



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 03:02 PM BST

PDB ID : 4V6U
EMDB ID: : EMD-2009
Title : Promiscuous behavior of proteins in archaeal ribosomes revealed by cryo-EM:
implications for evolution of eukaryotic ribosomes
Authors : Armache, J.-P.; Anger, A.M.; Marquez, V.; Frankenberg, S.; Froehlich, T.;
Villa, E.; Berninghausen, O.; Thomm, M.; Arnold, G.J.; Beckmann, R.; Wil-
son, D.N.
Deposited on : 2012-08-09
Resolution : 6.60 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

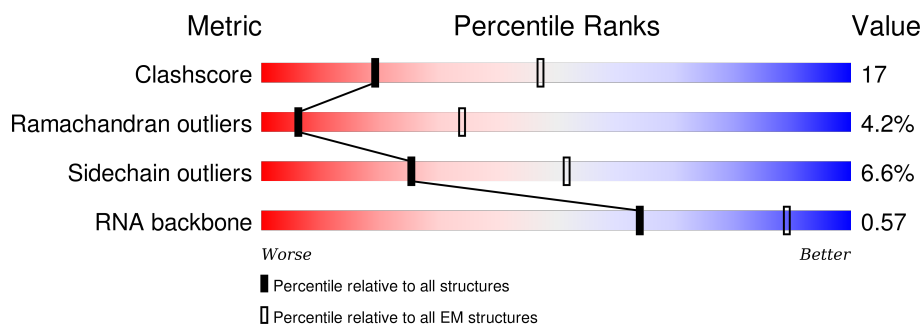
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.60 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	AQ	158	70% 24% 6%
2	AK	135	65% 25% 10%
3	AI	130	67% 28% ...
4	AG	125	44% 36% 14% 6%
5	AW	63	75% 21% 5%
6	AC	210	63% 20% 5% 11%
7	AB	202	68% 26% 5%
8	AR	113	66% 26% 8%





















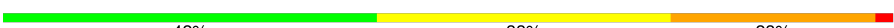




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Mol	Chain	Length	Quality of chain
9	A9	57	
10	AD	180	
11	A1	77	
12	AN	147	
13	AX	71	
14	AM	137	
15	AE	243	
16	AJ	127	
17	AO	148	
18	AF	236	
19	AS	67	
20	A3	123	
20	B4	123	
20	BG	123	
21	A2	1495	
22	AY	50	
23	AT	132	
24	AA	198	
25	AH	215	
26	AP	56	
27	A0	76	
28	AV	99	
28	B6	99	
29	AL	102	
30	AU	150	

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Mol	Chain	Length	Quality of chain
31	BY	155	
32	BO	203	
33	BC	365	
34	B5	83	
34	BK	83	
35	BL	147	
36	Bf	51	
37	BU	121	
38	Bb	130	
39	Be	62	
40	BE	186	
41	Ba	95	
42	BT	86	
43	Bk	339	
44	BW	72	
45	Bi	83	
46	BA	216	
47	BI	142	
48	BR	97	
49	BQ	150	
50	BV	66	
51	Bj	94	
52	BB	239	
53	BD	255	
54	BF	184	

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Mol	Chain	Length	Quality of chain
55	Bh	24	 92% 8%
56	BH	164	 40% 26% 10% 7% 18%
57	BZ	99	 66% 26% 6% •
58	BP	120	 69% 28% •
59	BM	194	 68% 27% • •
60	BS	155	 70% 21% 6% •
61	Bd	89	 52% 35% 10% •
62	BN	181	 65% 21% 7% • 7%
63	Bg	51	 43% 27% 12% 6% 12%
64	Bc	87	 63% 29% 7% •
65	BJ	141	 55% 32% 6% 6%
66	Bl	77	 71% 23% 5%
67	B1	3049	 • 57% 34% 8%
68	B3	126	 48% 38% 14%

2 Entry composition

There are 68 unique types of molecules in this entry. The entry contains 173979 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 30S ribosomal protein S15P/S13e.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AQ	158	Total	C	N	O	S	0	0
			1310	834	250	221	5		

- Molecule 2 is a protein called 30S ribosomal protein S9P.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AK	135	Total	C	N	O	S	0	0
			1072	671	205	190	6		

- Molecule 3 is a protein called 30S ribosomal protein S8P.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AI	129	Total	C	N	O	S	0	0
			1028	668	178	180	2		

- Molecule 4 is a protein called 30S ribosomal protein S6e.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AG	125	Total	C	N	O	S	0	0
			984	623	180	179	2		

- Molecule 5 is a protein called 30S ribosomal protein S27e.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AW	63	Total	C	N	O	S	0	0
			478	306	85	81	6		

- Molecule 6 is a protein called 30S ribosomal protein S3P.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AC	186	Total	C	N	O	S	0	0
			1459	933	271	251	4		

- Molecule 7 is a protein called 30S ribosomal protein S2P.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AB	202	Total	C	N	O	S	0	0
			1623	1046	282	290	5		

- Molecule 8 is a protein called 30S ribosomal protein S17P.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AR	113	Total	C	N	O	S	0	0
			934	592	177	160	5		

- Molecule 9 is a protein called unknown 30S ribosomal protein SX.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	A9	57	Total	C	N	O	0	0
			286	171	57	58		

- Molecule 10 is a protein called 30S ribosomal protein S4P.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AD	172	Total	C	N	O	S	0	0
			1434	902	273	255	4		

- Molecule 11 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	A1	77	Total	C	N	O	P	0	0
			1649	734	303	535	77		

- Molecule 12 is a protein called 30S ribosomal protein S12P.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AN	145	Total	C	N	O	S	0	0
			1140	722	222	193	3		

- Molecule 13 is a protein called 30S ribosomal protein S28e.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AX	71	Total	C	N	O	S	0	0
			568	345	115	107	1		

- Molecule 14 is a protein called 30S ribosomal protein S11P.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AM	133	Total	C	N	O	S	0	0
			1004	623	200	179	2		

- Molecule 15 is a protein called 30S ribosomal protein S4e.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AE	241	Total	C	N	O	S	0	0
			1976	1277	355	339	5		

- Molecule 16 is a protein called 30S ribosomal protein S8e.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AJ	127	Total	C	N	O	S	0	0
			1004	622	207	174	1		

- Molecule 17 is a protein called 30S ribosomal protein S13P.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AO	148	Total	C	N	O	S	0	0
			1189	746	237	200	6		

- Molecule 18 is a protein called 30S ribosomal protein S5P.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AF	217	Total	C	N	O	S	0	0
			1716	1084	319	305	8		

- Molecule 19 is a protein called 30S ribosomal protein S17e.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AS	67	Total	C	N	O	S	0	0
			556	353	105	95	3		

- Molecule 20 is a protein called 50S ribosomal protein L7Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	A3	123	Total	C	N	O	S	0	0
			939	599	155	181	4		
20	BG	123	Total	C	N	O	S	0	0
			939	599	155	181	4		
20	B4	123	Total	C	N	O	S	0	0
			939	599	155	181	4		

- Molecule 21 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	A2	1495	Total	C	N	O	P	0	0
			32135	14297	5954	10389	1495		

- Molecule 22 is a protein called 30S ribosomal protein S27ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AY	50	Total	C	N	O	S	0	0
			409	262	75	66	6		

- Molecule 23 is a protein called 30S ribosomal protein S19P.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AT	111	Total	C	N	O	S	0	0
			923	594	173	150	6		

- Molecule 24 is a protein called 30S ribosomal protein S3Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AA	190	Total	C	N	O	S	0	0
			1559	1007	273	274	5		

- Molecule 25 is a protein called 30S ribosomal protein S7P.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AH	215	Total	C	N	O	S	0	0
			1736	1100	326	302	8		

- Molecule 26 is a protein called 30S ribosomal protein S14P type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AP	56	Total	C	N	O	S	0	0
			462	292	95	69	6		

- Molecule 27 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A0	76	Total	C	N	O	P	0	0
			1625	722	291	536	76		

- Molecule 28 is a protein called 30S ribosomal protein S24e.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AV	99	Total	C	N	O	S	0	0
			823	532	134	154	3		
28	B6	94	Total	C	N	O	S	0	0
			782	508	127	144	3		

- Molecule 29 is a protein called 30S ribosomal protein S10P.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AL	102	Total	C	N	O	S	0	0
			822	507	159	152	4		

- Molecule 30 is a protein called SSU ribosomal protein S19E.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AU	144	Total	C	N	O	S	0	0
			1175	758	212	204	1		

- Molecule 31 is a protein called 50S ribosomal protein L30P.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BY	155	Total	C	N	O	S	0	0
			1243	788	235	213	7		

- Molecule 32 is a protein called 50S ribosomal protein L18P.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BO	197	Total	C	N	O	S	0	0
			1597	1021	299	274	3		

- Molecule 33 is a protein called 50S ribosomal protein L3P.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BC	365	Total	C	N	O	S	0	0
			2912	1870	527	500	15		

- Molecule 34 is a protein called 50S ribosomal protein L14e.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	B5	81	Total	C	N	O	S	0	0
			614	386	119	108	1		
34	BK	81	Total	C	N	O	S	0	0
			614	386	119	108	1		

- Molecule 35 is a protein called 50S ribosomal protein L15P.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BL	147	Total	C	N	O	S	0	0
			1154	727	227	195	5		

- Molecule 36 is a protein called 50S ribosomal protein L39e.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Bf	51	Total	C	N	O	S	0	0
			445	284	98	62	1		

- Molecule 37 is a protein called 50S ribosomal protein L24P.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BU	121	Total	C	N	O	S	0	0
			1008	637	195	172	4		

- Molecule 38 is a protein called 50S ribosomal protein L32e.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Bb	127	Total	C	N	O	S	0	0
			1074	689	217	167	1		

- Molecule 39 is a protein called 50S ribosomal protein L37e.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Be	62	Total	C	N	O	S	0	0
			506	312	111	78	5		

- Molecule 40 is a protein called 50S ribosomal protein L5P.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BE	186	Total	C	N	O	S	0	0
			1489	937	278	265	9		

- Molecule 41 is a protein called 50S ribosomal protein L31e.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	Ba	90	Total	C	N	O	0	0
			746	483	138	125		

- Molecule 42 is a protein called 50S ribosomal protein L23P.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	BT	84	Total	C	N	O		
			680	440	118	122	0	0

- Molecule 43 is a protein called Acidic ribosomal protein P0 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Bk	212	Total	C	N	O	S		
			1632	1051	272	303	6	0	0

- Molecule 44 is a protein called 50S ribosomal protein L29P.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	BW	72	Total	C	N	O	S	
			594	369	115	106	4	0

- Molecule 45 is a protein called 50S ribosomal protein L37Ae.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	Bi	78	Total	C	N	O	S	
			590	368	122	95	5	0

- Molecule 46 is a protein called 50S ribosomal protein L1P.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	BA	216	Total	C	N	O	S	
			1677	1068	300	304	5	0

- Molecule 47 is a protein called 50S ribosomal protein L13P.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	BI	142	Total	C	N	O	S	
			1150	737	215	195	3	0

- Molecule 48 is a protein called 50S ribosomal protein L21e.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	BR	95	Total	C	N	O	S	
			787	501	160	125	1	0

- Molecule 49 is a protein called 50S ribosomal protein L19e.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BQ	150	Total	C	N	O	S	0	0
			1256	794	255	202	5		

- Molecule 50 is a protein called 50S ribosomal protein L24e.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BV	66	Total	C	N	O	S	0	0
			555	351	106	91	7		

- Molecule 51 is a protein called 50S ribosomal protein L44E.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Bj	94	Total	C	N	O	S	0	0
			787	499	161	122	5		

- Molecule 52 is a protein called 50S ribosomal protein L2P.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BB	239	Total	C	N	O	S	0	0
			1838	1169	347	317	5		

- Molecule 53 is a protein called 50S ribosomal protein L4P.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BD	255	Total	C	N	O	S	0	0
			2026	1288	391	342	5		

- Molecule 54 is a protein called 50S ribosomal protein L6P.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BF	184	Total	C	N	O	S	0	0
			1476	956	252	266	2		

- Molecule 55 is a protein called 50S ribosomal protein L41e.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Bh	24	Total	C	N	O	S	0	0
			230	147	54	28	1		

- Molecule 56 is a protein called 50S ribosomal protein L11P.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BH	134	Total	C	N	O	S	0	0
			988	635	164	183	6		

- Molecule 57 is a protein called 50S ribosomal protein L30e.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BZ	99	Total	C	N	O	S	0	0
			754	489	121	142	2		

- Molecule 58 is a protein called 50S ribosomal protein L18e.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	BP	120	Total	C	N	O	S	0	0
			966	606	186	171	3		

- Molecule 59 is a protein called 50S ribosomal protein L15e.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	BM	194	Total	C	N	O	S	0	0
			1595	1020	316	253	6		

- Molecule 60 is a protein called 50S ribosomal protein L22P.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	BS	150	Total	C	N	O	S	0	0
			1200	764	230	202	4		

- Molecule 61 is a protein called 50S ribosomal protein L34e.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Bd	89	Total	C	N	O	S	0	0
			740	463	158	108	11		

- Molecule 62 is a protein called 50S ribosomal protein L10e.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	BN	168	Total	C	N	O	S	0	0
			1378	872	268	232	6		

- Molecule 63 is a protein called 50S ribosomal protein L40e.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Bg	45	Total	C	N	O	S	0	0
			371	236	76	55	4		

- Molecule 64 is a protein called 50S ribosomal protein L35Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Bc	87	Total	C	N	O	S	0	0
			685	434	132	117	2		

- Molecule 65 is a protein called 50S ribosomal protein L14P.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	BJ	132	Total	C	N	O	S	0	0
			1014	631	204	176	3		

- Molecule 66 is a protein called 50S ribosomal protein LX.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Bl	77	Total	C	N	O	S	0	0
			659	425	118	115	1		

- Molecule 67 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	B1	3049	Total	C	N	O	P	0	0
			65577	29172	12191	21165	3049		

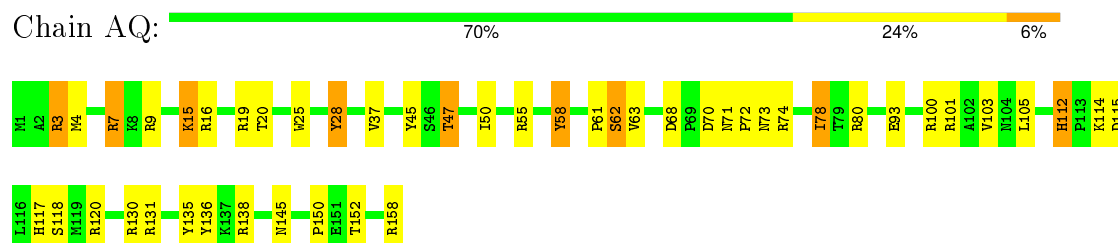
- Molecule 68 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	B3	126	Total	C	N	O	P	0	0
			2694	1199	492	877	126		

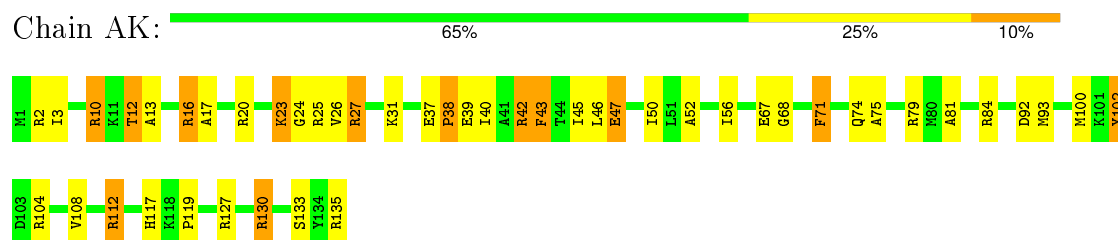
3 Residue-property plots [i](#)

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.

