



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 03:10 PM BST

PDB ID : 4UG0
EMDB ID: : EMD-2938
Title : STRUCTURE OF THE HUMAN 80S RIBOSOME
Authors : Khatter, H.; Myasnikov, A.G.; Natchiar, S.K.; Klaholz, B.P.
Deposited on : 2015-03-20
Resolution : unknown (reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

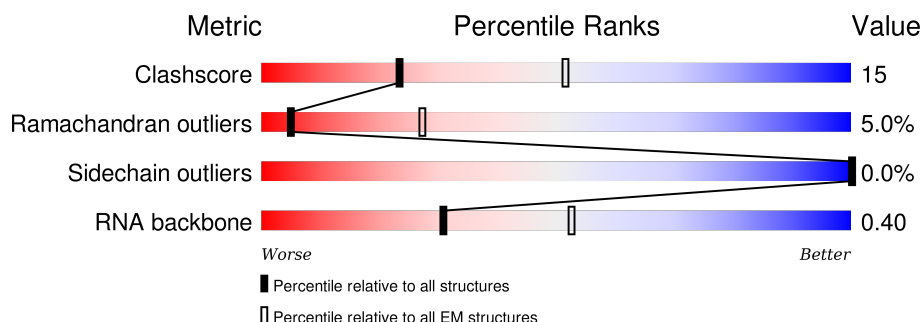
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is unknown.

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	L5	5070	<div> <div>31%</div> <div>30%</div> <div>13%</div> <div>26%</div> </div>
2	L7	121	<div> <div>57%</div> <div>35%</div> <div>7%</div> <div>.</div> </div>
3	L8	157	<div> <div>50%</div> <div>37%</div> <div>12%</div> <div>.</div> </div>
4	LA	257	<div> <div>60%</div> <div>34%</div> <div>.</div> <div>.</div> </div>
5	LB	403	<div> <div>61%</div> <div>36%</div> <div>.</div> </div>
6	LC	427	<div> <div>52%</div> <div>32%</div> <div>.</div> <div>14%</div> </div>
7	LD	297	<div> <div>66%</div> <div>30%</div> <div>.</div> <div>.</div> </div>
8	LE	288	<div> <div>49%</div> <div>31%</div> <div>.</div> <div>16%</div> </div>

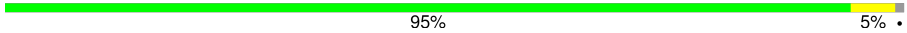
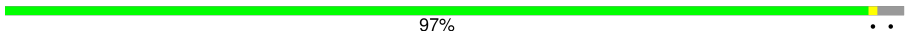
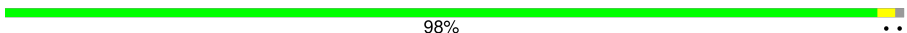












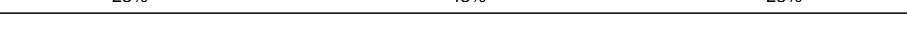









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Mol	Chain	Length	Quality of chain
9	LF	248	
10	LG	266	
11	LH	192	
12	LI	214	
13	LJ	178	
14	LL	211	
15	LM	215	
16	LN	204	
17	LO	203	
18	LP	184	
19	LQ	188	
20	LR	196	
21	LS	176	
22	LT	160	
23	LU	128	
24	LV	140	
25	LW	157	
26	LX	156	
27	LY	145	
28	LZ	136	
29	La	148	
30	Lb	159	
31	Lc	115	
32	Ld	125	
33	Le	135	


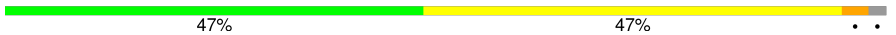











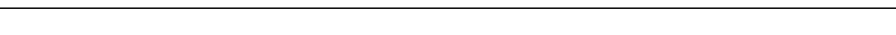

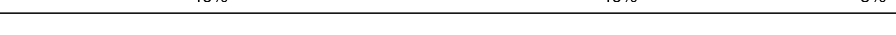





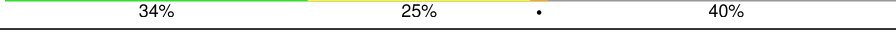
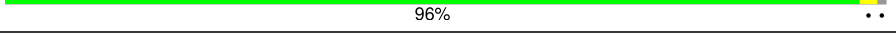
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Mol	Chain	Length	Quality of chain
34	Lf	110	
35	Lg	117	
36	Lh	123	
37	Li	105	
38	Lj	97	
39	Lk	70	
40	Ll	51	
41	Lm	128	
42	Ln	25	
43	Lo	106	
44	Lp	92	
45	Lr	137	
46	Lz	217	
47	S2	1869	
48	S6	75	
49	SA	295	
50	SB	264	
51	SD	243	
52	SE	263	
53	SF	204	
54	SH	194	
55	SI	208	
56	SK	165	
57	SL	158	
58	SP	145	

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Mol	Chain	Length	Quality of chain
59	SQ	146	
60	SR	135	
61	SS	152	
62	ST	145	
63	SU	119	
64	SV	83	
65	SX	143	
66	Sa	115	
67	Sc	69	
68	Sd	56	
69	Sf	156	
70	Sg	317	
71	SC	293	
72	SG	249	
73	SJ	194	
74	SM	132	
75	SN	151	
76	SO	151	
77	SW	130	
78	SY	133	
79	SZ	125	
80	Sb	84	
81	Se	59	

2 Entry composition

There are 83 unique types of molecules in this entry. The entry contains 218776 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 RNA (5070-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L5	3776	Total	C	N	O	P	0	0
			80184	35672	14597	26140	3775		

- Molecule 2 is a RNA chain called RNA (121-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 3 is a RNA chain called RNA (157-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 4 is a protein called 60S RIBOSOMAL PROTEIN L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LA	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 5 is a protein called 60S RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LB	402	Total	C	N	O	S	0	0
			3238	2060	608	556	14		

- Molecule 6 is a protein called 60S RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LC	367	Total	C	N	O	S	0	0
			2919	1835	582	488	14		

- Molecule 7 is a protein called 60S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LD	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 8 is a protein called 60S RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LE	242	Total	C	N	O	S	0	0
			1958	1257	372	325	4		

- Molecule 9 is a protein called 60S RIBOSOMAL PROTEIN L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 10 is a protein called 60S RIBOSOMAL PROTEIN L7A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LG	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		

- Molecule 11 is a protein called 60S RIBOSOMAL PROTEIN L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LH	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 12 is a protein called 60S RIBOSOMAL PROTEIN L10-LIKE.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LI	213	Total	C	N	O	S	0	0
			1711	1082	329	285	15		

- Molecule 13 is a protein called 60S RIBOSOMAL PROTEIN L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LJ	176	Total	C	N	O	S	0	0
			1410	888	263	253	6		

- Molecule 14 is a protein called 60S RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LL	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 15 is a protein called 60S RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LM	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	LN	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	LO	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 18 is a protein called 60S RIBOSOMAL PROTEIN L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LP	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	LQ	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	LR	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		

- Molecule 21 is a protein called 60S RIBOSOMAL PROTEIN L18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 22 is a protein called 60S RIBOSOMAL PROTEIN L21.

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

- Molecule 23 is a protein called 60S RIBOSOMAL PROTEIN L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LU	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 24 is a protein called 60S RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LV	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 25 is a protein called 60S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LW	124	Total	C	N	O	S	0	0
			1015	634	207	170	4		

- Molecule 26 is a protein called 60S RIBOSOMAL PROTEIN L23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LX	120	Total	C	N	O	S	0	0
			985	630	185	169	1		

- Molecule 27 is a protein called 60S RIBOSOMAL PROTEIN L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LY	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 28 is a protein called 60S RIBOSOMAL PROTEIN L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 29 is a protein called 60S RIBOSOMAL PROTEIN L27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	La	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	Lb	75	Total	C	N	O	S	0	0
			610	378	130	99	3		

- Molecule 31 is a protein called 60S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Lc	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 32 is a protein called 60S RIBOSOMAL PROTEIN L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ld	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 33 is a protein called 60S RIBOSOMAL PROTEIN L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Le	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 34 is a protein called 60S RIBOSOMAL PROTEIN L35A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lf	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	Lg	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	Lh	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	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 38 is a protein called 60S RIBOSOMAL PROTEIN L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lj	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 39 is a protein called 60S RIBOSOMAL PROTEIN L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lk	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	Ll	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	Lm	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 42 is a protein called 60S RIBOSOMAL PROTEIN L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 43 is a protein called 60S RIBOSOMAL PROTEIN L36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 44 is a protein called 60S RIBOSOMAL PROTEIN L37A.

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

- Molecule 45 is a protein called 60S RIBOSOMAL PROTEIN L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 46 is a protein called 60S RIBOSOMAL PROTEIN L10A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lz	217	Total	C	N	O	S	0	0
			1741	1113	312	307	9		

- Molecule 47 is a RNA chain called RNA (1869-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S2	1742	Total	C	N	O	P	0	0
			36900	16458	6595	12106	1741		

- Molecule 48 is a RNA chain called HUMAN INITIATOR MET-TRNA-I.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	S6	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

- Molecule 49 is a protein called 40S RIBOSOMAL PROTEIN SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SA	222	Total	C	N	O	S	0	0
			1747	1109	306	324	8		

- Molecule 50 is a protein called 40S RIBOSOMAL PROTEIN S3A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SB	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 51 is a protein called 40S RIBOSOMAL PROTEIN S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SD	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 52 is a protein called 40S RIBOSOMAL PROTEIN S4, X ISOFORM.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 53 is a protein called 40S RIBOSOMAL PROTEIN S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SF	191	Total	C	N	O	S	0	0
			1509	943	286	273	7		

- Molecule 54 is a protein called 40S RIBOSOMAL PROTEIN S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SH	189	Total	C	N	O	S	0	0
			1521	969	280	271	1		

- Molecule 55 is a protein called 40S RIBOSOMAL PROTEIN S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SI	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 56 is a protein called 40S RIBOSOMAL PROTEIN S10.

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

- Molecule 57 is a protein called 40S RIBOSOMAL PROTEIN S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SL	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		

- Molecule 58 is a protein called 40S RIBOSOMAL PROTEIN S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SP	97	Total	C	N	O	S	0	0
			804	505	155	138	6		

- Molecule 59 is a protein called 40S RIBOSOMAL PROTEIN S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SQ	146	Total	C	N	O	S	0	0
			1158	736	218	200	4		

- Molecule 60 is a protein called 40S RIBOSOMAL PROTEIN S17-LIKE.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SR	132	Total	C	N	O	S	0	0
			1072	673	199	195	5		

- Molecule 61 is a protein called 40S RIBOSOMAL PROTEIN S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SS	150	Total	C	N	O	S	0	0
			1235	776	250	208	1		

- Molecule 62 is a protein called 40S RIBOSOMAL PROTEIN S19.

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

- Molecule 63 is a protein called 40S RIBOSOMAL PROTEIN S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SU	104	Total	C	N	O	S	0	0
			821	514	155	148	4		

- Molecule 64 is a protein called 40S RIBOSOMAL PROTEIN S21.

