



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 04:25 AM UTC

PDB ID : 6M62 / pdb_00006m62
EMDB ID : EMD-30108
Title : Cryo-Em structure of eukaryotic pre-60S ribosome subunit from *Saccharomyces cerevisiae* rpf2 delta 255-344 strain, C4 state.
Authors : Li, Y.; Micic, J.
Deposited on : 2020-03-12
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

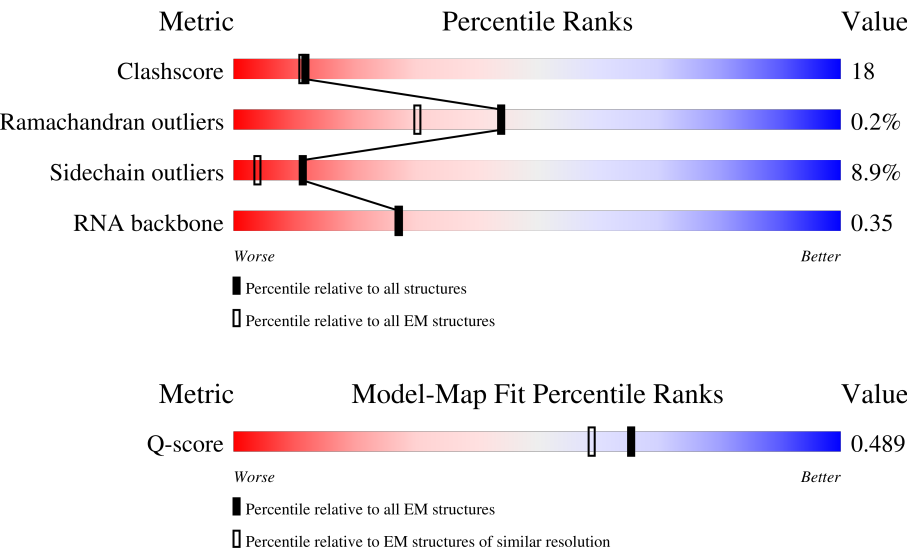
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.20 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	15020 (2.70 - 3.70)

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

Mol	Chain	Length	Quality of chain
1	1	3396	
2	2	158	
3	3	121	

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Mol	Chain	Length	Quality of chain
4	4	593	
5	5	120	
6	6	232	
7	A	254	
8	B	387	
9	C	362	
10	D	297	
11	E	176	
12	F	244	
13	G	256	
14	H	191	
15	I	166	
16	J	174	
17	K	376	
18	L	199	
19	M	138	
20	N	204	
21	O	199	
22	P	184	
23	Q	186	
24	R	189	
25	S	172	
26	T	160	
27	U	121	
28	V	137	

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Mol	Chain	Length	Quality of chain
29	W	236	
30	X	142	
31	Y	127	
32	Z	136	
33	a	149	
34	b	647	
35	c	105	
36	d	113	
37	e	130	
38	f	107	
39	g	121	
40	h	120	
41	i	100	
42	j	88	
43	k	78	
44	l	51	
45	m	486	
46	n	605	
47	o	220	
48	p	92	
49	q	455	
50	r	261	
51	s	520	
52	t	322	
53	u	199	

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Mol	Chain	Length	Quality of chain
54	v	254	
55	w	203	
56	x	515	
57	y	245	
58	z	106	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
60	GTP	b	701	-	-	X	-

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 153289 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 RDN25-1 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2972	Total	C	N	O	P	0	0
			63583	28398	11464	20749	2972		

- Molecule 2 is a RNA chain called RDN58-1 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 3 is a RNA chain called RDN5-2 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 4 is a protein called Probable metalloprotease ARX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	516	Total	C	N	O	S	0	0
			3999	2530	688	766	15		

- Molecule 5 is a protein called rRNA-processing protein CGR1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	73	Total	C	N	O	S	0	0
			645	395	133	114	3		

- Molecule 6 is a RNA chain called ITS2-1 miscRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	65	Total	C	N	O	P	0	0
			1370	614	228	463	65		

- Molecule 7 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	213	Total	C	N	O	S	0	0
			1634	1023	326	284	1		

- Molecule 8 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	386	Total	C	N	O	S	0	0
			3081	1956	584	533	8		

- Molecule 9 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	361	Total	C	N	O	S	0	0
			2749	1730	522	494	3		

- Molecule 10 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	276	Total	C	N	O	S	0	0
			2211	1397	391	421	2		

- Molecule 11 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 12 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 13 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	233	Total	C	N	O	S	0	0
			1817	1159	326	329	3		

- Molecule 14 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 15 is a protein called Bud site selection protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	I	131	Total	C	N	O	S	0	0
			1059	662	195	198	4		

- Molecule 16 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	J	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 17 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	K	256	Total	C	N	O	S	0	0
			2064	1332	342	387	3		

- Molecule 18 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	L	187	Total	C	N	O		0	0
			1499	934	307	258			

- Molecule 19 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	M	137	Total	C	N	O	S	0	0
			1059	678	200	179	2		

- Molecule 20 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	N	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 21 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	O	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 22 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	P	183	Total	C	N	O		0	0
			1442	896	287	259			

- Molecule 23 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Q	134	Total	C	N	O	S	0	0
			1035	659	196	179	1		

- Molecule 24 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	R	156	Total	C	N	O		0	0
			1258	781	265	212			

- Molecule 25 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 26 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	T	119	Total	C	N	O	S	0	0
			943	595	180	165	3		

- Molecule 27 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	U	106	Total	C	N	O		0	0
			844	545	138	161			

- Molecule 28 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	V	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 29 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	W	234	Total	C	N	O	S	0	0
			1885	1194	323	362	6		

- Molecule 30 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	X	141	Total	C	N	O	S	0	0
			1100	705	196	197	2		

- Molecule 31 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Y	126	Total	C	N	O		0	0
			993	625	192	176			

- Molecule 32 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Z	135	Total	C	N	O		0	0
			1092	710	202	180			

- Molecule 33 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	a	93	Total	C	N	O	S	0	0
			735	479	130	125	1		

- Molecule 34 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	b	642	Total	C	N	O	S	0	0
			5185	3251	938	970	26		

- Molecule 35 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	c	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 36 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	d	107	Total	C	N	O	S	0	0
			873	553	165	154	1		

- Molecule 37 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	e	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 38 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	f	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 39 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	g	112	Total	C	N	O	S	0	0
			881	546	179	152	4		

- Molecule 40 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	h	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 41 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	i	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 42 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	j	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 43 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	k	77	Total	C	N	O	S	0	0
			612	391	115	106			

- Molecule 44 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	l	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 45 is a protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	m	453	Total	C	N	O	S	0	0
			3648	2308	657	674	9		

- Molecule 46 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	n	371	Total	C	N	O	S	0	0
			3030	1963	523	534	10		

- Molecule 47 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	o	133	Total	C	N	O	S	0	0
			1107	716	198	189	4		

- Molecule 48 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	p	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 49 is a protein called Ribosome biogenesis protein NOP53.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	q	151	Total	C	N	O	S	0	0
			1258	793	226	238	1		

- Molecule 50 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	r	230	Total	C	N	O	S	0	0
			1860	1177	352	324	7		

- Molecule 51 is a protein called Nuclear GTP-binding protein NUG1.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	s	69	Total	C	N	O	S	0	0
			573	359	113	98	3		

- Molecule 52 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	t	287	Total	C	N	O	S	0	0
			2306	1459	427	417	3		

- Molecule 53 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	u	150	Total	C	N	O	S	0	0
			1265	793	253	210	9		

- Molecule 54 is a protein called Ribosome biogenesis protein RPF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	v	245	Total	C	N	O	S	0	0
			1985	1275	344	353	13		

- Molecule 55 is a protein called Regulator of ribosome biosynthesis.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	w	182	Total	C	N	O	S	0	0
			1448	911	261	271	5		

- Molecule 56 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	x	395	Total	C	N	O	S	0	0
			3093	1941	559	573	20		

- Molecule 57 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	y	244	Total	C	N	O	S	0	0
			1849	1146	319	377	7		

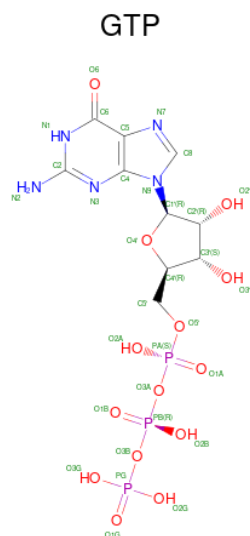
- Molecule 58 is a protein called UPF0642 protein YBL028C.

Mol	Chain	Residues	Atoms				AltConf	Trace
58	z	55	Total	C	N	O	0	0
			444	273	88	83		

- Molecule 59 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
59	I	1	Total	Zn	0
			1	1	
59	j	1	Total	Zn	0
			1	1	
59	p	1	Total	Zn	0
			1	1	
59	u	1	Total	Zn	0
			1	1	

- Molecule 60 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



Mol	Chain	Residues	Atoms					AltConf
60	b	1	Total 32	C 10	N 5	O 14	P 3	0
60	m	1	Total 32	C 10	N 5	O 14	P 3	0

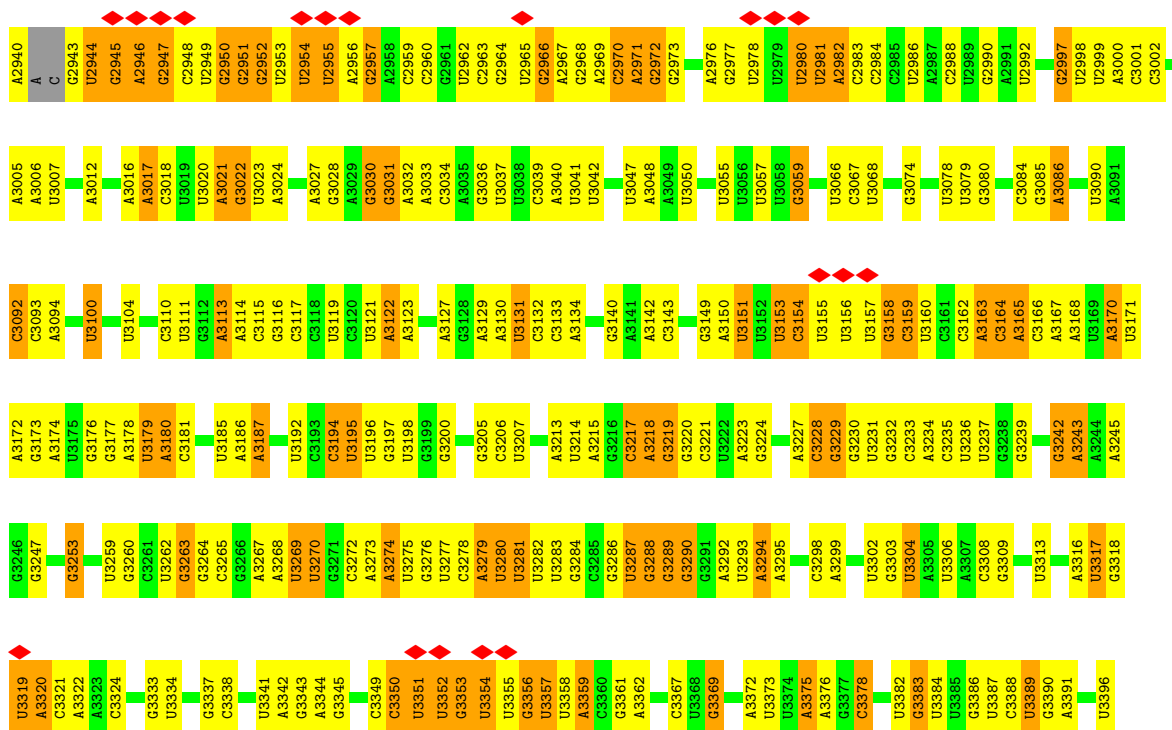
- Molecule 61 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
61	b	1	Total Mg 1 1	0
61	m	1	Total Mg 1 1	0



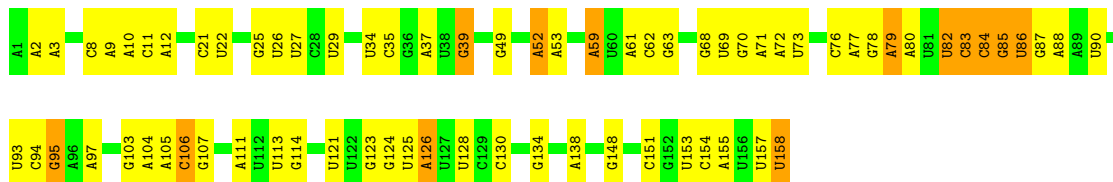


U2865	C2682	C2682	U2558	C	G2429	G2355	U	A	A	A2142	C	U
U2866	G2623	G2623	U2559	C	A2430	A2356	A	A	A	A2143	G	U
U2867	C2624	C2624	A2561	A	C2431	A2357	G	G	G	A2144	C	C
U2868	C2625	C2625	A2562	C	A2432	A2358	C	U	U		C	U
U2869	A2626	A2626		U	U2433		A	A	A	U2147	G	A
U2870	C2627	C2627		A	U2434		C	C	C	U2148	C	U
U2871	A2628	A2628	C2567	C	G2435	A2363	A	A	A	A2149	G	G
U2872	U2629	U2629	C2568	C	U2436	G2364	A	A	A		U	U
U2873	C2630	C2630	U2570	U	A2437	A2367	U	A	A	U2154	G	C
U2874	U2631	U2631	U2571	U	A2438		G	A	A	G2155	C	G
U2875	G2632	G2632	U2572	U	A2439		C	A	A	C2156	G	U
U2876	U2633	U2633	C2572	A	G2440	G2371	C	U	U	G2157	C	A
U2877	U2634	U2634	G2573	U2501	A2441	A	C	C	C	U2158	A	U
U2878	G2574	G2574	G2575	A2502	G2442	A	C	C	C	U2159	A	U
U2879	G2576	G2576	G2577	A2503	A2443	G	G	A	A	G2160	A	A
U2880	G2578	G2578	U2578	U2504	C2444	G2376	C	A	A	C2161	U	C
U2881	U2579	U2579	G2580	U2505	A2445	G2377	C	C	C	U2162	U	U
U2882	U2581	U2581	U2582	U2506	U		U	U	U	C2163	U	U
U2883	C2583	C2583	U2583	U2507	A		A	A	A	A2164	G	U
U2884	G2584	G2584	U2584	U2508	G	G2382	C	A	A	G2165	C	C
U2885	G2585	G2585	U2585	A2511	A	G2385	U	A	A	G2166	G	G
U2886	G2586	G2586	U2586	U2512	G	C2392	C	A	A	G2167	G	U
U2887	U2587	U2587	U2587	U2513	G	G2393	U	U	U	A2168	C	C
U2888	U2588	U2588	U2588	U2514	U	G2394	A	A	A	G2169	C	U
U2889	U2589	U2589	U2589	U2515	G	G2395	G	G	G	U2170	C	U
U2890	U2590	U2590	U2590	U2516	U	G2396	A	A	A		U	U
U2891	U2591	U2591	U2591	U2517	G	A2397	G	G	G	G2174	U	U
U2892	U2592	U2592	U2592	U2518	A	A2398	C	C	C	U2175	G	U
U2893	U2593	U2593	U2593	U2519	A	A2399	C	C	C	U2176	U	U
U2894	U2594	U2594	U2594	U2520	A	A2400	C	C	C	U2177	U	U
U2895	U2595	U2595	U2595	U2521	U	A2401	C	C	C	A2178	U	U
U2896	U2596	U2596	U2596	U2522	G	A2402	C	C	C	G2185	G	U
U2897	U2597	U2597	U2597	U2523	A	G2403	C	C	C	G2186	A	A
U2898	U2598	U2598	U2598	U2524	A	A2404	C	C	C	G2187	A	A
U2899	U2599	U2599	U2599	U2525	U	G2405	C	C	C	U2190	G	C
U2900	U2600	U2600	U2600	U2526	G	C2406	A	A	A	C2192	G	C
U2901	A2601	A2601	U2601	U2527	G	U2407	A	A	A	C2193	C	U
U2902	G2602	G2602	U2602	U2528	A	U2408	A	A	A	A2118	U	U
U2903	U2603	U2603	U2603	U2529	C	U2409	U	U	U	A2119	U	U
U2904	U2604	U2604	U2604	U2530	U	U2410	C	C	C	A2120	G	G
U2905	G2605	G2605	U2605	U2531	G	U2411	C	C	C	G2121	U	U
U2906	U2606	U2606	U2606	U2532	U	G2412	U	U	U	G2122	U	U
U2907	G2607	G2607	U2607	U2533	C	A2413	C	C	C	A2126	A	A
U2908	U2608	U2608	U2608	U2534	C	C2414	C	C	C	U2127	G	G
U2909	A2609	A2609	U2609	U2535	G	C2415	A	A	A	G2128	U	U
U2910	U2610	U2610	U2610	U2536	C	U2416	C	C	C	U2129	C	C
U2911	G2611	G2611	U2611	U2537	U	U2417	U	U	U	G2130	U	U
U2912	U2612	U2612	U2612	U2538	G	G2418	C	C	C	A2131	U	U
U2913	U2613	U2613	U2613	U2539	A	A2419	C	C	C	C2132	U	U
U2914	G2614	G2614	U2614	U2540	U	C2420	C	C	C	U2133	G	G
U2915	U2615	U2615	U2615	U2541	G	U2421	U	U	U		U	U
U2916	U2616	U2616	U2616	U2542	A	U2422	C	C	C	U2137	A	A
U2917	A2617	A2617	U2617	U2543	C	U2423	A	A	A	A2138	U	U
U2918	G2618	G2618	U2618	U2544	U	G2424	U	U	U	A2139	G	G
U2919	U2619	U2619	U2619	U2545	G	U2425	C	C	C	U2140	A	A
U2920	U2620	U2620	U2620	U2546	A	U2426	U	U	U	U2141	C	C
U2921	G2621	G2621	U2621	U2547	U	U2427	C	C	C			
U2922	U2622	U2622	U2622	U2548	A							
U2923	U2623	U2623	U2623	U2549	G							
U2924	A2624	A2624	U2624	U2550	A							
U2925	U2625	U2625	U2625	U2551	A							
U2926	G2626	G2626	U2626	U2552	A							
U2927	U2627	U2627	U2627	U2553	U							
U2928	A2628	A2628	U2628	U2554	A							
U2929	U2629	U2629	U2629	U2555	U							
U2930	G2630	G2630	U2630	U2556	A							
U2931	U2631	U2631	U2631	U2557	U							
U2932	A2632	A2632	U2632	U2558	A							
U2933	U2633	U2633	U2633	U2559	U							
U2934	G2634	G2634	U2634	U2560	A							
U2935	U2635	U2635	U2635	U2561	A							
U2936	A2636	A2636	U2636	U2562	U							
U2937	U2637	U2637	U2637	U2563	U							
U2938	G2638	G2638	U2638	U2564	A							
U2939	U2639	U2639	U2639	U2565	U							
U2940	A2640	A2640	U2640	U2566	A							
U2941	U2641	U2641	U2641	U2567	U							
U2942	G2642	G2642	U2642	U2568	A							
U2943	A2643	A2643	U2643	U2569	U							
U2944	G2644	G2644	U2644	U2570	A							
U2945	U2645	U2645	U2645	U2571	G							
U2946	A2646	A2646	U2646	U2572	A							
U2947	U2647	U2647	U2647	U2573	G							
U2948	G2648	G2648	U2648	U2574	A							
U2949	A2649	A2649	U2649	U2575	U							
U2950	U2650	U2650	U2650	U2576	A							
U2951	G2651	G2651	U2651	U2577	G							
U2952	A2652	A2652	U2652	U2578	A							
U2953	U2653	U2653	U2653	U2579	U							
U2954	G2654	G2654	U2654	U2580	A							
U2955	A2655	A2655	U2655	U2581	G							
U2956	U2656	U2656	U2656	U2582	A							
U2957	G2657	G2657	U2657	U2583	U							
U2958	A2658	A2658	U2658	U2584	A							
U2959	U2659	U2659	U2659	U2585	U							
U2960	G2660	G2660	U2660	U2586	A							
U2961	A2661	A2661	U2661	U2587	U							
U2962	U2662	U2662	U2662	U2588	G							
U2963	G2663	G2663	U2663	U2589	A							
U2964	U2664	U2664	U2664	U2590	U							
U2965	A2665	A2665	U2665	U2591	A							
U2966	U2666	U2666	U2666	U2592	G							
U2967	G2667	G2667	U2667	U2593	A							
U2968	A2668	A2668	U2668	U2594	U							
U2969	U2669	U2669	U2669	U2595	A							
U2970	G2670	G2670	U2670	U2596	A							
U2971	A2671	A2671	U2671	U2597	U							
U2972	U2672	U2672	U2672	U2598	G							
U2973	G2673	G2673	U2673	U2599	A							
U2974	A2674	A2674	U2674	U2600	U							
U2975	U2675	U2675	U2675	U2601	A							
U2976	G2676	G2676	U2676	U2602	G							
U2977	A2677	A2677	U2677	U2603	U							
U2978	U2678	U2678	U2678	U2604	C							
U2979	G2679	G2679	U2679	U2605	U							
U2980	A2680	A2680	U2680	U2606	G							
U2981	U2681	U2681	U2681	U2607	U							
U2982	G2682	G2682	U2682	U2608	C							
U2983	A2683	A2683	U2683	U2609	A							
U2984	U2684	U2684	U2684	U2610	U							
U2985	G2685	G2685	U2685	U2611	G							
U2986	A2686	A2686	U2686	U2612	U							
U2987	U2687	U2687	U2687	U2613	A							
U2988	G2688	G2688	U2688	U2614	G							
U2989	A2689	A2689	U2689	U2615	A							
U2990	U2690	U2690	U2690	U2616	U							
U2991	G2691	G2691	U2691	U2617	A							
U2992	A2692	A2692	U2692	U2618	U							
U2993	U2693	U2693	U2693	U2619	G							
U2994	G2694	G2694	U2694	U2620	U							
U2995	A2695	A2695	U2695	U2621	A							
U2996	U2696	U2696	U2696	U2622	U							



