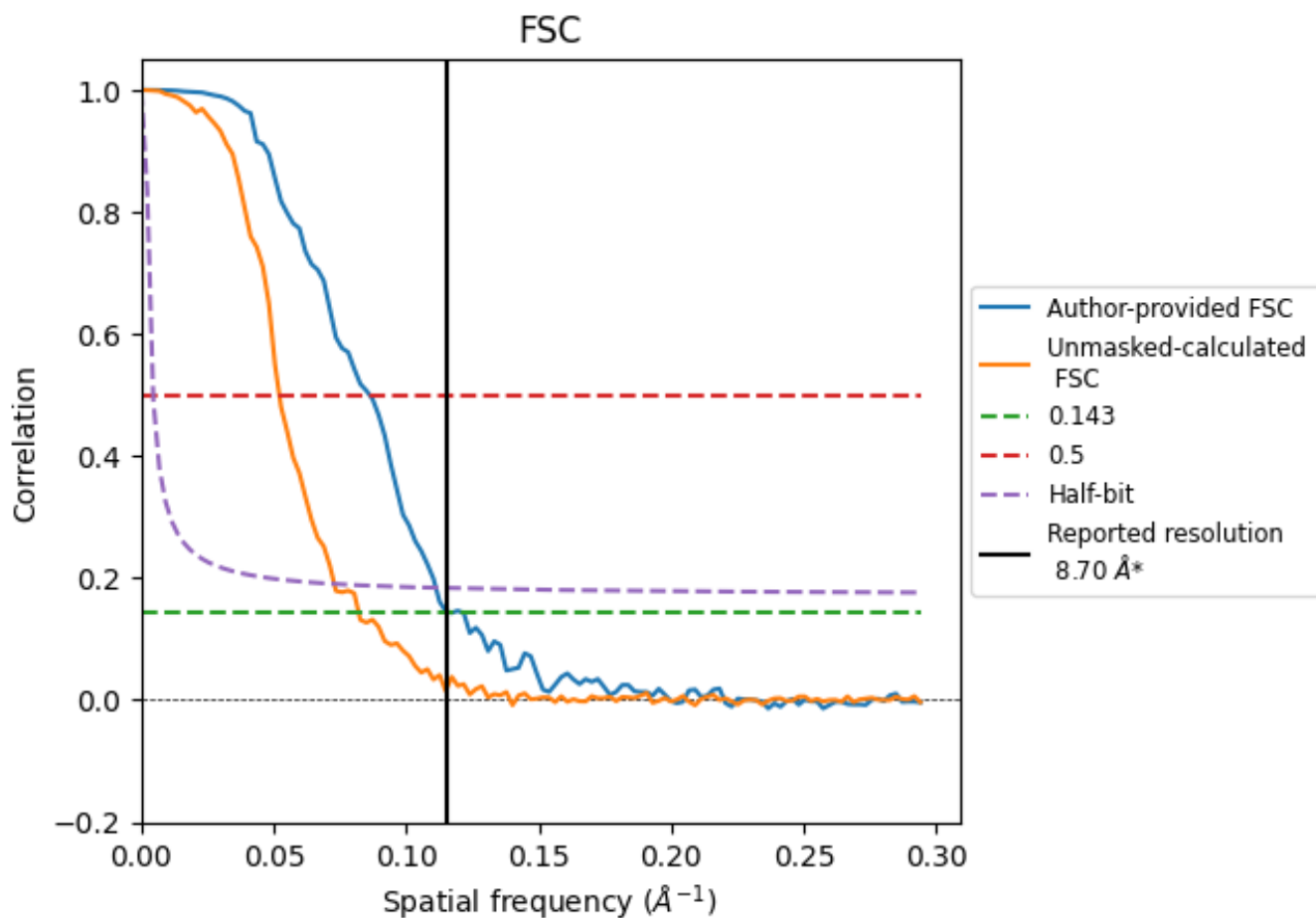


*Reported resolution corresponds to spatial frequency of 0.115 Å⁻¹

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 0.115 Å⁻¹

8.2 Resolution estimates [i](#)

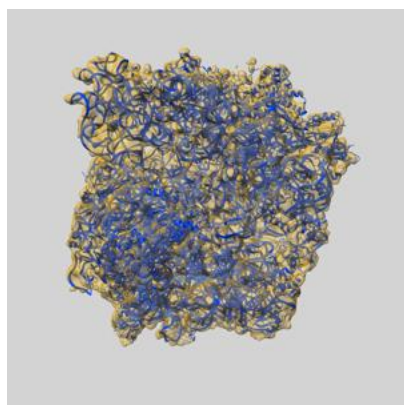
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	8.70	-	-
Author-provided FSC curve	8.55	11.60	8.99
Unmasked-calculated*	12.18	19.16	13.72

