



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 01:41 AM UTC

PDB ID : 9BUQ / pdb_00009buq
EMDB ID : EMD-44916
Title : Single particle cryoEM structure of the Pf80S ribosome in the POST state (nrt with P- and E-site tRNA)
Authors : Anton, L.; Haile, M.; Ho, C.M.
Deposited on : 2024-05-17
Resolution : 2.30 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

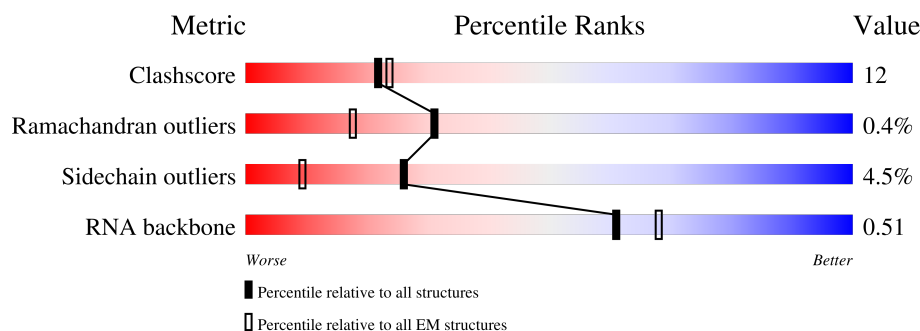
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.30 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.



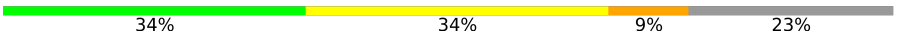
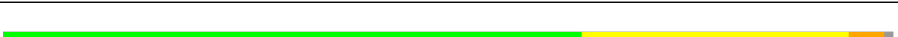
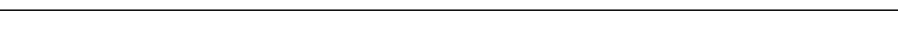
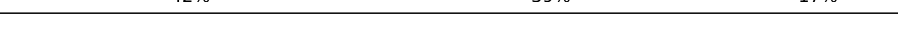
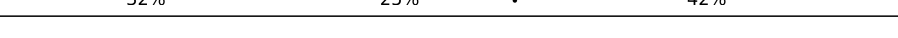
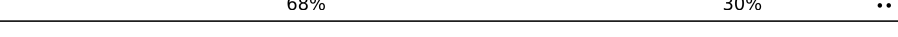
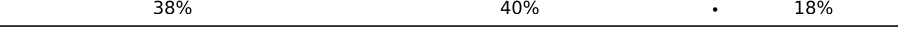
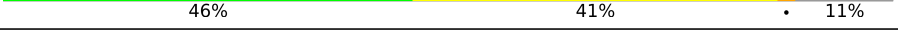
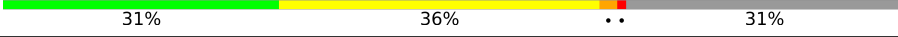
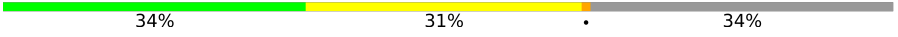
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	S1	133	56% 34% 10%
2	S2	105	30% 9% 61%
3	S3	107	63% 26% 11%
4	S4	82	60% 30% 7%
5	S5	67	55% 30% 12%
6	S6	58	48% 26% 26%
7	S7	74	30% 58% 12%

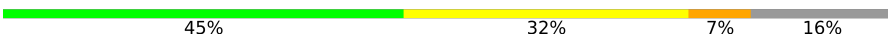
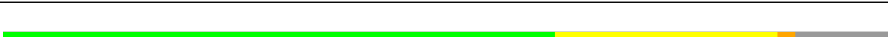
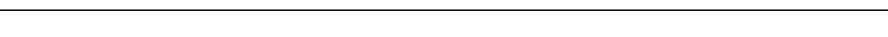
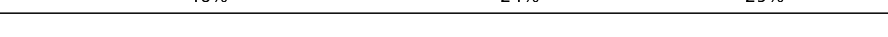
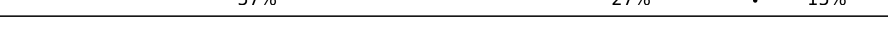
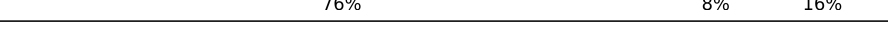
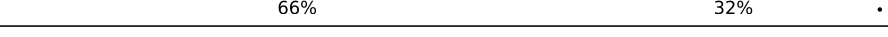
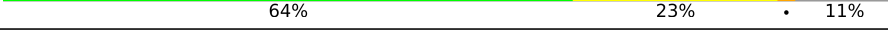
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Mol	Chain	Length	Quality of chain
8	SA	2092	
9	SB	262	
10	SC	263	
11	SD	221	
12	SE	189	
13	SF	261	
14	SG	272	
15	SH	306	
16	SI	195	
17	SJ	194	
18	SK	130	
19	SL	218	
20	SM	144	
21	SN	118	
22	SO	137	
23	SP	151	
24	SQ	145	
25	SR	141	
26	SS	156	
27	ST	54	
28	SU	151	
29	SV	161	
30	SW	137	
31	SX	145	
32	SY	170	

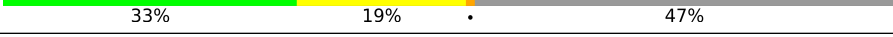
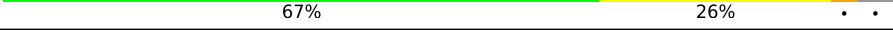
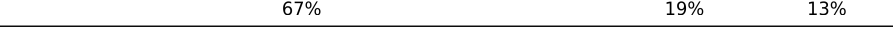
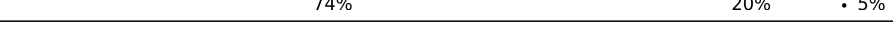
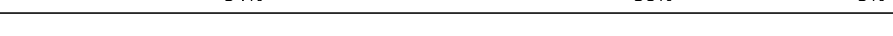
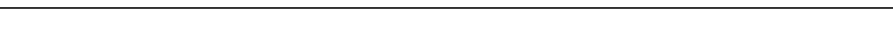
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Mol	Chain	Length	Quality of chain
33	SZ	82	
34	AA	3788	
35	AC	159	
36	AB	119	
37	AL	215	
38	A1	146	
39	A2	127	
40	A4	67	
41	A6	108	
42	A7	120	
43	AN	165	
44	A8	131	
45	A9	140	
46	Aa	150	
47	Ab	112	
48	Ad	87	
49	Ae	51	
50	Af	128	
51	AP	205	
52	Ah	96	
53	Ai	104	
54	AI	221	
55	AJ	283	
56	Ac	92	
57	AK	202	

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Mol	Chain	Length	Quality of chain
58	AM	139	
59	AS	187	
60	AO	148	
61	AQ	219	
62	AR	294	
63	AW	173	
64	AY	190	
65	AT	182	
66	AZ	126	
67	A3	124	
68	A5	257	
69	AD	260	
70	AE	386	
71	AF	411	
72	AG	173	
73	AU	184	
74	AH	190	
75	AV	161	
76	Ag	39	
77	AX	139	
78	A0	162	
79	S9	76	
80	mR	7	

2 Entry composition

There are 80 unique types of molecules in this entry. The entry contains 194758 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 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	S1	120	Total	C	N	O	S	0	0
			985	632	189	162	2		

- Molecule 2 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	S2	41	Total	C	N	O	0	0
			320	208	56	56		

- Molecule 3 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	S3	95	Total	C	N	O	S	0	0
			781	478	169	128	6		

- Molecule 4 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	S4	76	Total	C	N	O	S	0	0
			586	368	102	107	9		

- Molecule 5 is a protein called 40S ribosomal protein S28e.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	S5	59	Total	C	N	O	S	0	0
			465	290	94	80	1		

- Molecule 6 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	S6	43	Total	C	N	O	0	0
			345	213	75	57		

- Molecule 7 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	S7	74	Total	C	N	O	P	0	0
			1571	702	275	521	73		

- Molecule 8 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SA	1608	Total	C	N	O	P	0	0
			34208	15346	6106	11170	1586		

- Molecule 9 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SB	210	Total	C	N	O	S	0	0
			1713	1097	301	303	12		

- Molecule 10 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SC	195	Total	C	N	O	S	0	0
			1538	990	266	273	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SD	157	Total	C	N	O	S	0	0
			1228	782	225	214	7		

- Molecule 12 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SE	185	Total	C	N	O	S	0	0
			1514	962	290	260	2		

- Molecule 13 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SF	257	Total	C	N	O	S	0	0
			2061	1320	377	356	8		

- Molecule 14 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SG	224	Total	C	N	O	S	0	0
			1757	1132	307	309	9		

- Molecule 15 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SH	204	Total	C	N	O	S	0	0
			1651	1046	316	283	6		

- Molecule 16 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SI	180	Total	C	N	O	S	0	0
			1424	893	263	258	10		

- Molecule 17 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SJ	188	Total	C	N	O	S	0	0
			1528	982	264	278	4		

- Molecule 18 is a protein called 40S ribosomal protein S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SK	129	Total	C	N	O	S	0	0
			1037	665	189	178	5		

- Molecule 19 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SL	171	Total	C	N	O	S	0	0
			1383	872	264	243	4		

- Molecule 20 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	SM	138	Total	C	N	O	S	0	0
			1098	704	200	193	1		

- Molecule 21 is a protein called 40S ribosomal protein S20e.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	SN	98	Total	C	N	O	S	0	0
			772	484	135	148	5		

- Molecule 22 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	SO	79	Total	C	N	O	S	0	0
			686	450	116	118	2		

- Molecule 23 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SP	127	Total	C	N	O	S	0	0
			954	591	184	176	3		

- Molecule 24 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	SQ	144	Total	C	N	O	S	0	0
			1129	712	222	193	2		

- Molecule 25 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	SR	98	Total	C	N	O	S	0	0
			746	474	123	145	4		

- Molecule 26 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	SS	128	Total	C	N	O	S	0	0
			1046	657	205	180	4		

- Molecule 27 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	ST	48	Total	C	N	O	S	0	0
			405	252	85	64	4		

- Molecule 28 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	SU	149	Total	C	N	O	S	0	0
			1202	769	220	210	3		

- Molecule 29 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	SV	146	Total	C	N	O	S	0	0
			1206	772	227	200	7		

- Molecule 30 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	SW	95	Total	C	N	O	S	0	0
			785	498	149	135	3		

- Molecule 31 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	SX	96	Total	C	N	O	S	0	0
			776	497	137	138	4		

- Molecule 32 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	SY	154	Total	C	N	O	S	0	0
			1266	811	239	214	2		

- Molecule 33 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	SZ	72	Total	C	N	O	S	0	0
			557	346	102	105	4		

- Molecule 34 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AA	3193	Total	C	N	O	P	0	0
			67884	30446	12053	22224	3161		

- Molecule 35 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AC	151	Total	C	N	O	P	0	0
			3215	1444	589	1034	148		

- Molecule 36 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	AB	118	Total	C	N	O	P	0	0
			2517	1126	457	817	117		

- Molecule 37 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	AL	211	Total	C	N	O	S	0	0
			1761	1119	349	290	3		

- Molecule 38 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	A1	140	Total	C	N	O	S	0	0
			1134	736	204	191	3		

- Molecule 39 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	A2	105	Total	C	N	O	S	0	0
			837	534	152	148	3		

- Molecule 40 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	A4	66	Total	C	N	O	S	0	0
			555	347	116	90	2		

- Molecule 41 is a protein called 60S ribosomal protein L30e.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	A6	98	Total	C	N	O	S	0	0
			740	462	132	139	7		

- Molecule 42 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	A7	96	Total	C	N	O	S	0	0
			793	508	151	129	5		

- Molecule 43 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AN	147	Total	C	N	O	S	0	0
			1210	787	212	205	6		

- Molecule 44 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	A8	125	Total	C	N	O	S	0	0
			1036	660	206	163	7		

