



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Aug 21, 2017 – 12:21 PM EDT

PDB ID : 5AA0
EMDB ID: : EMD-6397
Title : Complex of Thermophilus thermophilus ribosome (A-and P-site tRNA) bound to BipA-GDPCP
Authors : Kumar, V.; Chen, Y.; Ahmed, T.; Tan, J.; Ero, R.; Bhushan, S.; Gao, Y.-G.
Deposited on : unknown
Resolution : 5.00 Å(reported)
Based on PDB ID : 4V4Y

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
Mogul : 1.7.2 (RC1), CSD as538be (2017)
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) : rb-20029824

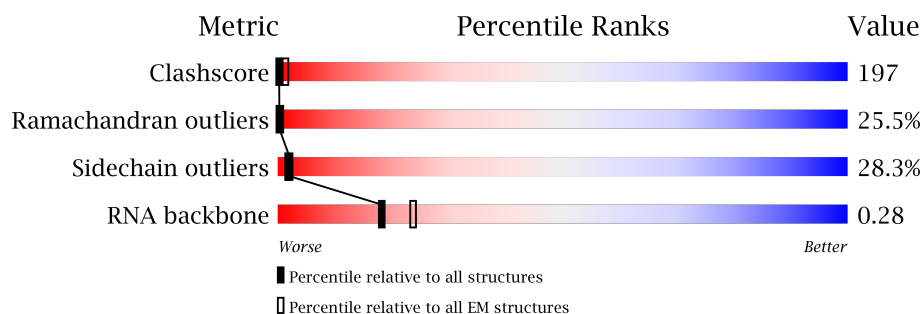
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.00 Å.

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







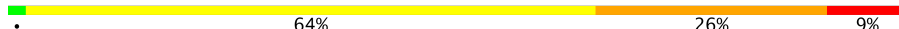
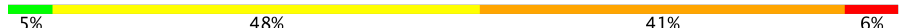



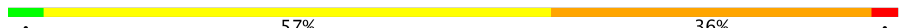
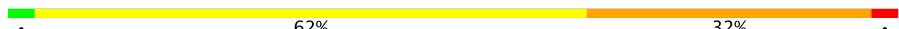
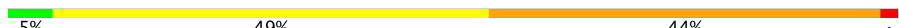




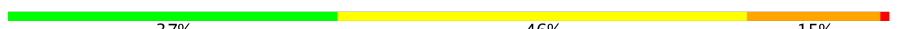
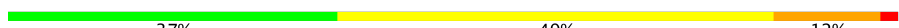
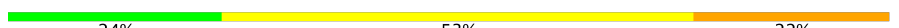



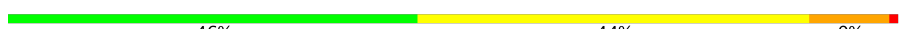


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

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	AA	2889	
2	AB	123	
3	AC	228	
4	AD	272	
5	AE	206	
6	AF	208	
7	AG	182	
8	AH	174	


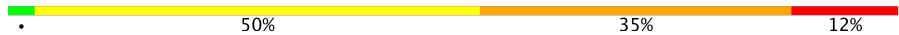
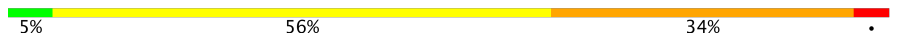



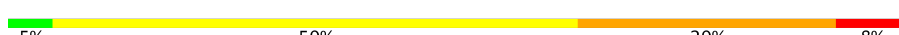
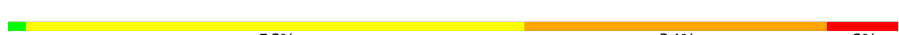



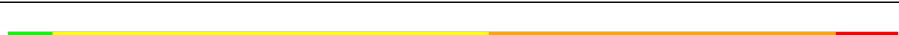

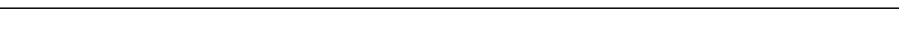
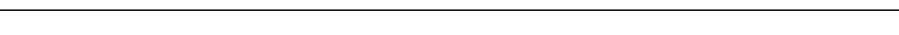
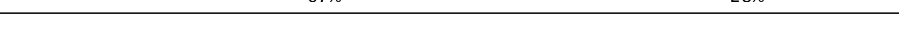

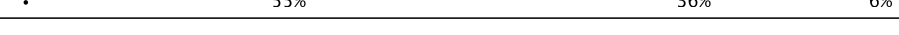







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Mol	Chain	Length	Quality of chain
9	AK	139	
10	AL	122	
11	AM	145	
12	AN	136	
13	AO	117	
14	AP	110	
15	AQ	117	
16	AR	117	
17	AS	101	
18	AT	110	
19	AU	94	
20	AV	110	
21	AW	180	
22	AX	85	
23	AY	67	
24	AZ	59	
25	Aa	71	
26	Ab	57	
27	Ac	49	
28	Ad	49	
29	Ae	64	
30	Af	37	
31	AI	153	
32	AJ	134	
33	Ag	128	

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Mol	Chain	Length	Quality of chain
34	BA	1515	
35	BF	234	
36	BG	206	
37	BH	208	
38	BI	150	
39	BJ	101	
40	BK	155	
41	BL	138	
42	BM	127	
43	BN	98	
44	BO	119	
45	BP	124	
46	BQ	114	
47	BR	60	
48	BS	88	
49	BT	83	
50	BU	104	
51	BV	73	
52	BW	80	
53	BX	99	
54	BY	24	
55	BC	76	
56	BD	75	
56	BE	75	
57	BZ	605	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
58	NMY	AA	3001	-	-	X	-
59	8AN	AA	3002	-	-	X	-
59	8AN	AA	3003	-	-	X	-
60	GCP	BZ	701	-	-	X	-

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 155482 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 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	2889	Total	C	N	O	P	0	0
			62218	27691	11629	20009	2889		

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AA	?	-	C	deletion	GB 37223181
AA	?	-	G	deletion	GB 37223181
AA	?	-	C	deletion	GB 37223181
AA	?	-	A	deletion	GB 37223181
AA	?	-	A	deletion	GB 37223181
AA	?	-	G	deletion	GB 37223181
AA	?	-	C	deletion	GB 37223181
AA	?	-	G	deletion	GB 37223181
AA	?	-	G	deletion	GB 37223181
AA	?	-	G	deletion	GB 37223181
AA	?	-	C	deletion	GB 37223181
AA	?	-	C	deletion	GB 37223181
AA	?	-	G	deletion	GB 37223181
AA	?	-	C	deletion	GB 37223181
AA	?	-	G	deletion	GB 37223181
AA	?	-	C	deletion	GB 37223181
AA	?	-	A	deletion	GB 37223181
AA	?	-	C	deletion	GB 37223181
AA	?	-	G	deletion	GB 37223181
AA	?	-	C	deletion	GB 37223181
AA	?	-	G	deletion	GB 37223181
AA	?	-	G	deletion	GB 37223181
AA	?	-	C	deletion	GB 37223181
AA	?	-	C	deletion	GB 37223181
AA	1134	G	UNK	conflict	GB 37223181

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	123	Total	C	N	O	P	0	0
			2641	1175	488	855	123		

- Molecule 3 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	228	Total	C	N	O	S	0	0
			1742	1102	318	319	3		

- Molecule 4 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AD	272	Total	C	N	O	S	0	0
			2124	1339	424	358	3		

- Molecule 5 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	206	Total	C	N	O	S	0	0
			1578	997	302	273	6		

- Molecule 6 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AF	208	Total	C	N	O	S	0	0
			1625	1034	303	286	2		

- Molecule 7 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	182	Total	C	N	O	S	0	0
			1482	947	269	261	5		

- Molecule 8 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AH	174	Total	C	N	O	S	0	0
			1328	844	248	235	1		

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AK	139	Total	C	N	O	S	0	0
			1113	717	207	186	3		

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AL	122	Total	C	N	O	S	0	0
			932	587	171	170	4		

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AM	145	Total	C	N	O	S	0	0
			1106	688	226	190	2		

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AN	136	Total	C	N	O	S	0	0
			1080	688	204	183	5		

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	AO	117	Total	C	N	O	0	0
			960	599	202	159		

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	AP	110	Total	C	N	O	0	0
			877	553	175	149		

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AQ	117	Total	C	N	O	S	0	0
			976	614	197	164	1		

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AR	117	Total	C	N	O	S	0	0
			964	610	202	151	1		

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AS	101	Total	C	N	O	S	0	0
			779	501	142	135	1		

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AT	110	Total	C	N	O	S	0	0
			876	552	171	151	2		

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AU	94	Total	C	N	O		0	0
			742	483	133	126			

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AV	110	Total	C	N	O	S	0	0
			844	539	158	141	6		

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AW	180	Total	C	N	O	S	0	0
			1435	916	256	260	3		

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AX	85	Total	C	N	O	S	0	0
			670	415	141	112	2		

- Molecule 23 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AY	67	Total	C	N	O	S	0	0
			567	350	116	99	2		

- Molecule 24 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AZ	59	Total	C	N	O		0	0
			469	298	90	81			

- Molecule 25 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Aa	71	Total	C	N	O	S	0	0
			581	364	108	104	5		

- Molecule 26 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Ab	57	Total	C	N	O	S	0	0
			445	279	87	74	5		

- Molecule 27 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Ac	49	Total	C	N	O	S	0	0
			426	265	87	70	4		

- Molecule 28 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Ad	49	Total	C	N	O	S	0	0
			430	263	108	57	2		

- Molecule 29 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Ae	64	Total	C	N	O	S	0	0
			515	331	102	79	3		

- Molecule 30 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Af	37	Total	C	N	O	S	0	0
			307	188	68	47	4		

- Molecule 31 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AI	153	Total	C	N	O	S	0	0
			752	446	153	153			

- Molecule 32 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	AJ	134	Total	C	N	O	S	0	0
			993	632	175	181	5		

- Molecule 33 is a protein called Unknown peptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ag	128	Total	C	N	O	S	0	5
			620	369	128	123			

- Molecule 34 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BA	1515	Total	C	N	O	P	0	0
			32554	14490	6022	10527	1515		

- Molecule 35 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BF	234	Total	C	N	O	S	0	0
			1900	1213	341	341	5		

- Molecule 36 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BG	206	Total	C	N	O	S	0	0
			1612	1016	314	281	1		

- Molecule 37 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BH	208	Total	C	N	O	S	0	0
			1703	1066	339	291	7		

- Molecule 38 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BI	150	Total	C	N	O	S	0	0
			1146	724	217	201	4		

- Molecule 39 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BJ	101	Total	C	N	O	S	0	0
			843	531	155	154	3		

- Molecule 40 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BK	155	Total	C	N	O	S	0	0
			1257	781	252	218	6		

- Molecule 41 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BL	138	Total	C	N	O	S	0	0
			1116	705	215	193	3		

- Molecule 42 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BM	127	Total	C	N	O	S	0	0
			1010	639	197	174			

- Molecule 43 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BN	98	Total	C	N	O	S	0	0
			794	499	156	138	1		

- Molecule 44 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BO	119	Total	C	N	O	S	0	0
			885	549	168	165	3		

- Molecule 45 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BP	124	Total	C	N	O	S	0	0
			970	611	195	163	1		

- Molecule 46 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BQ	114	Total	C	N	O	S	0	0
			914	565	189	158	2		

- Molecule 47 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BR	60	Total	C	N	O	S	0	0
			492	312	104	72	4		

- Molecule 48 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BS	88	Total	C	N	O	S	0	0
			734	459	147	126	2		

- Molecule 49 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BT	83	Total	C	N	O	S	0	0
			700	443	139	117	1		

- Molecule 50 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BU	104	Total	C	N	O	S	0	0
			857	547	161	147	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BU	96	GLN	GLU	conflict	UNP Q5SHP7

- Molecule 51 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	BV	73	Total	C	N	O	0	0
			597	380	118	99		

- Molecule 52 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BW	80	Total	C	N	O	S	0	0
			647	414	119	112	2		

- Molecule 53 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BX	99	Total	C	N	O	S	0	0
			763	470	162	129	2		

- Molecule 54 is a protein called 30S ribosomal protein Thx.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	BY	24	Total	C	N	O	0	0
			208	128	50	30		

- Molecule 55 is a RNA chain called tRNA chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BC	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

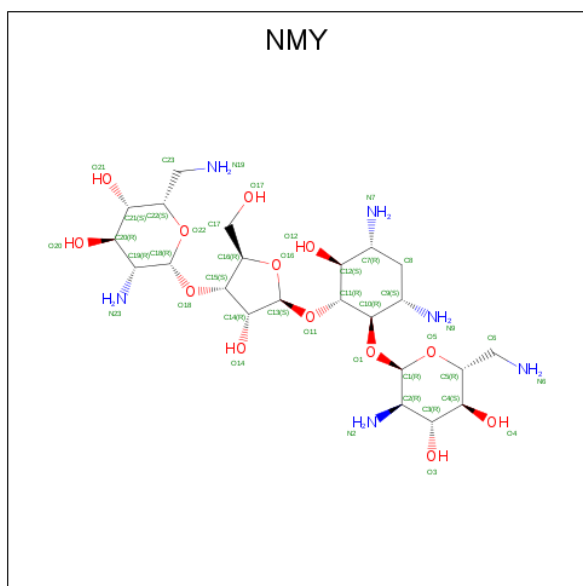
- Molecule 56 is a RNA chain called tRNA chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BD	75	Total	C	N	O	P	0	0
			1597	713	285	525	74		
56	BE	75	Total	C	N	O	P	0	0
			1597	713	285	525	74		

- Molecule 57 is a protein called GTP-binding protein.

