



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 04:50 AM UTC

PDB ID : 7BTB / pdb_00007btb
EMDB ID : EMD-30174
Title : Cryo-EM structure of pre-60S ribosome from *Saccharomyces cerevisiae* rpl4delta63-87 strain at 3.22 Angstroms resolution(state R2)
Authors : Li, Y.; Wilson, D.M.
Deposited on : 2020-04-01
Resolution : 3.22 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:

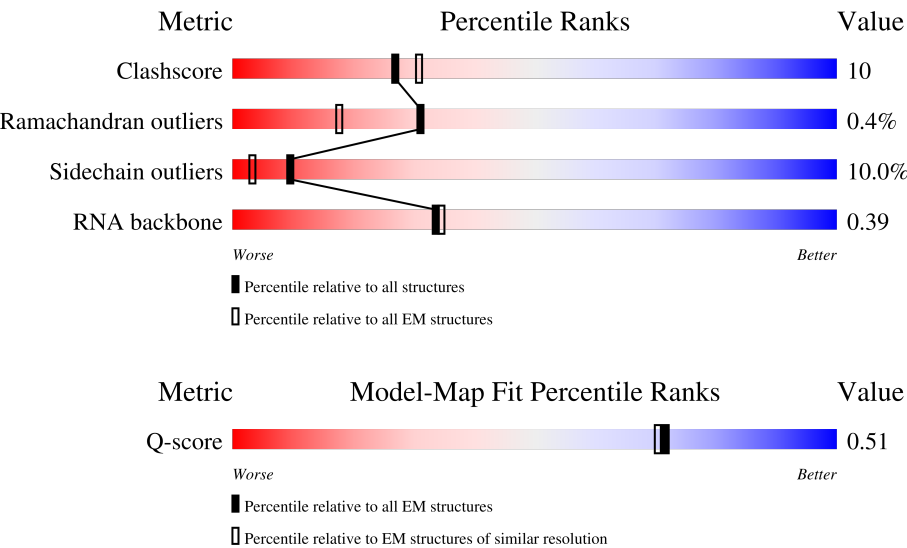
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.22 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.



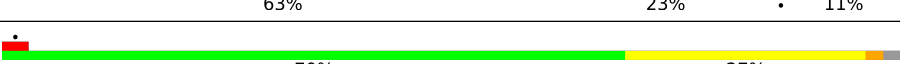
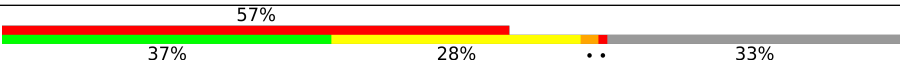
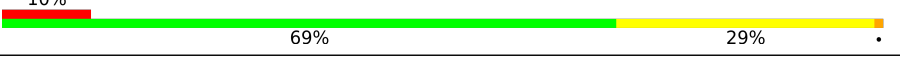
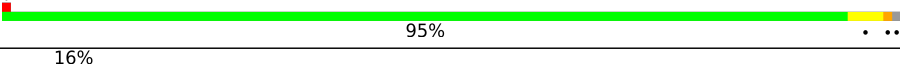
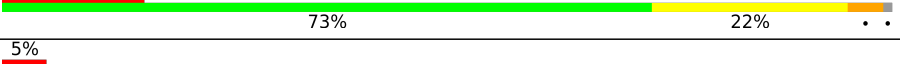
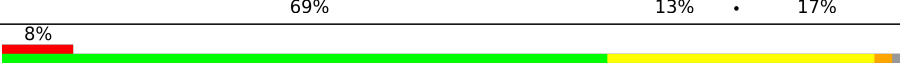
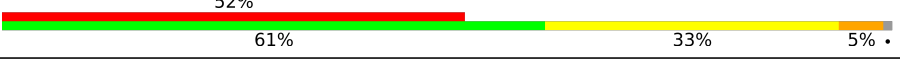
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14612 (2.72 - 3.72)

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	L	199	
2	a	149	
3	A	254	

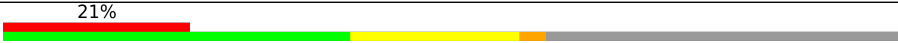
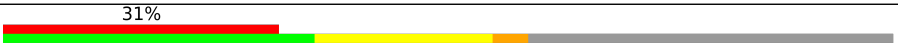
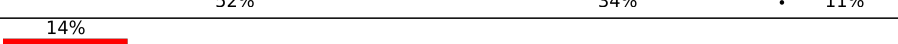
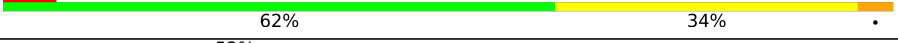
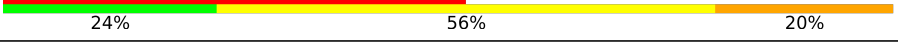
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Mol	Chain	Length	Quality of chain
4	B	387	
5	C	362	
6	D	297	
7	E	176	
8	F	244	
9	G	256	
10	H	191	
11	J	174	
12	K	376	
13	M	138	
14	N	204	
15	O	199	
16	P	184	
17	Q	186	
18	R	189	
19	S	172	
20	T	160	
21	U	121	
22	V	137	
23	W	236	
24	X	142	
25	Y	127	
26	Z	136	
27	b	647	
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	120	
34	i	100	
35	j	88	
36	k	78	
37	m	486	
38	n	605	
39	o	220	
40	p	92	
41	q	455	
42	r	261	
43	t	322	
44	u	199	
45	v	344	
46	w	203	
47	x	515	
48	y	245	
49	z	106	
50	1	3396	
51	2	158	
52	3	121	
53	6	232	

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 147931 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 protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	L	185	Total	C	N	O	0	0
			1484	923	305	256		

- Molecule 2 is a protein called 60S ribosomal protein L28.

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

- Molecule 3 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	A	193	Total	C	N	O	0	0
			1492	938	294	260		

- Molecule 4 is a protein called 60S ribosomal protein L3.

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

- Molecule 5 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	336	Total	C	N	O	S	0	0
			2576	1628	483	462	3		

- Molecule 6 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	274	Total	C	N	O	S	0	0
			2197	1388	388	419	2		

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

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

- Molecule 8 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 9 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	227	Total	C	N	O	S	0	0
			1775	1136	318	318	3		

- Molecule 10 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	188	Total	C	N	O	S	0	0
			1493	948	271	270	4		

- Molecule 11 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	167	Total	C	N	O	S	0	0
			1336	838	249	245	4		

- Molecule 12 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	253	Total	C	N	O	S	0	0
			2044	1318	339	384	3		

- Molecule 13 is a protein called 60S ribosomal protein L14-A.

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

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

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

- Molecule 15 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 16 is a protein called 60S ribosomal protein L17-A.

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

- Molecule 17 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 18 is a protein called 60S ribosomal protein L19-A.

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

- Molecule 19 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 20 is a protein called 60S ribosomal protein L21-A.

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
21	U	104	Total	C	N	O	0	0
			826	534	134	158		

- Molecule 22 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 23 is a protein called Ribosome assembly factor MRT4.

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

- Molecule 24 is a protein called 60S ribosomal protein L25.

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

- Molecule 25 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 26 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 27 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	509	Total	C	N	O	S	0	0
			4137	2624	723	771	19		

- 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
			743	479	124	139	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	105	Total	C	N	O	S	0	0
			856	544	163	148	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	125	Total	C	N	O	S	0	0
			1007	638	203	165	1		

- 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
			850	540	165	144	1		

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

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

- Molecule 33 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 34 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 35 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	85	Total	C	N	O	S	0	0
			670	408	146	111	5		

- Molecule 36 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	76	Total	C	N	O	S	0	0
			604	385	114	105			

- Molecule 37 is a protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	m	469	Total	C	N	O	S	0	0
			3774	2381	685	699	9		

- Molecule 38 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	n	366	Total	C	N	O	S	0	0
			2988	1936	517	525	10		

- Molecule 39 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	o	129	Total	C	N	O	S	0	0
			1064	685	192	183	4		

- Molecule 40 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 41 is a protein called Ribosome biogenesis protein NOP53.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	q	158	Total	C	N	O	S	0	0
			1313	827	235	250	1		

- Molecule 42 is a protein called Ribosome biogenesis protein NSA2.

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

- Molecule 43 is a protein called Ribosome biogenesis protein RLP7.

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

- Molecule 44 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	u	142	Total	C	N	O	S	0	0
			1196	751	239	197	9		

- Molecule 45 is a protein called Ribosome biogenesis protein RPF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	v	287	Total	C	N	O	S	0	0
			2318	1482	408	412	16		

- Molecule 46 is a protein called Regulator of ribosome biosynthesis.

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

- Molecule 47 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	x	488	Total	C	N	O	S	0	0
			3807	2398	677	711	21		

- Molecule 48 is a protein called Eukaryotic translation initiation factor 6.

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

- Molecule 49 is a protein called UPF0642 protein YBL028C.

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

- Molecule 50 is a RNA chain called RDN25-1 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	1	3058	Total	C	N	O	P	0	0
			65427	29223	11807	21339	3058		

- Molecule 51 is a RNA chain called RDN5.8-1 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	2	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

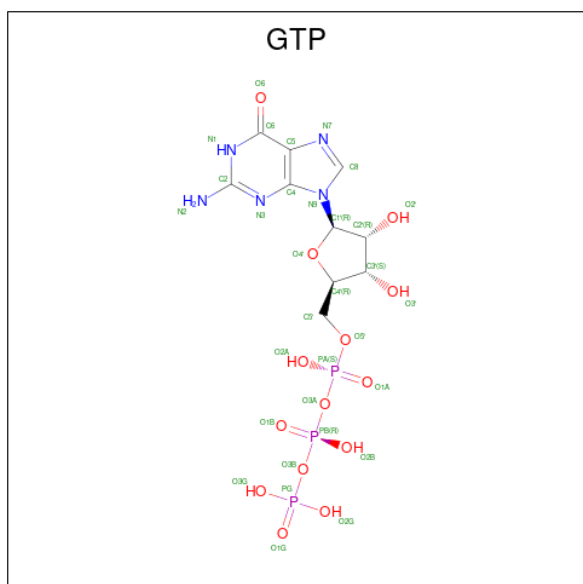
- Molecule 52 is a RNA chain called RDN5-2 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 53 is a RNA chain called ITS2-1 miscRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	6	65	Total	C	N	O	P	0	0
			1370	614	228	463	65		

- Molecule 54 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

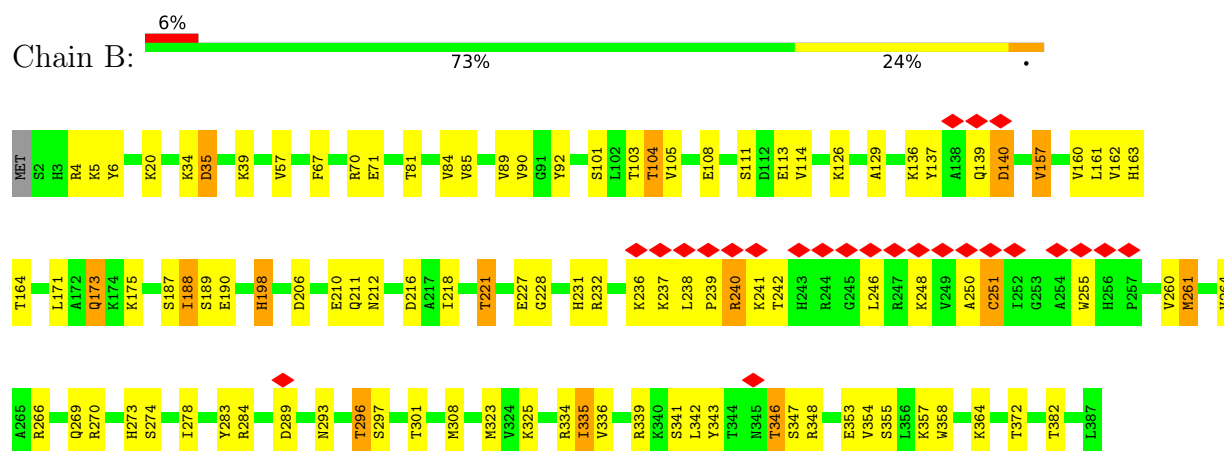
- Molecule 55 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

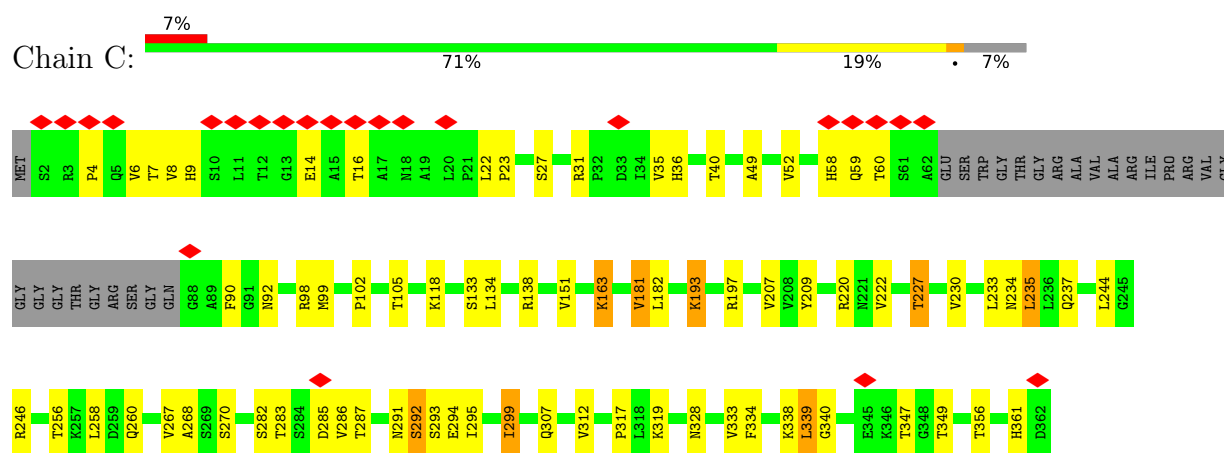
- Molecule 56 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

