



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 01:51 AM UTC

PDB ID : 3J9W / pdb_00003j9w
EMDB ID : EMD-6306
Title : Cryo-EM structure of the Bacillus subtilis MifM-stalled ribosome complex
Authors : Sohmen, D.; Chiba, S.; Shimokawa-Chiba, N.; Innis, C.A.; Berninghausen, O.; Beckmann, R.; Ito, K.; Wilson, D.N.
Deposited on : 2015-03-16
Resolution : 3.90 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

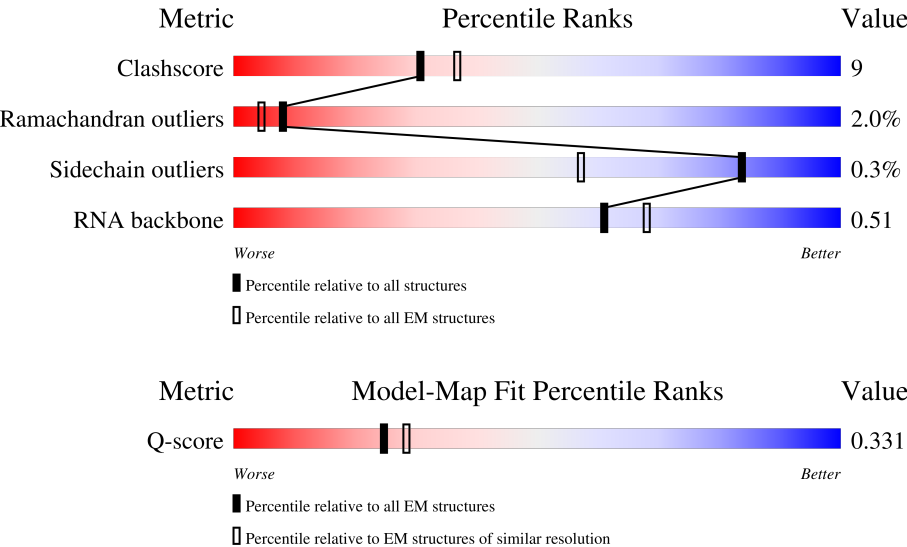
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.90 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	8855 (3.40 - 4.40)

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	AA	1555	
2	AB	246	
3	AC	218	

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Mol	Chain	Length	Quality of chain
4	AD	200	36% 96% .
5	AE	166	41% 95% 5% .
6	AF	95	12% 96% .
7	AG	156	21% 96% ..
8	AH	132	24% 98% ..
9	AI	130	41% 92% 5% .
10	AJ	102	65% 95% 5%
11	AK	131	17% 83% 7% 10%
12	AL	138	14% 93% 7% .
13	AM	121	20% 88% 8% ..
14	AN	61	26% 90% 7% ..
15	AO	89	6% 97% ..
16	AP	90	14% 97% ..
17	AQ	87	15% 97% ..
18	AR	79	25% 84% 5% 10%
19	AS	92	16% 86% 5% 9%
20	AT	88	14% 92% 6% .
21	AX	77	5% 61% 22% 17%
22	AY	19	11% 68% 58% 32%
23	AZ	95	13% 13% 11% .. 75%
24	B0	62	13% 58% 31% 5% 6%
25	B1	66	9% 67% 32% .
26	B2	59	7% 71% 25% ..
27	B3	66	48% 70% 26% ..
28	B4	59	8% 64% 27% 8%

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Mol	Chain	Length	Quality of chain
29	B5	49	
30	B6	44	
31	B7	66	
32	B8	37	
33	BA	2928	
34	BB	119	
35	BD	277	
36	BE	209	
37	BF	207	
38	BG	179	
39	BH	179	
40	BJ	166	
41	BK	141	
42	BM	145	
43	BN	122	
44	BO	146	
45	BP	144	
46	BQ	120	
47	BR	120	
48	BS	115	
49	BT	119	
50	BU	102	
51	BV	113	
52	BW	95	
53	BX	103	

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Mol	Chain	Length	Quality of chain
54	BZ	94	 A horizontal bar chart showing the quality of chain 54 (BZ, length 94). The bar is divided into three segments: green (64%), yellow (23%), and grey (13%). A small red flag icon is at the start of the bar.

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 135425 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 RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	1544	Total	C	N	O	P	0	0
			33115	14768	6067	10736	1544		

- Molecule 2 is a protein called 30S ribosomal protein uS2.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	AB	224	Total	C	N	O	0	0
			896	448	224	224		

- Molecule 3 is a protein called 30S ribosomal protein uS3.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	AC	210	Total	C	N	O	0	0
			840	420	210	210		

- Molecule 4 is a protein called 30S ribosomal protein uS4.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	AD	199	Total	C	N	O	0	0
			797	398	199	200		

- Molecule 5 is a protein called 30S ribosomal protein uS5.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	AE	165	Total	C	N	O	0	0
			661	330	165	166		

- Molecule 6 is a protein called 30S ribosomal protein bS6.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	AF	95	Total	C	N	O	0	0
			381	190	95	96		

- Molecule 7 is a protein called 30S ribosomal protein uS7.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	AG	153	Total	C	N	O	0	0
			613	306	153	154		

- Molecule 8 is a protein called 30S ribosomal protein uS8.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	AH	131	Total	C	N	O	0	0
			525	262	131	132		

- Molecule 9 is a protein called 30S ribosomal protein uS9.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	AI	130	Total	C	N	O	0	0
			521	260	130	131		

- Molecule 10 is a protein called 30S ribosomal protein uS10.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	AJ	102	Total	C	N	O	0	0
			409	204	102	103		

- Molecule 11 is a protein called 30S ribosomal protein uS11.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	AK	118	Total	C	N	O	0	0
			472	236	118	118		

- Molecule 12 is a protein called 30S ribosomal protein uS12.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	AL	137	Total	C	N	O	0	0
			549	274	137	138		

- Molecule 13 is a protein called 30S ribosomal protein uS13.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	AM	119	Total	C	N	O	0	0
			476	238	119	119		

- Molecule 14 is a protein called 30S ribosomal protein uS14.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	AN	60	Total	C	N	O	0	0
			241	120	60	61		

- Molecule 15 is a protein called 30S ribosomal protein uS15.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	AO	88	Total	C	N	O	0	0
			353	176	88	89		

- Molecule 16 is a protein called 30S ribosomal protein bS16.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	AP	89	Total	C	N	O	0	0
			357	178	89	90		

- Molecule 17 is a protein called 30S ribosomal protein uS17.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	AQ	86	Total	C	N	O	0	0
			345	172	86	87		

- Molecule 18 is a protein called 30S ribosomal protein bS18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	AR	71	Total	C	N	O	0	0
			285	142	71	72		

- Molecule 19 is a protein called 30S ribosomal protein uS19.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	AS	84	Total	C	N	O	0	0
			336	168	84	84		

- Molecule 20 is a protein called 30S ribosomal protein bS20.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	AT	86	Total	C	N	O	0	0
			345	172	86	87		

- Molecule 21 is a RNA chain called tRNA-Asp.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AX	77	Total	C	N	O	P	0	0
			1643	731	290	545	77		

- Molecule 22 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AY	19	Total	C	N	O	P	0	0
			415	185	82	129	19		

- Molecule 23 is a protein called MifM.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AZ	24	Total	C	N	O	S	0	0
			107	64	28	14	1		

- Molecule 24 is a protein called 50S ribosomal protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	B0	58	Total	C	N	O	S	0	0
			444	275	92	75	2		

- Molecule 25 is a protein called 50S ribosomal protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	B1	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

- Molecule 26 is a protein called 50S ribosomal protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	B2	58	Total	C	N	O	S	0	0
			455	281	89	84	1		

- Molecule 27 is a protein called 50S ribosomal protein bL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	B3	64	Total	C	N	O	S	0	0
			503	314	92	92	5		

- Molecule 28 is a protein called 50S ribosomal protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	B4	54	Total	C	N	O	S	0	0
			426	262	86	71	7		

- Molecule 29 is a protein called 50S ribosomal protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	B5	48	Total	C	N	O	S	0	0
			401	244	80	73	4		

- Molecule 30 is a protein called 50S ribosomal protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	B6	44	Total	C	N	O	S	0	0
			367	222	89	54	2		

- Molecule 31 is a protein called 50S ribosomal protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	B7	64	Total	C	N	O	S	0	0
			512	321	107	82	2		

- Molecule 32 is a protein called 50S ribosomal protein bL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	B8	36	Total	C	N	O	S	0	0
			288	181	59	44	4		

- Molecule 33 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BA	2923	Total	C	N	O	P	0	0
			62767	28002	11589	20253	2923		

- Molecule 34 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BB	112	Total	C	N	O	P	0	0
			2395	1068	435	780	112		

- Molecule 35 is a protein called 50S ribosomal protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BD	275	Total	C	N	O	S	0	0
			2111	1312	416	377	6		

- Molecule 36 is a protein called 50S ribosomal protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BE	207	Total	C	N	O	S	0	0
			1575	988	290	292	5		

- Molecule 37 is a protein called 50S ribosomal protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BF	205	Total	C	N	O	S	0	0
			1561	980	289	290	2		

- Molecule 38 is a protein called 50S ribosomal protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BG	178	Total	C	N	O	S	0	0
			1404	893	245	259	7		

- Molecule 39 is a protein called 50S ribosomal protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BH	175	Total	C	N	O	S	0	0
			1342	835	248	257	2		

- Molecule 40 is a protein called 50S ribosomal protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BJ	123	Total	C	N	O	S	0	0
			955	602	163	189	1		

- Molecule 41 is a protein called 50S ribosomal protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BK	133	Total	C	N	O	S	0	0
			981	617	173	185	6		

- Molecule 42 is a protein called 50S ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BM	142	Total	C	N	O	S	0	0
			1123	710	206	202	5		

- Molecule 43 is a protein called 50S ribosomal protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BN	122	Total	C	N	O	S	0	0
			920	571	173	172	4		

- Molecule 44 is a protein called 50S ribosomal protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BO	146	Total	C	N	O	S	0	0
			1081	671	207	201	2		

- Molecule 45 is a protein called 50S ribosomal protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BP	138	Total	C	N	O	S	0	0
			1097	703	208	181	5		

- Molecule 46 is a protein called 50S ribosomal protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BQ	119	Total	C	N	O	S	0	0
			953	583	186	180	4		

- Molecule 47 is a protein called 50S ribosomal protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BR	120	Total	C	N	O	S	0	0
			912	564	176	171	1		

- Molecule 48 is a protein called 50S ribosomal protein bL19.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	BS	114	Total	C	N	O	0	0
			936	595	184	157		

- Molecule 49 is a protein called 50S ribosomal protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BT	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 50 is a protein called 50S ribosomal protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BU	101	Total	C	N	O		0	0
			786	501	139	146			

- Molecule 51 is a protein called 50S ribosomal protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BV	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 52 is a protein called 50S ribosomal protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BW	93	Total	C	N	O	S	0	0
			752	472	137	139	4		

- Molecule 53 is a protein called 50S ribosomal protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BX	100	Total	C	N	O	S	0	0
			754	473	141	137	3		

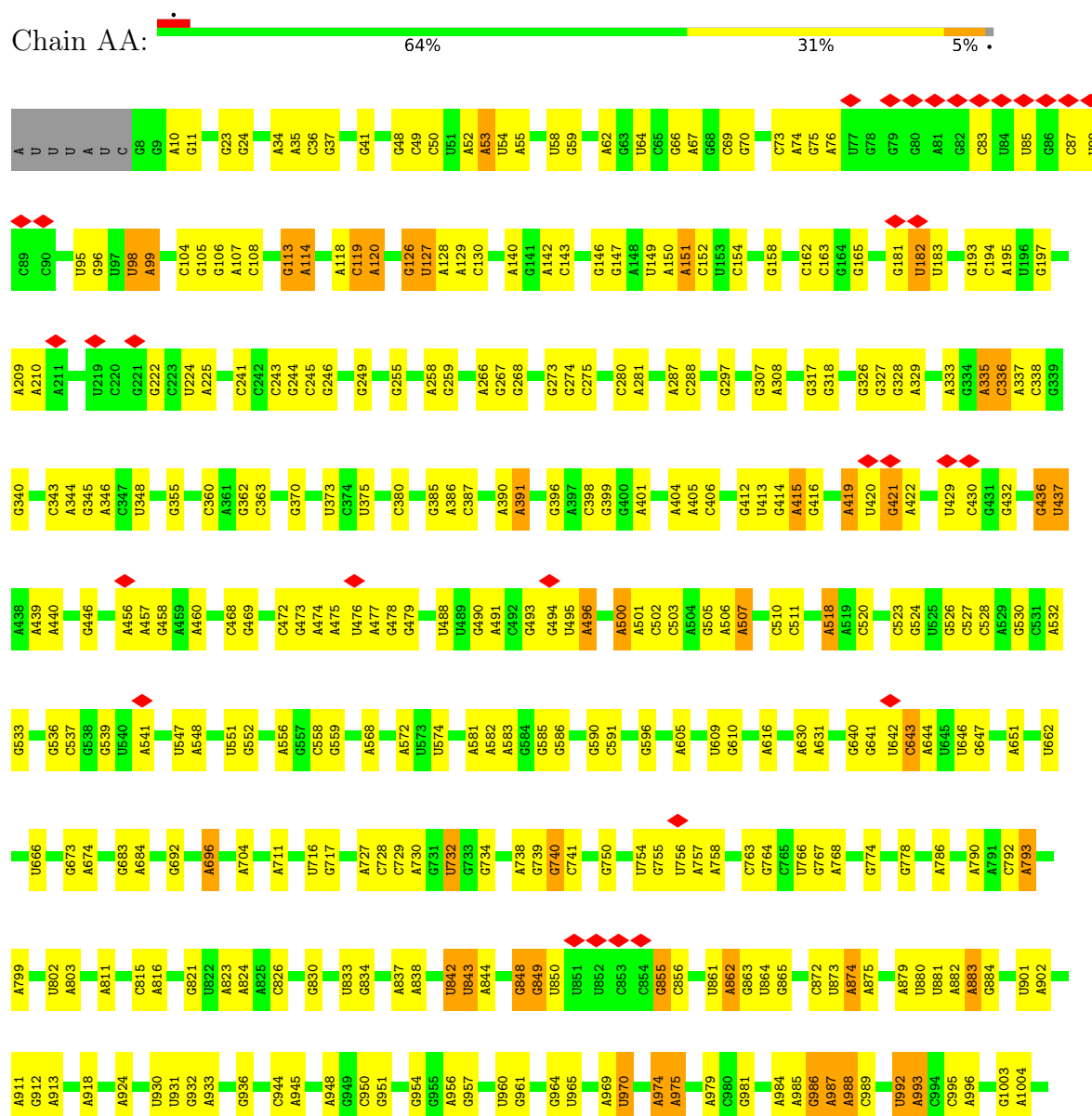
- Molecule 54 is a protein called 50S ribosomal protein bL27.

