



wwPDB EM Validation Summary Report ⓘ

Sep 15, 2026 – 10:43 PM EDT

PDB ID : 6ORL / pdb_00006orl
EMDB ID : EMD-20174
Title : RF1 pre-accommodated 70S complex at 24 ms
Authors : Fu, Z.; Indrisiunaite, G.; Kaledhonkar, S.; Shah, B.; Sun, M.; Chen, B.; Grassucci, R.A.; Ehrenberg, M.; Frank, J.
Deposited on : 2019-04-30
Resolution : 3.50 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:

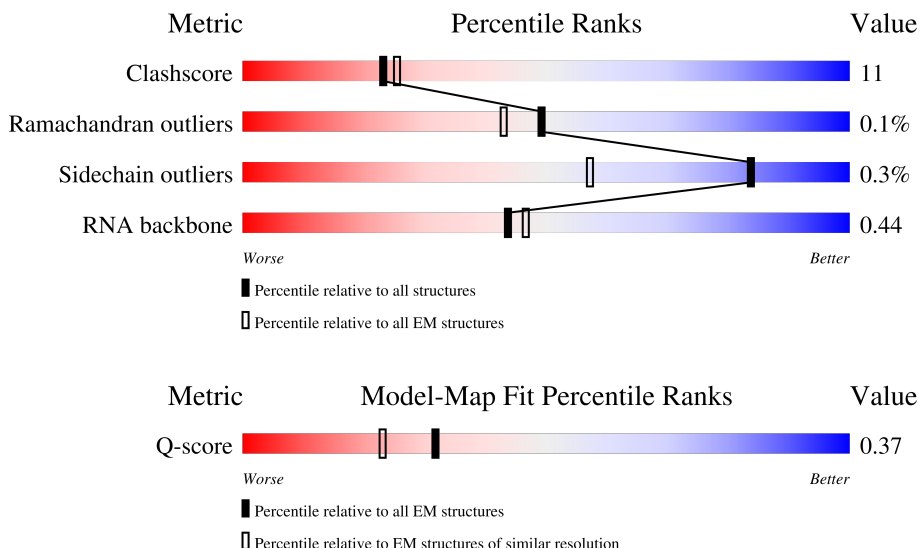
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 3.50 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.



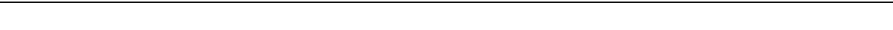
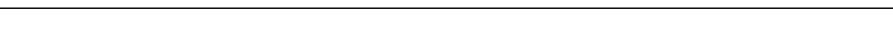
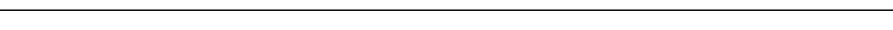
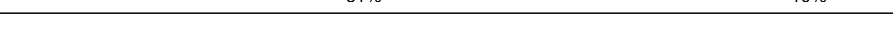
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	1	2903	
2	2	1534	
3	3	120	

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Mol	Chain	Length	Quality of chain
4	B	271	
5	C	209	
6	D	201	
7	E	177	
8	F	175	
9	G	149	
10	J	142	
11	K	123	
12	L	144	
13	M	136	
14	N	119	
15	O	116	
16	P	114	
17	Q	117	
18	R	103	
19	S	110	
20	T	94	
21	U	103	
22	V	94	
23	W	76	
24	X	77	
25	Y	62	
26	Z	58	
27	b	56	
28	c	52	

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Mol	Chain	Length	Quality of chain
29	d	46	
30	e	64	
31	f	38	
32	g	225	
33	h	208	
34	i	205	
35	j	156	
36	k	104	
37	l	151	
38	m	129	
39	n	127	
40	o	99	
41	p	117	
42	q	123	
43	r	116	
44	s	100	
45	t	88	
46	u	82	
47	v	80	
48	w	66	
49	x	83	
50	y	86	
51	z	70	
52	5	76	
53	H	3	

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Mol	Chain	Length	Quality of chain
54	A	257	33% 67% 28%
55	4	9	67% 22% 11%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 146039 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 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2903	Total	C	N	O	P	0	0
			62336	27816	11470	20147	2903		

- Molecule 2 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1534	Total	C	N	O	P	0	0
			32929	14693	6041	10661	1534		

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 4 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 5 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 6 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 7 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 8 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	F	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 9 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 10 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 11 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 12 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 13 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 14 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	119	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 15 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	116	Total	C	N	O		0	0
			892	552	178	162			

- Molecule 16 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 17 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	117	Total	C	N	O		0	0
			947	604	192	151			

- Molecule 18 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 19 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 20 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	94	Total	C	N	O	S	0	0
			746	470	140	134	2		

- Molecule 21 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	U	103	Total	C	N	O		
			788	498	148	142	0	0

- Molecule 22 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	94	Total	C	N	O	S		
			753	479	137	134	3	0	0

- Molecule 23 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	76	Total	C	N	O	S		
			582	360	117	104	1	0	0

- Molecule 24 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	77	Total	C	N	O	S		
			625	388	129	106	2	0	0

- Molecule 25 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	62	Total	C	N	O	S		
			501	308	98	94	1	0	0

- Molecule 26 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	58	Total	C	N	O	S		
			448	281	87	78	2	0	0

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	56	Total	C	N	O	S		
			444	269	94	80	1	0	0

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	c	52	Total	C	N	O	0	0
			426	275	78	73		

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	225	Total	C	N	O	S	0	0
			1760	1113	316	323	8		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h	208	Total	C	N	O	S	0	0
			1636	1036	307	290	3		

- Molecule 34 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 36 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	104	Total	C	N	O	S	0	0
			848	536	153	152	7		

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 38 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 39 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	99	Total	C	N	O	S	0	0
			790	495	151	143	1		

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	q	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	r	116	Total	C	N	O	S	0	0
			900	558	181	158	3		

- Molecule 44 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	s	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	t	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 46 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	u	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	v	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	w	66	Total	C	N	O	S	0	0
			544	344	102	97	1		

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	x	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	y	86	Total	C	N	O	S	0	0
			669	414	138	114	3		

- Molecule 51 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	z	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 52 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	5	76	Total	C	N	O	P	S	0	0
			1627	727	296	527	76	1		

- Molecule 53 is a protein called FME-PHE-PHE.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	H	3	Total	C	N	O	S	0	0
			32	24	3	4	1		

- Molecule 54 is a protein called Peptide chain release factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	A	246	Total	C	N	O	S	0	0
			1929	1186	364	371	8		

- Molecule 55 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	4	9	Total	C	N	O	P	0	0
			184	83	26	66	9		

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	1	283	Total 283	Mg 283	0
56	2	1	Total 1	Mg 1	0
56	3	8	Total 8	Mg 8	0
56	C	1	Total 1	Mg 1	0
56	b	1	Total 1	Mg 1	0
56	i	1	Total 1	Mg 1	0

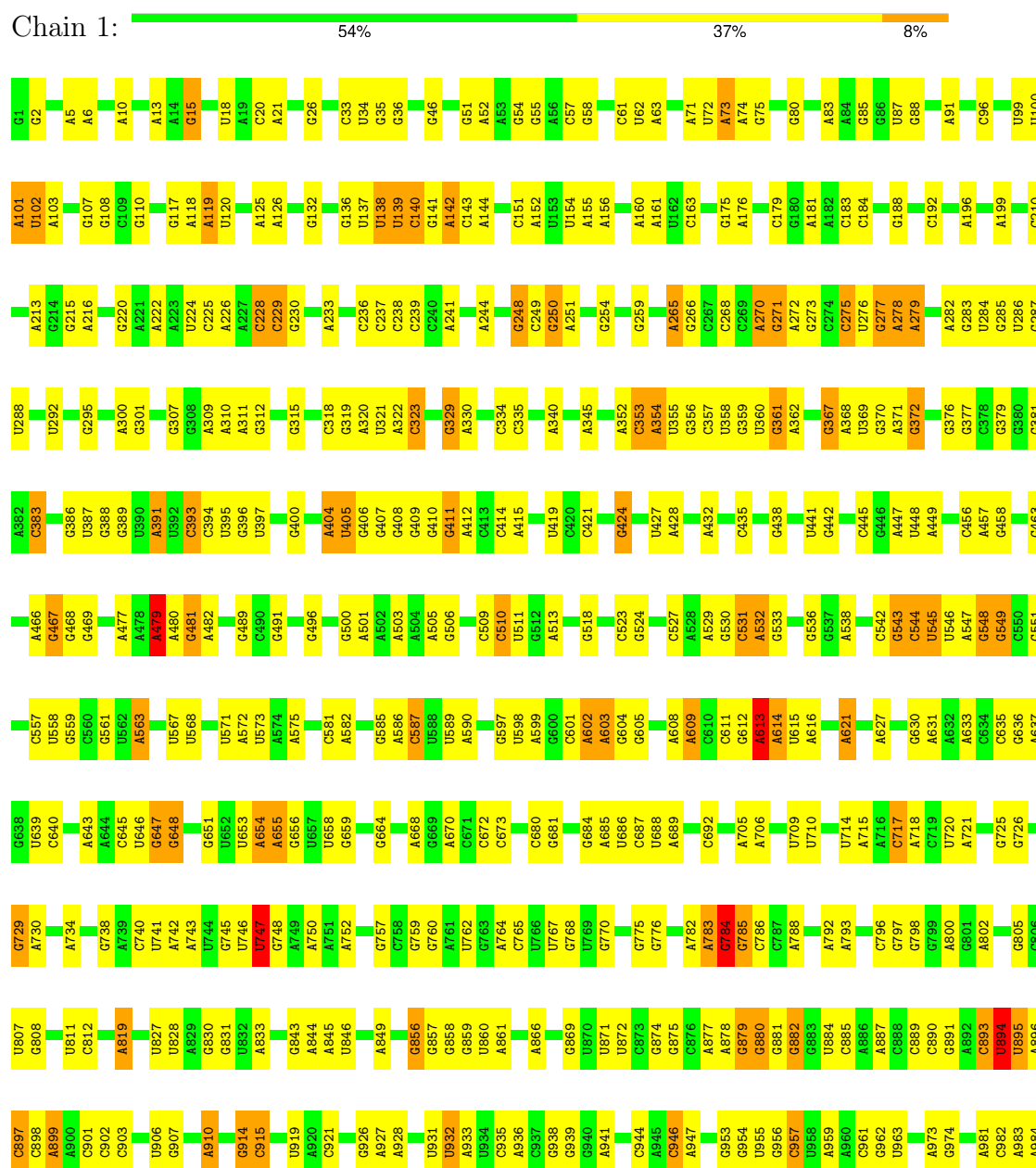
- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
57	f	1	Total 1	Zn 1	0

