



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 11:58 AM UTC

PDB ID : 6S05 / pdb_00006s05
EMDB ID : EMD-10071
Title : Cryo-EM structures of Lsg1-TAP pre-60S ribosomal particles
Authors : Kargas, V.; Warren, A.J.
Deposited on : 2019-06-13
Resolution : 3.90 Å(reported)
Based on initial model : 4V88

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

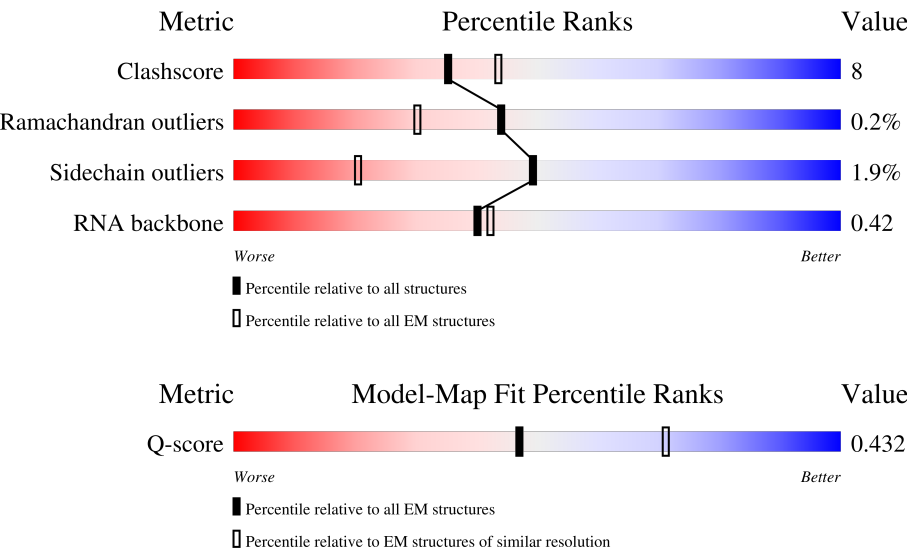
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



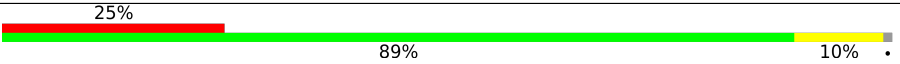
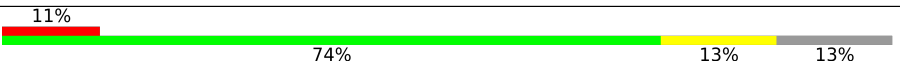
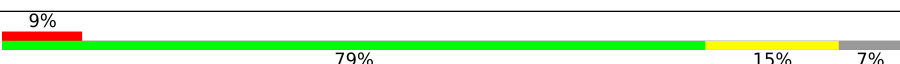
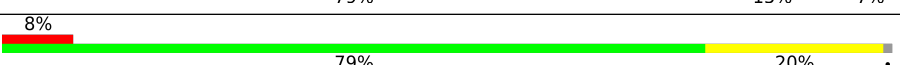
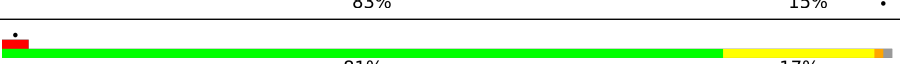
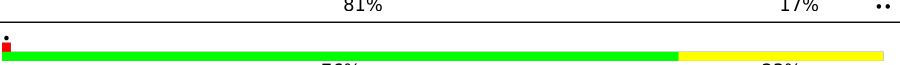
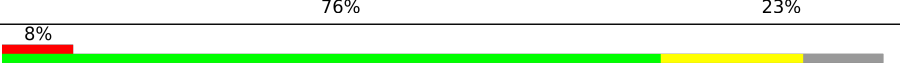
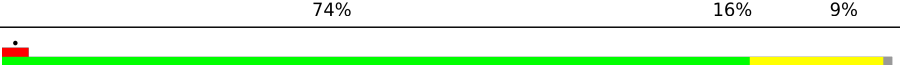
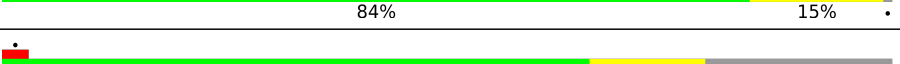
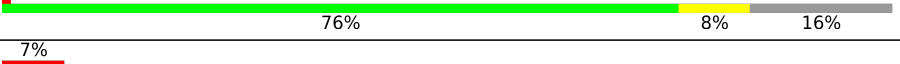
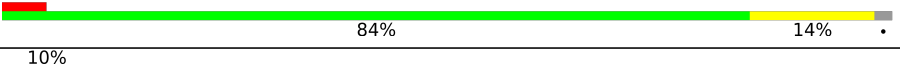
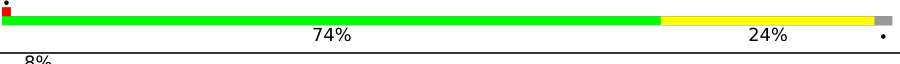
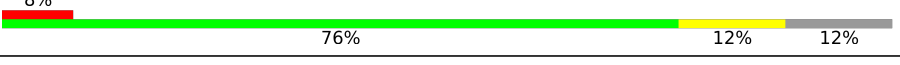
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8855 (3.40 - 4.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	3396	
2	B	254	
3	C	387	

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Mol	Chain	Length	Quality of chain
4	D	362	
5	E	174	
6	F	191	
7	G	176	
8	H	256	
9	J	198	
10	K	199	
11	L	137	
12	M	138	
13	N	149	
14	O	204	
15	P	297	
16	Q	186	
17	R	189	
18	S	172	
19	T	160	
20	U	184	
21	V	121	
22	W	142	
23	X	127	
24	Y	136	
25	Z	120	
26	a	59	
27	b	244	
28	c	105	

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Mol	Chain	Length	Quality of chain
29	d	113	
30	e	130	
31	f	107	
32	g	121	
33	h	100	
34	i	88	
35	j	78	
36	k	51	
37	l	106	
38	m	92	
39	n	245	
40	z	432	
41	w	518	
42	v	155	
43	o	640	
44	p	210	
45	s	364	
46	x	121	
47	y	158	

2 Entry composition

There are 48 unique types of molecules in this entry. The entry contains 129144 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 ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3146	Total	C	N	O	P	0	0
			67292	30062	12142	21944	3144		

- Molecule 2 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	247	Total	C	N	O	S	0	0
			1878	1170	381	326	1		

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	381	Total	C	N	O	S	0	0
			3039	1928	577	526	8		

- Molecule 4 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	361	Total	C	N	O	S	0	0
			2748	1730	522	493	3		

- Molecule 5 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	169	Total	C	N	O	S	0	0
			1352	847	253	248	4		

- Molecule 6 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	189	Total	C	N	O	S	0	0
			1502	953	272	273	4		

- Molecule 7 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	175	Total	C	N	O	S	0	0
			1399	902	251	245	1		

- Molecule 8 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	223	Total	C	N	O	S	0	0
			1742	1117	309	313	3		

- Molecule 9 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	197	Total	C	N	O	S	0	0
			1563	1005	292	265	1		

- Molecule 10 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	186	Total	C	N	O	S	0	0
			1486	929	304	253			

- Molecule 11 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	136	Total	C	N	O	S	0	0
			1002	628	189	178	7		

- Molecule 12 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	135	Total	C	N	O	S	0	0
			1045	669	197	177	2		

- Molecule 13 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	148	Total	C	N	O	S	0	0
			1172	749	231	189	3		

- Molecule 14 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	203	Total	C	N	O	S	0	0
			1719	1077	361	280	1		

- Molecule 15 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	269	Total	C	N	O	S	0	0
			2176	1378	375	421	2		

- Molecule 16 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	185	Total	C	N	O	S	0	0
			1440	908	290	240	2		

- Molecule 17 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	150	Total	C	N	O		0	0
			1209	752	257	200			

- Molecule 18 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	171	Total	C	N	O	S	0	0
			1436	925	266	242	3		

- Molecule 19 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	159	Total	C	N	O	S	0	0
			1275	805	246	220	4		

- Molecule 20 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	154	Total	C	N	O		0	0
			1222	761	237	224			

- Molecule 21 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	V	99	Total	C	N	O	0	0
			786	510	129	147		

- Molecule 22 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	120	Total	C	N	O	S	0	0
			958	617	168	171	2		

- Molecule 23 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	X	125	Total	C	N	O	0	0
			984	620	191	173		

- Molecule 24 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	Y	135	Total	C	N	O	0	0
			1091	710	202	179		

- Molecule 25 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	118	Total	C	N	O	S	0	0
			963	612	185	165	1		

- Molecule 26 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	a	52	Total	C	N	O	0	0
			415	259	90	66		

- Molecule 27 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	219	Total	C	N	O	S	0	0
			1760	1138	320	301	1		

- Molecule 28 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	97	Total	C	N	O	S	0	0
			741	479	124	137	1		

- Molecule 29 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	107	Total	C	N	O	S	0	0
			872	553	165	153	1		

- Molecule 30 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	127	Total	C	N	O	S	0	0
			1020	646	205	167	2		

- Molecule 31 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	106	Total	C	N	O	S	0	0
			849	540	165	143	1		

- Molecule 32 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	103	Total	C	N	O	S	0	0
			812	504	167	137	4		

- Molecule 33 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h	98	Total	C	N	O	S	0	0
			763	477	155	129	2		

- Molecule 34 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	84	Total	C	N	O	S	0	0
			665	405	145	110	5		

- Molecule 35 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	j	77	Total	C	N	O	0	0
			611	391	115	105		

- Molecule 36 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	50	Total	C	N	O	S	0	0
			435	272	97	64	2		

- Molecule 37 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	94	Total	C	N	O	S	0	0
			756	476	153	122	5		

- Molecule 38 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	89	Total	C	N	O	S	0	0
			680	421	136	117	6		

- Molecule 39 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	224	Total	C	N	O	S	0	0
			1691	1051	293	340	7		

- Molecule 40 is a protein called Cytoplasmic 60S subunit biogenesis factor REH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	z	58	Total	C	N	O	S	0	0
			491	301	100	87	3		

- Molecule 41 is a protein called 60S ribosomal export protein NMD3.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	w	389	Total	C	N	O	S	0	0
			3076	1955	530	571	20		

- Molecule 42 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	v	60	Total	C	N	O	S	0	0
			500	322	98	79	1		

- Molecule 43 is a protein called Large subunit GTPase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	o	322	Total	C	N	O	S	0	0
			2593	1660	449	477	7		

- Molecule 44 is a protein called uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	p	210	Total	C	N	O		0	0
			1050	630	210	210			

- Molecule 45 is a protein called Tyrosine-protein phosphatase YVH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	s	128	Total	C	N	O	S	0	0
			991	625	179	179	8		

- Molecule 46 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	x	121	Total	C	N	O	P	0	0
			2576	1152	461	843	120		

- Molecule 47 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	y	156	Total	C	N	O	P	0	0
			3310	1482	582	1091	155		

- Molecule 48 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
48	g	1	Total	Zn	0
			1	1	
48	i	1	Total	Zn	0
			1	1	
48	l	1	Total	Zn	0
			1	1	