- Molecule 45 is a protein called 60S ribosomal protein L35ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	A9	103	Total	C	N	O	S	0	0
			844	543	163	135	3		

- Molecule 46 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Aa	106	Total	C	N	O	S	0	0
			858	530	184	138	6		

- Molecule 47 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	Ab	95	Total	C	N	O	0	0
			756	477	150	129		

- Molecule 48 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Ad	72	Total	C	N	O	S	0	0
			603	395	107	99	2		

- Molecule 49 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Ae	43	Total	C	N	O	S	0	0
			388	243	92	52	1		

- Molecule 50 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Af	51	Total	C	N	O	S	0	0
			413	255	87	66	5		

- Molecule 51 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	AP	204	Total	C	N	O	S	0	0
			1697	1075	351	267	4		

- Molecule 52 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Ah	85	Total	C	N	O	S	0	0
			658	417	127	107	7		

- Molecule 53 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Ai	95	Total	C	N	O	S	0	0
			778	490	152	127	9		

- Molecule 54 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AI	207	Total	C	N	O	S	0	0
			1685	1096	298	286	5		

- Molecule 55 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	AJ	222	Total	C	N	O	S	0	0
			1813	1174	323	309	7		

- Molecule 56 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Ac	89	Total	C	N	O	S	0	0
			709	441	150	113	5		

- Molecule 57 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	AK	201	Total	C	N	O	S	0	0
			1659	1064	311	276	8		

- Molecule 58 is a protein called 60S ribosomal protein L23, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AM	132	Total	C	N	O	S	0	0
			996	631	179	178	8		

- Molecule 59 is a protein called 60S ribosomal protein L18-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AS	186	Total	C	N	O	S	0	0
			1503	958	299	241	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AO	147	Total	C	N	O	S	0	0
			1172	747	232	189	4		

- Molecule 61 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AQ	189	Total	C	N	O	S	0	0
			1544	984	291	261	8		

- Molecule 62 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AR	252	Total	C	N	O	S	0	0
			2049	1301	385	357	6		

- Molecule 63 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AW	170	Total	C	N	O	S	0	0
			1319	824	266	222	7		

- Molecule 64 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AY	101	Total	C	N	O	S	0	0
			796	502	144	144	6		

- Molecule 65 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AT	181	Total	C	N	O	S	0	0
			1509	952	309	244	4		

- Molecule 66 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AZ	121	Total	C	N	O	S	0	0
			1000	626	206	165	3		

- Molecule 67 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	A3	119	Total	C	N	O	S	0	0
			994	635	194	163	2		

- Molecule 68 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	A5	223	Total	C	N	O	S	0	0
			1879	1211	357	306	5		

- Molecule 69 is a protein called 60S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	AD	247	Total	C	N	O	S	0	0
			1866	1166	374	317	9		

- Molecule 70 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	AE	380	Total	C	N	O	S	0	0
			3061	1948	575	521	17		

- Molecule 71 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	AF	390	Total	C	N	O	S	0	0
			3094	1962	594	527	11		

- Molecule 72 is a protein called 60S ribosomal protein L11a.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	AG	124	Total	C	N	O	S	0	0
			1010	636	197	171	6		

- Molecule 73 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	AU	180	Total	C	N	O	S	0	0
			1497	946	289	255	7		

- Molecule 74 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	AH	185	Total	C	N	O	S	0	0
			1475	950	264	255	6		

- Molecule 75 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	AV	155	Total	C	N	O	S	0	0
			1275	814	241	214	6		

- Molecule 76 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Ag	37	Total	C	N	O	S	0	0
			343	210	86	45	2		

- Molecule 77 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	AX	97	Total	C	N	O	S	0	0
			824	548	135	139	2		

- Molecule 78 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	A0	62	Total	C	N	O	S	0	0
			521	336	97	87	1		

- Molecule 79 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	S9	76	Total	C	N	O	P	0	0
			1620	723	295	527	75		

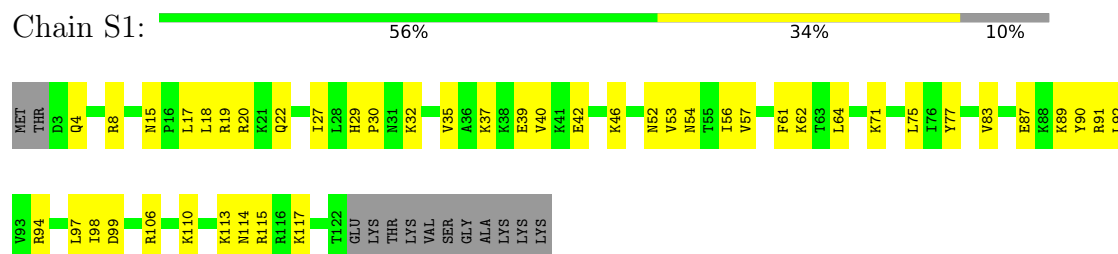
- Molecule 80 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	mR	7	Total	C	N	O	P	0	0
			145	65	21	52	7		

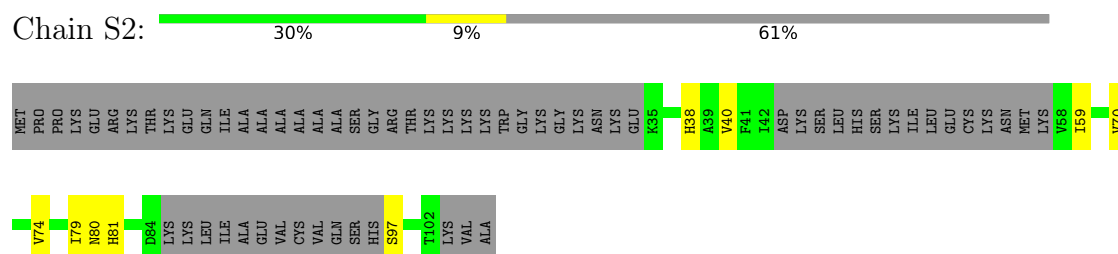
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

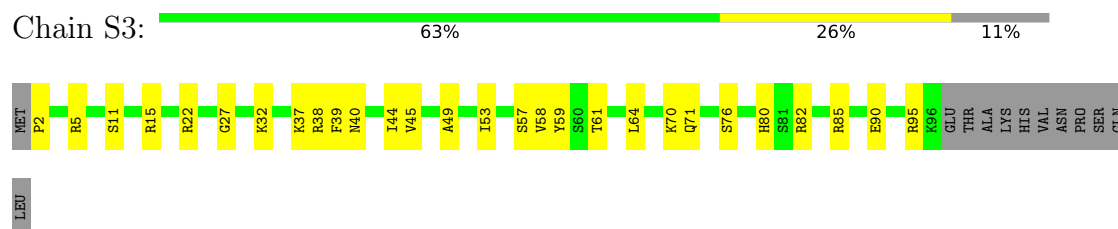
- Molecule 1: 40S ribosomal protein S24



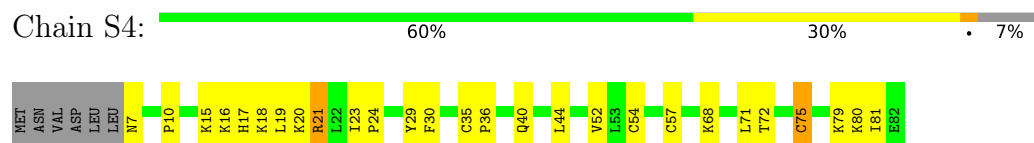
- Molecule 2: 40S ribosomal protein S25



- Molecule 3: 40S ribosomal protein S26



- Molecule 4: 40S ribosomal protein S27

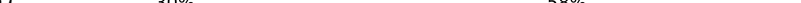


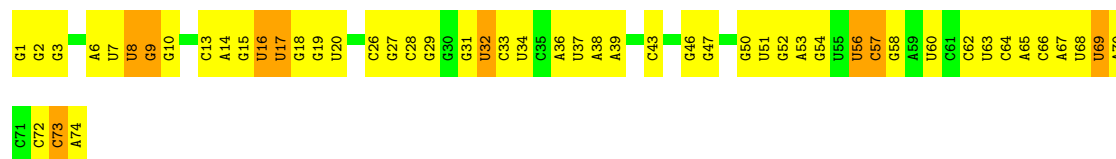
- Molecule 5: 40S ribosomal protein S28e

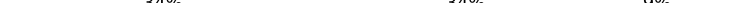
MT1	E2	K3	L6	A7	K8	V9	R15	R19	V25	R26	A27	Q28	F29	K30	GLY	ASP	ASP	SER	GLU	LEU	ALA	G37	R38	F39	L40	L41	R42	P47	V48	D52	I53	L54	A55	L56	R61	L66	A67
-----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

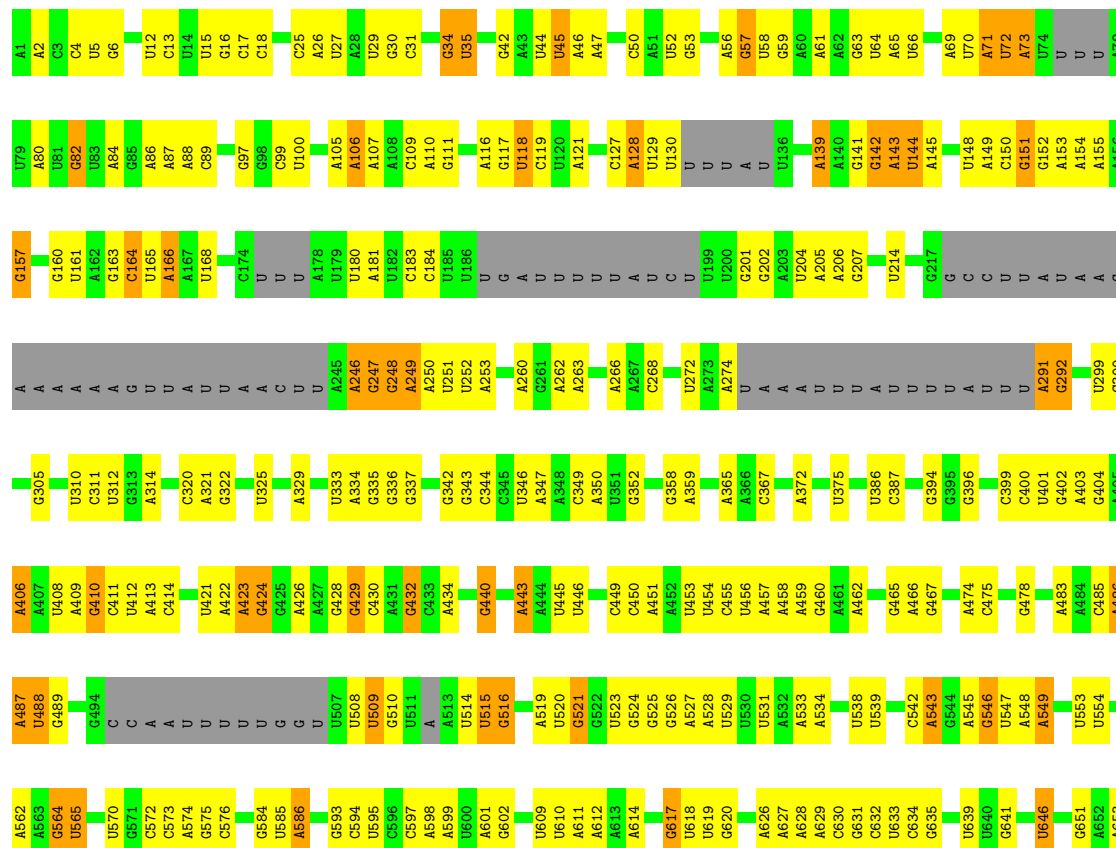
- Chain S6:



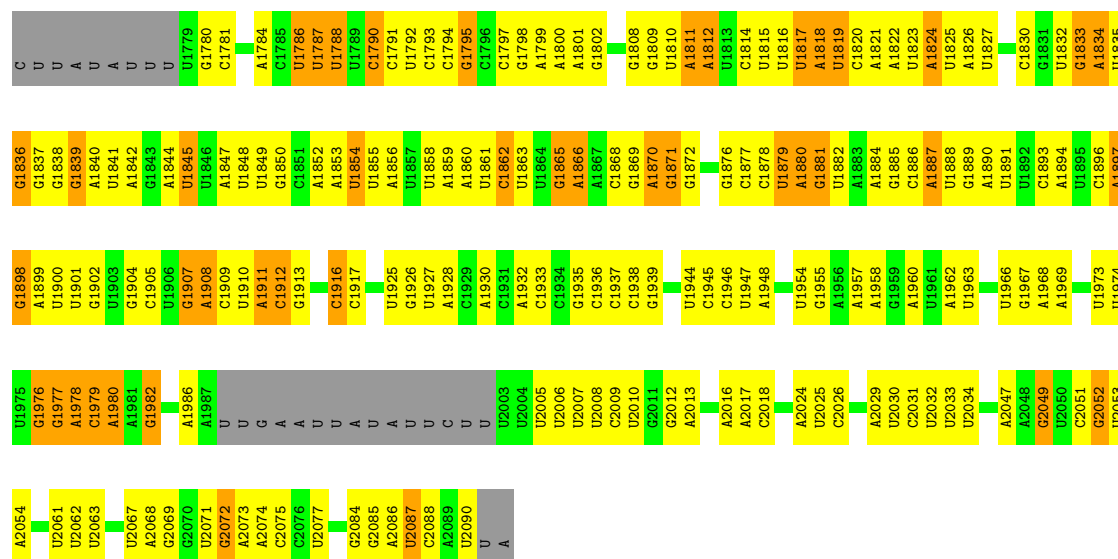
- Chain S7:  30% 58% 12%



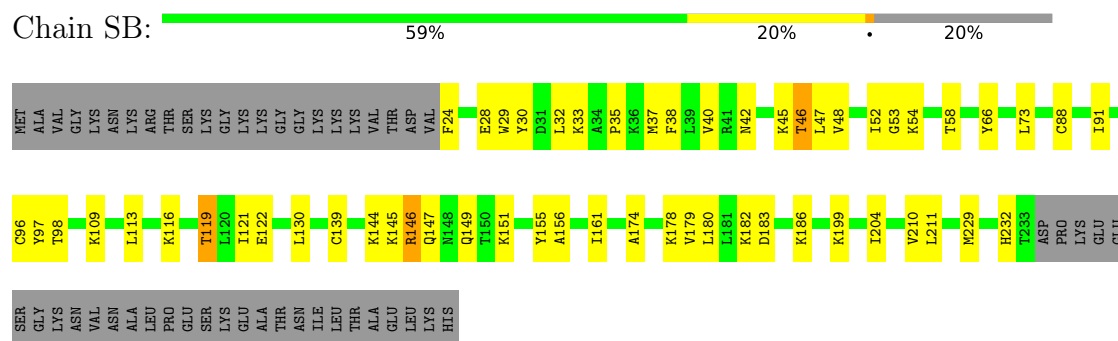
- Chain SA: 



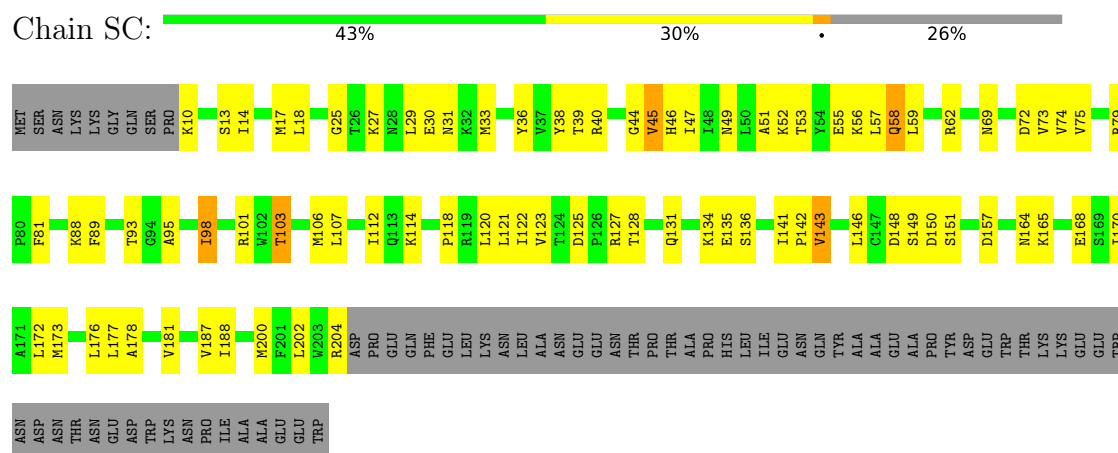
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G1710	U1646	C	A	U	A	G1254	U	U1098	A999	G921	U849	U887	U804	C	U854
U1711	A1647	U	A	U	G	A1258	G1165	U1099	A999	U922	U850	U888	A805	C	U855
G1712	U1648	C	A	U	A	A1258	C1166	A1000	A999	U922	U850	U888	A805	C	U855
C1713	C1649	U	A	U	G	C1260	U1167	G1101	A1001	U924	A851	U888	A805	C	U855
U1714	A1650	C	U	U	A	C1260	U1167	C1102	A1002	G925	A852	U888	A805	C	U855
A1715	C1651	U	U	U	A	A1261	C1169	U1107	C1003	G926	A857	U888	A805	C	U855
C1716	A1652	U	C	U	G	C1262	C1170	U1108	U1004	A927	U858	U888	A805	C	U855
A1717	A1653	C	A	U	G	C1263	U1171	A1109	U1005	U928	U859	U888	A805	C	U855
G1718	G1654	U	A	U	A	A1264	U1172	G1109	U1005	U928	U859	U888	A805	C	U855
U1719	G1655	U	U	U	U	G1265	C1173	G1110	U1005	U928	U859	U888	A805	C	U855
G1720	A1656	U	U	U	U	G1265	C1173	G1111	A1008	U932	U865	U888	A805	C	U855
A1721	A1657	U	U	U	U	C1267	A1177	U1112	A1009	U932	U865	U888	A805	C	U855
U1722	G1658	A	A	U	G	C1267	A1177	U1112	A1010	U932	U865	U888	A805	C	U855
A1723	U1659	A	A	U	A	G1268	A1182	G1116	G1011	A936	U867	U888	A805	C	U855
U1724	U1660	A	A	U	C	U1269	U1183	U1104	U1014	G937	U868	U888	A805	C	U855
A1725	U1661	G	A	U	A	G1270	U1183	U1104	U1014	U938	U869	U888	A805	C	U855
U1726	A1662	A	A	U	G	G1271	A1187	G1119	U1015	A939	U870	U888	A805	C	U855
A1727	A1663	A	A	U	A	A1272	A1187	A1120	U1016	A939	U870	U888	A805	C	U855
U1728	G1664	U	U	U	U	C1273	A1188	A1121	G1017	C941	U876	U888	A805	C	U855
A1729	G1665	C	C	U	U	G1274	A1189	A	U1018	U942	U877	U888	A805	C	U855
C1730	C1666	C	G	U	A	U1275	U1276	G1123	A1022	U943	U878	U888	A805	C	U855
G1731	C1667	C	A	U	A	U1276	G1277	U1124	A1023	G944	U879	U888	A805	C	U855
U1732	C1669	U	U	U	U	G1277	A1193	G	A1024	U944	U880	U888	A805	C	U855
A1733	C1670	U	U	U	A	C1278	A1193	U	A1024	U944	U880	U888	A805	C	U855
G1734	A1673	U	U	U	G	G1279	C1197	U	U1028	U944	U880	U888	A805	C	U855
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U	U1676	C	G	U	C	U1282	U1200	A	G1045	U944	U880	U888	A805	C	U855
U	C1677	C	U	U	U	A1283	G1201	A	U1035	U944	U880	U888	A805	C	U855
A	U1678	A	U	U	U	U1284	U1204	U	A1036	U944	U880	U888	A805	C	U855
U1741	G1679	U	U	U	C	A1285	U1204	U	U1037	U944	U880	U888	A805	C	U855
A1742	U1680	U	C	U	U	U1286	U1204	U	U1038	U944	U880	U888	A805	C	U855
U1745	G1681	G	C	U	U	C1293	G1209	A	A1039	U944	U880	U888	A805	C	U855
A1746	U1682	A	A	U	G	A1294	G1215	A	G1045	U944	U880	U888	A805	C	U855
U1747	U1683	A	C	U	A	A1295	G1215	A	U1039	U944	U880	U888	A805	C	U855
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G1749	U1685	A	A	U	U	A1297	U1218	C	G1049	U944	U880	U888	A805	C	U855
U1750	U1688	C	U	U	C	G1300	U1219	A	A1062	U944	U880	U888	A805	C	U855
A	U1689	U	A	U	U	G1301	U1220	U	A1062	U944	U880	U888	A805	C	U855
U	A1690	A	A	U	C	G1302	G1221	C	A1062	U944	U880	U888	A805	C	U855
A	G1691	U	U	U	U	G1303	G1221	U	A1062	U944	U880	U888	A805	C	U855
U	A1692	U	U	U	U	A1304	G1231	U	A1062	U944	U880	U888	A805	C	U855
A	U1693	U	U	U	U	A1305	A1234	C	A1062	U944	U880	U888	A805	C	U855
U	G1694	U	U	U	U	C1306	G1235	G	A1062	U944	U880	U888	A805	C	U855
U	A1695	G	C	U	A	U1307	G1235	A	A1062	U944	U880	U888	A805	C	U855
U	C1696	U	U	U	U	C1308	A1239	G	A1062	U944	U880	U888	A805	C	U855
G	U1697	U	U	U	U	A1309	A1239	U	A1062	U944	U880	U888	A805	C	U855
A	A1698	U	U	U	U	C1310	A1239	U	A1062	U944	U880	U888	A805	C	U855
U	U1699	U	U	U	U	U1311	A1239	G	A1062	U944	U880	U888	A805	C	U855
U	G1700	C	U	U	U	A1312	A1239	U	A1062	U944	U880	U888	A805	C	U855
C	C1701	A	A	U	A	G1313	A1239	G	A1062	U944	U880	U888	A805	C	U855
U	U1702	C	C	U	C	C1381	A1243	U	A1062	U944	U880	U888	A805	C	U855
U	G1703	U	A	U	A	G1382	A1244	A	A1062	U944	U880	U888	A805	C	U855
U	U1704	U	A	U	A	U1316	U1246	C	A1062	U944	U880	U888	A805	C	U855
G	G1705	C	A	U	U	A1317	G1247	U	A1062	U944	U880	U888	A805	C	U855
A	U1706	U	U	U	U	A1318	G1248	U	A1062	U944	U880	U888	A805	C	U855
U	C1707	A	U	U	U	A1319	G1249	U	A1062	U944	U880	U888	A805	C	U855
G	U1708	U	U	U	U	G1320	G1250	A	A1062	U944	U880	U888	A805	C	U855
						A1321	A1252	A	A1062	U944	U880	U888	A805	C	U855