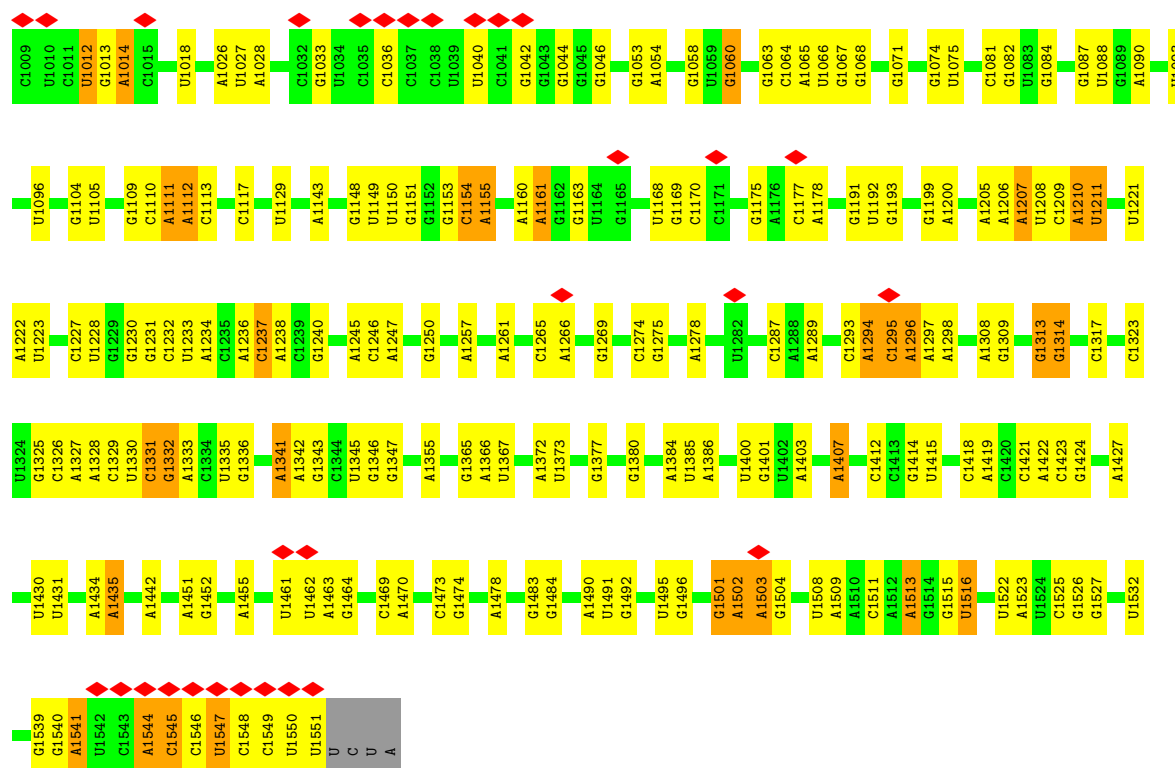
Mol	Chain	Residues	Atoms					AltConf	Trace
54	BZ	82	Total	C	N	O		0	0
			630	390	123	117			

3 Residue-property plots

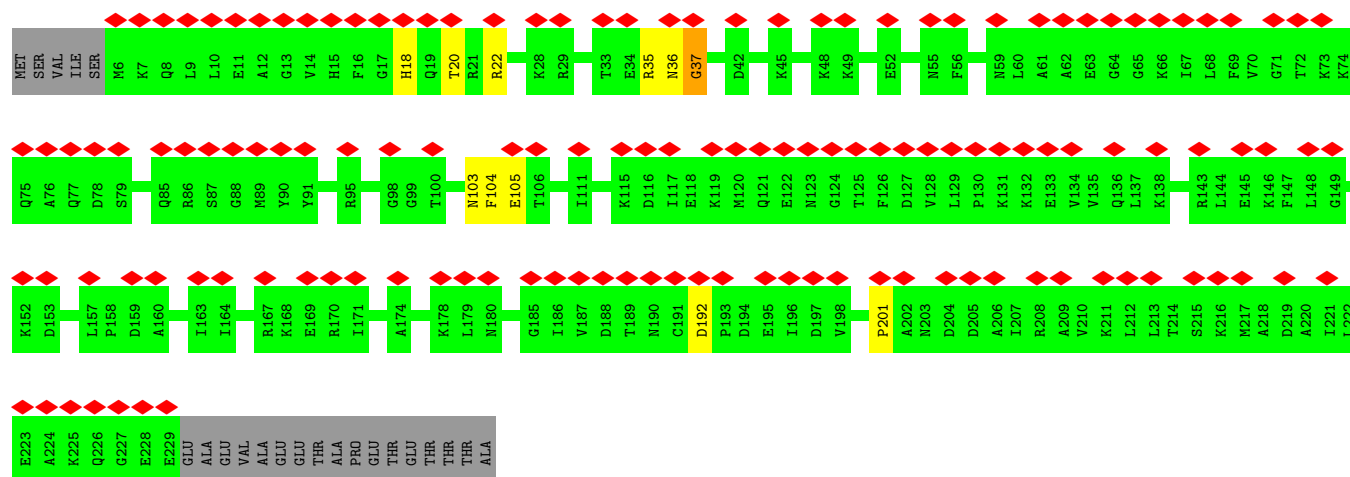
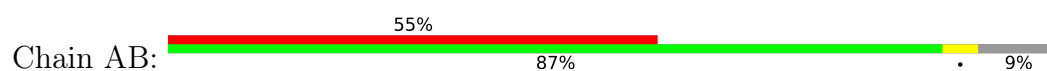
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 16S ribosomal RNA

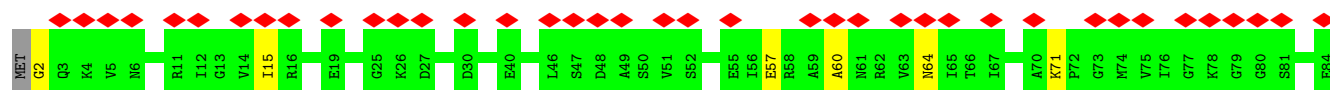
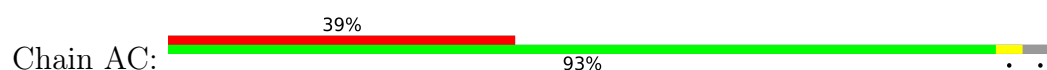


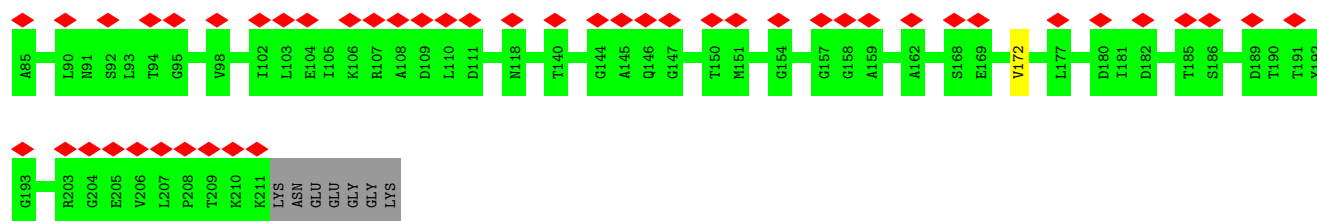


• Molecule 2: 30S ribosomal protein uS2

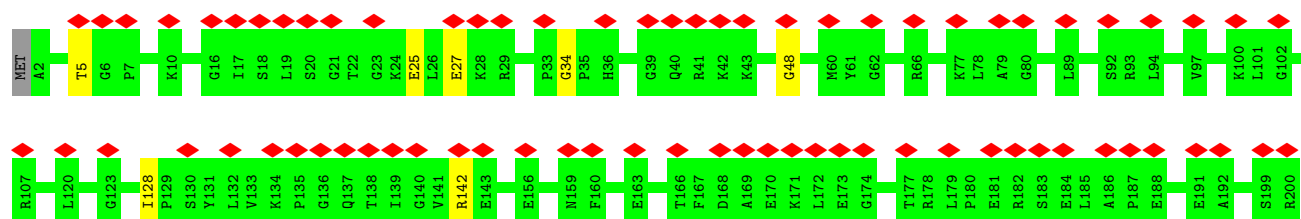


• Molecule 3: 30S ribosomal protein uS3

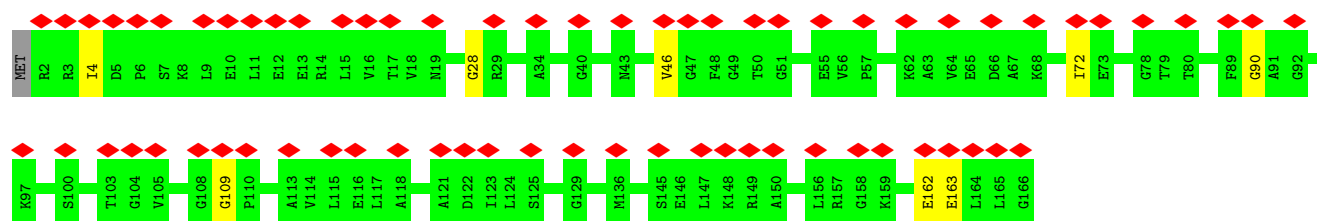
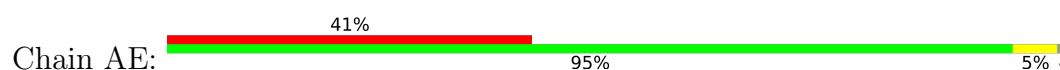




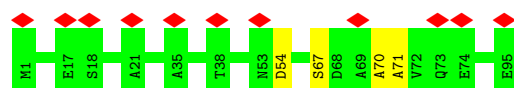
• Molecule 4: 30S ribosomal protein uS4



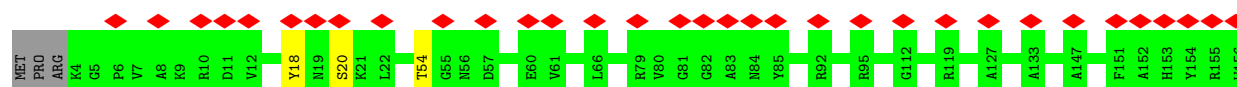
• Molecule 5: 30S ribosomal protein uS5



• Molecule 6: 30S ribosomal protein bS6

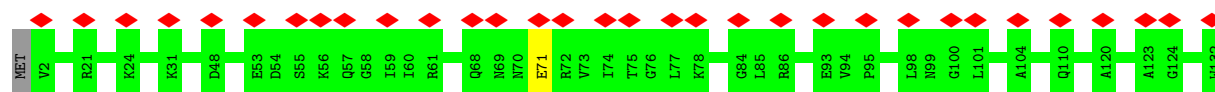


• Molecule 7: 30S ribosomal protein uS7

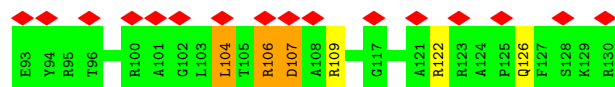
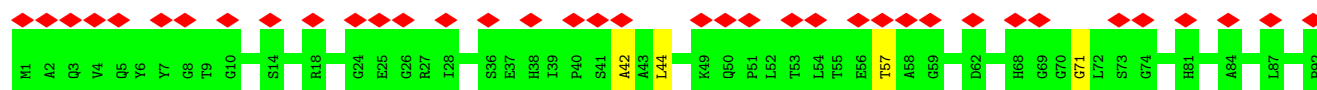
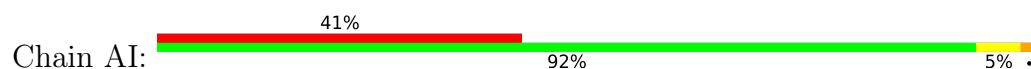


• Molecule 8: 30S ribosomal protein uS8

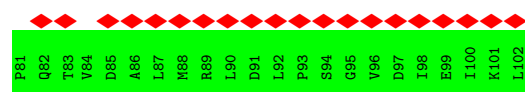
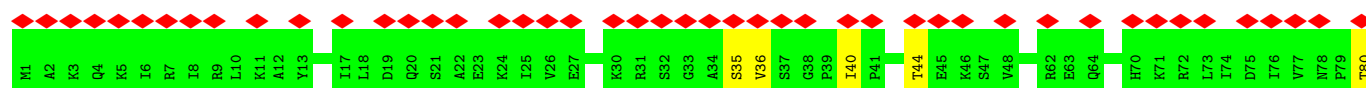




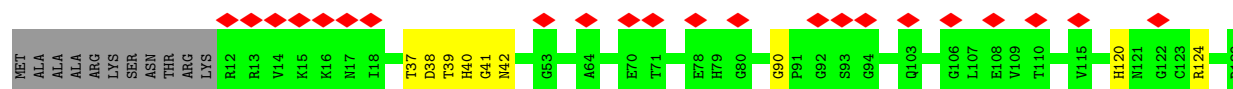
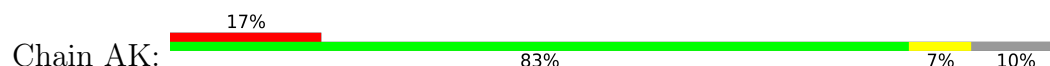
- Molecule 9: 30S ribosomal protein uS9



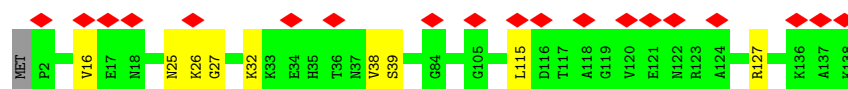
- Molecule 10: 30S ribosomal protein uS10



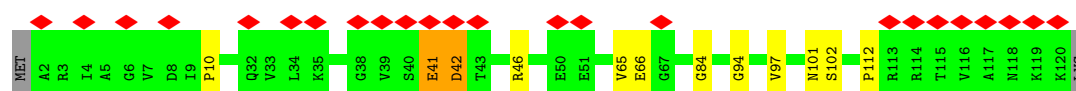
- Molecule 11: 30S ribosomal protein uS11



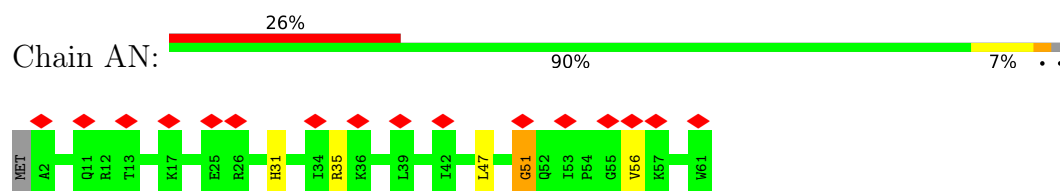
- Molecule 12: 30S ribosomal protein uS12