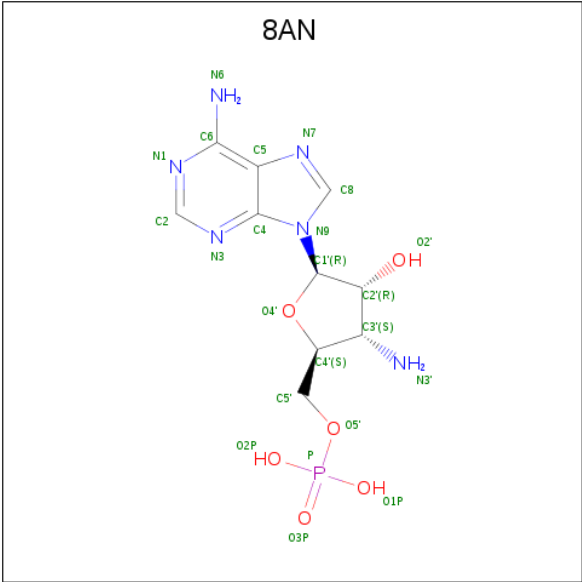
Mol	Chain	Residues	Atoms					AltConf	Trace
57	BZ	605	Total	C	N	O	S	0	0
			4610	2902	807	883	18		

- Molecule 58 is NEOMYCIN (three-letter code: NMY) (formula: $C_{23}H_{46}N_6O_{13}$).



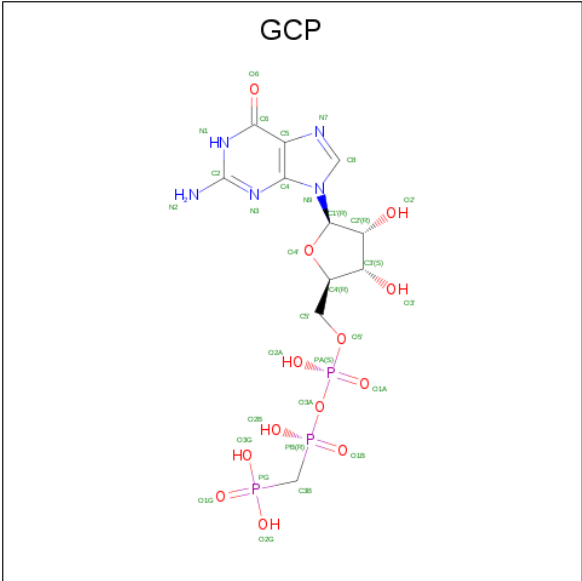
Mol	Chain	Residues	Atoms				AltConf
58	AA	1	Total	C	N	O	0
			42	23	6	13	
58	BA	1	Total	C	N	O	0
			42	23	6	13	

- Molecule 59 is 3'-amino-3'-deoxyadenosine 5'-(dihydrogen phosphate) (three-letter code: 8AN) (formula: $C_{10}H_{15}N_6O_6P$).



Mol	Chain	Residues	Atoms					AltConf
59	AA	1	Total	C	N	O	P	0
			44	20	12	10	2	
59	AA	1	Total	C	N	O	P	0
			44	20	12	10	2	

- Molecule 60 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (three-letter code: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃).

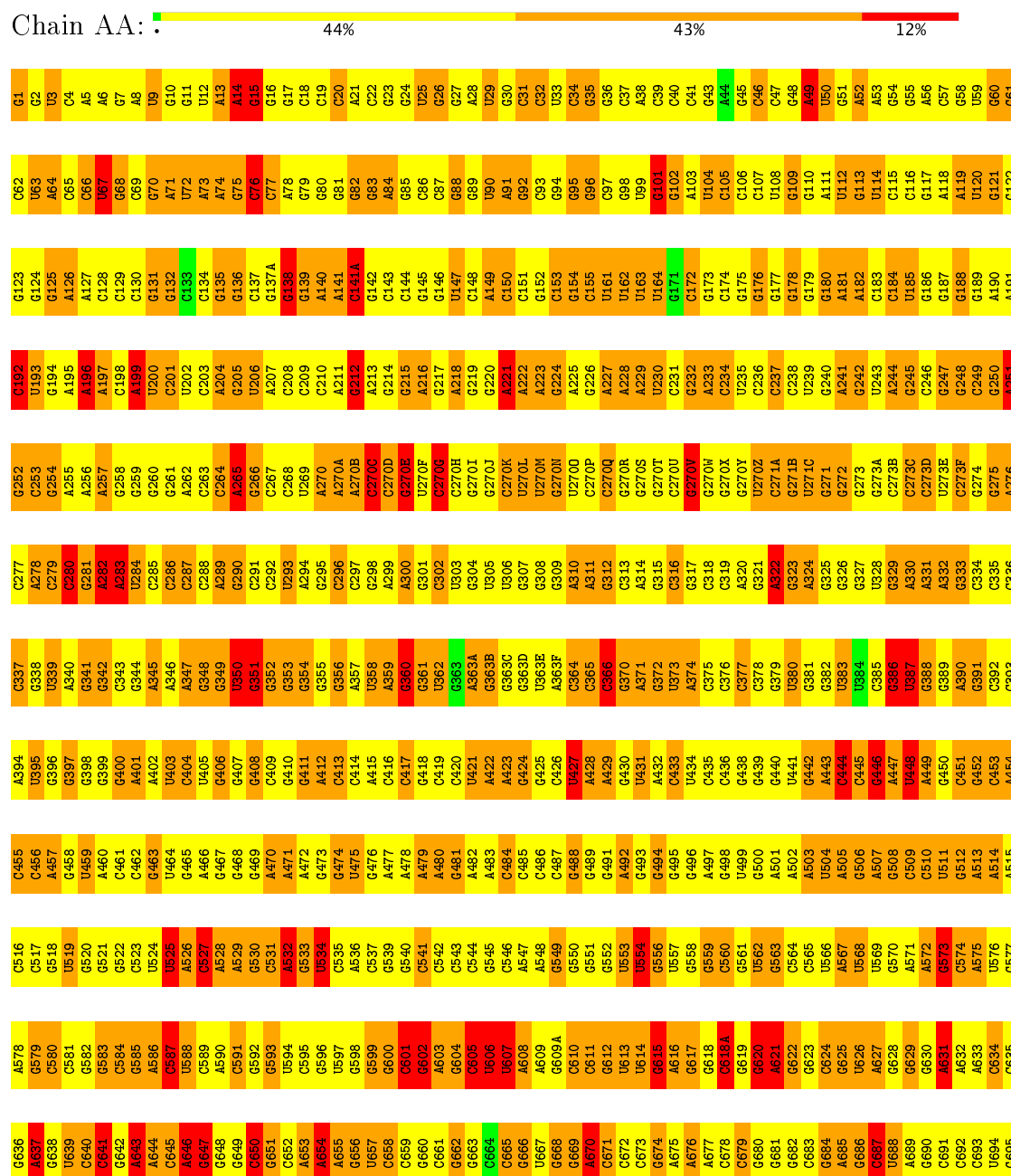


Mol	Chain	Residues	Atoms					AltConf
60	BZ	1	Total	C	N	O	P	0
			32	11	5	13	3	

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: 23S ribosomal RNA







C2652	U2712	C2771	G2834	U2895
U2653	A2712A	C2772	A2835	C2896
A2654	G2713	C2773	G2836	U2897
G2655	G2714	C2774	G2837	U2898
U2656	G2715	A2775	G2838	G2899
A2657	U2716	A2776	G2839	A2900
C2658	G2717	C2777	C2840	C2901
C2659	G2718	A2778	C2841	C2902
A2660	G2719	A2779	G2842	
C2661	U2720		G2843	
A2662	A2721	A2781	G2844	
G2663	G2722	G2782	G2845	
G2664	C2723	G2783	U2847	
A2665	C2724	C2784	G2848	
C2666	A2725	C2785	G2849	
C2667	U2726	U2786	A2850	
G2668	G2727	C2787	A2851	
C2669	U2728	C2788	G2852	
A2670	G2729	C2789	C2853	
A2671	C2730	A2790	G2854	
A2672	G2731	C2791	C2855	
G2673	G2732	G2792	C2856	
G2674	A2733	G2793	G2857	
A2675	G2734	C2794	C2858	
C2676	A2735	G2795	G2859	
C2677	G2736	U2797	A2860	
C2678	G2737	C2798	C2861	
A2679	A2738	A2799	G2862	
C2680	U2739	A2801	C2863	
C2681	A2740	C2802	C2864	
U2682	C2741	C2803	U2865	
C2683	C2742	C2804	U2866	
U2684	C2743	G2805	C2867	
G2685	G2744	U2808	A2868	
G2686	C2745	C2746	G2869	
U2687	U2746	A2809	C2870	
U2688	G2747	A2810	C2871	
U2689	A2748	G2811	G2872	
C2690	A2749	G2812	A2873	
C2691	A2750	A2813	C2874	
C2692	C2751	C2814	C2875	
A2693	C2752	C2815	G2876	
G2694	A2753	C2816	C2877	
C2695	U2754	G2817	U2878	
U2696	C2755	G2818	C2879	
G2697	U2756	A2820	C2880	
U2698	A2757	A2821	C2881	
C2699	A2758	G2822	A2882	
C2700	G2759	A2823	U2883	
C2701	C2760	C2824	C2884	
U2702	G2761	C2825	C2885	
C2703	G2762	A2826	G2886	
C2704	G2763	A2827	U2887	
A2705	A2764	A2765	C2888	
G2706	A2765	C2828	C2889	
G2707	G2766	C2829	C2891	
G2708	C2767	G2830	A2892	
G2709	C2768	U2831	G2893	
C2710	C2769	U2832	G2894	
A2711	G2770	G2833		

• Molecule 2: 5S ribosomal RNA

Chain AB:  52% 39% 9%

A-1	A59	G118
A0	C60	A119
U1	G61	U120
C2	C62	
C3	G63	
C4	C64	
C5	C65	
C6	A66	
G7	C68	
U8	G69	
C9	C70	
C10	G71	
C11	G72	
C12	A73	
A13	U74	
U14	G75	
G15	G76	
A16	U77	
C17	A78	
G18	C79	
C19	U80	
C20	C81	
G21	C82	
U22	G83	
C23	C84	
G24	A85	
A25	G86	
C26	C87	
C27	C88	
C28	G89	
A29	C90	
C30	C91	
C31	G92	
C32	C93	
G33	C94	
U34	U95	
C35	G96	
C36	C97	
C37	A98	
C38	C99	
A40	G100	
U41	A101	
C42	G102	
C43	U103	
G44	A104	
A45	G105	
A46	C106	
C47	U107	
A48	C108	
C49	G109	
G50	G110	
G51	U111	
A52	C112	
A53	G113	
G54	C114	
U55	G115	
G56	A116	
A57	G117	
A58		