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: 23S ribosomal RNA

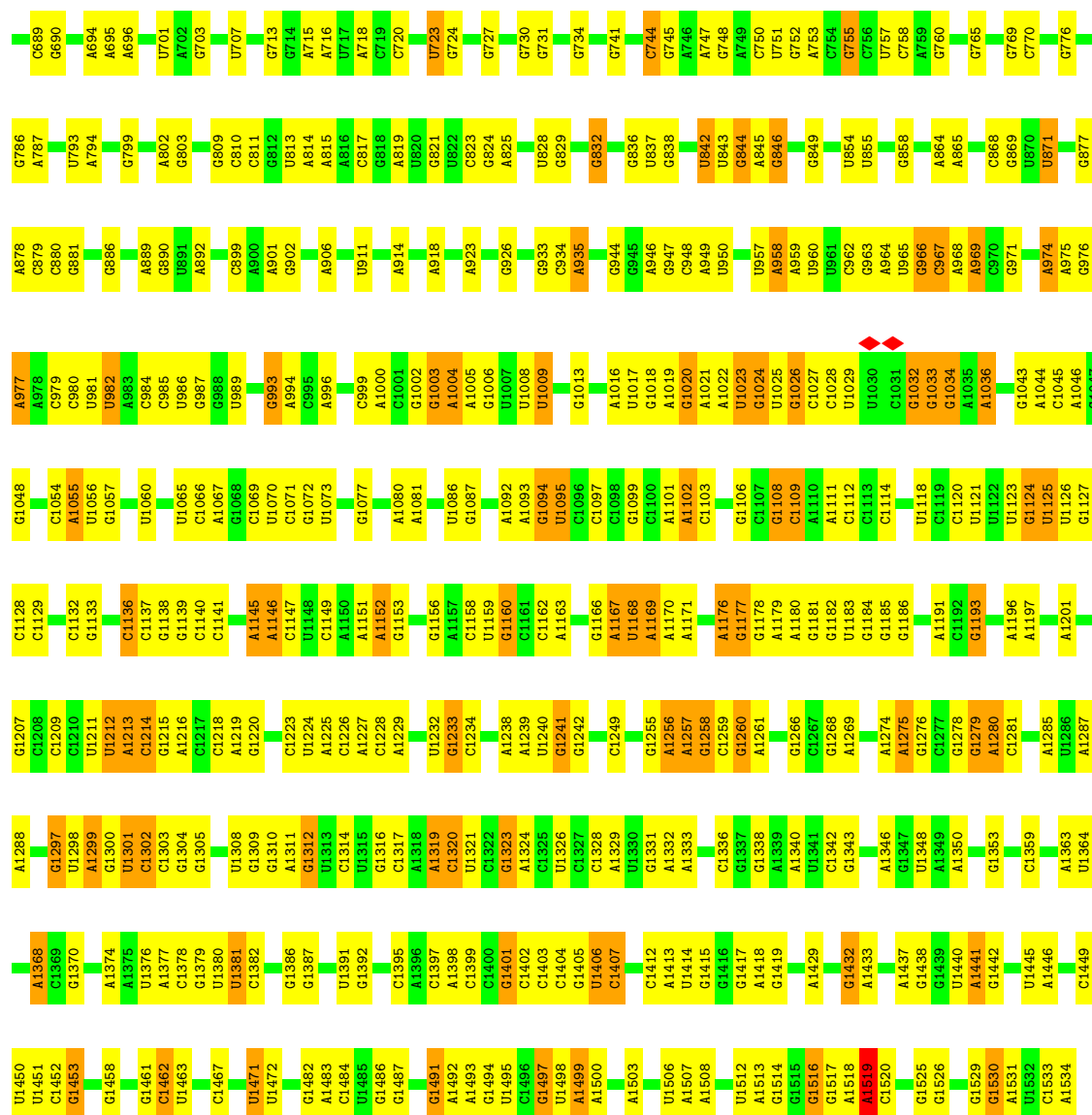


G2284	G2295	G2296	A2237	G2208	G2209	A2210	A2211	G2303	G2304	U2305	G2308	A2309	A2310	C2313	A2314	G2315	G2316	A2317	G2318	G2319	U2320	G2325	C2326	A2327	G2331	C2332	A2333	U2334	A2335	A2336	C2339	A2340	U2343	U2344	C2347	C2350	G2357	G2358	G2359	G2361	G2365	A2369	U2372	G2373	C2374	A2375	A2376	A2377																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
G2204	C2207	C2208	G2237	G2209	G2210	A2211	A2212	G2223	G2224	G2225	G2226	U2233	G2234	G2237	G2238	G2239	U2240	A2241	G2242	G2243	U2244	U2245	G2246	A2247	G2250	G2251	G2252	G2253	G2254	G2255	G2256	G2257	G2258	G2259	A2266	G2269	G2270	G2271	U2272	A2273	G2277	A2278	G2279	C2283	A2284	G2285	G2286	A2287	A2288	G2289	G2290	A2291	G2292	G2293																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
C2129	U2130	U2131	U2132	G2133	G2134	A2135	G2136	G2137	G2138	G2139	G2140	G2141	A2142	C2145	C2146	G2147	C2148	G2149	C2150	C2151	C2152	C2153	C2154	C2155	C2156	G2157	A2158	G2159	G2160	G2161	G2162	C2163	C2164	C2165	U2166	U2167	A2170	A2171	U2172	C2173	C2174	C2175	A2176	C2177	C2178	U2181	U2182	A2183	U2184	U2185	A2186	A2187	C2188	C2189	G2190	G2191	G2192	G2193	U2194	A2195	A2196	A2197	A2198	A2199	C2200	G2201	G2202	G2203	G2204	G2205	A2206	A2207	A2208	A2209	A2210	A2211	A2212	A2213	A2214	A2215	A2216	A2217	A2218	A2219	A2220	A2221	A2222	A2223	A2224	A2225	A2226	A2227	A2228	A2229	A2230	A2231	A2232	A2233	A2234	A2235	A2236	A2237	A2238	A2239	A2240	A2241	A2242	A2243	A2244	A2245	A2246	A2247	A2248	A2249	A2250	A2251	A2252	A2253	A2254	A2255	A2256	A2257	A2258	A2259	A2260	A2261	A2262	A2263	A2264	A2265	A2266	A2267	A2268	A2269	A2270	A2271	A2272	A2273	A2274	A2275	A2276	A2277	A2278	A2279	A2280	A2281	A2282	A2283	A2284	A2285	A2286	A2287	A2288	A2289	A2290	A2291	A2292	A2293	A2294	A2295	A2296	A2297	A2298	A2299	A2300	A2301	A2302	A2303	A2304	A2305	A2306	A2307	A2308	A2309	A2310	A2311	A2312	A2313	A2314	A2315	A2316	A2317	A2318	A2319	A2320	A2321	A2322	A2323	A2324	A2325	A2326	A2327	A2328	A2329	A2330	A2331	A2332	A2333	A2334	A2335	A2336	A2337	A2338	A2339	A2340	A2341	A2342	A2343	A2344	A2345	A2346	A2347	A2348	A2349	A2350	A2351	A2352	A2353	A2354	A2355	A2356	A2357	A2358	A2359	A2360	A2361	A2362	A2363	A2364	A2365	A2366	A2367	A2368	A2369	A2370	A2371	A2372	A2373	A2374	A2375	A2376	A2377	A2378	A2379	A2380	A2381	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	A2462	A2463	A2464	A2465	A2466	A2467	A2468	A2469	A2470	A2471	A2472	A2473	A2474	A2475	A2476	A2477	A2478	A2479	A2480	A2481	A2482	A2483	A2484	A2485	A2486	A2487	A2488	A2489	A2490	A2491	A2492	A2493	A2494	A2495	A2496	A2497	A2498	A2499	A2500	A2501	A2502	A2503	A2504	A2505	A2506	A2507	A2508	A2509	A2510	A2511	A2512	A2513	A2514	A2515	A2516	A2517	A2518	A2519	A2520	A2521	A2522	A2523	A2524	A2525	A2526	A2527	A2528	A2529	A2530	A2531	A2532	A2533	A2534	A2535	A2536	A2537	A2538	A2539	A2540	A2541	A2542	A2543	A2544	A2545	A2546	A2547	A2548	A2549	A2550	A2551	A2552	A2553	A2554	A2555	A2556	A2557	A2558	A2559	A2560	A2561	A2562	A2563	A2564	A2565	A2566	A2567	A2568	A2569	A2570	A2571	A2572	A2573	A2574	A2575	A2576	A2577	A2578	A2579	A2580	A2581	A2582	A2583	A2584	A2585	A2586	A2587	A2588	A2589	A2590	A2591	A2592	A2593	A2594	A2595	A2596	A2597	A2598	A2599	A2600	A2601	A2602	A2603	A2604	A2605	A2606	A2607	A2608	A2609	A2610	A2611	A2612	A2613	A2614	A2615	A2616	A2617	A2618	A2619	A2620	A2621	A2622	A2623	A2624	A2625	A2626	A2627	A2628	A2629	A2630	A2631	A2632	A2633	A2634	A2635	A2636	A2637	A2638	A2639	A2640	A2641	A2642	A2643	A2644	A2645	A2646	A2647	A2648	A2649	A2650	A2651	A2652	A2653	A2654	A2655	A2656	A2657	A2658	A2659	A2660	A2661	A2662	A2663	A2664	A2665	A2666	A2667	A2668	A2669	A2670	A2671	A2672	A2673	A2674	A2675	A2676	A2677	A2678	A2679	A2680	A2681	A2682	A2683	A2684	A2685	A2686	A2687	A2688	A2689	A2690	A2691	A2692	A2693	A2694	A2695	A2696	A2697	A2698	A2699	A2700	A2701	A2702	A2703	A2704	A2705	A2706	A2707	A2708	A2709	A2710	A2711	A2712	A2713	A2714	A2715	A2716	A2717	A2718	A2719	A2720	A2721	A2722	A2723	A2724	A2725	A2726	A2727	A2728	A2729	A2730	A2731	A2732	A2733	A2734	A2735	A2736	A2737	A2738	A2739	A2740	A2741	A2742	A2743	A2744	A2745	A2746	A2747	A2748	A2749	A2750	A2751	A2752	A2753	A2754	A2755	A2756	A2757	A2758	A2759	A2760	A2761	A2762	A2763	A2764	A2765	A2766	A2767	A2768	A2769	A2770	A2771	A2772	A2773	A2774	A2775	A2776	A2777	A2778	A2779	A2780	A2781	A2782	A2783	A2784	A2785	A2786	A2787	A2788	A2789	A2790	A2791	A2792	A2793	A2794	A2795	A2796	A2797	A2798	A2799	A2800	A2801	A2802	A2803	A2804	A2805	A2806	A2807	A2808	A2809	A2810	A2811	A2812	A2813	A2814	A2815	A2816	A2817	A2818	A2819	A2820	A2821	A2822	A2823	A2824	A2825	A2826	A2827	A2828	A2829	A2830	A2831	A2832	A2833	A2834	A2835	A2836	A2837	A2838	A2839	A2840	A2841	A2842	A2843	A2844	A2845	A2846	A2847	A2848	A2849	A2850	A2851	A2852	A2853	A2854	A2855	A2856	A2857	A2858	A2859	A2860	A2861	A2862	A2863	A2864	A2865	A2866	A2867	A2868	A2869	A2870	A2871	A2872	A2873	A2874	A2875	A2876	A2877	A2878	A2879	A2880	A2881	A2882	A2883	A2884	A2885	A2886	A2887	A2888	A2889	A2890	A2891	A2892	A2893	A2894	A2895	A2896	A2897	A2898	A2899	A2900	A2901	A2902	A2903	A2904	A2905	A2906	A2907	A2908	A2909	A2910	A2911	A2912	A2913	A2914	A2915	A2916	A2917	A2918	A2919	A2920	A2921	A2922	A2923	A2924	A2925	A2926	A2927	A2928	A2929	A2930	A2931	A2932	A2933	A2934	A2935	A2936	A2937	A2938	A2939	A2940	A2941	A2942	A2943	A2944	A2945	A2946	A2947	A2948	A2949	A2950	A2951	A2952	A2953	A2954	A2955	A2956	A2957	A2958	A2959	A2960	A2961	A2962	A2963	A2964	A2965	A2966	A2967	A2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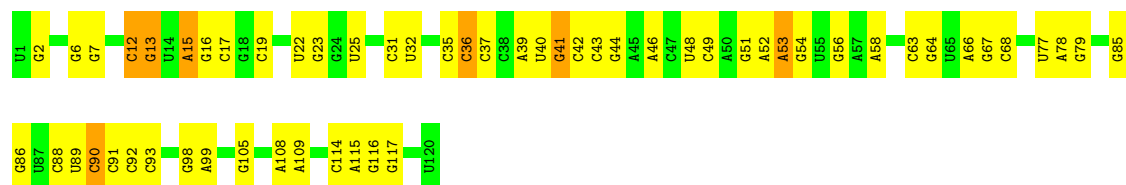
Response	Percentage
Yes	50%
No	41%
Don't know	9%