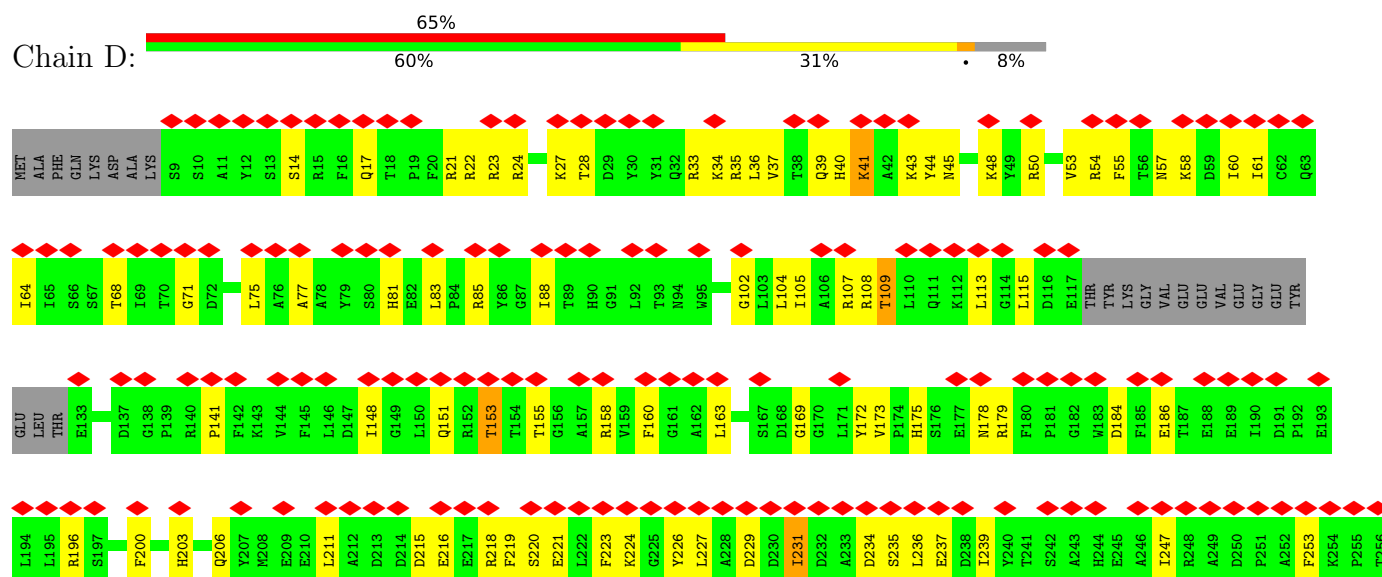
• Molecule 4: 60S ribosomal protein L3



• Molecule 5: 60S ribosomal protein L4-A

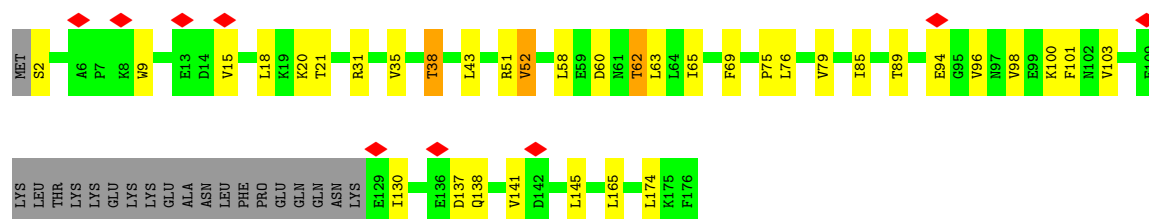


• Molecule 6: 60S ribosomal protein L5

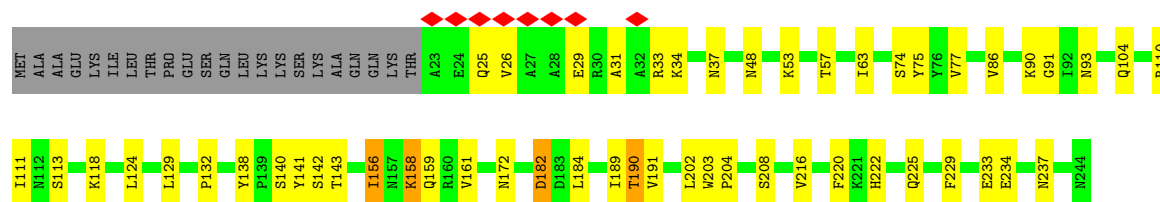




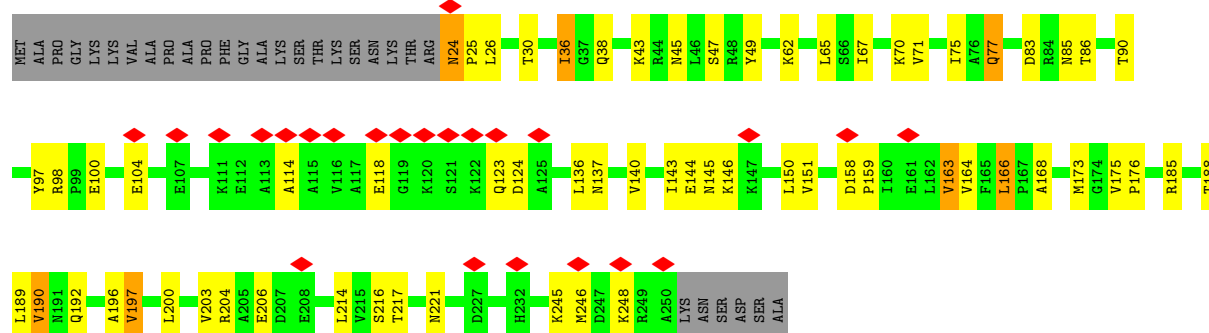
• Molecule 7: 60S ribosomal protein L6-A



• Molecule 8: 60S ribosomal protein L7-A

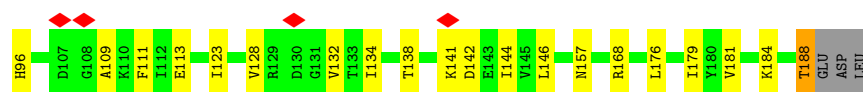


• Molecule 9: 60S ribosomal protein L8-A

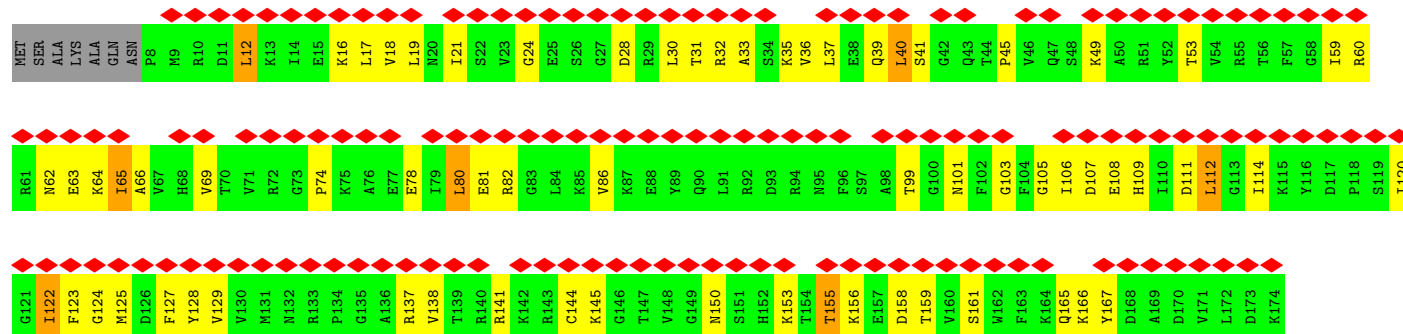
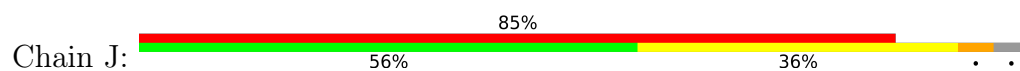


• Molecule 10: 60S ribosomal protein L9-A

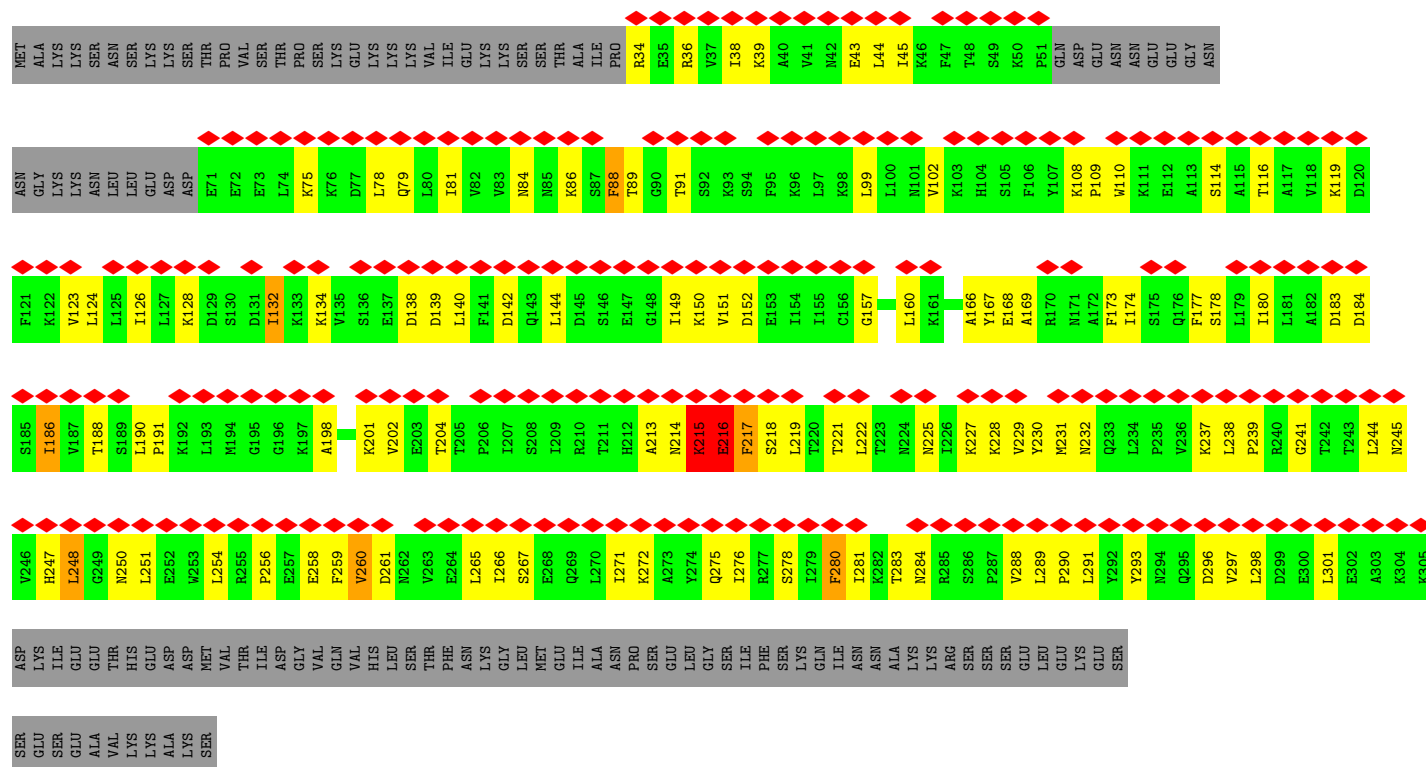




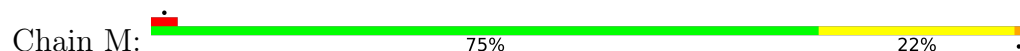
• Molecule 11: 60S ribosomal protein L11-A



• Molecule 12: Proteasome-interacting protein CIC1



• Molecule 13: 60S ribosomal protein L14-A





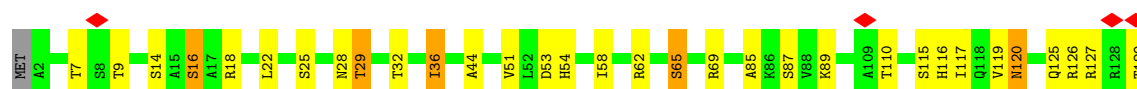
- Molecule 14: 60S ribosomal protein L15-A



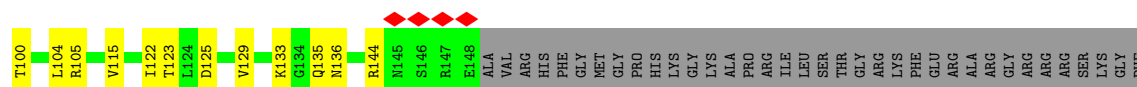
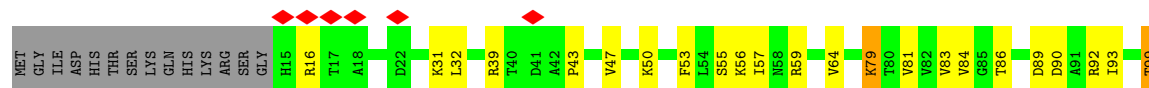
- Molecule 15: 60S ribosomal protein L16-A



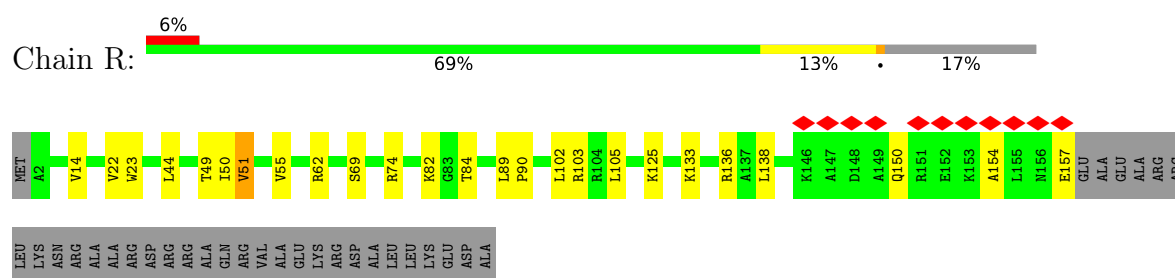
- Molecule 16: 60S ribosomal protein L17-A



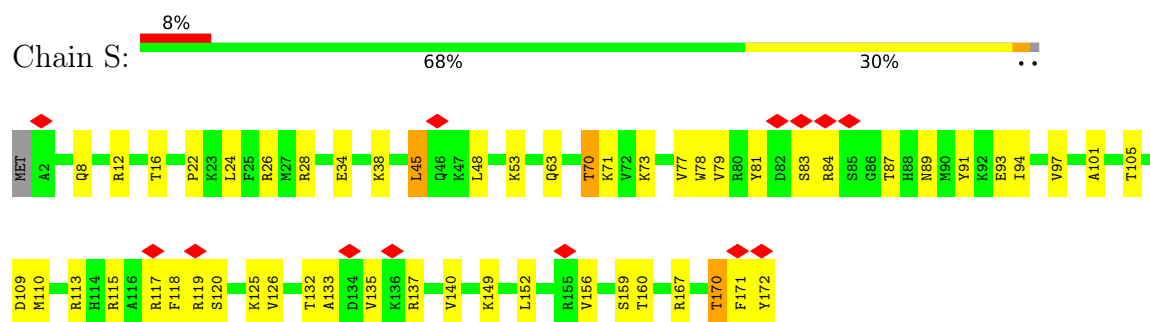
- Molecule 17: 60S ribosomal protein L18-A



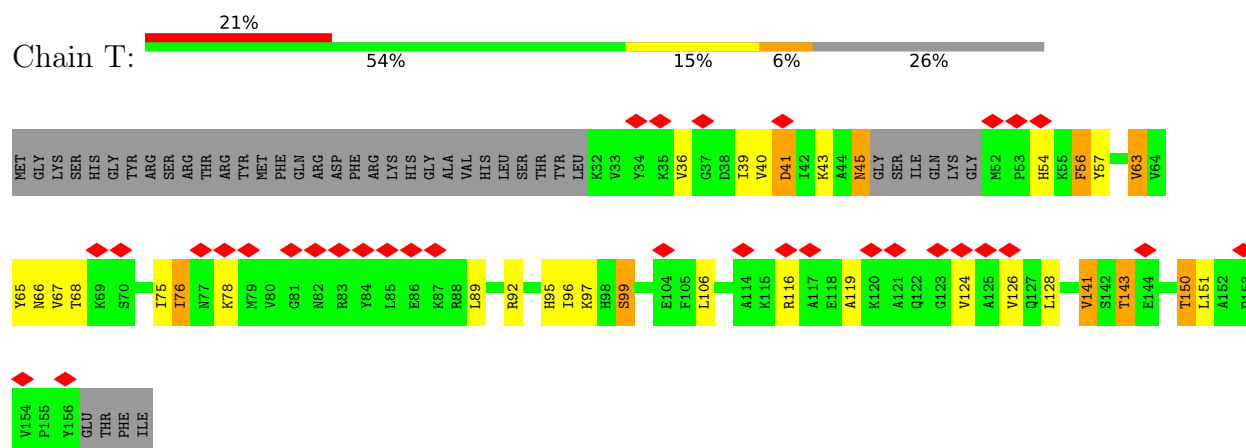
- Molecule 18: 60S ribosomal protein L19-A



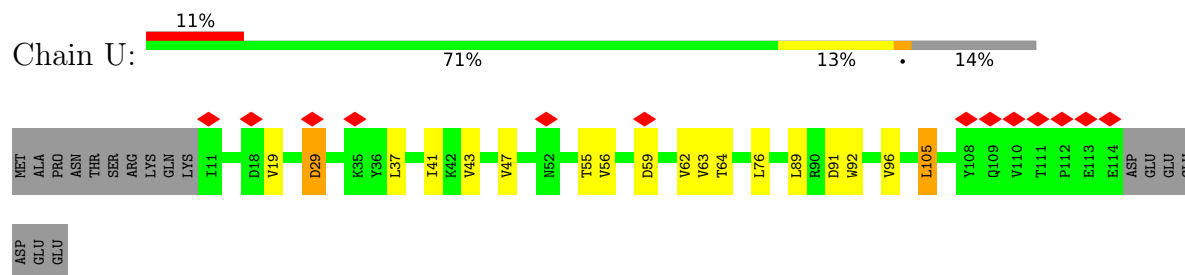
- Molecule 19: 60S ribosomal protein L20-A



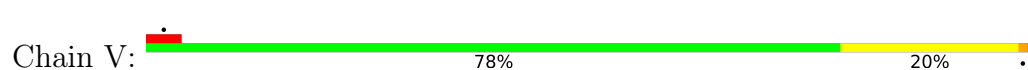
- Molecule 20: 60S ribosomal protein L21-A



