



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 01:07 PM UTC

PDB ID : 4UG0 / pdb_00004ug0
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 : 3.60 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:

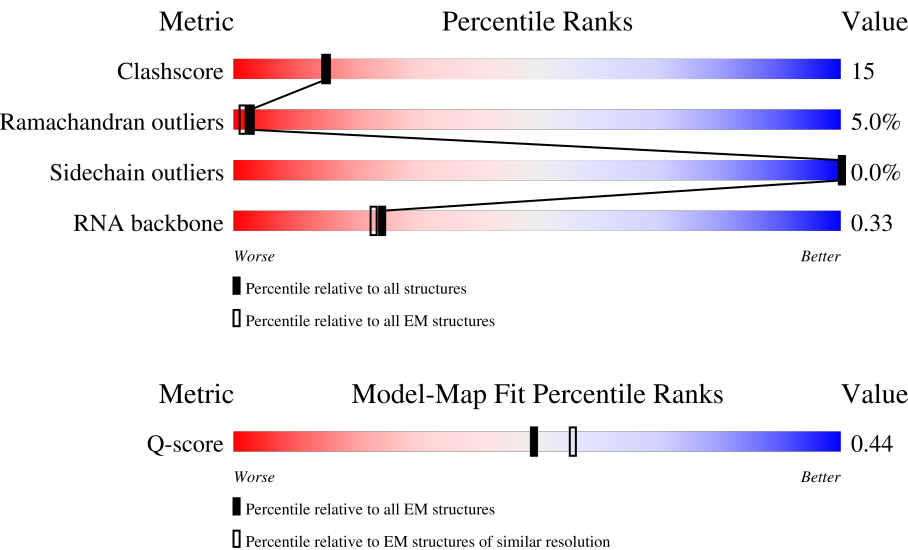
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.60 Å.

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



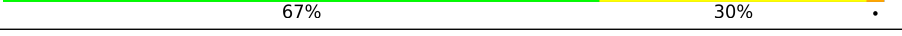
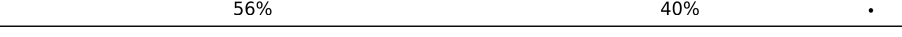
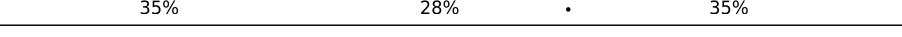
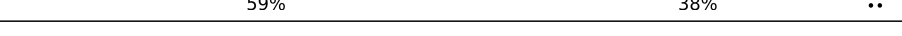
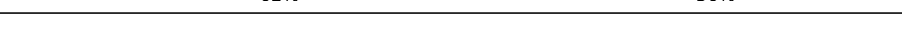
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12797 (3.10 - 4.10)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	L5	5070	30%30%14%26%
2	L7	121	55%36%7%
3	L8	157	46%40%13%

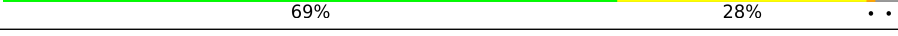
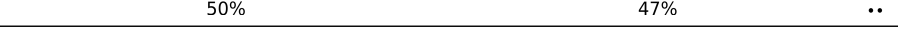
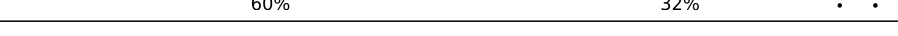
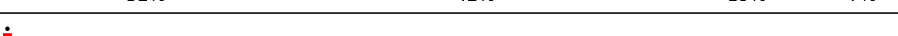
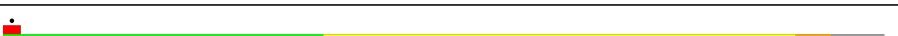
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Mol	Chain	Length	Quality of chain
4	LA	257	
5	LB	403	
6	LC	427	
7	LD	297	
8	LE	288	
9	LF	248	
10	LG	266	
11	LH	192	
12	LI	214	
13	LJ	178	
14	LL	211	
15	LM	215	
16	LN	204	
17	LO	203	
18	LP	184	
19	LQ	188	
20	LR	196	
21	LS	176	
22	LT	160	
23	LU	128	
24	LV	140	
25	LW	157	
26	LX	156	
27	LY	145	
28	LZ	136	

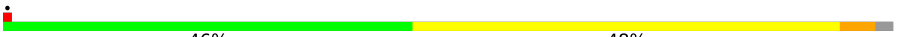
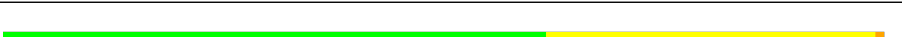
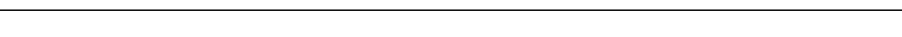
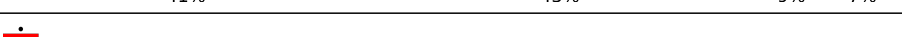
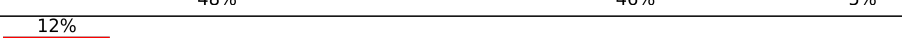
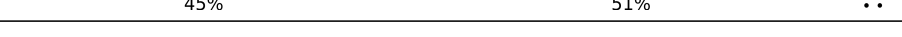
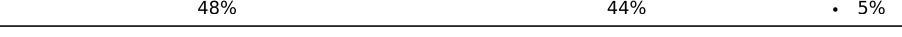
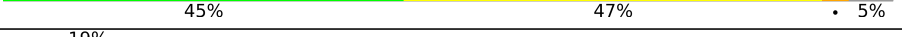
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Mol	Chain	Length	Quality of chain
29	La	148	
30	Lb	159	
31	Lc	115	
32	Ld	125	
33	Le	135	
34	Lf	110	
35	Lg	117	
36	Lh	123	
37	Li	105	
38	Lj	97	
39	Lk	70	
40	Ll	51	
41	Lm	128	
42	Ln	25	
43	Lo	106	
44	Lp	92	
45	Lr	137	
46	Lz	217	
47	S2	1869	
48	S6	75	
49	SA	295	
50	SB	264	
51	SD	243	
52	SE	263	
53	SF	204	

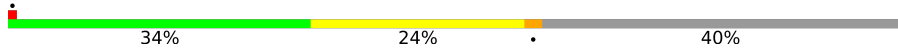
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Mol	Chain	Length	Quality of chain
54	SH	194	
55	SI	208	
56	SK	165	
57	SL	158	
58	SP	145	
59	SQ	146	
60	SR	135	
61	SS	152	
62	ST	145	
63	SU	119	
64	SV	83	
65	SX	143	
66	Sa	115	
67	Sc	69	
68	Sd	56	
69	Sf	156	
70	Sg	317	
71	SC	293	
72	SG	249	
73	SJ	194	
74	SM	132	
75	SN	151	
76	SO	151	
77	SW	130	
78	SY	133	

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Mol	Chain	Length	Quality of chain
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 28S ribosomal RNA.

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 5S ribosomal RNA.

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 5.8S ribosomal RNA.

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 18S ribosomal RNA.

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 (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
82	L5	149	Total	Mg	0
			149	149	
82	L7	5	Total	Mg	0
			5	5	
82	L8	2	Total	Mg	0
			2	2	
82	LA	1	Total	Mg	0
			1	1	
82	LB	1	Total	Mg	0
			1	1	
82	LH	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
82	LJ	1	Total 1	Mg 1	0
82	LN	1	Total 1	Mg 1	0
82	LP	1	Total 1	Mg 1	0
82	LQ	1	Total 1	Mg 1	0
82	La	1	Total 1	Mg 1	0
82	Le	1	Total 1	Mg 1	0
82	Ll	1	Total 1	Mg 1	0
82	S2	66	Total 66	Mg 66	0
82	S6	7	Total 7	Mg 7	0

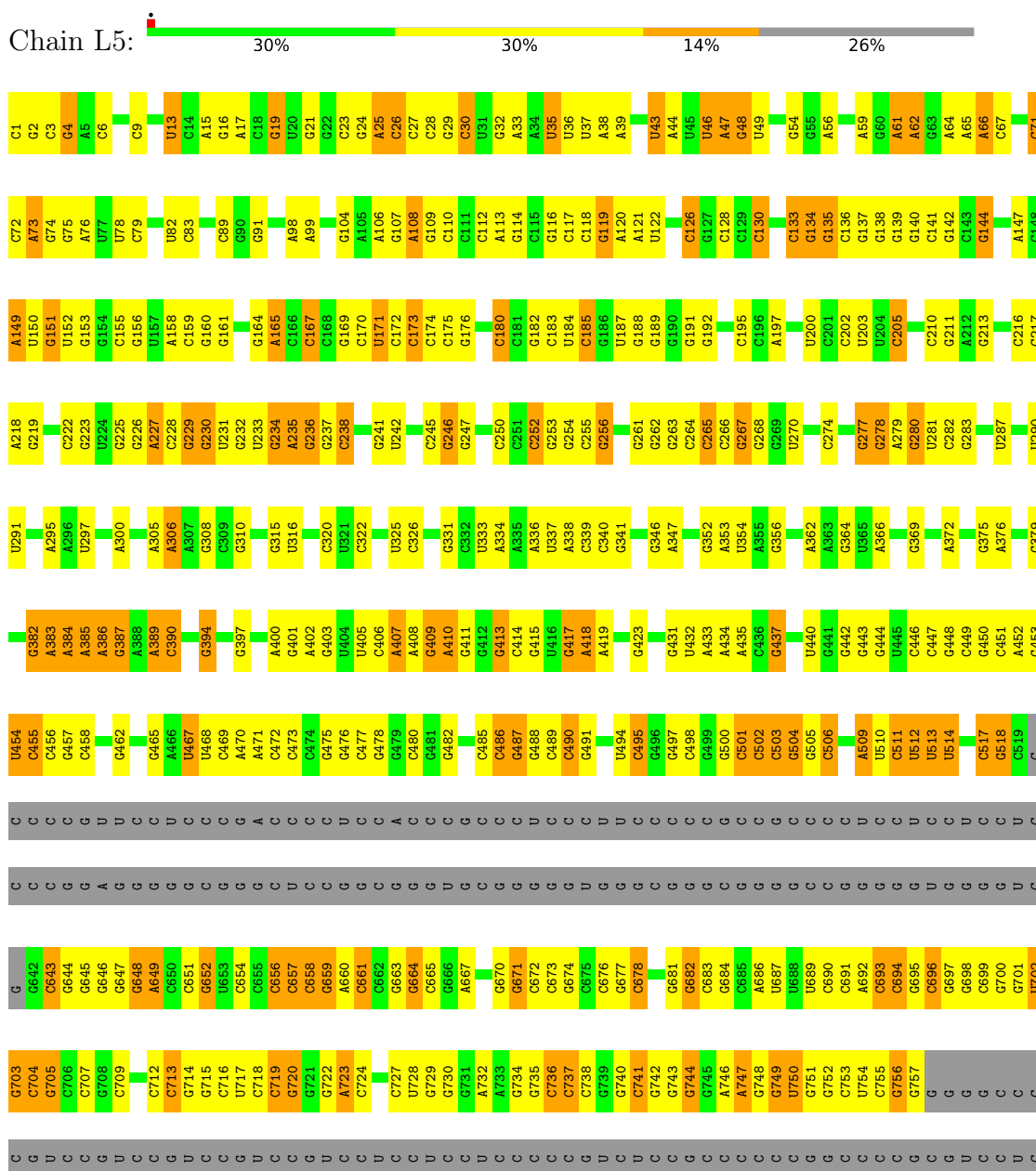
- Molecule 83 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
83	Lg	1	Total 1	Zn 1	0
83	Lj	1	Total 1	Zn 1	0
83	Lm	1	Total 1	Zn 1	0
83	Lo	1	Total 1	Zn 1	0
83	Lp	1	Total 1	Zn 1	0
83	Sa	1	Total 1	Zn 1	0

3 Residue-property plots

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 and atom inclusion in map density. 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. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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: 28S ribosomal RNA