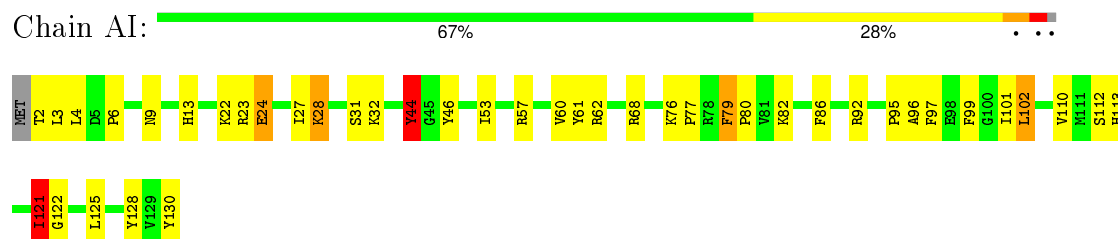
- Molecule 1: 30S ribosomal protein S15P/S13e



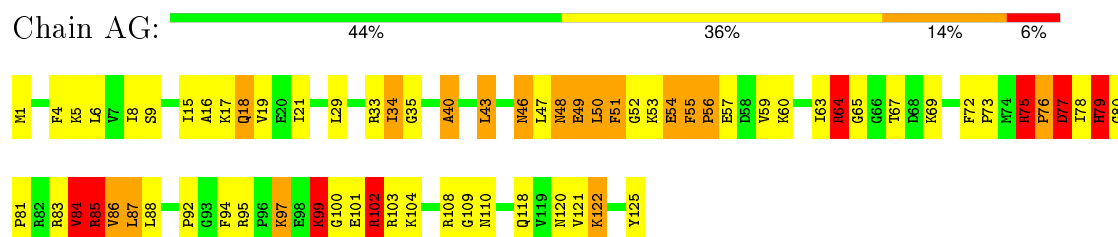
- Molecule 2: 30S ribosomal protein S9P



- Molecule 3: 30S ribosomal protein S8P



- Molecule 4: 30S ribosomal protein S6e



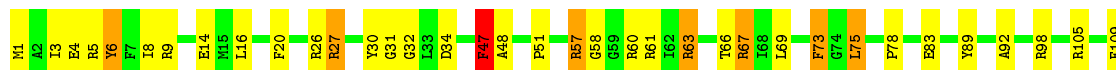
- Molecule 5: 30S ribosomal protein S27e

Chain AW:  75% 21% 5%



- Molecule 6: 30S ribosomal protein S3P

Chain AC:  63% 20% 5% 11%



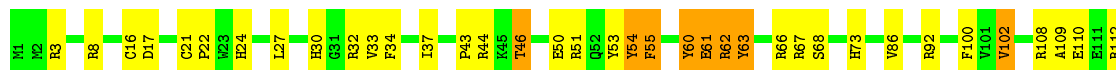
- Molecule 7: 30S ribosomal protein S2P

Chain AB:  68% 26% 5%



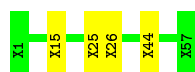
- Molecule 8: 30S ribosomal protein S17P

Chain AR:  66% 26% 8%



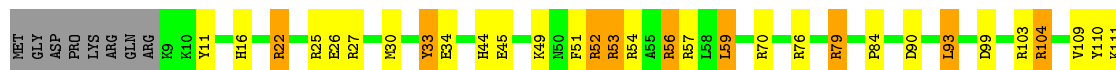
- Molecule 9: unknown 30S ribosomal protein SX

Chain A9:  93% 7%



- Molecule 10: 30S ribosomal protein S4P

Chain AD:  63% 25% 8% 4%

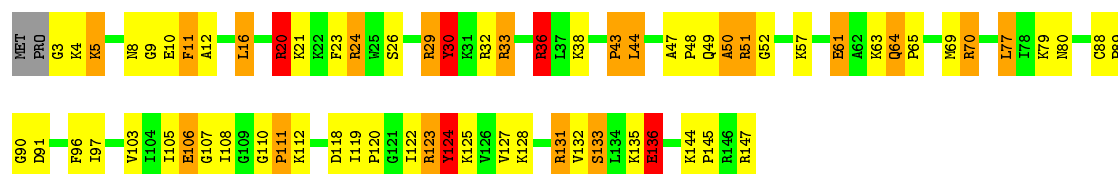




• Molecule 11: E-tRNA



• Molecule 12: 30S ribosomal protein S12P



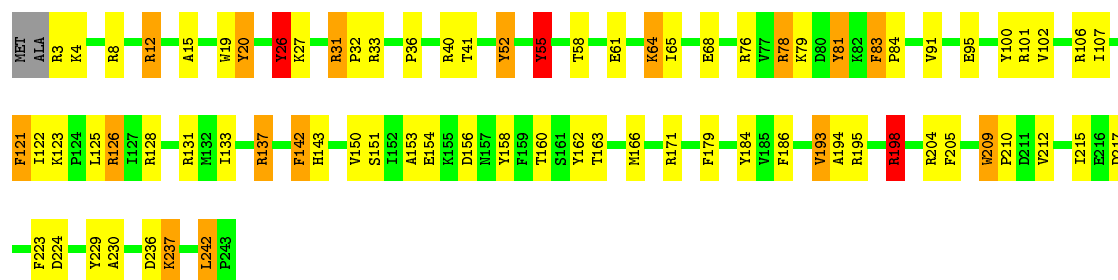
• Molecule 13: 30S ribosomal protein S28e



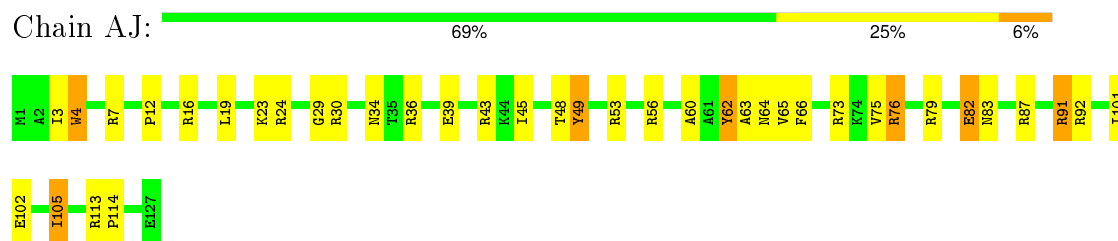
• Molecule 14: 30S ribosomal protein S11P



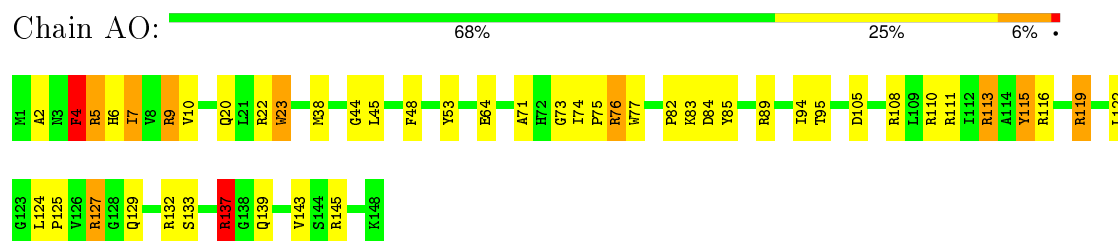
• Molecule 15: 30S ribosomal protein S4e



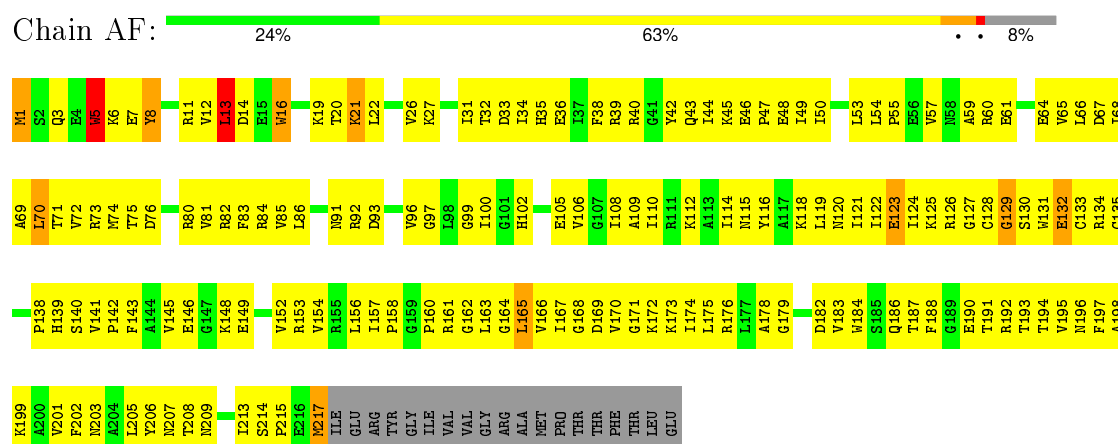
- Molecule 16: 30S ribosomal protein S8e



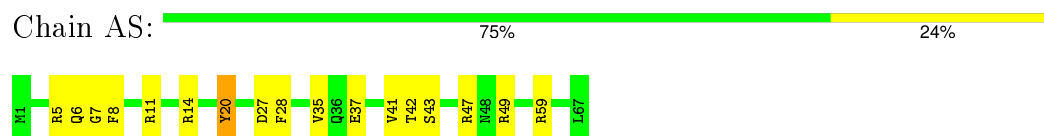
- Molecule 17: 30S ribosomal protein S13P



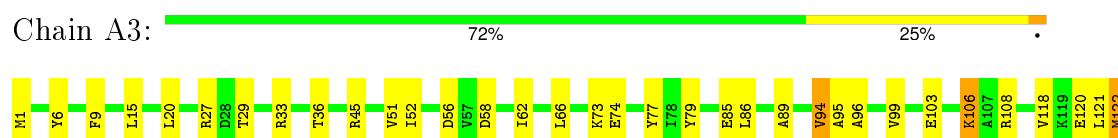
- Molecule 18: 30S ribosomal protein S5P



- Molecule 19: 30S ribosomal protein S17e

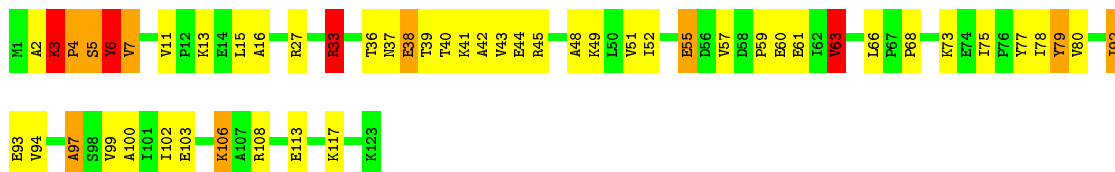


- Molecule 20: 50S ribosomal protein L7Ae




K123

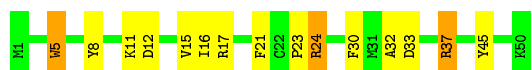
- Molecule 20: 50S ribosomal protein L7Ae