- Molecule 21: 60S ribosomal protein L22-A

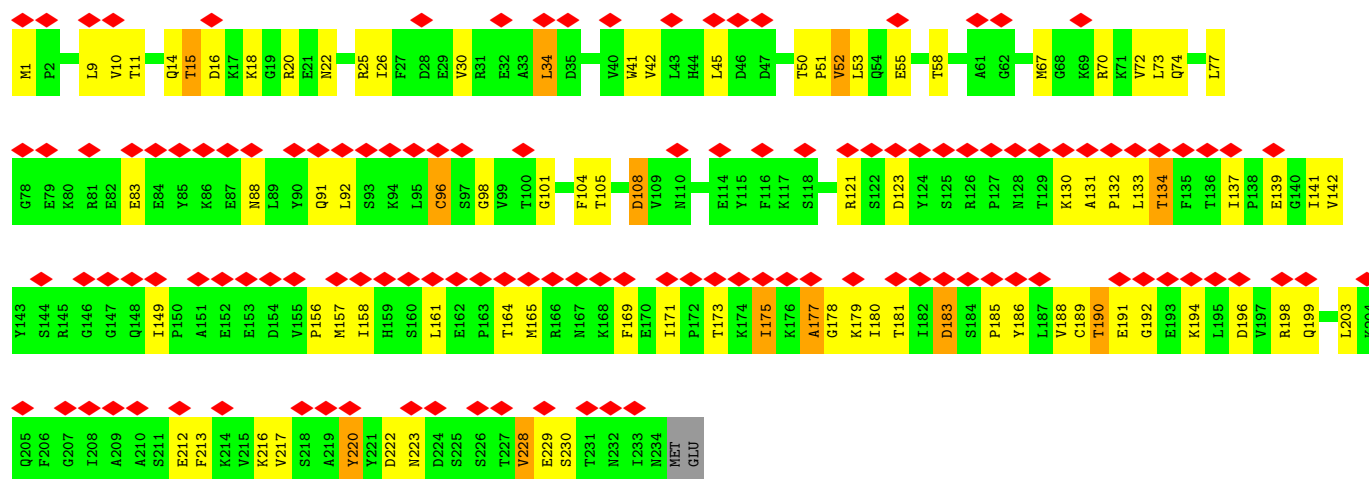


- Molecule 22: 60S ribosomal protein L23-A

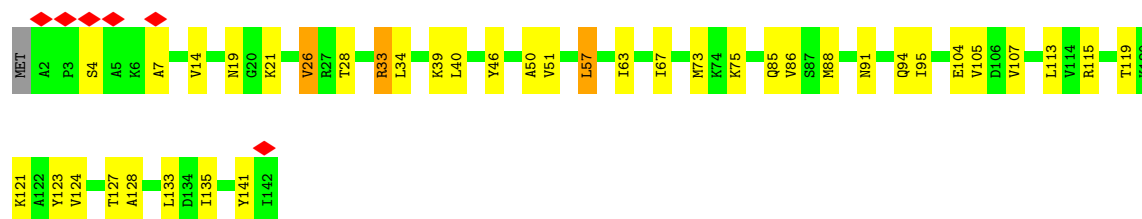




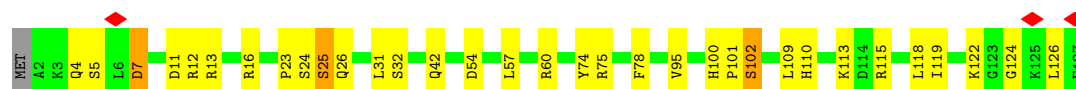
• Molecule 23: Ribosome assembly factor MRT4



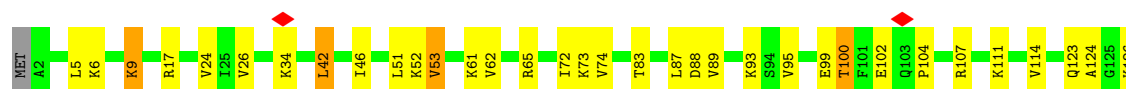
• Molecule 24: 60S ribosomal protein L25



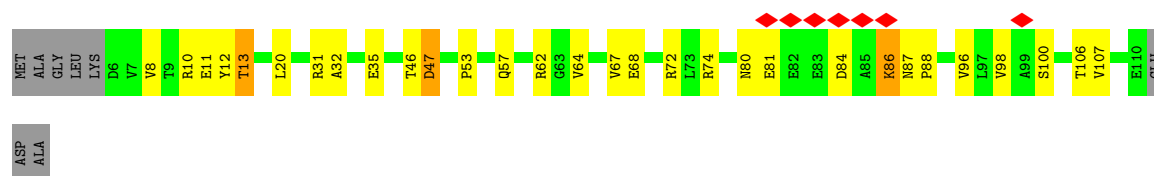
• Molecule 25: 60S ribosomal protein L26-A



• Molecule 26: 60S ribosomal protein L27-A







- Molecule 30: 60S ribosomal protein L32

Chain e: 78% 18%



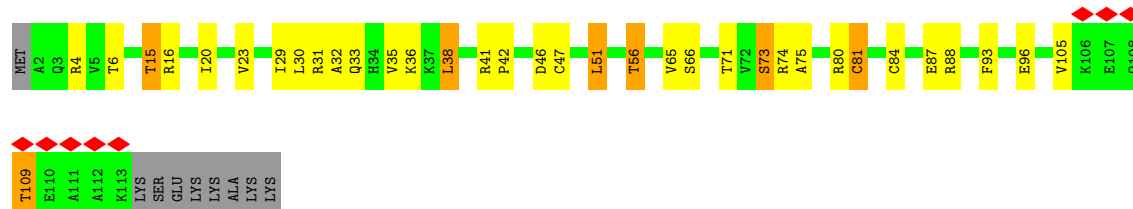
- Molecule 31: 60S ribosomal protein L33-A

Chain f: 78% 20%



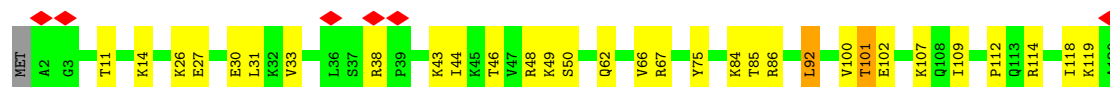
- Molecule 32: 60S ribosomal protein L34-A

Chain g: 7% 64% 23% 6% 7%



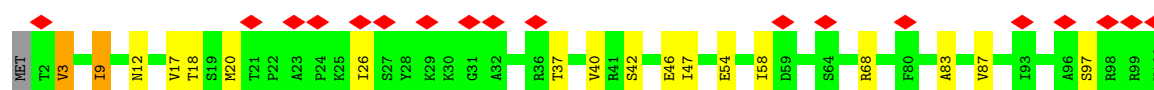
- Molecule 33: 60S ribosomal protein L35-A

Chain h: 5% 73% 24%



- Molecule 34: 60S ribosomal protein L36-A

Chain i: 18% 81% 16%



- Molecule 35: 60S ribosomal protein L37-A

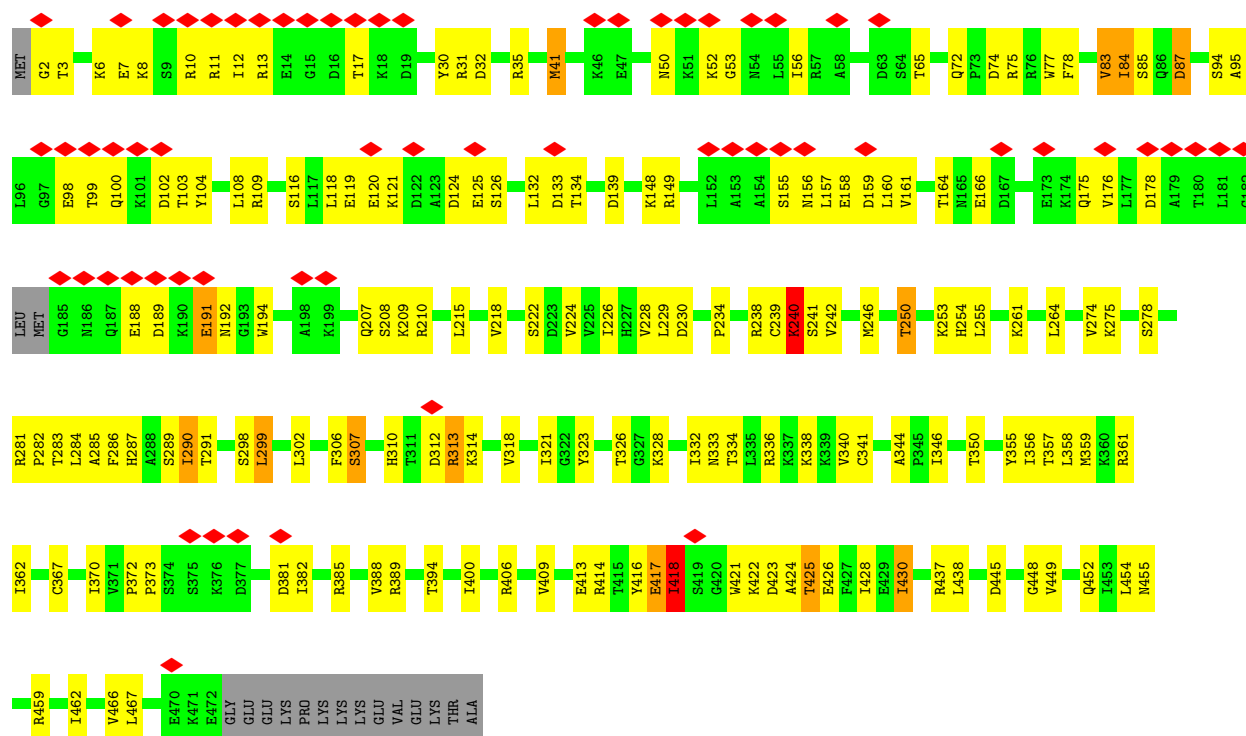
Chain j: 14% 65% 31%



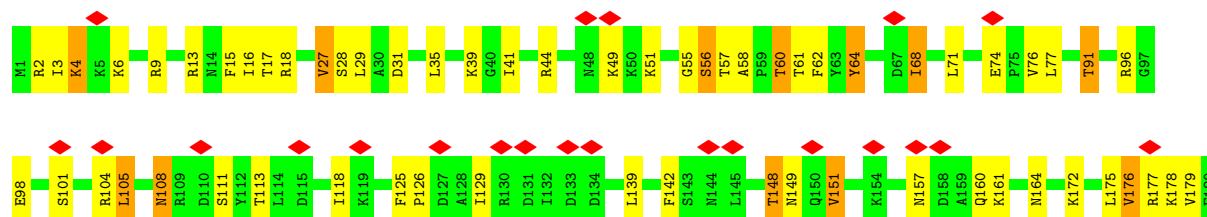
- Molecule 36: 60S ribosomal protein L38

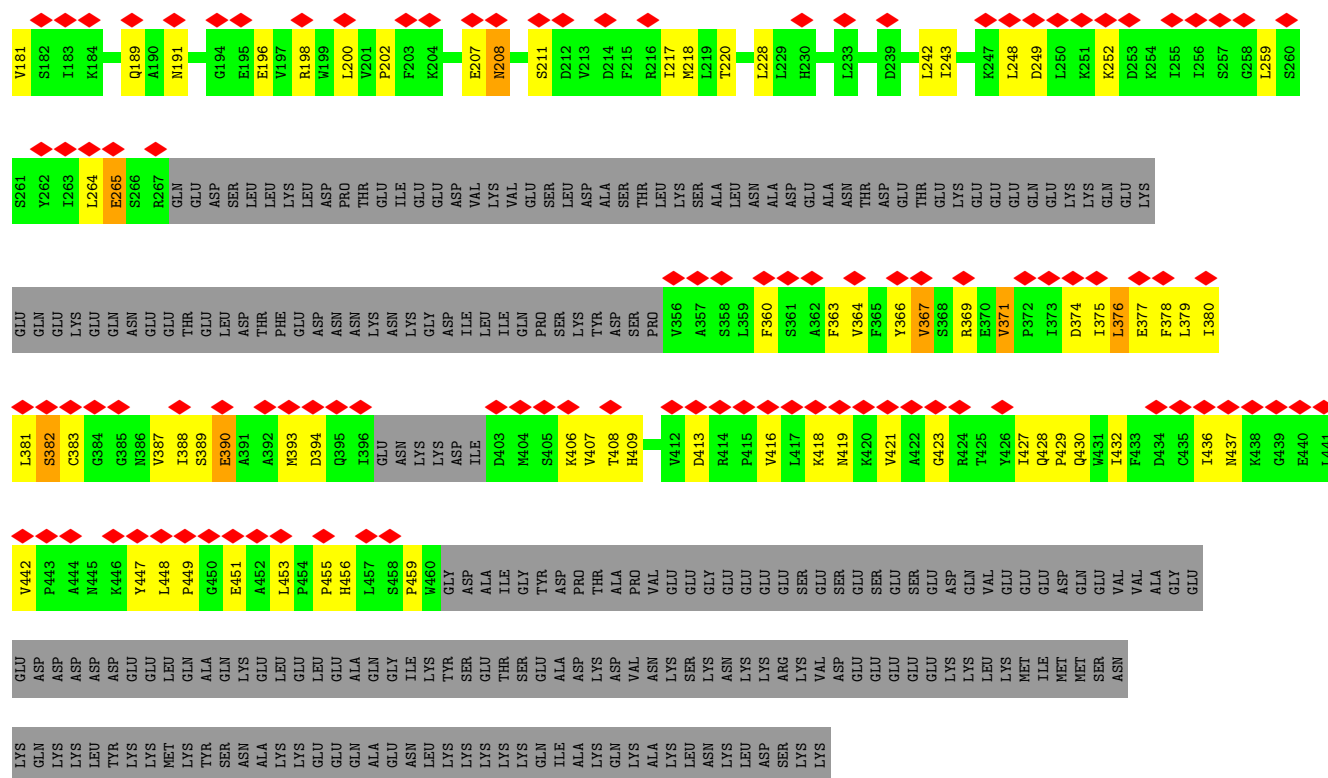


- Molecule 37: Nucleolar GTP-binding protein 2

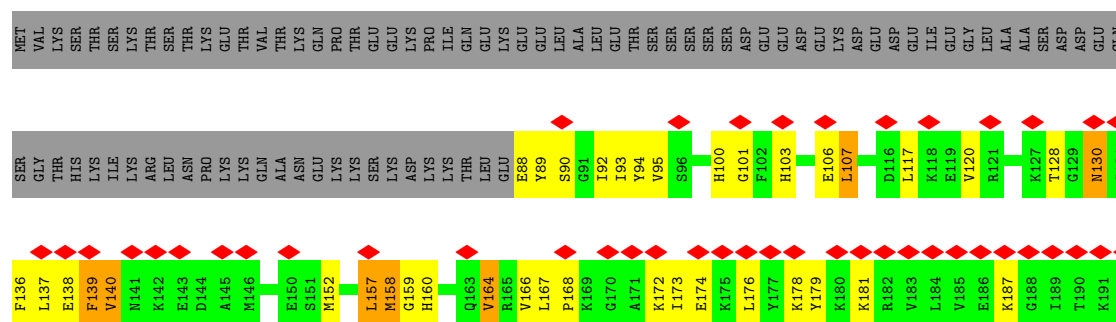
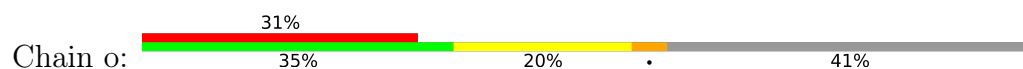