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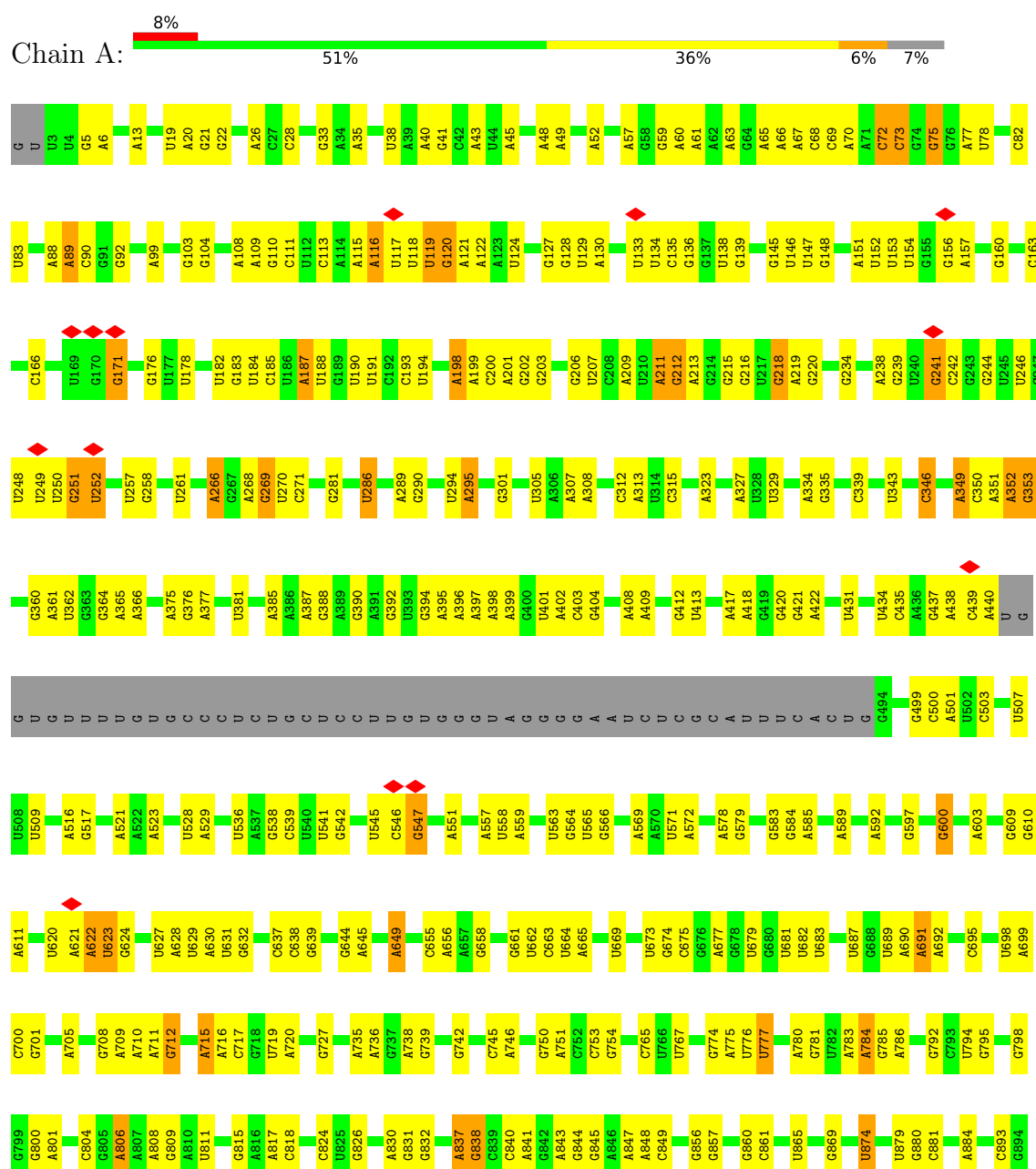
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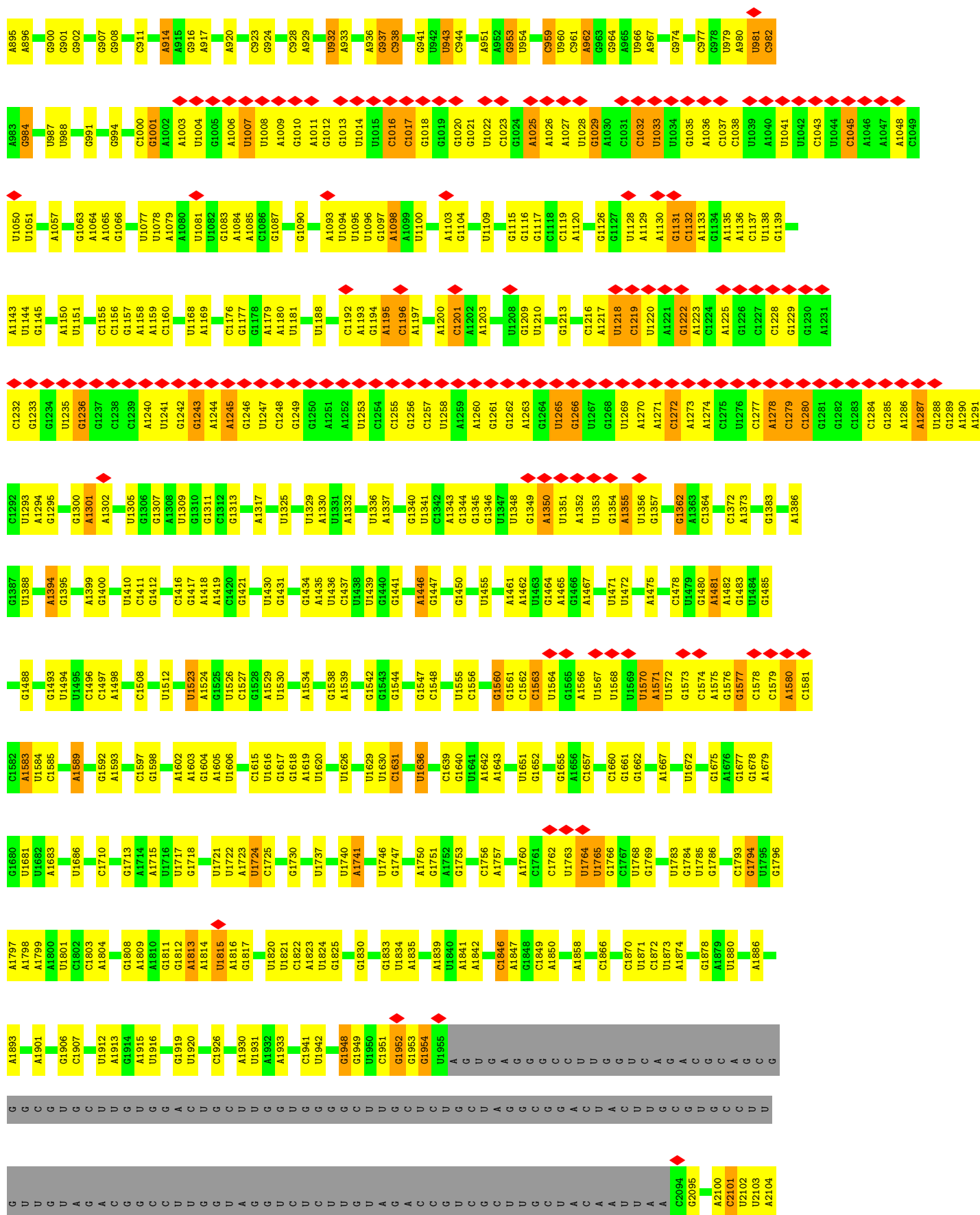
Mol	Chain	Residues	Atoms		AltConf
48	m	1	Total 1	Zn 1	0
48	w	2	Total 2	Zn 2	0
48	s	2	Total 2	Zn 2	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 25S ribosomal RNA



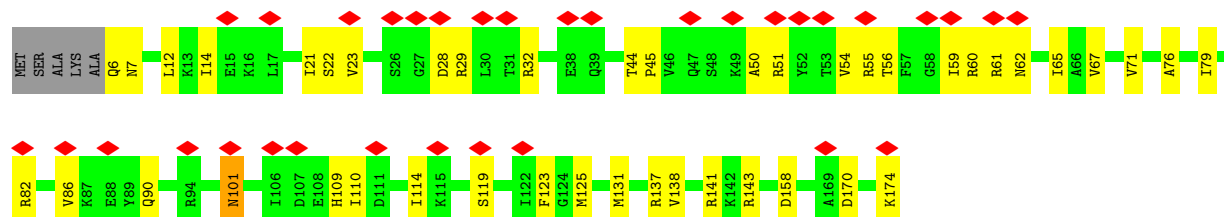


C3132	G3045	C2948	U2859	G2794	A2691	G2598	C2526	A2459	U2388	U2282	G2187	A2107
G3140	A3049	U2955	U2860	U2795	A2694	U2599	G2527	U2460	C2389	U2286	A2186	C2108
A3141	U3050	C2796	U2861	G2796	C2694	C2600	G2530	A2461	A2390	C2287	U2189	U2109
A3142	G3051	C2797	U2862	C2798	A2697	A2601	C	A2462	G2391	C2192	G2110	G2110
C3151	U3052	C2960	U2863	A2799	G2698	G2606	G	U2463	C2392	U2294	U2193	G2111
U3152	G3053	G2961	A2864	G2800	G2699	G2607	G	U2465	G2393	A2295	G2194	U2112
U3153	U3054	C2966	U2865	A2801	A2703	G2614	A	G2466	A2397	U2298	C2195	A2113
C3154	U3055	C2970	U2866	A2802	A2704	G2615	A	C2467	A2398	C2306	C2196	C2114
U3155	U3056	A2971	U2867	A2803	A2705	G2616	U	G2468	A2399	G2307	C2197	A2117
C3156	G3059	G2972	U2868	C2810	C2708	U2617	C	C2470	G2400	C2308	G2201	G2121
U3157	C3067	A2976	U2869	C2811	C2709	G2618	A	U2471	A2401	A2309	U2205	G2122
G3168	U3068	C2870	U2871	A2812	C2710	G2619	U	U2472	A2402	A2310	G2206	G2123
C3169	U3069	G2871	U2872	A2813	C2711	G2620	U	C2473	G2403	A2311	G2209	G2124
U3170	G3078	A2872	U2873	A2814	C2712	G2621	U	G2474	A2404	U2313	A2125	A2126
C3171	U3079	U2874	U2874	A2815	C2713	G2622	C	G2475	C2405	U2314	U2127	U2127
C3162	G3080	U2875	U2875	A2816	C2714	G2623	C	C2476	C2406	G2315	C2218	C2128
C3163	C3081	C2876	U2876	A2817	C2715	G2624	U	G2477	U2340	A2341	U2141	A2142
A3164	U3082	U2877	U2877	A2818	C2716	G2625	C	C2478	U2341	U2344	A2145	A2145
A3165	G3083	C2878	U2878	A2819	C2717	G2626	G2547	G2479	U2411	U2345	G2249	A2146
C3168	U3084	U2879	U2879	A2820	C2718	G2627	G2548	A2480	G2412	U2346	G2253	A2147
U3169	C3085	U2880	U2880	A2821	C2719	G2628	G2549	G2481	C2415	U2334	A2252	U2137
A3170	G3086	U2881	U2881	A2822	C2720	G2629	U2550	U2482	U2416	U2335	A2253	A2138
U3171	U3087	U2882	U2882	A2823	C2721	G2630	U2551	G2483	C2417	U2336	G2240	A2139
C3172	C3088	U2883	U2883	A2824	C2722	G2631	G2552	A2484	U2417	C2339	A2244	U2140
G3173	U3089	U2884	U2884	A2825	C2723	G2632	U2553	A2485	C2422	U2340	C2245	A2141
A3174	C3090	U2885	U2885	A2826	C2724	G2633	G2554	U2486	G2425	U2341	G2249	A2142
U3175	U3091	U2886	U2886	A2827	C2725	G2634	U2555	A2487	U2426	U2342	A2249	A2143
G3176	C3092	U2887	U2887	A2828	C2726	G2635	U2556	A2488	U2427	U2343	G2253	A2144
U3177	U3093	U2888	U2888	A2829	C2727	G2636	U2557	C2489	U2428	U2344	A2254	G2150
A3178	C3094	U2889	U2889	A2830	C2728	G2637	A2560	A2490	U2429	U2345	A2255	U2154
U3179	U3095	U2890	U2890	A2831	C2729	G2638	U2561	U2491	A2430	U2346	A2256	G2155
A3180	G3015	A2891	U2891	A2832	C2730	G2639	U2562	U2492	U2431	U2347	C2257	C2156
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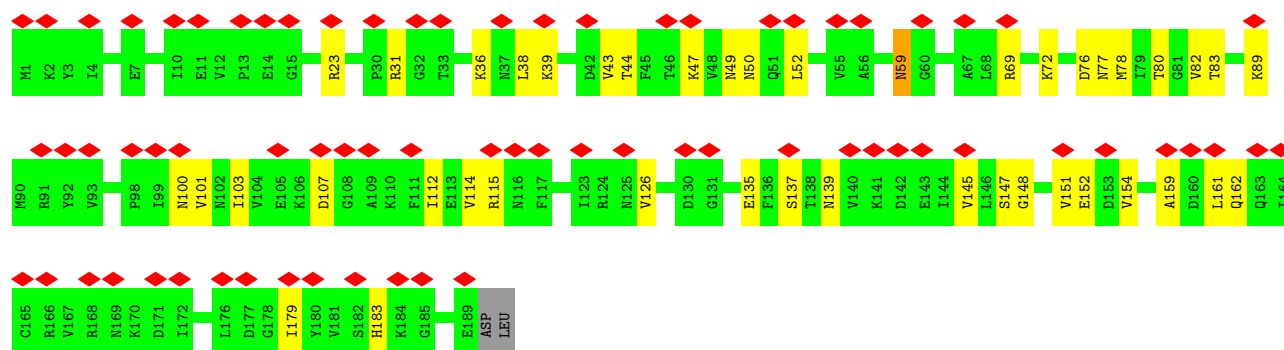
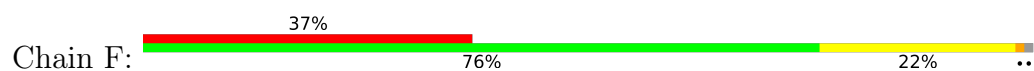