Chain BG:  58% 32% 7%

G1441	G1381	U1321	U1261	G1201	G1141	G1081	G1021	U961	G901	C841	U781	A721	C661	G601	G541
G1442	G1382	C1322	U1262	G1202	G1142	A1082	U1022	G962	U902	U842	A782	G722	C662	G602	G542
G1443	A1383	A1323	G1263	G1203	G1143	G1083	G1023	G963	G903	G843	G783	G723	G663	G603	G543
G1444	G1384	G1324	G1264	G1204	G1144	U1084	G1024	A964	G904	G844	G784	G724	G664	C604	C544
G1445	U1385	G1325	G1265	G1205	C1145	C1085	U1025	G965	A905	G845	G785	G725	G665	C605	C545
G1446	G1386	G1326	A1266	G1206	G1146	C1086	A1026	G966	G906	G846	G786	A726	G666	U606	C546
G1447	C1387	C1327	U1267	G1207	G1147	C1087	C1027	C967	C907	A847	G787	G727	G667	U607	U547
G1448	G1388	C1328	C1268	A1208	G1148	U1088	G1028	C968	G908	G848	G788	G728	G668	G608	A548
G1449	G1389	G1329	C1269	C1209	C1149	C1089	G1029	A969	U909	U849	G789	G729	A669	G609	A549
G1450	G1390	G1330	C1270	A1210	G1150	C1090	U1030	G970	G910	A850	G790	G670	G610	A610	U550
G1451	U1391	A1311	G1271	A1211	A1151	C1091	G1031	G971	C911	C851	G791	A731	C671	A611	U551
G1452	G1392	C1332	G1272	U1212	C1152	G1092	A1032	C972	G912	G852	G792	G732	G672	C612	C552
G1453	A1393	G1333	G1273	G1213	G1153	C1093	G1033	U973	G913	G853	G793	C733	G673	C613	C553
G1454	G1394	A1334	C1274	G1214	G1154	U1094	G1034	G974	U914	C854	A794	G734	G674	G614	C554
G1455	G1395	A1335	U1275	G1215	U1155	C1095	G1035	A975	U915	C855	A795	A735	A675	G615	U555
G1456	C1396	G1336	G1276	A1216	G1156	G1096	G1036	A976	U916	G856	C796	A736	G676	G616	A556
G1457	C1397	A1337	C1277	C1217	G1157	G1097	U1037	G977	A917	C857	G797	C737	U677	A617	U557
G1458	U1398	C1338	A1278	G1218	G1158	G1098	C1038	G978	A918	A858	U798	C738	G678	G618	C558
G1459	G1399	G1339	A1279	C1219	U1159	A1099	C1039	U979	U919	A859	C799	G739	G679	A619	C559
G1460	A1400	U1340	C1280	G1220	C1160	G1100	A1040	C980	U920	G860	G800	G740	C680	G620	A560
G1461	U1401	A1281	U1281	A1221	A1161	G1101	U1041	C981	G921	G861	A801	A741	C681	G621	A561
G1462	C1402	C1342	G1282	C1222	G1162	A1102	U1042	G982	G922	C862	G802	U742	A682	C622	A562
A1463	U1403	G1343	G1283	C1223	U1163	G1103	U1043	G983	A923	U863	C803	U743	A683	C623	U563
G1464	C1404	U1344	U1284	U1224	A1164	G1104	A1044	C984	U924	G864	U804	A744	G684	G624	C564
C1465	C1405	G1345	C1285	C1225	U1165	G1105	A1045	C985	U925	A865	C805	G745	G685	G625	C565
G1466	U1406	C1346	C1286	G1226	G1166	A1106	G1046	G986	C926	A866	G806	A746	C686	G626	C566
U1467	U1407	U1347	G1287	A1227	C1167	C1107	U1047	G987	A927	A867	C807	U747	G687	G627	A567
A1468	C1408	C1348	C1288	A1228	C1168	U1108	G1048	A988	A928	C868	C808	A748	G688	G628	C568
G1469	G1409	C1349	U1289	A1229	C1169	C1109	U1049	C989	C929	U869	C809	C749	C689	U629	C569
G1470	G1410	U1350	G1290	G1230	C1170	U1110	G1050	G990	G930	U870	G810	C750	C690	A630	A570
G1471	G1411	U1351	G1291	G1231	G1171	G1111	U1051	C991	C931	A871	C811	C751	G691	G631	C571
G1472	A1412	G1352	A1292	G1232	A1172	G1112	U1052	G992	C932	A872	U812	G752	G692	C632	U572
A1473	C1413	C1353	A1293	G1233	A1173	G1113	A1053	C993	G933	A873	G813	G753	C693	C633	C573
A1474	G1414	A1354	G1294	A1234	C1174	G1114	A1054	C994	G934	G874	C814	G754	U694	C634	A574
C1475	U1415	C1355	C1295	A1235	C1175	G1115	G1055	G995	G935	G875	C815	U755	G695	C635	A575
G1476	C1416	A1356	U1296	G1236	G1176	A1116	G1056	A996	A936	A876	G816	A756	G696	G636	C576
U1477	A1417	C1357	G1297	G1237	C1177	A1117	A1057	G997	A937	A877	U817	G757	A697	G637	C577
G1478	G1418	A1358	G1298	G1238	C1178	C1118	G1058	A998	C938	U878	A818	U758	A698	G638	C578
C1479	G1419	C1359	A1299	A1239	C1179	U1119	C1059	G999	C939	U879	G819	C759	C699	G639	U579
G1480	U1420	C1360	A1300	A1240	C1179	G1120	G1060	G1000	U940	G880	G820	G760	G700	U640	C580
C1481	G1421	G1361	U1301	U1241	G1181	C1121	A1061	A1001	C941	G881	G821	G761	G701	A641	C581
G1482	G1422	C1362	C1302	C1242	G1182	C1122	G1062	A1002	A942	C882	A822	G762	G702	G642	C582
U1483	A1423	C1363	C1303	C1243	C1183	G1123	A1063	G1003	C943	G883	A823	G763	G703	G643	C583
G1484	G1424	C1364	C1304	C1244	U1184	G1124	G1064	U1004	C944	G884	G824	C764	C704	G644	C584
G1485	C1425	G1365	U1305	C1245	A1185	C1125	C1065	G1005	G945	G885	C825	U765	C705	G645	C585
C1486	C1426	C1366	A1306	U1246	C1186	G1126	G1066	C1006	G946	G886	C826	G766	G706	U646	C586
U1487	G1427	G1367	G1307	A1247	A1187	A1127	G1067	A1007	G947	G887	G827	U767	A707	G647	C587
G1488	G1428	U1368	U1308	A1248	C1188	U1128	C1068	U1008	G948	A888	U828	A768	C708	A648	C588
A1489	G1429	C1369	A1309	A1249	G1189	A1129	G1069	G1009	G949	G889	U829	A769	A649	U589	C589
C1490	G1430	U1370	C1310	C1250	C1190	A1130	C1070	G1010	C950	C890	A830	A770	G710	A650	C590
C1491	G1431	C1371	C1311	C1251	G1191	G1131	C1071	C1011	G951	A891	A831	G771	U711	U651	C591
U1492	U1432	C1372	C1312	C1252	C1192	C1132	C1072	C1012	A952	C892	G832	G772	G712	C652	C592
C1493	C1433	G1373	G1313	G1253	G1193	C1133	C1073	G1013	C953	U893	C833	A773	A713	C653	C593
C1494	G1434	C1374	C1314	C1254	C1194	G1134	C1074	C1014	G954	A894	C834	U774	G714	U654	A594
G1495	G1435	C1375	G1315	C1255	U1195	G1135	A1075	G1015	C955	C895	C835	G775	C715	A655	U595
U1496	U1436	C1376	U1316	C1256	A1196	A1136	G1076	G1016	C956	A896	G836	C776	G716	U656	A596
G1497	G1437	G1377	G1317	U1257	C1197	G1137	U1077	U1017	A957	A897	C837	G777	C717	A657	C597
A1498	A1438	C1378	U1318	C1258	A1198	G1138	U1078	C1018	G958	G898	C838	G778	G718	A658	U598
G1499	G1439	G1379	C1319	A1259	A1199	G1139	G1079	U1019	G959	G899	C839	G779	G719	U659	C599
G1440	G1440	C1380	A1320	G1260	U1200	A1140	C1080	G1020	A960	G900	C840	C780	A720	C660	C540

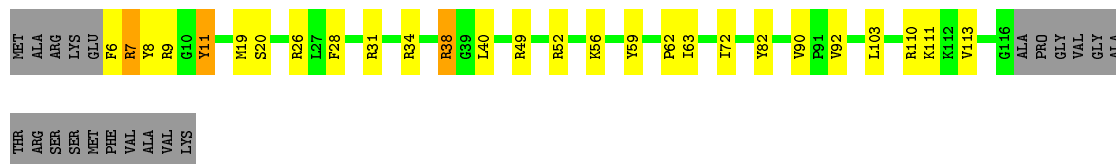
• Molecule 22: 30S ribosomal protein S27ae

Chain AY: 



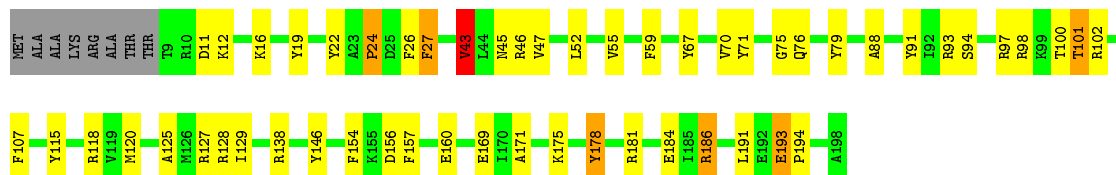
- Molecule 23: 30S ribosomal protein S19P

Chain AT: 



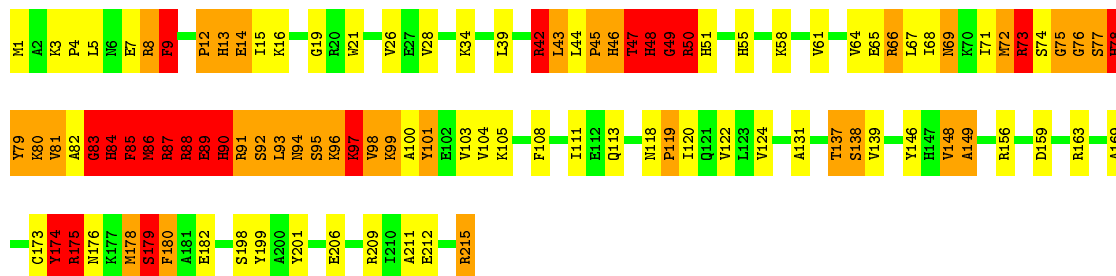
- Molecule 24: 30S ribosomal protein S3Ae

Chain AA: 



- Molecule 25: 30S ribosomal protein S7P

Chain AH: 




- Molecule 26: 30S ribosomal protein S14P type Z

Chain AP: 



- Molecule 27: P-tRNA

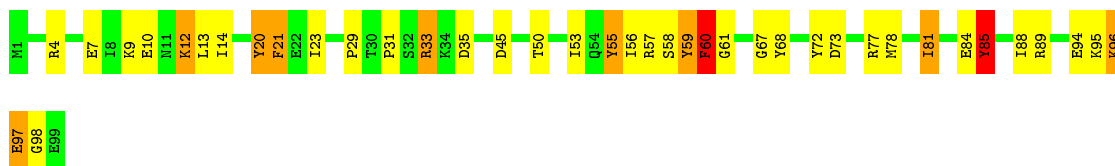
Chain A0: 





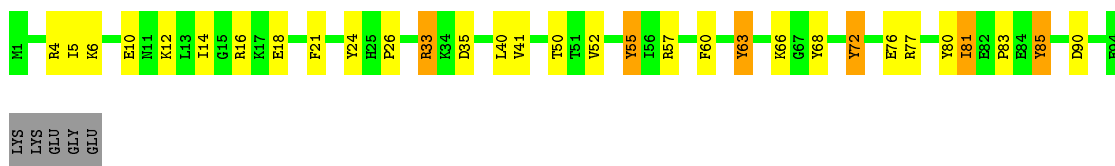
- Molecule 28: 30S ribosomal protein S24e

Chain AV: 60% 29% 9% •



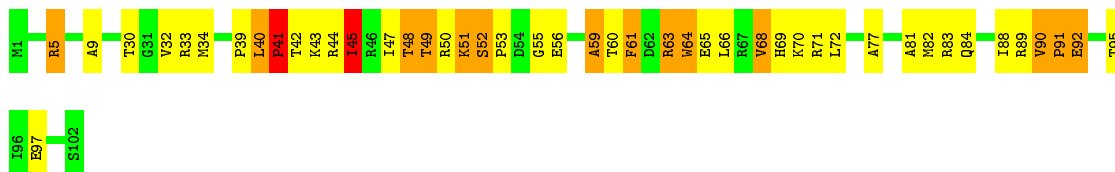
- Molecule 28: 30S ribosomal protein S24e

Chain B6: 64% 25% 6% 5%



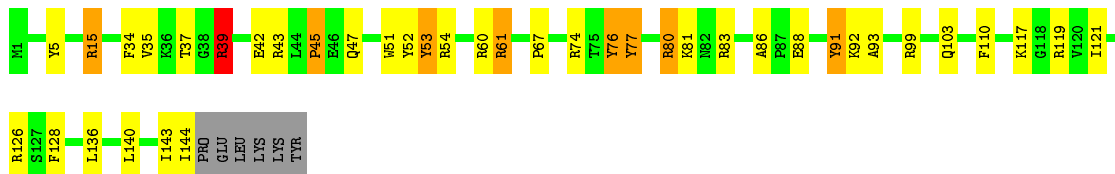
- Molecule 29: 30S ribosomal protein S10P

Chain AL: 55% 29% 14% •



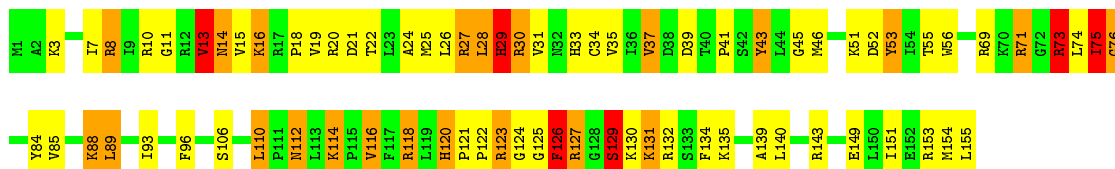
- Molecule 30: SSU ribosomal protein S19E

Chain AU: 69% 21% 5% •

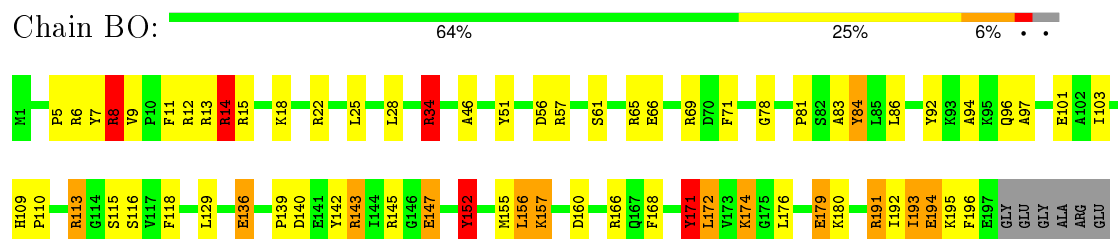


- Molecule 31: 50S ribosomal protein L30P

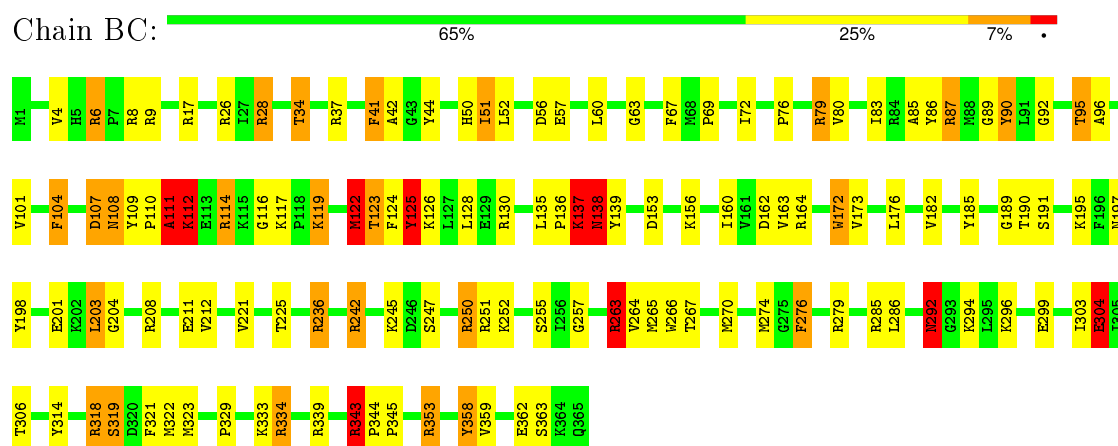
Chain BY: 51% 31% 14% •



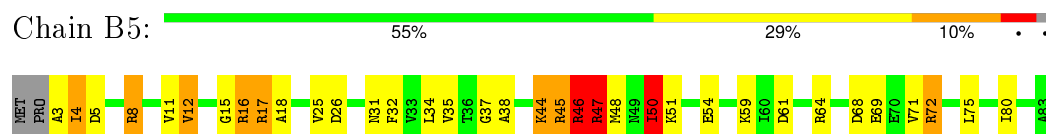
- Molecule 32: 50S ribosomal protein L18P



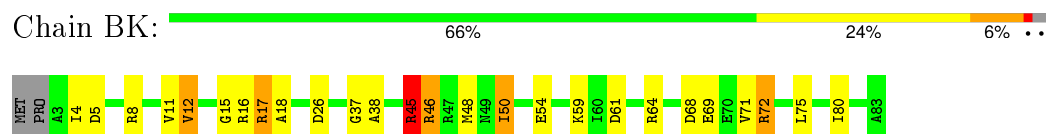
- Molecule 33: 50S ribosomal protein L3P



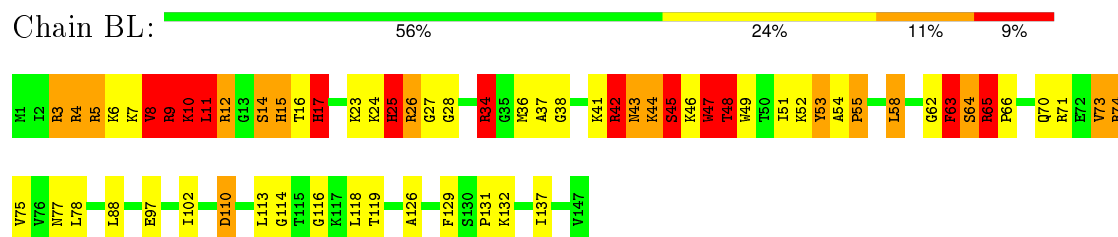
- Molecule 34: 50S ribosomal protein L14e