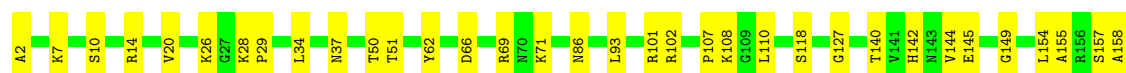
• Molecule 3: 5S ribosomal RNA

Chain 3: 52% 42% 6%



• Molecule 4: 50S ribosomal protein L2

Chain B: 79% 21%





• Molecule 5: 50S ribosomal protein L3

Chain C: 84% 15%



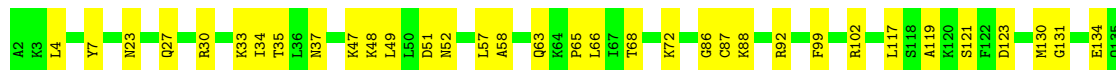
• Molecule 6: 50S ribosomal protein L4

Chain D: 81% 18%



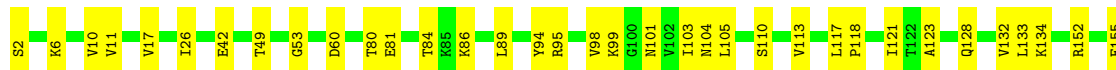
• Molecule 7: 50S ribosomal protein L5

Chain E: 74% 26%



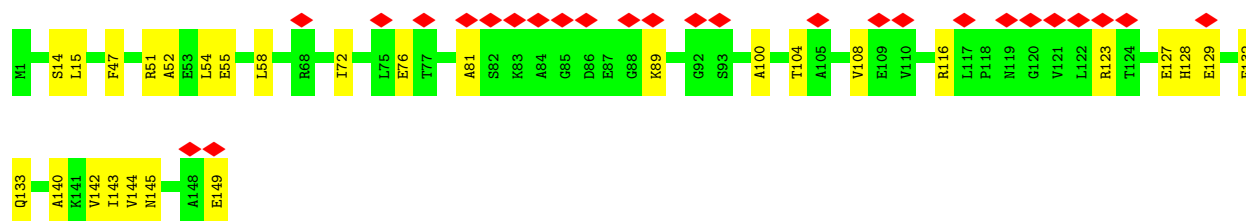
• Molecule 8: 50S ribosomal protein L6

Chain F: 77% 23%



• Molecule 9: 50S ribosomal protein L9

Chain G: 17% 81% 19%



- Molecule 10: 50S ribosomal protein L13

Chain J: 89% 11%



- Molecule 11: 50S ribosomal protein L14

Chain K: 85% 15%



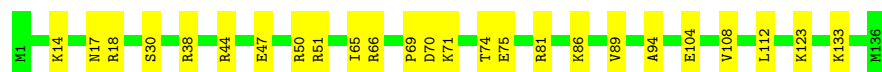
- Molecule 12: 50S ribosomal protein L15

Chain L: 85% 15%



- Molecule 13: 50S ribosomal protein L16

Chain M: 82% 18%



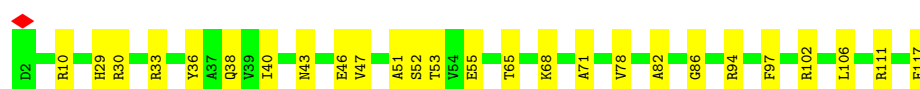
- Molecule 14: 50S ribosomal protein L17

Chain N: 87% 13%



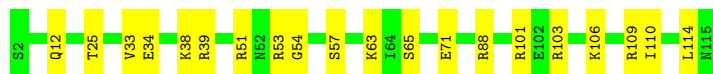
- Molecule 15: 50S ribosomal protein L18

Chain O: 78% 22%



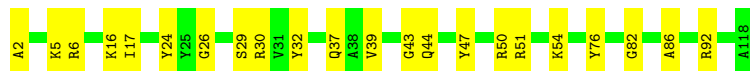
- Molecule 16: 50S ribosomal protein L19

Chain P:  82% 18%



- Molecule 17: 50S ribosomal protein L20

Chain Q:  81% 19%



- Molecule 18: 50S ribosomal protein L21

Chain R:  82% 15% . .



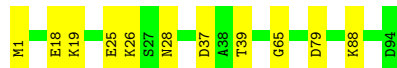
- Molecule 19: 50S ribosomal protein L22

Chain S:  81% 19%



- Molecule 20: 50S ribosomal protein L23

Chain T:  88% 12%



- Molecule 21: 50S ribosomal protein L24

Chain U:  77% 22% .



- Molecule 22: 50S ribosomal protein L25

Chain V:  82% 18%



- Molecule 23: 50S ribosomal protein L27

Chain W:  84% 16%



- Molecule 24: 50S ribosomal protein L28

Chain X:  70% 30%



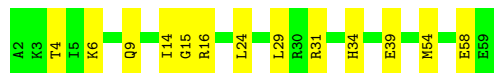
- Molecule 25: 50S ribosomal protein L29

Chain Y:  82% 18%



- Molecule 26: 50S ribosomal protein L30

Chain Z:  78% 22%



- Molecule 27: 50S ribosomal protein L32

Chain b:  73% 27%



- Molecule 28: 50S ribosomal protein L33

Chain c:  69% 31%



- Molecule 29: 50S ribosomal protein L34

Chain d:  85% 15%



- Molecule 30: 50S ribosomal protein L35

Chain e:  81% 17%



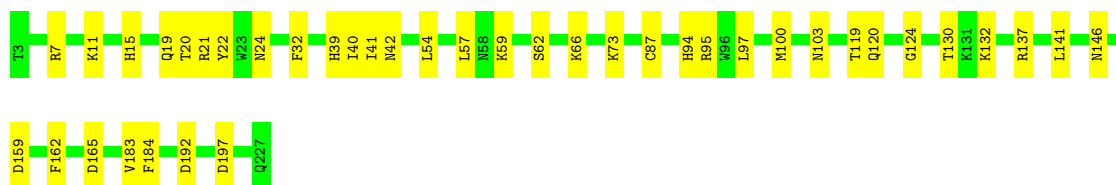
- Molecule 31: 50S ribosomal protein L36

Chain f:  71% 29%



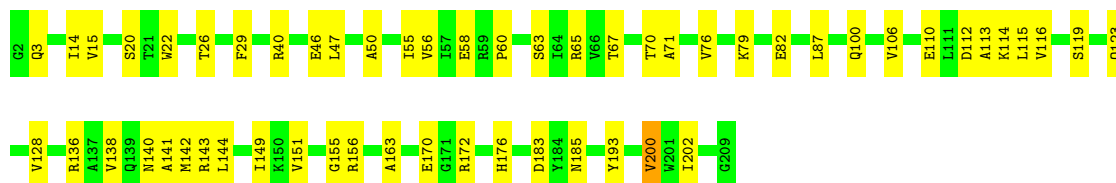
- Molecule 32: 30S ribosomal protein S2

Chain g:  82% 18%



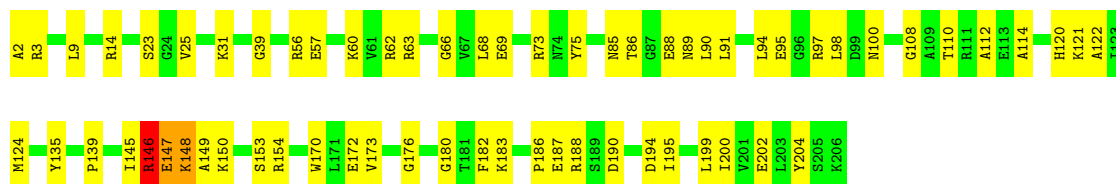
- Molecule 33: 30S ribosomal protein S3

Chain h:  74% 26%



- Molecule 34: 30S ribosomal protein S4

Chain i:  69% 30%



- Molecule 35: 30S ribosomal protein S5

Chain j:  78% 22%



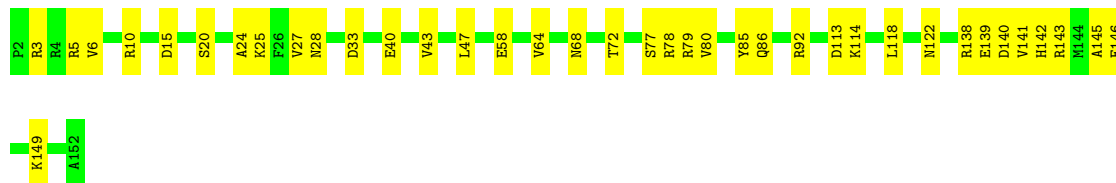
- Molecule 36: 30S ribosomal protein S6

Chain k:  75% 25%



- Molecule 37: 30S ribosomal protein S7

Chain l:  75% 25%



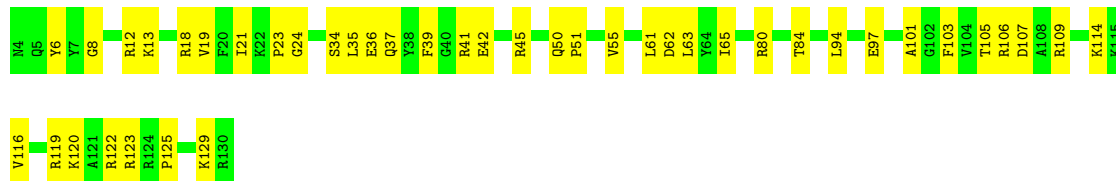
- Molecule 38: 30S ribosomal protein S8

Chain m:  80% 20%



- Molecule 39: 30S ribosomal protein S9

Chain n:  67% 33%



- Molecule 40: 30S ribosomal protein S10

Chain o:  67% 33%



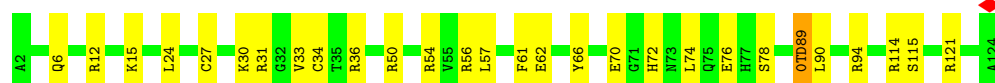
- Molecule 41: 30S ribosomal protein S11

Chain p:  76% 24%



- Molecule 42: 30S ribosomal protein S12

Chain q:  77% 22%



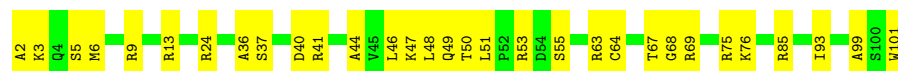
- Molecule 43: 30S ribosomal protein S13

Chain r:  74% 26%



- Molecule 44: 30S ribosomal protein S14

Chain s:  69% 31%



- Molecule 45: 30S ribosomal protein S15

Chain t:  84% 16%



- Molecule 46: 30S ribosomal protein S16

Chain u:  83% 17%



- Molecule 47: 30S ribosomal protein S17

Chain v:  71% 29%



- Molecule 48: 30S ribosomal protein S18

Chain w:  85% 15%



- Molecule 49: 30S ribosomal protein S19

Chain x:  78% 22%



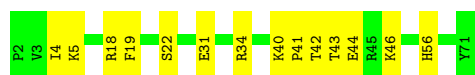
- Molecule 50: 30S ribosomal protein S20