• Molecule 9: 40S ribosomal protein S3a

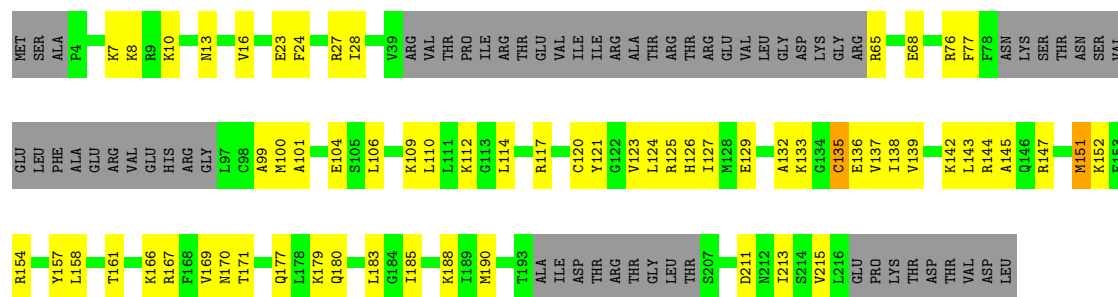


• Molecule 10: 40S ribosomal protein SA

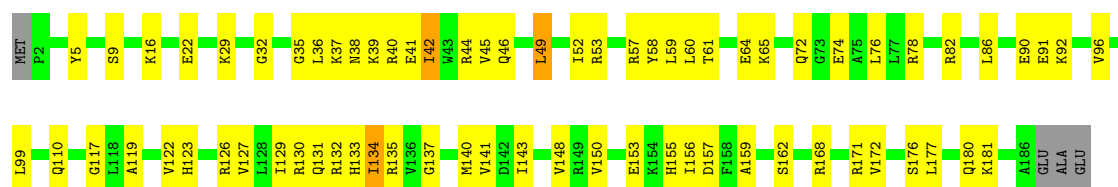


• Molecule 11: 40S ribosomal protein S3

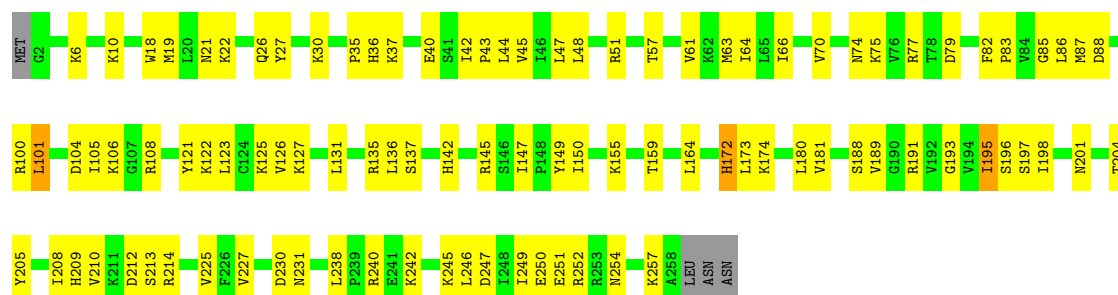




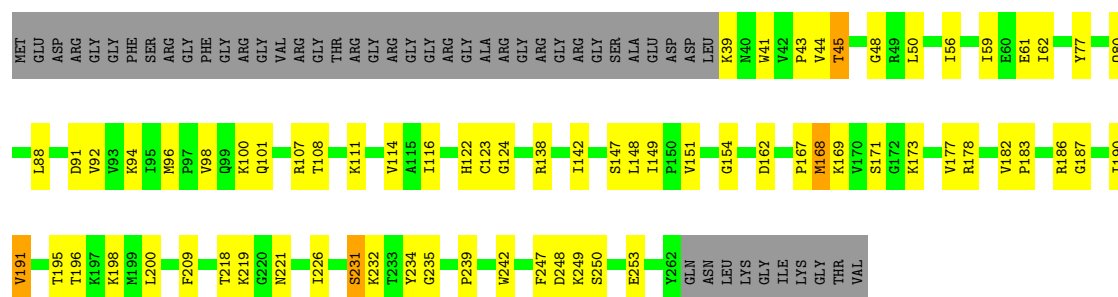
• Molecule 12: 40S ribosomal protein S9



• Molecule 13: 40S ribosomal protein S4



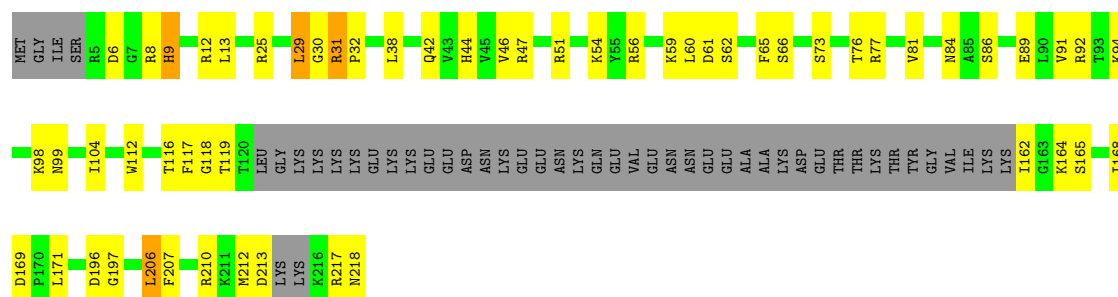
• Molecule 14: 40S ribosomal protein S5



• Molecule 15: 40S ribosomal protein S6

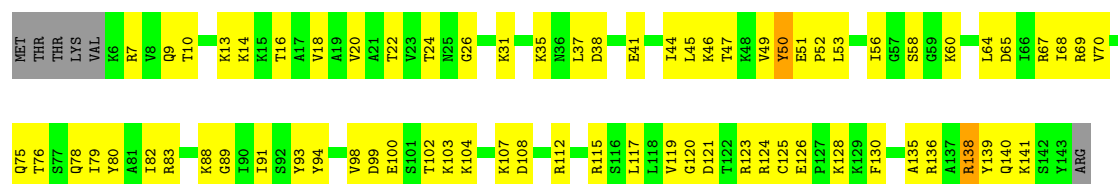


Chain SL:  52% 24% 22%



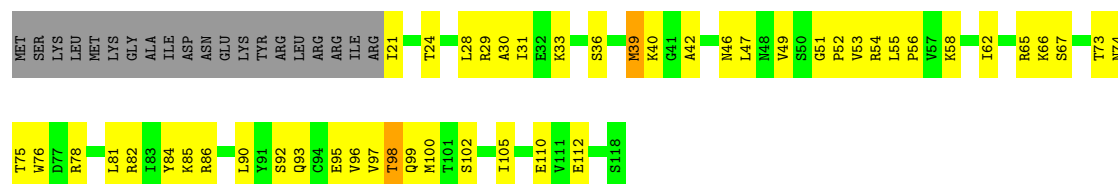
- Molecule 20: 40S ribosomal protein S16

Chain SM:  46% 49%

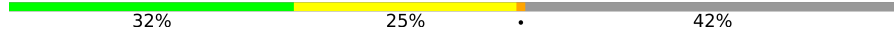


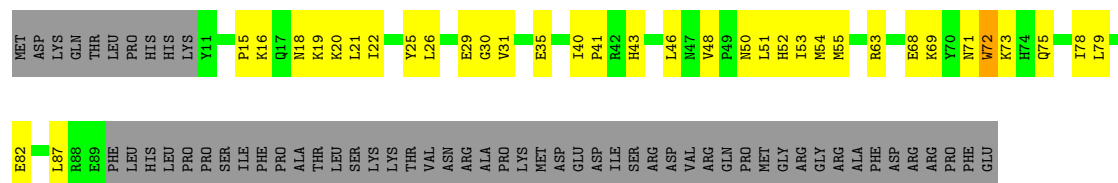
- Molecule 21: 40S ribosomal protein S20e

Chain SN:  42% 39% 17%



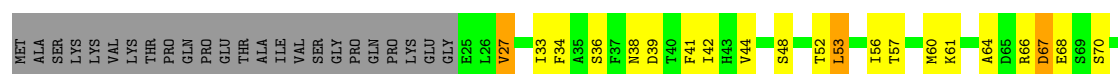
- Molecule 22: 40S ribosomal protein S10

Chain SO:  32% 25% 42%



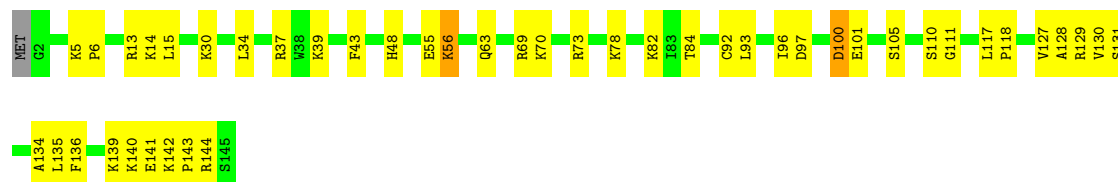
- Molecule 23: 40S ribosomal protein S11

Chain SP:  50% 31% 16%

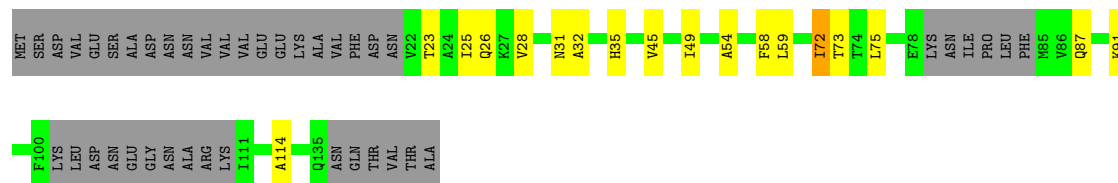




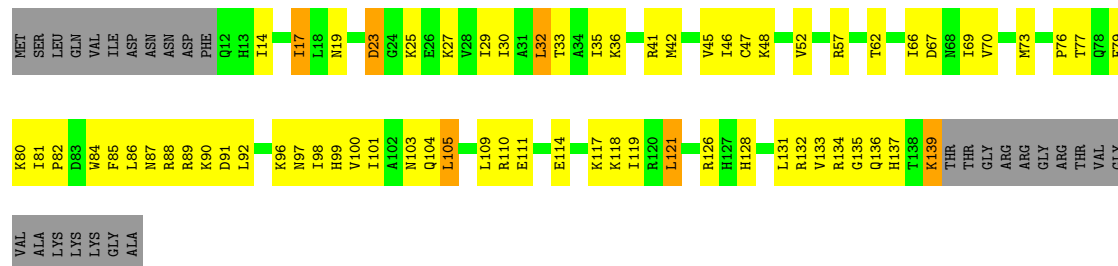
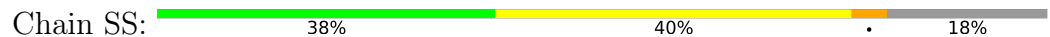
- Molecule 24: 40S ribosomal protein S23



- Molecule 25: 40S ribosomal protein S12



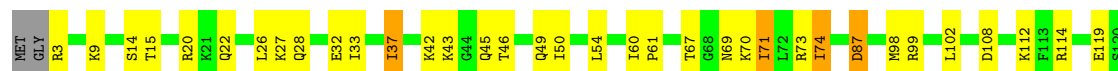
- Molecule 26: 40S ribosomal protein S18

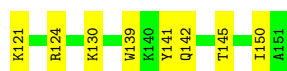


- Molecule 27: 40S ribosomal protein S29



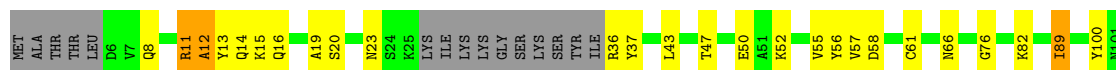
- Molecule 28: 40S ribosomal protein S15





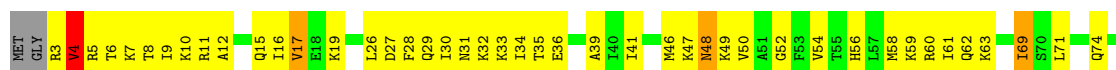
- Molecule 29: 40S ribosomal protein S11

Chain SV: 62% 27% 9%



- Molecule 30: 40S ribosomal protein S17

Chain SW: 31% 36% 31%



- Molecule 31: 40S ribosomal protein S19

Chain SX: 34% 31% 34%



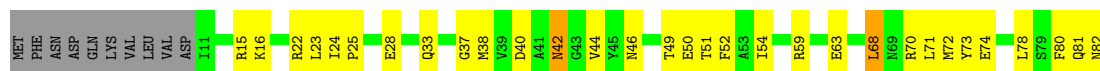
- Molecule 32: 40S ribosomal protein S19