• Molecule 3: 50S ribosomal protein L1

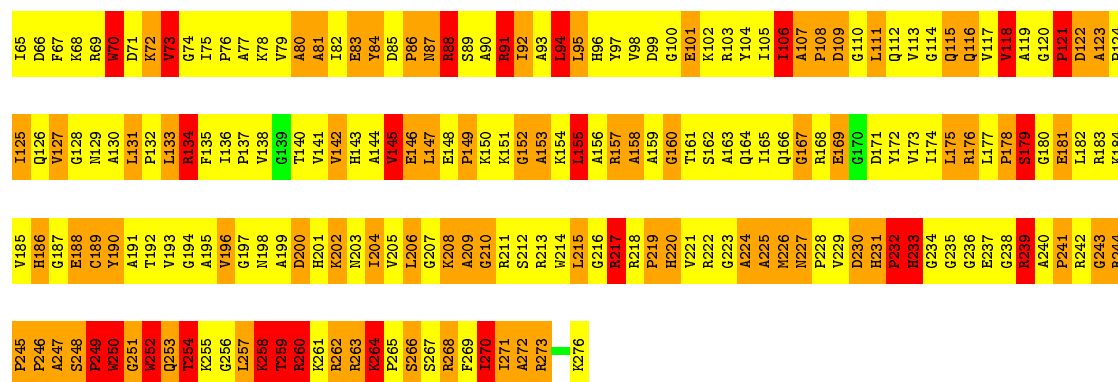
Chain AC:  6% 74% 18%

P1	T61	G121
K2	V62	A122
R3	S63	V123
G4	L64	G124
K5	P65	L125
R6	H66	K126
Y7	G67	L127
R8	L68	G128
A9	G69	L129
L10	K70	L130
L11	Q71	L131
E12	V72	G132
K13	R73	P133
V14	V74	R134
D15	L75	G135
A16	A76	L136
L17	I77	L137
K18	A78	P138
U19	K79	N139
I20	G80	P140
T21	E81	K141
D22	K82	A142
L23	I83	G143
E24	K84	T144
A25	G85	V145
A26	A86	G146
H27	E87	L147
L28	G88	N148
V29	A89	L149
K30	G90	G150
E31	A91	E151
L32	D92	L152
A33	Y93	L153
T34	V94	R154
A35	G95	E155
G36	G96	L156
F37	E97	K157
D38	G98	A158
E39	I99	G159
T40	I100	R160
V41	Q101	L161
E42	K102	F162
V43	I103	F163
H44	L104	R164
A45	D105	N165
K46	G106	D166
G48	W107	K167
L49	M108	T168
D50	D109	G169
P51	F110	A170
F52	D111	I171
R53	A112	H172
S54	V113	A173
D55	V114	P174
G56	A115	V175
N57	T116	G176
V58	P117	K177
R59	D118	A178
G60	V119	S179
	M120	F180

• Molecule 4: 50S ribosomal protein L2

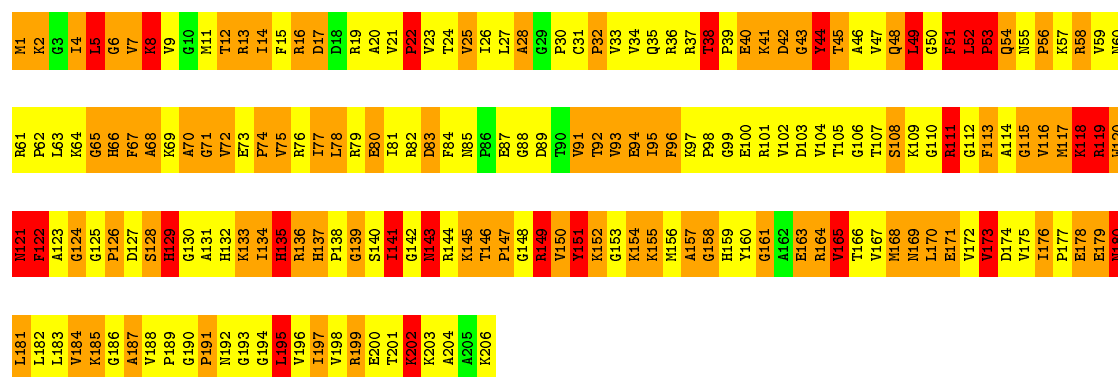
Chain AD:  53% 34% 11%

K5	F6	K7	P8	Y9	T10	P11	S12	K13	R14	F15	M16	T17	V18	A19	D20	F21	S22	E23	T24	K25	K26	T27	E28	P29	E30	R31	S32	L33	V34	K35	P36	L37	K38	K39	T40	G41	G42	R43	N44	N45	Q46	G47	R48	L49	T50	V51	R52	F53	R54	G55	G56	G57	H58	X59	R60	L61	V62	R63	L64
----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



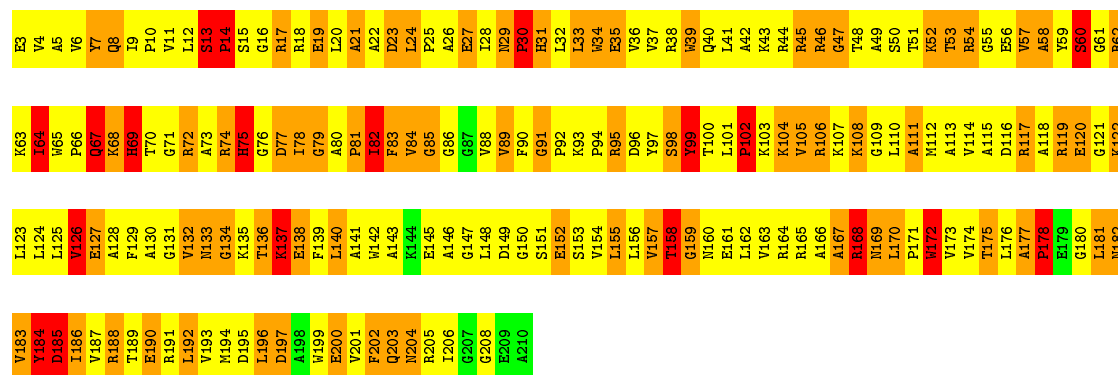
• Molecule 5: 50S ribosomal protein L3

Chain AE: 45% 39% 12%



• Molecule 6: 50S ribosomal protein L4

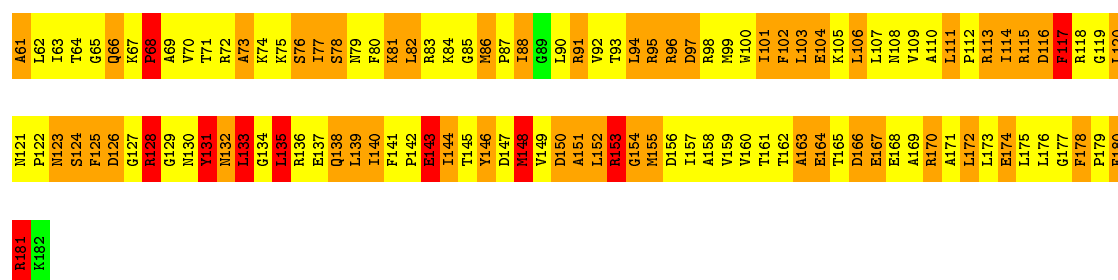
Chain AF: 51% 36% 9%



• Molecule 7: 50S ribosomal protein L5

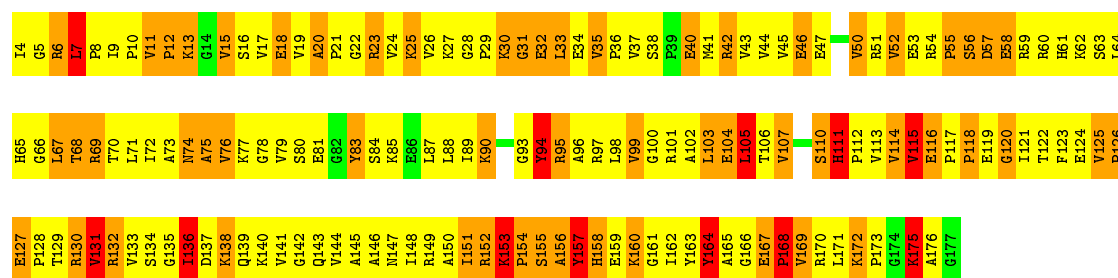
Chain AG: 54% 36% 9%





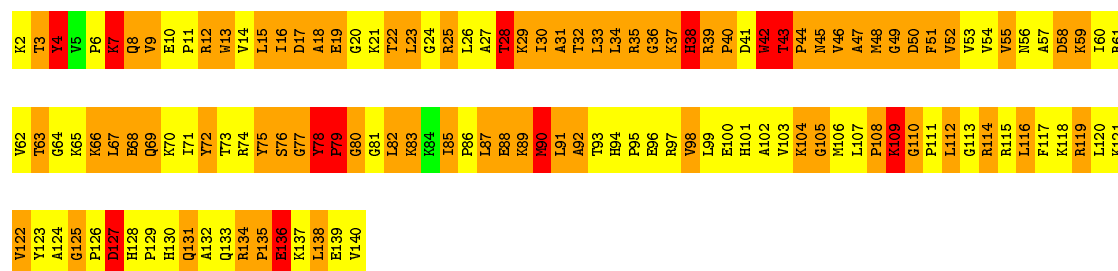
• Molecule 8: 50S ribosomal protein L6

Chain AH: 7% 53% 33% 7%



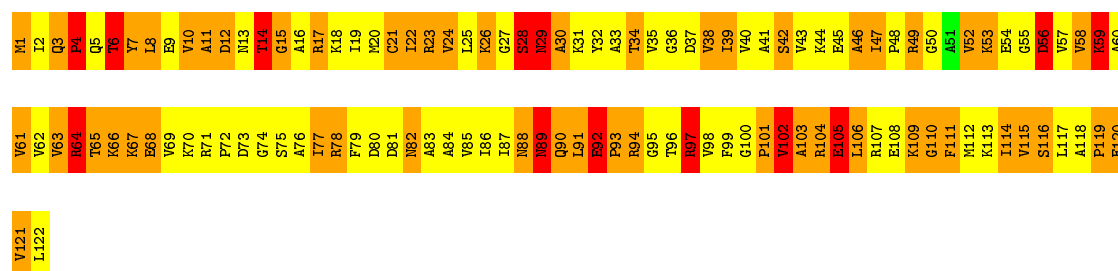
• Molecule 9: 50S ribosomal protein L13

Chain AK: 40% 50% 9%



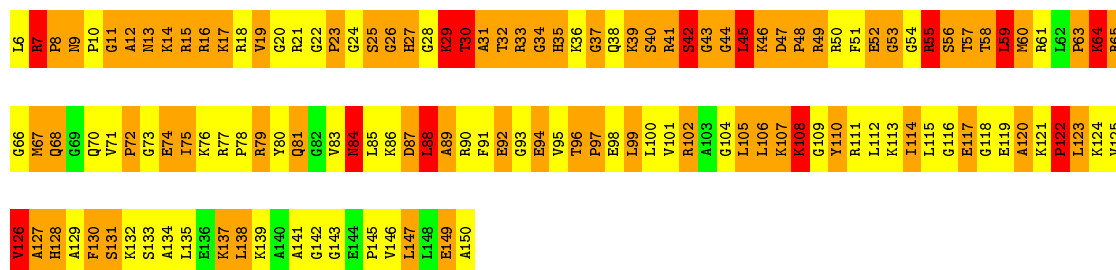
• Molecule 10: 50S ribosomal protein L14

Chain AL: 46% 43% 11%



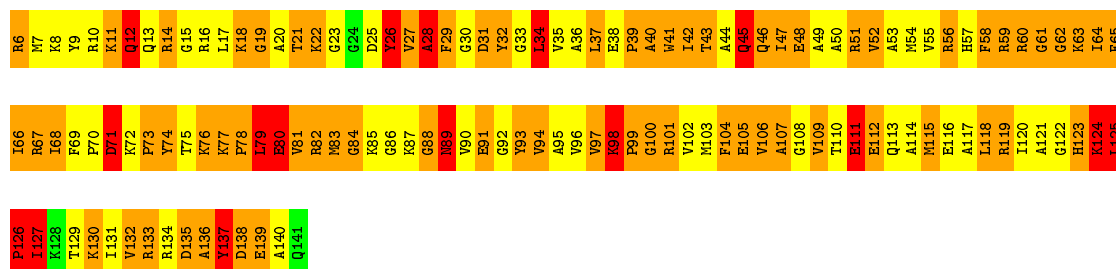
• Molecule 11: 50S ribosomal protein L15