Chain y:  84% 16%

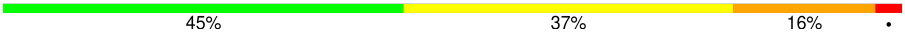


- Molecule 51: 30S ribosomal protein S21

Chain z:  80% 20%



- Molecule 52: P-tRNA

Chain 5:  45% 37% 16%



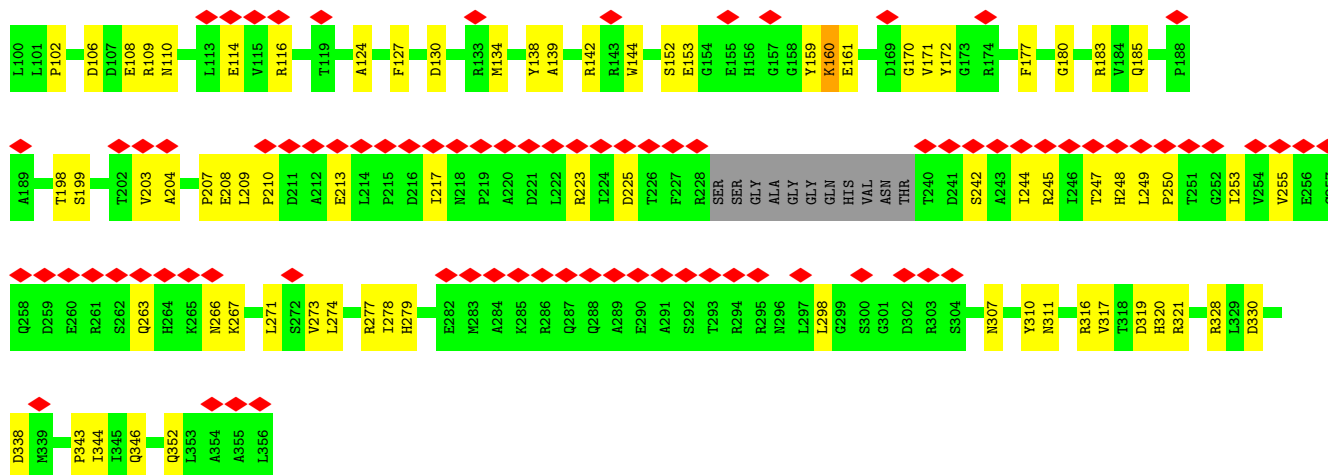
- Molecule 53: FME-PHE-PHE

Chain H:  33% 67%



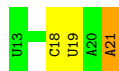
- Molecule 54: Peptide chain release factor 1

Chain A:  33% 67% 28%



- Molecule 55: mRNA

Chain 4:  67% 22% 11%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	48706	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	41.6	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.147	Depositor
Minimum map value	-0.667	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.138	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	424.96, 424.96, 424.96	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.66, 1.66, 1.66	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: OMC, 1MG, 4SU, 3TD, G7M, 7MG, 5MC, FME, H2U, PSU, 2MG, MG, UR3, OMG, ZN, 0TD, OMU, MA6, 4OC, 5MU, 2MA, 6MZ

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	1	0.54	0/69286	0.44	6/108087 (0.0%)
2	2	0.37	0/36590	0.38	0/57074
3	3	0.41	0/2872	0.41	0/4478
4	B	0.51	0/2121	0.61	0/2852
5	C	0.54	0/1586	0.61	0/2134
6	D	0.49	0/1571	0.56	0/2113
7	E	0.31	0/1434	0.54	0/1926
8	F	0.32	0/1333	0.46	0/1805
9	G	0.25	0/1122	0.53	0/1515
10	J	0.55	0/1152	0.56	0/1551
11	K	0.51	0/955	0.61	0/1279
12	L	0.47	0/1062	0.57	0/1413
13	M	0.49	0/1093	0.56	0/1460
14	N	0.52	0/964	0.65	0/1289
15	O	0.34	0/902	0.53	0/1209
16	P	0.48	0/929	0.55	0/1242
17	Q	0.58	0/960	0.60	0/1278
18	R	0.56	0/829	0.70	0/1107
19	S	0.55	0/864	0.52	0/1156
20	T	0.44	0/752	0.52	0/1005
21	U	0.43	0/796	0.57	0/1062
22	V	0.38	0/766	0.50	0/1025
23	W	0.51	0/589	0.56	0/779
24	X	0.46	0/635	0.54	0/848
25	Y	0.40	0/502	0.48	0/667
26	Z	0.50	0/452	0.57	0/605
27	b	0.55	0/450	0.59	0/599
28	c	0.37	0/433	0.50	0/576
29	d	0.58	0/380	0.62	0/498
30	e	0.53	0/513	0.64	0/676
31	f	0.45	0/303	0.59	0/397

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	g	0.30	0/1791	0.55	2/2413 (0.1%)
33	h	0.30	0/1663	0.48	0/2241
34	i	0.28	0/1665	0.50	0/2227
35	j	0.35	0/1165	0.55	0/1568
36	k	0.30	0/867	0.54	0/1171
37	l	0.27	0/1195	0.50	0/1602
38	m	0.31	0/989	0.47	0/1326
39	n	0.29	0/1034	0.57	0/1375
40	o	0.27	0/800	0.50	0/1082
41	p	0.31	0/893	0.47	0/1205
42	q	0.33	0/960	0.55	0/1286
43	r	0.28	0/909	0.57	0/1215
44	s	0.27	0/817	0.45	0/1088
45	t	0.33	0/722	0.51	0/964
46	u	0.28	0/659	0.55	0/884
47	v	0.27	0/657	0.49	0/881
48	w	0.29	0/553	0.45	0/743
49	x	0.23	0/680	0.46	0/915
50	y	0.26	0/675	0.43	0/895
51	z	0.28	0/597	0.50	0/792
52	5	0.30	0/1704	0.39	0/2654
53	H	0.52	0/23	0.45	0/29
54	A	0.27	0/1959	0.59	1/2638 (0.0%)
55	4	0.29	0/203	0.46	0/312
All	All	0.46	0/157376	0.45	9/235211 (0.0%)

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2425	A	C4'-C3'-O3'	7.71	120.97	109.40
1	1	784	G	C4'-C3'-O3'	6.48	122.73	113.00
1	1	894	U	C4'-C3'-O3'	6.17	118.65	109.40
1	1	1584	U	C4'-C3'-O3'	5.83	118.14	109.40
1	1	613	A	C4'-C3'-O3'	5.56	117.74	109.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	62336	0	31367	688	0
2	2	32929	0	16588	440	0
3	3	2569	0	1301	28	0
4	B	2082	0	2154	41	0
5	C	1565	0	1616	24	0
6	D	1552	0	1619	30	0
7	E	1410	0	1444	36	0
8	F	1313	0	1358	25	0
9	G	1111	0	1148	18	0
10	J	1129	0	1162	12	0
11	K	946	0	1023	12	0
12	L	1053	0	1129	18	0
13	M	1074	0	1157	18	0
14	N	951	0	994	12	0
15	O	892	0	923	19	0
16	P	917	0	962	17	0
17	Q	947	0	1019	16	0
18	R	816	0	839	19	0
19	S	857	0	922	13	0
20	T	746	0	811	8	0
21	U	788	0	843	16	0
22	V	753	0	780	10	0
23	W	582	0	599	8	0
24	X	625	0	652	16	0
25	Y	501	0	531	8	0
26	Z	448	0	488	8	0
27	b	444	0	458	12	0
28	c	426	0	464	8	0
29	d	377	0	418	7	0
30	e	504	0	572	10	0
31	f	302	0	340	11	0
32	g	1760	0	1787	25	0
33	h	1636	0	1710	38	0
34	i	1643	0	1707	50	0
35	j	1152	0	1196	20	0
36	k	848	0	846	16	0
37	l	1181	0	1238	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	m	979	0	1031	15	0
39	n	1022	0	1070	35	0
40	o	790	0	831	24	0
41	p	877	0	887	18	0
42	q	957	0	1017	23	0
43	r	900	0	965	23	0
44	s	805	0	844	29	0
45	t	714	0	734	11	0
46	u	649	0	666	12	0
47	v	648	0	691	17	0
48	w	544	0	560	7	0
49	x	663	0	688	15	0
50	y	669	0	719	10	0
51	z	589	0	629	10	0
52	5	1627	0	831	20	0
53	H	32	0	28	9	0
54	A	1929	0	1902	51	0
55	4	184	0	95	2	0
56	1	283	0	0	0	0
56	2	1	0	0	0	0
56	3	8	0	0	0	0
56	C	1	0	0	0	0
56	b	1	0	0	0	0
56	i	1	0	0	0	0
57	f	1	0	0	0	0
All	All	146039	0	98353	1812	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 11.

The worst 5 of 1812 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)
18:R:38:VAL:O	18:R:54:VAL:HG23	1.50	1.11
1:1:1380:G:H2'	1:1:1381:G:H8	1.18	1.07
1:1:1350:C:H2'	1:1:1351:C:C6	1.90	1.06
1:1:2451:A:C2	53:H:78:PHE:CE1	2.50	1.00
54:A:153:GLU:HG2	54:A:159:TYR:CD1	1.97	0.99

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	B	269/271 (99%)	247 (92%)	22 (8%)	0	100	100
5	C	207/209 (99%)	194 (94%)	12 (6%)	1 (0%)	24	57
6	D	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
7	E	175/177 (99%)	155 (89%)	19 (11%)	1 (1%)	21	54
8	F	173/175 (99%)	161 (93%)	12 (7%)	0	100	100
9	G	147/149 (99%)	133 (90%)	14 (10%)	0	100	100
10	J	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
11	K	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
12	L	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
13	M	134/136 (98%)	127 (95%)	7 (5%)	0	100	100
14	N	117/119 (98%)	109 (93%)	8 (7%)	0	100	100
15	O	114/116 (98%)	111 (97%)	3 (3%)	0	100	100
16	P	112/114 (98%)	108 (96%)	4 (4%)	0	100	100
17	Q	115/117 (98%)	113 (98%)	2 (2%)	0	100	100
18	R	101/103 (98%)	92 (91%)	7 (7%)	2 (2%)	6	32
19	S	108/110 (98%)	101 (94%)	7 (6%)	0	100	100
20	T	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
21	U	101/103 (98%)	89 (88%)	12 (12%)	0	100	100
22	V	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
23	W	74/76 (97%)	68 (92%)	6 (8%)	0	100	100
24	X	75/77 (97%)	71 (95%)	4 (5%)	0	100	100
25	Y	60/62 (97%)	58 (97%)	2 (3%)	0	100	100
26	Z	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
27	b	54/56 (96%)	51 (94%)	3 (6%)	0	100	100
28	c	50/52 (96%)	49 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	d	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
30	e	62/64 (97%)	57 (92%)	4 (6%)	1 (2%)	7	36
31	f	36/38 (95%)	36 (100%)	0	0	100	100
32	g	223/225 (99%)	201 (90%)	22 (10%)	0	100	100
33	h	206/208 (99%)	192 (93%)	14 (7%)	0	100	100
34	i	203/205 (99%)	188 (93%)	13 (6%)	2 (1%)	12	44
35	j	154/156 (99%)	140 (91%)	14 (9%)	0	100	100
36	k	102/104 (98%)	100 (98%)	2 (2%)	0	100	100
37	l	149/151 (99%)	144 (97%)	5 (3%)	0	100	100
38	m	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
39	n	125/127 (98%)	114 (91%)	11 (9%)	0	100	100
40	o	97/99 (98%)	90 (93%)	7 (7%)	0	100	100
41	p	115/117 (98%)	110 (96%)	5 (4%)	0	100	100
42	q	120/123 (98%)	109 (91%)	11 (9%)	0	100	100
43	r	114/116 (98%)	108 (95%)	6 (5%)	0	100	100
44	s	98/100 (98%)	95 (97%)	3 (3%)	0	100	100
45	t	86/88 (98%)	80 (93%)	6 (7%)	0	100	100
46	u	80/82 (98%)	74 (92%)	6 (8%)	0	100	100
47	v	78/80 (98%)	69 (88%)	9 (12%)	0	100	100
48	w	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
49	x	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
50	y	84/86 (98%)	81 (96%)	3 (4%)	0	100	100
51	z	68/70 (97%)	66 (97%)	2 (3%)	0	100	100
53	H	1/3 (33%)	1 (100%)	0	0	100	100
54	A	242/257 (94%)	236 (98%)	6 (2%)	0	100	100
All	All	5787/5901 (98%)	5433 (94%)	347 (6%)	7 (0%)	49	79

