



wwPDB EM Map/Model Validation Report

Apr 10, 2016 – 03:25 PM BST

PDB ID : 4V7E
EMDB ID: : EMD-1780
Title : Model of the small subunit RNA based on a 5.5 Å cryo-EM map of *Triticum aestivum* translating 80S ribosome
Authors : Barrio-Garcia, C.; Armache, J.-P.; Jarasch, A.; Anger, A.M.; Villa, E.; Becker, T.; Bhushan, S.; Jossinet, F.; Habeck, M.; Dindar, G.; Franckenberg, S.; Marquez, V.; Mielke, T.; Thomm, M.; Berninghausen, O.; Beatrix, B.; Soeding, J.; Westhof, E.; Wilson, D.N.; Beckmann, R.
Deposited on : 2013-11-22
Resolution : 5.50 Å(reported)

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) : trunk27241

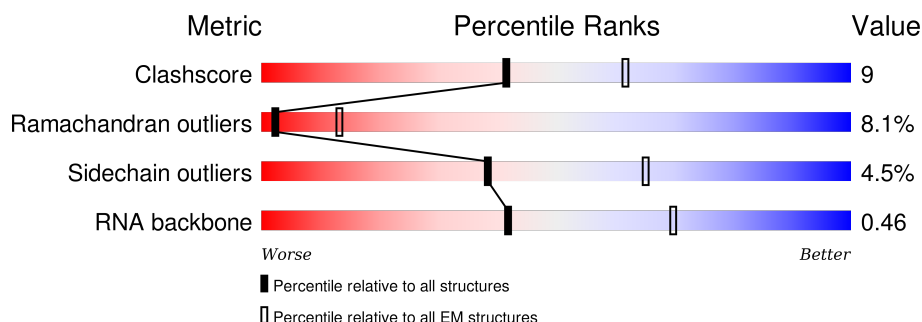
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.50 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.



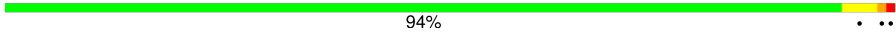









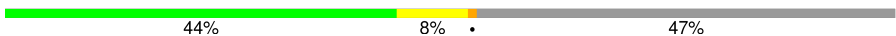






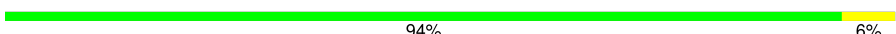







Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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	Ad	1810	
2	Ae	75	
3	Af	11	
4	BY	138	
5	BI	220	
6	BK	183	
7	BM	171	
8	Bf	155	






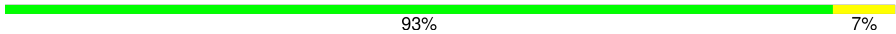



















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Mol	Chain	Length	Quality of chain
9	BX	142	 94% . . .
10	Bg	380	 92% 7% .
11	BD	208	 73% 24% .
12	BE	265	 70% 5% 25%
13	BF	191	 92% 7% .
14	BQ	149	 66% 15% . 15%
15	BU	128	 85% 12% .
16	BO	151	 66% 11% . 21%
17	BS	152	 76% 20% .
18	BN	151	 64% 15% . 20%
19	BL	160	 44% 8% . 47%
20	BT	146	 88% 10% .
21	BP	154	 49% 6% . . 41%
22	BZ	108	 74% 14% 5% 7%
23	Bc	65	 66% 18% 5% 11%
24	BW	130	 83% 15% .
25	Bd	56	 63% 16% 7% 14%
26	Bb	86	 94% 6%
27	Be	62	 89% 8% .
28	BA	260	 69% 7% 24%
29	BR	141	 73% 9% . 18%
30	BB	262	 68% 12% 19%
31	BV	82	 84% 9% 7%
32	Ba	133	 59% 11% . 30%
33	BJ	195	 90% . . .










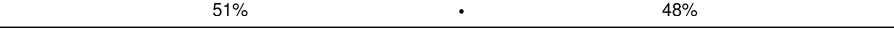
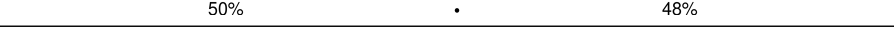
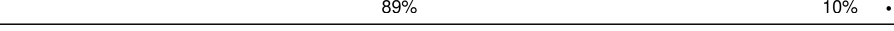





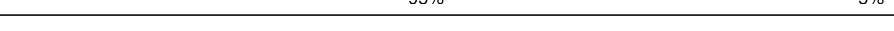

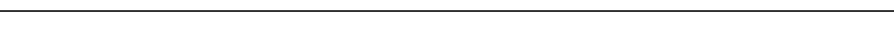

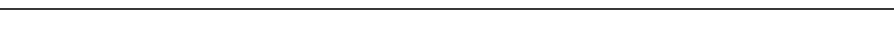
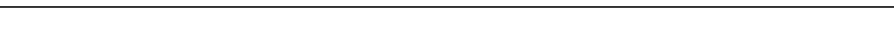


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Mol	Chain	Length	Quality of chain
34	BC	263	
35	BG	245	
36	BH	189	
37	CG	257	
38	CT	164	
39	CZ	136	
40	Cz	216	
41	CA	261	
42	CJ	180	
43	CH	190	
44	CV	140	
45	CN	200	
46	Ca	144	
47	CQ	188	
48	CD	304	
49	CR	209	
50	CP	171	
51	CX	152	
52	CW	162	
53	CY	150	
54	Cr	147	
55	Cc	112	
56	Cd	123	
57	Ce	133	
58	Cj	94	

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Mol	Chain	Length	Quality of chain
59	Cl	51	
60	Co	105	
61	CM	134	
62	CS	178	
63	CU	130	
64	Ci	112	
65	CK	166	
66	Cu	110	
66	Cv	110	
67	Cs	113	
67	Ct	113	
68	Ch	124	
69	CF	244	
70	Cq	319	
71	CB	389	
72	CC	405	
73	CO	206	
74	Cp	92	
75	CI	224	
76	Cn	25	
77	Cm	53	
78	CL	208	
79	CE	219	
80	Cf	111	
81	Ck	69	

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Mol	Chain	Length	Quality of chain
82	Cb	60	<div><div></div><div>90%</div><div></div><div></div><div></div></div>
83	Cg	119	<div><div></div><div>82%</div><div>10%</div><div>8%</div><div></div></div>
84	Aa	3391	<div><div></div><div>71%</div><div>25%</div><div></div><div></div></div>
85	Ac	160	<div><div></div><div>68%</div><div>28%</div><div></div><div></div></div>
86	Ab	120	<div><div></div><div>67%</div><div>32%</div><div></div><div></div></div>

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 212263 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 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Ad	1762	Total	C	N	O	P	0	0
			37584	16788	6708	12327	1761		

- Molecule 2 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Ae	75	Total	C	N	O	P	0	0
			1595	712	280	529	74		

- Molecule 3 is a RNA chain called 5'-R(*AP*AP*AP*AP*GP*AP*CP*UP*UP*CP*A)-3'.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Af	11	Total	C	N	O	P	0	0
			232	106	45	71	10		

- Molecule 4 is a protein called 40S ribosomal protein S24E.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	BY	138	Total	C	N	O	S	0	0
			1108	703	212	189	4		

- Molecule 5 is a protein called 40S ribosomal protein S8E.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	BI	66	Total	C	N	O	S	0	0
			533	330	105	95	3		

- Molecule 6 is a protein called 40S ribosomal protein S10E.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	BK	96	Total	C	N	O	S	0	0
			818	535	137	143	3		

- Molecule 7 is a protein called 40S ribosomal protein S12E.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	BM	123	Total	C	N	O	S	0	0
			924	577	159	179	9		

- Molecule 8 is a protein called 40S ribosomal protein S31e.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Bf	71	Total	C	N	O	S	0	0
			577	367	107	98	5		

- Molecule 9 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	BX	142	Total	C	N	O	S	0	0
			1103	698	214	187	4		

- Molecule 10 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Bg	380	Total	C	N	O	S	0	0
			2929	1813	530	567	19		

- Molecule 11 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	BD	208	Total	C	N	O	S	0	0
			1629	1029	294	297	9		

- Molecule 12 is a protein called 40S ribosomal protein S4E.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	BE	200	Total	C	N	O	S	0	0
			1607	1030	290	283	4		

- Molecule 13 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	BF	191	Total	C	N	O	S	0	0
			1489	928	281	273	7		

- Molecule 14 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	BQ	126	Total	C	N	O	S	0	0
			1017	648	195	170	4		

- Molecule 15 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	BU	128	Total	C	N	O	S	0	0
			982	613	176	187	6		

- Molecule 16 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	BO	119	Total	C	N	O	S	0	0
			899	550	178	167	4		

- Molecule 17 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	BS	152	Total	C	N	O	S	0	0
			1240	772	248	213	7		

- Molecule 18 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	BN	121	Total	C	N	O	S	0	0
			977	627	180	167	3		

- Molecule 19 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	BL	85	Total	C	N	O	S	0	0
			688	435	134	115	4		

- Molecule 20 is a protein called 40S ribosomal protein S19E.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	BT	146	Total	C	N	O	S	0	0
			1155	726	218	207	4		

- Molecule 21 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	BP	91	Total	C	N	O	S	0	0
			711	457	130	120	4		

- Molecule 22 is a protein called 40S ribosomal protein S25E.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BZ	100	Total	C	N	O	S	0	0
			779	489	146	144			

- Molecule 23 is a protein called 40S ribosomal protein S28E.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Bc	58	Total	C	N	O	S	0	0
			454	281	86	84	3		

- Molecule 24 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BW	130	Total	C	N	O	S	0	0
			1042	667	189	181	5		

- Molecule 25 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Bd	48	Total	C	N	O	S	0	0
			379	233	77	63	6		

- Molecule 26 is a protein called 40S ribosomal protein S27E.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Bb	86	Total	C	N	O	S	0	0
			663	414	119	122	8		

- Molecule 27 is a protein called 40S ribosomal protein S30E.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Be	60	Total	C	N	O	S	0	0
			469	289	104	75	1		

- Molecule 28 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BA	197	Total	C	N	O	S	0	0
			1537	969	280	278	10		

- Molecule 29 is a protein called 40S ribosomal protein S17E.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BR	116	Total	C	N	O	S	0	0
			945	589	178	171	7		

- Molecule 30 is a protein called 40S ribosomal protein S1E.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BB	211	Total	C	N	O	S	0	0
			1707	1089	308	302	8		

- Molecule 31 is a protein called 40S ribosomal protein S21E.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BV	76	Total	C	N	O	S	0	0
			601	371	112	115	3		

- Molecule 32 is a protein called 40S ribosomal protein S26E.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ba	93	Total	C	N	O	S	0	0
			753	461	163	122	7		

- Molecule 33 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BJ	187	Total	C	N	O	S	0	0
			1525	959	305	256	5		

- Molecule 34 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BC	214	Total	C	N	O	S	0	0
			1665	1074	297	287	7		

- Molecule 35 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BG	231	Total	C	N	O	S	0	0
			1867	1164	367	328	8		

- Molecule 36 is a protein called 40S ribosomal protein S7E.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BH	184	Total	C	N	O	S	0	0
			1508	962	278	266	2		

- Molecule 37 is a protein called 60S ribosomal protein L8E.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	CG	237	Total	C	N	O	S	0	0
			1906	1226	351	322	7		

- Molecule 38 is a protein called 60S ribosomal protein L21E.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	CT	160	Total	C	N	O	S	0	0
			1288	814	251	219	4		

- Molecule 39 is a protein called 60S ribosomal protein L27E.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	CZ	136	Total	C	N	O	S	0	0
			1090	704	205	176	5		

- Molecule 40 is a protein called 60S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Cz	216	Total	C	N	O	S	0	0
			1718	1092	309	304	13		