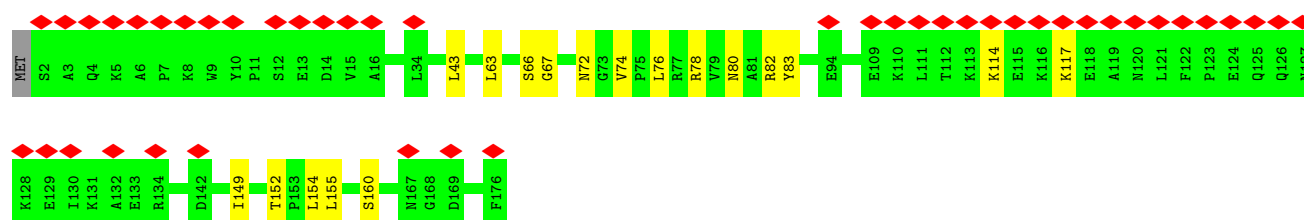
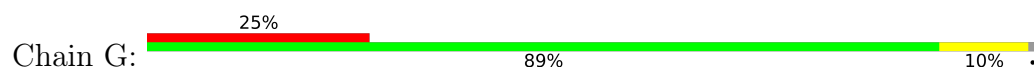
• Molecule 5: 60S ribosomal protein L11-A



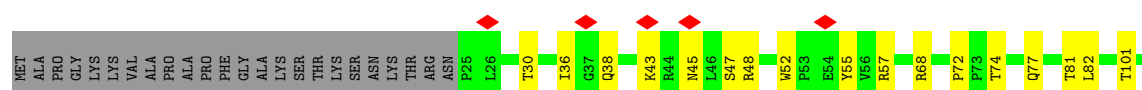
• Molecule 6: 60S ribosomal protein L9-A

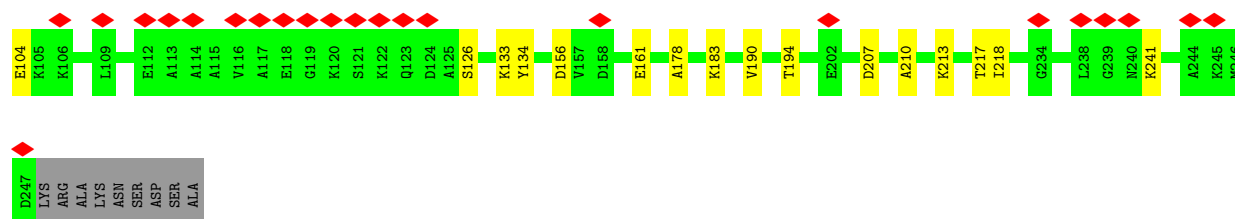


• Molecule 7: 60S ribosomal protein L6-A

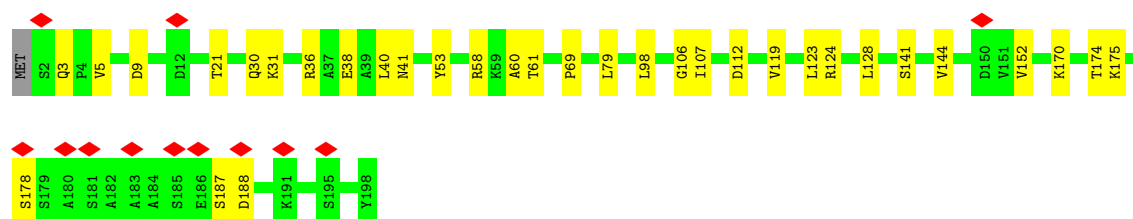
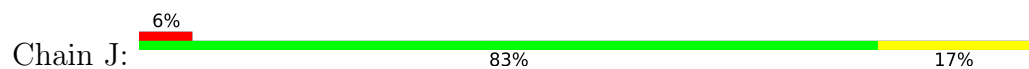


• Molecule 8: 60S ribosomal protein L8-A

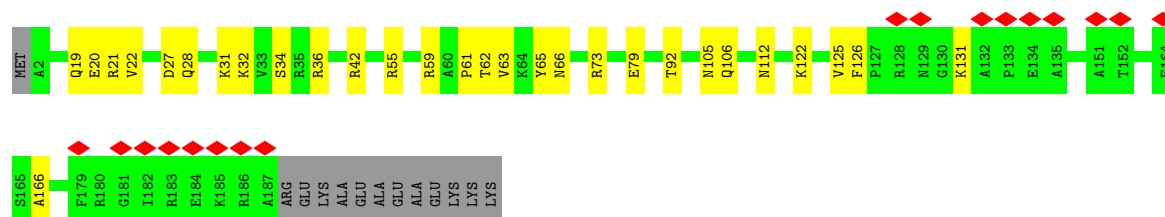
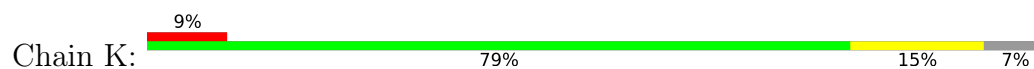




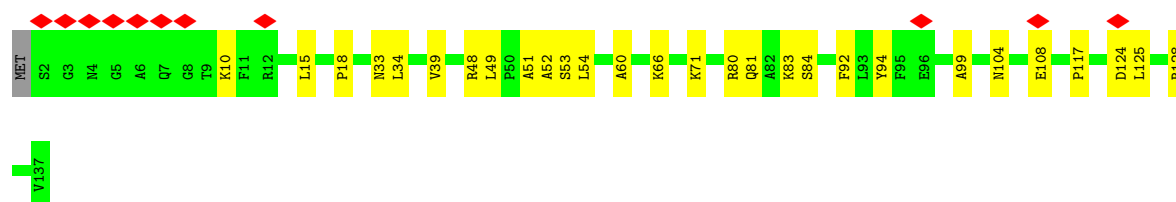
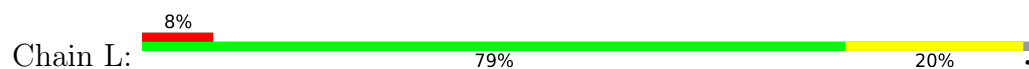
- Molecule 9: 60S ribosomal protein L16-B



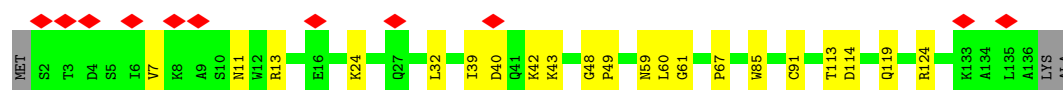
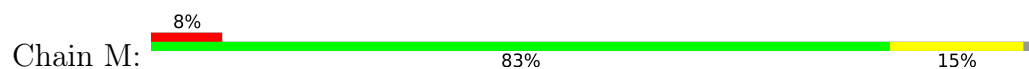
- Molecule 10: 60S ribosomal protein L13-A



- Molecule 11: 60S ribosomal protein L23-A

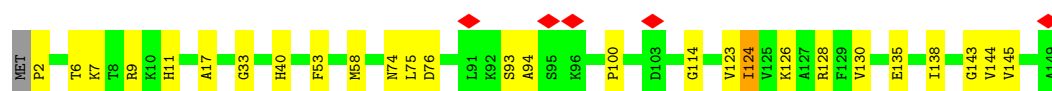


- Molecule 12: 60S ribosomal protein L14-A



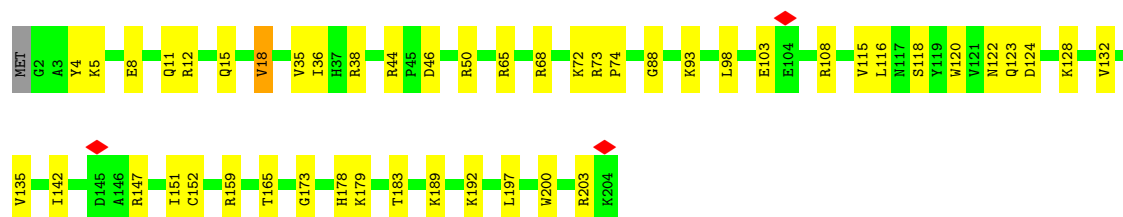
- Molecule 13: 60S ribosomal protein L28

Chain N:  81% 17% ..



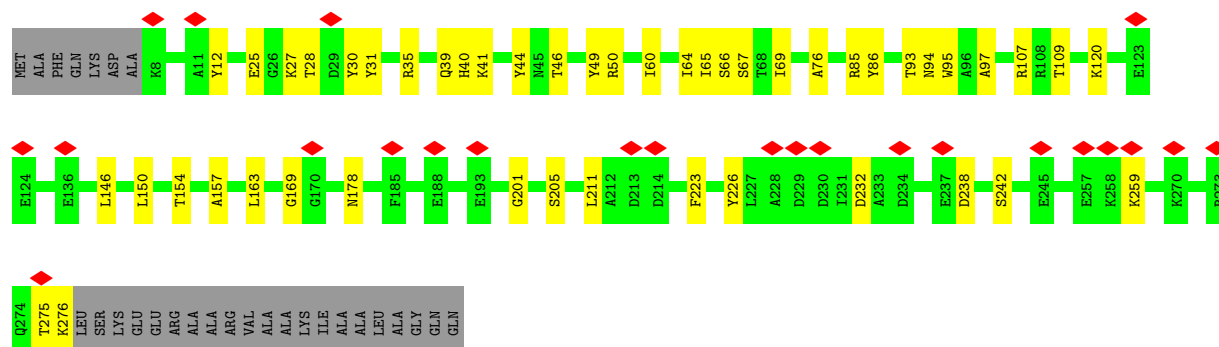
- Molecule 14: 60S ribosomal protein L15-A

Chain O:  76% 23%



- Molecule 15: 60S ribosomal protein L5

Chain P:  8% 74% 16% 9%



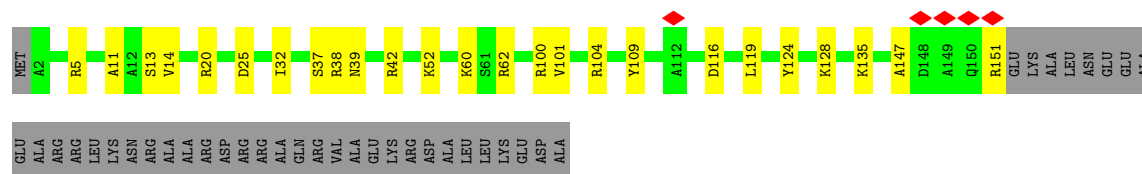
- Molecule 16: 60S ribosomal protein L18-A

Chain Q:  84% 15%



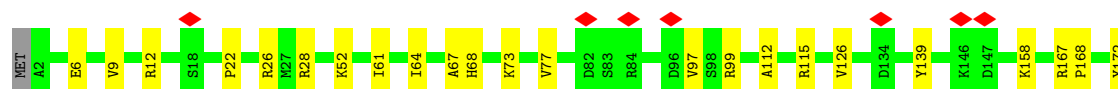
- Molecule 17: 60S ribosomal protein L19-A

Chain R:  66% 13% 21%



- Molecule 18: 60S ribosomal protein L20-A

Chain S:  86% 13% .



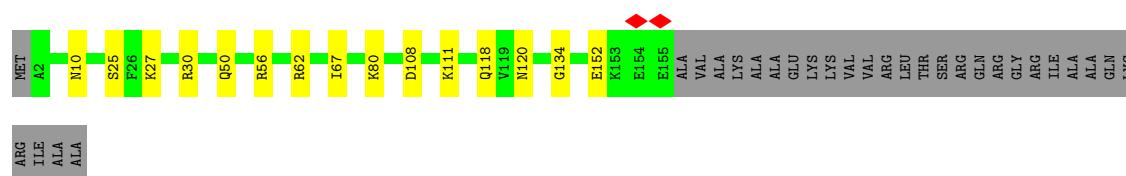
- Molecule 19: 60S ribosomal protein L21-A

Chain T:  9% 86% 13% ..