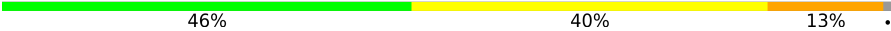


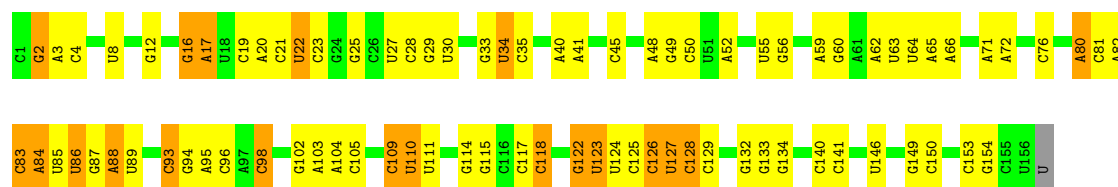
U1781	C	A1634	A1554	C1478	C1331	G1258	G1195	G1073	A	G950	G	C
A1788	G1718	A1638	G1555	G1479	C1332	G1259	G1196	G1074	A	G951	C	C
A1789	A1719	A1638	C1556	C1480	A1333	G1260	G1197	G1075	U	G952	G	U
A1793	G1720	G1641	A1562	C1481	U1339	G1261	G1198	C1076	C	G953	G	C
G1798	G1721	A1646	A1563	C1482	U1340	G1262	G1199	C1077	C	C954	C	G
G1799	A1722	A1646	A1564	C1483	U1341	C1264	G1200	A1078	C	G955	G	G
A1800	G1724	U1649	A1565	G1484	A1342	G1265	U1201	C1079	C	A956	G	G
A1801	U1725	A1650	A1566	C1485	A1343	G1266	C1202	C1080	C	G957	A	A
A1802	U1726	A1651	U1567	G1486	U1410	G1267	G1203	C1081	G	G958	G	G
A1803	U1727	G1651	C1568	G1487	U1411	C1268	C1204	U1082	C	G959	C	C
G1804	U1728	G1654	U1573	G1488	C1350	G1269	G1205	U1083	G	A960	C	G
A1805	A1729	C1655	G1574	G1489	G1351	G1270	U1209	C1084	A	G961	G	C
A1806	U1730	U1656	G1577	A1491	C1352	G1271	C1210	C1085	C	C962	A	C
C1807	C1731	G1657	U1578	G1492	A1354	G1272	G1211	C1086	C	G963	C	C
G1811	G1732	U1660	U1579	G1493	C1355	G1273	G1212	C1087	G	A964	A	A
G1815	G1733	C1661	C1579	U1494	U1356	G1274	G1213	C1088	C	G965	C	C
G1818	G1734	G1667	U1580	G1495	C1357	G1275	C1214	C1089	G	A966	C	G
G1819	U1735	U1670	G1581	G1496	G1358	G1276	G1215	C1090	C	C967	C	C
G1820	A1736	G1670	U1582	A1497	G1359	G1277	C1216	C1091	U	C968	C	G
G1821	A1737	G1670	U1591	G1501	G1360	C1278	G1217	C1092	C	C969	C	U
G1822	G1738	C1676	A1592	G1502	G1361	G1279	G1218	C1093	C	G970	C	C
G1823	G1739	U1677	A1593	A1503	G1362	C1280	G1219	A1095	C	C974	C	G
A1825	A1740	G1680	C1594	G1504	U1364	G1281	G1220	C1096	C	G975	G	G
G1829	A1741	G1681	U1595	C1505	C1365	U1285	A1222	C1097	C	G976	G	G
G1832	U1742	G1686	G1596	G1506	C1366	G1286	U1221	U1100	C	C977	U	C
G1833	U1743	G1687	C1597	A1508	C1367	G1287	G	C	C	G978	G	G
G1834	U1744	G1688	U1598	C1509	A1368	G1288	U	C	C	C979	A	C
G1835	U1745	G1691	C1599	G1510	C1369	G1289	U	C	C	U980	C	G
G1836	U1746	G1692	U1600	G1511	G1370	G1290	U	C	C	U981	C	G
G1837	U1747	G1693	A1601	U1512	A1371	U1291	C	C	C	U982	C	G
G1838	U1748	G1694	U1606	G1513	C1372	C1292	U	C	C	C983	C	C
G1839	U1749	U1695	C1607	U1514	C1373	C1293	U	C	C	C984	C	G
G1840	G1750	C1696	G1608	G1515	C1374	A1294	C	C	C	C985	C	C
C	G1751	A1699	U1609	C1520	C1375	G1295	G1232	C	C	C986	C	C
G1842	U1752	G	C1610	A1523	C1376	G1296	G1233	C	C	C987	C	C
U1852	U1753	A	G1611	G1524	G1377	U1297	G1234	C	C	C988	C	G
G1855	U1754	C	G1612	G1525	C1378	C1298	G1235	C	C	U989	C	C
G1856	U1755	C	G1613	A1527	C1379	C1301	C1236	C	C	C990	C	G
U1861	U1756	C	G1614	G1530	U1380	U1302	A1237	C	C	C991	C	G
U1862	A1757	C	G1615	A1534	G1381	U1303	C1238	C	C	G992	C	C
U1866	A1758	C	U1538	U1538	G1382	C1304	G1240	C	C	G993	G	G
A1867	G1759	C	G1539	C1540	U1383	G1305	G1241	C	C	G994	G	G
A1868	U1760	C	G1540	C1541	G1384	C1306	G1242	C	C	C995	C	U
G1869	U1761	C	U1541	A1547	A1387	U1317	C1243	C	C	G996	C	G
G1870	U1762	C	G1542	C1548	U1388	U1320	G1244	C	C	C	C	G
A1871	U1763	C	G1543	G1549	G1389	G1321	C1245	C	C	C	C	C
G1872	C1764	C	G1550	G1551	A1391	G1322	U1246	C	C	A	C	C
	U1765	C	C1551	C1552	A1392	A1321	C1247	C	C	C	C	C
	A1766	C	G1552	A1553	G1393	G1323	C1248	C	C	C	C	C
	U1767	C	G1553		A1394	A1324	G1249	C	C	C	C	C
	A1768	C	G1554		U1395	A1325	C1250	C	C	C	C	C
	G1769	C	G1555		G1396	G1326	C1251	C	C	C	C	C
	U1770	C	G1556		U1397	C1327	C1252	C	C	C	C	C
	U1771	C	G1557		A1398	G1328	A1254	C	C	C	C	C
	U1772	C	G1558		A1399	A1329	A1255	C	C	C	C	C
	U1773	C	G1559		G1400	A1330	A1256	C	C	C	C	C
	C1774	C	G1560		C1401		A1257	C	C	C	C	C
	U1775	C	G1561		C1402			C	C	C	C	C
	A1776	C	G1562		G1403			C	C	C	C	C
	G1777	C	G1563		G1404			C	C	C	C	C
	C1778	C	G1564		C1405			C	C	C	C	C
		C	G1565		C1406			C	C	C	C	C
		C	G1566		C1407			C	C	C	C	C
		C	G1567		G1408			C	C	C	C	C
		C	G1568		C1409			C	C	C	C	C
		C	G1569		U1410			C	C	C	C	C
		C	G1570		A1411			C	C	C	C	C
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		C	G1583		U1424			C	C	C	C	C
		C	G1584		G1425			C	C	C	C	C
		C	G1585		U1426			C	C	C	C	C
		C	G1586		G1427			C	C	C	C	C
		C	G1587		U1428			C	C	C	C	C
		C	G1588		G1429			C	C	C	C	C
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		C	G1594		G1435			C	C	C	C	C
		C	G1595		C1436			C	C	C	C	C
		C	G1596		U1437			C	C	C	C	C
		C	G1597		C1438			C	C	C	C	C
		C	G1598		U1439			C	C	C	C	C
		C	G1599		C1440			C	C	C	C	C
		C	G1600		G1441			C	C	C	C	C
		C	G1601		C1442			C	C	C	C	C
		C	G1602		G1443			C	C	C	C	C
		C	G1603		C1444			C	C	C	C	C
		C	G1604		U1445			C	C	C	C	C
		C	G1605		C1446			C	C	C	C	C
		C	G1606		G1447			C	C	C	C	C
		C	G1607		C1448			C	C	C	C	C
		C	G1608		U1449			C	C	C	C	C
		C	G1609		G1450			C	C	C	C	C
		C	G1610		C1451			C	C	C	C	C
		C	G1611		G1452			C	C	C	C	C
		C	G1612		C1453			C	C	C	C	C
		C	G1613		G1454			C	C	C	C	C
		C	G1614		C1455			C	C	C	C	C
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		C	G1617		U1458			C	C	C	C	C
		C	G1618		C1459			C	C	C	C	C
		C	G1619		G1460			C	C	C	C	C
		C	G1620		C1461			C	C	C	C	C
		C	G1621		U1462			C	C	C	C	C
		C	G1622		G1463			C	C	C	C	C
		C	G1623		C1464			C	C	C	C	C
		C	G1624		U1465			C	C	C	C	C
		C	G1625		C1466			C	C	C	C	C
		C	G1626		G1467			C	C	C	C	C
		C	G1627		A1468			C	C	C	C	C
		C	G1628		C1469			C	C	C	C	C
		C	G1629		U1470			C	C	C	C	C
		C	G1630		G1471			C	C	C	C	C
		C	G1631		C1472			C	C	C	C	C
		C	G1632		U1473			C	C	C	C	C
		C	G1633		G1474			C	C	C	C	C
		C	G1634		C1475			C	C	C	C	C
		C	G1635		U1476			C	C	C	C	C
		C	G1636		C1477			C	C	C	C	C
		C	G1637		G1478			C	C	C	C	C
		C	G1638		U1479			C	C	C	C	C
		C	G1639		C1480			C	C	C	C	C
		C	G1640		G1481			C	C	C	C	C
		C	G1641		C1482			C	C	C	C	C
		C	G1642		U1483			C	C	C	C	C
		C	G1643		G1484			C	C	C	C	C
		C	G1644		C1485			C	C	C	C	C
		C	G1645		U1486			C	C	C	C	C
		C	G1646		G1487			C	C	C	C	C
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		C	G1648		U1489			C	C	C	C	C
		C										





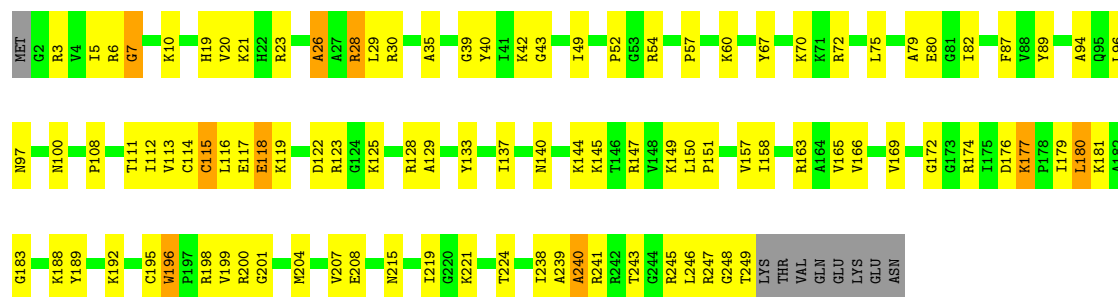


Chain L8:  46% 40% 13% .



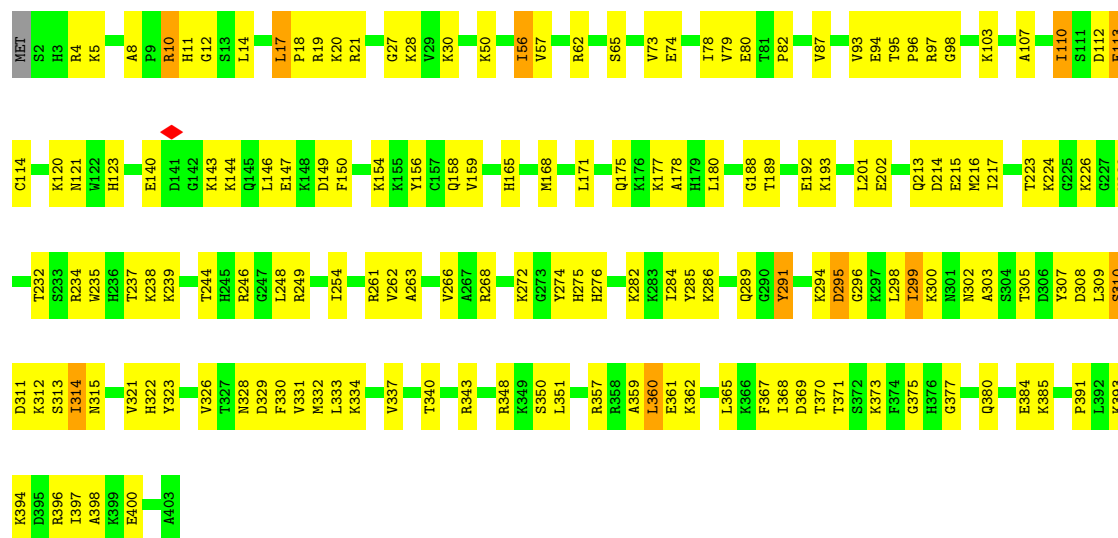
• Molecule 4: 60S RIBOSOMAL PROTEIN L8

Chain LA:  58% 35% . .



• Molecule 5: 60S RIBOSOMAL PROTEIN L3

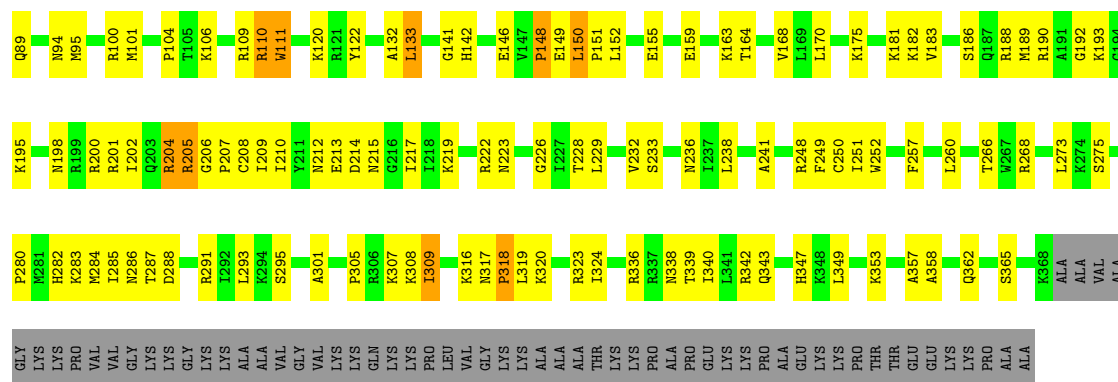
Chain LB:  60% 37% .