- Molecule 41 is a protein called 60S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	CA	255	Total	C	N	O	S	0	0
			1946	1210	399	328	9		

- Molecule 42 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	CJ	170	Total	C	N	O	S	0	0
			1380	869	256	246	9		

- Molecule 43 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	CH	190	Total	C	N	O	S	0	0
			1500	947	270	277	6		

- Molecule 44 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	CV	140	Total	C	N	O	S	0	0
			1048	658	199	181	10		

- Molecule 45 is a protein called 60S ribosomal protein L15E.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	CN	194	Total	C	N	O	S	0	0
			1630	1027	342	257	4		

- Molecule 46 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Ca	144	Total	C	N	O	S	0	0
			1114	710	223	175	6		

- Molecule 47 is a protein called 60S ribosomal protein L18E.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	CQ	163	Total	C	N	O	S	0	0
			1284	810	248	219	7		

- Molecule 48 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	CD	304	Total	C	N	O	S	0	0
			2444	1531	440	466	7		

- Molecule 49 is a protein called 60S ribosomal protein L19E.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	CR	189	Total	C	N	O	S	0	0
			1569	972	330	257	10		

- Molecule 50 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	CP	171	Total	C	N	O	S	0	0
			1372	852	271	244	5		

- Molecule 51 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	CX	122	Total	C	N	O	S	0	0
			987	634	178	173	2		

- Molecule 52 is a protein called 60S ribosomal protein L24E.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	CW	75	Total	C	N	O	S	0	0
			635	408	126	97	4		

- Molecule 53 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	CY	130	Total	C	N	O	S	0	0
			1048	647	220	178	3		

- Molecule 54 is a protein called 60S ribosomal protein L28E.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Cr	73	Total	C	N	O	S	0	0
			576	364	107	103	2		

- Molecule 55 is a protein called 60S ribosomal protein L30E.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Cc	112	Total	C	N	O	S	0	0
			857	540	149	161	7		

- Molecule 56 is a protein called 60S ribosomal protein L31E.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Cd	120	Total	C	N	O	S	0	0
			960	598	186	173	3		

- Molecule 57 is a protein called 60S ribosomal protein L32E.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Ce	133	Total	C	N	O	S	0	0
			1103	696	216	185	6		

- Molecule 58 is a protein called 60S ribosomal protein L37E.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Cj	94	Total	C	N	O	S	0	0
			755	459	166	123	7		

- Molecule 59 is a protein called 60S ribosomal protein L39E.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Cl	51	Total	C	N	O	S	0	0
			460	291	100	67	2		

- Molecule 60 is a protein called 60S ribosomal protein L44E.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Co	105	Total	C	N	O	S	0	0
			851	535	166	144	6		

- Molecule 61 is a protein called 60S ribosomal protein L14E.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	CM	134	Total	C	N	O	S	0	0
			1081	690	201	185	5		

- Molecule 62 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	CS	167	Total	C	N	O	S	0	0
			1419	916	263	233	7		

- Molecule 63 is a protein called 60S ribosomal protein L22E.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	CU	108	Total	C	N	O	S	0	0
			864	551	155	156	2		

- Molecule 64 is a protein called 60S ribosomal protein L36E.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Ci	77	Total	C	N	O	S	0	0
			613	383	128	100	2		

- Molecule 65 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	CK	128	Total	C	N	O	S	0	0
			960	602	177	177	4		

- Molecule 66 is a protein called 60S ribosomal protein P1.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Cu	58	Total	C	N	O	S	0	0
			432	283	69	79	1		
66	Cv	58	Total	C	N	O	S	0	0
			432	283	69	79	1		

- Molecule 67 is a protein called Acidic ribosomal protein P2.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Cs	59	Total	C	N	O	S	0	0
			441	278	69	90	4		
67	Ct	59	Total	C	N	O	S	0	0
			441	278	69	90	4		

- Molecule 68 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Ch	124	Total	C	N	O	S	0	0
			1012	636	202	173	1		

- Molecule 69 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	CF	244	Total	C	N	O	S	0	0
			1984	1271	368	339	6		

- Molecule 70 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Cq	262	Total	C	N	O	S	0	0
			1993	1278	330	377	8		

- Molecule 71 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	CB	389	Total	C	N	O	S	0	0
			3139	1997	584	540	18		

- Molecule 72 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	CC	372	Total	C	N	O	S	0	0
			2898	1823	556	510	9		

- Molecule 73 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	CO	206	Total	C	N	O	S	0	0
			1650	1045	320	274	11		

- Molecule 74 is a protein called 60S ribosomal protein L43E.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Cp	92	Total	C	N	O	S	0	0
			715	447	137	124	7		

- Molecule 75 is a protein called 60S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	CI	184	Total	C	N	O	S	0	0
			1490	941	290	247	12		

- Molecule 76 is a protein called 60S ribosomal protein L41E.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Cn	25	Total	C	N	O	S	0	0
			238	145	62	28	3		

- Molecule 77 is a protein called 60S ribosomal protein L40E.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Cm	52	Total	C	N	O	S	0	0
			428	267	90	66	5		

- Molecule 78 is a protein called 60S ribosomal protein L13E.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	CL	208	Total	C	N	O	S	0	0
			1691	1061	338	286	6		

- Molecule 79 is a protein called 60S ribosomal protein L6E.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	CE	219	Total	C	N	O	S	0	0
			1731	1106	314	307	4		

- Molecule 80 is a protein called 60S ribosomal protein L33E.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Cf	111	Total	C	N	O	S	0	0
			891	561	170	156	4		

- Molecule 81 is a protein called 60S ribosomal protein L38E.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Ck	69	Total	C	N	O	S	0	0
			564	360	104	97	3		

- Molecule 82 is a protein called 60S ribosomal protein L29E.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Cb	58	Total	C	N	O	S	0	0
			477	288	103	85	1		

- Molecule 83 is a protein called 60S ribosomal protein L34E.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Cg	110	Total	C	N	O	S	0	0
			897	567	182	146	2		

- Molecule 84 is a RNA chain called 60S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Aa	3391	Total	C	N	O	P	0	0
			72601	32373	13241	23598	3389		

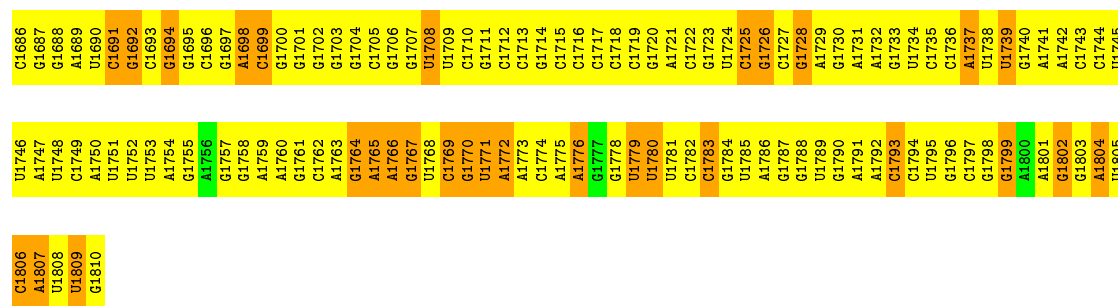
- Molecule 85 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	Ac	160	Total	C	N	O	P	0	0
			3408	1522	614	1113	159		

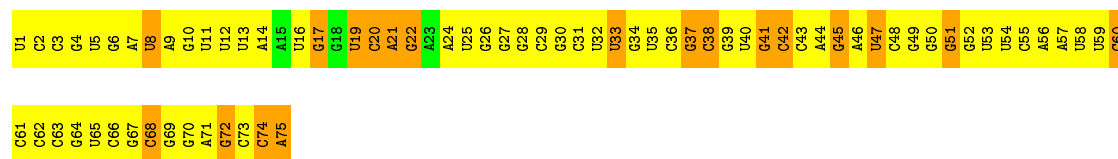
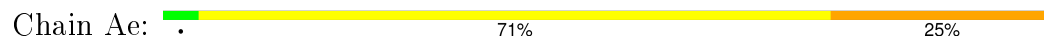
- Molecule 86 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	Ab	120	Total	C	N	O	P	0	0
			2561	1144	461	837	119		