Chain AM: 6% 39% 47% 9%



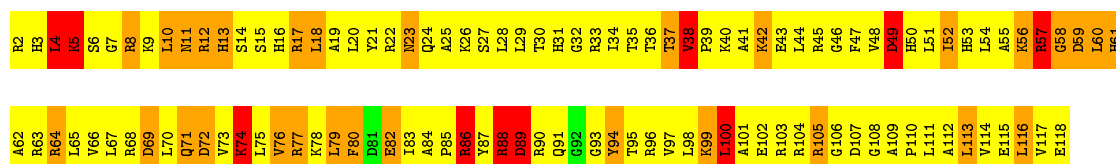
• Molecule 12: 50S ribosomal protein L16

Chain AN: . 36% 50% 12%



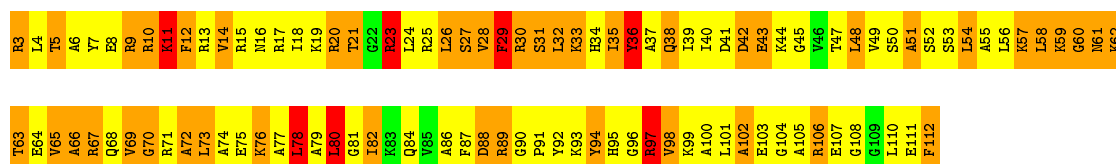
• Molecule 13: 50S ribosomal protein L17

Chain AO: . 64% 26% 9%



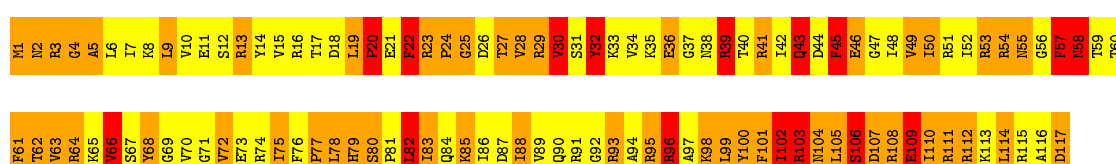
• Molecule 14: 50S ribosomal protein L18

Chain AP: . 5% 48% 41% 6%



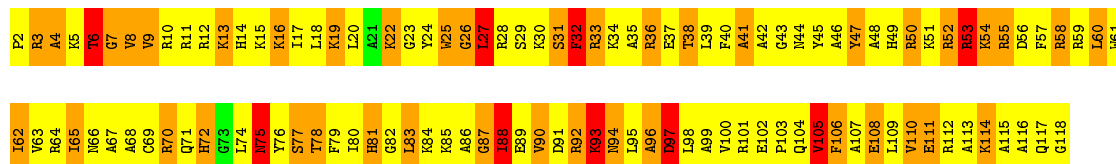
• Molecule 15: 50S ribosomal protein L19

Chain AQ: . 43% 44% 14%



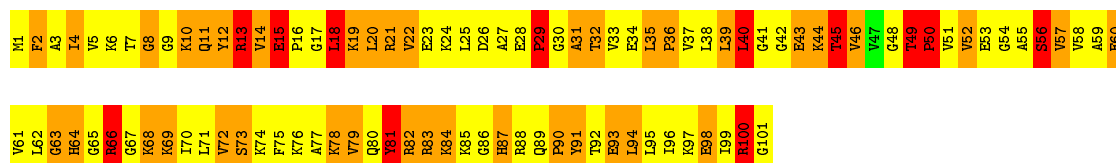
- Molecule 16: 50S ribosomal protein L20

Chain AR: 

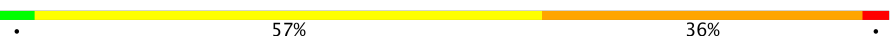


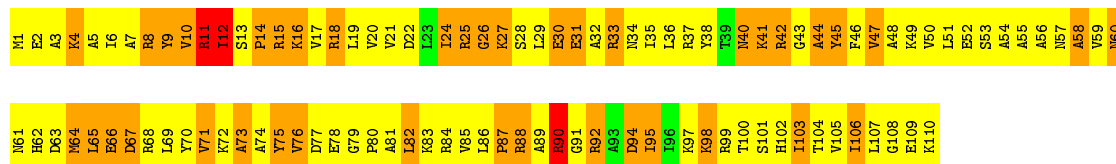
- Molecule 17: 50S ribosomal protein L21

Chain AS: 

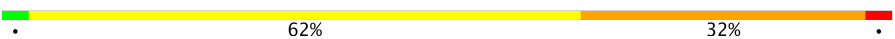


- Molecule 18: 50S ribosomal protein L22

Chain AT: 



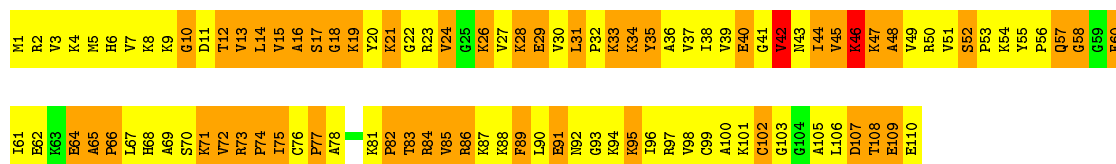
- Molecule 19: 50S ribosomal protein L23

Chain AU: 



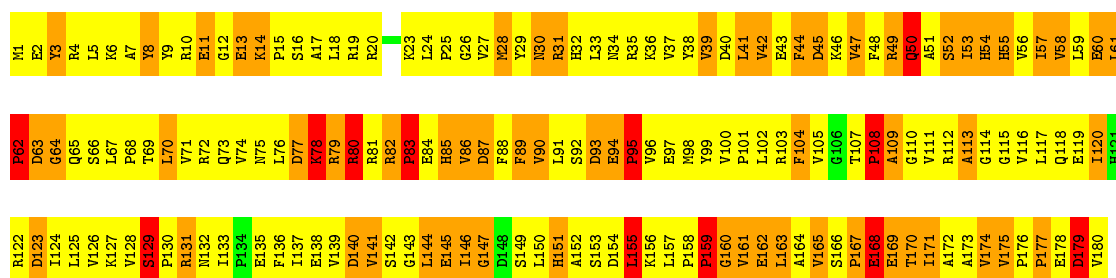
- Molecule 20: 50S ribosomal protein L24

Chain AV: 



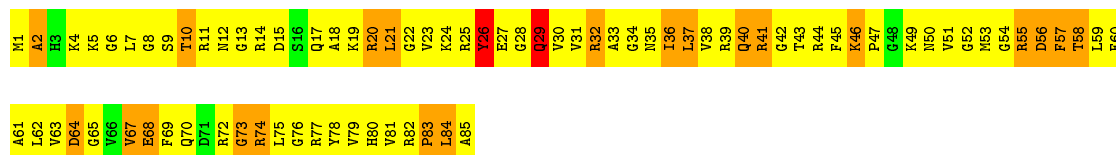
- Molecule 21: 50S ribosomal protein L25

Chain AW: 



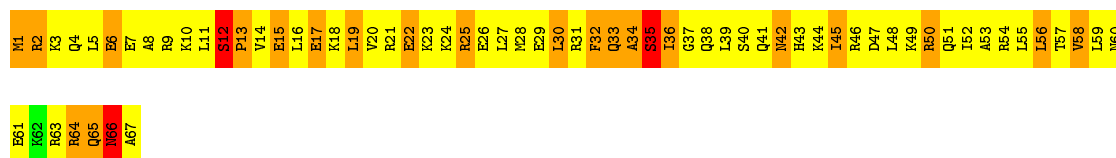
- Molecule 22: 50S ribosomal protein L27

Chain AX: 6% 67% 25%



- Molecule 23: 50S ribosomal protein L29

Chain AY: 63% 31%



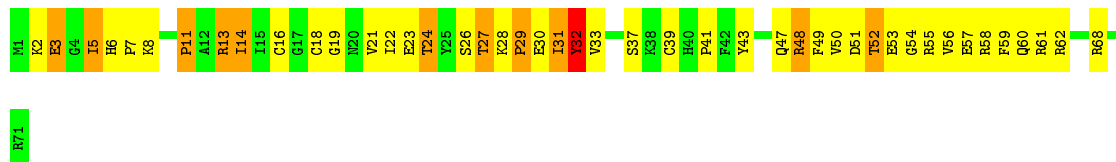
- Molecule 24: 50S ribosomal protein L30

Chain AZ: 5% 46% 44% 5%



- Molecule 25: 50S ribosomal protein L31

Chain Aa: 37% 46% 15%

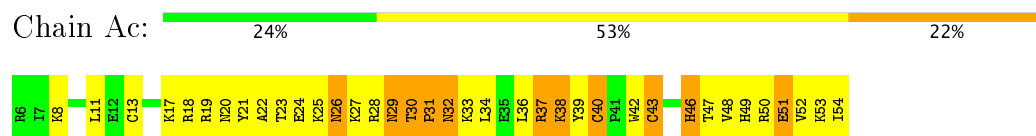


- Molecule 26: 50S ribosomal protein L32

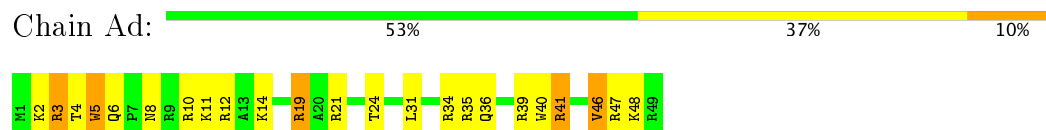
Chain Ab: 37% 49% 12%



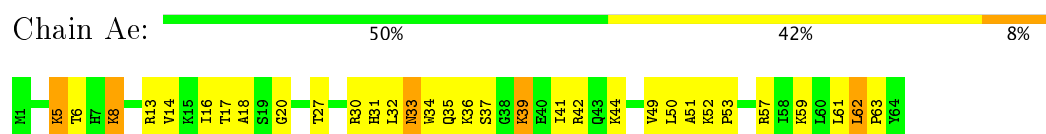
- Molecule 27: 50S ribosomal protein L33



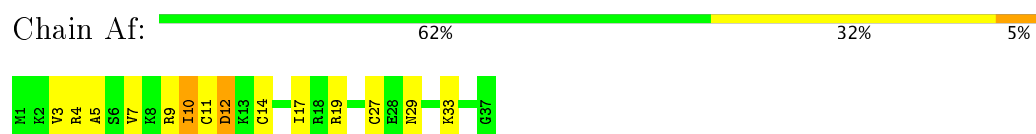
- Molecule 28: 50S ribosomal protein L34



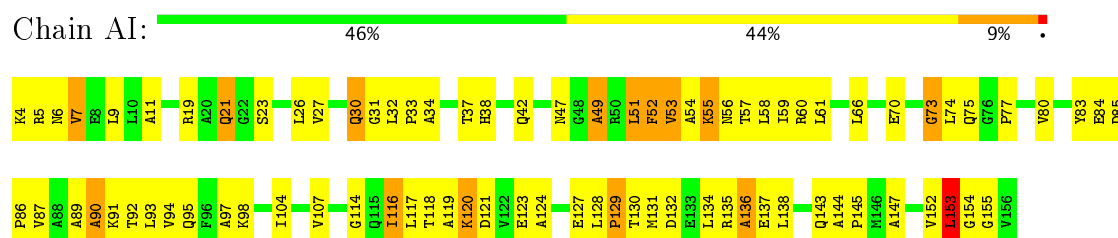
- Molecule 29: 50S ribosomal protein L35



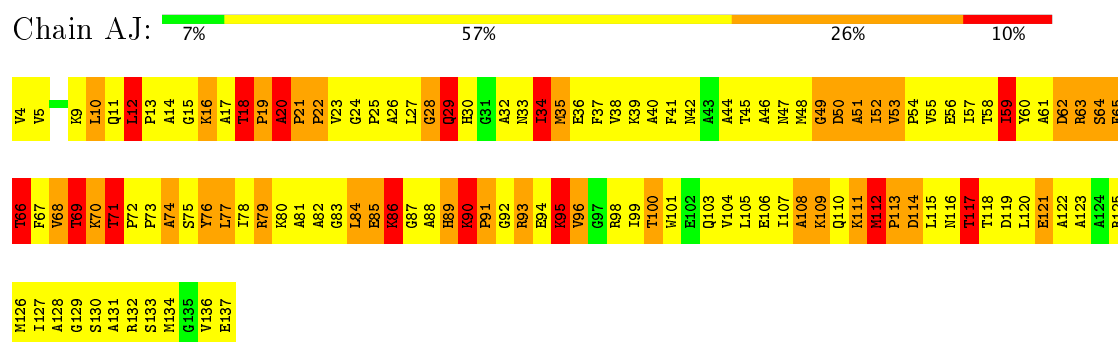
- Molecule 30: 50S ribosomal protein L36



- Molecule 31: 50S ribosomal protein L10



- Molecule 32: 50S ribosomal protein L11



- Molecule 33: Unknown peptide

Chain Ag:

100%

There are no outlier residues recorded for this chain.

