



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Jan 4, 2017 – 05:47 AM EST

PDB ID : 5AJ0
EMDB ID: : EMD-2875
Title : Cryo electron microscopy of actively translating human polysomes (POST state).
Authors : Behrmann, E.; Loerke, J.; Budkevich, T.V.; Yamamoto, K.; Schmidt, A.; Penczek, P.A.; Vos, M.R.; Burger, J.; Mielke, T.; Scheerer, P.; Spahn, C.M.T.
Deposited on : 2015-02-19
Resolution : 3.50 Å(reported)
Based on PDB ID : 4UJE

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

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

A user guide is available at

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

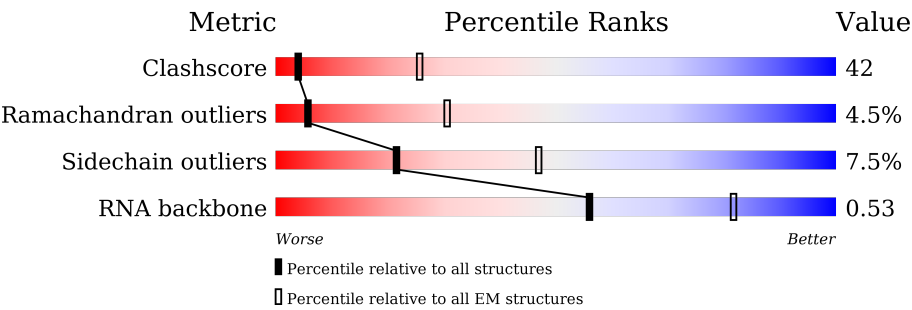
MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20028442

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 Å.

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








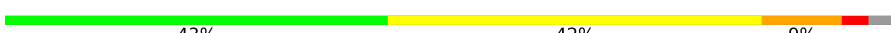
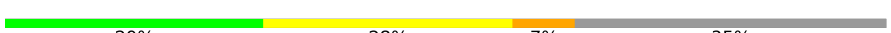




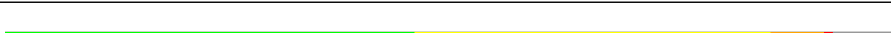



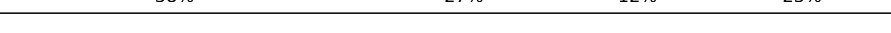









Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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	A3	194	<div><div>28%</div><div>28%</div><div>18%</div><div>7%</div><div>19%</div></div>
2	A4	121	<div><div>23%</div><div>38%</div><div>36%</div><div>• •</div></div>
3	AA	257	<div><div>54%</div><div>39%</div><div>5%</div><div>•</div></div>
4	AB	403	<div><div>41%</div><div>50%</div><div>5%</div><div>• •</div></div>
5	AC	427	<div><div>43%</div><div>35%</div><div>6%</div><div>•</div><div>15%</div></div>
6	AD	297	<div><div>53%</div><div>39%</div><div>7%</div><div>• •</div></div>
7	AE	288	<div><div>20%</div><div>30%</div><div>15%</div><div>•</div><div>33%</div></div>
8	AF	248	<div><div>52%</div><div>38%</div><div>• •</div><div>6%</div></div>







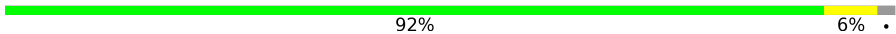

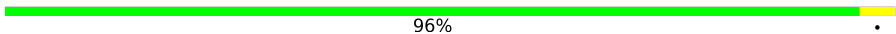


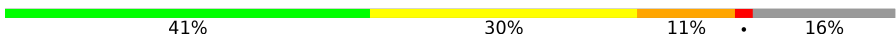



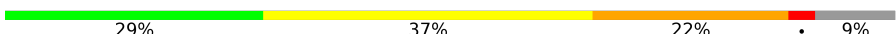
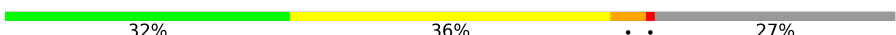
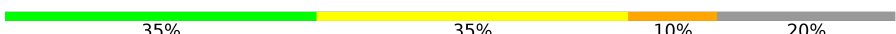







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Mol	Chain	Length	Quality of chain
9	AG	266	
10	AH	192	
11	AI	214	
12	AJ	178	
13	AK	317	
14	AL	211	
15	AM	215	
16	AN	204	
17	AO	203	
18	AP	184	
19	AQ	188	
20	AR	196	
21	AS	176	
22	AT	160	
23	AU	128	
24	AV	140	
25	AW	157	
26	AX	156	
27	AY	145	
28	AZ	136	
29	Aa	148	
30	Ab	159	
31	Ac	115	
32	Ad	125	
33	Ae	135	

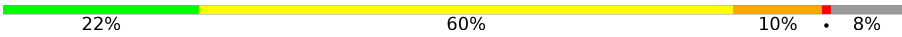
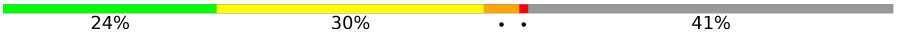



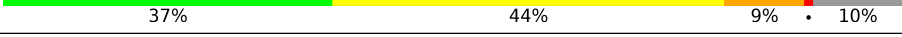
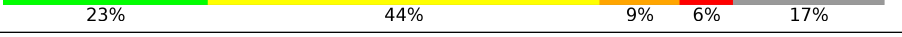

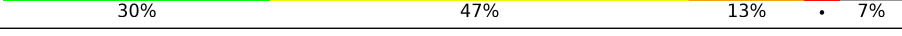

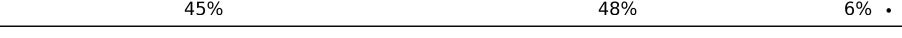
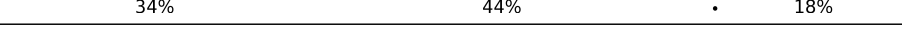

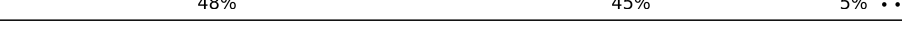


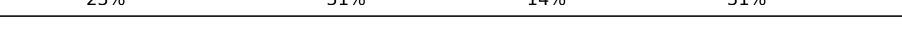

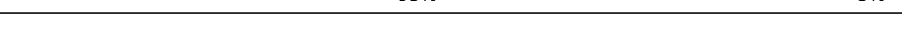




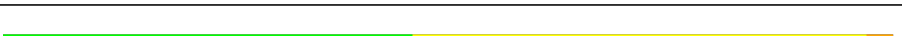

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Mol	Chain	Length	Quality of chain
34	Af	110	
35	Ag	117	
36	Ah	123	
37	Ai	105	
38	Aj	97	
39	Ak	70	
40	Al	51	
41	Am	128	
42	An	25	
43	Ao	106	
44	Ap	92	
45	Aq	165	
46	At	137	
47	Au	217	
48	A2	5029	
49	B1	1869	
50	BA	295	
51	BB	264	
52	BC	293	
53	BD	243	
54	BE	263	
55	BF	204	
56	BG	249	
57	BH	194	
58	BI	208	



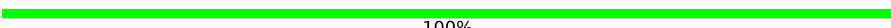
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Mol	Chain	Length	Quality of chain
59	BJ	194	
60	BK	165	
61	BL	158	
62	BM	132	
63	BN	151	
64	BO	151	
65	BP	145	
66	BQ	146	
67	BR	135	
68	BS	152	
69	BT	145	
70	BU	119	
71	BV	83	
72	BW	130	
73	BX	143	
74	BY	133	
75	BZ	125	
76	Ba	115	
77	Bb	84	
78	Bc	69	
79	Bd	56	
80	Be	59	
81	Bf	156	
82	Bg	317	
83	Bv	76	

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Mol	Chain	Length	Quality of chain
83	Bw	76	
84	Bx	28	
85	By	24	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
86	MG	B1	1941	-	-	X	-

2 Entry composition

There are 87 unique types of molecules in this entry. The entry contains 218559 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 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A3	157	Total	C	N	O	P	0	0
			3337	1489	587	1104	157		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A4	119	Total	C	N	O	P	0	0
			2541	1132	454	836	119		

- Molecule 3 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AA	252	Total	C	N	O	S	0	0
			1930	1209	395	320	6		

- Molecule 4 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AB	394	Total	C	N	O	S	0	0
			3178	2024	596	544	14		

- Molecule 5 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AC	363	Total	C	N	O	S	0	0
			2888	1817	577	480	14		

- Molecule 6 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AD	294	Total	C	N	O	S	0	0
			2392	1510	436	432	14		

- Molecule 7 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AE	194	Total	C	N	O	S	0	0
			1571	1013	294	263	1		

- Molecule 8 is a protein called 60S ribosomal protein L7.

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

- Molecule 9 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AG	234	Total	C	N	O	S	0	0
			1880	1197	362	317	4		

- Molecule 10 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AH	191	Total	C	N	O	S	0	0
			1526	960	285	275	6		

- Molecule 11 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AI	208	Total	C	N	O	S	0	0
			1692	1074	327	278	13		

- Molecule 12 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AJ	169	Total	C	N	O	S	0	0
			1353	855	252	240	6		

- Molecule 13 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AK	109	Total	C	N	O	S	0	0
			872	554	159	151	8		

- Molecule 14 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AL	205	Total	C	N	O	S	0	0
			1657	1036	344	273	4		

- Molecule 15 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 16 is a protein called 60S ribosomal protein L15.

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

- Molecule 17 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AO	195	Total	C	N	O	S	0	0
			1606	1034	315	252	5		

- Molecule 18 is a protein called 60S ribosomal protein L17.

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

- Molecule 19 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 20 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AR	181	Total	C	N	O	S	0	0
			1517	938	329	241	9		

- Molecule 21 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AS	175	Total	C	N	O	S	0	0
			1449	921	283	234	11		

- Molecule 22 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AT	157	Total	C	N	O	S	0	0
			1284	815	250	214	5		

- Molecule 23 is a protein called 60S ribosomal protein L22.

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

- Molecule 24 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AV	129	Total	C	N	O	S	0	0
			969	613	182	169	5		

- Molecule 25 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AW	121	Total	C	N	O	S	0	0
			989	617	202	167	3		

- Molecule 26 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AX	117	Total	C	N	O	S	0	0
			958	612	180	165	1		

- Molecule 27 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AY	127	Total	C	N	O	S	0	0
			1064	668	216	177	3		

- Molecule 28 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AZ	134	Total	C	N	O	S	0	0
			1103	712	207	181	3		

- Molecule 29 is a protein called 60S ribosomal protein L27a.

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

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Ab	68	Total	C	N	O	S	0	0
			559	344	122	90	3		

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Ac	103	Total	C	N	O	S	0	0
			801	508	141	145	7		

- Molecule 32 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ad	106	Total	C	N	O	S	0	0
			879	555	170	152	2		

- Molecule 33 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ae	129	Total	C	N	O	S	0	0
			1064	673	220	166	5		

- Molecule 34 is a protein called 60S ribosomal protein L35a.

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

- Molecule 35 is a protein called 60S ribosomal protein L34.

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

- Molecule 36 is a protein called 60S ribosomal protein L35.

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

- Molecule 37 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ai	97	Total	C	N	O	S	0	0
			794	497	168	124	5		

- Molecule 38 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Aj	84	Total	C	N	O	S	0	0
			689	423	152	109	5		

- Molecule 39 is a protein called 60S ribosomal protein L38.

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

- Molecule 40 is a protein called 60S ribosomal protein L39.

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

- Molecule 41 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Am	50	Total	C	N	O	S	0	0
			411	254	87	64	6		

- Molecule 42 is a protein called 60S ribosomal protein L41.

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

- Molecule 43 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Ao	105	Total	C	N	O	S	0	0
			863	542	175	140	6		

- Molecule 44 is a protein called 60S ribosomal protein L37a.

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

- Molecule 45 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Aq	138	Total	C	N	O	S	0	0
			1046	654	196	193	3		

- Molecule 46 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	At	122	Total	C	N	O	S	0	0
			980	607	204	165	4		

- Molecule 47 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Au	217	Total	C	N	O	S	0	0
			1744	1114	314	307	9		

- Molecule 48 is a RNA chain called Human 28S ribosomal RNA gene.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	A2	3612	Total	C	N	O	P	0	0
			77427	34482	14158	25175	3612		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A2	245	C	-	INSERTION	GB 337381
A2	246	C	-	INSERTION	GB 337381
A2	247	C	-	INSERTION	GB 337381
A2	4684	G	-	INSERTION	GB 337381

- Molecule 49 is a RNA chain called Human 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	B1	1708	Total	C	N	O	P	0	0
			36456	16274	6546	11928	1708		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BA	215	Total	C	N	O	S	0	0
			1704	1083	298	315	8		

- Molecule 51 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BB	212	Total	C	N	O	S	0	0
			1722	1093	308	307	14		

- Molecule 52 is a protein called 40S ribosomal protein S2.

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

- Molecule 53 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BD	220	Total	C	N	O	S	0	0
			1709	1090	308	304	7		

- Molecule 54 is a protein called 40S ribosomal protein S4, Y isoform 1.

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

- Molecule 55 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BF	190	Total	C	N	O	S	0	0
			1502	939	285	271	7		

- Molecule 56 is a protein called 40S ribosomal protein S6.

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

- Molecule 57 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BH	183	Total	C	N	O	S	0	0
			1479	941	272	265	1		

- Molecule 58 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	BI	207	Total	C	N	O	S	0	0
			1696	1064	334	293	5		

- Molecule 59 is a protein called 40S ribosomal protein S9.

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

- Molecule 60 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	BK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 61 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	BL	153	Total	C	N	O	S	0	0
			1258	804	235	213	6		

- Molecule 62 is a protein called 40S ribosomal protein S12.

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

- Molecule 63 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	BN	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 64 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	BO	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 65 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	BP	120	Total	C	N	O	S	0	0
			999	636	188	168	7		

- Molecule 66 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	BQ	139	Total	C	N	O	S	0	0
			1109	704	210	192	3		

- Molecule 67 is a protein called 40S ribosomal protein S17-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	BR	125	Total	C	N	O	S	0	0
			1011	634	187	186	4		

- Molecule 68 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	BS	139	Total	C	N	O	S	0	0
			1154	725	233	195	1		

- Molecule 69 is a protein called 40S ribosomal protein S19.

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

- Molecule 70 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	BU	97	Total	C	N	O	S	0	0
			769	483	144	138	4		

- Molecule 71 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	BV	81	Total	C	N	O	S	0	0
			617	380	114	118	5		

- Molecule 72 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	BW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 73 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	BX	139	Total	C	N	O	S	0	0
			1080	682	214	181	3		

- Molecule 74 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	BY	125	Total	C	N	O	S	0	0
			1015	642	199	169	5		

- Molecule 75 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	BZ	86	Total	C	N	O	S	0	0
			688	442	129	116	1		

- Molecule 76 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Ba	97	Total	C	N	O	S	0	0
			774	481	160	128	5		

- Molecule 77 is a protein called 40S ribosomal protein S27.