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

- Molecule 65 is a protein called 40S RIBOSOMAL PROTEIN S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 66 is a protein called 40S RIBOSOMAL PROTEIN S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Sa	107	Total	C	N	O	S	0	0
			847	528	176	138	5		

- Molecule 67 is a protein called 40S RIBOSOMAL PROTEIN S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Sc	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 68 is a protein called 40S RIBOSOMAL PROTEIN S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Sd	53	Total	C	N	O	S	0	0
			445	278	90	72	5		

- Molecule 69 is a protein called UBIQUITIN-40S RIBOSOMAL PROTEIN S27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Sf	71	Total	C	N	O	S	0	0
			581	367	109	98	7		

- Molecule 70 is a protein called GUANINE NUCLEOTIDE-BINDING PROTEIN SUBUNIT BETA-2-LIKE 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Sg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 71 is a protein called 40S RIBOSOMAL PROTEIN S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SC	222	Total	C	N	O	S	0	0
			1725	1115	298	302	10		

- Molecule 72 is a protein called 40S RIBOSOMAL PROTEIN S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 73 is a protein called 40S RIBOSOMAL PROTEIN S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SM	122	Total	C	N	O	S	0	0
			952	596	169	179	8		

- Molecule 75 is a protein called 40S RIBOSOMAL PROTEIN S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 76 is a protein called 40S RIBOSOMAL PROTEIN S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	SO	140	Total	C	N	O	S	0	0
			1049	642	204	197	6		

- Molecule 77 is a protein called 40S RIBOSOMAL PROTEIN S15A.

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

- Molecule 78 is a protein called 40S RIBOSOMAL PROTEIN S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	SY	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		

- Molecule 79 is a protein called 40S RIBOSOMAL PROTEIN S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	SZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 80 is a protein called 40S RIBOSOMAL PROTEIN S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 81 is a protein called 40S RIBOSOMAL PROTEIN S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Se	58	Total	C	N	O	S	0	0
			459	284	100	74	1		

- Molecule 82 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
82	L7	5	Total	Mg	0
			5	5	
82	L1	1	Total	Mg	0
			1	1	
82	LB	1	Total	Mg	0
			1	1	
82	S2	66	Total	Mg	0
			66	66	
82	L8	2	Total	Mg	0
			2	2	
82	Le	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
82	LN	1	Total 1	Mg 1	0
82	LQ	1	Total 1	Mg 1	0
82	LP	1	Total 1	Mg 1	0
82	La	1	Total 1	Mg 1	0
82	LH	1	Total 1	Mg 1	0
82	L5	149	Total 149	Mg 149	0
82	S6	7	Total 7	Mg 7	0
82	LA	1	Total 1	Mg 1	0
82	LJ	1	Total 1	Mg 1	0

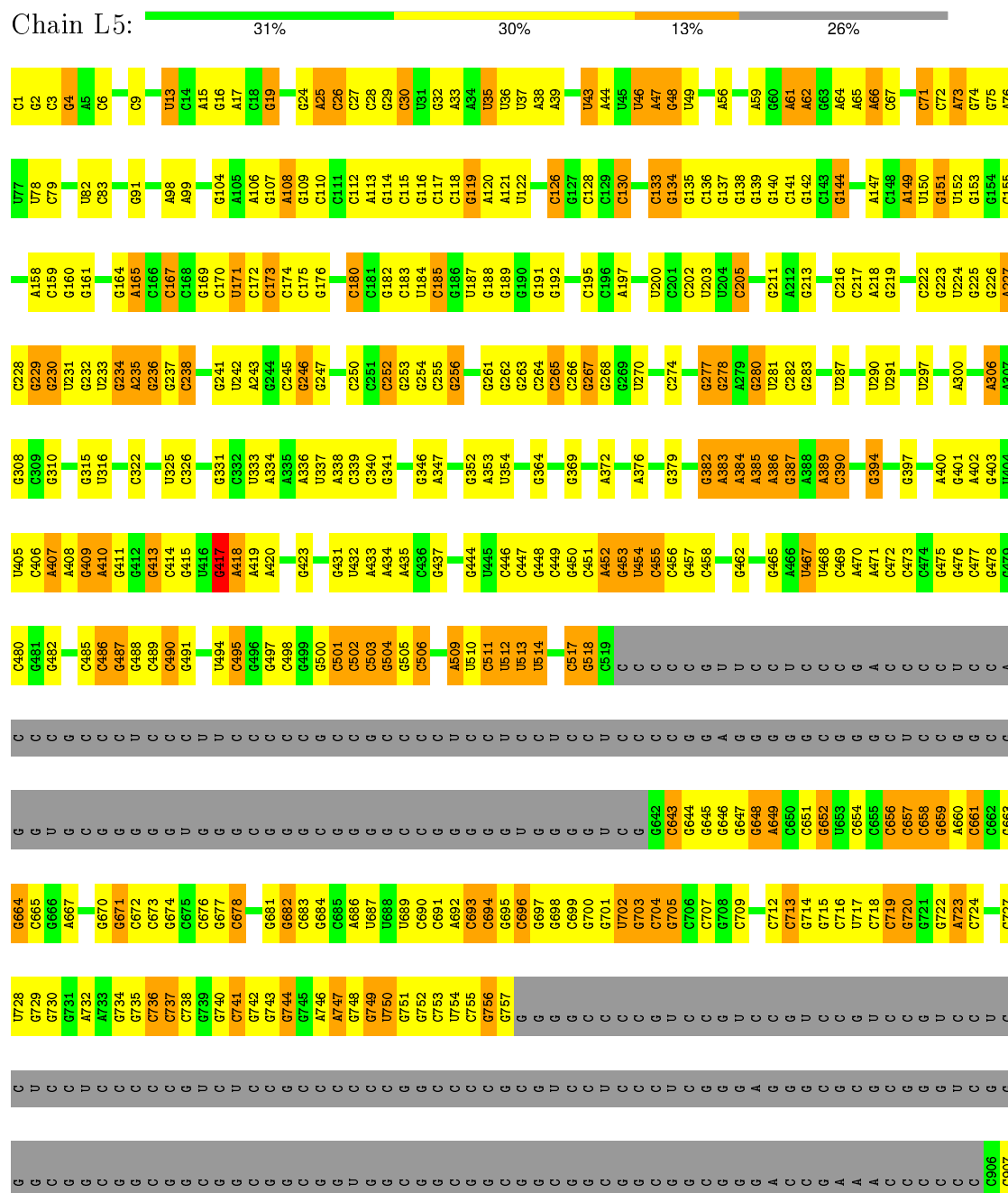
- Molecule 83 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
83	Lm	1	Total 1	Zn 1	0
83	Lo	1	Total 1	Zn 1	0
83	Lg	1	Total 1	Zn 1	0
83	Lp	1	Total 1	Zn 1	0
83	Sa	1	Total 1	Zn 1	0
83	Lj	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: RNA (5070-MER)







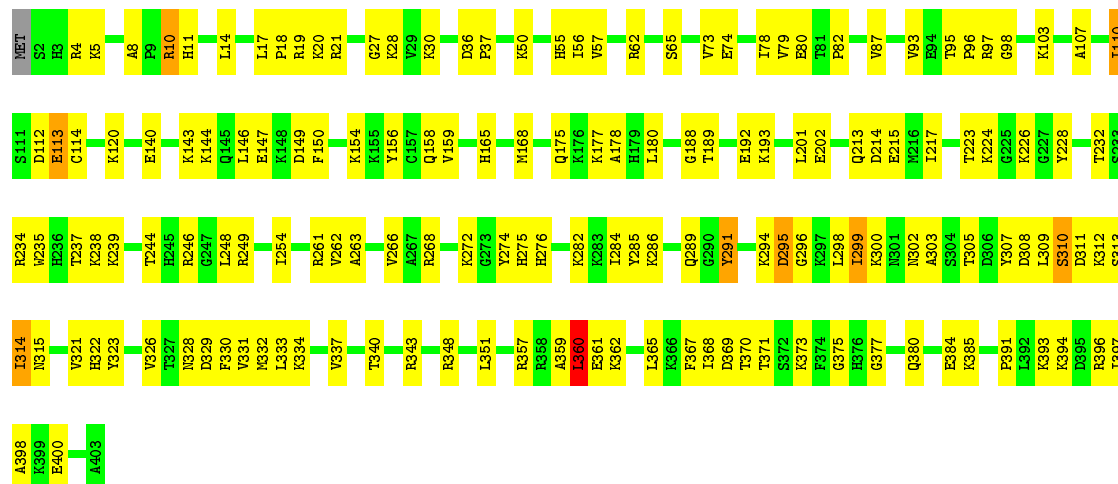






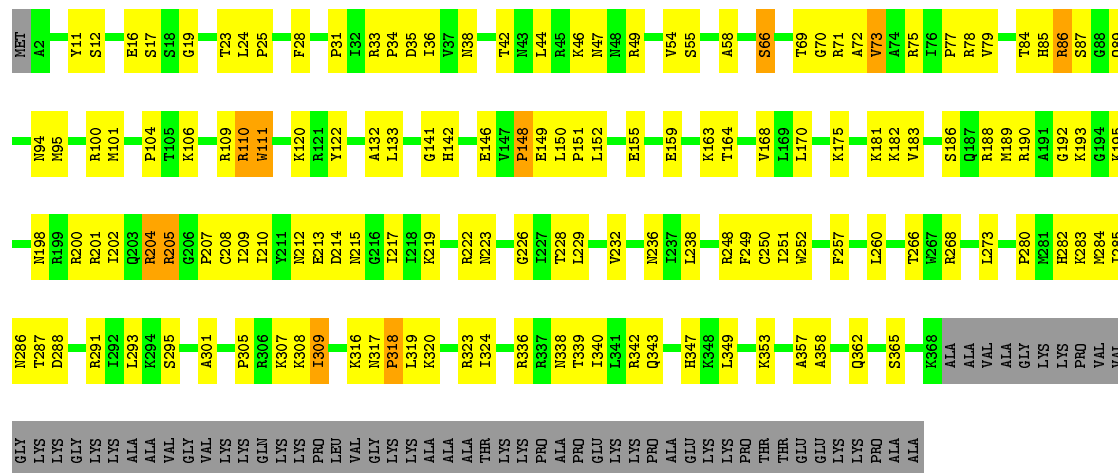

• Molecule 5: 60S RIBOSOMAL PROTEIN L3

Chain LB: 61% 36%



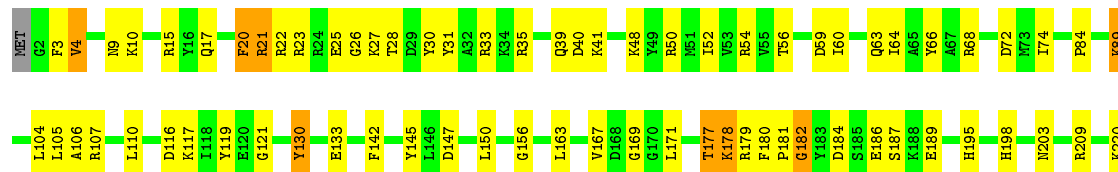
• Molecule 6: 60S RIBOSOMAL PROTEIN L4

Chain LC: 52% 32% 14%



• Molecule 7: 60S RIBOSOMAL PROTEIN L5

Chain LD: 66% 30%



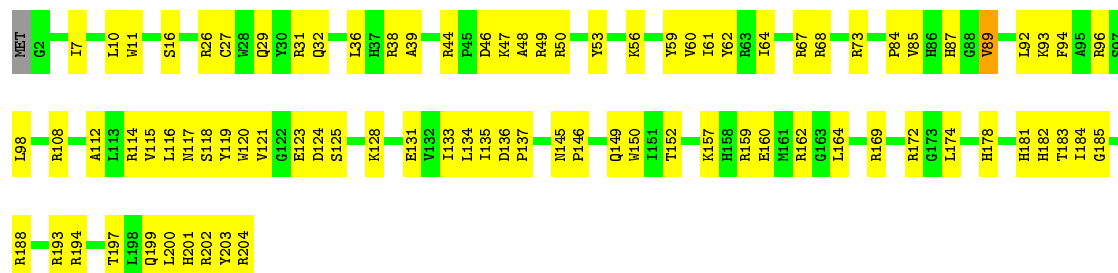




LYS
ILE
THR
ALA
SER
LYS
LYS
ALA
PRO
ALA
GLN
LYS
VAL
PRO
ALA
GLN
LYS
ALA
THR
GLY
GLN
LYS
ALA
ALA
PRO
ALA
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ALA
PRO
LYS
ALA
SER
GLY
LYS
LYS
ALA

