



wwPDB EM Validation Summary Report ⓘ

Oct 7, 2025 – 10:33 AM JST

PDB ID : 9V1L / pdb_00009v1l
EMDB ID : EMD-64697
Title : Cryo- EM structure of large subunit (LSU) of 75S ribosome with P- tRNA from *Entamoeba histolytica*
Authors : Sharma, S.; Mishra, S.; Gourinath, S.; Kaushal, P.S.
Deposited on : 2025-05-19
Resolution : 3.00 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.dev129
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.46

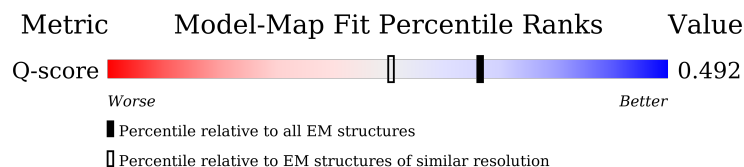
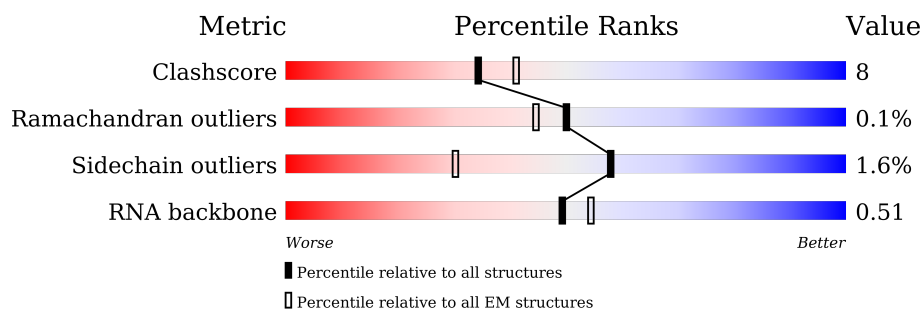
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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.











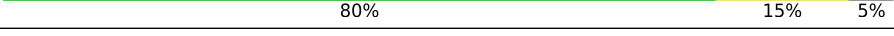

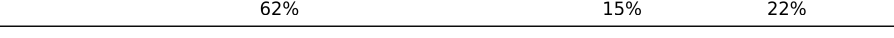
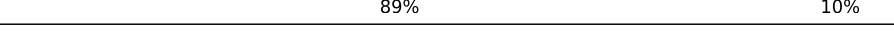

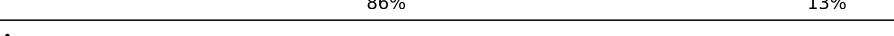


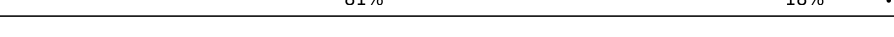

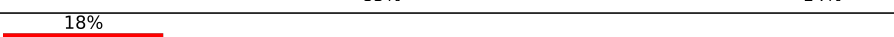






Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	1A	3503	
2	1B	155	
3	1C	117	













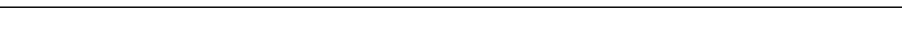



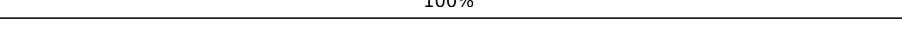
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Mol	Chain	Length	Quality of chain
4	ID	257	
5	IE	402	
6	IF	431	
7	IG	286	
8	IH	204	
9	II	230	
10	IJ	246	
11	IK	197	
12	IL	210	
13	IM	174	
14	IN	291	
15	IO	205	
16	IP	135	
17	IQ	205	
18	IR	179	
19	IS	168	
20	IT	173	
21	IU	198	
22	IV	166	
23	IW	137	
24	IX	140	
25	IY	121	
26	IZ	163	
27	la	213	
28	lb	139	

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Mol	Chain	Length	Quality of chain
29	lc	149	 85% 14% ..
30	ld	64	 75% 19% 6%
31	le	109	 67% 25% 8%
32	lf	150	 71% 15% 14%
33	lg	134	 86% 10% .
34	lh	137	 66% 10% 23%
35	li	122	 85% 15%
36	lj	106	 89% 10% .
37	lk	104	 68% 17% 14%
38	ll	77	 68% 25% . 6%
39	lm	93	 83% 13% ..
40	ln	84	 14% 64% 23% 13%
41	lo	51	 84% 14% .
42	lp	56	 71% 20% . 5%
43	lq	98	 77% 17% 6%
44	ls	14	 100%
45	sH	76	 12% 9% . 78%

2 Entry composition

There are 45 unique types of molecules in this entry. The entry contains 122723 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 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1A	3158	Total	C	N	O	P	0	0
			67497	30260	12256	21823	3158		

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1B	145	Total	C	N	O	P	0	0
			3097	1390	560	1002	145		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1C	117	Total	C	N	O	P	0	0
			2477	1108	425	827	117		

- Molecule 4 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	1D	246	Total	C	N	O	S	0	0
			1881	1165	382	326	8		

- Molecule 5 is a protein called 60S ribosomal protein L3, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	1E	388	Total	C	N	O	S	0	0
			3085	1961	579	530	15		

- Molecule 6 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	1F	424	Total	C	N	O	S	0	0
			3253	2069	619	551	14		

- Molecule 7 is a protein called 60S ribosomal protein L5, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	lG	280	Total	C	N	O	S	0	0
			2232	1427	403	394	8		

- Molecule 8 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	lH	168	Total	C	N	O	S	0	0
			1323	872	226	221	4		

- Molecule 9 is a protein called 60S ribosomal protein L7, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	lI	210	Total	C	N	O	S	0	0
			1658	1067	301	282	8		

- Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	lJ	178	Total	C	N	O	S	0	0
			1451	938	270	238	5		

- Molecule 11 is a protein called 60S ribosomal protein L9, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	lK	193	Total	C	N	O	S	0	0
			1538	974	279	279	6		

- Molecule 12 is a protein called Ribosomal protein L10, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	lL	200	Total	C	N	O	S	0	0
			1597	1017	302	264	14		

- Molecule 13 is a protein called 60S ribosomal protein L11, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	lM	170	Total	C	N	O	S	0	0
			1350	857	243	245	5		

- Molecule 14 is a protein called 60S ribosomal protein L13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	lN	226	Total	C	N	O	S	0	0
			1815	1151	356	301	7		

- Molecule 15 is a protein called 60S ribosomal protein L13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	lO	204	Total	C	N	O	S	0	0
			1616	1030	302	275	9		

- Molecule 16 is a protein called 60S ribosomal protein L14, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	lP	130	Total	C	N	O	S	0	0
			1020	654	188	174	4		

- Molecule 17 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	lQ	204	Total	C	N	O	S	0	0
			1676	1051	356	264	5		

- Molecule 18 is a protein called 60S ribosomal protein L17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	lR	155	Total	C	N	O	S	0	0
			1211	765	234	207	5		

- Molecule 19 is a protein called 60S ribosomal protein L18, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	lS	167	Total	C	N	O	S	0	0
			1316	832	257	218	9		

- Molecule 20 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	lT	173	Total	C	N	O	S	0	0
			1413	910	259	235	9		

- Molecule 21 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	IU	150	Total	C	N	O	S	0	0
			1235	787	246	197	5		

- Molecule 22 is a protein called 60S ribosomal protein L21, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	IV	165	Total	C	N	O	S	0	0
			1320	846	254	217	3		

- Molecule 23 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	IW	87	Total	C	N	O	S	0	0
			716	463	123	125	5		

- Molecule 24 is a protein called 60S ribosomal protein L23, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	IX	133	Total	C	N	O	S	0	0
			1015	629	196	182	8		

- Molecule 25 is a protein called Ribosomal protein L23A, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	IY	116	Total	C	N	O	S	0	0
			926	597	166	159	4		

- Molecule 26 is a protein called 60S ribosomal protein L24, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	IZ	57	Total	C	N	O	S	0	0
			481	318	88	73	2		

- Molecule 27 is a protein called 60S ribosomal protein L26, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	la	210	Total	C	N	O	S	0	0
			1651	1055	304	285	7		

- Molecule 28 is a protein called 60S ribosomal protein L27, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	lb	137	Total	C	N	O	S	0	0
			1094	707	196	187	4		

- Molecule 29 is a protein called Large ribosomal subunit protein uL15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	lc	148	Total	C	N	O	S	0	0
			1192	757	236	194	5		

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	ld	60	Total	C	N	O	S	0	0
			478	297	97	82	2		

- Molecule 31 is a protein called 60S ribosomal protein L30, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	le	100	Total	C	N	O	S	0	0
			748	475	128	143	2		

- Molecule 32 is a protein called 60S ribosomal protein L31, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	lf	129	Total	C	N	O	S	0	0
			1048	676	194	172	6		

- Molecule 33 is a protein called 60S ribosomal protein L32, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	lg	129	Total	C	N	O	S	0	0
			1058	672	209	172	5		

- Molecule 34 is a protein called 60S ribosomal protein L34, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	lh	105	Total	C	N	O	S	0	0
			820	512	169	133	6		

- Molecule 35 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	li	122	Total	C	N	O	S	0	0
			974	620	188	162	4		

- Molecule 36 is a protein called 60S ribosomal protein L35a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	lj	106	Total	C	N	O	S	0	0
			841	545	158	135	3		

- Molecule 37 is a protein called 60S ribosomal protein L36, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	lk	89	Total	C	N	O	S	0	0
			712	447	144	116	5		

- Molecule 38 is a protein called 60S ribosomal protein L37-A, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	ll	72	Total	C	N	O	S	0	0
			591	361	132	91	7		

- Molecule 39 is a protein called 60S ribosomal protein L37A, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	lm	90	Total	C	N	O	S	0	0
			688	428	135	119	6		

- Molecule 40 is a protein called 60S ribosomal protein L38, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	ln	73	Total	C	N	O	S	0	0
			584	378	104	100	2		

- Molecule 41 is a protein called Ribosomal protein L39, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	lo	50	Total	C	N	O	S	0	0
			432	275	91	63	3		

- Molecule 42 is a protein called 60S ribosomal protein L40, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	lp	53	Total	C	N	O	S	0	0
			420	259	86	69	6		

- Molecule 43 is a protein called 60S ribosomal protein L44, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	lq	92	Total	C	N	O	S	0	0
			756	480	148	122	6		

- Molecule 44 is a protein called Nascent peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	ls	14	Total	C	N	O	0	0
			76	45	17	14		

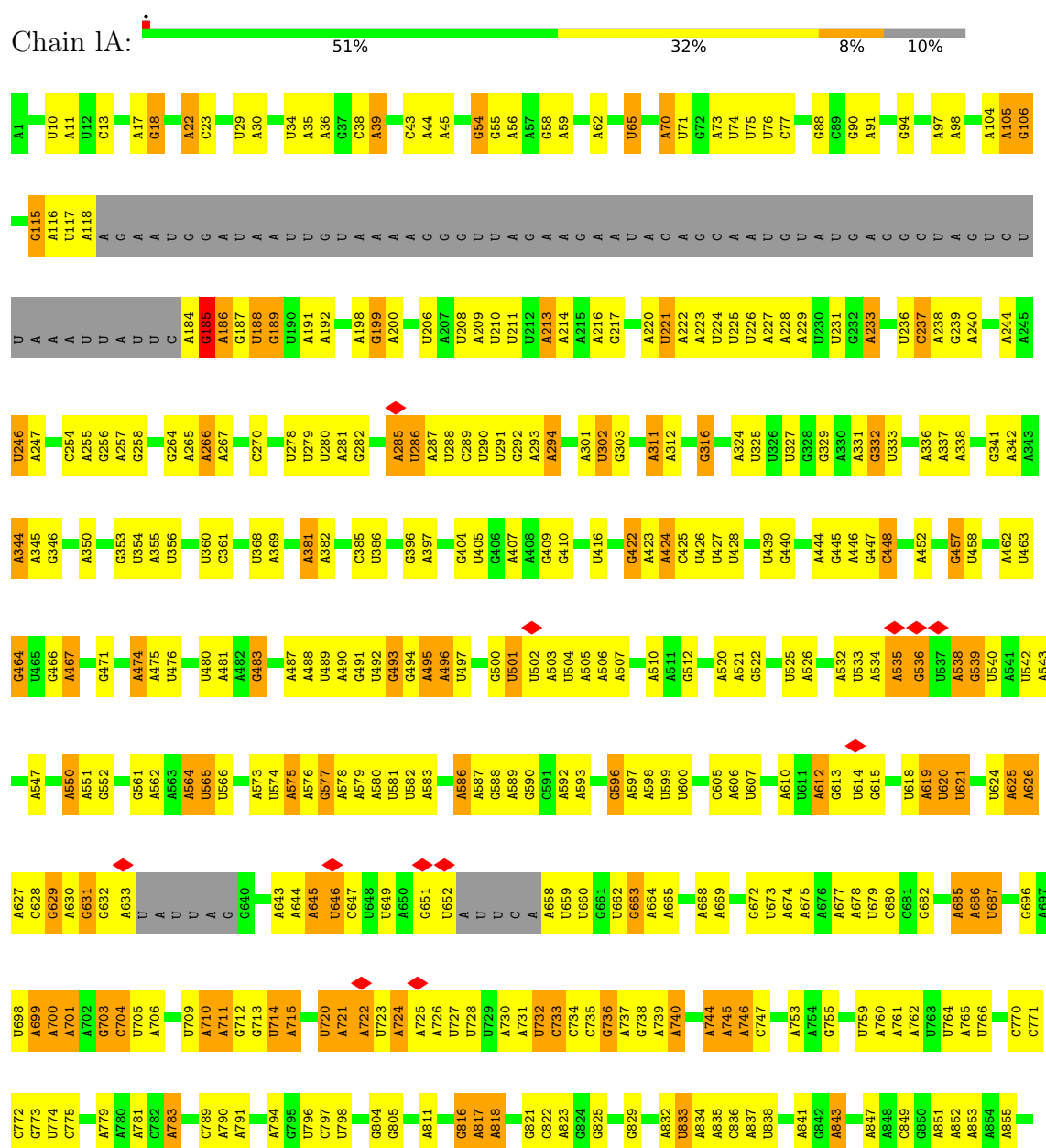
- Molecule 45 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	sH	17	Total	C	N	O	P	0	0
			361	162	66	116	17		