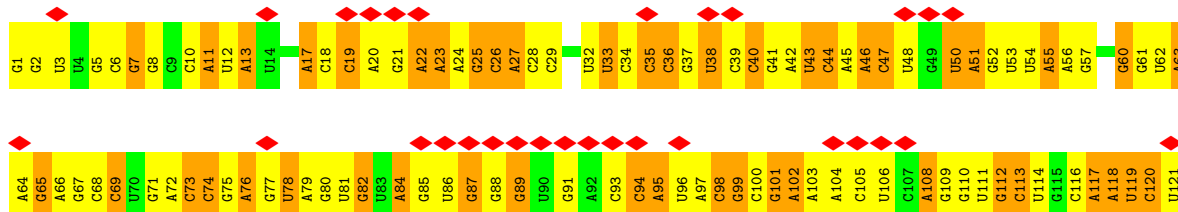
• Molecule 2: RDN58-1 rRNA

Chain 2: 55% 37% 8%



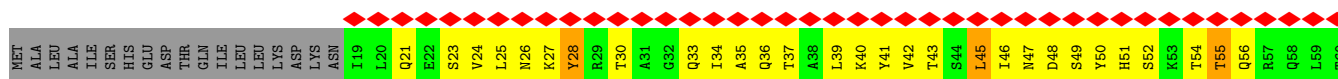
• Molecule 3: RDN5-2 rRNA

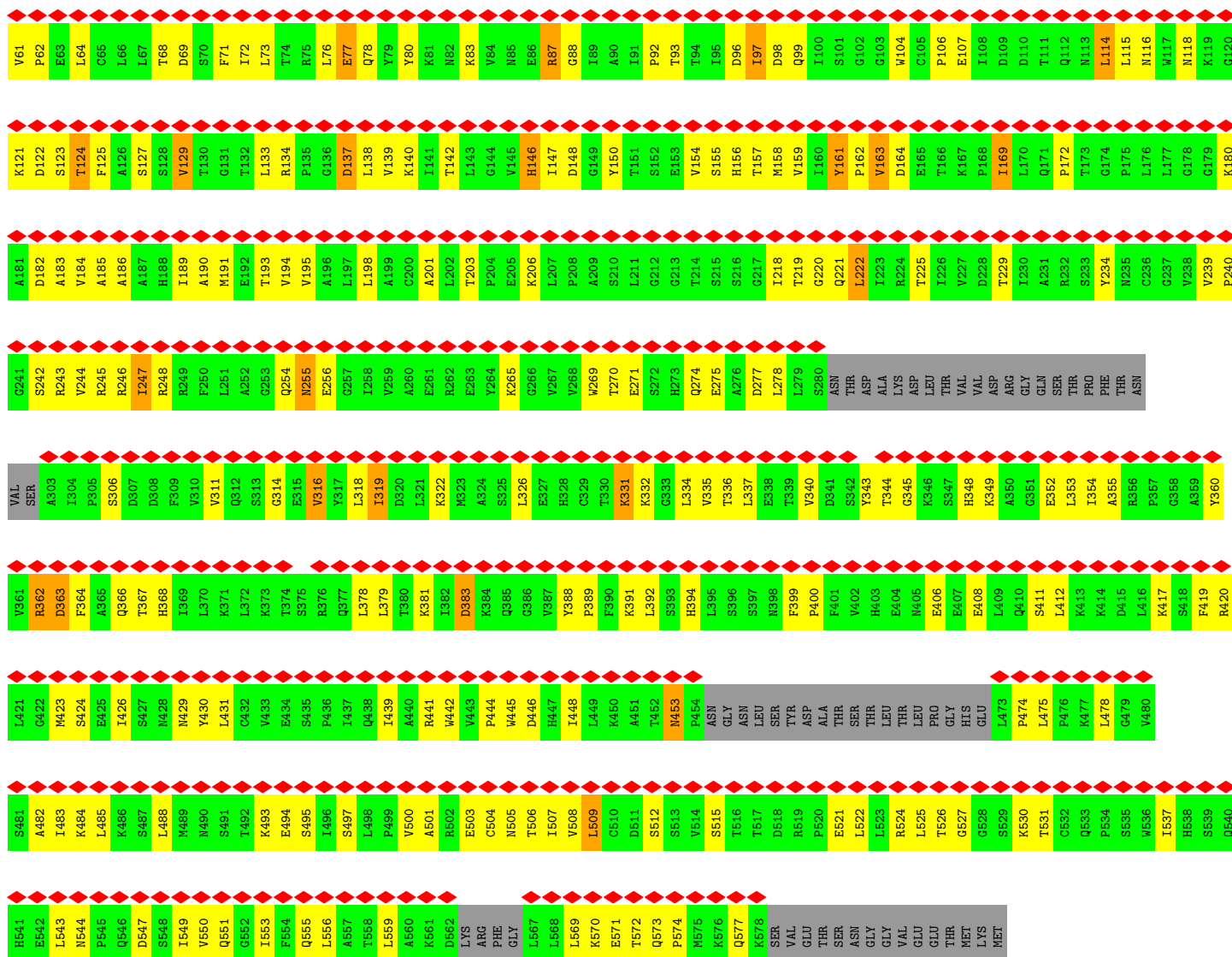
Chain 3: 25% 13% 48% 39%



• Molecule 4: Probable metalloprotease ARX1

Chain 4: 87% 46% 37% 13%

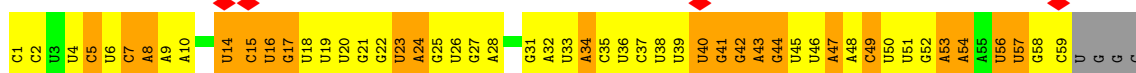


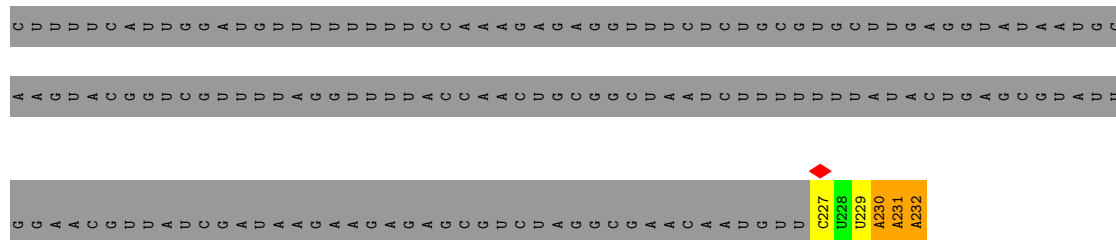


• Molecule 5: rRNA-processing protein CGR1

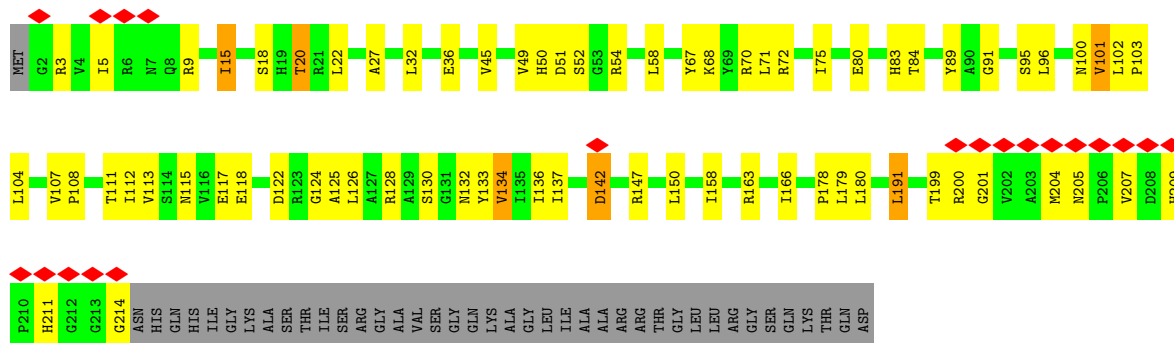


• Molecule 6: ITS2-1 miscRNA

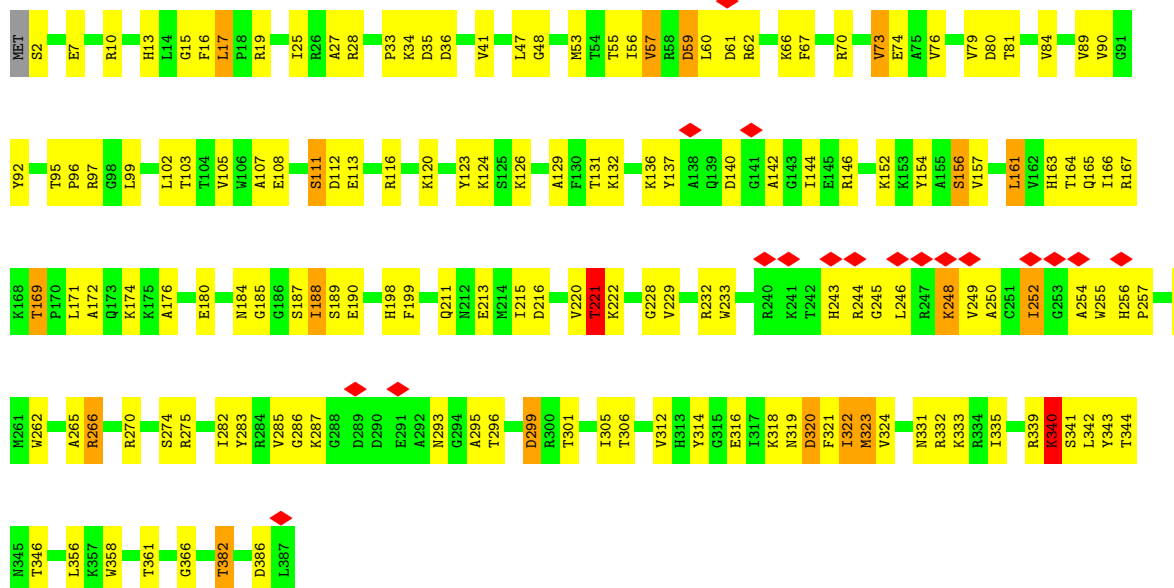




• Molecule 7: 60S ribosomal protein L2-A

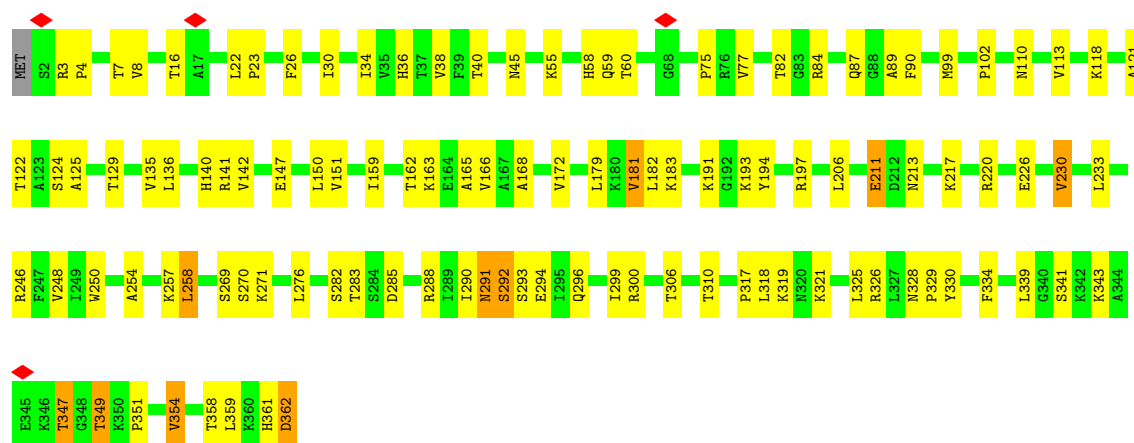


• Molecule 8: 60S ribosomal protein L3

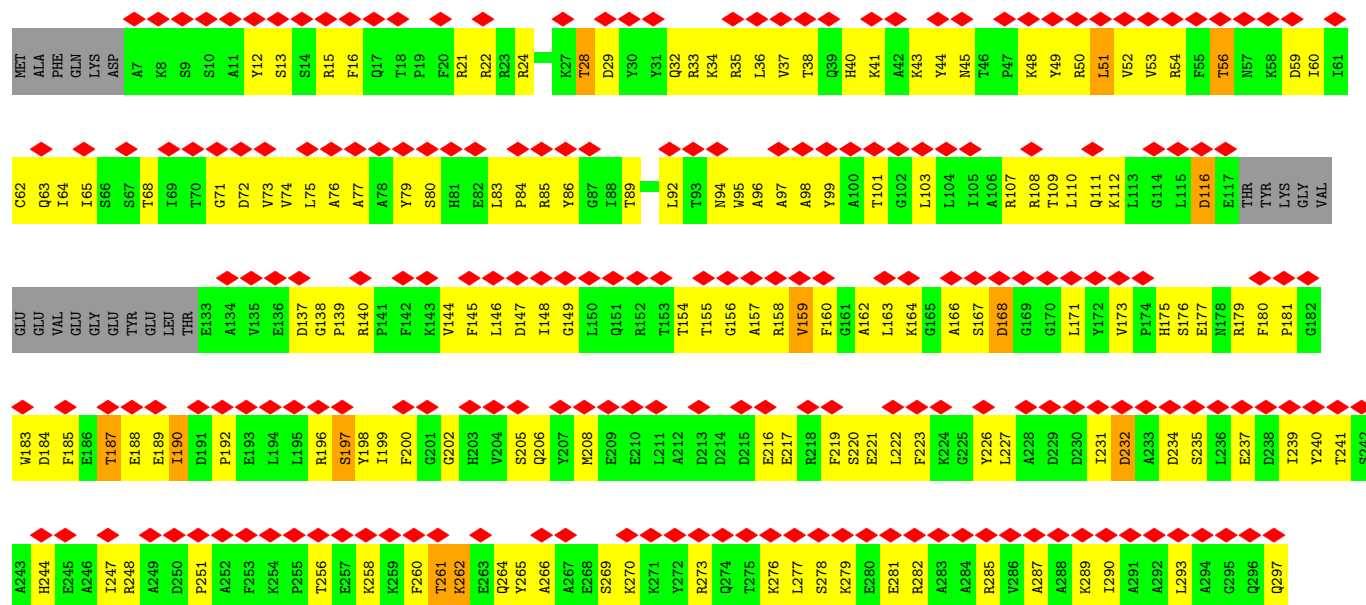
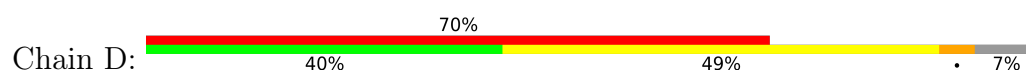


