



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 10:15 PM UTC

PDB ID : 9V25 / pdb_00009v25
EMDB ID : EMD-64717
Title : Cryo- EM structure of large subunit (LSU) of 75S ribosome with A/P- & P/E-tRNAs from Entamoeba histolytica
Authors : Sharma, S.; Mishra, S.; Gourinath, S.; Kaushal, P.S.
Deposited on : 2025-05-19
Resolution : 3.00 Å(reported)
Based on initial model : .

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

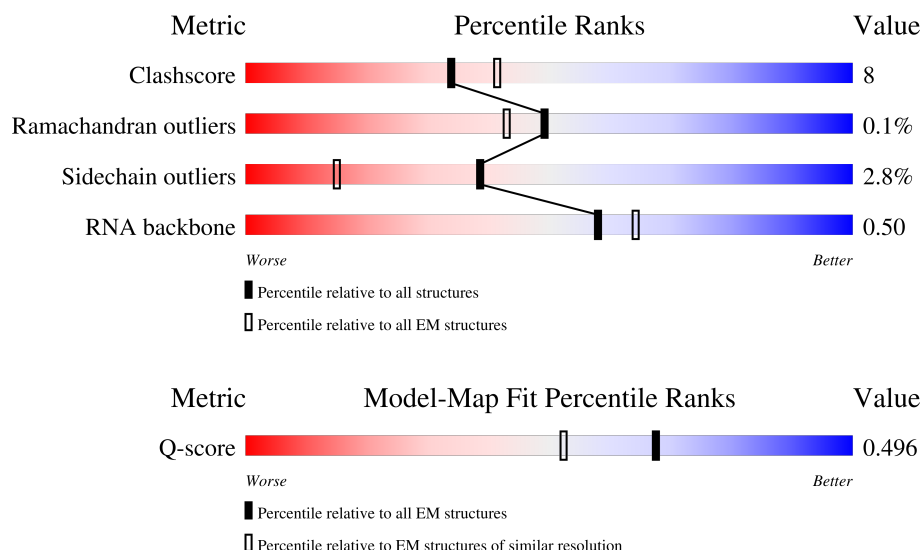
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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.



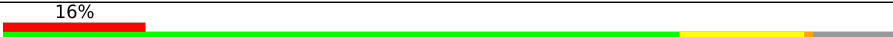
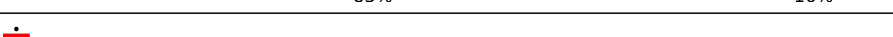
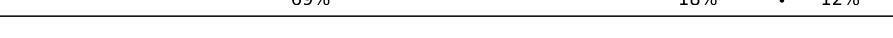
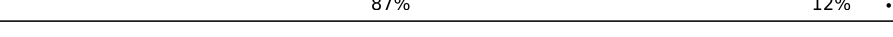
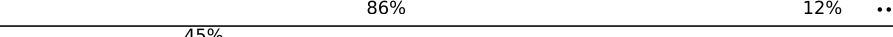
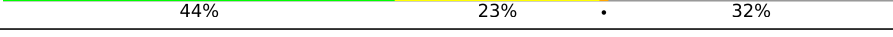
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	

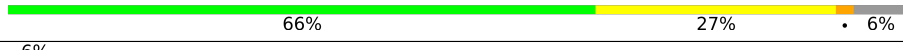
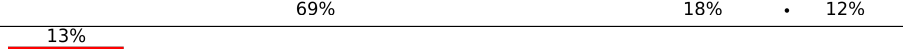
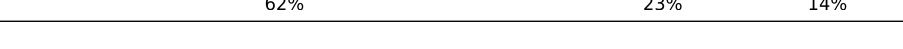
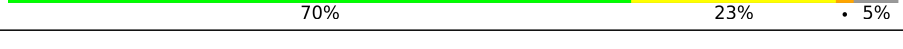
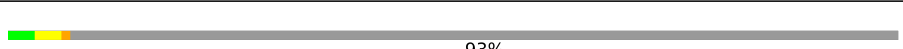
Continued on next page...

Continued from previous page...

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	286	
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	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	lc	149	
30	ld	64	
31	le	109	
32	lf	150	
33	lg	134	
34	lh	137	
35	li	122	
36	lj	108	
37	lk	104	
38	ll	77	
39	lm	93	
40	ln	77	
41	lo	51	
42	lp	56	
43	lq	98	
44	sH	6	
45	sI	76	
46	sJ	77	

2 Entry composition

There are 46 unique types of molecules in this entry. The entry contains 123062 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	lA	3140	Total	C	N	O	P	0	0
			67107	30085	12178	21704	3140		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	lB	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	lC	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	lD	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	lE	388	Total	C	N	O	S	0	0
			3085	1961	579	530	15		

- Molecule 6 is a protein called 60S ribosomal protein L4, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	lF	419	Total	C	N	O	S	0	0
			3229	2055	614	546	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
			2227	1424	401	394	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	lH	203	Total	C	N	O	S	0	0
			1608	1054	272	278	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	198	Total	C	N	O	S	0	0
			1606	1038	291	272	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	201	Total	C	N	O	S	0	0
			1608	1023	306	265	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	265	Total	C	N	O	S	0	0
			2104	1341	407	348	8		

- 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	158	Total	C	N	O	S	0	0
			1232	779	238	210	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	93	Total	C	N	O	S	0	0
			763	493	132	133	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	96	Total	C	N	O	S	0	0
			716	454	121	139	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	lf	124	Total	C	N	O	S	0	0
			1015	655	187	167	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 Unknown peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	sH	2	Total	C	N	O	0	0
			9	6	2	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
45	sI	5	Total	C	N	O	P	0	0
			104	47	19	33	5		

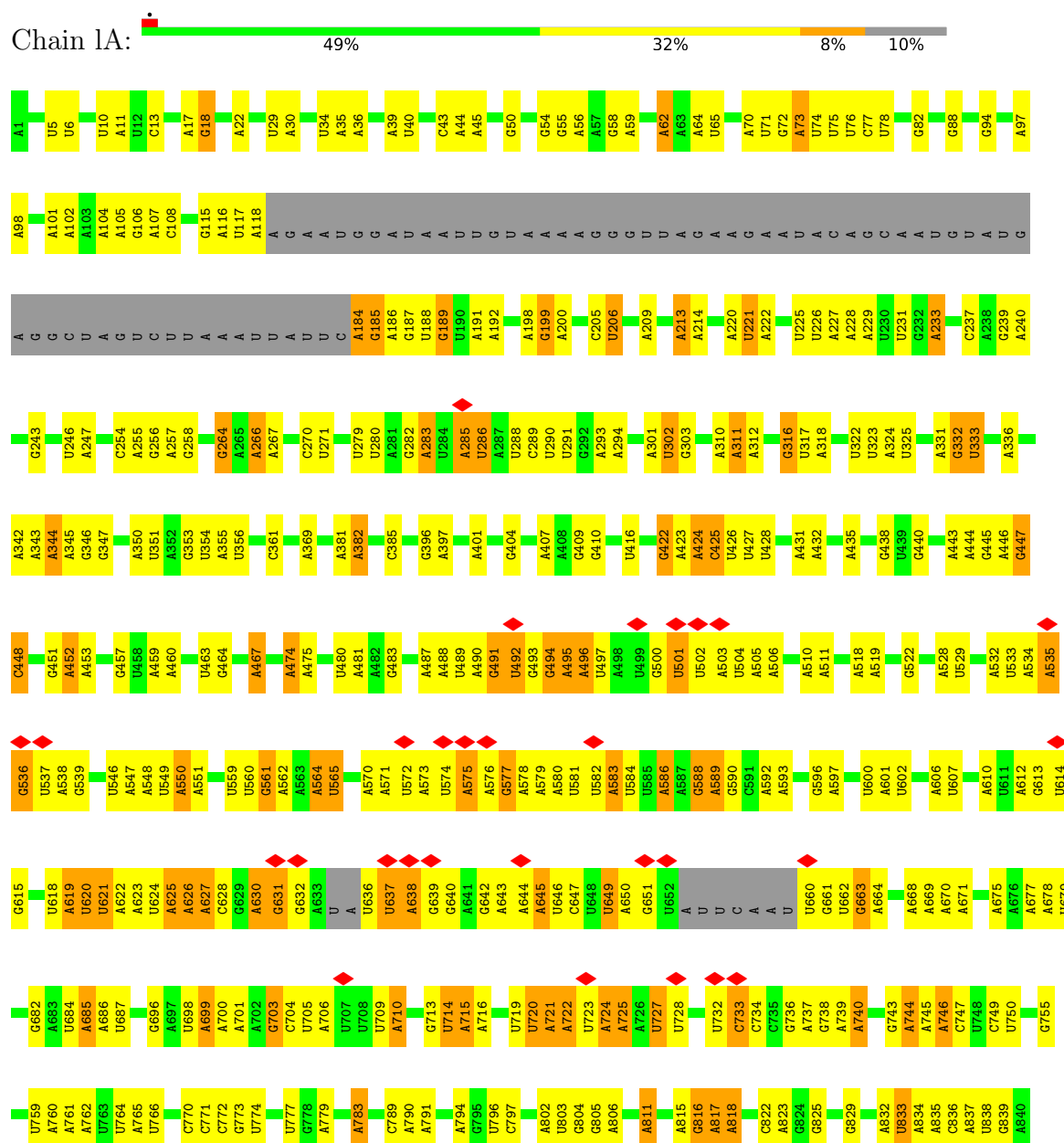
- Molecule 46 is a RNA chain called P/E- tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	sJ	16	Total	C	N	O	P	0	0
			339	152	61	110	16		

3 Residue-property plots

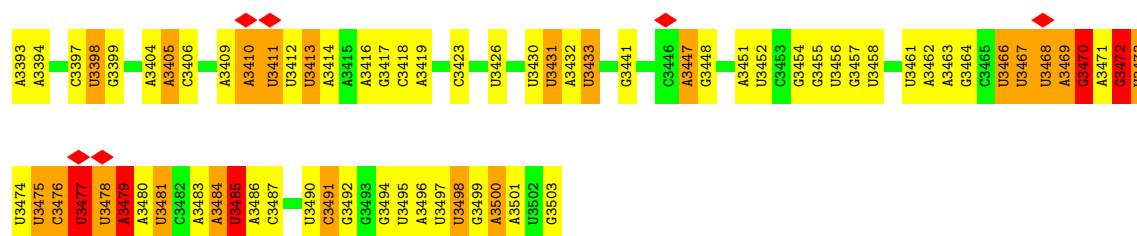
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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