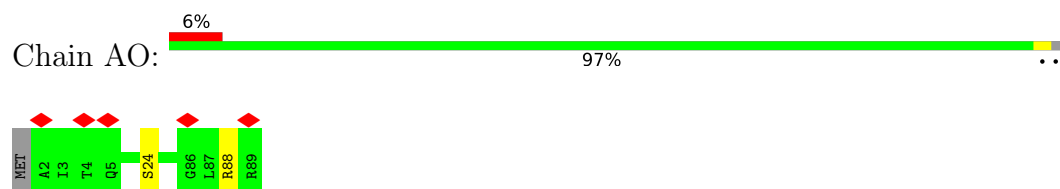
- Molecule 13: 30S ribosomal protein uS13



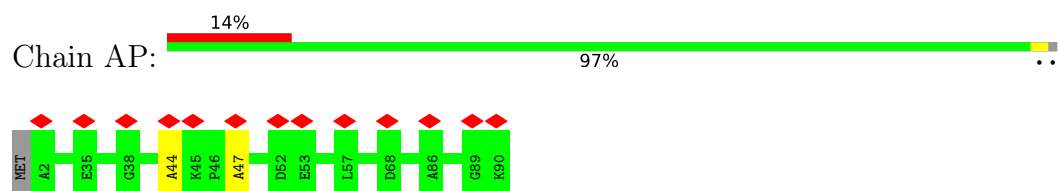
• Molecule 14: 30S ribosomal protein uS14



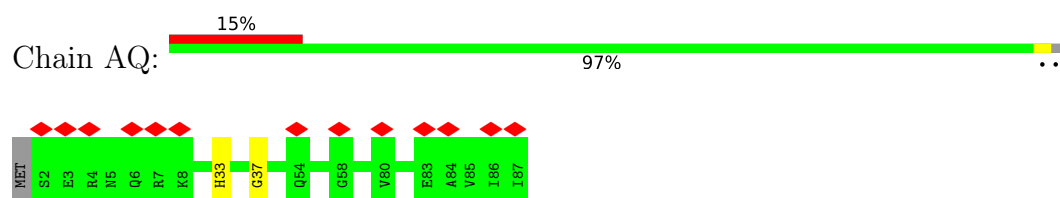
• Molecule 15: 30S ribosomal protein uS15



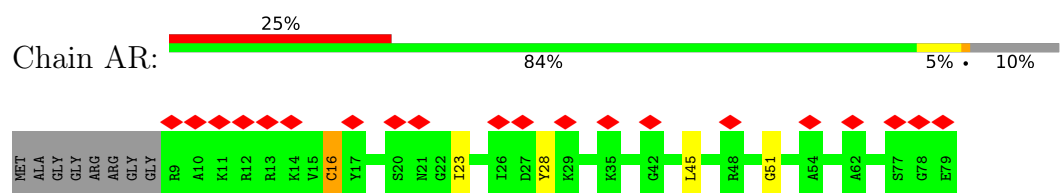
• Molecule 16: 30S ribosomal protein bS16



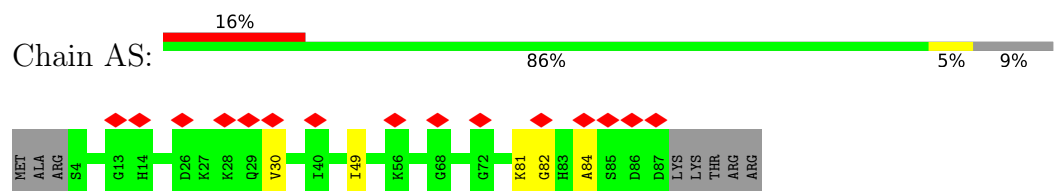
• Molecule 17: 30S ribosomal protein uS17



• Molecule 18: 30S ribosomal protein bS18

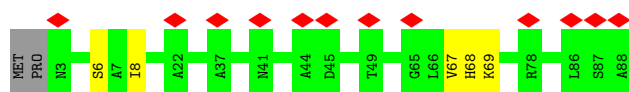


• Molecule 19: 30S ribosomal protein uS19

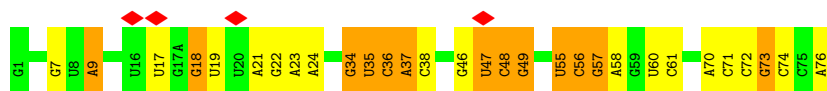


• Molecule 20: 30S ribosomal protein bS20

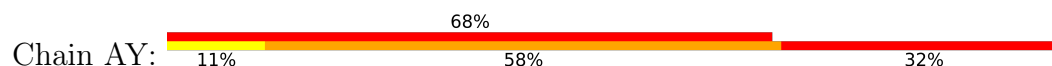




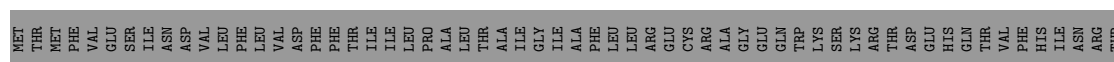
- Molecule 21: tRNA-Asp



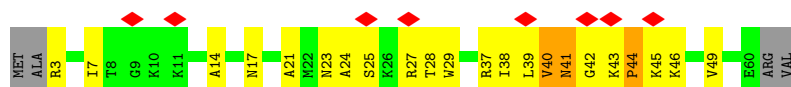
- Molecule 22: mRNA



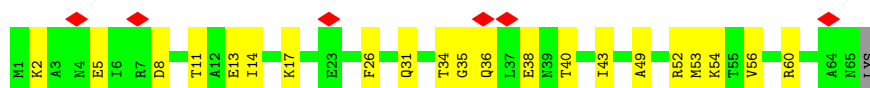
- Molecule 23: MifM



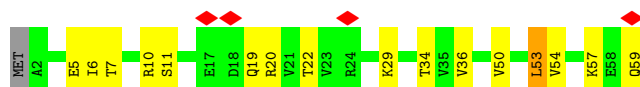
- Molecule 24: 50S ribosomal protein bL28



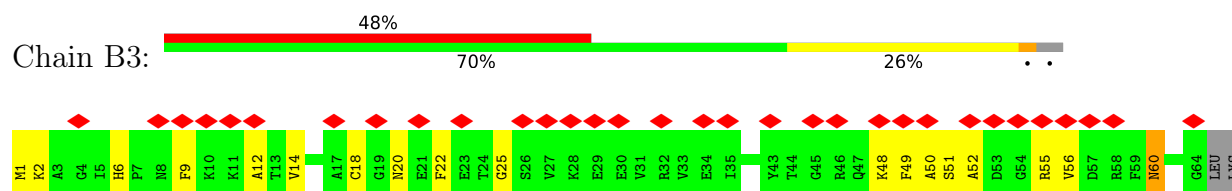
- Molecule 25: 50S ribosomal protein uL29



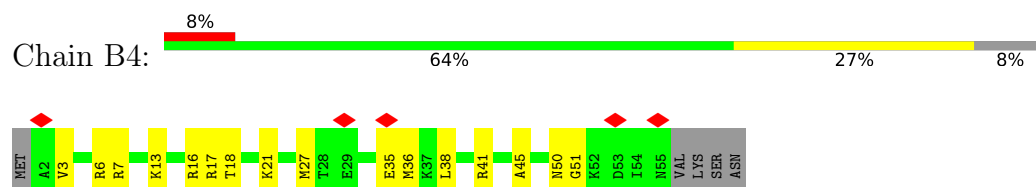
- Molecule 26: 50S ribosomal protein uL30



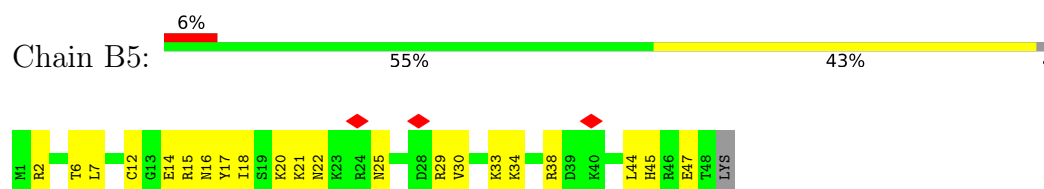
- Molecule 27: 50S ribosomal protein bL31



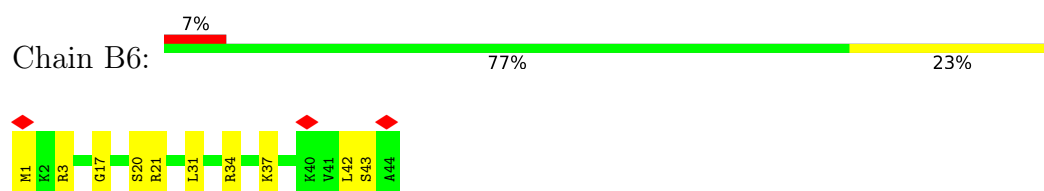
- Molecule 28: 50S ribosomal protein bL32



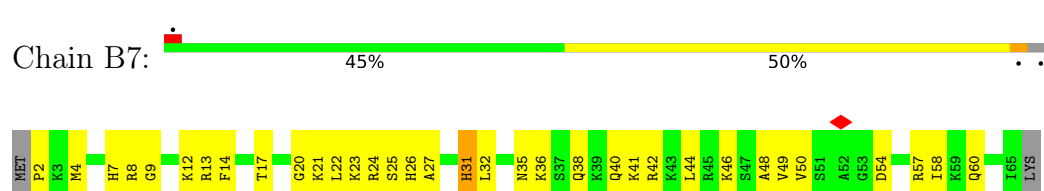
- Molecule 29: 50S ribosomal protein bL33



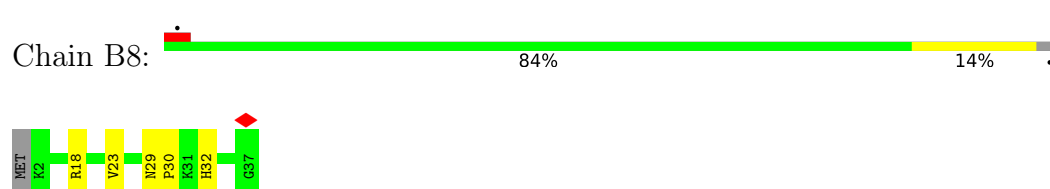
- Molecule 30: 50S ribosomal protein bL34