• Molecule 9: 60S ribosomal protein L4-A

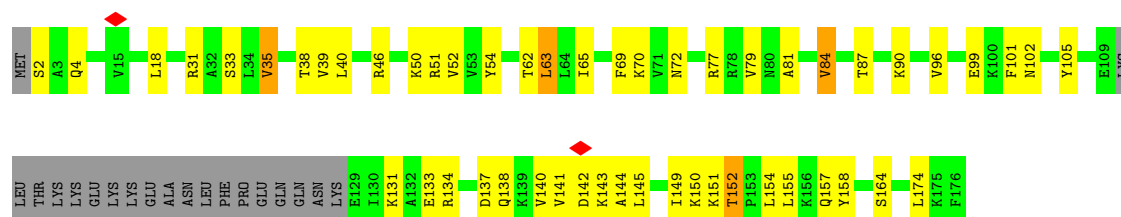




• Molecule 10: 60S ribosomal protein L5

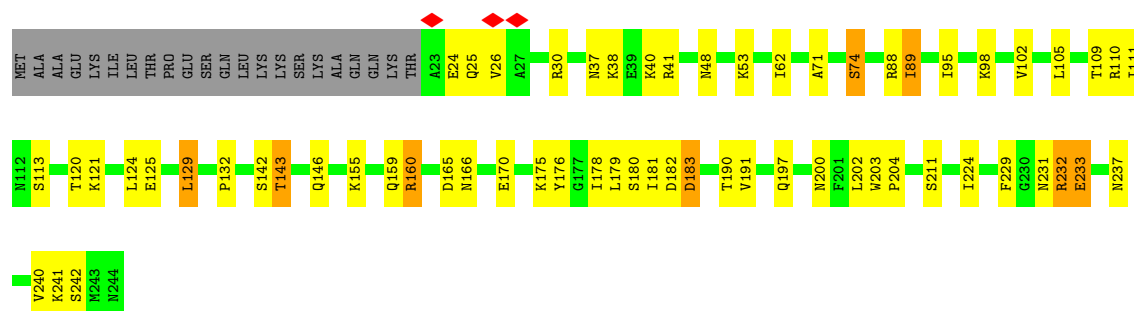


• Molecule 11: 60S ribosomal protein L6-A

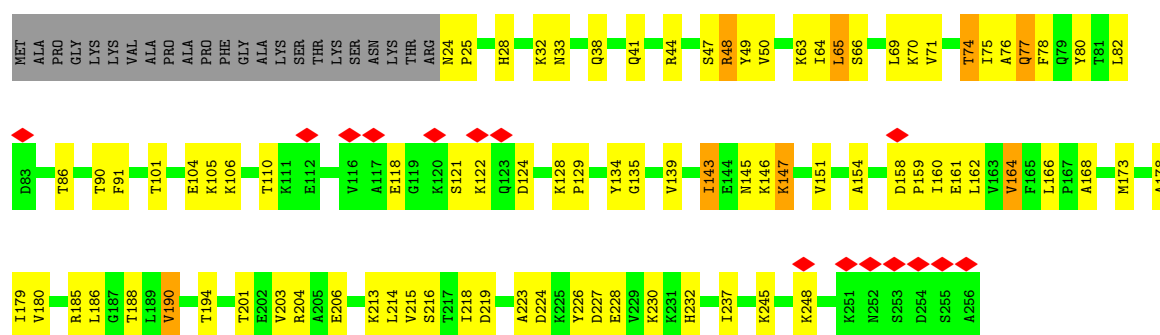


• Molecule 12: 60S ribosomal protein L7-A

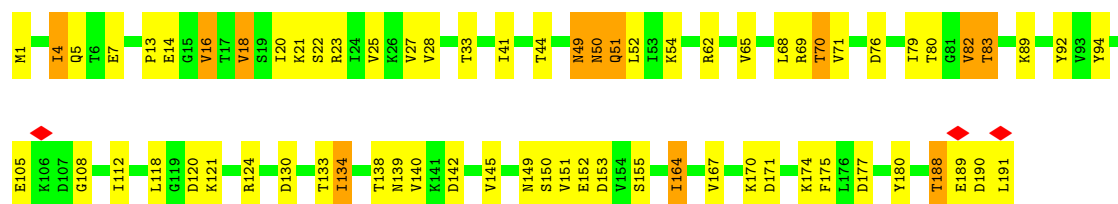




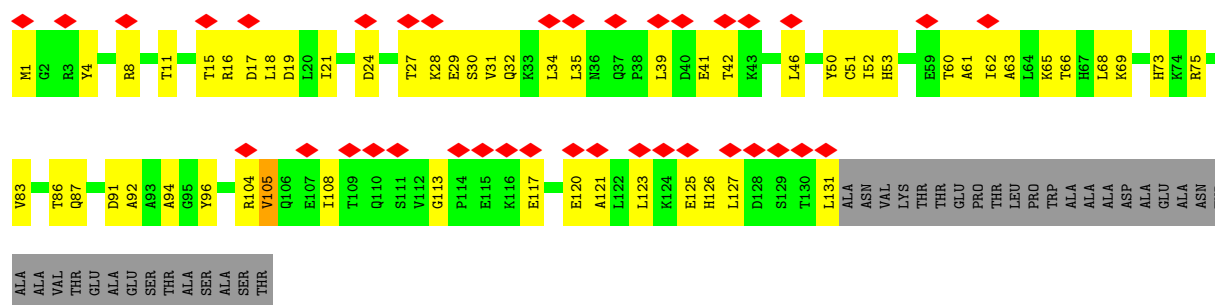
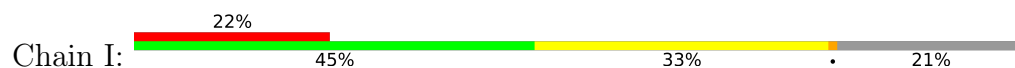
- Molecule 13: 60S ribosomal protein L8-A



- Molecule 14: 60S ribosomal protein L9-A

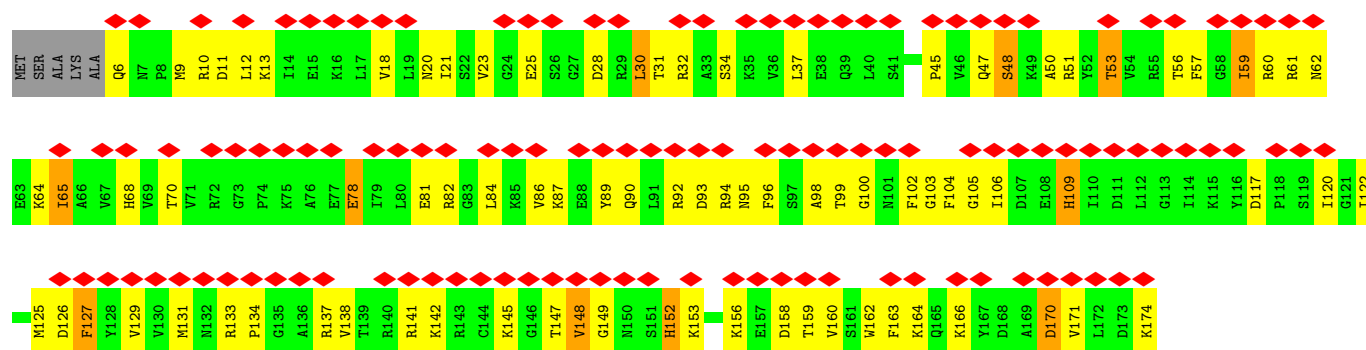


- Molecule 15: Bud site selection protein 20

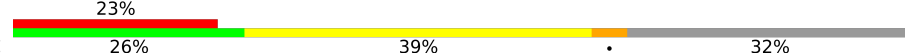


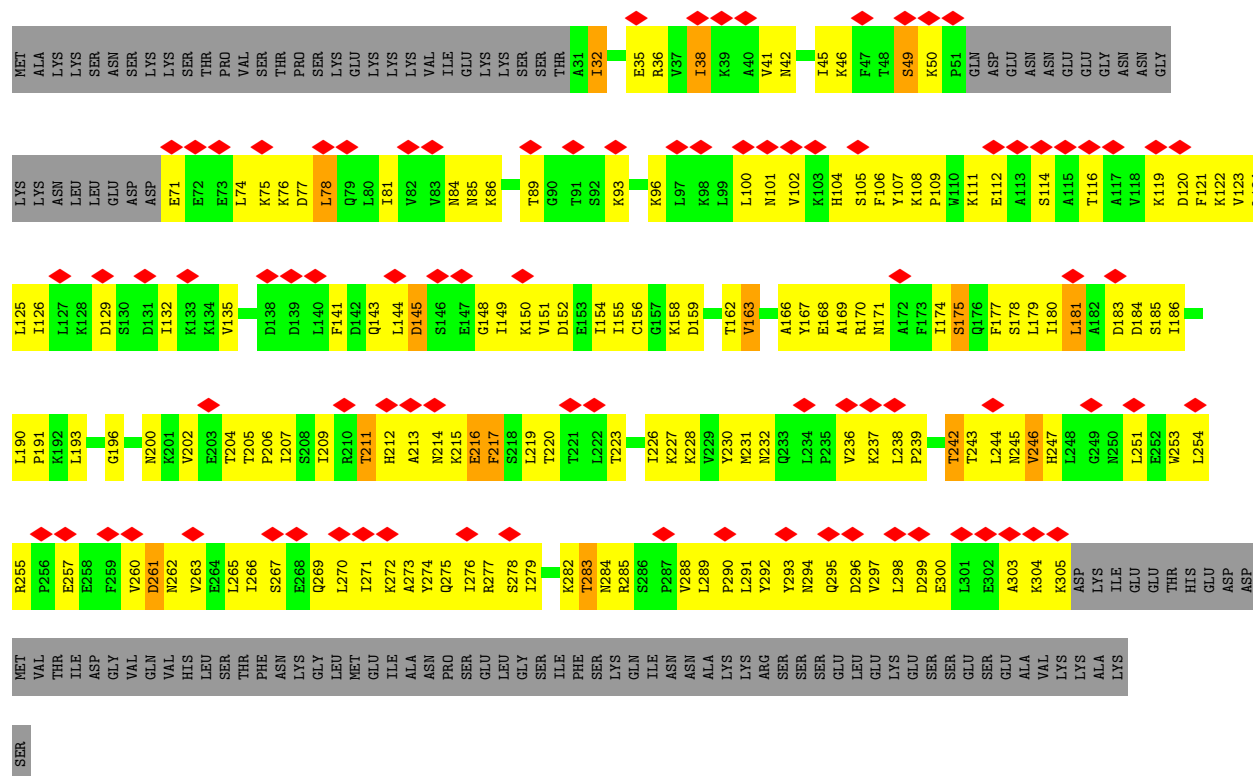
- Molecule 16: 60S ribosomal protein L11-A

Chain J: 



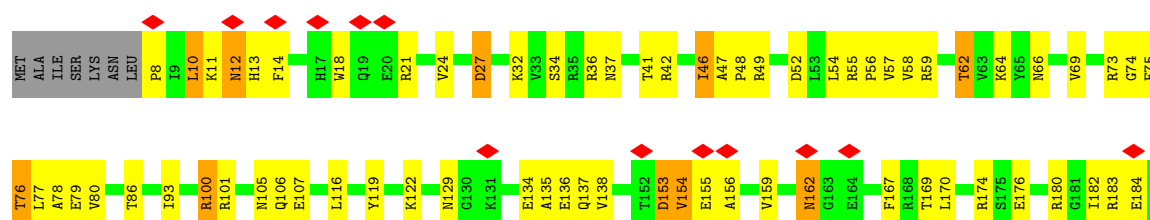
• Molecule 17: Proteasome-interacting protein CIC1

Chain K: 



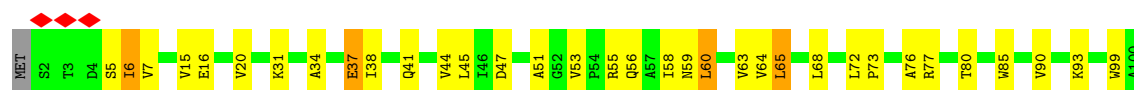
• Molecule 18: 60S ribosomal protein L13-A

Chain L: 

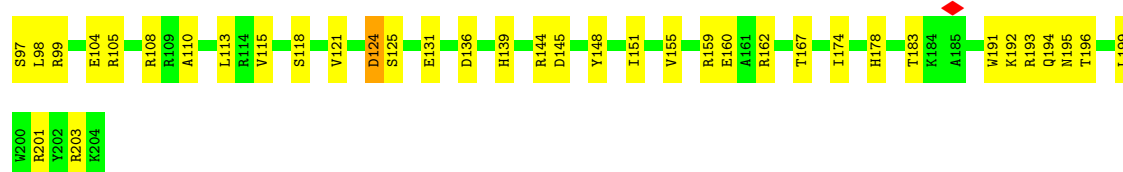
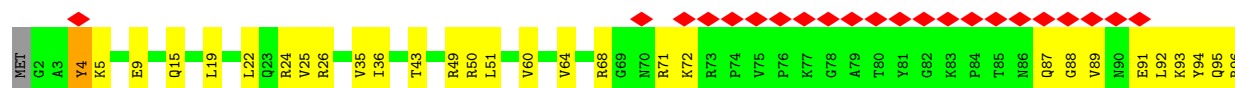




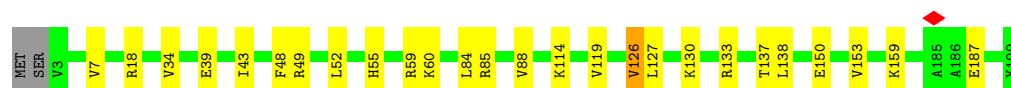
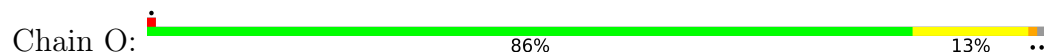
- Molecule 19: 60S ribosomal protein L14-A



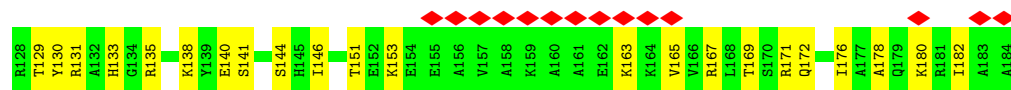
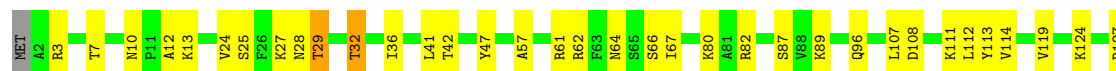
- Molecule 20: 60S ribosomal protein L15-A



- Molecule 21: 60S ribosomal protein L16-A

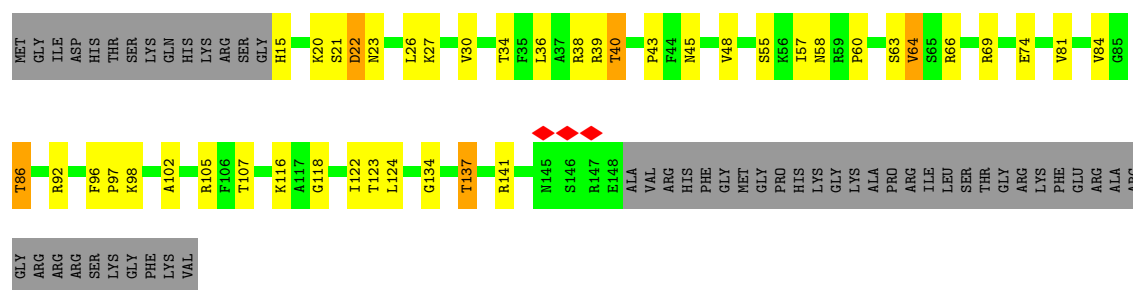


- Molecule 22: 60S ribosomal protein L17-A

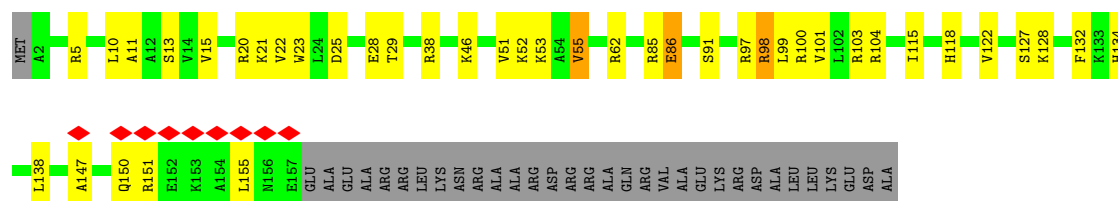


- Molecule 23: 60S ribosomal protein L18-A

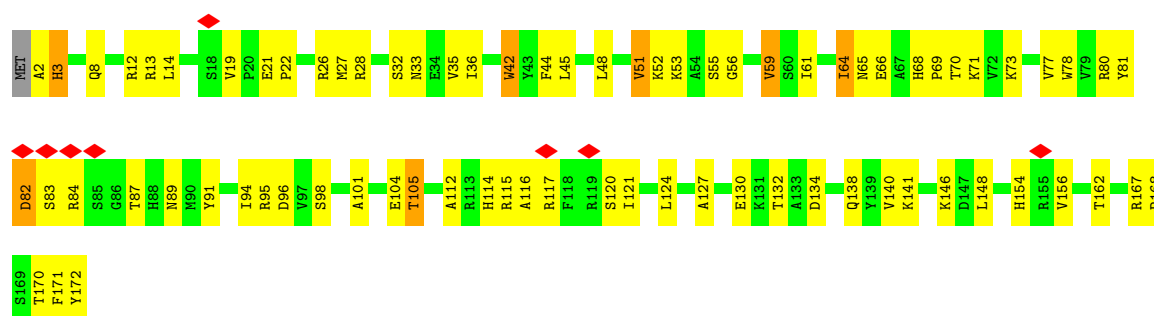




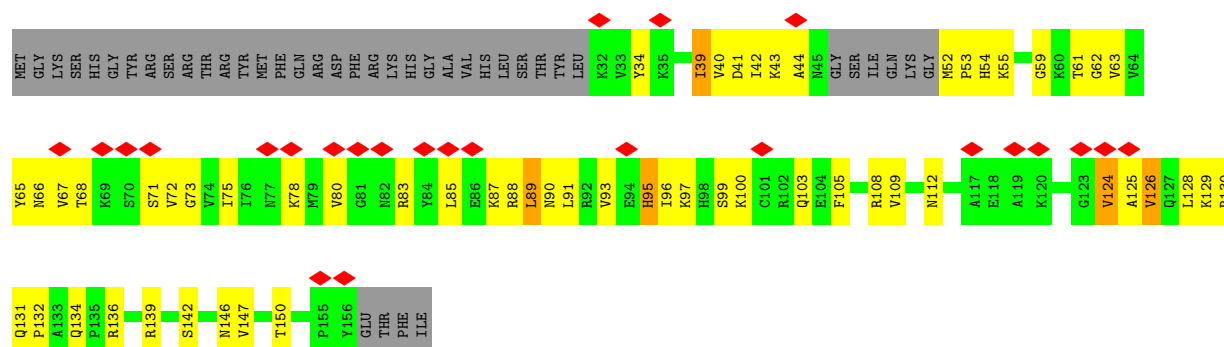
- Molecule 24: 60S ribosomal protein L19-A