• Molecule 6: 60S RIBOSOMAL PROTEIN L4

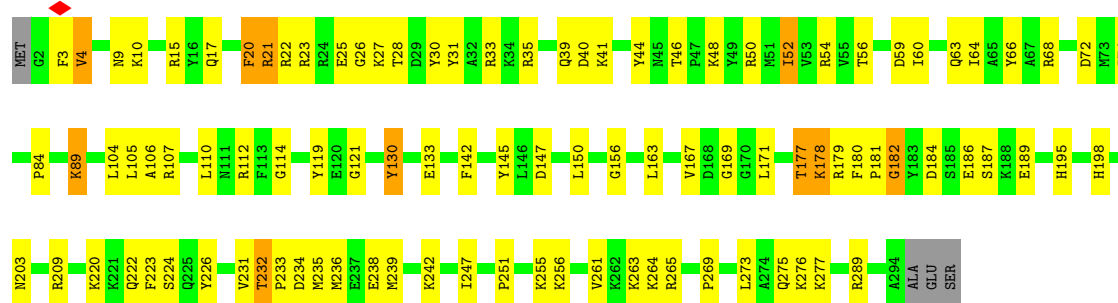
Chain LC:  51% 33% . 14%





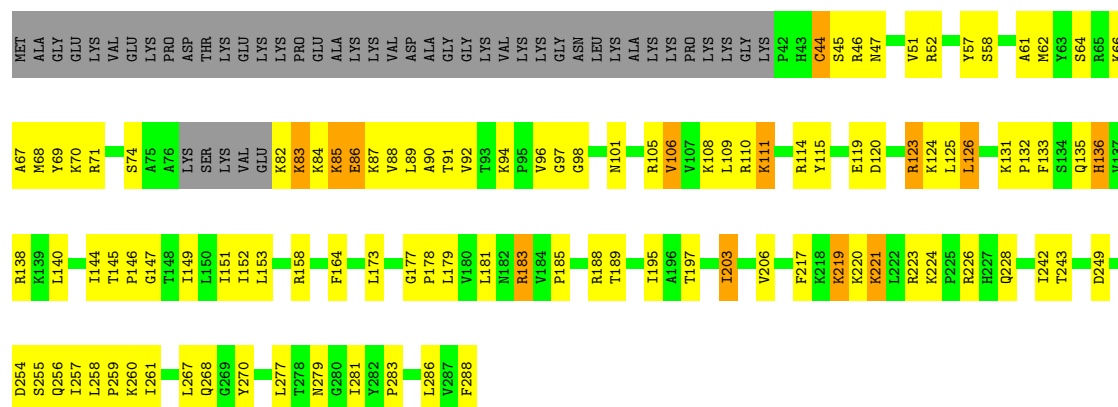
• Molecule 7: 60S RIBOSOMAL PROTEIN L5

Chain LD: 65% 30% ..



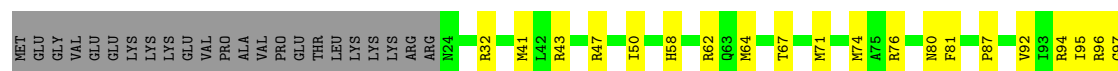
• Molecule 8: 60S RIBOSOMAL PROTEIN L6

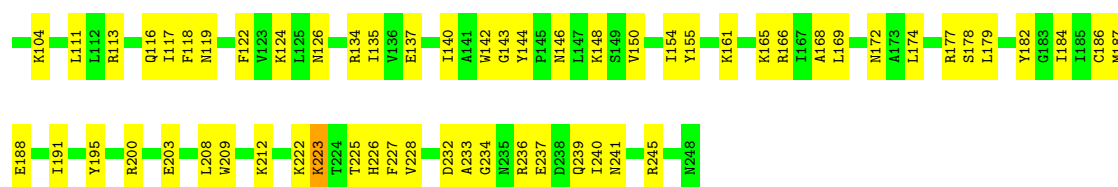
Chain LE: 47% 32% 5% 16%



• Molecule 9: 60S RIBOSOMAL PROTEIN L7

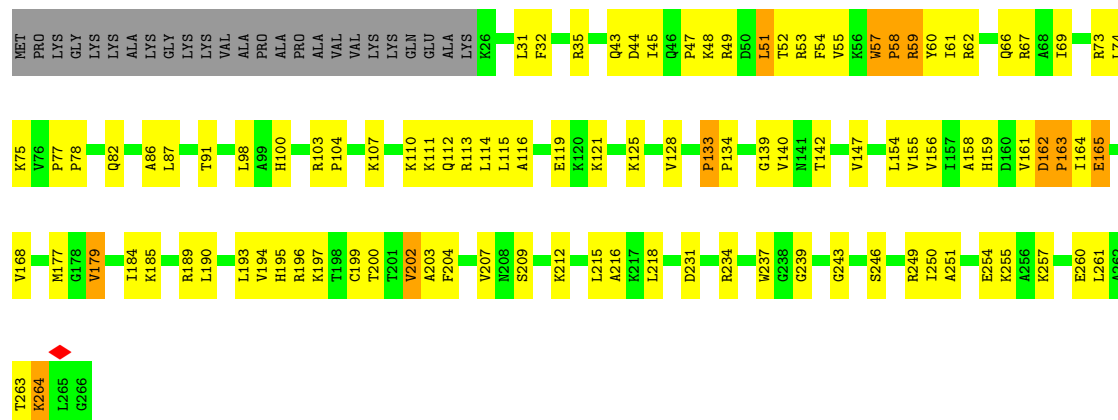
Chain LF: 59% 31% 9%





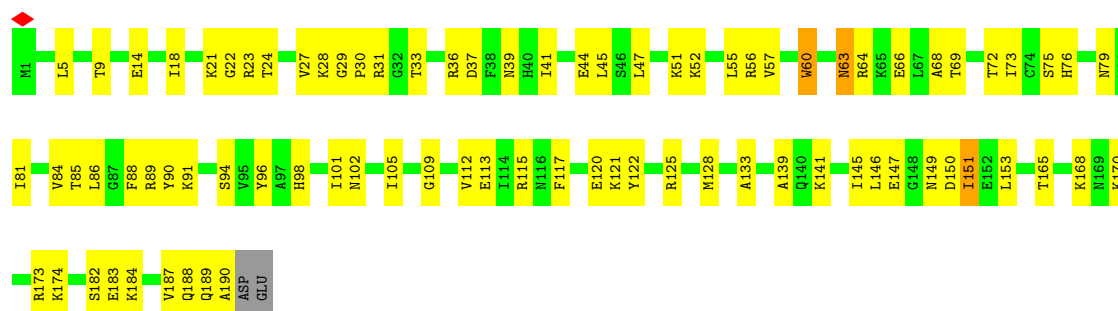
• Molecule 10: 60S RIBOSOMAL PROTEIN L7A

Chain LG: 52% 35% 9%



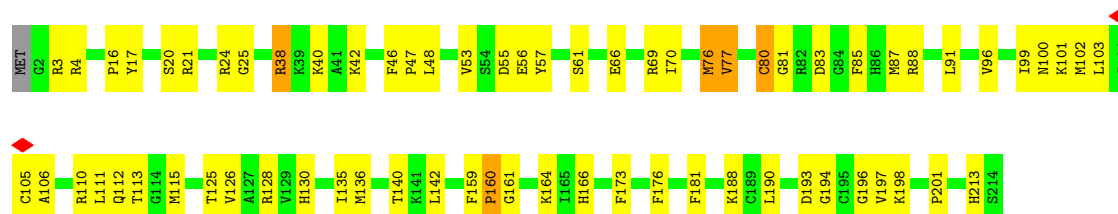
• Molecule 11: 60S RIBOSOMAL PROTEIN L9

Chain LH: 56% 42% 2%



• Molecule 12: 60S RIBOSOMAL PROTEIN L10-LIKE

Chain LI: 67% 30% 3%



• Molecule 13: 60S RIBOSOMAL PROTEIN L11

S158	T73	ME1
K159	V74	Q3
E150	L83	G6
M163	F84	E7
	K85	K8
F166	G86	E9
	L87	N10
K169	K88	P11
L174	E91	M12
L176		R13
P176	R95	
G177	K96	R16
K178	N98	
	F99	K19
	S100	L20
		C21
	M104	L22
	F105	M23
	G106	I24
	F107	
	G108	E28
	I109	S29
	Q110	G30
	E111	D31
	H112	R32
	I113	L33
	D114	T34
	L115	R35
	G116	A36
	Y119	L40
	S122	T44
		G45
	I125	Q46
	Y126	T47
	G127	P48
	L128	V49
		F50
	Y131	A53
	V132	R54
	V133	Y55
		T56
	P137	V57
	G138	R58
		S59
	K144	F60
	R146	G61
	R147	I62
		R63
		R64
	I151	K67
	G152	
	A153	V70
	K154	H71
	H155	C72

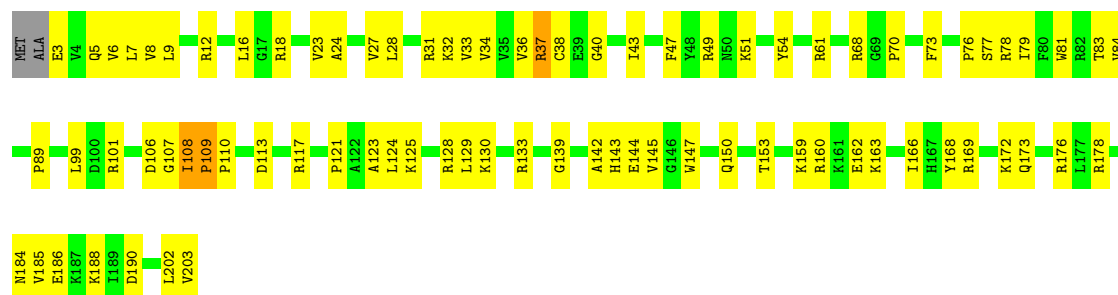
E171	K89	ME1
E172	V90	A2
E173	A91	P3
K174	R92	
	T93	K11
R186	I94	
	G95	W18
E204	I96	Q19
Q205	S97	
	V98	V22
E208	D99	
	P100	W25
K211	R101	
	S106	Q28
	T107	P29
	E108	A30
	S109	
	K123	R34
		R35
	L126	R36
	R129	
	S132	R39
	A133	O40
		A41
	G137	A43
	D138	R44
	S139	R45
	S140	T46
	E143	A47
		P48
	L146	R49
	A147	P50
	T148	A51
	Q149	S52
	L150	G53
	T151	P54
	G152	I55
	P153	R56
	V154	P57
	M155	T58
	P156	V59
	V157	R60
	R158	C61
	M159	P62
	V160	T63
	Y161	V64
	K162	R65
	E164	Y66
	K165	H67
	A166	T68
	R167	
	V168	G73
	I169	R74
	T170	G75
		F76
		S77
		E80

Lys	W86	MET
Lys	A87	V2
ILE	A88	F3
THR	T89	R4
ALA	R90	R5
ALA	W91	F6
SER		V7
Lys	K94	
Lys	I95	R11
ALA	E96	
PRO	A97	S16
ALA	R98	F17
GLN	E99	G18
Lys		P19
VAL	K103	H20
PRO		
ALA	F107	K23
GLN	D108	L24
Lys	R109	A25
ALA	F110	A26
THR	K111	I27
GLY		V28
GLN	K117	D29
Lys	M118	V30
ALA	R119	I31
ALA	N120	
PRO		N34
ALA	I123	R35
PRO		
Lys	E126	V38
ALA	V127	D39
GLN	K128	G40
Lys		P41
GLY	Q131	C42
GLN		T43
Lys	S139	R44
ALA	P140	V45
PRO	Lys	R46
ALA	Lys	R47
GLN	ALA	
Lys	PRO	P51
ALA	GLY	F52
PRO	THR	A53
ALA	Lys	C54
PRO	GLY	M55
Lys	THR	O56
ALA	ALA	L57
SER	ALA	
GLY	ALA	H69
Lys	ALA	Q70
Lys	ALA	K71
Lys	ALA	V72
ALA	ALA	V73
ALA	ALA	R74
ALA	ALA	Q75
ALA	ALA	A76
Lys	Lys	W77
VAL	VAL	
PRO	PRO	I82
ALA	ALA	

H181	A95	MET
H182	R96	G2
T183	S97	I7
I184	L98	L10
G185		M11
	R108	Q15
R188	A112	S16
R193	L113	R20
R194	R114	R26
T197	L116	C27
L198	S118	V28
Q199	S119	Q29
L200	V120	G30
H201	V121	R31
R202	G122	Q32
Y203	E123	L36
R204	D124	R37
	S125	R38
	K128	A39
	E131	R44
	V132	P45
	L133	D46
	L134	K47
	L135	A48
	D136	R49
	P137	R50
	N145	Y53
	P146	R56
	D147	Y59
T148	T148	V60
Q149	Q149	L61
V150	V150	Y62
I151	I151	R63
T152	T152	L64
	V155	R67
H156	H156	B68
K157	K157	R73
H158	H158	P84
R159	R159	V85
E160	E160	H86
H161	H161	H87
R162	R162	G88
G163	G163	V89
L164	L164	L92
R169	R169	R93
R172	R172	F94
G173	G173	
L174	L174	
H178	H178	

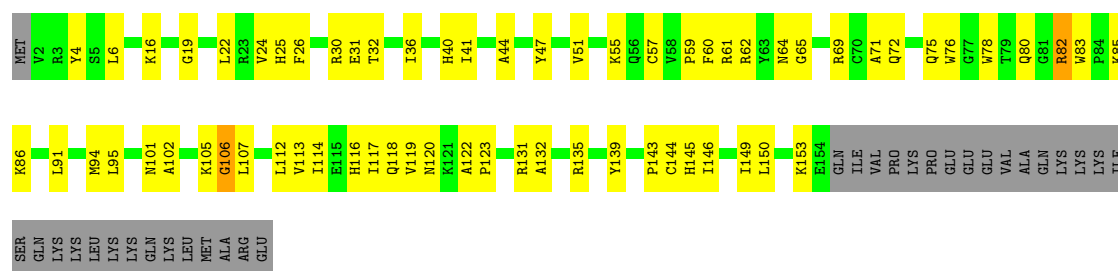
- Molecule 17: 60S RIBOSOMAL PROTEIN L13A