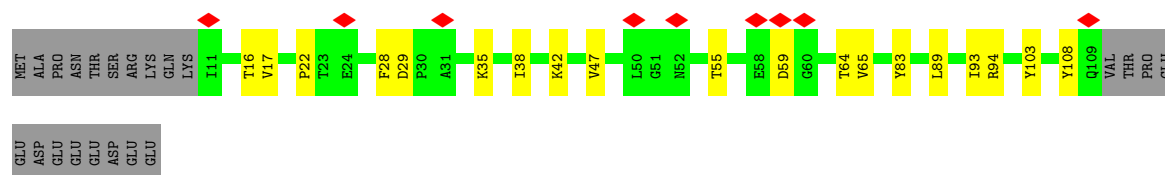
- Molecule 20: 60S ribosomal protein L17-A

Chain U:  76% 8% 16%



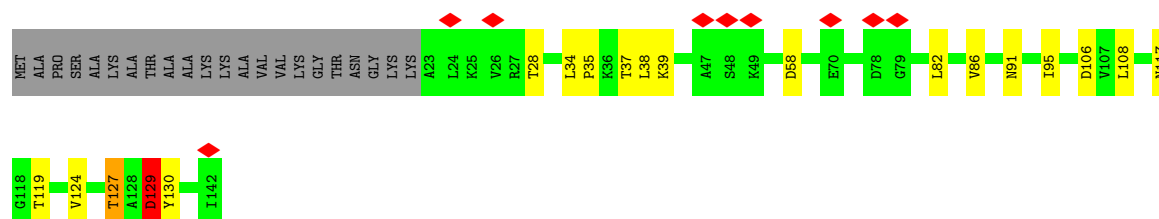
- Molecule 21: 60S ribosomal protein L22-A

Chain V:  7% 66% 16% 18%



- Molecule 22: 60S ribosomal protein L25

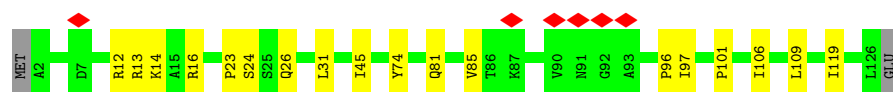
Chain W:  6% 71% 12% 15%



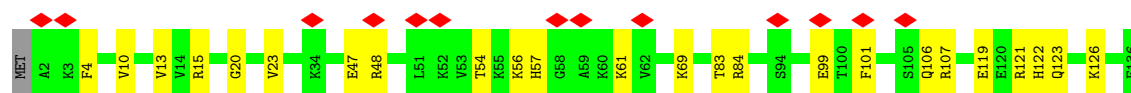
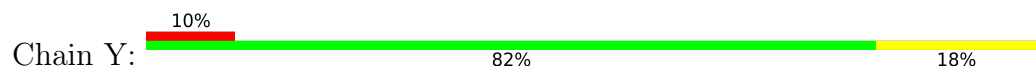
- Molecule 23: 60S ribosomal protein L26-A

Chain X:  5% 84% 14% .





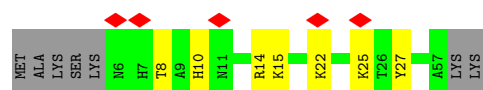
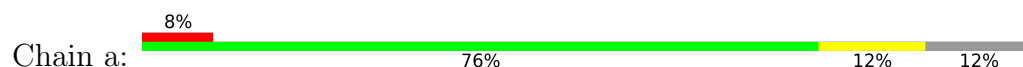
- Molecule 24: 60S ribosomal protein L27-A



- Molecule 25: 60S ribosomal protein L35-A



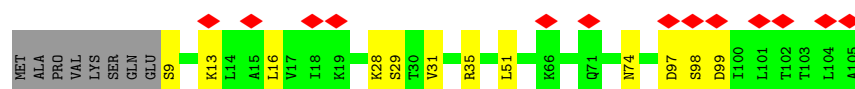
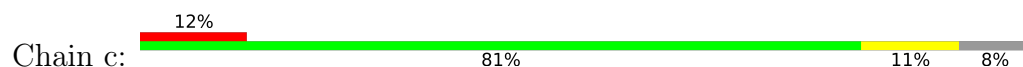
- Molecule 26: 60S ribosomal protein L29



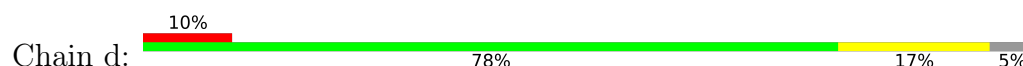
- Molecule 27: 60S ribosomal protein L7-A

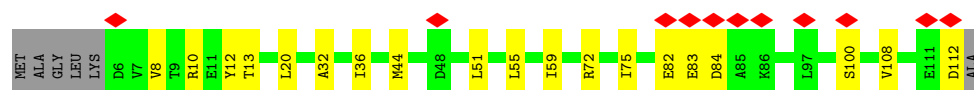


- Molecule 28: 60S ribosomal protein L30

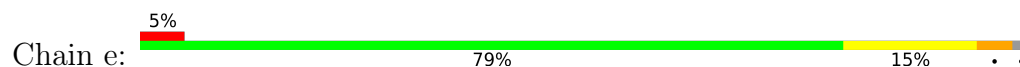


- Molecule 29: 60S ribosomal protein L31-A

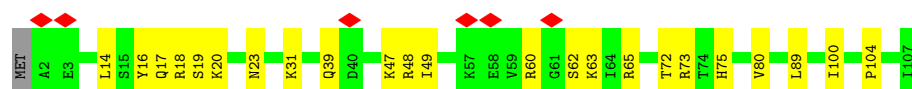
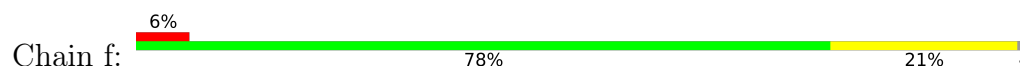




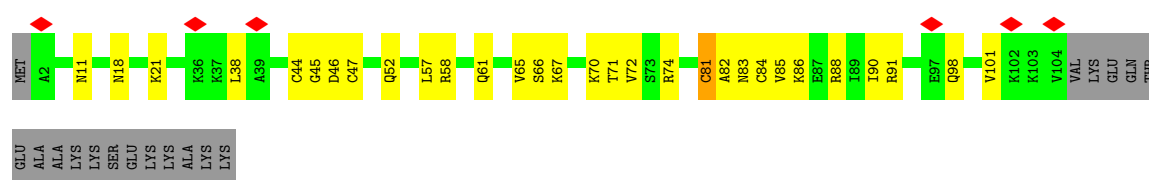
- Molecule 30: 60S ribosomal protein L32



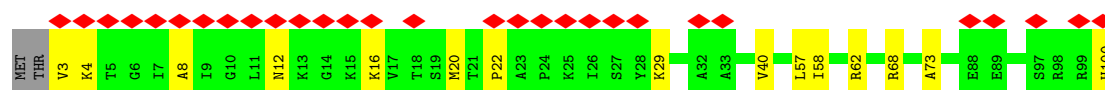
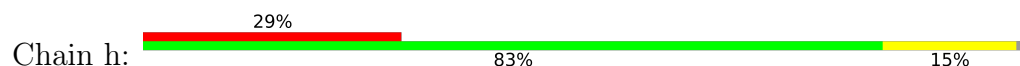
- Molecule 31: 60S ribosomal protein L33-A



- Molecule 32: 60S ribosomal protein L34-A



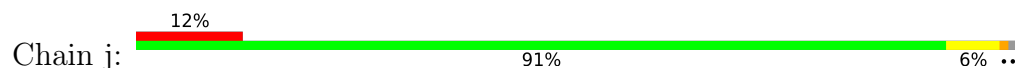
- Molecule 33: 60S ribosomal protein L36-A

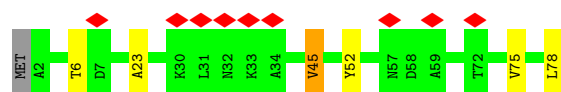


- Molecule 34: 60S ribosomal protein L37-A



- Molecule 35: 60S ribosomal protein L38





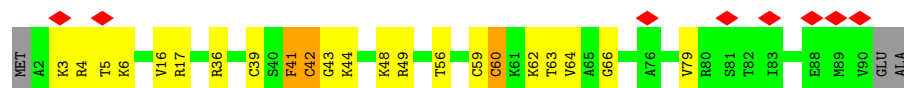
- Molecule 36: 60S ribosomal protein L39



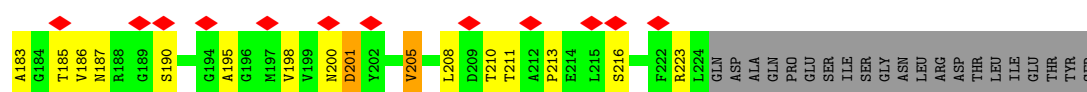
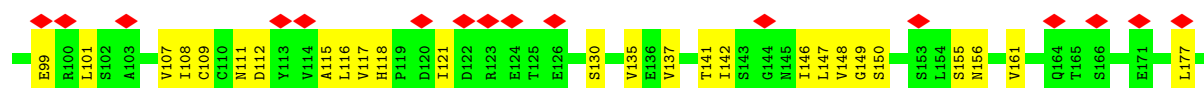
- Molecule 37: 60S ribosomal protein L42-A



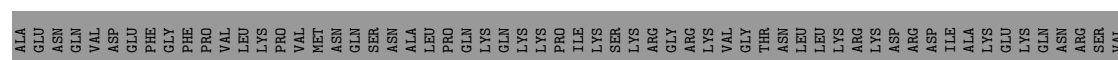
- Molecule 38: 60S ribosomal protein L43-A