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
18	R	54	VAL
34	i	146	ARG
18	R	52	PRO

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Mol	Chain	Res	Type
34	i	148	LYS
7	E	123	ASP

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	
4	B	216/216 (100%)	216 (100%)	0	100	100
5	C	164/164 (100%)	163 (99%)	1 (1%)	78	79
6	D	165/165 (100%)	163 (99%)	2 (1%)	63	73
7	E	148/148 (100%)	148 (100%)	0	100	100
8	F	136/136 (100%)	135 (99%)	1 (1%)	76	78
9	G	114/114 (100%)	114 (100%)	0	100	100
10	J	116/116 (100%)	116 (100%)	0	100	100
11	K	104/104 (100%)	104 (100%)	0	100	100
12	L	103/103 (100%)	103 (100%)	0	100	100
13	M	109/109 (100%)	109 (100%)	0	100	100
14	N	99/99 (100%)	99 (100%)	0	100	100
15	O	86/86 (100%)	86 (100%)	0	100	100
16	P	99/99 (100%)	98 (99%)	1 (1%)	68	75
17	Q	89/89 (100%)	89 (100%)	0	100	100
18	R	84/84 (100%)	81 (96%)	3 (4%)	31	57
19	S	93/93 (100%)	93 (100%)	0	100	100
20	T	81/81 (100%)	81 (100%)	0	100	100
21	U	84/84 (100%)	83 (99%)	1 (1%)	63	73
22	V	78/78 (100%)	77 (99%)	1 (1%)	61	72
23	W	58/58 (100%)	58 (100%)	0	100	100
24	X	67/67 (100%)	67 (100%)	0	100	100
25	Y	54/54 (100%)	54 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	Z	48/48 (100%)	48 (100%)	0	100	100
27	b	47/47 (100%)	47 (100%)	0	100	100
28	c	47/47 (100%)	47 (100%)	0	100	100
29	d	38/38 (100%)	38 (100%)	0	100	100
30	e	51/51 (100%)	51 (100%)	0	100	100
31	f	34/34 (100%)	33 (97%)	1 (3%)	37	60
32	g	187/187 (100%)	187 (100%)	0	100	100
33	h	171/171 (100%)	170 (99%)	1 (1%)	78	79
34	i	172/172 (100%)	170 (99%)	2 (1%)	63	73
35	j	119/119 (100%)	119 (100%)	0	100	100
36	k	91/91 (100%)	91 (100%)	0	100	100
37	l	124/124 (100%)	124 (100%)	0	100	100
38	m	104/104 (100%)	104 (100%)	0	100	100
39	n	105/105 (100%)	105 (100%)	0	100	100
40	o	86/86 (100%)	86 (100%)	0	100	100
41	p	90/90 (100%)	90 (100%)	0	100	100
42	q	102/102 (100%)	102 (100%)	0	100	100
43	r	94/94 (100%)	94 (100%)	0	100	100
44	s	83/83 (100%)	83 (100%)	0	100	100
45	t	76/76 (100%)	76 (100%)	0	100	100
46	u	65/65 (100%)	65 (100%)	0	100	100
47	v	74/74 (100%)	74 (100%)	0	100	100
48	w	57/57 (100%)	57 (100%)	0	100	100
49	x	72/72 (100%)	72 (100%)	0	100	100
50	y	65/65 (100%)	65 (100%)	0	100	100
51	z	60/60 (100%)	60 (100%)	0	100	100
53	H	2/2 (100%)	0	2 (100%)	0	0
54	A	201/208 (97%)	201 (100%)	0	100	100
All	All	4812/4819 (100%)	4796 (100%)	16 (0%)	84	83

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
53	H	78	PHE
34	i	147	GLU
21	U	52	LEU
34	i	146	ARG
18	R	80	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 63 such sidechains are listed below:

Mol	Chain	Res	Type
31	f	13	ASN
46	u	9	HIS
35	j	97	GLN
45	t	40	GLN
50	y	52	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2902/2903 (99%)	693 (23%)	15 (0%)
2	2	1532/1534 (99%)	363 (23%)	6 (0%)
3	3	119/120 (99%)	30 (25%)	0
52	5	75/76 (98%)	24 (32%)	1 (1%)
55	4	8/9 (88%)	2 (25%)	0
All	All	4636/4642 (99%)	1112 (23%)	22 (0%)

5 of 1112 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	G
1	1	10	A
1	1	15	G
1	1	34	U
1	1	35	G

5 of 22 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2756	U
2	2	966	2MG
2	2	516	PSU
2	2	1109	C

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Mol	Chain	Res	Type
1	1	654	A

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

40 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
52	H2U	5	20	52	18,21,22	3.31	5 (27%)	19,30,33	1.35	3 (15%)
2	5MC	2	967	2	19,22,23	3.83	8 (42%)	26,32,35	1.12	3 (11%)
1	5MU	1	747	1	19,22,23	4.48	7 (36%)	27,32,35	3.92	12 (44%)
2	2MG	2	1207	2	23,26,27	2.84	9 (39%)	33,38,41	2.57	12 (36%)
2	5MC	2	1407	2	19,22,23	3.69	8 (42%)	26,32,35	1.23	3 (11%)
1	2MG	1	2445	1	23,26,27	2.83	7 (30%)	33,38,41	2.42	9 (27%)
2	MA6	2	1518	2	23,26,27	1.63	5 (21%)	33,38,41	2.73	12 (36%)
52	PSU	5	55	52	18,21,22	1.20	1 (5%)	21,30,33	1.64	4 (19%)
2	PSU	2	516	2	18,21,22	1.05	1 (5%)	21,30,33	1.90	4 (19%)
1	PSU	1	746	56,1	18,21,22	1.12	2 (11%)	21,30,33	2.09	6 (28%)
2	MA6	2	1519	2	23,26,27	1.55	4 (17%)	33,38,41	2.74	13 (39%)
1	OMU	1	2552	1	19,22,23	2.80	8 (42%)	25,31,34	1.97	5 (20%)
2	UR3	2	1498	2	19,22,23	2.46	6 (31%)	26,32,35	1.64	3 (11%)
1	1MG	1	745	1	23,26,27	2.75	6 (26%)	33,39,42	2.25	9 (27%)
1	PSU	1	2605	1	18,21,22	1.09	2 (11%)	21,30,33	2.16	6 (28%)
53	FME	H	77	53	8,9,10	0.70	0	8,9,11	1.28	1 (12%)
42	0TD	q	89	42	8,9,10	1.83	2 (25%)	6,11,13	2.25	2 (33%)
1	OMG	1	2251	1,52	23,26,27	2.35	7 (30%)	32,38,41	1.95	8 (25%)
1	3TD	1	1915	1	19,22,23	4.26	5 (26%)	23,32,35	2.01	3 (13%)
1	6MZ	1	2030	1	22,25,26	2.85	7 (31%)	29,36,39	4.61	14 (48%)
1	2MG	1	1835	1	23,26,27	2.89	8 (34%)	33,38,41	2.36	9 (27%)
2	7MG	2	527	2	23,26,27	3.29	10 (43%)	27,39,42	2.00	8 (29%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	2MG	2	1516	2	23,26,27	2.92	8 (34%)	33,38,41	2.18	11 (33%)
1	5MU	1	1939	1	19,22,23	4.56	7 (36%)	27,32,35	4.00	10 (37%)
1	PSU	1	2580	1	18,21,22	1.20	3 (16%)	21,30,33	2.04	5 (23%)
1	G7M	1	2069	1	23,26,27	2.52	7 (30%)	34,39,42	2.43	10 (29%)
1	PSU	1	2504	1	18,21,22	1.07	2 (11%)	21,30,33	1.96	4 (19%)
52	4OC	5	32	52	20,23,24	3.02	8 (40%)	25,32,35	1.01	2 (8%)
52	5MU	5	54	52	19,22,23	4.81	7 (36%)	27,32,35	3.43	9 (33%)
52	4SU	5	8	52	18,21,22	3.69	7 (38%)	25,30,33	2.20	5 (20%)
1	6MZ	1	1618	1	22,25,26	2.86	6 (27%)	29,36,39	4.47	12 (41%)
1	PSU	1	2457	1	18,21,22	1.18	3 (16%)	21,30,33	2.44	6 (28%)
2	4OC	2	1402	2	20,23,24	2.87	8 (40%)	25,32,35	1.15	3 (12%)
1	2MA	1	2503	56,1	22,25,26	3.45	10 (45%)	32,37,40	1.96	9 (28%)
2	2MG	2	966	2	23,26,27	2.97	7 (30%)	33,38,41	2.42	7 (21%)
1	PSU	1	1911	1	18,21,22	1.09	2 (11%)	21,30,33	1.96	4 (19%)
1	PSU	1	955	1	18,21,22	1.09	2 (11%)	21,30,33	1.82	4 (19%)
1	PSU	1	1917	1	18,21,22	1.09	1 (5%)	21,30,33	2.03	4 (19%)
1	OMC	1	2498	56,1	19,22,23	2.76	7 (36%)	25,31,34	0.78	0
1	5MC	1	1962	1	19,22,23	3.62	8 (42%)	26,32,35	1.34	3 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
52	H2U	5	20	52	-	4/7/38/39	0/2/2/2
2	5MC	2	967	2	-	0/7/25/26	0/2/2/2
1	5MU	1	747	1	-	1/7/25/26	0/2/2/2
2	2MG	2	1207	2	-	0/9/27/28	0/3/3/3
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
1	2MG	1	2445	1	-	2/9/27/28	0/3/3/3
2	MA6	2	1518	2	-	0/11/29/30	0/3/3/3
52	PSU	5	55	52	-	2/7/25/26	0/2/2/2
2	PSU	2	516	2	-	2/7/25/26	0/2/2/2
1	PSU	1	746	56,1	-	4/7/25/26	0/2/2/2
2	MA6	2	1519	2	-	3/11/29/30	0/3/3/3
1	OMU	1	2552	1	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	UR3	2	1498	2	-	0/7/25/26	0/2/2/2
1	1MG	1	745	1	-	0/7/25/26	0/3/3/3
1	PSU	1	2605	1	-	0/7/25/26	0/2/2/2
53	FME	H	77	53	-	2/7/9/11	-
42	0TD	q	89	42	-	1/7/12/14	-
1	OMG	1	2251	1,52	-	0/9/27/28	0/3/3/3
1	3TD	1	1915	1	-	3/7/25/26	0/2/2/2
1	6MZ	1	2030	1	-	2/9/27/28	0/3/3/3
1	2MG	1	1835	1	-	0/9/27/28	0/3/3/3
2	7MG	2	527	2	-	3/7/37/38	0/3/3/3
2	2MG	2	1516	2	-	0/9/27/28	0/3/3/3
1	5MU	1	1939	1	-	0/7/25/26	0/2/2/2
1	PSU	1	2580	1	-	0/7/25/26	0/2/2/2
1	G7M	1	2069	1	-	0/7/25/26	0/3/3/3
1	PSU	1	2504	1	-	1/7/25/26	0/2/2/2
52	4OC	5	32	52	-	0/9/29/30	0/2/2/2
52	5MU	5	54	52	-	0/7/25/26	0/2/2/2
52	4SU	5	8	52	-	4/7/25/26	0/2/2/2
1	6MZ	1	1618	1	-	2/9/27/28	0/3/3/3
1	PSU	1	2457	1	-	2/7/25/26	0/2/2/2
2	4OC	2	1402	2	-	2/9/29/30	0/2/2/2
1	2MA	1	2503	56,1	-	3/7/25/26	0/3/3/3
2	2MG	2	966	2	-	3/9/27/28	0/3/3/3
1	PSU	1	1911	1	-	0/7/25/26	0/2/2/2
1	PSU	1	955	1	-	0/7/25/26	0/2/2/2
1	PSU	1	1917	1	-	0/7/25/26	0/2/2/2
1	OMC	1	2498	56,1	-	0/9/27/28	0/2/2/2
1	5MC	1	1962	1	-	3/7/25/26	0/2/2/2