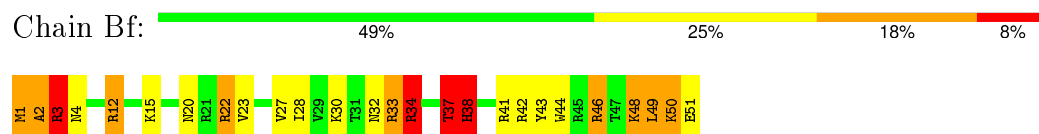
- Molecule 34: 50S ribosomal protein L14e



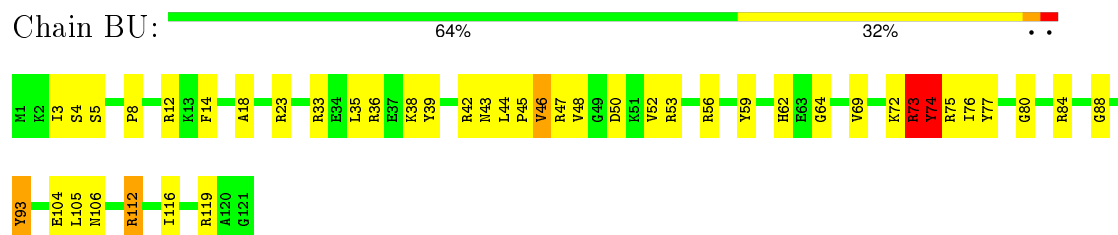
- Molecule 35: 50S ribosomal protein L15P



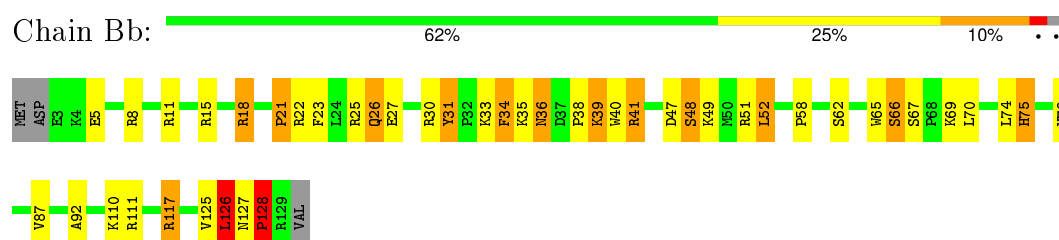
- Molecule 36: 50S ribosomal protein L39e



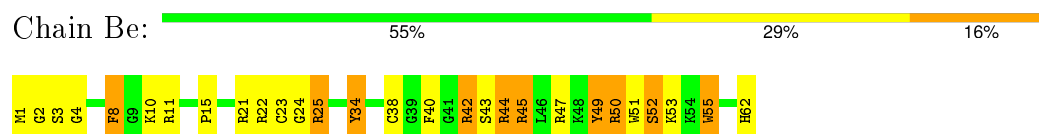
- Molecule 37: 50S ribosomal protein L24P



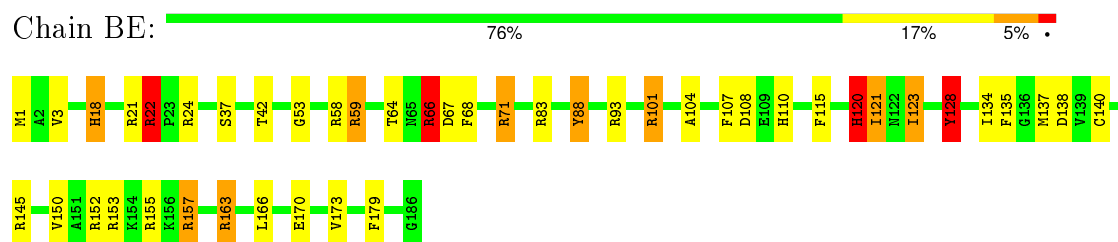
- Molecule 38: 50S ribosomal protein L32e



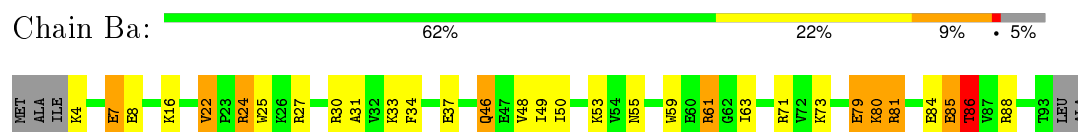
- Molecule 39: 50S ribosomal protein L37e




- Molecule 40: 50S ribosomal protein L5P



- Molecule 41: 50S ribosomal protein L31e



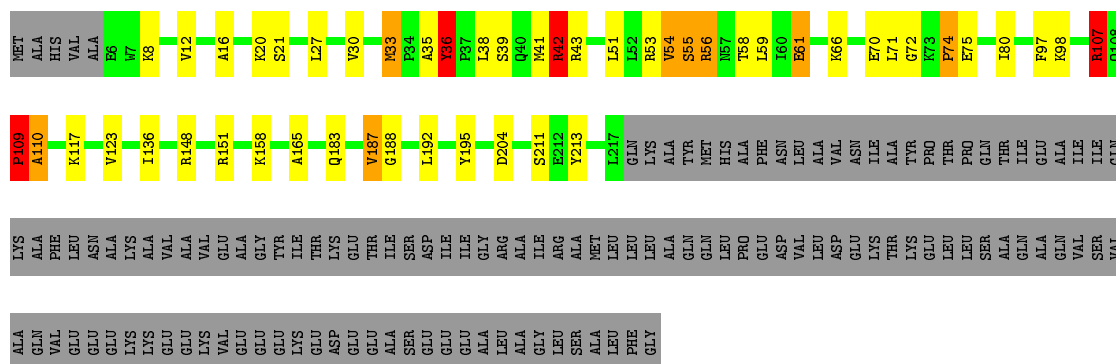
- Molecule 42: 50S ribosomal protein L23P

Chain BT:  73% 21% ..



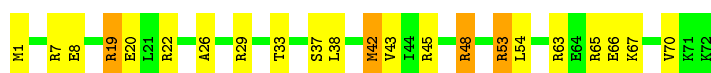
- Molecule 43: Acidic ribosomal protein P0 homolog

Chain Bk:  48% 11% .. 37%




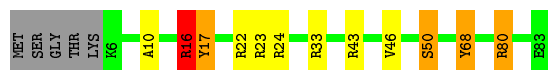
- Molecule 44: 50S ribosomal protein L29P

Chain BW:  69% 25% 6%



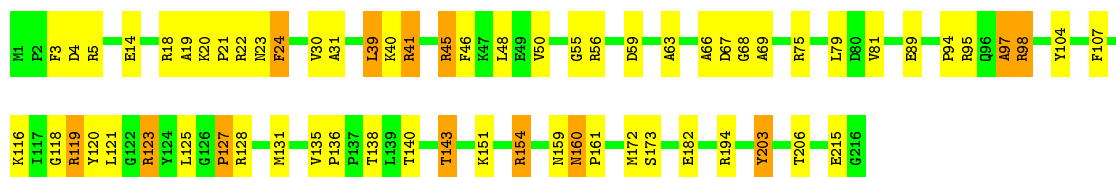
- Molecule 45: 50S ribosomal protein L37Ae

Chain Bi:  80% 8% 5% 6%



- Molecule 46: 50S ribosomal protein L1P

Chain BA:  70% 24% 6%



- Molecule 47: 50S ribosomal protein L13P

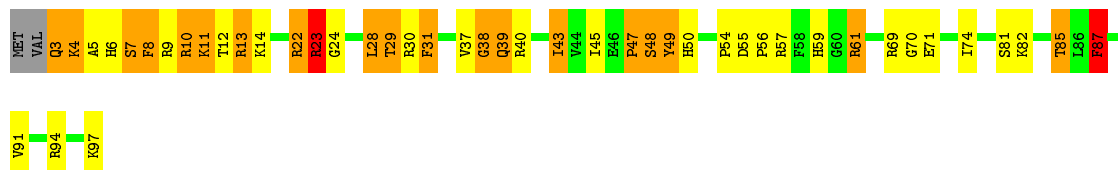
Chain BI:  70% 26% ..





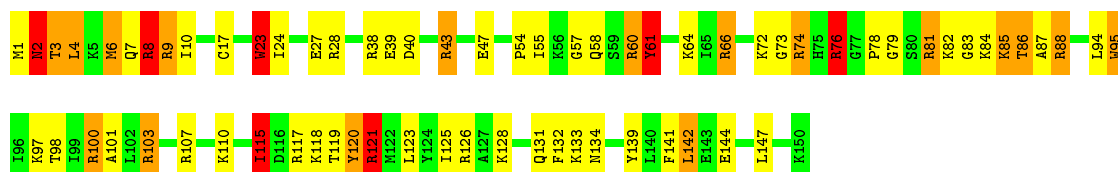
- Molecule 48: 50S ribosomal protein L21e

Chain BR: 51% 26% 20%



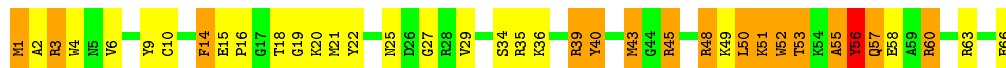
- Molecule 49: 50S ribosomal protein L19e

Chain BQ: 54% 30% 11% 5%



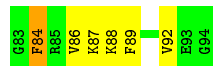
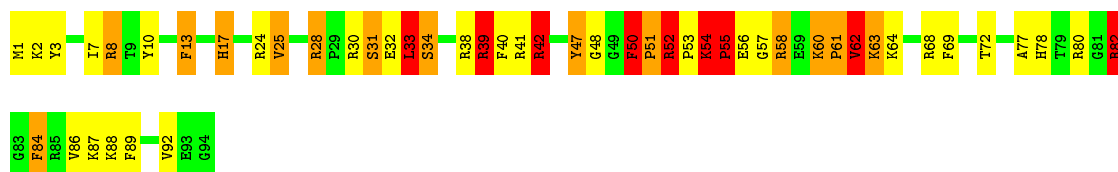
- Molecule 50: 50S ribosomal protein L24e

Chain BV: 42% 33% 23%



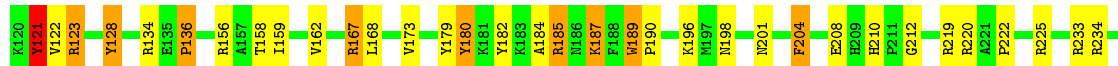
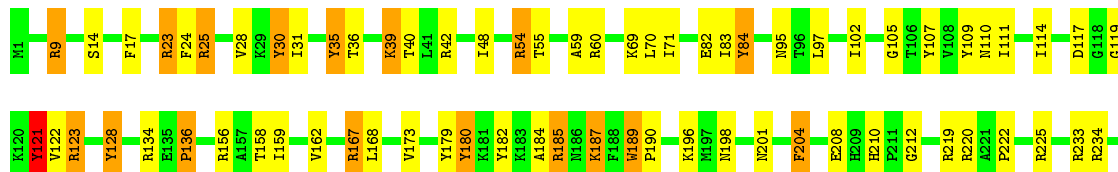
- Molecule 51: 50S ribosomal protein L44E

Chain Bj: 47% 29% 15% 10%



- Molecule 52: 50S ribosomal protein L2P

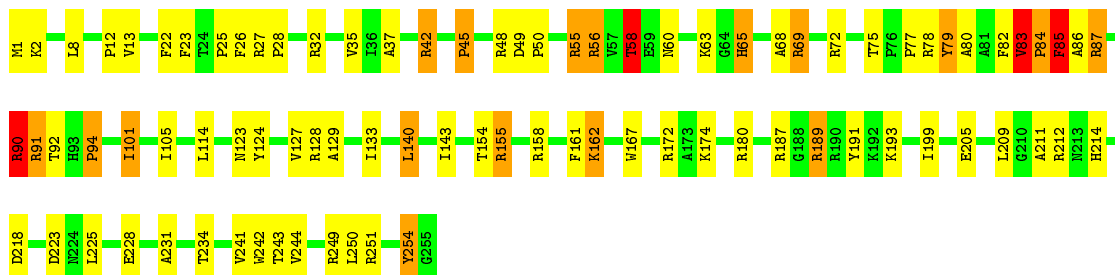
Chain BB: 70% 22% 8%





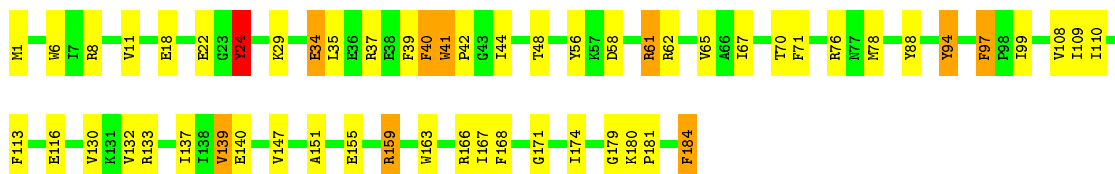
- Molecule 53: 50S ribosomal protein L4P

Chain BD: 66% 26% 7% •



- Molecule 54: 50S ribosomal protein L6P

Chain BF: 70% 25% 5% •



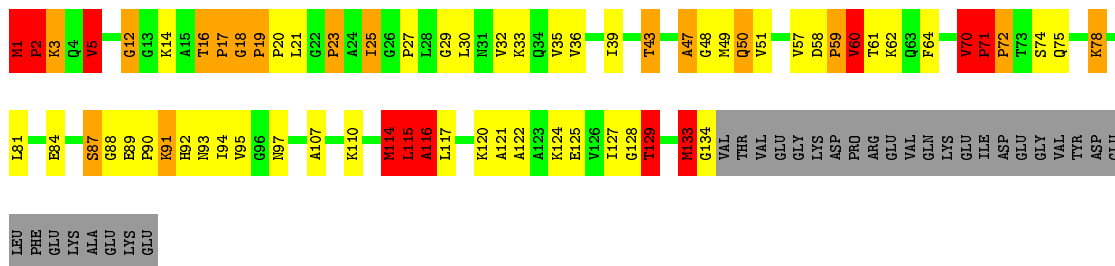
- Molecule 55: 50S ribosomal protein L41e