Chain LO:  59% 38%



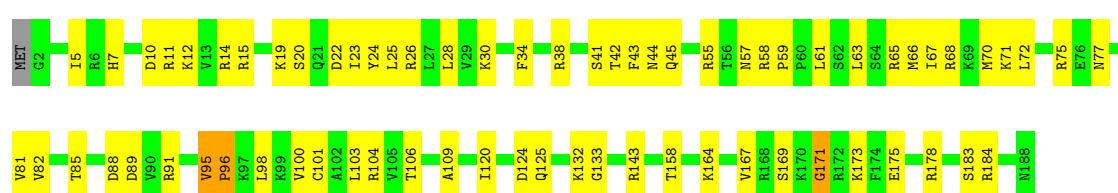
- Molecule 18: 60S RIBOSOMAL PROTEIN L17

Chain LP:  48% 34% 17%



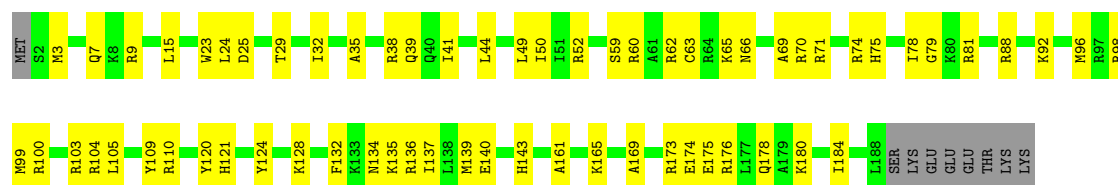
- Molecule 19: 60S RIBOSOMAL PROTEIN L18

Chain LQ:  63% 35%



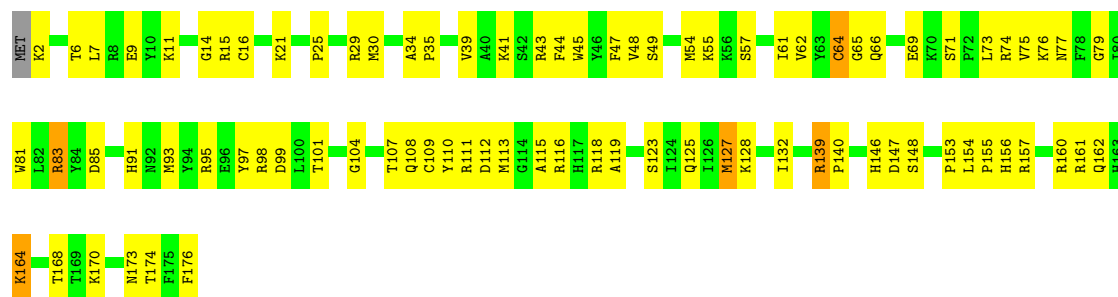
- Molecule 20: 60S RIBOSOMAL PROTEIN L19

Chain LR:  63% 33% 5%



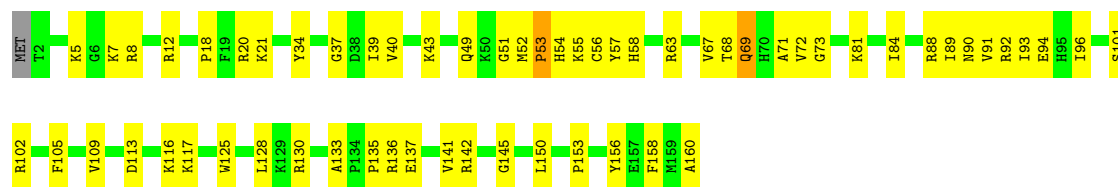
- Molecule 21: 60S RIBOSOMAL PROTEIN L18A

Chain LS:  52% 45%



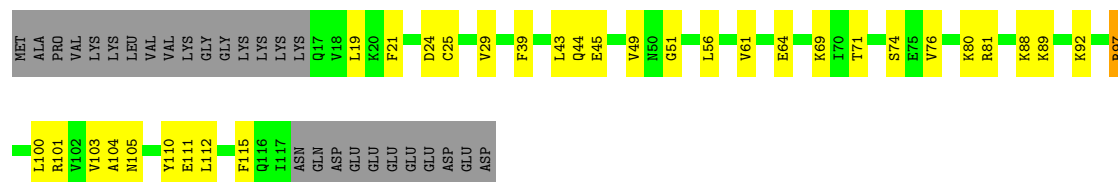
• Molecule 22: 60S RIBOSOMAL PROTEIN L21

Chain LT: 62% 36% ..



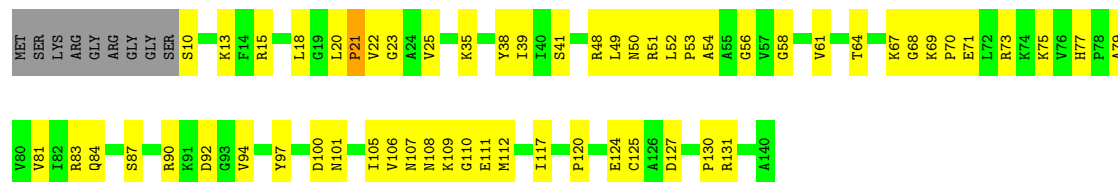
• Molecule 23: 60S RIBOSOMAL PROTEIN L22

Chain LU: 53% 25% 21%



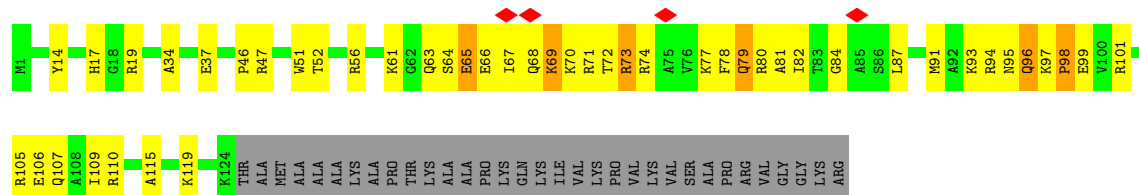
• Molecule 24: 60S RIBOSOMAL PROTEIN L23

Chain LV: 52% 41% 6%



• Molecule 25: 60S RIBOSOMAL PROTEIN L24

Chain LW: 49% 26% 21%



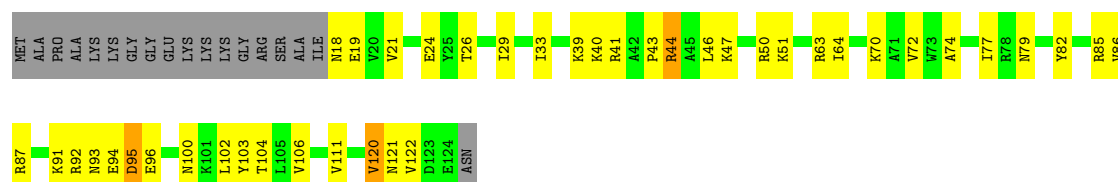
- Molecule 31: 60S RIBOSOMAL PROTEIN L30

Chain Lc: 



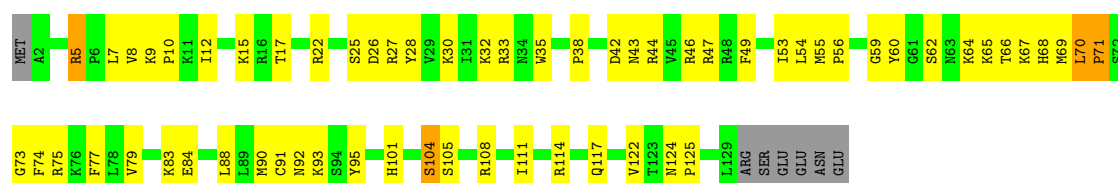
- Molecule 32: 60S RIBOSOMAL PROTEIN L31

Chain Ld: 



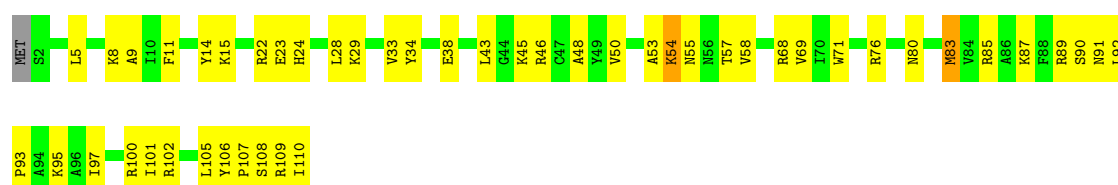
- Molecule 33: 60S RIBOSOMAL PROTEIN L32

Chain Le: 



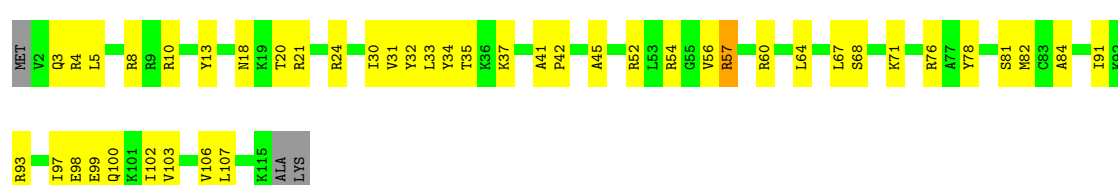
- Molecule 34: 60S RIBOSOMAL PROTEIN L35A

Chain Lf: 



- Molecule 35: 60S RIBOSOMAL PROTEIN L34

Chain Lg: 



[illegible]

- Molecule 42: 60S RIBOSOMAL PROTEIN L41

Chain Ln: 



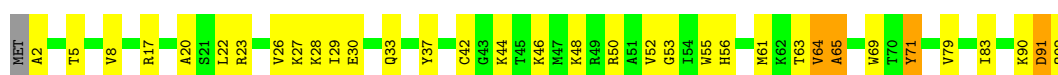
- Molecule 43: 60S RIBOSOMAL PROTEIN L36A

Chain Lo: 



- Molecule 44: 60S RIBOSOMAL PROTEIN L37A

Chain Lp: 



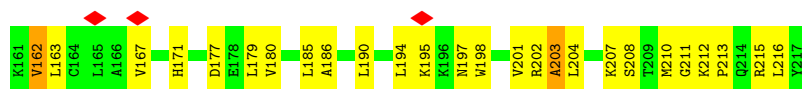
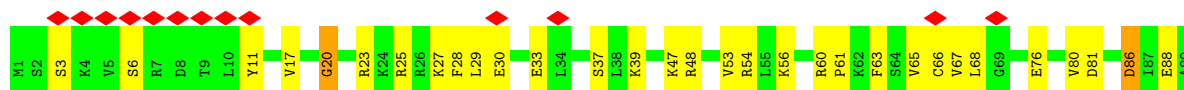
- Molecule 45: 60S RIBOSOMAL PROTEIN L28

Chain Lr: 

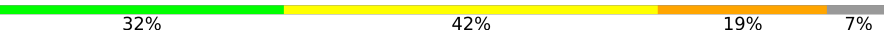


- Molecule 46: 60S RIBOSOMAL PROTEIN L10A

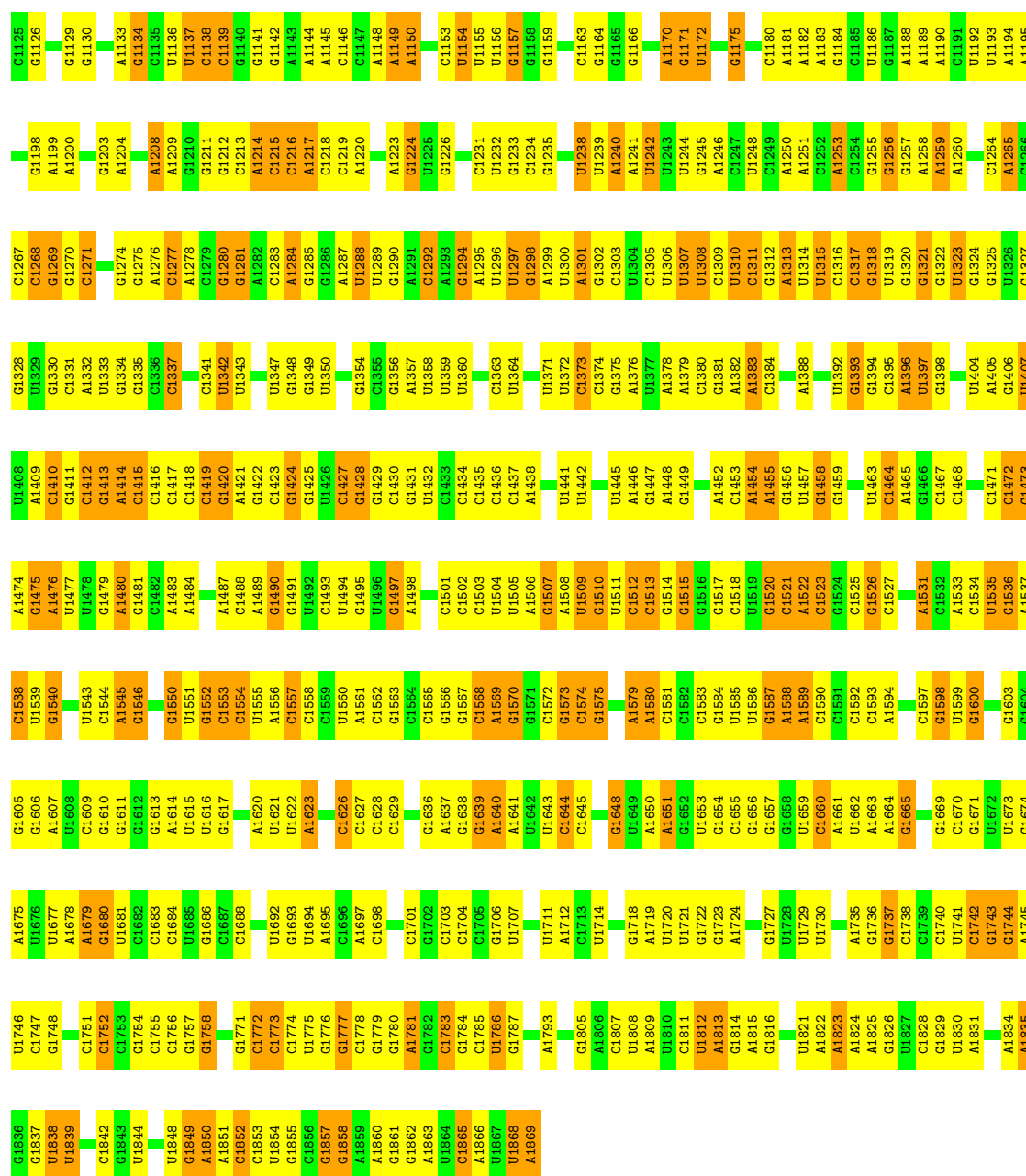
Chain Lz: 