The worst 5 of 221 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	1915	3TD	C6-C5	13.45	1.50	1.35
52	5	54	5MU	C2-N1	11.33	1.56	1.38
1	1	1618	6MZ	C6-N6	10.72	1.46	1.34
52	5	20	H2U	C2-N1	10.62	1.50	1.35
52	5	54	5MU	C6-N1	10.43	1.55	1.38

The worst 5 of 257 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2030	6MZ	C4-N9-C8	14.53	120.99	105.74
1	1	1618	6MZ	C4-N9-C8	13.72	120.14	105.74
1	1	1939	5MU	C5-C4-N3	12.60	126.28	115.32
1	1	747	5MU	C5-C4-N3	12.15	125.88	115.32
52	5	54	5MU	C5-C4-N3	11.65	125.44	115.32

There are no chirality outliers.

5 of 49 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1	746	PSU	C2'-C1'-C5-C4
1	1	746	PSU	C2'-C1'-C5-C6
1	1	1618	6MZ	C5-C6-N6-C9
1	1	1618	6MZ	N1-C6-N6-C9
1	1	1915	3TD	O4'-C1'-C5-C4

There are no ring outliers.

12 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1	747	5MU	1	0
2	2	1407	5MC	1	0
52	5	55	PSU	1	0
2	2	1519	MA6	1	0
42	q	89	0TD	1	0
1	1	2030	6MZ	1	0
2	2	527	7MG	1	0
2	2	1516	2MG	1	0
1	1	1939	5MU	1	0
52	5	8	4SU	1	0
1	1	2503	2MA	2	0
1	1	1962	5MC	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 296 ligands modelled in this entry, 296 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

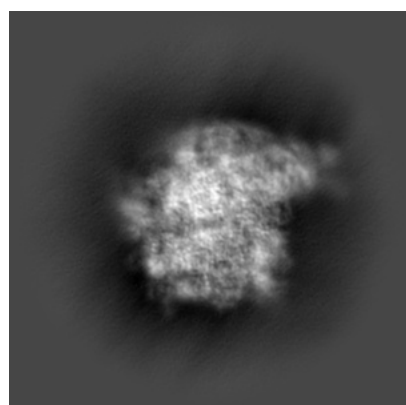
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20174. These allow visual inspection of the internal detail of the map and identification of artifacts.

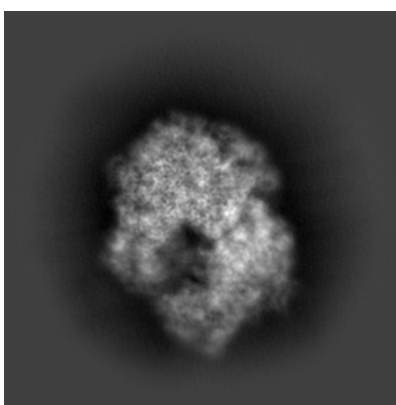
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

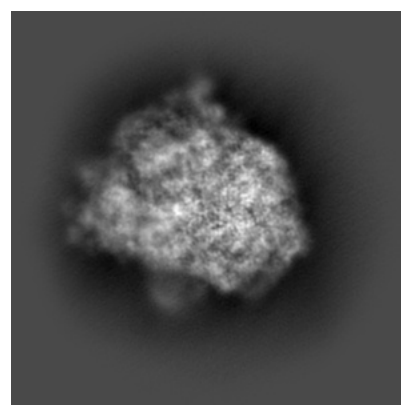
6.1.1 Primary map



X



Y

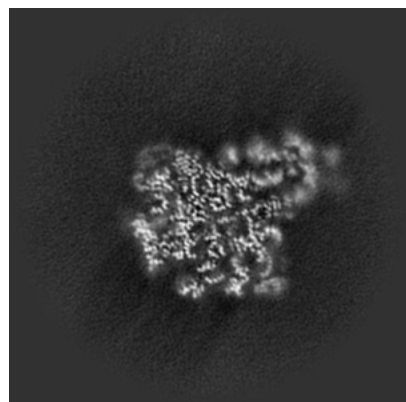


Z

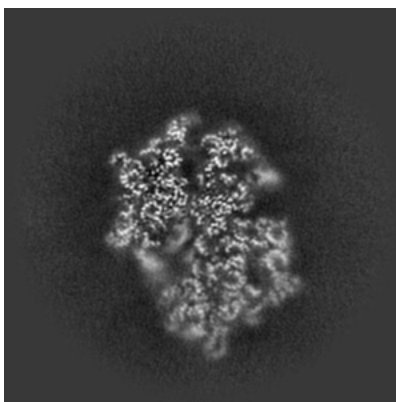
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

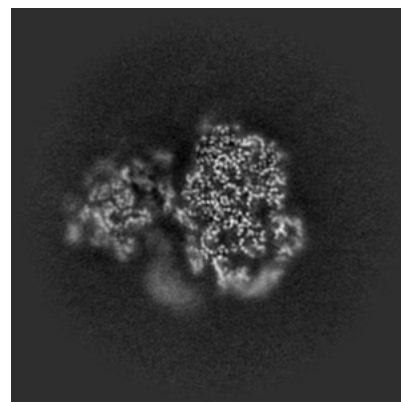
6.2.1 Primary map



X Index: 128



Y Index: 128

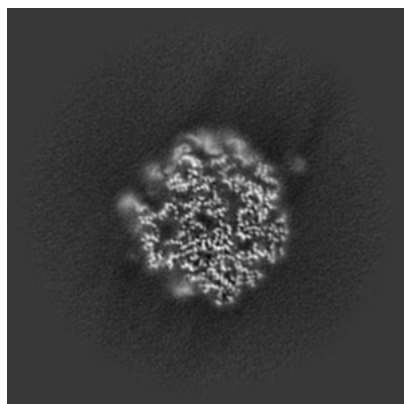


Z Index: 128

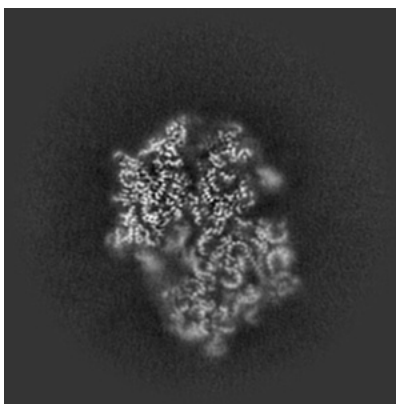
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

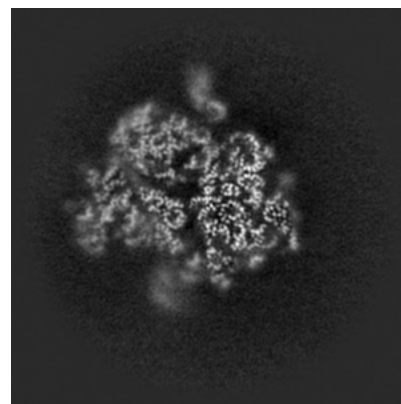
6.3.1 Primary map



X Index: 148



Y Index: 126

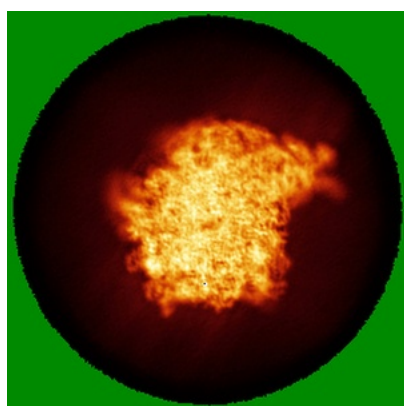


Z Index: 142

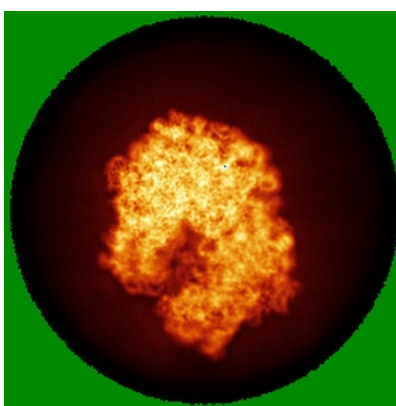
The images above show the largest variance slices of the map in three orthogonal directions.

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

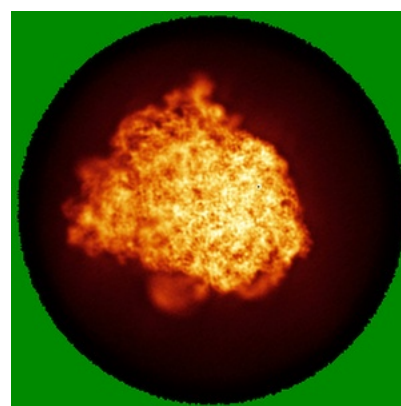
6.4.1 Primary map



X



Y

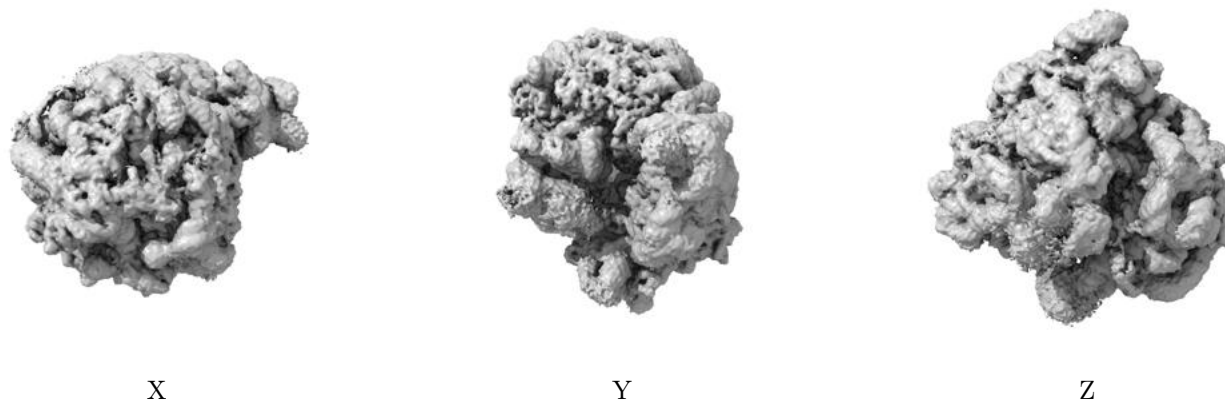


Z

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 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