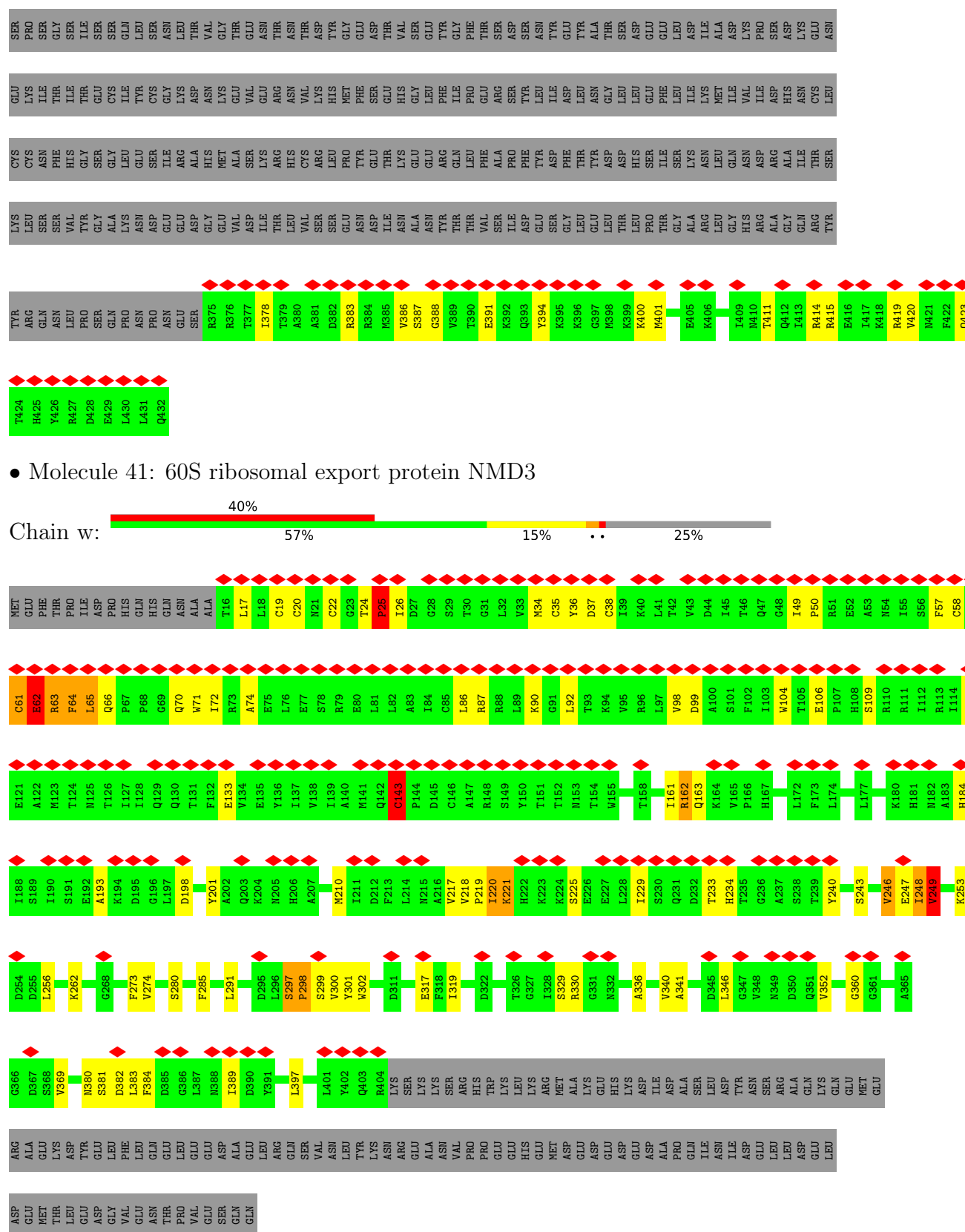


- Molecule 39: Eukaryotic translation initiation factor 6

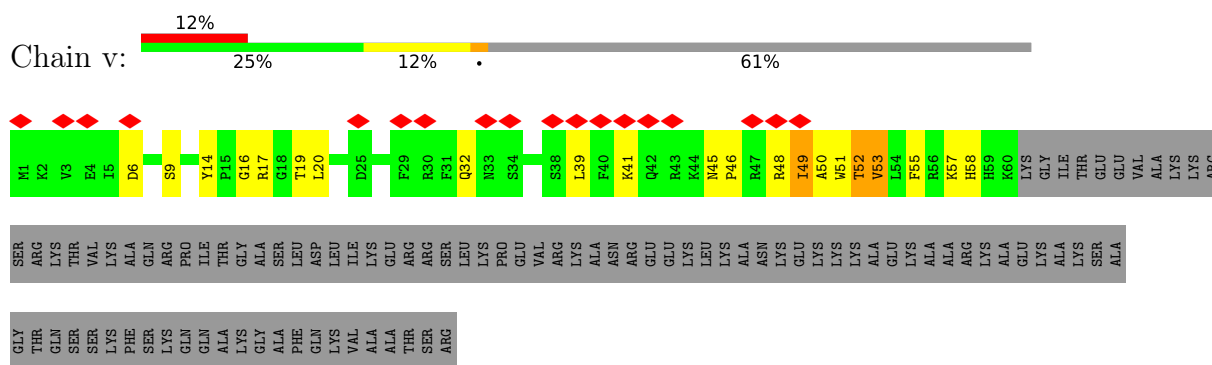


- Molecule 40: Cytoplasmic 60S subunit biogenesis factor REH1

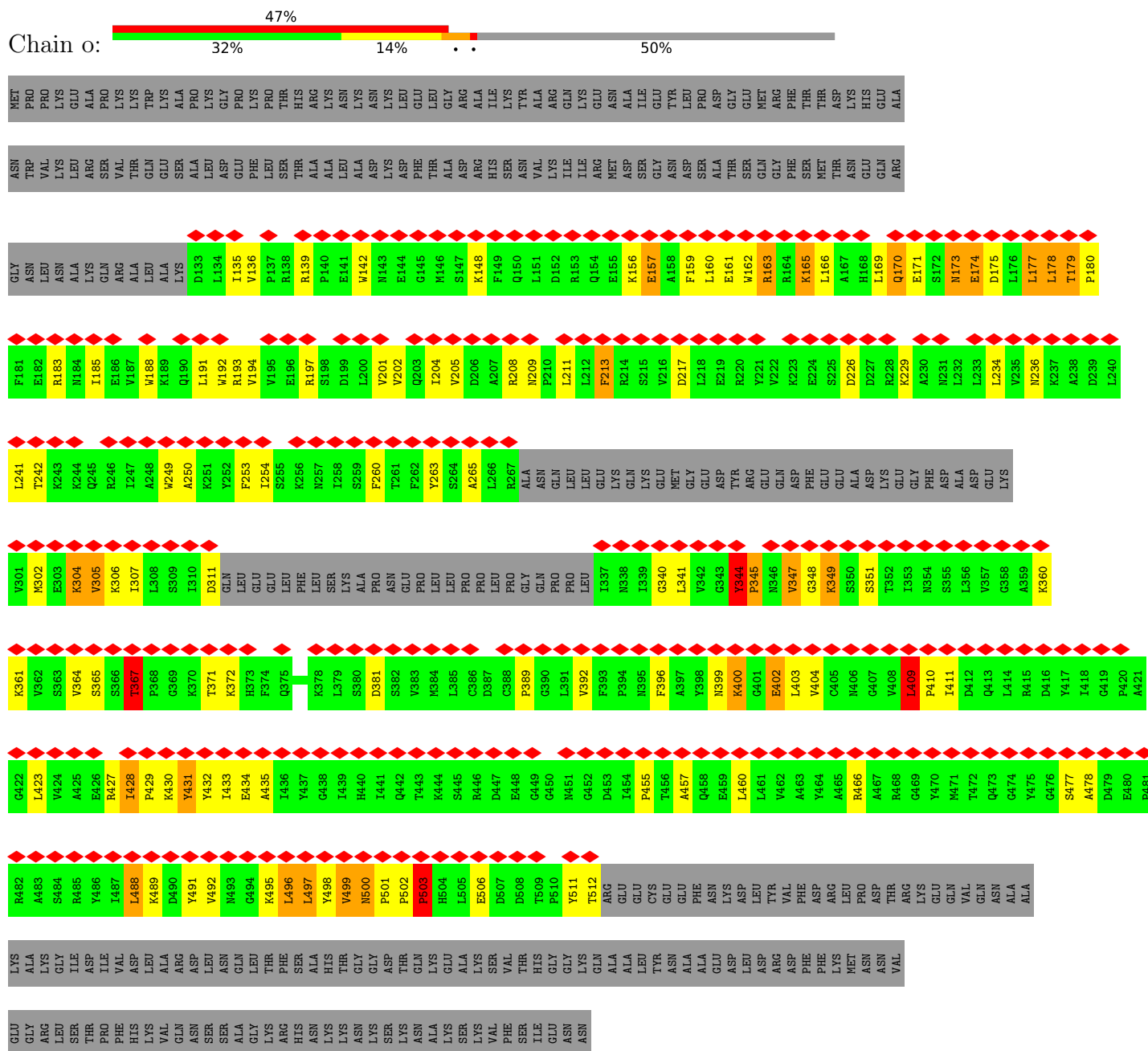




- Molecule 42: 60S ribosomal protein L24-A

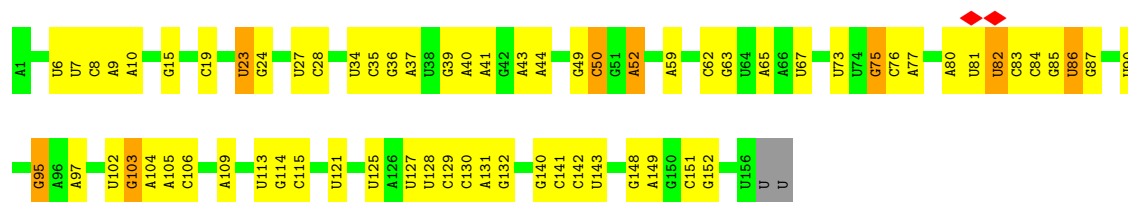


● Molecule 43: Large subunit GTPase 1



● Molecule 47: 5.8S ribosomal RNA

Chain y:  56% 38% 5%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	35152	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	63	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.460	Depositor
Minimum map value	-0.235	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.08	Depositor
Map size ($\text{\AA}$)	383.40002, 383.40002, 383.40002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.065, 1.065, 1.065	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	A	0.43	1/75327 (0.0%)	0.47	3/117440 (0.0%)
2	B	0.45	0/1912	0.61	0/2569
3	C	0.43	0/3110	0.64	5/4184 (0.1%)
4	D	0.45	0/2800	0.59	0/3791
5	E	0.28	0/1373	0.67	1/1841 (0.1%)
6	F	0.27	0/1523	0.61	0/2051
7	G	0.31	0/1423	0.54	0/1911
8	H	0.34	0/1774	0.56	0/2395
9	J	0.40	0/1593	0.57	0/2137
10	K	0.42	0/1511	0.59	0/2031
11	L	0.38	0/1017	0.65	0/1368
12	M	0.34	0/1060	0.57	0/1428
13	N	0.45	0/1203	0.62	0/1611
14	O	0.48	0/1756	0.63	1/2353 (0.0%)
15	P	0.34	0/2225	0.57	0/3004
16	Q	0.42	0/1464	0.55	0/1964
17	R	0.39	0/1226	0.53	0/1637
18	S	0.37	0/1472	0.60	0/1979
19	T	0.39	0/1299	0.55	0/1742
20	U	0.47	0/1245	0.57	0/1676
21	V	0.30	0/802	0.60	0/1087
22	W	0.41	0/973	0.70	1/1313 (0.1%)
23	X	0.41	0/995	0.57	0/1329
24	Y	0.30	0/1117	0.55	0/1496
25	Z	0.37	0/972	0.51	0/1293
26	a	0.29	0/426	0.54	0/570
27	b	0.47	0/1797	0.68	0/2419
28	c	0.31	0/749	0.51	0/1007
29	d	0.45	0/886	0.69	0/1190
30	e	0.49	0/1041	0.70	1/1393 (0.1%)
31	f	0.47	0/867	0.73	2/1167 (0.2%)
32	g	0.47	0/822	0.65	0/1099

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.33	0/770	0.53	0/1023
34	i	0.50	0/680	0.71	0/901
35	j	0.35	0/617	0.58	0/825
36	k	0.45	0/442	0.56	0/587
37	l	0.45	0/768	0.84	1/1016 (0.1%)
38	m	0.42	0/687	0.68	0/915
39	n	0.29	0/1712	0.56	0/2330
40	z	0.27	0/494	0.58	0/654
41	w	0.67	5/3135 (0.2%)	1.02	17/4255 (0.4%)
42	v	0.39	0/512	0.79	0/680
43	o	0.58	3/2647 (0.1%)	1.08	10/3582 (0.3%)
45	s	0.69	1/1016 (0.1%)	1.16	5/1368 (0.4%)
46	x	0.36	0/2880	0.39	0/4487
47	y	0.46	0/3699	0.48	0/5760
All	All	0.43	10/137819 (0.0%)	0.56	47/202858 (0.0%)

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	w	25	PRO	N-CA	18.21	1.70	1.47
41	w	298	PRO	N-CA	17.45	1.69	1.47
45	s	307	CYS	C-N	12.53	1.51	1.34
41	w	297	SER	C-N	10.51	1.45	1.34
41	w	143	CYS	C-N	7.32	1.50	1.33

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	w	297	SER	CA-C-N	18.57	140.09	120.04
41	w	297	SER	C-N-CA	18.57	140.09	120.04
45	s	247	ALA	N-CA-C	-15.40	83.63	108.73
43	o	367	THR	CA-C-N	14.11	137.47	119.84
43	o	367	THR	C-N-CA	14.11	137.47	119.84

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	67292	0	33821	648	0
2	B	1878	0	1946	45	0
3	C	3039	0	3113	54	0
4	D	2748	0	2863	59	0
5	E	1352	0	1383	29	0
6	F	1502	0	1572	31	0
7	G	1399	0	1501	11	0
8	H	1742	0	1834	25	0
9	J	1563	0	1665	20	0
10	K	1486	0	1554	28	0
11	L	1002	0	1048	21	0
12	M	1045	0	1136	14	0
13	N	1172	0	1215	22	0
14	O	1719	0	1779	39	0
15	P	2176	0	2116	32	0
16	Q	1440	0	1543	19	0
17	R	1209	0	1295	23	0
18	S	1436	0	1475	15	0
19	T	1275	0	1323	15	0
20	U	1222	0	1231	11	0
21	V	786	0	799	12	0
22	W	958	0	1023	21	0
23	X	984	0	1075	14	0
24	Y	1091	0	1155	14	0
25	Z	963	0	1073	25	0
26	a	415	0	429	6	0
27	b	1760	0	1843	41	0
28	c	741	0	797	9	0
29	d	872	0	914	12	0
30	e	1020	0	1091	23	0
31	f	849	0	880	14	0
32	g	812	0	875	19	0
33	h	763	0	842	11	0
34	i	665	0	668	15	0
35	j	611	0	682	2	0
36	k	435	0	475	12	0
37	l	756	0	817	19	0
38	m	680	0	725	20	0
39	n	1691	0	1687	53	0
40	z	491	0	518	16	0
41	w	3076	0	3107	137	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	v	500	0	524	32	0
43	o	2593	0	2625	180	0
44	p	1050	0	251	2	0
45	s	991	0	984	57	0
46	x	2576	0	1305	22	0
47	y	3310	0	1676	43	0
48	g	1	0	0	0	0
48	i	1	0	0	0	0
48	l	1	0	0	0	0
48	m	1	0	0	0	0
48	s	2	0	0	0	0
48	w	2	0	0	0	0
All	All	129144	0	94253	1688	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 1688 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)
41:w:65:LEU:HD13	41:w:71:TRP:CD2	1.43	1.50
38:m:42:CYS:SG	38:m:44:LYS:HG3	1.57	1.42
41:w:298:PRO:N	41:w:298:PRO:CA	1.69	1.42
42:v:46:PRO:C	42:v:49:ILE:HD11	1.43	1.41
43:o:344:TYR:HB3	43:o:345:PRO:CD	1.51	1.34