Chain Bh: 92% 8%



- Molecule 56: 50S ribosomal protein L11P

Chain BH: 40% 26% 10% 7% 18%

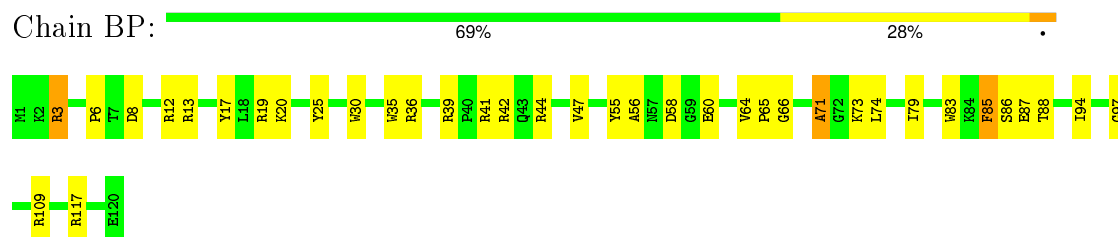


- Molecule 57: 50S ribosomal protein L30e

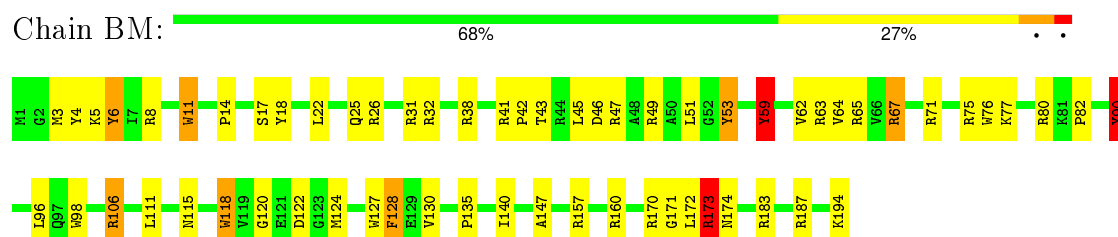
Chain BZ: 66% 26% 6% •



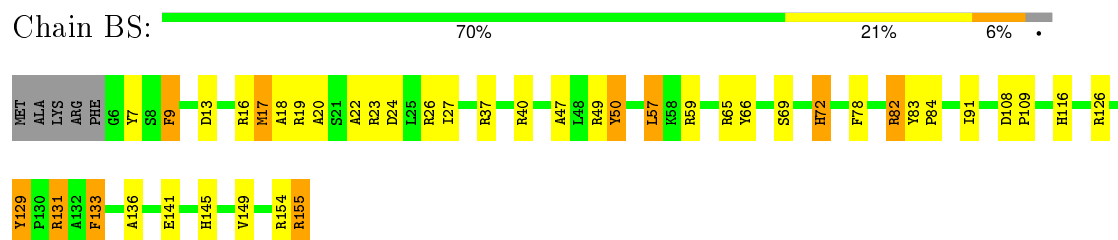
- Molecule 58: 50S ribosomal protein L18e



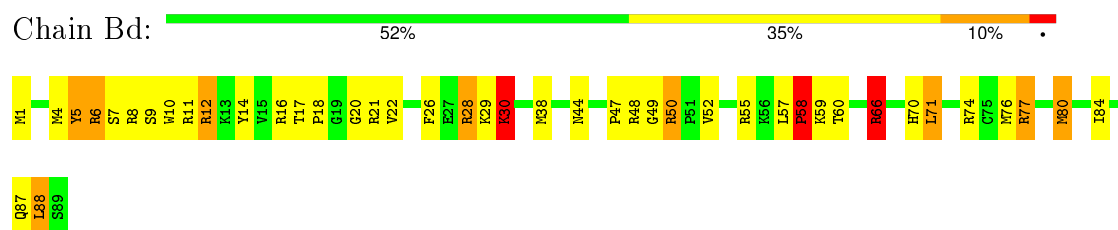
- Molecule 59: 50S ribosomal protein L15e



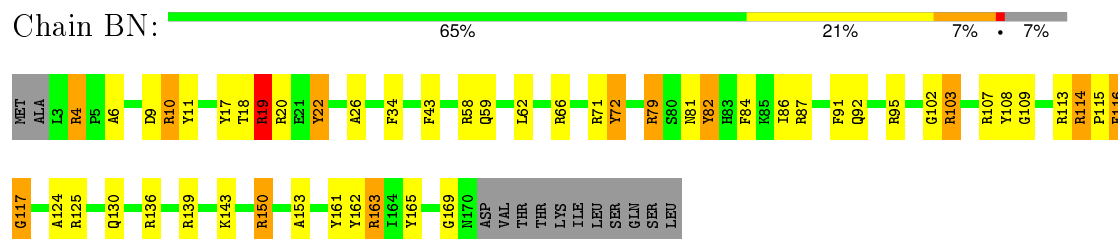
- Molecule 60: 50S ribosomal protein L22P



- Molecule 61: 50S ribosomal protein L34e



- Molecule 62: 50S ribosomal protein L10e



- Molecule 63: 50S ribosomal protein L40e

Chain Bg: 



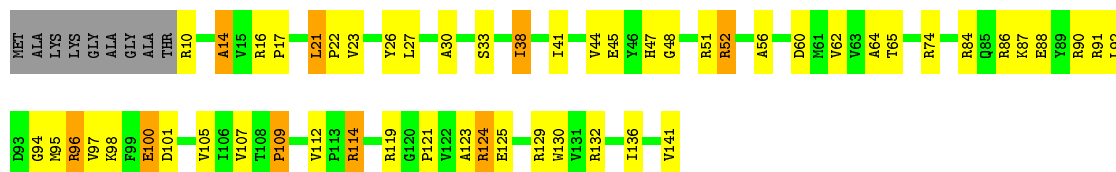
- Molecule 64: 50S ribosomal protein L35Ae

Chain Bc: 



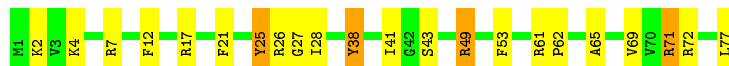
- Molecule 65: 50S ribosomal protein L14P

Chain BJ: 



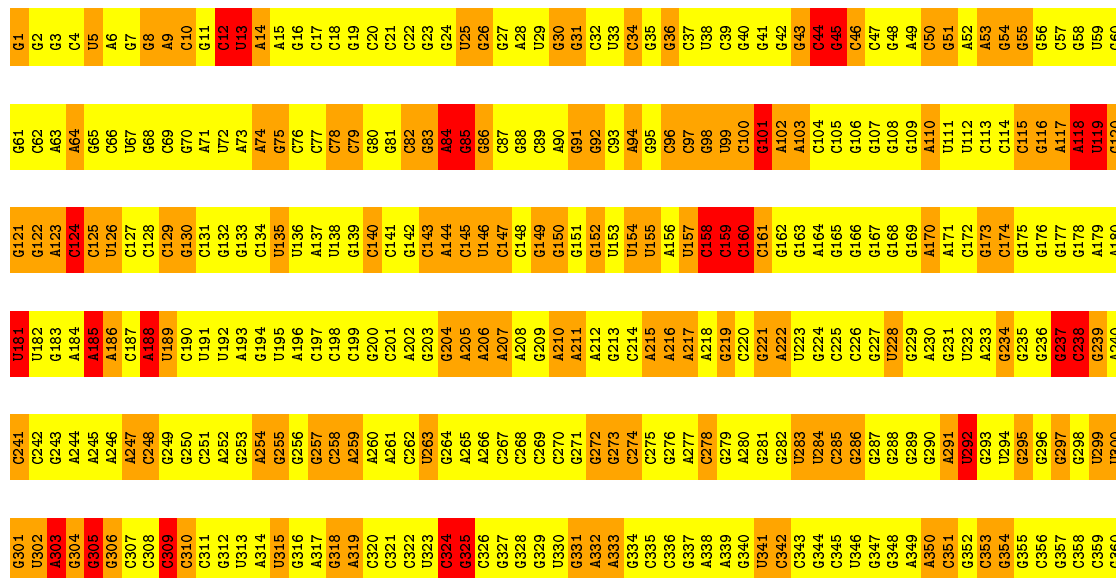
- Molecule 66: 50S ribosomal protein LX

Chain Bl: 



- Molecule 67: 23S rRNA

Chain B1: 



G1321	G1322	G1323	G1324	G1325	G1326	G1327	G1328	G1329	G1330	G1331	G1332	G1333	G1334	G1335	G1336	G1337	G1338	G1339	G1340	G1341	G1342	G1343	G1344	G1345	G1346	G1347	G1348	G1349	G1350	G1351	G1352	G1353	G1354	G1355	G1356	G1357	G1358	G1359	G1360	G1361	G1362	G1363	G1364	G1365	G1366	G1367	G1368	G1369	G1370	G1371	G1372	G1373	G1374	G1375	G1376	G1377	G1378	G1379	G1380																																																																																																																																																																																				
C1261	C1262	C1263	C1264	C1265	C1266	C1267	C1268	C1269	C1270	C1271	C1272	C1273	C1274	C1275	C1276	C1277	C1278	C1279	C1280	C1281	C1282	C1283	C1284	C1285	C1286	C1287	C1288	C1289	C1290	C1291	C1292	C1293	C1294	C1295	C1296	C1297	C1298	C1299	C1300	C1301	C1302	C1303	C1304	C1305	C1306	C1307	C1308	C1309	C1310	C1311	C1312	C1313	C1314	C1315	C1316	C1317	C1318	C1319	C1320																																																																																																																																																																																				
G1201	G1202	G1203	G1204	G1205	G1206	G1207	G1208	G1209	G1210	G1211	G1212	G1213	G1214	G1215	G1216	G1217	G1218	G1219	G1220	G1221	G1222	G1223	G1224	G1225	G1226	G1227	G1228	G1229	G1230	G1231	G1232	G1233	G1234	G1235	G1236	G1237	G1238	G1239	G1240	G1241	G1242	G1243	G1244	G1245	G1246	G1247	G1248	G1249	G1250	G1251	G1252	G1253	G1254	G1255	G1256	G1257	G1258	G1259	G1260																																																																																																																																																																																				
U1081	U1082	U1083	U1084	U1085	U1086	U1087	U1088	U1089	U1090	U1091	U1092	U1093	U1094	U1095	U1096	U1097	U1098	U1099	U1100	U1101	U1102	U1103	U1104	U1105	U1106	U1107	U1108	U1109	U1110	U1111	U1112	U1113	U1114	U1115	U1116	U1117	U1118	U1119	U1120	U1121	U1122	U1123	U1124	U1125	U1126	U1127	U1128	U1129	U1130	U1131	U1132	U1133	U1134	U1135	U1136	U1137	U1138	U1139	U1140																																																																																																																																																																																				
C1141	C1142	C1143	C1144	C1145	C1146	C1147	C1148	C1149	C1150	C1151	C1152	C1153	C1154	C1155	C1156	C1157	C1158	C1159	C1160	C1161	C1162	C1163	C1164	C1165	C1166	C1167	C1168	C1169	C1170	C1171	C1172	C1173	C1174	C1175	C1176	C1177	C1178	C1179	C1180	C1181	C1182	C1183	C1184	C1185	C1186	C1187	C1188	C1189	C1190	C1191	C1192	C1193	C1194	C1195	C1196	C1197	C1198	C1199	C1200																																																																																																																																																																																				
U0801	U0802	U0803	U0804	U0805	U0806	U0807	U0808	U0809	U0810	U0811	U0812	U0813	U0814	U0815	U0816	U0817	U0818	U0819	U0820	U0821	U0822	U0823	U0824	U0825	U0826	U0827	U0828	U0829	U0830	U0831	U0832	U0833	U0834	U0835	U0836	U0837	U0838	U0839	U0840	U0841	U0842	U0843	U0844	U0845	U0846	U0847	U0848	U0849	U0850	U0851	U0852	U0853	U0854	U0855	U0856	U0857	U0858	U0859	U0860																																																																																																																																																																																				
G0801	G0802	G0803	G0804	G0805	G0806	G0807	G0808	G0809	G0810	G0811	G0812	G0813	G0814	G0815	G0816	G0817	G0818	G0819	G0820	G0821	G0822	G0823	G0824	G0825	G0826	G0827	G0828	G0829	G0830	G0831	G0832	G0833	G0834	G0835	G0836	G0837	G0838	G0839	G0840	G0841	G0842	G0843	G0844	G0845	G0846	G0847	G0848	G0849	G0850	G0851	G0852	G0853	G0854	G0855	G0856	G0857	G0858	G0859	G0860																																																																																																																																																																																				
C901	C902	C903	C904	C905	C906	C907	C908	C909	C910	C911	C912	C913	C914	C915	C916	C917	C918	C919	C920	C921	C922	C923	C924	C925	C926	C927	C928	C929	C930	C931	C932	C933	C934	C935	C936	C937	C938	C939	C940	C941	C942	C943	C944	C945	C946	C947	C948	C949	C950	C951	C952	C953	C954	C955	C956	C957	C958	C959	C960																																																																																																																																																																																				
U841	U842	U843	U844	U845	U846	U847	U848	U849	U850	U851	U852	U853	U854	U855	U856	U857	U858	U859	U860	U861	U862	U863	U864	U865	U866	U867	U868	U869	U870	U871	U872	U873	U874	U875	U876	U877	U878	U879	U880	U881	U882	U883	U884	U885	U886	U887	U888	U889	U890	U891	U892	U893	U894	U895	U896	U897	U898	U899	C900																																																																																																																																																																																				
G701	G702	G703	G704	G705	G706	G707	G708	G709	G710	G711	G712	G713	G714	G715	G716	G717	G718	G719	G720	G721	G722	G723	G724	G725	G726	G727	G728	G729	G730	G731	G732	G733	G734	G735	G736	G737	G738	G739	G740	G741	G742	G743	G744	G745	G746	G747	G748	G749	G750	G751	G752	G753	G754	G755	G756	G757	G758	G759	G760	G761	G762	G763	G764	G765	G766	G767	G768	G769	G770	G771	G772	G773	G774	G775	G776	G777	G778	G779	G780																																																																																																																																																																
U701	U702	U703	U704	U705	U706	U707	U708	U709	U710	U711	U712	U713	U714	U715	U716	U717	U718	U719	U720	U721	U722	U723	U724	U725	U726	U727	U728	U729	U730	U731	U732	U733	U734	U735	U736	U737	U738	U739	U740	U741	U742	U743	U744	U745	U746	U747	U748	U749	U750	U751	U752	U753	U754	U755	U756	U757	U758	U759	U760	U761	U762	U763	U764	U765	U766	U767	U768	U769	U770	U771	U772	U773	U774	U775	U776	U777	U778	U779	U780																																																																																																																																																																
C601	C602	C603	C604	C605	C606	C607	C608	C609	C610	C611	C612	C613	C614	C615	C616	C617	C618	C619	C620	C621	C622	C623	C624	C625	C626	C627	C628	C629	C630	C631	C632	C633	C634	C635	C636	C637	C638	C639	C640	C641	C642	C643	C644	C645	C646	C647	C648	C649	C650	C651	C652	C653	C654	C655	C656	C657	C658	C659	C660	C661	C662	C663	C664	C665	C666	C667	C668	C669	C670	C671	C672	C673	C674	C675	C676	C677	C678	C679	C680	C681	C682	C683	C684	C685	C686	C687	C688	C689	C690	C691	C692	C693	C694	C695	C696	C697	C698	C699	C700	C701	C702	C703	C704	C705	C706	C707	C708	C709	C710	C711	C712	C713	C714	C715	C716	C717	C718	C719	C720																																																																																																																								
G601	G602	G603	G604	G605	G606	G607	G608	G609	G610	G611	G612	G613	G614	G615	G616	G617	G618	G619	G620	G621	G622	G623	G624	G625	G626	G627	G628	G629	G630	G631	G632	G633	G634	G635	G636	G637	G638	G639	G640	G641	G642	G643	G644	G645	G646	G647	G648	G649	G650	G651	G652	G653	G654	G655	G656	G657	G658	G659	G660	G661	G662	G663	G664	G665	G666	G667	G668	G669	G670	G671	G672	G673	G674	G675	G676	G677	G678	G679	G680	G681	G682	G683	G684	G685	G686	G687	G688	G689	G690	G691	G692	G693	G694	G695	G696	G697	G698	G699	G700	G701	G702	G703	G704	G705	G706	G707	G708	G709	G710	G711	G712	G713	G714	G715	G716	G717	G718	G719	G720																																																																																																																								
A541	A542	A543	A544	A545	A546	A547	A548	A549	A550	A551	A552	A553	A554	A555	A556	A557	A558	A559	A560	A561	A562	A563	A564	A565	A566	A567	A568	A569	A570	A571	A572	A573	A574	A575	A576	A577	A578	A579	A580	A581	A582	A583	A584	A585	A586	A587	A588	A589	A590	A591	A592	A593	A594	A595	A596	A597	A598	A599	A600	A601	A602	A603	A604	A605	A606	A607	A608	A609	A610	A611	A612	A613	A614	A615	A616	A617	A618	A619	A620	A621	A622	A623	A624	A625	A626	A627	A628	A629	A630	A631	A632	A633	A634	A635	A636	A637	A638	A639	A640	A641	A642	A643	A644	A645	A646	A647	A648	A649	A650	A651	A652	A653	A654	A655	A656	A657	A658	A659	A660	A661	A662	A663	A664	A665	A666	A667	A668	A669	A670	A671	A672	A673	A674	A675	A676	A677	A678	A679	A680	A681	A682	A683	A684	A685	A686	A687	A688	A689	A690	A691	A692	A693	A694	A695	A696	A697	A698	A699	A700	A701	A702	A703	A704	A705	A706	A707	A708	A709	A710	A711	A712	A713	A714	A715	A716	A717	A718	A719	A720																																																												
G481	G482	G483	G484	G485	G486	G487	G488	G489	G490	G491	G492	G493	G494	G495	G496	G497	G498	G499	G500	G501	G502	G503	G504	G505	G506	G507	G508	G509	G510	G511	G512	G513	G514	G515	G516	G517	G518	G519	G520	G521	G522	G523	G524	G525	G526	G527	G528	G529	G530	G531	G532	G533	G534	G535	G536	G537	G538	G539	G540	G541	G542	G543	G544	G545	G546	G547	G548	G549	G550	G551	G552	G553	G554	G555	G556	G557	G558	G559	G560	G561	G562	G563	G564	G565	G566	G567	G568	G569	G570	G571	G572	G573	G574	G575	G576	G577	G578	G579	G580	G581	G582	G583	G584	G585	G586	G587	G588	G589	G590	G591	G592	G593	G594	G595	G596	G597	G598	G599	G600	G601	G602	G603	G604	G605	G606	G607	G608	G609	G610	G611	G612	G613	G614	G615	G616	G617	G618	G619	G620	G621	G622	G623	G624	G625	G626	G627	G628	G629	G630	G631	G632	G633	G634	G635	G636	G637	G638	G639	G640	G641	G642	G643	G644	G645	G646	G647	G648	G649	G650	G651	G652	G653	G654	G655	G656	G657	G658	G659	G660	G661	G662	G663	G664	G665	G666	G667	G668	G669	G670	G671	G672	G673	G674	G675	G676	G677	G678	G679	G680	G681	G682	G683	G684	G685	G686	G687	G688	G689	G690	G691	G692	G693	G694	G695	G696	G697	G698	G699	G700	G701	G702	G703	G704	G705	G706	G707	G708	G709	G710	G711	G712	G713	G714	G715	G716	G717	G718	G719	G720
A481	A482	A483	A484	A485	A486	A487	A488	A489	A490	A491	A492	A493	A494	A495	A496	A497	A498	A499	A500	A501	A502	A503	A504	A505	A506	A507	A508	A509	A510	A511	A512	A513	A514	A515	A516	A517	A518	A519	A520	A521	A522	A523	A524	A525	A526	A527	A528	A529	A530	A531	A532	A533	A534	A535	A536	A537	A538	A539	A540	A541	A542	A543	A544	A545	A546	A547	A548	A549	A550	A551	A552	A553	A554	A555	A556	A557	A558	A559	A																																																																																																																																																																