- Molecule 31: 50S ribosomal protein bL35

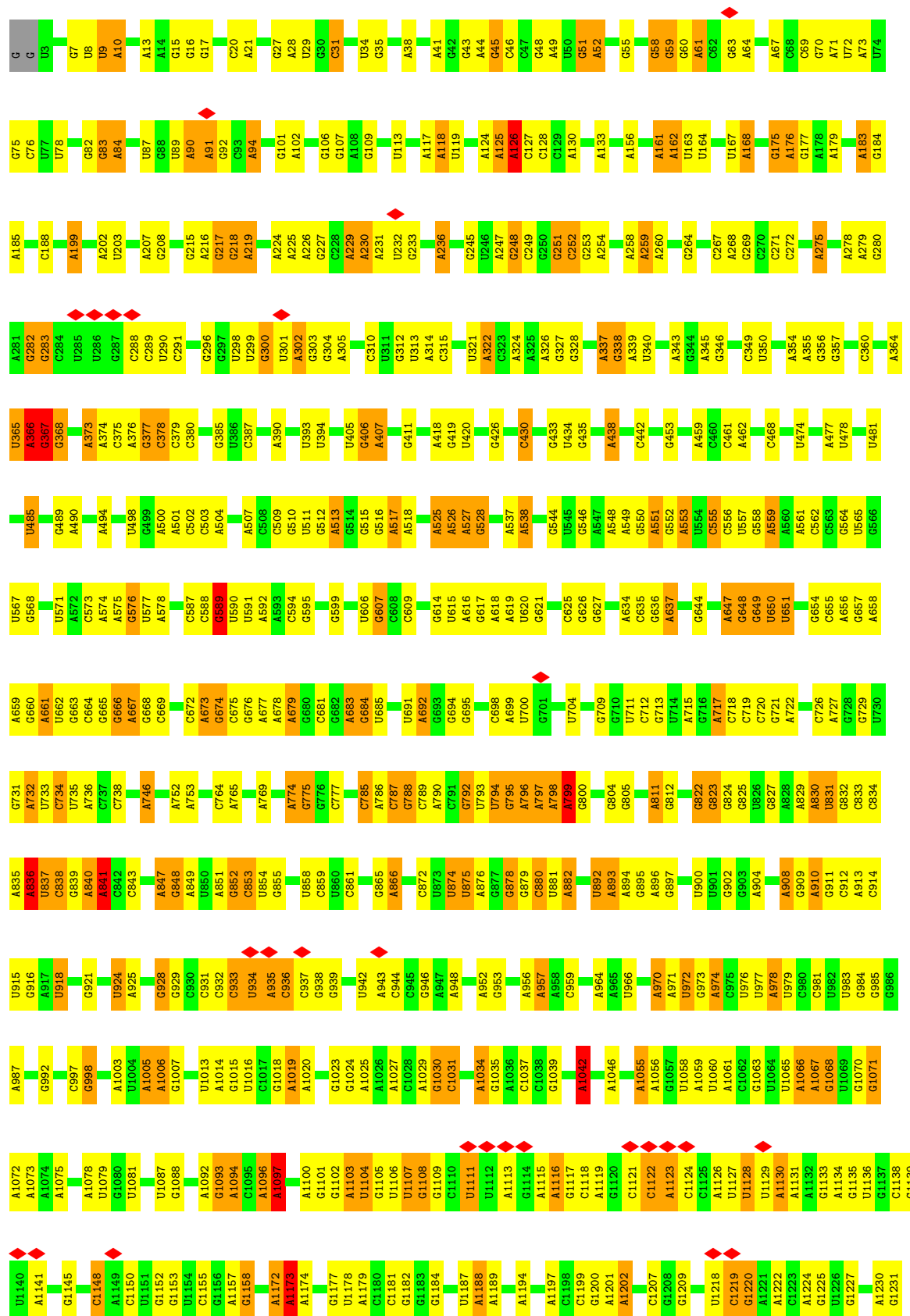


- Molecule 32: 50S ribosomal protein bL36

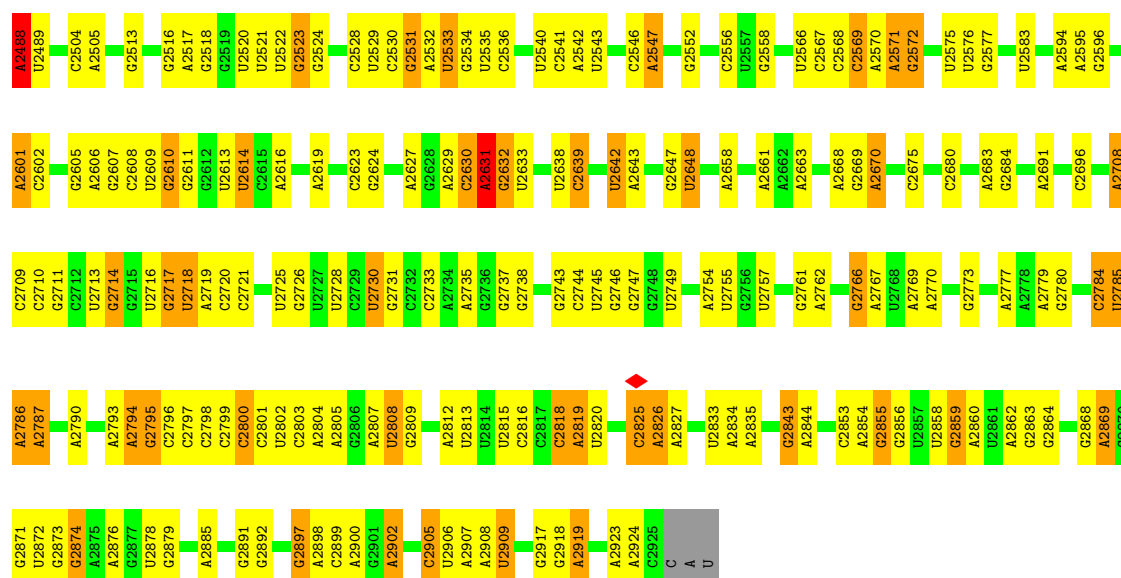


- Molecule 33: 23S ribosomal RNA

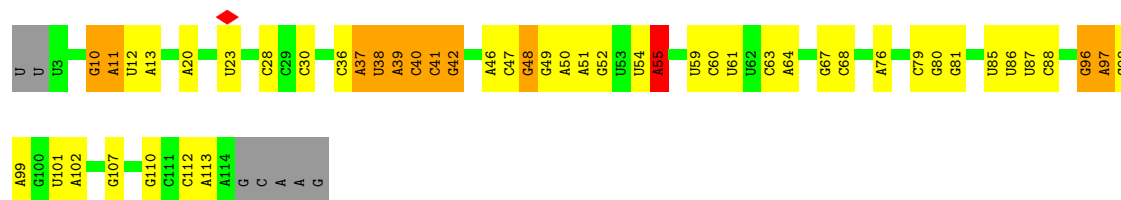




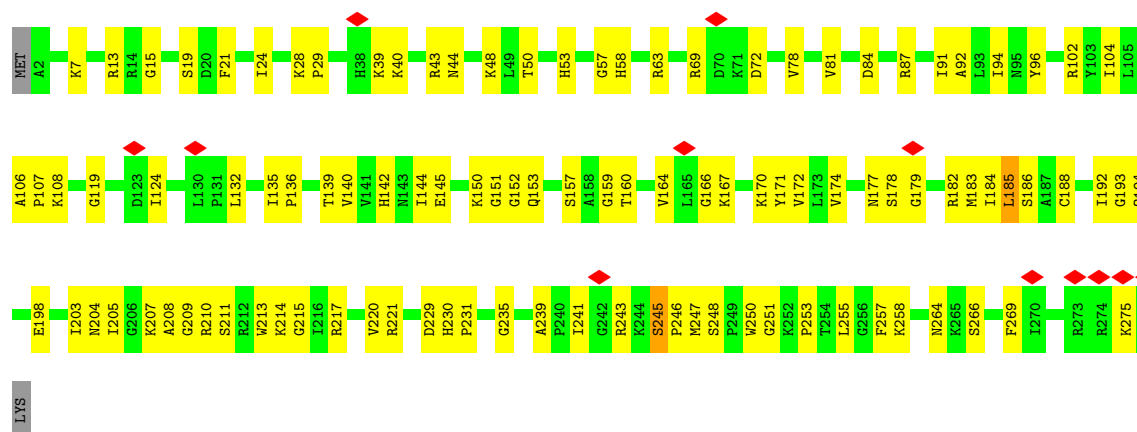
G2403	G2404	A2405	A2406	A2407	G2411	G2412	G2413	G2414	G2418	G2419	A2421	G2422	G2423	G2427	G2431	G2434	G2435	G2439	A2440	A2441	G2448	G2453	A2454	A2455	G2456	G2457	G2458	A2459	U2460	A2463	A2464	A2468	G2469	G2470	G2471	G2472	G2473	G2474	G2475	G2476	A2477	G2478	A2479	G2483	U2487								
U2330	U2331	G2332	G2333	U2334	U2335	G2336	G2337	A2338	U2339	A2340	U2341	G2342	A2343	A2344	U2345	A2346	G2347	G2348	A2349	G2350	A2351	G2352	U2355	A2356	A2357	A2358	G2359	A2362	G2363	A2364	A2369	G2370	G2371	U2372	U2373	G2374	A2375	G2376	U2377	G2378	G2379	G2382	A2383	U2386	A2387	G2388	A2389	A2390	G2393	G2394	A2395	G2400	
U2209	G2210	G2214	A2220	C2221	C2222	U2223	U2224	A2227	G2232	C2233	C2237	U2238	U2239	U2240	A2241	U2242	C2243	G2246	A2252	G2253	A2254	G2255	A2262	G2263	G2267	G2268	C2269	U2278	G2279	A2295	A2296	A2297	A2302	G2308	C2312	G2313	G2314	A2315	A2316	C2324	A2327	G2328	A2329	G2201	A2202	G2203	U2204	A2205	G2206	G2207	G2208		
A2059	A2060	A2062	A2066	G2067	U2070	A2071	C2072	A2078	G2082	A2083	G2084	G2085	A2088	A2089	G2090	A2091	C2092	G2098	G2099	G2100	G2101	U2105	G2109	C2110	A2111	G2116	U2121	G2122	A2123	A2124	U2125	U2128	G2129	C2133	A2134	G2135	C2136	U2137	U2138	G2139	U2140	A2141	C2142	G2143	G2144	G2145							
A2146	U2147	A2148	G2149	A2152	G2153	G2154	A2155	G2156	C2157	C2158	U2159	U2160	G2161	A2162	A2163	A2164	C2166	C2167	G2168	G2169	A2170	G2171	C2172	G2173	C2174	C2175	A2176	C2177	G2178	C2181	G2182	U2184	G2185	G2186	A2187	G2188	G2189	C2190	C2193	G2194	G2195	U2196	G2197	G2198	G2199	U2200	A2202	G2203	U2204	A2205	G2206	G2207	G2208
G2209	G2210	G2214	A2220	C2221	C2222	U2223	U2224	A2227	G2232	C2233	C2237	U2238	U2239	U2240	A2241	U2242	C2243	G2246	A2252	G2253	A2254	G2255	A2262	G2263	G2267	G2268	C2269	U2278	G2279	A2295	A2296	A2297	A2302	G2308	C2312	G2313	G2314	A2315	A2316	C2324	A2327	G2328	A2329	G2201	A2202	G2203	U2204	A2205	G2206	G2207	G2208		
A2330	U2331	G2332	G2333	U2334	U2335	G2336	G2337	A2338	U2339	A2340	U2341	G2342	A2343	A2344	U2345	A2346	G2347	G2348	A2349	G2350	A2351	G2352	U2355	A2356	A2357	A2358	G2359	A2362	G2363	A2364	A2369	G2370	G2371	U2372	U2373	G2374	A2375	G2376	U2377	G2378	G2379	G2382	A2383	U2386	A2387	G2388	A2389	A2390	G2393	G2394	A2395	G2400	



• Molecule 34: 5S ribosomal RNA

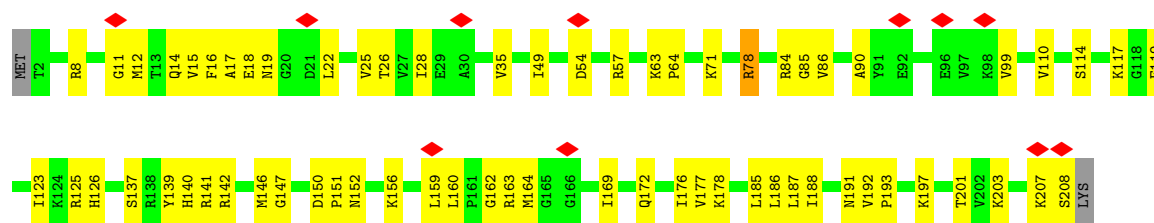


• Molecule 35: 50S ribosomal protein uL2

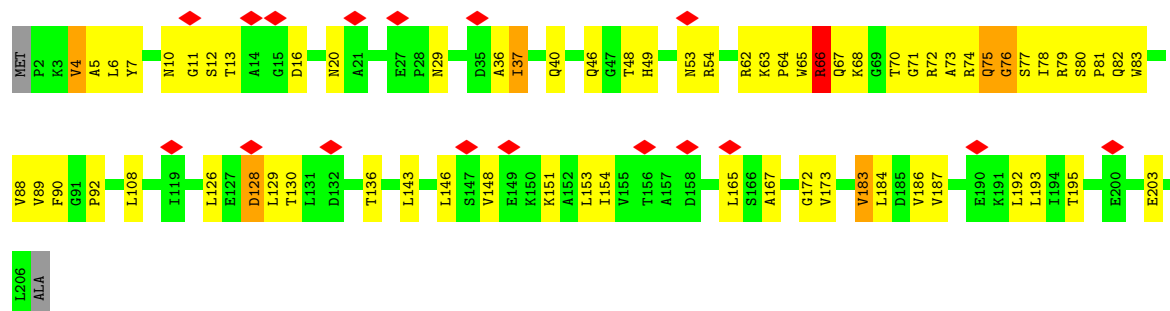


• Molecule 36: 50S ribosomal protein uL3

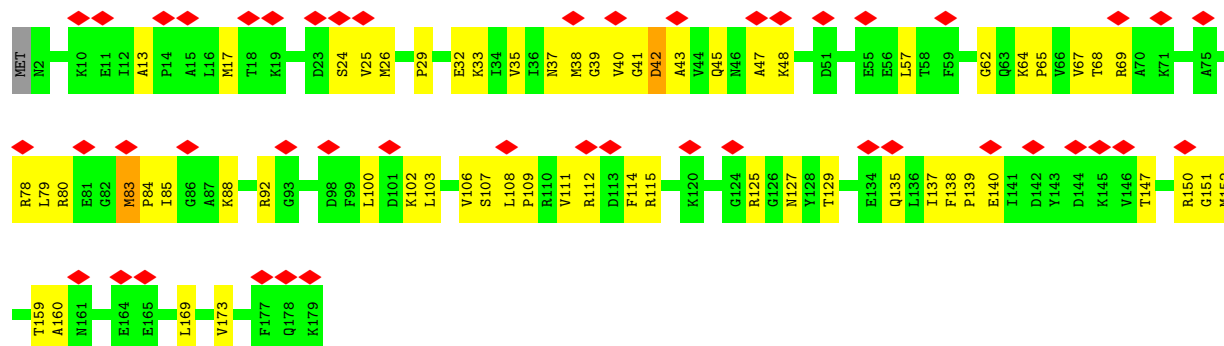




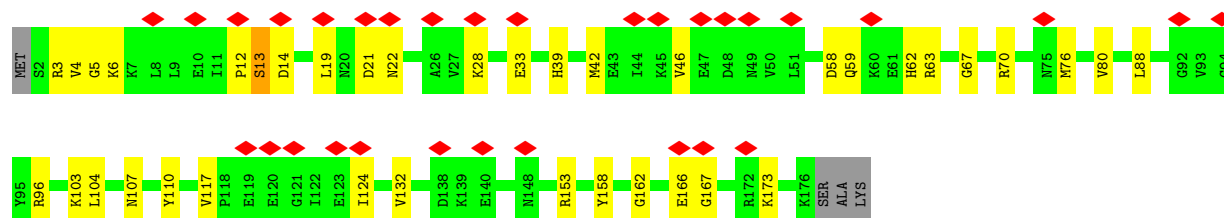
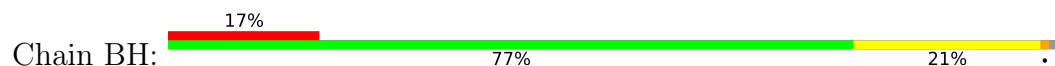
• Molecule 37: 50S ribosomal protein uL4



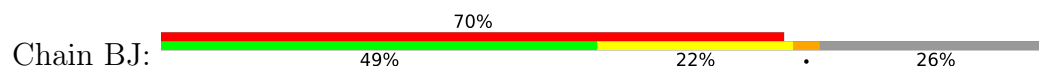
• Molecule 38: 50S ribosomal protein uL5

