



wwPDB EM Map/Model Validation Report ⓘ

May 19, 2016 – 08:33 PM EDT

PDB ID : 4UJC
EMDB ID: : EMD-2683
Title : mammalian 80S HCV-IRES initiation complex with eIF5B POST-like state
Authors : Yamamoto, H.; Unbehaun, A.; Loerke, J.; Behrmann, E.; Marianne, C.;
Burger, J.; Mielke, T.; Spahn, C.M.T.
Deposited on : 2014-06-18
Resolution : 9.50 Å(reported)
Based on PDB ID : 4CXC

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could
stem from errors in the original structure(s) used in the fitting.

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

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>

MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

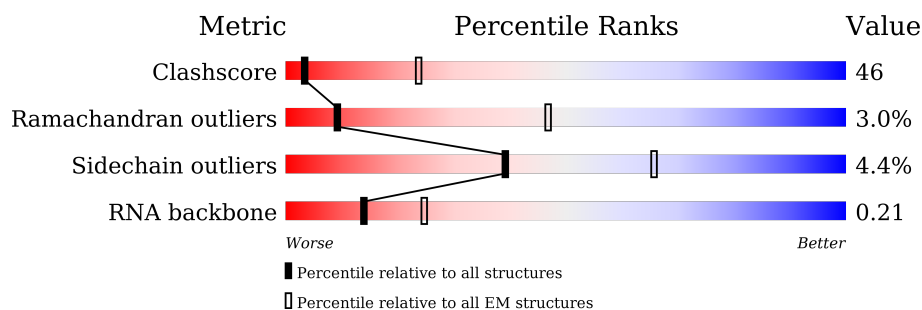
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 9.50 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.










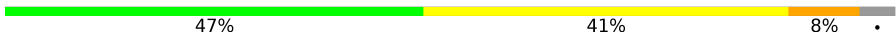

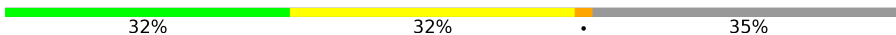


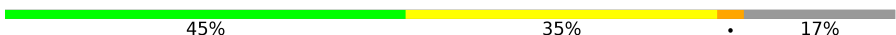










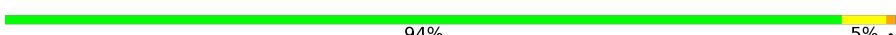

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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	76	13% 63% 22% .
2	AB	627	29% 58% 9% . .
3	AC	504	. 12% 23% 15% 48%
4	A2	5025	7% 28% 36% . 28%
5	A3	194	8% 37% 35% . 19%
6	A4	121	12% 36% 50% . .
7	BA	257	55% 40% . .
8	BB	403	56% 37% 5% .






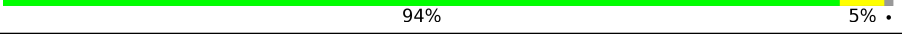


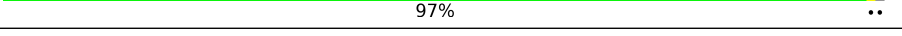
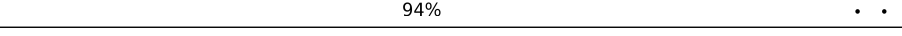
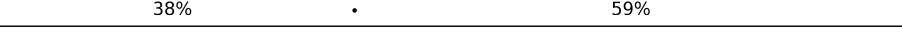
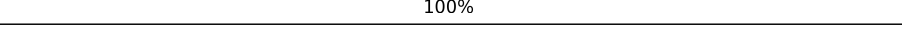
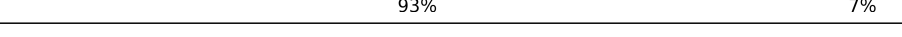
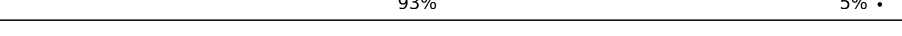


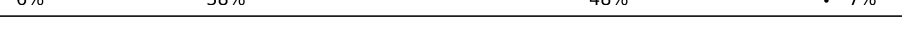

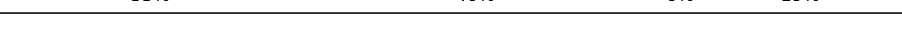




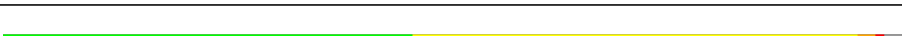

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Mol	Chain	Length	Quality of chain
9	BC	427	
10	BD	297	
11	BE	158	
12	BF	248	
13	BG	266	
14	BH	192	
15	BI	214	
16	BJ	178	
17	BL	211	
18	BM	215	
19	BN	204	
20	BO	203	
21	BP	184	
22	BQ	188	
23	BR	196	
24	BS	176	
25	BT	160	
26	BU	128	
27	BV	140	
28	BW	157	
29	BX	156	
30	BY	145	
31	BZ	136	
32	Ba	148	
33	Bb	159	











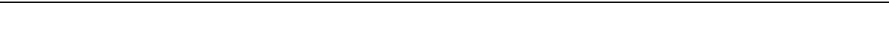

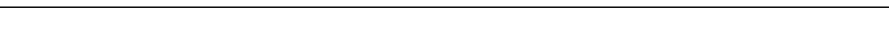
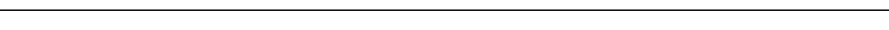











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Mol	Chain	Length	Quality of chain
34	Bc	115	
35	Bd	125	
36	Be	135	
37	Bf	110	
38	Bg	117	
39	Bh	123	
40	Bi	105	
41	Bj	97	
42	Bk	70	
43	Bl	51	
44	Bm	128	
45	Bn	25	
46	Bo	106	
47	Bp	92	
48	Bt	137	
49	Bu	210	
50	C1	1869	
51	CA	263	
52	CB	264	
53	CC	293	
54	CD	243	
55	CE	263	
56	CF	204	
57	CG	249	
58	CH	194	

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Mol	Chain	Length	Quality of chain
59	CI	208	
60	CJ	194	
61	CK	165	
62	CL	158	
63	CM	132	
64	CN	151	
65	CO	151	
66	CP	145	
67	CQ	146	
68	CR	135	
69	CS	152	
70	CT	145	
71	CU	119	
72	CV	83	
73	CW	130	
74	CX	143	
75	CY	133	
76	CZ	125	
77	Ca	115	
78	Cb	84	
79	Cc	69	
80	Cd	56	
81	Ce	59	
82	Cf	156	
83	Cg	317	

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 223911 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 TRNA.

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

- Molecule 2 is a protein called EIF5B.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	611	Total	C	N	O	S	0	0
			4846	3084	834	906	22		

- Molecule 3 is a RNA chain called HCV-IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	261	Total	C	N	O	P	0	0
			5574	2485	1001	1828	260		

- Molecule 4 is a RNA chain called 28S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A2	3616	Total	C	N	O	P	0	0
			77488	34508	14153	25212	3615		

- Molecule 5 is a RNA chain called 5.8S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A3	157	Total	C	N	O	P	0	0
			3334	1489	587	1102	156		

- Molecule 6 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A4	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

- Molecule 7 is a protein called 60S RIBOSOMAL PROTEIN L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	BA	247	Total	C	N	O	S	0	1
			1888	1183	388	311	6		

- Molecule 8 is a protein called 60S RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	BB	396	Total	C	N	O	S	0	1
			3190	2030	601	545	14		

- Molecule 9 is a protein called 60S RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	BC	364	Total	C	N	O	S	0	1
			2889	1817	578	480	14		

- Molecule 10 is a protein called 60S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	BD	290	Total	C	N	O	S	0	0
			2362	1489	431	428	14		

- Molecule 11 is a protein called 60S RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	BE	158	Total	C	N	O		0	0
			1287	834	238	215			

- Molecule 12 is a protein called 60S RIBOSOMAL PROTEIN L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	BF	234	Total	C	N	O	S	0	0
			1950	1252	376	313	9		

- Molecule 13 is a protein called 60S RIBOSOMAL PROTEIN L7A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	BG	235	Total	C	N	O	S	0	1
			1881	1197	363	317	4		

- Molecule 14 is a protein called 60S RIBOSOMAL PROTEIN L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	BH	192	Total	C	N	O	S	0	0
			1536	965	286	279	6		

- Molecule 15 is a protein called 60S RIBOSOMAL PROTEIN L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	BI	196	Total	C	N	O	S	0	0
			1605	1022	308	263	12		

- Molecule 16 is a protein called 60S RIBOSOMAL PROTEIN L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	BJ	170	Total	C	N	O	S	0	0
			1363	861	254	242	6		

- Molecule 17 is a protein called 60S RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	BL	200	Total	C	N	O	S	0	1
			1617	1013	335	265	4		

- Molecule 18 is a protein called 60S RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	BM	140	Total	C	N	O	S	0	1
			1139	730	219	183	7		

- Molecule 19 is a protein called 60S RIBOSOMAL PROTEIN L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	BN	204	Total	C	N	O	S	0	0
			1709	1077	360	267	5		

- Molecule 20 is a protein called 60S RIBOSOMAL PROTEIN L13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	BO	196	Total	C	N	O	S	0	1
			1607	1034	316	252	5		

- Molecule 21 is a protein called 60S RIBOSOMAL PROTEIN L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	BP	153	Total	C	N	O	S	0	1
			1234	771	241	213	9		

- Molecule 22 is a protein called 60S RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BQ	184	Total	C	N	O	S	0	0
			1494	933	311	245	5		

- Molecule 23 is a protein called 60S RIBOSOMAL PROTEIN L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	BR	183	Total	C	N	O	S	0	1
			1526	943	331	242	10		

- Molecule 24 is a protein called 60S RIBOSOMAL PROTEIN L18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BS	173	Total	C	N	O	S	0	0
			1439	916	280	233	10		

- Molecule 25 is a protein called 60S RIBOSOMAL PROTEIN L21.

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

- Molecule 26 is a protein called 60S RIBOSOMAL PROTEIN L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BU	102	Total	C	N	O	S	0	1
			827	529	146	150	2		

- Molecule 27 is a protein called 60S RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BV	128	Total	C	N	O	S	0	0
			964	610	181	168	5		

- Molecule 28 is a protein called 60S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BW	64	Total	C	N	O	S	0	1
			529	337	104	85	3		

- Molecule 29 is a protein called 60S RIBOSOMAL PROTEIN L23A.

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

- Molecule 30 is a protein called 60S RIBOSOMAL PROTEIN L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BY	128	Total	C	N	O	S	0	1
			1065	668	217	177	3		

- Molecule 31 is a protein called 60S RIBOSOMAL PROTEIN L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BZ	136	Total	C	N	O	S	0	0
			1115	719	209	183	4		

- Molecule 32 is a protein called 60S RIBOSOMAL PROTEIN L27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ba	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 33 is a protein called 60S RIBOSOMAL PROTEIN L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Bb	69	Total	C	N	O	S	0	1
			560	344	123	90	3		

- Molecule 34 is a protein called 60S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Bc	104	Total	C	N	O	S	0	1
			802	508	142	145	7		

- Molecule 35 is a protein called 60S RIBOSOMAL PROTEIN L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Bd	109	Total	C	N	O	S	0	0
			905	570	174	159	2		

- Molecule 36 is a protein called 60S RIBOSOMAL PROTEIN L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Be	128	Total	C	N	O	S	0	1
			1053	664	219	165	5		

- Molecule 37 is a protein called 60S RIBOSOMAL PROTEIN L35A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Bf	107	Total	C	N	O	S	0	0
			866	550	172	141	3		

- Molecule 38 is a protein called 60S RIBOSOMAL PROTEIN L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Bg	115	Total	C	N	O	S	0	1
			907	566	188	147	6		

- Molecule 39 is a protein called 60S RIBOSOMAL PROTEIN UL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Bh	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 40 is a protein called 60S RIBOSOMAL PROTEIN L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Bi	97	Total	C	N	O	S	0	1
			783	488	168	122	5		

- Molecule 41 is a protein called 60S RIBOSOMAL PROTEIN L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Bj	85	Total	C	N	O	S	0	1
			690	423	153	109	5		

- Molecule 42 is a protein called 60S RIBOSOMAL PROTEIN L38.

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

- Molecule 43 is a protein called 60S RIBOSOMAL PROTEIN L39.

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

- Molecule 44 is a protein called UBIQUITIN-60S RIBOSOMAL PROTEIN L40.

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

- Molecule 45 is a protein called 60S RIBOSOMAL PROTEIN L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Bn	25	Total	C	N	O	S	0	0
			240	145	64	28	3		

- Molecule 46 is a protein called 60S RIBOSOMAL PROTEIN L36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Bo	106	Total	C	N	O	S	0	0
			871	547	176	141	7		

- Molecule 47 is a protein called 60S RIBOSOMAL PROTEIN L37A.

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

- Molecule 48 is a protein called 60S RIBOSOMAL PROTEIN L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Bt	130	Total	C	N	O	S	0	1
			1043	646	220	172	5		

- Molecule 49 is a protein called 60S RIBOSOMAL PROTEIN L10A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Bu	210	Total	C	N	O	S	0	0
			1622	990	278	348	6		

- Molecule 50 is a RNA chain called 18S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	C1	1742	Total	C	N	O	P	0	0
			37159	16589	6665	12164	1741		

- Molecule 51 is a protein called 40S RIBOSOMAL PROTEIN US2.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	CA	218	Total	C	N	O	S	0	0
			1719	1091	301	319	8		

- Molecule 52 is a protein called 40S RIBOSOMAL PROTEIN ES1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	CB	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 53 is a protein called 40S RIBOSOMAL PROTEIN US5.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	CC	222	Total	C	N	O	S	0	0
			1724	1114	296	304	10		

- Molecule 54 is a protein called 40S RIBOSOMAL PROTEIN US3.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	CD	212	Total	C	N	O	S	0	0
			1646	1050	299	290	7		

- Molecule 55 is a protein called 40S RIBOSOMAL PROTEIN ES4.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	CE	257	Total	C	N	O	S	0	0
			2031	1298	381	344	8		

- Molecule 56 is a protein called 40S RIBOSOMAL PROTEIN US7.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	CF	188	Total	C	N	O	S	0	0
			1486	930	283	266	7		

- Molecule 57 is a protein called 40S RIBOSOMAL PROTEIN ES6.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	CG	232	Total	C	N	O	S	0	0
			1884	1176	379	322	7		

- Molecule 58 is a protein called 40S RIBOSOMAL PROTEIN ES7.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	CH	191	Total	C	N	O	S	0	0
			1535	978	282	274	1		

- Molecule 59 is a protein called 40S RIBOSOMAL PROTEIN ES8.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	CI	207	Total	C	N	O	S	0	0
			1695	1064	334	292	5		

- Molecule 60 is a protein called 40S RIBOSOMAL PROTEIN US4.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	CJ	179	Total	C	N	O	S	0	0
			1495	953	299	241	2		

- Molecule 61 is a protein called 40S RIBOSOMAL PROTEIN ES10.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	CK	94	Total	C	N	O	S	0	0
			791	519	138	129	5		

- Molecule 62 is a protein called 40S RIBOSOMAL PROTEIN US17.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	CL	146	Total	C	N	O	S	0	0
			1199	764	224	205	6		