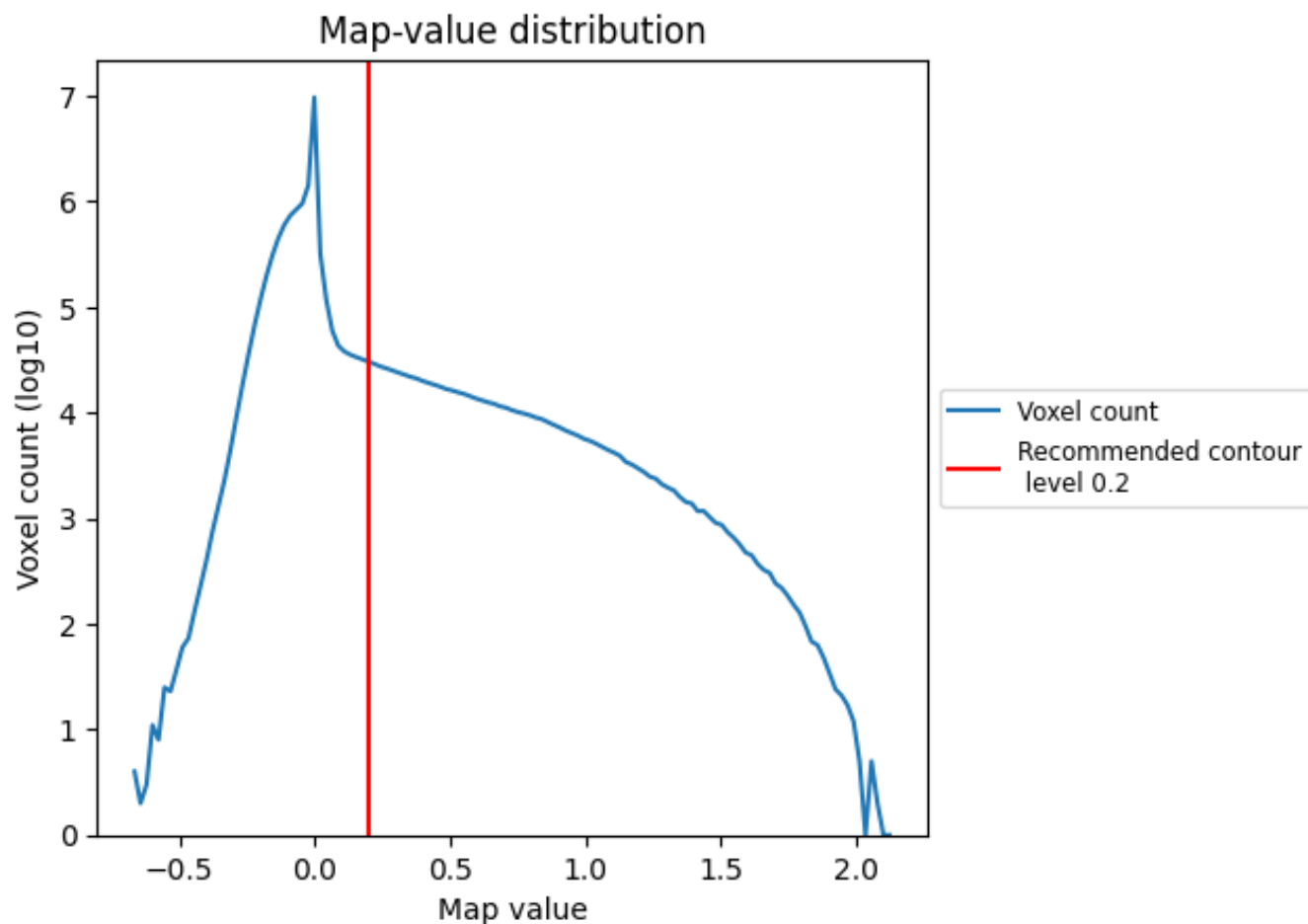
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

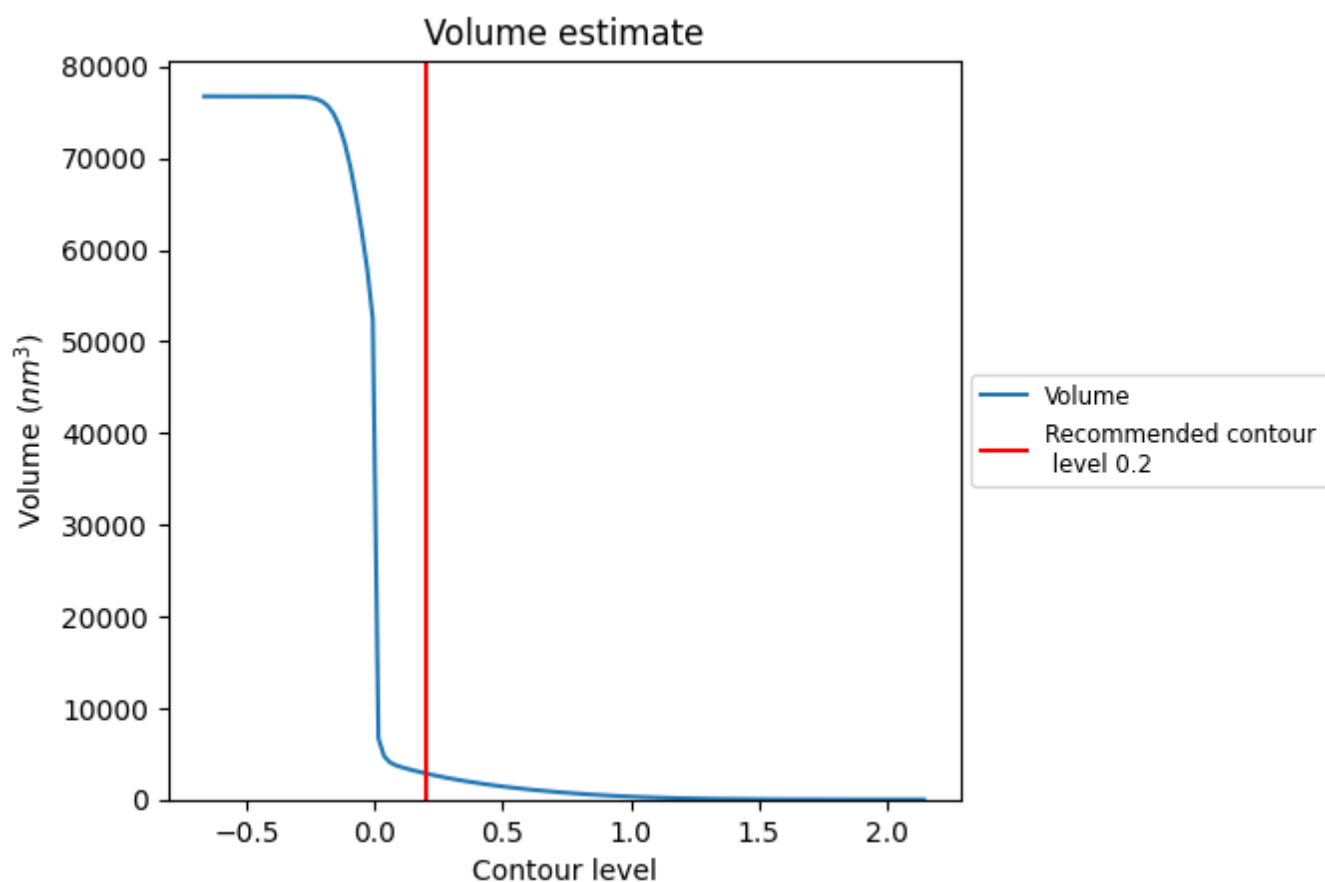
This section contains the results of statistical analysis of the map.

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.

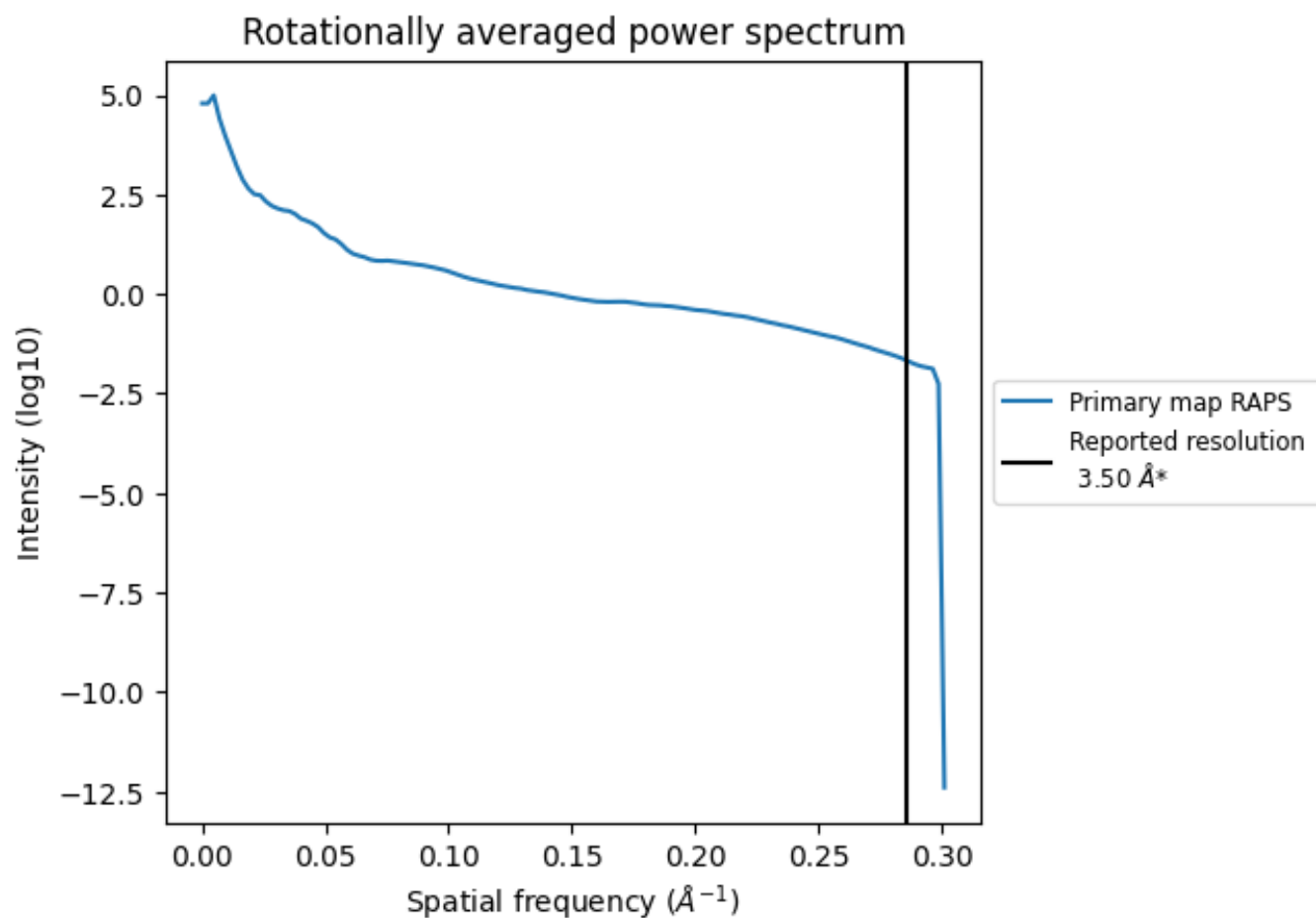
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2849 nm³; this corresponds to an approximate mass of 2574 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 0.286 Å⁻¹

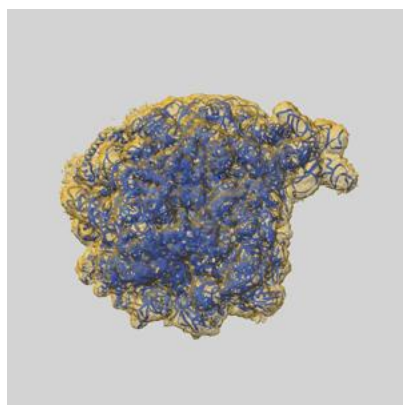
8 Fourier-Shell correlation

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

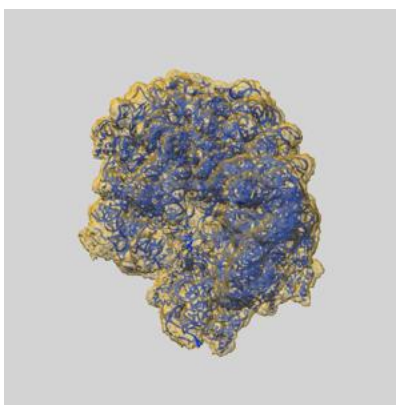
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20174 and PDB model 6ORL. Per-residue inclusion information can be found in section 3 on page 15.