G2282	C2222	A2161	A2101	U2041	G1981	U1921	G1861	C1801	C1741	G1681	G1561	G1501	C1441	C1381
C2283	G2223	G2162	C2102	A2042	C1982	A1922	G1862	G1802	C1742	G1682	G1562	C1502	C1442	C1382
C2284	G2224	G2163	C2103	A2043	C1983	A1923	G1863	U1803	C1743	C1683	G1563	C1503	G1443	G1383
G2285	G2225	G2164	G2104	C2044	G1984	A1924	A1864	G1804	A1744	C1684	U1624	C1504	U1444	C1384
U2286	G2226	A2165	A2105	C2045	G1985	A1925	U1865	U1805	U1745	G1685	G1565	U1505	G1445	C1385
C2287	G2227	C2166	G2106	C2046	U1986	A1926	G1866	C1806	C1746	C1686	A1626	U1506	G1446	G1386
C2288	G2228	C2167	G2107	U2047	A1987	C1927	C1867	G1807	C1747	G1687	G1527	A1507	G1447	U1387
C2289	G2229	C2168	U2108	C2048	U1988	A1928	C1868	G1808	C1748	C1688	A1628	A1508	G1448	U1388
U2290	G2230	C2169	C2109	U2049	U1989	C1929	U1869	G1809	C1749	G1689	C1629	C1509	C1449	C1389
G2291	G2231	C2170	G2110	U2050	U1990	A1930	U1870	G1810	C1750	U1690	C1570	U1510	C1450	U1390
C2292	U2232	G2171	C2111	A2051	G1991	G1931	C1871	G1811	G1751	U1691	G1571	C1511	A1451	U1391
G2293	G2233	C2172	C2112	A2052	A1992	G1932	G1872	A1812	C1752	A1692	C1572	G1512	G1452	C1392
A2294	C2234	U2173	G2053	G2053	A1993	C1933	G1873	A1813	C1753	G1693	U1573	G1513	G1453	C1393
C2295	G2235	G2174	G2114	G2054	G1994	C1934	G1874	A1814	A1754	G1694	A1574	C1514	G1454	G1394
A2296	C2236	G2175	U2115	U2055	C1995	C1935	U1875	C1815	C1755	G1695	G1575	G1515	U1455	G1395
C2297	A2237	G2176	A2056	A2056	C1996	C1936	G1876	C1816	G1756	G1696	U1576	C1516	U1456	A1396
G2298	G2238	A2177	U2117	C2057	C1997	A1937	C1877	C1817	G1757	G1697	C1577	G1517	C1457	U1397
C2299	C2239	A2178	C2118	C2058	G1998	G1938	G1878	G1818	U1758	G1698	C1578	G1518	C1458	C1398
C3300	G2240	G2179	C2119	G2059	G1999	C1939	U1879	C1819	A1759	G1699	G1579	G1519	A1459	C1399
C3301	U2241	C2180	C2120	A2060	G2000	U1940	A1880	C1820	C1760	U1700	G1580	C1520	C1460	U1400
C3302	A2242	G2181	A2061	A2061	U2001	A1941	A1881	C1821	C1761	C1641	G1581	G1521	G1461	C1401
A2303	G2243	A2182	G2122	A2062	A2002	G1942	C1882	G1822	G1762	C1702	G1582	A1522	G1462	C1402
C3304	G2244	C2183	G2123	U2063	C2003	C1943	C1883	A1823	A1763	G1703	G1583	A1523	C1463	C1403
U2305	G2245	G2184	C2124	U2064	A2004	C1944	C1884	G1824	C1764	C1644	G1584	A1524	A1464	G1404
C3306	G2246	A2185	C2125	C2065	A2005	C1945	C1885	G1825	A1765	C1705	U1585	G1525	A1465	G1405
C3307	G2247	C2186	G2126	C2066	C2006	G1946	C1886	A1826	A1766	G1706	G1586	C1526	C1466	G1406
C3308	G2248	C2187	G2127	U2067	C2007	A1947	A1887	A1827	C1767	A1587	C1587	G1527	G1467	A1407
C3309	A2249	C2188	G2128	U2068	G2008	A1948	G1888	A1828	C1768	C1648	C1588	G1528	C1468	U1408
G3310	G2250	G2189	G2129	G2069	G2009	A1949	G1889	C1829	G1769	C1649	U1589	A1529	U1469	U1409
C3311	G2251	A2190	C2130	U2070	G2010	G1950	U1890	U1830	A1770	C1710	C1590	A1530	C1470	A1410
U3312	C2252	U2191	C2131	C2071	U2011	G1951	C1891	C1831	C1771	C1711	A1651	G1531	G1471	C1411
C3313	G2253	G2192	C2132	G2072	C2012	G1952	C1892	G1832	A1772	U1712	U1592	C1532	U1472	C1412
U3314	U2254	G2193	G2133	G2073	A2013	U1953	C1893	G1833	C1773	G1713	C1593	G1533	C1473	G1413
G2315	C2255	A2194	G2134	U2074	A2014	U1954	A1894	C1834	A1774	G1714	G1594	G1534	A1474	G1414
U3316	G2256	G2195	C2135	U2075	G2015	U1955	G1895	A1835	G1775	G1715	G1595	U1535	G1475	C1415
G3317	A2257	C2196	G2136	A2076	C2016	G1956	U1896	A1836	C1776	G1716	C1596	U1536	C1476	C1416
C3318	A2258	U2197	A2137	A2077	A2017	U1957	C1897	A1837	U1777	G1717	G1597	U1537	C1477	U1417
C3319	G2259	U2198	A2138	C2078	C2018	A1958	A1898	C1838	C1778	C1718	U1598	A1538	G1478	A1418
U3320	C2260	U2199	C2019	U2079	C2019	C1959	C1899	U1839	C1779	G1719	G1599	U1539	U1479	G1419
A2321	C2261	A2200	C2140	G2080	G2020	U1960	U1900	G1840	C1780	G1720	G1600	A1540	G1480	U1420
C3322	C2262	C2201	C2141	C2081	G2021	G1961	A1901	G1841	C1781	U1721	A1661	U1541	C1481	C1421
C3323	G2263	U2202	U2142	C2082	U2022	G1962	G1902	C1842	C1782	G1722	C1662	U1542	G1482	G1422
C3324	G2264	U2203	C2143	G2083	A2023	G1963	G1903	C1843	U1783	A1723	C1663	C1543	U1483	G1423
C3325	C2265	A2205	U2144	A2084	A2024	G1964	G1904	C1844	G1784	A1724	G1664	C1544	U1484	G1424
C3326	G2266	G2206	C2145	C2085	A2025	C1965	G1905	C1845	G1785	A1725	G1665	C1545	U1485	U1425
C3327	U2267	C2207	C2146	C2086	C2026	C1966	G1906	G1846	G1786	A1726	G1666	G1546	G1486	G1426
G3328	C2268	C2208	C2147	U2087	G2027	G1967	G1907	U1847	U1787	G1727	C1667	U1547	U1487	A1427
A3329	C2269	U2209	U2148	C2088	G2028	A1968	C1908	A1848	C1788	C1728	G1668	U1548	C1488	G1428
C3330	G2270	G2210	G2149	C2089	C2029	C1969	C1909	A1849	A1789	C1729	A1669	C1549	G1489	A1429
C3331	C2271	C2210	G2150	A2090	G2030	G1970	C1910	C1850	G1790	C1730	C1670	C1550	U1490	A1430
G3332	G2272	C2212	U2091	U2091	C2031	C1971	G1911	U1851	A1791	U1731	A1671	G1551	U1491	U1431
C3333	C2273	G2213	G2152	C2092	G2032	C1972	A1912	U1852	G1792	C1732	G1672	C1552	C1492	C1432
C3334	C2274	U2214	C2153	A2093	C2033	U1973	C1913	C1853	G1793	C1733	C1673	G1553	C1493	C1433
G3335	G2275	U2215	G2154	A2094	G2034	G1974	U1914	G1854	C1794	G1734	G1674	G1554	U1494	C1434
C3336	G2276	G2216	C2155	U2095	U2035	C1975	G1915	G1855	C1795	G1735	G1675	G1555	A1495	G1435
C3337	G2277	C2217	A2156	C2096	A2036	C1976	G1916	C1856	U1796	G1736	G1676	G1556	A1496	A1436
A3338	U2278	C2218	U2157	G2097	A2037	C1977	A1917	A1857	A1797	A1737	G1677	G1557	C1497	C1437
C3339	G2279	A2219	G2158	C2098	C2038	C1978	U1918	G1858	A1798	A1738	A1678	U1558	C1498	C1438
U3340	G2280	C2220	C2159	G2099	U2039	G1979	A1919	A1859	G1799	U1739	U1679	C1559	C1499	C1439
C3341	C2281	C2221	C2160	U2100	A2040	U1980	A1920	A1860	C1800	U1700	C1620	C1560	C1500	C1440