- Molecule 38: Pescadillo homolog

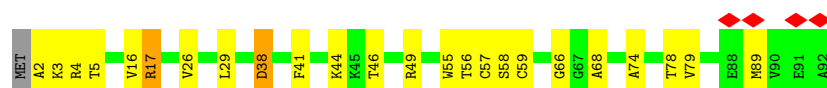




• Molecule 39: Ribosome biogenesis protein 15

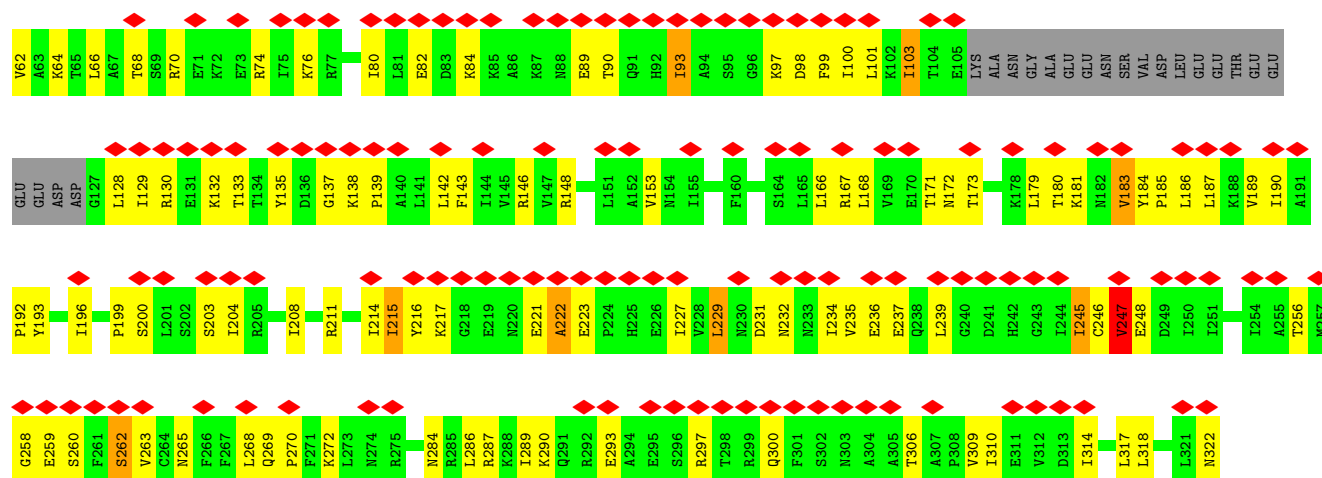


• Molecule 40: 60S ribosomal protein L43-A

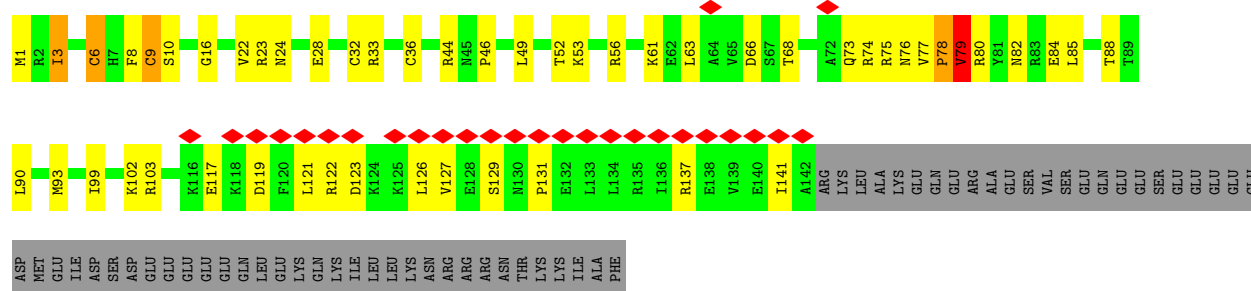
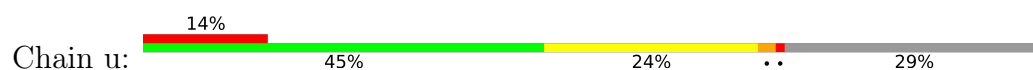


• Molecule 41: Ribosome biogenesis protein NOP53

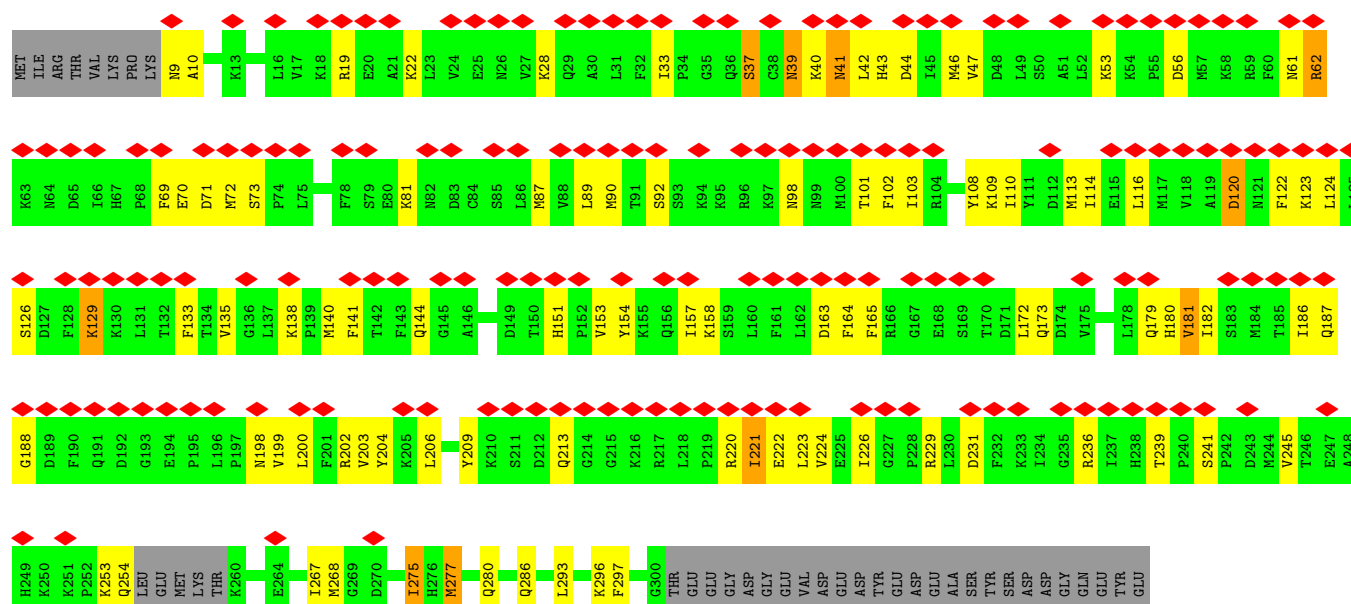




• Molecule 44: Ribosome biogenesis protein RLP24



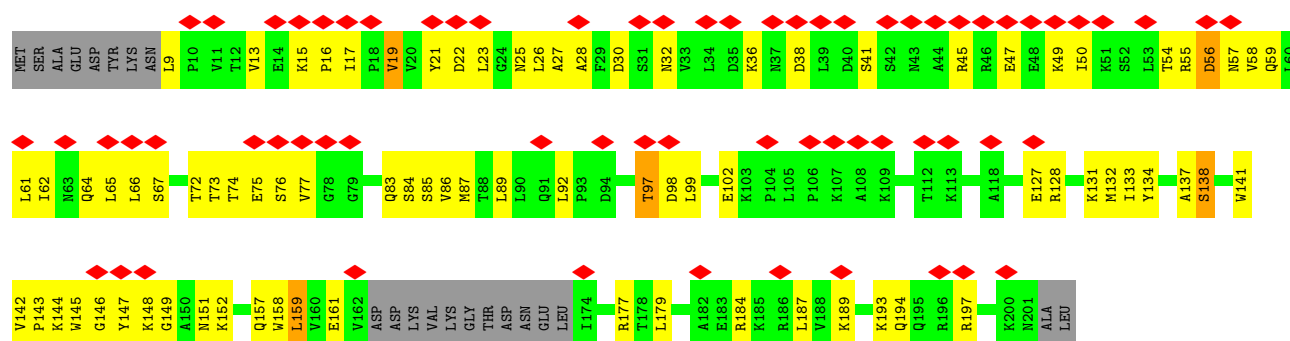
• Molecule 45: Ribosome biogenesis protein RPF2



GLU
GLU
PHE
VAL
SER
SER
ALA
THR
ASP
ILE
GLU
PRO
SER
ALA
LYS
ARG
GLN
LYS
LYS

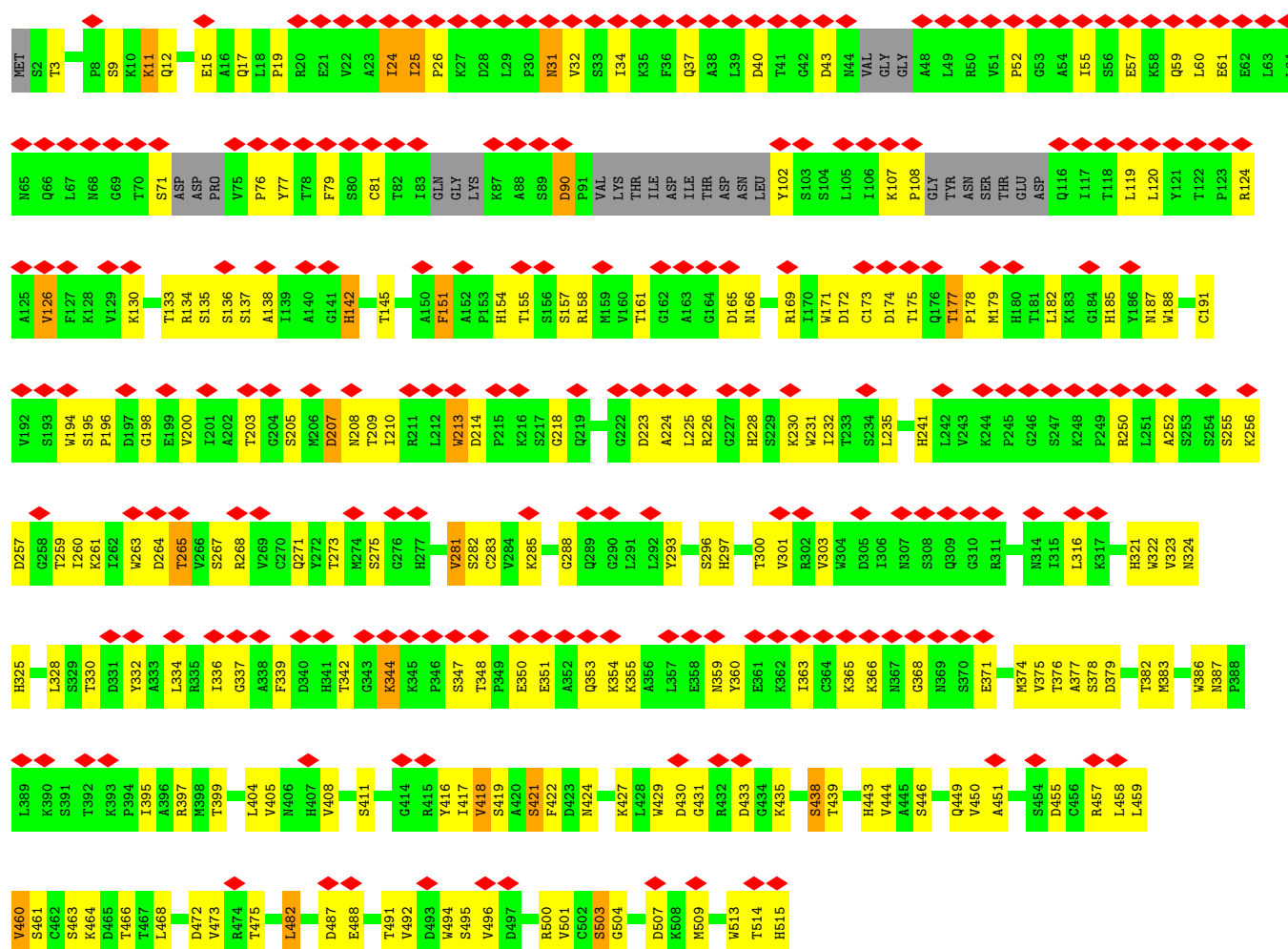
• Molecule 46: Regulator of ribosome biosynthesis

Chain w: 33% 49% 38% 10%



• Molecule 47: Ribosome assembly protein 4

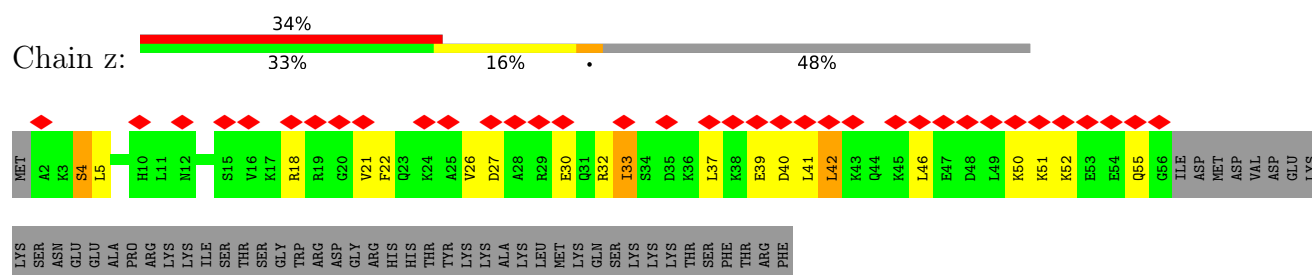
Chain x: 43% 53% 38% 5%



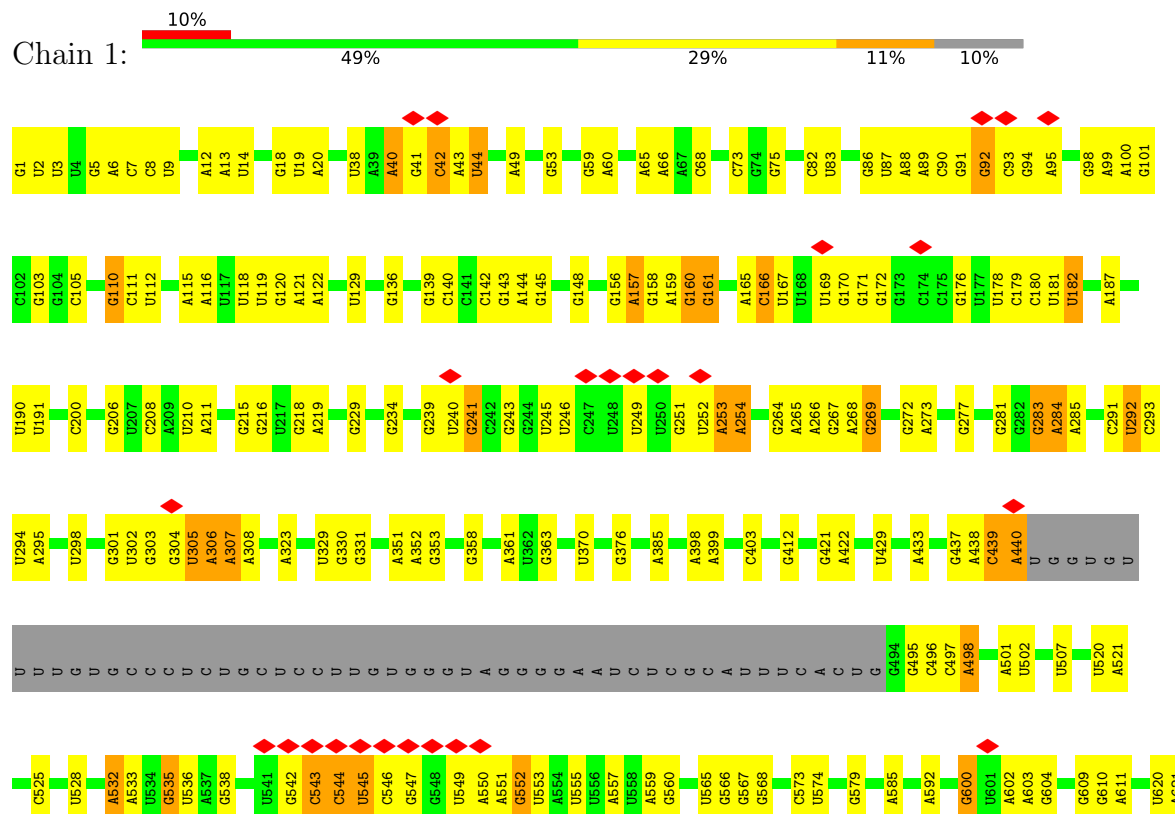
- Molecule 48: Eukaryotic translation initiation factor 6