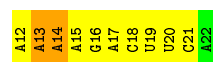
C1626	G1566	U1443	G1382	G1322	U1262	G1202	A1142	C1082	U1022	G962	C902	G842	G782	A722
C1627	G1567	G1444	U1383	U1323	C1263	G1203	A1143	C1083	C1023	U963	A903	G843	C783	A723
C1628	U1568	C1445	U1384	U1324	U1264	G1204	A1144	U1084	A1024	U964	A904	C844	C784	A724
U1629	U1569	C1446	C1385	A1325	G1265	G1205	G1145	U1085	A1025	U965	A905	C845	A785	U725
G1630	G1570	C1447	U1386	A1326	U1266	A1206	G1146	A1086	C1026	U966	G906	U846	C786	G726
C1631	G1571	U1387	C1327	C1327	G1267	A1207	A1147	U1087	C1027	C967	G907	U847	C787	G727
C1632	U1572	A1388	G1328	G1328	G1268	A1208	A1148	G1088	A1028	U968	U908	C848	C788	C728
C1633	C1573	G1389	A1329	A1329	G1269	C1209	U1149	A1089	U1029	U969	G909	C849	C789	C729
U1634	U1574	A1390	A1330	A1330	U1270	G1210	U1150	G1090	A1030	U970	A910	G850	C790	G730
U1635	U1575	C1391	C1331	C1331	G1271	U1211	G1151	A1091	A1031	A971	A911	G851	C791	G731
U1636	C1576	G1392	G1332	G1332	G1272	A1212	A1152	A1092	A1032	A972	A912	A852	C792	G732
G1637	A1577	G1393	A1333	A1333	U1273	C1213	G1153	A1093	C1033	U973	U913	U853	G793	U733
C1638	U1578	A1394	G1334	G1334	G1274	C1214	G1154	U1094	G1034	C974	U914	C854	C794	C734
A1639	C1579	C1395	A1335	A1335	G1275	A1215	G1155	C1095	A1035	A975	C915	G855	A795	G735
C1640	G1580	U1396	C1336	C1336	U1276	G1216	A1156	A1096	U1036	A976	U916	G856	U796	U736
A1641	U1581	C1397	C1337	C1337	G1277	G1217	A1157	A1097	G1037	G977	U917	A857	A797	G737
C1642	G1582	G1398	U1338	U1338	U1278	U1218	G1158	A1098	C1038	A978	G918	G858	C798	U738
A1643	G1583	G1399	C1339	C1339	A1279	C1219	G1159	G1099	A1039	A979	G919	U859	C799	U739
C1644	A1584	G1400	A1340	A1340	U1280	C1220	G1160	U1100	G1040	C980	A920	A860	U800	U740
C1645	A1585	C1401	G1341	G1341	G1281	A1221	C1161	C1101	A1041	G981	U921	A861	U801	C741
C1646	U1586	C1463	C1342	C1342	G1282	G1222	A1162	U1102	A1042	A982	U922	A862	A802	C742
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C1654	A1594	C1410	C1350	C1350	U1290	A1230	G1170	C1110	C1050	G990	A930	A870	A810	U750
U1655	A1595	G1471	U1351	U1351	A1291	A1231	C1171	C1111	G1051	G991	A931	A871	U811	U751
G1656	G1596	C1472	A1352	A1352	U1292	G1232	G1172	G1112	G1052	G992	C932	G872	A812	A752
C1657	U1597	U1474	C1353	C1353	U1293	G1233	U1173	G1113	C1053	C993	G933	G873	A813	C753
U1658	U1598	C1475	G1414	C1354	U1294	A1234	G1174	G1114	G1054	U994	A934	A874	C814	U754
C1659	C1599	A1476	U1355	U1355	G1295	U1235	G1175	G1115	G1055	C995	A935	C875	A815	U755
G1660	G1600	A1477	A1356	A1356	U1296	U1236	A1176	G1116	A1056	G996	C936	A876	U816	U756
C1661	A1601	C1478	G1417	U1357	U1297	G1237	G1177	G1117	U1057	A997	A937	C877	C817	G757
G1662	G1602	U1479	G1418	G1358	G1298	A1238	C1178	A1118	G1058	A998	A938	U878	A818	A758
A1663	U1541	G1480	U1419	C1359	G1299	C1239	C1179	G1119	U1059	C999	C939	C879	U819	A759
U1664	G1542	A1481	G1360	G1360	A1300	A1240	U1180	U1120	U1060	A1000	U940	G880	A820	G760
U1665	U1543	U1482	G1361	G1361	G1301	G1241	G1181	A1121	G1061	C1001	G941	G881	G821	A761
U1666	A1544	G1483	A1362	A1362	C1302	A1242	C1182	U1122	C1062	G1002	C942	G882	G822	A762
A1667	U1545	G1484	G1363	G1363	G1303	C1243	G1183	G1123	U1063	A1003	G943	G883	A823	A763
U1668	G1546	U1485	C1364	C1364	A1304	U1244	C1184	G1124	U1064	U1004	A944	G884	U824	U764
A1669	G1547	C1426	C1365	C1365	U1305	G1245	U1185	U1125	A1065	C1005	A945	C885	U825	U765
G1670	G1603	U1487	A1366	A1366	U1306	A1246	U1186	C1126	U1066	A1006	A946	A886	C826	A766
U1671	U1611	A1428	U1367	U1367	G1307	G1247	A1187	G1127	A1067	G1007	G947	U887	C827	G767
C1672	C1612	U1429	C1368	C1368	G1308	A1248	A1188	C1128	G1068	U888	C948	U888	G828	A768
C1673	G1613	A1430	C1369	C1369	U1309	G1249	U1189	A1129	G1069	C889	A949	C889	G829	G769
C1674	A1552	A1431	C1370	C1370	C1310	C1250	U1190	A1130	A1070	U950	U950	G890	U830	U770
G1675	U1554	G1492	U1371	U1371	U1311	U1251	U1191	G1131	C1071	C1011	U951	U891	C831	G771
U1676	A1555	A1493	C1372	C1372	G1312	C1252	G1192	G1132	U1072	C1012	U952	A892	C832	C772
C1677	U1617	G1494	C1373	C1373	G1313	U1253	G1193	A1133	C1073	G1013	G953	U893	C833	U773
G1678	G1618	U1495	G1374	G1374	U1314	U1254	C1194	U1134	C1074	U1014	C954	U894	A834	C774
A1679	U1496	U1436	C1375	C1375	U1315	U1255	U1195	G1135	G1075	C1015	C955	U895	U835	A775
C1680	C1620	U1497	A1376	A1376	A1316	C1256	C1196	A1136	C1076	U1016	A956	C896	U836	A776
G1681	U1498	U1438	G1377	G1377	U1317	U1257	A1197	A1137	C1077	U1017	A957	A897	G837	A777
U1682	A1622	U1499	C1378	C1378	U1318	U1258	A1198	A1138	G1078	A1018	G958	U898	U838	G778
G1683	C1623	A1500	U1379	U1379	U1319	G1259	C1199	C1139	G1079	G1019	G959	U899	C839	C779
U1684	G1624	C1441	A1380	A1380	C1320	A1260	A1200	U1140	C1080	U1020	A960	G900	U840	A780
U1685	U1625	A1442	G1381	G1381	C1321	U1261	C1201	U1141	A1081	C1021	U961	U901	U841	A781



- Molecule 2: P-site tRNA



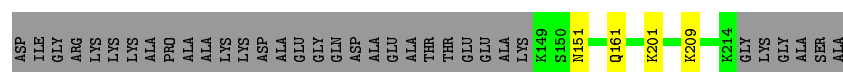
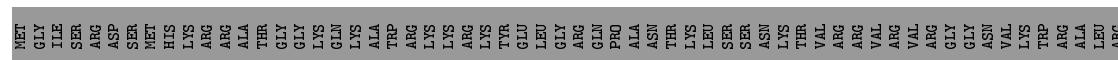
- Molecule 3: 5'-R(*AP*AP*AP*AP*GP*AP*CP*UP*UP*CP*A)-3'



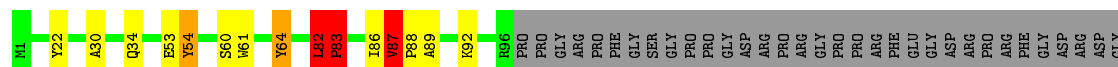
- Molecule 4: 40S ribosomal protein S24E



- Molecule 5: 40S ribosomal protein S8E

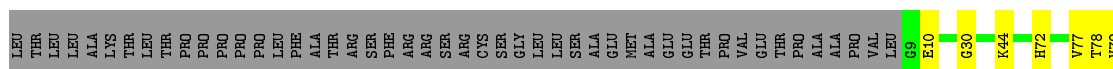


- Molecule 6: 40S ribosomal protein S10E

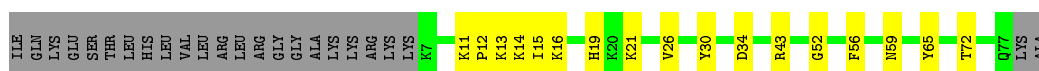
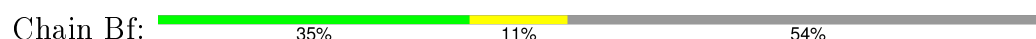




- Molecule 7: 40S ribosomal protein S12E



- Molecule 8: 40S ribosomal protein S31e



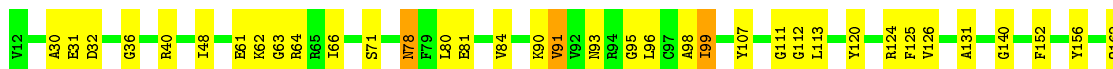
- Molecule 9: 40S ribosomal protein S12



- Molecule 10: RACK1

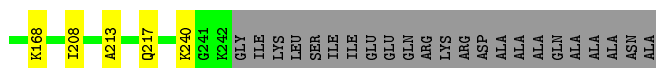
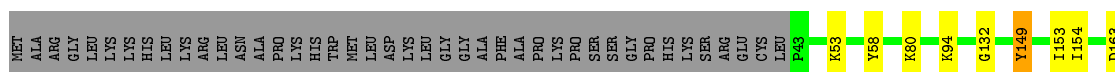


- Molecule 11: 40S ribosomal protein S3



- Molecule 12: 40S ribosomal protein S4E





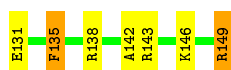
- Molecule 13: 40S ribosomal protein S7

Chain BF: 92% 7%



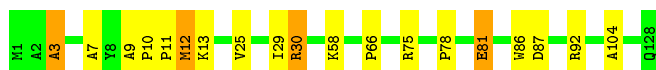
- Molecule 14: 40S ribosomal protein S9

Chain BQ: 66% 15% 15%



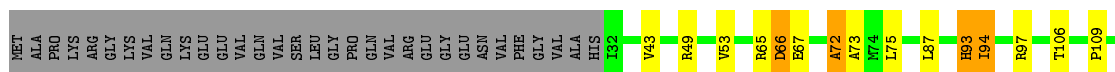
- Molecule 15: 40S ribosomal protein S10

Chain BU: 85% 12%



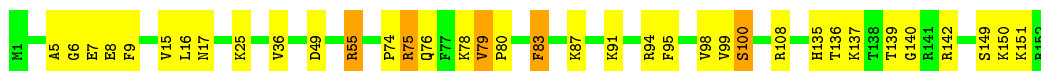
- Molecule 16: 40S ribosomal protein S11

Chain BO: 66% 11% 21%



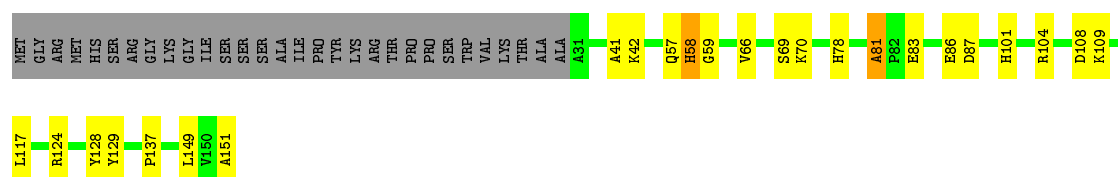
- Molecule 17: 40S ribosomal protein S13

Chain BS: 76% 20%

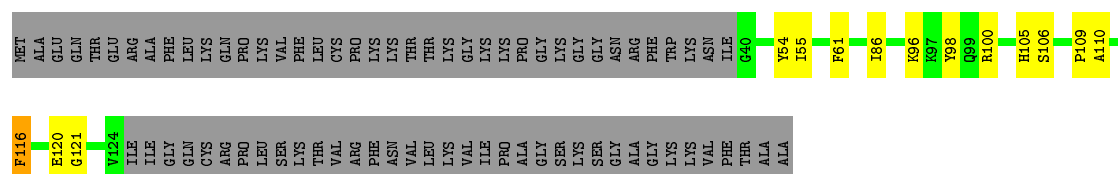


- Molecule 18: 40S ribosomal protein S15

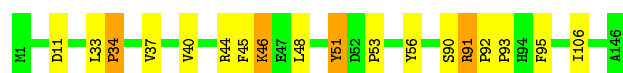
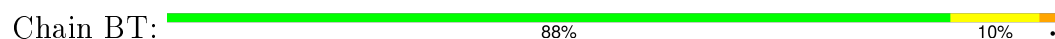
Chain BN: 64% 15% 20%



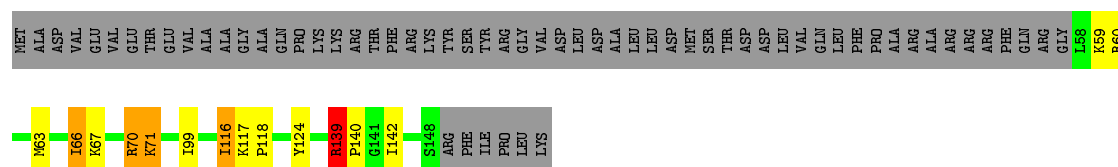
- Molecule 19: 40S ribosomal protein S17



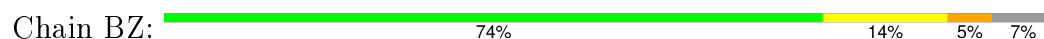
- Molecule 20: 40S ribosomal protein S19E



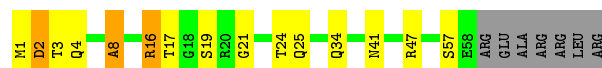
- Molecule 21: 40S ribosomal protein S19



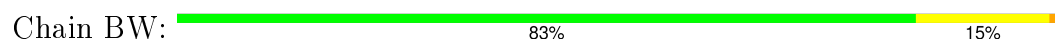
- Molecule 22: 40S ribosomal protein S25E



- Molecule 23: 40S ribosomal protein S28E

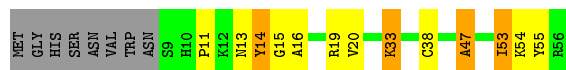


- Molecule 24: 40S ribosomal protein S8





- Molecule 25: 40S ribosomal protein S14



- Molecule 26: 40S ribosomal protein S27E



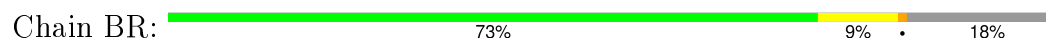
- Molecule 27: 40S ribosomal protein S30E