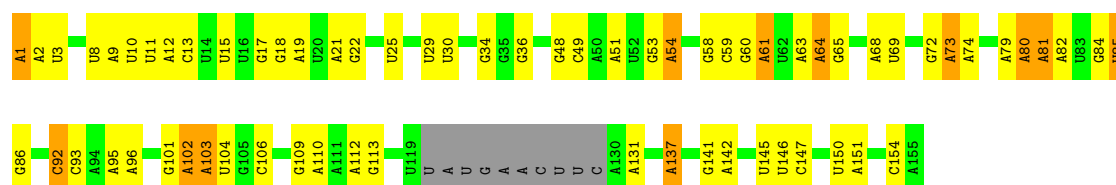


U3313	G3207	C3106	C2995	U2905	C2835	G2740	A	C	U2511	A2432	G2325	A2220	A2128
U3314	A3208	G3107	U3004	U2906	A2839	A2744	A	U	G2512	A2433	G2329	A2224	G2129
U3315	U3209	A3110	U3005	C2907	U2908	A2745	C	G	A2513	A2434	U2330	A2225	C2130
A3322	A3211	A3114	U3008	A2909	U2843	G2747	U	A	A2514	C2439	A2332	U2230	A2131
C3323	U3212	U3117	C3009	U2911	U2845	A2749	C	A	U2515	A2440	G2333	C2231	A2132
U3326	U3213	G3126	C3013	U2912	U2846	A2750		A	C	U2441	U2334	U2232	G2142
A3327	U3218	G3127	A3015	U2915	A2847	C2753		U	G	U2442	A2335	U2233	C2143
A3328	A3219	G3128	A3016	C2916	A2848	U2754		A	A	A2443	U2336	U2234	U2150
U3329	U3220	G3129	A3017	U2919	U2849	U2755		C	U	A2444	U2337	U2235	G2150
A3330	G3223	C3126	U3023	U2920	A2850	U2756		U	U	G2445	A2338	A2236	
C3331	C3227	C3127	C3024	A2921	A2851	G2757		U	U	G2446	C2339	A2237	U2153
A3332	A3227	G3128	U3025	A2925	G2855	U2758		U	U	A2449	U2340	A2238	U
A3333	A3228	U3129	U3026	U2926	G2856	U2759		U	U	C2450	C2341	U2239	C
U3334	G3232	G3133	C3027	U2929	A2857	A2760		G	C	U2451	U2342	U2240	C
U3335	G3232	G3134	U3028	C2931	U2858	A2761		U	U	G2452	U2343	U2241	U
A3336	G3232	U3135	A3030	C2932	U2859	A2762		A	A	U2453	U2344	U2242	U
A3337	G3232	G3136	U3031	U2937	U2860	U2763		U	U	G2454	U2345	A2245	G
A3338	A3245	U3140	C3032	U2938	A2861	A2764		U	U	U2456	A2346	G2246	U
U3344	C3243	G3141	C3033	U2939	A2862	A2765		A	A	G2457	A2347	U2251	A
A3345	A3245	U3142	U3034	G2940	A2863	A2766		G	C	U2458	U2348	U2252	A
G3349	A3245	U3143	A3034	U2941	A2864	G2768		C	C	G2459	G2352	A2254	A
U3350	C3247	U3144	C3038	A2942	A2865	A2774		U	U	U2460	A2355	G2257	G
U3351	A3248	U3145	A3039	U2943	C2866	A2775		A	A	U2461	A2356	G2257	A
G3352	U3254	U3146	U3040	A2944	A2867	A2776		G	G	G2462	U2357	G2261	U
U3353	U3254	U3147	G3041	U2945	U2868	U2781		U	U	U2463	A2358	U2262	U
A3354	A3260	A3151	G3044	A2946	A2869	U2782		G	G	A2473	C2360	G2263	A
U3355	A3261	A3152	U3047	U2951	U2870	G2784		A	A	U2474	U2374	A2264	A
U3356	C3265	U3153	U3048	C2952	G2873	U2791		U	U	A2475	U2269	U2270	A2173
A3358	U3266	U3154	U3066	U2953	U2874	G2792		G	A	G2476	G2271	G2270	U2174
U3359	G3267	U3155	U3067	C2954	U2875	U2793		G	A	U2477	G2381	U2271	C2175
U3360	A3268	G3159	C3068	A2955	U2876	A2797		U	C	C2481	G2382	A2274	A2178
A3361	U3276	U3160	A3069	C2956	U2877	G2798		U	U	U2482	G2383	U2281	U2179
U3364	C3277	A3165	C3070	G2957	A2878	U2799		U	U	U2483	A2385	U2282	A2183
U3365	A3278	G3166	U3073	U2958	U2879	C2805		C	G	U2484	U2386	U2283	A2184
G3366	G3284	G3167	U3074	A2959	C2880	G2815		U	U	G2485	G2387	U2284	A2190
U3367	A3285	A3168	U3078	U2960	U2884	A2816		C	C	U2486	A2388	U2285	G2193
U3368	A3286	C3170	A3079	U2961	G2887	A2817		A	A	U2487	G2389	U2286	G2197
U3369	U3287	G3176	A3083	C2977	U2888	U2818		C	C	G2488	A2390	U2287	A2198
U3370	U3288	U3177	A3084	C2978	A2889	G2819		U	U	U2489	U2391	U2288	A2199
U3371	G3299	A3178	C3085	U2981	G2890	A2820		A	A	G2490	G2392	A2289	A2190
U3372	U3302	G3185	G3090	C2982	A2893	U2822		C	C	U2491	A2393	A2290	G2193
C3374	A3303	U3194	C3091	C2983	C2894	G2823		U	G	G2492	C2394	G2291	G2197
U3375	C3304	G3195	U3096	U2984	G2895	U2824		U	U	U2493	A2395	A2292	A2198
G3376	U3305	U3196	U3097	C2985	U2896	C2825		A	A	U2494	C2396	A2293	A2207
A3380	U3306	C3197	U3098	A2988	U2897	A2826		A	A	A2500	U2410	A2294	G2210
A3381	U3307	U3198	U3099	U2989	U2898	U2827		U	U	U2501	G2411	A2295	U2213
A3382	A3308	G3199	U3100	A2990	U2899	A2828		A	A	U2502	U2412	A2296	A2214
A3383	U3309	C3199	C3103	C2991	G2899	C2829		C	C	U2503	C2413	A2297	A2215
A3384	C3310	U3199	G3104	C2992	U2901	G2730		C	C	A2504	C2414	A2298	A2216
G3385	U3311	G3200	U3105	A2994	A2902	G2731		A	A	U2505	C2415	A2299	U2217
G3392	U3312				A2903	A2732		C	C	C2507	U2416	A2300	A2218
						A2733		A	A	U2508	A2417	A2301	A2219
						U2739		C	A	U2509	U2418	U2318	



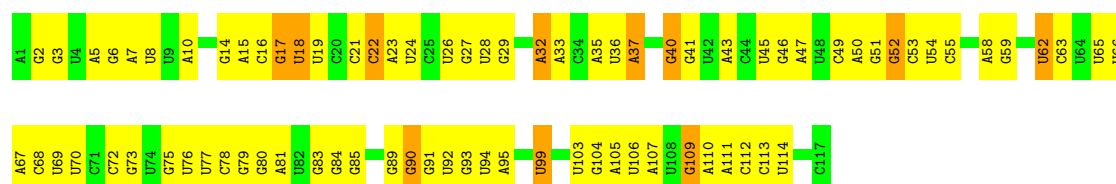
• Molecule 2: 5.8S rRNA

Chain IB: 50% 35% 8% 6%



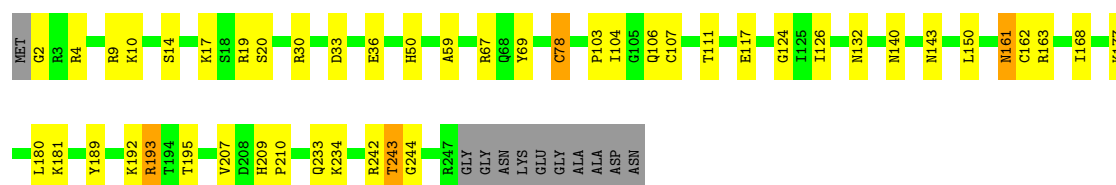
• Molecule 3: 5S rRNA

Chain IC: 32% 59% 9%



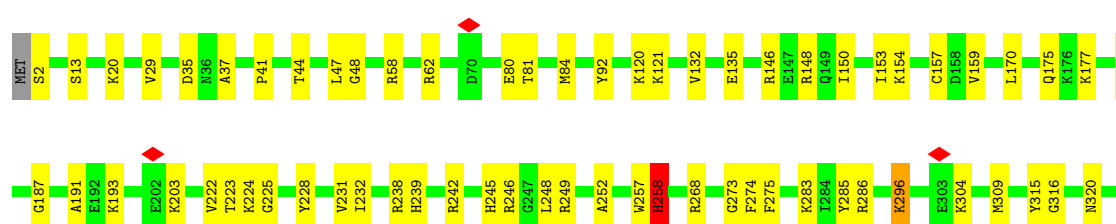
• Molecule 4: Large ribosomal subunit protein uL2

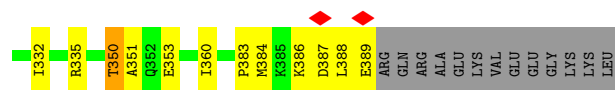
Chain ID: 77% 17%



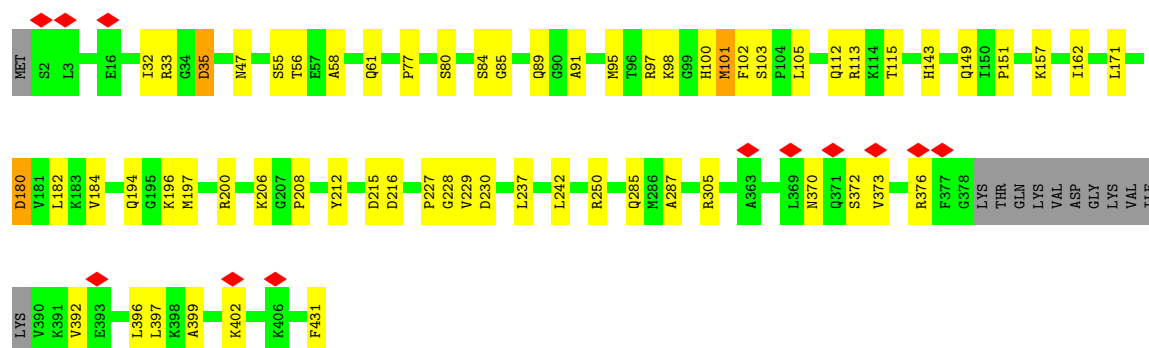
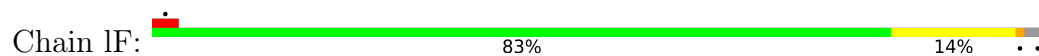
• Molecule 5: 60S ribosomal protein L3, putative

Chain IE: 77% 19%

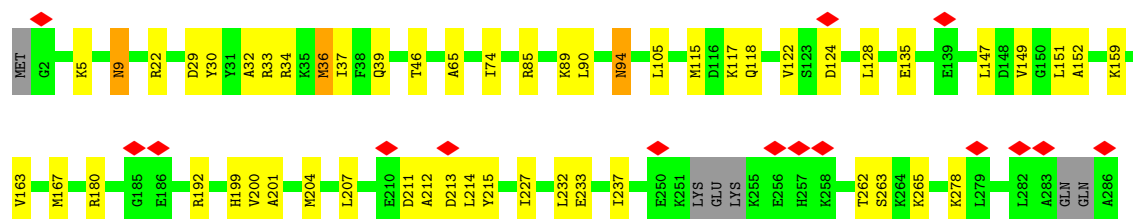
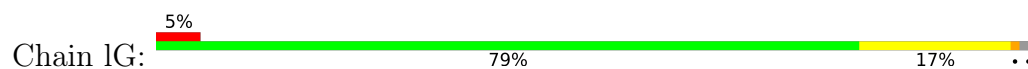




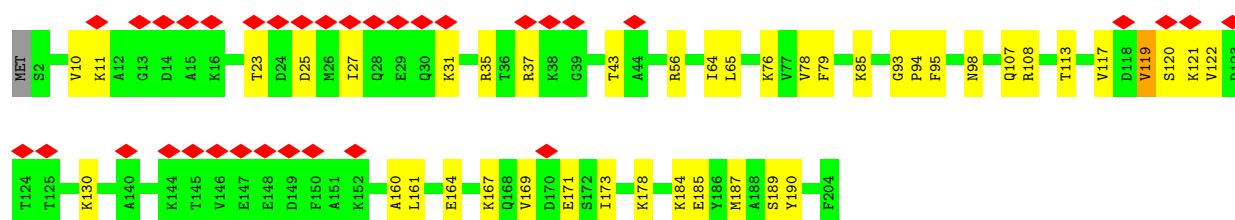
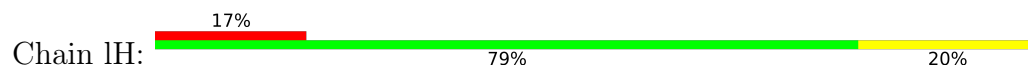
- Molecule 6: 60S ribosomal protein L4, putative



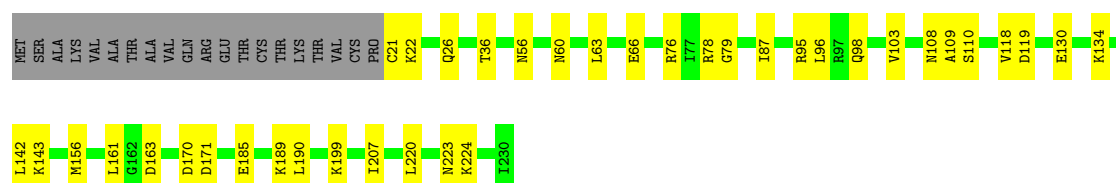
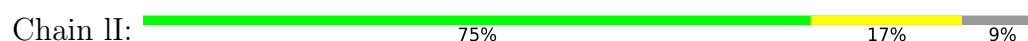
- Molecule 7: 60S ribosomal protein L5, putative