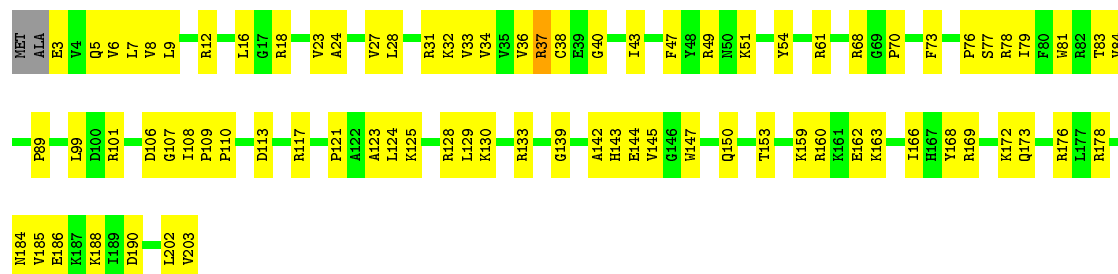
• Molecule 16: 60S RIBOSOMAL PROTEIN L15

Chain LN:  57% 42%



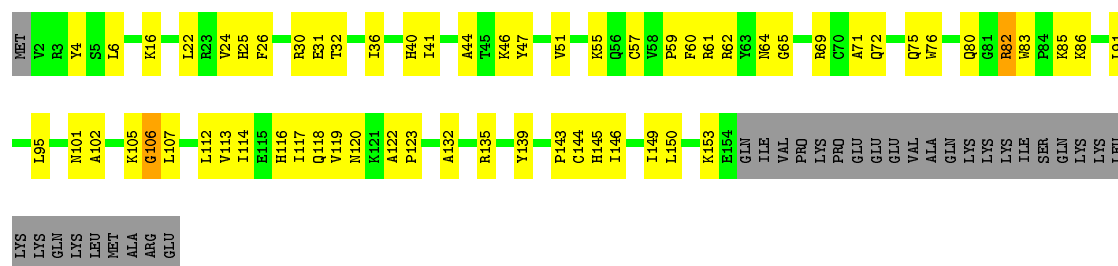
• Molecule 17: 60S RIBOSOMAL PROTEIN L13A

Chain LO:  59% 39%



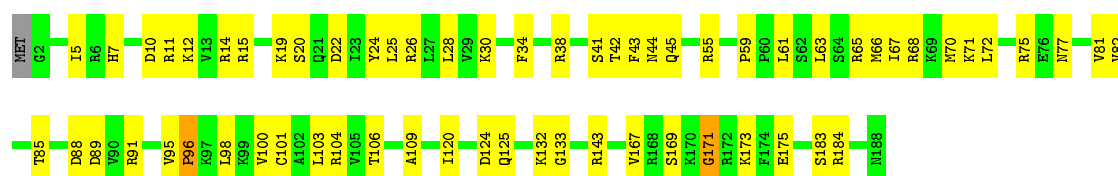
• Molecule 18: 60S RIBOSOMAL PROTEIN L17

Chain LP:  49% 33% 17%

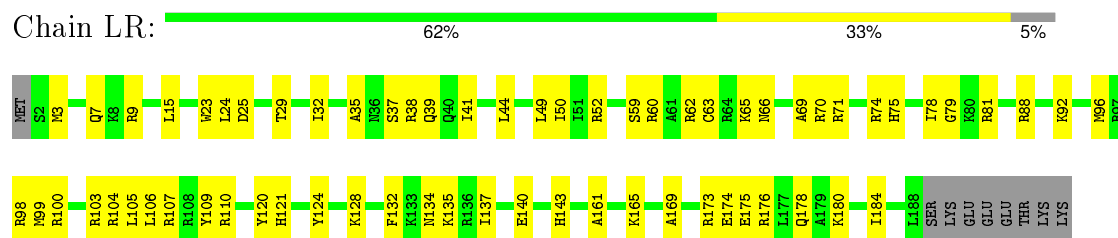


• Molecule 19: 60S RIBOSOMAL PROTEIN L18

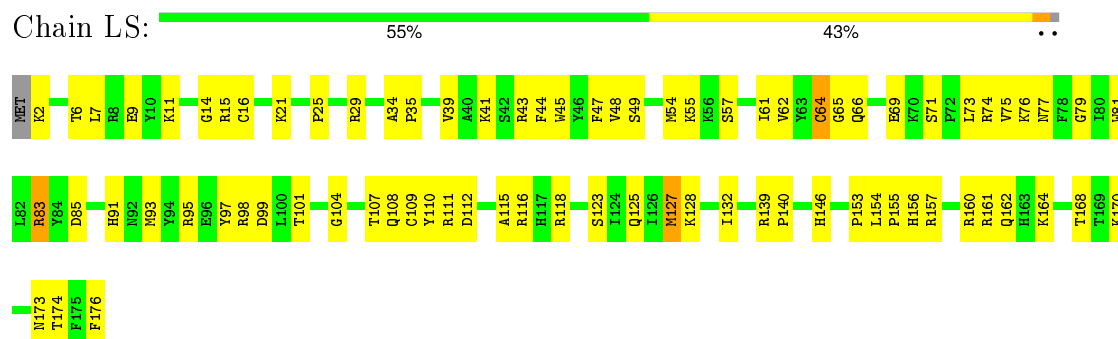
Chain LQ:  66% 32%



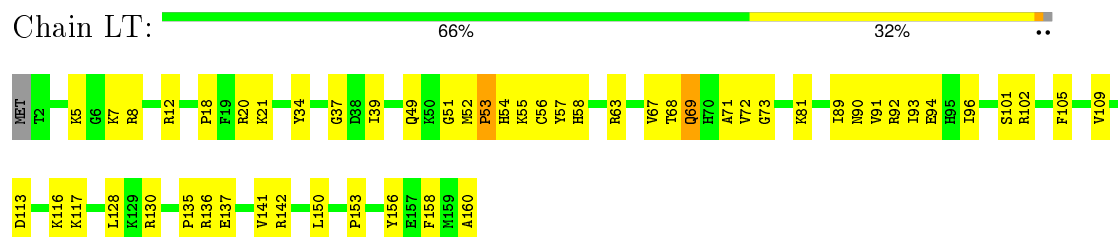
• Molecule 20: 60S RIBOSOMAL PROTEIN L19



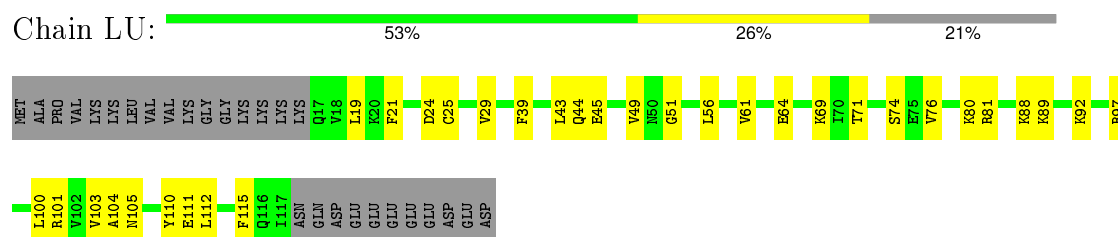
• Molecule 21: 60S RIBOSOMAL PROTEIN L18A



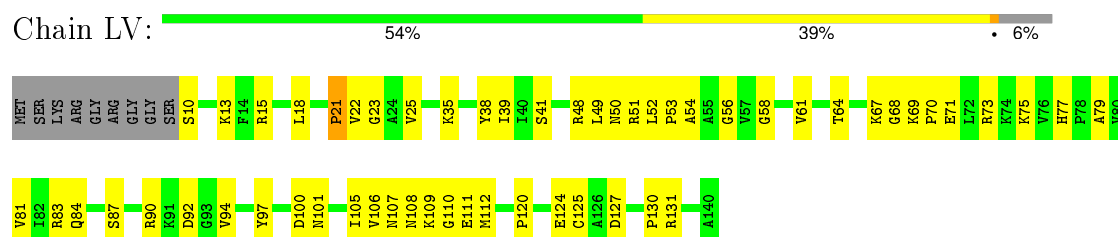
• Molecule 22: 60S RIBOSOMAL PROTEIN L21



• Molecule 23: 60S RIBOSOMAL PROTEIN L22




• Molecule 24: 60S RIBOSOMAL PROTEIN L23



• Molecule 25: 60S RIBOSOMAL PROTEIN L24


ALA
LYS
ASP
GLN
THR
LYS
ALA
GLN
ALA
ALA
ALA
ALA
PRO
ALA
SER
VAL
PRO
ALA
GLN
ALA
PRO
LYS
ARG
THR
GLN
ALA
PRO
THR
LYS
LYS
ALA
SER
GLU

• Molecule 31: 60S RIBOSOMAL PROTEIN L30

Chain Lc:  80% 5% 15%

MET
VAL
ALA
ALA
LYS
LYS
THR
LYS
R9
K23
N51
C52
P53
A54
S75
D101
R106
SER
MET
PRO
GLU
GLN
THR
GLY
GLU
LYS

• Molecule 32: 60S RIBOSOMAL PROTEIN L31

Chain Ld:  82% 14%

MET
ALA
PRO
ALA
LYS
LYS
GLY
GLY
GLU
LYS
LYS
LYS
GLY
ARG
SER
ALA
ALA
ILE
N18
V21
R44
Y82
E84
V120
E124
ASN

• Molecule 33: 60S RIBOSOMAL PROTEIN L32

Chain Le:  91% 5%

MET
A2
V8
S62
P71
S104
P125
L129
ARG
SER
GLU
GLU
ASN
GLU

• Molecule 34: 60S RIBOSOMAL PROTEIN L35A

Chain Lf:  95% 5%

MET
S2
L5
K54
M83
L105
P107
I110

• Molecule 35: 60S RIBOSOMAL PROTEIN L34

Chain Lg:  97%

MET
V2
R57
K115
ALA
LYS

• Molecule 36: 60S RIBOSOMAL PROTEIN L35

Chain Lh:  98%


MET
A2
G39
K37
A123

• Molecule 37: 60S RIBOSOMAL PROTEIN L36

Chain Li:  93%

MET
A2
L3
R4
C48
I73
K86
K103
LYS
ASP

• Molecule 38: 60S RIBOSOMAL PROTEIN L37

Chain Lj:  81% 7% 11%



- Molecule 39: 60S RIBOSOMAL PROTEIN L38

Chain Lk:  91% 7% .