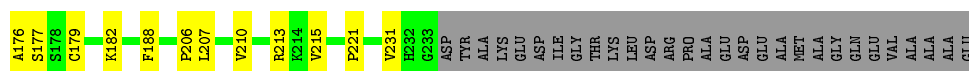
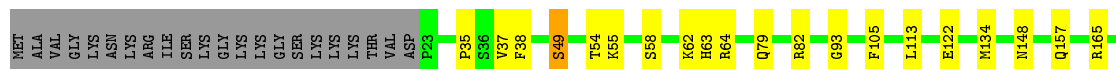
- Molecule 28: 40S ribosomal protein S2




- Molecule 29: 40S ribosomal protein S17E



- Molecule 30: 40S ribosomal protein S1E



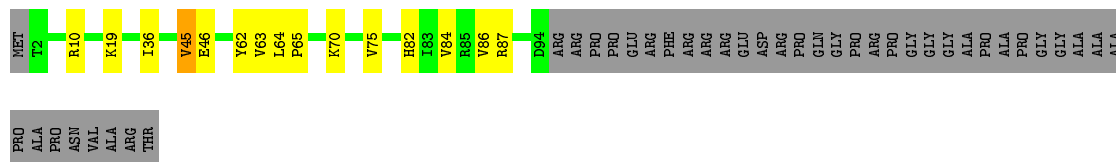
- Molecule 31: 40S ribosomal protein S21E

Chain BV:  84% 9% 7%



- Molecule 32: 40S ribosomal protein S26E

Chain Ba:  59% 11% 30%




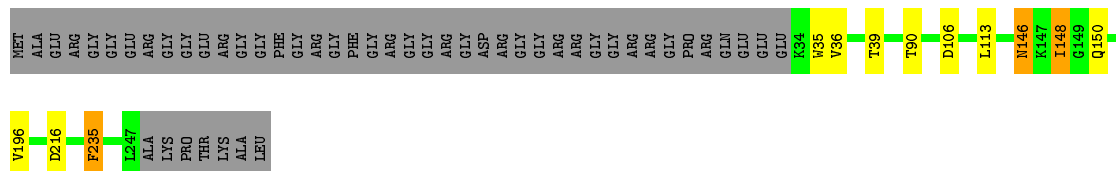
- Molecule 33: 40S ribosomal protein S4

Chain BJ:  90% . . .




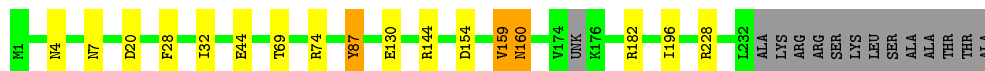
- Molecule 34: 40S ribosomal protein S5

Chain BC:  77% . . 19%




- Molecule 35: 40S ribosomal protein S6

Chain BG:  87% 6% 6%



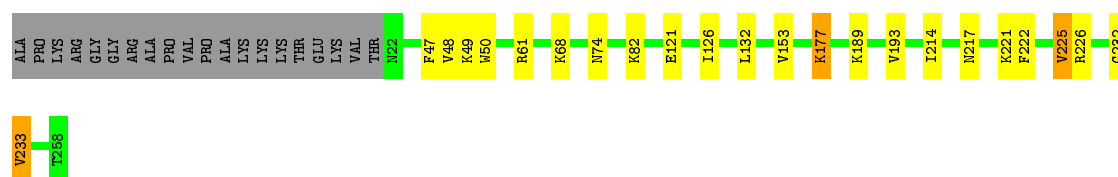
- Molecule 36: 40S ribosomal protein S7E

Chain BH:  81% 13% . . .



- Molecule 37: 60S ribosomal protein L8E

Chain CG:  83% 8% 8%



- Molecule 38: 60S ribosomal protein L21E

Chain CT: 84% 13% ..



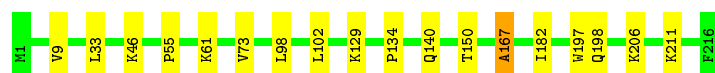
- Molecule 39: 60S ribosomal protein L27E

Chain CZ: 93% 7%



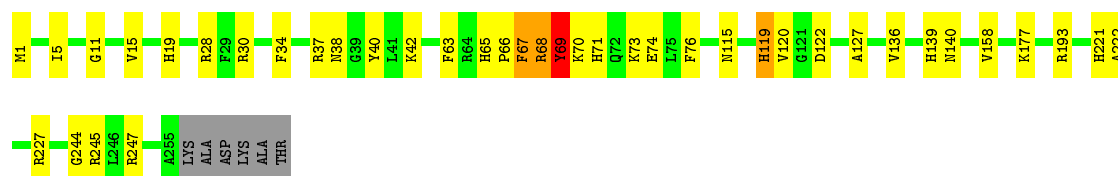
- Molecule 40: 60S ribosomal protein L1

Chain Cz: 92% 8%



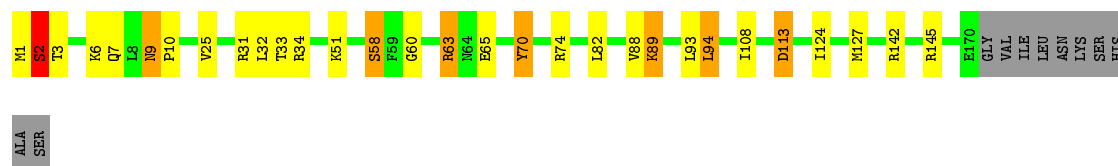
- Molecule 41: 60S ribosomal protein L2

Chain CA: 82% 14% ..



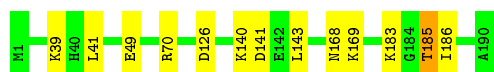
- Molecule 42: 60S ribosomal protein L5

Chain CJ: 78% 12% 6%



- Molecule 43: 60S ribosomal protein L6

Chain CH: 93% 6%



- Molecule 44: 60S ribosomal protein L14

Chain CV: 93% 7%



- Molecule 45: 60S ribosomal protein L15E

Chain CN: 88% 9% ..



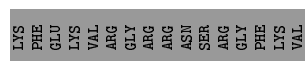
- Molecule 46: 60S ribosomal protein L15

Chain Ca: 77% 22% ..



- Molecule 47: 60S ribosomal protein L18E

Chain CQ: 72% 13% .. 13%



- Molecule 48: 60S ribosomal protein L18

Chain CD: 75% 18% 6% .

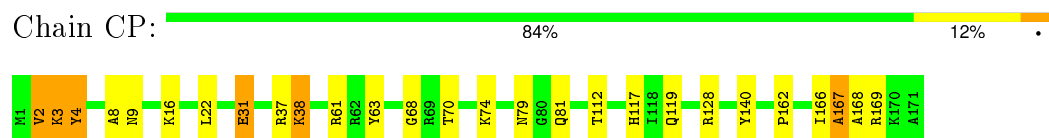


- Molecule 49: 60S ribosomal protein L19E

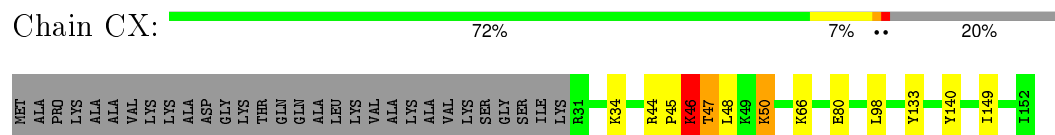
Chain CR: 80% 6% 5% 10%



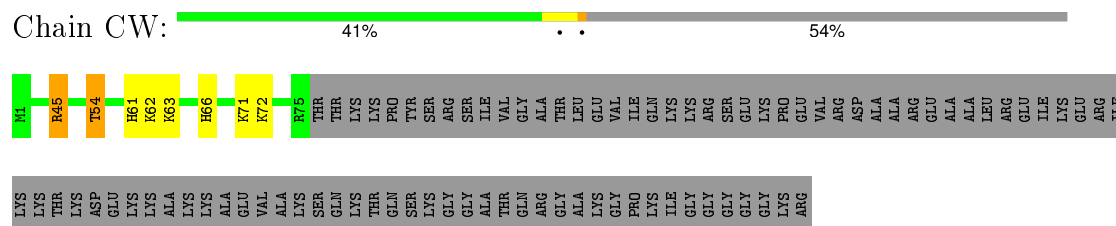
- Molecule 50: 60S ribosomal protein L22



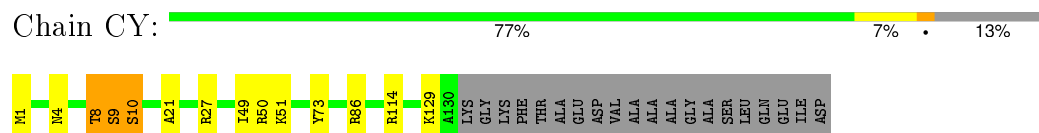
- Molecule 51: 60S ribosomal protein L23



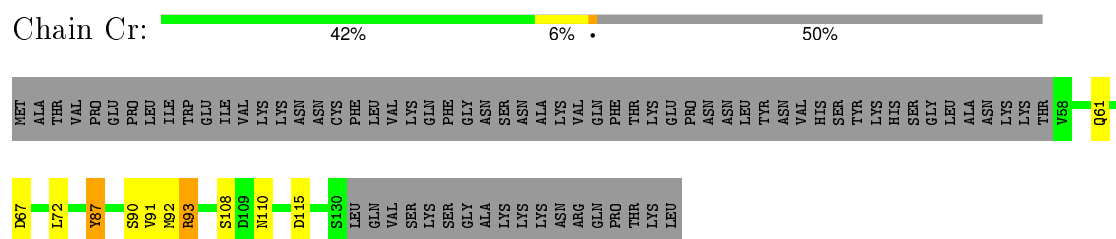
- Molecule 52: 60S ribosomal protein L24E



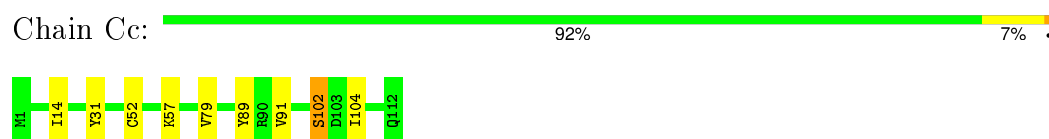
- Molecule 53: 60S ribosomal protein L24



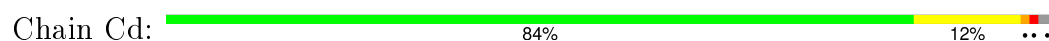
- Molecule 54: 60S ribosomal protein L28E



- Molecule 55: 60S ribosomal protein L30E



- Molecule 56: 60S ribosomal protein L31E





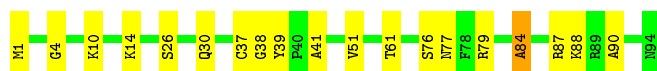
- Molecule 57: 60S ribosomal protein L32E

Chain Ce: 89% 8%



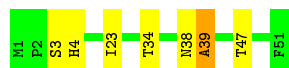
- Molecule 58: 60S ribosomal protein L37E

Chain Cj: 80% 19%



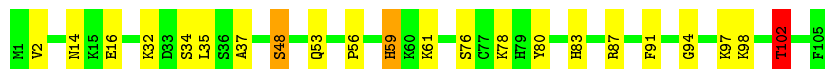
- Molecule 59: 60S ribosomal protein L39E