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: 25S rRNA



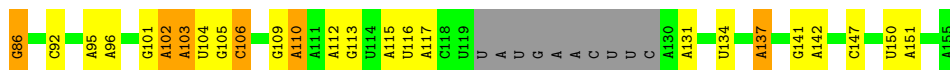


G3401	U3314	G3223	G3028	G2931	A2851	U2739	U	A	U2509	A2433	G2326	U2224
A3404	U3315	A3227	U3029	C2939	A2855	G2740	U	C	G2512	A2434	G2329	A2225
A3405	A3327	A3228	A3030	G2939	G2856	A2744	C	U	G2513	C2438	U2330	
C3406	G3328		U3031	U2940	A2857	C2745	G	A	A2514	A2439	A2331	U2230
	U3329		C3032	C2941	A2858	A2746		G	A2515	G2440	A	C2231
A3409	A3330	G3232	C3033	U2942	U2859	G2747	U2647		A2516	U2441	C	
A	C3331		C3038	G2943	U2860		U2648		C	C2442	U2334	A2234
U	A3332	G3239	G3041	G2943	U2861	U2753	A2651		G	A2443	U2335	U2235
U3412	A3333	A3240	A3041	A2945	A2862	C2754	G2655		A	A2444	U2336	A2236
U3413	U3334		G3044	A2946	A2863		G2656		U	G2445		A2237
A3414	U3335	G3243		A2951	A2864	A2759		A	U	G2446	C2343	C2240
U3415	U3336	U3244	U3047	C2952	A2865	A2760	U2660	U2582	U	A2449	U2344	U2241
A3416	A3337	A2445	U3047	C2953	C2866	A2761	U2661	U2583	U	C2450	U2345	
A3417	A3338	A3246	A3054	C2953	A2867	A2764	G2662		U	G2451	A2347	A2245
C3418	A3339	C3247	A3054	A2956	U2868	U2765	A2663	C2589	G	G2452	G2348	G2246
	A3340	A3248		A2957	A2869	A2766		U2591	G	G2453	G2349	
C3423			G3061	C2957	U2870	A2767	G2666	U2592	U	U2456		C2250
U3426	A3343	U3254	A3062	C2958	U2871	G2768		U2593	A		A2355	C2251
	U3344	G3255	U3066	C2959	U2871		U2670	C2594	G	G2462	A2356	U2252
U3430	A3345	A3256	U3067	A2960		A2774	A2671	G2595	G	A2463	A2357	
U3431	G3349			C2971	U2876				G	A2464		G2261
A3432	U3350	U3259	U3073	G2977	U2877	U2780	G2676	A2588	C	G2465	C2360	U2262
U3433	U3351	G3263	A3076	C2978		U2781	G2677	A2589	U	G2466	A2371	A2264
A3434	G3352	G3264	A3076	C2978	G2885				A			
G3435	U3353	U3265	A3077	C2979	U2886	G2784	U2681	A2606	G	G2469	U2374	U2269
A3436	G3267	G3267	A3079	A2981	U2887		U2682	A	U	G2470	G2381	C2271
C3437	A3268	A3267	A3083	G2982	U2888	U2790	U2683	A	U	G2471	G2382	C2272
	U3357		A3084	C2983	G2889	A2797	G2684	U	G	G2472	G2383	C2273
U3440	U3358	U3274	A3085	C2984	U2890	U2799	G2688	G	G	A2473	C2384	A2274
G3441	U3359		C3085	C2985	C2891		G2689	A	A		U2385	
A3442	A3361	C3277		U2986	A2892	G2815	A2696	U	G	A2478	U2386	U2281
G3443	U3362	A3278	G3088	C2987	C			U	U	G2479	G2282	G2282
A3448	C3363		A3089	A2988	G	A2818		U	C	A2480	A2283	A2283
A3450	U3367	A3285	G3090	C2991	U		U2701	U	U	G2481	U2389	A2284
A3451	G3368	A3286	C3091	G2992	A	U2822	G2702	U	U	C2482	U2390	A2284
U3452	U3369	U3287	G3092	C2993	A	G2823	U2703	C	U	U2483	G2391	U2285
C3453	A3370	U3288	C3093	G2993	G	G2824		U	U	U2484		G2286
G3454	U3371	U3289	U3098	A2994	U	C2825	A2707	U	G		U2394	A2289
G3455	U3372	C3290		C2995	G		A2708	U	U	U2487	A2395	A2289
U3456	A3373	G3291		C2995	U			U	C	G2488	A2396	A2290
G3457	C3374	U3292	C3103	U2998	G	A2832	U2711	A	A		C2397	A2290
U3458	U3375		G3104		A2903			A	A	A2489		A2294
	U3376	G3299	U3105	U3004	U2904	C2835	G2715	U	C	G2490	U2410	A2296
U3461	U3377	A3300	C3106	U3005	U2906			U	C	G2491	G2411	U2296
A3462		A3301	G3107	G3006	U2907	A2838	G2721	U	G	U2492	U2412	G2297
A3463	A3382	U3302	A3110	A3007	C2908	G2839	U2722	A2628	U	U2493	C2415	A2298
G3464	A3383	A3303	G3111	U3008	U2908	G2840		A2629	G	G2494	U2416	A2299
C3465	A3384	C3304	A3112	C3009	A2909		A2726		A	A2495		A2300
U3466	G3385		C3113	U3010	G2910	U2842	A2727	A2632	U	G2496	U2425	
U3467		U3306	A3114	A3015	U2911	U2843	A2730	A2633	A		U2426	A2304
	A3393	U3307	A3115	C3019	U2912	U2845	G2731	A2634	U	U2499	U2428	A2309
U3468	A3394	G3308	U3212	C3024	A2913	U2846	A2732	A2637	C	A2500	G2429	
A3469		U3309	U3213	U3025	C3016	A2847	A2733	A2638	C		U2430	A2309
G3470	C3397	C3310	U3218	U3026		A2848		A2639	C	U2504	G2431	C2324
A3471	U3398	U3311	A3219	C3027	U2920	U2849	A2737	A	A	A2506		G2325
G3472	G3399	U3312	U3220		A2921				C			
U3473	U3313								C			
U3474	A3400				A2925				C			
					U2926							



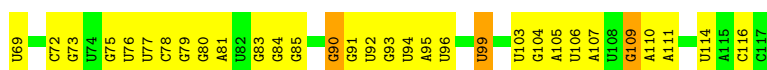
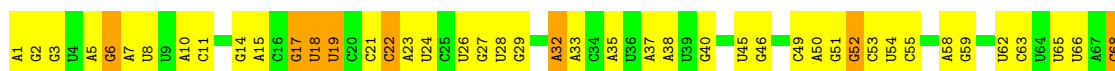
- Molecule 2: 5.8S rRNA

Chain 1B: 49% 35% 10% 6%



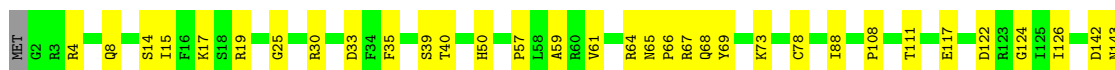
- Molecule 3: 5S rRNA

Chain 1C: 36% 55% 9%



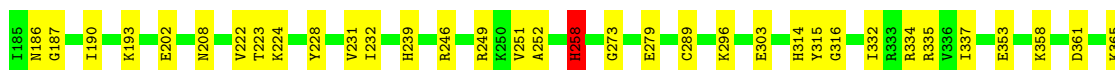
- Molecule 4: Large ribosomal subunit protein uL2

Chain 1D: 77% 18% 5%

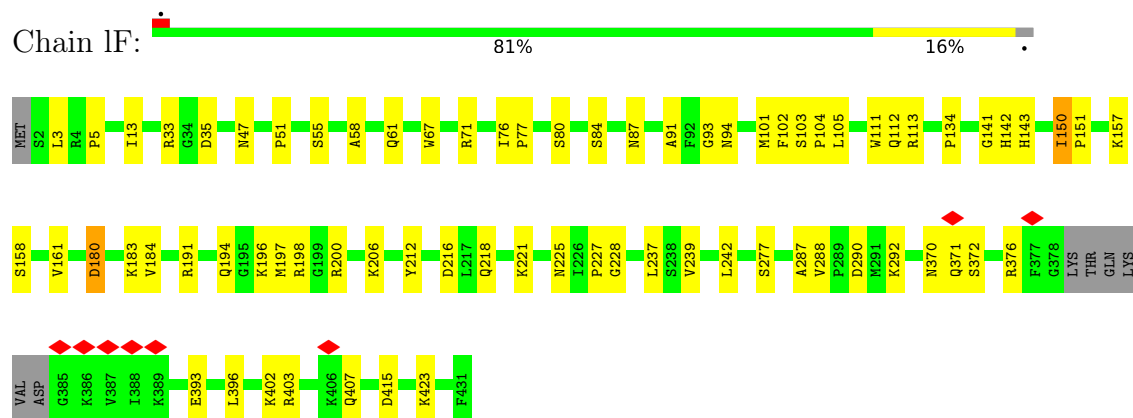


- Molecule 5: 60S ribosomal protein L3, putative

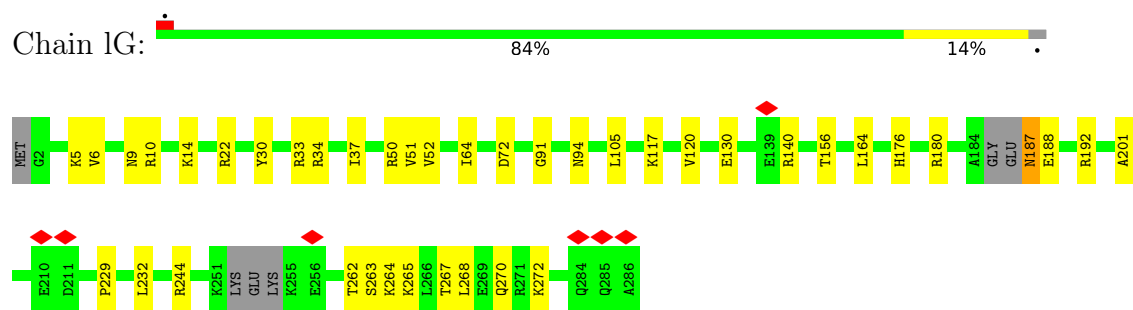
Chain 1E: 79% 17% 4%



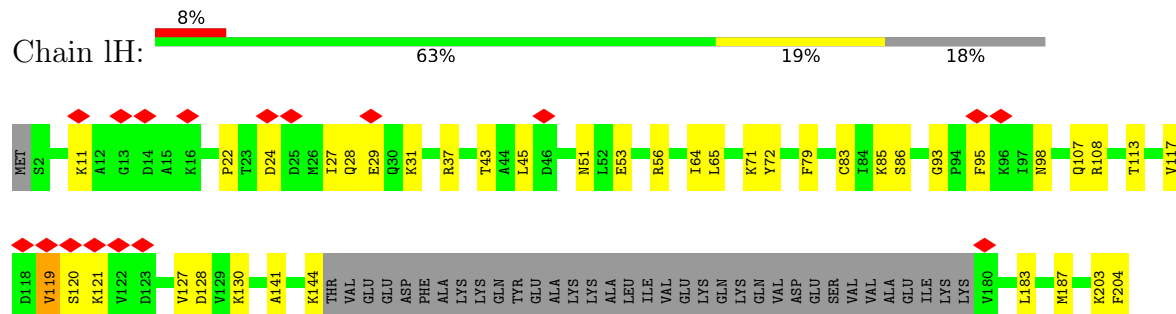
- Molecule 6: Large ribosomal subunit protein uL4