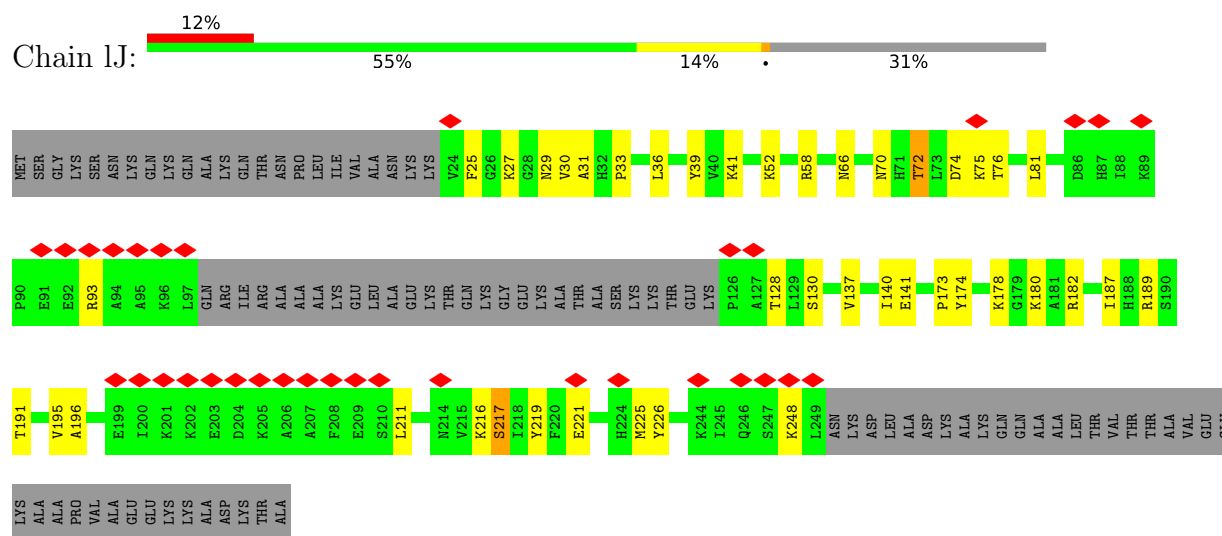
- Molecule 8: Large ribosomal subunit protein eL6



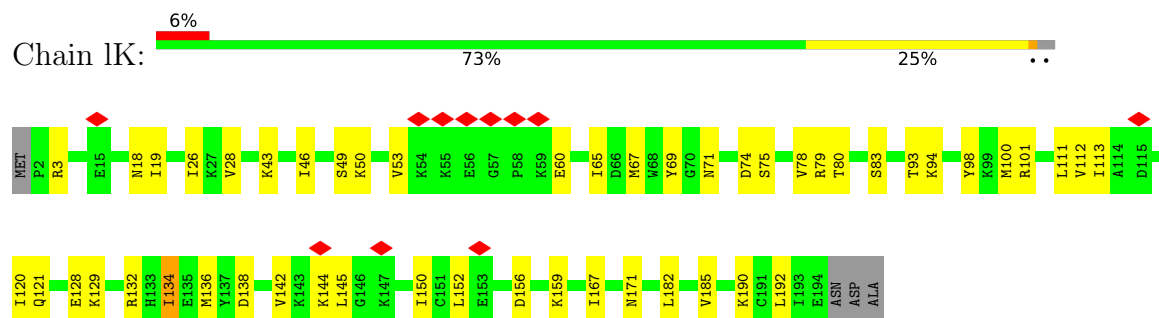
- Molecule 9: 60S ribosomal protein L7, putative



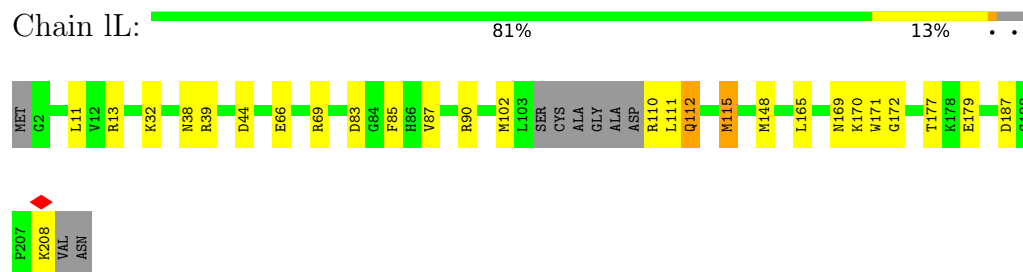
- Chain 1J:



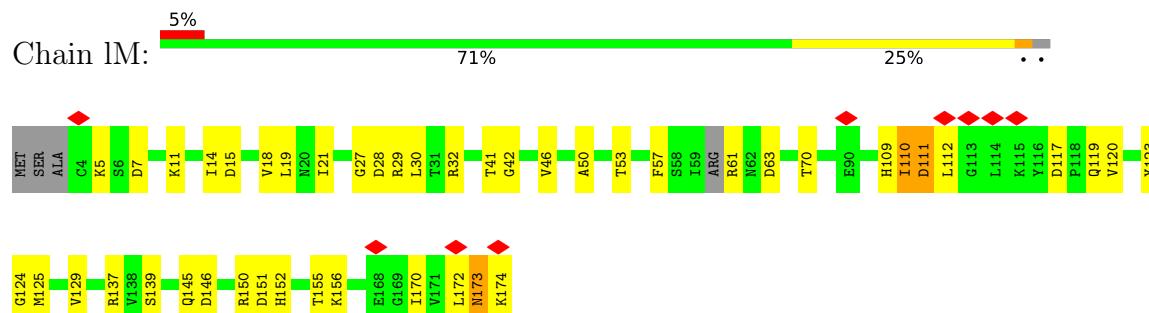
- Chain 1K:



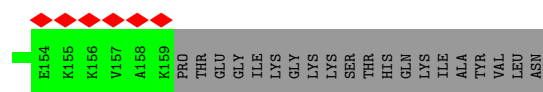
- Chain 1L:



- Chain 1M:



- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|----|----|----|----|----|--|-----|--|-----|-----|-----|-----|-----|--|-----|-----|-----|--|-----|--|-----|--|-----|--|-----|--|-----|-----|-----|-----|-----|--|-----|-----|--|-----|--|-----|-----|--|-----|--|-----|--|------|--|------|------|------|------|------|--|------|--|------|--|------|------|------|--|------|--|------|
| Met | V2 | K3 | K3 | Y4 | C5 | | K13 | | Q16 | A17 | R18 | G19 | D20 | | K27 | N28 | T29 | | D34 | | R37 | | V41 | | N60 | | I63 | K64 | K65 | E66 | I67 | | F60 | R61 | | N64 | | K70 | A71 | | Q72 | | R82 | | D100 | | S124 | S125 | R126 | R127 | R128 | | R131 | | F139 | | I146 | E147 | L148 | | I149 | | I150 |
|-----|----|----|----|----|----|--|-----|--|-----|-----|-----|-----|-----|--|-----|-----|-----|--|-----|--|-----|--|-----|--|-----|--|-----|-----|-----|-----|-----|--|-----|-----|--|-----|--|-----|-----|--|-----|--|-----|--|------|--|------|------|------|------|------|--|------|--|------|--|------|------|------|--|------|--|------|



- Molecule 19: 60S ribosomal protein L18, putative

Chain IS: 87% 12%



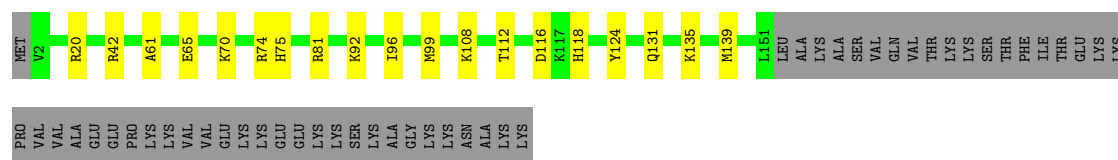
- Molecule 20: 60S ribosomal protein L18a

Chain IT: 87% 12%



- Molecule 21: Ribosomal protein L19

Chain IU: 66% 10% 24%



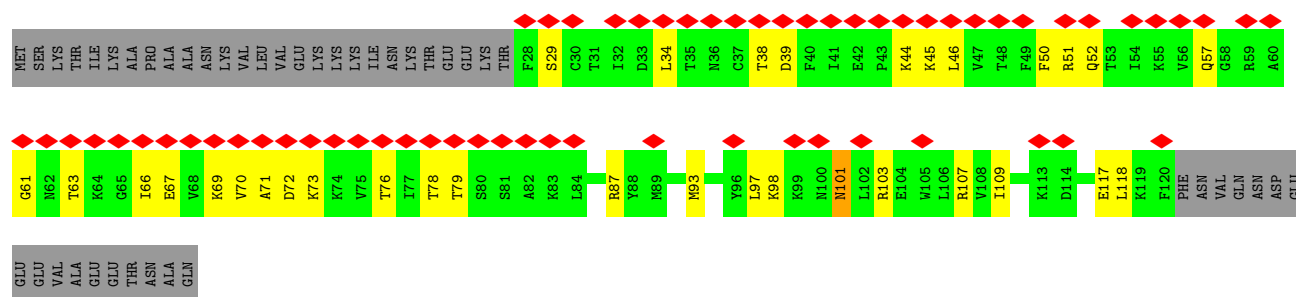
- Molecule 22: 60S ribosomal protein L21, putative

Chain IV: 86% 12%



- Molecule 23: Large ribosomal subunit protein eL22

Chain IW: 45% 44% 23% 32%



- Molecule 24: 60S ribosomal protein L23, putative

Chain IX: 



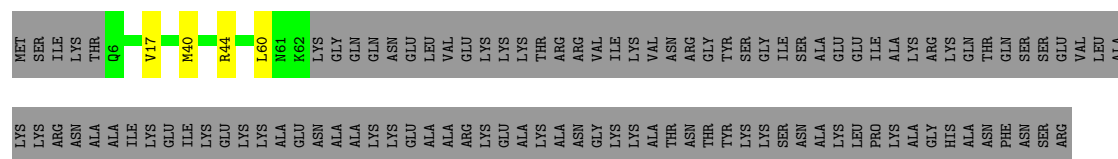
- Molecule 25: Ribosomal protein L23A, putative

Chain IY: 



- Molecule 26: 60S ribosomal protein L24, putative

Chain IZ: 



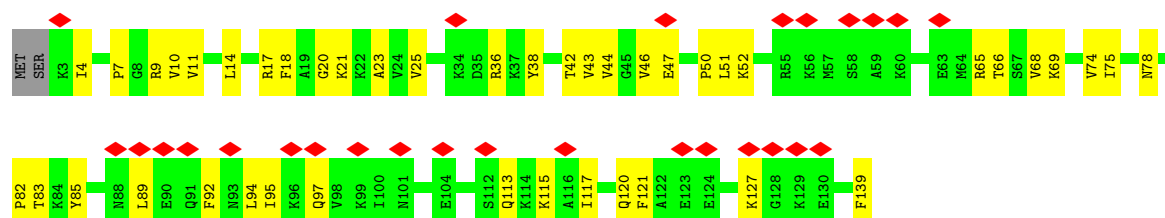
- Molecule 27: 60S ribosomal protein L26, putative

Chain Ia: 



- Molecule 28: 60S ribosomal protein L27, putative

Chain Ib: 

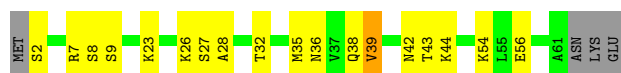


- Molecule 29: Large ribosomal subunit protein uL15A

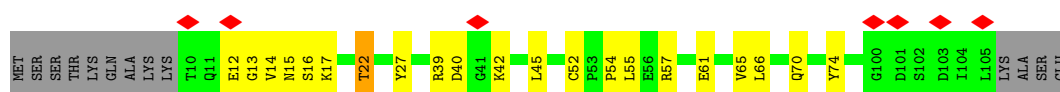
Chain Ic: 