- Molecule 47: 18S ribosomal RNA

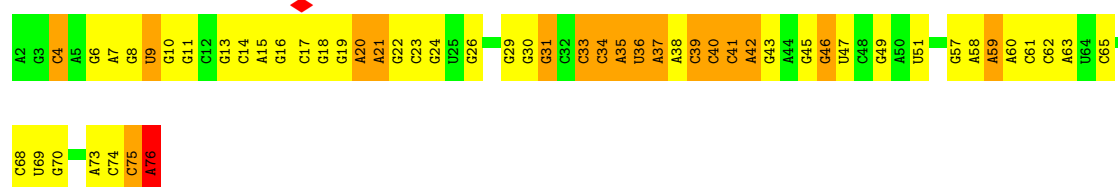
Chain S2: 

G1047	G970	A904	C833	U	C	A641	U566	G594	G431	U359	C293	A	G167	A77	U1
C1047	G971	C905	C834	C	C	U642	C570	G505	G432	A360	U294	C	C168	C76	A2
A1052	A972	U906	C835	U	G	A643	U571	G506	A433	C362	C295	C	U169	A79	C3
G1053	C973	G907	C836	U	C	G644	U572	G507	G434	C363		A	U170	C84	C4
G1054	C974	A908	A837	A	C	G645	U573	A508	A365	A508	A299	A	A171	A83	G7
G1055	G975	G909	C838	G	C	G646	U574	G509	G436	A364		C	U172	A84	U8
A1056	G976	G910	C839	C	C	U647	A574	G510	G437			C			U9
U1057	G977	C911	C840	U	G	A648	A575	U511	G438	U367		C	A175	U93	C14
C1057	G978	G912	G841	G	A	U649	A576		A439	U368		G	U176	G94	C17
G1058	C979	A913	C842	A	G	A650		U514	G440	C369		G	G177	C98	C18
A1059	A980	U914	C843	G	G	U651	U581	G515	C441	G370		U	C178	A99	G23
U1060	A981	U844	U844	U	C	U652	C582	A516		A371		C	G179	C17	U28
G1061	G982	C845	C845	G	G		C583	C517	A445			A	G180	G17	U29
A1062	A983	G846	G846	U	A	A655	G584	G518		U375		G	A181	A103	U31
	G986	A847	U848	C	G	G856	C585	A519	A448	A376		C	A182		G33
G1065	A920	C851	C851	C	G	U657	C586		A449	G377		C			A38
G1068	G921	C852	C852	C	C	U658	A587	A522	A450	G378		C	G184	U109	A39
U1069	A922	C853	C853	G	A	G659	A588	A523	C450	C379		C	G185	A25	A40
A1070	G923			G	C	C660	G589	U524	G451	G380		C	C186	U26	A41
G1071	G924			C	C	U661	A590	A525	G452	C381		U	G187	A27	G41
	G925			G	G	G662	A591	C526		C382		U	C188	U115	G42
G1076	A926	U863	U863	C	C		U591	C527	A459	U382		C	U189	U116	G43
A1077	C927	G864	G864	C	C	U666	C592	A528	A464	U383		C	C117	C117	U44
C1078	G928	A865	A865	C	C	U667	A594	A529	A465	U384		C	A191	U119	U45
G1079	G929			C	C	A668	U595	U530	G466	G385		G	C192		U46
A1080	C930	G868	G868	C	C	A689	U596	A531	G467	C387		C	C193	G122	A43
U1081	C931	A869	A869	G	C	U670	G597	C532	A468	U388		C	C194	G123	U44
U1082	G932	A870	A870	C	C	A671	G598	A533	A469	A389		C	C195		A45
A1083	G933	U871	U871	C	C	G672	A599	G534	G470	C390		C	C196	G126	A46
C1084	G934	A872	A872	C	C	U673	G600	C535	G471	C391		C	U197	C127	G41
G1085	C937	G873	G873	C	C	G674		A536	C472	G327		G	U198	U128	A42
U1086	A938	G874	G874	C	C	U675	A604	C537	A473	U328		C	C201	C129	U43
G1087	C939	A875	A875	C	C	A679	A605	U538	G474	C400		C	G202		U44
U1088	U940	C876	C876	U	U		G606	C539		A401		C	G203		U45
G1096	G941	C877	C877	C	C	U682	U607	U540	G477	C402		C	G204	C134	A50
U1017	C942	G878	G878	C	C	G683	U608	U541	G480	U406		G	G205		U53
U1018	U943	C880	C880	U	U	G684	G613	G543	C481	G407		G	G207	A141	G52
C1019	A944	G881	G881	U	U	U685	C614	G544	G482	A408		G	G208	C142	C53
G1020		U882	U882	C	C	U686	G617	G546	C483	C409		C	A209	U143	A54
U1021	C947	C884	C884	C	C	G687	U618	C547	A484	G410		C	G210	U144	U55
C1022	U950			C	C	U688	C619	C548	A485	G411		C	G211	G145	G56
U1023	C950	U887	U887	C	C	G689	U620	C549	A486	G412		C	C212	G146	U57
A1024	G952	U888	U888	C	C	U690	U621	C550	U487	G413		C	G213	A147	
	C953	U889	U889	C	C	G691		U551	A488	A414		G	U214	U148	G62
A1027	U954	U890	U890	C	C	G692	G626	U552	A489	A415		C	G215	A149	
U1028	A955	C891	C891	C	C	A693	U627	G553	U416	G416		C	C216		U63
G1029	G956	U892	U892	U	U	C694	A628	A554	C491	C417		C	A217	U152	A64
	A957	U893	U893	C	C	G695	U629	A555	C492	A418		G	U218	G153	C65
G1033	G958	C894	C894	C	C	G696	U630	U556	A493	G419		C	U219	U154	G66
U1115	G959	G895	G895	C	C	U697	U631	U557	G494	G420		C		G155	C87
A1034	U960	U896	U896	C	C	G698	U632	G558	U495	G421		C	U222	U156	A69
A1035	G961	U897	U897	C	C		C633	G559	C496	U422		U	G225	U160	C89
G1036	A962	U898	U898	U	U	G	A634	A560	C497	U423		U	A	U161	G71
U1037	G963	U899	U899	C	C	G	G498	G499	C498	U352		C	U	C162	C72
	A964	C900	C900	A	A	C	A561	A561	G499	C424		C	C	U163	C73
G1041	U965	G901	G901	U	U	C	G635	U562	G499	A426		C	A	A164	G74
A1042	U966	G902	G902	U	U	G	G636	G563	A500	C429		C	A	G165	G75
G1043		A830	A830	G	G		C639	G565	C501			U290	U	U166	
C1044	U969	A903	A903	C	C		A640		C503			A292	A	A166	U76

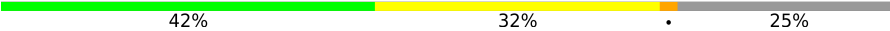


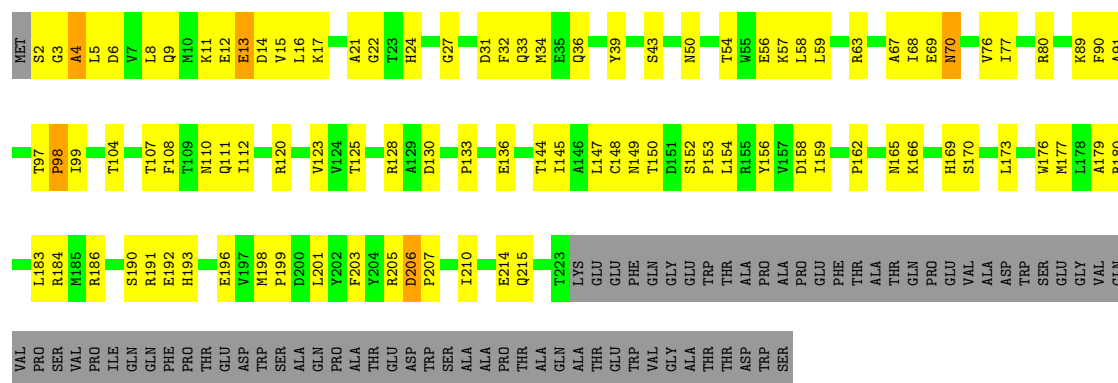
• Molecule 48: HUMAN INITIATOR MET-TRNA-I

Chain S6: 28% 48% 23%

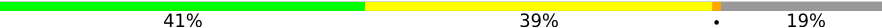


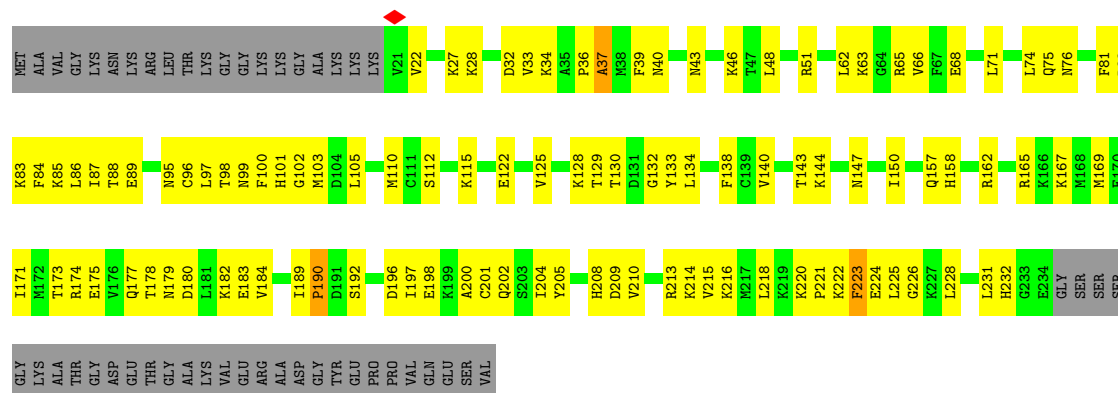
• Molecule 49: 40S RIBOSOMAL PROTEIN SA

Chain SA:  42% 32% 25%



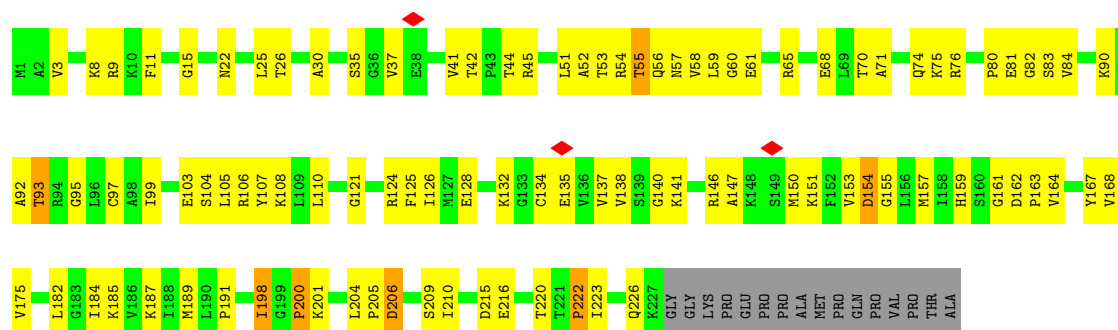
• Molecule 50: 40S RIBOSOMAL PROTEIN S3A