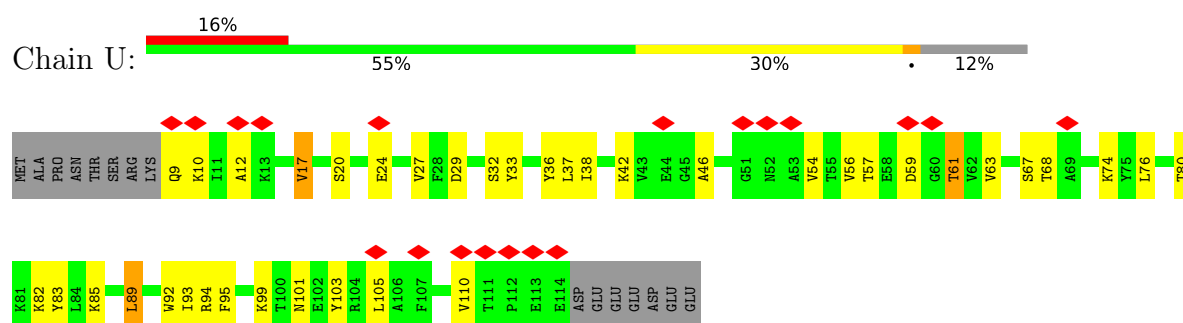
- Molecule 25: 60S ribosomal protein L20-A



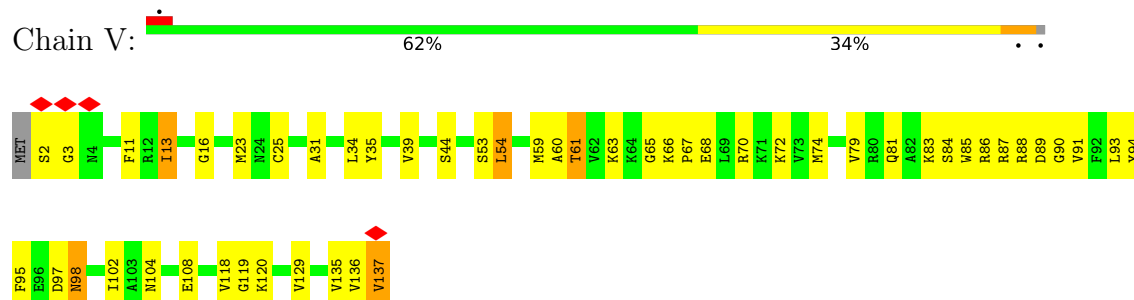
- Molecule 26: 60S ribosomal protein L21-A



- Molecule 27: 60S ribosomal protein L22-A



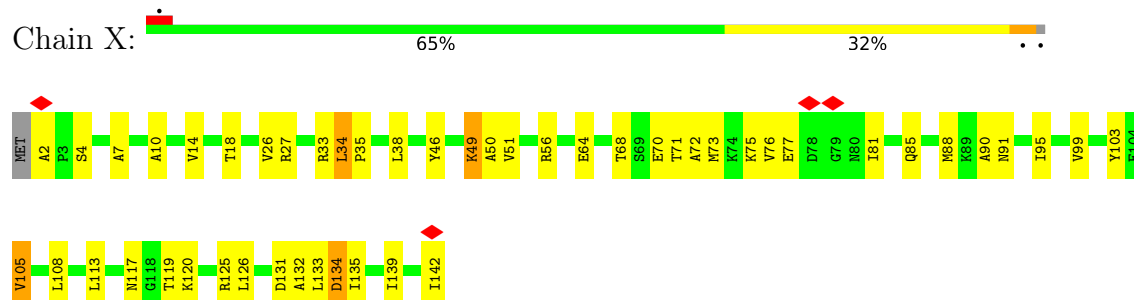
• Molecule 28: 60S ribosomal protein L23-A



• Molecule 29: Ribosome assembly factor MRT4

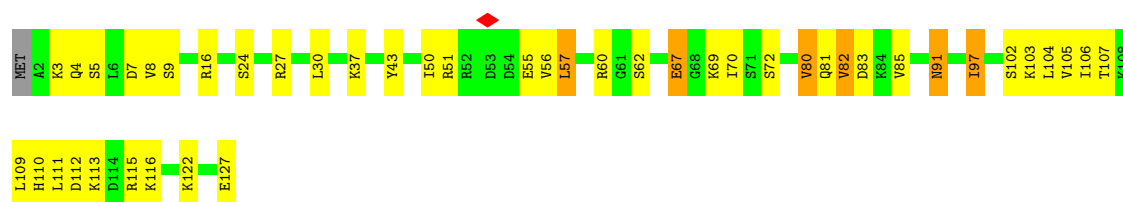


• Molecule 30: 60S ribosomal protein L25



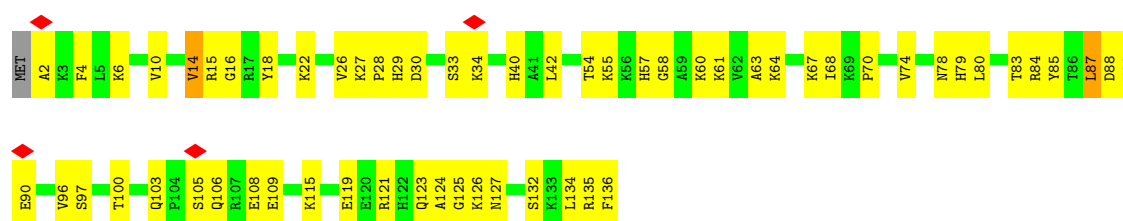
- Molecule 31: 60S ribosomal protein L26-A

Chain Y: 

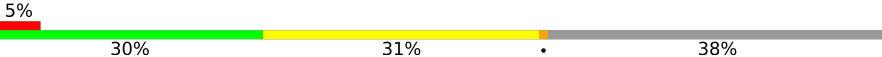


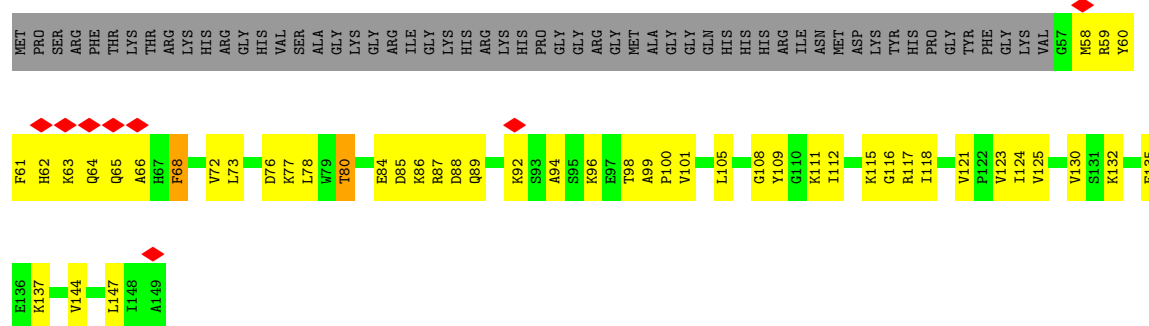
- Molecule 32: 60S ribosomal protein L27-A

Chain Z: 



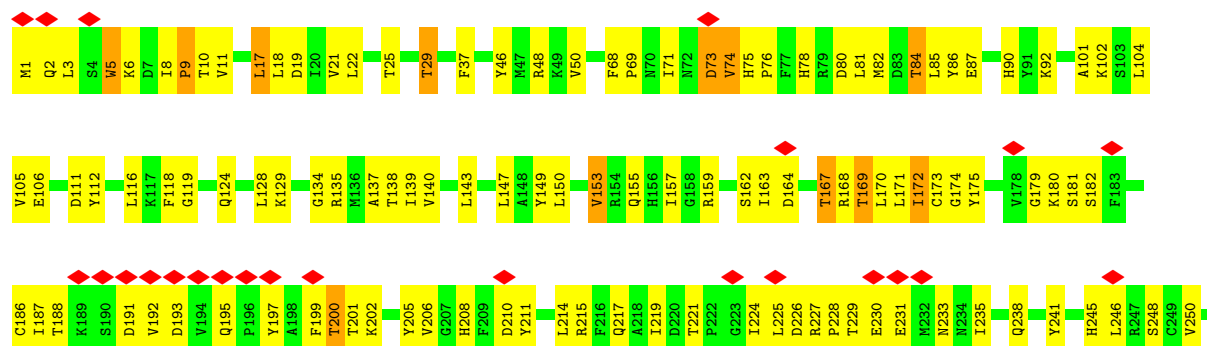
- Molecule 33: 60S ribosomal protein L28

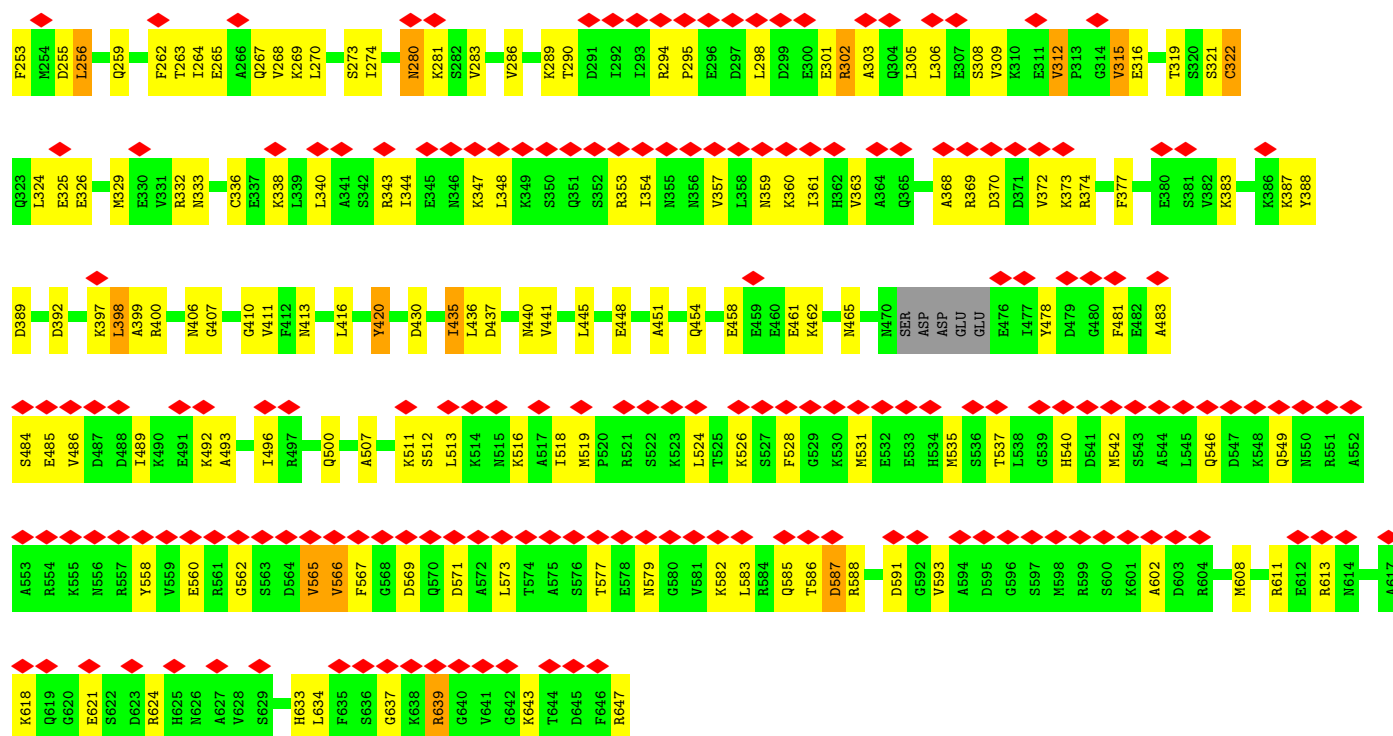
Chain a: 



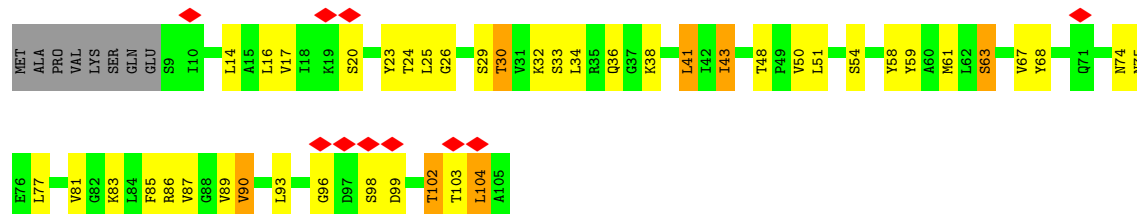
- Molecule 34: Nucleolar GTP-binding protein 1

Chain b: 

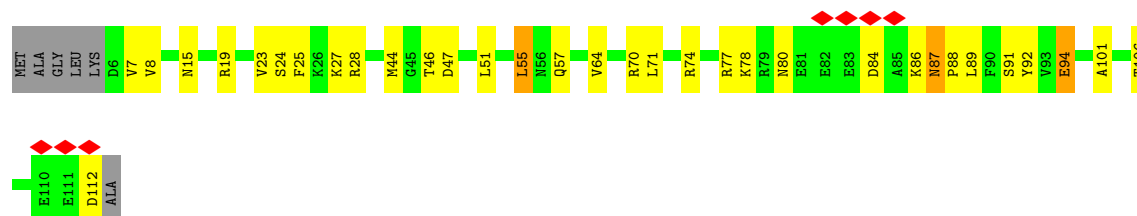




• Molecule 35: 60S ribosomal protein L30

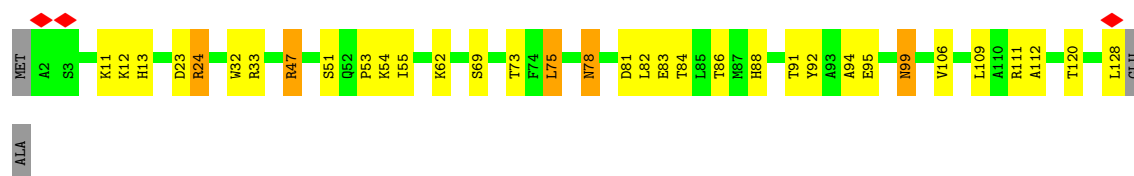


• Molecule 36: 60S ribosomal protein L31-A



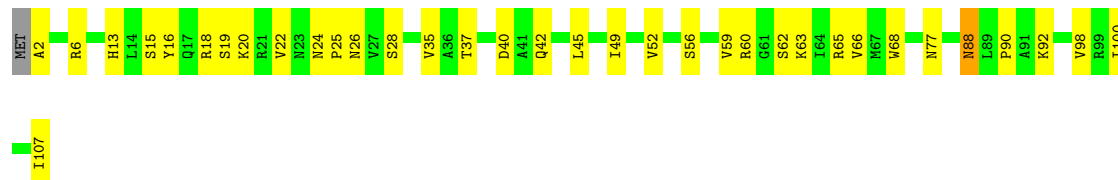
• Molecule 37: 60S ribosomal protein L32





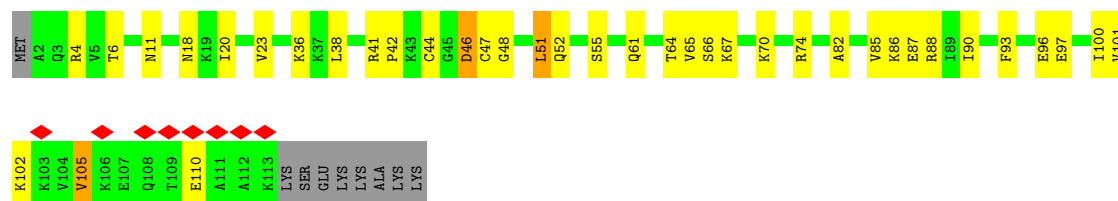
- Molecule 38: 60S ribosomal protein L33-A

Chain f: 66% 32% ..