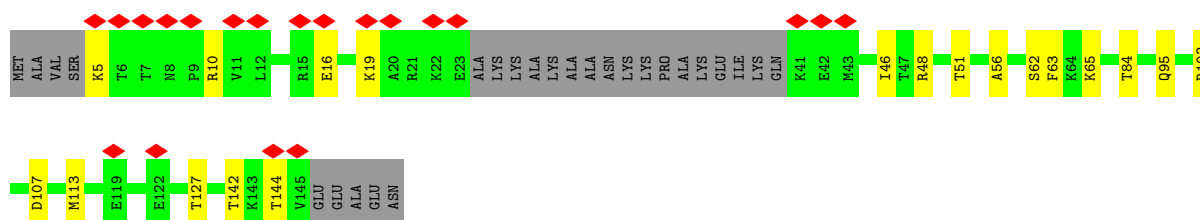
- Molecule 30: 60S ribosomal protein L29



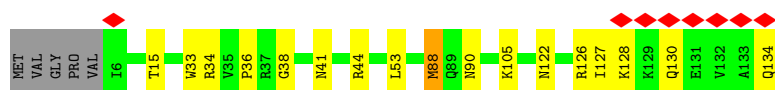
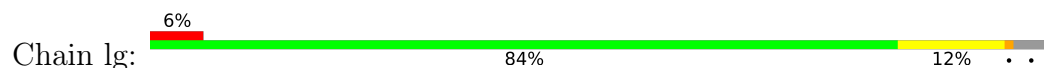
- Molecule 31: 60S ribosomal protein L30, putative



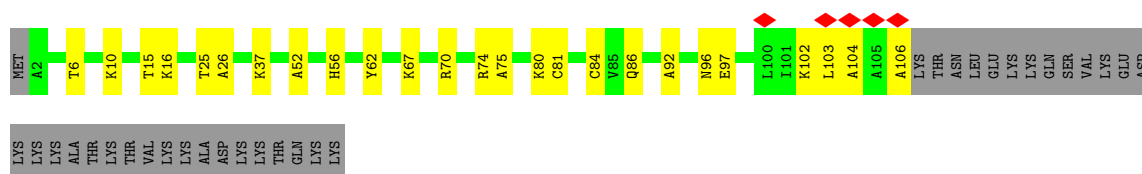
- Molecule 32: 60S ribosomal protein L31, putative



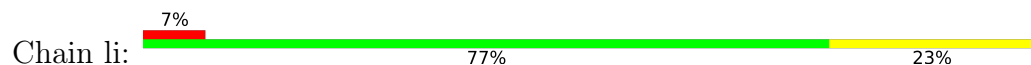
- Molecule 33: 60S ribosomal protein L32, putative



- Molecule 34: 60S ribosomal protein L34, putative

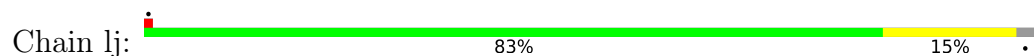


- Molecule 35: uL29





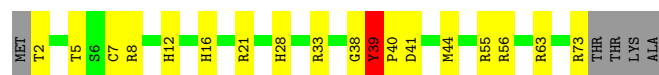
- Molecule 36: 60S ribosomal protein L35a, putative



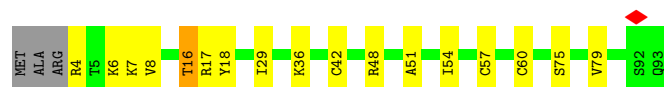
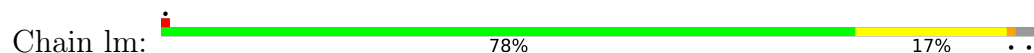
- Molecule 37: 60S ribosomal protein L36, putative



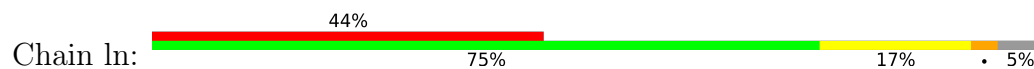
- Molecule 38: 60S ribosomal protein L37-A, putative



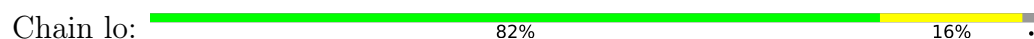
- Molecule 39: 60S ribosomal protein L37a, putative



- Molecule 40: 60S ribosomal protein L38 putative



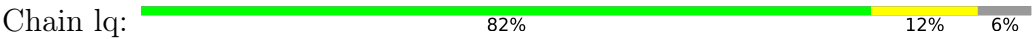
- Molecule 41: Ribosomal protein L39, putative



- Molecule 42: 60S ribosomal protein L40, putative



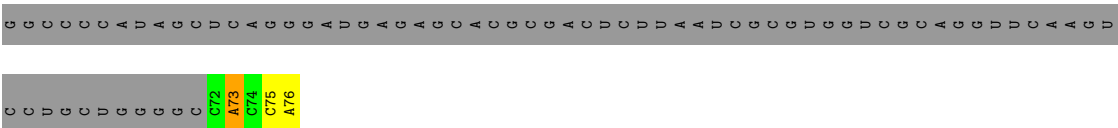
• Molecule 43: 60S ribosomal protein L44, putative



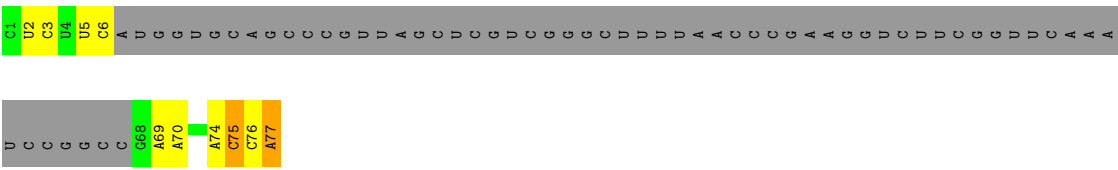
• Molecule 44: Unknown peptide



• Molecule 45: A/P- tRNA



• Molecule 46: P/E- tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	39958	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	16.259	Depositor
Minimum map value	-5.031	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2.8	Depositor
Map size ($\text{\AA}$)	374.50003, 374.50003, 374.50003	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	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	0.26	7/75197 (0.0%)	0.35	23/117139 (0.0%)
2	1B	0.24	1/3470 (0.0%)	0.30	0/5401
3	1C	0.23	0/2765	0.39	2/4303 (0.0%)
4	1D	0.21	0/1920	0.30	0/2582
5	1E	0.19	0/3149	0.28	0/4228
6	1F	0.19	0/3287	0.27	0/4413
7	1G	0.17	0/2265	0.29	0/3032
8	1H	0.15	0/1640	0.28	0/2204
9	1I	0.18	0/1680	0.26	0/2252
10	1J	0.15	0/1636	0.27	0/2199
11	1K	0.16	0/1562	0.24	0/2103
12	1L	0.18	0/1644	0.28	0/2198
13	1M	0.15	0/1369	0.27	0/1834
14	1N	0.17	0/2132	0.25	0/2844
15	1O	0.20	0/1646	0.28	0/2209
16	1P	0.18	0/1032	0.23	0/1388
17	1Q	0.22	0/1707	0.24	0/2276
18	1R	0.20	0/1251	0.26	0/1675
19	1S	0.20	0/1337	0.29	0/1789
20	1T	0.19	0/1445	0.27	0/1946
21	1U	0.17	0/1253	0.22	0/1666
22	1V	0.19	0/1351	0.26	0/1819
23	1W	0.11	0/774	0.31	0/1031
24	1X	0.20	0/1030	0.29	0/1384
25	1Y	0.17	0/941	0.26	0/1262
26	1Z	0.19	0/492	0.23	0/656
27	1a	0.16	0/1673	0.22	0/2236
28	1b	0.17	0/1112	0.28	0/1489
29	1c	0.23	0/1223	0.27	0/1636
30	1d	0.19	0/485	0.24	0/639
31	1e	0.16	0/724	0.26	0/977
32	1f	0.17	0/1034	0.22	0/1382
33	1g	0.20	0/1075	0.25	0/1434
34	1h	0.18	0/833	0.25	0/1115

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	li	0.15	0/984	0.22	0/1310
36	lj	0.22	0/862	0.29	0/1163
37	lk	0.15	0/721	0.22	0/955
38	ll	0.23	0/602	0.31	0/797
39	lm	0.21	0/696	0.35	0/928
40	ln	0.15	0/592	0.25	0/789
41	lo	0.21	0/444	0.23	0/587
42	lp	0.19	0/425	0.48	1/563 (0.2%)
43	lq	0.19	0/770	0.25	0/1019
45	sI	0.16	0/115	0.46	0/176
46	sJ	0.20	0/377	0.32	0/580
All	All	0.23	8/132722 (0.0%)	0.33	26/195608 (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

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	lA	3485	U	O3'-P	-6.57	1.51	1.61
1	lA	2511	U	O3'-P	-6.17	1.51	1.61
1	lA	2905	U	O3'-P	-5.71	1.52	1.61
1	lA	2903	A	O3'-P	-5.57	1.52	1.61
1	lA	2347	A	O3'-P	-5.30	1.53	1.61

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	lA	3473	U	C1'-C2'-O2'	-10.53	92.61	108.40
1	lA	2346	A	C3'-C2'-O2'	-9.46	96.52	110.70
3	lC	62	U	OP2-P-O3'	-8.96	81.13	108.00
1	lA	2902	G	C1'-C2'-O2'	-8.87	95.09	108.40
3	lC	62	U	OP1-P-O3'	-8.68	81.97	108.00

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	67107	0	33663	1017	0
2	lB	3097	0	1552	49	0
3	lC	2477	0	1252	88	0
4	lD	1881	0	1928	36	0
5	lE	3085	0	3215	61	0
6	lF	3229	0	3433	41	0
7	lG	2227	0	2308	34	0
8	lH	1608	0	1728	29	0
9	lI	1658	0	1802	25	0
10	lJ	1606	0	1708	24	0
11	lK	1538	0	1598	33	0
12	lL	1608	0	1667	22	0
13	lM	1350	0	1390	35	0
14	lN	2104	0	2297	38	0
15	lO	1616	0	1700	22	0
16	lP	1020	0	1104	23	0
17	lQ	1676	0	1777	21	0
18	lR	1232	0	1307	24	0
19	lS	1316	0	1420	15	0
20	lT	1413	0	1479	17	0
21	lU	1235	0	1369	13	0
22	lV	1320	0	1406	20	0
23	lW	763	0	818	22	0
24	lX	1015	0	1054	13	0
25	lY	926	0	997	15	0
26	lZ	481	0	518	1	0
27	la	1651	0	1822	24	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	lb	1094	0	1174	31	0
29	lc	1192	0	1205	16	0
30	ld	478	0	507	13	0
31	le	716	0	750	13	0
32	lf	1015	0	1086	10	0
33	lg	1058	0	1140	13	0
34	lh	820	0	864	18	0
35	li	974	0	1093	18	0
36	lj	841	0	878	11	0
37	lk	712	0	755	18	0
38	ll	591	0	617	16	0
39	lm	688	0	726	15	0
40	ln	584	0	643	7	0
41	lo	432	0	444	7	0
42	lp	420	0	450	12	0
43	lq	756	0	821	9	0
44	sH	9	0	4	0	0
45	sI	104	0	56	4	0
46	sJ	339	0	175	4	0
All	All	123062	0	89700	1701	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 1701 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)
1:1A:3139:G:H1'	2:1B:1:A:H2	1.11	1.14
5:1E:383:PRO:CB	5:1E:388:LEU:HD11	1.81	1.09
5:1E:383:PRO:HB2	5:1E:388:LEU:HD11	1.31	1.08
1:1A:3139:G:H1'	2:1B:1:A:C2	1.92	1.05
1:1A:869:G:H21	1:1A:872:A:N6	1.53	1.04