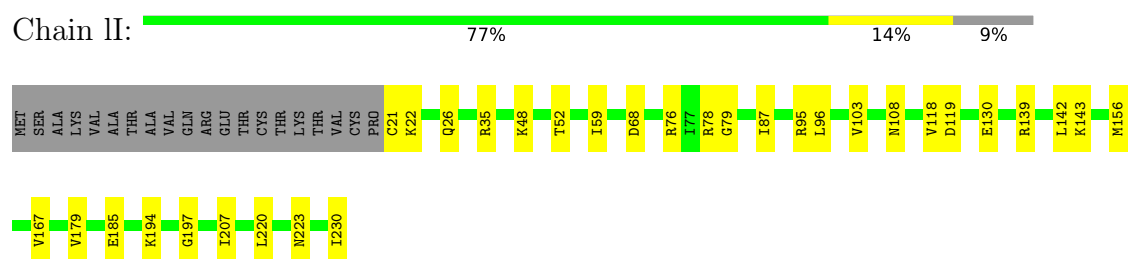
- Molecule 7: 60S ribosomal protein L5, putative



- Molecule 8: Large ribosomal subunit protein eL6



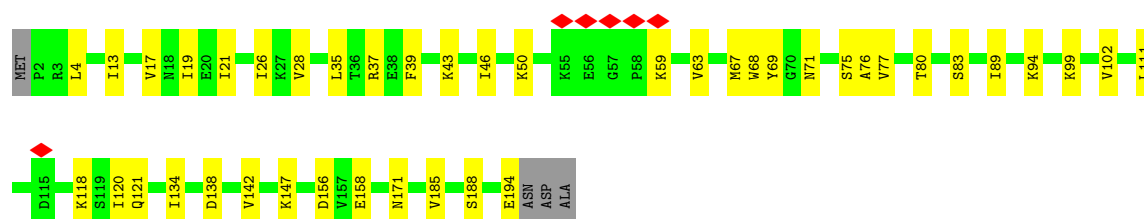
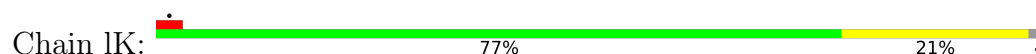
- Molecule 9: 60S ribosomal protein L7, putative



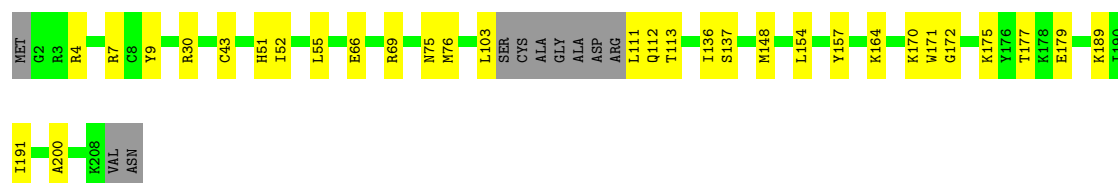
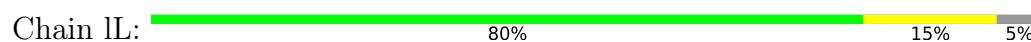
- Molecule 10: 60S ribosomal protein L7a



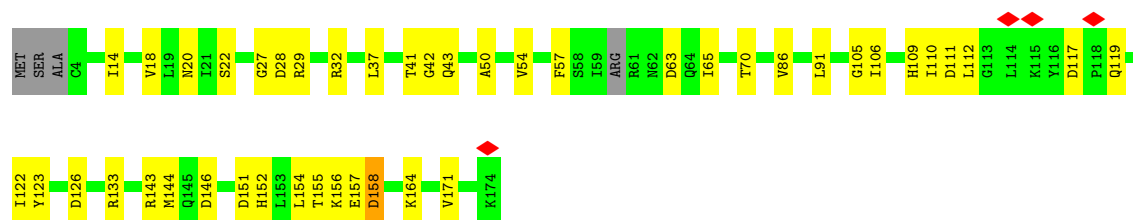
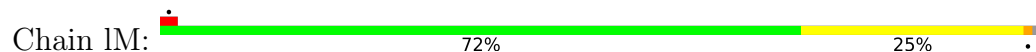
- Molecule 11: 60S ribosomal protein L9, putative



- Molecule 12: Ribosomal protein L10, putative



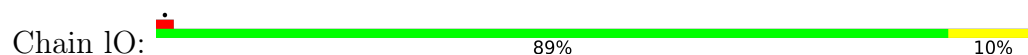
- Molecule 13: 60S ribosomal protein L11, putative



- Molecule 14: 60S ribosomal protein L13, putative



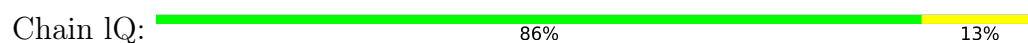
- Molecule 15: 60S ribosomal protein L13, putative



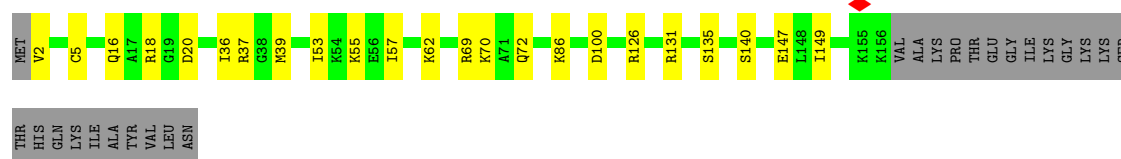
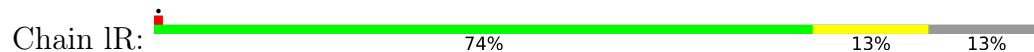
- Molecule 16: 60S ribosomal protein L14, putative



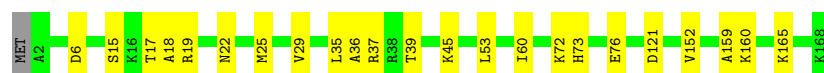
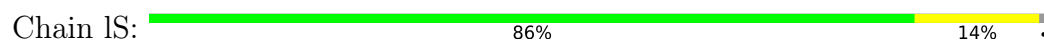
- Molecule 17: Ribosomal protein L15



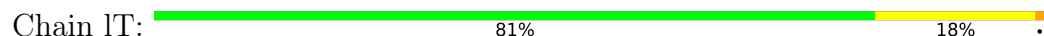
- Molecule 18: 60S ribosomal protein L17, putative

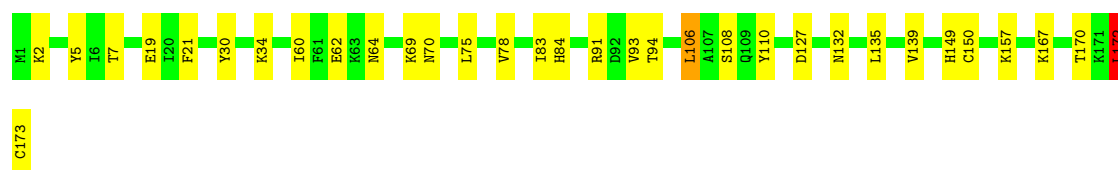


- Molecule 19: 60S ribosomal protein L18, putative

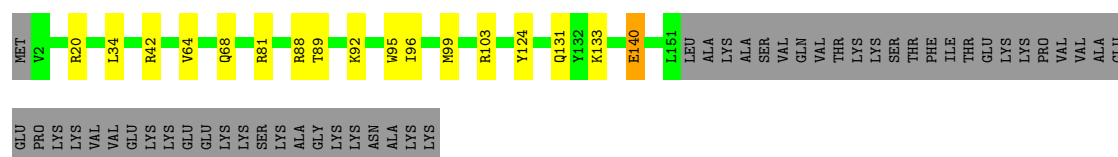


- Molecule 20: 60S ribosomal protein L18a

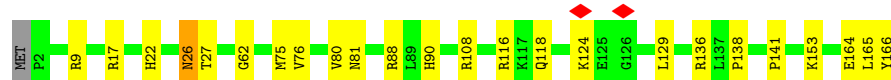
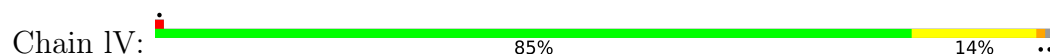




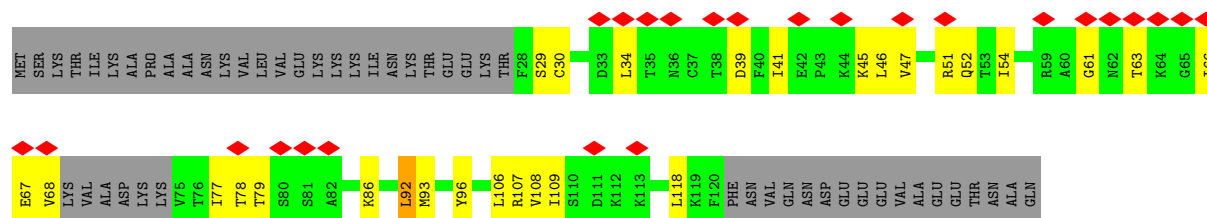
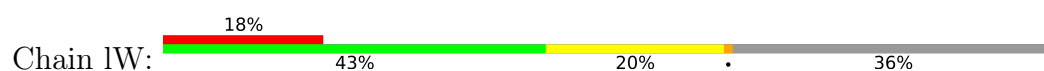
- Molecule 21: Ribosomal protein L19



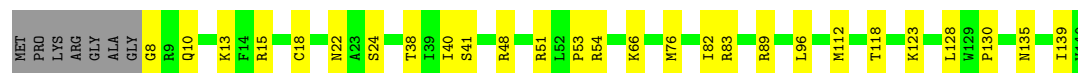
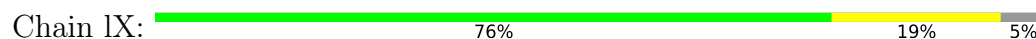
- Molecule 22: 60S ribosomal protein L21, putative



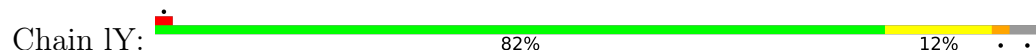
- Molecule 23: Large ribosomal subunit protein eL22



- Molecule 24: 60S ribosomal protein L23, putative

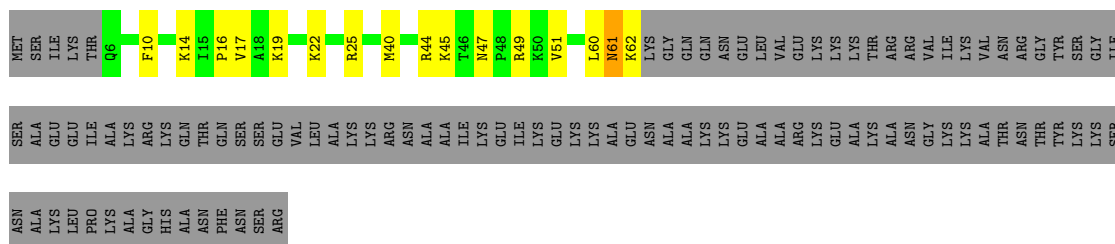


- Molecule 25: Ribosomal protein L23A, putative




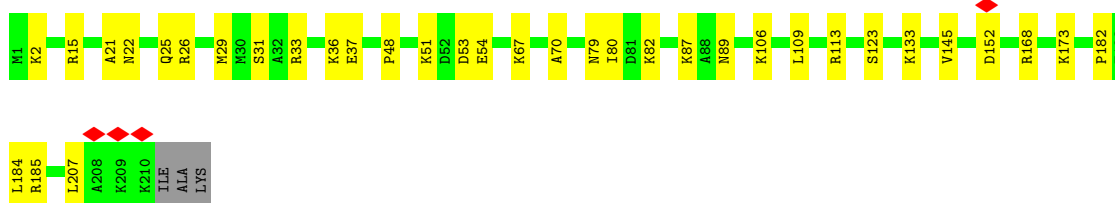
- Molecule 26: 60S ribosomal protein L24, putative

Chain lZ: 