Chain SY: 55% 35% 9%

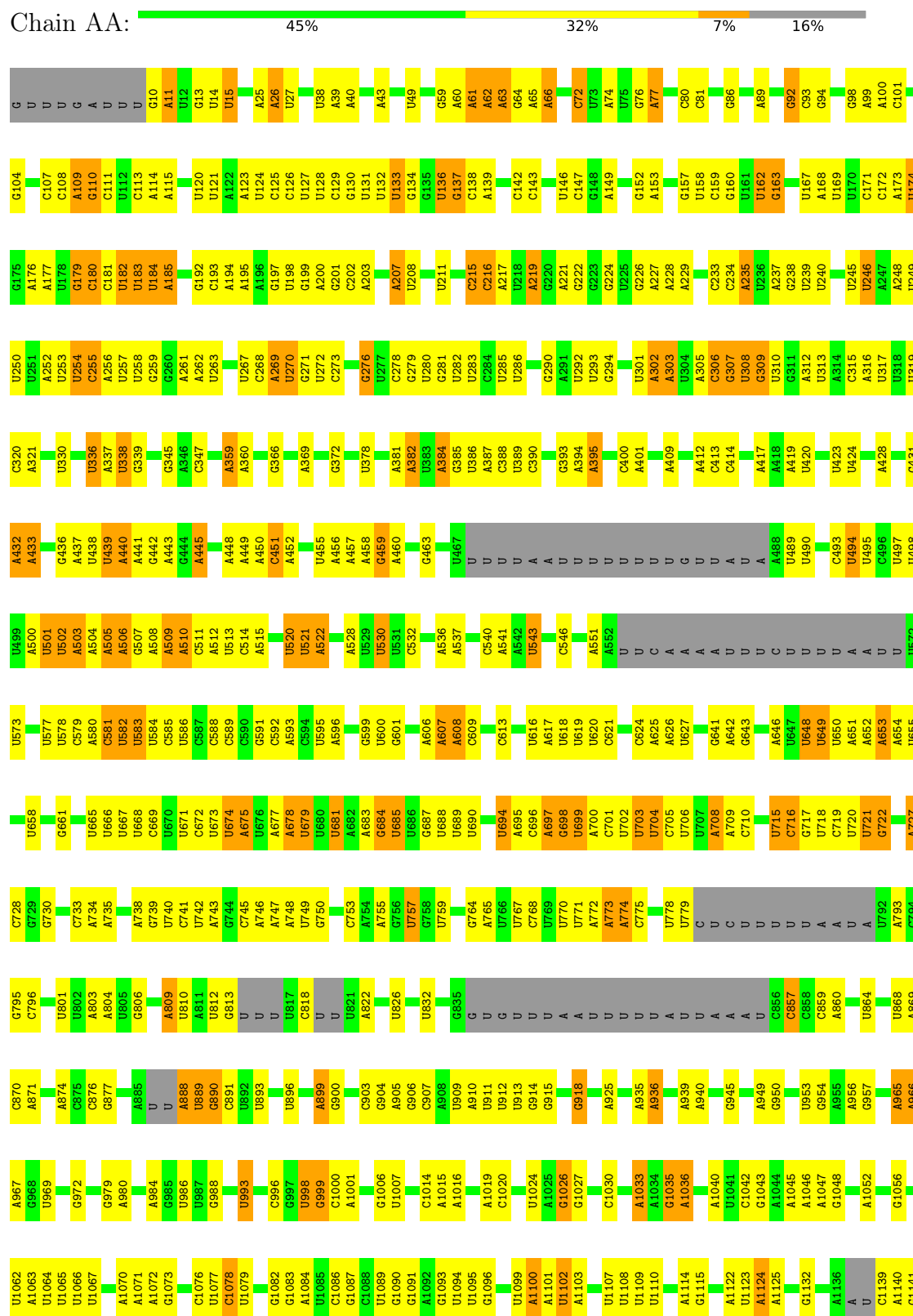


- Molecule 33: 40S ribosomal protein S21

Chain SZ: 50% 35% 12%



● Molecule 34: 28S ribosomal RNA



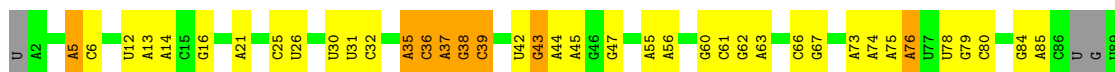






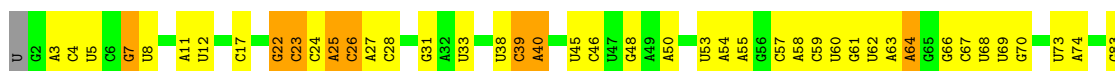
• Molecule 35: 5.8S ribosomal RNA

Chain AC: 50% 35% 10% 5%



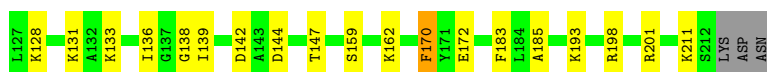
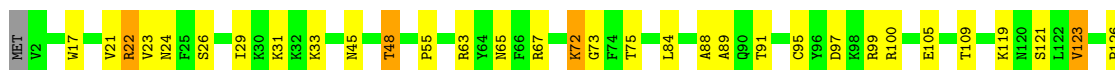
• Molecule 36: 5S ribosomal RNA

Chain AB: 57% 34% 8%



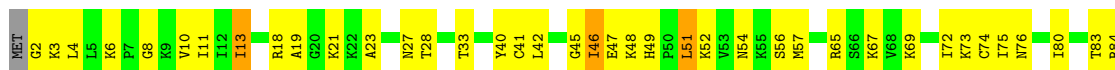
• Molecule 37: 60S ribosomal protein L13

Chain AL: 74% 21% 5%



• Molecule 38: 60S ribosomal protein L27

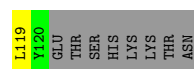
Chain A1: 59% 34% 7%



• Molecule 39: 60S ribosomal protein L28

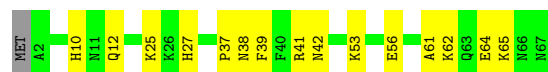
Chain A2: 61% 20% 17%





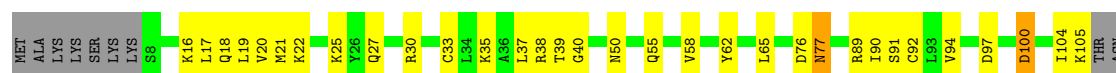
- Molecule 40: 60S ribosomal protein L29

Chain A4: 76% 22% .



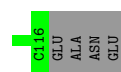
- Molecule 41: 60S ribosomal protein L30e

Chain A6: 61% 28% . 9%



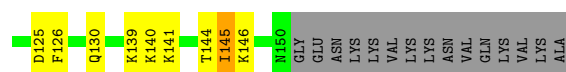
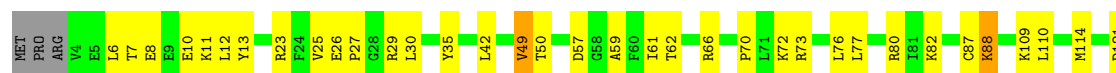
- Molecule 42: 60S ribosomal protein L31

Chain A7: 62% 17% . 20%



- Molecule 43: 60S ribosomal protein L14

Chain AN: 62% 25% . 11%



- Molecule 44: 60S ribosomal protein L32

Chain A8: 58% 35% . 5%

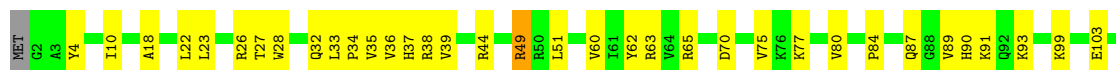


- Chain Af: 31% 8% 60%



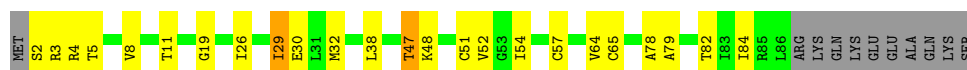
• Molecule 51: Ribosomal protein L15

Chain AP: 66% 32%



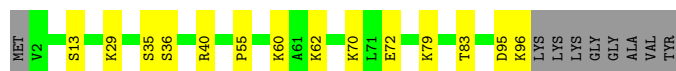
• Molecule 52: Large ribosomal subunit protein eL43

Chain Ah: 64% 23% 11%



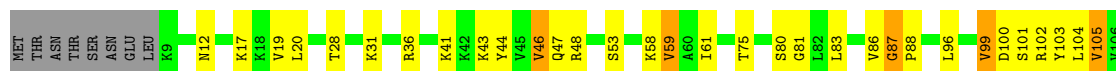
• Molecule 53: Large ribosomal subunit protein eL42

Chain Ai: 78% 13% 9%



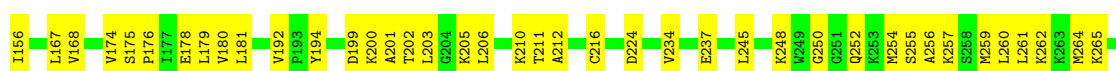
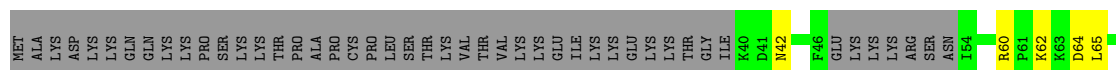
• Molecule 54: 60S ribosomal protein L6

Chain AI: 66% 24% 6%



• Molecule 55: 60S ribosomal protein L7a

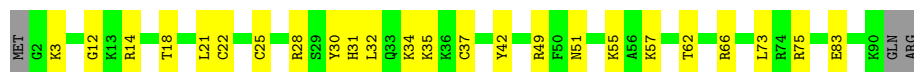
Chain AJ: 51% 26% 22%





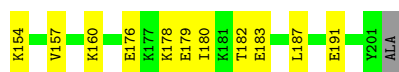
- Molecule 56: Ribosomal protein L37

Chain Ac: 71% 26%



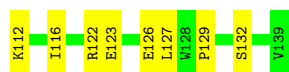
- Molecule 57: 60S ribosomal protein L13

Chain AK: 76% 23%



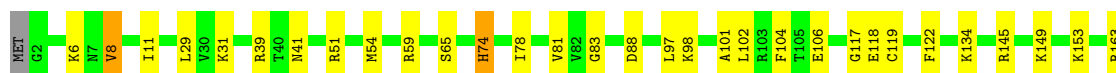
- Molecule 58: 60S ribosomal protein L23, putative

Chain AM: 66% 27% 5%



- Molecule 59: 60S ribosomal protein L18-2

Chain AS: 78% 20%



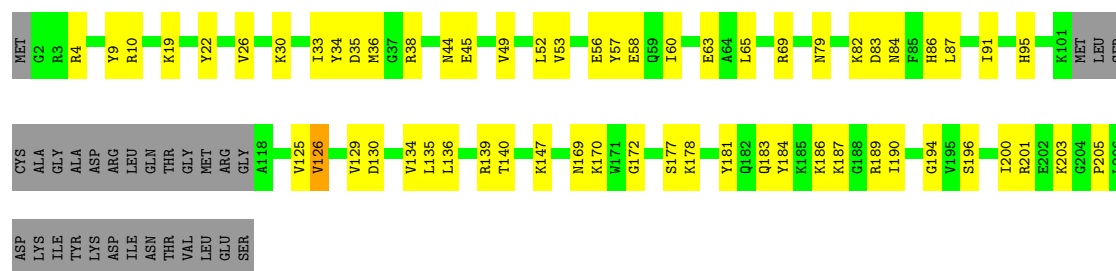
- Molecule 60: 60S ribosomal protein L27a

Chain AO: 81% 16%



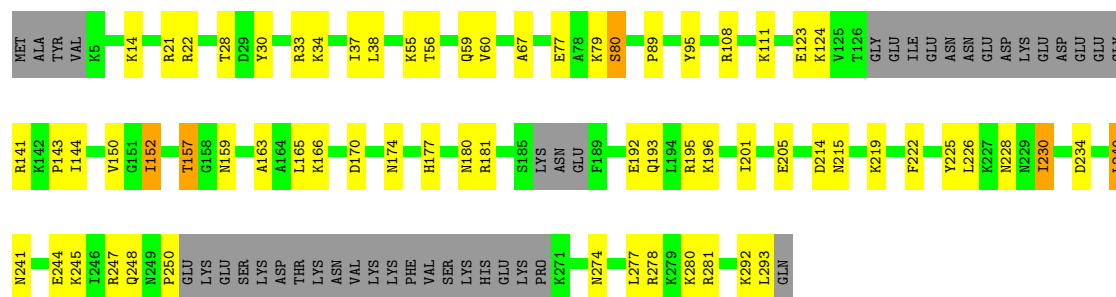
- Molecule 61: 60S ribosomal protein L10