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%)	233 (96%)	11 (4%)	0	100	100
5	IE	386/402 (96%)	372 (96%)	14 (4%)	0	100	100
6	IF	415/431 (96%)	395 (95%)	20 (5%)	0	100	100
7	IG	275/286 (96%)	256 (93%)	19 (7%)	0	100	100
8	IH	201/204 (98%)	185 (92%)	15 (8%)	1 (0%)	24	60
9	II	208/230 (90%)	200 (96%)	8 (4%)	0	100	100
10	IJ	194/286 (68%)	186 (96%)	8 (4%)	0	100	100
11	IK	191/197 (97%)	183 (96%)	7 (4%)	1 (0%)	24	60
12	IL	197/210 (94%)	188 (95%)	9 (5%)	0	100	100
13	IM	166/174 (95%)	157 (95%)	8 (5%)	1 (1%)	21	56
14	IN	259/291 (89%)	248 (96%)	11 (4%)	0	100	100
15	IO	202/205 (98%)	197 (98%)	5 (2%)	0	100	100
16	IP	128/135 (95%)	125 (98%)	3 (2%)	0	100	100
17	IQ	202/205 (98%)	195 (96%)	7 (4%)	0	100	100
18	IR	156/179 (87%)	154 (99%)	2 (1%)	0	100	100
19	IS	165/168 (98%)	154 (93%)	11 (7%)	0	100	100
20	IT	171/173 (99%)	160 (94%)	11 (6%)	0	100	100
21	IU	148/198 (75%)	147 (99%)	1 (1%)	0	100	100
22	IV	163/166 (98%)	158 (97%)	5 (3%)	0	100	100
23	IW	91/137 (66%)	85 (93%)	6 (7%)	0	100	100
24	IX	131/140 (94%)	125 (95%)	6 (5%)	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%)	201 (97%)	7 (3%)	0	100	100
28	lb	135/139 (97%)	132 (98%)	3 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	lc	146/149 (98%)	138 (94%)	8 (6%)	0	100	100
30	ld	58/64 (91%)	55 (95%)	3 (5%)	0	100	100
31	le	94/109 (86%)	88 (94%)	6 (6%)	0	100	100
32	lf	120/150 (80%)	115 (96%)	5 (4%)	0	100	100
33	lg	127/134 (95%)	122 (96%)	5 (4%)	0	100	100
34	lh	103/137 (75%)	97 (94%)	6 (6%)	0	100	100
35	li	120/122 (98%)	117 (98%)	2 (2%)	1 (1%)	16	50
36	lj	104/108 (96%)	99 (95%)	5 (5%)	0	100	100
37	lk	83/104 (80%)	82 (99%)	1 (1%)	0	100	100
38	ll	70/77 (91%)	65 (93%)	3 (4%)	2 (3%)	3	20
39	lm	88/93 (95%)	82 (93%)	6 (7%)	0	100	100
40	ln	71/77 (92%)	69 (97%)	2 (3%)	0	100	100
41	lo	48/51 (94%)	48 (100%)	0	0	100	100
42	lp	51/56 (91%)	49 (96%)	2 (4%)	0	100	100
43	lq	90/98 (92%)	86 (96%)	4 (4%)	0	100	100
All	All	6178/6839 (90%)	5913 (96%)	259 (4%)	6 (0%)	49	80

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
38	ll	40	PRO
35	li	-6	LYS
38	ll	39	TYR
8	lH	119	VAL
11	lK	134	ILE

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%)	190 (97%)	5 (3%)	40	72

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	lE	331/343 (96%)	324 (98%)	7 (2%)	47	75
6	lF	332/345 (96%)	321 (97%)	11 (3%)	33	67
7	lG	225/231 (97%)	215 (96%)	10 (4%)	25	60
8	lH	172/173 (99%)	168 (98%)	4 (2%)	44	74
9	lI	178/195 (91%)	173 (97%)	5 (3%)	38	70
10	lJ	174/242 (72%)	165 (95%)	9 (5%)	21	55
11	lK	171/174 (98%)	164 (96%)	7 (4%)	27	61
12	lL	170/176 (97%)	165 (97%)	5 (3%)	37	70
13	lM	144/147 (98%)	138 (96%)	6 (4%)	26	61
14	lN	220/243 (90%)	217 (99%)	3 (1%)	59	80
15	lO	167/168 (99%)	163 (98%)	4 (2%)	43	73
16	lP	113/118 (96%)	112 (99%)	1 (1%)	70	85
17	lQ	171/172 (99%)	165 (96%)	6 (4%)	32	65
18	lR	129/147 (88%)	126 (98%)	3 (2%)	44	74
19	lS	141/143 (99%)	137 (97%)	4 (3%)	38	70
20	lT	156/156 (100%)	155 (99%)	1 (1%)	78	88
21	lU	132/174 (76%)	132 (100%)	0	100	100
22	lV	144/145 (99%)	140 (97%)	4 (3%)	38	70
23	lW	86/125 (69%)	84 (98%)	2 (2%)	44	74
24	lX	109/113 (96%)	104 (95%)	5 (5%)	24	58
25	lY	99/102 (97%)	94 (95%)	5 (5%)	21	55
26	lZ	52/137 (38%)	50 (96%)	2 (4%)	29	63
27	la	177/179 (99%)	173 (98%)	4 (2%)	44	74
28	lb	121/123 (98%)	119 (98%)	2 (2%)	53	78
29	lc	120/121 (99%)	115 (96%)	5 (4%)	26	61
30	ld	50/54 (93%)	48 (96%)	2 (4%)	28	62
31	le	81/92 (88%)	78 (96%)	3 (4%)	30	64
32	lf	109/128 (85%)	105 (96%)	4 (4%)	30	64
33	lg	112/116 (97%)	109 (97%)	3 (3%)	39	71
34	lh	86/116 (74%)	84 (98%)	2 (2%)	44	74
35	li	103/103 (100%)	102 (99%)	1 (1%)	68	84

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	lj	89/91 (98%)	88 (99%)	1 (1%)	65	83
37	lk	71/82 (87%)	69 (97%)	2 (3%)	38	70
38	ll	60/64 (94%)	60 (100%)	0	100	100
39	lm	72/75 (96%)	70 (97%)	2 (3%)	38	70
40	ln	63/66 (96%)	57 (90%)	6 (10%)	8	31
41	lo	44/45 (98%)	43 (98%)	1 (2%)	44	74
42	lp	45/48 (94%)	45 (100%)	0	100	100
43	lq	85/91 (93%)	84 (99%)	1 (1%)	63	82
All	All	5299/5764 (92%)	5151 (97%)	148 (3%)	38	70

5 of 148 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	lc	8	THR
40	ln	38	ASN
29	lc	148	THR
33	lg	53	LEU
10	lJ	128	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
20	lT	136	HIS
34	lh	98	HIS
22	lV	22	HIS
31	le	11	GLN
37	lk	74	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	lA	3126/3503 (89%)	590 (18%)	0
2	lB	143/155 (92%)	31 (21%)	0
3	lC	116/117 (99%)	19 (16%)	0
45	sI	4/76 (5%)	2 (50%)	0
46	sJ	14/77 (18%)	7 (50%)	0
All	All	3403/3928 (86%)	649 (19%)	0

5 of 649 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	lA	18	G
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.

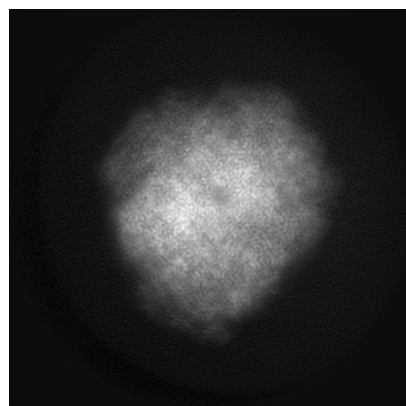
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64717. These allow visual inspection of the internal detail of the map and identification of artifacts.

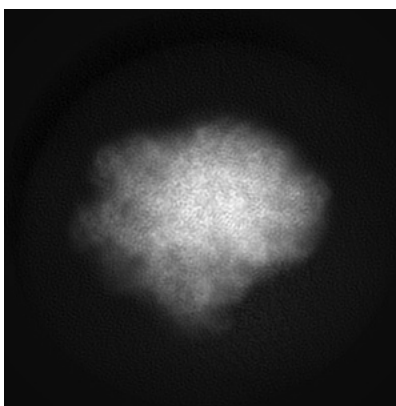
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

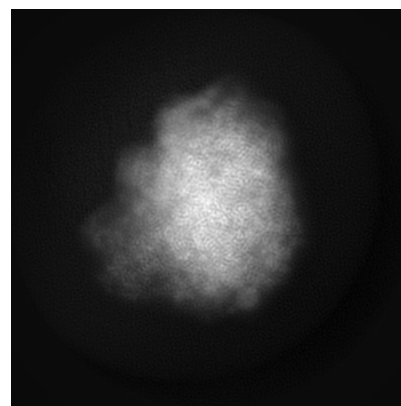
6.1.1 Primary map



X

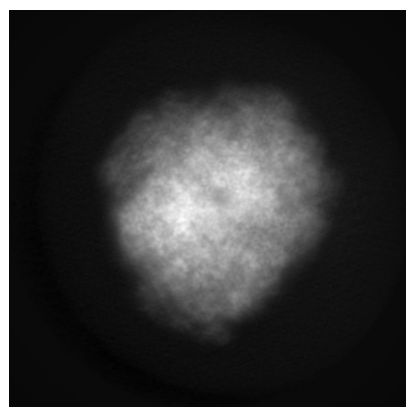


Y

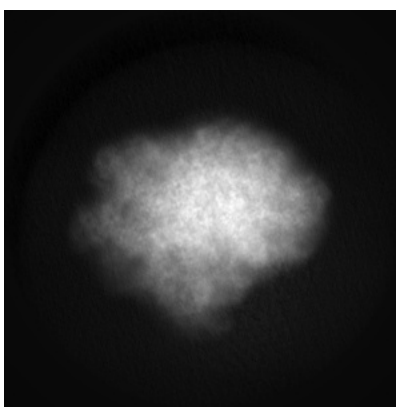


Z

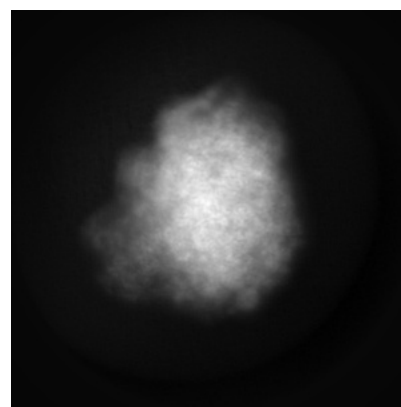
6.1.2 Raw map



X



Y

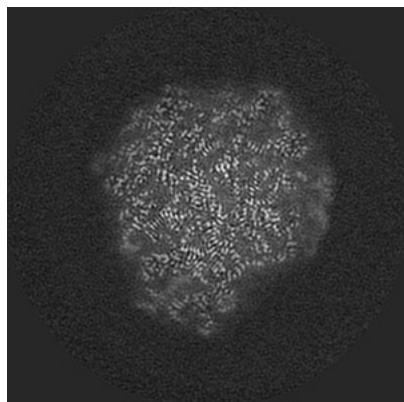


Z

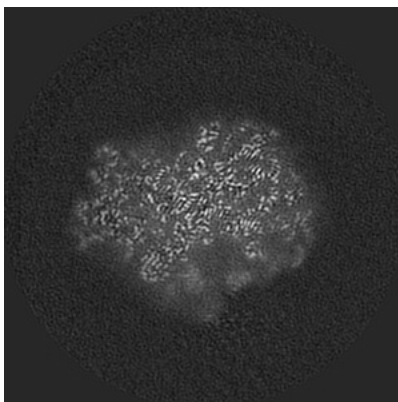
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