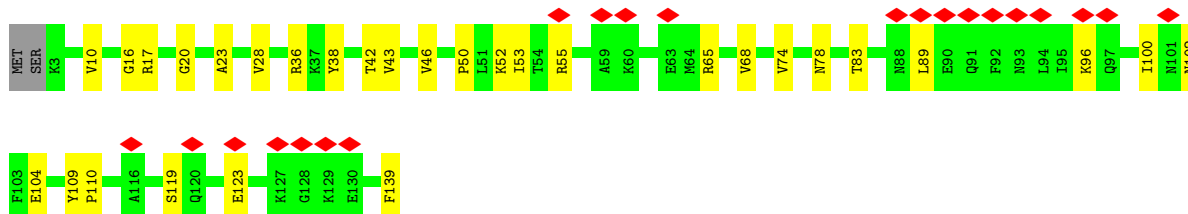
- Molecule 27: 60S ribosomal protein L26, putative

Chain la: 




- Molecule 28: 60S ribosomal protein L27, putative

Chain lb: 



- Molecule 29: Large ribosomal subunit protein uL15A

Chain lc: 



- Molecule 30: 60S ribosomal protein L29

Chain ld: 

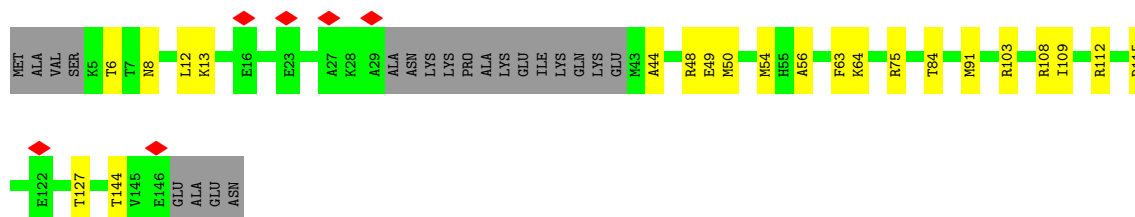


- Molecule 31: 60S ribosomal protein L30, putative

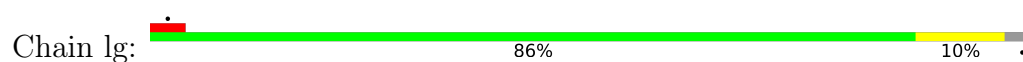
Chain le: 



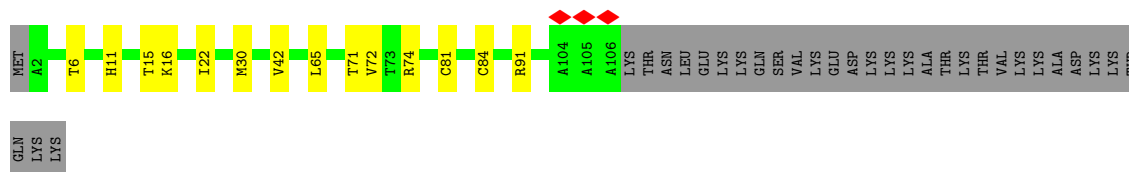
- Molecule 32: 60S ribosomal protein L31, putative



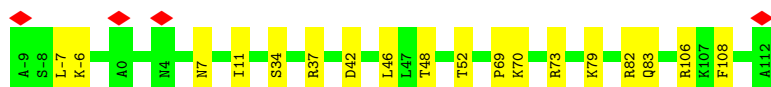
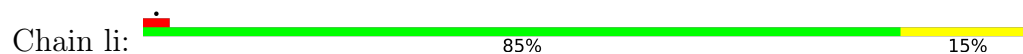
- Molecule 33: 60S ribosomal protein L32, putative



- Molecule 34: 60S ribosomal protein L34, putative



- Molecule 35: uL29

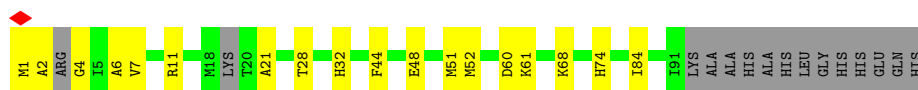


- Molecule 36: 60S ribosomal protein L35a, putative



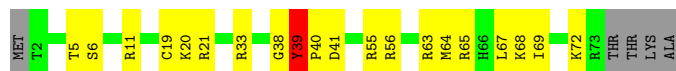
- Molecule 37: 60S ribosomal protein L36, putative





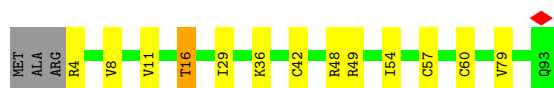
- Molecule 38: 60S ribosomal protein L37-A, putative

Chain ll: 68% 25% 6%



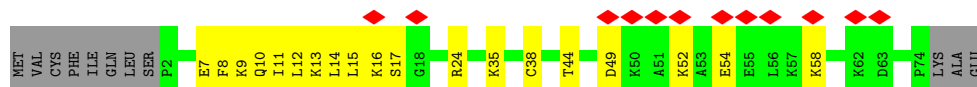
- Molecule 39: 60S ribosomal protein L37A, putative

Chain lm: 83% 13% 4%



- Molecule 40: 60S ribosomal protein L38, putative

Chain ln: 14% 64% 23% 13%



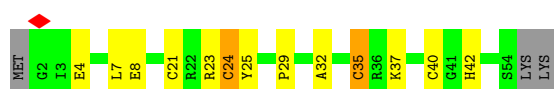
- Molecule 41: Ribosomal protein L39, putative

Chain lo: 84% 14% 2%



- Molecule 42: 60S ribosomal protein L40, putative

Chain lp: 71% 20% 5%



- Molecule 43: 60S ribosomal protein L44, putative

Chain lq: 77% 17% 6%



- Molecule 44: Nascent peptide

Chain ls:

100%

There are no outlier residues recorded for this chain.

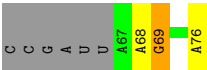
● Molecule 45: P-tRNA

Chain sH:

12%

9%

78%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	53764	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.106	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	15.718	Depositor
Minimum map value	-3.902	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2.5	Depositor
Map size (Å)	374.50003, 374.50003, 374.50003	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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	1A	0.25	5/75634 (0.0%)	0.33	10/117816 (0.0%)
2	1B	0.24	0/3470	0.32	1/5401 (0.0%)
3	1C	0.25	0/2765	0.39	2/4303 (0.0%)
4	1D	0.22	0/1920	0.31	0/2582
5	1E	0.21	0/3149	0.27	0/4228
6	1F	0.20	0/3311	0.27	0/4446
7	1G	0.19	0/2270	0.30	0/3039
8	1H	0.17	0/1352	0.30	0/1819
9	1I	0.20	0/1680	0.26	0/2252
10	1J	0.17	0/1477	0.32	0/1983
11	1K	0.18	0/1562	0.25	0/2103
12	1L	0.19	0/1633	0.28	0/2184
13	1M	0.17	0/1369	0.27	0/1834
14	1N	0.20	0/1842	0.29	0/2460
15	1O	0.20	0/1646	0.28	0/2209
16	1P	0.20	0/1032	0.25	0/1388
17	1Q	0.23	0/1707	0.24	0/2276
18	1R	0.21	0/1230	0.24	0/1647
19	1S	0.22	0/1337	0.27	0/1789
20	1T	0.21	0/1445	0.27	0/1946
21	1U	0.20	0/1253	0.27	0/1666
22	1V	0.20	0/1351	0.26	0/1819
23	1W	0.12	0/726	0.30	0/967
24	1X	0.22	0/1030	0.28	0/1384
25	1Y	0.17	0/941	0.25	0/1262
26	1Z	0.21	0/492	0.24	0/656
27	1a	0.17	0/1673	0.24	0/2236
28	1b	0.16	0/1112	0.25	0/1489
29	1c	0.23	0/1223	0.26	0/1636
30	1d	0.22	0/485	0.29	0/639
31	1e	0.19	0/756	0.35	0/1017
32	1f	0.19	0/1067	0.25	0/1425
33	1g	0.21	0/1075	0.24	0/1434
34	1h	0.20	0/833	0.27	0/1115

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	li	0.16	0/984	0.25	0/1310
36	lj	0.23	0/862	0.29	0/1163
37	lk	0.16	0/721	0.26	0/955
38	ll	0.24	0/602	0.31	0/797
39	lm	0.22	0/696	0.33	0/928
40	ln	0.17	0/592	0.29	0/789
41	lo	0.23	0/444	0.22	0/587
42	lp	0.21	0/425	0.52	2/563 (0.4%)
43	lq	0.20	0/770	0.24	0/1019
44	ls	0.99	0/10	1.39	0/11
45	sH	0.15	0/402	0.24	0/621
All	All	0.23	5/132356 (0.0%)	0.31	15/195193 (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
5	lE	0	1
20	lT	0	1
38	ll	0	1
All	All	0	3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	lA	2150	G	O3'-P	-7.93	1.49	1.61
1	lA	3469	A	C1'-N9	-6.04	1.38	1.48
1	lA	2905	U	O3'-P	-5.88	1.52	1.61
1	lA	3473	U	C1'-N1	5.79	1.57	1.48
1	lA	3465	C	C1'-N1	5.17	1.56	1.48

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	lC	62	U	OP1-P-O3'	-8.82	81.55	108.00
3	lC	62	U	OP2-P-O3'	-8.72	81.85	108.00
1	lA	3477	U	C4'-C3'-O3'	7.06	119.99	109.40
1	lA	185	G	C4'-C3'-O3'	-7.02	102.47	113.00
42	lp	24	CYS	CA-CB-SG	6.73	129.88	114.40

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	lE	258	HIS	Peptide
20	lT	172	LEU	Peptide
38	lI	39	TYR	Peptide

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	lA	67497	0	33861	968	0
2	lB	3097	0	1552	44	0
3	lC	2477	0	1252	87	0
4	lD	1881	0	1928	34	0
5	lE	3085	0	3215	52	0
6	lF	3253	0	3444	52	0
7	lG	2232	0	2315	26	0
8	lH	1323	0	1425	30	0
9	lI	1658	0	1802	20	0
10	lJ	1451	0	1562	21	0
11	lK	1538	0	1598	26	0
12	lL	1597	0	1654	22	0
13	lM	1350	0	1390	29	0
14	lN	1815	0	1964	40	0
15	lO	1616	0	1700	16	0
16	lP	1020	0	1104	22	0
17	lQ	1676	0	1777	19	0
18	lR	1211	0	1280	19	0
19	lS	1316	0	1420	18	0
20	lT	1413	0	1479	21	0
21	lU	1235	0	1369	13	0
22	lV	1320	0	1406	17	0
23	lW	716	0	760	23	0
24	lX	1015	0	1054	19	0
25	lY	926	0	997	14	0
26	lZ	481	0	518	8	0
27	la	1651	0	1822	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	lb	1094	0	1174	24	0
29	lc	1192	0	1205	17	0
30	ld	478	0	507	8	0
31	le	748	0	794	21	0
32	lf	1048	0	1127	14	0
33	lg	1058	0	1140	14	0
34	lh	820	0	864	11	0
35	li	974	0	1093	12	0
36	lj	841	0	878	10	0
37	lk	712	0	755	13	0
38	ll	591	0	617	14	0
39	lm	688	0	728	13	0
40	ln	584	0	643	16	0
41	lo	432	0	444	6	0
42	lp	420	0	450	11	0
43	lq	756	0	821	13	0
44	ls	76	0	34	0	0
45	sH	361	0	186	5	0
All	All	122723	0	89108	1644	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 8.