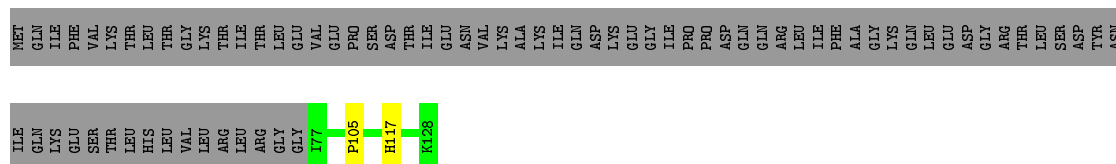
- Molecule 40: 60S RIBOSOMAL PROTEIN L39

Chain Ll:  96% . .



- Molecule 41: UBIQUITIN-60S RIBOSOMAL PROTEIN L40

Chain Lm:  39% . 59%



- Molecule 42: 60S RIBOSOMAL PROTEIN L41

Chain Ln:  96% .



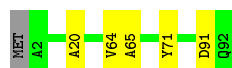
- Molecule 43: 60S RIBOSOMAL PROTEIN L36A

Chain Lo:  96% . .




- Molecule 44: 60S RIBOSOMAL PROTEIN L37A

Chain Lp:  93% 5% .



- Molecule 45: 60S RIBOSOMAL PROTEIN L28

Chain Lr:  87% 9%



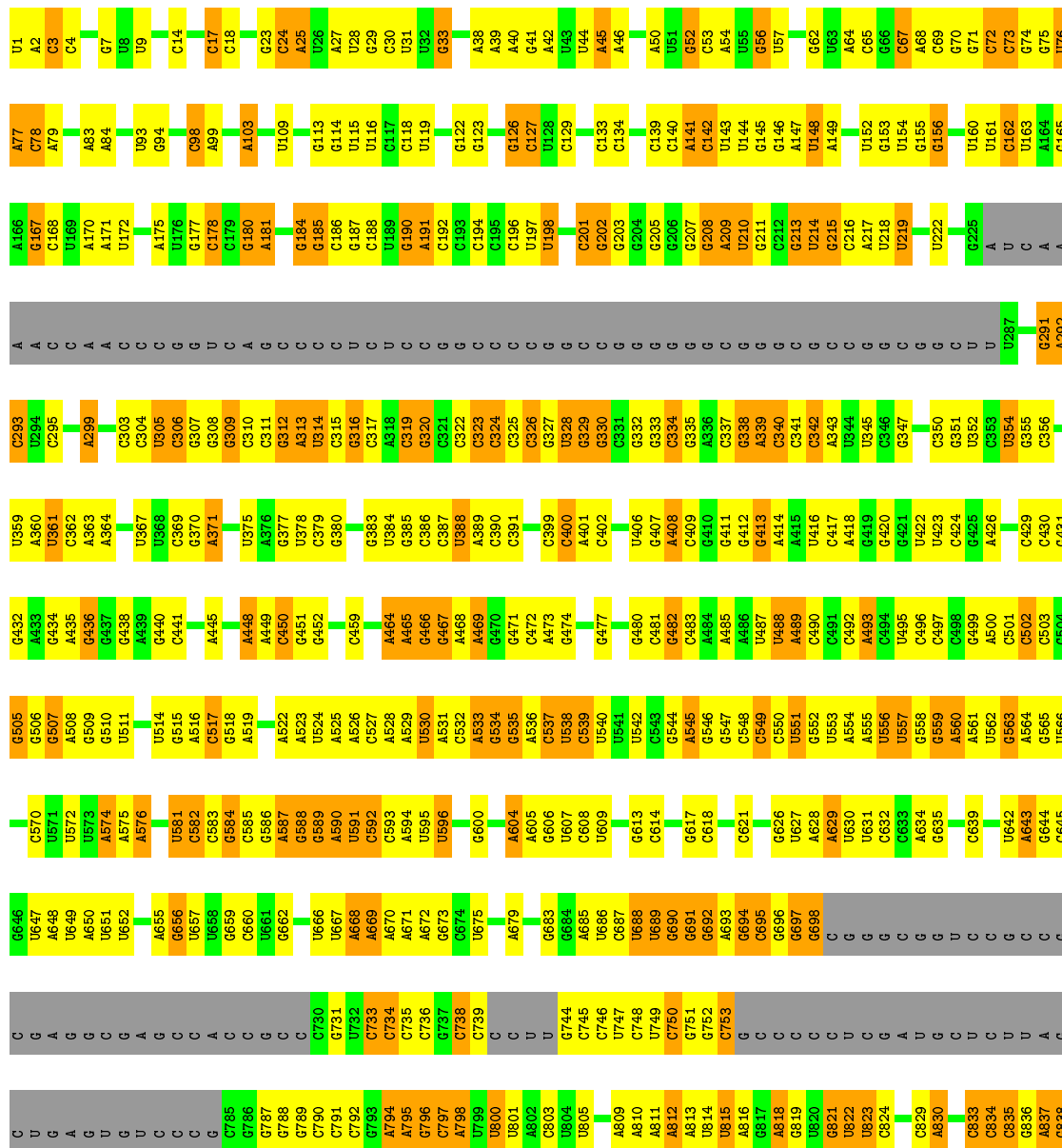
• Molecule 46: 60S RIBOSOMAL PROTEIN L10A

Chain Lz:  93% 7%



• Molecule 47: RNA (1869-MER)

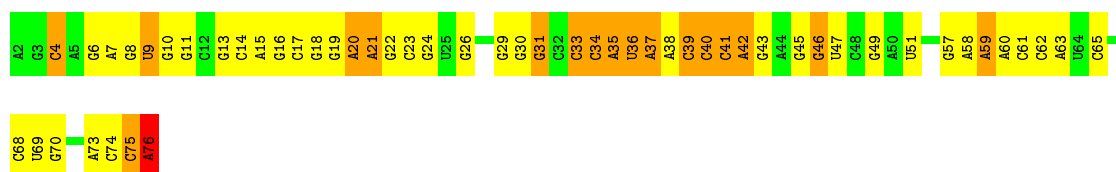
Chain S2:  32% 42% 19% 7%



U1848	G1849	G1758	G1686	U1615	U1551	A1484	C1418	C1341	A1278	U1136	G1057	G977	G910	C839
A1850	G1850	G1771	C1688	U1616	G1552	A1487	C1419	U1342	C1279	U1137	A1058	G978	C911	C840
A1851	G1851	G1772	C1688	G1617	C1553	C1488	A1420	U1343	G1280	C1138	G1059	G979	C912	C841
C1852	G1852	C1773	A1620	A1621	C1554	A1489	A1421	U1343	G1281	C1139	A1060	A980	A913	C842
C1853	G1853	C1774	A1621	A1622	C1555	A1490	A1422	U1347	A1282	G1140	U1061	A981	U914	C843
U1854	G1854	G1775	A1622	G1623	C1557	G1491	G1424	G1348	A1284	G1141	A1062	A982	U917	U844
C1855	G1855	G1776	A1623	A1624	C1558	U1492	G1425	G1349	G1285	G1142		A983	U918	G845
								U1350	G1286	A1143	G1065		U919	G846
										A1144		G986	A919	A847
										A1145	G1068		A920	U848
										G1146	U1069	A990	G921	
										C1147	A1070	G991	A922	C851
										U1148	G1071	A992	G923	C852
										A1149		A996	G924	C853
										A1150	G1076		A925	U863
										C1153	C1078	G999	G926	A864
										U1154	C1079	G999	G927	A865
										U1155	A1080	A1001	G928	
										U1156	U1081	A1002	G929	
										G1157	U1082	U1003	G930	C868
										G1158	A1083	U1004	G933	A869
										G1159	A1084	G1005	G934	A870
											C1085			U871
										C1163	G1086	A1008	C937	A872
										G1164	A1087		A938	G873
										G1166	U1089		U939	G874
													U940	A875
										A1170	G1096	U1016	C941	C877
										G1171	C1093	U1017	G942	G878
										U1172	G1099	U1018	U943	C879
												U1019	A944	C880
										G1175	G1102	A1020	G947	G881
										C1180	C1103	U1021	C950	U882
										A1181	G1104	A1023	C951	C884
										A1182		A1024	G952	
										C1183	G1110		G953	U887
										G1184	U1111	A1028	C954	U888
										U1186	A1112	G1029	A955	U889
										G1187	A1113		G956	C891
										U1188	U1114	G1033	A957	U892
										A1189	U1115	A1034	G958	U893
										C1191	C1116	A1035	G959	G894
										U1192	C1117	G1037	G961	U896
										U1193	U1120	A1036	A962	U897
										A1194	G1121	G1041	A963	U898
										A1195		A1042	A964	U899
											C1124	G1043	U865	C900
										G1198	C1125	G1044	U869	G901
										A1200	G1126	C1047	G970	G902
										G1203	G1129	A1052	G971	A904
										A1204	G1130	C1053	C973	U906
										G1274	G1134	G1054	C974	G907
										A1276		A1055	G975	A908
										C1277	C1135	U1056	G976	G909

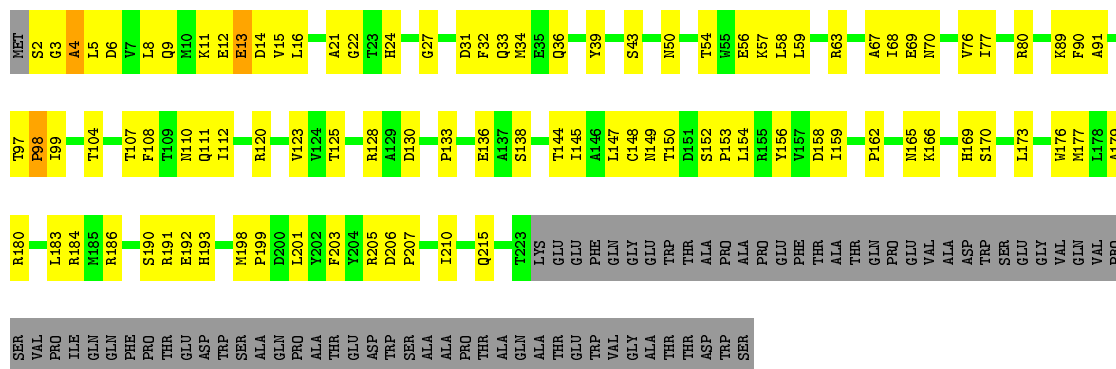
• Molecule 48: HUMAN INITIATOR MET-TRNA-I