Chain Cl: 86% 12%



- Molecule 60: 60S ribosomal protein L44E

Chain Co: 79% 18%



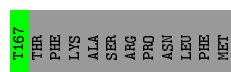
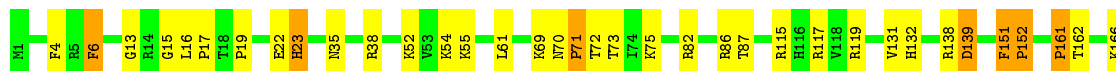
- Molecule 61: 60S ribosomal protein L14E

Chain CM: 82% 15%



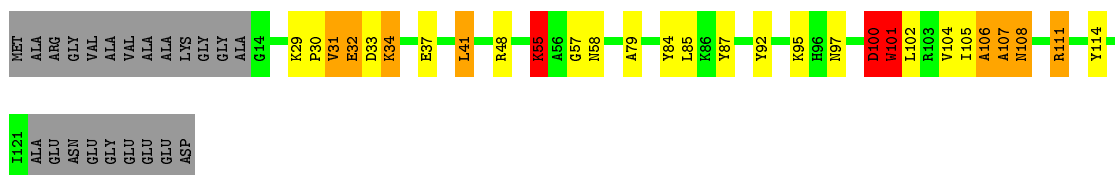
- Molecule 62: 60S ribosomal protein L20

Chain CS: 74% 16% 6%



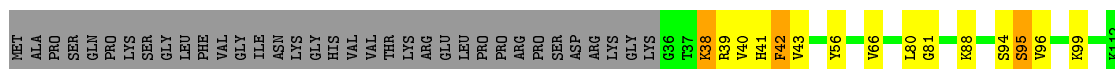
- Molecule 63: 60S ribosomal protein L22E

Chain CU: 61% 14% 6% 17%



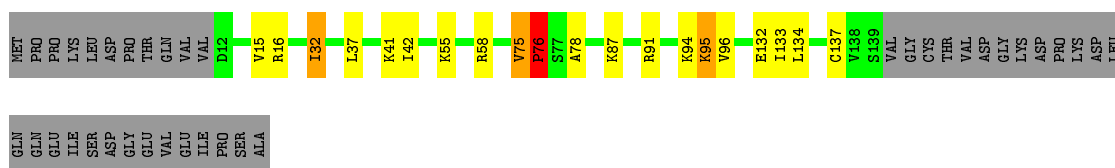
- Molecule 64: 60S ribosomal protein L36E

Chain Ci: 55% 11% 31%



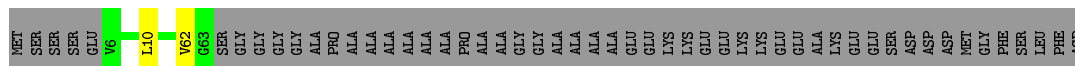
- Molecule 65: 60S ribosomal protein L11

Chain CK: 65% 10% 23%



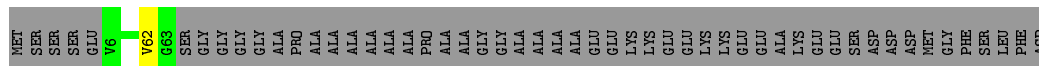
- Molecule 66: 60S ribosomal protein P1

Chain Cu: 51% 47%



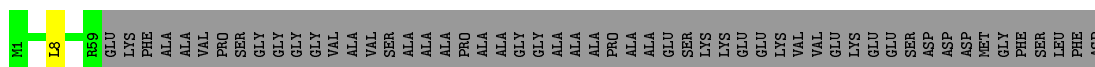
- Molecule 66: 60S ribosomal protein P1

Chain Cv: 52% 47%



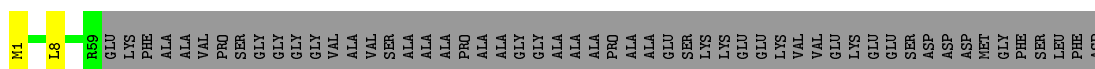
- Molecule 67: Acidic ribosomal protein P2

Chain Cs: 51% 48%




- Molecule 67: Acidic ribosomal protein P2

Chain Ct: 50% 48%



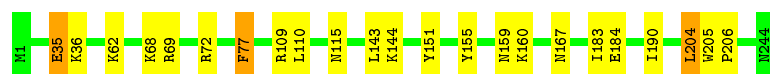
- Molecule 68: 60S ribosomal protein L29

Chain Ch:  89% 10%




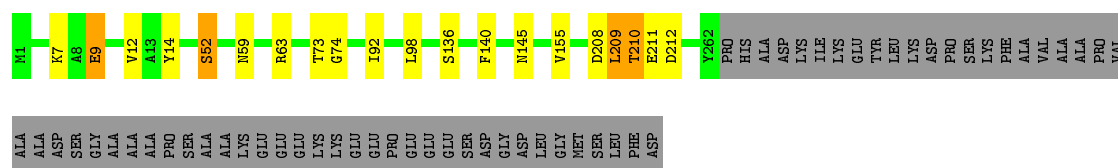
- Molecule 69: 60S ribosomal protein L30

Chain CF:  91% 8%




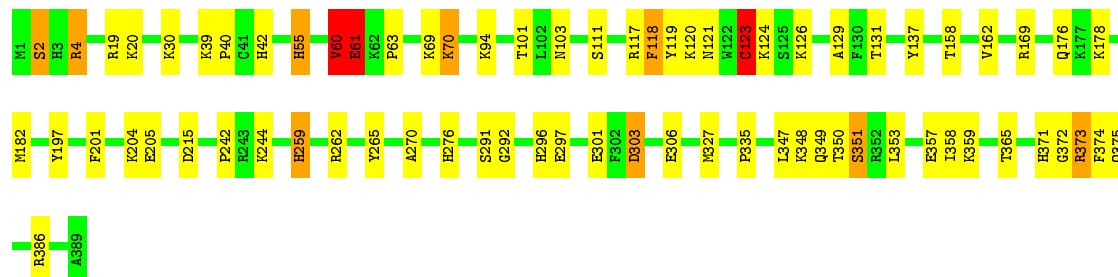
- Molecule 70: 60S acidic ribosomal protein P0

Chain Cq:  76% 5% 18%




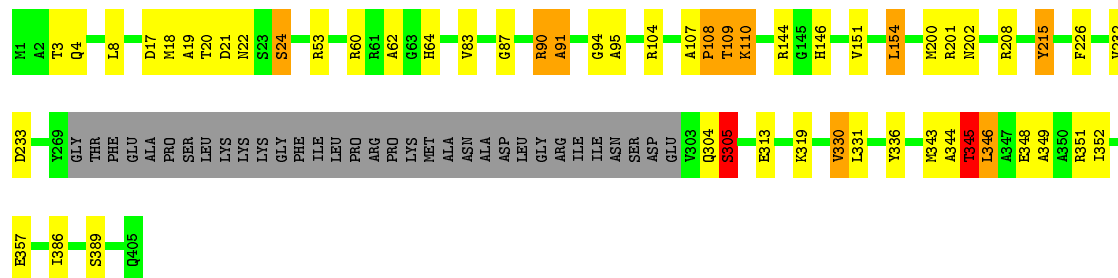
- Molecule 71: 60S ribosomal protein L3

Chain CB:  81% 15%




- Molecule 72: 60S ribosomal protein L4

Chain CC:  78% 11% 8%



- Molecule 73: 60S ribosomal protein L13

Chain CO:  87% 9%



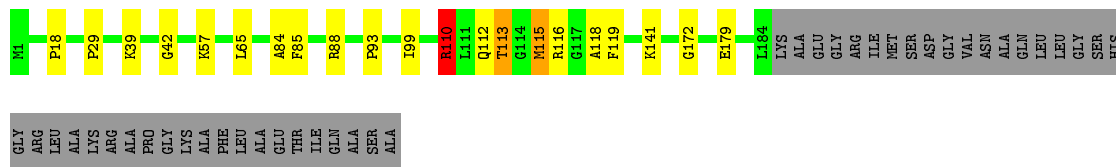
- Molecule 74: 60S ribosomal protein L43E

Chain Cp: 95% 5%



- Molecule 75: 60S ribosomal protein L16

Chain CI: 73% 8% 18%



- Molecule 76: 60S ribosomal protein L41E

Chain Cn: 92% 8%



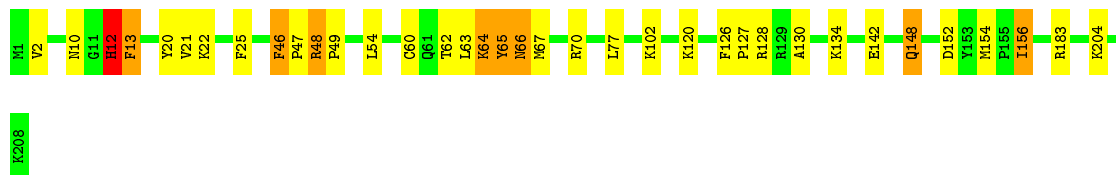
- Molecule 77: 60S ribosomal protein L40E

Chain Cm: 94% 4% 2%



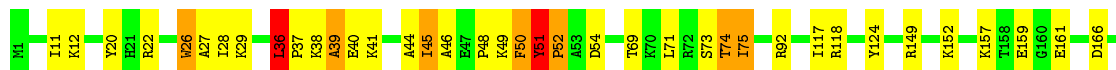
- Molecule 78: 60S ribosomal protein L13E

Chain CL: 83% 13% 4%



- Molecule 79: 60S ribosomal protein L6E

Chain CE: 80% 15% 5%





- Molecule 80: 60S ribosomal protein L33E

Chain Cf: 94% 5% •



- Molecule 81: 60S ribosomal protein L38E

Chain Ck: 90% 10%



- Molecule 82: 60S ribosomal protein L29E

Chain Cb: 90% • • •



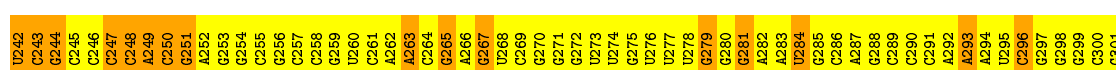
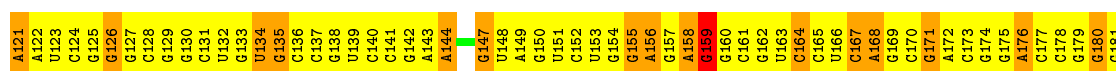
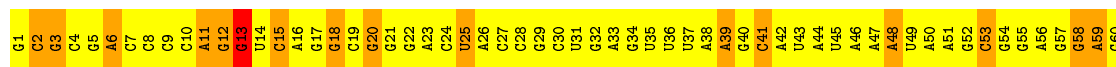
- Molecule 83: 60S ribosomal protein L34E