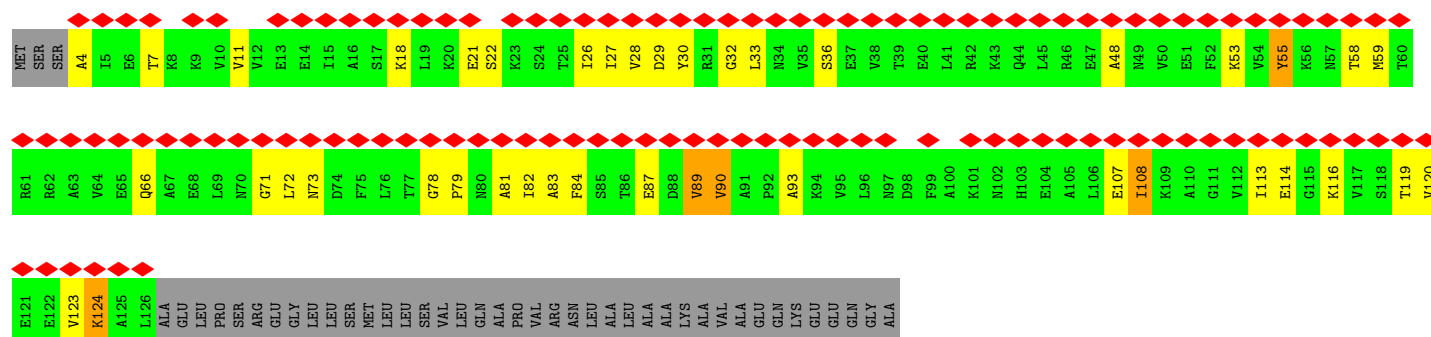


• Molecule 39: 50S ribosomal protein uL6

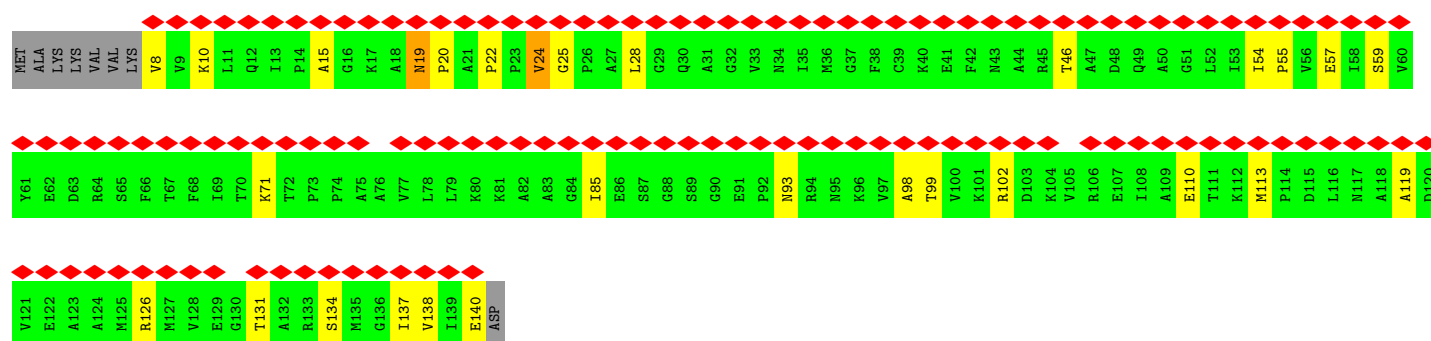
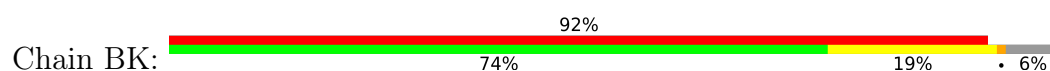


• Molecule 40: 50S ribosomal protein uL10

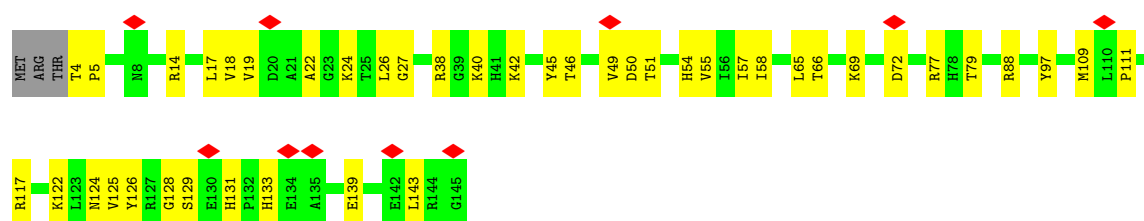




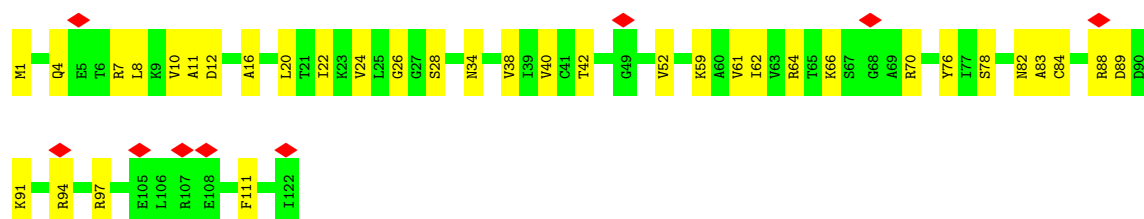
• Molecule 41: 50S ribosomal protein uL11



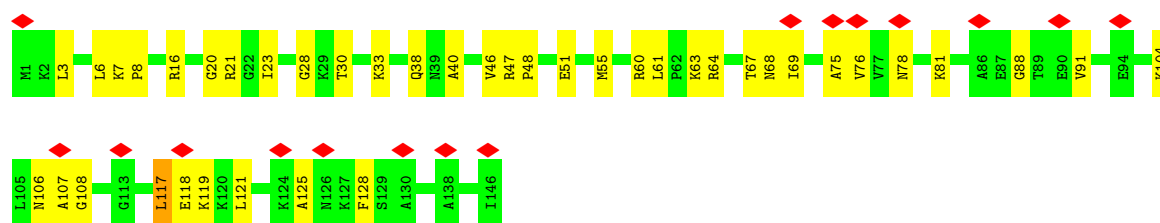
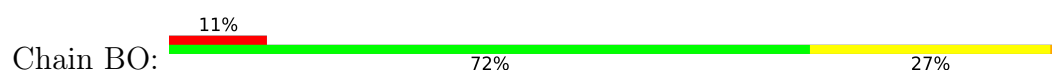
• Molecule 42: 50S ribosomal protein uL13



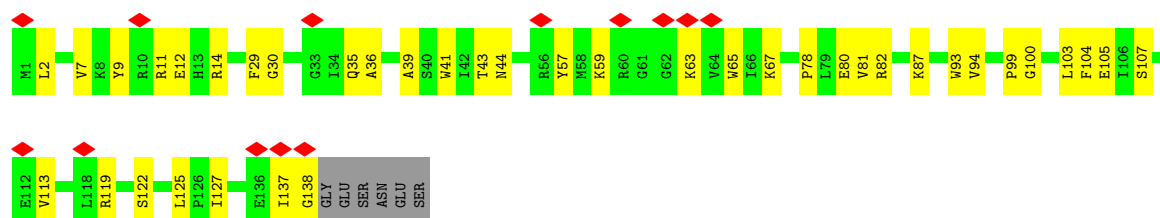
• Molecule 43: 50S ribosomal protein uL14



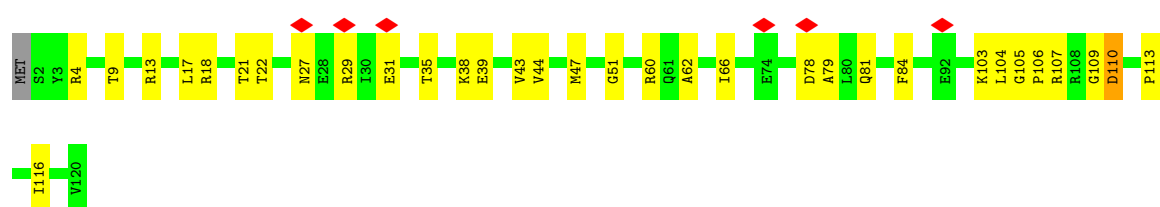
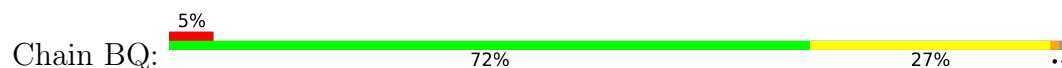
• Molecule 44: 50S ribosomal protein uL15



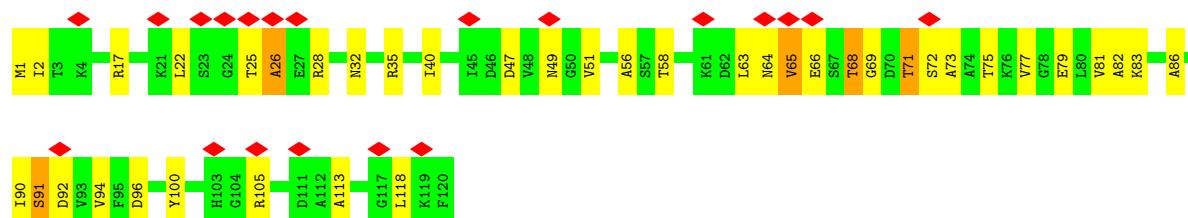
- Molecule 45: 50S ribosomal protein uL16



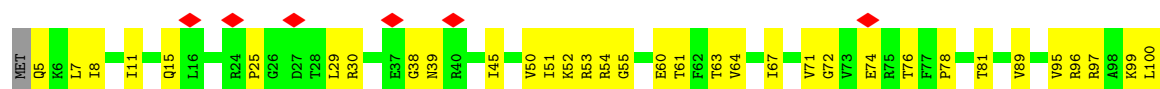
- Molecule 46: 50S ribosomal protein bL17

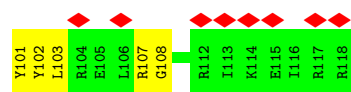


- Molecule 47: 50S ribosomal protein uL18

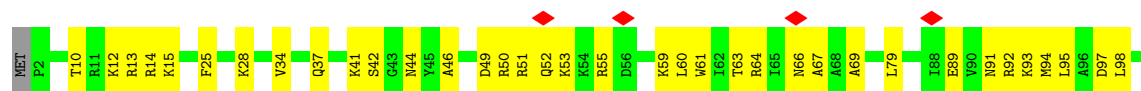


- Molecule 48: 50S ribosomal protein bL19

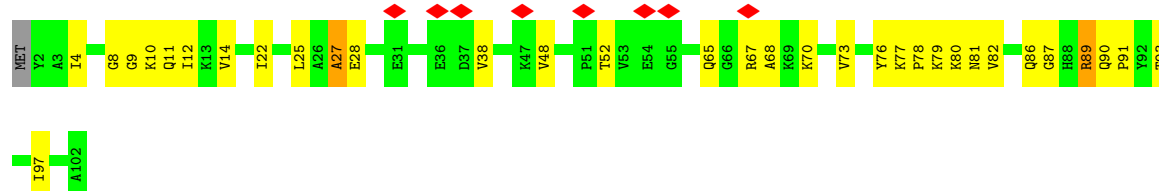




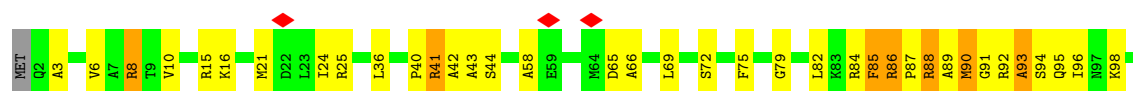
- Molecule 49: 50S ribosomal protein bL20



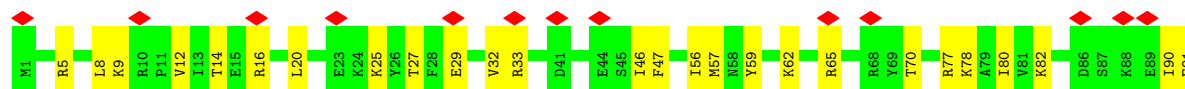
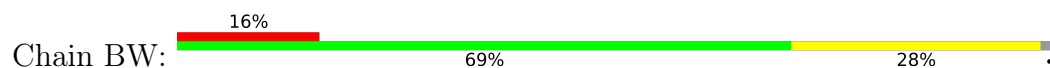
- Molecule 50: 50S ribosomal protein bL21



- Molecule 51: 50S ribosomal protein uL22

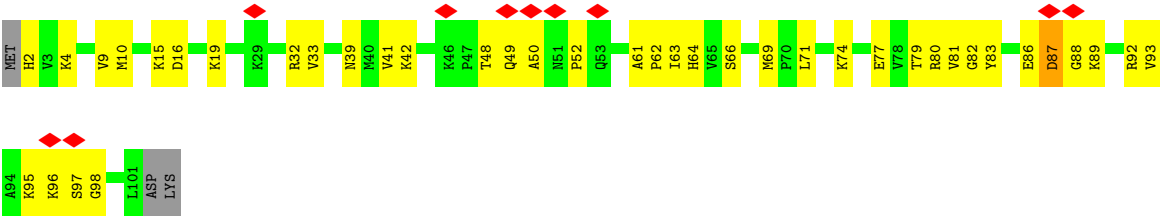


- Molecule 52: 50S ribosomal protein uL23

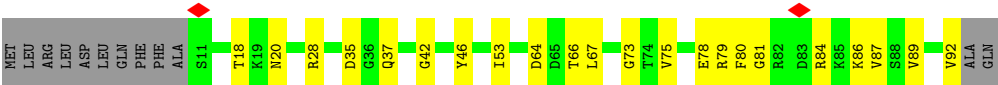


- Molecule 53: 50S ribosomal protein uL24





• Molecule 54: 50S ribosomal protein bL27



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	305045	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	defocus groups	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	28	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	125085	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.009	Depositor
Minimum map value	-0.005	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.00155	Depositor
Map size ($\text{\AA}$)	407.74402, 407.74402, 407.74402	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.108, 1.108, 1.108	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	AA	0.52	0/37074	0.53	0/57834
2	AB	0.52	0/895	0.94	2/1117 (0.2%)
3	AC	0.47	0/839	0.92	3/1047 (0.3%)
4	AD	0.44	0/796	1.03	4/992 (0.4%)
5	AE	0.45	0/660	1.05	1/822 (0.1%)
6	AF	0.51	0/380	1.00	2/472 (0.4%)
7	AG	0.43	0/612	0.82	0/762
8	AH	0.41	0/524	0.95	0/652
9	AI	0.44	0/520	0.97	1/647 (0.2%)
10	AJ	0.49	0/408	1.01	2/507 (0.4%)
11	AK	0.43	0/471	1.15	4/587 (0.7%)
12	AL	0.42	0/548	1.12	0/682
13	AM	0.48	0/475	0.99	1/592 (0.2%)
14	AN	0.38	0/240	1.02	0/297
15	AO	0.42	0/352	0.83	0/437
16	AP	0.45	0/356	0.95	0/442
17	AQ	0.44	0/344	0.90	0/427
18	AR	0.48	0/284	0.96	2/352 (0.6%)
19	AS	0.53	0/335	0.99	1/417 (0.2%)
20	AT	0.43	0/344	0.74	0/427
21	AX	0.41	0/1834	0.47	0/2858
22	AY	0.48	0/466	0.87	3/726 (0.4%)
23	AZ	0.78	0/106	1.66	3/122 (2.5%)
24	B0	0.38	0/448	0.89	2/596 (0.3%)
25	B1	0.29	0/531	0.65	0/707
26	B2	0.32	0/457	0.69	0/613
27	B3	0.35	0/513	0.75	0/683
28	B4	0.30	0/433	0.76	0/574
29	B5	0.34	0/406	0.69	0/540
30	B6	0.26	0/370	0.76	1/483 (0.2%)
31	B7	0.28	0/519	0.64	0/680
32	B8	0.26	0/291	0.75	0/383
33	BA	0.54	0/70307	0.57	22/109687 (0.0%)
34	BB	0.49	0/2678	0.52	0/4174

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	BD	0.37	0/2148	0.85	2/2881 (0.1%)
36	BE	0.39	0/1597	0.76	2/2140 (0.1%)
37	BF	0.37	0/1580	0.80	3/2132 (0.1%)
38	BG	0.40	0/1423	0.81	5/1910 (0.3%)
39	BH	0.33	0/1360	0.76	0/1832
40	BJ	0.38	0/963	0.73	0/1298
41	BK	0.41	0/995	0.90	5/1346 (0.4%)
42	BM	0.36	0/1146	0.77	2/1542 (0.1%)
43	BN	0.40	0/927	0.80	1/1245 (0.1%)
44	BO	0.30	0/1093	0.78	2/1457 (0.1%)
45	BP	0.29	0/1120	0.72	1/1496 (0.1%)
46	BQ	0.35	0/960	0.69	0/1284
47	BR	0.44	0/921	0.84	1/1236 (0.1%)
48	BS	0.33	0/949	0.73	0/1269
49	BT	0.34	0/952	0.66	0/1266
50	BU	0.38	0/797	0.81	2/1070 (0.2%)
51	BV	0.53	1/851 (0.1%)	0.88	2/1146 (0.2%)
52	BW	0.40	0/759	0.74	0/1011
53	BX	0.37	0/764	0.88	0/1022
54	BZ	0.39	0/638	0.77	0/847
All	All	0.50	1/147759 (0.0%)	0.63	82/221768 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	0	36
21	AX	0	2
22	AY	0	7
33	BA	0	84
34	BB	0	2
37	BF	0	1
51	BV	0	2
All	All	0	134

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	BV	95	GLN	CA-C	-6.25	1.45	1.52

The worst 5 of 82 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	BA	589	G	C4'-C3'-O3'	20.99	140.88	109.40
33	BA	83	G	C4'-C3'-O3'	-17.76	82.76	109.40
33	BA	82	G	C4'-C3'-O3'	-15.30	90.05	113.00
33	BA	2487	U	C4'-C3'-O3'	14.71	131.47	109.40
33	BA	366	A	C4'-C3'-O3'	12.42	128.03	109.40

There are no chirality outliers.