Chain S6: 28% 48% 23%



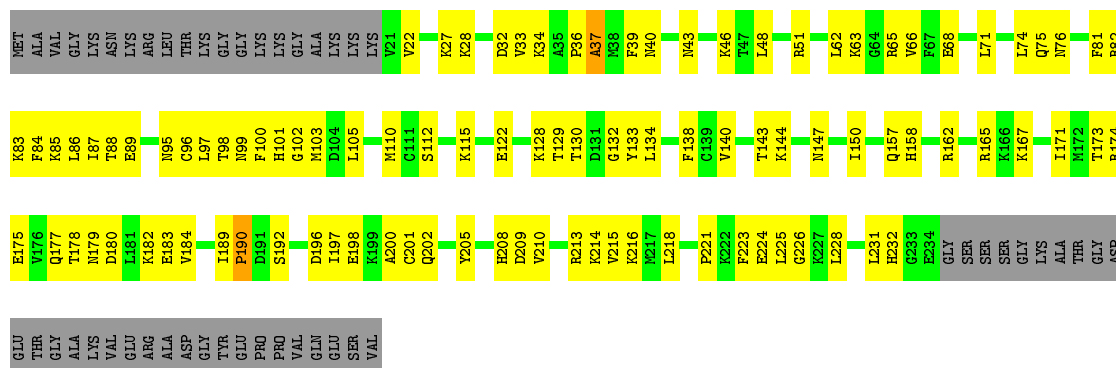
• Molecule 49: 40S RIBOSOMAL PROTEIN SA

Chain SA: 43% 32% 25%



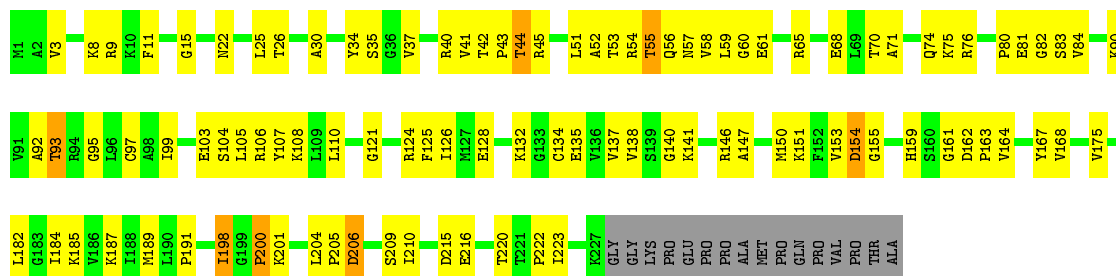
• Molecule 50: 40S RIBOSOMAL PROTEIN S3A

Chain SB: 43% 37% 19%

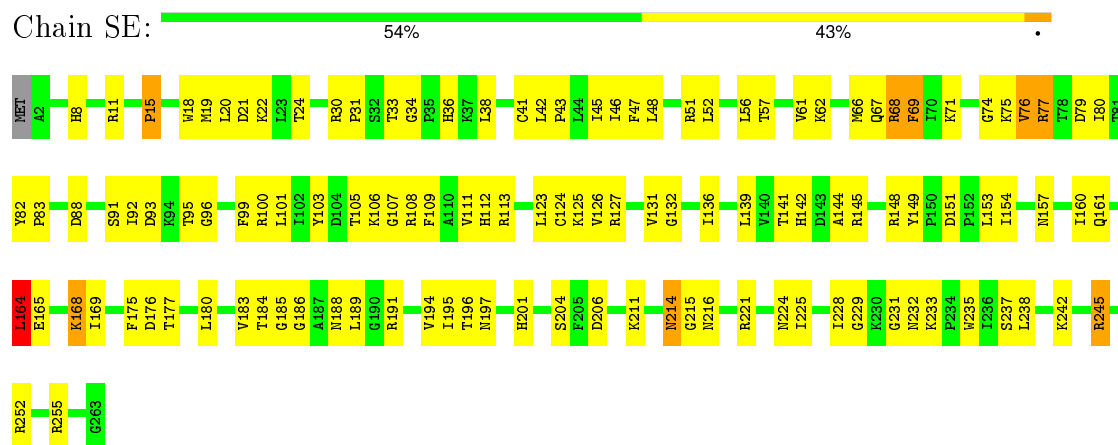


• Molecule 51: 40S RIBOSOMAL PROTEIN S3

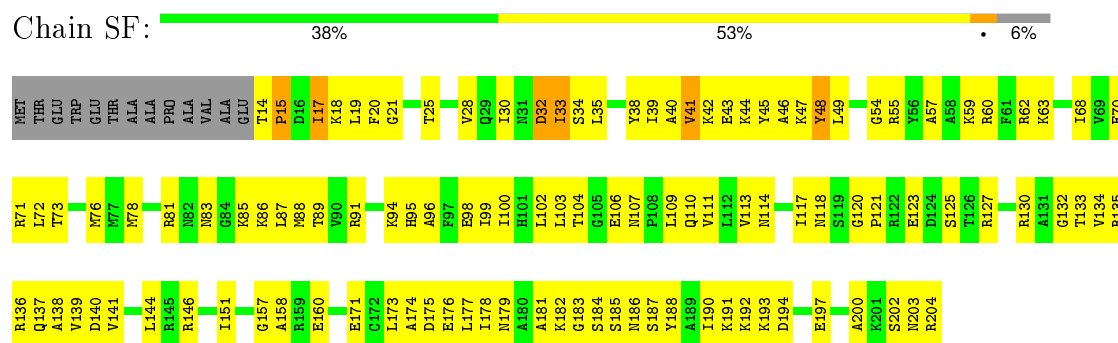
Chain SD: 52% 38% 7%



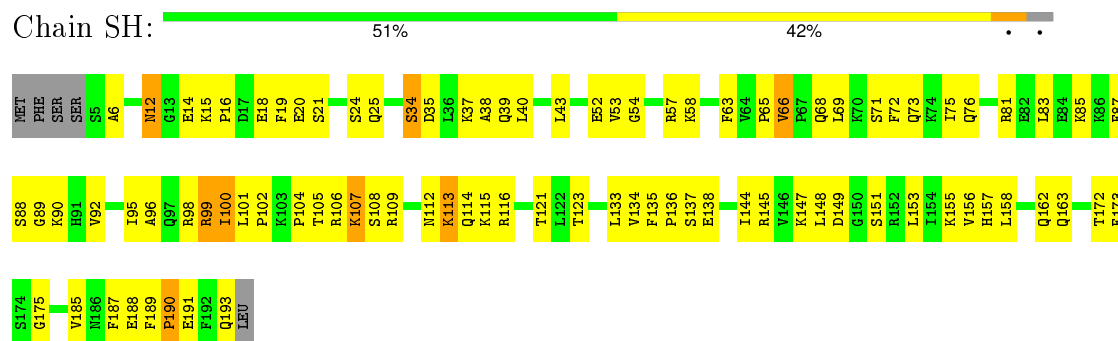
• Molecule 52: 40S RIBOSOMAL PROTEIN S4, X ISOFORM



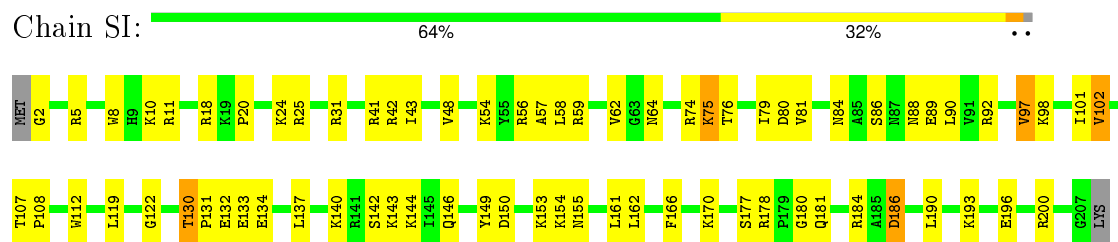
- Molecule 53: 40S RIBOSOMAL PROTEIN S5



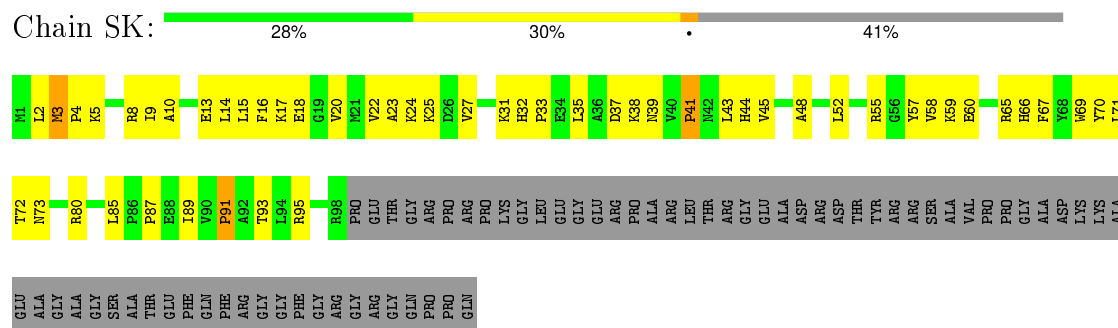
- Molecule 54: 40S RIBOSOMAL PROTEIN S7



- Molecule 55: 40S RIBOSOMAL PROTEIN S8



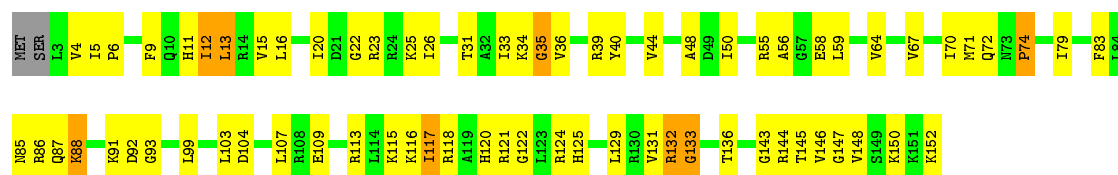
- Molecule 56: 40S RIBOSOMAL PROTEIN S10





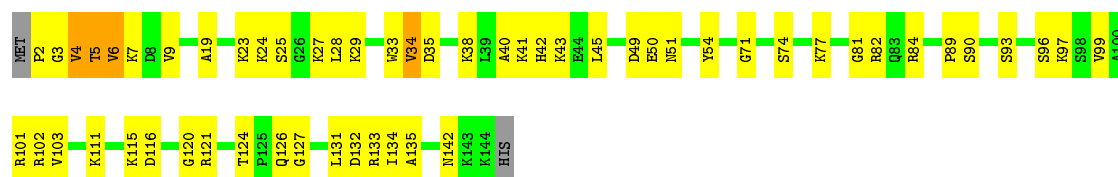
• Molecule 61: 40S RIBOSOMAL PROTEIN S18

Chain SS: 52% 41% 5%



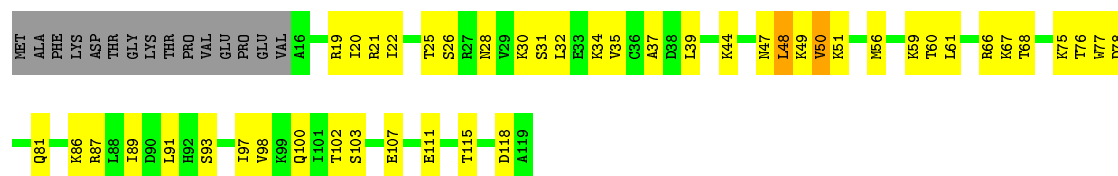
• Molecule 62: 40S RIBOSOMAL PROTEIN S19

Chain ST: 60% 36%



• Molecule 63: 40S RIBOSOMAL PROTEIN S20

Chain SU: 49% 37% 13%



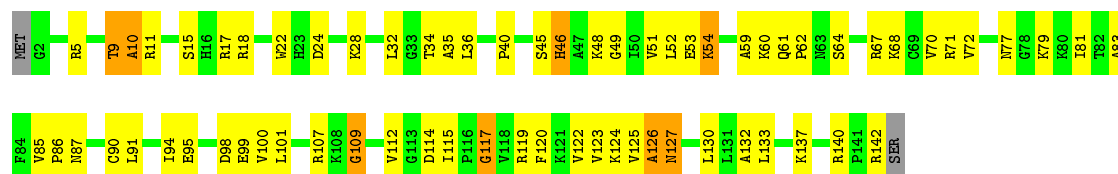
• Molecule 64: 40S RIBOSOMAL PROTEIN S21

