



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Mar 2, 2017 – 11:57 am GMT

PDB ID : 3J7Q
EMDB ID: : EMD-2650
Title : Structure of the idle mammalian ribosome-Sec61 complex
Authors : Voorhees, R.M.; Fernandez, I.S.; Scheres, S.H.W.; Hegde, R.S.
Deposited on : 2014-08-01
Resolution : 3.50 Å(reported)
Based on PDB ID : 3J3B, 3J3F

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB entry.

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

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

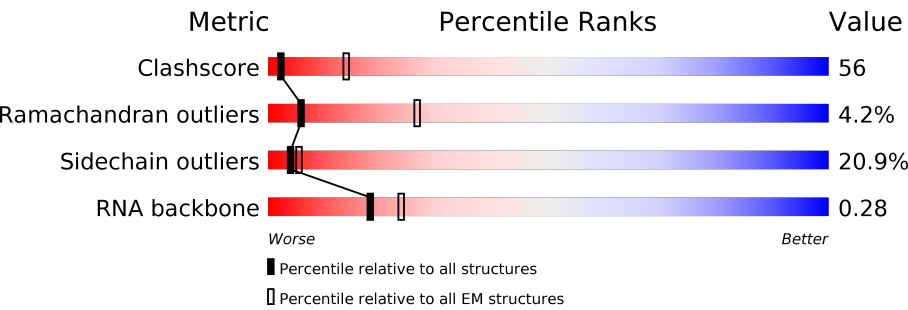
MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : recalc29047

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 3.50 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.









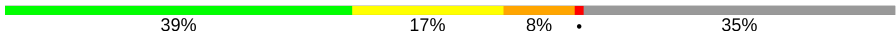





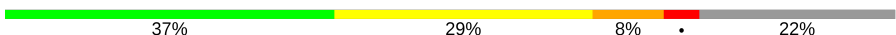












Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	5	3722	9% 46% 33% 11% .
2	7	120	18% 57% 22% .
3	8	156	8% 54% 25% 13%
4	A	257	50% 28% 12% 6% 5%
5	B	394	48% 34% 13% 5%
6	C	367	55% 31% 11% .
7	D	297	46% 35% 12% 5% .
8	E	236	47% 27% 19% 7%

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Mol	Chain	Length	Quality of chain
9	F	225	
10	G	266	
11	H	192	
12	I	213	
13	J	178	
14	L	211	
15	M	213	
16	N	204	
17	O	204	
18	P	153	
19	Q	188	
20	R	196	
21	S	224	
22	T	160	
23	U	128	
24	V	140	
25	W	157	
26	X	156	
27	Y	145	
28	Z	136	
29	a	148	
30	b	160	
31	c	115	
32	d	125	
33	e	135	

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Mol	Chain	Length	Quality of chain
34	f	110	 78%15%5% ..
35	g	117	 77%19% ..
36	h	123	 80%12%6% ..
37	i	105	 76%17% ..
38	j	86	 73%21%6%
39	k	70	 71%27% ..
40	l	51	 76%20% ..
41	m	128	 31%8%59% .
42	n	25	 72%20%8%
43	o	106	 69%23%6% ...
44	p	91	 82%15% ..
45	r	125	 73%23% ..
46	1	476	 60%19%18% .
47	2	68	 71%18%9% .
48	3	36	 94%6%

2 Entry composition

There are 50 unique types of molecules in this entry. The entry contains 140540 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 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	3662	Total	C	N	O	P	0	0
			78486	34947	14363	25515	3661		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 4 is a protein called Ribosomal protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	244	Total	C	N	O	S	0	0
			1868	1171	382	309	6		

- Molecule 5 is a protein called Ribosomal protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	394	Total	C	N	O	S	0	0
			3147	2005	591	538	13		

- Molecule 6 is a protein called Ribosomal protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	367	Total	C	N	O	S	0	0
			2919	1836	582	486	15		

- Molecule 7 is a protein called Ribosomal protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	292	Total	C	N	O	S	0	0
			2380	1508	434	426	12		

- Molecule 8 is a protein called Ribosomal protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	236	Total	C	N	O	S	0	0
			1904	1219	364	316	5		

- Molecule 9 is a protein called Ribosomal protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 10 is a protein called Ribosomal protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	241	Total	C	N	O	S	0	0
			1934	1232	372	326	4		

- Molecule 11 is a protein called Ribosomal protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 12 is a protein called Ribosomal protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	213	Total	C	N	O	S	0	0
			1713	1083	331	284	15		

- Molecule 13 is a protein called Ribosomal protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	170	Total	C	N	O	S	0	0
			1359	856	256	241	6		

- Molecule 14 is a protein called Ribosomal protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L	210	Total	C	N	O	S	0	0
			1703	1064	354	280	5		

- Molecule 15 is a protein called Ribosomal protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M	138	Total	C	N	O	S	0	0
			1131	727	216	181	7		

- Molecule 16 is a protein called Ribosomal protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	N	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 17 is a protein called Ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	201	Total	C	N	O	S	0	0
			1651	1063	323	260	5		

- Molecule 18 is a protein called Ribosomal protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	P	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 19 is a protein called Ribosomal protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Q	187	Total	C	N	O	S	0	0
			1506	941	311	249	5		

- Molecule 20 is a protein called Ribosomal protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 21 is a protein called Ribosomal protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S	175	Total	C	N	O	S	0	0
			1454	925	284	235	10		

- Molecule 22 is a protein called Ribosomal protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	T	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 23 is a protein called Ribosomal protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U	99	Total	C	N	O	S	0	0
			808	518	141	147	2		

- Molecule 24 is a protein called Ribosomal protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 25 is a protein called Ribosomal protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 26 is a protein called Ribosomal protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	X	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 27 is a protein called Ribosomal protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 28 is a protein called Ribosomal protein eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Z	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 29 is a protein called Ribosomal protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	a	147	Total	C	N	O	S	0	0
			1163	735	239	185	4		

- Molecule 30 is a protein called Ribosomal protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	b	75	Total	C	N	O	S	0	0
			610	378	130	99	3		

- Molecule 31 is a protein called Ribosomal protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	c	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

- Molecule 32 is a protein called Ribosomal protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 33 is a protein called Ribosomal protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 34 is a protein called Ribosomal protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 35 is a protein called Ribosomal protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 36 is a protein called Ribosomal protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	122	Total	C	N	O	S	0	0
			1015	642	205	167	1		

- Molecule 37 is a protein called Ribosomal protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 38 is a protein called Ribosomal protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	86	Total	C	N	O	S	0	0
			706	436	155	110	5		

- Molecule 39 is a protein called Ribosomal protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	k	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 40 is a protein called Ribosomal protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	l	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 41 is a protein called Ribosomal protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	m	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 42 is a protein called Ribosomal protein eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	n	23	Total	C	N	O	S	0	0
			222	134	61	25	2		

- Molecule 43 is a protein called Ribosomal protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 44 is a protein called Ribosomal protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 45 is a protein called Ribosomal protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	125	Total	C	N	O	S	0	0
			1001	622	206	168	5		

- Molecule 46 is a protein called Sec61 alpha subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	1	392	Total	C	N	O	S	0	0
			3051	2007	493	532	19		

- Molecule 47 is a protein called Sec61 gamma subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	2	62	Total	C	N	O	S	0	0
			494	326	86	79	3		

- Molecule 48 is a protein called Sec61 beta subunit.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	3	36	Total	C	N	O	0	0
			180	108	36	36		

- Molecule 49 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
49	8	4	Total 4	Mg 4	0
49	7	5	Total 5	Mg 5	0
49	P	1	Total 1	Mg 1	0
49	V	1	Total 1	Mg 1	0
49	5	119	Total 119	Mg 119	0