5 of 134 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	209	A	Sidechain
1	AA	308	A	Sidechain
1	AA	335	A	Sidechain
1	AA	53	A	Sidechain
1	AA	76	A	Sidechain

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	AA	33115	0	16676	248	0
2	AB	896	0	244	3	0
3	AC	840	0	241	3	0
4	AD	797	0	224	3	0
5	AE	661	0	197	2	0
6	AF	381	0	104	0	0
7	AG	613	0	164	1	0
8	AH	525	0	146	0	0
9	AI	521	0	155	4	0
10	AJ	409	0	104	0	0
11	AK	472	0	135	7	0
12	AL	549	0	157	1	0
13	AM	476	0	137	2	0
14	AN	241	0	62	2	0
15	AO	353	0	94	0	0
16	AP	357	0	95	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	AQ	345	0	90	1	0
18	AR	285	0	76	1	0
19	AS	336	0	93	2	0
20	AT	345	0	89	2	0
21	AX	1643	0	830	30	0
22	AY	415	0	207	79	0
23	AZ	107	0	58	9	0
24	B0	444	0	486	60	0
25	B1	530	0	568	14	0
26	B2	455	0	491	12	0
27	B3	503	0	494	12	0
28	B4	426	0	445	16	0
29	B5	401	0	413	18	0
30	B6	367	0	410	20	0
31	B7	512	0	564	32	0
32	B8	288	0	330	3	0
33	BA	62767	0	31584	785	0
34	BB	2395	0	1212	21	0
35	BD	2111	0	2200	87	0
36	BE	1575	0	1642	51	0
37	BF	1561	0	1647	93	0
38	BG	1404	0	1467	47	0
39	BH	1342	0	1388	26	0
40	BJ	955	0	990	28	0
41	BK	981	0	1020	28	0
42	BM	1123	0	1162	32	0
43	BN	920	0	977	21	0
44	BO	1081	0	1132	40	0
45	BP	1097	0	1165	25	0
46	BQ	953	0	983	29	0
47	BR	912	0	947	36	0
48	BS	936	0	1008	31	0
49	BT	940	0	1005	41	0
50	BU	786	0	826	40	0
51	BV	842	0	899	50	0
52	BW	752	0	802	22	0
53	BX	754	0	809	31	0
54	BZ	630	0	644	16	0
All	All	135425	0	80088	1887	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 9.

The worst 5 of 1887 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)
23:AZ:74:ILE:CA	51:BV:85:PHE:HE2	1.11	1.60
23:AZ:74:ILE:CA	51:BV:85:PHE:CE2	1.99	1.44
24:B0:37:ARG:NH1	24:B0:44:PRO:HG3	1.37	1.40
37:BF:80:SER:OG	37:BF:81:PRO:HD2	1.30	1.29
41:BK:15:ALA:HB1	41:BK:46:THR:CG2	1.62	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	
2	AB	222/246 (90%)	204 (92%)	13 (6%)	5 (2%)	5	30
3	AC	208/218 (95%)	193 (93%)	14 (7%)	1 (0%)	24	59
4	AD	197/200 (98%)	191 (97%)	4 (2%)	2 (1%)	12	45
5	AE	163/166 (98%)	150 (92%)	9 (6%)	4 (2%)	4	29
6	AF	93/95 (98%)	88 (95%)	3 (3%)	2 (2%)	5	31
7	AG	151/156 (97%)	144 (95%)	6 (4%)	1 (1%)	18	53
8	AH	129/132 (98%)	123 (95%)	5 (4%)	1 (1%)	16	50
9	AI	128/130 (98%)	113 (88%)	10 (8%)	5 (4%)	2	21
10	AJ	100/102 (98%)	88 (88%)	8 (8%)	4 (4%)	2	21
11	AK	116/131 (88%)	106 (91%)	9 (8%)	1 (1%)	14	47
12	AL	135/138 (98%)	119 (88%)	9 (7%)	7 (5%)	1	17
13	AM	117/121 (97%)	94 (80%)	13 (11%)	10 (8%)	0	10
14	AN	58/61 (95%)	51 (88%)	4 (7%)	3 (5%)	1	17
15	AO	86/89 (97%)	82 (95%)	2 (2%)	2 (2%)	5	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	AP	87/90 (97%)	82 (94%)	3 (3%)	2 (2%)	5	30
17	AQ	84/87 (97%)	78 (93%)	6 (7%)	0	100	100
18	AR	69/79 (87%)	64 (93%)	2 (3%)	3 (4%)	2	20
19	AS	82/92 (89%)	75 (92%)	5 (6%)	2 (2%)	4	29
20	AT	84/88 (96%)	77 (92%)	6 (7%)	1 (1%)	10	41
23	AZ	22/95 (23%)	17 (77%)	2 (9%)	3 (14%)	0	3
24	B0	56/62 (90%)	53 (95%)	1 (2%)	2 (4%)	2	23
25	B1	63/66 (96%)	60 (95%)	3 (5%)	0	100	100
26	B2	56/59 (95%)	54 (96%)	1 (2%)	1 (2%)	6	34
27	B3	62/66 (94%)	56 (90%)	4 (6%)	2 (3%)	3	25
28	B4	52/59 (88%)	47 (90%)	4 (8%)	1 (2%)	6	33
29	B5	46/49 (94%)	44 (96%)	2 (4%)	0	100	100
30	B6	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
31	B7	62/66 (94%)	56 (90%)	5 (8%)	1 (2%)	7	36
32	B8	34/37 (92%)	33 (97%)	1 (3%)	0	100	100
35	BD	273/277 (99%)	264 (97%)	8 (3%)	1 (0%)	30	64
36	BE	205/209 (98%)	189 (92%)	11 (5%)	5 (2%)	4	29
37	BF	203/207 (98%)	184 (91%)	16 (8%)	3 (2%)	8	37
38	BG	176/179 (98%)	154 (88%)	18 (10%)	4 (2%)	5	30
39	BH	173/179 (97%)	165 (95%)	7 (4%)	1 (1%)	21	55
40	BJ	121/166 (73%)	97 (80%)	14 (12%)	10 (8%)	0	10
41	BK	131/141 (93%)	122 (93%)	7 (5%)	2 (2%)	8	37
42	BM	140/145 (97%)	130 (93%)	9 (6%)	1 (1%)	18	53
43	BN	120/122 (98%)	112 (93%)	6 (5%)	2 (2%)	7	35
44	BO	144/146 (99%)	132 (92%)	10 (7%)	2 (1%)	9	38
45	BP	136/144 (94%)	129 (95%)	7 (5%)	0	100	100
46	BQ	117/120 (98%)	109 (93%)	7 (6%)	1 (1%)	14	47
47	BR	118/120 (98%)	106 (90%)	7 (6%)	5 (4%)	2	20
48	BS	112/115 (97%)	100 (89%)	12 (11%)	0	100	100
49	BT	115/119 (97%)	112 (97%)	3 (3%)	0	100	100
50	BU	99/102 (97%)	82 (83%)	15 (15%)	2 (2%)	6	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	BV	107/113 (95%)	96 (90%)	8 (8%)	3 (3%)	4	27
52	BW	91/95 (96%)	86 (94%)	5 (6%)	0	100	100
53	BX	98/103 (95%)	87 (89%)	8 (8%)	3 (3%)	3	25
54	BZ	80/94 (85%)	77 (96%)	3 (4%)	0	100	100
All	All	5563/5920 (94%)	5116 (92%)	336 (6%)	111 (2%)	8	32

5 of 111 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	AE	4	ILE
6	AF	70	ALA
12	AL	127	ARG
13	AM	101	ASN
23	AZ	78	PHE

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	
23	AZ	6/87 (7%)	4 (67%)	2 (33%)	0	2
24	B0	47/50 (94%)	47 (100%)	0	100	100
25	B1	56/57 (98%)	56 (100%)	0	100	100
26	B2	52/53 (98%)	51 (98%)	1 (2%)	50	66
27	B3	53/55 (96%)	53 (100%)	0	100	100
28	B4	48/53 (91%)	48 (100%)	0	100	100
29	B5	46/47 (98%)	46 (100%)	0	100	100
30	B6	39/39 (100%)	39 (100%)	0	100	100
31	B7	54/56 (96%)	54 (100%)	0	100	100
32	B8	34/35 (97%)	34 (100%)	0	100	100
35	BD	223/225 (99%)	222 (100%)	1 (0%)	84	83
36	BE	168/170 (99%)	168 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	BF	169/170 (99%)	167 (99%)	2 (1%)	63	72
38	BG	153/154 (99%)	153 (100%)	0	100	100
39	BH	148/151 (98%)	148 (100%)	0	100	100
40	BJ	105/138 (76%)	105 (100%)	0	100	100
41	BK	103/110 (94%)	103 (100%)	0	100	100
42	BM	120/123 (98%)	120 (100%)	0	100	100
43	BN	101/101 (100%)	101 (100%)	0	100	100
44	BO	110/110 (100%)	110 (100%)	0	100	100
45	BP	111/116 (96%)	111 (100%)	0	100	100
46	BQ	99/100 (99%)	99 (100%)	0	100	100
47	BR	93/93 (100%)	93 (100%)	0	100	100
48	BS	99/100 (99%)	99 (100%)	0	100	100
49	BT	96/98 (98%)	96 (100%)	0	100	100
50	BU	83/84 (99%)	83 (100%)	0	100	100
51	BV	90/93 (97%)	89 (99%)	1 (1%)	65	74
52	BW	84/85 (99%)	84 (100%)	0	100	100
53	BX	84/87 (97%)	84 (100%)	0	100	100
54	BZ	64/74 (86%)	64 (100%)	0	100	100
All	All	2738/2914 (94%)	2731 (100%)	7 (0%)	84	85

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	BD	185	LEU
37	BF	37	ILE
51	BV	90	MET
37	BF	66	ARG
26	B2	53	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
44	BO	106	ASN
51	BV	60	HIS
46	BQ	27	ASN

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Mol	Chain	Res	Type
49	BT	37	GLN
53	BX	2	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1543/1555 (99%)	235 (15%)	17 (1%)
21	AX	76/77 (98%)	15 (19%)	1 (1%)
22	AY	18/19 (94%)	14 (77%)	3 (16%)
33	BA	2922/2928 (99%)	792 (27%)	80 (2%)
34	BB	111/119 (93%)	32 (28%)	4 (3%)
All	All	4670/4698 (99%)	1088 (23%)	105 (2%)

5 of 1088 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	10	A
1	AA	11	G
1	AA	34	A
1	AA	41	G
1	AA	49	C

5 of 105 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
33	BA	1173	A
33	BA	1652	C
33	BA	2807	A
33	BA	1250	G
33	BA	1455	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.

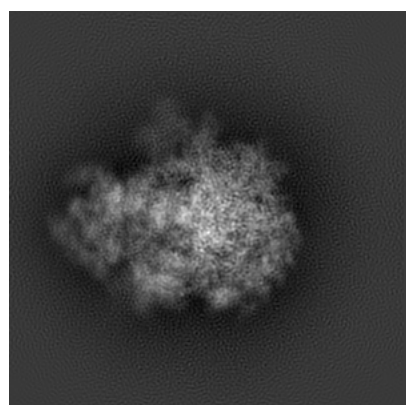
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6306. These allow visual inspection of the internal detail of the map and identification of artifacts.