Chain SB:  41% 39% 19%



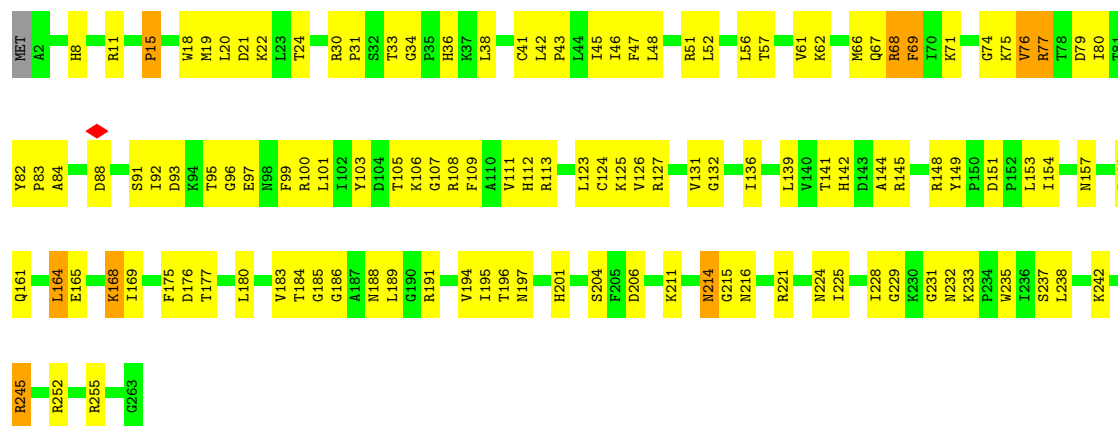
• Molecule 51: 40S RIBOSOMAL PROTEIN S3

Chain SD:  53% 38% 7%

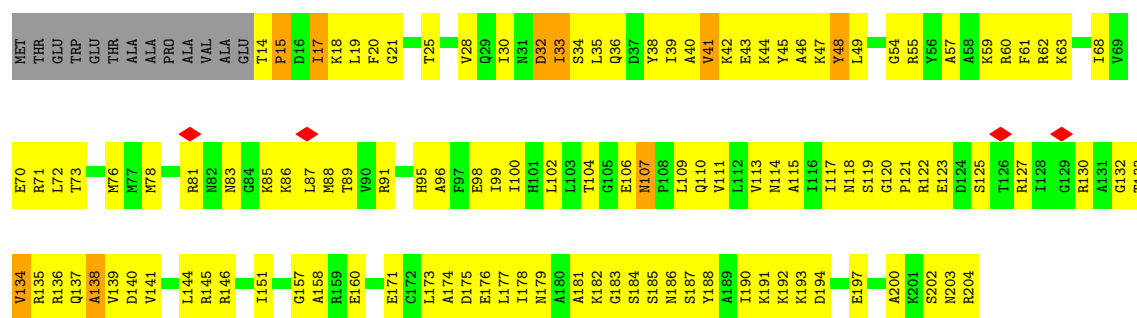


• Molecule 52: 40S RIBOSOMAL PROTEIN S4, X ISOFORM

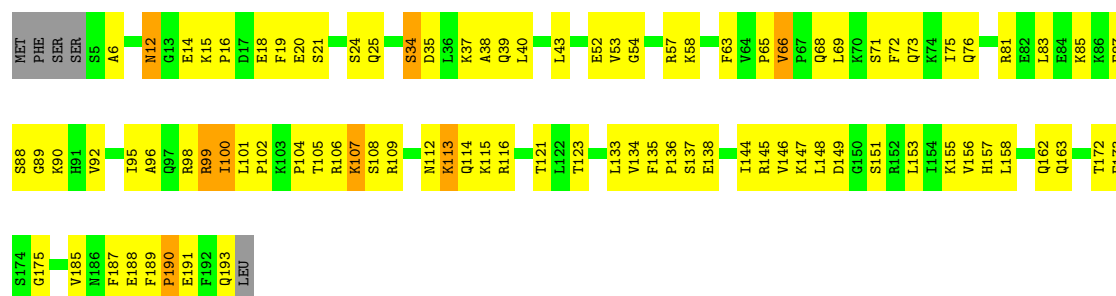
Chain SE:  53% 43%



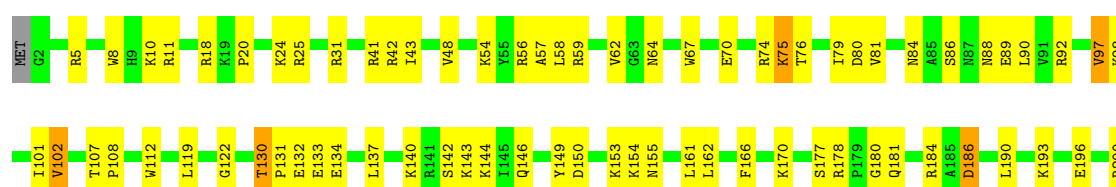
• Molecule 53: 40S RIBOSOMAL PROTEIN S5



• Molecule 54: 40S RIBOSOMAL PROTEIN S7



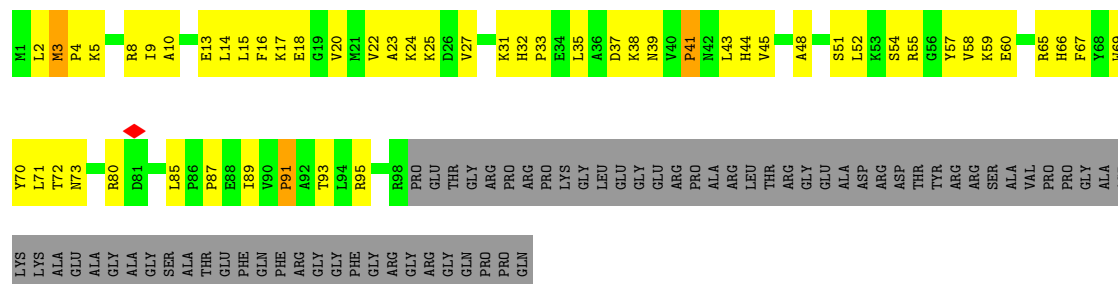
• Molecule 55: 40S RIBOSOMAL PROTEIN S8





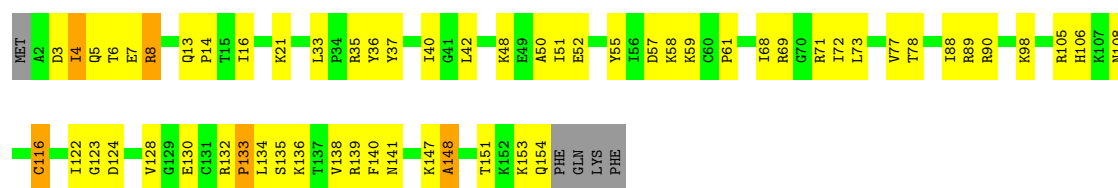
• Molecule 56: 40S RIBOSOMAL PROTEIN S10

Chain SK: 27% 31% 41%



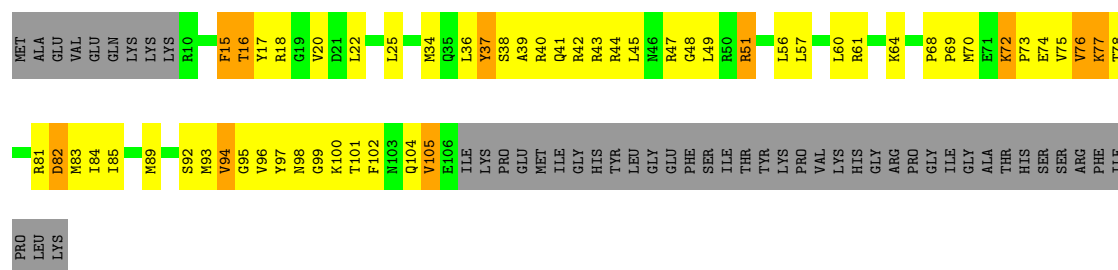
• Molecule 57: 40S RIBOSOMAL PROTEIN S11

Chain SL: 59% 34%



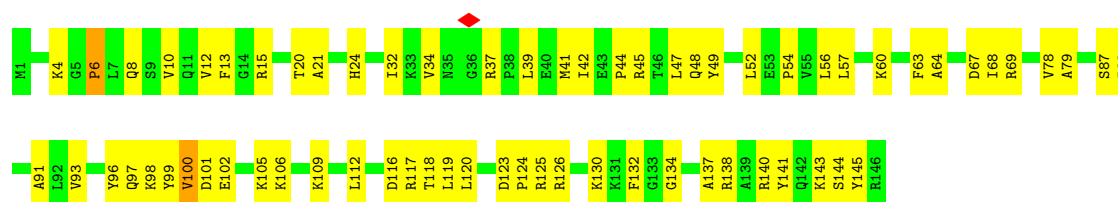
• Molecule 58: 40S RIBOSOMAL PROTEIN S15

Chain SP: 28% 32% 7% 33%



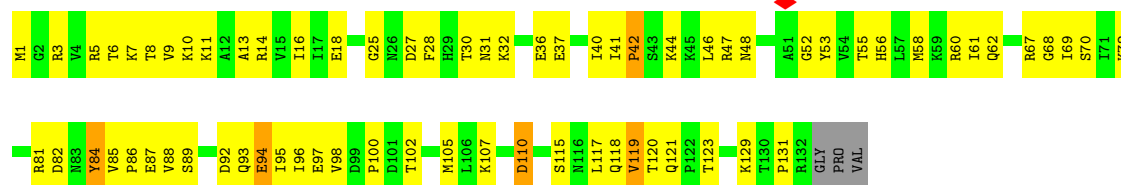
• Molecule 59: 40S RIBOSOMAL PROTEIN S16

Chain SQ: 54% 45%



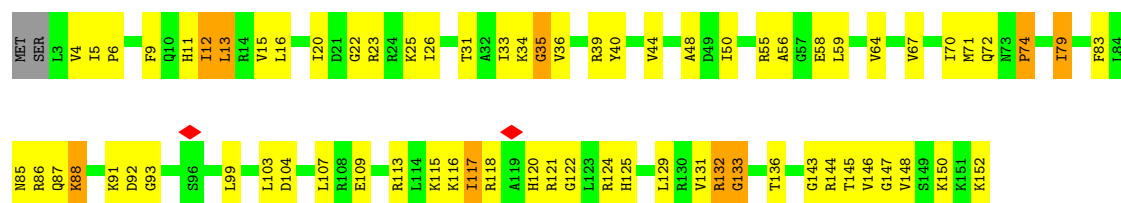
• Molecule 60: 40S RIBOSOMAL PROTEIN S17-LIKE

Chain SR:  46% 48%



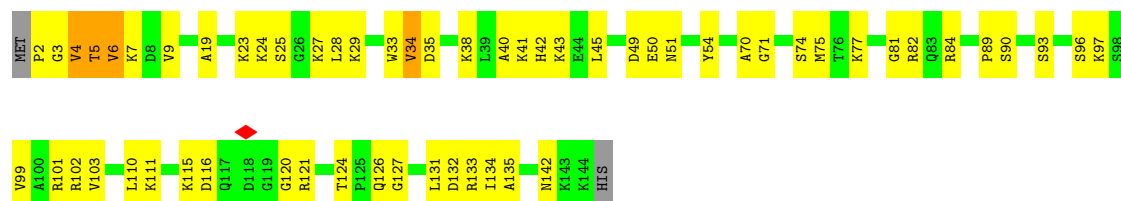
• Molecule 61: 40S RIBOSOMAL PROTEIN S18

Chain SS:  52% 41% 6%

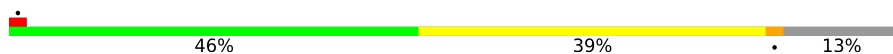


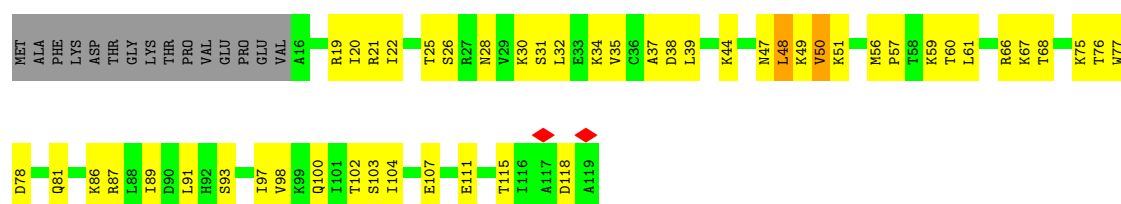
• Molecule 62: 40S RIBOSOMAL PROTEIN S19

Chain ST:  58% 38%



• Molecule 63: 40S RIBOSOMAL PROTEIN S20

Chain SU:  46% 39% 13%



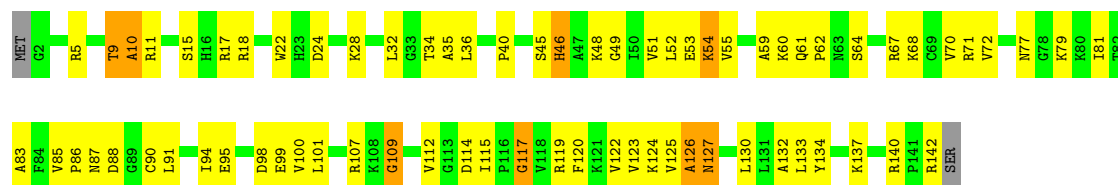
• Molecule 64: 40S RIBOSOMAL PROTEIN S21

Chain SV:  61% 37%



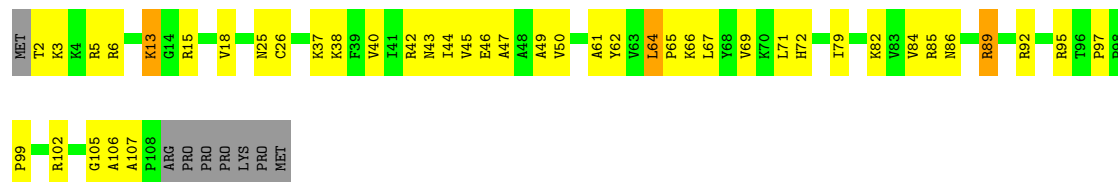
• Molecule 65: 40S RIBOSOMAL PROTEIN S23

Chain SX:  49% 44% 6%



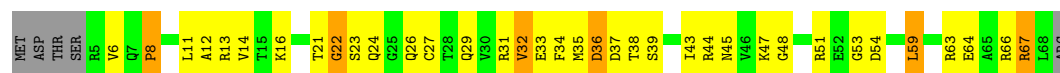
• Molecule 66: 40S RIBOSOMAL PROTEIN S26

Chain Sa: 56% 35% 7%



• Molecule 67: 40S RIBOSOMAL PROTEIN S28

Chain Sc: 41% 43% 9% 7%



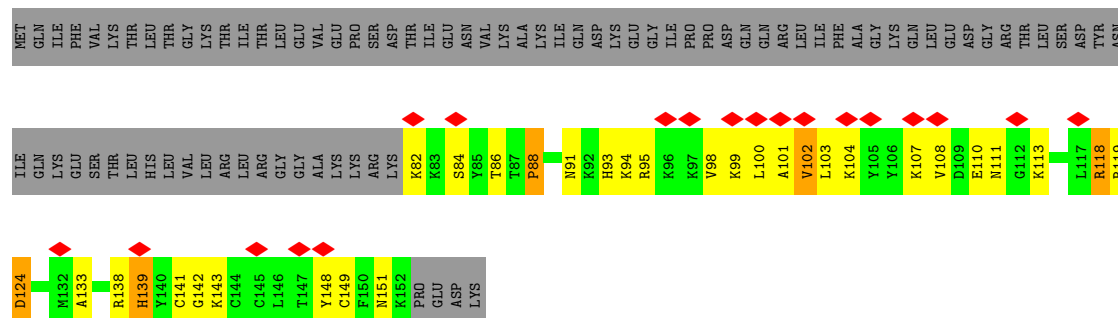
• Molecule 68: 40S RIBOSOMAL PROTEIN S29