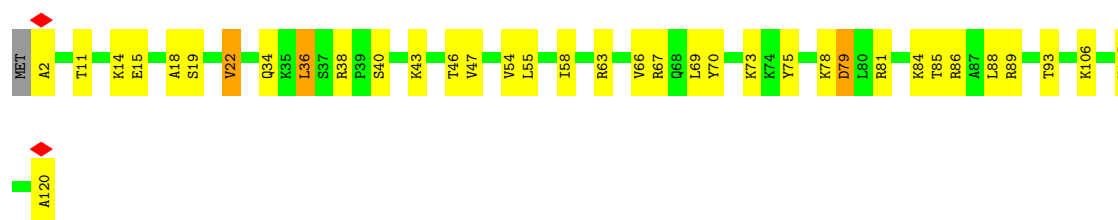
- Molecule 39: 60S ribosomal protein L34-A

Chain g: 7% 61% 29% 7%



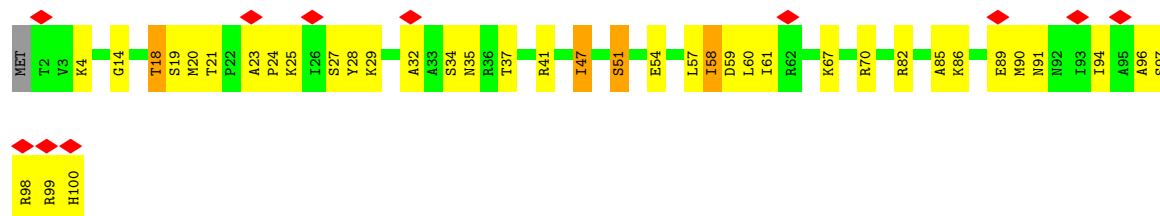
- Molecule 40: 60S ribosomal protein L35-A

Chain h: 69% 28% ..

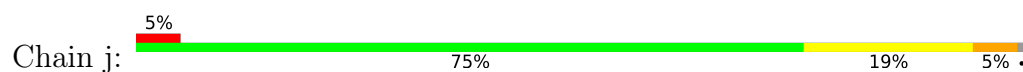


- Molecule 41: 60S ribosomal protein L36-A

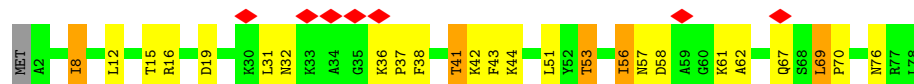
Chain i: 11% 60% 35%



- Molecule 42: 60S ribosomal protein L37-A



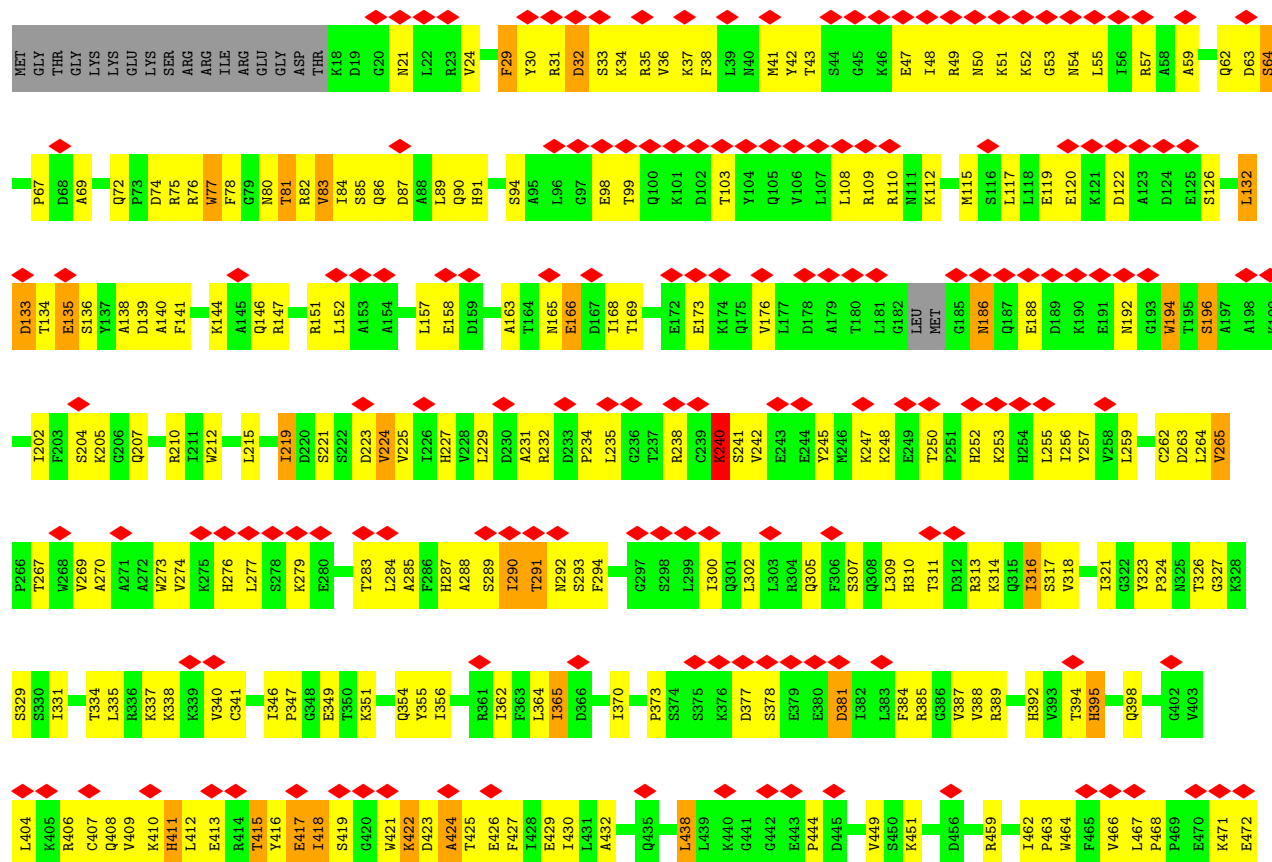
- Molecule 43: 60S ribosomal protein L38



- Molecule 44: 60S ribosomal protein L39

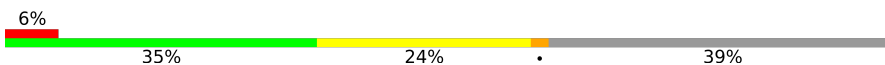


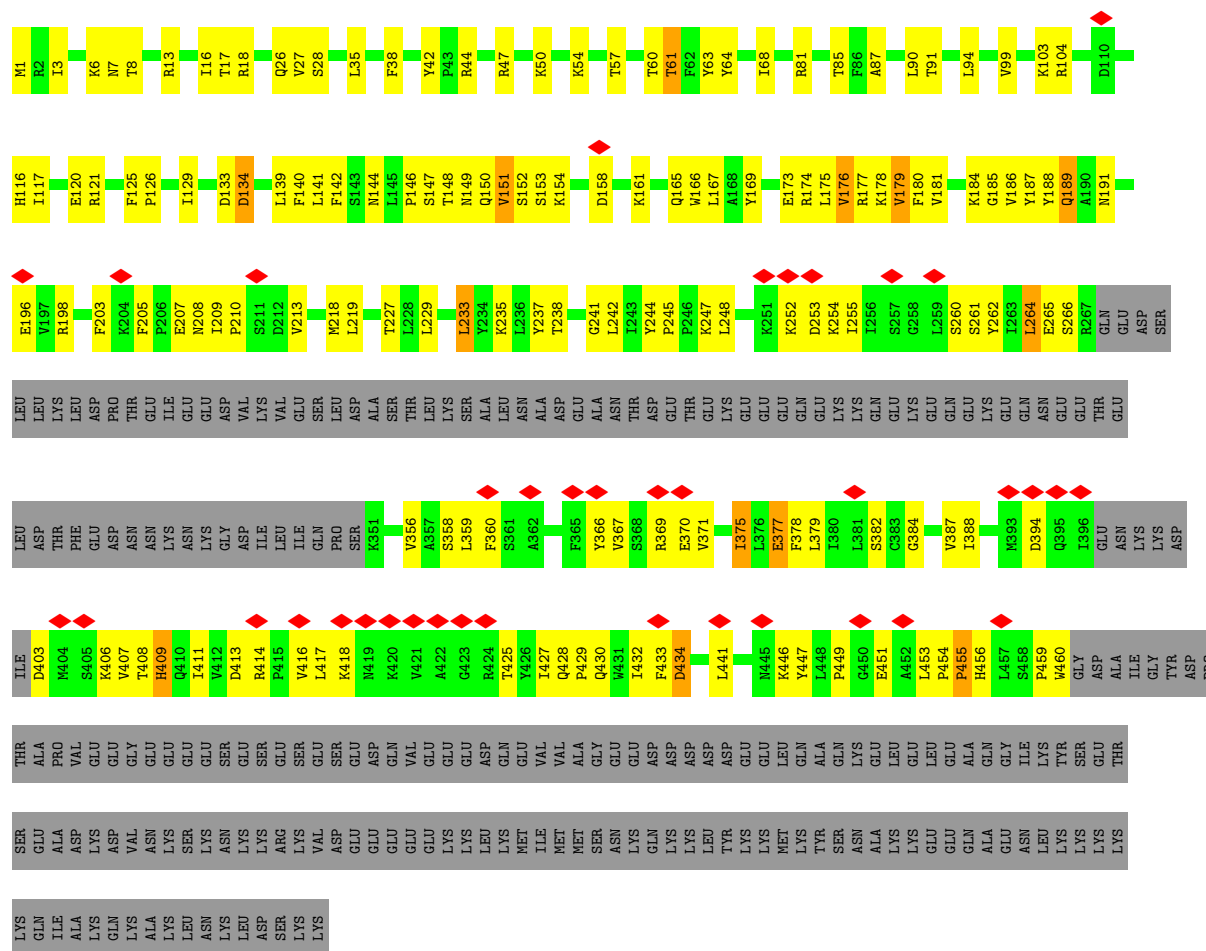
- Molecule 45: Nucleolar GTP-binding protein 2



GLY
GLU
GLU
LYS
PRO
LYS
LYS
LYS
VAL
GLU
GLU
LYS
THR
ALA

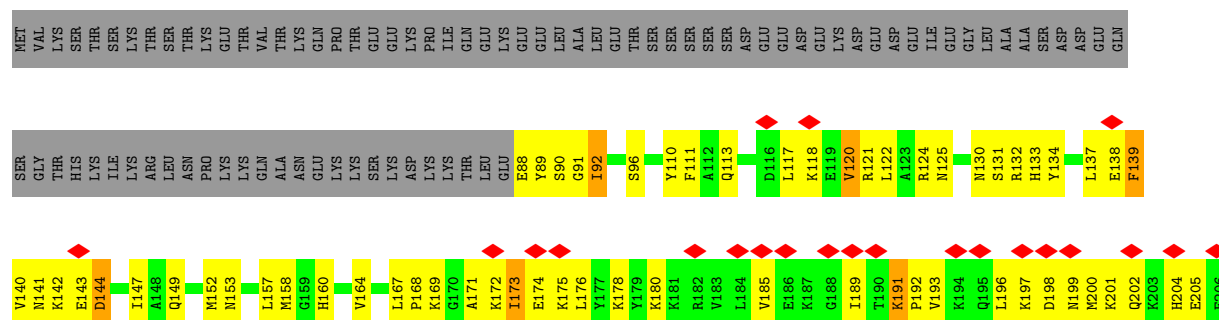
• Molecule 46: Pescadillo homolog

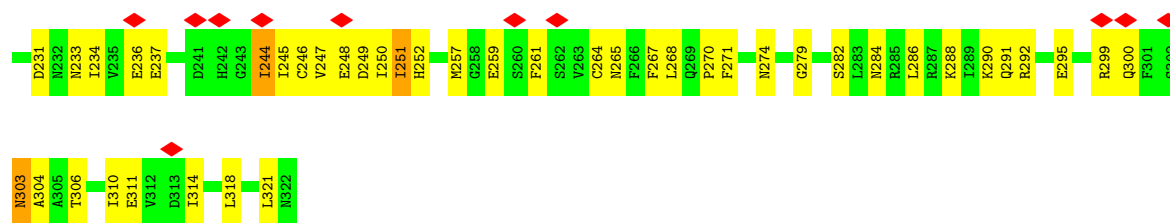
Chain n: 



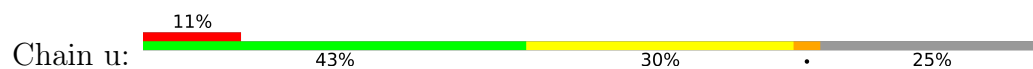
• Molecule 47: Ribosome biogenesis protein 15

Chain o: 

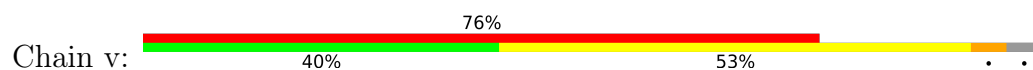




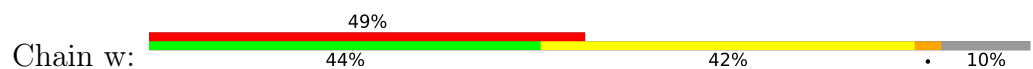
• Molecule 53: Ribosome biogenesis protein RLP24

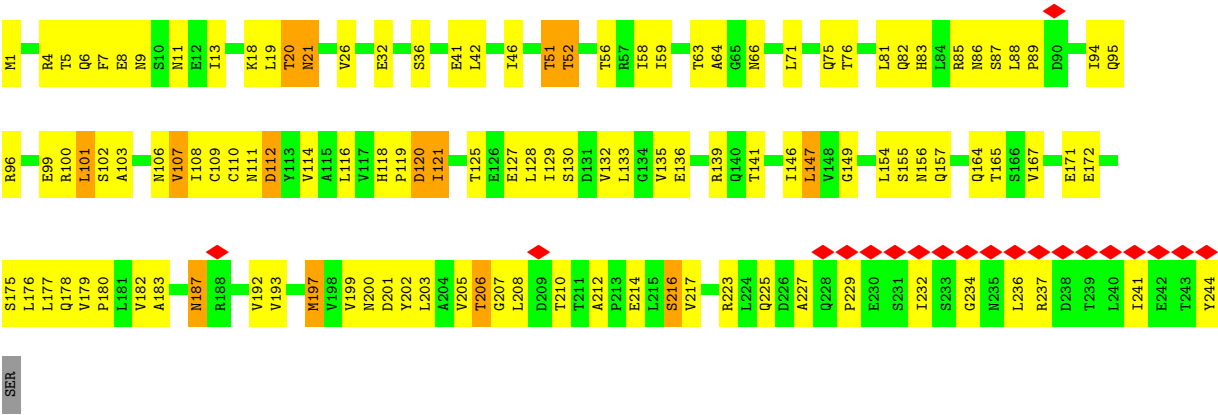


• Molecule 54: Ribosome biogenesis protein RPF2

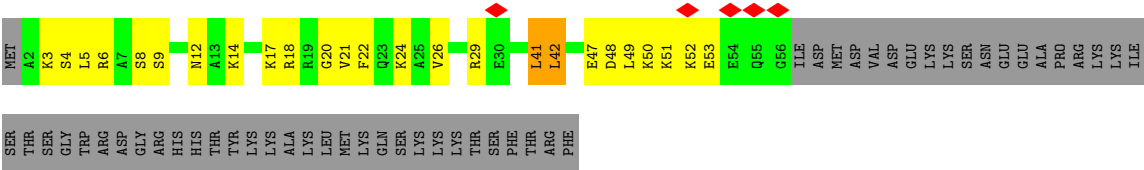
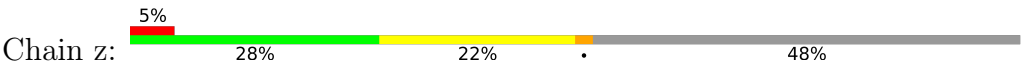


• Molecule 55: Regulator of ribosome biosynthesis





● Molecule 58: UPF0642 protein YBL028C



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	53177	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.9	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.164	Depositor
Minimum map value	-0.090	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	422.80002, 422.80002, 422.80002	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.057, 1.057, 1.057	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.69	0/71167	0.52	1/110944 (0.0%)
2	2	0.88	0/3746	0.52	0/5832
3	3	0.25	0/2883	0.45	0/4491
4	4	0.26	0/4069	0.54	0/5520
5	5	0.26	0/649	0.53	0/848
6	6	0.36	0/1527	0.62	0/2371
7	A	0.59	0/1666	0.59	0/2241
8	B	0.68	0/3152	0.61	0/4239
9	C	0.70	0/2801	0.59	0/3792
10	D	0.25	0/2257	0.50	0/3043
11	E	0.52	0/1260	0.54	0/1694
12	F	0.67	0/1821	0.55	0/2451
13	G	0.63	0/1849	0.63	0/2495
14	H	0.60	0/1539	0.60	0/2073
15	I	0.35	0/1075	0.53	0/1443
16	J	0.24	0/1374	0.51	0/1842
17	K	0.30	0/2098	0.52	0/2830
18	L	0.58	0/1524	0.61	0/2046
19	M	0.61	1/1074 (0.1%)	0.57	0/1446
20	N	0.82	0/1757	0.67	0/2354
21	O	0.85	0/1585	0.60	0/2128
22	P	0.69	0/1465	0.59	0/1968
23	Q	0.58	0/1050	0.55	0/1419
24	R	0.55	0/1275	0.58	0/1702
25	S	0.58	0/1473	0.59	0/1980
26	T	0.36	0/957	0.51	0/1285
27	U	0.39	0/861	0.55	0/1167
28	V	0.61	0/1018	0.61	1/1369 (0.1%)
29	W	0.32	0/1918	0.52	0/2586
30	X	0.67	0/1116	0.59	0/1503
31	Y	0.59	0/1004	0.54	0/1341
32	Z	0.49	0/1118	0.53	0/1497

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	a	0.51	0/751	0.58	0/1013
34	b	0.41	0/5270	0.54	0/7080
35	c	0.44	0/751	0.47	0/1008
36	d	0.62	0/887	0.56	0/1191
37	e	0.80	0/1041	0.57	0/1394
38	f	0.83	0/868	0.60	0/1168
39	g	0.68	0/891	0.64	0/1191
40	h	0.63	0/978	0.62	0/1301
41	i	0.39	0/778	0.56	0/1034
42	j	0.89	0/696	0.63	0/923
43	k	0.45	0/618	0.52	0/826
44	l	0.63	0/443	0.54	0/588
45	m	0.34	0/3722	0.55	0/5017
46	n	0.49	0/3101	0.58	0/4187
47	o	0.38	0/1129	0.58	0/1502
48	p	0.54	0/701	0.56	0/934
49	q	0.36	0/1279	0.52	0/1710
50	r	0.52	0/1892	0.61	0/2528
51	s	0.43	0/577	0.52	0/752
52	t	0.39	0/2333	0.58	0/3128
53	u	0.51	0/1287	0.61	1/1711 (0.1%)
54	v	0.26	0/2027	0.49	0/2718
55	w	0.29	0/1471	0.51	0/1980
56	x	0.29	0/3174	0.54	0/4305
57	y	0.48	0/1872	0.54	0/2548
58	z	0.51	0/445	0.60	0/585
All	All	0.61	1/163110 (0.0%)	0.54	3/236262 (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
4	4	0	3
8	B	0	2
9	C	0	1
12	F	0	1
16	J	0	1
18	L	0	1
28	V	0	1
36	d	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
45	m	0	6
46	n	0	1
47	o	0	1
50	r	0	1
53	u	0	1
56	x	0	1
All	All	0	22

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	M	60	LEU	CA-C	-5.08	1.46	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	u	80	ARG	N-CA-C	7.05	124.34	113.28
28	V	129	VAL	N-CA-C	-6.55	106.18	111.81
1	1	994	G	O4'-C1'-N9	-5.34	100.19	108.20

There are no chirality outliers.