- Molecule 63 is a protein called 40S RIBOSOMAL PROTEIN ES12.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	CM	120	Total	C	N	O	S	0	0
			931	584	164	174	9		

- Molecule 64 is a protein called 40S RIBOSOMAL PROTEIN US15.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	CN	150	Total	C	N	O	S	0	0
			1207	773	229	204	1		

- Molecule 65 is a protein called 40S RIBOSOMAL PROTEIN US11.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	CO	137	Total	C	N	O	S	0	0
			1023	627	200	190	6		

- Molecule 66 is a protein called 40S RIBOSOMAL PROTEIN US19.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	CP	118	Total	C	N	O	S	0	0
			981	625	183	166	7		

- Molecule 67 is a protein called 40S RIBOSOMAL PROTEIN US9.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	CQ	139	Total	C	N	O	S	0	0
			1108	704	210	191	3		

- Molecule 68 is a protein called 40S RIBOSOMAL PROTEIN ES17.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	CR	109	Total	C	N	O	S	0	0
			893	561	170	159	3		

- Molecule 69 is a protein called 40S RIBOSOMAL PROTEIN US13.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	CS	142	Total	C	N	O	S	0	0
			1172	736	236	199	1		

- Molecule 70 is a protein called 40S RIBOSOMAL PROTEIN ES19.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	CT	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

- Molecule 71 is a protein called 40S RIBOSOMAL PROTEIN US10.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	CU	101	Total	C	N	O	S	0	0
			803	502	153	144	4		

- Molecule 72 is a protein called 40S RIBOSOMAL PROTEIN ES21.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	CV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 73 is a protein called 40S RIBOSOMAL PROTEIN US8.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	CW	129	Total	C	N	O	S	0	0
			1033	659	193	175	6		

- Molecule 74 is a protein called 40S RIBOSOMAL PROTEIN US12.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	CX	134	Total	C	N	O	S	0	0
			1046	663	205	176	2		

- Molecule 75 is a protein called 40S RIBOSOMAL PROTEIN ES24.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	CY	122	Total	C	N	O	S	0	0
			1002	635	196	166	5		

- Molecule 76 is a protein called 40S RIBOSOMAL PROTEIN ES25.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	CZ	76	Total	C	N	O	S	0	0
			605	387	112	105	1		

- Molecule 77 is a protein called 40S RIBOSOMAL PROTEIN ES26.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Ca	96	Total	C	N	O	S	0	0
			767	476	159	127	5		

- Molecule 78 is a protein called 40S RIBOSOMAL PROTEIN ES27.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Cb	80	Total	C	N	O	S	0	0
			625	391	116	111	7		

- Molecule 79 is a protein called 40S RIBOSOMAL PROTEIN ES28.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Cc	62	Total	C	N	O	S	0	0
			490	298	99	91	2		

- Molecule 80 is a protein called 40S RIBOSOMAL PROTEIN US14.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Cd	53	Total	C	N	O	S	0	0
			444	278	90	71	5		

- Molecule 81 is a protein called 40S RIBOSOMAL PROTEIN ES30.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Ce	51	Total	C	N	O	S	0	0
			412	258	90	63	1		

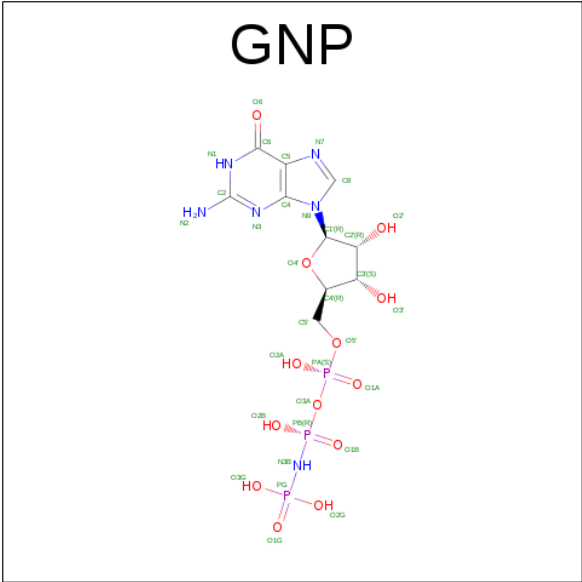
- Molecule 82 is a protein called 40S RIBOSOMAL PROTEIN ES31.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Cf	61	Total	C	N	O	S	0	0
			497	312	94	84	7		

- Molecule 83 is a protein called 40S RIBOSOMAL PROTEIN RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Cg	314	Total	C	N	O	S	0	0
			2440	1537	425	466	12		

- Molecule 84 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula: C₁₀H₁₇N₆O₁₃P₃).



Mol	Chain	Residues	Atoms					AltConf
84	AB	1	Total	C	N	O	P	0
			32	10	6	13	3	

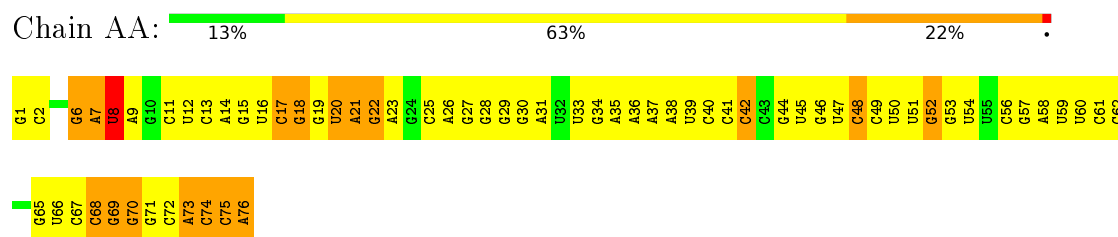
- Molecule 85 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
85	AB	1	Total	Mg	0
			1	1	

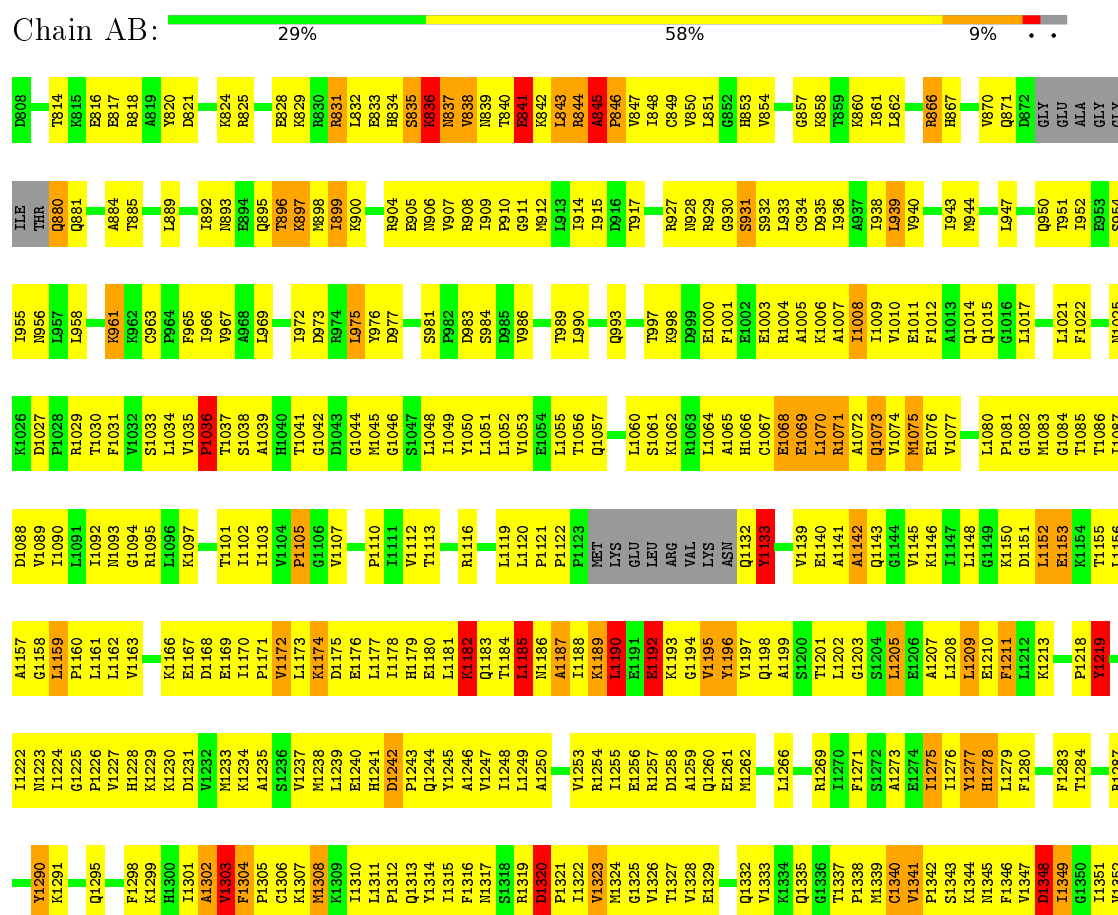
3 Residue-property plots

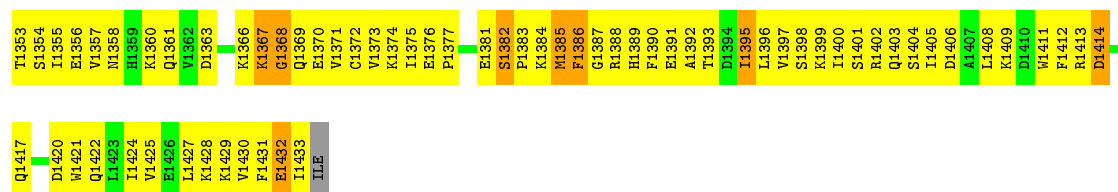
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric 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: TRNA