● Molecule 34: 16S ribosomal RNA

Chain BA:

56%

36%

7%

6803	U743	6683	C623	A563	C503	A493	G371	C311	G251	C186E	C131	U65	U5
U804	C744	A684	C624	A564	C504	A494	C372	C312	U252	C186F	C132	G66	G6
C805	C745	G685	G625	U565	C505	C495	A373	A303	U253	C187	U133	C67	G7
A806	A746	U686	U626	G566	G506	U494	A374	C314	G254	U188	A134	G68	A8
C747	C747	A687	G627	G567	C507	C496	U375	A315	G255	U189	C135	G69	G9
C808	C748	G688	G628	G568	C508	C497	G376	G316	U256	G190	C136	G73	G10
C809	C749	C689	G629	C569	A509	U437	C377	G317	G257	G191A	C137	C74	G11
C810	C750	G690	C630	C570	A510	C438	C378	G318	G258	G191B	C138		
C811	U751	G691	G631	U571	C511	A439	C379	G319	G259	G191C	C139	U12	U12
C812	G752	U692	A632	U572	U512	A440	G380	C320	G260	U191D	A140	G77	U13
A813	A753	G693	G633	A573	C513	C442	C381	A321	U261	G191E	A141	G78	U14
A814	C754	A694	C634	A574	C514	C443	A382	C322	A262	U191F	A142	G79	G15
A815	C755	A695	G635	G575	G515	C444	A383	U323	A263	G191	A143	G80	U16
A816	C756	A696	U636	G576	U516	C445	C384	G324	U264	U192	C144	G81	C18
C817	U757	U697	G637	G577	C517	C446	C385	A325	G265	C193	G145	U82	C19
G818	G758	G698	G638	C578	C518	C447	C386	G326	G266	C194	G146	U84	U20
A819	A759	C699	G639	G579	C519	A448	U387	A327	G267	A195	G147	U85	G21
U820	G760	G700	A640	U580	A520	C449	G388	C328	C268	A196	G148	U86	G22
G821	G761	C701	U641	G581	G521	C450	A389	A329	C269	A197	A149	A87	C23
C822	C762	A642	C642	U582	C522	A491	C390	C330	A270	G198	C150	C88	U24
G823	G763	C703	C643	A583	A523	A492	C391	G331	C271	G199	A151	U89	C25
C824	C764	A704	G644	G584	G524	A493	G392	G332	C272	G200	A152	C90	A26
G825	G765	U705	C645	G585	C525	C494	A393	G333	C273	C201	C153	C91	G27
C826	A766	A706	U646	G586	C526	C495	G394	C334	A274	U208	C154	G92	G28
A767	A767	C707	C647	G587	G527	C496	C395	C335	G275	G209	C155	U93	G29
A828	A768	G708	A648	G588	C528	C497	C396	C336	G276	U210	G156	G95	G31
C829	G769	C709	G649	C589	G529	C498	A397	C337	C277	G216	G157	G96	G32
G830	G770	G710	G650	C590	G530	A499	C398	A338	G278	C217	G158	U97	A32
C771	C771	C651	U651	U591	U531	C499	C399	C339	A279	C218	G159	C99	A33
G772	U772	A712	U652	G592	A532	C499	C400	U340	C280	C219	A160	A101	C34
C833	C773	G713	A653	G593	C533	C497	C401	C341	G281	G220	A161	G102	G35
C834	C774	A654	U654	U594	U534	A498	A402	C342	A282	C221	A162	C103	C36
U835	C775	A715	A655	G595	C535	C497	C403	U343	C283	U222	C163	G104	U37
G776	G776	A716	C656	C596	C536	C497	A404	A344	G284	U223	U164	G105	G38
C837	A777	G717	G657	G597	G537	C497	A405	C345	G285	C224	C165	G106	G39
C838	C778	G718	G658	U598	G538	C497	A406	G346	G286	C225	G166	G107	C40
U841	C779	C719	C659	U599	A539	A497	G407	C347	U287	G226	G167	G108	C41
C842	A780	C720	G660	C600	G540	C497	A408	G348	A288	G227	G168	A109	G42
U843	C781	G721	G661	C601	G541	U498	A409	A349	G289	A228	C169	C110	C43
C848	A782	A722	G662	A602	G542	C498	A410	G350	C290	U229	U170	G111	G44
C849	C783	U723	A663	U603	C543	A498	A411	C351	C291	G230	A171	G112	U45
U850	C784	G724	G664	C604	G544	C498	A412	C352	G292	C231	A172	G113	G46
G851	G785	G725	A665	U605	C545	C498	G413	A353	G293	G232	U173	G114	G47
C852	C786	G726	G666	G606	G546	C498	A414	C354	U294	C233	C174	G115	C48
G853	A787	G727	A667	A607	G547	C498	A415	C355	C295	C234	C175	U49	G49
U854	C788	A728	G668	A608	G548	A497	A416	A356	U296	C235	C176	G117	A50
G855	U789	U669	U669	A609	C549	C498	C417	G357	G297	G236	C177	U118	A51
C856	A790	G730	G670	G610	G550	C499	C418	U358	A298	C237	C178	A119	G52
C857	G791	G731	G671	A611	U551	C499	C419	U359	G299	G238	A179	A120	A53
G858	A792	C732	U672	C612	U552	C499	A420	A360	C300	G239	C180	C54	G54
C859	C793	A733	G673	C613	A553	C499	U421	G361	G301	G240	G181	G122	A55
A860	A794	G734	G674	A614	C554	C499	C422	A362	G302	C242	U182	C123	G56
C795	C795	C735	A675	C615	C555	U494	A423	G363	A303	A243	G183	G124	U57
G861	G796	C736	A676	G616	C556	A495	G424	A364	U304	U244	G184	U125	C58
C862	C797	A737	G677	G617	G557	A496	G425	U365	G305	C245	A185	G126	A59
U863	A798	C738	U678	C618	G558	U497	G426	C366	G306	A246	C186	G127	G60
C864	C799	G739	C679	U619	A559	A498	U427	G367	C307	G247	C187	G128	C61
A865	G800	U740	C680	U560	C560	G500	G428	U368	C308	C248	C188	U129	G62
C866	C801	G741	C681	A621	U561	C501	U429	C369	G309	U249	G189	C129A	G63
G867	U801	C742	C682	A622	C562	C502	A430	C370	C210	G250	C190	A130	C64
C868	C802	A743	C683	C623	C503	A493	G371	C311	G251	C186E	C131	U65	U5

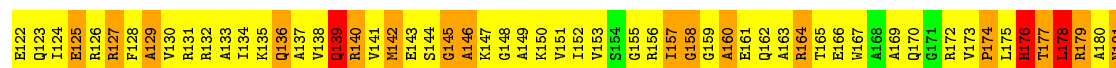
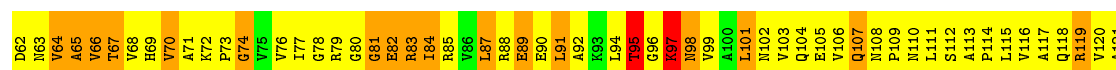
- Molecule 35: 30S ribosomal protein S2

Chain BF: 



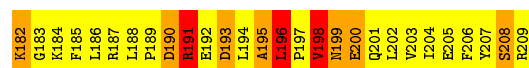
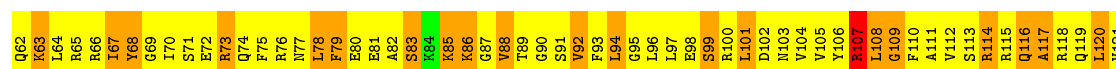
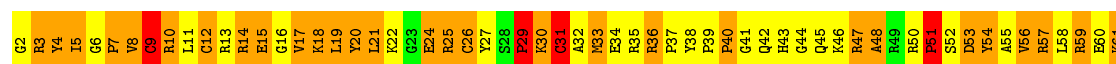
• Molecule 36: 30S ribosomal protein S3

Chain BG: 5% 56% 34%



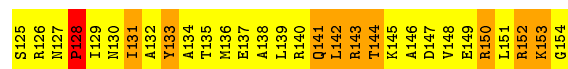
• Molecule 37: 30S ribosomal protein S4

Chain BH: 54% 37% 7%



• Molecule 38: 30S ribosomal protein S5

Chain BI: 63% 33%



• Molecule 39: 30S ribosomal protein S6

Chain BJ: 53% 37% 7%

M1 R2 R3 Y4 E5 V6 W7 I8 V9 L10 L11 N12 M13 M14 L15 D16 Q16 S17 Q18 Q19 L20 A20 L21 L22 E23 K23 E24 I25 I26 Q27 R28 A29 L30 L31 R32 N33 Y33 G34 A35 A36 V37 E38 R39 V40 E41 E42 L43 G44 L45 R46 R47 L48 A49 Y50 Y51 P51 I52 A53 K54 D55 P56 Q57 G58 Y59 F60

L61 M62 Y63 Q64 V65 E66 W67 P68 E69 D70 R71 R72 N73 D74 L75 A76 R77 R78 E79 R80 L81 R82 D83 N84 R85 R86 R87 V88 A89 V90 V91 R92 R93 Q96 Q97 Q98 E99 P96 F97 L98 A99 N100 A101

• Molecule 40: 30S ribosomal protein S7

Chain BK: 5% 59% 29% 8%

A2 R3 R4 R5 R6 A7 E8 V9 R10 R11 Q12 L13 Q14 D15 L16 V17 Y18 G19 D20 V21 L22 R23 Y24 A25 R26 T27 N28 V29 R30 R31 R32 R33 Q34 Q35 Q36 R37 L38 A39 R40 R41 L42 L43 V44 A45 A46 Q47 R48 Q49 R50 Q51 T54 G55 A56 E57 E58 P58 V61 F62 E63

Q64 A65 E66 E67 V68 W69 R70 R71 R72 R73 V74 D75 S77 R78 R79 V80 G81 G82 A83 N84 R85 Q86 V87 A88 R89 E90 V91 R92 R93 R94 R95 Q96 Q97 Q98 S98 L99 A100 L101 R102 V103 L104 V105 Q106 A107 A108 N109 Q110 R111 R112 R113 R114 R115 G116 A117 E118 R119 I120 A121 E122 E123

L124 M125 D126 A127 A128 E129 G130 K131 G132 G133 A134 V135 K136 K137 K138 E139 D140 V141 E142 R143 M144 A145 E146 A147 N148 R149 R150 Y151 A152 H153 R154 R155 W156

• Molecule 41: 30S ribosomal protein S8

Chain BL: 56% 34% 8%

M1 L2 T3 D4 P5 I6 A7 D8 M9 L10 T11 T12 R13 I14 R15 A16 T17 T18 V19 Y20 R21 K22 E23 S23 T24 R25 D26 V27 P27 R28 A29 S29 R30 R31 R32 R33 E34 I35 L36 R37 R38 L39 A40 R41 E42 G43 A44 I45 K46 G47 Y48 E49 R50 V51 D52 V53 D54 G55 G56 P57 Y58 L59 R60