Chain Sd: 48% 46% 5%



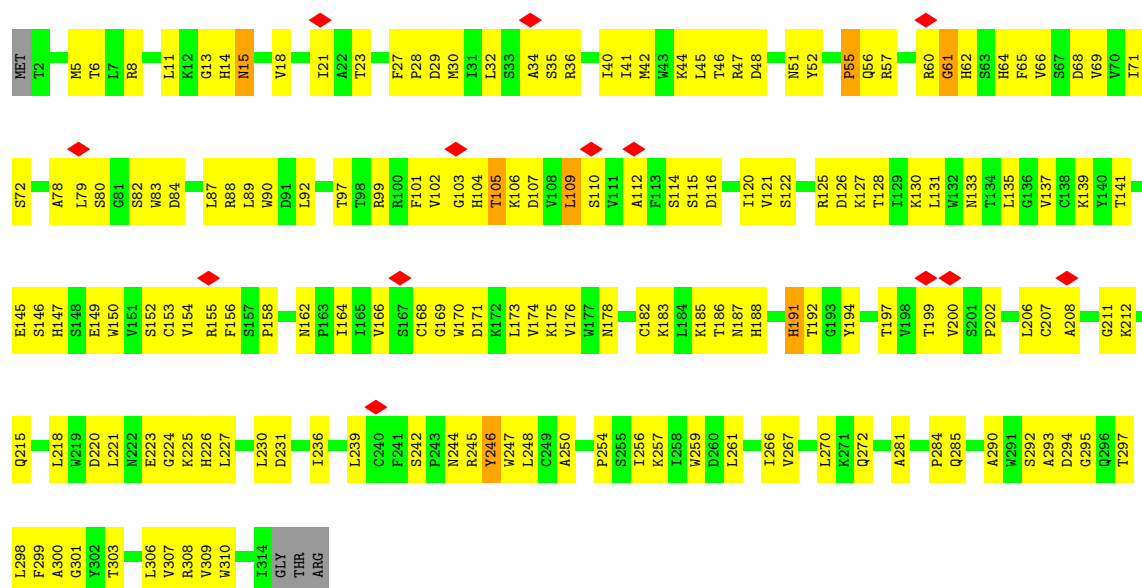
• Molecule 69: UBIQUITIN-40S RIBOSOMAL PROTEIN S27A

Chain Sf: 12% 23% 19% 54%



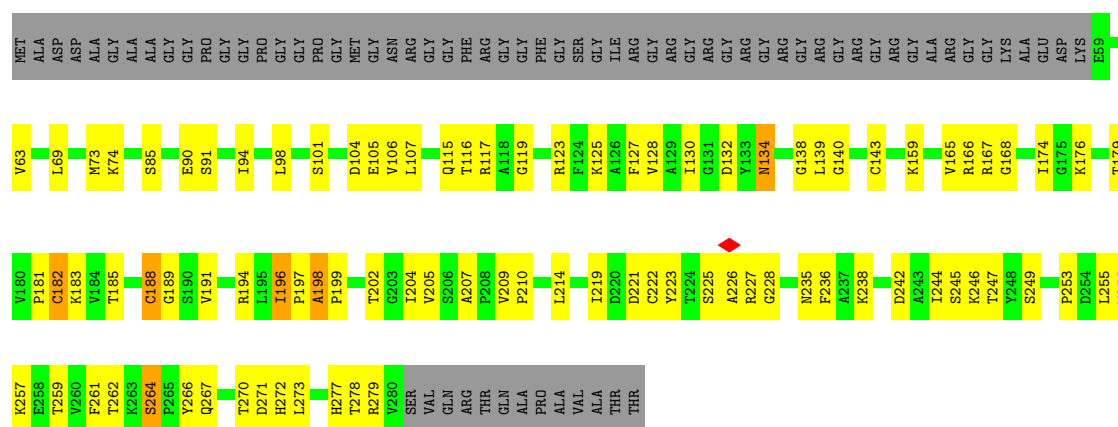
• Molecule 70: GUANINE NUCLEOTIDE-BINDING PROTEIN SUBUNIT BETA-2-LIKE 1

Chain Sg: 45% 51% 2%



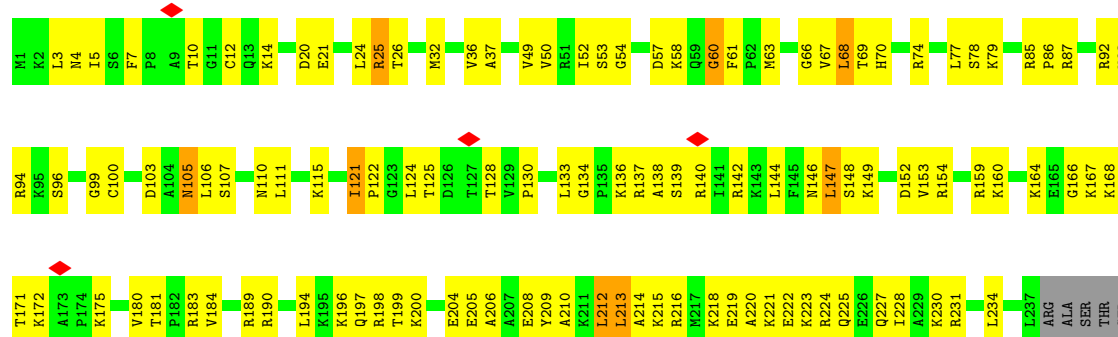
• Molecule 71: 40S RIBOSOMAL PROTEIN S2

Chain SC: 45% 29% 24%



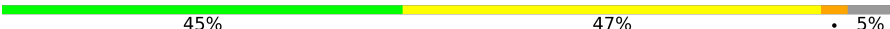
• Molecule 72: 40S RIBOSOMAL PROTEIN S6

Chain SG: 48% 44% 5%



LYS
SER
GLU
SER
SER
GLN
LYS

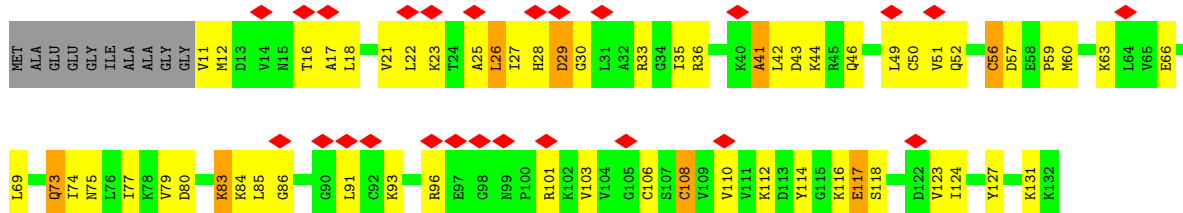
• Molecule 73: 40S RIBOSOMAL PROTEIN S9

Chain SJ:  45% 47% 5%



• Molecule 74: 40S RIBOSOMAL PROTEIN

Chain SM:  19% 47% 39% 6% 8%

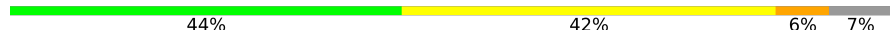


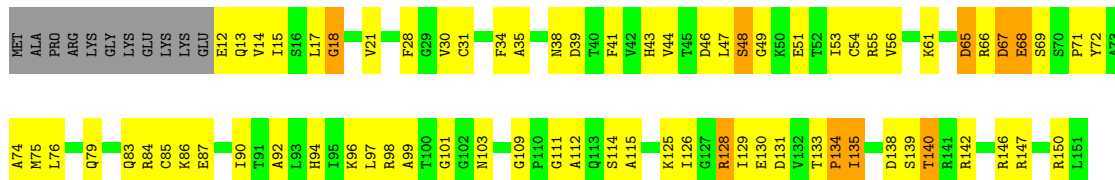
• Molecule 75: 40S RIBOSOMAL PROTEIN S13

Chain SN:  56% 42% 2%



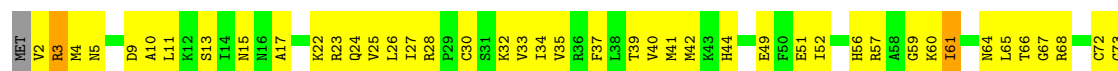
• Molecule 76: 40S RIBOSOMAL PROTEIN S14

Chain SO:  44% 42% 6% 7%



• Molecule 77: 40S RIBOSOMAL PROTEIN S15A

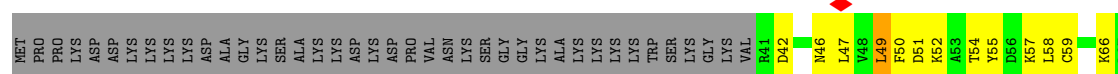
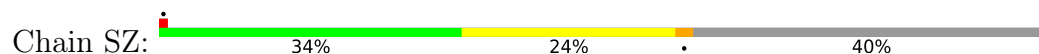
Chain SW:  49% 48% 3%



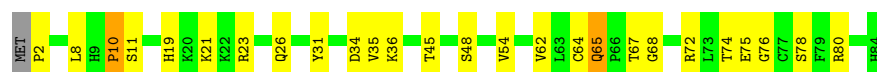
• Molecule 78: 40S RIBOSOMAL PROTEIN S24



• Molecule 79: 40S RIBOSOMAL PROTEIN S25



• Molecule 80: 40S RIBOSOMAL PROTEIN S27



• Molecule 81: 40S RIBOSOMAL PROTEIN S30



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	24000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.362	Depositor
Minimum map value	-0.237	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.020	Depositor
Recommended contour level	0.01	Depositor
Map size ($\text{\AA}$)	330.0, 330.0, 330.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1, 1.1, 1.1	Depositor

5 Model quality

5.1 Standard geometry

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

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	L5	0.20	0/89645	0.29	0/139764
2	L7	0.17	0/2858	0.22	0/4455
3	L8	0.19	0/3701	0.26	0/5766
4	LA	0.44	0/1936	0.91	3/2596 (0.1%)
5	LB	0.37	0/3306	0.82	6/4424 (0.1%)
6	LC	0.40	0/2973	0.86	9/3992 (0.2%)
7	LD	0.37	0/2428	0.81	6/3252 (0.2%)
8	LE	0.38	0/1996	0.94	8/2673 (0.3%)
9	LF	0.39	0/1905	0.80	0/2539
10	LG	0.39	0/1960	0.87	7/2637 (0.3%)
11	LH	0.34	0/1537	0.80	2/2066 (0.1%)
12	LI	0.40	0/1751	0.84	5/2340 (0.2%)
13	LJ	0.34	0/1433	0.80	0/1915
14	LL	0.39	0/1732	0.90	8/2315 (0.3%)
15	LM	0.38	0/1161	0.80	2/1554 (0.1%)
16	LN	0.42	0/1746	0.87	4/2338 (0.2%)
17	LO	0.42	0/1682	0.84	4/2250 (0.2%)
18	LP	0.41	0/1268	0.85	2/1701 (0.1%)
19	LQ	0.39	0/1537	0.91	7/2052 (0.3%)
20	LR	0.38	0/1582	0.80	0/2091
21	LS	0.38	0/1493	0.79	2/2003 (0.1%)
22	LT	0.40	0/1326	0.93	4/1770 (0.2%)
23	LU	0.32	0/839	0.75	1/1126 (0.1%)
24	LV	0.39	0/993	0.82	2/1332 (0.2%)
25	LW	0.38	0/1030	0.93	8/1364 (0.6%)
26	LX	0.38	0/1002	0.87	3/1345 (0.2%)
27	LY	0.36	0/1132	0.85	2/1504 (0.1%)
28	LZ	0.38	0/1130	0.77	0/1507
29	La	0.39	0/1191	0.80	0/1591
30	Lb	0.35	0/620	0.76	2/819 (0.2%)
31	Lc	0.37	0/774	0.75	0/1038
32	Ld	0.38	0/903	0.80	1/1216 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.42	0/1071	0.87	5/1429 (0.3%)
34	Lf	0.38	0/895	0.87	1/1198 (0.1%)
35	Lg	0.37	0/916	0.78	0/1220
36	Lh	0.35	0/1023	0.79	0/1351
37	Li	0.39	0/843	0.78	2/1115 (0.2%)
38	Lj	0.41	0/720	0.87	1/952 (0.1%)
39	Lk	0.37	0/575	0.88	3/761 (0.4%)
40	Ll	0.38	0/454	0.81	0/599
41	Lm	0.36	0/435	0.95	3/575 (0.5%)
42	Ln	0.40	0/231	0.89	1/294 (0.3%)
43	Lo	0.37	0/875	0.81	0/1153
44	Lp	0.42	0/718	0.81	0/953
45	Lr	0.37	0/1017	0.83	3/1364 (0.2%)
46	Lz	0.34	0/1769	0.81	1/2371 (0.0%)
47	S2	0.16	0/41243	0.26	0/64257
48	S6	0.21	1/1795 (0.1%)	0.36	1/2798 (0.0%)
49	SA	0.35	0/1784	0.83	5/2424 (0.2%)
50	SB	0.36	0/1765	0.78	0/2362
51	SD	0.37	0/1793	0.79	0/2414
52	SE	0.34	0/2118	0.84	1/2849 (0.0%)
53	SF	0.40	0/1531	0.86	4/2059 (0.2%)
54	SH	0.34	0/1544	0.80	0/2068
55	SI	0.34	0/1715	0.76	0/2287
56	SK	0.36	0/851	0.91	0/1147
57	SL	0.36	0/1268	0.76	0/1696
58	SP	0.38	0/815	0.87	1/1087 (0.1%)
59	SQ	0.33	0/1177	0.80	2/1575 (0.1%)
60	SR	0.39	0/1086	0.92	3/1457 (0.2%)
61	SS	0.33	0/1253	0.86	2/1676 (0.1%)
62	ST	0.34	0/1131	0.81	1/1515 (0.1%)
63	SU	0.37	0/831	0.89	0/1115
64	SV	0.34	0/643	0.72	1/860 (0.1%)
65	SX	0.39	0/1116	0.79	0/1490
66	Sa	0.41	0/862	0.81	0/1156
67	Sc	0.36	0/508	0.88	3/680 (0.4%)
68	Sd	0.30	0/455	0.76	0/603
69	Sf	0.33	0/593	0.77	0/786
70	Sg	0.31	0/2493	0.81	2/3394 (0.1%)
71	SC	0.37	0/1762	0.87	9/2381 (0.4%)
72	SG	0.34	0/1946	0.92	9/2590 (0.3%)
73	SJ	0.35	0/1550	0.77	0/2069
74	SM	0.32	0/962	0.80	1/1290 (0.1%)
75	SN	0.40	0/1232	0.81	1/1656 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SO	0.41	0/1062	0.95	7/1425 (0.5%)
77	SW	0.39	0/1051	0.86	1/1406 (0.1%)
78	SY	0.35	0/1083	0.76	0/1438
79	SZ	0.36	0/604	0.91	1/810 (0.1%)
80	Sb	0.35	0/665	0.88	2/891 (0.2%)
81	Se	0.34	0/465	0.69	0/612
All	All	0.28	1/234864 (0.0%)	0.56	175/344993 (0.1%)