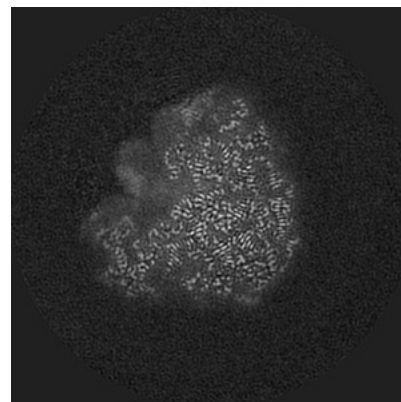
6.2.1 Primary map



X Index: 175

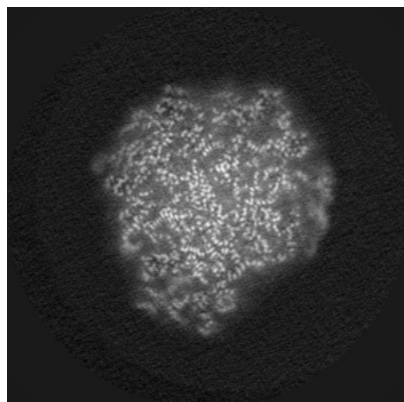


Y Index: 175

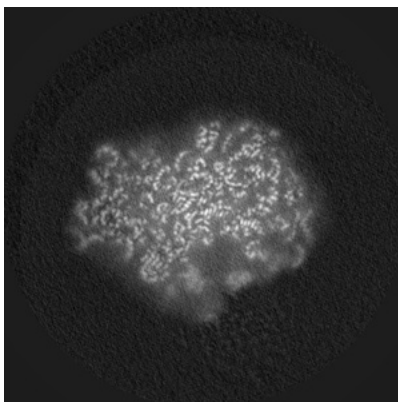


Z Index: 175

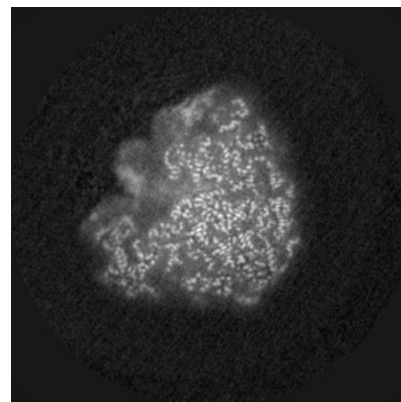
6.2.2 Raw map



X Index: 175



Y Index: 175

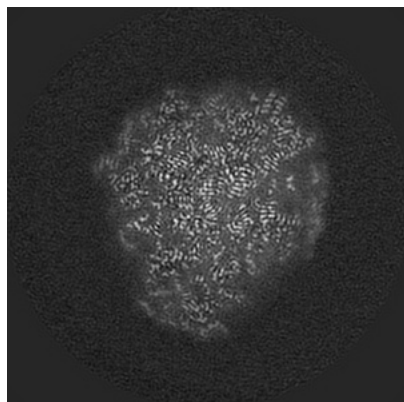


Z Index: 175

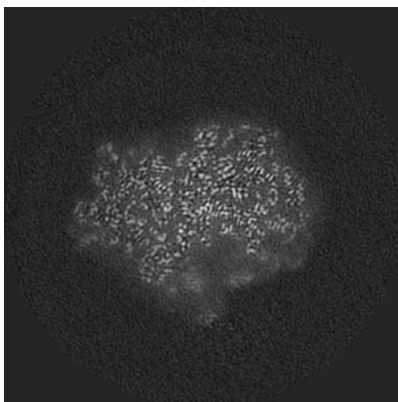
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

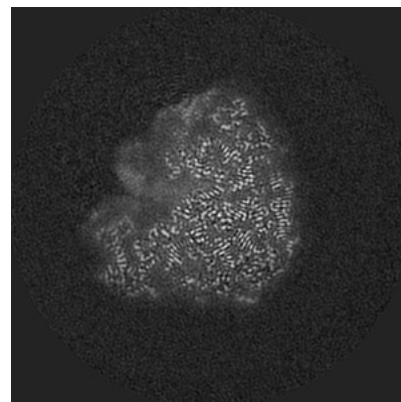
6.3.1 Primary map



X Index: 169

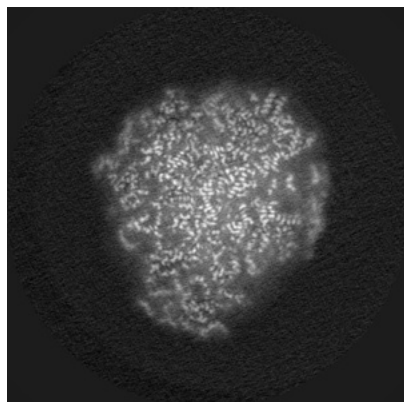


Y Index: 173

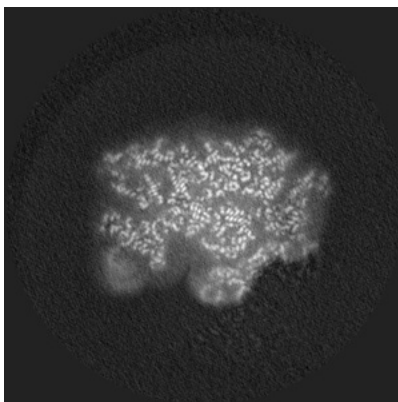


Z Index: 174

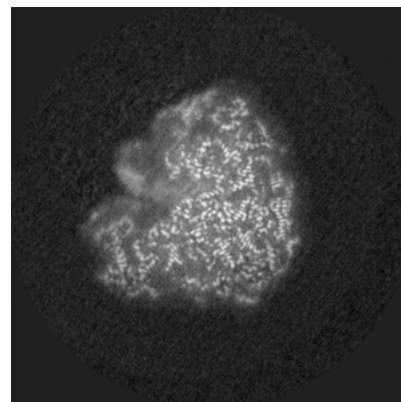
6.3.2 Raw map



X Index: 169



Y Index: 206

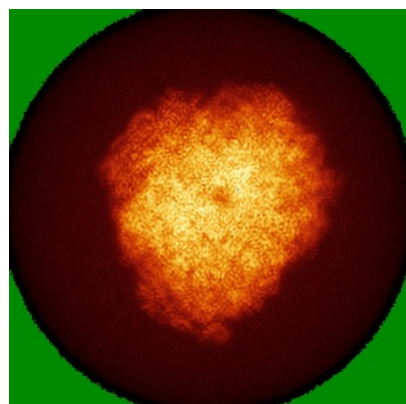


Z Index: 174

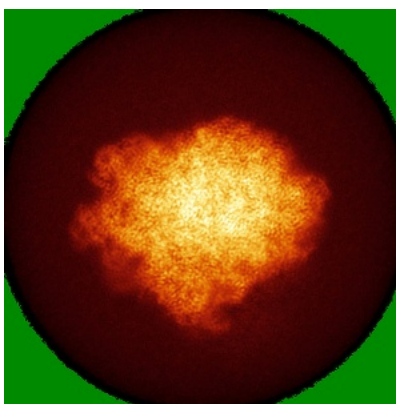
The images above show the largest variance slices of the map in three orthogonal directions.

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

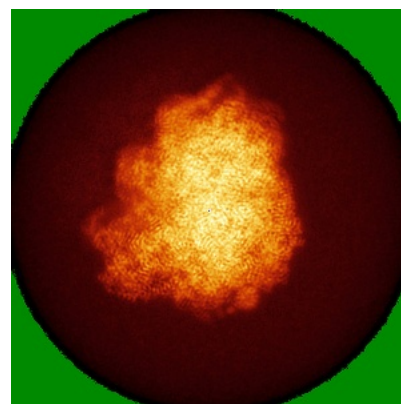
6.4.1 Primary map



X

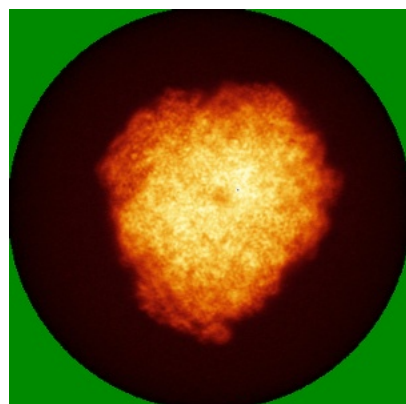


Y

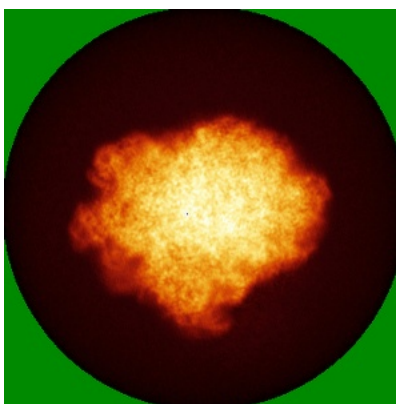


Z

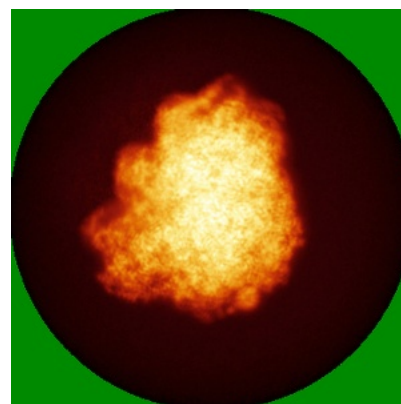
6.4.2 Raw map



X



Y

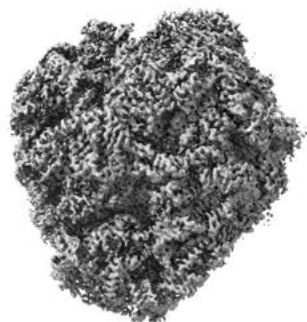


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



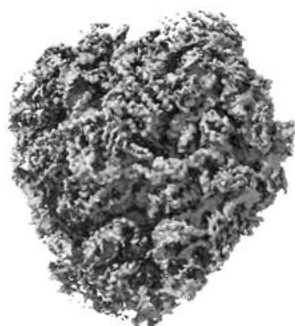
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.8. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

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

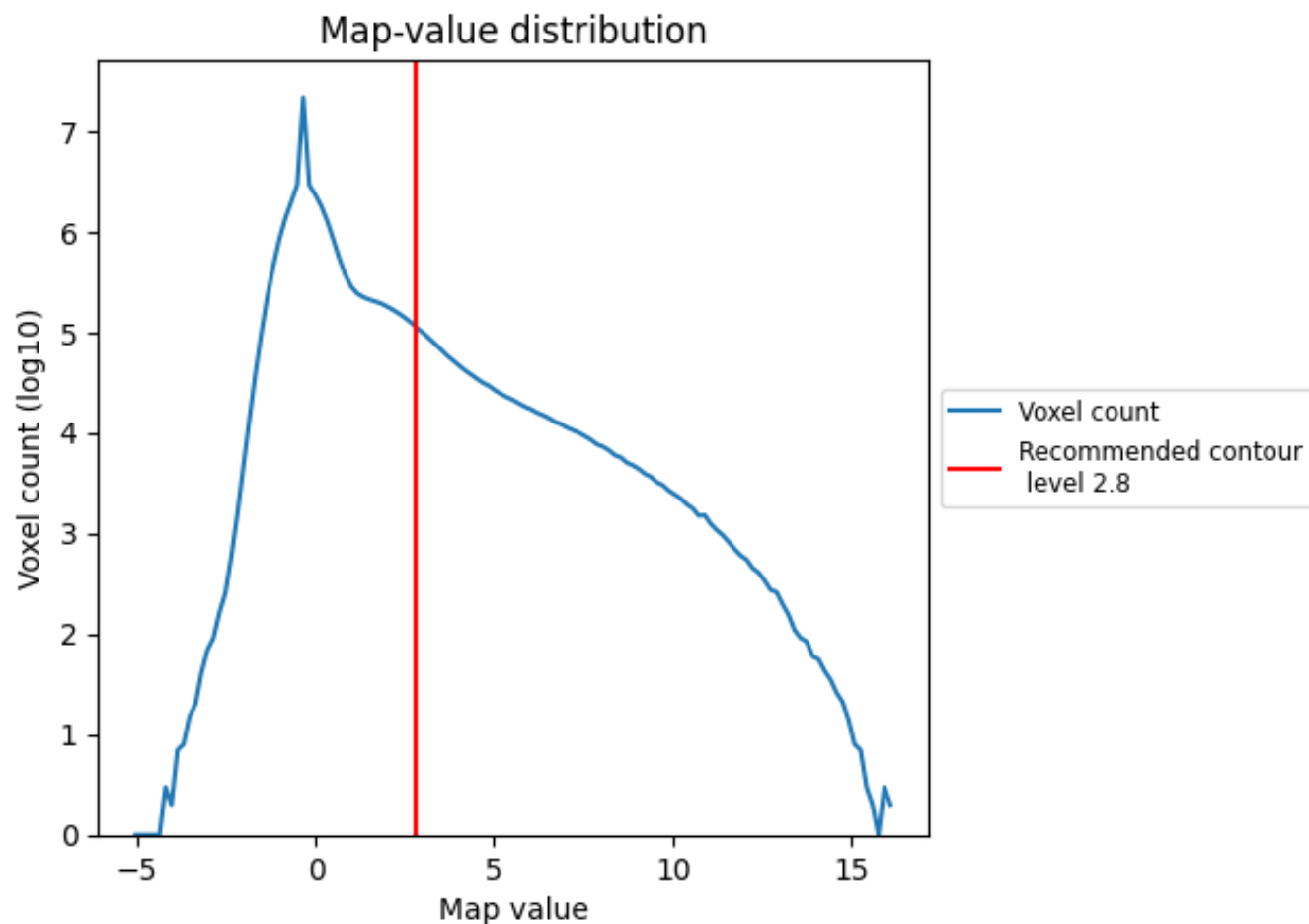
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