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	245/254 (96%)	217 (89%)	28 (11%)	0	100	100
3	C	379/387 (98%)	338 (89%)	40 (11%)	1 (0%)	36	69
4	D	359/362 (99%)	331 (92%)	28 (8%)	0	100	100
5	E	167/174 (96%)	153 (92%)	14 (8%)	0	100	100
6	F	187/191 (98%)	177 (95%)	10 (5%)	0	100	100
7	G	173/176 (98%)	153 (88%)	20 (12%)	0	100	100
8	H	221/256 (86%)	207 (94%)	14 (6%)	0	100	100
9	J	195/198 (98%)	187 (96%)	8 (4%)	0	100	100
10	K	184/199 (92%)	165 (90%)	19 (10%)	0	100	100
11	L	134/137 (98%)	124 (92%)	10 (8%)	0	100	100
12	M	133/138 (96%)	125 (94%)	8 (6%)	0	100	100
13	N	146/149 (98%)	124 (85%)	22 (15%)	0	100	100
14	O	201/204 (98%)	188 (94%)	13 (6%)	0	100	100
15	P	267/297 (90%)	251 (94%)	16 (6%)	0	100	100
16	Q	183/186 (98%)	169 (92%)	14 (8%)	0	100	100
17	R	148/189 (78%)	144 (97%)	4 (3%)	0	100	100
18	S	169/172 (98%)	161 (95%)	8 (5%)	0	100	100
19	T	157/160 (98%)	142 (90%)	15 (10%)	0	100	100
20	U	152/184 (83%)	138 (91%)	14 (9%)	0	100	100
21	V	97/121 (80%)	88 (91%)	9 (9%)	0	100	100
22	W	118/142 (83%)	106 (90%)	11 (9%)	1 (1%)	16	50
23	X	123/127 (97%)	114 (93%)	9 (7%)	0	100	100
24	Y	133/136 (98%)	121 (91%)	12 (9%)	0	100	100
25	Z	116/120 (97%)	106 (91%)	10 (9%)	0	100	100
26	a	50/59 (85%)	42 (84%)	8 (16%)	0	100	100
27	b	217/244 (89%)	197 (91%)	20 (9%)	0	100	100
28	c	95/105 (90%)	93 (98%)	2 (2%)	0	100	100
29	d	105/113 (93%)	88 (84%)	17 (16%)	0	100	100
30	e	125/130 (96%)	112 (90%)	12 (10%)	1 (1%)	16	50
31	f	104/107 (97%)	93 (89%)	11 (11%)	0	100	100
32	g	101/121 (84%)	87 (86%)	14 (14%)	0	100	100
33	h	96/100 (96%)	90 (94%)	6 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	i	82/88 (93%)	72 (88%)	9 (11%)	1 (1%)	10	41
35	j	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
36	k	48/51 (94%)	40 (83%)	8 (17%)	0	100	100
37	l	92/106 (87%)	84 (91%)	8 (9%)	0	100	100
38	m	87/92 (95%)	77 (88%)	10 (12%)	0	100	100
39	n	222/245 (91%)	195 (88%)	27 (12%)	0	100	100
40	z	56/432 (13%)	47 (84%)	9 (16%)	0	100	100
41	w	387/518 (75%)	347 (90%)	37 (10%)	3 (1%)	16	50
42	v	58/155 (37%)	57 (98%)	1 (2%)	0	100	100
43	o	316/640 (49%)	252 (80%)	58 (18%)	6 (2%)	6	33
45	s	126/364 (35%)	99 (79%)	24 (19%)	3 (2%)	4	29
All	All	6829/8407 (81%)	6174 (90%)	639 (9%)	16 (0%)	44	74

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	18	PRO
22	W	129	ASP
30	e	7	PRO
41	w	61	CYS
41	w	62	GLU

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	
2	B	189/196 (96%)	186 (98%)	3 (2%)	55	69
3	C	317/323 (98%)	313 (99%)	4 (1%)	61	71
4	D	288/289 (100%)	281 (98%)	7 (2%)	43	63
5	E	147/150 (98%)	144 (98%)	3 (2%)	48	65
6	F	169/171 (99%)	167 (99%)	2 (1%)	63	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	G	152/153 (99%)	151 (99%)	1 (1%)	76	78
8	H	183/208 (88%)	183 (100%)	0	100	100
9	J	163/164 (99%)	161 (99%)	2 (1%)	63	72
10	K	149/159 (94%)	149 (100%)	0	100	100
11	L	104/105 (99%)	103 (99%)	1 (1%)	68	75
12	M	107/109 (98%)	107 (100%)	0	100	100
13	N	118/119 (99%)	117 (99%)	1 (1%)	73	77
14	O	175/176 (99%)	174 (99%)	1 (1%)	78	80
15	P	227/245 (93%)	226 (100%)	1 (0%)	84	83
16	Q	150/151 (99%)	149 (99%)	1 (1%)	76	78
17	R	124/154 (80%)	124 (100%)	0	100	100
18	S	155/156 (99%)	154 (99%)	1 (1%)	78	80
19	T	136/137 (99%)	133 (98%)	3 (2%)	45	64
20	U	125/146 (86%)	125 (100%)	0	100	100
21	V	86/107 (80%)	86 (100%)	0	100	100
22	W	104/118 (88%)	103 (99%)	1 (1%)	68	75
23	X	108/110 (98%)	108 (100%)	0	100	100
24	Y	115/116 (99%)	115 (100%)	0	100	100
25	Z	104/105 (99%)	104 (100%)	0	100	100
26	a	41/47 (87%)	41 (100%)	0	100	100
27	b	184/205 (90%)	183 (100%)	1 (0%)	81	82
28	c	81/88 (92%)	81 (100%)	0	100	100
29	d	94/97 (97%)	92 (98%)	2 (2%)	47	65
30	e	109/111 (98%)	105 (96%)	4 (4%)	30	53
31	f	90/91 (99%)	90 (100%)	0	100	100
32	g	88/103 (85%)	86 (98%)	2 (2%)	44	63
33	h	80/82 (98%)	79 (99%)	1 (1%)	61	71
34	i	69/71 (97%)	68 (99%)	1 (1%)	59	71
35	j	68/69 (99%)	65 (96%)	3 (4%)	25	49
36	k	45/46 (98%)	44 (98%)	1 (2%)	45	64
37	l	81/91 (89%)	78 (96%)	3 (4%)	30	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	m	70/72 (97%)	64 (91%)	6 (9%)	10	33
39	n	192/211 (91%)	189 (98%)	3 (2%)	55	69
40	z	53/392 (14%)	53 (100%)	0	100	100
41	w	348/467 (74%)	336 (97%)	12 (3%)	32	55
42	v	53/129 (41%)	48 (91%)	5 (9%)	8	29
43	o	284/555 (51%)	256 (90%)	28 (10%)	7	28
45	s	110/323 (34%)	102 (93%)	8 (7%)	13	39
All	All	5835/7117 (82%)	5723 (98%)	112 (2%)	49	66

5 of 112 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	n	201	ASP
45	s	325	SER
42	v	19	THR
45	s	307	CYS
43	o	496	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 48 such sidechains are listed below:

Mol	Chain	Res	Type
29	d	105	GLN
40	z	402	GLN
30	e	98	HIS
38	m	34	HIS
41	w	130	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3141/3396 (92%)	811 (25%)	17 (0%)
46	x	120/121 (99%)	29 (24%)	0
47	y	155/158 (98%)	32 (20%)	0
All	All	3416/3675 (92%)	872 (25%)	17 (0%)

5 of 872 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	5	G
1	A	6	A
1	A	22	G
1	A	26	A
1	A	38	U

5 of 17 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	3121	U
1	A	3303	G
1	A	1355	A
1	A	1815	U
1	A	2101	C

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](#)

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

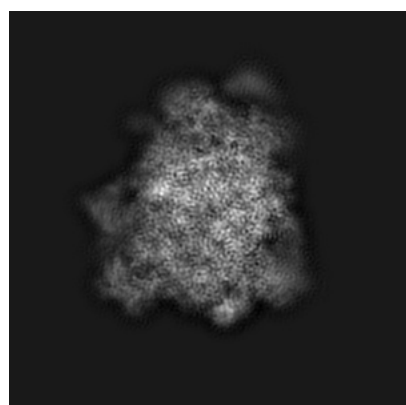
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10071. These allow visual inspection of the internal detail of the map and identification of artifacts.

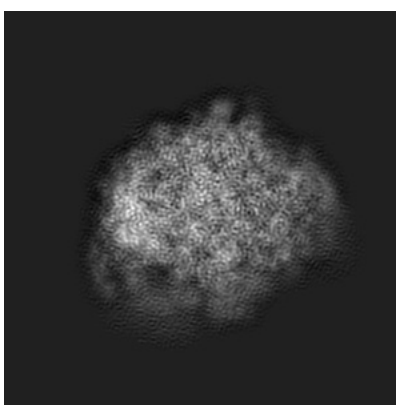
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

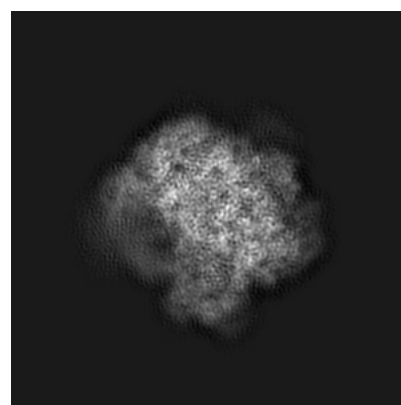
6.1.1 Primary map



X



Y

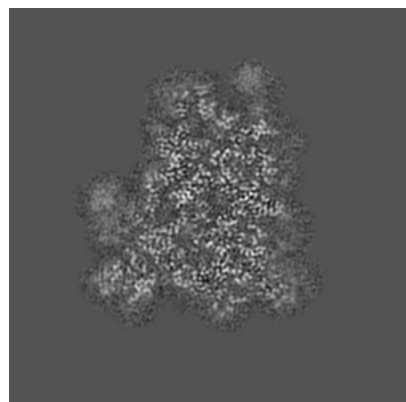


Z

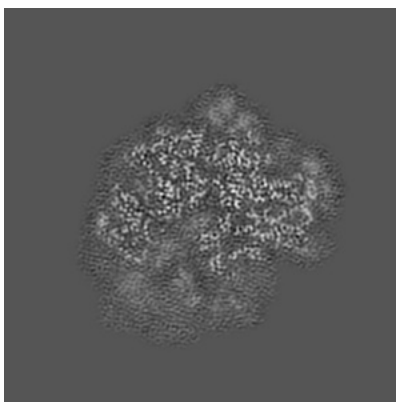
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

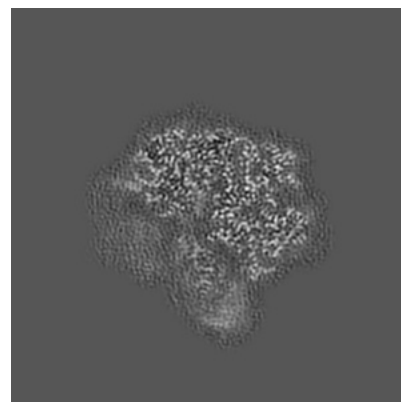
6.2.1 Primary map



X Index: 180



Y Index: 180

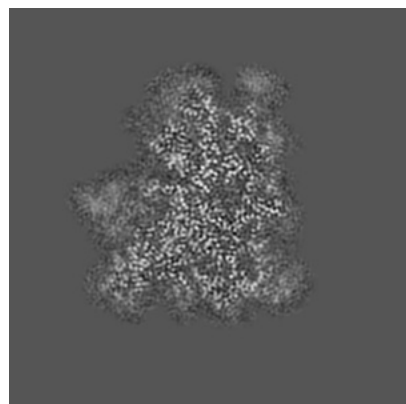


Z Index: 180

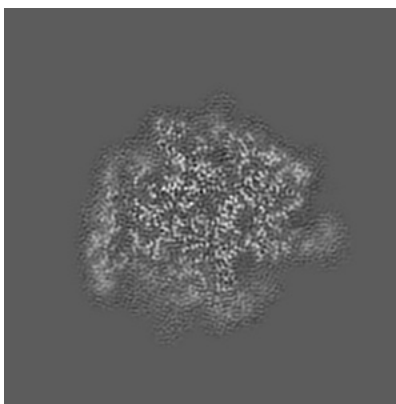
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