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

- Molecule 78 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Bc	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 79 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Bd	51	Total	C	N	O	S	0	0
			427	269	87	66	5		

- Molecule 80 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Be	55	Total	C	N	O	S	0	0
			437	272	96	68	1		

- Molecule 81 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Bf	73	Total	C	N	O	S	0	0
			601	379	115	100	7		

- Molecule 82 is a protein called Guanine nucleotide-binding protein subunit beta-2-like 1.

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

- Molecule 83 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Bv	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		
83	Bw	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		

- Molecule 84 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Bx	28	Total	C	N	O	P	0	0
			561	252	56	225	28		

- Molecule 85 is a protein called NASCENT CHAIN.

Mol	Chain	Residues	Atoms				AltConf	Trace
85	By	24	Total	C	N	O	0	0
			120	72	24	24		

- Molecule 86 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
86	An	1	Total	Mg	0
			1	1	
86	Bx	1	Total	Mg	0
			1	1	
86	Ae	2	Total	Mg	0
			2	2	
86	AB	2	Total	Mg	0
			2	2	
86	BD	1	Total	Mg	0
			1	1	
86	Bv	2	Total	Mg	0
			2	2	
86	AA	1	Total	Mg	0
			1	1	
86	A4	9	Total	Mg	0
			9	9	
86	BX	1	Total	Mg	0
			1	1	
86	AN	2	Total	Mg	0
			2	2	
86	B1	72	Total	Mg	0
			72	72	

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Mol	Chain	Residues	Atoms		AltConf
86	A2	220	Total 220	Mg 220	0
86	AY	1	Total 1	Mg 1	0
86	A3	8	Total 8	Mg 8	0
86	Aa	3	Total 3	Mg 3	0

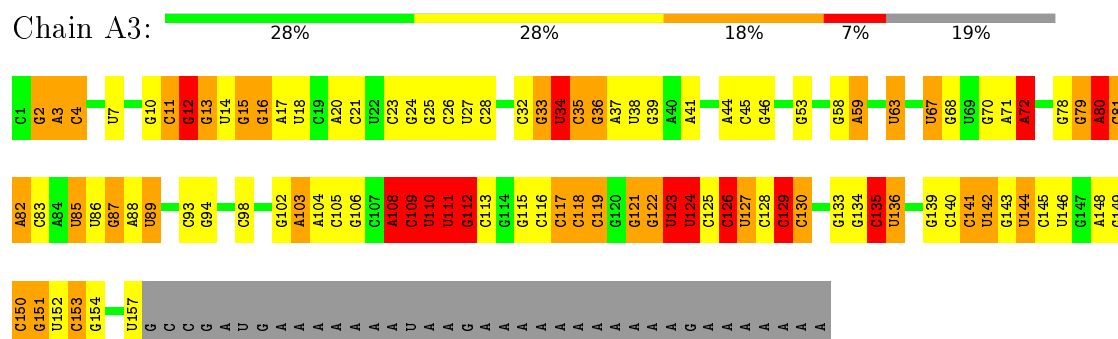
- Molecule 87 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
87	Ap	1	Total 1	Zn 1	0
87	Ao	1	Total 1	Zn 1	0
87	Aj	1	Total 1	Zn 1	0
87	Bd	1	Total 1	Zn 1	0
87	Ba	1	Total 1	Zn 1	0

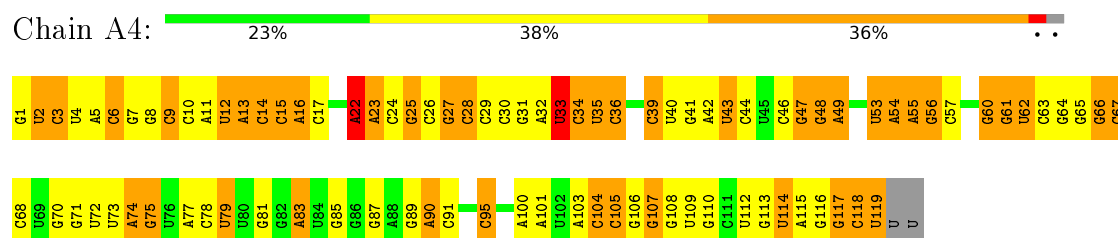
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

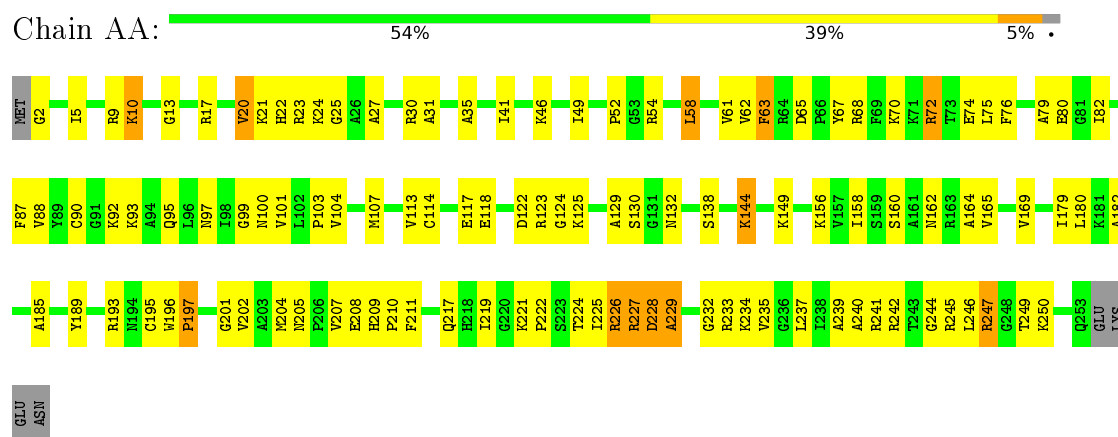
• Molecule 1: 5.8S rRNA



• Molecule 2: 5S Ribosomal RNA

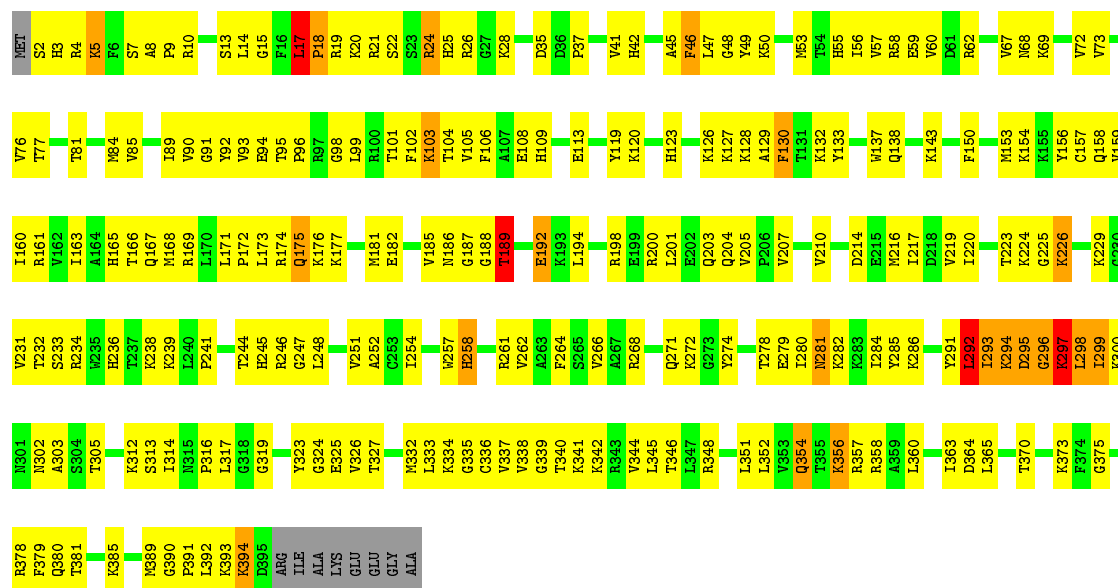


• Molecule 3: 60S ribosomal protein L8



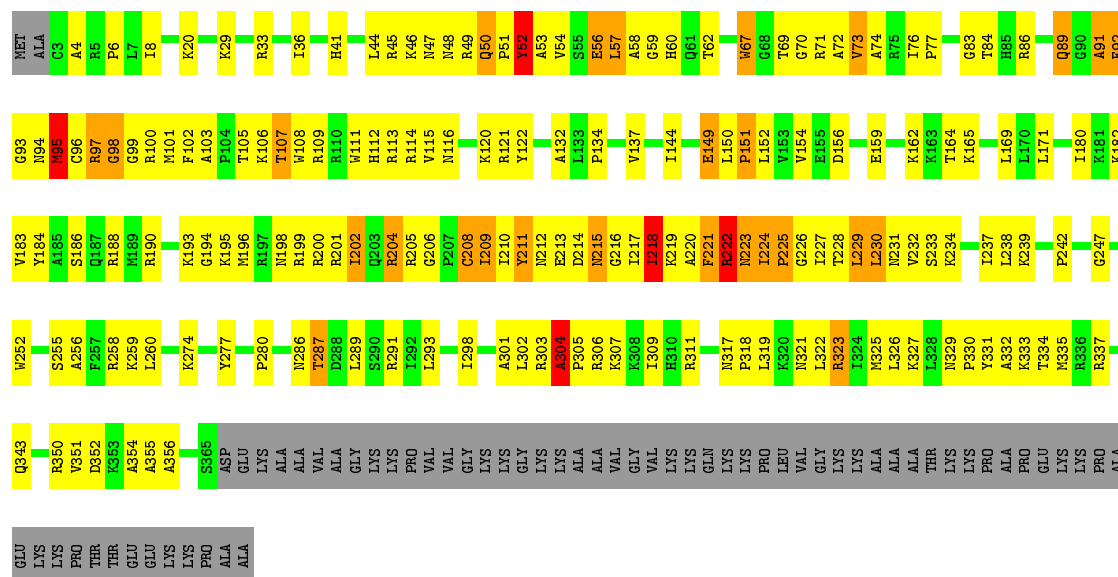
• Molecule 4: 60S ribosomal protein L3

Chain AB: 



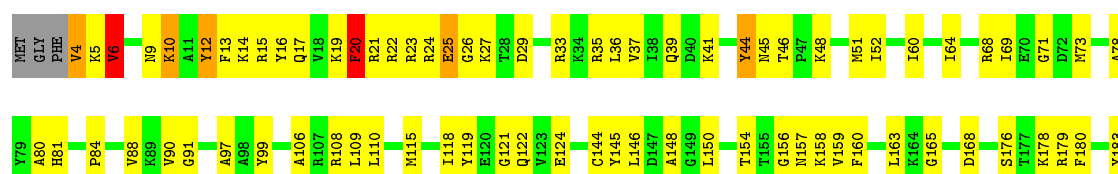
• Molecule 5: 60S ribosomal protein L4

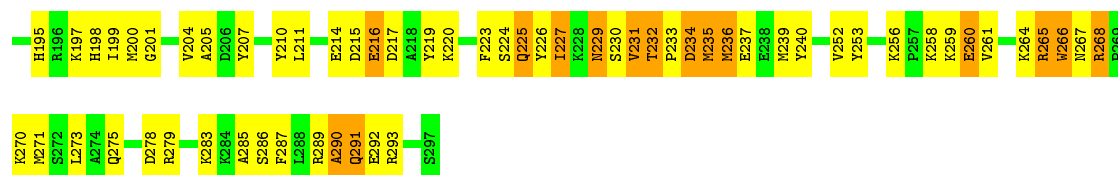
Chain AC: 



• Molecule 6: 60S ribosomal protein L5

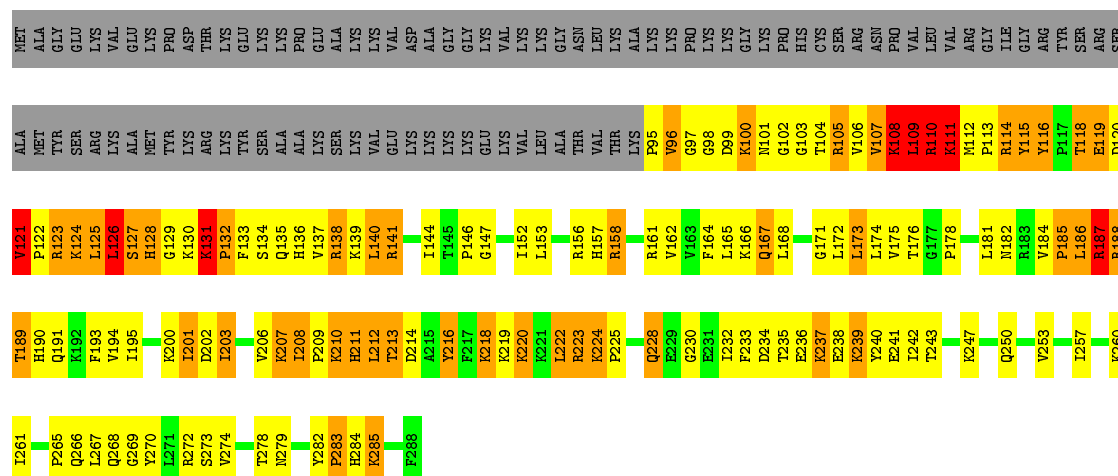
Chain AD: 