V61 V62 L63 M64 V65 G66 R67 R68 R69 Q70 G71 G72 F73 D74 F75 R76 R77 Q78 V79 R80 R81 H81 R82 R83 R84 R85 V86 S87 R88 R89 P89 Q90 Q91 D92 R93 R94 Y94 Y95 G96 V97 R98 E99 T100 P101 R102 V103 V104 R105 G106 L107 G108 T109 A110 T111 L112 S113 T114 S115 K116 G117 V118 L119 T120

D121 R122 E123 A124 R125 K126 L127 G128 G129 G130 G131 G132 E133 E134 C135 E136 V137 W138

• Molecule 42: 30S ribosomal protein S9

Chain BM: 61% 31% 6%

E2 Q3 Y4 Y5 G6 T7 G8 R9 R10 K11 E12 E13 A14 V14 A15 R16 V17 F18 F19 L19 R20 R21 F22 G22 R23 G24 K25 K26 V26 T27 V28 N29 R30 G31 Q32 R33 R34 N34 E35 Y36 F37 R38 Q38 R39 L40 V41 R42 R43 A44 A45 A46 L47 E48 V49 P49 L50 R51 R52 A52 V53 D54 A55 G55 L56 G57 H58 H59 D60 A61

Y62 I63 T64 V65 R66 G67 G68 G69 R70 S71 R72 G73 Q74 V74 D75 A76 I77 R78 R79 G80 R81 A82 R83 A84 K85 V86 Q87 Y88 N89 R90 P90 D91 Q92 R93 R94 A94 R95 L96 R97 R98 L99 G100 F101 L102 R103 R104 D105 A106 A107 R108 V108 V109 E110 R111 K112 K113 Y114 G115 K116 H117 K118 A119 R120 R121

A122 F123 Q124 Y125 S126 K127 R128

• Molecule 43: 30S ribosomal protein S10

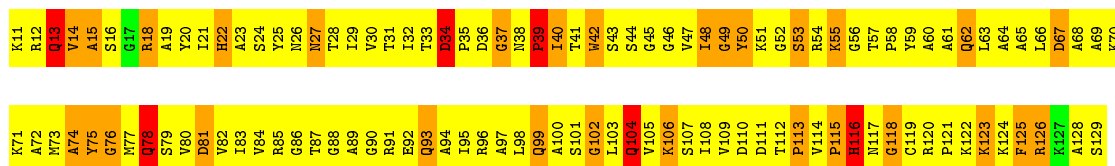
Chain BN: 55% 39%

K3 L4 I6 K7 L8 R9 G10 F11 D12 R13 H13 K14 T15 L16 D17 A18 S19 A20 Q21 Q22 I23 V24 E25 A26 A27 R28 R29 S30 G31 A32 Q33 Q34 S35 G36 P37 I38 R39 L40 P41 T42 R43 V44 R45 R46 F47 T48 V49 I50 R51 G52 P53 F54 K55 H56 K57 D58 S59 R60 E61 H62



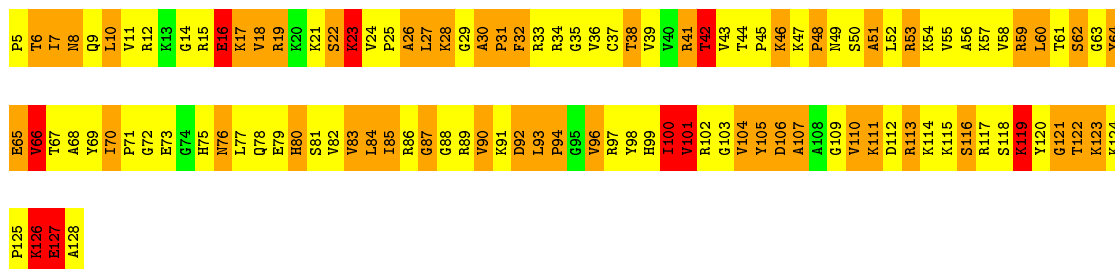
• Molecule 44: 30S ribosomal protein S11

Chain BO: . 69% 24% 5%



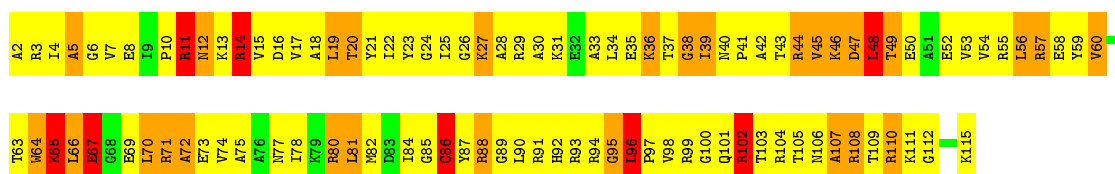
• Molecule 45: 30S ribosomal protein S12

Chain BP: 5% 49% 39% 7%



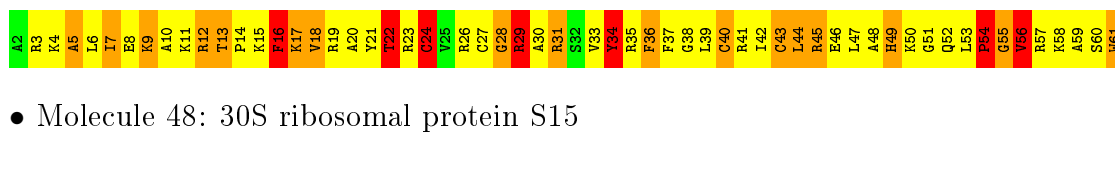
• Molecule 46: 30S ribosomal protein S13

Chain BQ: 10% 59% 25% 7%



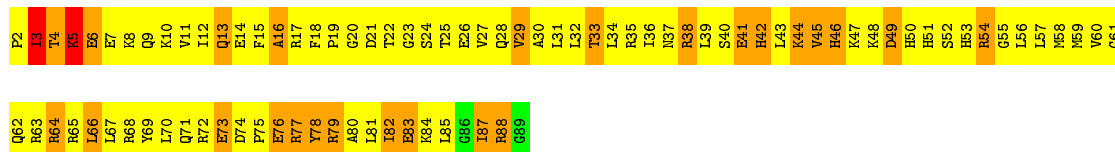
• Molecule 47: 30S ribosomal protein S14 type Z

Chain BR: 5% 55% 28% 12%

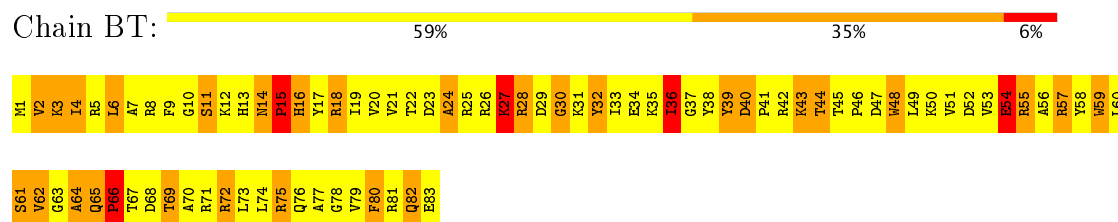


• Molecule 48: 30S ribosomal protein S15

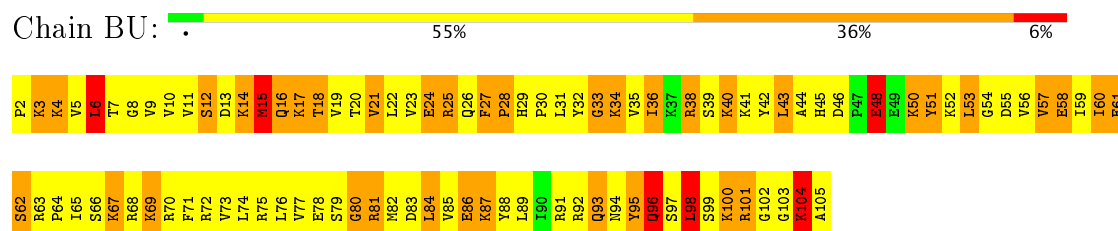
Chain BS: . 67% 28%



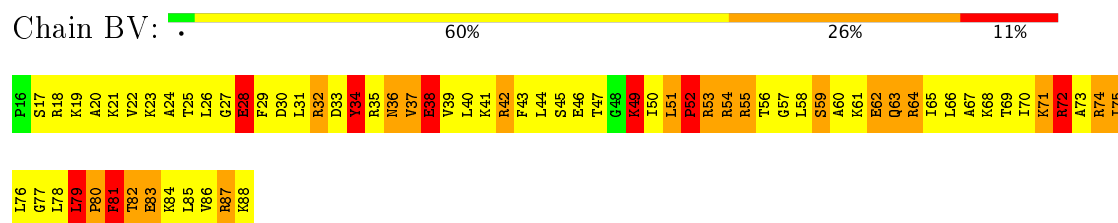
- Molecule 49: 30S ribosomal protein S16



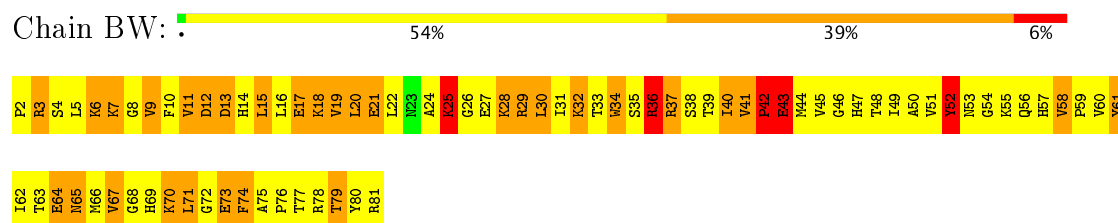
- Molecule 50: 30S ribosomal protein S17



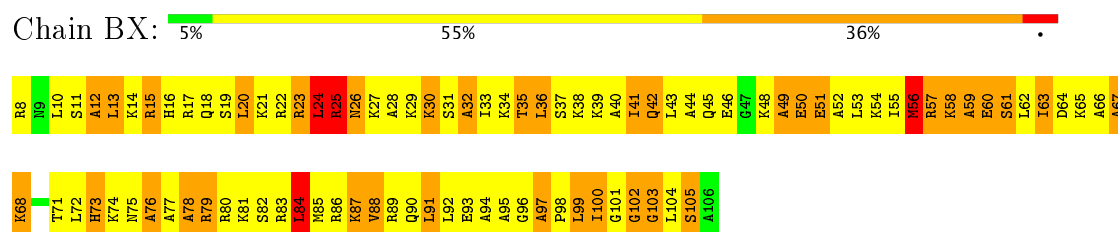
- Molecule 51: 30S ribosomal protein S18



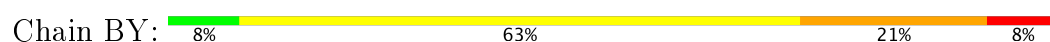
- Molecule 52: 30S ribosomal protein S19

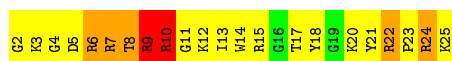


- Molecule 53: 30S ribosomal protein S20



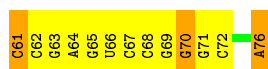
- Molecule 54: 30S ribosomal protein Thx





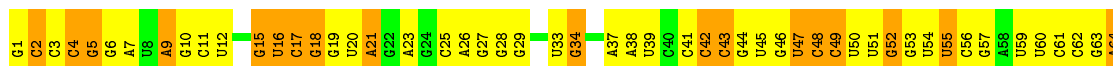
- Molecule 55: tRNA chain 1

Chain BC: 11% 57% 33%



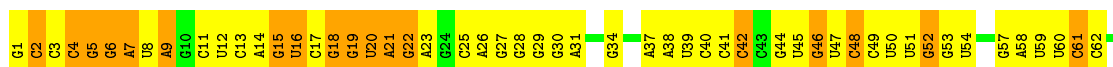
- Molecule 56: tRNA chain 2

Chain BD: 16% 48% 36%



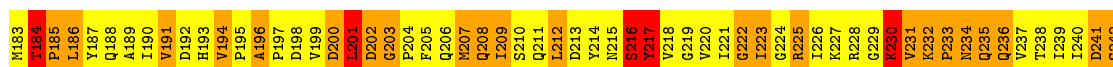
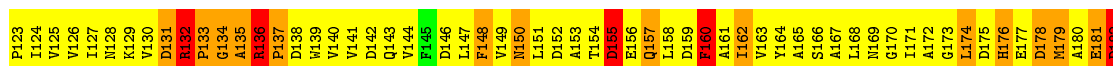
- Molecule 56: tRNA chain 2