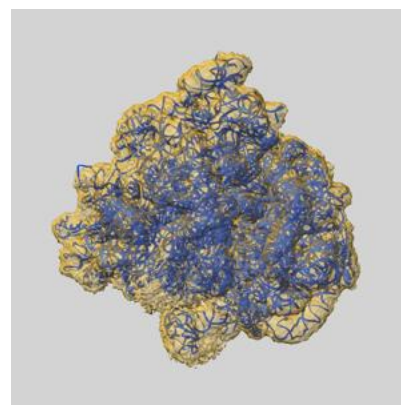
9.1 Map-model overlay [i](#)



X



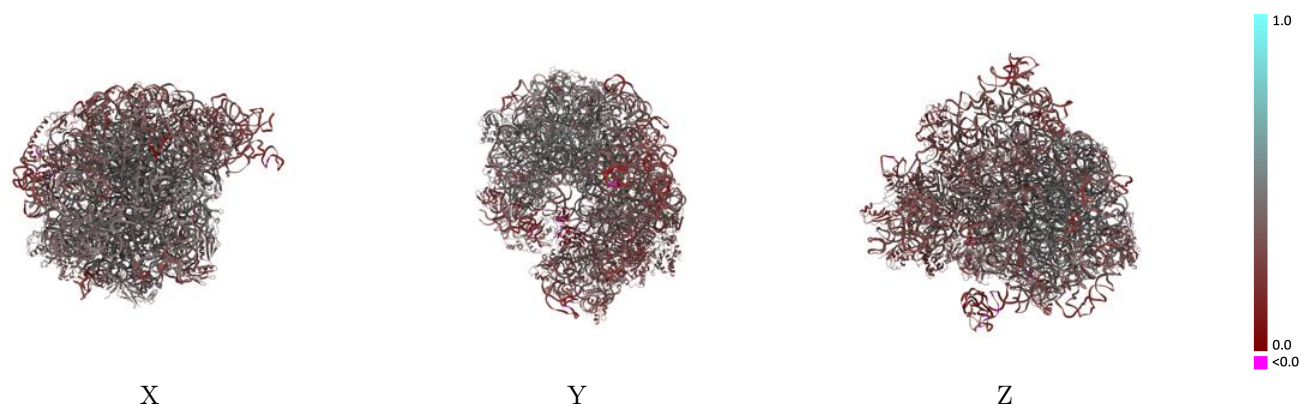
Y



Z

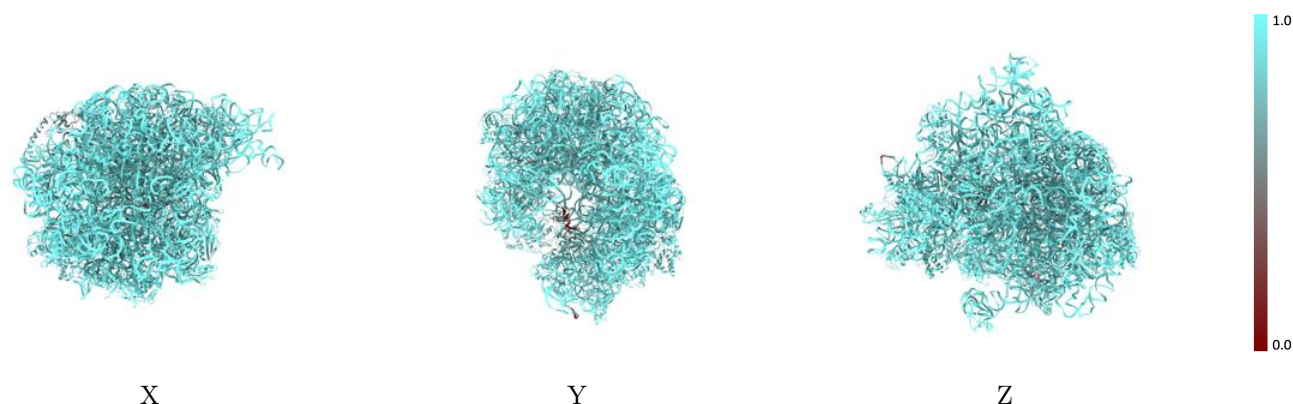
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



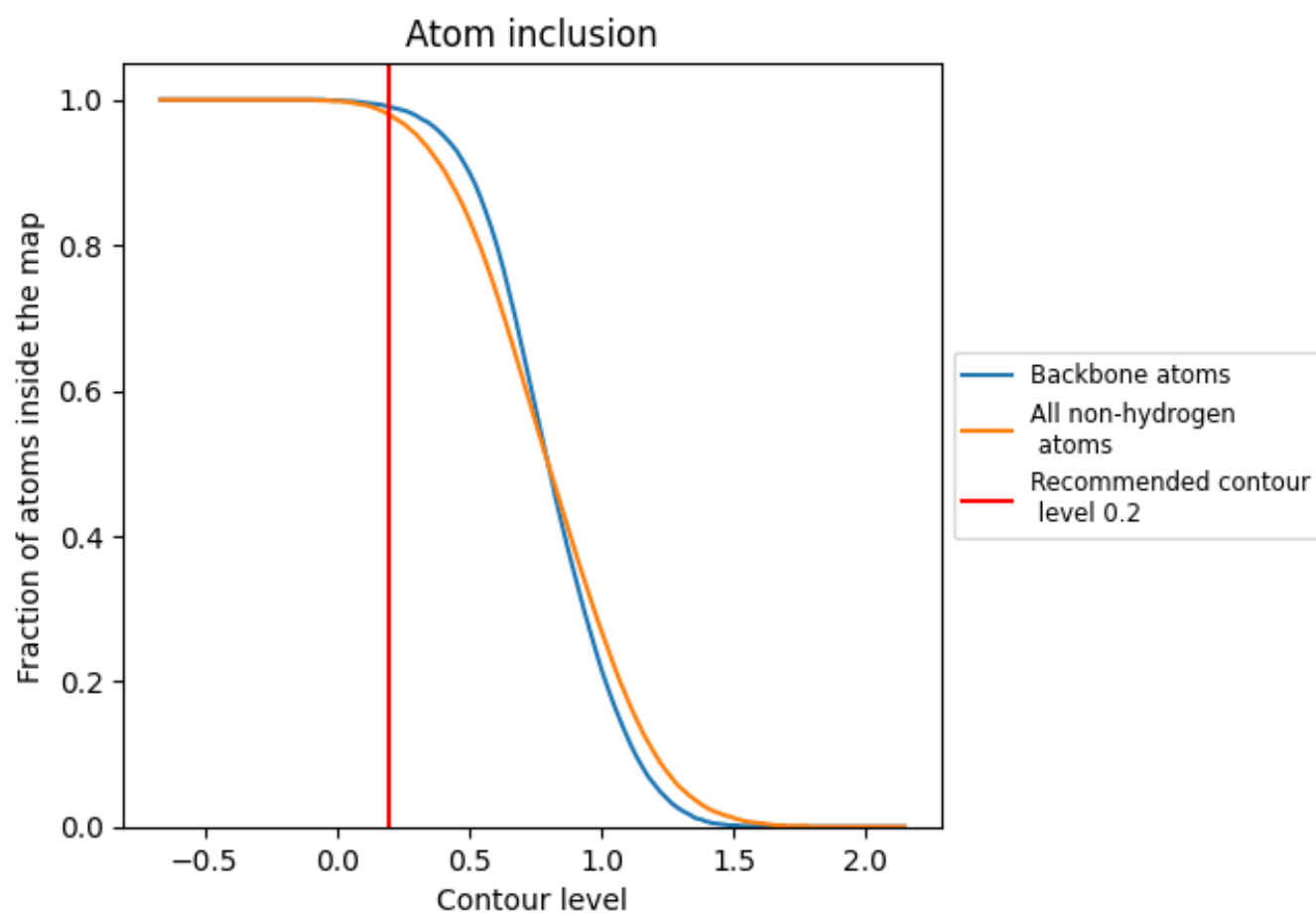
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 98% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9790	 0.3700
1	 0.9990	 0.3980
2	 0.9970	 0.3440
3	 0.9990	 0.3330
4	 1.0000	 0.3850
5	 0.9630	 0.2890
A	 0.5300	 0.1470
B	 0.9620	 0.4470
C	 0.9680	 0.4550
D	 0.9490	 0.4140
E	 0.9370	 0.2860
F	 0.9810	 0.3490
G	 0.7100	 0.2710
H	 0.9380	 0.2890
J	 0.9620	 0.4370
K	 0.9160	 0.4320
L	 0.9770	 0.4340
M	 0.9540	 0.4240
N	 0.9810	 0.4340
O	 0.9510	 0.3320
P	 0.9510	 0.4300
Q	 0.9760	 0.4280
R	 0.9550	 0.4400
S	 0.9590	 0.4450
T	 0.9470	 0.4050
U	 0.9640	 0.3850
V	 0.9770	 0.3640
W	 0.9540	 0.4400
X	 0.9620	 0.4050
Y	 0.9610	 0.3160
Z	 0.9310	 0.4230
b	 0.9770	 0.4290
c	 0.9710	 0.3990
d	 0.9610	 0.4380
e	 0.9330	 0.4330



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Chain	Atom inclusion	Q-score
f	 0.9630	 0.4030
g	 0.9560	 0.3030
h	 0.9540	 0.3380
i	 0.9740	 0.2700
j	 0.9770	 0.3610
k	 0.9720	 0.3300
l	 0.9560	 0.2770
m	 0.9740	 0.3540
n	 0.9850	 0.2890
o	 0.9580	 0.2920
p	 0.9840	 0.3530
q	 0.9170	 0.3580
r	 0.9450	 0.2770
s	 0.9760	 0.3240
t	 0.9680	 0.3250
u	 0.9750	 0.3400
v	 0.9680	 0.3120
w	 0.9920	 0.3140
x	 0.9720	 0.2870
y	 0.9450	 0.2680
z	 0.9610	 0.2880