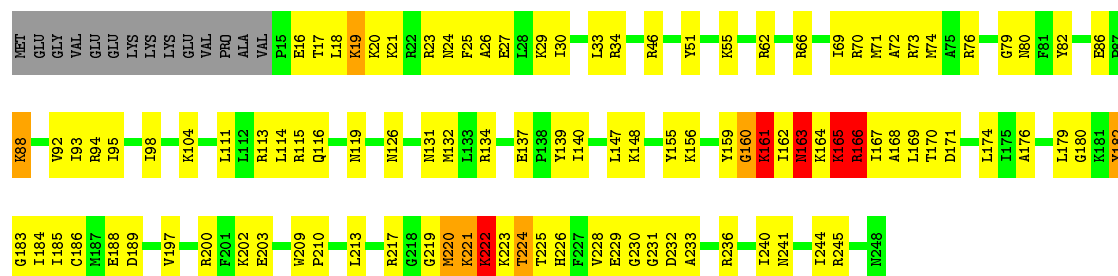
• Molecule 7: 60S ribosomal protein L6

Chain AE: 20% 30% 15% 33%



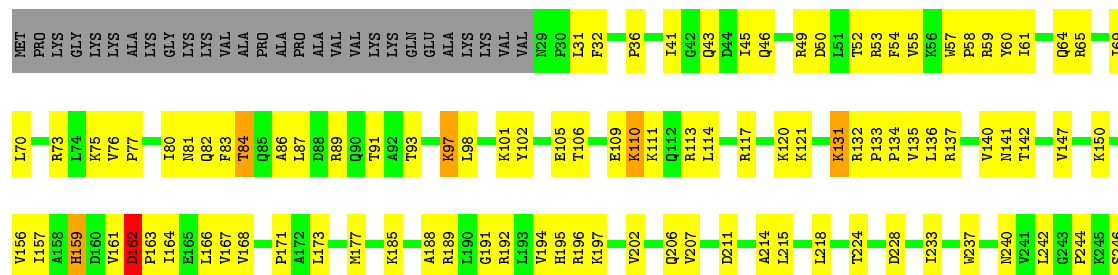
• Molecule 8: 60S ribosomal protein L7

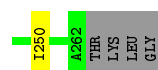
Chain AF: 52% 38% 6%



• Molecule 9: 60S ribosomal protein L7a

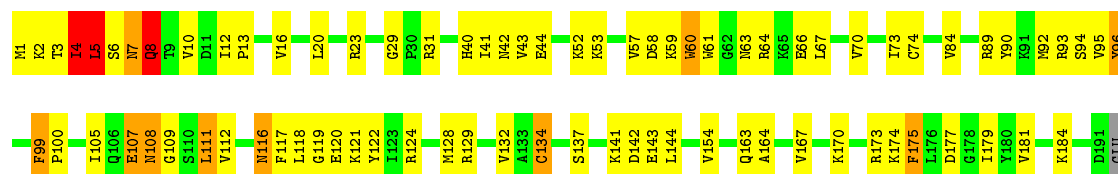
Chain AG: 50% 35% 12%





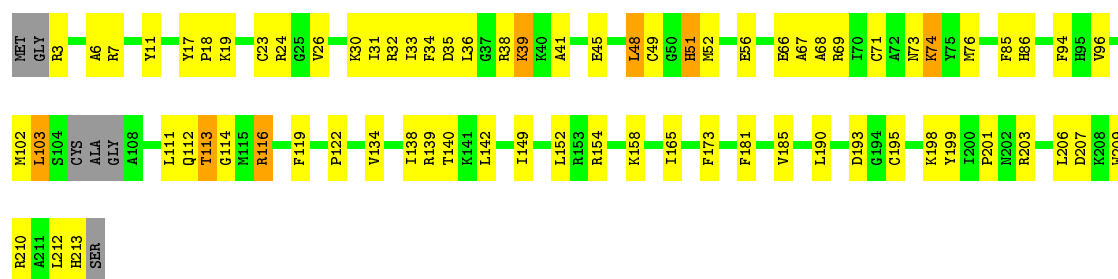
- Molecule 10: 60S ribosomal protein L9

Chain AH: 58% 35% 5% ..



- Molecule 11: 60S ribosomal protein L10

Chain AI: 63% 31% ..



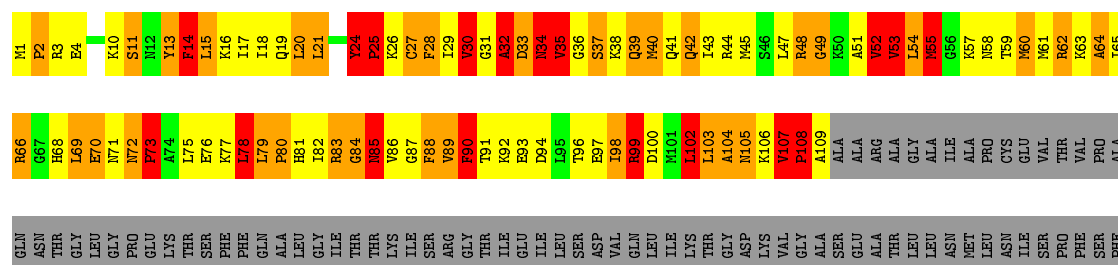
- Molecule 12: 60S ribosomal protein L11

Chain AJ: 56% 35% .. 5%



- Molecule 13: 60S acidic ribosomal protein P0

Chain AK: 5% 14% 10% 6% 66%



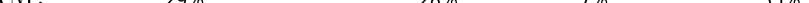
GLU	SER	ASP	GLU	ASP	MET	GLY	PHE	GLY	LEU	PHE	ASP	GLY	SER	ILE	TYR	ASN	PRO	GLU	VAL	LEU	ASP	THR	GLU	GLU	THR	LEU	HIS	SER	ARG	PHE	LEU	GLY	VAL	ARG	ASN	VAL	ALA	SER	SER	VAL	CYS	LEU	GLN	ILE	GLY	PRO	THR	VAL	ALA	SER	VAL	PRO	HIS	SER	ILE	ILE	ASN	GLY
LYS	ARG	VAL	LEU	ALA	LEU	SER	VAL	THR	GLU	THR	ASP	THR	THR	PHE	PRO	LEU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

- Molecule 14: 60S ribosomal protein L13

Chain AL:  43% 42% 9% . .

P156	R157	R158	M159	P160	Y161	K162	E163	E164	K165	A166	R167	T170	E171	E172	E173	K174	M175	F176	K177	A178	F179	A180	R183	R185	A186	K187	R188	D206	VAL	GLU	LYS	LYS	LYS																		
G75	S77	L78	E79	E80	L81	A84	V80	A91	I94	G95	I96	D99	R102	R103	N104	K105	L110	K118	L124	I125	L126	F127	P128	R129	K130	P131	S132	A133	P134	K135	K136	G137	D138	S139	S140	A141	E142	E143	L144	K145	L146	A147	T148	Q149	L150	T151	V154				
F76	S77	L78	E79	E80	L81	A84	V80	A91	I94	G95	I96	D99	R102	R103	N104	K105	L110	K118	L124	I125	L126	F127	P128	R129	K130	P131	S132	A133	P134	K135	K136	G137	D138	S139	S140	A141	E142	E143	L144	K145	L146	A147	T148	Q149	L150	T151	V154				
MET	A2	M8	V9	L10	K11	P12	H13	F14	H15	K16	D17	V18	Q19	R20	R21	W25	F26	N27	Q28	P29	A30	R31	R35	R36	Q40	A41	K42	A43	R44	R45	I46	A47	P48	R49	P50	A51	S52	G53	P54	R55	P57	L58	V59	R60	C61	P62	T63	Y66	V70	R71	A72

- Molecule 15: 60S ribosomal protein L14

Chain AM: 

[illegible]

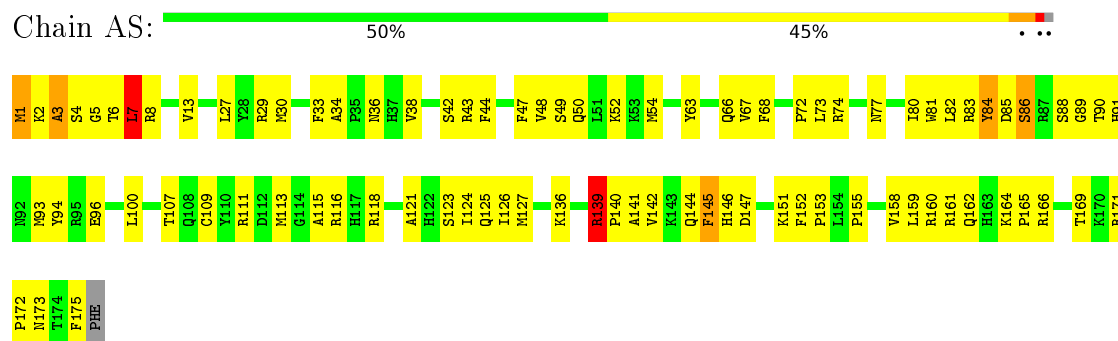
- Molecule 16: 60S ribosomal protein L15

Chain AN:  59% 36% 5%

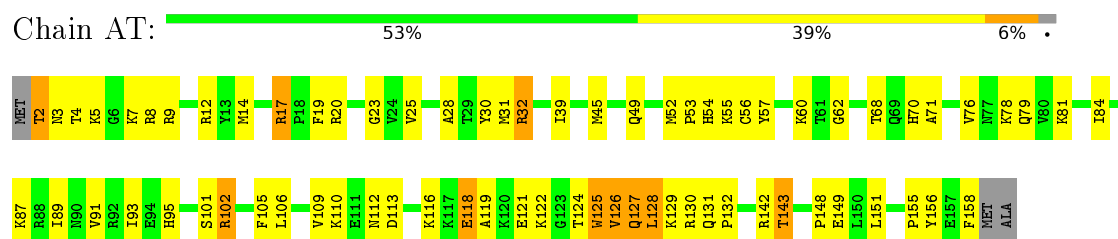
S187	R96	ME1
R188	S97	G2
R189	L98	A3
	Q99	
R193	S100	I7
R194	V101	Q8
R195	A102	
		R12
L200	R108	K13
H201		K14
R202	L113	
R203	R114	M19
R204	V115	R20
		F21
	E123	
	D124	V25
		R26
	K128	
	F129	Y30
	F130	
	L134	R38
		A39
	P137	P40
	F138	
	R144	A48
	N145	R49
	P146	R50
	D147	
	T148	Y63
Q149	K157	R94
W150		A55
I151		
		Y59
		V60
		L61
	P154	Y62
	V155	R63
	H156	I64
	K157	
	H158	R67
	R159	R68
	E160	
	M161	
	G168	
		R71
	S171	K72
	R172	R73
		P74
		T80
	K176	P84
	G177	V85
	H178	H86
	K179	H87
	F180	G88
	H181	V89
	H182	
	T183	L92
	I184	K93
	G185	R94

- Molecule 17: 60S ribosomal protein L13a

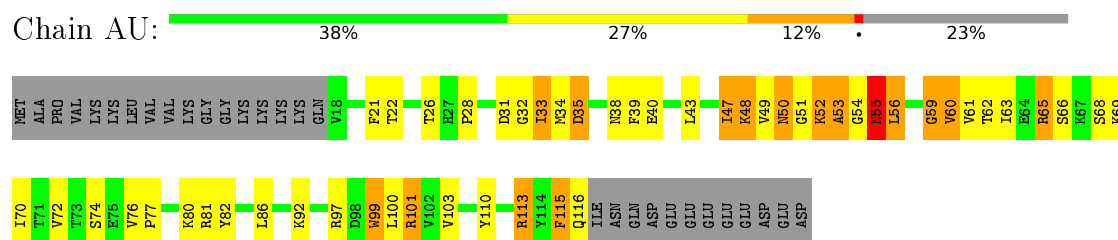
- Molecule 21: 60S ribosomal protein L18a



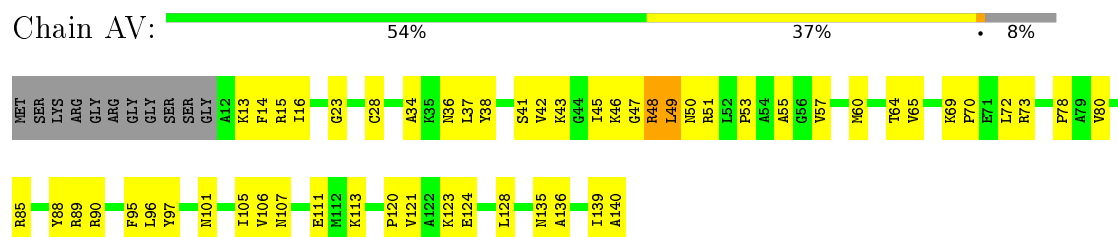
- Molecule 22: 60S ribosomal protein L21



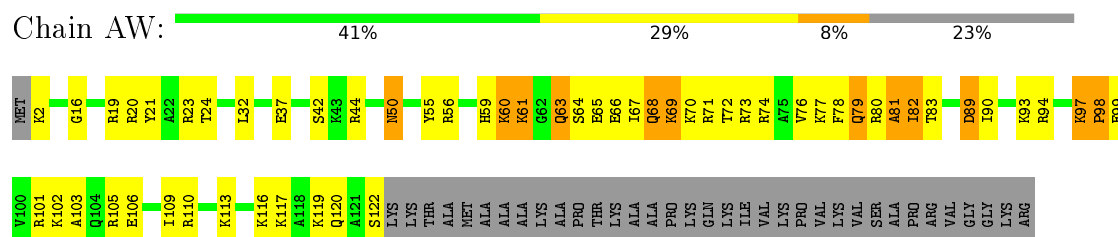
- Molecule 23: 60S ribosomal protein L22



- Molecule 24: 60S ribosomal protein L23

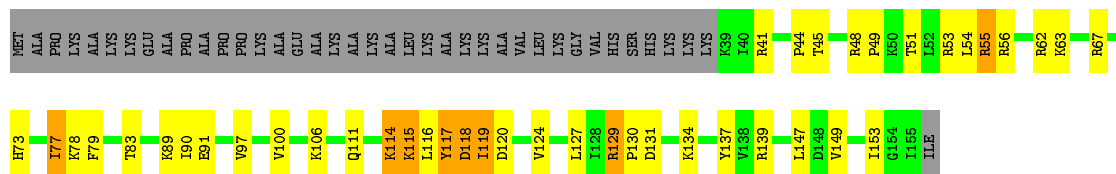


- Molecule 25: 60S ribosomal protein L24



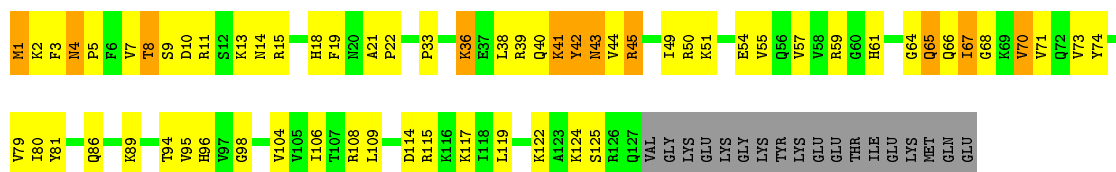
- Molecule 26: 60S ribosomal protein L23a

Category	Percentage
Very good	47%
Good	22%
Not good	5%
Very bad	25%



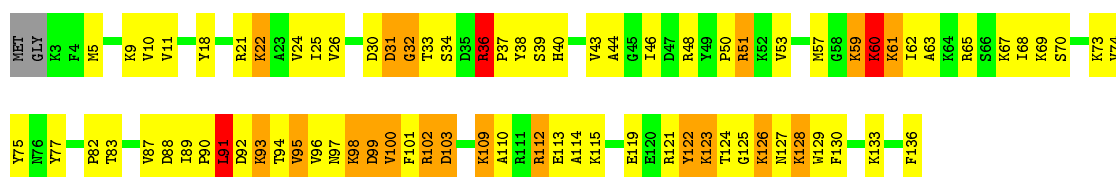
- Molecule 27: 60S ribosomal protein L26

Response	Percentage
Yes, U.S. should take action to reduce greenhouse gas emissions	43%
No, U.S. should not take action to reduce greenhouse gas emissions	37%
Don't know	8%
Refuse to answer	12%



- Molecule 28: 60S ribosomal protein L27

10% 43% 14% ...