- Molecule 49: UPF0642 protein YBL028C

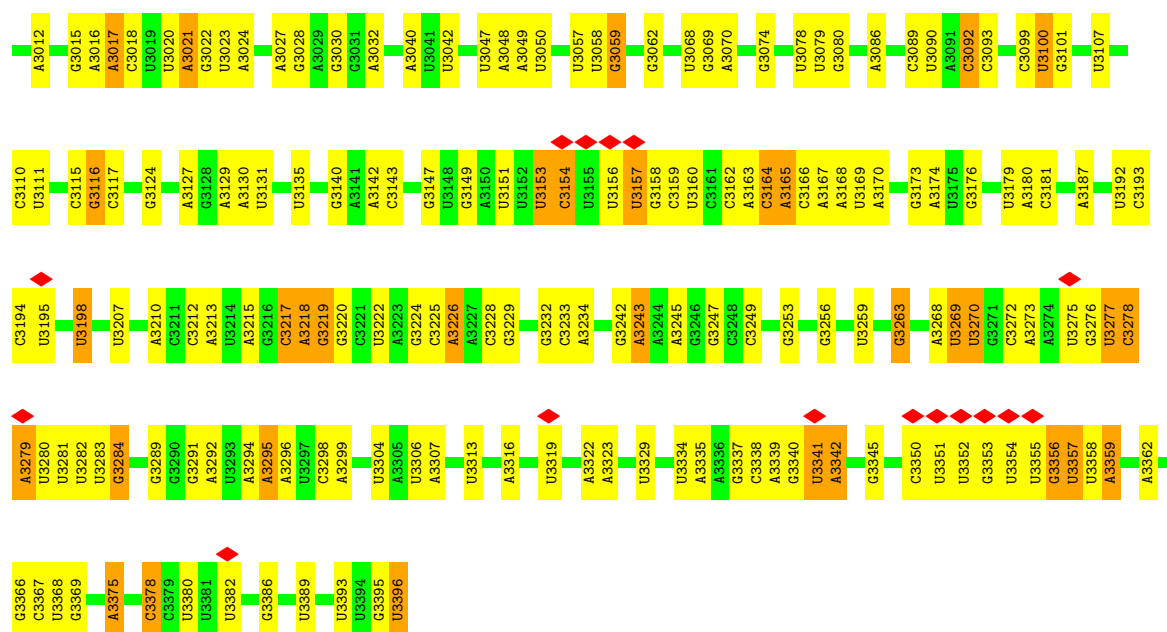


- Molecule 50: RDN25-1 rRNA

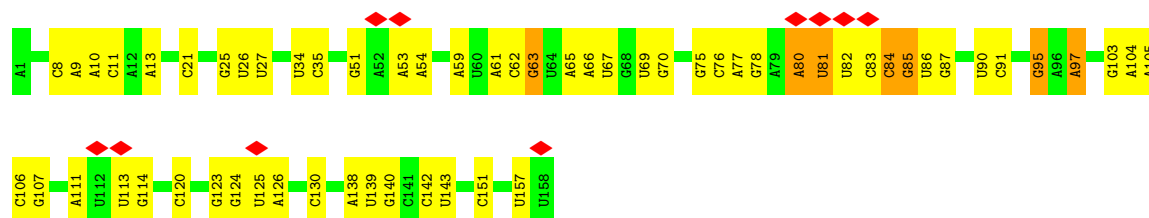




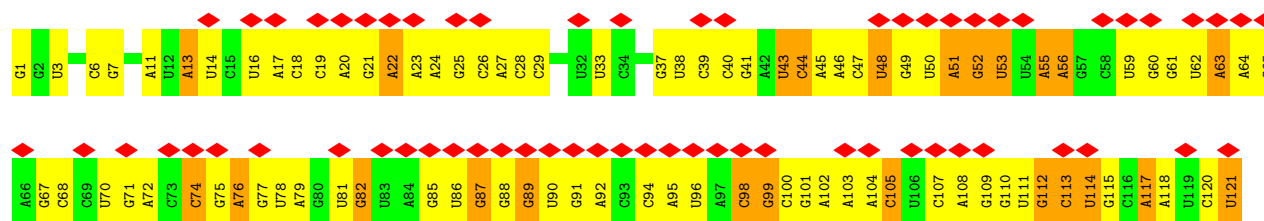
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G2922	A2837	G2770	G2700	C2638	A2566	A	A2419	U2318	U2258	G	G2219	G2194	A2094	C
U2923	G2838	U2771	U2701	G2639	C2566	C	C2420	U2319	C2259	C	U2220	C2195	U2095	G
U2924	G2839	U2772	A2702	A2640	C2567	C	C2422	A2321	U2260	A	C2196	C2196	A2096	G
C2925	C2773	C2772	A2703	U2641	C2568	A	U2423	C2333	G2261	C	C2197	A2261	A2097	C
A2926	C2774	C2773	A2704	A2642	A2569	U	A2424	U2334	A2262	C	A2198	A2262	U2097	C
C2927	U2775	U2774	A2705	A2643	U2570	A	G2425	G2335	U2263	C	U2199	A2263	C2098	G
C2928	U2843	U2775	G2706	A2644	U2571	C	U2426	U2336	U2264	C	U2200	U2264	U2098	G
C2929	U2844	G2776	G2706	C2644	U2572	U	U2427	C2339	U2265	C	G2201	U2265	G2099	G
A2930	C2844	G2777	G2706	G2645	G2573	U	U2428	U2340	C2267	C	U2202	U2266	A2099	G
U2935	A2845	G2778	U2712	A2646	G2576	A	A2438	U2347	U2268	C	U2203	U2267	G2099	G
U2936	A2780	A2779	U2713	G2648	C2577	U	A2439	U2347	U2269	C	U2204	U2268	A2096	G
A2940	U2781	G2779	G2714	A2649	G2585	U	G2442	A2357	U2270	C	U2205	U2269	U2097	C
C	U2782	U2783	U2715	G2650	G2586	U	C2444	A2358	A2271	C	U2206	U2270	U2098	G
G2943	U2783	G2784	U2716	G2651	G2587	U	U2445	C2359	G2272	C	U2207	U2271	C2101	G
U2944	G2786	A2785	U2717	G2652	G2588	U	A	C2362	G2273	C	U2208	U2272	U2102	G
G2945	G2787	G2786	U2718	U2653	G2589	U	G	A2363	G2274	C	U2209	U2273	U2103	G
U2946	C2788	U2789	U2719	C2654	A2593	U	U	G2364	A2275	C	U2210	U2274	A2112	G
A2947	U2789	A2790	U2720	U2655	C2594	U	G	U2370	G2276	C	U2211	U2275	A2113	G
C2948	G2791	G2792	U2721	A2656	U2595	U	A	G2371	G2277	C	U2212	U2276	A2114	G
U2949	A2792	G2793	U2722	G2657	U2596	U	G	A	C2278	C	U2213	U2277	A2115	G
G2950	G2794	G2794	U2723	U2658	U2597	U	G	C2376	A2279	C	U2214	U2278	A2116	G
U2951	U2795	G2795	U2724	G2659	A2601	U	U	G2377	A2280	C	U2215	U2279	A2117	G
G2952	U2796	U2796	U2725	U2660	G2602	U	A	A	A2281	C	U2216	U2280	A2118	G
U2953	G2797	G2797	U2726	G2661	G2603	U	G	C	A2282	C	U2217	U2281	A2119	G
U2954	U2798	U2798	U2727	G2662	U2604	U	U	G	A2283	C	U2218	U2282	A2120	G
C2955	C2799	A2800	U2728	U2663	G2605	U	U	C	U2284	C	U2219	U2283	A2121	G
U2956	U2801	G2801	U2729	G2664	G2606	U	G	G2385	U2285	C	U2220	U2284	A2122	G
C2957	A2802	A2802	U2730	U2665	G2607	U	A	U2388	U2286	C	U2221	U2285	A2123	G
G2961	U2807	U2807	U2731	A2666	G2608	U	U	C2389	U2287	C	U2222	U2286	U2137	G
U2962	A2808	A2808	U2732	U2667	A2609	U	U	U2390	U2288	C	U2223	U2287	A2138	G
C2963	C2809	C2809	U2733	A2668	G2610	U	G	C2391	U2289	C	U2224	U2288	U2139	G
U2965	G2810	G2810	U2734	U2669	U2611	U	U	U2392	U2290	C	U2225	U2289	U2140	G
U2966	U2811	U2811	U2735	A2670	U2612	U	G	U2393	U2291	C	U2226	U2290	U2141	G
A2967	C2812	C2812	U2736	U2671	G2613	U	U	U2394	U2292	C	U2227	U2291	A2142	G
G2968	G2813	G2813	U2737	U2672	G2614	C	G	G2395	U2293	C	U2228	U2292	U2143	G
A2969	U2814	U2814	U2738	A2673	G2615	U	U	U2396	U2294	C	U2229	U2293	U2144	G
C2970	G2815	G2815	U2739	U2674	U2616	G	G	A2397	U2295	C	U2230	U2294	U2145	G
A2971	U2816	U2816	U2740	A2675	U2617	U	U	U2398	U2296	C	U2231	U2295	A2158	G
G2977	G2817	G2817	U2741	G2676	U2618	G	G	A2399	U2297	C	U2232	U2296	C2163	G
U2978	U2818	U2818	U2742	A2677	U2619	U	U	U2400	U2298	C	U2233	U2297	G2169	G
U2979	A2819	A2819	U2743	U2678	G2620	G	G	U2401	U2299	C	U2234	U2298	U2170	G
U2980	C2820	C2820	U2744	U2679	G2621	U	U	A2402	U2300	C	U2235	U2299	G2174	G
U2981	U2821	U2821	U2745	A2680	C2622	G	G	G2403	U2301	C	U2236	U2300	U2175	G
C2982	G2822	G2822	U2746	U2681	U2623	U	U	U2404	U2302	C	U2237	U2301	U2176	G
A2983	U2823	U2823	U2747	U2682	C2624	G	G	A2405	U2303	C	U2238	U2302	G2177	G
C2984	C2824	C2824	U2748	U2683	C2625	C	C	G2406	U2304	C	U2239	U2303	A2178	G
G2988	U2825	U2825	U2749	U2684	U2626	U	U	U2407	U2305	C	U2240	U2304	U2184	G
A2989	C2826	C2826	U2750	U2685	A2627	G	G	G2408	U2306	C	U2241	U2305	A2242	G
C2990	U2827	U2827	U2751	U2686	U2628	U	U	U2409	U2307	C	U2242	U2306	A2243	G
U2991	G2828	G2828	U2752	U2687	C2629	G	G	U2410	U2308	C	U2243	U2307	A2244	G
C2992	U2829	U2829	U2753	U2688	U2630	U	U	U2411	U2309	C	U2244	U2308	G2245	G
G2993	G2830	G2830	U2754	U2689	U2631	U	U	G2412	U2310	C	U2245	U2309	G2246	G
C2994	U2831	U2831	U2755	U2690	U2632	U	U	A2413	U2311	C	U2246	U2310	G2247	G
U2995	C2832	C2832	U2756	U2691	G2633	U	U	G2414	U2312	C	U2247	U2311	G2248	G
A2996	U2833	U2833	U2757	U2692	U2634	U	U	U2415	U2313	C	U2248	U2312	G2249	G
C2997	C2834	C2834	U2758	U2693	A2635	U	U	U2416	U2314	C	U2249	U2313	A2255	G
U2998	U2835	U2835	U2759	U2694	U2636	U	U	U2417	U2315	C	U2250	U2314	A2256	G



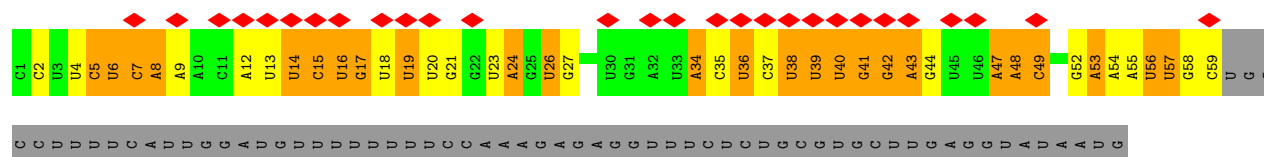
• Molecule 51: RDN5.8-1 rRNA

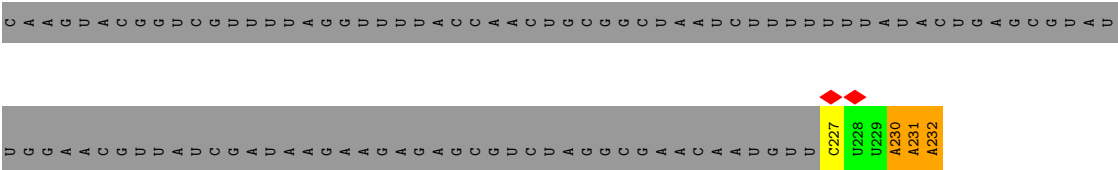


• Molecule 52: RDN5-2 rRNA



• Molecule 53: ITS2-1 miscRNA





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	47025	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	0.208	Depositor
Minimum map value	-0.120	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	412.02, 412.02, 412.02	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3734, 1.3734, 1.3734	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, MG, 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	L	0.31	0/1508	0.59	0/2024
2	a	0.29	0/751	0.47	0/1013
3	A	0.34	0/1520	0.52	0/2043
4	B	0.34	0/3152	0.52	0/4239
5	C	0.34	0/2624	0.55	0/3553
6	D	0.21	0/2243	0.48	0/3025
7	E	0.28	0/1260	0.48	0/1694
8	F	0.33	0/1821	0.51	0/2451
9	G	0.30	0/1807	0.56	2/2439 (0.1%)
10	H	0.31	0/1514	0.45	0/2039
11	J	0.18	0/1357	0.49	0/1818
12	K	0.20	0/2077	0.53	2/2800 (0.1%)
13	M	0.30	0/1074	0.48	0/1446
14	N	0.34	0/1757	0.55	0/2354
15	O	0.37	0/1585	0.47	0/2128
16	P	0.32	0/1465	0.51	0/1968
17	Q	0.29	0/1050	0.46	0/1419
18	R	0.33	0/1275	0.45	0/1702
19	S	0.31	0/1473	0.54	0/1980
20	T	0.23	0/957	0.52	0/1285
21	U	0.26	0/843	0.47	0/1144
22	V	0.34	0/1018	0.48	0/1369
23	W	0.22	0/1918	0.49	0/2586
24	X	0.31	0/1116	0.46	0/1503
25	Y	0.31	0/1004	0.51	0/1341
26	Z	0.30	0/1118	0.57	0/1497
27	b	0.28	0/4211	0.52	0/5675
28	c	0.28	0/751	0.40	0/1008
29	d	0.34	0/870	0.48	0/1168
30	e	0.34	0/1028	0.45	0/1376
31	f	0.35	0/868	0.48	0/1168
32	g	0.38	0/891	0.54	0/1191

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.31	0/978	0.49	0/1301
34	i	0.25	0/778	0.53	0/1034
35	j	0.34	0/685	0.48	0/908
36	k	0.28	0/610	0.50	0/815
37	m	0.30	0/3848	0.56	0/5181
38	n	0.25	0/3057	0.54	0/4127
39	o	0.23	0/1083	0.53	0/1440
40	p	0.36	0/701	0.51	0/934
41	q	0.21	0/1336	0.49	0/1788
42	r	0.32	0/1892	0.60	2/2528 (0.1%)
43	t	0.22	0/2333	0.54	0/3128
44	u	0.29	0/1218	0.56	2/1621 (0.1%)
45	v	0.22	0/2361	0.46	0/3153
46	w	0.23	0/1471	0.49	0/1980
47	x	0.22	0/3897	0.53	2/5282 (0.0%)
48	y	0.30	0/1872	0.50	0/2548
49	z	0.18	0/445	0.38	0/585
50	1	0.32	0/73234	0.39	0/114167
51	2	0.34	0/3746	0.37	0/5832
52	3	0.17	0/2883	0.36	0/4491
53	6	0.19	0/1527	0.43	0/2371
All	All	0.30	0/157861	0.45	10/229660 (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
1	L	0	1
4	B	0	2
8	F	0	1
11	J	0	1
12	K	0	1
23	W	0	1
29	d	0	1
32	g	0	1
37	m	0	3
38	n	0	3
39	o	0	1
41	q	0	2
42	r	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
44	u	0	2
47	x	0	1
All	All	0	23

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	x	213	TRP	CA-C-N	10.43	135.50	121.74
47	x	213	TRP	C-N-CA	10.43	135.50	121.74
42	r	202	LYS	CA-C-N	6.52	132.00	121.83
42	r	202	LYS	C-N-CA	6.52	132.00	121.83
44	u	79	VAL	CA-C-N	5.62	132.28	121.54

There are no chirality outliers.

5 of 23 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	B	221	THR	Peptide
4	B	346	THR	Peptide
8	F	158	LYS	Peptide
11	J	167	TYR	Peptide
1	L	46	ILE	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L	1484	0	1539	34	0
2	a	735	0	776	17	0
3	A	1492	0	1548	35	0
4	B	3081	0	3165	64	0
5	C	2576	0	2692	42	0
6	D	2197	0	2157	82	0
7	E	1239	0	1326	22	0
8	F	1784	0	1862	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	G	1775	0	1870	41	0
10	H	1493	0	1566	32	0
11	J	1336	0	1370	54	0
12	K	2044	0	2133	79	0
13	M	1059	0	1154	20	0
14	N	1720	0	1779	40	0
15	O	1555	0	1659	4	0
16	P	1442	0	1485	28	0
17	Q	1035	0	1115	18	0
18	R	1258	0	1342	14	0
19	S	1437	0	1475	30	0
20	T	943	0	994	23	0
21	U	826	0	834	3	0
22	V	1003	0	1048	14	0
23	W	1885	0	1921	60	0
24	X	1100	0	1187	24	0
25	Y	993	0	1081	21	0
26	Z	1092	0	1155	22	0
27	b	4137	0	4199	114	0
28	c	743	0	797	14	0
29	d	856	0	904	18	0
30	e	1007	0	1074	9	0
31	f	850	0	880	16	0
32	g	881	0	945	19	0
33	h	969	0	1078	17	0
34	i	771	0	849	11	0
35	j	670	0	673	18	0
36	k	604	0	671	8	0
37	m	3774	0	3835	119	0
38	n	2988	0	3069	79	0
39	o	1064	0	1121	41	0
40	p	694	0	736	15	0
41	q	1313	0	1344	36	0
42	r	1860	0	1965	70	0
43	t	2306	0	2454	79	0
44	u	1196	0	1239	34	0
45	v	2318	0	2398	78	0
46	w	1448	0	1510	74	0
47	x	3807	0	3790	142	0
48	y	1849	0	1836	60	0
49	z	444	0	478	13	0
50	1	65427	0	32879	836	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
51	2	3353	0	1695	30	0
52	3	2579	0	1304	98	0
53	6	1370	0	692	47	0
54	b	32	0	12	3	0
54	m	32	0	12	2	0
55	b	1	0	0	0	0
55	m	1	0	0	0	0
56	j	1	0	0	0	0
56	p	1	0	0	0	0
56	u	1	0	0	0	0
All	All	147931	0	114672	2557	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 10.