5 of 22 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	4	26	ASN	Peptide
4	4	362	ARG	Peptide
4	4	97	ILE	Peptide
8	B	221	THR	Peptide
8	B	340	LYS	Peptide

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	1	63583	0	31950	1616	0
2	2	3353	0	1695	48	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	3	2579	0	1304	170	0
4	4	3999	0	4088	196	0
5	5	645	0	688	33	0
6	6	1370	0	692	71	0
7	A	1634	0	1685	53	0
8	B	3081	0	3165	116	0
9	C	2749	0	2863	76	0
10	D	2211	0	2175	148	0
11	E	1239	0	1326	42	0
12	F	1784	0	1862	43	0
13	G	1817	0	1908	58	0
14	H	1518	0	1587	45	0
15	I	1059	0	1089	38	0
16	J	1353	0	1383	77	0
17	K	2064	0	2156	134	0
18	L	1499	0	1558	63	0
19	M	1059	0	1154	32	0
20	N	1720	0	1779	46	0
21	O	1555	0	1659	20	0
22	P	1442	0	1485	45	0
23	Q	1035	0	1115	26	0
24	R	1258	0	1342	32	0
25	S	1437	0	1475	64	0
26	T	943	0	994	41	0
27	U	844	0	855	32	0
28	V	1003	0	1048	35	0
29	W	1885	0	1921	103	0
30	X	1100	0	1187	35	0
31	Y	993	0	1081	30	0
32	Z	1092	0	1155	50	0
33	a	735	0	776	41	0
34	b	5185	0	5251	239	0
35	c	743	0	797	32	0
36	d	873	0	914	22	0
37	e	1020	0	1090	21	0
38	f	850	0	880	25	0
39	g	881	0	945	26	0
40	h	969	0	1078	28	0
41	i	771	0	849	30	0
42	j	681	0	683	17	0
43	k	612	0	682	18	0
44	l	436	0	475	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
45	m	3648	0	3701	197	0
46	n	3030	0	3107	111	0
47	o	1107	0	1159	76	0
48	p	694	0	735	31	0
49	q	1258	0	1292	62	0
50	r	1860	0	1965	87	0
51	s	573	0	644	30	0
52	t	2306	0	2454	101	0
53	u	1265	0	1315	52	0
54	v	1985	0	2037	137	0
55	w	1448	0	1510	90	0
56	x	3093	0	3041	213	0
57	y	1849	0	1836	93	0
58	z	444	0	478	20	0
59	I	1	0	0	0	0
59	j	1	0	0	0	0
59	p	1	0	0	0	0
59	u	1	0	0	0	0
60	b	32	0	12	9	0
60	m	32	0	12	3	0
61	b	1	0	0	0	0
61	m	1	0	0	0	0
All	All	153289	0	121142	4722	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 18.

The worst 5 of 4722 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)
1:1:2623:G:N2	1:1:2756:C:C2	1.89	1.35
1:1:1200:A:C2	1:1:2824:G:N1	2.09	1.20
1:1:1200:A:H2	1:1:2824:G:N1	1.41	1.19
1:1:3158:G:N1	1:1:3292:A:C2	2.21	1.08
1:1:91:G:N2	1:1:95:A:N7	2.06	1.02

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	4	508/593 (86%)	423 (83%)	84 (16%)	1 (0%)	43	73
5	5	71/120 (59%)	69 (97%)	2 (3%)	0	100	100
7	A	211/254 (83%)	173 (82%)	38 (18%)	0	100	100
8	B	384/387 (99%)	322 (84%)	59 (15%)	3 (1%)	16	50
9	C	359/362 (99%)	297 (83%)	61 (17%)	1 (0%)	36	68
10	D	272/297 (92%)	223 (82%)	48 (18%)	1 (0%)	30	62
11	E	152/176 (86%)	137 (90%)	15 (10%)	0	100	100
12	F	220/244 (90%)	197 (90%)	23 (10%)	0	100	100
13	G	231/256 (90%)	194 (84%)	37 (16%)	0	100	100
14	H	189/191 (99%)	161 (85%)	27 (14%)	1 (0%)	24	59
15	I	129/166 (78%)	113 (88%)	15 (12%)	1 (1%)	16	50
16	J	167/174 (96%)	134 (80%)	33 (20%)	0	100	100
17	K	252/376 (67%)	219 (87%)	33 (13%)	0	100	100
18	L	185/199 (93%)	151 (82%)	33 (18%)	1 (0%)	24	59
19	M	135/138 (98%)	119 (88%)	16 (12%)	0	100	100
20	N	201/204 (98%)	176 (88%)	24 (12%)	1 (0%)	24	59
21	O	195/199 (98%)	184 (94%)	11 (6%)	0	100	100
22	P	181/184 (98%)	156 (86%)	25 (14%)	0	100	100
23	Q	132/186 (71%)	116 (88%)	16 (12%)	0	100	100
24	R	154/189 (82%)	141 (92%)	13 (8%)	0	100	100
25	S	169/172 (98%)	141 (83%)	28 (17%)	0	100	100
26	T	115/160 (72%)	103 (90%)	12 (10%)	0	100	100
27	U	104/121 (86%)	89 (86%)	15 (14%)	0	100	100
28	V	134/137 (98%)	120 (90%)	14 (10%)	0	100	100
29	W	232/236 (98%)	201 (87%)	31 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	X	139/142 (98%)	122 (88%)	17 (12%)	0	100	100
31	Y	124/127 (98%)	111 (90%)	13 (10%)	0	100	100
32	Z	133/136 (98%)	110 (83%)	23 (17%)	0	100	100
33	a	91/149 (61%)	74 (81%)	17 (19%)	0	100	100
34	b	638/647 (99%)	525 (82%)	110 (17%)	3 (0%)	24	59
35	c	95/105 (90%)	84 (88%)	11 (12%)	0	100	100
36	d	105/113 (93%)	87 (83%)	18 (17%)	0	100	100
37	e	125/130 (96%)	112 (90%)	13 (10%)	0	100	100
38	f	104/107 (97%)	91 (88%)	13 (12%)	0	100	100
39	g	110/121 (91%)	98 (89%)	12 (11%)	0	100	100
40	h	117/120 (98%)	110 (94%)	7 (6%)	0	100	100
41	i	97/100 (97%)	84 (87%)	13 (13%)	0	100	100
42	j	85/88 (97%)	76 (89%)	9 (11%)	0	100	100
43	k	75/78 (96%)	69 (92%)	6 (8%)	0	100	100
44	l	48/51 (94%)	41 (85%)	7 (15%)	0	100	100
45	m	449/486 (92%)	358 (80%)	86 (19%)	5 (1%)	11	43
46	n	365/605 (60%)	307 (84%)	56 (15%)	2 (0%)	24	59
47	o	131/220 (60%)	106 (81%)	25 (19%)	0	100	100
48	p	89/92 (97%)	77 (86%)	12 (14%)	0	100	100
49	q	147/455 (32%)	120 (82%)	26 (18%)	1 (1%)	18	52
50	r	224/261 (86%)	185 (83%)	38 (17%)	1 (0%)	30	62
51	s	65/520 (12%)	57 (88%)	8 (12%)	0	100	100
52	t	283/322 (88%)	239 (84%)	42 (15%)	2 (1%)	18	52
53	u	148/199 (74%)	129 (87%)	19 (13%)	0	100	100
54	v	243/254 (96%)	201 (83%)	42 (17%)	0	100	100
55	w	178/203 (88%)	143 (80%)	35 (20%)	0	100	100
56	x	393/515 (76%)	316 (80%)	77 (20%)	0	100	100
57	y	242/245 (99%)	203 (84%)	39 (16%)	0	100	100
58	z	53/106 (50%)	51 (96%)	2 (4%)	0	100	100
All	All	10178/12418 (82%)	8645 (85%)	1509 (15%)	24 (0%)	44	73

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	C	4	PRO
20	N	95	GLN
34	b	9	PRO
34	b	399	ALA
46	n	153	SER

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	4	453/520 (87%)	413 (91%)	40 (9%)	9	35
5	5	67/106 (63%)	66 (98%)	1 (2%)	57	76
7	A	166/196 (85%)	150 (90%)	16 (10%)	8	32
8	B	322/323 (100%)	282 (88%)	40 (12%)	4	21
9	C	288/289 (100%)	268 (93%)	20 (7%)	14	45
10	D	227/245 (93%)	207 (91%)	20 (9%)	9	35
11	E	134/153 (88%)	128 (96%)	6 (4%)	24	58
12	F	186/205 (91%)	170 (91%)	16 (9%)	10	36
13	G	191/208 (92%)	170 (89%)	21 (11%)	6	26
14	H	171/171 (100%)	150 (88%)	21 (12%)	4	22
15	I	117/141 (83%)	109 (93%)	8 (7%)	14	46
16	J	147/150 (98%)	135 (92%)	12 (8%)	10	39
17	K	236/346 (68%)	208 (88%)	28 (12%)	5	23
18	L	149/159 (94%)	130 (87%)	19 (13%)	4	20
19	M	108/109 (99%)	95 (88%)	13 (12%)	5	23
20	N	175/176 (99%)	164 (94%)	11 (6%)	16	48
21	O	160/162 (99%)	149 (93%)	11 (7%)	14	45
22	P	145/146 (99%)	135 (93%)	10 (7%)	14	45
23	Q	110/151 (73%)	100 (91%)	10 (9%)	9	34
24	R	129/154 (84%)	120 (93%)	9 (7%)	14	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	S	155/156 (99%)	139 (90%)	16 (10%)	7	28
26	T	102/137 (74%)	92 (90%)	10 (10%)	7	31
27	U	93/107 (87%)	88 (95%)	5 (5%)	20	53
28	V	104/105 (99%)	93 (89%)	11 (11%)	6	27
29	W	211/213 (99%)	195 (92%)	16 (8%)	12	42
30	X	117/118 (99%)	105 (90%)	12 (10%)	7	28
31	Y	109/110 (99%)	98 (90%)	11 (10%)	7	30
32	Z	115/116 (99%)	111 (96%)	4 (4%)	32	64
33	a	76/119 (64%)	72 (95%)	4 (5%)	20	53
34	b	568/573 (99%)	522 (92%)	46 (8%)	11	39
35	c	81/88 (92%)	71 (88%)	10 (12%)	4	22
36	d	94/97 (97%)	86 (92%)	8 (8%)	10	37
37	e	109/111 (98%)	96 (88%)	13 (12%)	5	23
38	f	90/91 (99%)	84 (93%)	6 (7%)	15	47
39	g	95/103 (92%)	85 (90%)	10 (10%)	6	28
40	h	104/105 (99%)	97 (93%)	7 (7%)	15	47
41	i	81/82 (99%)	72 (89%)	9 (11%)	6	25
42	j	70/71 (99%)	63 (90%)	7 (10%)	7	30
43	k	68/69 (99%)	61 (90%)	7 (10%)	7	28
44	l	45/46 (98%)	44 (98%)	1 (2%)	45	71
45	m	400/428 (94%)	352 (88%)	48 (12%)	5	23
46	n	334/548 (61%)	306 (92%)	28 (8%)	10	38
47	o	118/199 (59%)	107 (91%)	11 (9%)	8	33
48	p	71/72 (99%)	66 (93%)	5 (7%)	14	45
49	q	140/420 (33%)	134 (96%)	6 (4%)	26	59
50	r	203/229 (89%)	176 (87%)	27 (13%)	4	19
51	s	62/445 (14%)	55 (89%)	7 (11%)	5	24
52	t	256/287 (89%)	243 (95%)	13 (5%)	21	54
53	u	133/180 (74%)	127 (96%)	6 (4%)	24	58
54	v	222/231 (96%)	207 (93%)	15 (7%)	14	46
55	w	161/179 (90%)	147 (91%)	14 (9%)	9	36

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
56	x	344/451 (76%)	305 (89%)	39 (11%)	5	24
57	y	210/211 (100%)	187 (89%)	23 (11%)	6	26
58	z	48/95 (50%)	45 (94%)	3 (6%)	16	48
All	All	8870/10702 (83%)	8080 (91%)	790 (9%)	11	34

5 of 790 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
34	b	587	ASP
45	m	291	THR
35	c	104	LEU
34	b	571	ASP
40	h	93	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 133 such sidechains are listed below:

Mol	Chain	Res	Type
54	v	173	GLN
55	w	63	ASN
57	y	178	GLN
23	Q	23	ASN
22	P	45	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2962/3396 (87%)	915 (30%)	58 (1%)
2	2	157/158 (99%)	33 (21%)	2 (1%)
3	3	120/121 (99%)	54 (45%)	0
6	6	63/232 (27%)	33 (52%)	5 (7%)
All	All	3302/3907 (84%)	1035 (31%)	65 (1%)

5 of 1035 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	U
1	1	5	G
1	1	6	A
1	1	18	G

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Mol	Chain	Res	Type
1	1	26	A

5 of 65 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	3351	U
2	2	123	G
1	1	1329	U
1	1	1307	G
6	6	16	U

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, 6 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
60	GTP	m	501	61	33,34,34	0.95	2 (6%)	50,54,54	1.71	10 (20%)
60	GTP	b	701	61	33,34,34	0.91	0	50,54,54	1.63	8 (16%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
60	GTP	m	501	61	-	6/22/38/38	0/3/3/3
60	GTP	b	701	61	-	7/22/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	m	501	GTP	C5-N7	-2.11	1.34	1.39
60	m	501	GTP	C2-N3	2.06	1.38	1.33

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	b	701	GTP	C5-C4-N3	-5.18	120.15	128.39
60	m	501	GTP	C5-C4-N3	-5.05	120.36	128.39
60	b	701	GTP	C2-N3-C4	4.86	120.66	112.30
60	m	501	GTP	C2-N3-C4	4.72	120.43	112.30
60	b	701	GTP	N9-C4-N3	3.50	132.95	125.95

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
60	b	701	GTP	C5'-O5'-PA-O3A
60	b	701	GTP	C5'-O5'-PA-O1A
60	b	701	GTP	C5'-O5'-PA-O2A
60	b	701	GTP	C3'-C4'-C5'-O5'
60	b	701	GTP	O4'-C4'-C5'-O5'

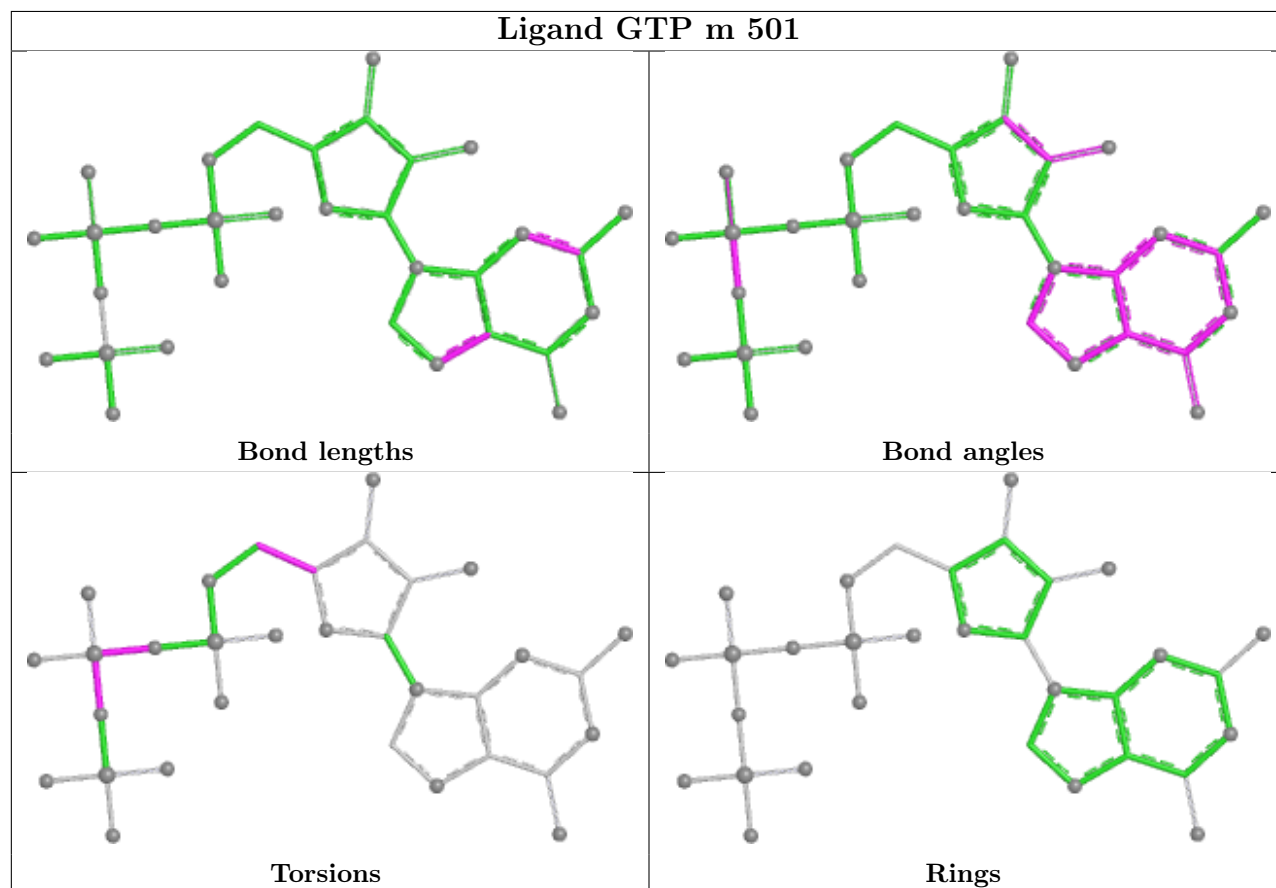
There are no ring outliers.