Chain AQ:  59% 27% 14%



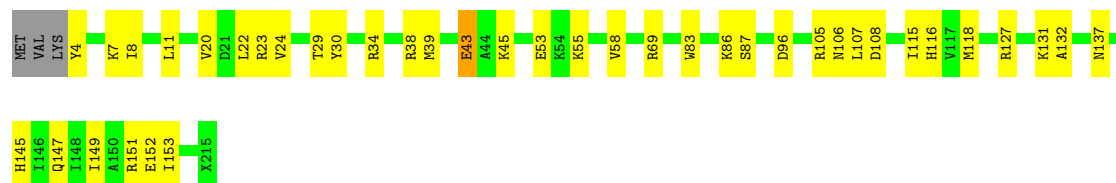
- Molecule 62: 60S ribosomal protein L5

Chain AR:  63% 21% 14%

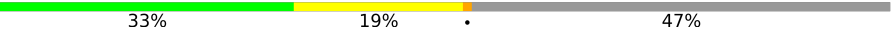


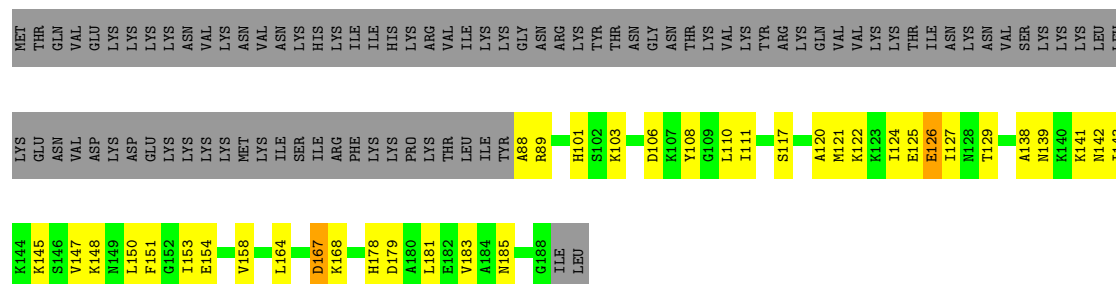
- Molecule 63: 60S ribosomal protein L17

Chain AW:  75% 23% ..



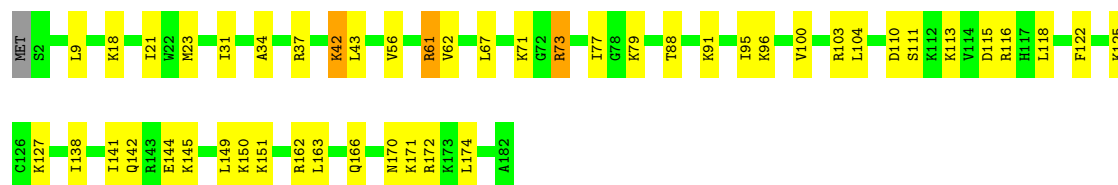
- Molecule 64: 60S ribosomal protein L23

Chain AY:  33% 19% 47%



- Molecule 65: 60S ribosomal protein L19

Chain AT:  73% 25% ..



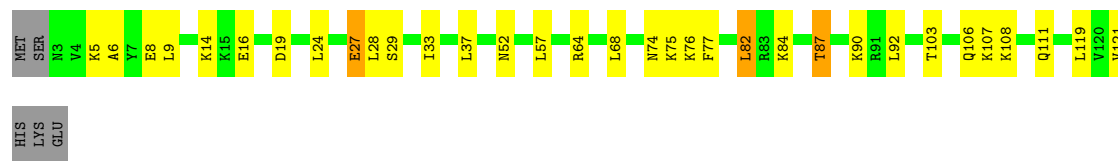
- Molecule 66: 60S ribosomal protein L26

Chain AZ: 67% 26% • •



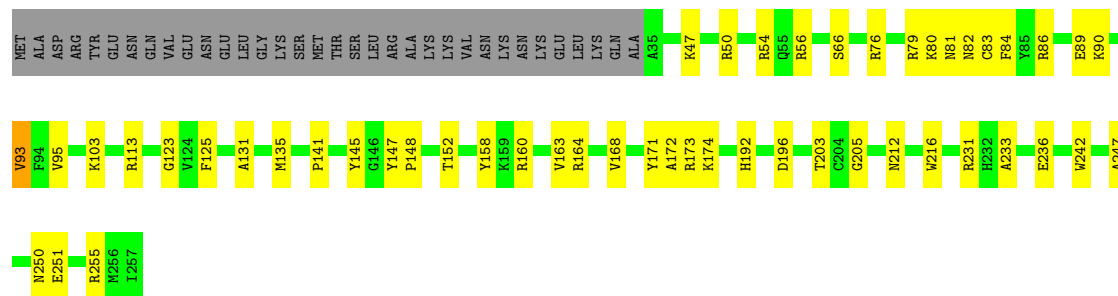
- Molecule 67: 60S ribosomal protein L35

Chain A3: 69% 24% • •



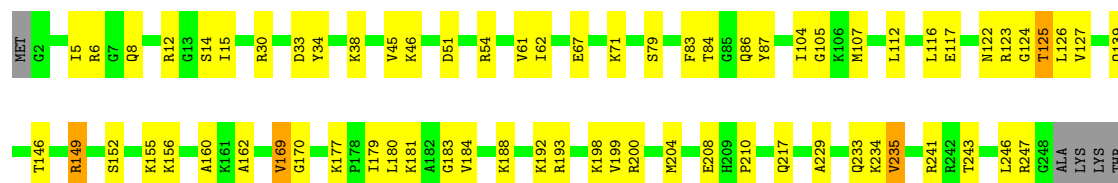
- Molecule 68: 60S ribosomal protein L7

Chain A5: 67% 19% 13%



- Molecule 69: 60S ribosomal protein L2

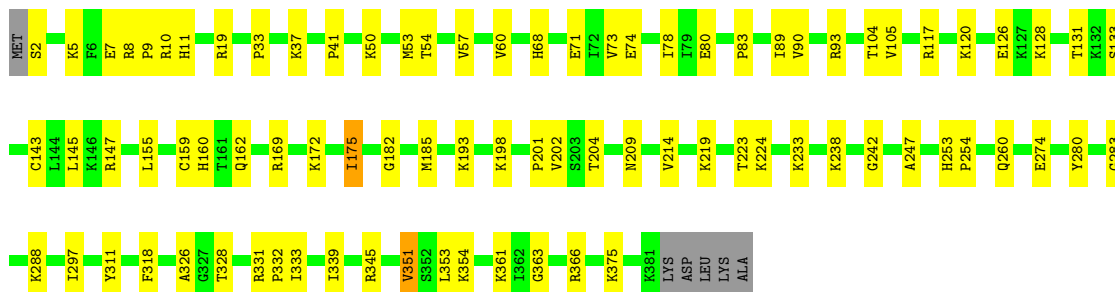
Chain AD: 68% 25% 5% •



LYS
LEU
VAL
GLY
LYS
SER
GLU
GLU

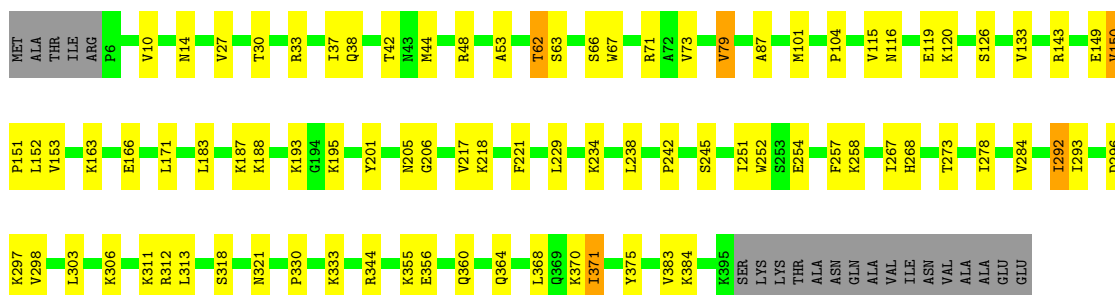
• Molecule 70: 60S ribosomal protein L3

Chain AE:  77% 21% ..

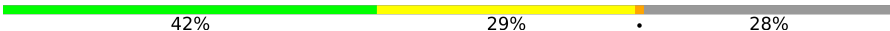


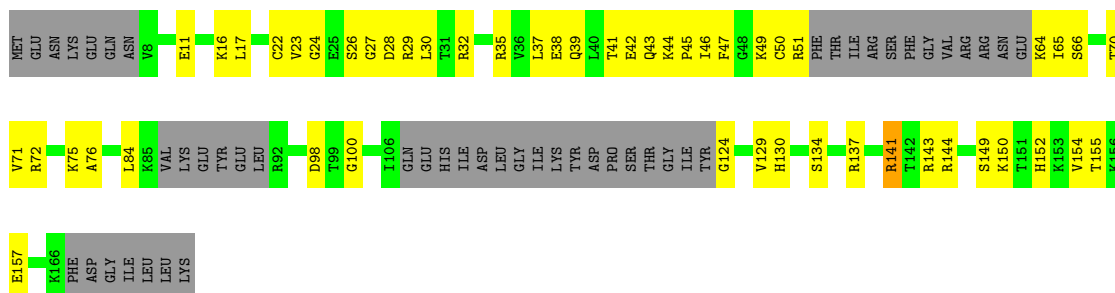
• Molecule 71: 60S ribosomal protein L4

Chain AF:  74% 20% 5%



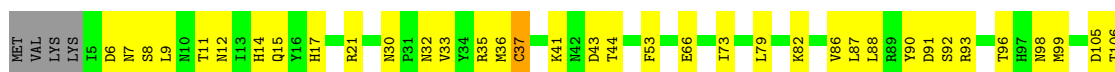
• Molecule 72: 60S ribosomal protein L11a

Chain AG:  42% 29% 28%

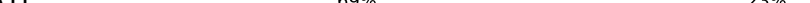


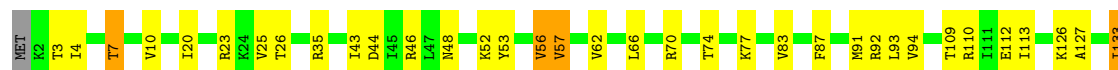
• Molecule 73: 60S ribosomal protein L18a

Chain AU:  67% 30% ..

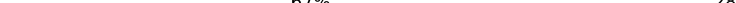


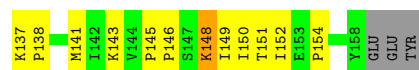
- Molecule 74: 60S ribosomal protein L6

Chain AH:  69% 23% 5%

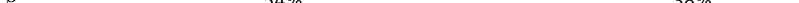


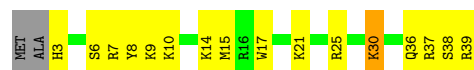
- Molecule 75: 60S ribosomal protein L21

Chain AV:  67% 28% ..