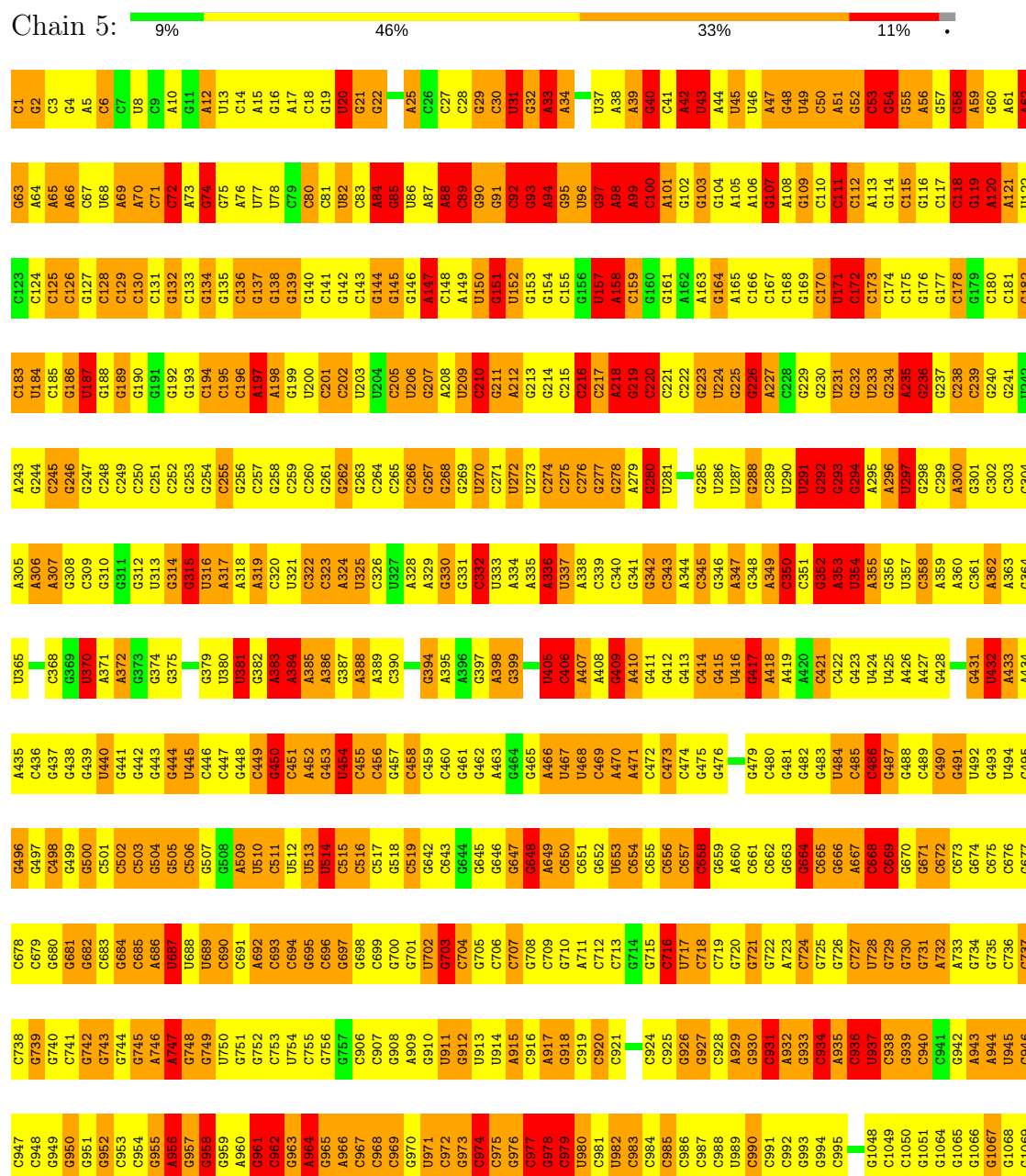
- Molecule 50 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
50	o	1	Total 1	Zn 1	0
50	j	1	Total 1	Zn 1	0
50	m	1	Total 1	Zn 1	0

3 Residue-property plots

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

• Molecule 1: 28S ribosomal RNA





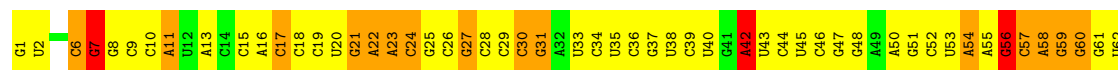

A3856	U3796	U3734	G3674	G3614	C2875	G2808	A2745	G2682	G2619	C2558	C2497	C2437	C2373	U2312	G2252
G3857	C3797	G3735	G3675	G3615	G2876	G2811	A2746	G2683	G2620	C2559	C2498	A2438	C2376	A2313	A2253
G3858	U3798	A3736	G3676	U3616	G2877	A2812	U2747	C2684	A2621	C2560	C2499	U2440	A2376	G2314	G2254
A3859	A3737	G2878	U3677	G3617	G2879	A2813	C2748	C2685	G2622	C2561	G2502	U2441	C2378	G2315	C2255
A3860	A3800	A2879	G3678	G3618	A2880	G2814	G2751	G2686	A2623	C2562	G2503	G2442	G2318	G2316	G2256
A3861	U3801	G3739	U3679	G3619	G2881	A2815	G2752	U2687	G2624	G2563	C2504	G2443	A2382	C2317	C2257
A3862	U3802	G3740	U3680	G3620	G2882	G2816	G2753	G2688	C2627	G2564	C2505	U2444	C2383	G2318	G2258
A3863	A3803	C3741	G3681	A3621	G2884	G2817	G2754	G2689	U2628	A2565	C2506	U2445	C2384	G2319	G2259
A3864	G3804	G3742	A3682	C3622	G2885	G2818	A2755	G2690	G2629	U2566	U2507	C2446	U2385	G2320	G2260
A3865	U3805	G3743	G3683	G3623	G2886	G2819	G2756	C2691	U2630	C2567	U2508	U2447	U2386	G2321	G2261
A3866	G3806	G3744	G3684	A3624	G2889	G2820	A2757	U2692	U2631	C2568	C2509	U2448	G2387	G2322	G2262
A3867	A3807	U3745	G3685	G3625	C2890	G2821	G2758	G2693	U2632	C2569	G2510	A2449	G2388	G2323	A2263
A3868	C3808	A3746	G3686	G3626	U2891	G2822	G2759	G2694	U2633	C2571	G2511	G2450	A2389	C2324	C2264
C3869	G3809	A3747	A3687	G3627	C2892	G2823	G2760	A2695	U2634	C2572	A2512	G2451	G2390	C2325	G2265
A3870	G3810	A3748	U3688	G3628	G2893	G2824	A2761	A2696	G2635	C2573	A2513	G2452	G2391	G2326	G2266
A3871	G3811	C3749	G3689	A3629	A2895	G2825	U2762	A2697	U2636	C2574	G2514	G2453	C2392	G2327	U2267
A3872	C3812	G3750	U3690	A3630	G2896	A2826	G2763	C2698	U2637	U2575	G2515	U2454	C2393	G2328	A2268
A3873	A3813	G3751	G3691	G3631	G2897	G2827	U2764	C2699	G2638	U2576	G2516	G2455	G2394	U2329	C2269
A3874	U3814	C3752	A3692	C3632	C2898	G2828	A2765	G2700	U2639	G2577	A2517	G2456	A2395	G2330	G2270
A3875	G3815	G3753	U3693	G3633	C2899	U2829	A2766	G2701	U2640	C2578	G2518	G2457	A2396	G2331	C2271
A3876	A3816	G3754	G3694	A3634	U2900	U2830	A2767	G2702	A2641	C2579	U2519	C2458	U2398	G2332	C2272
A3877	U3817	G3755	U3695	A3635	G2905	G2831	C2768	G2703	A2642	U2580	C2520	G2459	C2399	G2333	C2273
A3878	G3818	A3756	C3696	C3636	C2906	G2832	G2769	G2704	G2643	A2581	G2521	A2460	G2401	G2334	C2274
A3879	G3819	G3757	G3697	G3637	G2907	A2833	C2770	G2705	G2644	A2582	G2522	G2461	G2402	G2335	A2276
G3880	G3820	U3758	G3698	G3638	C2908	G2834	G2771	G2706	G2645	C2583	G2523	C2462	G2403	C2336	G2277
A3881	A3821	A3759	C3699	U3639	G2909	G2835	G2772	U2707	U2646	C2584	U2524	G2463	A2404	C2339	G2278
C3882	U3822	A3760	C3700	U3640	U2908	A2836	G2773	U2708	A2647	C2585	U2525	G2464	G2405	G2340	A2279
A3883	G3823	C3761	G3701	G3641	C2909	G2837	G2774	G2709	G2648	C2586	C2526	G2465	G2406	C2341	G2280
A3884	A3824	A3762	A3702	A3642	G2910	G2838	C2775	C2710	U2649	A2587	U2527	G2466	G2407	A2342	U2281
A3885	G3825	A3763	G3703	G3643	C3583	U2839	G2776	G2711	G2650	C2588	G2528	U2467	U2408	G2343	A2282
A3886	C3826	U3764	U3704	U3644	C3584	G2840	U2777	G2712	C2651	C2589	U2529	U2468	U2409	G2344	G2283
A3887	G3827	G3765	C3706	A3646	G3585	G2841	C2778	G2713	G2652	C2590	U2530	C2469	U2410	U2345	A2284
A3888	A3828	U3766	U3707	A3647	G3586	G2842	C2779	G2714	C2653	C2591	C2531	G2470	C2411	G2346	A2285
A3889	G3829	C3767	G3708	A3648	C3587	U2843	A2782	G2715	G2654	U2592	C2532	A2471	C2412	A2347	G2286
A3890	A3830	U3770	U3709	A3649	G3588	G2844	A2783	G2716	U2655	C2593	C2533	A2472	U2413	G2348	G2287
A3891	U3831	G3771	G3710	A3650	G3589	A2845	C2784	G2656	G2657	C2594	G2534	A2473	U2414	G2349	G2288
A3892	C3832	U3772	A3711	A3651	C3591	G2846	C2785	G2658	G2659	C2595	G2535	G2474	G2415	A2350	C2289
A3893	G3833	U3773	A3712	A3652	G3592	A2849	C2786	G2721	A2660	C2596	A2536	G2475	U2416	G2351	G2290
A3894	C3834	A3774	U3713	A3653	C3593	G2850	A2787	G2722	U2661	C2597	U2537	G2476	G2417	C2352	C2291
A3895	A3835	G3775	G3714	G3654	C3594	G2851	U2788	G2723	U2662	C2598	U2538	A2477	A2418	U2353	C2292
A3896	G3836	A3776	U3715	C3655	U3595	U2852	A2789	G2724	U2661	C2599	C2539	C2478	C2419	U2354	U2293
A3897	C3837	G3777	G3716	A3656	A3596	G2853	U2790	A2725	G2662	A2600	G2540	G2479	A2419	G2354	G2294
A3898	U3838	U3778	A3717	U3657	G3597	G2854	C2791	G2726	G2663	A2601	G2541	G2480	A2420	C2295	C2295
A3899	G3839	U3779	G3718	U3658	C3598	G2855	C2792	G2727	G2664	G2602	G2542	G2481	G2421	G2296	G2296
U3900	U3840	A3779	A3718	C3658	C3599	G2856	C2793	U2728	U2665	C2603	A2543	G2482	C2422	G2297	G2297
A3901	C3841	G3780	U3719	G3659	A3599	A2857	G2794	G2729	G2666	C2604	G2544	G2483	A2423	U2359	U2298
A3902	G3842	C3781	G3720	C3660	G3600	G2858	C2795	G2730	C2667	C2605	U2545	A2484	G2424	A2360	G2299
A3903	C3843	G3782	U3721	G3661	C3601	A2859	G2796	G2731	G2668	G2606	G2546	U2485	U2425	G2361	A2300
A3904	U3844	A3783	G3722	A3662	C3602	G2860	C2797	U2734	C2669	C2607	G2547	G2486	U2426	U2362	G2301
A3905	A3845	A3784	A3723	A3663	G3603	C2861	A2798	U2735	C2670	G2608	C2548	G2487	G2427	A2363	C2302
A3906	C3846	U3785	A3724	G3664	A3604	G2862	G2799	G2736	C2671	C2488	G2549	A2488	A2428	G2364	C2303
A3907	G3847	A3786	G3725	C3665	C3605	G2863	G2799	G2737	G2672	C2489	G2550	C2489	A2429	C2365	U2304
A3908	U3848	C3787	A3726	G3666	U3606	G2864	G2800	C2738	C2673	A2611	G2551	C2490	C2430	A2366	U2305
A3909	A3849	U3788	G3727	C3667	G3607	G2865	U2801	U2739	G2674	C2612	A2552	U2490	A2431	A2367	U2306
C3910	C3850	G3789	A3728	G3668	U3608	G2866	U2802	U2740	A2675	C2613	G2553	C2491	U2432	A2368	A2307
C3911	U3851	C3791	G3729	G3669	G3609	G2867	U2803	U2741	G2676	C2614	U2554	C2492	U2433	U2369	A2308
A3912	A3852	G3792	U3730	C3670	A3610	A2871	C2804	U2742	A2677	C2615	U2555	G2493	G2434	U2370	A2309
A3913	G3853	U3793	C3731	G3671	A3611	G2872	C2805	G2743	G2678	C2616	G2556	U2494	G2435	U2371	G2310
A3914	C3854	C3794	A3732	C3672	A2806	U2873	A2806	A2743	G2679	G2617	G2557	G2496	U2436	U2372	C2311
A3915	G3855	A3795	A3733	C3673	U3613	U2874	A2807	A2744	G2679	G2618					