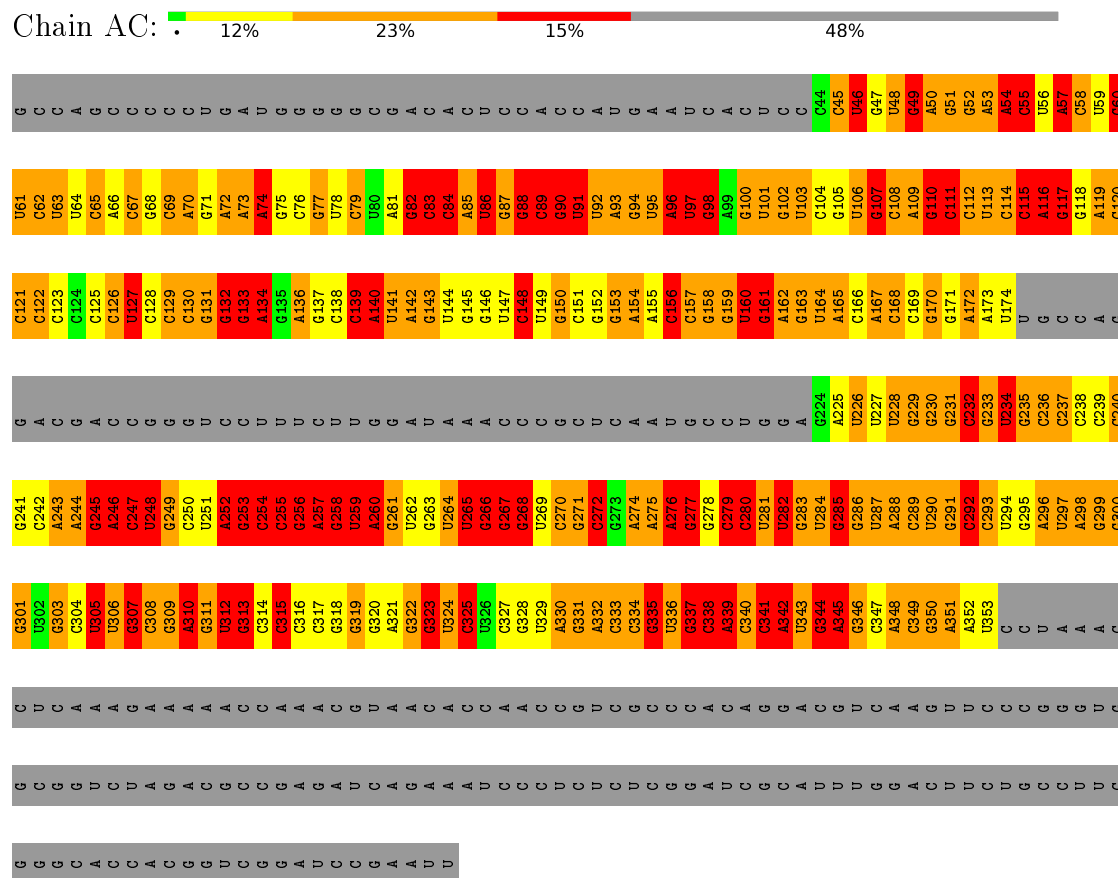


• Molecule 2: EIF5B

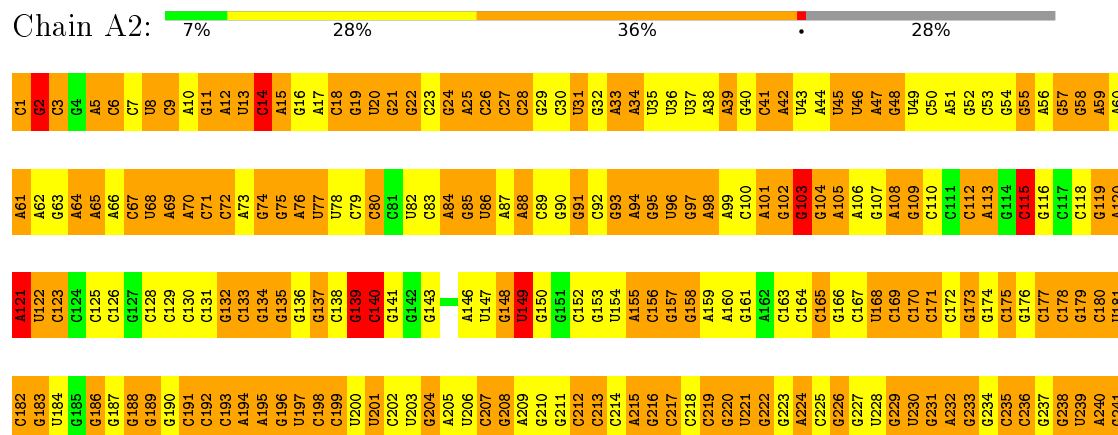




• Molecule 3: HCV-IRES



• Molecule 4: 28S RIBOSOMAL RNA



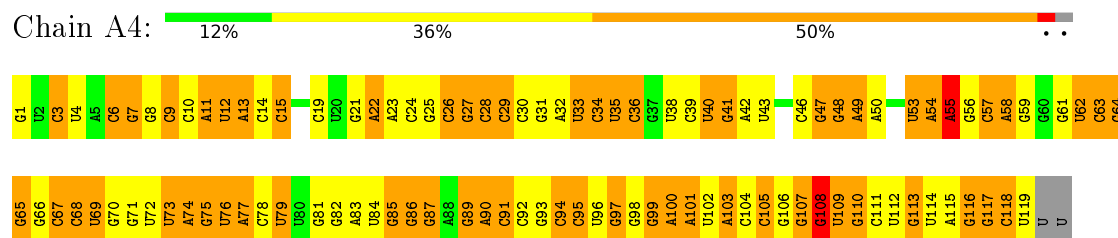
A1218	U1157	C1095	G	C974	G914	U	C	G731	C668	G	C	U483	G422	A362	G302	C242
C1219	G1158	C1096	U	C975	C915	G	C	G732	G669	C	C	G484	U423	A363	G303	G243
G1220	U1159	C1097	C	C976	A916	G	G	A733	C670	G	G	C486	A424	G364	U304	G244
C1221	C1160	C	U	C977	G917	C	G	G734	C671	G	C	G487	A425	G365	G305	C245
G1222	C1161	C	C	C978	C918	G	G	A735	G672	G	G	G488	A426	G366	G306	C246
C1223	C1162	C	C	C979	A919	G	G	G736	G673	G	G	G489	C427	A367	U307	C247
G1224	C1163	G	U	G	C920	C	C	G737	G674	G	C	C490	G428	A368	A308	C248
C1225	A1164	C	C	C	U921	G	C	U738	C675	G	C	G491	G429	A369	A309	C249
G1226	G1165	C	G	C	C922	G	C	G739	G676	G	C	G496	U431	G370	A310	G250
U1227	U1166	C	U	C	C923	C	C	G740	A678	C	C	A500	U432	U371	C311	C251
G1228	G1167	C	C	A	C924	G	G	C741	U679	C	C	U501	G433	U372	U312	G252
C1229	C1170	C	C	C	C925	G	C	U742	U680	G	C	G502	G434	G373	C313	C253
C1230	C1171	C	C	C	A927	G	C	U743	U681	G	C	U503	G435	A374	C314	G254
C1231	C1172	C	C	C	U928	G	C	G744	U682	G	C	C504	U436	A375	A315	C255
G1232	C1173	C	C	C	C929	G	C	G745	C683	G	C	C505	C437	A376	U316	C256
A	G1174	C	U	C	C930	G	U	G746	C684	G	C	C506	U438	A377	C317	C257
A	G1175	C	G	C	C931	G	C	G	A684	U	C	U504	C439	G378	U318	G258
G	G1176	C	C	C	C932	C	C	G	G689	U	C	U505	U440	A379	A320	G259
A	C1177	C	C	C	G933	G	C	C	U690	G	C	C507	C441	A380	A321	G260
G1238	G1178	G	C	G	G934	G	U	C	G691	G	C	C508	C442	U382	G322	U261
G1239	C1179	A	C	A	G935	C	G	C	C692	G	C	C509	A443	U383	C323	G262
G1240	G1180	C	C	A	G936	G	C	G	G693	U	C	C510	G444	U384	U324	U263
G1241	U1181	G	U	U	C937	G	C	U	C694	C	C	C	U445	G385	A325	U264
G1242	C1182	G	C	C	C938	G	A	C	C695	G	C	C	U446	A386	A326	C265
A1243	G1183	G	C	C	G939	A	G	C	G696	G633	C	C	C447	A387	A327	C266
G1244	C1184	G	C	C	A940	C	C	C	C697	G634	C	C	G448	G388	U328	G268
G1245	G1185	G	C	C	G941	C	C	U	G698	G635	G	C	G449	A389	A329	G269
G1246	C1186	A	C	C	G942	G	C	C	A699	G636	G	C	C450	G390	A330	A270
C1247	C1187	G	C	C	G943	A	C	C	C700	G637	A	U	C451	A391	G331	G271
G1248	G1188	G	C	C	A944	A	C	G	C701	G638	G	U	A454	G392	G332	U272
G1249	U1189	U	C	C	G945	A	C	U	G702	G639	G	C	G455	A393	G333	C273
C1250	C1190	G	C	U	C946	C	C	C	G703	G640	G	C	G456	C394	C334	G274
G1251	G1191	C	C	G	G947	C	C	C	C704	C641	C	U	G457	U395	A335	G275
C1252	C1192	C	C	G	A948	C	G	C	U705	C642	G	C	U458	G396	C336	G276
G1253	G1193	G	C	G	G949	U	C	U	C706	G643	C	C	U459	A397	G337	U277
A1254	C1194	C	C	G	A950	C	U	C	C707	U644	C	C	C460	A398	A338	U278
G1255	C1195	G	C	G	C951	C	C	C	G708	C645	G	G	C461	A399	G339	G279
C1256	C1196	C	U	U	C952	C	G	U	G709	C646	G	A	A462	G400	A340	C280
G1257	G1197	G	C	U	C953	C	C	C	G710	C647	G	C	G463	A401	C341	U281
C1258	C1198	C	C	U	G954	G	C	C	A711	C648	U	C	C464	G402	C342	U282
G1259	G1199	G	C	C	U955	A993	G	U	C712	C649	C	C	U465	G403	G343	G283
C1260	G1200	G1137	C	C1015	G956	G894	G	C	G713	G650	C	C	G466	G404	A344	G284
G1261	G1201	G1138	C	C1016	G957	U895	G	C	G714	A652	C	U	G467	C405	U345	G285
C1262	A1202	U1139	C	C1017	C958	G896	G	U	C715	G653	G	C	C468	G406	A346	A286
G1263	G1203	G1140	C	C1019	C959	U897	C	C	U716	C654	G	C	G469	U407	G347	A287
C1264	C1204	G1141	C	G1020	G960	U898	G	C	G717	G655	G	A	G470	A408	U348	U288
U1265	U1205	G1142	C	G	C961	A899	G	C	G718	G656	G	C	C471	A409	C349	G289
C1266	U1206	G1143	C	C	G962	C900	C	C	G719	G657	C	C	G472	A410	A350	C290
G1267	C1207	G1144	G	C	C963	A901	G	C	A720	C658	U	C	G473	A411	A351	A291
C1268	U1208	G1145	C	C	U964	G902	C	G	A721	G659	C	G	G474	C412	C352	G292
G1269	C1209	G1146	G	G	C965	C903	C	U	G722	A659	C	C	C475	C413	A353	C293
G1270	U1210	C1147	G	C	U966	C904	G	C	G723	C660	C	C	U476	G414	A354	C294
G1271	C1211	G1148	C	U	C967	C905	G	U	C724	C661	G	C	C477	U415	G355	C295
C1272	G1212	G1149	C	C	C968	C906	C	C	G725	G662	U	C	G478	U416	U356	A296
G1273	G1213	C1090	C	C	C969	C907	G	C	C726	G663	G	C	G479	A417	A357	A297
A1274	G1214	U1091	C	C	C970	G	G	G	G727	C664	G	C	G480	A418	C358	A298
C1275	G1215	C1092	G	G	C971	C	C	C	G728	C665	U	C	C481	G419	G299	C300
G1276	C1216	A1155	C	C	C972	G	C	C	C729	G666	U	C	G482	A420	G360	C301
U1277	C1217	C1156	C	C	U973	A913	G	C	G730	C667	G	C		G421	U361	G302



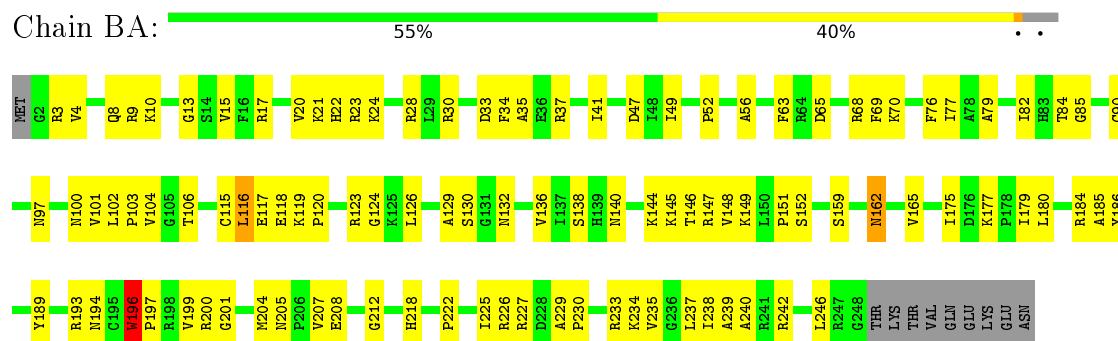

WORLDWIDE
PDB
PROTEIN DATA BANK

 **EMDDataBank**
Unified Data Resource for 3DEM

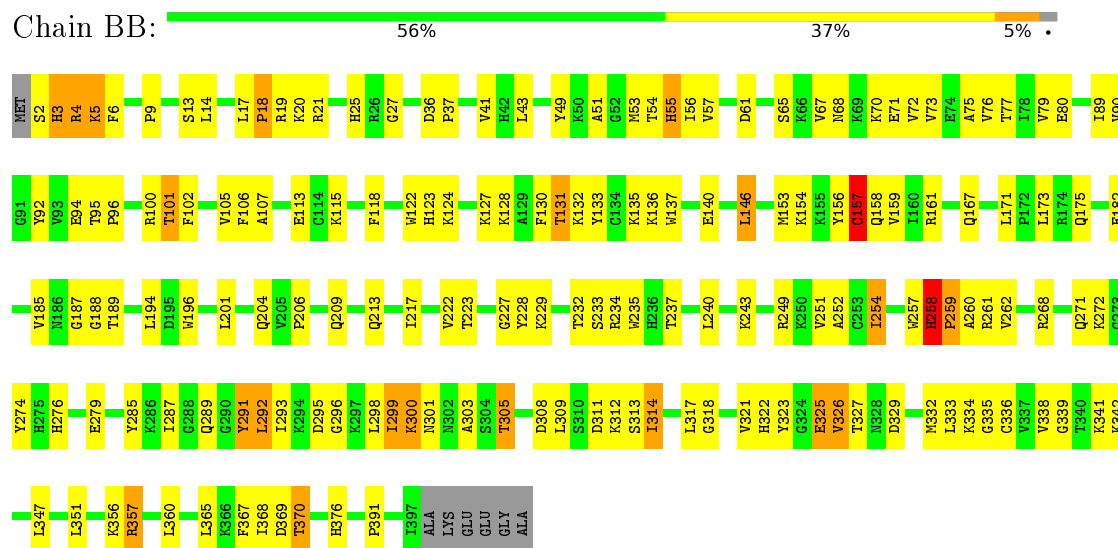


• Molecule 7: 60S RIBOSOMAL PROTEIN L8

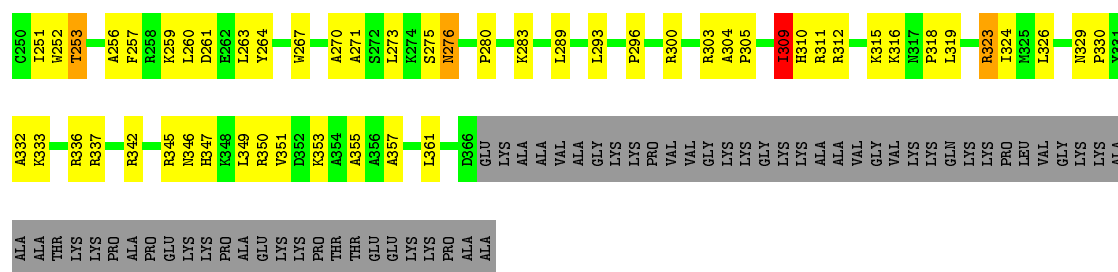


• Molecule 8: 60S RIBOSOMAL PROTEIN L3



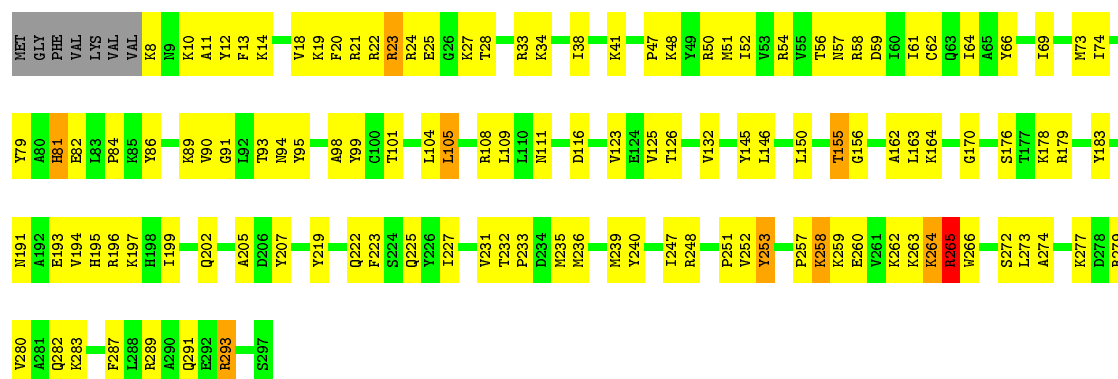
• Molecule 9: 60S RIBOSOMAL PROTEIN L4





• Molecule 10: 60S RIBOSOMAL PROTEIN L5

Chain BD: 57% 38%



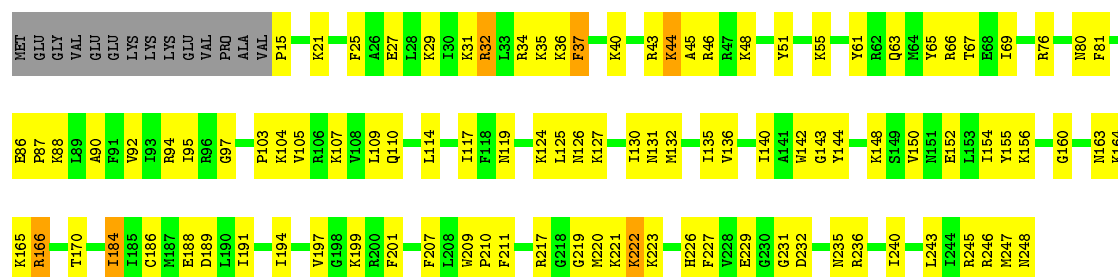
• Molecule 11: 60S RIBOSOMAL PROTEIN L6

Chain BE: 39% 54% 7%



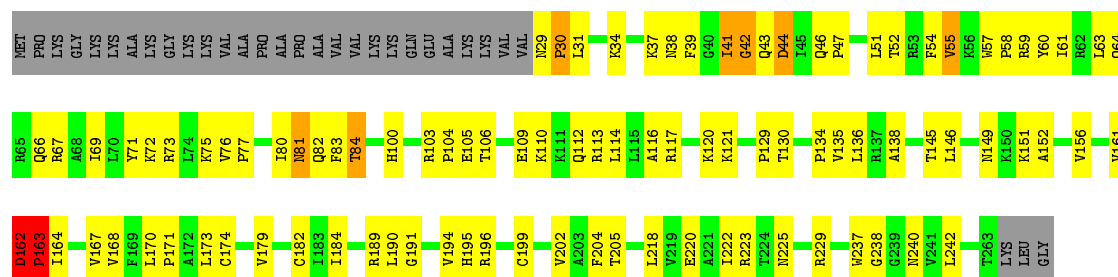
• Molecule 12: 60S RIBOSOMAL PROTEIN L7

Chain BF: 53% 39% 6%



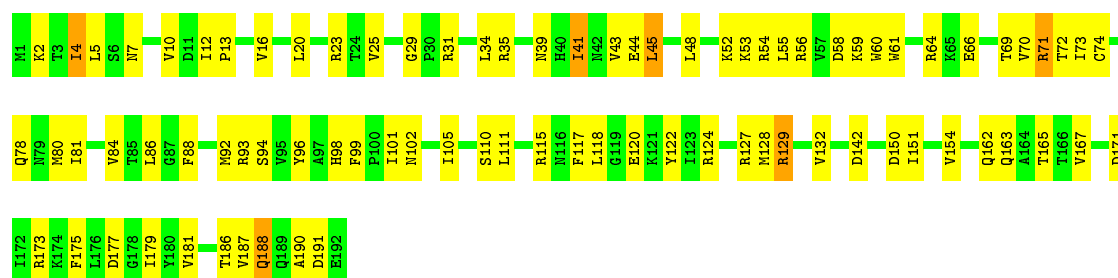
• Molecule 13: 60S RIBOSOMAL PROTEIN L7A

Chain BG:  52% 33% 2% 2% 11%



- Molecule 14: 60S RIBOSOMAL PROTEIN L9

Chain BH: 56% 41% .