Chain BE: 15% 55% 31%



- Molecule 57: GTP-binding protein

Chain BZ: 8% 54% 31% 6%



P305	E371	D432	Q493	B553
T306	N372	G433	G494	A554
S307	M373	K434	K495	V555
S308	R374	G435	A496	V556
	R375	R436	V497	L557
F310	E376	V437	A498	V558
F311	G377	R438	F499	P559
C312	F378	L439	A500	P560
C313	E379	D440	L501	L561
N314	L380	Y441	F502	N562
T315	A381	G442	G503	N563
S316	V382	I443	L504	T564
P317	S383	P444	Q505	L565
F318	R384	S445	D506	B566
C319	P385	R446	R507	Q567
G320	K386	G447	G508	A568
K321	V387	L448	K509	L569
E322	I388	T449	L510	B570
G323	F389	G450	F511	F571
K324	R390	F451	L512	L572
F325	E391	R452	G513	D573
V326	I392	H453	H514	D574
T327	D393	E454	G515	D575
S328	G394	F455	A516	B576
R329	R395	M456	B517	L577
Q330	K396	T457	V518	V578
I331	Q397	M458	Y519	B579
L332	E398	T459	B520	V580
D333	P399	S460	G521	T581
	Y400	G461	Q522	P582
E338	E401	T462	I523	T583
L339	N402	G463	I524	S584
V340	V403	L464	G525	L585
H341	T404	L465	I526	B586
	L405	Y466	H527	L587
V343	D406	S467	S528	B588
A344	Y407	T468	R529	K589
L345	E408	F469	S530	B590
R346	E409	S470	N531	B591
	Q410	H471	D532	L592
E351	H411	Y472	L533	T593
D352	Q412	D473	T534	
A353	G413	D474	V535	D596
D354	S414	V475	N536	B597
A355	V415	R476	C537	B598
F356	M416	P477	L538	B599
R357	Q417		T539	A600
V358	A418		G540	N601
S359	L419		K541	B602
G360			K542	A603
R361			L543	P604
G362	R422		T544	R605
E363	K423		Q494	
L364	G424		N485	
H365	D425		M546	
L366	L426		V437	
S367	K427		L488	
V368	N428		I489	
L369	M429		G550	
P431	N430		A551	
			D552	

4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	77127	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	CTFFIND3	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	73684	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: GCP, 8AN, NMY

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	AA	1.00	107/69678 (0.2%)	1.08	348/108758 (0.3%)
10	AL	0.92	1/942 (0.1%)	1.31	10/1268 (0.8%)
11	AM	0.71	0/1123	1.12	5/1493 (0.3%)
12	AN	0.72	0/1100	1.19	8/1470 (0.5%)
13	AO	0.70	0/974	1.06	2/1302 (0.2%)
14	AP	0.72	0/887	1.06	4/1180 (0.3%)
15	AQ	0.85	0/990	1.31	9/1325 (0.7%)
16	AR	0.76	0/982	1.08	0/1306
17	AS	0.87	1/790 (0.1%)	1.28	9/1057 (0.9%)
18	AT	0.66	0/886	1.04	1/1189 (0.1%)
19	AU	0.57	0/756	0.93	0/1015
2	AB	0.83	4/2954 (0.1%)	0.99	7/4606 (0.2%)
20	AV	0.54	0/857	1.05	2/1142 (0.2%)
21	AW	0.66	0/1467	1.11	7/1992 (0.4%)
22	AX	0.65	0/679	1.04	1/902 (0.1%)
23	AY	0.59	0/569	0.88	0/751
24	AZ	0.59	0/474	1.10	2/635 (0.3%)
25	Aa	0.84	1/594 (0.2%)	1.31	8/795 (1.0%)
26	Ab	0.72	0/459	1.16	3/621 (0.5%)
27	Ac	0.85	1/433 (0.2%)	1.36	5/576 (0.9%)
28	Ad	0.73	0/438	1.01	0/575
29	Ae	0.59	0/523	1.14	5/690 (0.7%)
3	AC	0.54	0/1772	0.87	0/2383
30	Af	0.59	0/310	1.08	1/407 (0.2%)
31	AI	0.50	1/751 (0.1%)	0.82	4/1042 (0.4%)
32	AJ	0.52	0/1012	0.64	8/1373 (0.6%)
34	BA	0.92	26/36437 (0.1%)	1.10	139/56865 (0.2%)
35	BF	0.65	0/1935	1.00	4/2609 (0.2%)
36	BG	0.55	0/1636	0.92	4/2205 (0.2%)
37	BH	0.64	1/1733 (0.1%)	0.98	3/2318 (0.1%)
38	BI	0.63	0/1162	1.01	3/1564 (0.2%)
39	BJ	0.60	0/856	0.95	0/1154

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
4	AD	0.72	2/2174 (0.1%)	1.19	13/2927 (0.4%)
40	BK	0.57	0/1276	0.90	3/1709 (0.2%)
41	BL	0.62	0/1136	1.01	3/1527 (0.2%)
42	BM	0.54	0/1029	0.83	0/1379
43	BN	0.48	0/807	0.89	1/1085 (0.1%)
44	BO	0.62	0/900	0.98	0/1213
45	BP	0.60	0/986	1.00	3/1320 (0.2%)
46	BQ	0.33	0/924	0.45	2/1238 (0.2%)
47	BR	0.55	0/501	0.97	1/664 (0.2%)
48	BS	0.62	0/745	0.95	0/992
49	BT	0.62	0/716	0.95	1/963 (0.1%)
5	AE	0.75	0/1611	1.16	13/2171 (0.6%)
50	BU	0.68	1/870 (0.1%)	0.99	2/1159 (0.2%)
51	BV	0.59	0/603	1.01	1/799 (0.1%)
52	BW	0.53	1/661 (0.2%)	1.34	5/890 (0.6%)
53	BX	0.65	0/765	1.00	2/1007 (0.2%)
54	BY	0.45	0/212	0.80	0/277
55	BC	0.36	0/1809	0.67	0/2819
56	BD	0.37	0/1784	0.68	0/2780
56	BE	0.35	0/1784	0.70	0/2780
57	BZ	0.37	0/4678	0.50	16/6310 (0.3%)
6	AF	0.64	0/1660	1.03	4/2247 (0.2%)
7	AG	0.62	0/1507	1.06	4/2027 (0.2%)
8	AH	0.59	0/1354	0.98	4/1831 (0.2%)
9	AK	0.78	1/1140 (0.1%)	1.16	8/1537 (0.5%)
All	All	0.86	148/167791 (0.1%)	1.05	688/250219 (0.3%)

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	AA	0	432
12	AN	0	1
15	AQ	0	1
17	AS	0	1
2	AB	0	17
25	Aa	0	1
26	Ab	0	1
3	AC	0	1
31	AI	0	2

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Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
34	BA	0	170
37	BH	0	1
39	BJ	0	1
44	BO	0	1
47	BR	0	1
5	AE	0	1
6	AF	0	1
9	AK	0	1
All	All	0	634

The worst 5 of 148 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AA	1060	U	O3'-P	-80.27	0.64	1.61
34	BA	1317	C	O3'-P	-70.10	0.77	1.61
1	AA	1203	G	O3'-P	-34.75	1.19	1.61
34	BA	1167	A	O3'-P	20.86	1.86	1.61
1	AA	2500	U	C4-O4	18.56	1.38	1.23

The worst 5 of 688 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	BA	1064	G	N1-C2-N2	-71.66	51.71	116.20
34	BA	1064	G	N3-C2-N2	57.63	160.24	119.90
34	BA	1317	C	P-O3'-C3'	-48.78	61.17	119.70
34	BA	1317	C	O3'-P-O5'	30.58	162.11	104.00
1	AA	1060	U	O3'-P-O5'	28.68	158.49	104.00

There are no chirality outliers.

5 of 634 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	14	A	Sidechain
1	AA	25	U	Sidechain
1	AA	3	U	Sidechain
1	AA	31	C	Sidechain
1	AA	9	U	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	AA	62218	0	31250	16189	0
2	AB	2641	0	1337	612	0
3	AC	1742	0	1779	1073	0
4	AD	2124	0	2207	1489	0
5	AE	1578	0	1647	1111	0
6	AF	1625	0	1666	824	0
7	AG	1482	0	1546	878	0
8	AH	1328	0	1407	716	0
9	AK	1113	0	1183	775	0
10	AL	932	0	992	735	0
11	AM	1106	0	1183	771	0
12	AN	1080	0	1127	743	0
13	AO	960	0	1021	592	0
14	AP	877	0	938	509	0
15	AQ	976	0	1031	647	0
16	AR	964	0	1022	730	0
17	AS	779	0	852	567	0
18	AT	876	0	941	442	0
19	AU	742	0	800	355	0
20	AV	844	0	930	431	0
21	AW	1435	0	1463	733	0
22	AX	670	0	700	380	0
23	AY	567	0	621	306	0
24	AZ	469	0	518	322	0
25	Aa	581	0	577	0	0
26	Ab	445	0	459	0	0
27	Ac	426	0	452	0	0
28	Ad	430	0	480	0	0
29	Ae	515	0	587	0	0
30	Af	307	0	335	0	0
31	AI	752	0	363	165	0
32	AJ	993	0	1019	739	0
33	Ag	620	0	132	0	0
34	BA	32554	0	16390	7456	0
35	BF	1900	0	1951	1054	0
36	BG	1612	0	1677	720	0
37	BH	1703	0	1763	850	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	BI	1146	0	1207	586	0
39	BJ	843	0	857	393	0
40	BK	1257	0	1296	564	0
41	BL	1116	0	1177	722	0
42	BM	1010	0	1035	505	0
43	BN	794	0	840	371	0
44	BO	885	0	904	471	0
45	BP	970	0	1057	519	0
46	BQ	914	0	954	640	0
47	BR	492	0	529	283	0
48	BS	734	0	771	348	0
49	BT	700	0	720	351	0
50	BU	857	0	930	454	0
51	BV	597	0	666	373	0
52	BW	647	0	653	536	0
53	BX	763	0	857	410	0
54	BY	208	0	221	88	0
55	BC	1619	0	819	220	0
56	BD	1597	0	802	300	0
56	BE	1597	0	799	357	0
57	BZ	4610	0	4492	2673	0
58	AA	42	0	46	25	0
58	BA	42	0	46	15	0
59	AA	44	0	18	80	0
60	BZ	32	0	14	38	0
All	All	155482	0	106056	49352	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 197.