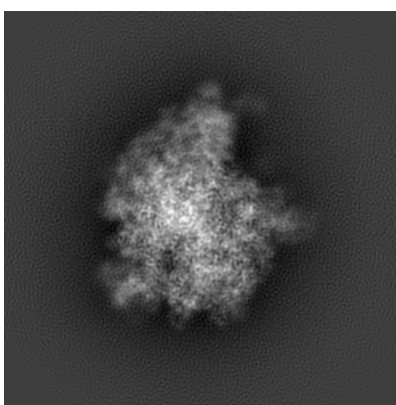
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

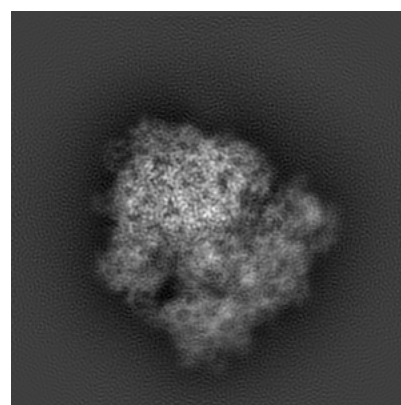
6.1.1 Primary map



X



Y

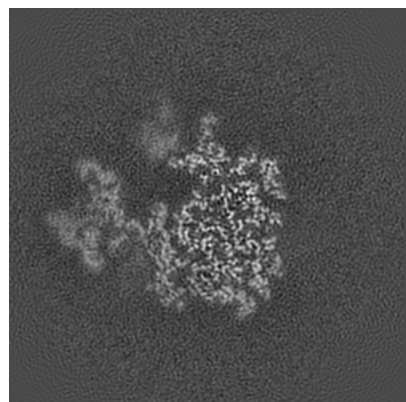


Z

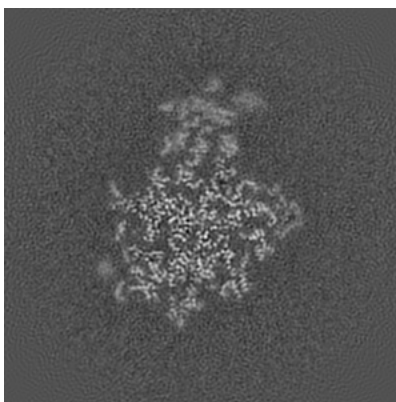
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

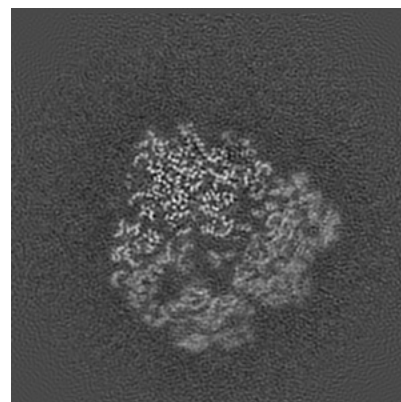
6.2.1 Primary map



X Index: 184



Y Index: 184

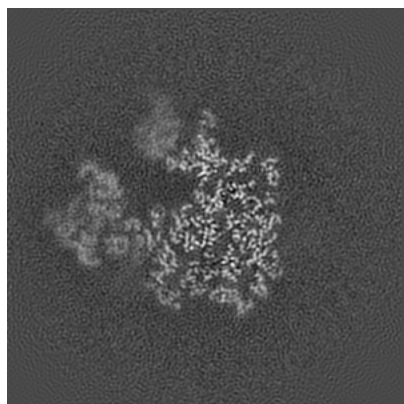


Z Index: 184

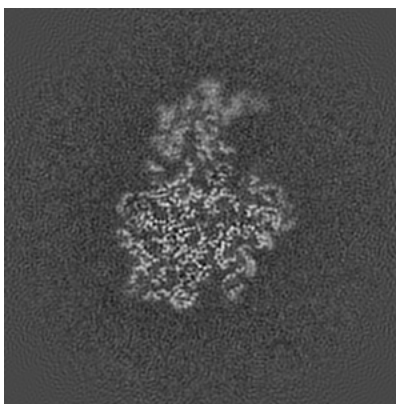
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

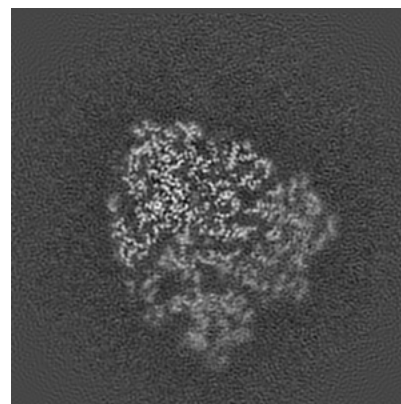
6.3.1 Primary map



X Index: 181



Y Index: 176

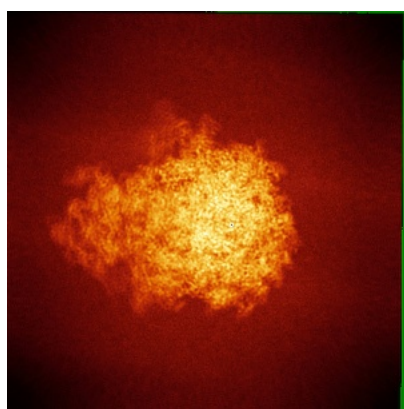


Z Index: 179

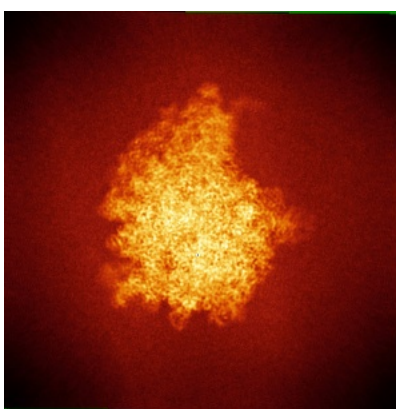
The images above show the largest variance slices of the map in three orthogonal directions.

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

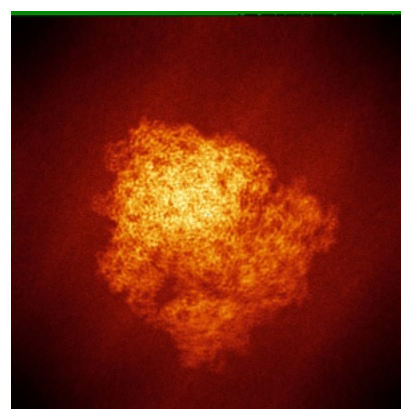
6.4.1 Primary map



X



Y

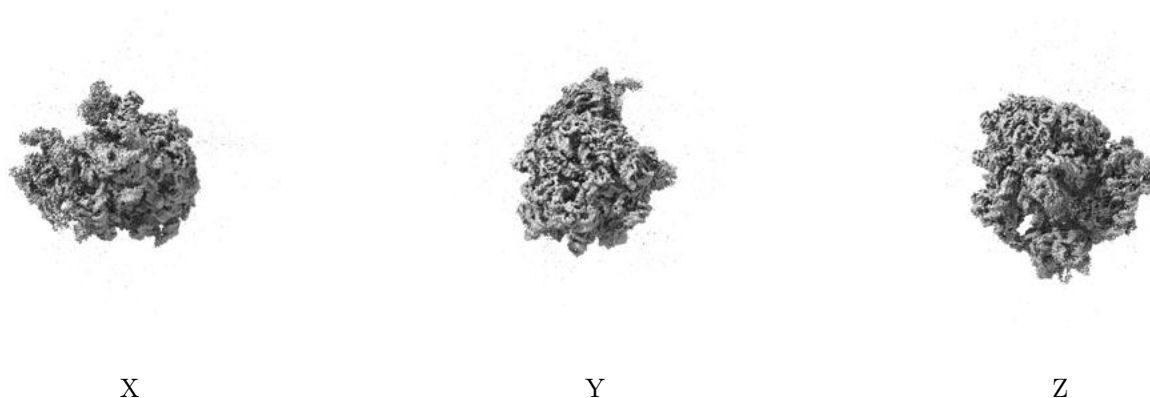


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00155. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

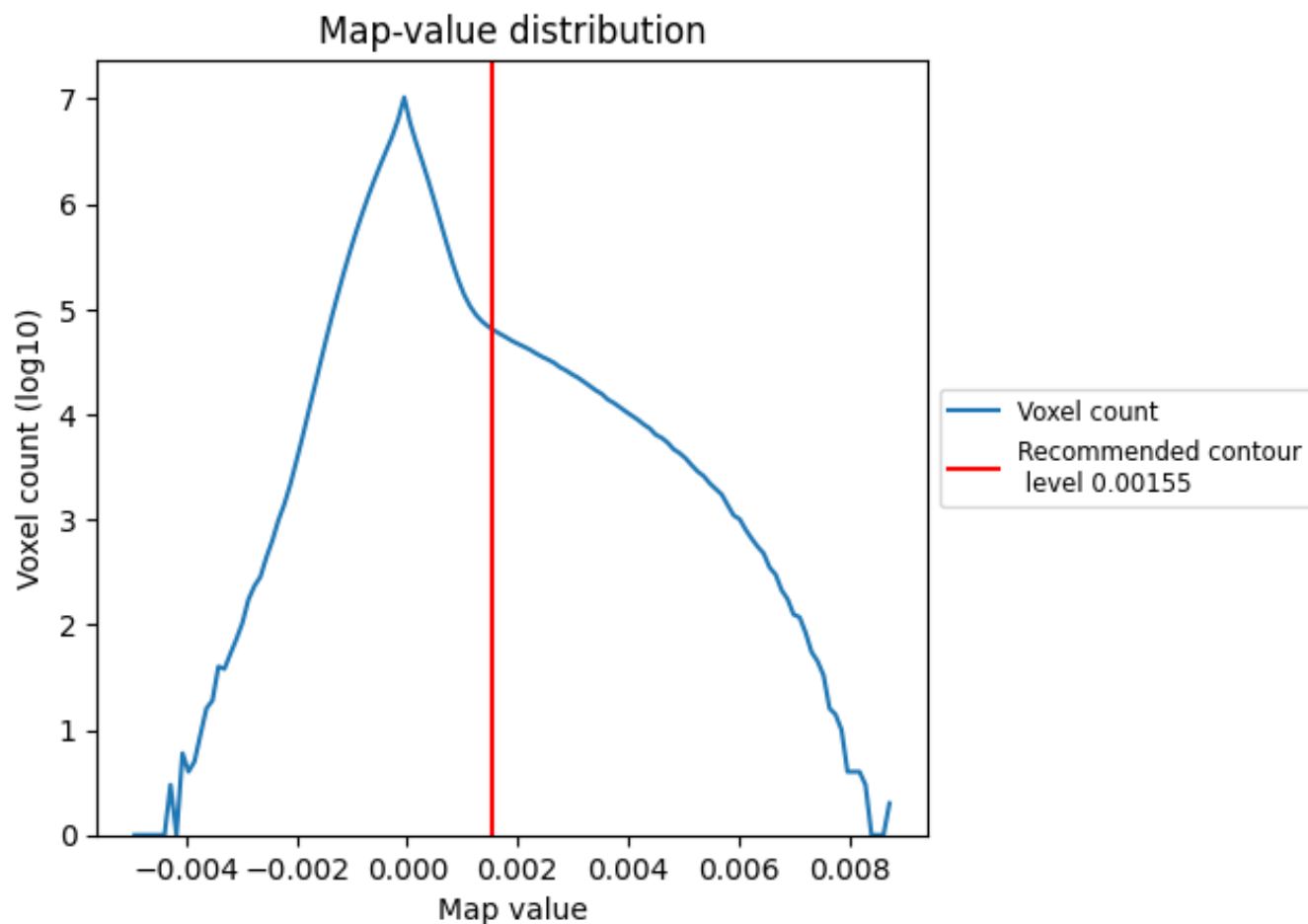
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

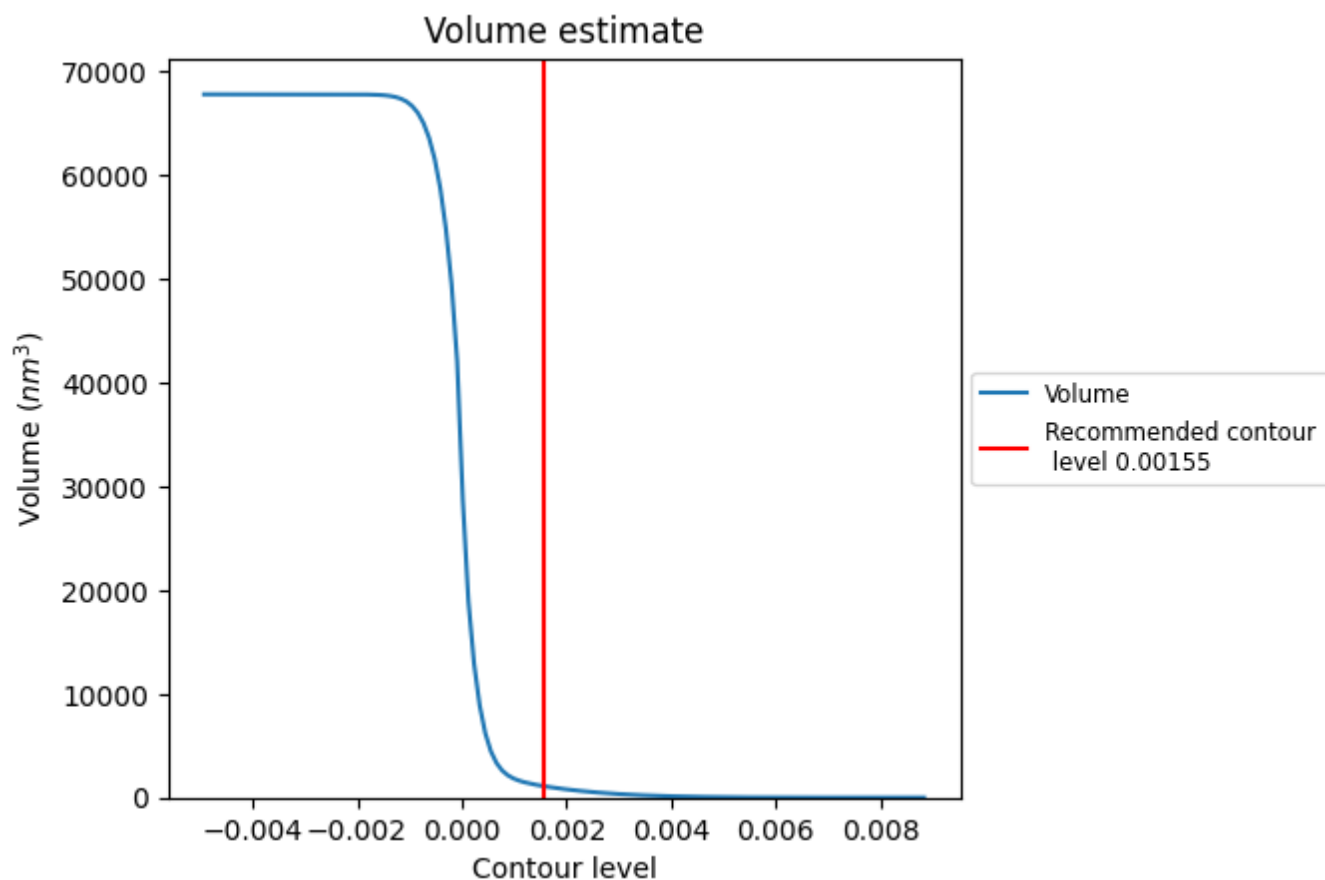
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