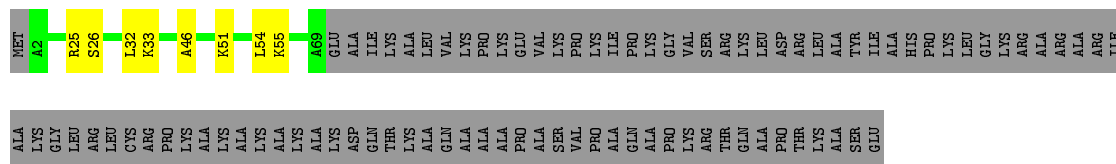
- Molecule 29: 60S ribosomal protein L27a

90% 9% ...



- Molecule 30: 60S ribosomal protein L29

Response	Percentage
Yes	38%
No	5%
Don't know	57%




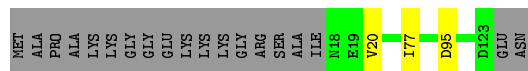
- Molecule 31: 60S ribosomal protein L30

85% • 10%



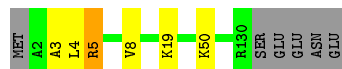
- Molecule 32: 60S ribosomal protein L31

Chain Ad:  82% 15%



- Molecule 33: 60S ribosomal protein L32

Chain Ae:  91%



- Molecule 34: 60S ribosomal protein L35a

Chain Af:  90% 6%




- Molecule 35: 60S ribosomal protein L34

Chain Ag:  91% 6%




- Molecule 36: 60S ribosomal protein L35

Chain Ah:  83% 16%



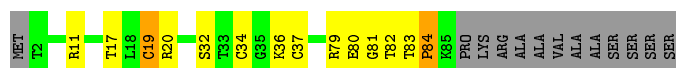
- Molecule 37: 60S ribosomal protein L36

Chain Ai:  85% 8% 8%




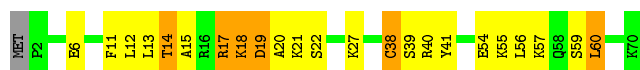
- Molecule 38: 60S ribosomal protein L37

Chain Aj:  72% 12% 13%



- Molecule 39: 60S ribosomal protein L38

Chain Ak:  66% 24% 9% .



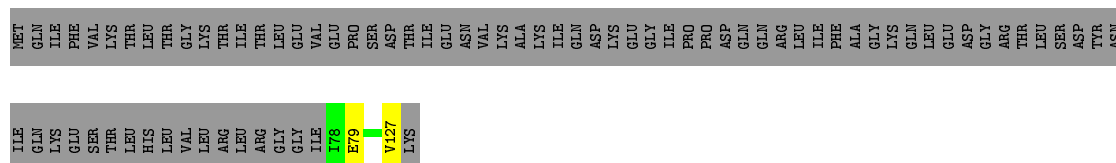
- Molecule 40: 60S ribosomal protein L39

Chain Al:  92% 6% .



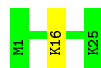
- Molecule 41: Ubiquitin-60S ribosomal protein L40

Chain Am:  38% 61% .




- Molecule 42: 60S ribosomal protein L41

Chain An:  96% .



- Molecule 43: 60S ribosomal protein L36a

Chain Ao:  88% 11% .



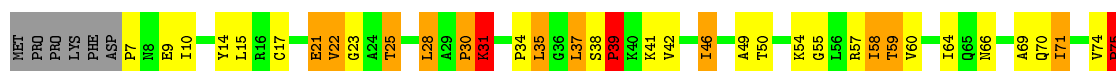
- Molecule 44: 60S ribosomal protein L37a

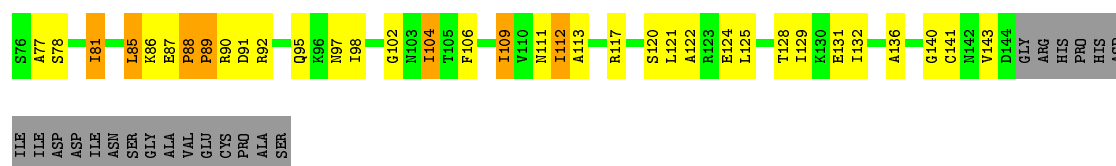
Chain Ap:  93% 5% .



- Molecule 45: 60S ribosomal protein L12

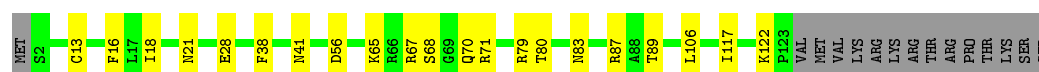
Chain Aq:  41% 30% 11% 16% .





- Molecule 46: 60S ribosomal protein L28

Chain At: 74% 15% 11%



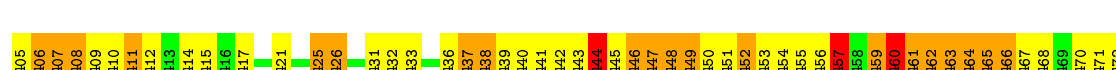
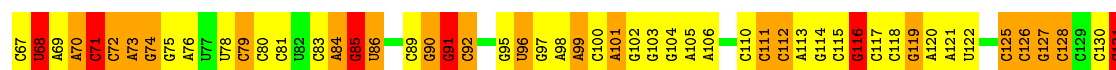
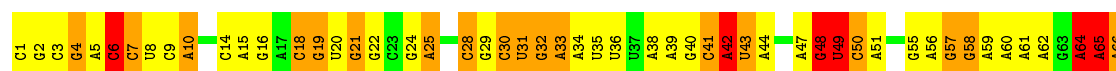
- Molecule 47: 60S ribosomal protein L10a

Chain Au: 87% 10% 3%



- Molecule 48: Human 28S ribosomal RNA gene

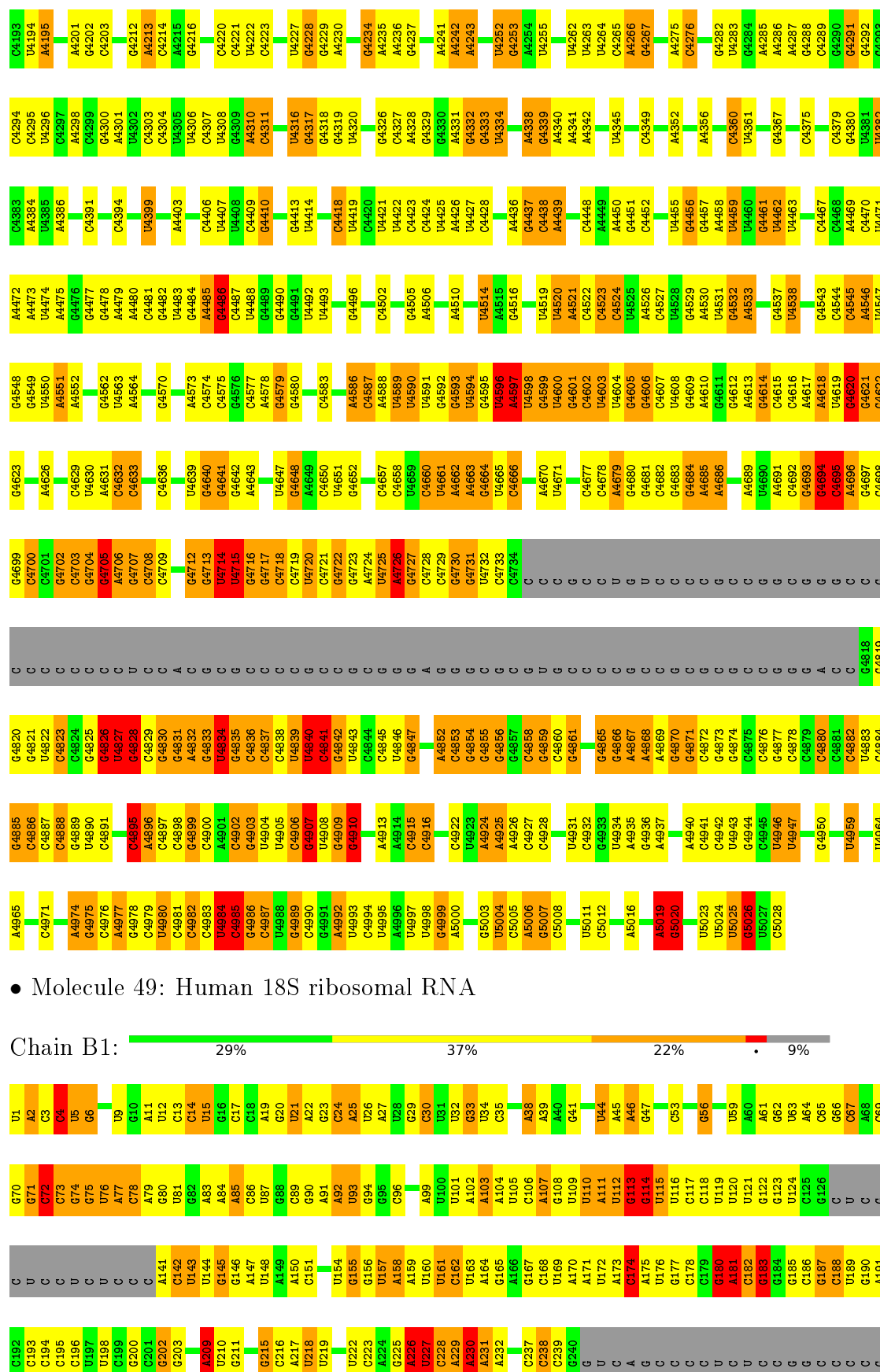
Chain A2: 25% 26% 17% 28%



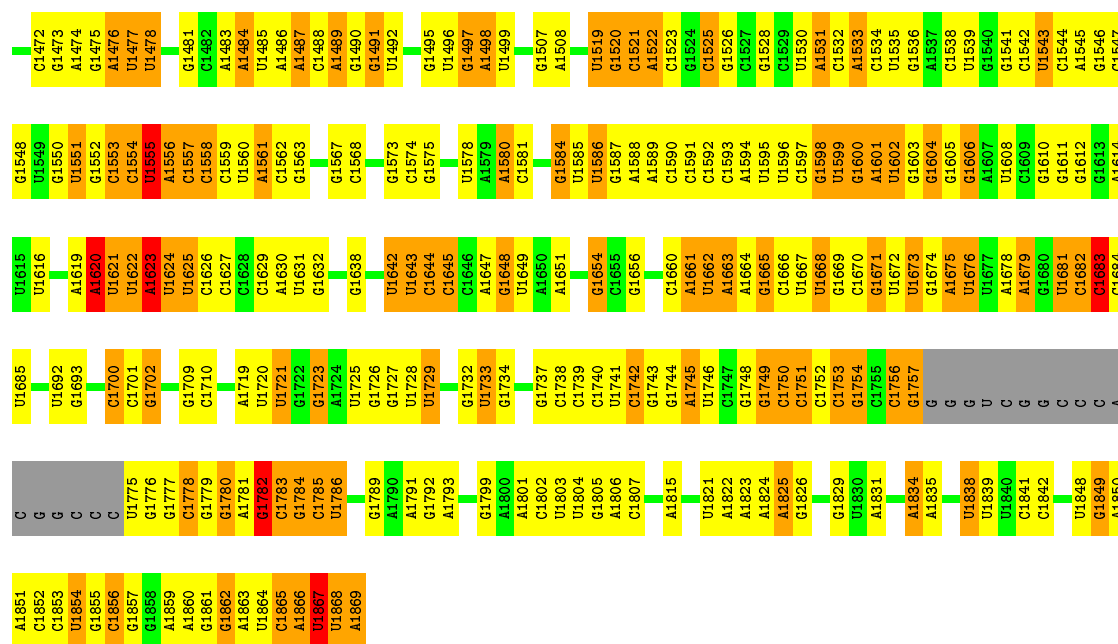
A1725	C1643	G1556	A1435	A1355	C1289	C1226	G1156	U	C	C	U967	C907	G	G	G658	G
U1726	C1644	G1559	G1436	A1356	A1290	G1227	G1157	C	G	G	C968	C908	G	G	G659	G
G1727	C1645	U1560	G1438	G1357	C1291	C1228	A1158	U	C	U	C969	C909	C	C	G660	C
A1730	U1646	C1561	G1439	C1358	C1292	G1233	U1159	C	G	C	C970	C910	G	G	G661	G
A1731	C1657	G1569	C1440	C1359	G1293	C	U1160	C	C	U	C971	C911	C	C	G662	G
G1732	C1658	C1570	A1441	C1361	A1295	C	U1161	C	C	U	C972	C912	C	C	G663	G
A1733	U1659	C1571	A1442	C1362	C1296	A	U1162	C	C	C	C973	C913	C	C	G664	U
G1734	C1659	C1572	C1460	G1363	C1297	A	C1163	C	G	G	C974	C914	G	G	G665	U
U1735	U1669	U1573	G1461	C1364	C1298	A	C1164	C	C	C	C975	C915	C	C	G666	C
U1736	G1670	U1574	C1462	G1365	C1299	G	C1165	C	G	G	U976	A916	G	G	G	C
U1737	G1673	A1575	C1463	G1368	U1300	A	C1166	C	U	C	C	C917	G	G	G669	G
U1738	G1673	A1575	C1463	G1368	A1306	G	C1167	C	C	C	C	C918	U	C	G670	G
U1739	G1673	C1576	G1464	C1369	A1307	G1243	U1168	C	C	U	C	A919	G	C	G671	G
G1740	C1676	U1577	C1465	A1370	C1308	G1244	G1170	C	U	C	G	G920	G	C	G672	G
G1741	U1677	U1578	G1466	C1371	C1309	C1245	C1171	C	C	C	C	A922	C	G	G673	U
G1742	C1678	C1580	C1467	A1374	A1310	G1246	G1172	C	U	C	C	C923	C	G	G674	G
G1743	C1678	G1581	C1468	G1375	C1311	C1247	C1185	C	U	C	C	U924	C	C	G675	G
C1744	G1679	A1582	A1479	G1376	G1312	G1248	G1186	C	G	C	C	C925	G	C	G676	G
C1745	G1680	A1582	G1480	C1379	A1313	G1249	G1187	C	G	C	C	C926	G	C	G677	C
G1746	A	U1583	C1483	A1380	C1314	C1250	G1188	C	G	C	A	C927	C	G	G678	G
A1747	G	C1584	C1484	A1381	C1315	G1251	G1189	C	C	C	C	C928	G	C	G679	G
A1748	C	U1585	A1485	A1316	A1317	G1252	C1190	C	C	C	C	A930	G	C	A681	C
A1749	C	G1586	A1485	C1388	A1253	G1253	C1191	C	C	C	C	A931	G	C	U682	G
C1750	C	U1587	G1486	C1389	G1318	G1254	G1192	C	C	C	C	U932	G	C	U683	G
G1751	C	U1588	G1487	C1390	G1319	C1255	C1193	C	C	C	C	C933	G	C	U684	G
U1752	G	C1589	G1488	C1391	A1320	G1256	C1194	C	C	C	C	C934	G	C	G689	C
U1753	C	U1590	C1489	C1392	G1321	G1257	G1195	C	C	C	C	C935	G	C	G690	C
C1754	C	G1592	C1490	U1393	U1322	G1258	G1196	C	C	C	C	G936	C	C	G691	G
U1755	C	C1593	C1394	C1323	C1323	C1259	G1198	C	C	C	C	G937	G	C	G692	G
C1756	C	U1594	C1395	U1324	U1324	G1260	C1197	C	C	C	C	G938	G	C	U693	G
A1757	C	A1595	U1496	C1396	A1325	G1261	C1198	C	C	C	A	G939	C	C	G694	G
U1758	C	C1596	A1497	C1397	A1326	C1262	C1199	C	C	C	U	C940	G	C	G695	G
C1759	C	U1597	G1498	G1402	G1327	G1263	G1200	C	C	C	U	C941	G	C	C	C
C1760	C	A1500	G1499	C1403	C1327	G1264	G1201	C	C	C	C	G942	G	C	C	C
U1761	C	C1501	A1500	U1403	U1331	G1265	G1202	C	C	C	C	A943	A	C	C	C
A1762	C	C1502	C1502	G1408	G1332	G1266	G	C	C	C	C	G944	C	C	G698	G
U1763	C	U1506	A1506	G1409	C1333	G1267	G	C	C	C	C	G945	C	C	G699	G
U1764	C	A1507	A1507	A1410	G1334	U1268	A	C	C	C	C	G946	C	C	C700	C
G1765	C	U1516	U1524	U1411	C1335	G1269	G	C	C	C	C	A947	A	C	G701	C
A1768	C	U1516	U1524	C1413	G1336	G1270	G	C	C	C	C	G948	A	C	A702	C
A1769	C	U1516	U1524	C1414	G1337	G1271	U	C	C	C	C	C949	A	C	C703	C
A1770	C	U1516	U1524	C1415	C1338	G1272	U	C	C	C	C	G950	C	C	G704	C
C1771	C	U1520	U1520	G1415	U1339	C1273	C	C	C	C	C	A951	C	C	G705	C
U1772	C	C1523	C1523	A1416	G1341	G1274	U	C	C	C	C	G952	C	C	G706	C
U1773	C	U1524	U1524	C1420	G1342	G1275	U	C	C	C	C	C953	C	C	U707	C
U1774	C	U1525	U1525	U1421	G1343	G1276	U	C	C	C	C	C954	C	C	C709	C
A1775	C	U1529	A1529	C1425	G1344	A1277	G	C	C	C	C	C955	C	C	G710	C
A1776	C	G1623	G1623	A1426	G1345	C1278	G1216	C	C	C	C	C956	C	C	G711	C
A1777	C	A1624	G1630	G1427	G1346	U1280	G1217	C	C	C	C	G957	C	C	G712	C
G1779	C	C1627	G1531	G1428	U1347	U1281	G1218	C	C	C	C	C958	C	C	G713	C
A1783	C	U1631	G1532	C1430	C1348	G1282	C1219	C	C	C	C	C959	C	C	A714	C
A1784	C	U1631	G1533	C1431	G1349	G1283	G1220	C	C	C	C	C960	C	C	C715	C
G1785	C	A1632	G1534	C1432	C1350	G1284	G1221	C	C	C	C	C961	C	C	G716	C
A1786	C	C1548	U1548	G1433	A1351	U1285	C1222	C	C	C	C	C962	C	C	G717	C
A1787	C	G1633	C1548	C1432	A1352	A1286	G1223	C	C	C	C	G963	C	C	C718	C
G1788	C	G1636	G1555	G1434	A1354	C1288	G1225	C	C	C	C	C964	C	C	U719	C
															G720	C
															G721	C