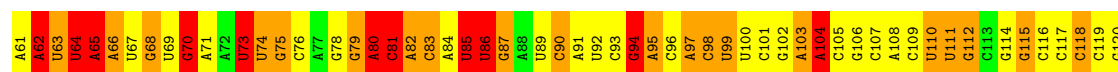
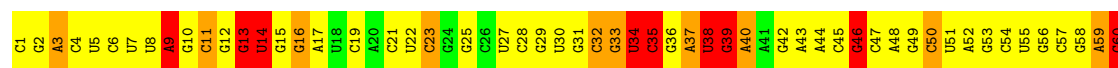

• Molecule 2: 5S ribosomal RNA

Chain 7: 18% 57% 22%



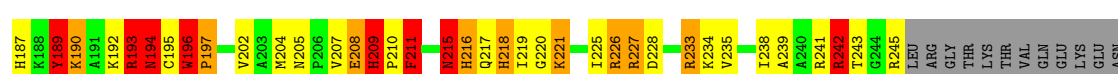
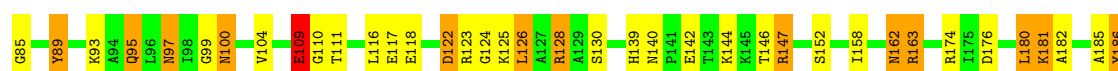
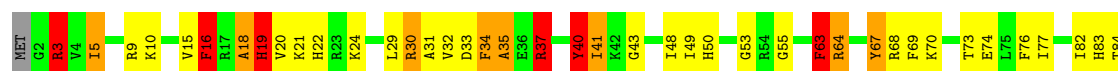
• Molecule 3: 5.8S ribosomal RNA