*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 12.18 differs from the reported value 8.7 by more than 10 %

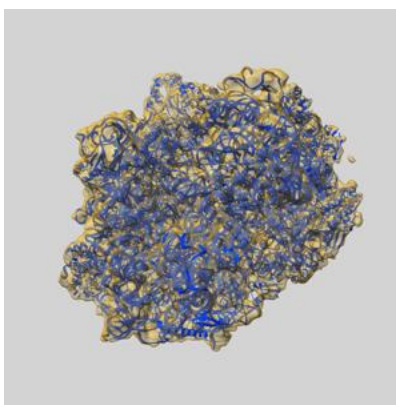
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13410 and PDB model 7PH9. Per-residue inclusion information can be found in section 3 on page 13.

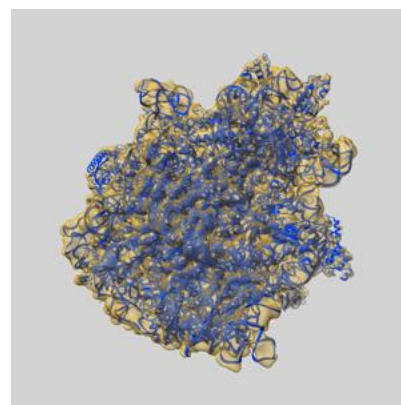
9.1 Map-model overlay [i](#)