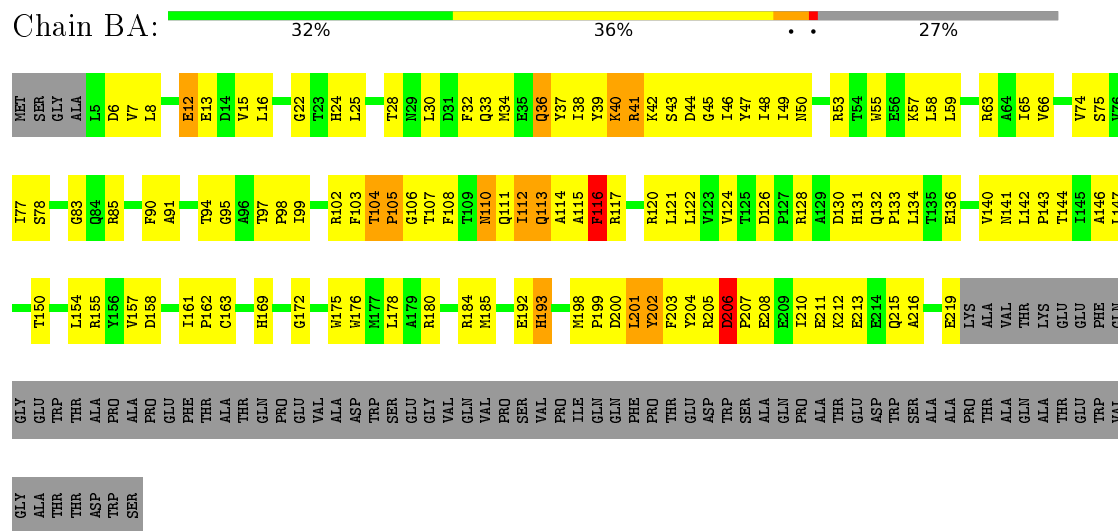

[illegible]



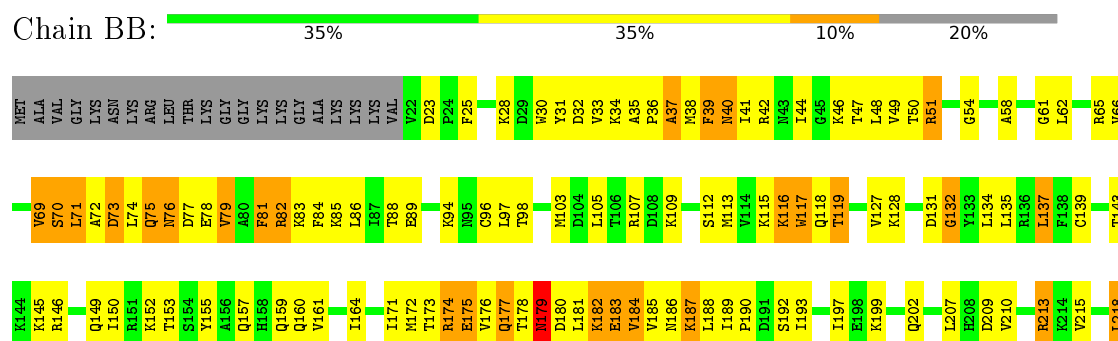


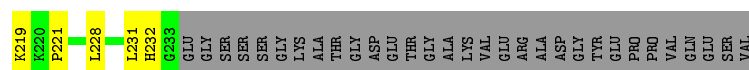



• Molecule 50: 40S ribosomal protein SA



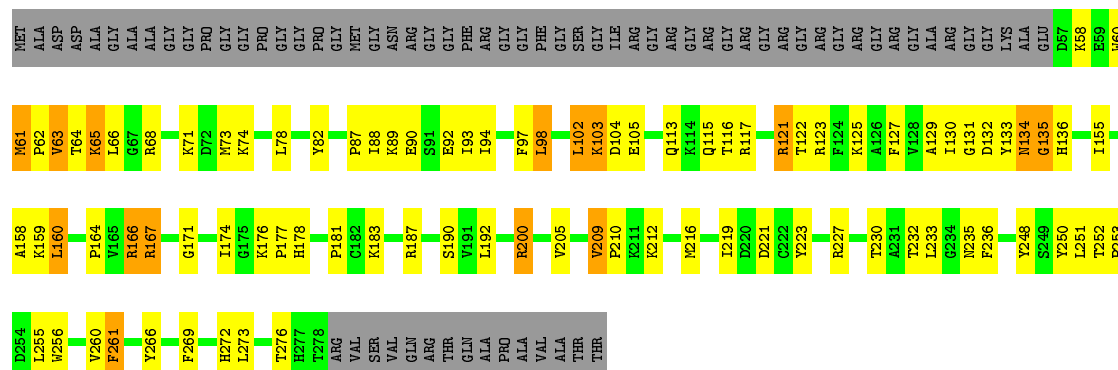
• Molecule 51: 40S ribosomal protein S3a





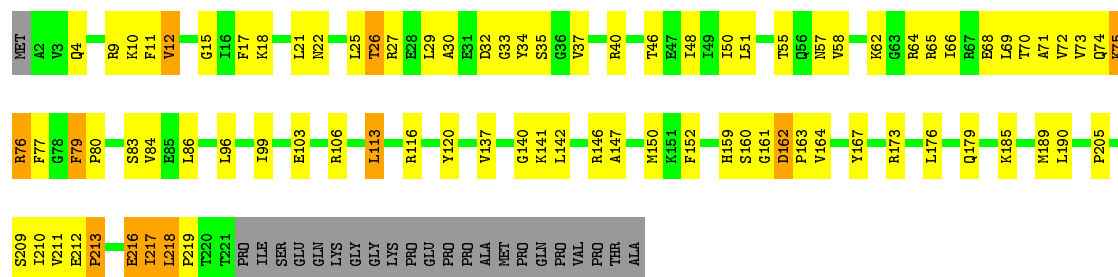
- Molecule 52: 40S ribosomal protein S2

Chain BC: 45% 26% 5% 24%



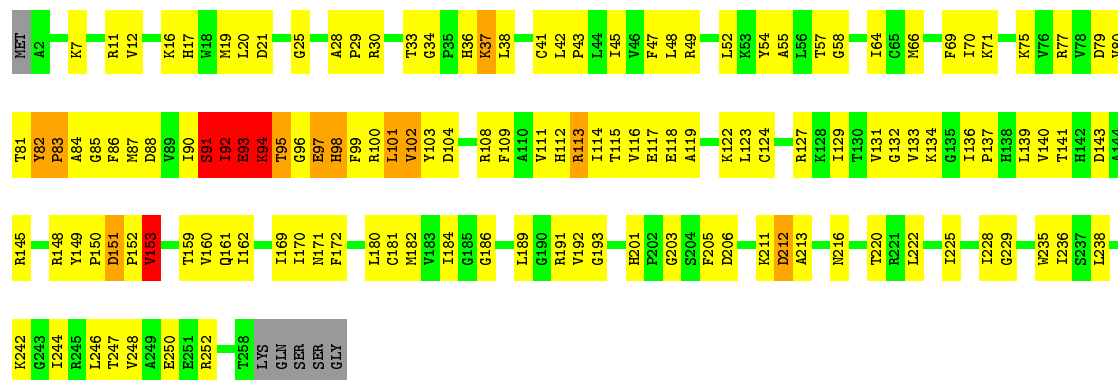
- Molecule 53: 40S ribosomal protein S3

Chain BD: 56% 30% 5% 9%



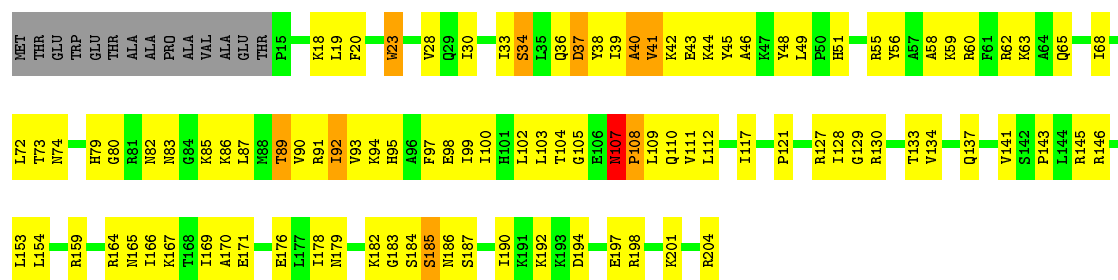
- Molecule 54: 40S ribosomal protein S4, Y isoform 1