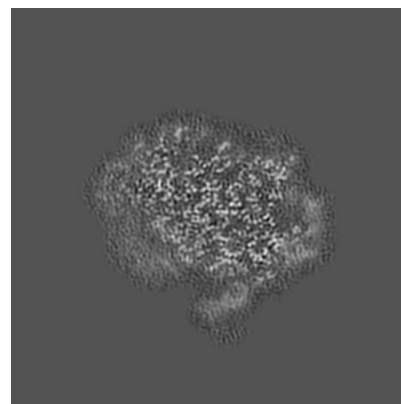
6.3.1 Primary map



X Index: 190



Y Index: 196

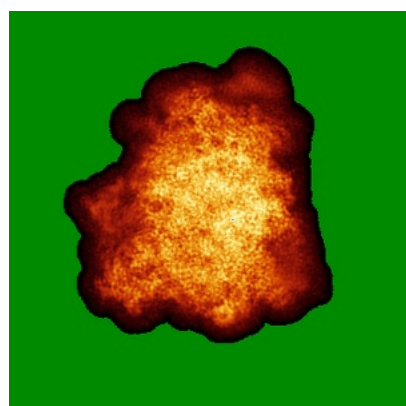


Z Index: 199

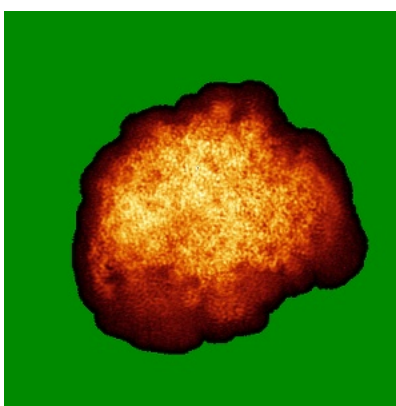
The images above show the largest variance slices of the map in three orthogonal directions.

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

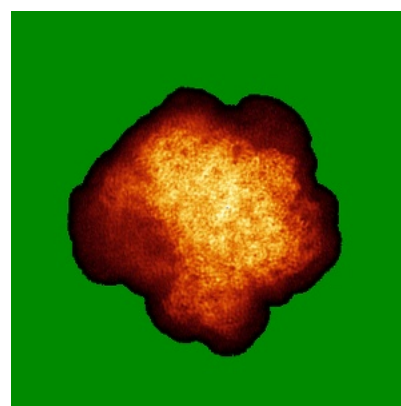
6.4.1 Primary map



X



Y

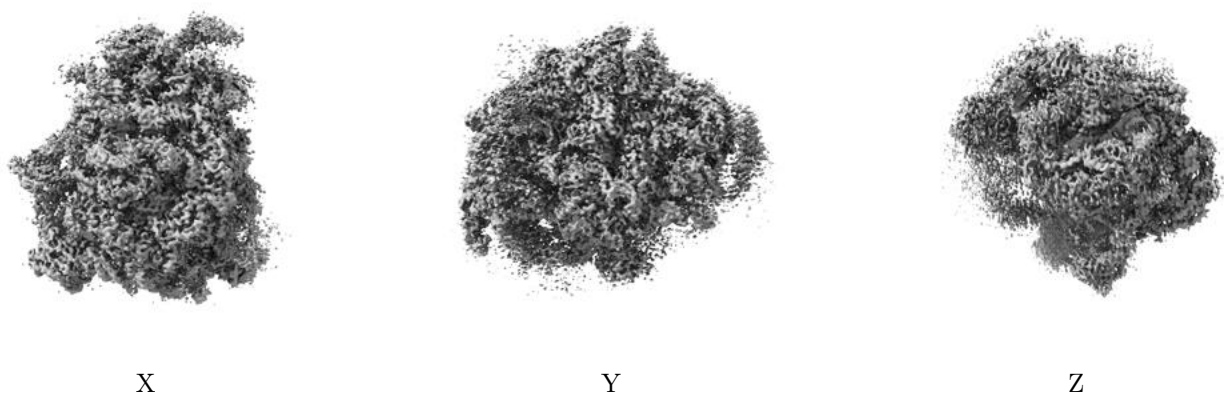


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.08. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

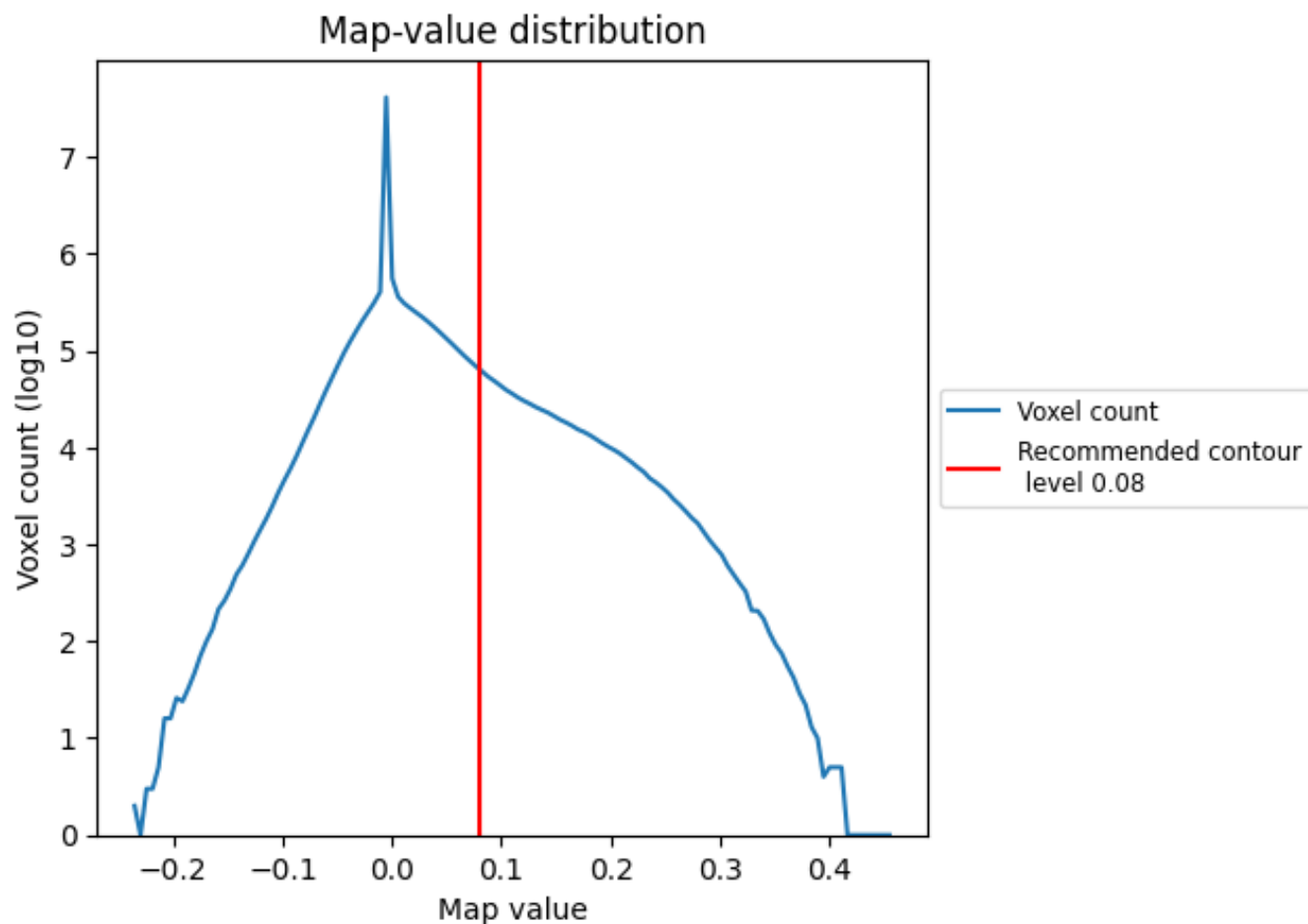
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

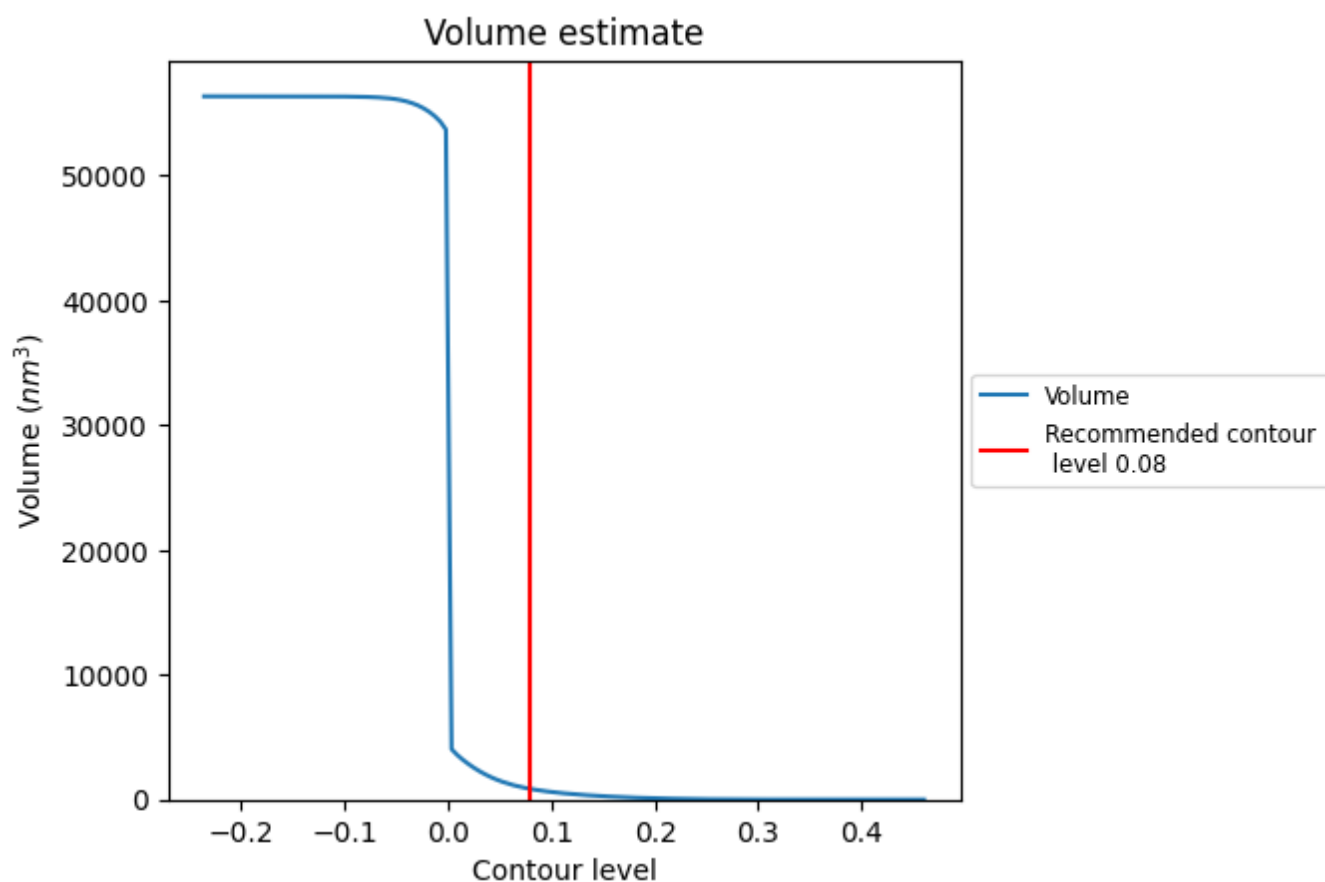
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