Chain Cg: 82% 10% 8%



- Molecule 84: 60S ribosomal RNA

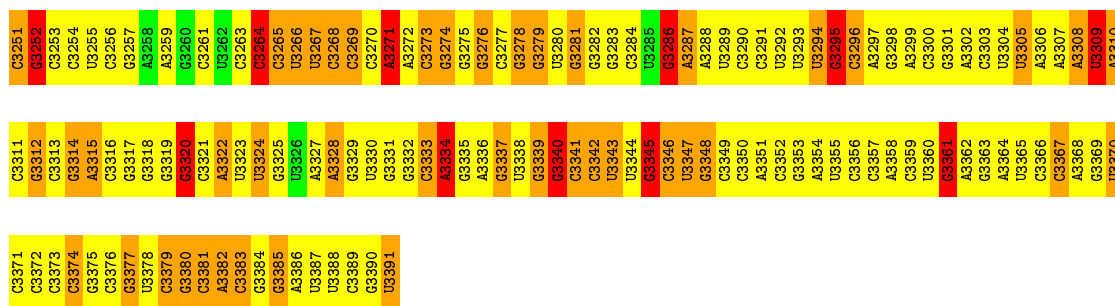
Chain Aa: 71% 25% •



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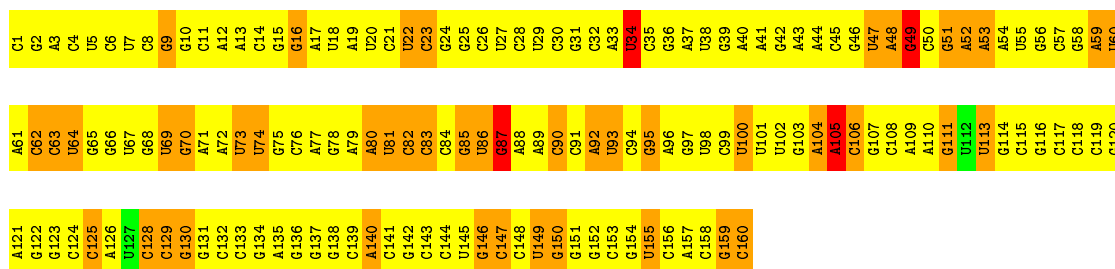
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C1987	A2047	C2048	G2049	G2050	G2051	G2052	A2053	A2054	U2055	C2056	G2057	C2058	A2059	C2060	U2061	C2062	U2063	C2064	G2065	G2066	C2067	G2068	G2069	C2070	U2071	U2072	U2073	C2074	C2075	C2076	C2077	G2078	A2079	G2080	A2081	A2082	U2083	U2084	A2085	A2086	A2087	C2088	A2089	G2090	U2091	C2092	G2093	A2094	C2095	U2096	C2097	A2098	G2099	A2100	A2101	C2102	U2103	G2104	G2105	U2106
A2107	C2108	G2109	G2110	A2111	C2112	A2113	G2114	G2115	G2116	G2117	G2118	A2119	A2120	U2121	C2122	C2123	G2124	A2125	C2126	U2127	G2128	U2129	U2130	U2131	A2132	A2133	G2134	U2135	U2136	C2137	A2138	U2139	C2140	A2141	A2142	A2143	G2144	C2145	A2146	U2147	U2148	A2149	C2150	G2151	A2152	G2153	A2154	G2155	U2156	C2157	C2158	A2159	C2160	U2161	C2162	G2163	A2164	G2165	U2166	
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G3197	G3137	C3077	A3017	U2957	G2897	G2836	U2776	U2716	C2656	A2596	G2536	G2476	G2413	C2353	U2293
C3198	U3138	A3078	A3018	A2958	A2898	C2837	U2777	G2717	C2657	C2597	G2537	G2477	C2414	C2354	A2294
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C3206	C3146	G3086	C3026	G2966	U2906	U2845	U2785	U2725	A2665	G2605	C2545	G2485	U2422	A2362	G2302
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G3222	G3162	G3102	U3042	U2982	U2922	U2861	A2801	G2741	A2681	G2621	A2561	U2501	A2438	U2378	U2318
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C3229	C3169	G3109	A3049	A2989	C2929	C2869	U2808	G2748	G2688	C2628	G2568	U2508	U2445	A2385	A2325
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C3231	C3171	C3111	U3051	U2991	C2931	G2871	A2810	U2750	G2690	A2630	U2570	U2510	A2447	U2387	U2327
C3232	G3172	U3112	U3052	G2992	A2932	C2872	A2811	A2751	U2691	A2631	C2571	U2511	G2448	C2388	C2328
C3233	A3173	G3113	G3053	A2993	C2933	G2873	C2812	G2752	G2692	U2632	U2572	U2512	A2449	A2389	C2329
G3234	C3174	A3114	G3054	U2994	C2934	A2874	A2813	C2753	G2693	C2633	U2573	U2513	G2450	C2390	C2330
A3235	C3175	A3115	U3055	G2995	A2935	U2875	C2814	G2754	A2694	U2634	A2574	A2514	G2451	C2391	A2331
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G3239	G3179	G3119	C3059	G2999	G2939	G2879	G2818	C2758	A2698	A2638	G2578	A2518	A2455	G2395	U2335
C3240	U3180	U3120	G3060	U3000	G2940	G2880	A2819	C2759	A2699	A2639	G2579	U2519	G2456	A2396	C2336
C3241	U3181	C3121	C3061	G3001	G2941	U2881	U2820	U2760	A2700	A2640	C2580	U2520	G2457	A2397	C2337
G3242	A3182	U3122	G3062	U3002	A2942	C2882	U2821	A2761	G2701	A2641	C2581	C2521	A2458	A2398	U2338
C3243	G3183	A3123	C3063	C3003	A2943	U2883	A2822	G2762	G2702	G2642	G2582	C2522	U2459	U2399	U2339
G3244	C3184	A3124	U3064	C2944	C2944	U2884	C2763	C2763	G2703	A2643	A2583	G2523	A2460	A2400	G2340
G3245	G3185	G3125	U3065	C3005	G2945	U2885	U2824	U2764	U2704	U2644	U2584	U2524	A2461	U2341	U2341
U3246	G3186	U3126	G3066	U3006	U2946	C2886	G2825	A2765	A2705	A2645	C2585	G2525	G2462	G2402	C2342
C3247	C3187	C3127	G3067	A3007	G2947	C2887	G2826	U2766	A2706	A2646	C2586	G2526	U2463	A2403	U2343
G3248	G3188	U3128	U3068	U3008	A2948	U2888	C2827	G2767	A2707	C2647	G2587	U2527	G2464	C2404	A2344
C3249	C3189	G3129	U3069	A3009	G2949	A2889	U2828	C2768	A2708	G2648	G2588	U2528	G2465	C2405	C2345
C3250	U3190	A3130	G3070	G3010	C2950	U2890	U2829	U2769	G2709	C2649	G2589	C2529	G2466	C2406	G2346



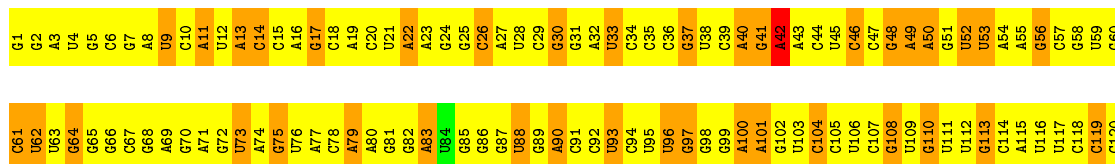
- Molecule 85: 5.8S ribosomal RNA

Chain Ac: . 68% 28% .



- Molecule 86: 5S ribosomal RNA

Chain Ab: . 67% 32% .



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	2108230	Depositor
Resolution determination method	FSC 0.5	Depositor
CTF correction method	Wiener Filter on 3D volumes (SPIDER)	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	39000	Depositor
Image detector	Kodak SO-163 film	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	Ad	2.49	2030/42036 (4.8%)	2.11	2382/65520 (3.6%)
10	Bg	0.97	0/2988	1.06	3/4049 (0.1%)
11	BD	1.01	0/1652	1.20	4/2222 (0.2%)
12	BE	0.99	0/1637	1.07	0/2202
13	BF	0.98	0/1509	1.00	3/2034 (0.1%)
14	BQ	1.11	0/1034	1.19	6/1379 (0.4%)
15	BU	0.93	0/995	1.14	3/1338 (0.2%)
16	BO	1.05	0/909	1.11	2/1217 (0.2%)
17	BS	1.04	0/1258	1.15	5/1674 (0.3%)
18	BN	0.96	0/994	1.13	5/1332 (0.4%)
19	BL	1.04	0/704	1.15	3/944 (0.3%)
2	Ae	2.62	95/1781 (5.3%)	2.13	105/2775 (3.8%)
20	BT	1.01	0/1179	1.08	3/1586 (0.2%)
21	BP	0.91	0/727	1.11	2/975 (0.2%)
22	BZ	0.94	0/791	1.18	7/1057 (0.7%)
23	Bc	1.04	0/455	1.26	2/609 (0.3%)
24	BW	1.02	0/1060	1.16	6/1419 (0.4%)
25	Bd	1.11	0/386	1.25	4/510 (0.8%)
26	Bb	0.92	0/674	1.04	0/905
27	Be	1.07	0/476	1.01	0/627
28	BA	0.96	0/1567	1.06	4/2121 (0.2%)
29	BR	1.03	0/955	1.03	1/1273 (0.1%)
3	Af	2.45	12/260 (4.6%)	2.06	16/403 (4.0%)
30	BB	0.96	0/1736	1.12	4/2329 (0.2%)
31	BV	1.00	0/610	1.07	0/820
32	Ba	1.07	0/766	1.13	0/1023
33	BJ	1.09	0/1553	1.05	4/2079 (0.2%)
34	BC	0.93	0/1701	1.05	3/2298 (0.1%)
35	BG	1.06	0/1888	1.05	4/2507 (0.2%)
36	BH	3.40	1/1535 (0.1%)	1.14	4/2065 (0.2%)
37	CG	0.94	0/1939	1.01	5/2598 (0.2%)
38	CT	0.99	0/1316	1.11	2/1772 (0.1%)
39	CZ	1.00	0/1110	1.02	2/1480 (0.1%)
4	BY	0.99	0/1123	1.10	1/1487 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
40	Cz	0.89	0/1741	1.00	1/2323 (0.0%)
41	CA	1.05	0/1992	1.15	10/2681 (0.4%)
42	CJ	1.06	0/1401	1.14	7/1869 (0.4%)
43	CH	0.96	0/1519	1.03	0/2042
44	CV	0.99	0/1064	1.07	0/1425
45	CN	1.12	0/1669	1.07	6/2235 (0.3%)
46	Ca	0.98	0/1143	1.17	4/1527 (0.3%)
47	CQ	1.04	0/1303	1.11	5/1748 (0.3%)
48	CD	1.00	0/2489	1.23	22/3342 (0.7%)
49	CR	1.09	0/1590	1.06	4/2100 (0.2%)
5	BI	1.05	0/539	0.95	0/712
50	CP	1.03	0/1397	1.14	6/1871 (0.3%)
51	CX	0.90	0/1002	1.03	3/1340 (0.2%)
52	CW	1.04	0/649	1.07	1/861 (0.1%)
53	CY	1.10	0/1061	1.08	4/1418 (0.3%)
54	Cr	0.98	0/585	1.16	1/786 (0.1%)
55	Cc	0.86	0/869	0.98	1/1169 (0.1%)
56	Cd	1.01	0/970	1.10	4/1295 (0.3%)
57	Ce	1.01	0/1122	1.06	4/1497 (0.3%)
58	Cj	1.17	0/769	1.16	1/1019 (0.1%)
59	Cl	1.14	0/472	1.12	1/627 (0.2%)
6	BK	0.93	0/840	1.21	6/1135 (0.5%)
60	Co	0.93	0/867	1.12	3/1144 (0.3%)
61	CM	0.99	0/1094	1.10	4/1461 (0.3%)
62	CS	1.01	0/1457	1.16	3/1957 (0.2%)
63	CU	0.98	0/876	1.27	12/1170 (1.0%)
64	Ci	1.07	0/618	1.16	5/809 (0.6%)
65	CK	0.92	0/968	1.11	1/1299 (0.1%)
66	Cu	0.78	0/438	0.91	0/596
66	Cv	0.79	0/438	0.90	0/596
67	Cs	0.83	0/444	0.82	0/596
67	Ct	0.84	0/444	0.81	0/596
68	Ch	1.02	0/1023	1.05	2/1359 (0.1%)
69	CF	0.98	0/2020	1.00	4/2708 (0.1%)
7	BM	0.82	0/936	1.11	2/1260 (0.2%)
70	Cq	0.87	0/2023	0.96	5/2739 (0.2%)
71	CB	0.97	0/3207	1.14	16/4289 (0.4%)
72	CC	1.01	0/2951	1.11	8/3972 (0.2%)
73	CO	1.03	0/1678	1.07	6/2246 (0.3%)
74	Cp	1.00	0/724	1.02	1/958 (0.1%)
75	CI	1.01	0/1523	1.00	1/2036 (0.0%)
76	Cn	1.34	0/239	1.04	0/302
77	Cm	1.01	0/434	0.95	0/574