Chain BE: 47% 45%



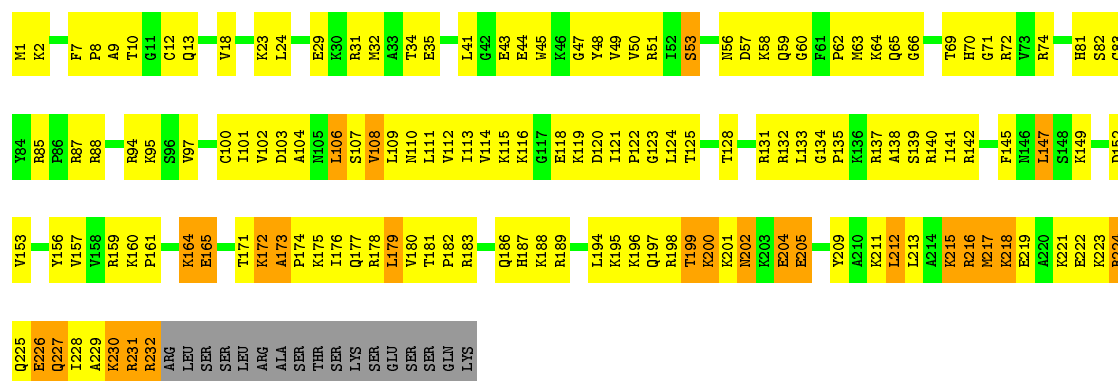
- Molecule 55: 40S ribosomal protein S5

Chain BF: 44% 45% 7%



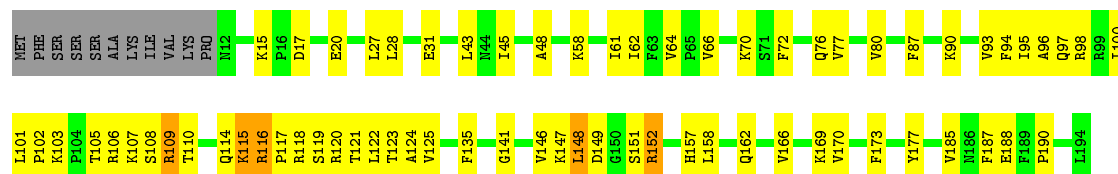
- Molecule 56: 40S ribosomal protein S6

Chain BG: 34% 49% 10% 7%



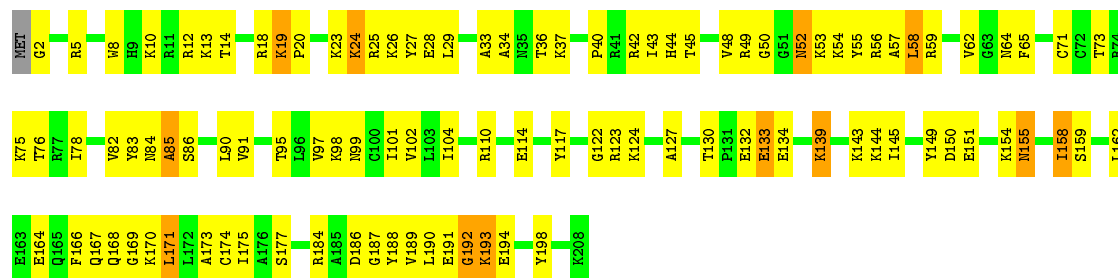
- Molecule 57: 40S ribosomal protein S7

Chain BH: 59% 33% 6%



- Molecule 58: 40S ribosomal protein S8

Chain BI: 50% 44% 6%



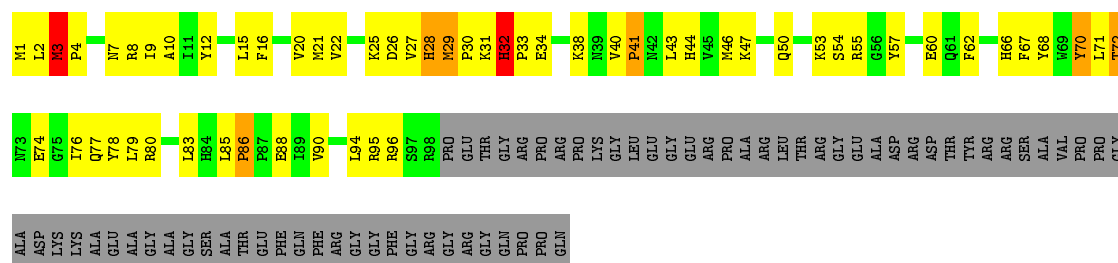
- Molecule 59: 40S ribosomal protein S9

Chain BJ: 22% 60% 10% 8%



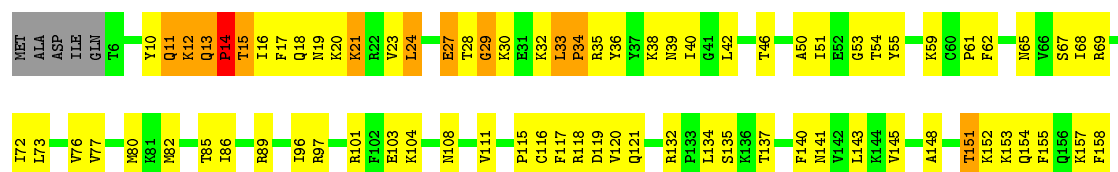
• Molecule 60: 40S ribosomal protein S10

Chain BK: 24% 30% 41%



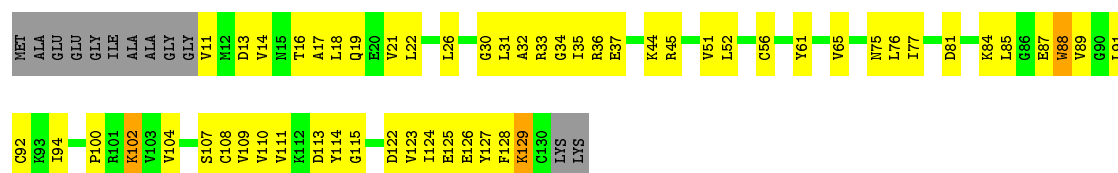
• Molecule 61: 40S ribosomal protein S11

Chain BL: 47% 42% 7%



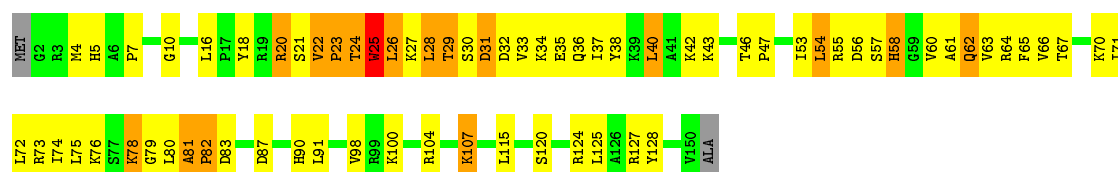
• Molecule 62: 40S ribosomal protein S12

Chain BM: 48% 40% 9%

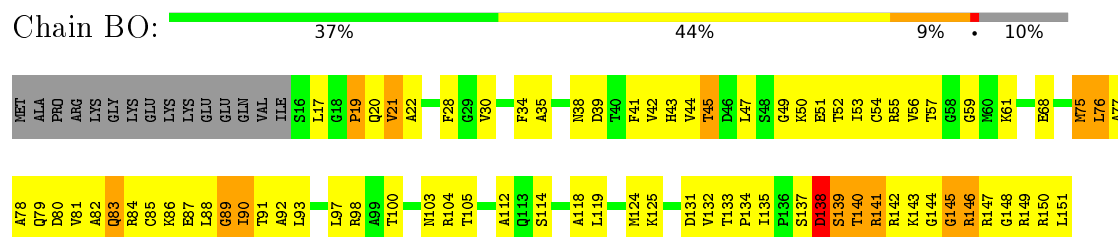


• Molecule 63: 40S ribosomal protein S13

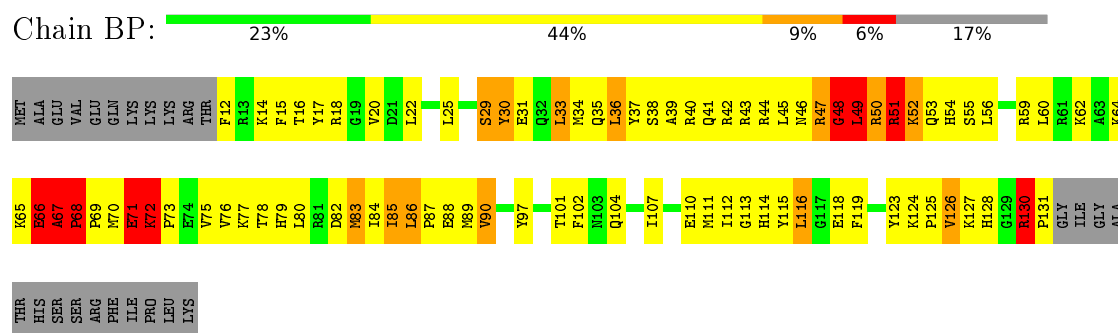
Chain BN: 52% 35% 11%



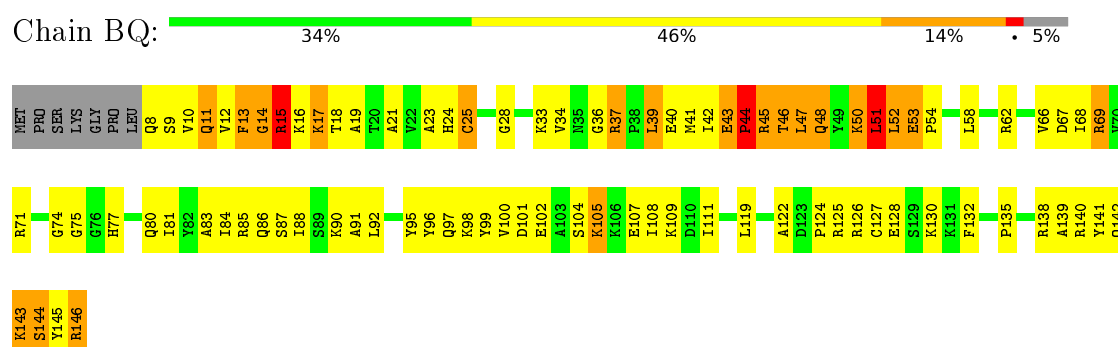
- Molecule 64: 40S ribosomal protein S14



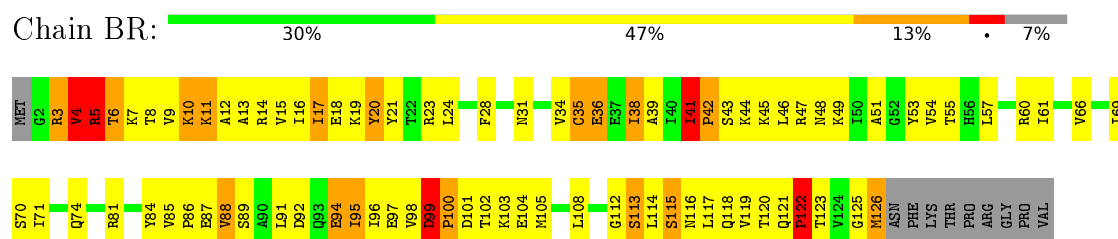
- Molecule 65: 40S ribosomal protein S15



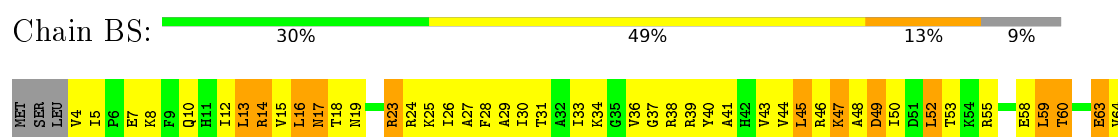
- Molecule 66: 40S ribosomal protein S16

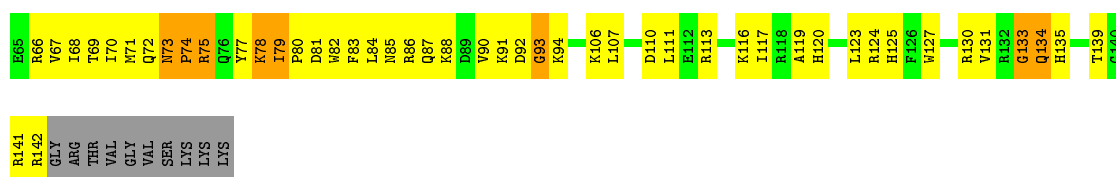


- Molecule 67: 40S ribosomal protein S17-like



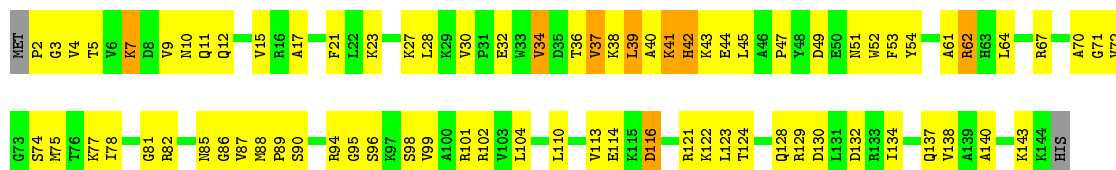
- Molecule 68: 40S ribosomal protein S18





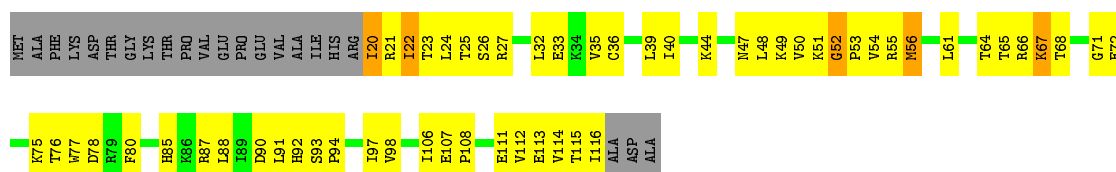
- Molecule 69: 40S ribosomal protein S19

Chain BT: 45% 48% 6% .



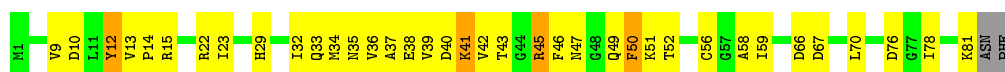
- Molecule 70: 40S ribosomal protein S20

Chain BU: 34% 44% 18% .



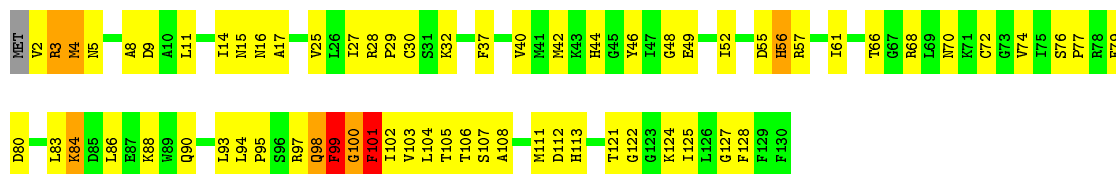
- Molecule 71: 40S ribosomal protein S21

Chain BV: 53% 40% 5% .



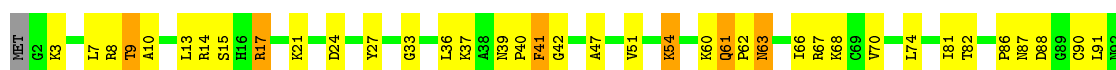
- Molecule 72: 40S ribosomal protein S15a

Chain BW: 48% 45% 5% ..



- Molecule 73: 40S ribosomal protein S23

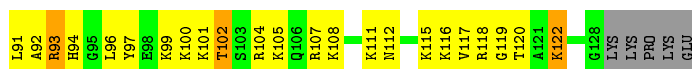
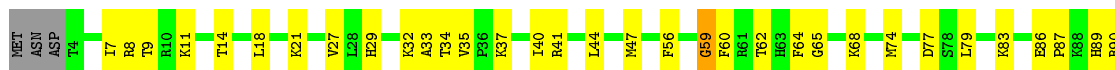
Chain BX: 51% 38% 8% ..