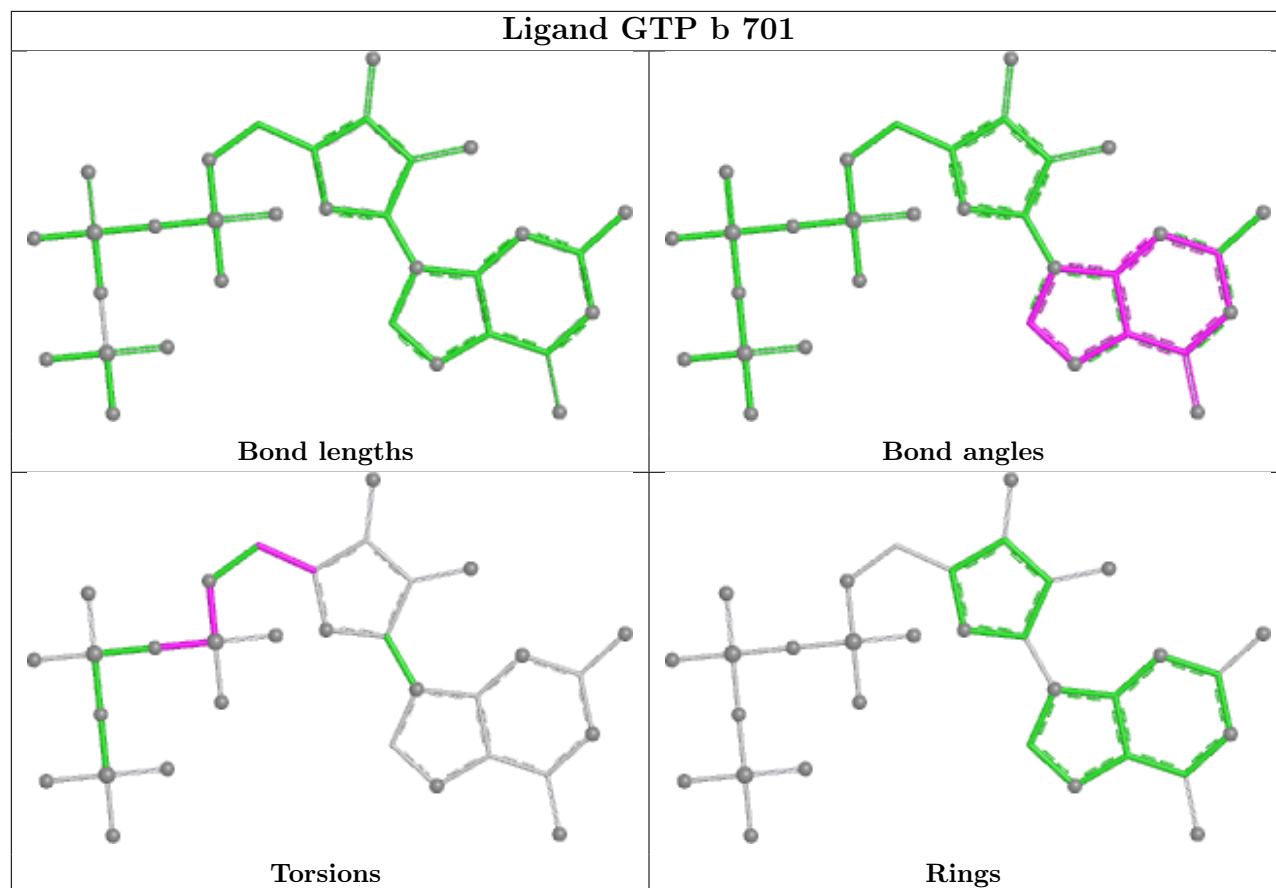
2 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	m	501	GTP	3	0
60	b	701	GTP	9	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring

in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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.

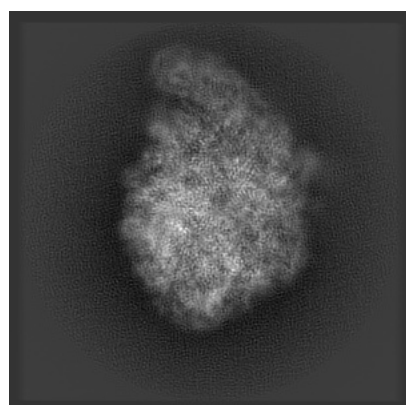
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30108. These allow visual inspection of the internal detail of the map and identification of artifacts.

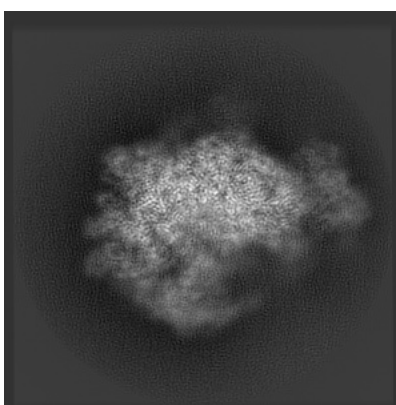
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

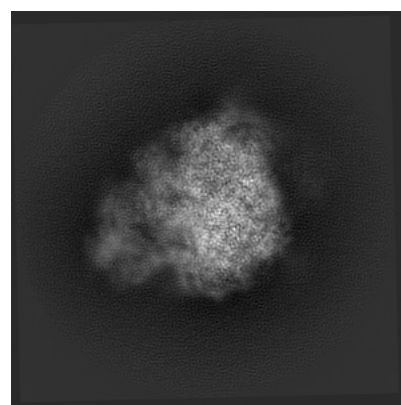
6.1.1 Primary map



X



Y

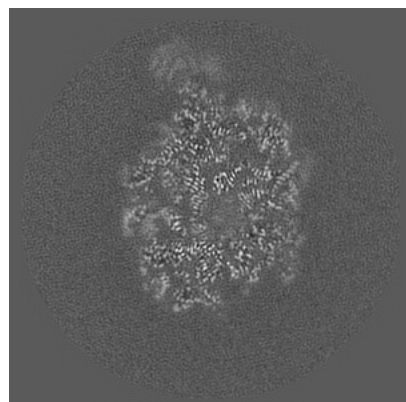


Z

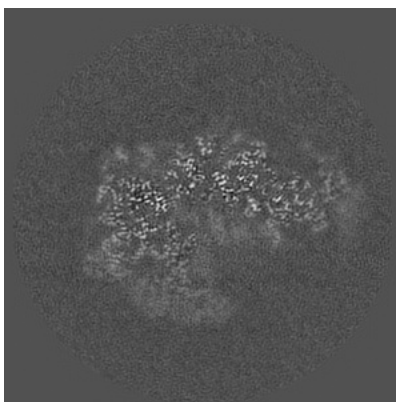
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

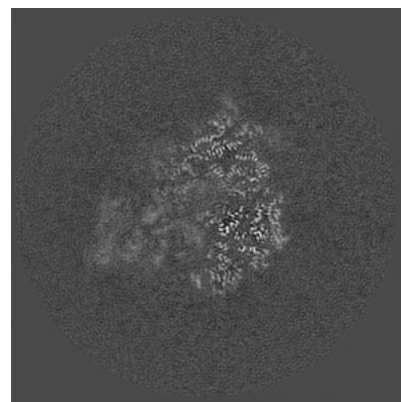
6.2.1 Primary map



X Index: 200



Y Index: 200

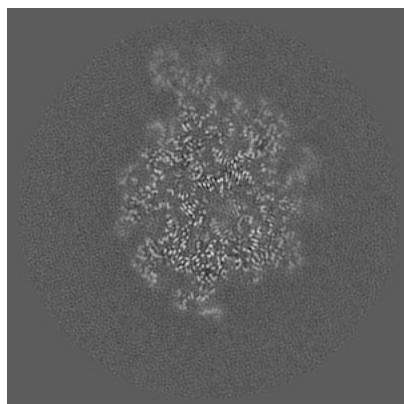


Z Index: 200

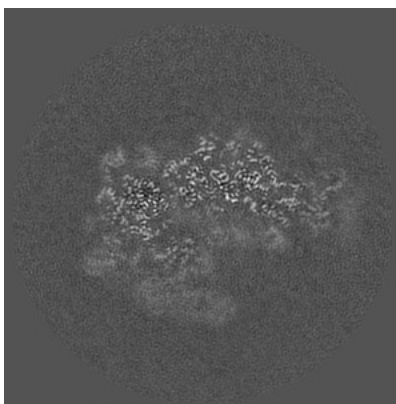
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

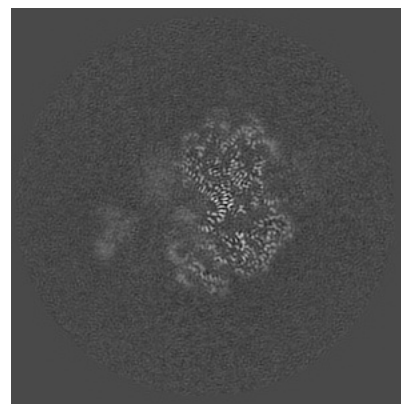
6.3.1 Primary map



X Index: 210



Y Index: 197

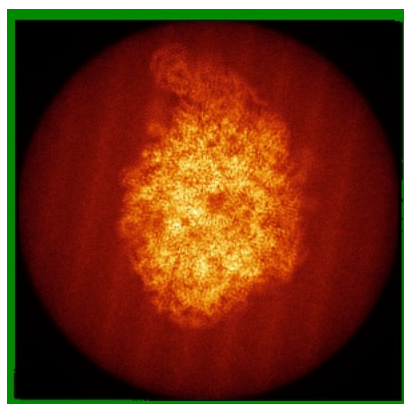


Z Index: 223

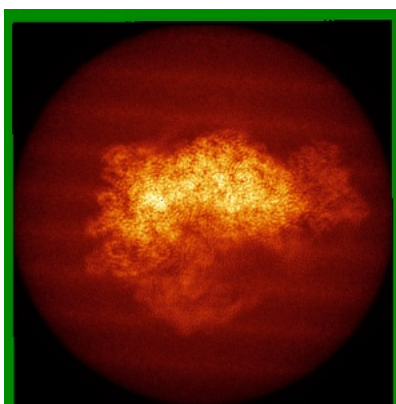
The images above show the largest variance slices of the map in three orthogonal directions.

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

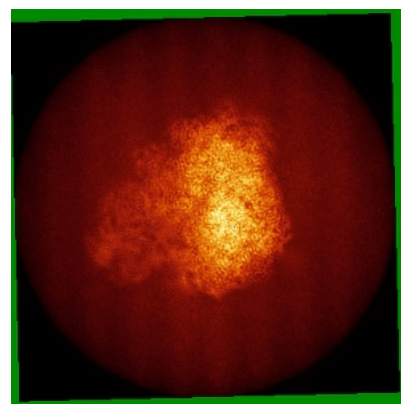
6.4.1 Primary map



X



Y

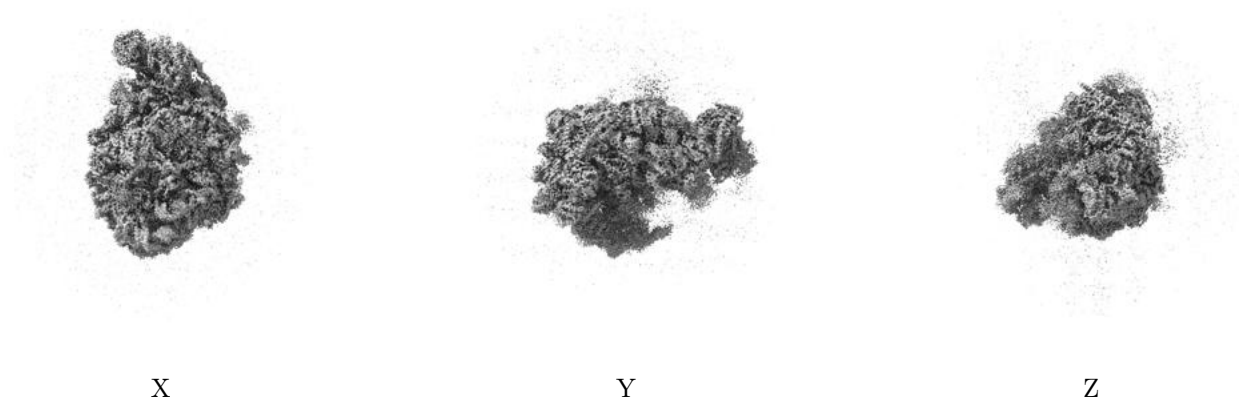


Z

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

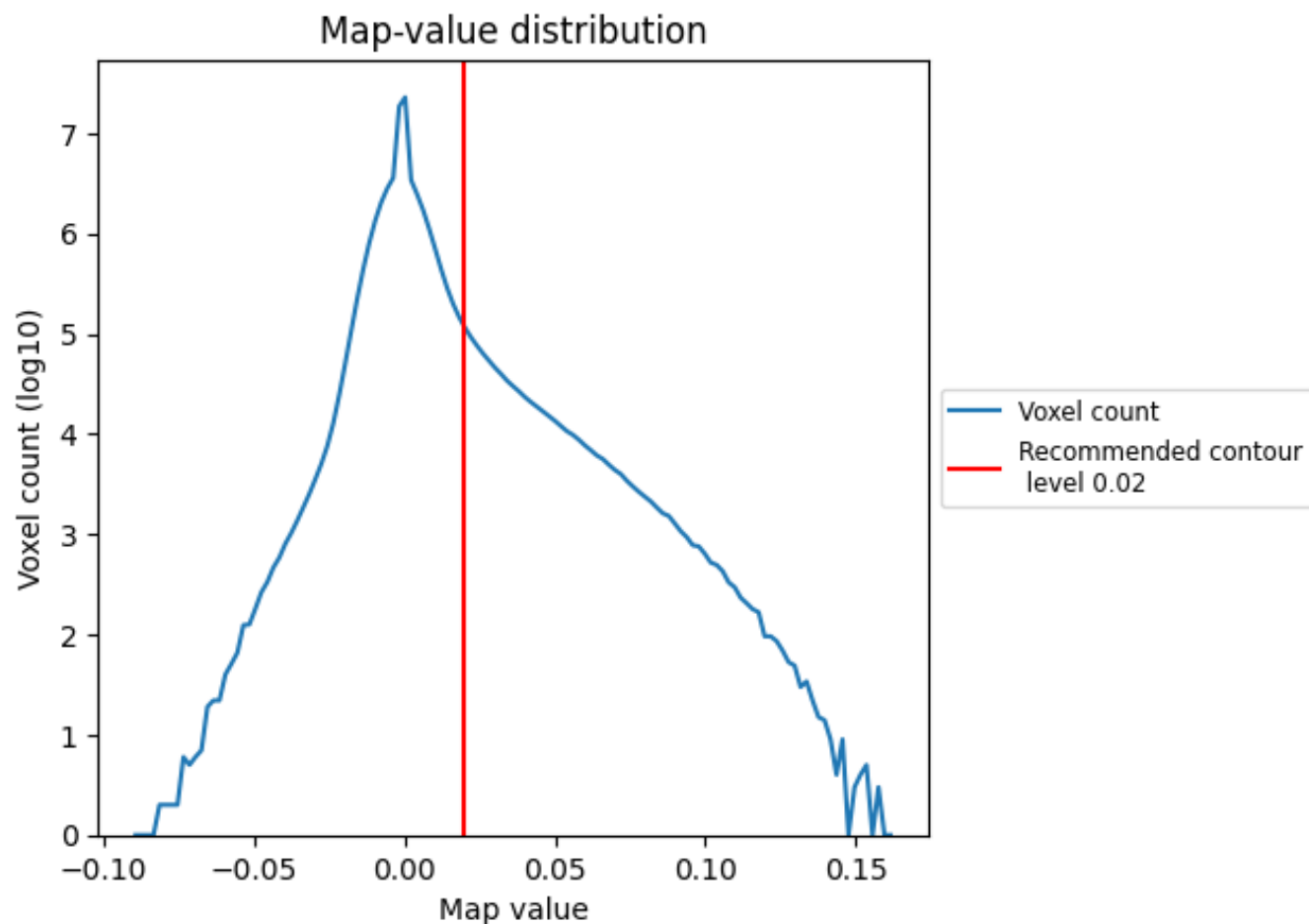
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