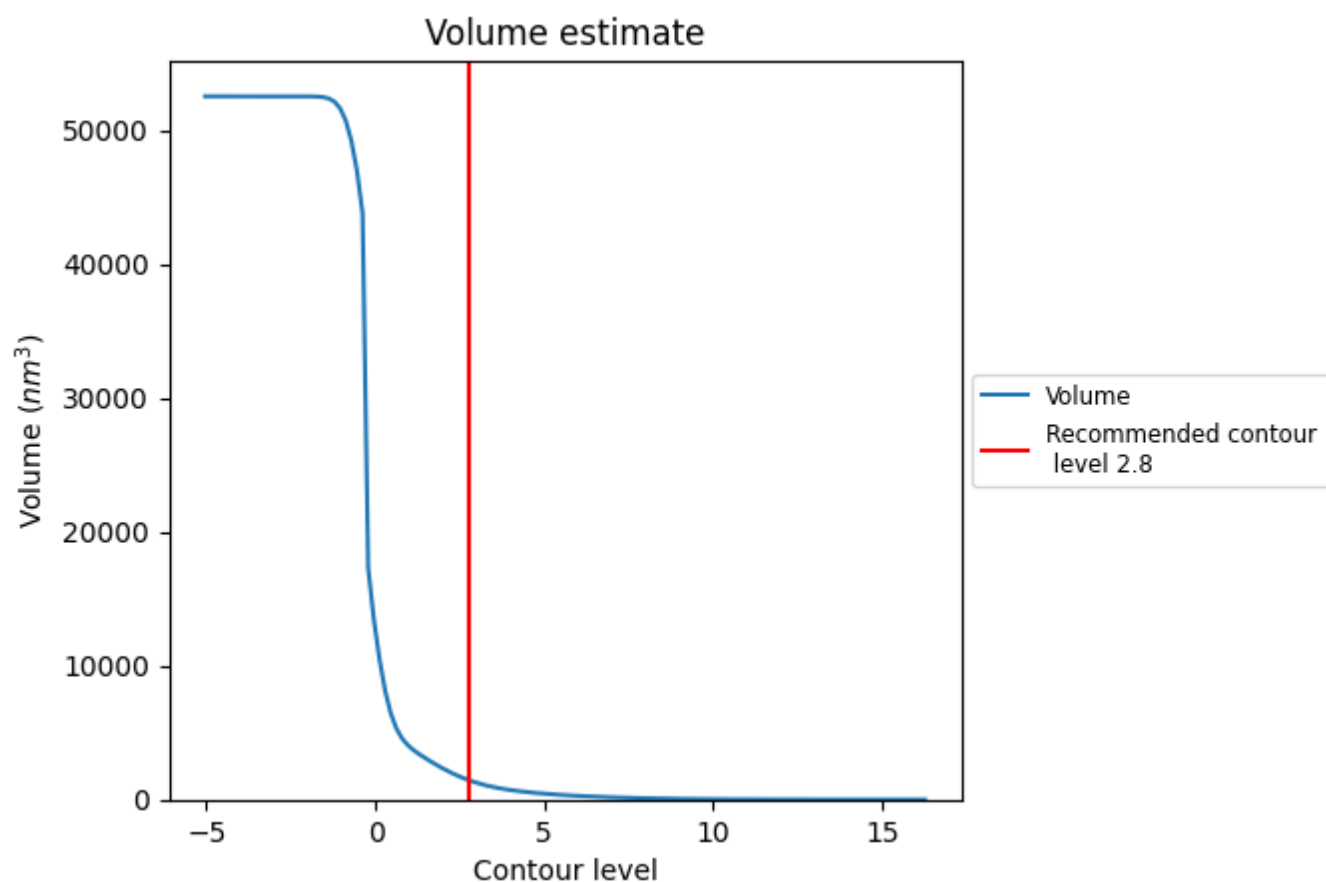
This section contains the results of statistical analysis of the map.

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.

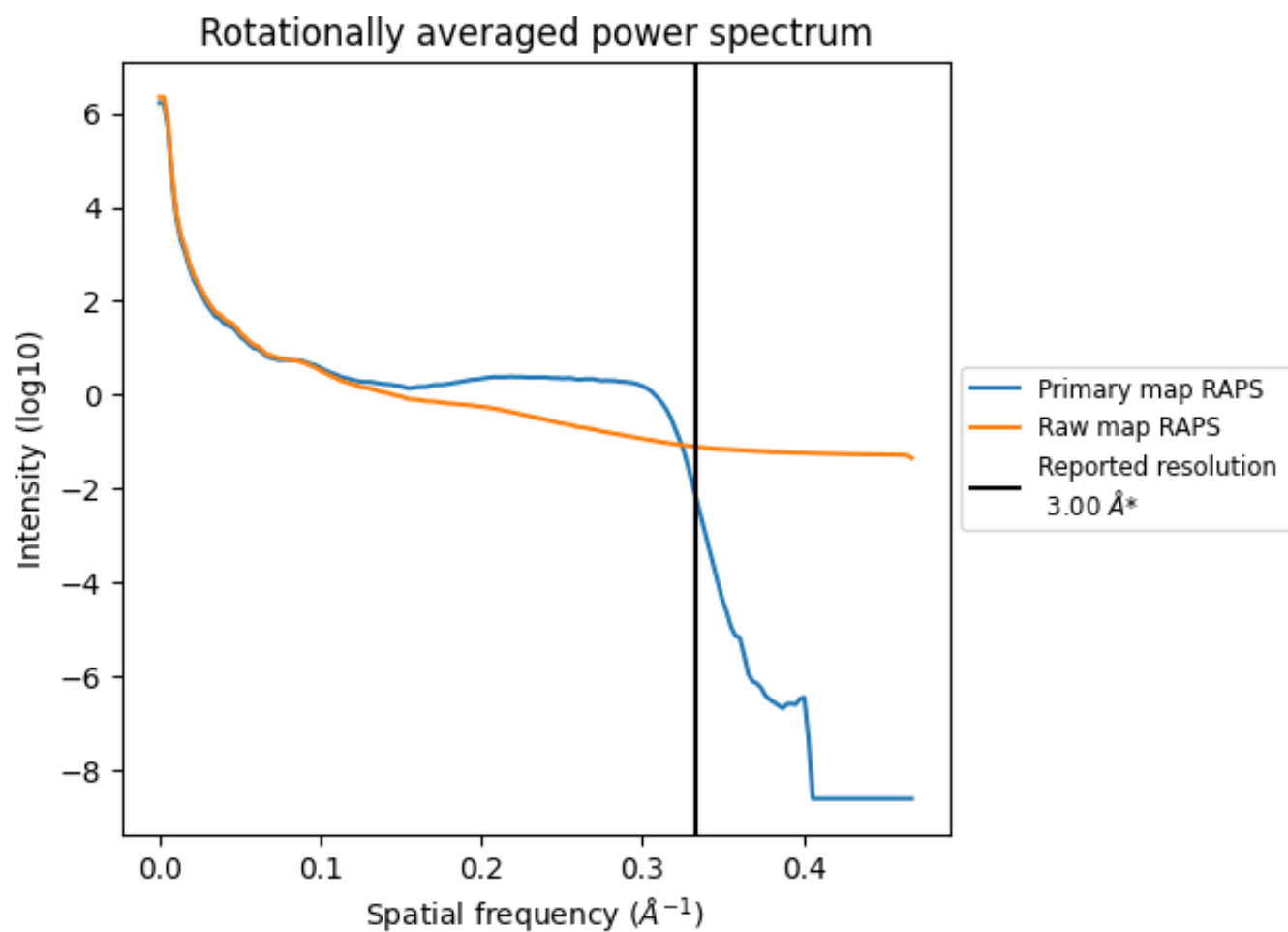
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1417 nm³; this corresponds to an approximate mass of 1280 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 ⓘ

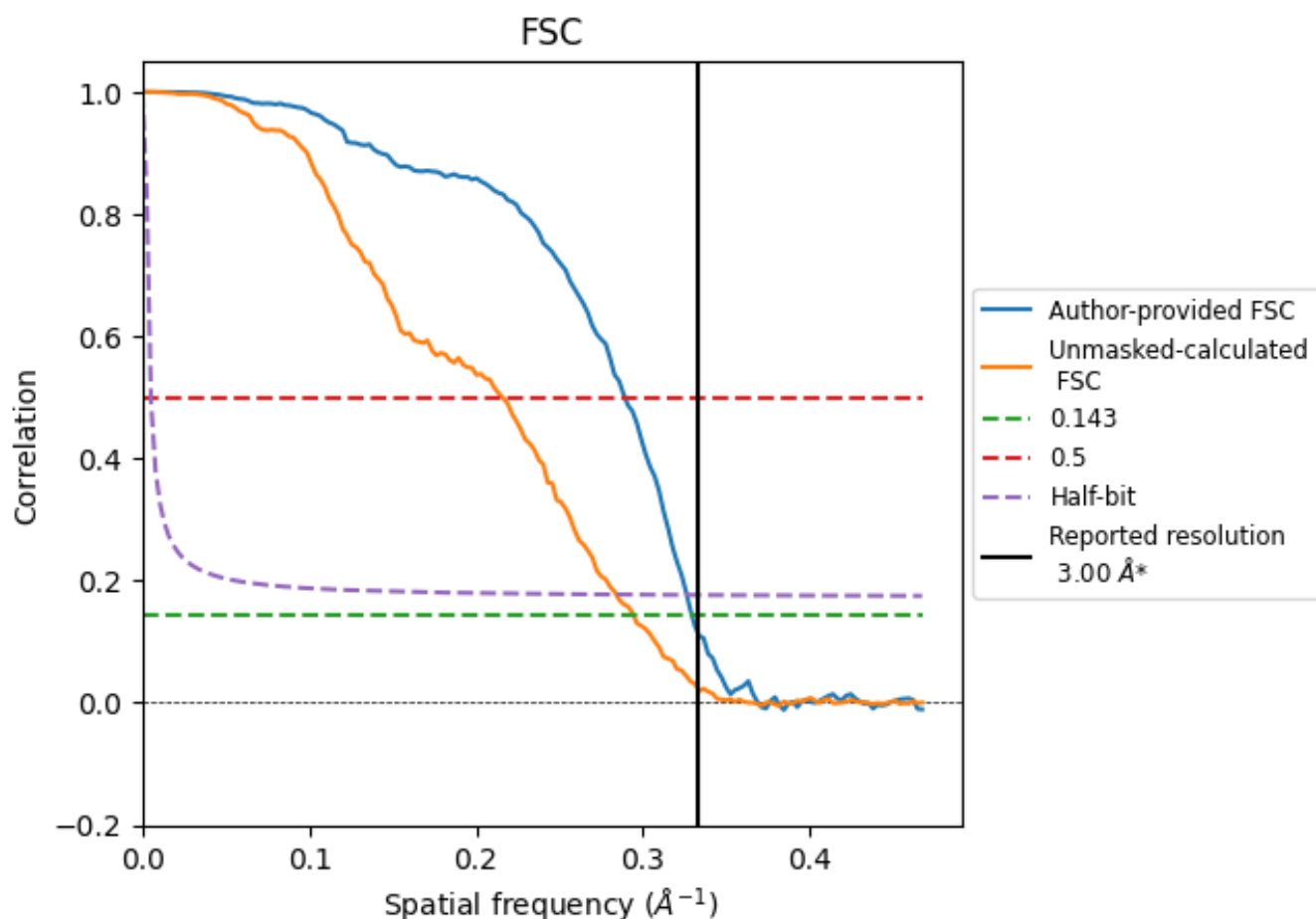


*Reported resolution corresponds to spatial frequency of $0.333 \text{ \AA}^{-1}$