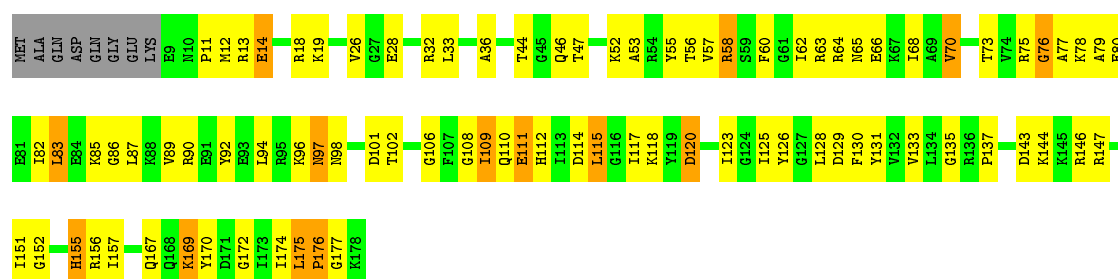
- Molecule 15: 60S RIBOSOMAL PROTEIN L10

Chain BI:  51% 38% 8%

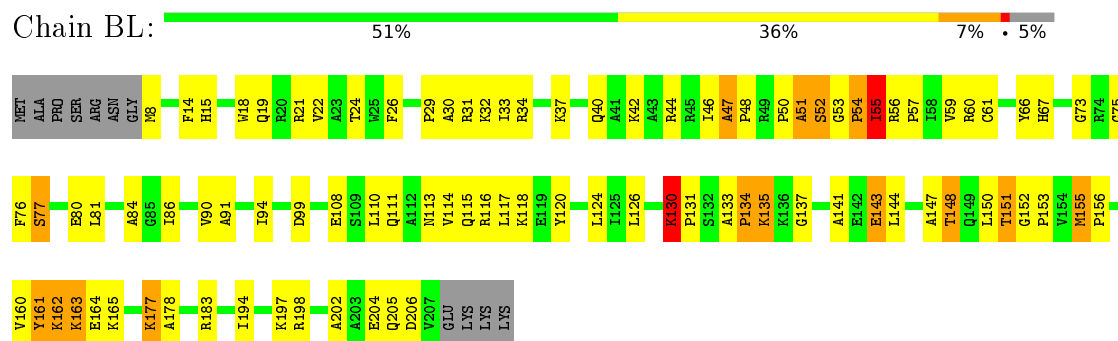


- Molecule 16: 60S RIBOSOMAL PROTEIN L11

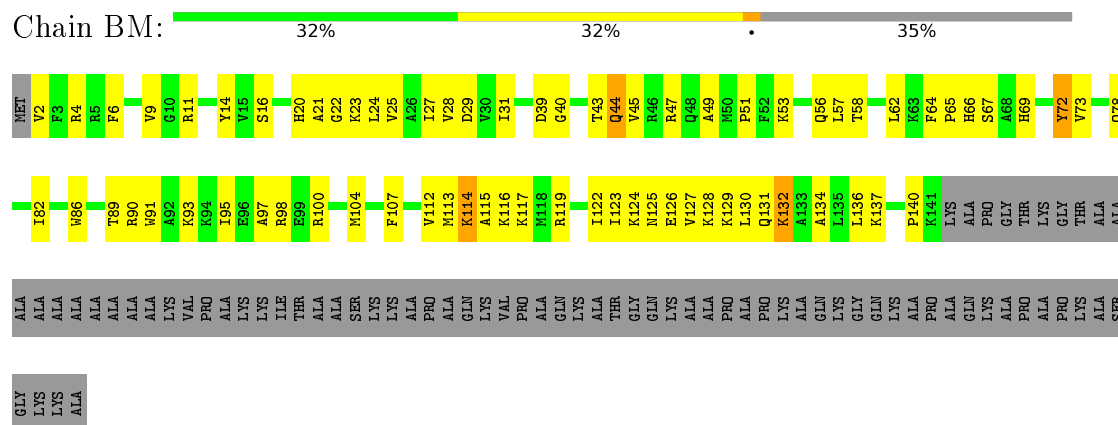
Chain BJ:  47% 41% 8% .



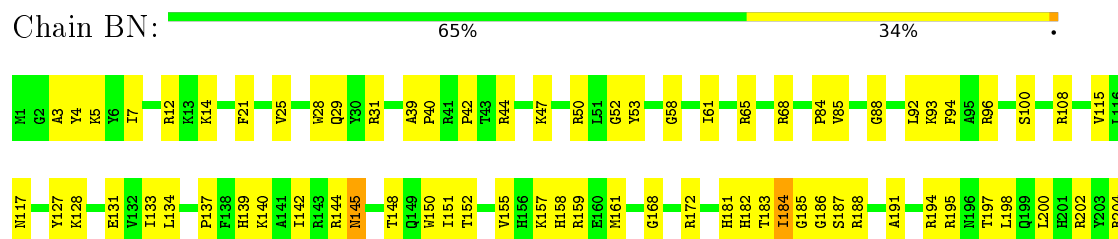
- Molecule 17: 60S RIBOSOMAL PROTEIN L13



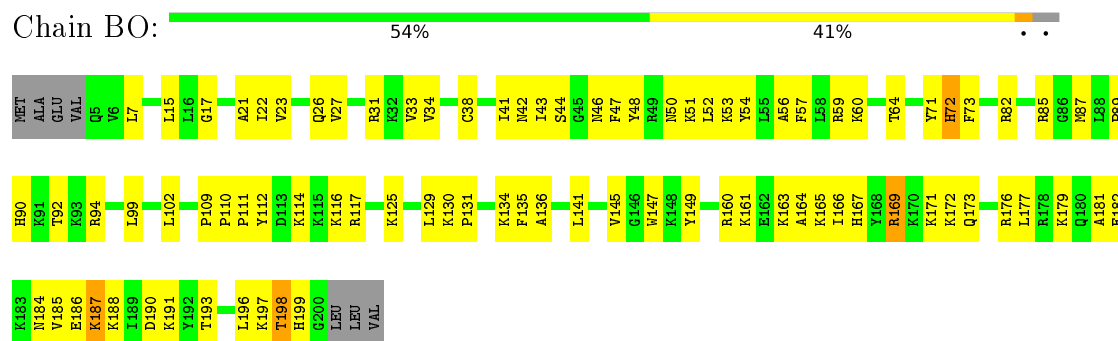
- Molecule 18: 60S RIBOSOMAL PROTEIN L14



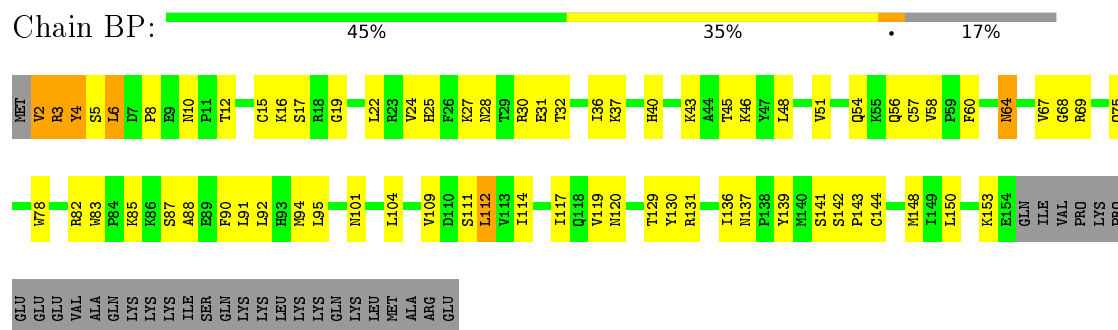
- Molecule 19: 60S RIBOSOMAL PROTEIN L15



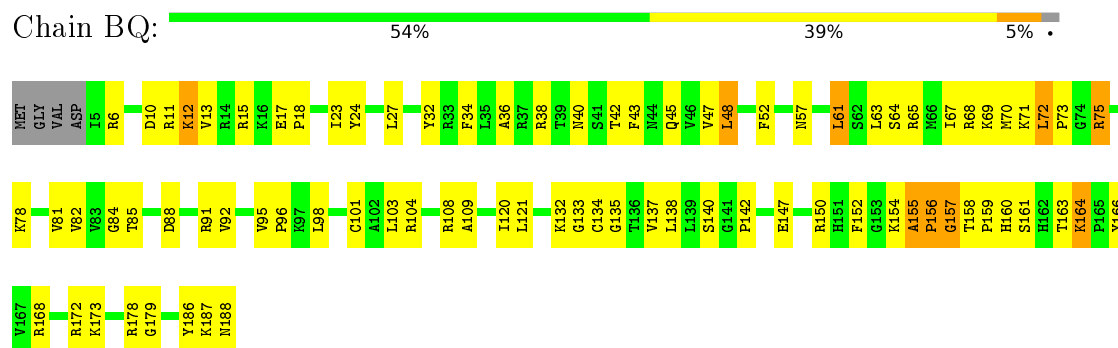
• Molecule 20: 60S RIBOSOMAL PROTEIN L13A



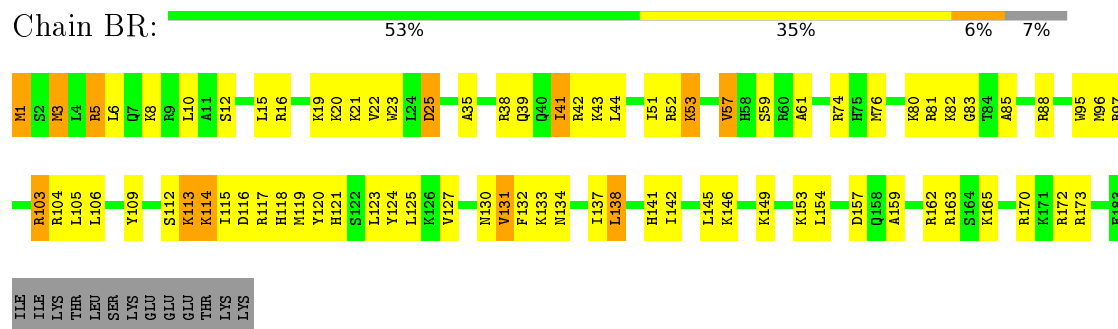
- Molecule 21: 60S RIBOSOMAL PROTEIN L17



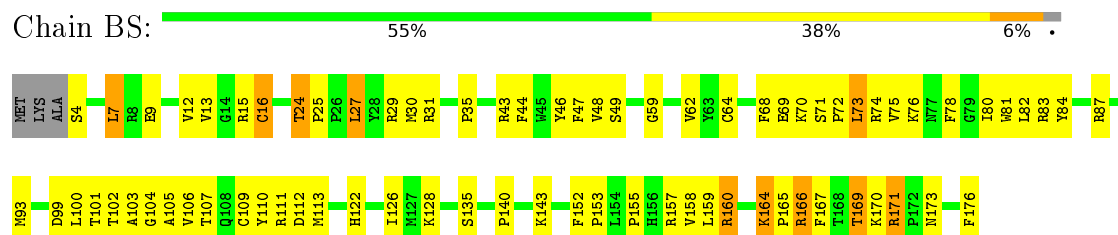
• Molecule 22: 60S RIBOSOMAL PROTEIN L18



• Molecule 23: 60S RIBOSOMAL PROTEIN L19

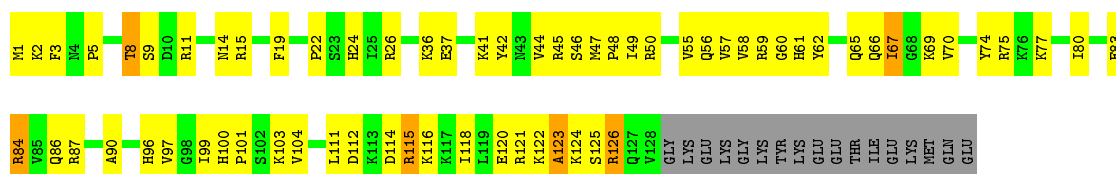


• Molecule 24: 60S RIBOSOMAL PROTEIN L18A



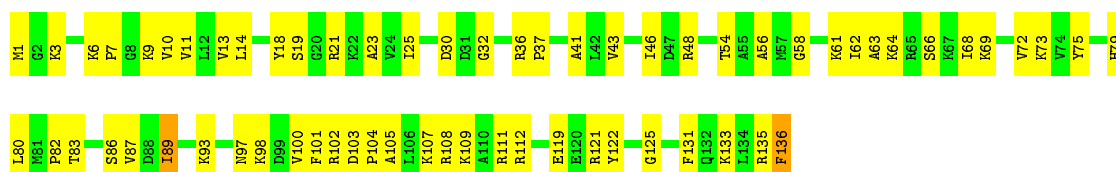
• Molecule 25: 60S RIBOSOMAL PROTEIN L21





• Molecule 31: 60S RIBOSOMAL PROTEIN L27

Chain BZ: 53% 46%



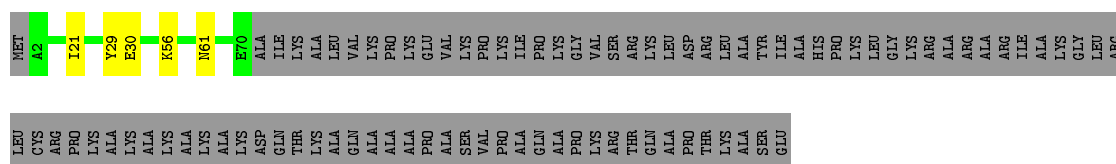
• Molecule 32: 60S RIBOSOMAL PROTEIN L27A

Chain Ba: 94% 5%



• Molecule 33: 60S RIBOSOMAL PROTEIN L29

Chain Bb: 40% 57%



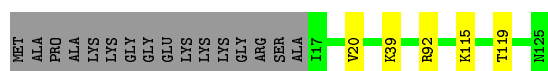
• Molecule 34: 60S RIBOSOMAL PROTEIN L30

Chain Bc: 88% 10%



• Molecule 35: 60S RIBOSOMAL PROTEIN L31

Chain Bd: 83% 13%




• Molecule 36: 60S RIBOSOMAL PROTEIN L32

Chain Be: 90% 5%




- Molecule 37: 60S RIBOSOMAL PROTEIN L35A

Chain Bf:  86% 10% ..



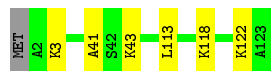
- Molecule 38: 60S RIBOSOMAL PROTEIN L34

Chain Bg:  87% 10% ..