- Molecule 74: 40S ribosomal protein S24

Chain BY: 52% 39% 6%



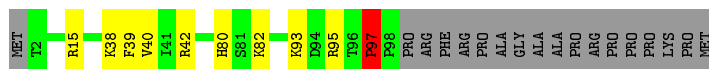
- Molecule 75: 40S ribosomal protein S25

Chain BZ: 23% 31% 14% 31%



- Molecule 76: 40S ribosomal protein S26

Chain Ba: 76% 8% 16%



- Molecule 77: 40S ribosomal protein S27

Chain Bb: 93% 5%



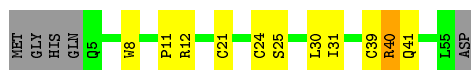
- Molecule 78: 40S ribosomal protein S28

Chain Bc: 84% 10% 6%




- Molecule 79: 40S ribosomal protein S29

Chain Bd: 71% 18% 9%



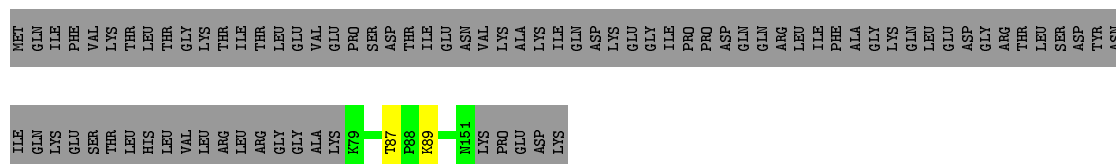
- Molecule 80: 40S ribosomal protein S30

Chain Be:  80% 14% 7%



- Molecule 81: Ubiquitin-40S ribosomal protein S27a

Chain Bf:  46% 53%



- Molecule 82: Guanine nucleotide-binding protein subunit beta-2-like 1

Chain Bg:  96%



- Molecule 83: tRNA

Chain Bv:  46% 51%



- Molecule 83: tRNA

Chain Bw:  51% 49%



- Molecule 84: mRNA

Chain Bx:  18% 82%



- Molecule 85: NASCENT CHAIN

Chain By:  100%

There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	313321	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20.00	Depositor
Minimum defocus (nm)	2000.00	Depositor
Maximum defocus (nm)	4500.00	Depositor
Magnification	205000	Depositor
Image detector	TVIPS TEMCAM-F416 (4K X 4K)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
1	A3	1.12	40/3726 (1.1%)	1.17	52/5804 (0.9%)
10	AH	0.38	0/1545	0.54	1/2077 (0.0%)
11	AI	0.41	0/1730	0.61	1/2311 (0.0%)
12	AJ	0.39	0/1376	0.59	0/1841
13	AK	0.85	3/886 (0.3%)	1.53	23/1188 (1.9%)
14	AL	0.48	3/1688 (0.2%)	0.73	5/2260 (0.2%)
15	AM	0.39	0/1161	0.64	0/1554
16	AN	0.39	0/1746	0.57	0/2338
17	AO	0.37	0/1638	0.60	0/2191
18	AP	0.42	0/1268	0.70	0/1701
19	AQ	0.47	2/1537 (0.1%)	0.63	3/2052 (0.1%)
2	A4	1.10	32/2839 (1.1%)	1.13	40/4425 (0.9%)
20	AR	0.38	0/1533	0.63	1/2025 (0.0%)
21	AS	0.38	1/1488 (0.1%)	0.60	1/1997 (0.1%)
22	AT	0.38	0/1312	0.60	0/1753
23	AU	0.35	0/822	0.58	0/1103
24	AV	0.37	0/983	0.55	0/1319
25	AW	0.42	1/1004 (0.1%)	0.74	3/1332 (0.2%)
26	AX	0.34	0/975	0.51	0/1312
27	AY	0.35	0/1081	0.56	0/1439
28	AZ	0.42	0/1126	0.69	2/1502 (0.1%)
29	Aa	0.50	0/1191	0.70	1/1591 (0.1%)
3	AA	0.44	0/1968	0.65	1/2639 (0.0%)
30	Ab	0.36	0/569	0.58	0/750
31	Ac	0.38	0/812	0.60	0/1089
32	Ad	0.38	0/894	0.58	0/1204
33	Ae	0.42	0/1082	0.58	1/1443 (0.1%)
34	Af	0.47	0/895	0.73	2/1198 (0.2%)
35	Ag	0.39	0/916	0.58	0/1220
36	Ah	0.37	0/1023	0.63	1/1351 (0.1%)
37	Ai	0.35	0/805	0.58	0/1065
38	Aj	0.47	1/703 (0.1%)	0.92	3/929 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z > 2	RMSZ	# Z > 2
39	AK	0.51	0/575	0.74	0/761
4	AB	0.39	0/3246	0.64	0/4345
40	AI	0.37	0/454	0.54	0/599
41	AM	0.42	0/417	0.59	0/553
42	AN	0.36	0/241	0.60	0/305
43	AO	0.39	0/877	0.66	0/1156
44	AP	0.39	0/718	0.60	0/953
45	AQ	0.89	3/1058 (0.3%)	1.93	34/1424 (2.4%)
46	AT	0.41	0/995	0.69	0/1334
47	AU	0.73	1/1772 (0.1%)	1.28	17/2375 (0.7%)
48	A2	0.98	666/86613 (0.8%)	1.13	1094/135108 (0.8%)
49	B1	0.96	275/40767 (0.7%)	1.13	515/63536 (0.8%)
5	AC	0.41	1/2942 (0.0%)	0.62	3/3951 (0.1%)
50	BA	0.52	1/1741 (0.1%)	0.72	5/2366 (0.2%)
51	BB	0.42	0/1749	0.62	0/2340
52	BC	0.37	0/1761	0.58	0/2379
53	BD	0.44	1/1736 (0.1%)	0.63	1/2338 (0.0%)
54	BE	0.41	1/2072 (0.0%)	0.59	1/2793 (0.0%)
55	BF	0.40	1/1524 (0.1%)	0.62	1/2048 (0.0%)
56	BG	0.41	0/1907	0.62	1/2538 (0.0%)
57	BH	0.43	0/1501	0.64	1/2009 (0.0%)
58	BI	0.41	0/1725	0.59	0/2298
59	BJ	0.36	0/1520	0.55	1/2030 (0.0%)
6	AD	0.42	0/2437	0.65	2/3262 (0.1%)
60	BK	0.43	0/851	0.68	0/1147
61	BL	0.44	1/1281 (0.1%)	0.65	2/1710 (0.1%)
62	BM	0.39	0/941	0.63	0/1264
63	BN	0.40	1/1226 (0.1%)	0.57	1/1649 (0.1%)
64	BO	0.43	0/1029	0.64	0/1380
65	BP	0.50	1/1019 (0.1%)	0.74	3/1361 (0.2%)
66	BQ	0.38	0/1126	0.58	2/1506 (0.1%)
67	BR	0.49	3/1023 (0.3%)	0.68	3/1373 (0.2%)
68	BS	0.42	1/1172 (0.1%)	0.63	1/1570 (0.1%)
69	BT	0.36	0/1131	0.60	0/1515
7	AE	0.50	0/1603	0.80	4/2153 (0.2%)
70	BU	0.45	0/778	0.65	1/1045 (0.1%)
71	BV	0.41	0/623	0.60	1/833 (0.1%)
72	BW	0.37	0/1051	0.55	0/1406
73	BX	0.44	1/1097 (0.1%)	0.61	1/1464 (0.1%)
74	BY	0.40	0/1032	0.64	0/1371
75	BZ	0.43	0/696	0.62	0/929
76	Ba	0.49	0/786	0.75	2/1053 (0.2%)
77	Bb	0.42	0/637	0.59	0/854

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
78	Bc	0.40	0/490	0.66	0/656
79	Bd	0.54	0/437	0.89	3/580 (0.5%)
8	AF	0.37	0/1986	0.57	0/2644
80	Be	0.37	0/443	0.60	0/583
81	Bf	0.44	0/613	0.62	0/811
82	Bg	0.40	0/2497	0.60	0/3399
83	Bv	0.58	4/1813 (0.2%)	0.84	5/2823 (0.2%)
83	Bw	0.43	2/1813 (0.1%)	0.90	4/2823 (0.1%)
84	Bx	0.60	2/616 (0.3%)	1.20	11/948 (1.2%)
9	AG	0.38	0/1913	0.57	0/2576
All	All	0.80	1049/234393 (0.4%)	0.98	1861/344230 (0.5%)

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	AH	0	3
13	AK	0	3
14	AL	0	6
39	AK	0	1
4	AB	0	3
48	A2	2	3
49	B1	1	0
5	AC	0	2
54	BE	0	6
63	BN	0	2
64	BO	0	2
65	BP	0	11
66	BQ	0	6
7	AE	0	1
72	BW	0	3
76	Ba	0	1
79	Bd	0	1
8	AF	0	2
All	All	3	56

The worst 5 of 1049 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	A2	3612	U	O3'-P	-21.32	1.35	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	B1	842	C	O3'-P	20.18	1.85	1.61
48	A2	2689	C	O3'-P	-19.59	1.37	1.61
49	B1	558	G	O3'-P	19.39	1.84	1.61
49	B1	497	C	O3'-P	18.59	1.83	1.61

The worst 5 of 1861 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	Aq	75	PRO	CA-N-CD	-36.28	60.70	111.50
48	A2	1225	G	O5'-P-OP1	-28.99	75.91	110.70
48	A2	131	C	C4'-C3'-O3'	28.78	170.56	113.00
49	B1	558	G	P-O3'-C3'	-28.42	85.60	119.70
48	A2	137	G	C4'-C3'-O3'	26.49	165.98	113.00

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
48	A2	131	C	C3'
48	A2	137	G	C3'
49	B1	1289	U	C4'

5 of 56 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	AB	295	ASP	Peptide
4	AB	296	GLY	Peptide
4	AB	297	LYS	Peptide
5	AC	98	GLY	Peptide
5	AC	99	GLY	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	A3	3337	0	1691	157	0
2	A4	2541	0	1284	156	0
3	AA	1930	0	2030	181	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	AB	3178	0	3314	339	0
5	AC	2888	0	3064	417	0
6	AD	2392	0	2424	334	0
7	AE	1571	0	1698	425	0
8	AF	1950	0	2093	284	0
9	AG	1880	0	2018	144	0
10	AH	1526	0	1605	143	0
11	AI	1692	0	1744	81	0
12	AJ	1353	0	1386	93	0
13	AK	872	0	916	335	0
14	AL	1657	0	1764	228	0
15	AM	1138	0	1204	155	0
16	AN	1701	0	1748	129	0
17	AO	1606	0	1745	137	0
18	AP	1242	0	1269	94	0
19	AQ	1513	0	1628	198	0
20	AR	1517	0	1665	229	0
21	AS	1449	0	1493	160	0
22	AT	1284	0	1352	163	0
23	AU	808	0	831	79	0
24	AV	969	0	1031	88	0
25	AW	989	0	1041	154	0
26	AX	958	0	1029	87	0
27	AY	1064	0	1145	97	0
28	AZ	1103	0	1179	144	0
29	Aa	1162	0	1213	0	0
30	Ab	559	0	590	0	0
31	Ac	801	0	845	0	0
32	Ad	879	0	924	0	0
33	Ae	1064	0	1160	0	0
34	Af	876	0	912	0	0
35	Ag	906	0	1002	0	0
36	Ah	1015	0	1147	0	0
37	Ai	794	0	870	0	0
38	Aj	689	0	717	0	0
39	Ak	569	0	637	0	0
40	Al	444	0	483	0	0
41	Am	411	0	443	0	0
42	An	240	0	289	0	0
43	Ao	863	0	929	0	0
44	Ap	708	0	756	0	0
45	Aq	1046	0	1116	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
46	At	980	0	1041	0	0
47	Au	1744	0	1859	0	0
48	A2	77427	0	39103	3881	0
49	B1	36456	0	18412	2354	0
50	BA	1704	0	1703	312	0
51	BB	1722	0	1794	286	0
52	BC	1724	0	1808	188	0
53	BD	1709	0	1801	206	0
54	BE	2031	0	2138	314	0
55	BF	1502	0	1557	161	0
56	BG	1884	0	2044	369	0
57	BH	1479	0	1563	129	0
58	BI	1696	0	1785	187	0
59	BJ	1495	0	1615	387	0
60	BK	827	0	854	142	0
61	BL	1258	0	1334	137	0
62	BM	931	0	961	107	0
63	BN	1202	0	1289	165	0
64	BO	1016	0	1039	143	0
65	BP	999	0	1046	250	0
66	BQ	1109	0	1174	257	0
67	BR	1011	0	1063	313	0
68	BS	1154	0	1210	231	0
69	BT	1112	0	1146	159	0
70	BU	769	0	837	119	0
71	BV	617	0	622	77	0
72	BW	1034	0	1080	130	0
73	BX	1080	0	1147	120	0
74	BY	1015	0	1085	160	0
75	BZ	688	0	766	176	0
76	Ba	774	0	821	0	0
77	Bb	625	0	646	0	0
78	Bc	488	0	514	0	0
79	Bd	427	0	426	0	0
80	Be	437	0	483	0	0
81	Bf	601	0	625	0	0
82	Bg	2440	0	2396	0	0
83	Bv	1623	0	820	0	0
83	Bw	1623	0	821	0	0
84	Bx	561	0	281	0	0
85	By	120	0	32	0	0
86	A2	220	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	A3	8	0	0	0	0
86	A4	9	0	0	0	0
86	AA	1	0	0	0	0
86	AB	2	0	0	0	0
86	AN	2	0	0	0	0
86	AY	1	0	0	0	0
86	Aa	3	0	0	0	0
86	Ae	2	0	0	0	0
86	An	1	0	0	0	0
86	B1	72	0	0	2	0
86	BD	1	0	0	0	0
86	BX	1	0	0	0	0
86	Bv	2	0	0	0	0
86	Bx	1	0	0	0	0
87	Aj	1	0	0	0	0
87	Ao	1	0	0	0	0
87	Ap	1	0	0	0	0
87	Ba	1	0	0	0	0
87	Bd	1	0	0	0	0
All	All	218559	0	162165	13081	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 42.