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 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

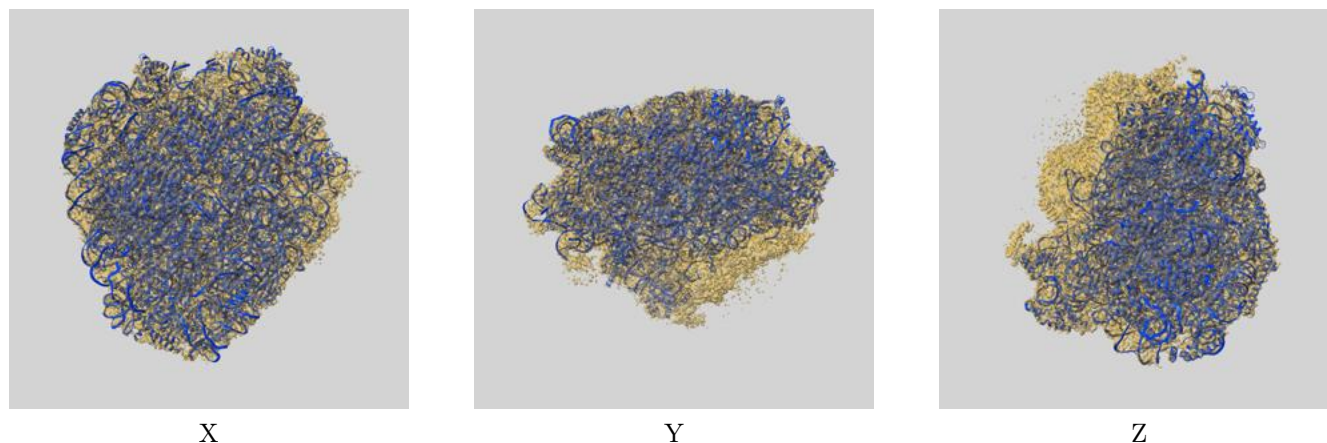
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.04	3.46	3.06
Unmasked-calculated*	3.40	4.63	3.52

*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 3.40 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

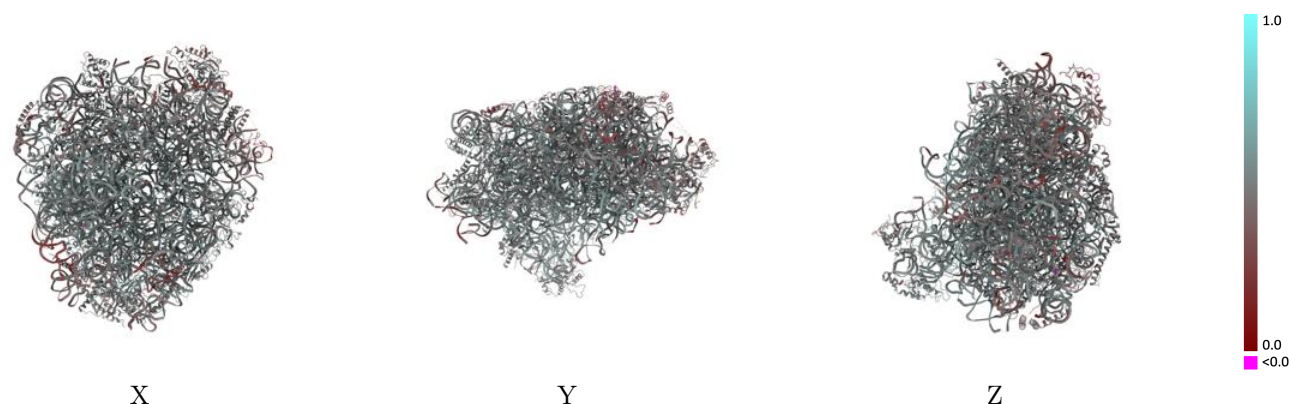
This section contains information regarding the fit between EMDB map EMD-64717 and PDB model 9V25. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

9.1 Map-model overlay [i](#)



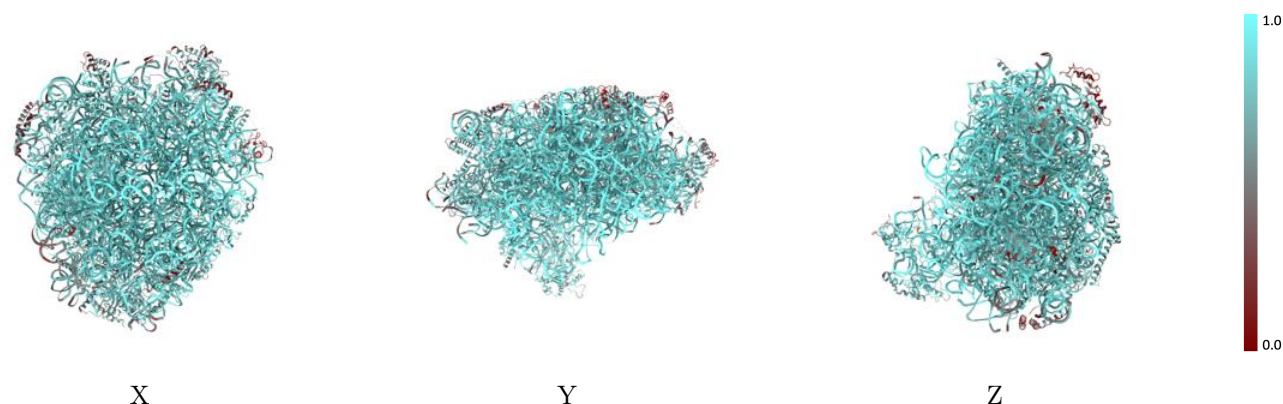
The images above show the 3D surface view of the map at the recommended contour level 2.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



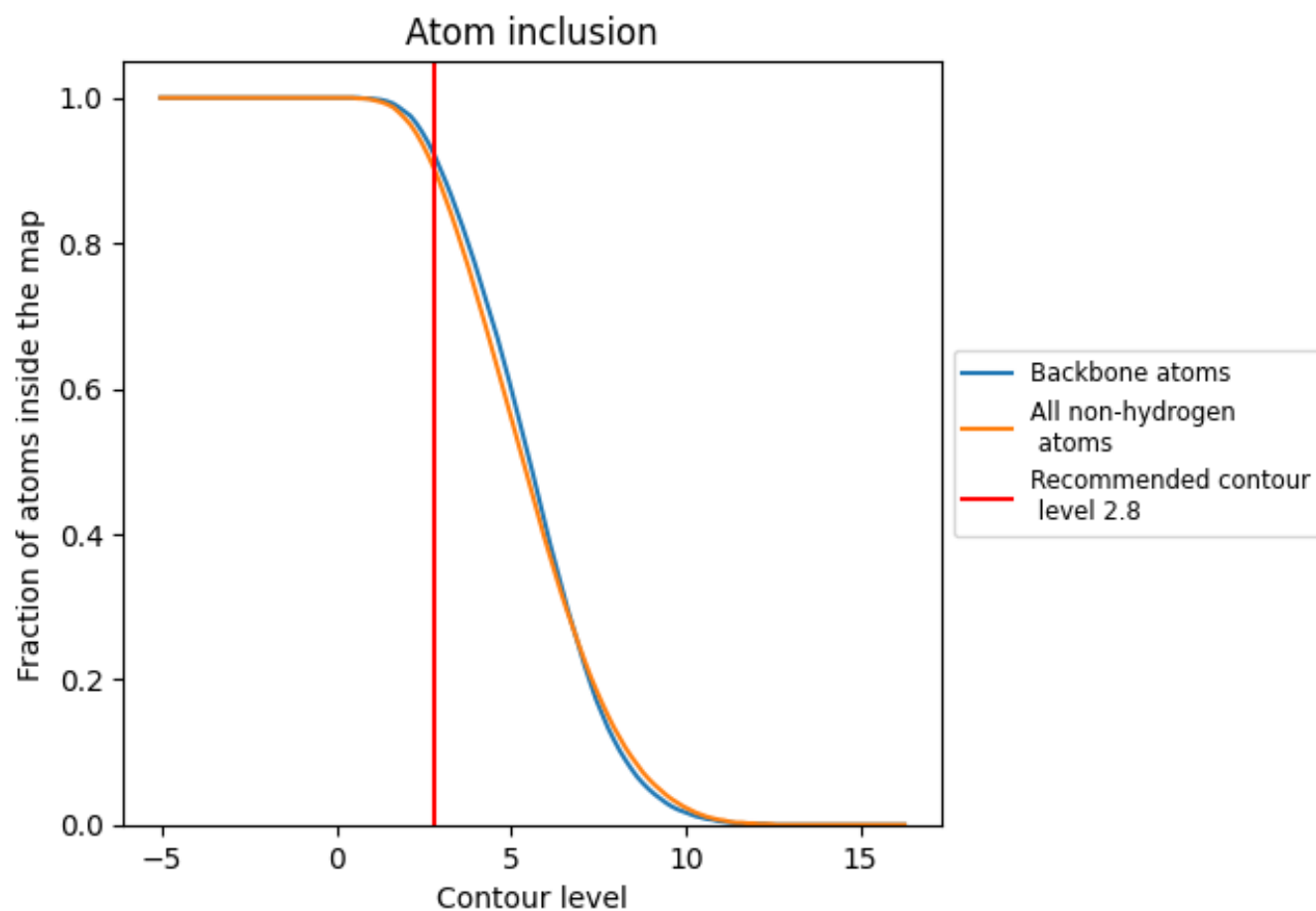
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.8).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 90% 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 (2.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9020	 0.4960
1A	 0.9380	 0.4960
1B	 0.9500	 0.5010
1C	 0.9670	 0.5030
1D	 0.9610	 0.5030
1E	 0.8990	 0.5040
1F	 0.8630	 0.5150
1G	 0.8100	 0.5180
1H	 0.6650	 0.4770
1I	 0.9070	 0.5290
1J	 0.6940	 0.4650
1K	 0.8040	 0.5000
1L	 0.9390	 0.5120
1M	 0.8160	 0.4700
1N	 0.7190	 0.4840
1O	 0.8940	 0.5160
1P	 0.8430	 0.5210
1Q	 0.9620	 0.5180
1R	 0.8920	 0.4980
1S	 0.9490	 0.5300
1T	 0.9290	 0.5380
1U	 0.8720	 0.4700
1V	 0.9180	 0.5340
1W	 0.3320	 0.3140
1X	 0.9600	 0.5010
1Y	 0.7960	 0.4720
1Z	 0.9400	 0.4920
1a	 0.7960	 0.4880
1b	 0.6100	 0.4200
1c	 0.9370	 0.5360
1d	 0.9550	 0.5380
1e	 0.7700	 0.4550
1f	 0.7570	 0.4370
1g	 0.8950	 0.5100
1h	 0.8840	 0.4760



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
li	 0.7910	 0.4740
lj	 0.9250	 0.5290
lk	 0.8550	 0.4950
ll	 0.9840	 0.5120
lm	 0.9410	 0.4850
ln	 0.4710	 0.4010
lo	 0.9760	 0.5080
lp	 0.8760	 0.4980
lq	 0.9530	 0.5270
sH	 1.0000	 0.4900
sI	 0.9900	 0.3750
sJ	 0.9850	 0.4850