A121	C61	A3002	G2942	G2882	G2762	A2702	C9642	C9582	C9522	U2462	A2402	C2342
C122	A62	A3003	G2943	G2823	U2763	G2703	U2643	G2583	C2523	G2463	G2403	G2343
U123	G63	C3004	G2944	G2824	G2764	A2704	G2644	A2584	C2524	G2464	G2404	G2344
A124	C64	C3005	A2945	A2825	G2765	C2705	G2645	G2585	C2525	A2465	U2405	U2345
U125	G65	C3006	C2946	U2826	G2766	G2706	A2946	A2586	C2526	C2466	C2406	C2346
C126	A66	A3007	G2947	G2827	G2767	G2707	G2647	A2587	G2527	G2467	G2407	G2347
	U67	C3008	A2948	G2828	G2768	U2708	C2648	C2588	U2528	C2468	G2408	G2348
	C68	C3009	G2949	C2829	U2769	C2709	A2649	C2589	U2529	C2469	C2409	U2349
	C69	C3010	G2950	C2830	A2770	G2710	G2650	C2590	G2530	U2470	C2410	G2350
	U10	G3011	G2951	G2831	G2771	U2711	G2651	A2591	G2531	A2471	C2411	G2351
	A11	C3012	C2952	G2832	U2772	G2712	G2652	U2592	G2532	A2472	A2412	C2352
	G12	U3013	U2953	G2833	A2773	A2713	G2653	A2593	G2533	C2473	G2413	C2353
	C13	U3014	C2954	C2834	C2774	G2714	C2654	U2594	C2534	A2474	G2414	C2354
	U73	A3015	G2955	A2835	G2775	A2715	C2655	C2595	C2535	G2475	C2415	G2355
	U74	G3016	G2956	G2836	U2776	C2716	A2656	G2596	A2536	A2476	G2416	U2356
	G75	U3017	C2957	C2837	G2777	A2717	A2657	U2597	G2537	G2477	G2417	U2357
	U76	U3018	U2958	U2838	A2778	G2718	G2658	C2598	G2538	G2478	G2418	U2358
	A77	C3019	A2959	A2839	G2779	G2719	G2659	C2599	G2539	C2479	U2419	C2359
	C78	G3020	G2960	C2840	G2780	U2720	G2660	C2600	A2540	G2480	C2420	G2360
	U79	G3021	A2961	G2841	A2781	C2721	U2661	C2601	U2541	G2481	A2421	U2361
	G80	C3022	A2962	C2842	A2782	G2722	G2662	G2602	G2542	G2482	A2422	C2362
	C81	G3023	G2963	C2843	G2783	G2723	G2663	A2603	A2543	U2483	G2423	G2363
	C82	C3024	A2964	G2844	A2784	A2724	G2664	C2604	C2544	C2484	A2424	G2364
	C83	C3025	C2965	G2845	G2785	U2725	G2665	G2605	C2545	C2485	A2425	G2365
	U84	C3026	C2966	A2846	G2786	G2726	G2666	C2606	G2546	U2486	U2426	G2366
	G85	C3027	C2967	G2847	G2787	C2727	U2667	U2607	A2547	G2487	C2427	C2367
	C86	U3028	G2968	C2848	U2788	U2728	G2668	U2608	A2548	C2488	C2428	G2368
	G87	A3029	C2969	C2849	G2789	A2729	U2669	C2609	U2549	G2489	G2429	G2369
	A88	U3030	U2970	G2850	G2790	U2730	U2670	C2610	A2550	C2490	C2430	C2370
	G89	A3031	C2971	A2851	C2791	C2731	G2671	U2611	G2551	C2491	C2431	A2371
	A90	U3032	G2972	U2852	G2792	U2732	A2672	A2612	C2552	G2492	G2432	C2372
	G91	C3033	A2973	A2853	G2793	A2733	C2673	C2613	U2553	A2493	U2433	C2373
	C92	U3034	U2974	C2854	G2794	G2734	A2674	C2614	A2554	A2494	A2434	C2374
	U93	C3035	A2975	G2855	G2795	G2735	C2675	U2615	C2555	A2495	G2435	C2375
	C94	C3036	G2976	G2856	G2796	G2736	A2676	C2616	C2556	G2496	A2436	U2376
	A95	U3037	G2977	C2857	C2797	G2737	U2677	G2617	C2557	G2497	G2437	C2377
	G96	G3038	G2978	C2858	U2798	G2738	U2678	C2618	U2558	G2498	U2438	C2378
	U97	C3039	C2979	U2859	C2799	G2739	A2679	U2619	G2559	U2499	G2439	G2379
	C98	G3040	G2980	G2860	U2800	G2740	A2680	C2620	G2560	G2500	C2440	A2380
	G99	U3041	G2981	A2861	G2801	U2741	A2681	U2621	G2561	A2441	A2441	A2381
	A100	C3042	G2982	A2862	G2802	G2742	G2682	C2622	C2562	C2502	A2442	A2382
	A101	C3043	G2983	A2863	U2803	U2743	G2683	G2623	C2563	C2503	G2443	A2383
	G102	U3044	A2984	G2864	C2804	U2744	G2684	C2624	U2564	G2444	G2444	G2384
	C103	G3045	U2985	C2865	U2805	G2745	G2685	C2625	A2565	A2505	G2445	G2385
	C104	C3046	G2986	A2866	G2746	G2746	A2686	U2626	A2566	G2506	C2446	U2386
	G105	U3047	U2987	U2867	C2807	C2747	A2687	C2627	C2567	C2507	A2447	A2387
	G106	C3048	A2988	C2868	C2808	C2748	G2688	U2628	A2568	G2508	A2448	U2388
	U107	G3049	A2989	U2869	G2809	G2749	G2689	U2629	C2569	A2509	A2449	C2389
	A108	C3050	G2990	A2870	G2810	C2750	U2690	C2630	A2570	A2510	A2450	G2390
	A109	U3051	C2991	A2871	U2811	C2751	G2691	C2631	G2571	C2511	G2451	G2391
	C110	G3052	G2992	G2872	U2812	U2752	A2692	C2632	U2572	C2512	C2452	A2392
	U111	C3053	G2993	G2873	G2813	G2753	G2693	A2633	C2573	C2513	C2453	G2393
	C112	U3054	G2994	C2874	U2814	A2754	C2694	U2634	C2574	G2514	G2454	G2394
	A113	G3055	A2995	C2875	G2815	G2755	G2695	C2635	U2575	U2515	G2455	C2395
	G114	U3056	A2996	G2876	C2816	G2756	G2696	C2636	C2576	G2516	C2456	G2396
	C115	C3057	U2997	A2877	U2817	G2757	G2697	U2637	U2577	U2517	G2457	C2397
	U116	G3058	G2998	A2878	C2818	G2758	G2698	G2638	C2578	G2518	U2458	C2398
	G117	C3059	U2999	G2879	C2819	A2759	U2699	G2639	G2579	C2519	G2459	C2399
	C118	U3000	C3000	C2880	G2820	A2760	U2700	C2640	C2580	C2520	A2460	U2400
	U119	C3001	A2941	G2881	G2821	G2761	U2701	C2641	G2581	U2521	C2461	A2401

• Molecule 68: 5S rRNA

Chain B3:



C1	G1
G2	G2
C3	G3
C4	C4
G5	G5
G6	G6
C7	C7
C8	C8
A9	A9
U10	U10
A11	A11
G12	G12
C13	C13
G14	G14
G15	G15
G16	G16
G17	G17
G18	G18
C19	C19
U19	U19
G20	G20
C21	C21
C22	C22
C83	C83
A23	A23
C24	C24
A25	A25
C26	C26
C86	C86
G87	G87
A88	A88
G89	G89
A90	A90
G91	G91
G92	G92
C93	C93
C94	C94
A95	A95
G96	G96
C97	C97
U98	U98
C99	C99
A100	A100
G101	G101
G102	G102
C103	C103
C104	C104
C45	C45
G106	G106
G107	G107
G108	G108
A109	A109
C110	C110
G111	G111
C112	C112
U52	U52
A53	A53
G114	G114
C115	C115
C116	C116
C56	C56
C57	C57
C58	C58
C119	C119
C120	C120

4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	10000	Depositor
Resolution determination method	FSC at 0.5 cut-off	Depositor
CTF correction method	Wiener Filter	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	3600	Depositor
Magnification	75000	Depositor
Image detector	TemCam-F416 CMOS camera	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	AQ	1.71	11/1338 (0.8%)	1.93	30/1797 (1.7%)
10	AD	1.73	15/1457 (1.0%)	1.93	36/1953 (1.8%)
11	A1	3.43	155/1843 (8.4%)	2.59	167/2873 (5.8%)
12	AN	1.58	12/1156 (1.0%)	1.95	31/1535 (2.0%)
13	AX	1.92	9/570 (1.6%)	2.14	19/760 (2.5%)
14	AM	1.71	11/1022 (1.1%)	1.98	27/1375 (2.0%)
15	AE	1.80	28/2025 (1.4%)	2.16	66/2732 (2.4%)
16	AJ	1.85	16/1013 (1.6%)	2.04	20/1349 (1.5%)
17	AO	1.88	16/1208 (1.3%)	2.11	39/1619 (2.4%)
18	AF	1.23	5/1745 (0.3%)	1.38	18/2350 (0.8%)
19	AS	1.71	8/562 (1.4%)	1.86	14/744 (1.9%)
2	AK	1.74	12/1088 (1.1%)	2.01	32/1455 (2.2%)
20	A3	1.67	7/951 (0.7%)	1.95	24/1281 (1.9%)
20	B4	1.41	2/951 (0.2%)	1.64	11/1281 (0.9%)
20	BG	1.34	0/951	1.79	21/1281 (1.6%)
21	A2	3.29	2781/35966 (7.7%)	2.59	3540/56138 (6.3%)
22	AY	1.72	4/421 (1.0%)	1.85	8/558 (1.4%)
23	AT	1.81	7/942 (0.7%)	1.95	24/1257 (1.9%)
24	AA	1.71	13/1585 (0.8%)	2.12	53/2124 (2.5%)
25	AH	1.62	20/1773 (1.1%)	2.11	75/2381 (3.1%)
26	AP	1.87	6/471 (1.3%)	2.06	15/620 (2.4%)
27	A0	3.33	158/1814 (8.7%)	2.51	182/2828 (6.4%)
28	AV	1.57	7/839 (0.8%)	1.75	17/1122 (1.5%)
28	B6	1.73	9/798 (1.1%)	2.09	32/1071 (3.0%)
29	AL	1.52	3/830 (0.4%)	2.03	28/1113 (2.5%)
3	AI	1.54	5/1049 (0.5%)	1.70	9/1408 (0.6%)
30	AU	1.79	14/1203 (1.2%)	2.05	29/1621 (1.8%)
31	BY	1.73	13/1262 (1.0%)	2.04	31/1687 (1.8%)
32	BO	1.85	29/1635 (1.8%)	1.96	37/2196 (1.7%)
33	BC	1.72	27/2978 (0.9%)	2.06	96/4003 (2.4%)
34	B5	1.76	7/618 (1.1%)	2.12	24/829 (2.9%)
34	BK	1.80	8/618 (1.3%)	1.98	19/829 (2.3%)
35	BL	1.71	13/1175 (1.1%)	2.07	46/1563 (2.9%)
36	Bf	1.94	13/453 (2.9%)	2.75	38/603 (6.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
37	BU	1.77	16/1024 (1.6%)	2.05	29/1365 (2.1%)
38	Bb	1.77	12/1099 (1.1%)	2.14	36/1466 (2.5%)
39	Be	1.82	10/517 (1.9%)	2.11	19/681 (2.8%)
4	AG	1.48	3/999 (0.3%)	1.97	31/1337 (2.3%)
40	BE	1.72	12/1513 (0.8%)	1.99	39/2026 (1.9%)
41	Ba	1.61	1/760 (0.1%)	2.04	30/1019 (2.9%)
42	BT	1.66	5/689 (0.7%)	1.97	19/924 (2.1%)
43	Bk	1.48	8/1659 (0.5%)	1.82	44/2253 (2.0%)
44	BW	1.85	13/595 (2.2%)	2.02	19/784 (2.4%)
45	Bi	1.57	0/599	1.85	16/798 (2.0%)
46	BA	1.73	23/1702 (1.4%)	1.98	46/2293 (2.0%)
47	BI	1.80	18/1168 (1.5%)	1.96	30/1561 (1.9%)
48	BR	1.65	4/808 (0.5%)	1.92	22/1080 (2.0%)
49	BQ	1.69	15/1272 (1.2%)	2.17	43/1676 (2.6%)
5	AW	1.76	3/485 (0.6%)	1.86	11/651 (1.7%)
50	BV	1.67	3/570 (0.5%)	2.07	23/758 (3.0%)
51	Bj	1.75	6/805 (0.7%)	2.36	51/1064 (4.8%)
52	BB	1.77	19/1883 (1.0%)	2.08	56/2540 (2.2%)
53	BD	1.81	25/2068 (1.2%)	1.99	57/2787 (2.0%)
54	BF	1.74	13/1507 (0.9%)	2.01	44/2033 (2.2%)
55	Bh	1.34	2/233 (0.9%)	1.11	3/301 (1.0%)
56	BH	1.46	5/1001 (0.5%)	1.88	31/1351 (2.3%)
57	BZ	1.69	6/764 (0.8%)	1.99	20/1028 (1.9%)
58	BP	1.89	12/980 (1.2%)	1.97	24/1313 (1.8%)
59	BM	1.84	23/1634 (1.4%)	1.97	35/2179 (1.6%)
6	AC	1.81	19/1480 (1.3%)	1.99	34/1985 (1.7%)
60	BS	1.76	7/1226 (0.6%)	2.16	38/1649 (2.3%)
61	Bd	1.60	5/758 (0.7%)	2.22	41/1007 (4.1%)
62	BN	1.86	16/1409 (1.1%)	2.09	51/1890 (2.7%)
63	Bg	1.58	2/380 (0.5%)	2.02	17/504 (3.4%)
64	Bc	1.67	6/694 (0.9%)	2.12	30/926 (3.2%)
65	BJ	1.88	14/1027 (1.4%)	1.95	24/1385 (1.7%)
66	Bl	1.81	7/669 (1.0%)	1.92	15/884 (1.7%)
67	B1	3.31	5858/73410 (8.0%)	2.59	7158/114595 (6.2%)
68	B3	3.47	234/3010 (7.8%)	2.74	322/4693 (6.9%)
7	AB	1.79	18/1654 (1.1%)	2.06	51/2233 (2.3%)
8	AR	1.83	14/956 (1.5%)	2.07	35/1287 (2.7%)
All	All	2.81	9901/187317 (5.3%)	2.41	13452/276642 (4.9%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AQ	0	7
10	AD	0	6
12	AN	0	10
13	AX	0	7
14	AM	0	2
15	AE	0	11
16	AJ	0	4
17	AO	0	11
18	AF	0	1
19	AS	0	1
2	AK	0	4
20	B4	0	1
20	BG	0	3
21	A2	1	7
22	AY	0	4
23	AT	0	5
24	AA	0	2
25	AH	4	21
26	AP	0	6
28	AV	0	10
28	B6	0	2
29	AL	1	5
3	AI	0	5
30	AU	0	6
31	BY	0	7
32	BO	0	11
33	BC	0	18
34	B5	1	3
34	BK	1	1
35	BL	3	12
36	Bf	0	13
37	BU	0	3
38	Bb	0	10
39	Be	1	12
4	AG	1	9
40	BE	0	6
41	Ba	0	7
42	BT	0	3
43	Bk	0	10
44	BW	0	2
45	Bi	0	4
46	BA	0	4
47	BI	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
48	BR	0	6
49	BQ	3	10
5	AW	0	2
50	BV	1	4
51	Bj	1	18
52	BB	0	16
53	BD	0	8
54	BF	0	8
56	BH	1	9
57	BZ	0	1
58	BP	0	2
59	BM	0	7
6	AC	0	11
60	BS	0	7
61	Bd	1	7
62	BN	0	8
63	Bg	1	4
64	Bc	1	7
65	BJ	0	3
66	Bl	0	3
67	B1	0	12
7	AB	0	6
8	AR	0	3
9	A9	0	1
All	All	22	442

The worst 5 of 9901 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
67	B1	1565	G	O4'-C1'	51.72	2.08	1.41
67	B1	2507	C	O4'-C1'	37.95	1.91	1.41
67	B1	1570	C	O4'-C1'	37.84	1.90	1.41
67	B1	1642	G	C2'-C1'	35.02	1.91	1.53
21	A2	85	A	C2'-C1'	34.42	1.91	1.53

The worst 5 of 13452 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
67	B1	2363	G	O4'-C1'-N9	44.16	143.53	108.20
67	B1	1754	A	O4'-C1'-N9	36.92	137.74	108.20
21	A2	1207	G	O4'-C1'-N9	31.50	133.40	108.20
11	A1	49	C	O4'-C1'-N1	30.68	132.75	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
67	B1	2174	G	O4'-C1'-N9	30.40	132.52	108.20

5 of 22 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	AG	53	LYS	CA
21	A2	1317	G	C1'
25	AH	85	PHE	CA
25	AH	86	MET	CA
25	AH	87	ARG	CA

5 of 442 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AQ	28	TYR	Sidechain
1	AQ	3	ARG	Sidechain
1	AQ	58	TYR	Sidechain
1	AQ	68	ASP	Peptide
1	AQ	74	ARG	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AQ	1310	0	1392	8	0
2	AK	1072	0	1128	99	0
3	AI	1028	0	1065	121	0
4	AG	984	0	1043	182	0
5	AW	478	0	524	18	0
6	AC	1459	0	1549	17	0
7	AB	1623	0	1685	17	0
8	AR	934	0	959	25	0
9	A9	286	0	62	4	0
10	AD	1434	0	1498	43	0
11	A1	1649	0	838	18	0
12	AN	1140	0	1235	116	0
13	AX	568	0	600	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	AM	1004	0	1041	15	0
15	AE	1976	0	2046	29	0
16	AJ	1004	0	1088	5	0
17	AO	1189	0	1248	2	0
18	AF	1716	0	1768	360	0
19	AS	556	0	604	0	0
20	A3	939	0	994	3	0
20	B4	939	0	994	12	0
20	BG	939	0	994	72	0
21	A2	32135	0	16230	1011	0
22	AY	409	0	410	1	0
23	AT	923	0	986	0	0
24	AA	1559	0	1648	3	0
25	AH	1736	0	1787	359	0
26	AP	462	0	492	43	0
27	A0	1625	0	824	12	0
28	AV	823	0	847	77	0
28	B6	782	0	806	1	0
29	AL	822	0	870	73	0
30	AU	1175	0	1216	36	0
31	BY	1243	0	1326	109	0
32	BO	1597	0	1639	10	0
33	BC	2912	0	3073	40	0
34	B5	614	0	670	67	0
34	BK	614	0	670	3	0
35	BL	1154	0	1217	268	0
36	Bf	445	0	510	0	0
37	BU	1008	0	1077	8	0
38	Bb	1074	0	1167	0	0
39	Be	506	0	528	0	0
40	BE	1489	0	1550	22	0
41	Ba	746	0	808	0	0
42	BT	680	0	739	0	0
43	Bk	1632	0	1725	0	0
44	BW	594	0	665	1	0
45	Bi	590	0	631	0	0
46	BA	1677	0	1796	30	0
47	BI	1150	0	1240	10	0
48	BR	787	0	827	88	0
49	BQ	1256	0	1389	84	0
50	BV	555	0	548	67	0
51	Bj	787	0	837	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	BB	1838	0	1914	20	0
53	BD	2026	0	2134	42	0
54	BF	1476	0	1518	24	0
55	Bh	230	0	269	0	0
56	BH	988	0	1077	84	0
57	BZ	754	0	804	49	0
58	BP	966	0	1019	10	0
59	BM	1595	0	1695	46	0
60	BS	1200	0	1255	4	0
61	Bd	740	0	806	0	0
62	BN	1378	0	1405	4	0
63	Bg	371	0	395	0	0
64	Bc	685	0	743	0	0
65	BJ	1014	0	1073	72	0
66	Bl	659	0	699	0	0
67	B1	65577	0	33094	1346	0
68	B3	2694	0	1371	60	0
All	All	173979	0	126374	3655	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 17.