The worst 5 of 1644 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:IW:47:VAL:HG13	23:IW:68:VAL:CG1	1.53	1.37
1:1A:3454:G:N1	1:1A:3501:A:C2	2.16	1.14
1:1A:3454:G:N1	1:1A:3501:A:H2	1.47	1.13
1:1A:3469:A:N6	1:1A:3485:U:H3	1.46	1.12
3:1C:79:G:N1	3:1C:95:A:H2	1.45	1.12

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	ID	244/257 (95%)	228 (93%)	16 (7%)	0	100	100
5	IE	386/402 (96%)	372 (96%)	13 (3%)	1 (0%)	37	70
6	IF	420/431 (97%)	401 (96%)	19 (4%)	0	100	100
7	IG	274/286 (96%)	258 (94%)	15 (6%)	1 (0%)	30	66
8	IH	164/204 (80%)	145 (88%)	17 (10%)	2 (1%)	11	41
9	II	208/230 (90%)	199 (96%)	8 (4%)	1 (0%)	25	61
10	IJ	172/246 (70%)	166 (96%)	6 (4%)	0	100	100
11	IK	191/197 (97%)	183 (96%)	7 (4%)	1 (0%)	25	61
12	IL	196/210 (93%)	184 (94%)	12 (6%)	0	100	100
13	IM	166/174 (95%)	159 (96%)	7 (4%)	0	100	100
14	IN	222/291 (76%)	213 (96%)	9 (4%)	0	100	100
15	IO	202/205 (98%)	197 (98%)	5 (2%)	0	100	100
16	IP	128/135 (95%)	124 (97%)	4 (3%)	0	100	100
17	IQ	202/205 (98%)	194 (96%)	8 (4%)	0	100	100
18	IR	153/179 (86%)	150 (98%)	3 (2%)	0	100	100
19	IS	165/168 (98%)	154 (93%)	11 (7%)	0	100	100
20	IT	171/173 (99%)	163 (95%)	8 (5%)	0	100	100
21	IU	148/198 (75%)	147 (99%)	1 (1%)	0	100	100
22	IV	163/166 (98%)	160 (98%)	3 (2%)	0	100	100
23	IW	83/137 (61%)	79 (95%)	4 (5%)	0	100	100
24	IX	131/140 (94%)	126 (96%)	5 (4%)	0	100	100
25	IY	114/121 (94%)	111 (97%)	3 (3%)	0	100	100
26	IZ	55/163 (34%)	54 (98%)	1 (2%)	0	100	100
27	la	208/213 (98%)	199 (96%)	9 (4%)	0	100	100
28	lb	135/139 (97%)	132 (98%)	3 (2%)	0	100	100
29	lc	146/149 (98%)	138 (94%)	8 (6%)	0	100	100
30	ld	58/64 (91%)	57 (98%)	1 (2%)	0	100	100
31	le	98/109 (90%)	90 (92%)	8 (8%)	0	100	100
32	lf	125/150 (83%)	124 (99%)	1 (1%)	0	100	100
33	lg	127/134 (95%)	120 (94%)	7 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	lh	103/137 (75%)	99 (96%)	4 (4%)	0	100	100
35	li	120/122 (98%)	117 (98%)	2 (2%)	1 (1%)	16	51
36	lj	104/106 (98%)	102 (98%)	2 (2%)	0	100	100
37	lk	83/104 (80%)	83 (100%)	0	0	100	100
38	ll	70/77 (91%)	63 (90%)	5 (7%)	2 (3%)	3	20
39	lm	88/93 (95%)	79 (90%)	9 (10%)	0	100	100
40	ln	71/84 (84%)	68 (96%)	3 (4%)	0	100	100
41	lo	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
42	lp	51/56 (91%)	50 (98%)	1 (2%)	0	100	100
43	lq	90/98 (92%)	86 (96%)	4 (4%)	0	100	100
44	ls	1/14 (7%)	0	1 (100%)	0	100	100
All	All	6084/6818 (89%)	5821 (96%)	254 (4%)	9 (0%)	50	81

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
38	ll	40	PRO
5	lE	387	ASP
38	ll	39	TYR
35	li	-6	LYS
8	lH	119	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	lD	195/201 (97%)	192 (98%)	3 (2%)	60	83
5	lE	331/343 (96%)	327 (99%)	4 (1%)	67	86
6	lF	332/345 (96%)	325 (98%)	7 (2%)	48	77
7	lG	226/231 (98%)	222 (98%)	4 (2%)	54	80
8	lH	141/173 (82%)	140 (99%)	1 (1%)	81	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	II	178/195 (91%)	175 (98%)	3 (2%)	56	81
10	IJ	157/212 (74%)	154 (98%)	3 (2%)	52	79
11	IK	171/174 (98%)	169 (99%)	2 (1%)	67	86
12	IL	169/176 (96%)	169 (100%)	0	100	100
13	IM	144/147 (98%)	139 (96%)	5 (4%)	31	65
14	IN	193/243 (79%)	187 (97%)	6 (3%)	35	68
15	IO	167/168 (99%)	167 (100%)	0	100	100
16	IP	113/118 (96%)	112 (99%)	1 (1%)	75	89
17	IQ	171/172 (99%)	170 (99%)	1 (1%)	84	93
18	IR	127/147 (86%)	127 (100%)	0	100	100
19	IS	141/143 (99%)	141 (100%)	0	100	100
20	IT	156/156 (100%)	152 (97%)	4 (3%)	41	72
21	IU	132/174 (76%)	128 (97%)	4 (3%)	36	69
22	IV	144/145 (99%)	141 (98%)	3 (2%)	48	77
23	IW	81/125 (65%)	76 (94%)	5 (6%)	15	45
24	IX	109/113 (96%)	109 (100%)	0	100	100
25	IY	99/102 (97%)	96 (97%)	3 (3%)	36	69
26	IZ	52/137 (38%)	47 (90%)	5 (10%)	7	27
27	la	177/179 (99%)	176 (99%)	1 (1%)	84	93
28	lb	121/123 (98%)	120 (99%)	1 (1%)	79	90
29	lc	120/121 (99%)	116 (97%)	4 (3%)	33	67
30	ld	50/54 (93%)	48 (96%)	2 (4%)	27	61
31	le	84/92 (91%)	84 (100%)	0	100	100
32	lf	111/128 (87%)	110 (99%)	1 (1%)	75	89
33	lg	112/116 (97%)	112 (100%)	0	100	100
34	lh	86/116 (74%)	85 (99%)	1 (1%)	67	86
35	li	103/103 (100%)	103 (100%)	0	100	100
36	lj	89/89 (100%)	87 (98%)	2 (2%)	47	76
37	lk	71/82 (87%)	70 (99%)	1 (1%)	62	83
38	ll	60/64 (94%)	59 (98%)	1 (2%)	56	81
39	lm	72/74 (97%)	71 (99%)	1 (1%)	62	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	ln	63/73 (86%)	63 (100%)	0	100	100
41	lo	44/45 (98%)	43 (98%)	1 (2%)	45	75
42	lp	45/48 (94%)	44 (98%)	1 (2%)	47	76
43	lq	85/91 (93%)	84 (99%)	1 (1%)	67	86
44	ls	1/1 (100%)	1 (100%)	0	100	100
All	All	5223/5739 (91%)	5141 (98%)	82 (2%)	58	82

5 of 82 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
25	lY	109	VAL
30	ld	35	MET
26	lZ	17	VAL
28	lb	28	VAL
36	lj	38	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
34	lh	40	ASN
41	lo	18	HIS
41	lo	36	ASN
17	lQ	67	HIS
17	lQ	32	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	lA	3141/3503 (89%)	588 (18%)	0
2	lB	143/155 (92%)	35 (24%)	0
3	lC	116/117 (99%)	19 (16%)	0
45	sH	15/76 (19%)	4 (26%)	0
All	All	3415/3851 (88%)	646 (18%)	0

5 of 646 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	lA	18	G

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Mol	Chain	Res	Type
1	lA	22	A
1	lA	29	U
1	lA	30	A
1	lA	36	A

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

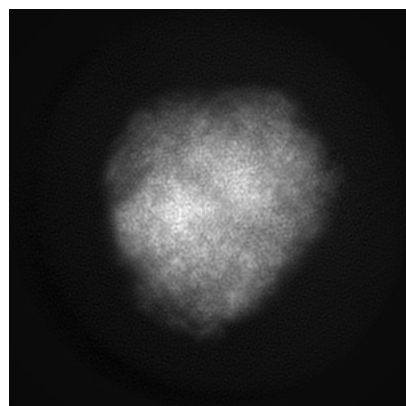
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64697. These allow visual inspection of the internal detail of the map and identification of artifacts.

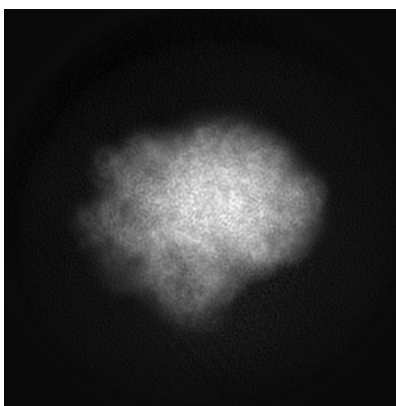
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

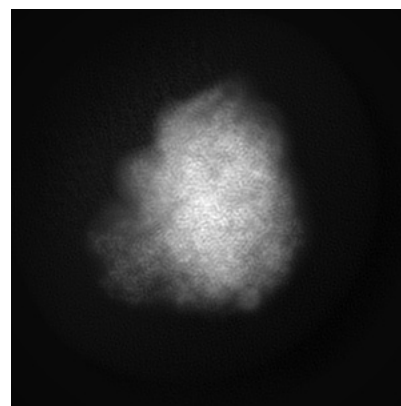
6.1.1 Primary map



X

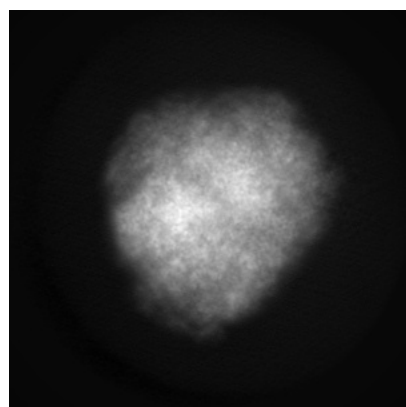


Y

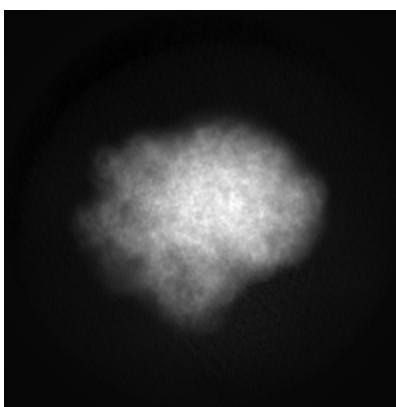


Z

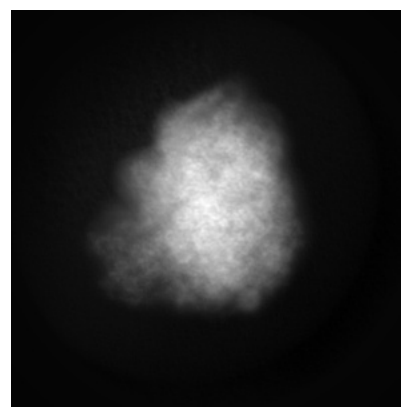
6.1.2 Raw map



X



Y

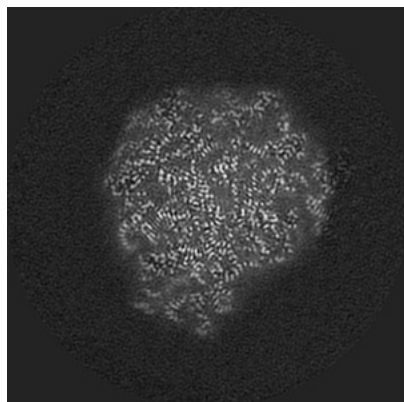


Z

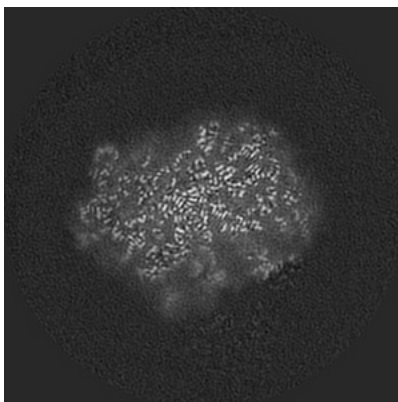
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