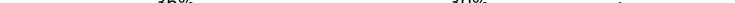


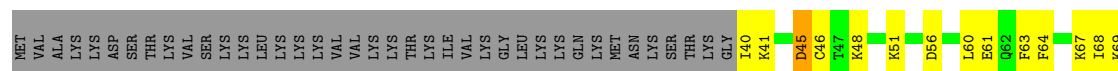
- Molecule 76: 60S ribosomal protein L41

Chain Ag:  54% 38% 5%

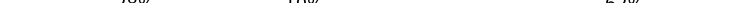


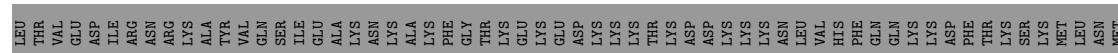
- Molecule 77: 60S ribosomal protein L22

Chain AX: 



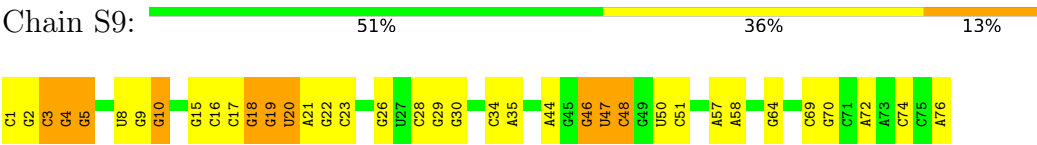
- Molecule 78: 60S ribosomal protein L24

Chain A0:  28% 10% 62%

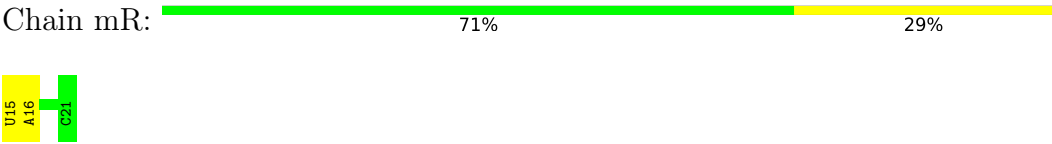


ALA
LYS
SER
LYS
LYS
MET
HIS
LYS
LYS
MET
MET
LYS
LYS

● Molecule 79: P-site tRNA



● Molecule 80: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	261029	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	$\# Z > 5$	RMSZ	$\# Z > 5$
1	S1	0.17	0/998	0.37	0/1321
2	S2	0.12	0/323	0.27	0/435
3	S3	0.21	0/793	0.37	0/1055
4	S4	0.17	0/597	0.45	0/801
5	S5	0.13	0/466	0.38	0/616
6	S6	0.16	0/348	0.51	0/458
7	S7	0.14	0/1754	0.23	0/2732
8	SA	0.20	0/38276	0.29	0/59598
9	SB	0.24	0/1737	0.51	1/2321 (0.0%)
10	SC	0.19	0/1569	0.47	0/2129
11	SD	0.14	0/1240	0.38	0/1652
12	SE	0.20	0/1538	0.45	0/2055
13	SF	0.20	0/2097	0.40	0/2819
14	SG	0.22	0/1799	0.42	0/2429
15	SH	0.16	0/1668	0.42	0/2214
16	SI	0.16	0/1443	0.42	0/1936
17	SJ	0.17	0/1544	0.44	0/2064
18	SK	0.23	0/1054	0.45	0/1411
19	SL	0.22	0/1407	0.44	0/1879
20	SM	0.14	0/1113	0.38	0/1487
21	SN	0.15	0/780	0.41	0/1053
22	SO	0.15	0/705	0.46	0/950
23	SP	0.22	0/966	0.44	0/1295
24	SQ	0.20	0/1149	0.39	0/1532
25	SR	0.09	0/754	0.25	0/1013
26	SS	0.15	0/1062	0.49	0/1425
27	ST	0.14	0/412	0.28	0/544
28	SU	0.24	0/1223	0.39	0/1634
29	SV	0.22	0/1233	0.39	0/1645
30	SW	0.17	0/792	0.50	0/1053
31	SX	0.13	0/787	0.40	0/1050
32	SY	0.15	0/1294	0.38	0/1742
33	SZ	0.20	0/565	0.38	0/758
34	AA	0.27	0/75947	0.32	0/118255

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	AC	0.26	0/3599	0.31	0/5603
36	AB	0.24	0/2816	0.28	0/4388
37	AL	0.22	0/1793	0.39	0/2387
38	A1	0.21	0/1151	0.40	0/1531
39	A2	0.22	0/846	0.42	0/1124
40	A4	0.20	0/564	0.37	0/737
41	A6	0.23	0/748	0.37	0/1001
42	A7	0.21	0/805	0.33	0/1073
43	AN	0.21	0/1226	0.36	0/1632
44	A8	0.25	0/1053	0.45	0/1399
45	A9	0.28	0/864	0.46	0/1160
46	Aa	0.24	0/871	0.32	0/1161
47	Ab	0.21	0/762	0.44	0/1008
48	Ad	0.21	0/611	0.42	0/812
49	Ae	0.22	0/396	0.29	0/521
50	Af	0.23	0/418	0.38	0/556
51	AP	0.26	0/1735	0.46	1/2320 (0.0%)
52	Ah	0.22	0/667	0.34	0/887
53	Ai	0.22	0/788	0.33	0/1032
54	AI	0.22	0/1708	0.41	0/2274
55	AJ	0.22	0/1840	0.47	0/2456
56	Ac	0.25	0/722	0.44	0/951
57	AK	0.23	0/1689	0.34	0/2260
58	AM	0.25	0/1012	0.42	0/1363
59	AS	0.23	0/1531	0.37	0/2040
60	AO	0.24	0/1199	0.37	0/1597
61	AQ	0.19	0/1579	0.34	0/2113
62	AR	0.20	0/2078	0.34	0/2776
63	AW	0.23	0/1244	0.40	0/1663
64	AY	0.22	0/805	0.40	0/1074
65	AT	0.23	0/1525	0.41	0/2016
66	AZ	0.22	0/1012	0.48	0/1339
67	A3	0.21	0/1004	0.35	0/1329
68	A5	0.23	0/1917	0.42	0/2562
69	AD	0.25	0/1901	0.40	0/2544
70	AE	0.23	0/3129	0.33	0/4195
71	AF	0.22	0/3144	0.36	0/4205
72	AG	0.22	0/1020	0.44	0/1349
73	AU	0.23	0/1527	0.35	0/2043
74	AH	0.22	0/1500	0.38	0/2025
75	AV	0.23	0/1300	0.41	0/1732
76	Ag	0.22	0/348	0.44	0/448
77	AX	0.22	0/841	0.50	0/1125

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	A0	0.22	0/533	0.45	0/711
79	S9	0.13	0/1810	0.26	0/2821
80	mR	0.12	0/160	0.22	0/246
All	All	0.23	0/209224	0.35	2/306950 (0.0%)

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
9	SB	0	1
29	SV	0	1
54	AI	0	1
All	All	0	3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	SB	54	LYS	N-CA-C	-9.08	104.27	114.62
51	AP	156	VAL	N-CA-C	-6.95	106.45	113.47

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
54	AI	87	GLY	Peptide
9	SB	53	GLY	Peptide
29	SV	12	ALA	Peptide

5.2 Too-close contacts [i](#)

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	S1	985	0	1076	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	S2	320	0	338	6	0
3	S3	781	0	820	25	0
4	S4	586	0	604	20	0
5	S5	465	0	505	18	0
6	S6	345	0	381	12	0
7	S7	1571	0	797	43	0
8	SA	34208	0	17266	768	0
9	SB	1713	0	1838	32	0
10	SC	1538	0	1600	62	0
11	SD	1228	0	1311	50	0
12	SE	1514	0	1605	49	0
13	SF	2061	0	2200	70	0
14	SG	1757	0	1811	47	0
15	SH	1651	0	1807	70	0
16	SI	1424	0	1471	86	0
17	SJ	1528	0	1680	51	0
18	SK	1037	0	1099	28	0
19	SL	1383	0	1434	39	0
20	SM	1098	0	1183	56	0
21	SN	772	0	813	47	0
22	SO	686	0	695	27	0
23	SP	954	0	997	40	0
24	SQ	1129	0	1196	30	0
25	SR	746	0	754	9	0
26	SS	1046	0	1101	63	0
27	ST	405	0	419	30	0
28	SU	1202	0	1299	41	0
29	SV	1206	0	1239	35	0
30	SW	785	0	858	53	0
31	SX	776	0	832	38	0
32	SY	1266	0	1316	53	0
33	SZ	557	0	558	25	0
34	AA	67884	0	34243	1041	0
35	AC	3215	0	1633	53	0
36	AB	2517	0	1275	44	0
37	AL	1761	0	1896	45	0
38	A1	1134	0	1245	45	0
39	A2	837	0	896	18	0
40	A4	555	0	599	10	0
41	A6	740	0	763	26	0
42	A7	793	0	869	17	0
43	AN	1210	0	1329	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	A8	1036	0	1139	39	0
45	A9	844	0	886	23	0
46	Aa	858	0	912	28	0
47	Ab	756	0	842	19	0
48	Ad	603	0	686	21	0
49	Ae	388	0	421	4	0
50	Af	413	0	452	9	0
51	AP	1697	0	1802	50	0
52	Ah	658	0	727	17	0
53	Ai	778	0	859	10	0
54	AI	1685	0	1849	39	0
55	AJ	1813	0	1985	65	0
56	Ac	709	0	761	21	0
57	AK	1659	0	1782	34	0
58	AM	996	0	1044	25	0
59	AS	1503	0	1636	26	0
60	AO	1172	0	1230	25	0
61	AQ	1544	0	1582	35	0
62	AR	2049	0	2145	50	0
63	AW	1319	0	1303	27	0
64	AY	796	0	850	29	0
65	AT	1509	0	1682	36	0
66	AZ	1000	0	1099	29	0
67	A3	994	0	1121	21	0
68	A5	1879	0	2005	36	0
69	AD	1866	0	1964	52	0
70	AE	3061	0	3205	61	0
71	AF	3094	0	3333	67	0
72	AG	1010	0	1073	37	0
73	AU	1497	0	1556	48	0
74	AH	1475	0	1574	37	0
75	AV	1275	0	1355	31	0
76	Ag	343	0	388	14	0
77	AX	824	0	882	35	0
78	A0	521	0	539	13	0
79	S9	1620	0	827	28	0
80	mR	145	0	74	1	0
All	All	194758	0	145221	3875	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 12.

The worst 5 of 3875 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)
34:AA:11:A:N6	35:AC:154:G:H1	1.40	1.20
50:Af:10:ALA:O	50:Af:14:ASN:HB2	1.57	1.02
34:AA:3636:U:H3	34:AA:3649:G:H1	1.02	1.00
7:S7:8:U:H3	7:S7:14:A:H62	1.06	0.99
34:AA:3641:U:H3	34:AA:3644:G:H1	1.02	0.98