Chain SV: 63% 36%



• Molecule 65: 40S RIBOSOMAL PROTEIN S23

Chain SX: 51% 42% 6%



• Molecule 66: 40S RIBOSOMAL PROTEIN S26

MET	T2	K3	K4	R5	K13	V18	E46	A61	Y62	V63	L64	R89	A106	A107	P108	ARG	PRQ	PRQ	PRQ	LYS	PRQ	MET
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MET	Q4	D56
GLY		
HIS		

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

ILE	GLN	GLN	LYS	GLU	SER	THR	LEU	HIS	LEU	VAL	LEU	ARG	LEU	ARG	GLY	GLY	ALA	LYS	LYS	ARG	LYS	LYS	K92	T96	T97	P98	H93	V98	K99	L100	A101	L102	L103	K104	R118	S123	D124	H139	K152	P160	GLU	ASP	LYS
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MET	T2	G13	H14	N15	P28	P55	Q56	G61	R99	V102	T105	E145	H191	N244	R245	Y246	L261	V267	A281	T314	GLY	THR	ARG
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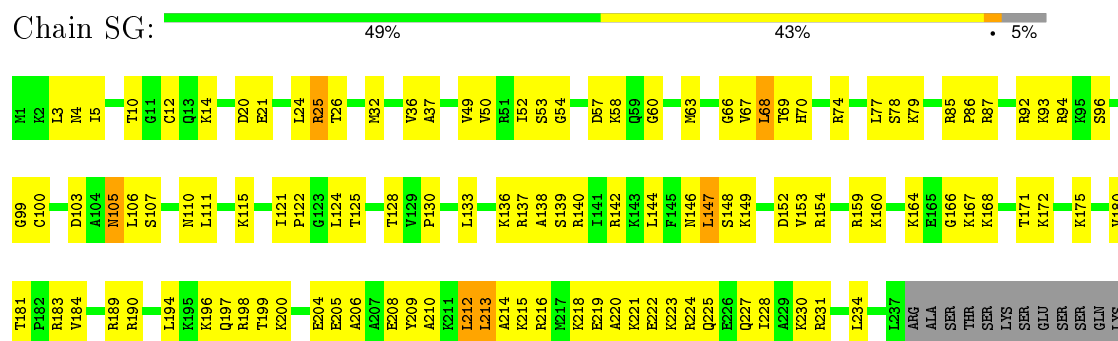
MET	ALA	ASP	ASP	ALA	GLY	ALA	ALA	ALA	GLY	GLY	PRO	PRO	GLY	GLY	GLY	PRO	PRO	GLY	MET	GLY	ASN	ARG	ARG	GLY	GLY	PHE	GLY	GLY	PHE	GLY	SER	GLY	ILE	ARG	ARG	GLY	GLY	GLY	GLY	ARG	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LYS	ALA	GLU	ASP	ASN	LNS	E30
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

V63	L69	M73 K14	S85	E90 S91	I94	L98	S101	D104 E105 V106 L107	Q115 T116 R117	A118	G119	R123	F124 T125	A126	F127	V128 A129	I130 G131	D132 Y133	M134	G138	L139 G140	C143	K159	V165	R166 R167	G168	I174 G175	K176	T179
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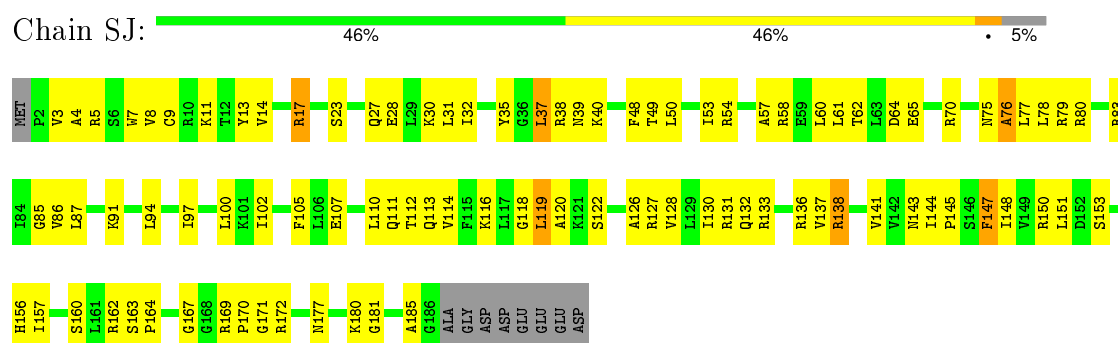
P180	P181	P182	P183	P184	P185	P188	P189	P190	P191	P194	P195	P196	P197	P198	P199	T202	G203	L204	V205	S206	A207	P210	L214	I219	D220	D221	C222	G223	T224	S225	A226	D237	K238	D242	L243	L244	S245	K246	T247	G248	S249	P253	V256	T258
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

V260	F261	T262	K263	S264	P265	Y266	Q267	T270	D271	K272	L273	H277	T278	R279	V280	SER	VAL	GLN	ARG	THR	GLN	GLN	ALA	PRO	ALA	VAL	ALA	THR	THR
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

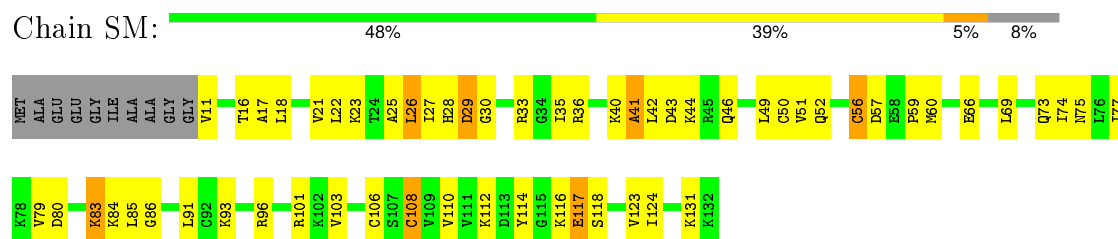
- Molecule 72: 40S RIBOSOMAL PROTEIN S6



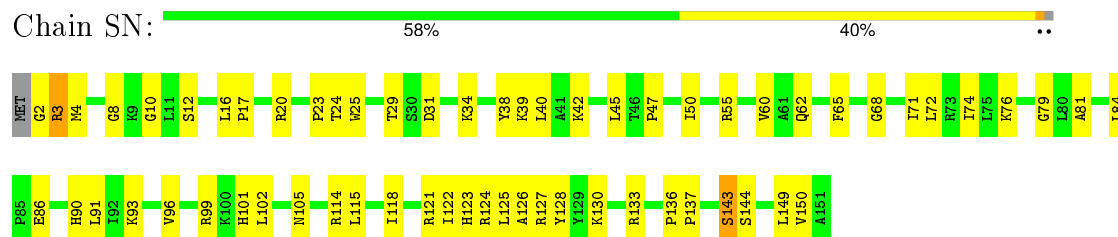
- Molecule 73: 40S RIBOSOMAL PROTEIN S9



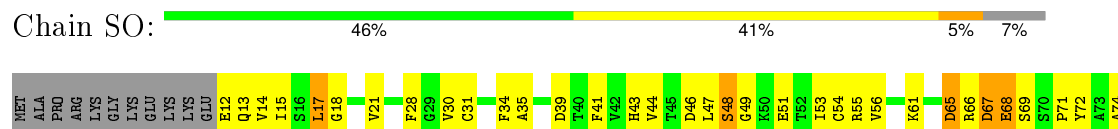
- Molecule 74: 40S RIBOSOMAL PROTEIN



- Molecule 75: 40S RIBOSOMAL PROTEIN S13



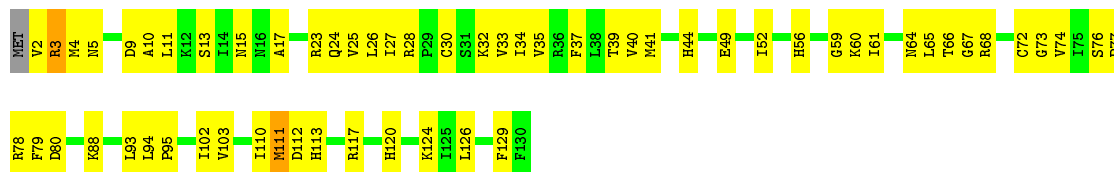
- Molecule 76: 40S RIBOSOMAL PROTEIN S14





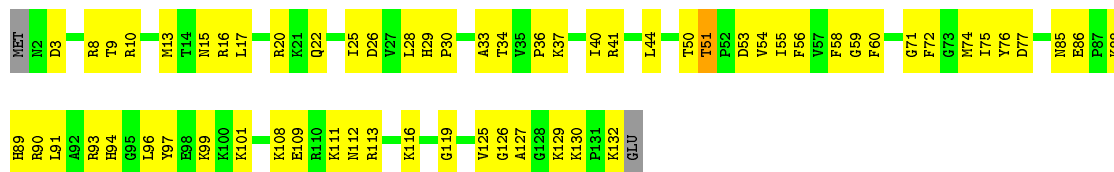
• Molecule 77: 40S RIBOSOMAL PROTEIN S15A

Chain SW: 53% 45%



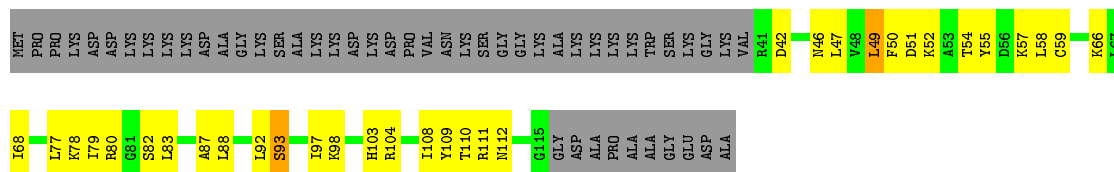
• Molecule 78: 40S RIBOSOMAL PROTEIN S24

Chain SY: 52% 46%



• Molecule 79: 40S RIBOSOMAL PROTEIN S25

Chain SZ: 34% 25% 40%



• Molecule 80: 40S RIBOSOMAL PROTEIN S27

Chain Sb: 96%



• Molecule 81: 40S RIBOSOMAL PROTEIN S30

Chain Se: 92% 7%



4 Experimental information ⓘ

Property	Value	Source
Reconstruction method	Not provided	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	Not provided	Depositor
Microscope	Not provided	Depositor
Voltage (kV)	Not provided	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	Not provided	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	L5	0.42	0/89645	0.79	26/139764 (0.0%)
10	LG	0.27	0/1960	0.50	0/2637
11	LH	0.26	0/1537	0.48	0/2066
12	LI	0.30	0/1751	0.50	0/2340
13	LJ	0.26	0/1433	0.49	0/1915
14	LL	0.30	0/1732	0.53	0/2315
15	LM	0.28	0/1161	0.46	0/1554
16	LN	0.33	0/1746	0.51	0/2338
17	LO	0.31	0/1682	0.47	0/2250
18	LP	0.31	0/1268	0.49	0/1701
19	LQ	0.30	0/1537	0.49	0/2052
2	L7	0.37	0/2858	0.73	0/4455
20	LR	0.28	0/1582	0.49	0/2091
21	LS	0.31	0/1493	0.48	0/2003
22	LT	0.32	0/1326	0.52	0/1770
23	LU	0.27	0/839	0.47	0/1126
24	LV	0.31	0/993	0.49	0/1332
25	LW	0.29	0/1030	0.57	0/1364
26	LX	0.29	0/1002	0.49	0/1345
27	LY	0.28	0/1132	0.47	0/1504
28	LZ	0.29	0/1130	0.47	0/1507
29	La	0.31	0/1191	0.50	0/1591
3	L8	0.40	0/3701	0.76	0/5766
30	Lb	0.26	0/620	0.44	0/819
31	Lc	0.29	0/774	0.48	0/1038
32	Ld	0.29	0/903	0.50	0/1216
33	Le	0.33	0/1071	0.53	0/1429
34	Lf	0.30	0/895	0.51	0/1198
35	Lg	0.28	0/916	0.49	0/1220
36	Lh	0.28	0/1023	0.46	0/1351
37	Li	0.28	0/843	0.47	0/1115
38	Lj	0.35	0/720	0.55	0/952