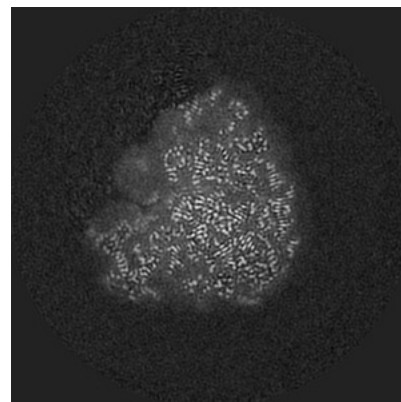
6.2.1 Primary map



X Index: 175

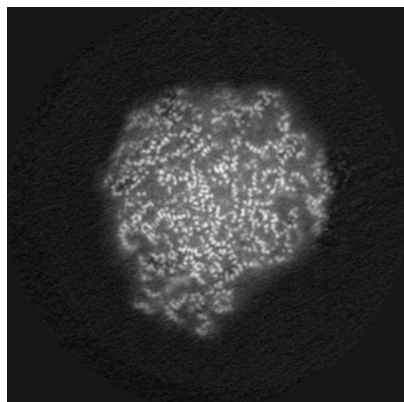


Y Index: 175

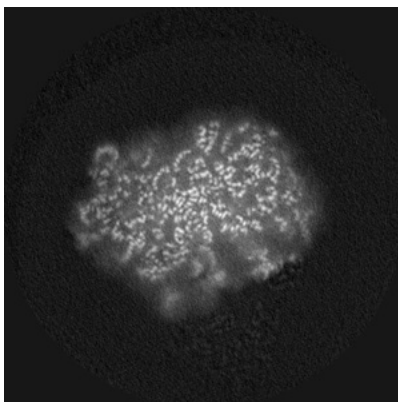


Z Index: 175

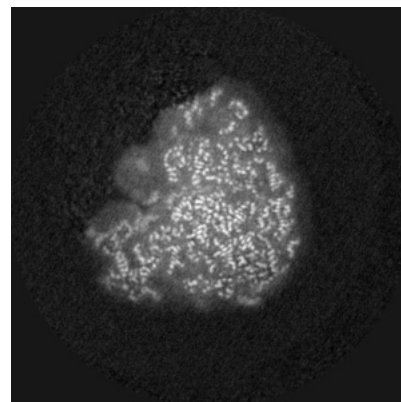
6.2.2 Raw map



X Index: 175



Y Index: 175

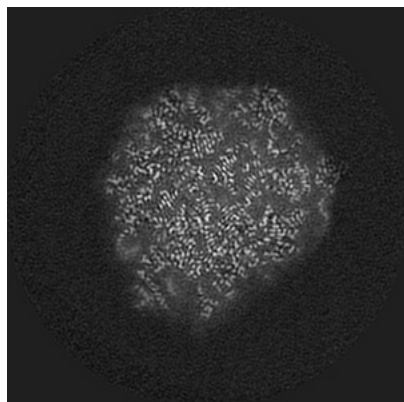


Z Index: 175

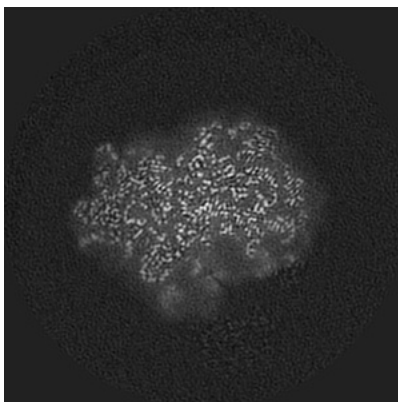
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

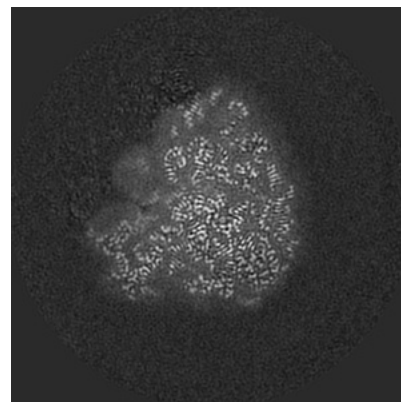
6.3.1 Primary map



X Index: 181

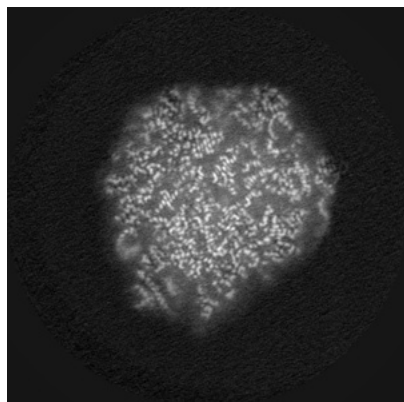


Y Index: 171

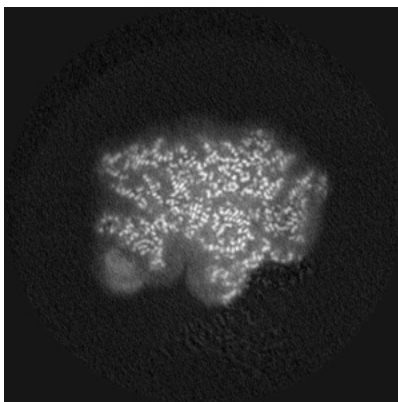


Z Index: 176

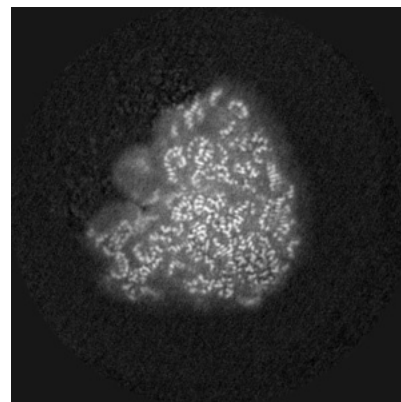
6.3.2 Raw map



X Index: 181



Y Index: 205

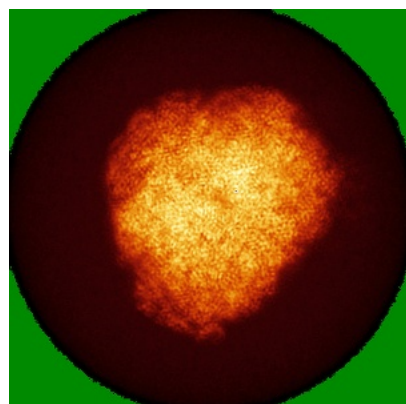


Z Index: 176

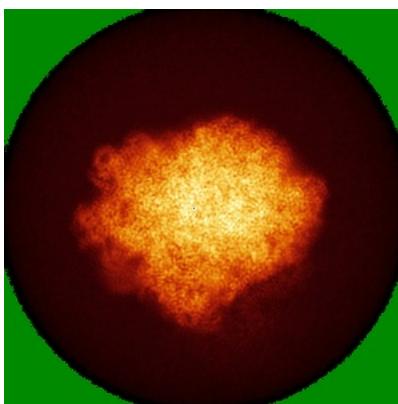
The images above show the largest variance slices of the map in three orthogonal directions.

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

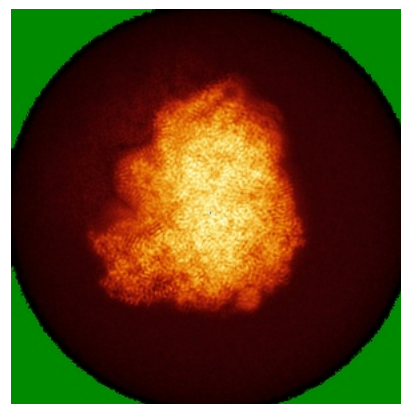
6.4.1 Primary map



X

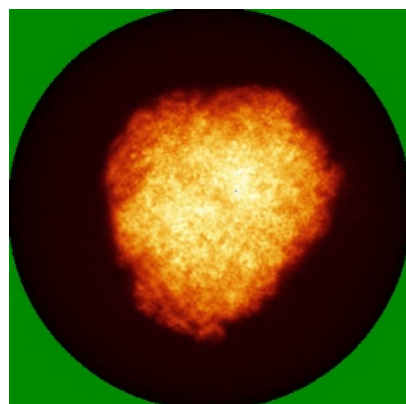


Y

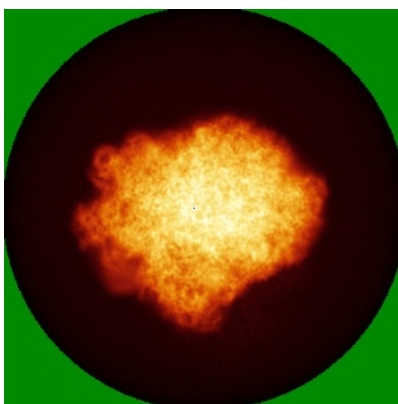


Z

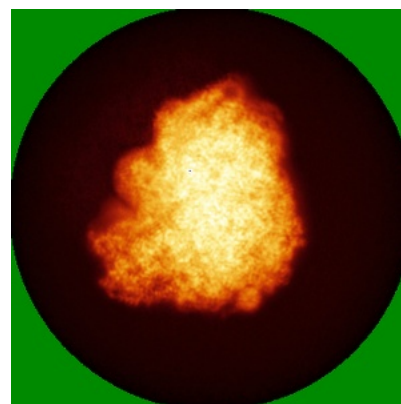
6.4.2 Raw map



X



Y

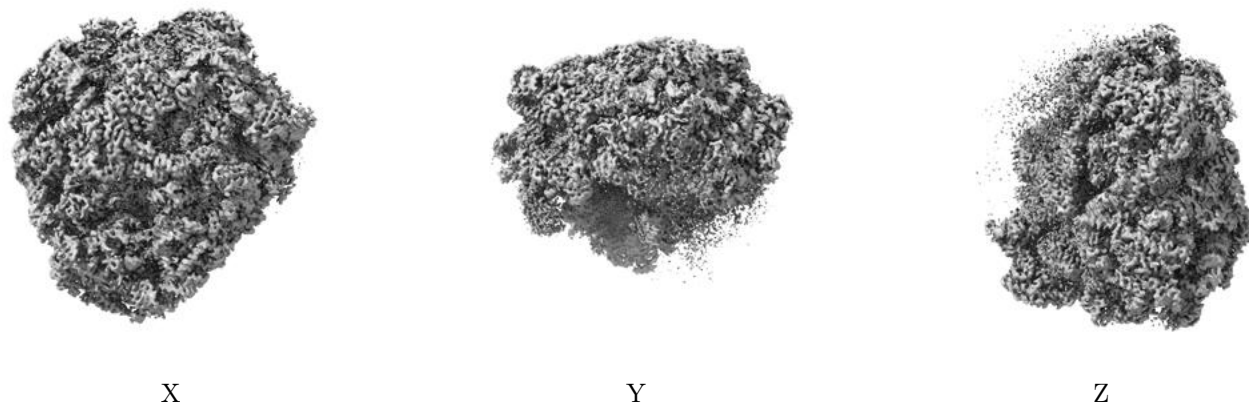


Z

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

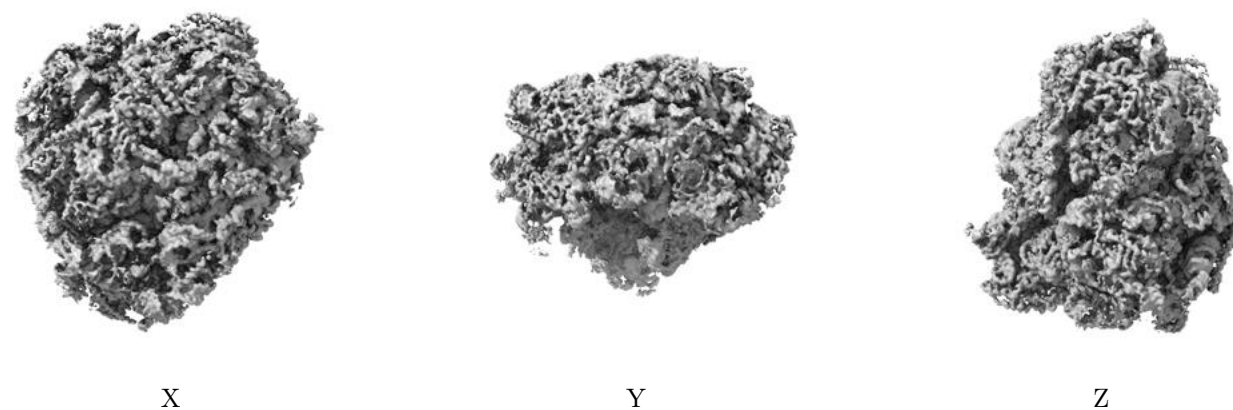
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