The worst 5 of 2557 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)
50:1:3222:U:H3	50:1:3263:G:H1	1.05	0.99
50:1:1001:G:C6	50:1:1050:U:O2	2.17	0.97
50:1:2426:U:H3	50:1:2603:G:H1	1.01	0.95
52:3:79:A:H62	52:3:101:G:H21	1.02	0.94
52:3:67:G:H1	52:3:111:U:H3	1.05	0.94

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	
1	L	183/199 (92%)	157 (86%)	25 (14%)	1 (0%)	24	58
2	a	91/149 (61%)	79 (87%)	11 (12%)	1 (1%)	11	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	A	191/254 (75%)	172 (90%)	19 (10%)	0	100	100
4	B	384/387 (99%)	330 (86%)	51 (13%)	3 (1%)	16	48
5	C	332/362 (92%)	282 (85%)	47 (14%)	3 (1%)	14	46
6	D	270/297 (91%)	246 (91%)	24 (9%)	0	100	100
7	E	152/176 (86%)	136 (90%)	16 (10%)	0	100	100
8	F	220/244 (90%)	204 (93%)	16 (7%)	0	100	100
9	G	225/256 (88%)	196 (87%)	29 (13%)	0	100	100
10	H	186/191 (97%)	169 (91%)	16 (9%)	1 (0%)	24	58
11	J	165/174 (95%)	136 (82%)	29 (18%)	0	100	100
12	K	249/376 (66%)	217 (87%)	30 (12%)	2 (1%)	16	48
13	M	135/138 (98%)	124 (92%)	11 (8%)	0	100	100
14	N	201/204 (98%)	185 (92%)	14 (7%)	2 (1%)	12	44
15	O	195/199 (98%)	188 (96%)	7 (4%)	0	100	100
16	P	181/184 (98%)	163 (90%)	18 (10%)	0	100	100
17	Q	132/186 (71%)	120 (91%)	12 (9%)	0	100	100
18	R	154/189 (82%)	145 (94%)	9 (6%)	0	100	100
19	S	169/172 (98%)	154 (91%)	15 (9%)	0	100	100
20	T	115/160 (72%)	98 (85%)	17 (15%)	0	100	100
21	U	102/121 (84%)	90 (88%)	12 (12%)	0	100	100
22	V	134/137 (98%)	124 (92%)	10 (8%)	0	100	100
23	W	232/236 (98%)	209 (90%)	22 (10%)	1 (0%)	30	61
24	X	139/142 (98%)	131 (94%)	8 (6%)	0	100	100
25	Y	124/127 (98%)	118 (95%)	6 (5%)	0	100	100
26	Z	133/136 (98%)	113 (85%)	18 (14%)	2 (2%)	8	36
27	b	505/647 (78%)	430 (85%)	72 (14%)	3 (1%)	21	55
28	c	95/105 (90%)	91 (96%)	4 (4%)	0	100	100
29	d	103/113 (91%)	91 (88%)	12 (12%)	0	100	100
30	e	123/130 (95%)	113 (92%)	10 (8%)	0	100	100
31	f	104/107 (97%)	99 (95%)	5 (5%)	0	100	100
32	g	110/121 (91%)	103 (94%)	7 (6%)	0	100	100
33	h	117/120 (98%)	106 (91%)	10 (8%)	1 (1%)	14	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	i	97/100 (97%)	86 (89%)	11 (11%)	0	100	100
35	j	83/88 (94%)	75 (90%)	8 (10%)	0	100	100
36	k	74/78 (95%)	67 (90%)	7 (10%)	0	100	100
37	m	465/486 (96%)	389 (84%)	70 (15%)	6 (1%)	9	39
38	n	360/605 (60%)	311 (86%)	46 (13%)	3 (1%)	16	48
39	o	127/220 (58%)	110 (87%)	16 (13%)	1 (1%)	16	48
40	p	89/92 (97%)	80 (90%)	9 (10%)	0	100	100
41	q	154/455 (34%)	128 (83%)	24 (16%)	2 (1%)	9	39
42	r	224/261 (86%)	188 (84%)	33 (15%)	3 (1%)	9	39
43	t	283/322 (88%)	238 (84%)	42 (15%)	3 (1%)	11	42
44	u	140/199 (70%)	126 (90%)	14 (10%)	0	100	100
45	v	283/344 (82%)	265 (94%)	18 (6%)	0	100	100
46	w	178/203 (88%)	158 (89%)	20 (11%)	0	100	100
47	x	476/515 (92%)	422 (89%)	54 (11%)	0	100	100
48	y	242/245 (99%)	213 (88%)	29 (12%)	0	100	100
49	z	53/106 (50%)	51 (96%)	2 (4%)	0	100	100
All	All	9279/11058 (84%)	8226 (89%)	1015 (11%)	38 (0%)	31	61

5 of 38 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	C	339	LEU
12	K	216	GLU
26	Z	102	GLU
37	m	241	SER
1	L	63	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	L	147/159 (92%)	128 (87%)	19 (13%)	4	19
2	a	76/119 (64%)	63 (83%)	13 (17%)	2	10
3	A	152/196 (78%)	136 (90%)	16 (10%)	6	27
4	B	322/323 (100%)	282 (88%)	40 (12%)	4	21
5	C	273/289 (94%)	248 (91%)	25 (9%)	8	32
6	D	226/245 (92%)	212 (94%)	14 (6%)	16	47
7	E	134/153 (88%)	122 (91%)	12 (9%)	9	33
8	F	186/205 (91%)	169 (91%)	17 (9%)	9	32
9	G	186/208 (89%)	168 (90%)	18 (10%)	8	31
10	H	168/171 (98%)	152 (90%)	16 (10%)	8	31
11	J	145/150 (97%)	136 (94%)	9 (6%)	16	47
12	K	234/346 (68%)	213 (91%)	21 (9%)	9	33
13	M	108/109 (99%)	97 (90%)	11 (10%)	7	28
14	N	175/176 (99%)	161 (92%)	14 (8%)	11	38
15	O	160/162 (99%)	154 (96%)	6 (4%)	29	60
16	P	145/146 (99%)	126 (87%)	19 (13%)	4	19
17	Q	110/151 (73%)	96 (87%)	14 (13%)	4	20
18	R	129/154 (84%)	120 (93%)	9 (7%)	14	43
19	S	155/156 (99%)	138 (89%)	17 (11%)	6	25
20	T	102/137 (74%)	87 (85%)	15 (15%)	3	14
21	U	91/107 (85%)	76 (84%)	15 (16%)	2	10
22	V	104/105 (99%)	96 (92%)	8 (8%)	12	40
23	W	211/213 (99%)	187 (89%)	24 (11%)	5	23
24	X	117/118 (99%)	105 (90%)	12 (10%)	7	27
25	Y	109/110 (99%)	101 (93%)	8 (7%)	13	42
26	Z	115/116 (99%)	105 (91%)	10 (9%)	9	35
27	b	457/573 (80%)	414 (91%)	43 (9%)	8	31
28	c	81/88 (92%)	71 (88%)	10 (12%)	4	21
29	d	92/97 (95%)	82 (89%)	10 (11%)	6	25
30	e	108/111 (97%)	95 (88%)	13 (12%)	5	22
31	f	90/91 (99%)	85 (94%)	5 (6%)	19	50
32	g	95/103 (92%)	81 (85%)	14 (15%)	3	14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	h	104/105 (99%)	90 (86%)	14 (14%)	4	18
34	i	81/82 (99%)	75 (93%)	6 (7%)	13	41
35	j	69/71 (97%)	61 (88%)	8 (12%)	5	23
36	k	67/69 (97%)	61 (91%)	6 (9%)	9	33
37	m	413/428 (96%)	369 (89%)	44 (11%)	6	26
38	n	329/548 (60%)	288 (88%)	41 (12%)	4	20
39	o	114/199 (57%)	101 (89%)	13 (11%)	5	23
40	p	71/72 (99%)	64 (90%)	7 (10%)	7	29
41	q	147/420 (35%)	133 (90%)	14 (10%)	8	31
42	r	203/229 (89%)	183 (90%)	20 (10%)	7	29
43	t	256/287 (89%)	233 (91%)	23 (9%)	9	33
44	u	126/180 (70%)	118 (94%)	8 (6%)	16	46
45	v	258/309 (84%)	234 (91%)	24 (9%)	8	32
46	w	161/179 (90%)	149 (92%)	12 (8%)	12	40
47	x	428/451 (95%)	386 (90%)	42 (10%)	7	30
48	y	210/211 (100%)	187 (89%)	23 (11%)	6	25
49	z	48/95 (50%)	41 (85%)	7 (15%)	3	15
All	All	8088/9522 (85%)	7279 (90%)	809 (10%)	9	29

5 of 809 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	d	106	THR
37	m	462	ILE
48	y	226	ASP
30	e	120	THR
29	d	100	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 167 such sidechains are listed below:

Mol	Chain	Res	Type
39	o	204	HIS
44	u	130	ASN
41	q	264	HIS
43	t	157	ASN

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Mol	Chain	Res	Type
46	w	91	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	1	3048/3396 (89%)	815 (26%)	64 (2%)
51	2	157/158 (99%)	32 (20%)	1 (0%)
52	3	120/121 (99%)	33 (27%)	1 (0%)
53	6	63/232 (27%)	33 (52%)	2 (3%)
All	All	3388/3907 (86%)	913 (26%)	68 (2%)

5 of 913 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	1	5	G
50	1	7	C
50	1	14	U
50	1	18	G
50	1	38	U

5 of 68 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	1	2857	C
50	1	2875	U
52	3	52	G
50	1	1307	G
50	1	1302	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 7 ligands modelled in this entry, 5 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	$\# Z > 2$
54	GTP	b	701	55	33,34,34	0.92	0	50,54,54	1.59	8 (16%)
54	GTP	m	501	-	33,34,34	0.92	2 (6%)	50,54,54	1.73	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
54	GTP	b	701	55	-	3/22/38/38	0/3/3/3
54	GTP	m	501	-	-	8/22/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	m	501	GTP	O4'-C4'	-2.04	1.40	1.45
54	m	501	GTP	C2-N3	2.03	1.38	1.33

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	m	501	GTP	C5-C4-N3	-5.39	119.82	128.39
54	b	701	GTP	C5-C4-N3	-4.72	120.88	128.39
54	m	501	GTP	C2-N3-C4	4.70	120.40	112.30
54	b	701	GTP	C2-N3-C4	4.54	120.12	112.30
54	m	501	GTP	N9-C4-N3	3.66	133.26	125.95

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
54	m	501	GTP	O4'-C4'-C5'-O5'
54	m	501	GTP	C3'-C4'-C5'-O5'
54	b	701	GTP	C3'-C4'-C5'-O5'
54	b	701	GTP	O4'-C4'-C5'-O5'
54	m	501	GTP	PB-O3B-PG-O1G

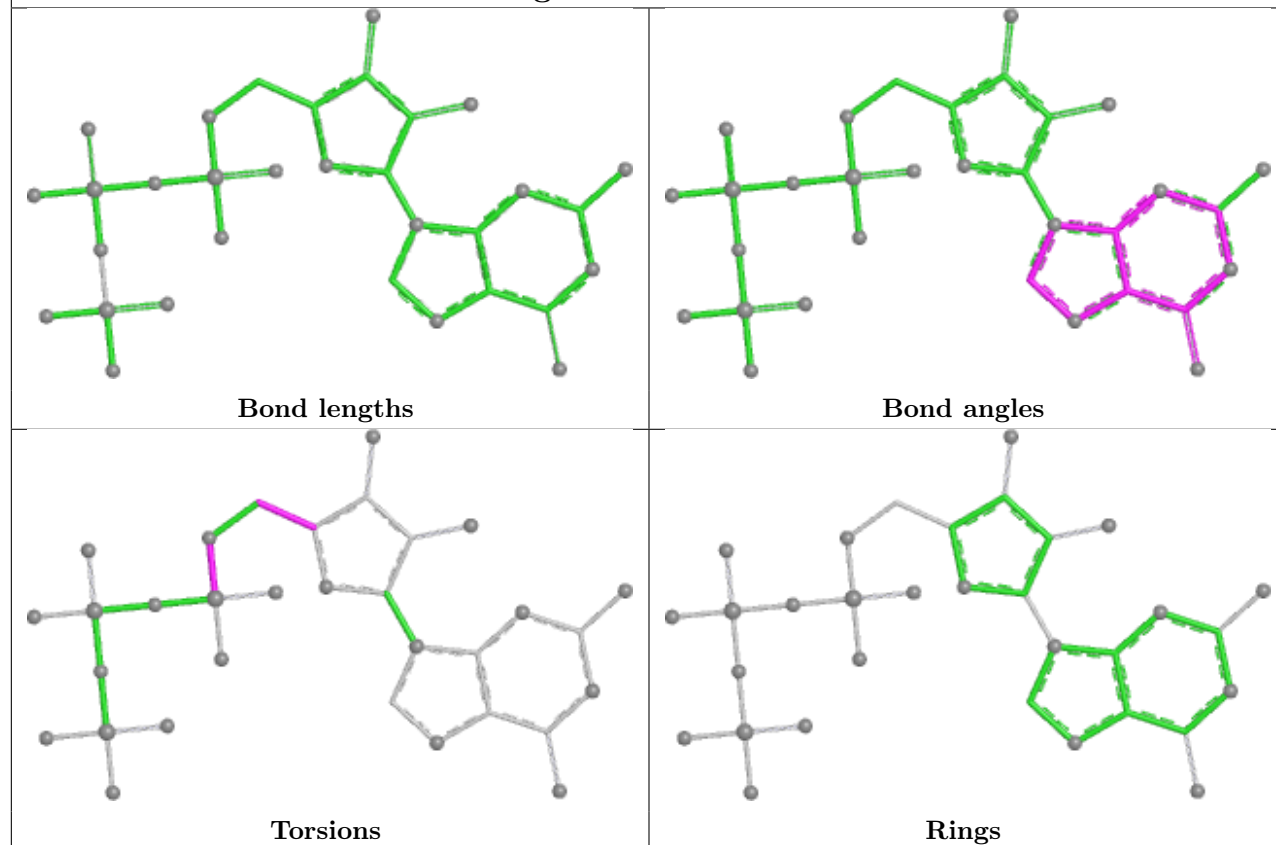
There are no ring outliers.