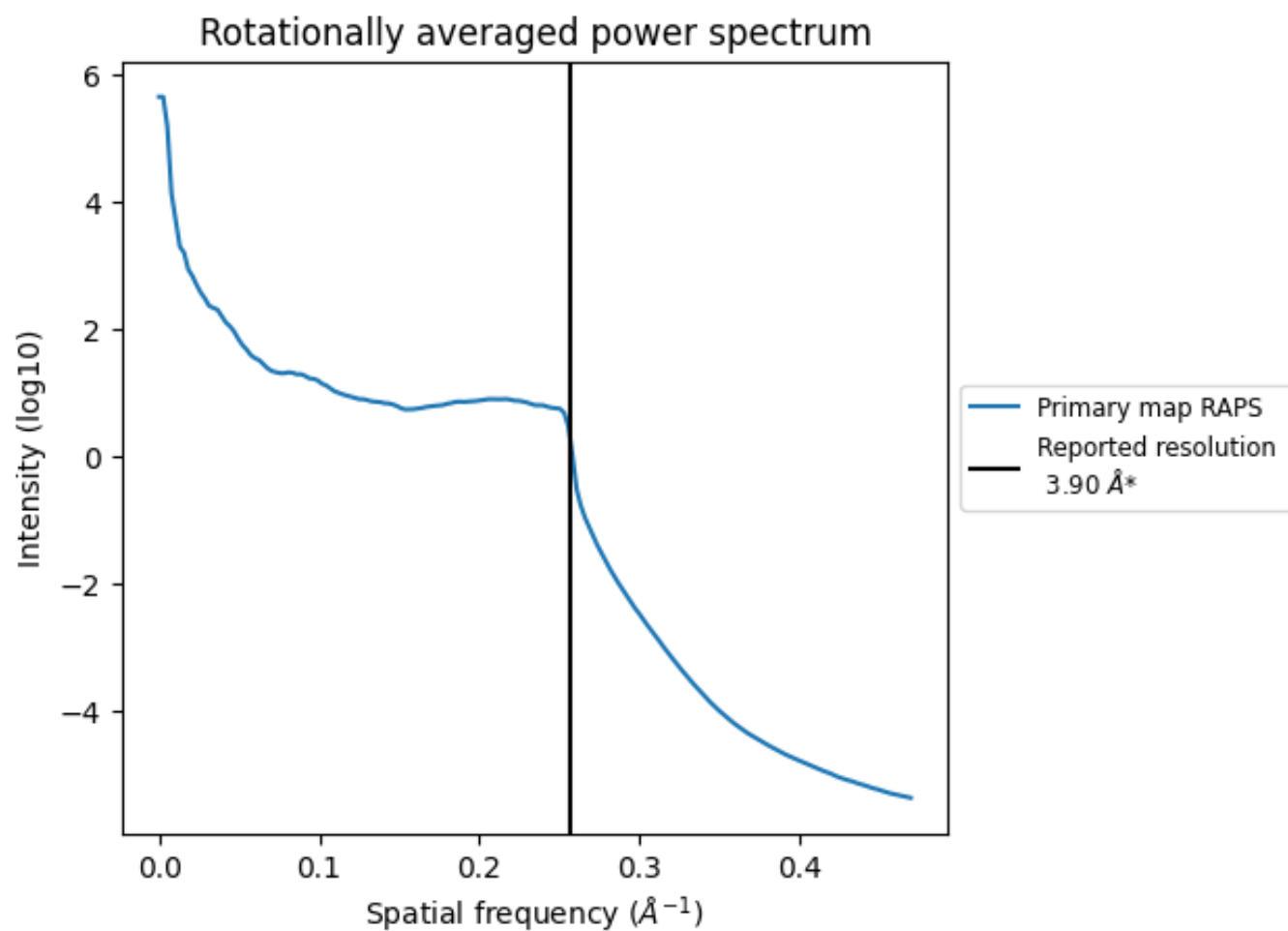
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 854 nm³; this corresponds to an approximate mass of 771 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

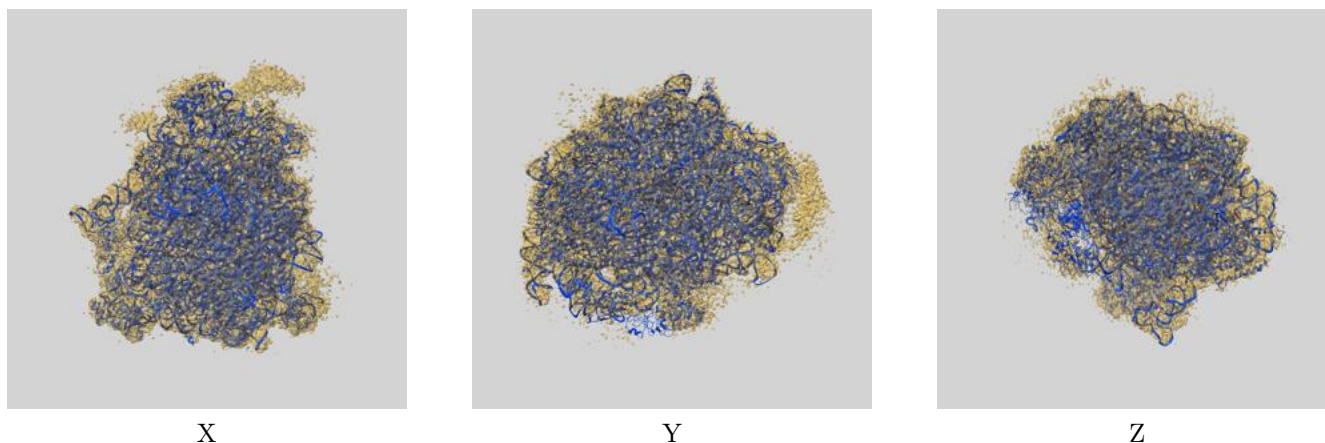
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

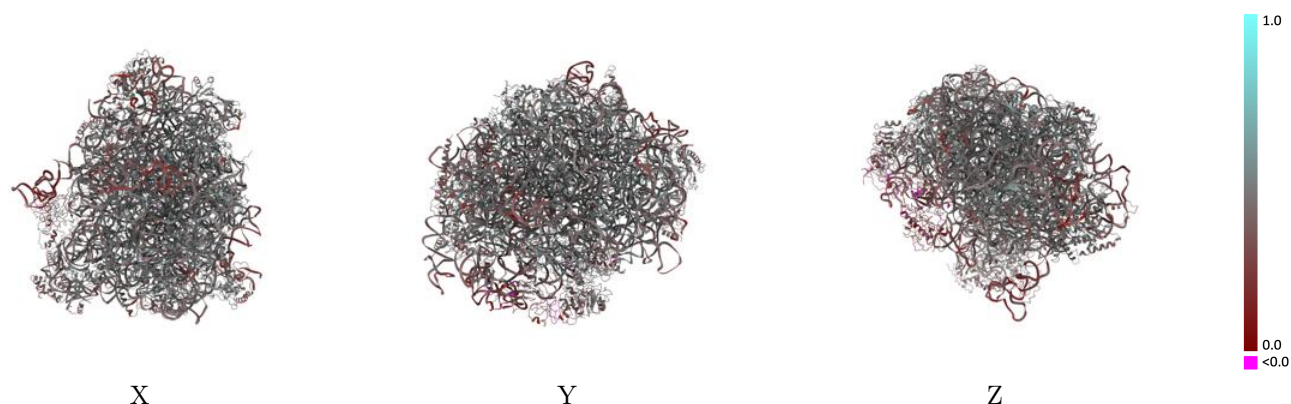
This section contains information regarding the fit between EMDB map EMD-10071 and PDB model 6S05. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.08 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](#)

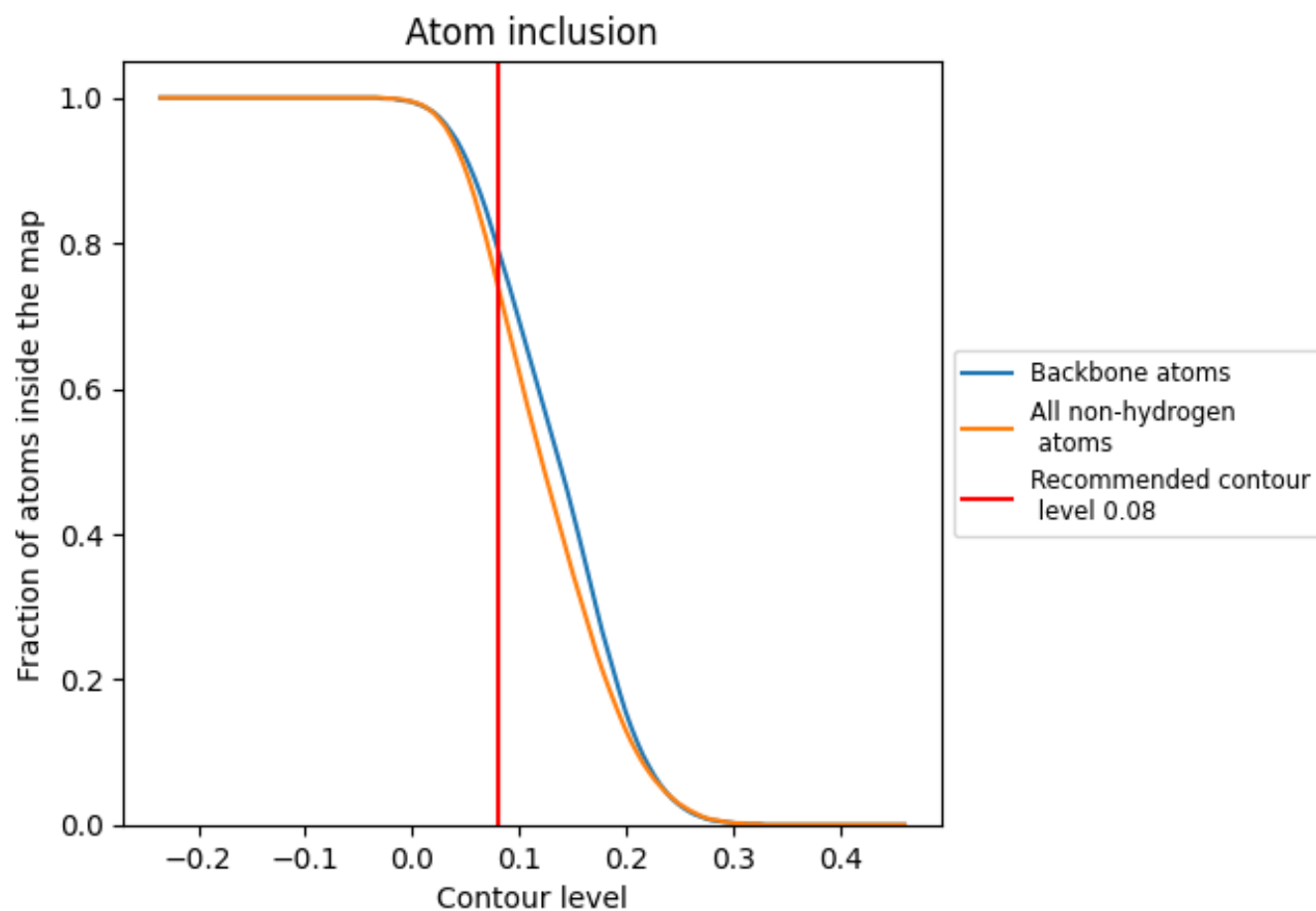


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 74% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7420	 0.4320
A	 0.8030	 0.4180
B	 0.7560	 0.4960
C	 0.7700	 0.4860
D	 0.7750	 0.4980
E	 0.6160	 0.3770
F	 0.4650	 0.3880
G	 0.5860	 0.4140
H	 0.6890	 0.4450
J	 0.7260	 0.4850
K	 0.7290	 0.4740
L	 0.6770	 0.4880
M	 0.7120	 0.4610
N	 0.7760	 0.4970
O	 0.7810	 0.5080
P	 0.7290	 0.4370
Q	 0.7860	 0.5120
R	 0.7740	 0.4820
S	 0.7250	 0.4790
T	 0.7190	 0.4770
U	 0.8030	 0.5060
V	 0.6850	 0.4450
W	 0.7270	 0.4830
X	 0.7880	 0.4920
Y	 0.6830	 0.4340
Z	 0.7880	 0.4830
a	 0.6720	 0.4740
b	 0.7710	 0.4730
c	 0.6720	 0.4210
d	 0.7330	 0.4880
e	 0.7510	 0.5050
f	 0.7610	 0.4960
g	 0.7460	 0.4890
h	 0.5780	 0.4430
i	 0.8110	 0.5150



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Chain	Atom inclusion	Q-score
j	 0.6540	 0.4560
k	 0.7490	 0.5190
l	 0.7370	 0.4990
m	 0.7200	 0.4840
n	 0.5690	 0.4060
o	 0.1270	 0.2660
p	 0.4740	 0.3440
s	 0.0150	 0.1980
v	 0.5290	 0.4540
w	 0.3740	 0.3650
x	 0.9090	 0.4310
y	 0.8960	 0.4560
z	 0.2580	 0.4300