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
78	CL	1.03	0/1721	1.13	6/2299 (0.3%)
79	CE	0.95	0/1766	1.16	8/2374 (0.3%)
8	Bf	0.93	0/590	1.17	1/788 (0.1%)
80	Cf	1.05	0/908	1.13	3/1215 (0.2%)
81	Ck	0.98	0/572	1.09	0/763
82	Cb	0.98	0/486	1.06	2/641 (0.3%)
83	Cg	1.07	0/913	1.02	0/1223
84	Aa	1.61	170/81235 (0.2%)	2.52	9121/126706 (7.2%)
85	Ac	1.61	7/3809 (0.2%)	2.48	426/5936 (7.2%)
86	Ab	2.31	125/2864 (4.4%)	2.91	380/4464 (8.5%)
9	BX	0.96	0/1122	1.05	4/1492 (0.3%)
All	All	1.65	2440/227878 (1.1%)	2.00	12710/334219 (3.8%)

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
10	Bg	0	1
11	BD	0	3
12	BE	0	2
13	BF	0	2
14	BQ	0	1
15	BU	0	2
17	BS	0	1
19	BL	0	1
20	BT	0	4
23	Bc	0	1
24	BW	0	1
25	Bd	0	1
26	Bb	0	2
29	BR	0	1
30	BB	0	1
32	Ba	0	1
35	BG	0	1
36	BH	0	4
37	CG	0	2
4	BY	0	1
41	CA	0	4
42	CJ	0	2
43	CH	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
45	CN	0	1
46	Ca	0	7
47	CQ	0	6
48	CD	0	13
49	CR	0	3
50	CP	0	1
51	CX	0	1
55	Cc	0	1
57	Ce	0	1
58	Cj	0	1
59	Cl	0	1
6	BK	0	4
60	Co	0	2
61	CM	0	4
62	CS	0	3
63	CU	0	2
65	CK	0	2
68	Ch	0	1
69	CF	0	3
7	BM	0	1
70	Cq	0	2
71	CB	0	9
72	CC	0	4
73	CO	0	4
74	Cp	0	1
75	CI	0	4
78	CL	0	5
79	CE	0	7
8	Bf	0	1
80	Cf	0	2
83	Cg	0	1
84	Aa	0	309
85	Ac	0	18
86	Ab	0	19
All	All	0	486

The worst 5 of 2440 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	BH	117	ARG	CZ-NH2	127.06	2.98	1.33
1	Ad	1203	G	C2'-C1'	23.55	1.79	1.53
2	Ae	28	G	C2'-C1'	-23.31	1.27	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Ad	218	G	C2'-C1'	-23.01	1.28	1.53
1	Ad	999	G	C2'-C1'	-22.88	1.28	1.53

The worst 5 of 12710 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Ad	1005	C	O4'-C1'-N1	31.46	133.37	108.20
1	Ad	1462	C	O4'-C1'-N1	29.23	131.58	108.20
1	Ad	547	C	O4'-C1'-N1	28.96	131.37	108.20
1	Ad	1765	A	O4'-C1'-N9	28.77	131.22	108.20
84	Aa	2162	C	P-O3'-C3'	27.64	152.86	119.70

There are no chirality outliers.

5 of 486 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	BK	22	TYR	Sidechain
6	BK	83	PRO	Peptide
6	BK	86	ILE	Peptide
6	BK	87	VAL	Peptide
4	BY	48	LYS	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Ad	37584	0	18947	0	0
2	Ae	1595	0	808	0	0
3	Af	232	0	121	0	0
4	BY	1108	0	1200	1	0
5	BI	533	0	551	0	0
6	BK	818	0	831	1	0
7	BM	924	0	939	1	0
8	Bf	577	0	589	0	0
9	BX	1103	0	1170	1	0
10	Bg	2929	0	2843	0	0
11	BD	1629	0	1694	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	BE	1607	0	1678	0	0
13	BF	1489	0	1537	2	0
14	BQ	1017	0	1080	4	0
15	BU	982	0	1032	1	0
16	BO	899	0	936	3	0
17	BS	1240	0	1293	3	0
18	BN	977	0	1057	2	0
19	BL	688	0	704	1	0
20	BT	1155	0	1175	1	0
21	BP	711	0	759	4	0
22	BZ	779	0	833	2	0
23	Bc	454	0	489	0	0
24	BW	1042	0	1086	2	0
25	Bd	379	0	378	0	0
26	Bb	663	0	680	0	0
27	Be	469	0	506	0	0
28	BA	1537	0	1557	0	0
29	BR	945	0	1002	0	0
30	BB	1707	0	1783	1	0
31	BV	601	0	588	0	0
32	Ba	753	0	769	0	0
33	BJ	1525	0	1600	3	0
34	BC	1665	0	1751	0	0
35	BG	1867	0	1990	1	0
36	BH	1508	0	1572	2	0
37	CG	1906	0	2064	3	0
38	CT	1288	0	1341	3	0
39	CZ	1090	0	1183	2	0
40	Cz	1718	0	1841	0	0
41	CA	1946	0	1974	5	0
42	CJ	1380	0	1422	0	0
43	CH	1500	0	1564	0	0
44	CV	1048	0	1116	0	0
45	CN	1630	0	1704	1	0
46	Ca	1114	0	1166	0	0
47	CQ	1284	0	1376	1	0
48	CD	2444	0	2418	1	0
49	CR	1569	0	1695	3	0
50	CP	1372	0	1410	3	0
51	CX	987	0	1082	18	0
52	CW	635	0	677	2	0
53	CY	1048	0	1130	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
54	Cr	576	0	616	0	0
55	Cc	857	0	904	0	0
56	Cd	960	0	1025	0	0
57	Ce	1103	0	1177	0	0
58	Cj	755	0	782	0	0
59	Cl	460	0	490	0	0
60	Co	851	0	909	0	0
61	CM	1081	0	1171	1	0
62	CS	1419	0	1466	3	0
63	CU	864	0	910	22	0
64	Ci	613	0	684	0	0
65	CK	960	0	1042	0	0
66	Cu	432	0	463	0	0
66	Cv	432	0	463	0	0
67	Cs	441	0	453	0	0
67	Ct	441	0	453	0	0
68	Ch	1012	0	1112	0	0
69	CF	1984	0	2092	2	0
70	Cq	1993	0	2086	0	0
71	CB	3139	0	3258	4	0
72	CC	2898	0	3023	6	0
73	CO	1650	0	1770	3	0
74	Cp	715	0	758	0	0
75	CI	1490	0	1539	25	0
76	Cn	238	0	289	0	0
77	Cm	428	0	470	0	0
78	CL	1691	0	1788	2	0
79	CE	1731	0	1825	1	0
80	Cf	891	0	928	0	0
81	Ck	564	0	612	0	0
82	Cb	477	0	483	0	0
83	Cg	897	0	983	0	0
84	Aa	72601	0	36663	0	0
85	Ac	3408	0	1732	0	0
86	Ab	2561	0	1295	0	0
All	All	212263	0	158405	149	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 9.

The worst 5 of 149 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)
75:CI:115:MET:HB2	75:CI:116:ARG:CA	1.60	1.29
63:CU:31:VAL:CG2	63:CU:101:TRP:CD1	2.22	1.22
63:CU:31:VAL:HG21	63:CU:101:TRP:CG	1.74	1.21
63:CU:31:VAL:HG21	63:CU:101:TRP:CD1	1.76	1.19
75:CI:112:GLN:O	75:CI:113:THR:HG23	1.43	1.18