The worst 5 of 49352 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)
32:AJ:112:MET:SD	32:AJ:122:ALA:HB2	1.28	1.70
3:AC:171:ILE:CD1	3:AC:192:PHE:CZ	1.75	1.70
34:BA:1226:C:C4	46:BQ:104:ARG:HG3	1.16	1.69
1:AA:716:A:C2	48:BS:44:LYS:HG3	1.30	1.67
32:AJ:75:SER:HB3	32:AJ:130:SER:CB	1.24	1.66

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	AC	220/228 (96%)	153 (70%)	39 (18%)	28 (13%)	0	7
4	AD	270/272 (99%)	125 (46%)	59 (22%)	86 (32%)	0	0
5	AE	204/206 (99%)	117 (57%)	31 (15%)	56 (28%)	0	0
6	AF	206/208 (99%)	109 (53%)	46 (22%)	51 (25%)	0	1
7	AG	180/182 (99%)	79 (44%)	47 (26%)	54 (30%)	0	0
8	AH	172/174 (99%)	80 (46%)	46 (27%)	46 (27%)	0	1
9	AK	137/139 (99%)	64 (47%)	28 (20%)	45 (33%)	0	0
10	AL	120/122 (98%)	59 (49%)	23 (19%)	38 (32%)	0	0
11	AM	143/145 (99%)	57 (40%)	36 (25%)	50 (35%)	0	0
12	AN	134/136 (98%)	49 (37%)	33 (25%)	52 (39%)	0	0
13	AO	115/117 (98%)	57 (50%)	39 (34%)	19 (16%)	0	4
14	AP	108/110 (98%)	48 (44%)	28 (26%)	32 (30%)	0	0
15	AQ	115/117 (98%)	52 (45%)	26 (23%)	37 (32%)	0	0
16	AR	115/117 (98%)	35 (30%)	50 (44%)	30 (26%)	0	1
17	AS	99/101 (98%)	52 (52%)	19 (19%)	28 (28%)	0	0
18	AT	108/110 (98%)	63 (58%)	24 (22%)	21 (19%)	0	3
19	AU	92/94 (98%)	57 (62%)	16 (17%)	19 (21%)	0	2
20	AV	108/110 (98%)	43 (40%)	32 (30%)	33 (31%)	0	0
21	AW	178/180 (99%)	96 (54%)	43 (24%)	39 (22%)	0	2
22	AX	83/85 (98%)	52 (63%)	21 (25%)	10 (12%)	0	7
23	AY	65/67 (97%)	36 (55%)	20 (31%)	9 (14%)	0	6
24	AZ	57/59 (97%)	34 (60%)	8 (14%)	15 (26%)	0	1
25	Aa	69/71 (97%)	23 (33%)	15 (22%)	31 (45%)	0	0
26	Ab	55/57 (96%)	14 (26%)	19 (34%)	22 (40%)	0	0
27	Ac	47/49 (96%)	14 (30%)	7 (15%)	26 (55%)	0	0

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	Ad	47/49 (96%)	20 (43%)	12 (26%)	15 (32%)	0	0
29	Ae	62/64 (97%)	23 (37%)	17 (27%)	22 (36%)	0	0
30	Af	35/37 (95%)	20 (57%)	5 (14%)	10 (29%)	0	0
31	AI	151/153 (99%)	89 (59%)	33 (22%)	29 (19%)	0	3
32	AJ	132/134 (98%)	56 (42%)	44 (33%)	32 (24%)	0	1
35	BF	232/234 (99%)	114 (49%)	41 (18%)	77 (33%)	0	0
36	BG	204/206 (99%)	107 (52%)	46 (22%)	51 (25%)	0	1
37	BH	206/208 (99%)	95 (46%)	58 (28%)	53 (26%)	0	1
38	BI	148/150 (99%)	93 (63%)	38 (26%)	17 (12%)	0	8
39	BJ	99/101 (98%)	58 (59%)	19 (19%)	22 (22%)	0	2
40	BK	153/155 (99%)	73 (48%)	45 (29%)	35 (23%)	0	2
41	BL	136/138 (99%)	68 (50%)	35 (26%)	33 (24%)	0	1
42	BM	125/127 (98%)	62 (50%)	33 (26%)	30 (24%)	0	2
43	BN	96/98 (98%)	52 (54%)	20 (21%)	24 (25%)	0	1
44	BO	117/119 (98%)	65 (56%)	29 (25%)	23 (20%)	0	3
45	BP	122/124 (98%)	50 (41%)	30 (25%)	42 (34%)	0	0
46	BQ	112/114 (98%)	64 (57%)	28 (25%)	20 (18%)	0	3
47	BR	58/60 (97%)	24 (41%)	16 (28%)	18 (31%)	0	0
48	BS	86/88 (98%)	36 (42%)	35 (41%)	15 (17%)	0	3
49	BT	81/83 (98%)	42 (52%)	24 (30%)	15 (18%)	0	3
50	BU	102/104 (98%)	62 (61%)	23 (22%)	17 (17%)	0	4
51	BV	71/73 (97%)	26 (37%)	26 (37%)	19 (27%)	0	1
52	BW	78/80 (98%)	30 (38%)	25 (32%)	23 (30%)	0	0
53	BX	97/99 (98%)	38 (39%)	32 (33%)	27 (28%)	0	0
54	BY	22/24 (92%)	9 (41%)	6 (27%)	7 (32%)	0	0
57	BZ	603/605 (100%)	280 (46%)	200 (33%)	123 (20%)	0	2
All	All	6575/6683 (98%)	3224 (49%)	1675 (26%)	1676 (26%)	0	1

5 of 1676 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AC	35	ALA
3	AC	39	GLU

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Mol	Chain	Res	Type
3	AC	54	SER
3	AC	61	THR
3	AC	72	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	
3	AC	180/180 (100%)	151 (84%)	29 (16%)	3	18
4	AD	215/215 (100%)	153 (71%)	62 (29%)	0	3
5	AE	166/166 (100%)	102 (61%)	64 (39%)	0	0
6	AF	164/164 (100%)	105 (64%)	59 (36%)	0	1
7	AG	156/156 (100%)	112 (72%)	44 (28%)	0	3
8	AH	143/143 (100%)	108 (76%)	35 (24%)	1	5
9	AK	118/118 (100%)	79 (67%)	39 (33%)	0	2
10	AL	100/100 (100%)	69 (69%)	31 (31%)	0	2
11	AM	111/111 (100%)	71 (64%)	40 (36%)	0	1
12	AN	106/106 (100%)	65 (61%)	41 (39%)	0	0
13	AO	100/100 (100%)	71 (71%)	29 (29%)	0	3
14	AP	87/87 (100%)	63 (72%)	24 (28%)	0	4
15	AQ	105/105 (100%)	68 (65%)	37 (35%)	0	1
16	AR	93/93 (100%)	64 (69%)	29 (31%)	0	2
17	AS	82/82 (100%)	57 (70%)	25 (30%)	0	2
18	AT	90/90 (100%)	64 (71%)	26 (29%)	0	3
19	AU	76/76 (100%)	57 (75%)	19 (25%)	1	5
20	AV	91/91 (100%)	72 (79%)	19 (21%)	1	8
21	AW	159/159 (100%)	120 (76%)	39 (24%)	1	5
22	AX	67/67 (100%)	51 (76%)	16 (24%)	1	6
23	AY	62/62 (100%)	44 (71%)	18 (29%)	0	3

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	AZ	51/51 (100%)	36 (71%)	15 (29%)	0	3
25	Aa	63/63 (100%)	45 (71%)	18 (29%)	0	3
26	Ab	50/50 (100%)	31 (62%)	19 (38%)	0	1
27	Ac	48/48 (100%)	32 (67%)	16 (33%)	0	2
28	Ad	42/42 (100%)	29 (69%)	13 (31%)	0	2
29	Ae	54/54 (100%)	44 (82%)	10 (18%)	2	13
30	Af	34/34 (100%)	29 (85%)	5 (15%)	3	21
32	AJ	101/101 (100%)	71 (70%)	30 (30%)	0	3
35	BF	202/202 (100%)	138 (68%)	64 (32%)	0	2
36	BG	160/160 (100%)	123 (77%)	37 (23%)	1	6
37	BH	180/180 (100%)	131 (73%)	49 (27%)	0	4
38	BI	115/115 (100%)	78 (68%)	37 (32%)	0	2
39	BJ	90/90 (100%)	61 (68%)	29 (32%)	0	2
40	BK	126/126 (100%)	93 (74%)	33 (26%)	0	4
41	BL	119/119 (100%)	86 (72%)	33 (28%)	0	4
42	BM	98/98 (100%)	73 (74%)	25 (26%)	0	5
43	BN	88/88 (100%)	67 (76%)	21 (24%)	1	6
44	BO	90/90 (100%)	73 (81%)	17 (19%)	2	11
45	BP	104/104 (100%)	81 (78%)	23 (22%)	1	8
46	BQ	92/92 (100%)	67 (73%)	25 (27%)	0	4
47	BR	49/49 (100%)	36 (74%)	13 (26%)	0	4
48	BS	79/79 (100%)	64 (81%)	15 (19%)	2	11
49	BT	72/72 (100%)	49 (68%)	23 (32%)	0	2
50	BU	96/96 (100%)	67 (70%)	29 (30%)	0	3
51	BV	64/64 (100%)	48 (75%)	16 (25%)	1	5
52	BW	71/71 (100%)	52 (73%)	19 (27%)	0	4
53	BX	76/76 (100%)	59 (78%)	17 (22%)	1	7
54	BY	19/19 (100%)	17 (90%)	2 (10%)	8	33
57	BZ	486/514 (95%)	338 (70%)	148 (30%)	0	2
All	All	5390/5418 (100%)	3864 (72%)	1526 (28%)	2	3

5 of 1526 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
21	AW	179	ASP
35	BF	20	GLU
57	BZ	115	LYS
23	AY	12	SER
26	Ab	51	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 192 such sidechains are listed below:

Mol	Chain	Res	Type
29	Ae	35	GLN
36	BG	170	GLN
57	BZ	150	ASN
30	Af	36	GLN
35	BF	204	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	2881/2889 (99%)	1265 (43%)	253 (8%)
2	AB	122/123 (99%)	46 (37%)	3 (2%)
34	BA	1514/1515 (99%)	484 (31%)	140 (9%)
55	BC	75/76 (98%)	26 (34%)	0
56	BD	74/75 (98%)	31 (41%)	2 (2%)
56	BE	74/75 (98%)	23 (31%)	1 (1%)
All	All	4740/4753 (99%)	1875 (39%)	399 (8%)

5 of 1875 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	13	A
1	AA	14	A
1	AA	15	G
1	AA	20	C
1	AA	26	G

5 of 399 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	2021	C
1	AA	2503	A
34	BA	1239	A

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Mol	Chain	Res	Type
1	AA	2047	U
1	AA	2240	C

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

5 ligands are modelled in this entry.

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
58	NMY	AA	3001	-	45,45,45	0.51	0	59,67,67	1.20	7 (11%)
59	8AN	AA	3002	1,56	17,24,25	1.18	1 (5%)	14,35,38	2.25	5 (35%)
59	8AN	AA	3003	1,56,22	17,24,25	1.17	1 (5%)	14,35,38	2.25	5 (35%)
58	NMY	BA	1601	-	45,45,45	0.51	0	59,67,67	1.10	6 (10%)
60	GCP	BZ	701	-	25,34,34	2.78	9 (36%)	28,54,54	1.22	2 (7%)

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
58	NMY	AA	3001	-	-	0/18/94/94	1/4/4/4
59	8AN	AA	3002	1,56	-	0/3/25/26	0/3/3/3
59	8AN	AA	3003	1,56,22	-	0/3/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	NMY	BA	1601	-	-	0/18/94/94	0/4/4/4
60	GCP	BZ	701	-	-	0/18/38/38	0/3/3/3

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	BZ	701	GCP	C4-N9	-10.39	1.33	1.47
60	BZ	701	GCP	C8-N9	-3.87	1.35	1.46
60	BZ	701	GCP	PG-O2G	-2.75	1.48	1.54
60	BZ	701	GCP	C5-C6	-2.45	1.48	1.53
60	BZ	701	GCP	C2-N1	-2.18	1.35	1.44

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	AA	3003	8AN	N3-C2-N1	-5.93	123.69	128.86
59	AA	3002	8AN	N3-C2-N1	-5.89	123.73	128.86
60	BZ	701	GCP	PA-O3A-PB	-3.69	120.51	132.39
59	AA	3003	8AN	C4-C5-N7	-2.90	106.61	109.41
59	AA	3002	8AN	C4-C5-N7	-2.89	106.62	109.41

There are no chirality outliers.

There are no torsion outliers.

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	AA	3001	NMY	C10-C11-C12-C7-C8-C9

5 monomers are involved in 158 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	AA	3001	NMY	25	0
59	AA	3002	8AN	45	0
59	AA	3003	8AN	35	0
58	BA	1601	NMY	15	0
60	BZ	701	GCP	38	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	AA	7
34	BA	3
33	Ag	2
3	AC	2
31	AI	1

The worst 5 of 15 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Ag	30:UNK	C	123:UNK	N	31.39
1	AA	164:U	O3'	171:G	P	7.68
1	AA	2893:G	O3'	2894:G	P	5.34
1	BA	1308:U	O3'	1309:G	P	3.99
1	Ag	153:UNK	C	154:UNK	N	3.23