2 monomers are involved in 5 short contacts:

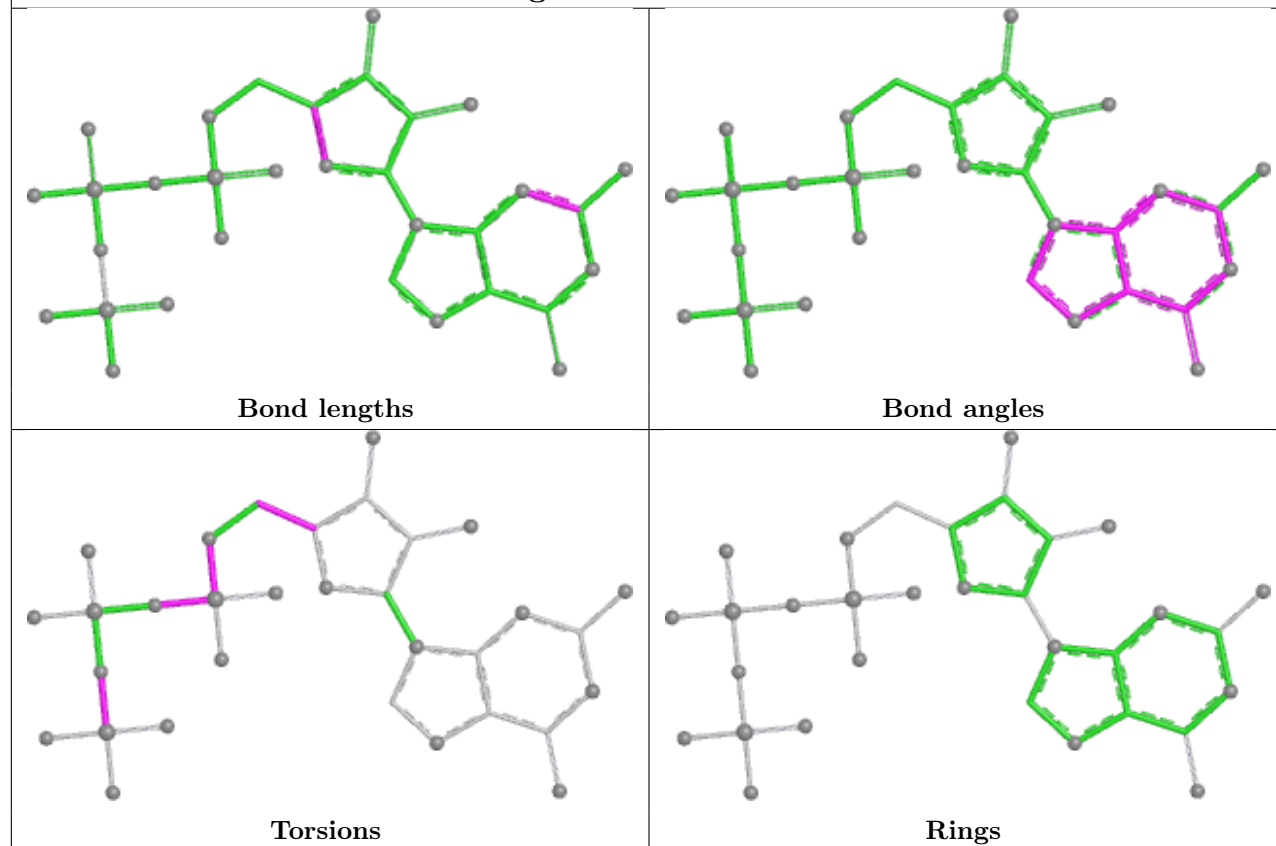
Mol	Chain	Res	Type	Clashes	Symm-Clashes
54	b	701	GTP	3	0
54	m	501	GTP	2	0

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.

Ligand GTP b 701



Ligand GTP m 501



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.

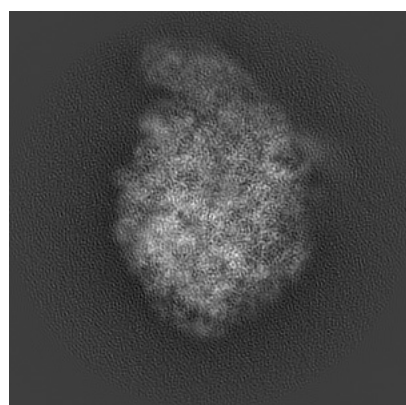
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30174. These allow visual inspection of the internal detail of the map and identification of artifacts.

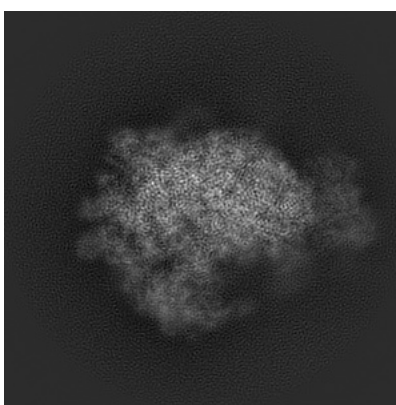
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

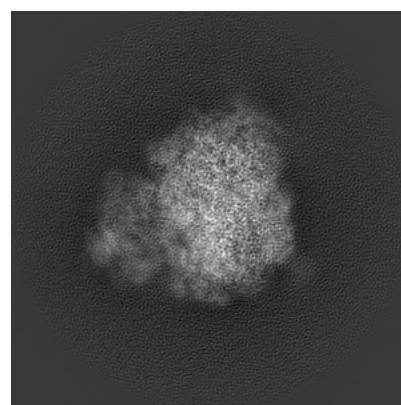
6.1.1 Primary map



X



Y

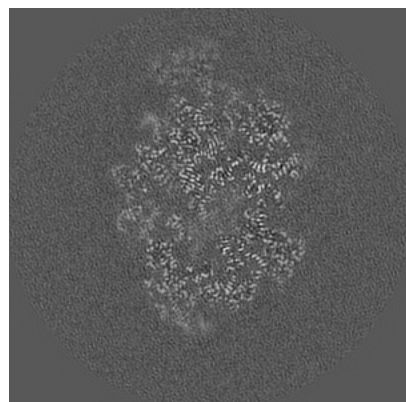


Z

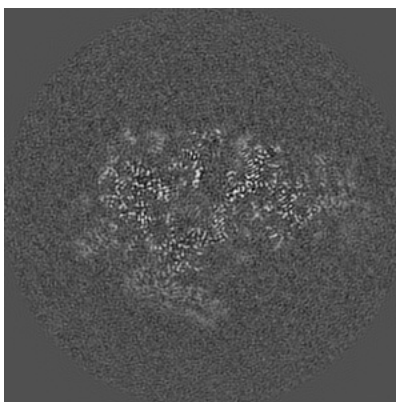
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

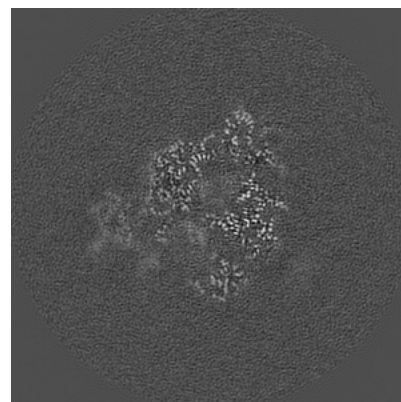
6.2.1 Primary map



X Index: 150



Y Index: 150

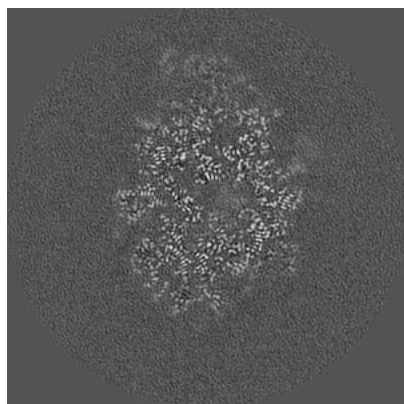


Z Index: 150

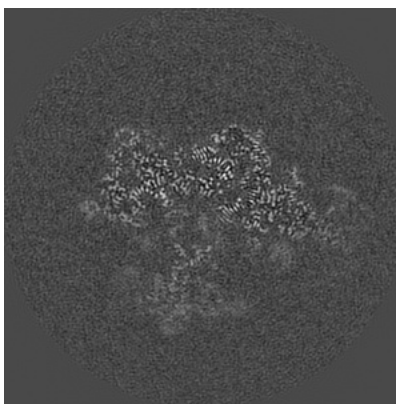
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

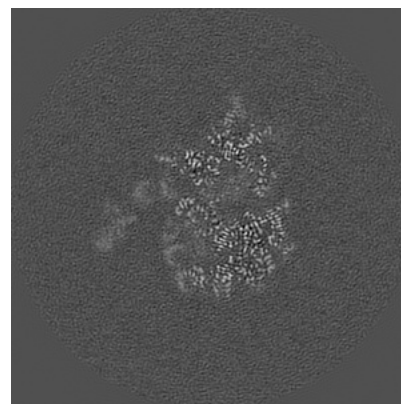
6.3.1 Primary map



X Index: 162



Y Index: 133

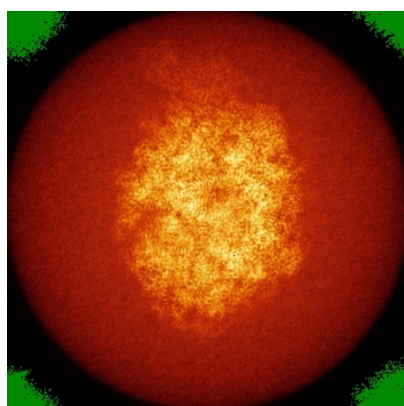


Z Index: 162

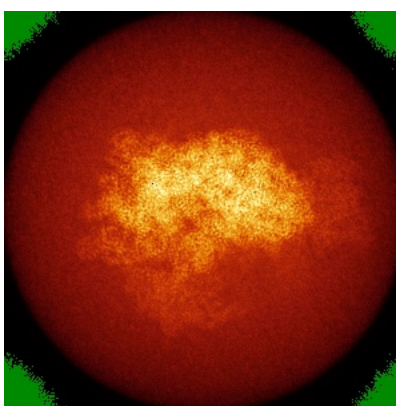
The images above show the largest variance slices of the map in three orthogonal directions.

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

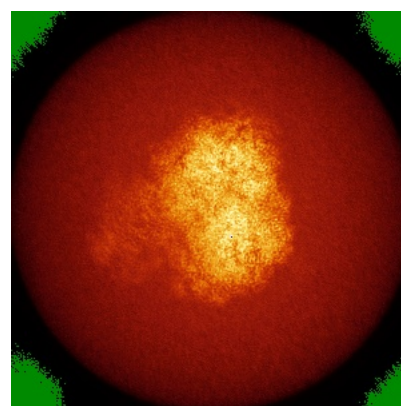
6.4.1 Primary map



X



Y

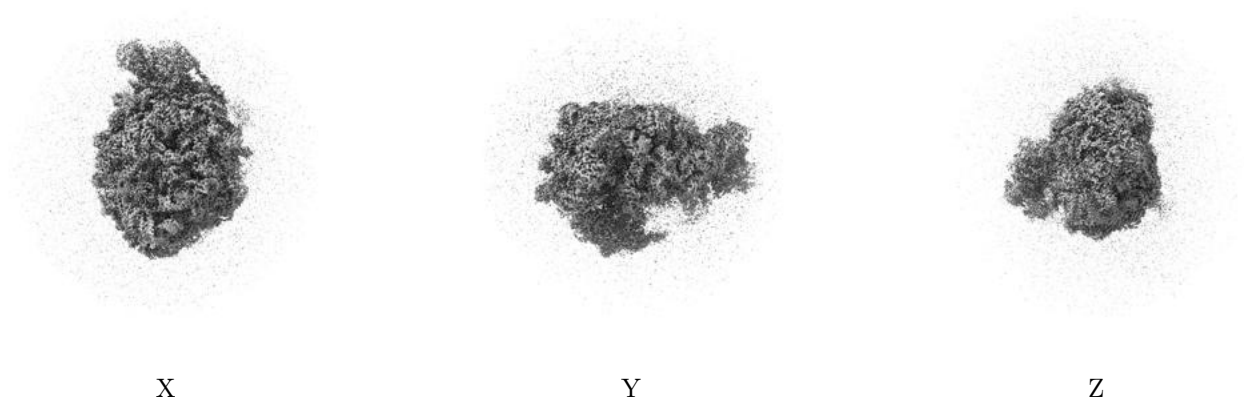


Z

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

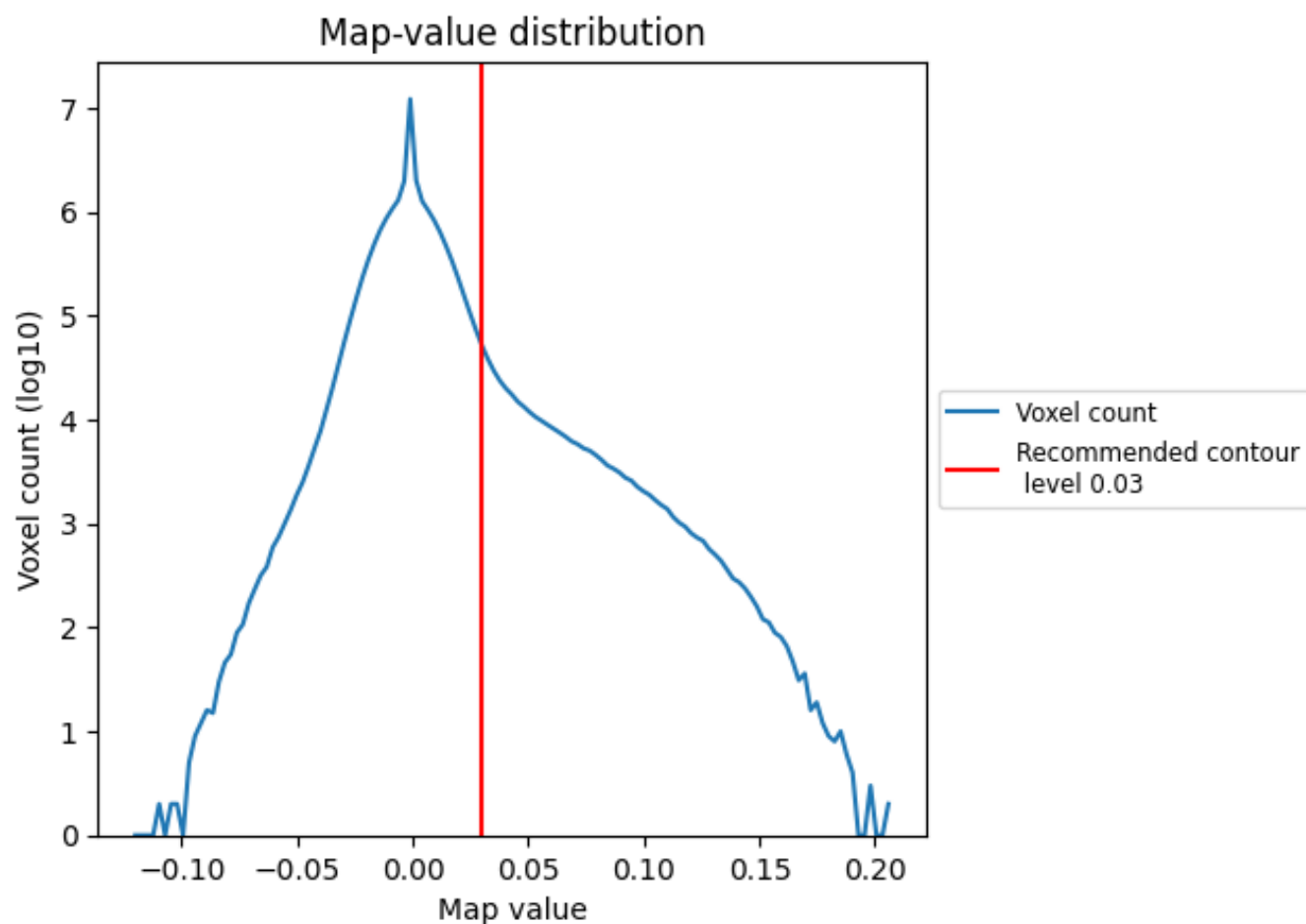
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

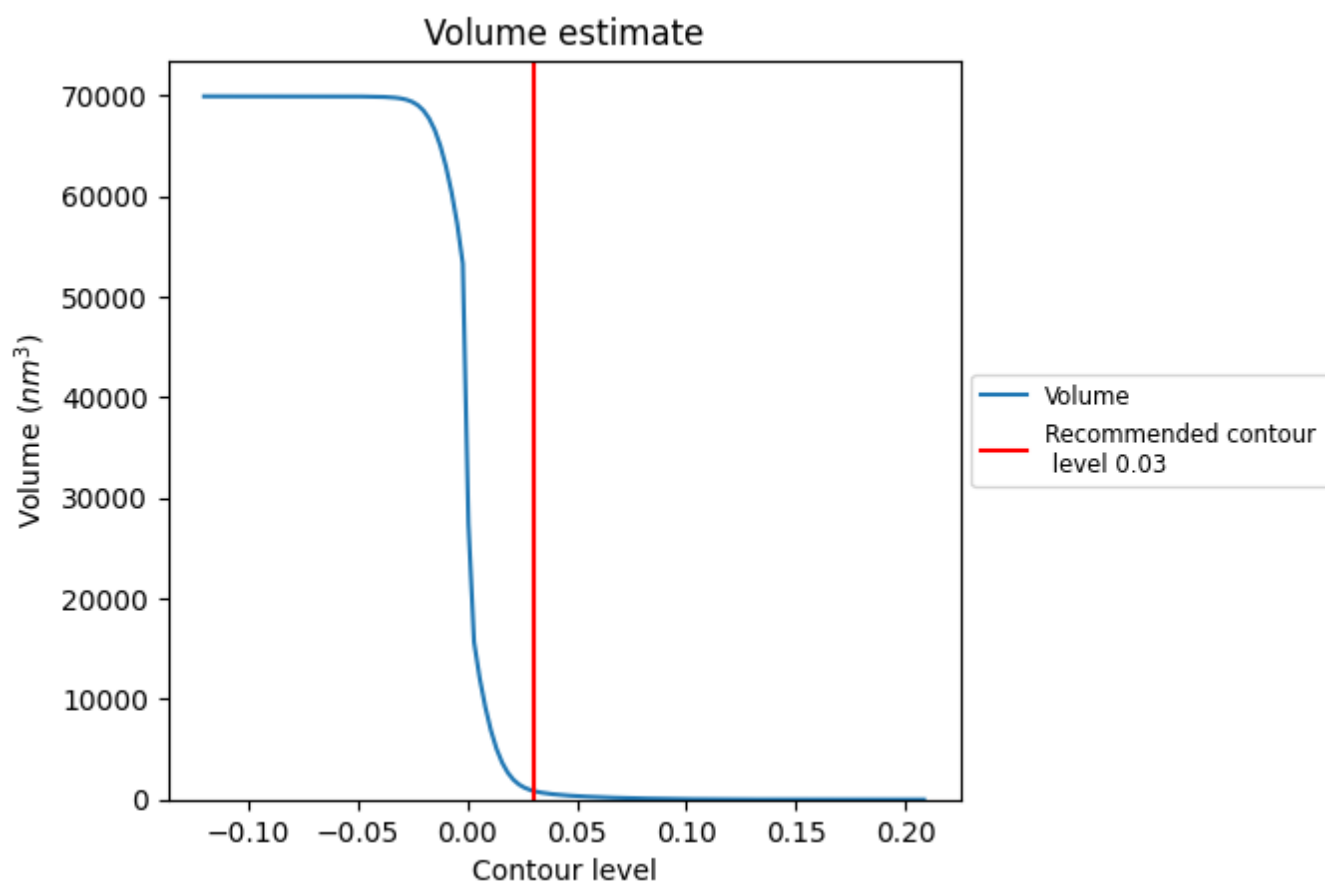
This section contains the results of statistical analysis of the map.