The worst 5 of 3655 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)
21:A2:340:A:C1'	21:A2:340:A:C2'	1.74	1.63
67:B1:404:G:C2'	67:B1:404:G:C1'	1.76	1.62
68:B3:35:A:C2'	68:B3:35:A:C1'	1.78	1.61
67:B1:2554:A:C2'	67:B1:2554:A:C1'	1.79	1.61
21:A2:1458:A:C1'	21:A2:1458:A:C2'	1.74	1.61

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AQ	156/158 (99%)	139 (89%)	8 (5%)	9 (6%)	2	27
2	AK	133/135 (98%)	119 (90%)	12 (9%)	2 (2%)	13	57
3	AI	127/130 (98%)	121 (95%)	4 (3%)	2 (2%)	12	56
4	AG	123/125 (98%)	103 (84%)	11 (9%)	9 (7%)	1	21
5	AW	61/63 (97%)	55 (90%)	4 (7%)	2 (3%)	5	40
6	AC	184/210 (88%)	175 (95%)	6 (3%)	3 (2%)	12	56
7	AB	200/202 (99%)	177 (88%)	19 (10%)	4 (2%)	9	51
8	AR	111/113 (98%)	100 (90%)	9 (8%)	2 (2%)	11	53
10	AD	170/180 (94%)	151 (89%)	14 (8%)	5 (3%)	6	43
12	AN	143/147 (97%)	129 (90%)	8 (6%)	6 (4%)	3	34
13	AX	69/71 (97%)	59 (86%)	4 (6%)	6 (9%)	1	17
14	AM	131/137 (96%)	118 (90%)	8 (6%)	5 (4%)	4	37
15	AE	239/243 (98%)	210 (88%)	23 (10%)	6 (2%)	7	46
16	AJ	125/127 (98%)	101 (81%)	18 (14%)	6 (5%)	3	32
17	AO	146/148 (99%)	122 (84%)	15 (10%)	9 (6%)	2	26
18	AF	215/236 (91%)	191 (89%)	22 (10%)	2 (1%)	21	67
19	AS	65/67 (97%)	64 (98%)	0	1 (2%)	13	57
20	A3	121/123 (98%)	105 (87%)	8 (7%)	8 (7%)	1	24
20	B4	121/123 (98%)	113 (93%)	6 (5%)	2 (2%)	11	55
20	BG	121/123 (98%)	109 (90%)	8 (7%)	4 (3%)	5	40
22	AY	48/50 (96%)	43 (90%)	3 (6%)	2 (4%)	3	34
23	AT	109/132 (83%)	98 (90%)	9 (8%)	2 (2%)	11	53
24	AA	188/198 (95%)	170 (90%)	12 (6%)	6 (3%)	5	41
25	AH	213/215 (99%)	181 (85%)	14 (7%)	18 (8%)	1	17
26	AP	54/56 (96%)	43 (80%)	8 (15%)	3 (6%)	2	28
28	AV	97/99 (98%)	86 (89%)	6 (6%)	5 (5%)	2	30
28	B6	92/99 (93%)	84 (91%)	4 (4%)	4 (4%)	3	34
29	AL	100/102 (98%)	92 (92%)	1 (1%)	7 (7%)	1	22
30	AU	142/150 (95%)	134 (94%)	5 (4%)	3 (2%)	9	50
31	BY	153/155 (99%)	143 (94%)	5 (3%)	5 (3%)	5	40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
32	BO	195/203 (96%)	164 (84%)	17 (9%)	14 (7%)	1	22
33	BC	363/365 (100%)	303 (84%)	34 (9%)	26 (7%)	1	22
34	B5	79/83 (95%)	69 (87%)	5 (6%)	5 (6%)	2	25
34	BK	79/83 (95%)	68 (86%)	6 (8%)	5 (6%)	2	25
35	BL	145/147 (99%)	128 (88%)	8 (6%)	9 (6%)	2	26
36	Bf	49/51 (96%)	37 (76%)	8 (16%)	4 (8%)	1	18
37	BU	119/121 (98%)	113 (95%)	3 (2%)	3 (2%)	7	46
38	Bb	125/130 (96%)	102 (82%)	13 (10%)	10 (8%)	1	19
39	Be	60/62 (97%)	45 (75%)	11 (18%)	4 (7%)	1	24
40	BE	184/186 (99%)	170 (92%)	8 (4%)	6 (3%)	5	40
41	Ba	88/95 (93%)	74 (84%)	7 (8%)	7 (8%)	1	19
42	BT	82/86 (95%)	78 (95%)	3 (4%)	1 (1%)	16	61
43	Bk	210/339 (62%)	187 (89%)	12 (6%)	11 (5%)	2	30
44	BW	70/72 (97%)	70 (100%)	0	0	100	100
45	Bi	76/83 (92%)	70 (92%)	6 (8%)	0	100	100
46	BA	214/216 (99%)	190 (89%)	12 (6%)	12 (6%)	2	28
47	BI	140/142 (99%)	129 (92%)	7 (5%)	4 (3%)	6	43
48	BR	93/97 (96%)	85 (91%)	6 (6%)	2 (2%)	8	49
49	BQ	148/150 (99%)	141 (95%)	4 (3%)	3 (2%)	9	51
50	BV	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
51	Bj	92/94 (98%)	71 (77%)	8 (9%)	13 (14%)	0	6
52	BB	237/239 (99%)	213 (90%)	17 (7%)	7 (3%)	5	42
53	BD	253/255 (99%)	218 (86%)	21 (8%)	14 (6%)	2	29
54	BF	182/184 (99%)	169 (93%)	13 (7%)	0	100	100
55	Bh	22/24 (92%)	21 (96%)	1 (4%)	0	100	100
56	BH	132/164 (80%)	108 (82%)	14 (11%)	10 (8%)	1	20
57	BZ	97/99 (98%)	84 (87%)	7 (7%)	6 (6%)	2	26
58	BP	118/120 (98%)	102 (86%)	13 (11%)	3 (2%)	7	46
59	BM	192/194 (99%)	173 (90%)	17 (9%)	2 (1%)	19	65
60	BS	148/155 (96%)	137 (93%)	8 (5%)	3 (2%)	9	51
61	Bd	87/89 (98%)	78 (90%)	6 (7%)	3 (3%)	5	40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
62	BN	166/181 (92%)	137 (82%)	20 (12%)	9 (5%)	2	29
63	Bg	43/51 (84%)	31 (72%)	3 (7%)	9 (21%)	0	3
64	Bc	85/87 (98%)	74 (87%)	7 (8%)	4 (5%)	3	32
65	BJ	130/141 (92%)	124 (95%)	4 (3%)	2 (2%)	13	57
66	Bl	75/77 (97%)	69 (92%)	4 (5%)	2 (3%)	6	45
All	All	8599/9048 (95%)	7630 (89%)	608 (7%)	361 (4%)	6	34

5 of 361 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AQ	78	ILE
2	AK	133	SER
3	AI	121	ILE
4	AG	48	ASN
4	AG	50	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	
1	AQ	143/143 (100%)	138 (96%)	5 (4%)	43	74
2	AK	111/111 (100%)	105 (95%)	6 (5%)	27	64
3	AI	107/108 (99%)	100 (94%)	7 (6%)	21	58
4	AG	108/108 (100%)	88 (82%)	20 (18%)	2	14
5	AW	54/54 (100%)	52 (96%)	2 (4%)	41	73
6	AC	145/167 (87%)	143 (99%)	2 (1%)	74	89
7	AB	173/173 (100%)	164 (95%)	9 (5%)	29	65
8	AR	102/102 (100%)	101 (99%)	1 (1%)	82	92
10	AD	153/160 (96%)	147 (96%)	6 (4%)	39	72
12	AN	118/121 (98%)	104 (88%)	14 (12%)	6	31
13	AX	60/60 (100%)	55 (92%)	5 (8%)	14	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	AM	100/104 (96%)	94 (94%)	6 (6%)	24	60
15	AE	212/213 (100%)	198 (93%)	14 (7%)	21	57
16	AJ	103/103 (100%)	98 (95%)	5 (5%)	31	66
17	AO	122/122 (100%)	119 (98%)	3 (2%)	55	81
18	AF	181/197 (92%)	176 (97%)	5 (3%)	51	78
19	AS	61/61 (100%)	61 (100%)	0	100	100
20	A3	99/99 (100%)	95 (96%)	4 (4%)	38	71
20	B4	99/99 (100%)	95 (96%)	4 (4%)	38	71
20	BG	99/99 (100%)	92 (93%)	7 (7%)	18	55
22	AY	41/41 (100%)	39 (95%)	2 (5%)	31	66
23	AT	99/114 (87%)	99 (100%)	0	100	100
24	AA	166/171 (97%)	163 (98%)	3 (2%)	66	87
25	AH	184/184 (100%)	166 (90%)	18 (10%)	10	39
26	AP	46/46 (100%)	39 (85%)	7 (15%)	3	22
28	AV	89/89 (100%)	81 (91%)	8 (9%)	12	44
28	B6	85/89 (96%)	78 (92%)	7 (8%)	14	49
29	AL	91/91 (100%)	82 (90%)	9 (10%)	10	39
30	AU	121/127 (95%)	114 (94%)	7 (6%)	25	61
31	BY	133/133 (100%)	112 (84%)	21 (16%)	3	21
32	BO	166/169 (98%)	157 (95%)	9 (5%)	27	64
33	BC	312/312 (100%)	293 (94%)	19 (6%)	23	60
34	B5	64/66 (97%)	60 (94%)	4 (6%)	22	59
34	BK	64/66 (97%)	62 (97%)	2 (3%)	47	77
35	BL	117/117 (100%)	102 (87%)	15 (13%)	5	29
36	Bf	47/47 (100%)	40 (85%)	7 (15%)	4	23
37	BU	110/110 (100%)	106 (96%)	4 (4%)	42	74
38	Bb	114/117 (97%)	105 (92%)	9 (8%)	15	51
39	Be	51/51 (100%)	46 (90%)	5 (10%)	10	39
40	BE	158/158 (100%)	152 (96%)	6 (4%)	40	73
41	Ba	80/83 (96%)	71 (89%)	9 (11%)	7	33
42	BT	75/77 (97%)	72 (96%)	3 (4%)	38	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	Bk	179/280 (64%)	159 (89%)	20 (11%)	7	33
44	BW	66/66 (100%)	63 (96%)	3 (4%)	34	69
45	Bi	57/61 (93%)	55 (96%)	2 (4%)	43	74
46	BA	182/182 (100%)	174 (96%)	8 (4%)	35	69
47	BI	122/122 (100%)	119 (98%)	3 (2%)	55	81
48	BR	85/87 (98%)	75 (88%)	10 (12%)	6	31
49	BQ	130/130 (100%)	121 (93%)	9 (7%)	19	56
50	BV	56/56 (100%)	54 (96%)	2 (4%)	42	74
51	Bj	82/83 (99%)	65 (79%)	17 (21%)	1	10
52	BB	189/189 (100%)	180 (95%)	9 (5%)	31	67
53	BD	213/213 (100%)	197 (92%)	16 (8%)	17	53
54	BF	156/156 (100%)	150 (96%)	6 (4%)	40	73
55	Bh	23/23 (100%)	23 (100%)	0	100	100
56	BH	110/137 (80%)	96 (87%)	14 (13%)	5	29
57	BZ	80/80 (100%)	73 (91%)	7 (9%)	12	45
58	BP	101/101 (100%)	98 (97%)	3 (3%)	48	77
59	BM	162/162 (100%)	152 (94%)	10 (6%)	23	60
60	BS	126/130 (97%)	121 (96%)	5 (4%)	38	71
61	Bd	81/81 (100%)	66 (82%)	15 (18%)	2	14
62	BN	140/152 (92%)	138 (99%)	2 (1%)	74	89
63	Bg	37/39 (95%)	29 (78%)	8 (22%)	1	9
64	Bc	74/74 (100%)	65 (88%)	9 (12%)	6	31
65	BJ	104/108 (96%)	99 (95%)	5 (5%)	31	67
66	Bl	72/72 (100%)	68 (94%)	4 (6%)	26	62
All	All	7390/7646 (97%)	6904 (93%)	486 (7%)	25	57

5 of 486 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
34	B5	45	ARG
41	Ba	53	LYS
61	Bd	66	ARG
35	BL	34	ARG
37	BU	93	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 65 such sidechains are listed below:

Mol	Chain	Res	Type
32	BO	43	HIS
38	Bb	26	GLN
61	Bd	25	HIS
33	BC	50	HIS
34	B5	31	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	A1	76/77 (98%)	15 (19%)	3 (3%)
21	A2	1494/1495 (99%)	260 (17%)	118 (7%)
27	A0	75/76 (98%)	18 (24%)	3 (4%)
67	B1	3047/3049 (99%)	603 (19%)	194 (6%)
68	B3	126/126 (100%)	35 (27%)	13 (10%)
All	All	4818/4823 (99%)	931 (19%)	331 (6%)

5 of 931 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	A1	8	U
11	A1	9	A
11	A1	10	G
11	A1	16	C
11	A1	21	G

5 of 331 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
67	B1	410	C
67	B1	1038	U
67	B1	2892	A
67	B1	471	U
67	B1	700	A

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

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

5.5 Carbohydrates [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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
53	BD	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BD	91:ARG	C	92:THR	N	0.93