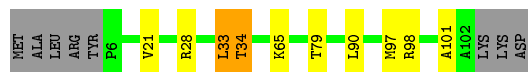
- Molecule 39: 60S RIBOSOMAL PROTEIN UL29

Chain Bh:  94% 5% .




- Molecule 40: 60S RIBOSOMAL PROTEIN L36

Chain Bi:  83% 8% . 8%



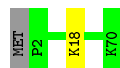
- Molecule 41: 60S RIBOSOMAL PROTEIN L37

Chain Bj:  84% 12%



- Molecule 42: 60S RIBOSOMAL PROTEIN L38

Chain Bk:  97% ..



- Molecule 43: 60S RIBOSOMAL PROTEIN L39

Chain Bl:  94% ..



- Molecule 44: UBIQUITIN-60S RIBOSOMAL PROTEIN L40

Chain Bm:  38% 59%

MET GLN ILE PHE VAL LYS THR LEU THR GLY LYS THR ILE THR LEU GLY VAL PRO SER ASP THR ILE GLU ASN VAL LYS ALA LYS ILE GLN ASP LYS GLY ILE PRO PRO ASP GLN ARG LEU ILE PHE ALA GLY LYS LYS LEU GLU ASP GLY ARG THR LEU SER ASP TYR ASN

ILE GLN LYS SER THR LEU HIS LEU VAL LYS ARG LEU ARG GLY I77 I78 E79 K112 C115 T118 K128

- Molecule 45: 60S RIBOSOMAL PROTEIN L41

Chain Bn:  100%

There are no outlier residues recorded for this chain.

- Molecule 46: 60S RIBOSOMAL PROTEIN L36A

Chain Bo:  93% 7%


MH SS2 L33 Y34 L43 L93 R99 K100 G101 F106

- Molecule 47: 60S RIBOSOMAL PROTEIN L37A

Chain Bp:  93% 5%

MET A2 G12 G19 Y29 A51 V52 Q92

- Molecule 48: 60S RIBOSOMAL PROTEIN L28

Chain Bt:  86% 7% 5%

MET S2 A3 H4 I18 K19 R20 I44 H45 V61 S76 Y77 V78 R79 T80 T81 T89 P104 T131 ARG PRO THR LYS SER SER

- Molecule 49: 60S RIBOSOMAL PROTEIN L10A

Chain Bu:  92% 8%

A1 D2 Q3 F21 T24 N30 P39 T53 T57 V60 T101 L110 M145 R156 R157 K190 L193 T197 V210

- Molecule 50: 18S RIBOSOMAL RNA

Chain C1:  6% 38% 48% 7%

U1 A2 C3 C4 U5 G6 G7 U8 U9 G10 A11 G11 U12 C13 C14 U15 U16 G16 U17 C17 C18 A19 G20 U21 U22 A23 G23 C24 A25 U26 A27 U28 G29 C30 U31 U32 G33 U34 C35 C36 U37 C37 U38 A39 A40 G41 A42 A43 U44 A45 A46 G47 C48 C49 A50 U51 U52 G52 C53 A54 U55 U56 G56 U57 C58 U59 A60

A61 G62 U63 A64 C65 G66 C67 U68 A69 G70 G71 G72 C73 G74 G75 U76 U77 C78 A79 G80 G81 U81 A82 A83 A84 A85 C86 U87 U88 G89 A90 A91 A92 U93 G94 G95 G96 C97 U97 C98 A99 U100 U101 A102 A103 U104 A105 U106 A107 G108 C109 U109 U110 A111 U112 G113 G114 U115 U116 G117 C118 U119 U120

U121 G122 U123 U124 C125 G126 C127 U128 C129 G130 G131 G132 U133 C134 U135 C136 U137 C138 A139 C140 A141 C142 U143 A144 U145 G146 A147 U148 A149 A150 A151 U152 G153 U154 G155 G156 U157 A158 A159 U160 U161 C162 A163 U164 A165 G166 A167 C168 U169 U170 A171 U172 A173 C174 U175 A176 G177 C178 U179 G180

A1149	G1089	A1027	U965	C905	U844	G	A664	A604	G544	A484	C424	U361	A301	A181
A1150	C1090	A1028	U966	U906	G845	C	G665	A605	A945	A485	G425	C362	A302	C182
G1151	C1091	A1029	C967	G907	G846	C	G666	G606	G546	A486	G426	C363	A303	G183
U1152	G1092	A1030	U968	A908	A847	G	U667	U607	G547	U487	U427	G364	C304	G184
C1153	A1093	A1031	U969	G909	U848	C	A668	C608	C548	U488	U428	U365	U305	G185
U1154	C1094	G1032	G970	G910	A849	C	A669	U609	C549	A489	C429	U366	C306	C186
C1155	C1095	G1033	G971	C911	C850	C	A670	G610	C550	C490	C430	U367	G307	G187
U1156	G1096	A1034	C851	C912	C851	G	A671	G611	U551	C491	G431	U368	G308	C188
G1157	C1097	A1035	G852	A913	G852	U	A672	U612	G552	C492	G432	C369	G309	C189
U1158	G1098	A1036	C853	A914	C853	C	G673	G613	U553	A493	A433	G370	C310	G190
G1159	C1099	G1037	G854	G915	A854	C	C674	C614	G554	C494	G434	A371	C311	A191
U1160	A1100	U1038	G855	A916	G855	C	U675	C615	A555	U495	A435	U372	G312	C192
U1161	U1101	C1039	C856	U917	C856	C	G676	A616	U556	C496	G436	U373	A313	C193
C1162	G1102	G1040	U857	U918	U857	G	G677	G617	U557	C497	G437	G374	U314	C194
C1163	C1103	G1041	A858	A919	A858	C	U678	C618	G558	C498	G438	U375	C315	C195
G1164	G1104	A1042	C859	A920	G859	U	A679	A619	G559	G499	A439	A376	G316	C196
G1165	G1105	G1043	G860	G921	G860	C	G680	G620	A560	A500	G440	G377	C317	C197
G1166	C1106	G1044	A861	A922	A861	C	U741	C621	A561	C501	C441	U378	A318	U198
G1167	G1107	U1045	A862	G923	U862	U	U682	C622	U562	G502	C442	C379	C319	C199
G1168	G1108	U1046	U863	G924	G863	C	G683	G623	G563	C503	U443	C380	G320	C200
G1169	C1109	G1047	A864	G925	A864	C	U744	C624	G564	C504	G444	C381	G321	C201
A1170	G1110	G1048	G865	A926	U865	C	C745	G625	G565	G505	A445	C382	C322	G202
G1171	U1111	A1049	U866	C927	U866	C	C746	G626	U566	G506	G446	G383	C323	G203
U1172	U1112	A1050	G867	G928	G867	C	U747	U627	C567	A507	A447	U384	C324	G204
A1173	G1113	G1051	C868	G929	G868	C	U688	A628	C568	A508	A448	G385	C325	G205
U1174	U1114	A1052	A869	C930	A869	C	U749	A629	A569	G509	A449	C386	G326	G206
G1175	U1115	C1053	G870	G931	U870	C	C750	U630	C570	U510	C450	C387	G327	G207
G1176	C1116	G1054	U871	G932	U871	C	G651	C631	U571	U511	G451	U388	U328	G208
U1177	C1117	A1055	A872	A933	A872	C	G652	C632	U572	A512	C452	G389	G329	A209
U1178	G1118	U1056	G873	G934	G873	C	C653	C633	U573	G513	G453	C390	G330	U210
U1179	U1119	G1057	G874	G935	G874	C	G654	A634	A574	U514	U454	C391	C331	G211
C1180	U1120	A1058	A875	G936	A875	C	C655	G635	A575	G515	A455	U393	G332	G212
A1181	G1121	G1059	C876	C937	C876	C	G656	C636	A576	A516	C456	G394	G333	G213
A1182	C1122	A1060	C877	U938	C877	C	U657	U637	U577	C517	C457	G395	C334	U214
A1183	C1123	U1061	G878	A939	G878	C	C658	C638	C578	G518	A458	U396	G335	G215
G1184	C1124	C879	C879	U940	C879	C	C659	C639	C579	A519	C459	G397	A336	C216
G1185	C1125	G1063	U1003	C941	G880	U	G660	A640	U580	A520	A460	A398	G337	G217
U1186	G1126	C1064	U1004	G942	G880	C	A641	U641	U581	A521	U461	C399	G338	C218
G1187	C1127	G1065	G999	C943	U883	G	U642	U642	U582	A522	C462	C400	A339	U219
A1188	C1128	U1066	C1000	U943	U884	A	A643	U643	U583	A523	C463	A401	C340	G220
A1189	G1129	C1067	A1001	A944	C884	U	G644	C644	C584	A524	A464	C402	C341	C221
G1190	C1130	A1068	U1007	U945	U885	G	C645	C645	C585	A525	A465	C342	G222	U222
A1191	G1131	U1069	A1008	U946	A886	C	U646	G646	G586	A526	G466	U343	G223	C223
C1132	C1132	G1070	G1010	G947	U887	U	U647	U647	A587	C527	G467	U344	A224	G224
U1193	A1133	G1071	A1011	G949	U888	C	C648	A648	G588	A528	A468	U345	G225	C225
A1194	G1134	U1072	C950	C950	U889	U	U649	U649	G589	A529	A469	C346	U226	A226
A1195	C1135	U1013	C951	C951	G891	U	A650	U650	A590	U530	G470	G347	U227	U227
A1196	U1136	C1075	G1014	G952	U892	A	U651	U651	U591	A531	G471	A348	C228	G228
G1197	U1137	G1076	U1015	C953	U893	C	U652	U652	C592	C532	G472	A349	A229	G229
A1198	C1138	U1016	G944	U954	G894	C	A653	C653	C593	A533	A473	C350	U230	A230
C1199	C1139	U1017	G895	A955	U895	U	A654	A654	A594	G534	G474	G351	G231	A231
A1200	G1140	A1080	U956	G956	U896	G	A655	A655	U595	G535	C475	U352	A232	A232
U1201	G1141	U1081	C1018	A957	U897	A	G656	C656	U596	A536	A476	C353	C233	C233
U1202	G1142	A1082	U958	G958	U898	G	U657	U657	G597	C537	G477	U354	C234	C234
G1203	A1143	A1083	U959	G959	G898	U	G658	U658	A598	U538	A478	G355	A235	A235
A1204	U1204	A1084	C900	U960	C900	C	G659	G659	A599	C539	C479	C356	A236	A236
C1205	A1145	C1085	G901	G961	G901	A	U660	C660	G600	U540	G480	C357	C237	C237
G1206	C1146	U1086	A902	A962	G902	C	G661	U661	G601	U541	C481	C358	G238	G238
G1207	C1147	A1087	U1025	A963	A903	C	C662	G662	G602	U542	U422	U359	A239	G239
A1208	U1148	U1088	A904	A964	C904	C	C663	C663	C603	C543	C483	U423	U300	G240

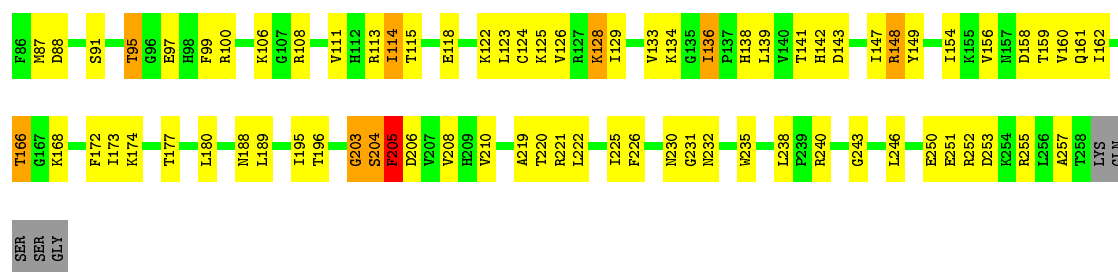
PRO	L178	R85	RET	A1824	C1635	G1575	G1514	C1453	G1393	C1331	G1269	A1209
SER	A179	A86	G1760	A1825	G1636	G1576	G1515	A1454	G1394	A1332	G1270	G1210
VAL	E180	B87	G1761	A1826	G1637	A1637	G1516	A1455	G1395	A1333	G1271	G1211
PRO	E181	L88	G1762	A1827	G1638	U1578	G1517	G1456	A1396	G1334	C1272	G1212
ILE	K99	L89	G1763	U1827	G1639	A1699	C1518	G1457	A1397	G1335	G1273	C1213
GLN	V182	F90	G1764	A1828	A1640	A1580	C1519	U1457	G1398	C1336	G1274	A1214
GLN	L183	V91	G1765	G1829	A1641	C1581	G1520	G1458	G1399	C1337	G1275	C1215
GLN	R184	T99	G1766	A1830	A1642	C1582	G1521	U1459	U1400	C1338	A1276	C1216
PHE	M185	Q9	G1767	A1831	G1643	C1583	A1522	G1462	A1401	G1339	G1277	A1217
PRO	T189	R102	G1768	A1832	G1644	G1584	C1523	U1463	A1402	U1340	A1278	C1218
	S190	F103	G1769	C1833	C1645	U1585	C1524	U1464	C1403	C1341	C1279	C1219
	R191	T104	G1770	A1834	C1646	U1586	C1525	A1465	U1404	U1342	G1280	A1220
	P199	P105	G1771	A1835	A1647	G1587	U1526	G1466	U1405	U1343	G1281	G1221
	D200	G106	C1772	G1836	G1648	A1588	G1528	C1467	G1406	A1344	A1282	G1222
	L201	T107	U1775	G1837	U1649	A1589	G1529	C1468	U1407	G1345	A1283	A1223
	F202	F108	U1776	U1838	A1650	C1590	U1530	A1469	U1408	U1346	A1284	G1224
	F203	T109	G1777	U1839	A1651	C1591	A1531	C1470	A1409	U1347	G1285	U1225
	F204	N110	U1778	U1840	G1652	C1592	C1532	C1471	C1410	G1348	G1286	G1226
	R205	Q111	C1778	C1841	U1653	C1593	A1533	C1472	G1411	G1349	A1287	G1227
	R206	I112	G1779	C1842	G1654	A1594	C1534	C1473	C1412	U1350	U1288	A1228
	P207	Q113	G1780	U1843	G1655	U1595	U1535	A1474	G1413	G1351	G1229	C1230
	E208	A114	A1781	U1844	G1656	U1596	G1536	A1475	A1414	G1352	G1290	C1231
		F116	G1782	A1845	G1657	C1597	A1537	A1476	G1415	A1353	A1291	C1232
		R117	G1783	G1846	G1658	G1598	C1538	U1477	C1416	G1354	C1292	G1233
		R117	G1784	G1847	U1659	U1599	U1539	U1478	C1417	C1355	G1234	G1234
		E118	G1785	U1848	C1660	G1600	G1540	G1479	C1418	G1356	U1296	C1235
		P119	G1786	G1849	A1661	A1601	G1541	A1480	C1419	U1357	U1297	G1236
		R120	G1787	A1850	U1662	U1602	G1542	G1481	G1420	U1358	G1298	G1237
		R41	U1788	A1851	A1663	G1603	U1543	C1482	U1359	A1299	G1238	U1238
		L122	G1789	G1852	G1664	G1604	C1544	A1483	U1360	U1300	U1239	U1239
		K42	U1790	C1853	G1665	G1605	A1545	A1484	G1361	A1301	G1302	A1240
		S43	A1791	U1854	C1666	G1606	G1546	U1485	U1362	G1303	C1303	A1241
		H131	G1792	G1855	U1667	A1607	G1547	A1486	G1425	U1363	U1242	U1242
		Q132	A1793	C1856	G1668	U1608	G1548	A1487	C1426	U1364	U1243	U1243
		P133	G1794	G1857	G1669	C1609	U1549	C1488	C1427	U1306	G1305	U1244
		L48	G1795	G1858	C1670	G1610	G1550	A1489	G1428	U1307	G1245	G1245
		E136	G1796	A1859	G1671	G1611	U1551	G1490	G1429	U1308	A1246	A1246
		Y139	G1799	A1860	U1672	G1612	G1552	G1491	C1430	A1370	C1247	C1247
		R53	A1800	G1861	U1673	G1613	C1553	U1492	G1431	U1371	C1309	U1248
		T54	A1801	G1862	G1674	A1614	C1554	C1493	U1432	U1372	C1310	C1249
		P143	C1802	A1863	U1675	U1615	U1555	U1494	C1433	C1373	C1311	A1250
		L142	U1803	U1864	G1676	U1616	A1556	G1495	C1434	C1374	G1312	A1251
		L147	U1804	C1865	U1677	G1617	C1557	U1496	C1435	G1375	A1313	C1252
		L58	U1805	A1866	U1678	G1618	C1558	G1497	C1436	A1376	U1314	A1253
		C148	C1807	U1867	A1679	A1619	C1559	A1498	C1437	U1377	U1315	G1254
		N149	U1808	U1868	G1680	A1620	U1560	U1499	A1438	A1378	C1316	G1255
		L154	A1809	G1869	U1681	U1621	A1561	G1500	A1379	A1379	G1317	G1256
		C163	U1810	C1870	G1682	U1622	C1562	C1501	G1380	G1380	G1318	G1257
		N164	U1811	C1871	C1683	A1623	G1563	U1502	G1381	U1319	G1257	A1258
		A168	U1812	U1872	C1684	U1624	C1564	C1503	U1442	A1382	G1320	A1259
		V66	A1813	U1873	U1685	U1625	C1565	U1504	C1443	A1383	G1321	A1260
		A67	G1814	G1874	G1686	C1626	G1566	U1505	U1444	C1384	G1322	C1261
		B69	A1815	U1875	C1687	C1627	G1567	A1506	U1445	U1385	U1323	C1262
		T77	G1816	C1876	C1688	C1628	C1568	G1507	A1446	A1386	G1324	C1263
		N81	G1817	U1877	C1689	C1629	A1569	A1508	G1447	G1387	G1325	C1264
		T82	A1818	C1877	U1690	A1630	G1570	A1509	A1448	A1388	U1326	A1265
		G83	U1819	C1753	U1691	U1631	G1571	G1510	C1389	C1389	G1327	A1266
		Q84	G1820	G1754	U1692	C1632	C1572	G1450	U1390	C1390	G1328	C1267
			U1821	C1755	A1693	G1633	G1573	U1511	C1391	C1391	U1329	C1268
			A1822	C1756	U1694	A1634	C1574	A1513	A1452	U1392	G1330	