Chain 8: 8% 54% 25% 13%



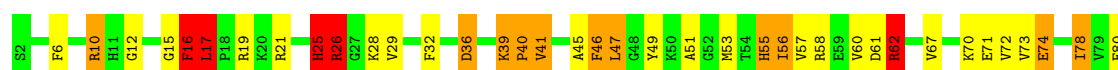
• Molecule 4: Ribosomal protein uL2

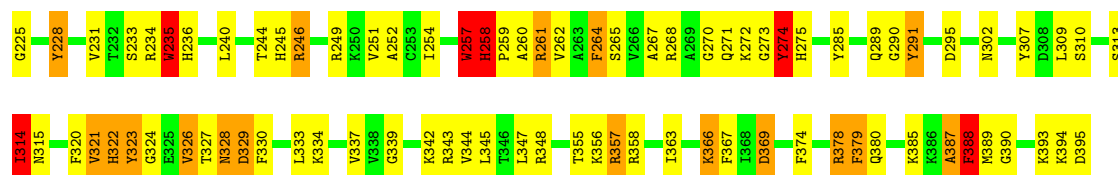
Chain A: 50% 28% 12% 6% 5%



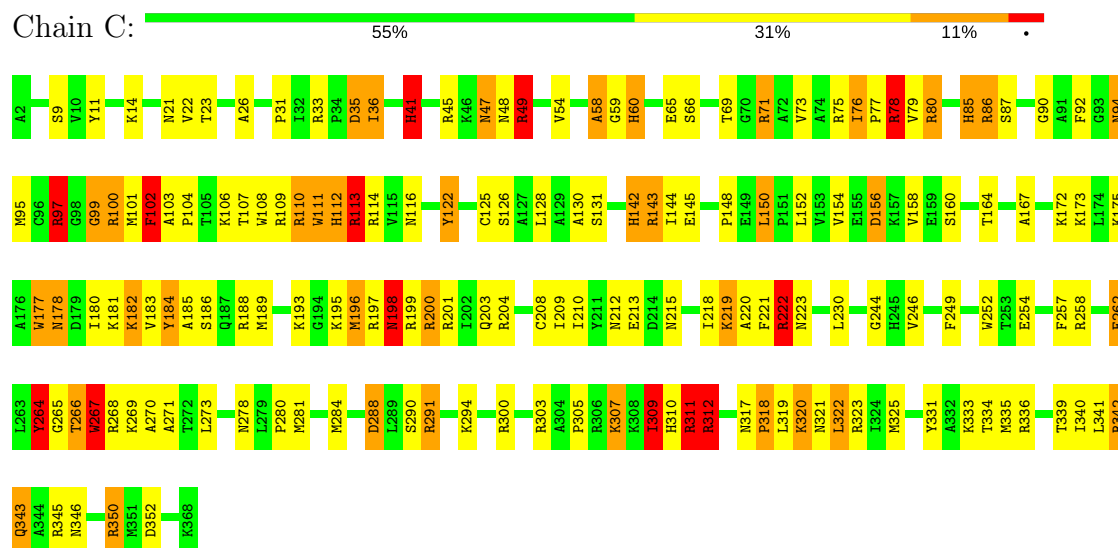
• Molecule 5: Ribosomal protein uL3

Chain B: 48% 34% 13% 5%

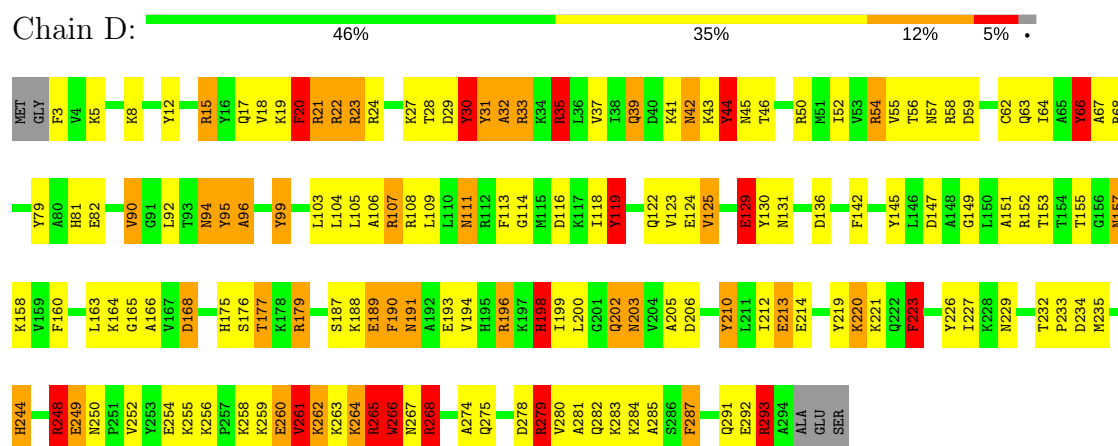




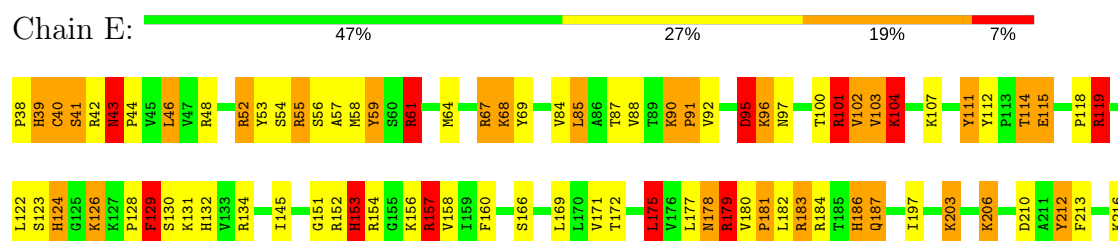
• Molecule 6: Ribosomal protein uL4



• Molecule 7: Ribosomal protein uL18



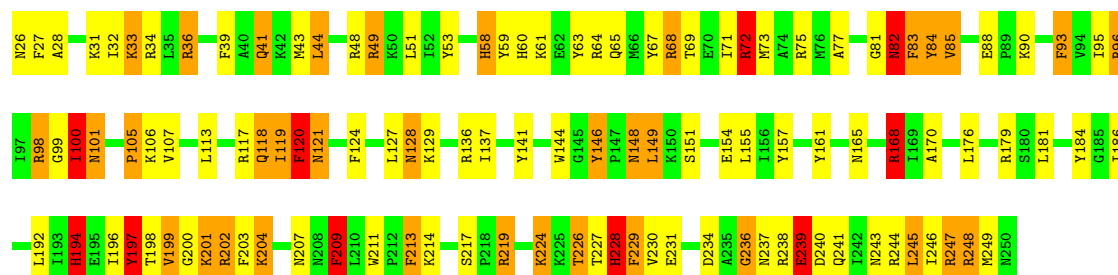
• Molecule 8: Ribosomal protein eL6





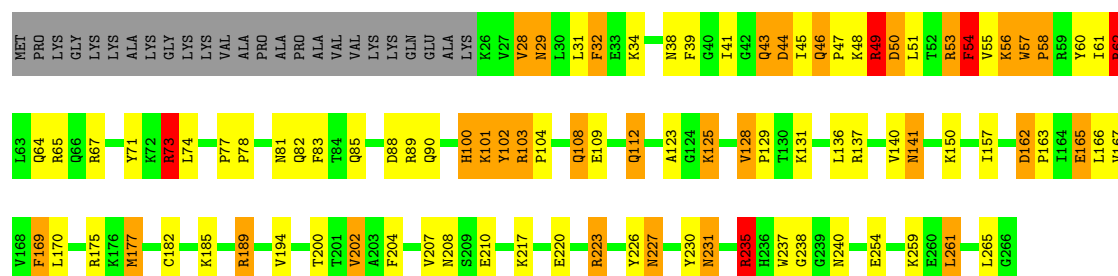
• Molecule 9: Ribosomal protein uL30

Chain F: 48% 32% 16%



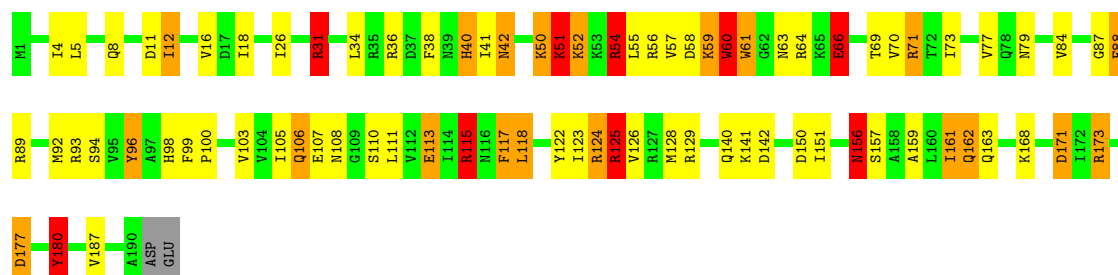
• Molecule 10: Ribosomal protein eL8

Chain G: 55% 22% 11% 9%



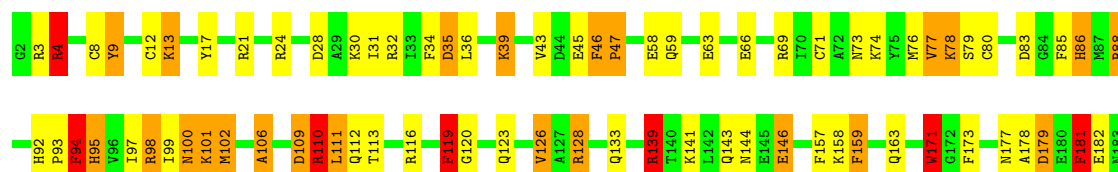
• Molecule 11: Ribosomal protein uL6

Chain H: 57% 27% 10% 5%

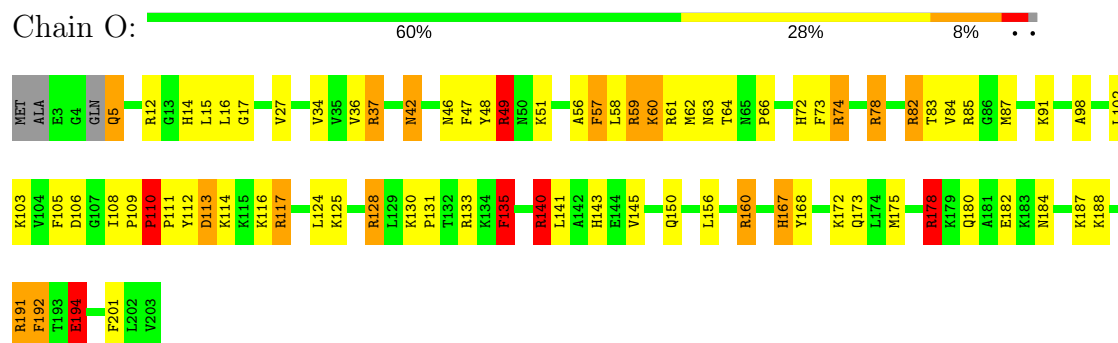