X



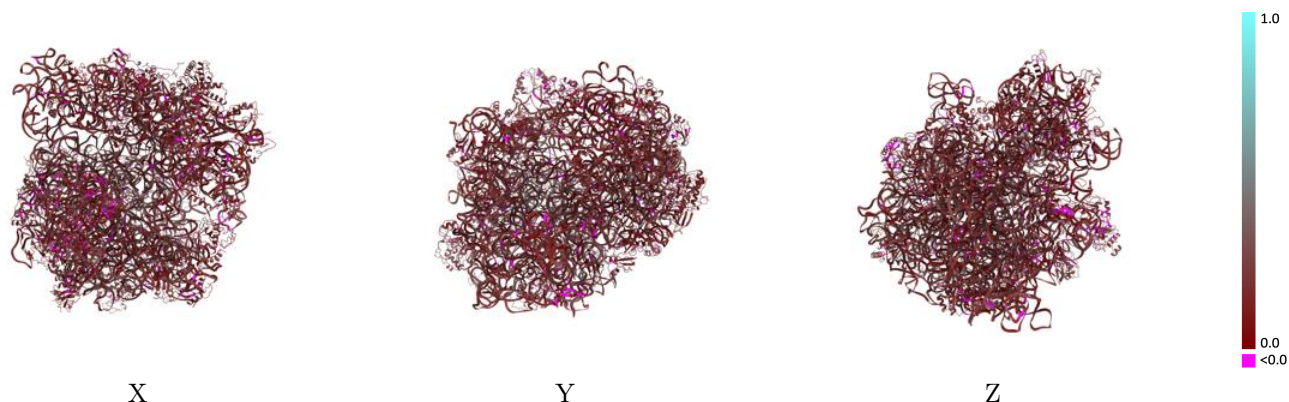
Y



Z

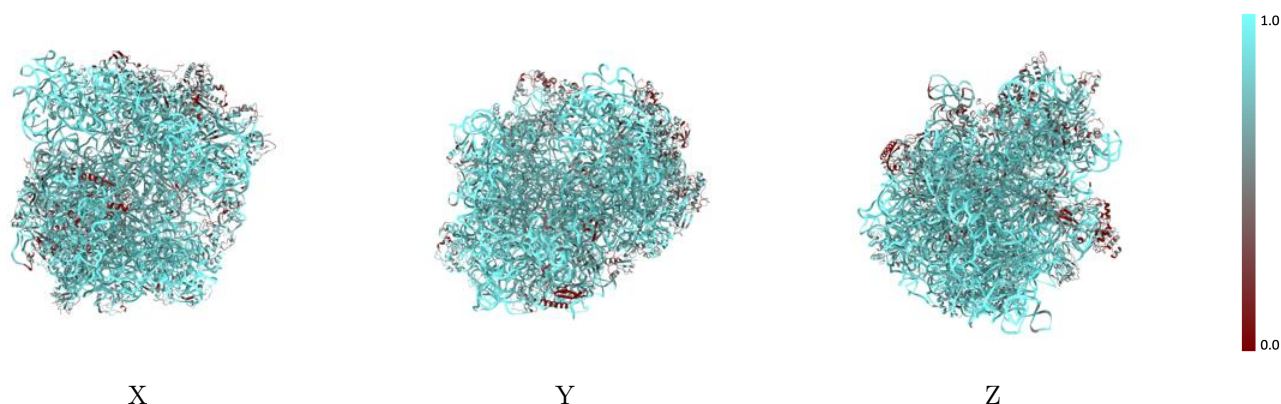
The images above show the 3D surface view of the map at the recommended contour level 0.45 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