• Molecule 51: 40S RIBOSOMAL PROTEIN US2

Chain CA:  47% 34% 17%

L178	R85	RET
A179	A86	S2
E181	R87	G3
L182	L88	A4
L183	K89	L5
L184	F90	D6
M185		V7
	I99	L8
		Q9
L189	R102	M10
S190	F103	K11
R191	T104	E12
	P105	
P199	G106	V15
D200	T107	
L201	F108	L19
Y202	T109	
F203	N110	L25
R204	Q111	G26
R205	I112	L30
D206	Q113	D31
P207	A114	F32
E208	A115	F33
	F116	Q33
	R117	P34
	E118	E35
LVS	P119	
ALA	R120	Y39
VAL	A121	K40
THR	L121	R41
LVS	L122	K42
GLU		S43
GLU	D130	
PHE	H131	I46
GLN	Q132	Y47
GLY	P133	I48
GLU		I49
TRP	E136	N50
THR		
ALA	Y139	R53
PRO		T54
ALA	L142	S55
PRO	P143	
GLU		L58
PHE	L147	
THR	C148	A62
ALA	N149	R63
THR		A64
GLN	L154	I65
PRO		V66
GLU	C163	A67
VAL	N164	I68
ALA		E69
ASP	A168	
TRP		
SER	V171	I77
GLU		
GLY	M174	N81
VAL	T175	T82
GLN	G176	G83
GLN	M177	O84

Chain CE:



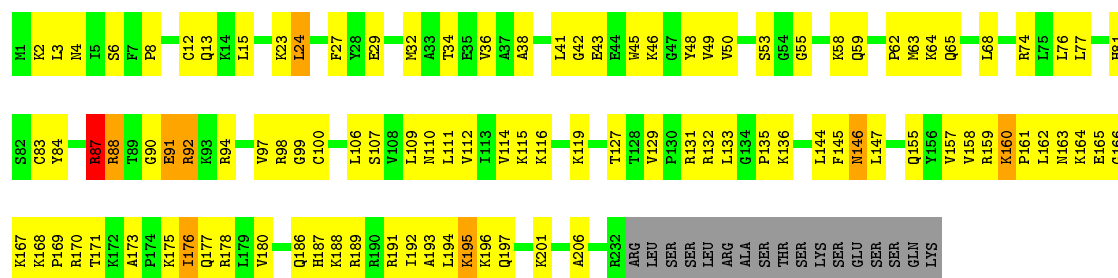
- Molecule 56: 40S RIBOSOMAL PROTEIN US7

Chain CF: 48% 38% 7% 8%



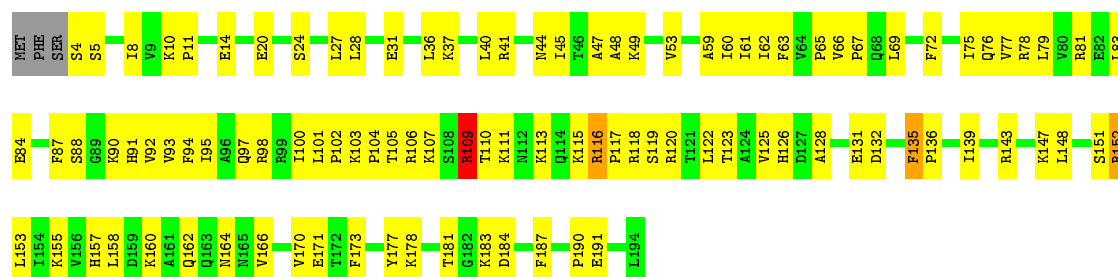
- Molecule 57: 40S RIBOSOMAL PROTEIN ES6

Chain CG: 51% 39% 7%



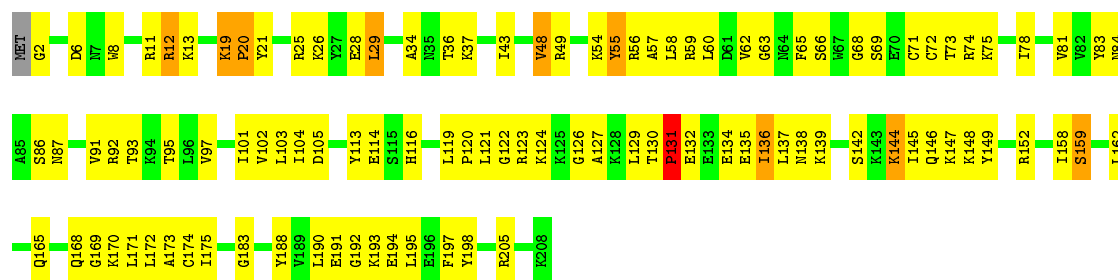
- Molecule 58: 40S RIBOSOMAL PROTEIN ES7

Chain CH: 46% 50%



- Molecule 59: 40S RIBOSOMAL PROTEIN ES8

Chain CI: 49% 46%



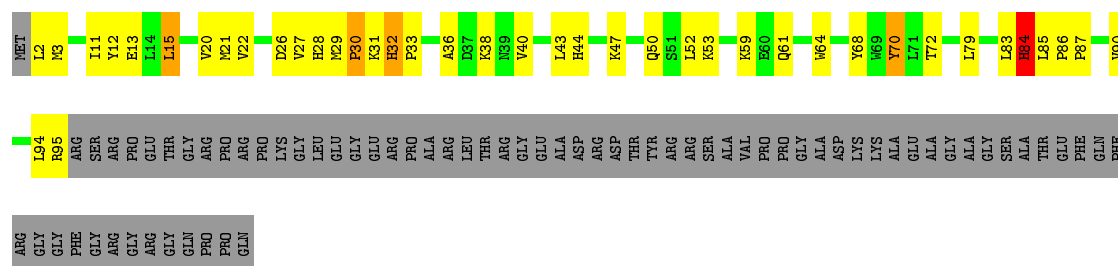
• Molecule 60: 40S RIBOSOMAL PROTEIN US4

Chain CJ: 51% 36% 6% 8%



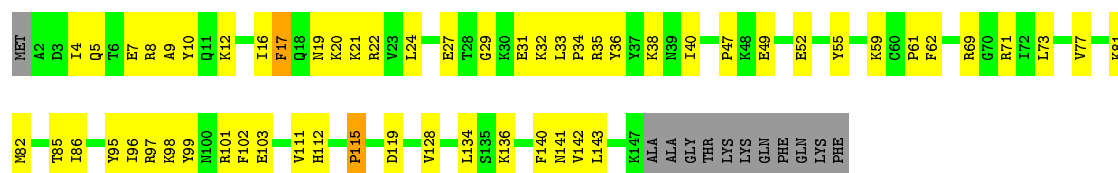
• Molecule 61: 40S RIBOSOMAL PROTEIN ES10

Chain CK: 32% 22% 43%



• Molecule 62: 40S RIBOSOMAL PROTEIN US17

Chain CL: 56% 35% 8%



• Molecule 63: 40S RIBOSOMAL PROTEIN ES12

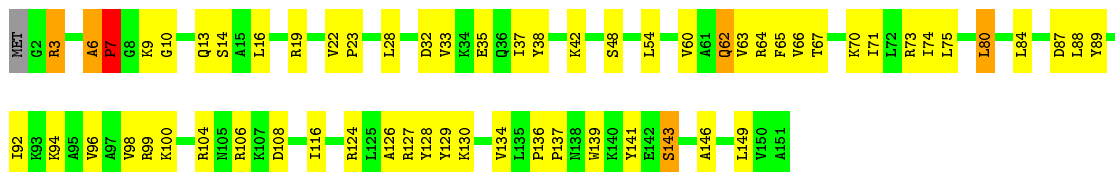
Chain CM: 55% 33% 9%





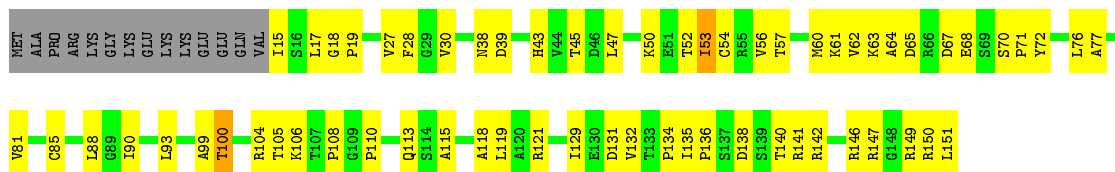
• Molecule 64: 40S RIBOSOMAL PROTEIN US15

Chain CN: 59% 36%



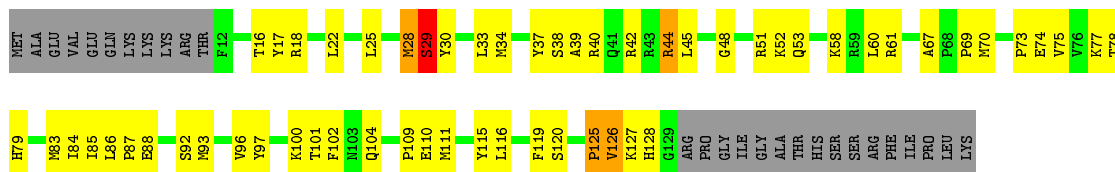
• Molecule 65: 40S RIBOSOMAL PROTEIN US11

Chain CO: 49% 40% 9%



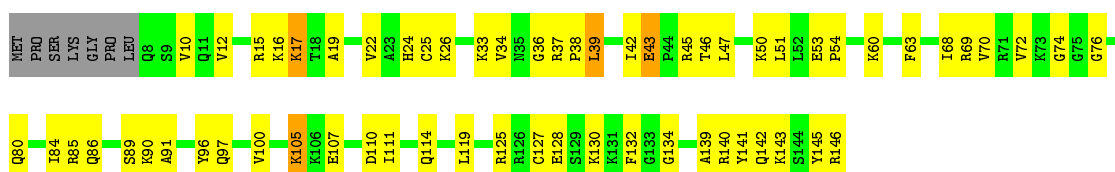
• Molecule 66: 40S RIBOSOMAL PROTEIN US19

Chain CP: 41% 37% 19%



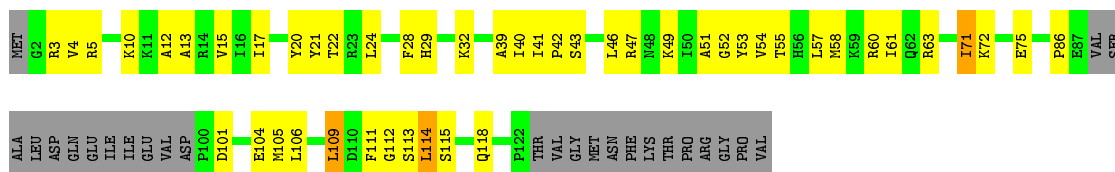
• Molecule 67: 40S RIBOSOMAL PROTEIN US9