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	BY	136/138 (99%)	118 (87%)	8 (6%)	10 (7%)	1	20
5	BI	64/220 (29%)	61 (95%)	2 (3%)	1 (2%)	12	56
6	BK	94/183 (51%)	66 (70%)	17 (18%)	11 (12%)	0	9
7	BM	121/171 (71%)	84 (69%)	20 (16%)	17 (14%)	0	6
8	Bf	69/155 (44%)	46 (67%)	10 (14%)	13 (19%)	0	3
9	BX	140/142 (99%)	124 (89%)	11 (8%)	5 (4%)	4	38
10	Bg	378/380 (100%)	334 (88%)	26 (7%)	18 (5%)	3	31
11	BD	206/208 (99%)	125 (61%)	34 (16%)	47 (23%)	0	2
12	BE	198/265 (75%)	173 (87%)	16 (8%)	9 (4%)	3	33
13	BF	189/191 (99%)	162 (86%)	20 (11%)	7 (4%)	4	38
14	BQ	124/149 (83%)	93 (75%)	15 (12%)	16 (13%)	0	7
15	BU	126/128 (98%)	102 (81%)	14 (11%)	10 (8%)	1	19
16	BO	117/151 (78%)	91 (78%)	12 (10%)	14 (12%)	0	8
17	BS	150/152 (99%)	109 (73%)	16 (11%)	25 (17%)	0	5
18	BN	119/151 (79%)	92 (77%)	14 (12%)	13 (11%)	0	11
19	BL	83/160 (52%)	61 (74%)	16 (19%)	6 (7%)	1	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	BT	144/146 (99%)	123 (85%)	13 (9%)	8 (6%)	2	28
21	BP	89/154 (58%)	69 (78%)	12 (14%)	8 (9%)	1	17
22	BZ	98/108 (91%)	75 (76%)	10 (10%)	13 (13%)	0	7
23	Bc	56/65 (86%)	40 (71%)	5 (9%)	11 (20%)	0	3
24	BW	128/130 (98%)	101 (79%)	16 (12%)	11 (9%)	1	17
25	Bd	46/56 (82%)	29 (63%)	6 (13%)	11 (24%)	0	2
26	Bb	84/86 (98%)	75 (89%)	6 (7%)	3 (4%)	4	38
27	Be	58/62 (94%)	49 (84%)	5 (9%)	4 (7%)	1	22
28	BA	195/260 (75%)	176 (90%)	10 (5%)	9 (5%)	3	32
29	BR	114/141 (81%)	89 (78%)	15 (13%)	10 (9%)	1	17
30	BB	209/262 (80%)	153 (73%)	31 (15%)	25 (12%)	0	8
31	BV	74/82 (90%)	62 (84%)	9 (12%)	3 (4%)	3	34
32	Ba	91/133 (68%)	65 (71%)	13 (14%)	13 (14%)	0	6
33	BJ	185/195 (95%)	162 (88%)	16 (9%)	7 (4%)	4	37
34	BC	212/263 (81%)	189 (89%)	16 (8%)	7 (3%)	5	40
35	BG	227/245 (93%)	211 (93%)	10 (4%)	6 (3%)	7	45
36	BH	182/189 (96%)	154 (85%)	10 (6%)	18 (10%)	1	14
37	CG	235/257 (91%)	205 (87%)	24 (10%)	6 (3%)	7	45
38	CT	158/164 (96%)	137 (87%)	6 (4%)	15 (10%)	1	15
39	CZ	134/136 (98%)	123 (92%)	10 (8%)	1 (1%)	26	71
40	Cz	214/216 (99%)	197 (92%)	9 (4%)	8 (4%)	4	38
41	CA	253/261 (97%)	219 (87%)	19 (8%)	15 (6%)	2	26
42	CJ	168/180 (93%)	132 (79%)	14 (8%)	22 (13%)	0	7
43	CH	188/190 (99%)	167 (89%)	16 (8%)	5 (3%)	6	44
44	CV	138/140 (99%)	124 (90%)	7 (5%)	7 (5%)	2	29
45	CN	192/200 (96%)	168 (88%)	18 (9%)	6 (3%)	5	42
46	Ca	142/144 (99%)	101 (71%)	24 (17%)	17 (12%)	0	8
47	CQ	161/188 (86%)	127 (79%)	18 (11%)	16 (10%)	1	14
48	CD	302/304 (99%)	213 (70%)	35 (12%)	54 (18%)	0	4
49	CR	187/209 (90%)	163 (87%)	14 (8%)	10 (5%)	2	29
50	CP	169/171 (99%)	140 (83%)	12 (7%)	17 (10%)	1	13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	CX	120/152 (79%)	100 (83%)	17 (14%)	3 (2%)	7	46
52	CW	73/162 (45%)	55 (75%)	12 (16%)	6 (8%)	1	18
53	CY	128/150 (85%)	114 (89%)	8 (6%)	6 (5%)	3	32
54	Cr	71/147 (48%)	49 (69%)	13 (18%)	9 (13%)	0	7
55	Cc	110/112 (98%)	96 (87%)	10 (9%)	4 (4%)	4	38
56	Cd	118/123 (96%)	98 (83%)	8 (7%)	12 (10%)	1	13
57	Ce	131/133 (98%)	113 (86%)	10 (8%)	8 (6%)	2	25
58	Cj	92/94 (98%)	58 (63%)	19 (21%)	15 (16%)	0	5
59	Cl	49/51 (96%)	36 (74%)	8 (16%)	5 (10%)	1	13
60	Co	103/105 (98%)	76 (74%)	13 (13%)	14 (14%)	0	6
61	CM	132/134 (98%)	101 (76%)	14 (11%)	17 (13%)	0	7
62	CS	165/178 (93%)	122 (74%)	20 (12%)	23 (14%)	0	6
63	CU	106/130 (82%)	76 (72%)	13 (12%)	17 (16%)	0	5
64	Ci	75/112 (67%)	59 (79%)	5 (7%)	11 (15%)	0	6
65	CK	126/166 (76%)	94 (75%)	17 (14%)	15 (12%)	0	8
66	Cu	56/110 (51%)	54 (96%)	1 (2%)	1 (2%)	11	53
66	Cv	56/110 (51%)	53 (95%)	2 (4%)	1 (2%)	11	53
67	Cs	57/113 (50%)	54 (95%)	3 (5%)	0	100	100
67	Ct	57/113 (50%)	54 (95%)	3 (5%)	0	100	100
68	Ch	122/124 (98%)	103 (84%)	11 (9%)	8 (7%)	1	24
69	CF	242/244 (99%)	217 (90%)	16 (7%)	9 (4%)	4	38
70	Cq	260/319 (82%)	233 (90%)	15 (6%)	12 (5%)	3	32
71	CB	387/389 (100%)	307 (79%)	43 (11%)	37 (10%)	1	14
72	CC	368/405 (91%)	311 (84%)	27 (7%)	30 (8%)	1	18
73	CO	204/206 (99%)	179 (88%)	14 (7%)	11 (5%)	2	29
74	Cp	90/92 (98%)	81 (90%)	7 (8%)	2 (2%)	8	49
75	CI	182/224 (81%)	147 (81%)	24 (13%)	11 (6%)	2	26
76	Cn	23/25 (92%)	21 (91%)	1 (4%)	1 (4%)	3	34
77	Cm	50/53 (94%)	46 (92%)	3 (6%)	1 (2%)	9	51
78	CL	206/208 (99%)	168 (82%)	13 (6%)	25 (12%)	0	8
79	CE	217/219 (99%)	177 (82%)	14 (6%)	26 (12%)	0	8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
80	Cf	109/111 (98%)	103 (94%)	5 (5%)	1 (1%)	21	66
81	Ck	67/69 (97%)	63 (94%)	2 (3%)	2 (3%)	5	42
82	Cb	56/60 (93%)	48 (86%)	4 (7%)	4 (7%)	1	21
83	Cg	108/119 (91%)	96 (89%)	8 (7%)	4 (4%)	4	38
All	All	11663/13543 (86%)	9641 (83%)	1083 (9%)	939 (8%)	2	18

5 of 939 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	BY	2	ALA
4	BY	39	ASN
4	BY	41	SER
4	BY	46	LYS
4	BY	49	LEU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	BY	116/116 (100%)	110 (95%)	6 (5%)	29	65
5	BI	56/179 (31%)	53 (95%)	3 (5%)	27	64
6	BK	90/146 (62%)	88 (98%)	2 (2%)	60	83
7	BM	101/142 (71%)	101 (100%)	0	100	100
8	Bf	62/135 (46%)	60 (97%)	2 (3%)	46	77
9	BX	113/113 (100%)	111 (98%)	2 (2%)	66	87
10	Bg	323/323 (100%)	310 (96%)	13 (4%)	38	71
11	BD	175/175 (100%)	170 (97%)	5 (3%)	50	78
12	BE	176/225 (78%)	172 (98%)	4 (2%)	58	83
13	BF	159/159 (100%)	153 (96%)	6 (4%)	40	73
14	BQ	103/120 (86%)	97 (94%)	6 (6%)	25	62
15	BU	113/113 (100%)	107 (95%)	6 (5%)	28	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	BO	94/120 (78%)	90 (96%)	4 (4%)	35	70
17	BS	133/133 (100%)	125 (94%)	8 (6%)	24	61
18	BN	106/130 (82%)	101 (95%)	5 (5%)	32	68
19	BL	74/135 (55%)	70 (95%)	4 (5%)	27	64
20	BT	121/121 (100%)	115 (95%)	6 (5%)	30	66
21	BP	77/130 (59%)	71 (92%)	6 (8%)	16	52
22	BZ	87/93 (94%)	84 (97%)	3 (3%)	44	76
23	Bc	52/58 (90%)	48 (92%)	4 (8%)	16	53
24	BW	113/113 (100%)	109 (96%)	4 (4%)	43	75
25	Bd	40/47 (85%)	39 (98%)	1 (2%)	55	81
26	Bb	78/78 (100%)	78 (100%)	0	100	100
27	Be	47/49 (96%)	46 (98%)	1 (2%)	61	85
28	BA	161/204 (79%)	153 (95%)	8 (5%)	30	66
29	BR	105/127 (83%)	103 (98%)	2 (2%)	65	86
30	BB	188/226 (83%)	186 (99%)	2 (1%)	80	91
31	BV	63/68 (93%)	59 (94%)	4 (6%)	22	59
32	Ba	80/107 (75%)	78 (98%)	2 (2%)	55	81
33	BJ	160/167 (96%)	157 (98%)	3 (2%)	65	86
34	BC	182/211 (86%)	177 (97%)	5 (3%)	52	79
35	BG	201/210 (96%)	192 (96%)	9 (4%)	34	69
36	BH	164/168 (98%)	157 (96%)	7 (4%)	35	70
37	CG	205/220 (93%)	194 (95%)	11 (5%)	27	64
38	CT	139/141 (99%)	135 (97%)	4 (3%)	50	78
39	CZ	113/113 (100%)	109 (96%)	4 (4%)	43	75
40	Cz	192/192 (100%)	182 (95%)	10 (5%)	29	65
41	CA	195/199 (98%)	184 (94%)	11 (6%)	26	63
42	CJ	149/157 (95%)	139 (93%)	10 (7%)	20	57
43	CH	164/164 (100%)	158 (96%)	6 (4%)	41	74
44	CV	109/109 (100%)	106 (97%)	3 (3%)	51	79
45	CN	167/173 (96%)	161 (96%)	6 (4%)	42	74
46	Ca	110/110 (100%)	101 (92%)	9 (8%)	14	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
47	CQ	138/160 (86%)	132 (96%)	6 (4%)	35	70
48	CD	251/251 (100%)	234 (93%)	17 (7%)	20	57
49	CR	166/183 (91%)	154 (93%)	12 (7%)	18	55
50	CP	144/144 (100%)	139 (96%)	5 (4%)	43	75
51	CX	109/130 (84%)	102 (94%)	7 (6%)	22	59
52	CW	66/133 (50%)	65 (98%)	1 (2%)	72	89
53	CY	115/128 (90%)	110 (96%)	5 (4%)	35	70
54	Cr	64/131 (49%)	61 (95%)	3 (5%)	32	68
55	Cc	98/98 (100%)	94 (96%)	4 (4%)	37	71
56	Cd	103/106 (97%)	98 (95%)	5 (5%)	31	67
57	Ce	122/122 (100%)	116 (95%)	6 (5%)	31	67
58	Cj	77/77 (100%)	74 (96%)	3 (4%)	39	72
59	Cl	48/48 (100%)	47 (98%)	1 (2%)	61	85
60	Co	94/94 (100%)	87 (93%)	7 (7%)	17	54
61	CM	116/116 (100%)	110 (95%)	6 (5%)	29	65
62	CS	153/163 (94%)	145 (95%)	8 (5%)	29	65
63	CU	94/106 (89%)	86 (92%)	8 (8%)	13	48
64	Ci	62/92 (67%)	59 (95%)	3 (5%)	31	67
65	CK	105/139 (76%)	98 (93%)	7 (7%)	20	57
66	Cu	46/77 (60%)	45 (98%)	1 (2%)	60	83
66	Cv	46/77 (60%)	46 (100%)	0	100	100
67	Cs	48/82 (58%)	47 (98%)	1 (2%)	61	85
67	Ct	48/82 (58%)	46 (96%)	2 (4%)	36	70
68	Ch	109/109 (100%)	103 (94%)	6 (6%)	27	64
69	CF	206/206 (100%)	199 (97%)	7 (3%)	44	76
70	Cq	222/265 (84%)	216 (97%)	6 (3%)	52	79
71	CB	335/335 (100%)	315 (94%)	20 (6%)	24	61
72	CC	302/329 (92%)	286 (95%)	16 (5%)	28	65
73	CO	173/173 (100%)	160 (92%)	13 (8%)	17	54
74	Cp	73/73 (100%)	72 (99%)	1 (1%)	74	89
75	CI	156/183 (85%)	152 (97%)	4 (3%)	54	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
76	Cn	24/24 (100%)	23 (96%)	1 (4%)	36	70
77	Cm	47/48 (98%)	46 (98%)	1 (2%)	61	85
78	CL	175/175 (100%)	166 (95%)	9 (5%)	29	66
79	CE	185/185 (100%)	169 (91%)	16 (9%)	13	47
80	Cf	96/96 (100%)	93 (97%)	3 (3%)	47	77
81	Ck	63/63 (100%)	58 (92%)	5 (8%)	15	51
82	Cb	51/53 (96%)	51 (100%)	0	100	100
83	Cg	98/107 (92%)	91 (93%)	7 (7%)	18	56
All	All	10084/11382 (89%)	9634 (96%)	450 (4%)	38	69

5 of 450 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
45	CN	116	LEU
49	CR	153	LYS
78	CL	120	LYS
46	Ca	26	ARG
48	CD	158	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 129 such sidechains are listed below:

Mol	Chain	Res	Type
41	CA	209	HIS
46	Ca	69	HIS
79	CE	67	HIS
41	CA	216	HIS
42	CJ	153	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	Ad	1760/1810 (97%)	458 (26%)	0
2	Ae	74/75 (98%)	19 (25%)	0
3	Af	10/11 (90%)	2 (20%)	0
84	Aa	3389/3391 (99%)	748 (22%)	0
85	Ac	159/160 (99%)	35 (22%)	0
86	Ab	119/120 (99%)	23 (19%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	5511/5567 (98%)	1285 (23%)	0

5 of 1285 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	Ad	4	C
1	Ad	8	U
1	Ad	16	G
1	Ad	25	C
1	Ad	26	A

There are no RNA pucker outliers to report.

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](#)

There are no ligands in this entry.

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.