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	S1	118/133 (89%)	116 (98%)	2 (2%)	0	100	100
2	S2	35/105 (33%)	35 (100%)	0	0	100	100
3	S3	93/107 (87%)	84 (90%)	9 (10%)	0	100	100
4	S4	74/82 (90%)	62 (84%)	12 (16%)	0	100	100
5	S5	55/67 (82%)	45 (82%)	9 (16%)	1 (2%)	6	6
6	S6	41/58 (71%)	38 (93%)	2 (5%)	1 (2%)	4	4
9	SB	208/262 (79%)	198 (95%)	9 (4%)	1 (0%)	24	31
10	SC	193/263 (73%)	179 (93%)	13 (7%)	1 (0%)	24	31
11	SD	149/221 (67%)	147 (99%)	2 (1%)	0	100	100
12	SE	183/189 (97%)	172 (94%)	11 (6%)	0	100	100
13	SF	255/261 (98%)	237 (93%)	17 (7%)	1 (0%)	30	38
14	SG	222/272 (82%)	211 (95%)	11 (5%)	0	100	100
15	SH	200/306 (65%)	189 (94%)	11 (6%)	0	100	100
16	SI	176/195 (90%)	165 (94%)	11 (6%)	0	100	100
17	SJ	186/194 (96%)	169 (91%)	16 (9%)	1 (0%)	24	31
18	SK	127/130 (98%)	117 (92%)	9 (7%)	1 (1%)	16	20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	SL	165/218 (76%)	151 (92%)	13 (8%)	1 (1%)	21	27
20	SM	136/144 (94%)	130 (96%)	5 (4%)	1 (1%)	18	23
21	SN	96/118 (81%)	92 (96%)	4 (4%)	0	100	100
22	SO	77/137 (56%)	71 (92%)	5 (6%)	1 (1%)	9	10
23	SP	125/151 (83%)	115 (92%)	10 (8%)	0	100	100
24	SQ	142/145 (98%)	135 (95%)	7 (5%)	0	100	100
25	SR	92/141 (65%)	86 (94%)	6 (6%)	0	100	100
26	SS	126/156 (81%)	110 (87%)	14 (11%)	2 (2%)	7	7
27	ST	46/54 (85%)	45 (98%)	1 (2%)	0	100	100
28	SU	147/151 (97%)	137 (93%)	10 (7%)	0	100	100
29	SV	142/161 (88%)	135 (95%)	6 (4%)	1 (1%)	18	23
30	SW	91/137 (66%)	79 (87%)	9 (10%)	3 (3%)	3	2
31	SX	92/145 (63%)	84 (91%)	8 (9%)	0	100	100
32	SY	152/170 (89%)	146 (96%)	6 (4%)	0	100	100
33	SZ	70/82 (85%)	66 (94%)	4 (6%)	0	100	100
37	AL	209/215 (97%)	202 (97%)	7 (3%)	0	100	100
38	A1	136/146 (93%)	124 (91%)	11 (8%)	1 (1%)	18	23
39	A2	97/127 (76%)	93 (96%)	3 (3%)	1 (1%)	12	15
40	A4	64/67 (96%)	60 (94%)	4 (6%)	0	100	100
41	A6	96/108 (89%)	92 (96%)	4 (4%)	0	100	100
42	A7	92/120 (77%)	91 (99%)	1 (1%)	0	100	100
43	AN	145/165 (88%)	135 (93%)	10 (7%)	0	100	100
44	A8	123/131 (94%)	113 (92%)	10 (8%)	0	100	100
45	A9	101/140 (72%)	91 (90%)	10 (10%)	0	100	100
46	Aa	104/150 (69%)	98 (94%)	6 (6%)	0	100	100
47	Ab	91/112 (81%)	83 (91%)	7 (8%)	1 (1%)	11	13
48	Ad	68/87 (78%)	67 (98%)	1 (2%)	0	100	100
49	Ae	39/51 (76%)	38 (97%)	1 (3%)	0	100	100
50	Af	49/128 (38%)	45 (92%)	4 (8%)	0	100	100
51	AP	202/205 (98%)	182 (90%)	18 (9%)	2 (1%)	12	15
52	Ah	83/96 (86%)	80 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	Ai	93/104 (89%)	87 (94%)	6 (6%)	0	100	100
54	AI	203/221 (92%)	190 (94%)	12 (6%)	1 (0%)	24	31
55	AJ	216/283 (76%)	209 (97%)	6 (3%)	1 (0%)	24	31
56	Ac	87/92 (95%)	80 (92%)	7 (8%)	0	100	100
57	AK	199/202 (98%)	194 (98%)	4 (2%)	1 (0%)	24	31
58	AM	130/139 (94%)	124 (95%)	5 (4%)	1 (1%)	16	20
59	AS	184/187 (98%)	177 (96%)	6 (3%)	1 (0%)	24	31
60	AO	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
61	AQ	185/219 (84%)	174 (94%)	9 (5%)	2 (1%)	11	13
62	AR	244/294 (83%)	236 (97%)	7 (3%)	1 (0%)	30	38
63	AW	149/173 (86%)	143 (96%)	6 (4%)	0	100	100
64	AY	99/190 (52%)	96 (97%)	3 (3%)	0	100	100
65	AT	179/182 (98%)	177 (99%)	2 (1%)	0	100	100
66	AZ	119/126 (94%)	115 (97%)	4 (3%)	0	100	100
67	A3	117/124 (94%)	109 (93%)	8 (7%)	0	100	100
68	A5	221/257 (86%)	205 (93%)	16 (7%)	0	100	100
69	AD	245/260 (94%)	231 (94%)	12 (5%)	2 (1%)	16	20
70	AE	378/386 (98%)	364 (96%)	13 (3%)	1 (0%)	36	46
71	AF	388/411 (94%)	373 (96%)	14 (4%)	1 (0%)	36	46
72	AG	116/173 (67%)	106 (91%)	8 (7%)	2 (2%)	7	7
73	AU	178/184 (97%)	171 (96%)	6 (3%)	1 (1%)	21	27
74	AH	183/190 (96%)	169 (92%)	14 (8%)	0	100	100
75	AV	153/161 (95%)	148 (97%)	5 (3%)	0	100	100
76	Ag	35/39 (90%)	28 (80%)	7 (20%)	0	100	100
77	AX	95/139 (68%)	92 (97%)	3 (3%)	0	100	100
78	A0	60/162 (37%)	58 (97%)	2 (3%)	0	100	100
All	All	10114/12049 (84%)	9533 (94%)	545 (5%)	36 (0%)	31	38

5 of 36 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	SB	146	ARG
17	SJ	112	ILE

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Mol	Chain	Res	Type
19	SL	168	ILE
20	SM	41	GLU
26	SS	101	ILE

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	S1	104/115 (90%)	102 (98%)	2 (2%)	50	69
2	S2	35/88 (40%)	35 (100%)	0	100	100
3	S3	87/98 (89%)	84 (97%)	3 (3%)	32	49
4	S4	70/76 (92%)	67 (96%)	3 (4%)	26	39
5	S5	48/54 (89%)	47 (98%)	1 (2%)	47	66
6	S6	36/47 (77%)	34 (94%)	2 (6%)	19	28
9	SB	195/238 (82%)	184 (94%)	11 (6%)	19	28
10	SC	167/227 (74%)	160 (96%)	7 (4%)	26	40
11	SD	132/188 (70%)	122 (92%)	10 (8%)	12	16
12	SE	161/167 (96%)	152 (94%)	9 (6%)	19	28
13	SF	233/237 (98%)	219 (94%)	14 (6%)	17	25
14	SG	191/222 (86%)	180 (94%)	11 (6%)	18	26
15	SH	182/279 (65%)	175 (96%)	7 (4%)	29	44
16	SI	154/165 (93%)	148 (96%)	6 (4%)	28	43
17	SJ	177/183 (97%)	167 (94%)	10 (6%)	19	28
18	SK	115/116 (99%)	106 (92%)	9 (8%)	11	16
19	SL	151/193 (78%)	142 (94%)	9 (6%)	17	25
20	SM	116/122 (95%)	112 (97%)	4 (3%)	32	49
21	SN	91/109 (84%)	88 (97%)	3 (3%)	33	50
22	SO	76/129 (59%)	71 (93%)	5 (7%)	15	21
23	SP	99/119 (83%)	94 (95%)	5 (5%)	21	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	SQ	120/121 (99%)	117 (98%)	3 (2%)	42	60
25	SR	83/121 (69%)	80 (96%)	3 (4%)	31	47
26	SS	114/136 (84%)	102 (90%)	12 (10%)	6	8
27	ST	43/48 (90%)	42 (98%)	1 (2%)	44	63
28	SU	132/133 (99%)	128 (97%)	4 (3%)	36	53
29	SV	131/144 (91%)	125 (95%)	6 (5%)	24	36
30	SW	86/127 (68%)	84 (98%)	2 (2%)	44	63
31	SX	88/130 (68%)	86 (98%)	2 (2%)	44	63
32	SY	137/151 (91%)	130 (95%)	7 (5%)	21	32
33	SZ	60/70 (86%)	55 (92%)	5 (8%)	10	14
37	AL	190/194 (98%)	184 (97%)	6 (3%)	34	51
38	A1	127/132 (96%)	120 (94%)	7 (6%)	19	28
39	A2	98/118 (83%)	95 (97%)	3 (3%)	35	52
40	A4	60/61 (98%)	60 (100%)	0	100	100
41	A6	83/92 (90%)	79 (95%)	4 (5%)	23	35
42	A7	90/112 (80%)	87 (97%)	3 (3%)	33	50
43	AN	136/152 (90%)	131 (96%)	5 (4%)	30	45
44	A8	114/120 (95%)	107 (94%)	7 (6%)	17	24
45	A9	90/127 (71%)	87 (97%)	3 (3%)	33	50
46	Aa	89/128 (70%)	84 (94%)	5 (6%)	19	28
47	Ab	82/97 (84%)	78 (95%)	4 (5%)	22	34
48	Ad	69/83 (83%)	66 (96%)	3 (4%)	26	39
49	Ae	40/48 (83%)	40 (100%)	0	100	100
50	Af	45/114 (40%)	44 (98%)	1 (2%)	45	65
51	AP	179/180 (99%)	170 (95%)	9 (5%)	22	33
52	Ah	70/80 (88%)	65 (93%)	5 (7%)	13	19
53	Ai	87/93 (94%)	85 (98%)	2 (2%)	44	63
54	AI	189/203 (93%)	177 (94%)	12 (6%)	16	23
55	AJ	204/260 (78%)	197 (97%)	7 (3%)	32	49
56	Ac	74/77 (96%)	73 (99%)	1 (1%)	59	76
57	AK	181/182 (100%)	175 (97%)	6 (3%)	33	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	AM	106/110 (96%)	100 (94%)	6 (6%)	18	27
59	AS	158/159 (99%)	152 (96%)	6 (4%)	29	44
60	AO	121/122 (99%)	118 (98%)	3 (2%)	42	60
61	AQ	165/190 (87%)	161 (98%)	4 (2%)	43	62
62	AR	215/254 (85%)	207 (96%)	8 (4%)	30	45
63	AW	128/131 (98%)	123 (96%)	5 (4%)	28	43
64	AY	90/177 (51%)	83 (92%)	7 (8%)	11	16
65	AT	162/163 (99%)	152 (94%)	10 (6%)	16	24
66	AZ	111/115 (96%)	105 (95%)	6 (5%)	20	29
67	A3	110/115 (96%)	106 (96%)	4 (4%)	31	47
68	A5	201/231 (87%)	196 (98%)	5 (2%)	42	60
69	AD	191/202 (95%)	185 (97%)	6 (3%)	35	52
70	AE	335/340 (98%)	325 (97%)	10 (3%)	36	53
71	AF	336/352 (96%)	325 (97%)	11 (3%)	33	50
72	AG	110/155 (71%)	104 (94%)	6 (6%)	19	28
73	AU	162/166 (98%)	156 (96%)	6 (4%)	30	45
74	AH	168/173 (97%)	153 (91%)	15 (9%)	9	12
75	AV	140/144 (97%)	130 (93%)	10 (7%)	13	19
76	Ag	34/35 (97%)	31 (91%)	3 (9%)	9	12
77	AX	92/131 (70%)	83 (90%)	9 (10%)	7	10
78	A0	53/146 (36%)	52 (98%)	1 (2%)	50	69
All	All	9099/10617 (86%)	8689 (96%)	410 (4%)	26	37

5 of 410 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
51	AP	80	VAL
61	AQ	126	VAL
76	Ag	38	SER
52	Ah	47	THR
55	AJ	192	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 93 such sidechains are listed below:

Mol	Chain	Res	Type
55	AJ	240	ASN
62	AR	114	ASN
56	Ac	31	HIS
59	AS	18	HIS
65	AT	170	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	AA	3163/3788 (83%)	607 (19%)	69 (2%)
35	AC	148/159 (93%)	31 (20%)	5 (3%)
36	AB	117/119 (98%)	20 (17%)	3 (2%)
7	S7	73/74 (98%)	24 (32%)	0
79	S9	75/76 (98%)	15 (20%)	2 (2%)
8	SA	1588/2092 (75%)	355 (22%)	28 (1%)
80	mR	6/7 (85%)	1 (16%)	0
All	All	5170/6315 (81%)	1053 (20%)	107 (2%)

5 of 1053 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	S7	8	U
7	S7	9	G
7	S7	10	G
7	S7	16	U
7	S7	17	U

5 of 107 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	AA	721	U
34	AA	1841	U
35	AC	134	G
34	AA	859	C
34	AA	1222	U

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 oligosaccharides 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
63	AW	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AW	154:ASN	C	197:UNK	N	31.42

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-44916. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis ⓘ

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.