Chain CQ: 53% 40% 5%

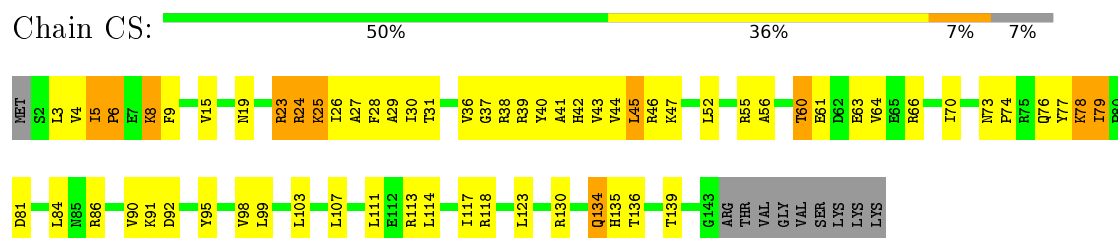


• Molecule 68: 40S RIBOSOMAL PROTEIN ES17

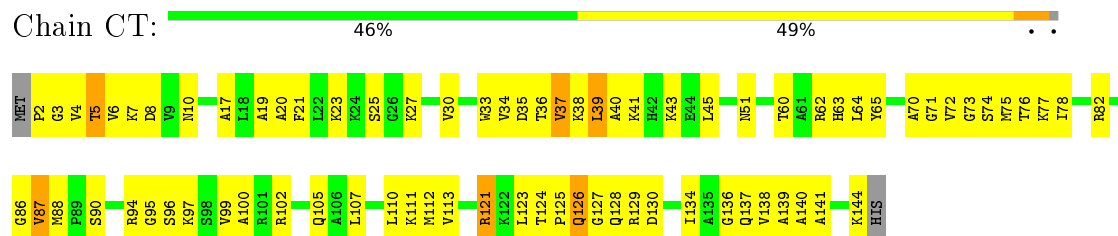
Chain CR: 45% 33% 19%



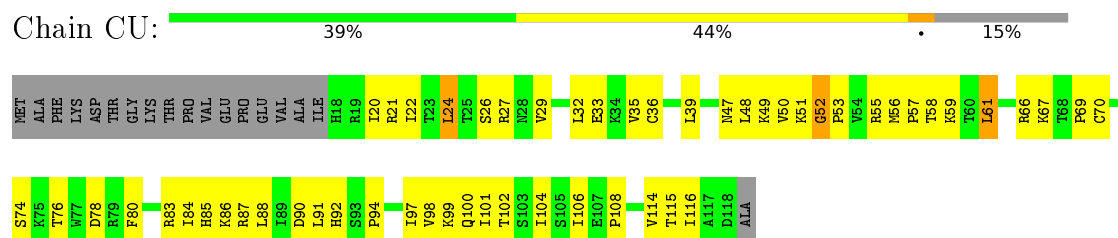
- Molecule 69: 40S RIBOSOMAL PROTEIN US13



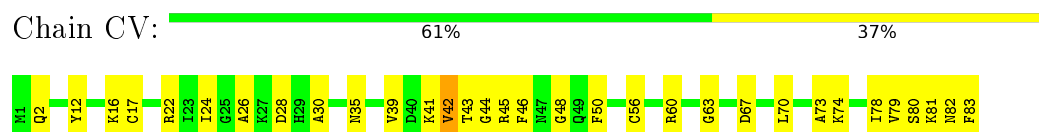
- Molecule 70: 40S RIBOSOMAL PROTEIN ES19



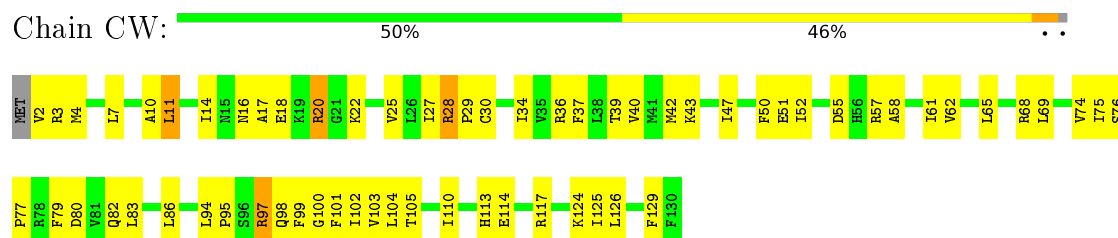
- Molecule 71: 40S RIBOSOMAL PROTEIN US10



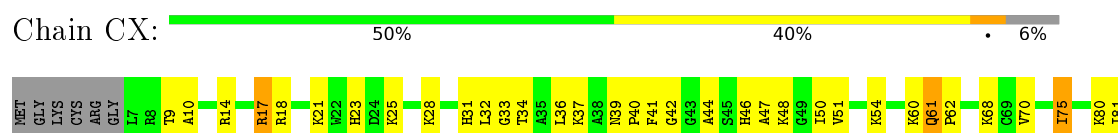
- Molecule 72: 40S RIBOSOMAL PROTEIN ES21

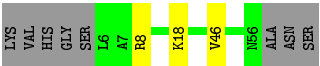
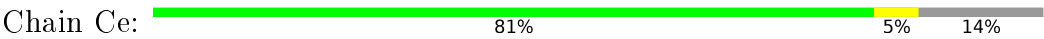


- Molecule 73: 40S RIBOSOMAL PROTEIN US8

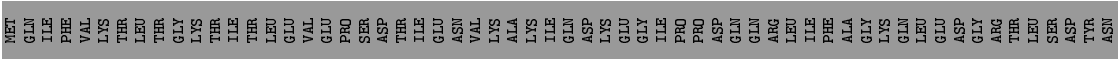


- Molecule 74: 40S RIBOSOMAL PROTEIN US12





● Molecule 82: 40S RIBOSOMAL PROTEIN ES31



● Molecule 83: 40S RIBOSOMAL PROTEIN RACK1



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	CTFFIND3	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	115000	Depositor
Image detector	TVIPS TEMCAM-F416 (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: GNP, 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	AA	0.53	0/1809	1.02	17/2819 (0.6%)
10	BD	0.49	2/2407 (0.1%)	0.70	1/3221 (0.0%)
11	BE	0.52	0/1312	0.73	0/1763
12	BF	0.45	0/1986	0.68	0/2644
13	BG	0.46	0/1914	0.72	0/2578
14	BH	0.43	0/1555	0.69	0/2089
15	BI	0.42	0/1643	0.67	0/2194
16	BJ	0.49	0/1386	0.71	0/1852
17	BL	0.53	2/1647 (0.1%)	0.73	3/2205 (0.1%)
18	BM	0.49	0/1162	0.70	0/1556
19	BN	0.43	0/1754	0.65	0/2348
2	AB	0.65	1/4926 (0.0%)	1.15	29/6641 (0.4%)
20	BO	0.44	0/1639	0.69	0/2193
21	BP	0.44	0/1260	0.70	0/1691
22	BQ	0.45	0/1518	0.74	0/2026
23	BR	0.41	0/1542	0.64	0/2037
24	BS	0.44	0/1479	0.73	0/1985
25	BT	0.46	0/1326	0.71	0/1770
26	BU	0.47	0/841	0.71	0/1128
27	BV	0.43	0/978	0.63	0/1312
28	BW	0.43	0/542	0.59	0/722
29	BX	0.41	0/993	0.67	0/1334
3	AC	1.52	10/6230 (0.2%)	2.37	535/9712 (5.5%)
30	BY	0.47	0/1082	0.72	1/1441 (0.1%)
31	BZ	0.47	0/1138	0.79	0/1517
32	Ba	0.45	0/1191	0.71	0/1591
33	Bb	0.45	0/570	0.72	0/752
34	Bc	0.46	0/813	0.70	0/1091
35	Bd	0.45	0/920	0.67	0/1238
36	Be	0.45	0/1071	0.68	0/1428
37	Bf	0.50	0/885	0.81	0/1185
38	Bg	0.48	0/917	0.74	0/1222

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	Bh	0.38	0/1023	0.64	0/1351
4	A2	0.41	23/86672 (0.0%)	0.81	40/135198 (0.0%)
40	Bi	0.43	0/793	0.75	0/1048
41	Bj	0.49	0/704	0.76	0/931
42	Bk	0.43	0/575	0.73	0/761
43	Bl	0.41	0/454	0.61	0/599
44	Bm	0.42	0/435	0.70	0/575
45	Bn	0.40	0/241	0.51	0/305
46	Bo	0.45	0/885	0.74	0/1166
47	Bp	0.40	0/718	0.61	0/953
48	Bt	0.48	0/1058	0.75	0/1416
49	Bu	0.45	0/1639	0.69	1/2222 (0.0%)
5	A3	0.36	0/3723	0.79	1/5800 (0.0%)
50	C1	0.37	2/41550 (0.0%)	0.80	6/64763 (0.0%)
51	CA	0.51	0/1756	0.68	0/2386
52	CB	0.51	0/1756	0.75	1/2350 (0.0%)
53	CC	0.42	0/1761	0.65	0/2379
54	CD	0.40	0/1672	0.66	0/2250
55	CE	0.47	0/2072	0.70	0/2793
56	CF	0.43	0/1507	0.74	0/2026
57	CG	0.48	0/1907	0.74	0/2538
58	CH	0.46	0/1558	0.74	1/2087 (0.0%)
59	CI	0.47	0/1724	0.72	0/2298
6	A4	0.38	0/2836	0.81	3/4421 (0.1%)
60	CJ	0.46	0/1520	0.77	0/2030
61	CK	0.48	0/815	0.68	0/1101
62	CL	0.45	0/1220	0.72	0/1633
63	CM	0.48	0/941	0.72	0/1264
64	CN	0.43	0/1231	0.73	1/1656 (0.1%)
65	CO	0.46	0/1036	0.71	0/1391
66	CP	0.43	0/1000	0.67	0/1335
67	CQ	0.43	0/1125	0.66	0/1506
68	CR	0.42	0/904	0.67	0/1208
69	CS	0.42	0/1190	0.68	0/1594
7	BA	0.44	0/1926	0.67	0/2583
70	CT	0.44	0/1131	0.69	0/1515
71	CU	0.50	0/813	0.70	0/1092
72	CV	0.47	0/643	0.71	0/860
73	CW	0.44	0/1050	0.69	0/1406
74	CX	0.46	0/1063	0.70	0/1421
75	CY	0.45	0/1019	0.70	0/1354
76	CZ	0.46	0/611	0.71	0/820
77	Ca	0.48	0/778	0.75	1/1041 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
78	Cb	0.48	0/637	0.68	0/854
79	Cc	0.46	0/492	0.74	0/657
8	BB	0.45	0/3258	0.73	2/4361 (0.0%)
80	Cd	0.51	0/454	0.76	0/603
81	Ce	0.45	0/417	0.69	0/548
82	Cf	0.53	0/507	0.84	1/673 (0.1%)
83	Cg	0.45	0/2497	0.67	0/3399
9	BC	0.47	0/2943	0.73	0/3953
All	All	0.49	40/240676 (0.0%)	0.86	644/353759 (0.2%)

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
2	AB	0	14
3	AC	0	105
4	A2	0	35
5	A3	0	2
50	C1	0	24
All	All	0	180

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A2	1701	C	C5'-C4'	18.44	1.73	1.51
4	A2	1673	C	C3'-O3'	15.36	1.63	1.42
4	A2	1701	C	O5'-C5'	14.46	1.67	1.44
4	A2	1673	C	O3'-P	14.13	1.78	1.61
4	A2	1701	C	P-O5'	13.49	1.73	1.59

The worst 5 of 644 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A2	1701	C	O4'-C4'-C3'	-15.17	88.83	104.00
2	AB	1133	TYR	CB-CG-CD2	-14.76	112.14	121.00
8	BB	258	HIS	C-N-CD	-13.97	89.87	120.60
1	AA	8	U	C5'-C4'-C3'	13.49	137.58	116.00
4	A2	1701	C	O4'-C1'-N1	12.28	118.02	108.20

There are no chirality outliers.

5 of 180 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AB	1105	PRO	Mainchain
2	AB	834	HIS	Peptide
2	AB	836	LYS	Peptide
2	AB	880	GLN	Mainchain
2	AB	899	ILE	Mainchain

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	1619	0	814	327	0
2	AB	4846	0	4956	1414	0
3	AC	5574	0	2810	338	0
4	A2	77488	0	39154	7347	0
5	A3	3334	0	1693	288	0
6	A4	2538	0	1286	246	0
7	BA	1888	0	1983	131	0
8	BB	3190	0	3327	184	0
9	BC	2889	0	3064	239	0
10	BD	2362	0	2385	139	0
11	BE	1287	0	1398	154	0
12	BF	1950	0	2093	142	0
13	BG	1881	0	2018	121	0
14	BH	1536	0	1611	101	0
15	BI	1605	0	1651	79	0
16	BJ	1363	0	1397	123	0
17	BL	1617	0	1725	100	0
18	BM	1139	0	1204	130	0
19	BN	1709	0	1761	82	0
20	BO	1607	0	1745	125	0
21	BP	1234	0	1263	72	0
22	BQ	1494	0	1612	96	0
23	BR	1526	0	1681	99	0
24	BS	1439	0	1472	87	0
25	BT	1298	0	1366	107	0
26	BU	827	0	852	27	0
27	BV	964	0	1026	42	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	BW	529	0	541	31	0
29	BX	976	0	1053	43	0
30	BY	1065	0	1145	85	0
31	BZ	1115	0	1194	73	0
32	Ba	1162	0	1213	0	0
33	Bb	560	0	590	0	0
34	Bc	802	0	845	0	0
35	Bd	905	0	947	0	0
36	Be	1053	0	1144	0	0
37	Bf	866	0	904	0	0
38	Bg	907	0	1002	0	0
39	Bh	1015	0	1148	0	0
40	Bi	783	0	862	0	0
41	Bj	690	0	719	0	0
42	Bk	569	0	637	0	0
43	Bl	444	0	483	0	0
44	Bm	429	0	466	0	0
45	Bn	240	0	287	0	0
46	Bo	871	0	943	0	0
47	Bp	708	0	760	0	0
48	Bt	1043	0	1120	0	0
49	Bu	1622	0	1563	0	0
50	C1	37159	0	18774	3943	0
51	CA	1719	0	1717	127	0
52	CB	1729	0	1803	138	0
53	CC	1724	0	1808	117	0
54	CD	1646	0	1737	86	0
55	CE	2031	0	2138	116	0
56	CF	1486	0	1543	116	0
57	CG	1884	0	2044	154	0
58	CH	1535	0	1632	130	0
59	CI	1695	0	1783	123	0
60	CJ	1495	0	1615	91	0
61	CK	791	0	811	44	0
62	CL	1199	0	1269	67	0
63	CM	931	0	961	42	0
64	CN	1207	0	1292	64	0
65	CO	1023	0	1050	88	0
66	CP	981	0	1026	54	0
67	CQ	1108	0	1172	88	0
68	CR	893	0	946	58	0
69	CS	1172	0	1229	75	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
70	CT	1112	0	1146	115	0
71	CU	803	0	866	69	0
72	CV	636	0	637	42	0
73	CW	1033	0	1080	64	0
74	CX	1046	0	1110	78	0
75	CY	1002	0	1075	66	0
76	CZ	605	0	665	58	0
77	Ca	767	0	816	0	0
78	Cb	625	0	640	0	0
79	Cc	490	0	520	0	0
80	Cd	444	0	442	0	0
81	Ce	412	0	463	0	0
82	Cf	497	0	497	0	0
83	Cg	2440	0	2396	0	0
84	AB	32	0	13	7	0
85	AB	1	0	0	0	0
All	All	223911	0	165629	16508	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 46.