• Molecule 12: Ribosomal protein uL16

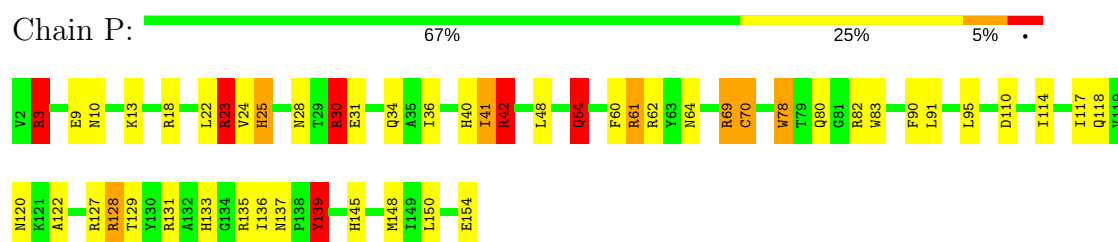
Chain I: 58% 28% 11%



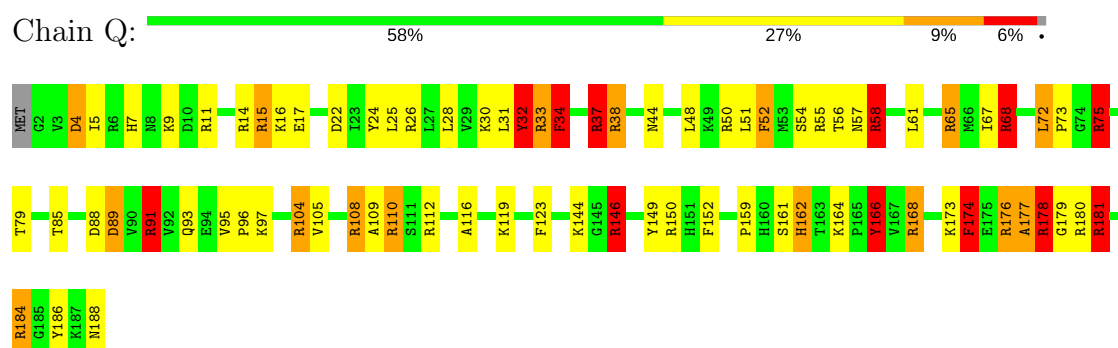
- Molecule 17: Ribosomal protein uL13



- Molecule 18: Ribosomal protein uL22



- Molecule 19: Ribosomal protein eL18

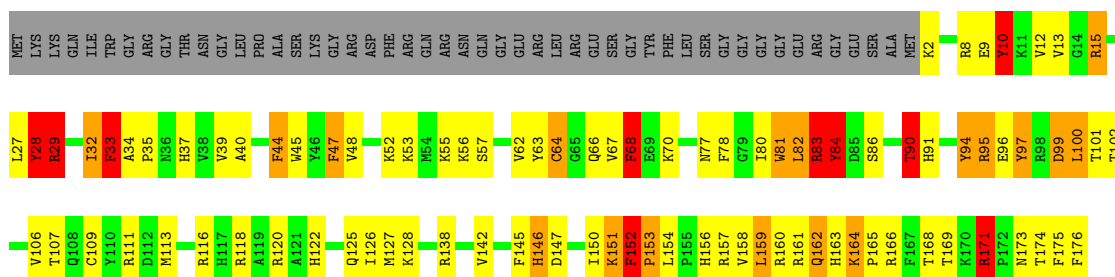
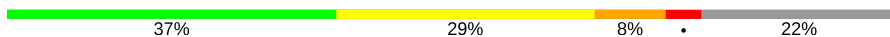


- Molecule 20: Ribosomal protein eL19



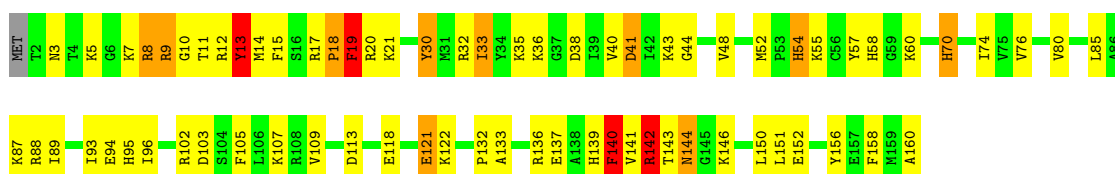
- Molecule 21: Ribosomal protein eL20

Chain S:



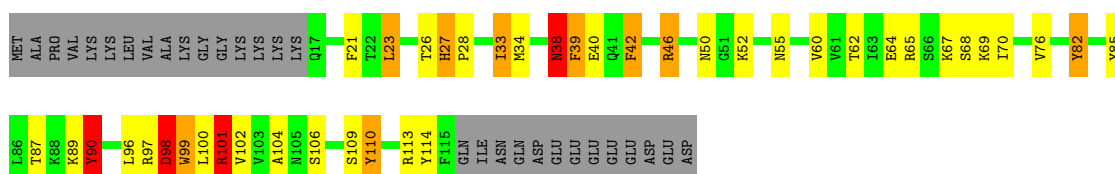
- Molecule 22: Ribosomal protein eL21

Chain T:



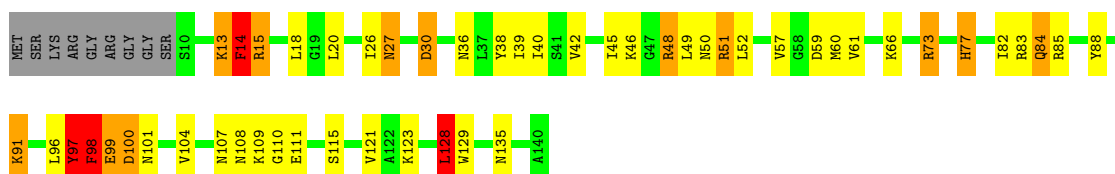
- Molecule 23: Ribosomal protein eL22

Chain U:



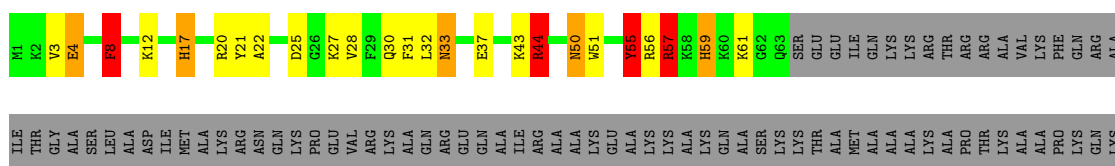
- Molecule 24: Ribosomal protein uL14

Chain V:



- Molecule 25: Ribosomal protein eL24

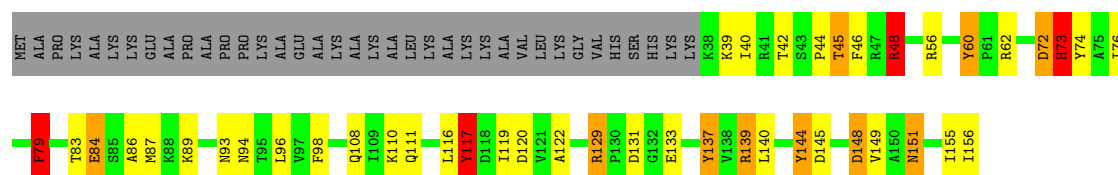
Chain W:



ILE
VAL
LYS
PRO
LYS
VAL
LYS
VAL
SER
ALA
PRO
ARG
VAL
GLY
LYS
ARG

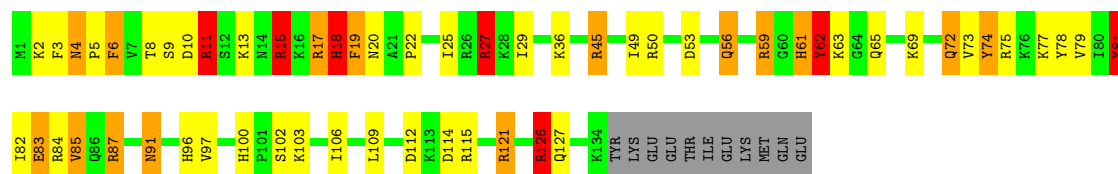
• Molecule 26: Ribosomal protein uL23

Chain X: 47% 20% 6% 24%



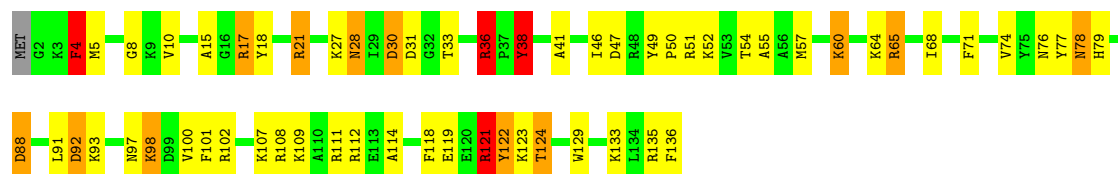
• Molecule 27: Ribosomal protein uL24

Chain Y: 52% 25% 10% 5% 8%



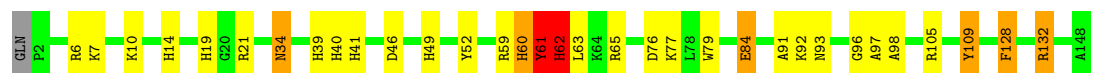
• Molecule 28: Ribosomal protein eL27

Chain Z: 55% 32% 9% 2%



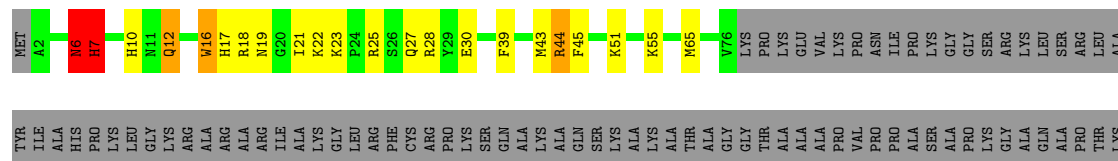
• Molecule 29: Ribosomal protein uL15

Chain a: 77% 17% 2%



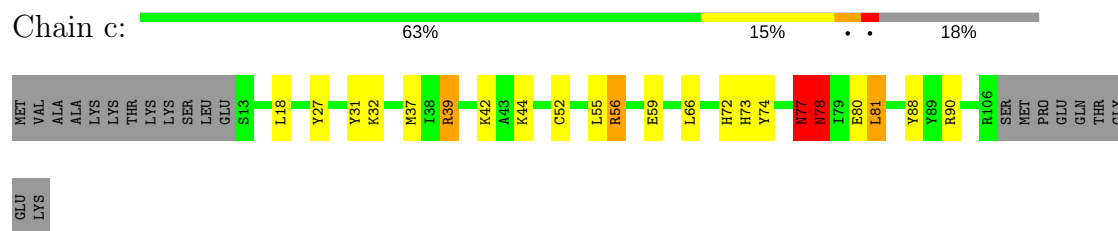
• Molecule 30: Ribosomal protein eL29

Chain b: 33% 11% 2% 53%

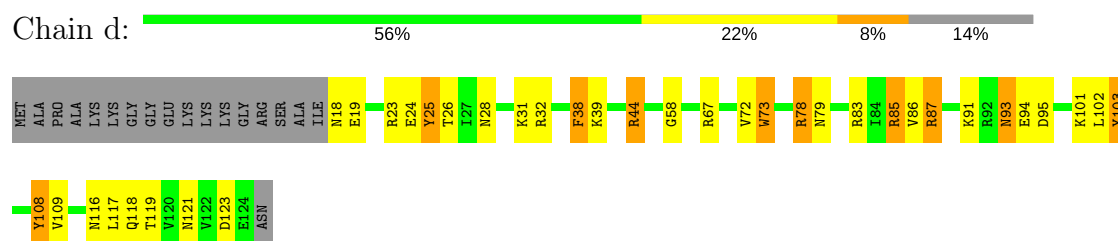


ALA
PRO
GLN

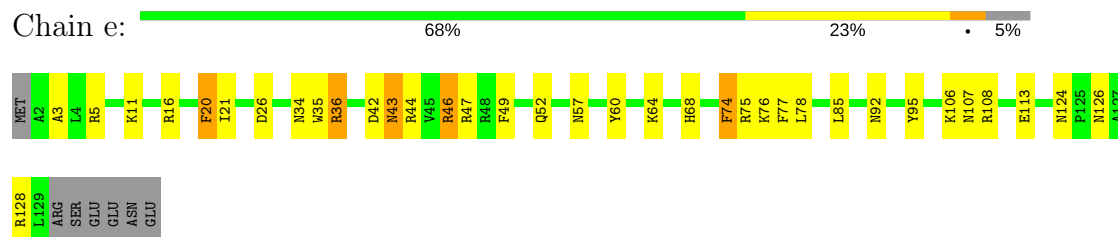
- Molecule 31: Ribosomal protein eL30



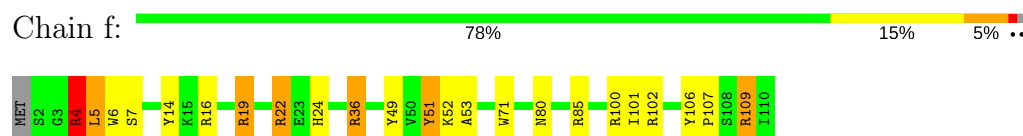
- Molecule 32: Ribosomal protein eL31



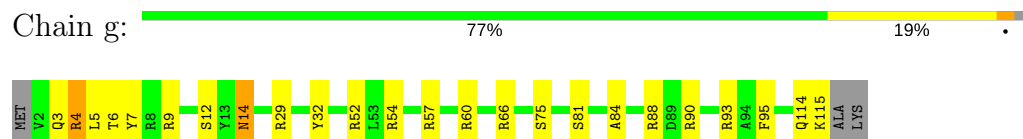
- Molecule 33: Ribosomal protein eL32



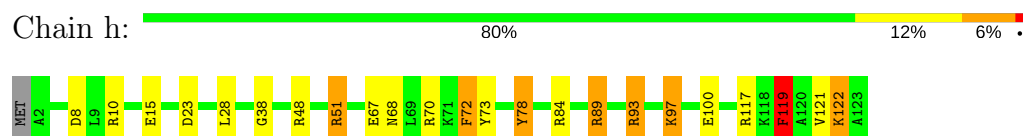
- Molecule 34: Ribosomal protein eL33



- Molecule 35: Ribosomal protein eL34



- Molecule 36: Ribosomal protein uL29



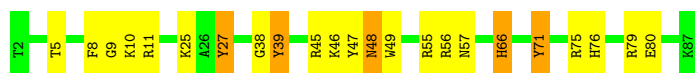
- Molecule 37: Ribosomal protein eL36

Chain i:  76% 17% . .



- Molecule 38: Ribosomal protein eL37

Chain j:  73% 21% 6%



- Molecule 39: Ribosomal protein eL38

Chain k:  71% 27% .



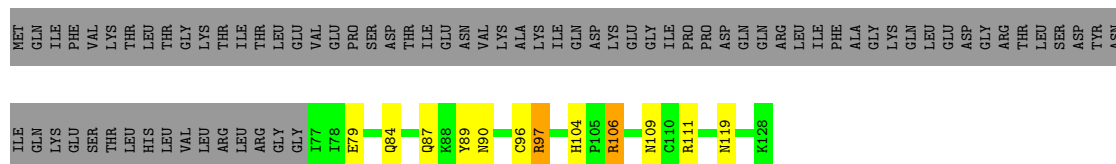
- Molecule 40: Ribosomal protein eL39

Chain l:  76% 20% . .



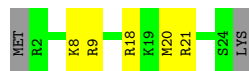
- Molecule 41: Ribosomal protein eL40

Chain m:  31% 8% 59%



- Molecule 42: Ribosomal protein eL41

Chain n:  72% 20% 8%




- Molecule 43: Ribosomal protein eL42

Chain o:  69% 23% 6% . .