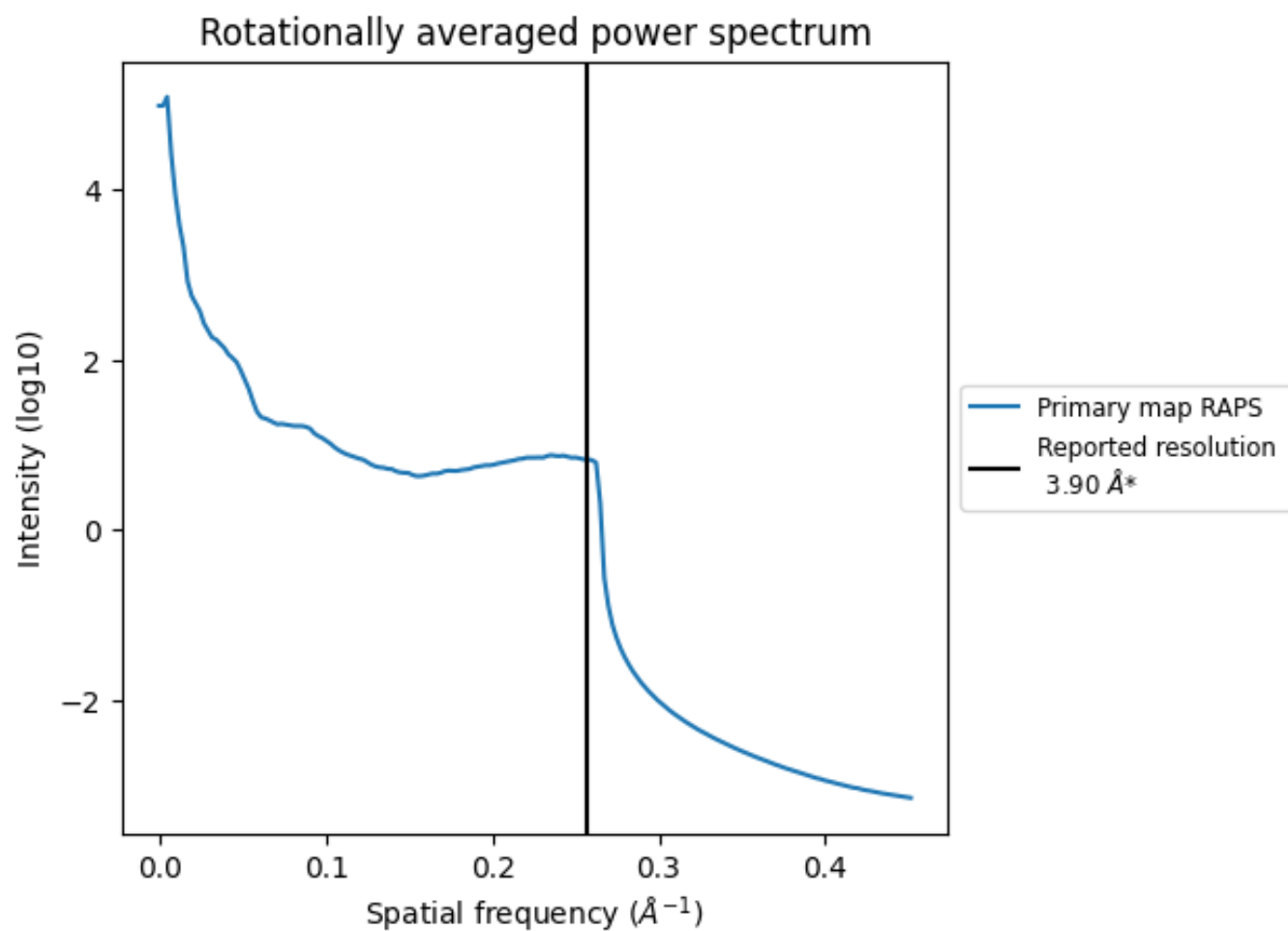
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1114 nm³; this corresponds to an approximate mass of 1007 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 0.256 Å⁻¹

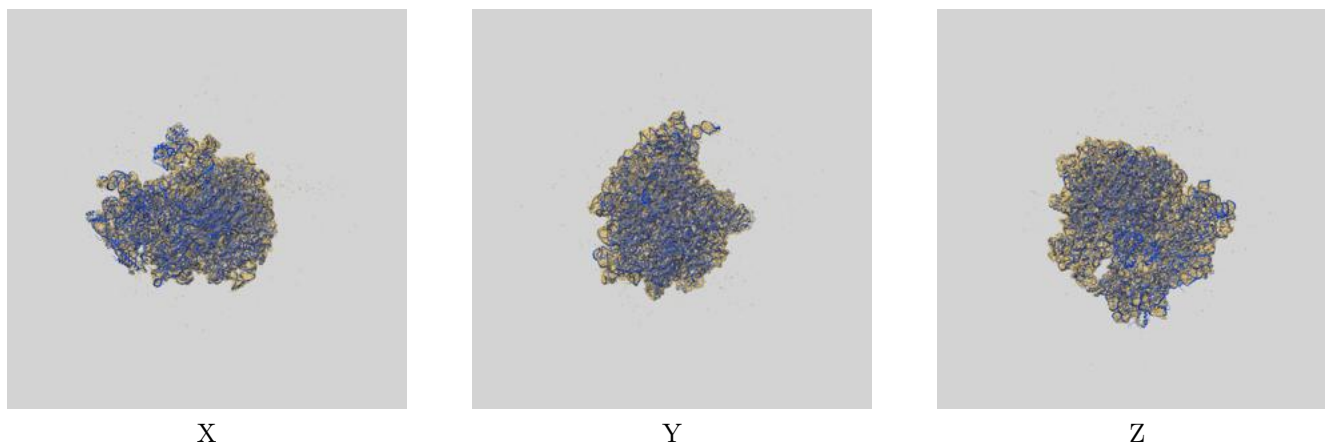
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

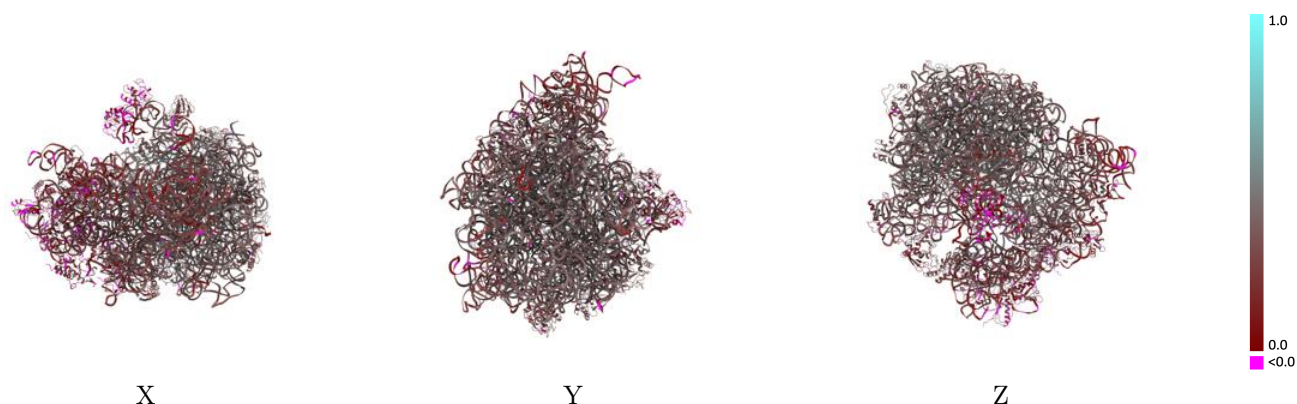
This section contains information regarding the fit between EMDB map EMD-6306 and PDB model 3J9W. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



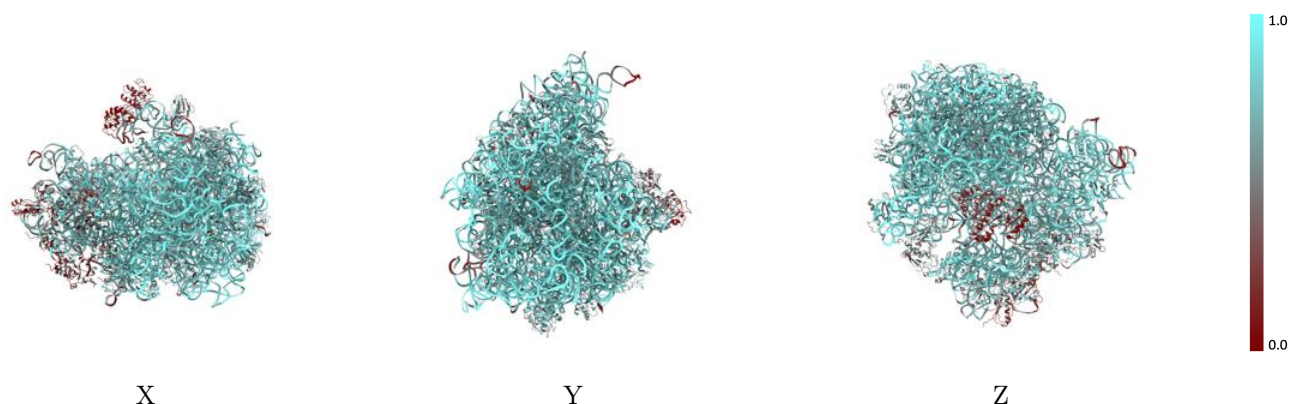
The images above show the 3D surface view of the map at the recommended contour level 0.00155 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



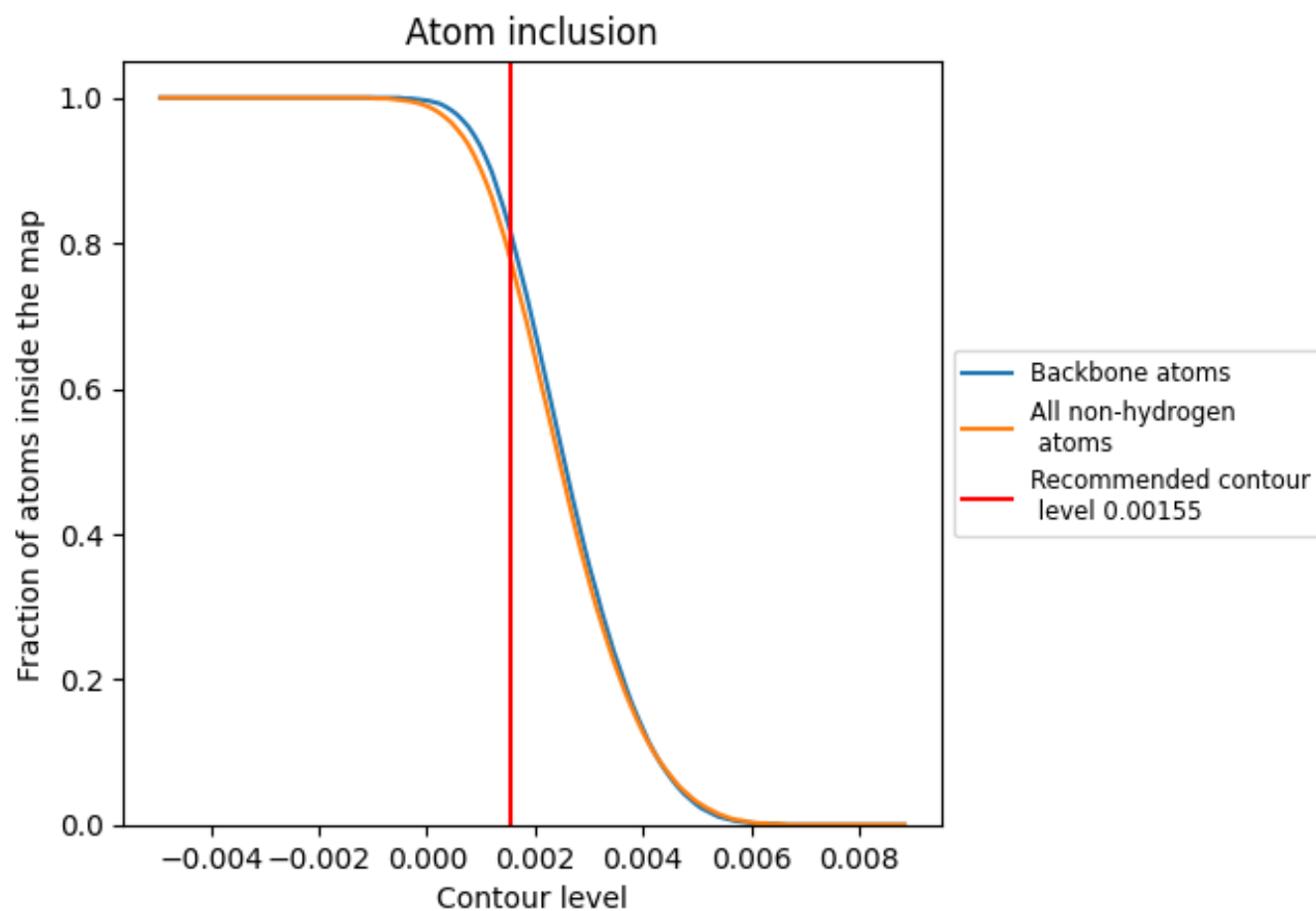
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00155).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 78% 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 (0.00155) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7770	 0.3310
AA	 0.8030	 0.2870
AB	 0.3240	 0.1870
AC	 0.4710	 0.2100
AD	 0.5060	 0.2030
AE	 0.4780	 0.2410
AF	 0.7580	 0.3250
AG	 0.6720	 0.2690
AH	 0.6100	 0.2660
AI	 0.4300	 0.1660
AJ	 0.3010	 0.1370
AK	 0.6610	 0.3210
AL	 0.7050	 0.3380
AM	 0.6930	 0.2840
AN	 0.6100	 0.2250
AO	 0.8440	 0.3280
AP	 0.6920	 0.3000
AQ	 0.7100	 0.3010
AR	 0.6250	 0.2540
AS	 0.6610	 0.2440
AT	 0.7650	 0.2640
AX	 0.8170	 0.3370
AY	 0.3640	 0.1620
AZ	 0.5710	 0.4570
B0	 0.5830	 0.3470
B1	 0.5990	 0.2730
B2	 0.6720	 0.3690
B3	 0.4000	 0.1850
B4	 0.7050	 0.3740
B5	 0.6460	 0.3430
B6	 0.6960	 0.3790
B7	 0.7150	 0.4180
B8	 0.6700	 0.3790
BA	 0.8610	 0.3720
BB	 0.8870	 0.3550



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Chain	Atom inclusion	Q-score
BD	 0.6890	 0.3790
BE	 0.6840	 0.3720
BF	 0.6630	 0.3510
BG	 0.5290	 0.2470
BH	 0.5960	 0.2850
BJ	 0.1040	 0.0480
BK	 0.0360	 0.0280
BM	 0.6790	 0.3530
BN	 0.6510	 0.3710
BO	 0.6420	 0.3440
BP	 0.6770	 0.3780
BQ	 0.6890	 0.3560
BR	 0.5990	 0.2690
BS	 0.6260	 0.3180
BT	 0.7070	 0.3500
BU	 0.6660	 0.3550
BV	 0.6870	 0.3880
BW	 0.6050	 0.3330
BX	 0.6080	 0.3180
BZ	 0.6760	 0.3730