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	Lk	0.28	0/575	0.54	0/761
4	LA	0.34	0/1936	0.56	1/2596 (0.0%)
40	Ll	0.28	0/454	0.48	0/599
41	Lm	0.29	0/435	0.47	0/575
42	Ln	0.29	0/231	0.53	0/294
43	Lo	0.31	0/875	0.49	0/1153
44	Lp	0.36	0/718	0.51	0/953
45	Lr	0.27	0/1017	0.50	0/1364
46	Lz	0.24	0/1769	0.49	0/2371
47	S2	0.35	0/41243	0.77	11/64257 (0.0%)
48	S6	0.32	1/1795 (0.1%)	0.80	1/2798 (0.0%)
49	SA	0.26	0/1784	0.49	0/2424
5	LB	0.30	0/3306	0.52	1/4424 (0.0%)
50	SB	0.28	0/1765	0.52	0/2362
51	SD	0.26	0/1793	0.49	0/2414
52	SE	0.26	0/2118	0.53	1/2849 (0.0%)
53	SF	0.27	0/1531	0.52	0/2059
54	SH	0.26	0/1544	0.50	0/2068
55	SI	0.27	0/1715	0.48	0/2287
56	SK	0.27	0/851	0.50	0/1147
57	SL	0.29	0/1268	0.51	1/1696 (0.1%)
58	SP	0.26	0/815	0.56	0/1087
59	SQ	0.26	0/1177	0.48	0/1575
6	LC	0.29	0/2973	0.50	0/3992
60	SR	0.27	0/1086	0.57	0/1457
61	SS	0.25	0/1253	0.52	0/1676
62	ST	0.25	0/1131	0.48	0/1515
63	SU	0.26	0/831	0.56	0/1115
64	SV	0.26	0/643	0.44	0/860
65	SX	0.29	0/1116	0.47	0/1490
66	Sa	0.31	0/862	0.52	0/1156
67	Sc	0.25	0/508	0.51	0/680
68	Sd	0.26	0/455	0.42	0/603
69	Sf	0.25	0/593	0.47	0/786
7	LD	0.29	0/2428	0.47	0/3252
70	Sg	0.24	0/2493	0.50	0/3394
71	SC	0.29	0/1762	0.49	0/2381
72	SG	0.25	0/1946	0.52	0/2590
73	SJ	0.26	0/1550	0.47	0/2069
74	SM	0.23	0/962	0.53	0/1290
75	SN	0.28	0/1232	0.48	0/1656
76	SO	0.29	0/1062	0.57	1/1425 (0.1%)
77	SW	0.30	0/1051	0.52	0/1406

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
78	SY	0.26	0/1083	0.47	0/1438
79	SZ	0.26	0/604	0.57	0/810
8	LE	0.27	0/1996	0.59	0/2673
80	Sb	0.27	0/665	0.51	0/891
81	Se	0.24	0/465	0.43	0/612
9	LF	0.31	0/1905	0.49	0/2539
All	All	0.36	1/234864 (0.0%)	0.69	43/344993 (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
34	Lf	0	1
58	SP	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	S6	76	A	C4'-O4'	-5.87	1.38	1.45

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	S6	76	A	C5'-C4'-O4'	13.26	125.02	109.10
1	L5	4083	U	N1-C2-O2	8.35	128.64	122.80
1	L5	4083	U	C2-N1-C1'	8.04	127.35	117.70
1	L5	4937	C	C2-N1-C1'	7.68	127.25	118.80
1	L5	1367	C	N1-C2-O2	7.38	123.33	118.90

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
34	Lf	105	LEU	Peptide
58	SP	72	LYS	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L5	80184	0	40397	1417	0
2	L7	2558	0	1296	34	0
3	L8	3314	0	1683	42	0
4	LA	1898	0	1993	79	0
5	LB	3238	0	3376	117	0
6	LC	2919	0	3092	112	0
7	LD	2382	0	2410	80	0
8	LE	1958	0	2126	76	0
9	LF	1870	0	1996	68	0
10	LG	1927	0	2074	78	0
11	LH	1518	0	1601	57	0
12	LI	1711	0	1749	44	0
13	LJ	1410	0	1441	55	0
14	LL	1701	0	1818	52	0
15	LM	1138	0	1204	53	0
16	LN	1701	0	1749	74	0
17	LO	1650	0	1794	61	0
18	LP	1242	0	1269	45	0
19	LQ	1513	0	1628	49	0
20	LR	1566	0	1729	51	0
21	LS	1453	0	1490	60	0
22	LT	1298	0	1366	49	0
23	LU	825	0	850	22	0
24	LV	979	0	1039	42	0
25	LW	1015	0	1079	50	0
26	LX	985	0	1066	35	0
27	LY	1115	0	1205	40	0
28	LZ	1107	0	1182	41	0
29	La	1162	0	1213	0	0
30	Lb	610	0	650	0	0
31	Lc	764	0	804	0	0
32	Ld	888	0	930	0	0
33	Le	1053	0	1147	0	0
34	Lf	876	0	912	0	0
35	Lg	906	0	1000	0	0
36	Lh	1015	0	1148	0	0
37	Li	832	0	917	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	Lj	705	0	738	0	0
39	Lk	569	0	637	0	0
40	Ll	444	0	483	0	0
41	Lm	429	0	466	0	0
42	Ln	230	0	276	0	0
43	Lo	862	0	932	0	0
44	Lp	708	0	757	0	0
45	Lr	1002	0	1068	0	0
46	Lz	1741	0	1854	0	0
47	S2	36900	0	18598	741	0
48	S6	1604	0	816	42	0
49	SA	1747	0	1751	71	0
50	SB	1738	0	1809	76	0
51	SD	1765	0	1865	72	0
52	SE	2076	0	2177	97	0
53	SF	1509	0	1563	97	0
54	SH	1521	0	1616	69	0
55	SI	1686	0	1772	55	0
56	SK	827	0	854	41	0
57	SL	1247	0	1323	44	0
58	SP	804	0	841	53	0
59	SQ	1158	0	1232	43	0
60	SR	1072	0	1130	54	0
61	SS	1235	0	1309	64	0
62	ST	1112	0	1146	45	0
63	SU	821	0	883	40	0
64	SV	636	0	637	25	0
65	SX	1098	0	1167	52	0
66	Sa	847	0	896	0	0
67	Sc	506	0	536	0	0
68	Sd	445	0	442	0	0
69	Sf	581	0	597	0	0
70	Sg	2436	0	2393	0	0
71	SC	1725	0	1813	59	0
72	SG	1923	0	2089	103	0
73	SJ	1525	0	1640	81	0
74	SM	952	0	983	46	0
75	SN	1208	0	1294	44	0
76	SO	1049	0	1073	55	0
77	SW	1034	0	1080	53	0
78	SY	1065	0	1142	55	0
79	SZ	598	0	656	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	Sb	651	0	672	0	0
81	Se	459	0	503	0	0
82	L5	149	0	0	0	0
82	L7	5	0	0	0	0
82	L8	2	0	0	0	0
82	LA	1	0	0	0	0
82	LB	1	0	0	0	0
82	LH	1	0	0	0	0
82	LJ	1	0	0	0	0
82	LN	1	0	0	0	0
82	LP	1	0	0	0	0
82	LQ	1	0	0	0	0
82	La	1	0	0	0	0
82	Le	1	0	0	0	0
82	Ll	1	0	0	0	0
82	S2	66	0	0	0	0
82	S6	7	0	0	0	0
83	Lg	1	0	0	0	0
83	Lj	1	0	0	0	0
83	Lm	1	0	0	0	0
83	Lo	1	0	0	0	0
83	Lp	1	0	0	0	0
83	Sa	1	0	0	0	0
All	All	218776	0	161932	4534	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 15.

The worst 5 of 4534 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)
25:LW:69:LYS:H	25:LW:70:LYS:HB2	1.28	0.98
1:L5:747:A:H62	1:L5:916:C:H42	1.12	0.95
47:S2:122:G:H4'	52:SE:145:ARG:HG2	1.48	0.94
58:SP:96:VAL:HG11	61:SS:118:ARG:HG3	1.53	0.91
25:LW:77:LYS:HB3	25:LW:78:PHE:HB3	1.54	0.90