The worst 5 of 16508 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)
2:AB:1116:ARG:CD	50:C1:488:U:C6	1.76	1.69
2:AB:1116:ARG:CB	50:C1:488:U:C5	1.78	1.62
1:AA:75:C:H5	2:AB:1316:PHE:CD2	1.14	1.62
2:AB:817:GLU:CB	2:AB:1172:VAL:HG12	1.27	1.60
2:AB:927:ARG:HH12	2:AB:1158:GLY:CA	1.16	1.59

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AB	605/627 (96%)	523 (86%)	50 (8%)	32 (5%)	2	29
7	BA	245/257 (95%)	236 (96%)	6 (2%)	3 (1%)	16	61
8	BB	394/403 (98%)	369 (94%)	11 (3%)	14 (4%)	4	38
9	BC	362/427 (85%)	338 (93%)	9 (2%)	15 (4%)	3	35
10	BD	288/297 (97%)	279 (97%)	4 (1%)	5 (2%)	11	55
11	BE	156/158 (99%)	141 (90%)	8 (5%)	7 (4%)	3	33
12	BF	232/248 (94%)	225 (97%)	3 (1%)	4 (2%)	11	55
13	BG	233/266 (88%)	217 (93%)	7 (3%)	9 (4%)	4	36
14	BH	190/192 (99%)	184 (97%)	3 (2%)	3 (2%)	12	56
15	BI	192/214 (90%)	187 (97%)	2 (1%)	3 (2%)	12	56
16	BJ	168/178 (94%)	153 (91%)	3 (2%)	12 (7%)	1	22
17	BL	198/211 (94%)	178 (90%)	9 (4%)	11 (6%)	2	28
18	BM	138/215 (64%)	132 (96%)	4 (3%)	2 (1%)	14	58
19	BN	202/204 (99%)	193 (96%)	6 (3%)	3 (2%)	13	57
20	BO	194/203 (96%)	187 (96%)	4 (2%)	3 (2%)	13	57
21	BP	151/184 (82%)	141 (93%)	7 (5%)	3 (2%)	9	51
22	BQ	182/188 (97%)	169 (93%)	7 (4%)	6 (3%)	5	40
23	BR	181/196 (92%)	175 (97%)	3 (2%)	3 (2%)	11	55
24	BS	171/176 (97%)	158 (92%)	7 (4%)	6 (4%)	4	39
25	BT	157/160 (98%)	150 (96%)	4 (2%)	3 (2%)	10	52
26	BU	100/128 (78%)	97 (97%)	3 (3%)	0	100	100
27	BV	126/140 (90%)	119 (94%)	5 (4%)	2 (2%)	12	56
28	BW	62/157 (40%)	61 (98%)	1 (2%)	0	100	100
29	BX	117/156 (75%)	113 (97%)	4 (3%)	0	100	100
30	BY	126/145 (87%)	119 (94%)	4 (3%)	3 (2%)	7	47
31	BZ	134/136 (98%)	125 (93%)	5 (4%)	4 (3%)	5	42
32	Ba	145/148 (98%)	134 (92%)	6 (4%)	5 (3%)	5	40
33	Bb	67/159 (42%)	60 (90%)	3 (4%)	4 (6%)	2	26
34	Bc	102/115 (89%)	99 (97%)	1 (1%)	2 (2%)	9	51
35	Bd	107/125 (86%)	103 (96%)	3 (3%)	1 (1%)	21	67

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	Be	126/135 (93%)	117 (93%)	6 (5%)	3 (2%)	7	47
37	Bf	105/110 (96%)	96 (91%)	4 (4%)	5 (5%)	3	32
38	Bg	113/117 (97%)	103 (91%)	6 (5%)	4 (4%)	4	39
39	Bh	120/123 (98%)	112 (93%)	5 (4%)	3 (2%)	7	46
40	Bi	95/105 (90%)	85 (90%)	4 (4%)	6 (6%)	2	25
41	Bj	83/97 (86%)	75 (90%)	6 (7%)	2 (2%)	7	47
42	Bk	67/70 (96%)	64 (96%)	2 (3%)	1 (2%)	13	57
43	Bl	48/51 (94%)	46 (96%)	1 (2%)	1 (2%)	9	50
44	Bm	50/128 (39%)	48 (96%)	1 (2%)	1 (2%)	9	51
45	Bn	23/25 (92%)	23 (100%)	0	0	100	100
46	Bo	104/106 (98%)	98 (94%)	4 (4%)	2 (2%)	10	52
47	Bp	89/92 (97%)	83 (93%)	3 (3%)	3 (3%)	5	40
48	Bt	128/137 (93%)	112 (88%)	9 (7%)	7 (6%)	2	29
49	Bu	208/210 (99%)	199 (96%)	6 (3%)	3 (1%)	14	58
51	CA	216/263 (82%)	209 (97%)	5 (2%)	2 (1%)	21	67
52	CB	211/264 (80%)	176 (83%)	18 (8%)	17 (8%)	1	19
53	CC	220/293 (75%)	213 (97%)	2 (1%)	5 (2%)	8	48
54	CD	210/243 (86%)	201 (96%)	4 (2%)	5 (2%)	7	47
55	CE	255/263 (97%)	237 (93%)	13 (5%)	5 (2%)	9	51
56	CF	186/204 (91%)	163 (88%)	12 (6%)	11 (6%)	2	27
57	CG	230/249 (92%)	216 (94%)	5 (2%)	9 (4%)	4	36
58	CH	189/194 (97%)	178 (94%)	7 (4%)	4 (2%)	9	50
59	CI	205/208 (99%)	184 (90%)	14 (7%)	7 (3%)	5	40
60	CJ	177/194 (91%)	169 (96%)	5 (3%)	3 (2%)	11	55
61	CK	92/165 (56%)	84 (91%)	1 (1%)	7 (8%)	1	20
62	CL	144/158 (91%)	133 (92%)	5 (4%)	6 (4%)	3	34
63	CM	118/132 (89%)	111 (94%)	1 (1%)	6 (5%)	2	30
64	CN	148/151 (98%)	138 (93%)	5 (3%)	5 (3%)	5	40
65	CO	135/151 (89%)	129 (96%)	3 (2%)	3 (2%)	8	49
66	CP	116/145 (80%)	106 (91%)	5 (4%)	5 (4%)	3	34
67	CQ	137/146 (94%)	129 (94%)	6 (4%)	2 (2%)	13	57

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
68	CR	105/135 (78%)	99 (94%)	4 (4%)	2 (2%)	10	52
69	CS	140/152 (92%)	125 (89%)	7 (5%)	8 (6%)	2	28
70	CT	141/145 (97%)	135 (96%)	4 (3%)	2 (1%)	14	58
71	CU	99/119 (83%)	95 (96%)	3 (3%)	1 (1%)	19	65
72	CV	81/83 (98%)	78 (96%)	1 (1%)	2 (2%)	7	46
73	CW	127/130 (98%)	118 (93%)	7 (6%)	2 (2%)	12	56
74	CX	132/143 (92%)	120 (91%)	5 (4%)	7 (5%)	2	29
75	CY	120/133 (90%)	114 (95%)	2 (2%)	4 (3%)	5	40
76	CZ	74/125 (59%)	71 (96%)	0	3 (4%)	3	35
77	Ca	94/115 (82%)	85 (90%)	5 (5%)	4 (4%)	3	34
78	Cb	78/84 (93%)	70 (90%)	8 (10%)	0	100	100
79	Cc	60/69 (87%)	57 (95%)	1 (2%)	2 (3%)	5	40
80	Cd	51/56 (91%)	44 (86%)	7 (14%)	0	100	100
81	Ce	49/59 (83%)	43 (88%)	5 (10%)	1 (2%)	9	51
82	Cf	59/156 (38%)	53 (90%)	6 (10%)	0	100	100
83	Cg	312/317 (98%)	291 (93%)	14 (4%)	7 (2%)	8	49
All	All	11795/13363 (88%)	11000 (93%)	439 (4%)	356 (3%)	9	42

5 of 356 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	835	SER
2	AB	838	VAL
2	AB	843	LEU
2	AB	897	LYS
2	AB	931	SER

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AB	540/552 (98%)	517 (96%)	23 (4%)	35	70
7	BA	189/199 (95%)	184 (97%)	5 (3%)	54	80
8	BB	344/349 (99%)	326 (95%)	18 (5%)	29	65
9	BC	302/348 (87%)	284 (94%)	18 (6%)	24	60
10	BD	244/250 (98%)	237 (97%)	7 (3%)	50	78
11	BE	143/143 (100%)	135 (94%)	8 (6%)	26	62
12	BF	203/215 (94%)	196 (97%)	7 (3%)	44	75
13	BG	199/223 (89%)	192 (96%)	7 (4%)	43	74
14	BH	171/171 (100%)	164 (96%)	7 (4%)	37	71
15	BI	170/181 (94%)	161 (95%)	9 (5%)	28	64
16	BJ	143/149 (96%)	137 (96%)	6 (4%)	36	70
17	BL	167/177 (94%)	156 (93%)	11 (7%)	21	57
18	BM	118/161 (73%)	114 (97%)	4 (3%)	44	75
19	BN	172/172 (100%)	170 (99%)	2 (1%)	78	90
20	BO	168/174 (97%)	166 (99%)	2 (1%)	78	90
21	BP	133/163 (82%)	126 (95%)	7 (5%)	28	64
22	BQ	162/165 (98%)	157 (97%)	5 (3%)	47	77
23	BR	161/175 (92%)	150 (93%)	11 (7%)	20	57
24	BS	155/157 (99%)	148 (96%)	7 (4%)	34	69
25	BT	139/140 (99%)	134 (96%)	5 (4%)	42	74
26	BU	91/115 (79%)	88 (97%)	3 (3%)	45	76
27	BV	100/107 (94%)	99 (99%)	1 (1%)	82	92
28	BW	55/126 (44%)	52 (94%)	3 (6%)	27	63
29	BX	107/133 (80%)	105 (98%)	2 (2%)	65	86
30	BY	119/135 (88%)	115 (97%)	4 (3%)	44	75
31	BZ	118/118 (100%)	112 (95%)	6 (5%)	29	66
32	Ba	120/121 (99%)	116 (97%)	4 (3%)	45	76
33	Bb	58/126 (46%)	57 (98%)	1 (2%)	68	87
34	Bc	88/97 (91%)	87 (99%)	1 (1%)	80	91
35	Bd	100/110 (91%)	96 (96%)	4 (4%)	38	71
36	Be	115/121 (95%)	112 (97%)	3 (3%)	54	80
37	Bf	87/89 (98%)	79 (91%)	8 (9%)	11	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	Bg	98/100 (98%)	88 (90%)	10 (10%)	9	37
39	Bh	109/110 (99%)	106 (97%)	3 (3%)	51	78
40	Bi	82/89 (92%)	76 (93%)	6 (7%)	17	54
41	Bj	71/80 (89%)	69 (97%)	2 (3%)	51	78
42	Bk	64/65 (98%)	64 (100%)	0	100	100
43	Bl	47/48 (98%)	46 (98%)	1 (2%)	61	84
44	Bm	48/116 (41%)	45 (94%)	3 (6%)	22	59
45	Bn	24/24 (100%)	24 (100%)	0	100	100
46	Bo	94/94 (100%)	89 (95%)	5 (5%)	28	64
47	Bp	74/75 (99%)	72 (97%)	2 (3%)	52	79
48	Bt	113/121 (93%)	106 (94%)	7 (6%)	23	60
49	Bu	177/177 (100%)	163 (92%)	14 (8%)	15	51
51	CA	181/219 (83%)	176 (97%)	5 (3%)	51	78
52	CB	194/231 (84%)	183 (94%)	11 (6%)	25	62
53	CC	188/225 (84%)	181 (96%)	7 (4%)	41	73
54	CD	175/202 (87%)	166 (95%)	9 (5%)	29	66
55	CE	220/225 (98%)	208 (94%)	12 (6%)	27	63
56	CF	158/170 (93%)	151 (96%)	7 (4%)	35	69
57	CG	202/218 (93%)	195 (96%)	7 (4%)	43	74
58	CH	171/174 (98%)	167 (98%)	4 (2%)	58	83
59	CI	179/180 (99%)	167 (93%)	12 (7%)	20	57
60	CJ	160/168 (95%)	150 (94%)	10 (6%)	22	59
61	CK	85/136 (62%)	82 (96%)	3 (4%)	43	74
62	CL	133/142 (94%)	131 (98%)	2 (2%)	72	88
63	CM	102/108 (94%)	96 (94%)	6 (6%)	24	61
64	CN	130/131 (99%)	128 (98%)	2 (2%)	72	88
65	CO	107/119 (90%)	100 (94%)	7 (6%)	21	58
66	CP	107/130 (82%)	102 (95%)	5 (5%)	32	68
67	CQ	115/121 (95%)	111 (96%)	4 (4%)	43	74
68	CR	99/122 (81%)	94 (95%)	5 (5%)	29	66
69	CS	123/132 (93%)	114 (93%)	9 (7%)	17	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
70	CT	113/115 (98%)	106 (94%)	7 (6%)	23	60
71	CU	93/107 (87%)	89 (96%)	4 (4%)	35	70
72	CV	67/67 (100%)	66 (98%)	1 (2%)	72	88
73	CW	112/113 (99%)	107 (96%)	5 (4%)	34	69
74	CX	108/115 (94%)	103 (95%)	5 (5%)	33	68
75	CY	107/115 (93%)	101 (94%)	6 (6%)	26	62
76	CZ	67/103 (65%)	63 (94%)	4 (6%)	24	60
77	Ca	83/98 (85%)	76 (92%)	7 (8%)	14	48
78	Cb	72/76 (95%)	68 (94%)	4 (6%)	26	62
79	Cc	55/62 (89%)	52 (94%)	3 (6%)	27	63
80	Cd	47/49 (96%)	43 (92%)	4 (8%)	13	48
81	Ce	42/48 (88%)	40 (95%)	2 (5%)	31	67
82	Cf	54/140 (39%)	51 (94%)	3 (6%)	26	62
83	Cg	272/275 (99%)	260 (96%)	12 (4%)	35	69
All	All	10303/11397 (90%)	9847 (96%)	456 (4%)	39	69

5 of 456 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	Bf	89	ARG
49	Bu	110	LEU
77	Ca	21	ILE
38	Bg	36	LYS
44	Bm	112	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 227 such sidechains are listed below:

Mol	Chain	Res	Type
29	BX	111	GLN
40	Bi	80	HIS
75	CY	19	GLN
30	BY	72	GLN
33	Bb	50	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	75/76 (98%)	14 (18%)	1 (1%)
3	AC	259/504 (51%)	135 (52%)	40 (15%)
4	A2	3605/5025 (71%)	2041 (56%)	325 (9%)
5	A3	156/194 (80%)	82 (52%)	6 (3%)
50	C1	1738/1869 (92%)	1038 (59%)	151 (8%)
6	A4	118/121 (97%)	68 (57%)	9 (7%)
All	All	5951/7789 (76%)	3378 (56%)	532 (8%)

5 of 3378 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	2	C
1	AA	17	C
1	AA	18	G
1	AA	19	G
1	AA	20	U

5 of 532 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	A2	2703	G
4	A2	4236	G
50	C1	1411	G
4	A2	2749	C
4	A2	3845	A

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](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length

(or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
84	GNP	AB	2434	85	29,34,34	2.75	8 (27%)	28,54,54	1.83	6 (21%)

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
84	GNP	AB	2434	85	-	0/16/38/38	0/3/3/3

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	AB	2434	GNP	C4-N9	-9.56	1.35	1.47
84	AB	2434	GNP	C5-C6	-4.95	1.44	1.53
84	AB	2434	GNP	C8-N9	-3.50	1.36	1.47
84	AB	2434	GNP	C2'-C1'	-3.02	1.43	1.53
84	AB	2434	GNP	PB-O3A	-2.74	1.55	1.59

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	AB	2434	GNP	O6-C6-N1	-2.77	119.17	122.80
84	AB	2434	GNP	O2G-PG-O1G	2.26	119.53	113.58
84	AB	2434	GNP	O2A-PA-O3A	2.41	115.59	105.27
84	AB	2434	GNP	O3A-PB-N3B	2.41	112.71	106.07
84	AB	2434	GNP	O6-C6-C5	3.84	127.03	119.69

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
84	AB	2434	GNP	7	0

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.