- Molecule 44: Ribosomal protein eL43

Chain p:  82% 15%



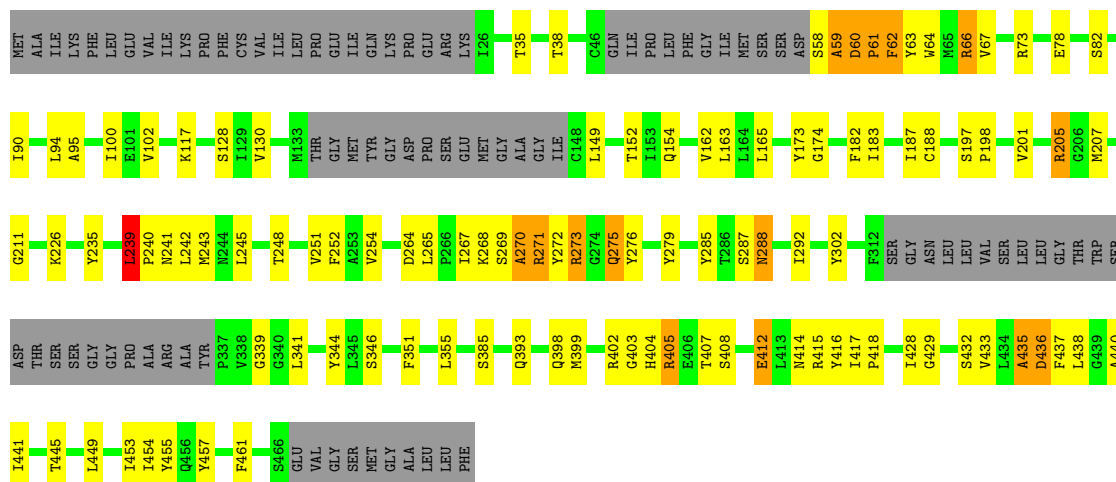
- Molecule 45: Ribosomal protein eL28

Chain r:  73% 23%



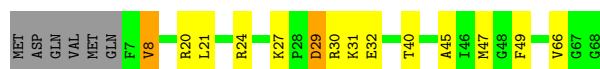
- Molecule 46: Sec61 alpha subunit

Chain 1:  60% 19% 18%



- Molecule 47: Sec61 gamma subunit

Chain 2:  71% 18% 9%



- Molecule 48: Sec61 beta subunit

Chain 3:  94% 6%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	80019	Depositor
Resolution determination method	FSC 0.143	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	27	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	104478	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	$\# Z > 2$	RMSZ	$\# Z > 2$
1	5	0.64	80/87792 (0.1%)	1.13	742/136945 (0.5%)
10	G	0.76	4/1966 (0.2%)	1.09	14/2645 (0.5%)
11	H	0.77	3/1537 (0.2%)	1.17	10/2066 (0.5%)
12	I	0.66	1/1753 (0.1%)	1.11	12/2343 (0.5%)
13	J	0.63	1/1382 (0.1%)	1.04	11/1849 (0.6%)
14	L	0.71	2/1734 (0.1%)	1.12	15/2318 (0.6%)
15	M	0.76	2/1152 (0.2%)	1.11	5/1539 (0.3%)
16	N	0.84	4/1746 (0.2%)	1.33	23/2338 (1.0%)
17	O	0.72	3/1684 (0.2%)	1.11	12/2251 (0.5%)
18	P	0.74	2/1268 (0.2%)	1.10	9/1701 (0.5%)
19	Q	0.69	0/1530	1.35	31/2041 (1.5%)
2	7	0.54	1/2858 (0.0%)	0.96	9/4455 (0.2%)
20	R	0.79	3/1524 (0.2%)	1.27	21/2013 (1.0%)
21	S	0.95	8/1493 (0.5%)	1.30	19/2002 (0.9%)
22	T	0.67	1/1326 (0.1%)	1.04	7/1770 (0.4%)
23	U	0.63	1/822 (0.1%)	1.03	2/1103 (0.2%)
24	V	0.89	4/993 (0.4%)	1.11	7/1332 (0.5%)
25	W	0.71	0/541	1.23	5/720 (0.7%)
26	X	0.64	0/993	1.09	10/1334 (0.7%)
27	Y	0.72	0/1132	1.24	19/1504 (1.3%)
28	Z	0.63	0/1130	1.11	8/1507 (0.5%)
29	a	0.93	6/1192 (0.5%)	1.37	17/1591 (1.1%)
3	8	0.68	3/3701 (0.1%)	1.20	42/5766 (0.7%)
30	b	0.88	2/620 (0.3%)	1.17	5/819 (0.6%)
31	c	0.70	0/742	1.14	5/996 (0.5%)
32	d	0.84	3/903 (0.3%)	1.37	16/1216 (1.3%)
33	e	0.90	3/1071 (0.3%)	1.23	15/1429 (1.0%)
34	f	1.02	2/895 (0.2%)	1.34	17/1198 (1.4%)
35	g	0.65	0/916	1.08	5/1220 (0.4%)
36	h	0.63	0/1023	1.21	13/1350 (1.0%)
37	i	0.63	0/843	1.19	8/1115 (0.7%)
38	j	0.97	1/721 (0.1%)	1.43	11/953 (1.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	k	0.59	0/575	0.97	1/761 (0.1%)
4	A	0.80	3/1906 (0.2%)	1.26	21/2556 (0.8%)
40	l	0.68	0/454	1.07	3/599 (0.5%)
41	m	0.57	0/435	1.02	3/575 (0.5%)
42	n	0.48	0/223	1.02	0/284
43	o	0.64	0/864	1.27	9/1140 (0.8%)
44	p	0.64	1/718 (0.1%)	1.00	3/953 (0.3%)
45	r	0.68	0/1017	1.12	8/1365 (0.6%)
46	1	0.45	0/3114	0.63	0/4218
47	2	0.47	0/504	0.71	1/673 (0.1%)
5	B	0.81	8/3214 (0.2%)	1.16	26/4308 (0.6%)
6	C	0.73	4/2973 (0.1%)	1.12	18/3990 (0.5%)
7	D	0.73	2/2426 (0.1%)	1.23	27/3252 (0.8%)
8	E	0.73	5/1941 (0.3%)	1.21	20/2601 (0.8%)
9	F	0.80	2/1905 (0.1%)	1.27	26/2539 (1.0%)
All	All	0.68	165/151252 (0.1%)	1.14	1311/223243 (0.6%)

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	5	1	158
10	G	0	3
11	H	0	3
12	I	0	5
13	J	0	2
14	L	0	5
15	M	0	4
16	N	0	11
17	O	0	3
18	P	0	1
19	Q	0	5
2	7	0	2
20	R	0	6
21	S	0	11
22	T	0	2
23	U	0	2
24	V	0	3
25	W	0	1
26	X	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
27	Y	0	4
29	a	0	9
3	8	0	11
30	b	0	1
31	c	0	2
32	d	0	4
33	e	0	4
34	f	0	2
35	g	0	1
36	h	0	3
37	i	0	3
38	j	0	4
39	k	0	1
4	A	0	6
43	o	0	6
44	p	0	1
45	r	0	5
46	1	0	1
47	2	0	1
5	B	0	13
6	C	0	5
7	D	0	8
8	E	0	12
9	F	0	5
All	All	1	340

The worst 5 of 165 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	5	1823	G	O3'-P	41.48	2.10	1.61
10	G	109	GLU	CD-OE2	16.17	1.43	1.25
11	H	66	GLU	CD-OE1	15.86	1.43	1.25
34	f	6	TRP	CB-CG	-15.77	1.21	1.50
30	b	16	TRP	CB-CG	-13.52	1.25	1.50

The worst 5 of 1311 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	8	60	G	N9-C1'-C2'	16.16	135.01	114.00
38	j	11	ARG	NE-CZ-NH2	-13.83	113.38	120.30
19	Q	37	ARG	NE-CZ-NH2	12.90	126.75	120.30
1	5	92	C	N1-C1'-C2'	-12.62	97.59	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	I	139	ARG	CG-CD-NE	12.29	137.61	111.80

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	5	1992	U	C1'

5 of 340 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	5	22	G	Sidechain
1	5	31	U	Sidechain
1	5	42	A	Sidechain
1	5	43	U	Sidechain
1	5	53	C	Sidechain

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	5	78486	0	39661	10163	0
2	7	2558	0	1296	307	0
3	8	3314	0	1683	481	0
4	A	1868	0	1959	156	0
5	B	3147	0	3280	217	0
6	C	2919	0	3100	162	0
7	D	2380	0	2412	171	0
8	E	1904	0	2055	132	0
9	F	1870	0	1996	174	0
10	G	1934	0	2086	102	0
11	H	1518	0	1601	84	0
12	I	1713	0	1752	88	0
13	J	1359	0	1390	63	0
14	L	1703	0	1818	87	0
15	M	1131	0	1209	68	0
16	N	1701	0	1749	116	0
17	O	1651	0	1786	86	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	P	1242	0	1269	56	0
19	Q	1506	0	1623	74	0
20	R	1508	0	1664	98	0
21	S	1454	0	1496	120	0
22	T	1298	0	1366	74	0
23	U	808	0	831	25	0
24	V	979	0	1039	51	0
25	W	528	0	541	52	0
26	X	976	0	1053	64	0
27	Y	1115	0	1205	60	0
28	Z	1107	0	1182	49	0
29	a	1163	0	1211	0	0
30	b	610	0	650	0	0
31	c	732	0	769	0	0
32	d	888	0	930	0	0
33	e	1053	0	1147	0	0
34	f	876	0	912	0	0
35	g	906	0	1002	0	0
36	h	1015	0	1149	0	0
37	i	832	0	917	0	0
38	j	706	0	743	0	0
39	k	569	0	637	0	0
40	l	444	0	483	0	0
41	m	429	0	466	0	0
42	n	222	0	264	0	0
43	o	851	0	922	0	0
44	p	708	0	760	0	0
45	r	1001	0	1062	0	0
46	1	3051	0	3158	175	0
47	2	494	0	527	23	0
48	3	180	0	40	1	0
49	5	119	0	0	0	0
49	7	5	0	0	0	0
49	8	4	0	0	0	0
49	P	1	0	0	0	0
49	V	1	0	0	0	0
50	j	1	0	0	0	0
50	m	1	0	0	0	0
50	o	1	0	0	0	0
All	All	140540	0	101851	12655	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 56.