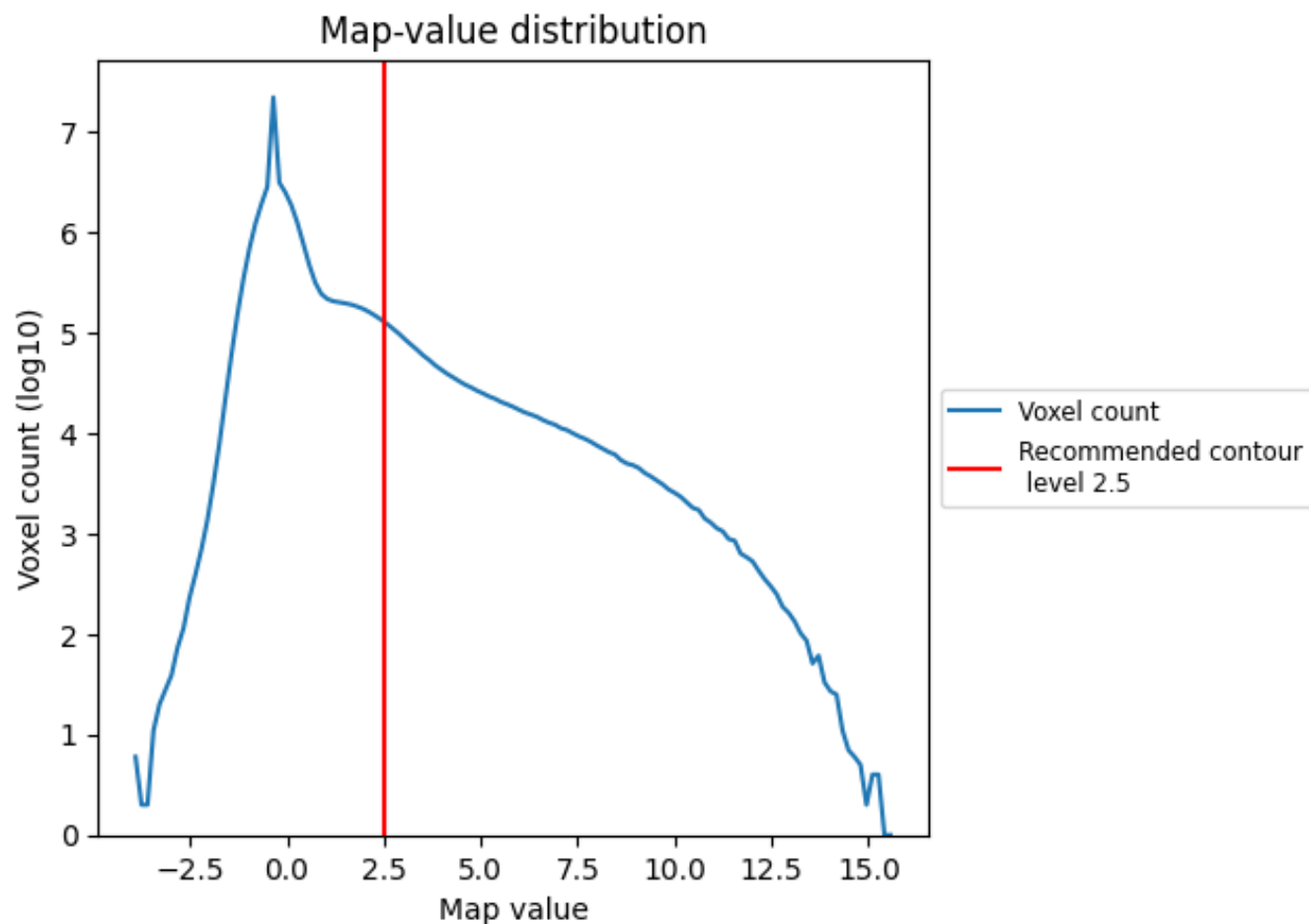
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

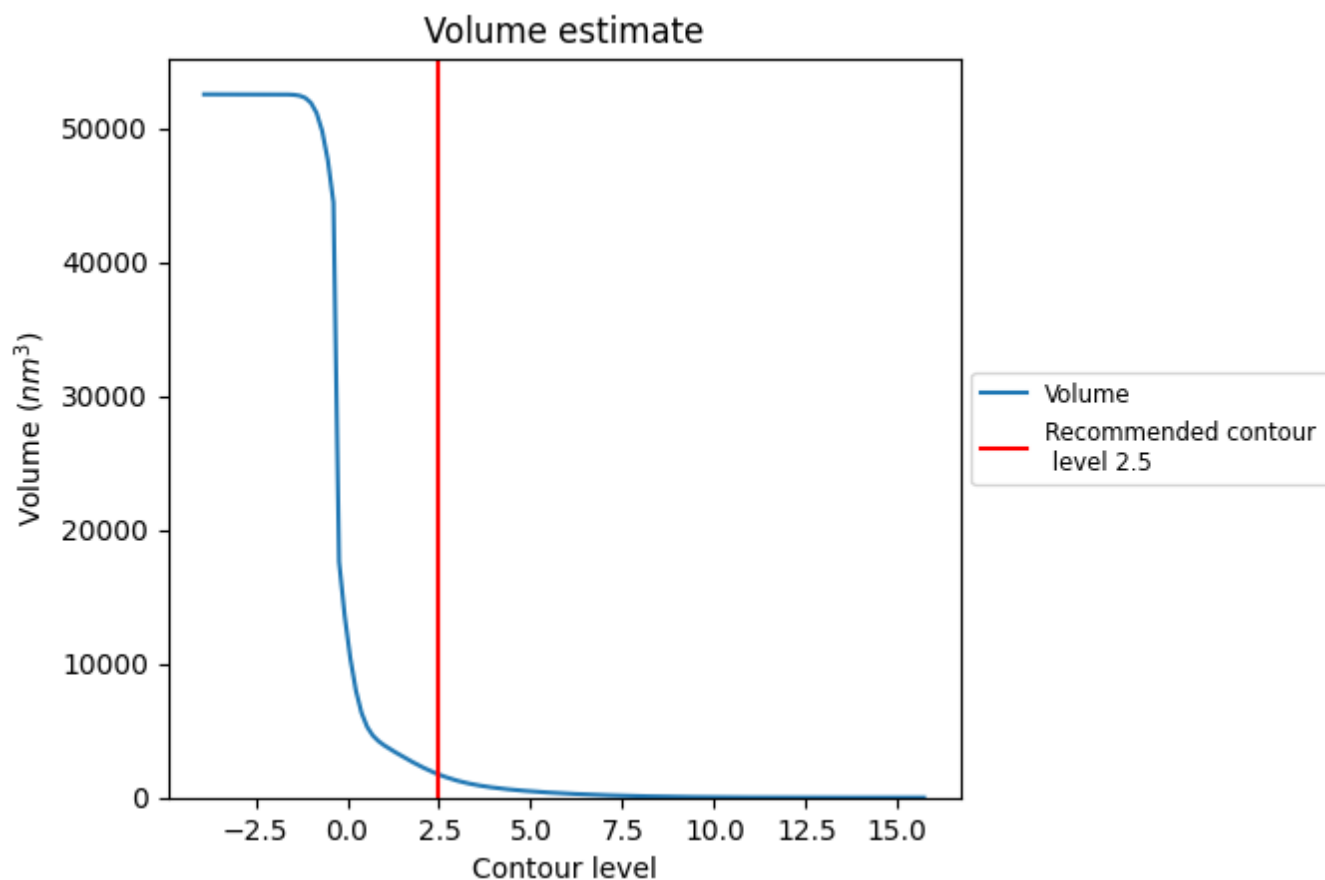
This section contains the results of statistical analysis of the map.

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.

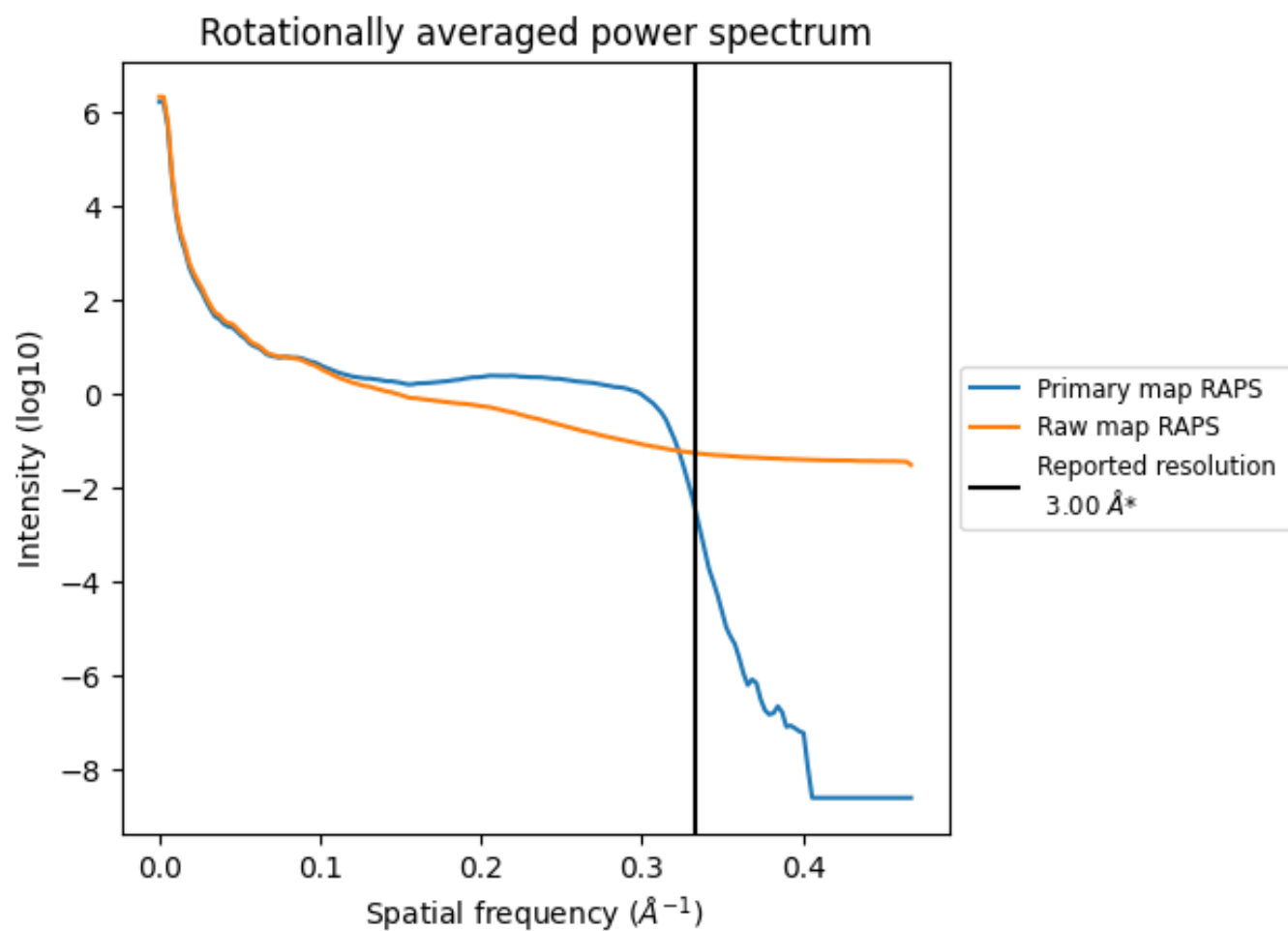
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1716 nm^3 ; this corresponds to an approximate mass of 1550 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 ⓘ