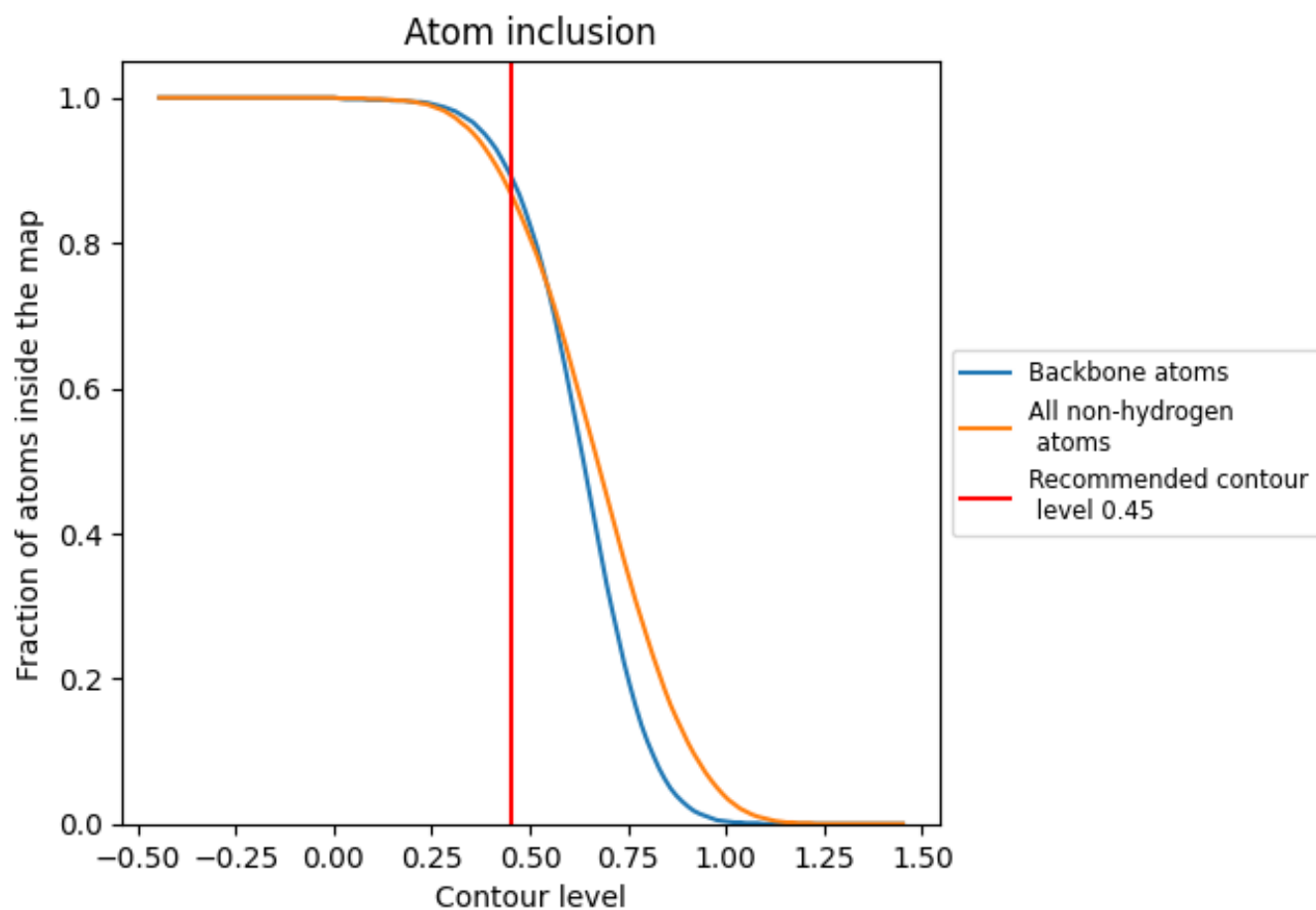
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.45).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 87% 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 (0.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8700	 0.1850
0	 0.8770	 0.1650
1	 0.7980	 0.1470
2	 0.7870	 0.1410
3	 0.9660	 0.1970
4	 0.9750	 0.1960
5	 0.9660	 0.1930
7	 0.9410	 0.1970
A	 0.5760	 0.1900
B	 0.6120	 0.1820
C	 0.5990	 0.1570
D	 0.6760	 0.1710
E	 0.5490	 0.1860
F	 0.6270	 0.1670
G	 0.6480	 0.1710
H	 0.6360	 0.1500
I	 0.5740	 0.1700
J	 0.6070	 0.1580
K	 0.6960	 0.1550
L	 0.6370	 0.1760
M	 0.7230	 0.1370
N	 0.6890	 0.1820
O	 0.7870	 0.1680
P	 0.6560	 0.1560
Q	 0.7210	 0.1670
R	 0.6990	 0.1370
S	 0.8230	 0.1840
T	 0.7430	 0.2190
a	 0.7920	 0.1520
b	 0.6980	 0.1390
c	 0.7590	 0.1810
d	 0.6600	 0.1690
e	 0.5970	 0.1770
f	 0.2590	 0.1090
g	 0.4200	 0.1510



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Chain	Atom inclusion	Q-score
h	 0.2740	 0.1120
i	 0.7750	 0.1700
j	 0.6400	 0.1580
k	 0.7740	 0.1540
l	 0.7800	 0.1570
m	 0.7510	 0.1570
n	 0.7220	 0.1800
o	 0.6720	 0.1770
p	 0.7930	 0.1670
q	 0.6860	 0.1580
r	 0.8260	 0.1720
s	 0.7390	 0.1790
t	 0.6410	 0.1740
u	 0.7780	 0.1430
v	 0.7580	 0.1460
w	 0.7180	 0.1980
x	 0.5360	 0.1720
y	 0.7880	 0.1470
z	 0.7680	 0.1700