The worst 5 of 12655 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)
1:5:100:C:C5	1:5:101:A:C8	2.00	1.49
1:5:1174:G:N2	1:5:1175:A:N7	1.67	1.41
1:5:2526:C:C5	46:1:405:ARG:CZ	2.04	1.41
1:5:1266:G:N2	1:5:2111:G:N3	1.67	1.39
1:5:2361:G:O6	18:P:25:HIS:CD2	1.74	1.38

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	
4	A	242/257 (94%)	203 (84%)	30 (12%)	9 (4%)	4	32
5	B	392/394 (100%)	319 (81%)	40 (10%)	33 (8%)	1	11
6	C	365/367 (100%)	304 (83%)	46 (13%)	15 (4%)	3	29
7	D	290/297 (98%)	235 (81%)	33 (11%)	22 (8%)	1	13
8	E	232/236 (98%)	150 (65%)	51 (22%)	31 (13%)	0	4
9	F	223/225 (99%)	190 (85%)	23 (10%)	10 (4%)	3	27
10	G	239/266 (90%)	200 (84%)	32 (13%)	7 (3%)	5	38
11	H	188/192 (98%)	164 (87%)	20 (11%)	4 (2%)	8	45
12	I	211/213 (99%)	168 (80%)	30 (14%)	13 (6%)	2	19
13	J	168/178 (94%)	137 (82%)	23 (14%)	8 (5%)	2	25
14	L	208/211 (99%)	172 (83%)	25 (12%)	11 (5%)	2	22
15	M	136/213 (64%)	118 (87%)	16 (12%)	2 (2%)	12	52
16	N	201/204 (98%)	172 (86%)	23 (11%)	6 (3%)	5	37
17	O	199/204 (98%)	182 (92%)	14 (7%)	3 (2%)	12	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	P	151/153 (99%)	140 (93%)	9 (6%)	2 (1%)	14	55
19	Q	185/188 (98%)	160 (86%)	20 (11%)	5 (3%)	6	40
20	R	178/196 (91%)	153 (86%)	21 (12%)	4 (2%)	8	44
21	S	173/224 (77%)	146 (84%)	24 (14%)	3 (2%)	11	49
22	T	157/160 (98%)	128 (82%)	26 (17%)	3 (2%)	9	47
23	U	97/128 (76%)	74 (76%)	21 (22%)	2 (2%)	8	45
24	V	129/140 (92%)	112 (87%)	14 (11%)	3 (2%)	7	43
25	W	61/157 (39%)	57 (93%)	3 (5%)	1 (2%)	11	50
26	X	117/156 (75%)	108 (92%)	7 (6%)	2 (2%)	11	49
27	Y	132/145 (91%)	112 (85%)	14 (11%)	6 (4%)	3	27
28	Z	133/136 (98%)	113 (85%)	15 (11%)	5 (4%)	4	31
29	a	145/148 (98%)	111 (77%)	26 (18%)	8 (6%)	2	22
30	b	73/160 (46%)	58 (80%)	11 (15%)	4 (6%)	2	22
31	c	92/115 (80%)	78 (85%)	10 (11%)	4 (4%)	3	28
32	d	105/125 (84%)	85 (81%)	16 (15%)	4 (4%)	4	31
33	e	126/135 (93%)	110 (87%)	15 (12%)	1 (1%)	22	65
34	f	107/110 (97%)	95 (89%)	7 (6%)	5 (5%)	3	26
35	g	112/117 (96%)	103 (92%)	7 (6%)	2 (2%)	10	48
36	h	120/123 (98%)	103 (86%)	14 (12%)	3 (2%)	6	41
37	i	100/105 (95%)	91 (91%)	7 (7%)	2 (2%)	9	46
38	j	84/86 (98%)	67 (80%)	13 (16%)	4 (5%)	2	25
39	k	67/70 (96%)	55 (82%)	7 (10%)	5 (8%)	1	13
40	l	48/51 (94%)	42 (88%)	4 (8%)	2 (4%)	3	28
41	m	50/128 (39%)	44 (88%)	6 (12%)	0	100	100
42	n	21/25 (84%)	21 (100%)	0	0	100	100
43	o	102/106 (96%)	85 (83%)	11 (11%)	6 (6%)	2	20
44	p	89/91 (98%)	79 (89%)	9 (10%)	1 (1%)	17	59
45	r	123/125 (98%)	97 (79%)	20 (16%)	6 (5%)	2	24
46	1	384/476 (81%)	325 (85%)	42 (11%)	17 (4%)	3	27
47	2	60/68 (88%)	51 (85%)	6 (10%)	3 (5%)	2	24
All	All	6815/7604 (90%)	5717 (84%)	811 (12%)	287 (4%)	6	28

5 of 287 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	19	HIS
4	A	197	PRO
5	B	16	PHE
5	B	40	PRO
5	B	108	GLU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	A	187/199 (94%)	139 (74%)	48 (26%)	0	4
5	B	335/335 (100%)	265 (79%)	70 (21%)	1	7
6	C	305/305 (100%)	239 (78%)	66 (22%)	1	6
7	D	246/250 (98%)	178 (72%)	68 (28%)	0	3
8	E	209/209 (100%)	157 (75%)	52 (25%)	1	4
9	F	194/194 (100%)	145 (75%)	49 (25%)	0	4
10	G	206/226 (91%)	158 (77%)	48 (23%)	1	4
11	H	169/171 (99%)	125 (74%)	44 (26%)	0	3
12	I	180/180 (100%)	136 (76%)	44 (24%)	1	4
13	J	143/149 (96%)	115 (80%)	28 (20%)	1	8
14	L	176/177 (99%)	135 (77%)	41 (23%)	1	4
15	M	116/160 (72%)	95 (82%)	21 (18%)	2	11
16	N	171/172 (99%)	129 (75%)	42 (25%)	1	4
17	O	172/174 (99%)	146 (85%)	26 (15%)	3	19
18	P	134/134 (100%)	112 (84%)	22 (16%)	2	15
19	Q	163/164 (99%)	132 (81%)	31 (19%)	2	9
20	R	159/175 (91%)	120 (76%)	39 (24%)	1	4
21	S	156/192 (81%)	121 (78%)	35 (22%)	1	5
22	T	139/140 (99%)	112 (81%)	27 (19%)	1	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	U	89/114 (78%)	67 (75%)	22 (25%)	1	4
24	V	101/107 (94%)	77 (76%)	24 (24%)	1	4
25	W	55/126 (44%)	42 (76%)	13 (24%)	1	4
26	X	107/133 (80%)	89 (83%)	18 (17%)	2	14
27	Y	124/135 (92%)	96 (77%)	28 (23%)	1	5
28	Z	117/118 (99%)	94 (80%)	23 (20%)	1	8
29	a	119/120 (99%)	102 (86%)	17 (14%)	4	22
30	b	63/123 (51%)	45 (71%)	18 (29%)	0	3
31	c	79/97 (81%)	60 (76%)	19 (24%)	1	4
32	d	98/110 (89%)	66 (67%)	32 (33%)	0	2
33	e	114/121 (94%)	89 (78%)	25 (22%)	1	6
34	f	88/89 (99%)	73 (83%)	15 (17%)	2	14
35	g	98/100 (98%)	79 (81%)	19 (19%)	1	8
36	h	109/110 (99%)	92 (84%)	17 (16%)	3	18
37	i	86/89 (97%)	71 (83%)	15 (17%)	2	13
38	j	73/73 (100%)	60 (82%)	13 (18%)	2	12
39	k	64/65 (98%)	52 (81%)	12 (19%)	2	9
40	l	47/48 (98%)	39 (83%)	8 (17%)	2	14
41	m	48/116 (41%)	36 (75%)	12 (25%)	1	4
42	n	22/24 (92%)	17 (77%)	5 (23%)	1	5
43	o	92/94 (98%)	70 (76%)	22 (24%)	1	4
44	p	74/74 (100%)	61 (82%)	13 (18%)	2	12
45	r	109/109 (100%)	85 (78%)	24 (22%)	1	6
46	1	330/398 (83%)	309 (94%)	21 (6%)	20	58
47	2	53/59 (90%)	50 (94%)	3 (6%)	24	61
All	All	5919/6458 (92%)	4680 (79%)	1239 (21%)	4	7

5 of 1239 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
15	M	17	PHE
19	Q	119	LYS
41	m	97	ARG

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Mol	Chain	Res	Type
15	M	91	TRP
17	O	62	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 188 such sidechains are listed below:

Mol	Chain	Res	Type
16	N	178	HIS
20	R	66	ASN
45	r	6	GLN
16	N	182	HIS
18	P	54	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3645/3722 (97%)	1611 (44%)	0
2	7	119/120 (99%)	31 (26%)	0
3	8	155/156 (99%)	61 (39%)	0
All	All	3919/3998 (98%)	1703 (43%)	0

5 of 1703 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	2	G
1	5	5	A
1	5	6	C
1	5	8	U
1	5	12	A

There are no RNA pucker outliers to report.

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 133 ligands modelled in this entry, 133 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.