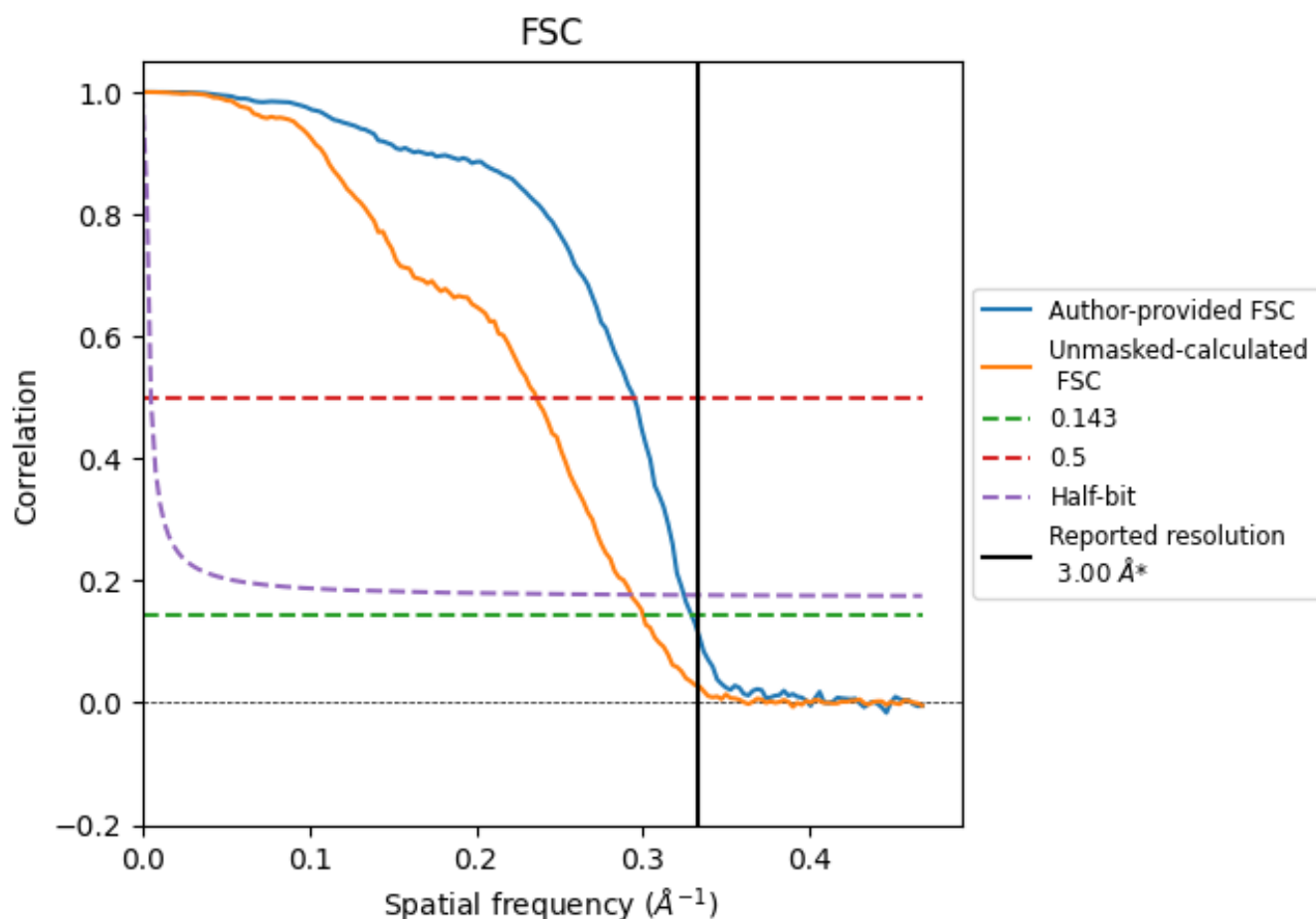


*Reported resolution corresponds to spatial frequency of 0.333 \AA^{-1}

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.333 \AA^{-1}

8.2 Resolution estimates [i](#)

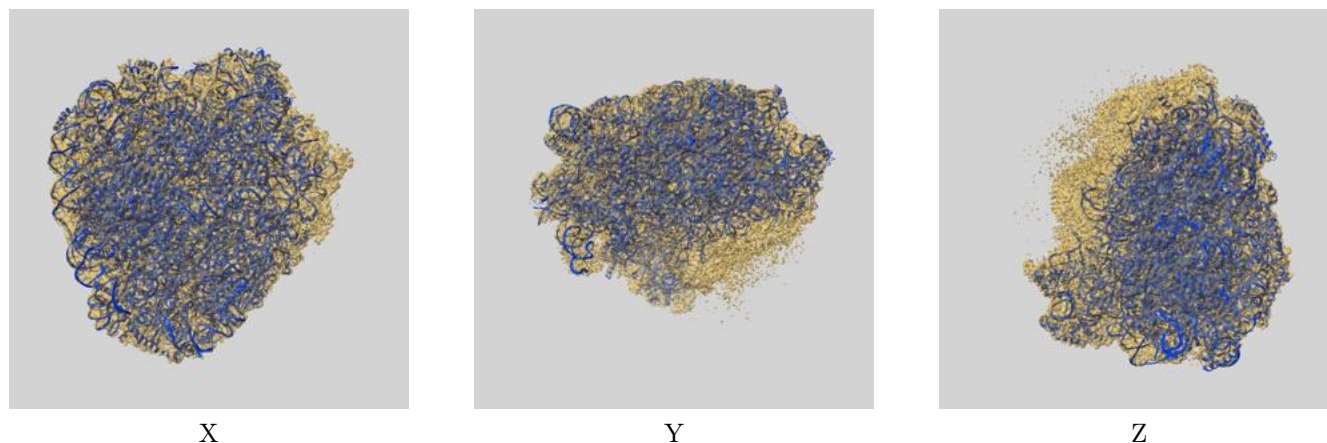
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.04	3.39	3.08
Unmasked-calculated*	3.33	4.24	3.41

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.33 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

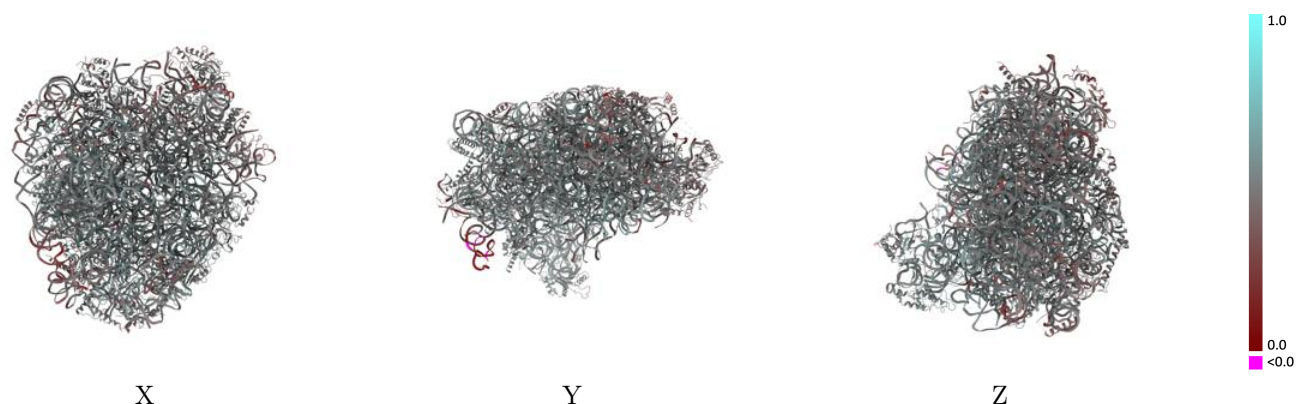
This section contains information regarding the fit between EMDB map EMD-64697 and PDB model 9V1L. Per-residue inclusion information can be found in section [3](#) on page [12](#).

9.1 Map-model overlay [i](#)



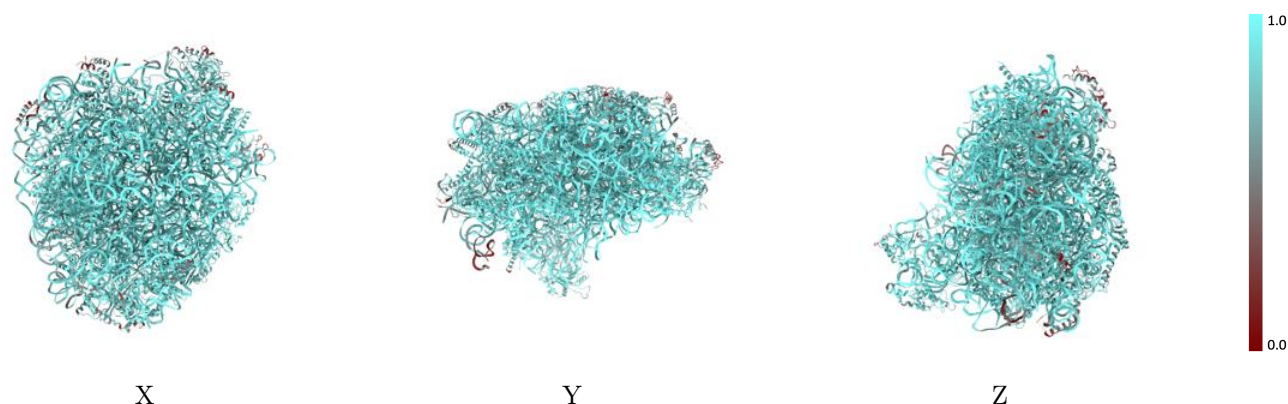
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



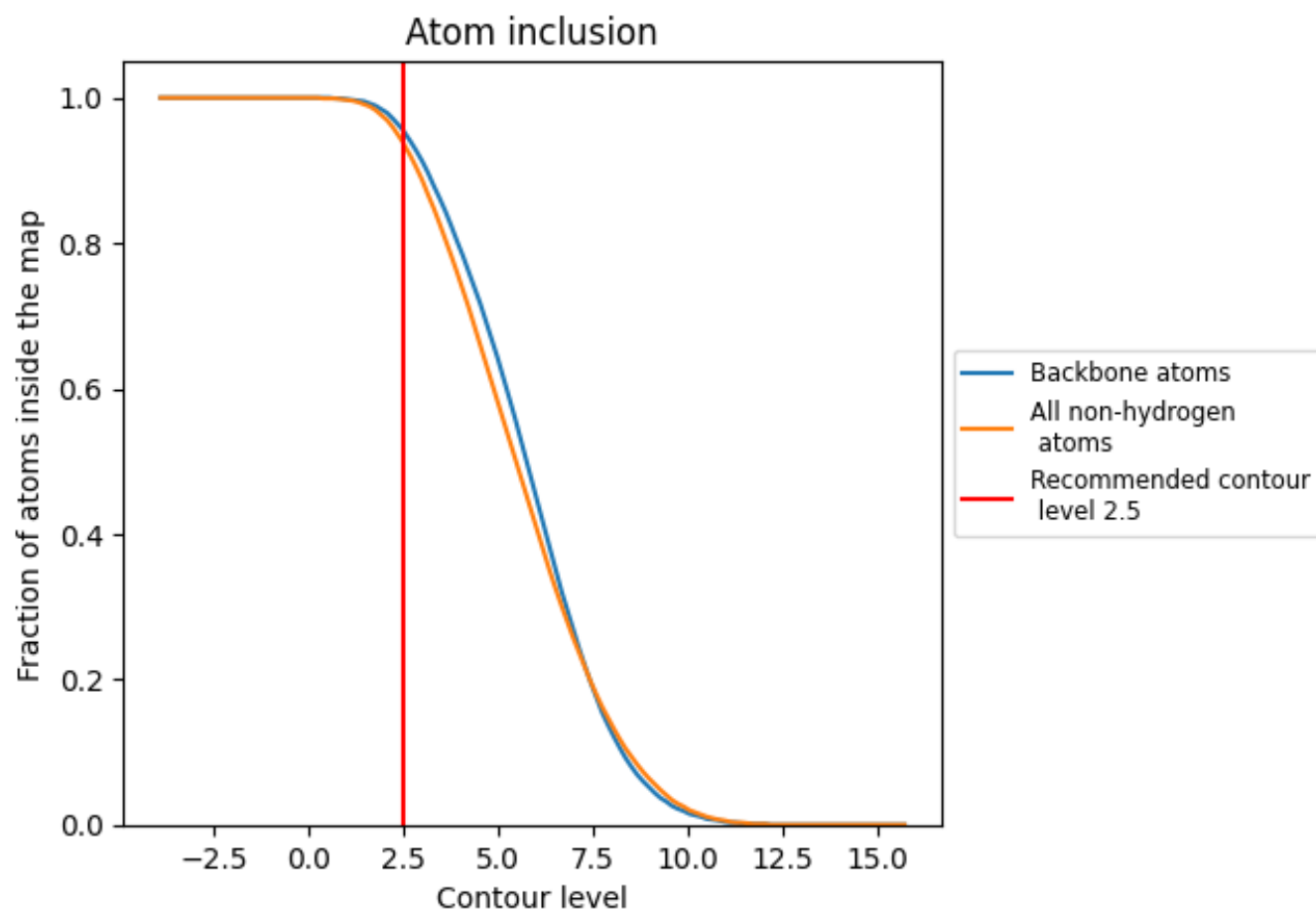
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2.5).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 96% of all backbone atoms, 94% 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 (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9380	 0.4920
1A	 0.9590	 0.4890
1B	 0.9780	 0.4930
1C	 0.9830	 0.5010
1D	 0.9840	 0.5000
1E	 0.9370	 0.5030
1F	 0.8990	 0.5110
1G	 0.8770	 0.5210
1H	 0.7640	 0.4840
1I	 0.9510	 0.5280
1J	 0.7680	 0.4580
1K	 0.8630	 0.4920
1L	 0.9760	 0.5150
1M	 0.8820	 0.4780
1N	 0.8330	 0.4800
1O	 0.9260	 0.5150
1P	 0.9140	 0.5170
1Q	 0.9760	 0.5140
1R	 0.9540	 0.4970
1S	 0.9710	 0.5280
1T	 0.9680	 0.5330
1U	 0.9350	 0.4650
1V	 0.9470	 0.5320
1W	 0.5710	 0.3520
1X	 0.9790	 0.4990
1Y	 0.8780	 0.4570
1Z	 0.9680	 0.4910
1a	 0.8670	 0.4790
1b	 0.6920	 0.4270
1c	 0.9580	 0.5330
1d	 0.9700	 0.5280
1e	 0.8600	 0.4520
1f	 0.8670	 0.4710
1g	 0.9180	 0.4980
1h	 0.9360	 0.4720



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Chain	Atom inclusion	Q-score
li	 0.8600	 0.4650
lj	 0.9670	 0.5280
lk	 0.9100	 0.4930
ll	 0.9960	 0.5130
lm	 0.9710	 0.4830
ln	 0.6540	 0.4030
lo	 0.9880	 0.4980
lp	 0.9360	 0.4960
lq	 0.9720	 0.5270
ls	 1.0000	 0.4720
sH	 0.9970	 0.4560