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	
4	LA	246/257 (96%)	207 (84%)	25 (10%)	14 (6%)	2	2
5	LB	400/403 (99%)	344 (86%)	42 (10%)	14 (4%)	4	4
6	LC	365/427 (86%)	311 (85%)	30 (8%)	24 (7%)	1	1
7	LD	291/297 (98%)	258 (89%)	22 (8%)	11 (4%)	4	4
8	LE	238/288 (83%)	182 (76%)	37 (16%)	19 (8%)	1	1
9	LF	223/248 (90%)	201 (90%)	18 (8%)	4 (2%)	11	11
10	LG	239/266 (90%)	205 (86%)	19 (8%)	15 (6%)	2	2
11	LH	188/192 (98%)	162 (86%)	18 (10%)	8 (4%)	3	3
12	LI	211/214 (99%)	177 (84%)	26 (12%)	8 (4%)	4	4
13	LJ	174/178 (98%)	147 (84%)	19 (11%)	8 (5%)	3	3
14	LL	208/211 (99%)	179 (86%)	18 (9%)	11 (5%)	2	2
15	LM	137/215 (64%)	115 (84%)	16 (12%)	6 (4%)	3	3
16	LN	201/204 (98%)	180 (90%)	18 (9%)	3 (2%)	13	13
17	LO	199/203 (98%)	180 (90%)	15 (8%)	4 (2%)	9	9
18	LP	151/184 (82%)	130 (86%)	16 (11%)	5 (3%)	5	5
19	LQ	185/188 (98%)	159 (86%)	22 (12%)	4 (2%)	8	8
20	LR	185/196 (94%)	168 (91%)	17 (9%)	0	100	100
21	LS	173/176 (98%)	141 (82%)	21 (12%)	11 (6%)	2	2
22	LT	157/160 (98%)	134 (85%)	18 (12%)	5 (3%)	5	5
23	LU	99/128 (77%)	81 (82%)	17 (17%)	1 (1%)	19	19
24	LV	129/140 (92%)	105 (81%)	18 (14%)	6 (5%)	3	3
25	LW	122/157 (78%)	96 (79%)	22 (18%)	4 (3%)	5	5
26	LX	118/156 (76%)	103 (87%)	13 (11%)	2 (2%)	11	11
27	LY	132/145 (91%)	118 (89%)	10 (8%)	4 (3%)	5	5
28	LZ	133/136 (98%)	118 (89%)	12 (9%)	3 (2%)	8	8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	La	145/148 (98%)	122 (84%)	18 (12%)	5 (3%)	5	5
30	Lb	73/159 (46%)	62 (85%)	9 (12%)	2 (3%)	6	6
31	Lc	96/115 (84%)	81 (84%)	9 (9%)	6 (6%)	2	2
32	Ld	105/125 (84%)	85 (81%)	15 (14%)	5 (5%)	3	3
33	Le	126/135 (93%)	107 (85%)	14 (11%)	5 (4%)	4	4
34	Lf	107/110 (97%)	87 (81%)	16 (15%)	4 (4%)	4	4
35	Lg	112/117 (96%)	103 (92%)	8 (7%)	1 (1%)	21	21
36	Lh	120/123 (98%)	110 (92%)	8 (7%)	2 (2%)	11	11
37	Li	100/105 (95%)	92 (92%)	4 (4%)	4 (4%)	4	4
38	Lj	84/97 (87%)	67 (80%)	10 (12%)	7 (8%)	1	1
39	Lk	67/70 (96%)	50 (75%)	12 (18%)	5 (8%)	1	1
40	Ll	48/51 (94%)	44 (92%)	3 (6%)	1 (2%)	9	9
41	Lm	50/128 (39%)	43 (86%)	5 (10%)	2 (4%)	4	4
42	Ln	22/25 (88%)	20 (91%)	2 (9%)	0	100	100
43	Lo	102/106 (96%)	85 (83%)	15 (15%)	2 (2%)	9	9
44	Lp	89/92 (97%)	71 (80%)	13 (15%)	5 (6%)	2	2
45	Lr	123/137 (90%)	102 (83%)	15 (12%)	6 (5%)	3	3
46	Lz	215/217 (99%)	168 (78%)	31 (14%)	16 (7%)	1	1
49	SA	220/295 (75%)	187 (85%)	27 (12%)	6 (3%)	6	6
50	SB	212/264 (80%)	174 (82%)	30 (14%)	8 (4%)	4	4
51	SD	225/243 (93%)	183 (81%)	24 (11%)	18 (8%)	1	1
52	SE	260/263 (99%)	215 (83%)	30 (12%)	15 (6%)	2	2
53	SF	189/204 (93%)	144 (76%)	31 (16%)	14 (7%)	1	1
54	SH	187/194 (96%)	145 (78%)	27 (14%)	15 (8%)	1	1
55	SI	204/208 (98%)	168 (82%)	24 (12%)	12 (6%)	2	2
56	SK	96/165 (58%)	76 (79%)	16 (17%)	4 (4%)	3	3
57	SL	151/158 (96%)	130 (86%)	11 (7%)	10 (7%)	1	1
58	SP	95/145 (66%)	61 (64%)	21 (22%)	13 (14%)	0	0
59	SQ	144/146 (99%)	114 (79%)	20 (14%)	10 (7%)	1	1
60	SR	130/135 (96%)	104 (80%)	17 (13%)	9 (7%)	1	1
61	SS	148/152 (97%)	121 (82%)	13 (9%)	14 (10%)	1	1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
62	ST	141/145 (97%)	119 (84%)	16 (11%)	6 (4%)	3	3
63	SU	102/119 (86%)	86 (84%)	11 (11%)	5 (5%)	3	3
64	SV	81/83 (98%)	65 (80%)	11 (14%)	5 (6%)	2	2
65	SX	139/143 (97%)	114 (82%)	12 (9%)	13 (9%)	1	1
66	Sa	103/115 (90%)	77 (75%)	16 (16%)	10 (10%)	1	1
67	Sc	62/69 (90%)	47 (76%)	9 (14%)	6 (10%)	1	1
68	Sd	51/56 (91%)	44 (86%)	7 (14%)	0	100	100
69	Sf	69/156 (44%)	47 (68%)	10 (14%)	12 (17%)	0	0
70	Sg	311/317 (98%)	237 (76%)	58 (19%)	16 (5%)	2	2
71	SC	220/293 (75%)	188 (86%)	23 (10%)	9 (4%)	3	3
72	SG	235/249 (94%)	198 (84%)	26 (11%)	11 (5%)	3	3
73	SJ	183/194 (94%)	157 (86%)	16 (9%)	10 (6%)	2	2
74	SM	120/132 (91%)	79 (66%)	29 (24%)	12 (10%)	1	1
75	SN	148/151 (98%)	133 (90%)	8 (5%)	7 (5%)	3	3
76	SO	138/151 (91%)	101 (73%)	24 (17%)	13 (9%)	1	1
77	SW	127/130 (98%)	109 (86%)	13 (10%)	5 (4%)	4	4
78	SY	129/133 (97%)	108 (84%)	16 (12%)	5 (4%)	4	4
79	SZ	73/125 (58%)	59 (81%)	11 (15%)	3 (4%)	3	3
80	Sb	81/84 (96%)	67 (83%)	12 (15%)	2 (2%)	7	7
81	Se	56/59 (95%)	41 (73%)	11 (20%)	4 (7%)	1	1
All	All	11518/12905 (89%)	9598 (83%)	1346 (12%)	574 (5%)	5	3

5 of 574 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	LA	118	GLU
5	LB	360	LEU
6	LC	23	THR
6	LC	148	PRO
6	LC	186	SER

5.3.2 Protein sidechains ⓘ

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	LA	190/199 (96%)	189 (100%)	1 (0%)	92	92
5	LB	348/349 (100%)	348 (100%)	0	100	100
6	LC	305/348 (88%)	305 (100%)	0	100	100
7	LD	246/250 (98%)	246 (100%)	0	100	100
8	LE	215/252 (85%)	215 (100%)	0	100	100
9	LF	194/215 (90%)	194 (100%)	0	100	100
10	LG	203/223 (91%)	203 (100%)	0	100	100
11	LH	169/171 (99%)	169 (100%)	0	100	100
12	LI	180/181 (99%)	180 (100%)	0	100	100
13	LJ	148/149 (99%)	148 (100%)	0	100	100
14	LL	176/177 (99%)	176 (100%)	0	100	100
15	LM	118/161 (73%)	118 (100%)	0	100	100
16	LN	171/172 (99%)	171 (100%)	0	100	100
17	LO	173/174 (99%)	173 (100%)	0	100	100
18	LP	134/163 (82%)	134 (100%)	0	100	100
19	LQ	164/165 (99%)	164 (100%)	0	100	100
20	LR	166/175 (95%)	166 (100%)	0	100	100
21	LS	156/157 (99%)	156 (100%)	0	100	100
22	LT	139/140 (99%)	139 (100%)	0	100	100
23	LU	91/115 (79%)	91 (100%)	0	100	100
24	LV	101/107 (94%)	101 (100%)	0	100	100
25	LW	103/126 (82%)	103 (100%)	0	100	100
26	LX	108/133 (81%)	108 (100%)	0	100	100
27	LY	124/135 (92%)	124 (100%)	0	100	100
28	LZ	117/118 (99%)	117 (100%)	0	100	100
29	La	120/121 (99%)	120 (100%)	0	100	100
30	Lb	63/126 (50%)	63 (100%)	0	100	100
31	Lc	83/97 (86%)	83 (100%)	0	100	100
32	Ld	98/110 (89%)	98 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	Le	114/121 (94%)	114 (100%)	0	100	100
34	Lf	88/89 (99%)	88 (100%)	0	100	100
35	Lg	98/100 (98%)	98 (100%)	0	100	100
36	Lh	109/110 (99%)	109 (100%)	0	100	100
37	Li	86/89 (97%)	86 (100%)	0	100	100
38	Lj	73/80 (91%)	73 (100%)	0	100	100
39	Lk	64/65 (98%)	64 (100%)	0	100	100
40	Ll	47/48 (98%)	47 (100%)	0	100	100
41	Lm	48/116 (41%)	48 (100%)	0	100	100
42	Ln	23/24 (96%)	23 (100%)	0	100	100
43	Lo	93/94 (99%)	92 (99%)	1 (1%)	80	80
44	Lp	74/75 (99%)	74 (100%)	0	100	100
45	Lr	109/121 (90%)	109 (100%)	0	100	100
46	Lz	195/196 (100%)	195 (100%)	0	100	100
49	SA	184/243 (76%)	184 (100%)	0	100	100
50	SB	195/231 (84%)	195 (100%)	0	100	100
51	SD	190/202 (94%)	190 (100%)	0	100	100
52	SE	224/225 (100%)	224 (100%)	0	100	100
53	SF	161/170 (95%)	161 (100%)	0	100	100
54	SH	169/174 (97%)	169 (100%)	0	100	100
55	SI	178/180 (99%)	178 (100%)	0	100	100
56	SK	89/136 (65%)	89 (100%)	0	100	100
57	SL	137/142 (96%)	137 (100%)	0	100	100
58	SP	87/130 (67%)	87 (100%)	0	100	100
59	SQ	121/121 (100%)	121 (100%)	0	100	100
60	SR	120/122 (98%)	120 (100%)	0	100	100
61	SS	130/132 (98%)	130 (100%)	0	100	100
62	ST	113/115 (98%)	113 (100%)	0	100	100
63	SU	94/107 (88%)	94 (100%)	0	100	100
64	SV	67/67 (100%)	67 (100%)	0	100	100
65	SX	113/115 (98%)	113 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
66	Sa	90/98 (92%)	90 (100%)	0	100	100
67	Sc	57/62 (92%)	57 (100%)	0	100	100
68	Sd	47/49 (96%)	47 (100%)	0	100	100
69	Sf	64/140 (46%)	64 (100%)	0	100	100
70	Sg	272/275 (99%)	272 (100%)	0	100	100
71	SC	188/225 (84%)	188 (100%)	0	100	100
72	SG	207/218 (95%)	207 (100%)	0	100	100
73	SJ	161/168 (96%)	161 (100%)	0	100	100
74	SM	104/108 (96%)	104 (100%)	0	100	100
75	SN	130/131 (99%)	130 (100%)	0	100	100
76	SO	110/119 (92%)	110 (100%)	0	100	100
77	SW	112/113 (99%)	112 (100%)	0	100	100
78	SY	113/115 (98%)	113 (100%)	0	100	100
79	SZ	66/103 (64%)	66 (100%)	0	100	100
80	Sb	75/76 (99%)	75 (100%)	0	100	100
81	Se	47/48 (98%)	47 (100%)	0	100	100
All	All	10039/10997 (91%)	10037 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	LA	215	ASN
43	Lo	31	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 95 such sidechains are listed below:

Mol	Chain	Res	Type
25	LW	96	GLN
45	Lr	6	GLN
75	SN	58	HIS
29	La	41	HIS
33	Le	117	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3707/5070 (73%)	1303 (35%)	56 (1%)
2	L7	119/121 (98%)	21 (17%)	0
3	L8	155/157 (98%)	44 (28%)	2 (1%)
47	S2	1716/1869 (91%)	677 (39%)	22 (1%)
48	S6	74/75 (98%)	28 (37%)	2 (2%)
All	All	5771/7292 (79%)	2073 (35%)	82 (1%)

5 of 2073 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	4	G
1	L5	6	C
1	L5	9	C
1	L5	13	U
1	L5	17	A

5 of 82 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	3625	G
1	L5	4600	G
47	S2	1404	U
1	L5	3673	C
1	L5	3784	A

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 245 ligands modelled in this entry, 245 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
43	Lo	1
66	Sa	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Lo	105:GLN	C	106:PHE	N	3.21
1	Sa	99:PRO	C	100:ARG	N	3.14