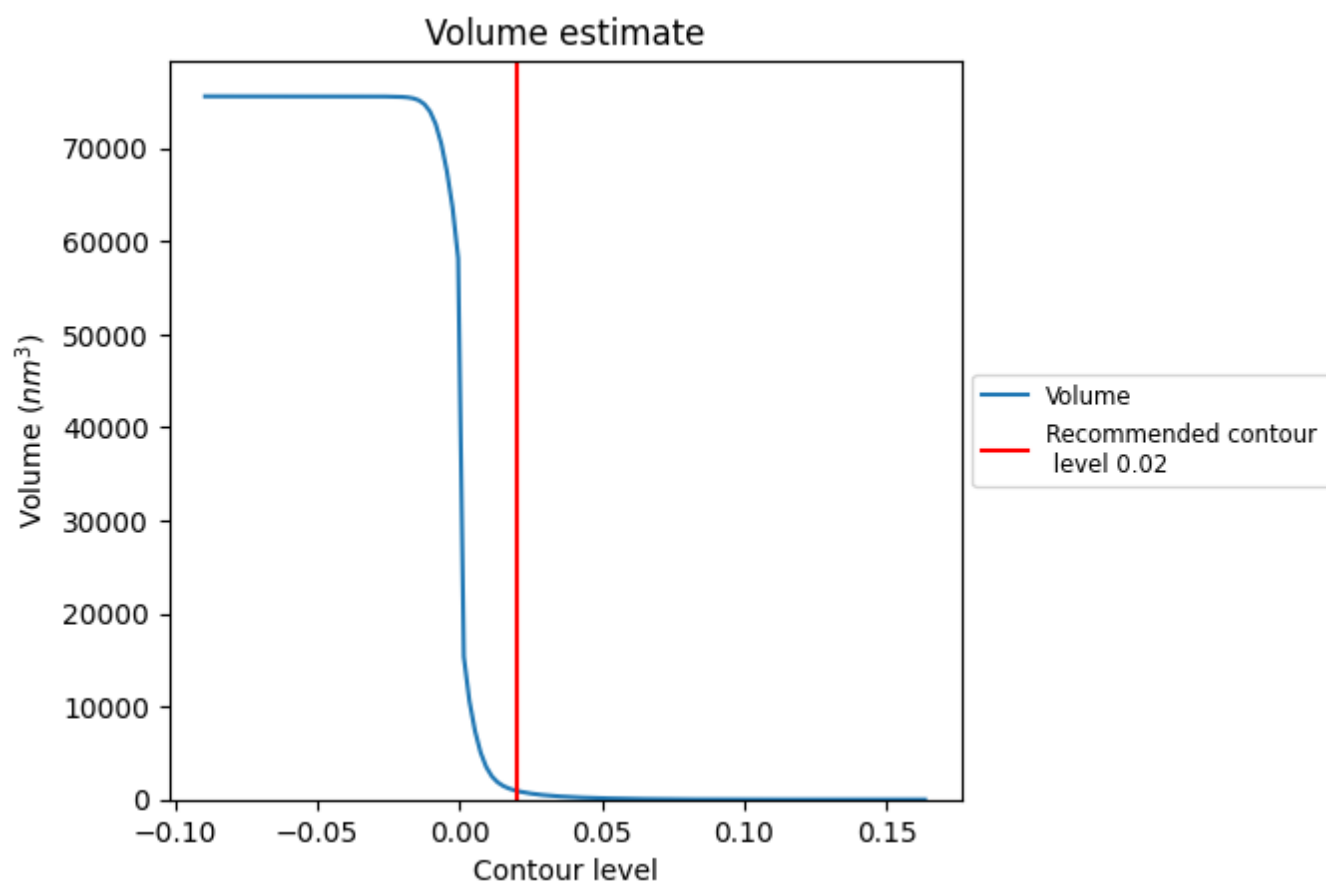
This section contains the results of statistical analysis of the map.

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.

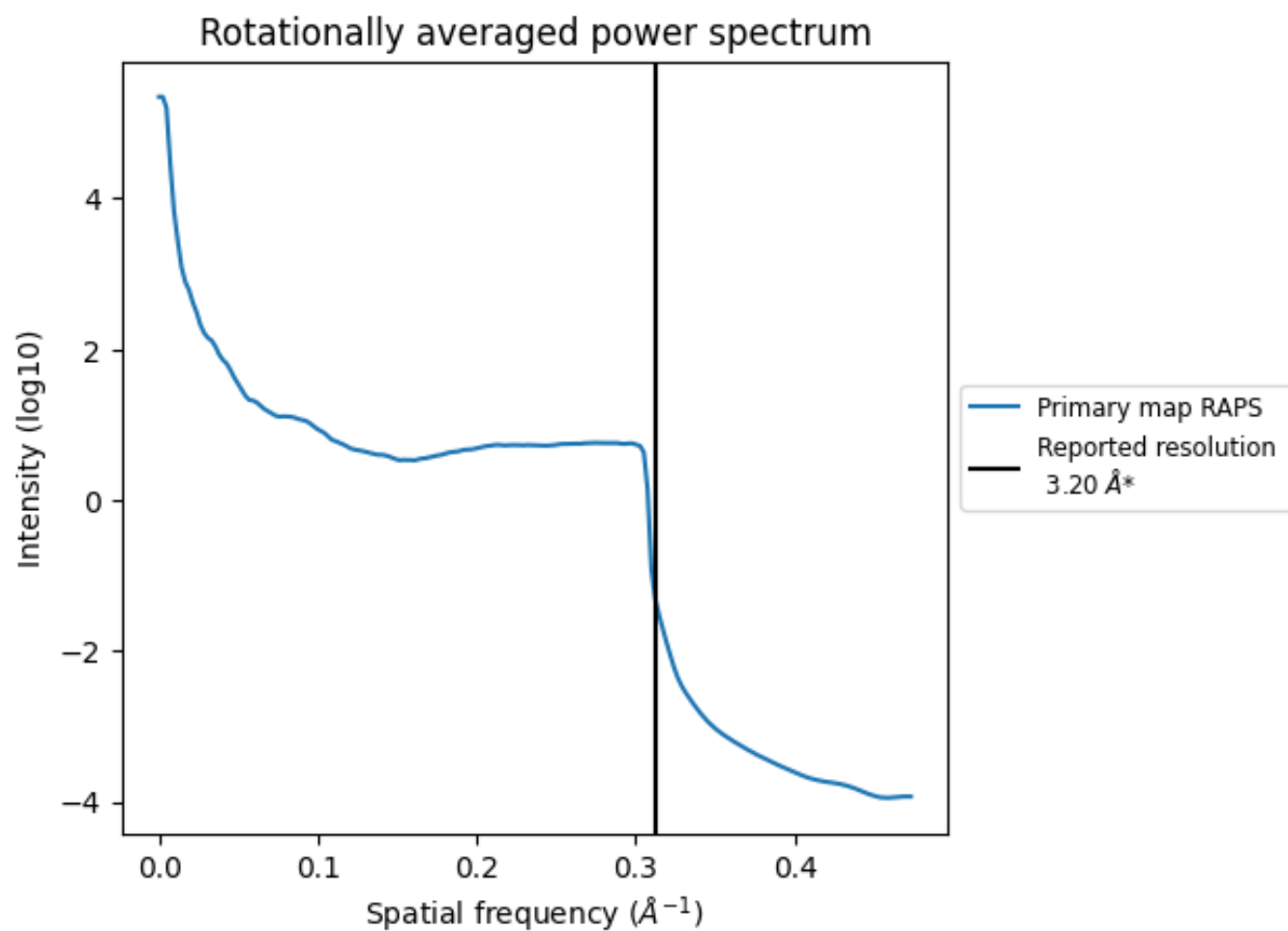
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 950 nm^3 ; this corresponds to an approximate mass of 858 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 0.312 Å⁻¹

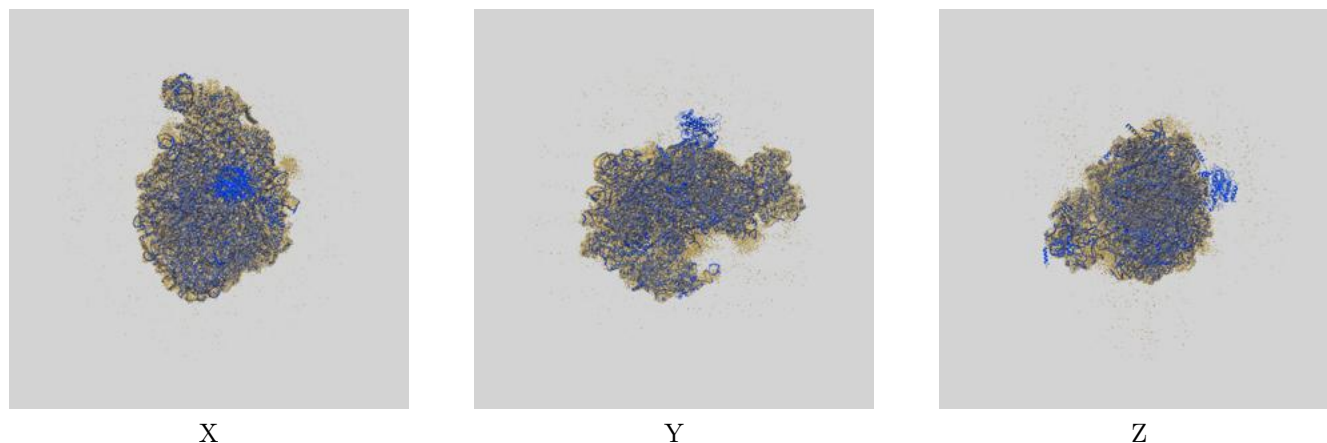
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

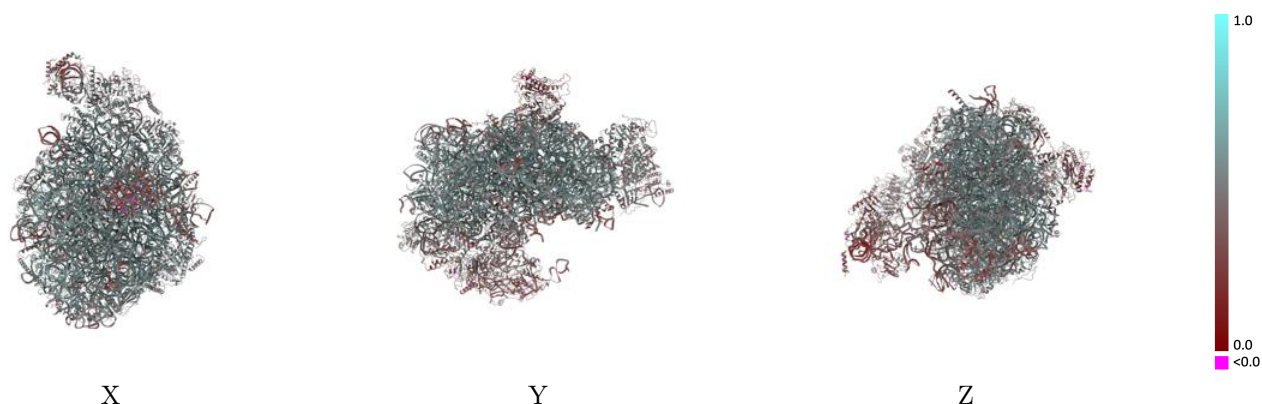
This section contains information regarding the fit between EMDB map EMD-30108 and PDB model 6M62. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

9.1 Map-model overlay [i](#)



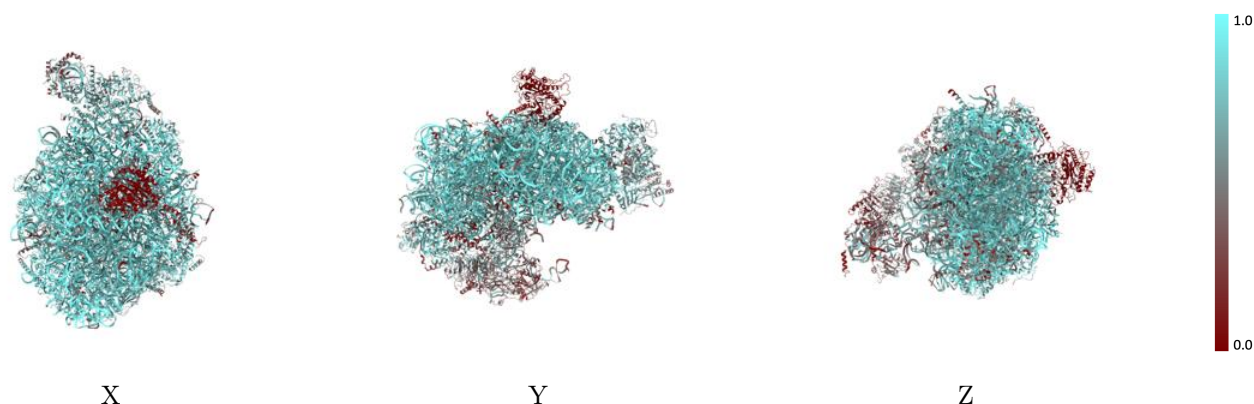
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



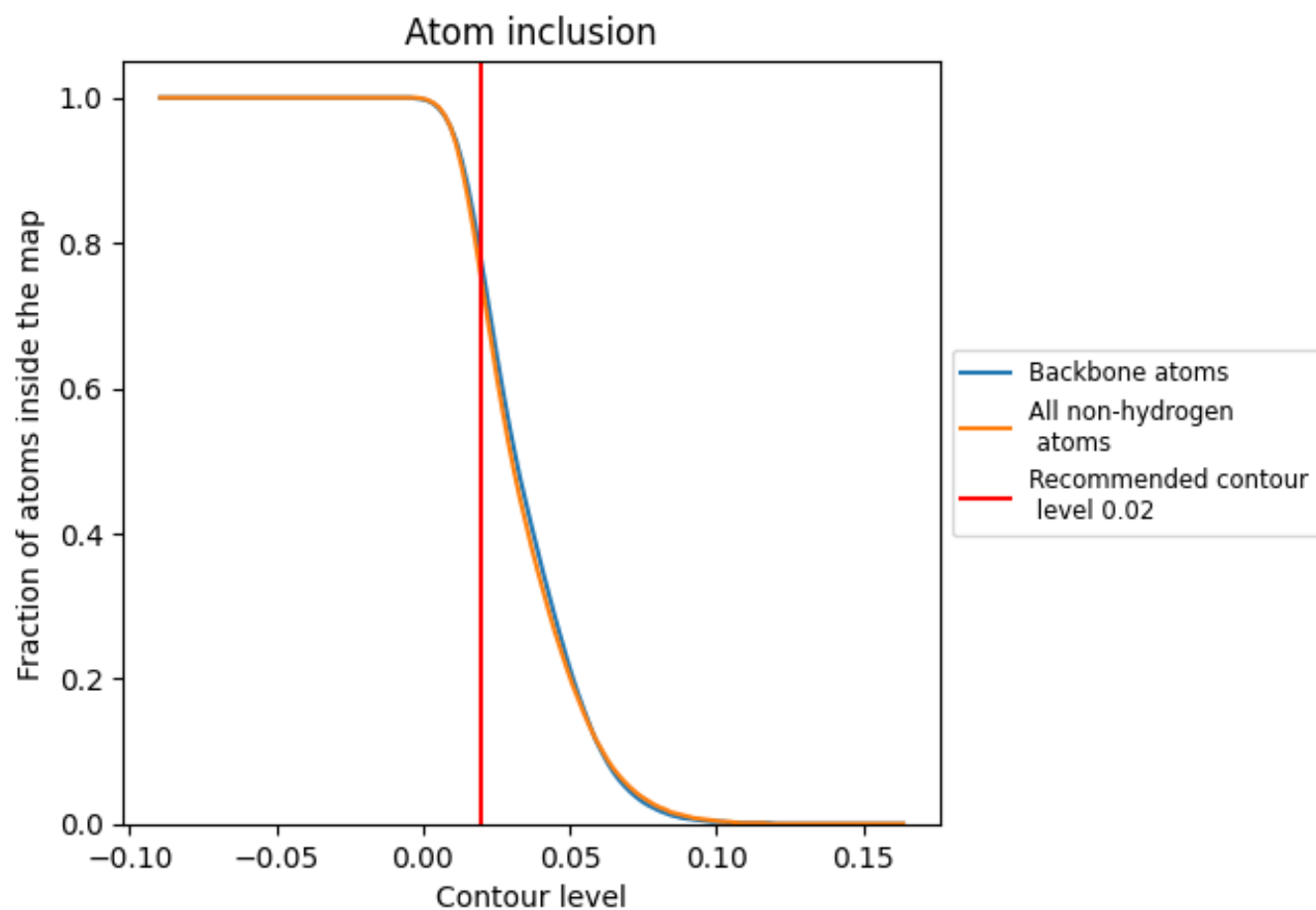
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 75% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7480	 0.4890
1	 0.8740	 0.5000
2	 0.9570	 0.5640
3	 0.5200	 0.2580
4	 0.0370	 0.3610
5	 0.1160	 0.3560
6	 0.7430	 0.3920
A	 0.7900	 0.5510
B	 0.8520	 0.5600
C	 0.8660	 0.5630
D	 0.2650	 0.3260
E	 0.8130	 0.5210
F	 0.8640	 0.5550
G	 0.7970	 0.5310
H	 0.8320	 0.5470
I	 0.5330	 0.4990
J	 0.2780	 0.3250
K	 0.4980	 0.4020
L	 0.7680	 0.5200
M	 0.8540	 0.5470
N	 0.8150	 0.5530
O	 0.9110	 0.5790
P	 0.8200	 0.5550
Q	 0.8460	 0.5460
R	 0.8090	 0.5400
S	 0.8260	 0.5300
T	 0.6140	 0.4590
U	 0.6510	 0.4460
V	 0.8360	 0.5670
W	 0.5800	 0.4320
X	 0.8560	 0.5630
Y	 0.8390	 0.5520
Z	 0.8210	 0.5340
a	 0.7670	 0.4900
b	 0.5660	 0.4620



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Chain	Atom inclusion	Q-score
c	 0.7250	 0.5110
d	 0.8150	 0.5580
e	 0.8780	 0.5810
f	 0.9160	 0.5930
g	 0.8300	 0.5600
h	 0.8430	 0.5580
i	 0.6900	 0.4810
j	 0.9050	 0.5940
k	 0.7280	 0.5070
l	 0.8410	 0.5840
m	 0.4920	 0.4490
n	 0.7120	 0.5030
o	 0.5790	 0.4420
p	 0.8070	 0.5450
q	 0.5500	 0.4670
r	 0.7400	 0.5170
s	 0.5360	 0.5010
t	 0.6300	 0.4750
u	 0.7460	 0.5000
v	 0.2510	 0.3450
w	 0.4100	 0.4000
x	 0.4720	 0.3840
y	 0.7390	 0.5050
z	 0.7350	 0.5190