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.

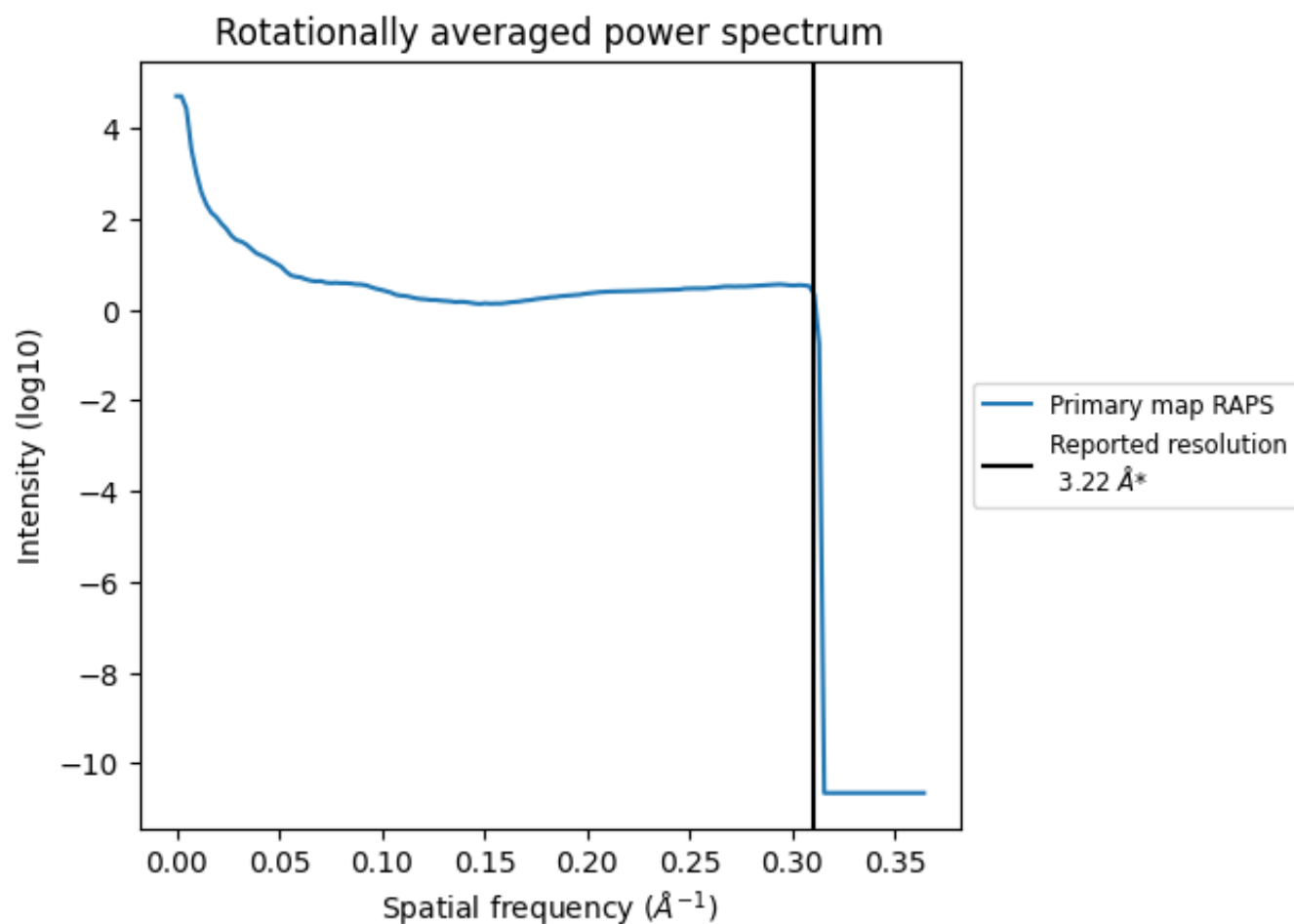
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 879 nm³; this corresponds to an approximate mass of 794 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 0.311 Å⁻¹

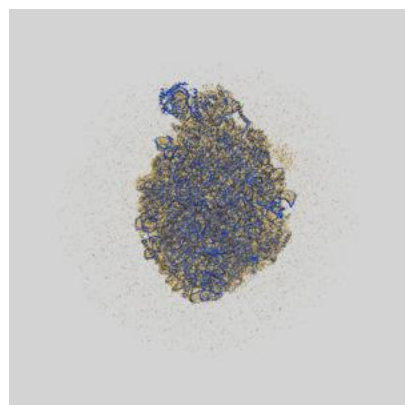
8 Fourier-Shell correlation

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

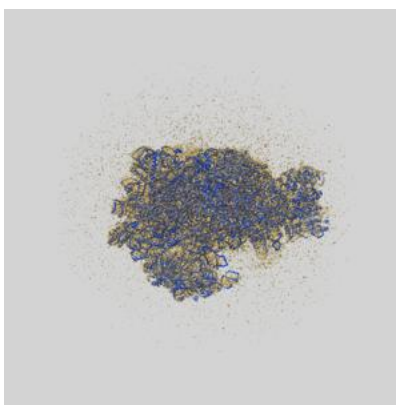
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-30174 and PDB model 7BTB. Per-residue inclusion information can be found in section 3 on page 14.

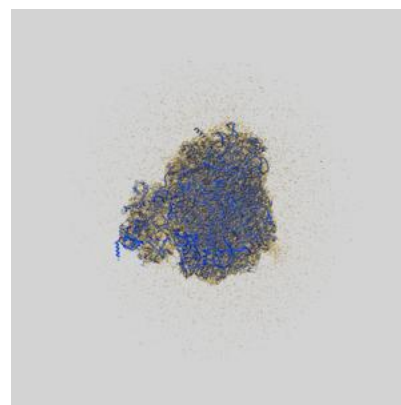
9.1 Map-model overlay [i](#)



X



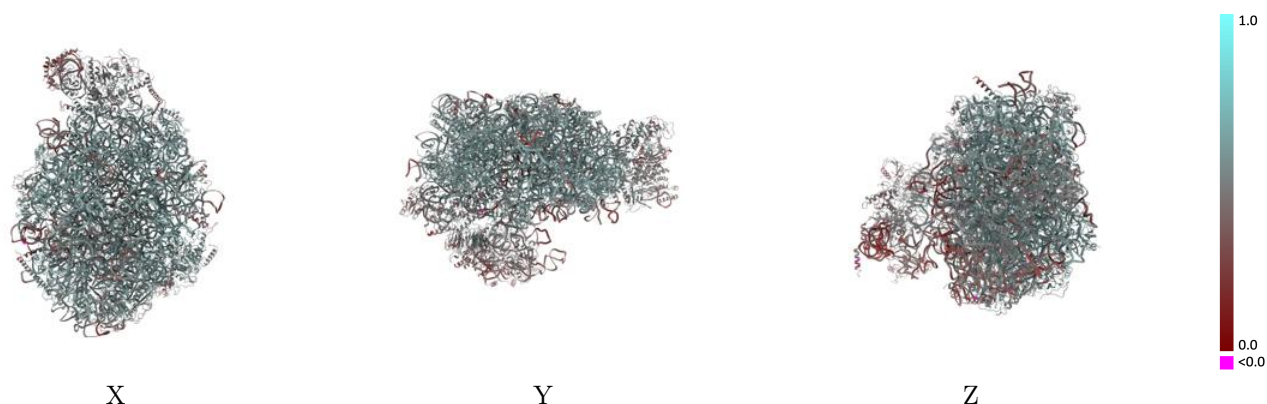
Y



Z

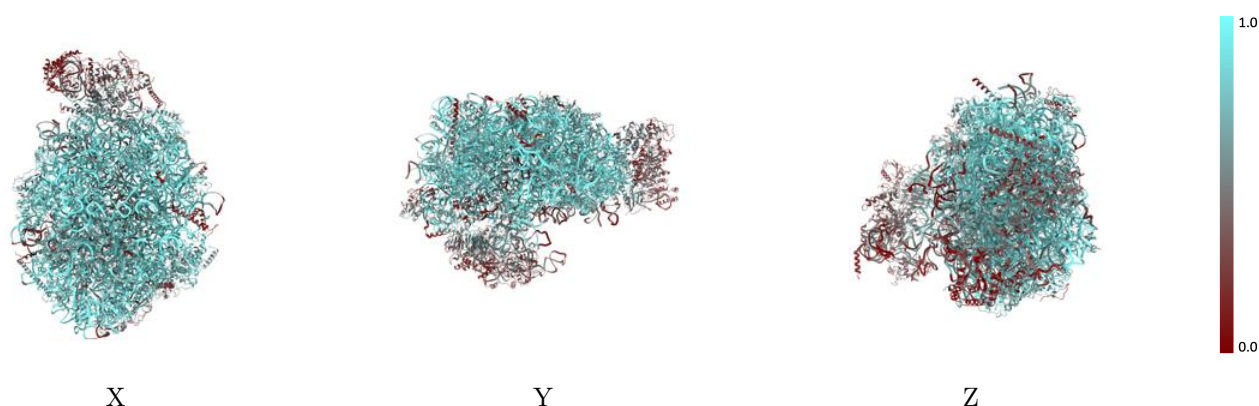
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



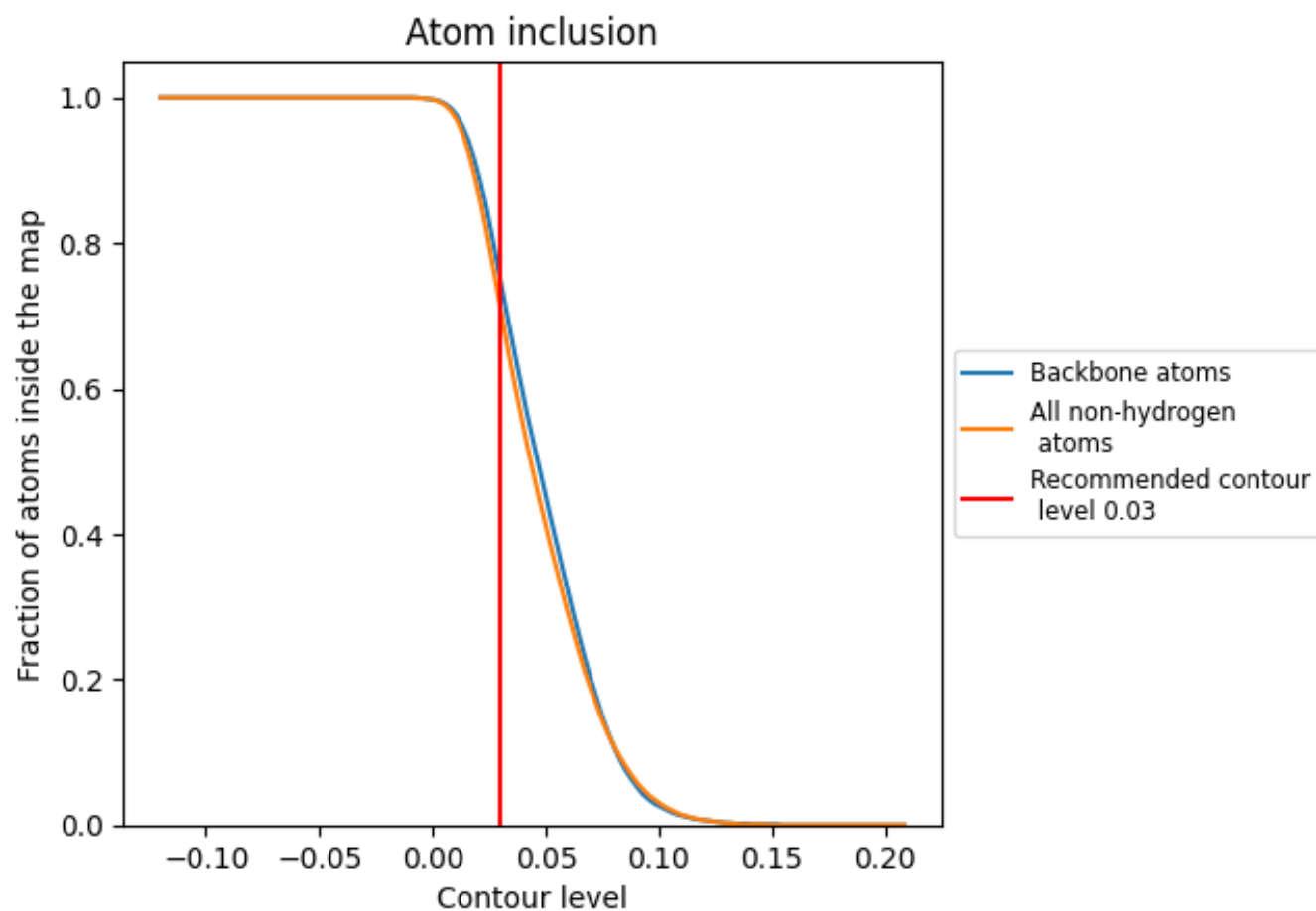
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 71% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7110	 0.5100
1	 0.8040	 0.5140
2	 0.8900	 0.5560
3	 0.3970	 0.2790
6	 0.4140	 0.3910
A	 0.8090	 0.5840
B	 0.8060	 0.5650
C	 0.7910	 0.5630
D	 0.2930	 0.3840
E	 0.7340	 0.5370
F	 0.8030	 0.5620
G	 0.7080	 0.5340
H	 0.8120	 0.5680
J	 0.1700	 0.3260
K	 0.2040	 0.4020
L	 0.7400	 0.5360
M	 0.8010	 0.5580
N	 0.7700	 0.5650
O	 0.8500	 0.5860
P	 0.7340	 0.5480
Q	 0.7600	 0.5520
R	 0.7990	 0.5600
S	 0.7320	 0.5350
T	 0.5200	 0.4760
U	 0.6560	 0.5090
V	 0.8210	 0.5790
W	 0.4070	 0.4260
X	 0.7970	 0.5710
Y	 0.8060	 0.5730
Z	 0.7780	 0.5560
a	 0.7180	 0.5340
b	 0.6150	 0.5010
c	 0.7500	 0.5470
d	 0.7960	 0.5680
e	 0.8180	 0.5740



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Chain	Atom inclusion	Q-score
f	 0.8690	 0.6000
g	 0.8000	 0.5670
h	 0.7890	 0.5530
i	 0.6310	 0.5020
j	 0.7640	 0.5670
k	 0.6750	 0.5310
m	 0.7100	 0.5360
n	 0.5060	 0.4950
o	 0.3810	 0.4530
p	 0.8130	 0.5690
q	 0.4080	 0.4910
r	 0.7590	 0.5550
t	 0.3730	 0.4630
u	 0.7060	 0.5380
v	 0.3920	 0.4360
w	 0.4820	 0.4560
x	 0.4330	 0.4390
y	 0.7380	 0.5430
z	 0.3430	 0.4870