The worst 5 of 13081 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)
6:AD:286:SER:HB3	48:A2:1163:C:C5'	1.21	1.68
64:BO:54:CYS:SG	64:BO:81:VAL:HG22	1.31	1.67
10:AH:5:LEU:HD13	10:AH:60:TRP:CH2	1.32	1.65
75:BZ:79:ILE:HG21	75:BZ:83:LEU:CD1	1.18	1.64
10:AH:5:LEU:HB3	10:AH:60:TRP:CZ3	1.14	1.63

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	AA	250/257 (97%)	237 (95%)	7 (3%)	6 (2%)	7	47
4	AB	392/403 (97%)	370 (94%)	10 (3%)	12 (3%)	5	41
5	AC	361/427 (84%)	333 (92%)	13 (4%)	15 (4%)	3	32
6	AD	292/297 (98%)	270 (92%)	14 (5%)	8 (3%)	6	44
7	AE	192/288 (67%)	161 (84%)	12 (6%)	19 (10%)	1	10
8	AF	232/248 (94%)	213 (92%)	10 (4%)	9 (4%)	4	34
9	AG	232/266 (87%)	217 (94%)	10 (4%)	5 (2%)	8	49
10	AH	189/192 (98%)	175 (93%)	8 (4%)	6 (3%)	5	40
11	AI	204/214 (95%)	192 (94%)	7 (3%)	5 (2%)	7	46
12	AJ	167/178 (94%)	154 (92%)	7 (4%)	6 (4%)	4	37
13	AK	107/317 (34%)	34 (32%)	37 (35%)	36 (34%)	0	0
14	AL	203/211 (96%)	175 (86%)	14 (7%)	14 (7%)	1	18
15	AM	137/215 (64%)	127 (93%)	5 (4%)	5 (4%)	4	37
16	AN	201/204 (98%)	193 (96%)	6 (3%)	2 (1%)	19	66
17	AO	193/203 (95%)	187 (97%)	3 (2%)	3 (2%)	12	55
18	AP	151/184 (82%)	147 (97%)	4 (3%)	0	100	100
19	AQ	185/188 (98%)	163 (88%)	10 (5%)	12 (6%)	1	20
20	AR	179/196 (91%)	171 (96%)	4 (2%)	4 (2%)	8	49
21	AS	173/176 (98%)	156 (90%)	11 (6%)	6 (4%)	4	38
22	AT	155/160 (97%)	144 (93%)	6 (4%)	5 (3%)	5	40
23	AU	97/128 (76%)	81 (84%)	7 (7%)	9 (9%)	1	11
24	AV	127/140 (91%)	125 (98%)	2 (2%)	0	100	100
25	AW	119/157 (76%)	96 (81%)	18 (15%)	5 (4%)	3	32
26	AX	115/156 (74%)	113 (98%)	2 (2%)	0	100	100
27	AY	125/145 (86%)	119 (95%)	2 (2%)	4 (3%)	5	40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	AZ	132/136 (97%)	118 (89%)	6 (4%)	8 (6%)	2	21
29	Aa	145/148 (98%)	135 (93%)	6 (4%)	4 (3%)	6	43
30	Ab	66/159 (42%)	57 (86%)	5 (8%)	4 (6%)	2	21
31	Ac	101/115 (88%)	97 (96%)	2 (2%)	2 (2%)	9	51
32	Ad	104/125 (83%)	99 (95%)	3 (3%)	2 (2%)	10	51
33	Ae	127/135 (94%)	116 (91%)	6 (5%)	5 (4%)	4	34
34	Af	107/110 (97%)	93 (87%)	5 (5%)	9 (8%)	1	13
35	Ag	112/117 (96%)	107 (96%)	3 (3%)	2 (2%)	11	53
36	Ah	120/123 (98%)	112 (93%)	2 (2%)	6 (5%)	3	27
37	Ai	95/105 (90%)	83 (87%)	7 (7%)	5 (5%)	2	25
38	Aj	82/97 (84%)	69 (84%)	7 (8%)	6 (7%)	1	16
39	Ak	67/70 (96%)	50 (75%)	7 (10%)	10 (15%)	0	3
40	Al	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
41	Am	48/128 (38%)	44 (92%)	3 (6%)	1 (2%)	9	50
42	An	23/25 (92%)	23 (100%)	0	0	100	100
43	Ao	103/106 (97%)	94 (91%)	5 (5%)	4 (4%)	4	34
44	Ap	89/92 (97%)	84 (94%)	3 (3%)	2 (2%)	8	49
45	Aq	136/165 (82%)	40 (29%)	47 (35%)	49 (36%)	0	0
46	At	120/137 (88%)	107 (89%)	10 (8%)	3 (2%)	7	46
47	Au	215/217 (99%)	185 (86%)	20 (9%)	10 (5%)	3	29
50	BA	213/295 (72%)	197 (92%)	12 (6%)	4 (2%)	10	51
51	BB	210/264 (80%)	180 (86%)	12 (6%)	18 (9%)	1	12
52	BC	220/293 (75%)	204 (93%)	7 (3%)	9 (4%)	3	33
53	BD	218/243 (90%)	201 (92%)	10 (5%)	7 (3%)	5	40
54	BE	255/263 (97%)	230 (90%)	14 (6%)	11 (4%)	3	31
55	BF	188/204 (92%)	163 (87%)	15 (8%)	10 (5%)	2	25
56	BG	230/249 (92%)	211 (92%)	11 (5%)	8 (4%)	4	38
57	BH	181/194 (93%)	169 (93%)	8 (4%)	4 (2%)	8	49
58	BI	205/208 (99%)	175 (85%)	20 (10%)	10 (5%)	3	27
59	BJ	177/194 (91%)	137 (77%)	28 (16%)	12 (7%)	1	19
60	BK	96/165 (58%)	84 (88%)	7 (7%)	5 (5%)	2	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
61	BL	151/158 (96%)	133 (88%)	11 (7%)	7 (5%)	3	29
62	BM	118/132 (89%)	113 (96%)	1 (1%)	4 (3%)	5	39
63	BN	147/151 (97%)	126 (86%)	13 (9%)	8 (5%)	2	25
64	BO	134/151 (89%)	113 (84%)	11 (8%)	10 (8%)	1	15
65	BP	118/145 (81%)	100 (85%)	9 (8%)	9 (8%)	1	15
66	BQ	137/146 (94%)	120 (88%)	10 (7%)	7 (5%)	2	26
67	BR	123/135 (91%)	106 (86%)	9 (7%)	8 (6%)	1	20
68	BS	137/152 (90%)	125 (91%)	7 (5%)	5 (4%)	4	37
69	BT	141/145 (97%)	131 (93%)	6 (4%)	4 (3%)	6	43
70	BU	95/119 (80%)	91 (96%)	2 (2%)	2 (2%)	9	50
71	BV	79/83 (95%)	77 (98%)	2 (2%)	0	100	100
72	BW	127/130 (98%)	120 (94%)	3 (2%)	4 (3%)	5	41
73	BX	137/143 (96%)	124 (90%)	8 (6%)	5 (4%)	4	37
74	BY	123/133 (92%)	116 (94%)	6 (5%)	1 (1%)	24	70
75	BZ	84/125 (67%)	80 (95%)	1 (1%)	3 (4%)	4	37
76	Ba	95/115 (83%)	87 (92%)	7 (7%)	1 (1%)	17	63
77	Bb	78/84 (93%)	72 (92%)	4 (5%)	2 (3%)	7	45
78	Bc	60/69 (87%)	57 (95%)	1 (2%)	2 (3%)	5	39
79	Bd	49/56 (88%)	42 (86%)	4 (8%)	3 (6%)	2	21
80	Be	53/59 (90%)	49 (92%)	2 (4%)	2 (4%)	4	35
81	Bf	71/156 (46%)	63 (89%)	7 (10%)	1 (1%)	14	58
82	Bg	312/317 (98%)	292 (94%)	12 (4%)	8 (3%)	7	45
All	All	11580/13387 (86%)	10401 (90%)	657 (6%)	522 (4%)	6	30

5 of 522 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AA	138	SER
3	AA	144	LYS
3	AA	197	PRO
4	AB	189	THR
4	AB	356	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	AA	194/199 (98%)	185 (95%)	9 (5%)	33	72
4	AB	343/349 (98%)	323 (94%)	20 (6%)	25	65
5	AC	302/348 (87%)	278 (92%)	24 (8%)	15	53
6	AD	248/250 (99%)	229 (92%)	19 (8%)	16	54
7	AE	174/252 (69%)	127 (73%)	47 (27%)	0	4
8	AF	203/215 (94%)	193 (95%)	10 (5%)	31	70
9	AG	199/223 (89%)	192 (96%)	7 (4%)	43	78
10	AH	170/171 (99%)	160 (94%)	10 (6%)	24	65
11	AI	178/181 (98%)	174 (98%)	4 (2%)	60	85
12	AJ	142/149 (95%)	138 (97%)	4 (3%)	51	82
13	AK	95/258 (37%)	70 (74%)	25 (26%)	0	4
14	AL	171/177 (97%)	156 (91%)	15 (9%)	12	48
15	AM	118/161 (73%)	104 (88%)	14 (12%)	6	31
16	AN	171/172 (99%)	163 (95%)	8 (5%)	32	72
17	AO	168/174 (97%)	164 (98%)	4 (2%)	57	85
18	AP	134/163 (82%)	123 (92%)	11 (8%)	14	51
19	AQ	164/165 (99%)	144 (88%)	20 (12%)	6	29
20	AR	160/175 (91%)	145 (91%)	15 (9%)	11	44
21	AS	156/157 (99%)	149 (96%)	7 (4%)	34	73
22	AT	138/140 (99%)	126 (91%)	12 (9%)	13	48
23	AU	89/115 (77%)	78 (88%)	11 (12%)	6	29
24	AV	100/107 (94%)	98 (98%)	2 (2%)	63	87
25	AW	100/126 (79%)	94 (94%)	6 (6%)	24	64
26	AX	105/133 (79%)	95 (90%)	10 (10%)	11	43
27	AY	119/135 (88%)	109 (92%)	10 (8%)	14	50
28	AZ	117/118 (99%)	100 (86%)	17 (14%)	4	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	Aa	120/121 (99%)	110 (92%)	10 (8%)	14	50
30	Ab	58/126 (46%)	54 (93%)	4 (7%)	19	59
31	Ac	88/97 (91%)	85 (97%)	3 (3%)	44	79
32	Ad	97/110 (88%)	96 (99%)	1 (1%)	82	93
33	Ae	115/121 (95%)	114 (99%)	1 (1%)	84	94
34	Af	88/89 (99%)	85 (97%)	3 (3%)	44	79
35	Ag	98/100 (98%)	93 (95%)	5 (5%)	29	69
36	Ah	109/110 (99%)	96 (88%)	13 (12%)	6	31
37	Ai	83/89 (93%)	80 (96%)	3 (4%)	42	77
38	Aj	71/80 (89%)	65 (92%)	6 (8%)	13	49
39	Ak	64/65 (98%)	46 (72%)	18 (28%)	0	3
40	Al	47/48 (98%)	44 (94%)	3 (6%)	22	62
41	Am	46/116 (40%)	45 (98%)	1 (2%)	60	85
42	An	24/24 (100%)	23 (96%)	1 (4%)	36	74
43	Ao	93/94 (99%)	85 (91%)	8 (9%)	13	49
44	Ap	74/75 (99%)	71 (96%)	3 (4%)	37	74
45	Aq	114/137 (83%)	90 (79%)	24 (21%)	1	8
46	At	106/121 (88%)	88 (83%)	18 (17%)	2	15
47	Au	196/196 (100%)	180 (92%)	16 (8%)	14	51
50	BA	180/243 (74%)	165 (92%)	15 (8%)	14	50
51	BB	193/231 (84%)	177 (92%)	16 (8%)	14	50
52	BC	188/225 (84%)	177 (94%)	11 (6%)	24	65
53	BD	183/202 (91%)	175 (96%)	8 (4%)	35	73
54	BE	220/225 (98%)	213 (97%)	7 (3%)	46	80
55	BF	160/170 (94%)	155 (97%)	5 (3%)	47	81
56	BG	202/218 (93%)	177 (88%)	25 (12%)	6	29
57	BH	164/174 (94%)	160 (98%)	4 (2%)	57	85
58	BI	179/180 (99%)	175 (98%)	4 (2%)	60	85
59	BJ	160/168 (95%)	151 (94%)	9 (6%)	26	66
60	BK	89/136 (65%)	83 (93%)	6 (7%)	20	61
61	BL	138/142 (97%)	134 (97%)	4 (3%)	50	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
62	BM	102/108 (94%)	101 (99%)	1 (1%)	82	93
63	BN	130/131 (99%)	122 (94%)	8 (6%)	23	63
64	BO	106/119 (89%)	99 (93%)	7 (7%)	21	61
65	BP	109/130 (84%)	93 (85%)	16 (15%)	4	22
66	BQ	115/121 (95%)	102 (89%)	13 (11%)	7	34
67	BR	113/122 (93%)	97 (86%)	16 (14%)	4	24
68	BS	121/132 (92%)	106 (88%)	15 (12%)	6	29
69	BT	113/115 (98%)	102 (90%)	11 (10%)	10	42
70	BU	90/107 (84%)	85 (94%)	5 (6%)	26	66
71	BV	65/67 (97%)	59 (91%)	6 (9%)	11	45
72	BW	112/113 (99%)	108 (96%)	4 (4%)	42	77
73	BX	111/115 (96%)	101 (91%)	10 (9%)	12	46
74	BY	107/115 (93%)	103 (96%)	4 (4%)	41	76
75	BZ	75/103 (73%)	57 (76%)	18 (24%)	1	5
76	Ba	84/98 (86%)	75 (89%)	9 (11%)	8	37
77	Bb	72/76 (95%)	72 (100%)	0	100	100
78	Bc	55/62 (89%)	52 (94%)	3 (6%)	27	67
79	Bd	45/49 (92%)	40 (89%)	5 (11%)	8	35
80	Be	44/48 (92%)	38 (86%)	6 (14%)	5	26
81	Bf	66/140 (47%)	65 (98%)	1 (2%)	72	90
82	Bg	272/275 (99%)	268 (98%)	4 (2%)	72	90
All	All	10112/11392 (89%)	9354 (92%)	758 (8%)	21	55

5 of 758 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	Aa	27	LYS
45	Aq	9	GLU
73	BX	54	LYS
30	Ab	33	LYS
38	Aj	11	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 196 such sidechains are listed below:

Mol	Chain	Res	Type
30	Ab	12	GLN
45	Aq	70	GLN
72	BW	70	ASN
32	Ad	79	ASN
40	Al	19	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A3	156/194 (80%)	28 (17%)	4 (2%)
2	A4	118/121 (97%)	23 (19%)	1 (0%)
48	A2	3600/5029 (71%)	695 (19%)	48 (1%)
49	B1	1701/1869 (91%)	290 (17%)	19 (1%)
83	Bv	75/76 (98%)	38 (50%)	0
83	Bw	75/76 (98%)	34 (45%)	0
84	Bx	27/28 (96%)	18 (66%)	0
All	All	5752/7393 (77%)	1126 (19%)	72 (1%)

5 of 1126 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A3	2	G
1	A3	12	G
1	A3	16	G
1	A3	35	C
1	A3	59	A

5 of 72 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
48	A2	2485	G
48	A2	4026	A
49	B1	869	A
48	A2	2508	A
48	A2	3595	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](#)

Of 331 ligands modelled in this entry, 331 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
49	B1	8
48	A2	5

The worst 5 of 13 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B1	842:C	O3'	843:C	P	1.85
1	B1	558:G	O3'	559:G	P	1.84
1	B1	497:C	O3'	498:C	P	1.83
1	B1	72:C	O3'	73:C	P	1.82
1	B1	1253:A	O3'	1254:C	P	1.82