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'	-5.29	1.38	1.45

The worst 5 of 175 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	LQ	58	ARG	CA-C-N	12.44	128.74	119.66
19	LQ	58	ARG	C-N-CA	12.44	128.74	119.66
48	S6	76	A	C5'-C4'-O4'	10.61	125.02	109.10
6	LC	206	GLY	CA-C-N	9.77	129.82	119.76
6	LC	206	GLY	C-N-CA	9.77	129.82	119.76

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	1527	0
2	L7	2558	0	1296	34	0
3	L8	3314	0	1683	56	0
4	LA	1898	0	1993	86	0
5	LB	3238	0	3376	118	0
6	LC	2919	0	3092	115	0
7	LD	2382	0	2410	79	0
8	LE	1958	0	2126	82	0
9	LF	1870	0	1996	68	0
10	LG	1927	0	2074	77	0
11	LH	1518	0	1601	55	0
12	LI	1711	0	1749	45	0
13	LJ	1410	0	1441	59	0
14	LL	1701	0	1818	66	0
15	LM	1138	0	1204	53	0
16	LN	1701	0	1749	77	0
17	LO	1650	0	1794	61	0
18	LP	1242	0	1269	44	0
19	LQ	1513	0	1628	54	0
20	LR	1566	0	1729	49	0
21	LS	1453	0	1490	66	0
22	LT	1298	0	1366	54	0
23	LU	825	0	850	23	0
24	LV	979	0	1039	44	0
25	LW	1015	0	1079	51	0
26	LX	985	0	1066	37	0
27	LY	1115	0	1205	42	0
28	LZ	1107	0	1182	42	0
29	La	1162	0	1213	42	0
30	Lb	610	0	650	18	0
31	Lc	764	0	804	22	0
32	Ld	888	0	930	31	0
33	Le	1053	0	1147	50	0
34	Lf	876	0	912	34	0
35	Lg	906	0	1000	38	0
36	Lh	1015	0	1148	50	0
37	Li	832	0	917	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	Lj	705	0	738	32	0
39	Lk	569	0	637	22	0
40	Ll	444	0	483	13	0
41	Lm	429	0	466	13	0
42	Ln	230	0	276	9	0
43	Lo	862	0	932	21	0
44	Lp	708	0	757	29	0
45	Lr	1002	0	1068	42	0
46	Lz	1741	0	1854	58	0
47	S2	36900	0	18598	792	0
48	S6	1604	0	816	43	0
49	SA	1747	0	1751	72	0
50	SB	1738	0	1809	81	0
51	SD	1765	0	1865	74	0
52	SE	2076	0	2177	98	0
53	SF	1509	0	1563	103	0
54	SH	1521	0	1616	71	0
55	SI	1686	0	1772	55	0
56	SK	827	0	854	45	0
57	SL	1247	0	1323	44	0
58	SP	804	0	841	55	0
59	SQ	1158	0	1232	45	0
60	SR	1072	0	1130	55	0
61	SS	1235	0	1309	65	0
62	ST	1112	0	1146	46	0
63	SU	821	0	883	46	0
64	SV	636	0	637	24	0
65	SX	1098	0	1167	57	0
66	Sa	847	0	896	25	0
67	Sc	506	0	536	23	0
68	Sd	445	0	442	31	0
69	Sf	581	0	597	25	0
70	Sg	2436	0	2393	125	0
71	SC	1725	0	1813	60	0
72	SG	1923	0	2089	105	0
73	SJ	1525	0	1640	84	0
74	SM	952	0	983	49	0
75	SN	1208	0	1294	48	0
76	SO	1049	0	1073	58	0
77	SW	1034	0	1080	59	0
78	SY	1065	0	1142	54	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	19	0
81	Se	459	0	503	17	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	5392	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 5392 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
1:L5:1961:G:H1	1:L5:2024:G:HO2'	1.12	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%)	1	13
5	LB	400/403 (99%)	344 (86%)	42 (10%)	14 (4%)	3	23
6	LC	365/427 (86%)	311 (85%)	30 (8%)	24 (7%)	1	12
7	LD	291/297 (98%)	258 (89%)	22 (8%)	11 (4%)	2	21
8	LE	238/288 (83%)	182 (76%)	37 (16%)	19 (8%)	1	8
9	LF	223/248 (90%)	201 (90%)	18 (8%)	4 (2%)	6	34
10	LG	239/266 (90%)	205 (86%)	19 (8%)	15 (6%)	1	12
11	LH	188/192 (98%)	162 (86%)	18 (10%)	8 (4%)	2	18
12	LI	211/214 (99%)	177 (84%)	26 (12%)	8 (4%)	2	21
13	LJ	174/178 (98%)	147 (84%)	19 (11%)	8 (5%)	2	17
14	LL	208/211 (99%)	179 (86%)	18 (9%)	11 (5%)	1	14
15	LM	137/215 (64%)	115 (84%)	16 (12%)	6 (4%)	2	18
16	LN	201/204 (98%)	180 (90%)	18 (9%)	3 (2%)	8	37
17	LO	199/203 (98%)	180 (90%)	15 (8%)	4 (2%)	6	32
18	LP	151/184 (82%)	130 (86%)	16 (11%)	5 (3%)	3	24
19	LQ	185/188 (98%)	159 (86%)	22 (12%)	4 (2%)	5	30
20	LR	185/196 (94%)	168 (91%)	17 (9%)	0	100	100
21	LS	173/176 (98%)	141 (82%)	21 (12%)	11 (6%)	1	12
22	LT	157/160 (98%)	134 (85%)	18 (12%)	5 (3%)	3	24
23	LU	99/128 (77%)	81 (82%)	17 (17%)	1 (1%)	12	45
24	LV	129/140 (92%)	105 (81%)	18 (14%)	6 (5%)	2	17
25	LW	122/157 (78%)	96 (79%)	22 (18%)	4 (3%)	3	24
26	LX	118/156 (76%)	103 (87%)	13 (11%)	2 (2%)	7	35
27	LY	132/145 (91%)	118 (89%)	10 (8%)	4 (3%)	3	25
28	LZ	133/136 (98%)	118 (89%)	12 (9%)	3 (2%)	5	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	La	145/148 (98%)	122 (84%)	18 (12%)	5 (3%)	3	23
30	Lb	73/159 (46%)	62 (85%)	9 (12%)	2 (3%)	4	27
31	Lc	96/115 (84%)	81 (84%)	9 (9%)	6 (6%)	1	12
32	Ld	105/125 (84%)	85 (81%)	15 (14%)	5 (5%)	2	16
33	Le	126/135 (93%)	107 (85%)	14 (11%)	5 (4%)	2	20
34	Lf	107/110 (97%)	87 (81%)	16 (15%)	4 (4%)	2	21
35	Lg	112/117 (96%)	103 (92%)	8 (7%)	1 (1%)	14	46
36	Lh	120/123 (98%)	110 (92%)	8 (7%)	2 (2%)	7	35
37	Li	100/105 (95%)	92 (92%)	4 (4%)	4 (4%)	2	20
38	Lj	84/97 (87%)	67 (80%)	10 (12%)	7 (8%)	0	8
39	Lk	67/70 (96%)	50 (75%)	12 (18%)	5 (8%)	1	9
40	Ll	48/51 (94%)	44 (92%)	3 (6%)	1 (2%)	5	31
41	Lm	50/128 (39%)	43 (86%)	5 (10%)	2 (4%)	2	20
42	Ln	22/25 (88%)	20 (91%)	2 (9%)	0	100	100
43	Lo	102/106 (96%)	85 (83%)	15 (15%)	2 (2%)	6	32
44	Lp	89/92 (97%)	71 (80%)	13 (15%)	5 (6%)	1	14
45	Lr	123/137 (90%)	102 (83%)	15 (12%)	6 (5%)	1	16
46	Lz	215/217 (99%)	168 (78%)	31 (14%)	16 (7%)	1	9
49	SA	220/295 (75%)	187 (85%)	27 (12%)	6 (3%)	4	27
50	SB	212/264 (80%)	174 (82%)	30 (14%)	8 (4%)	2	21
51	SD	225/243 (93%)	183 (81%)	24 (11%)	18 (8%)	1	8
52	SE	260/263 (99%)	215 (83%)	30 (12%)	15 (6%)	1	13
53	SF	189/204 (93%)	144 (76%)	31 (16%)	14 (7%)	1	9
54	SH	187/194 (96%)	145 (78%)	27 (14%)	15 (8%)	1	8
55	SI	204/208 (98%)	168 (82%)	24 (12%)	12 (6%)	1	13
56	SK	96/165 (58%)	76 (79%)	16 (17%)	4 (4%)	2	19
57	SL	151/158 (96%)	130 (86%)	11 (7%)	10 (7%)	1	12
58	SP	95/145 (66%)	61 (64%)	21 (22%)	13 (14%)	0	3
59	SQ	144/146 (99%)	114 (79%)	20 (14%)	10 (7%)	1	11
60	SR	130/135 (96%)	104 (80%)	17 (13%)	9 (7%)	1	11
61	SS	148/152 (97%)	121 (82%)	13 (9%)	14 (10%)	0	6

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
62	ST	141/145 (97%)	119 (84%)	16 (11%)	6 (4%)	2	18
63	SU	102/119 (86%)	86 (84%)	11 (11%)	5 (5%)	1	16
64	SV	81/83 (98%)	65 (80%)	11 (14%)	5 (6%)	1	12
65	SX	139/143 (97%)	114 (82%)	12 (9%)	13 (9%)	0	6
66	Sa	103/115 (90%)	77 (75%)	16 (16%)	10 (10%)	0	6
67	Sc	62/69 (90%)	47 (76%)	9 (14%)	6 (10%)	0	6
68	Sd	51/56 (91%)	44 (86%)	7 (14%)	0	100	100
69	Sf	69/156 (44%)	47 (68%)	10 (14%)	12 (17%)	0	1
70	Sg	311/317 (98%)	237 (76%)	58 (19%)	16 (5%)	1	15
71	SC	220/293 (75%)	188 (86%)	23 (10%)	9 (4%)	2	19
72	SG	235/249 (94%)	198 (84%)	26 (11%)	11 (5%)	2	17
73	SJ	183/194 (94%)	157 (86%)	16 (9%)	10 (6%)	1	14
74	SM	120/132 (91%)	79 (66%)	29 (24%)	12 (10%)	0	5
75	SN	148/151 (98%)	133 (90%)	8 (5%)	7 (5%)	2	17
76	SO	138/151 (91%)	101 (73%)	24 (17%)	13 (9%)	0	6
77	SW	127/130 (98%)	109 (86%)	13 (10%)	5 (4%)	2	20
78	SY	129/133 (97%)	108 (84%)	16 (12%)	5 (4%)	2	20
79	SZ	73/125 (58%)	59 (81%)	11 (15%)	3 (4%)	2	19
80	Sb	81/84 (96%)	67 (83%)	12 (15%)	2 (2%)	4	28
81	Se	56/59 (95%)	41 (73%)	11 (20%)	4 (7%)	1	10
All	All	11518/12905 (89%)	9598 (83%)	1346 (12%)	574 (5%)	3	16

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%)	81	80
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%)	245 (100%)	1 (0%)	84	81
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%)	107 (99%)	1 (1%)	70	76
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%)	65	74
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%)	10035 (100%)	4 (0%)	100	100

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	LA	215	ASN
7	LD	52	ILE
26	LX	40	ILE
43	Lo	38	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 144 such sidechains are listed below:

Mol	Chain	Res	Type
65	SX	87	ASN
81	Se	56	ASN
68	Sd	4	GLN
73	SJ	113	GLN
21	LS	117	HIS

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	1714/1869 (91%)	676 (39%)	22 (1%)
48	S6	74/75 (98%)	28 (37%)	2 (2%)
All	All	5769/7292 (79%)	2072 (35%)	82 (1%)

5 of 2072 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
3	L8	87	G
47	S2	912	C
47	S2	213	G
47	S2	606	G
47	S2	1404	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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

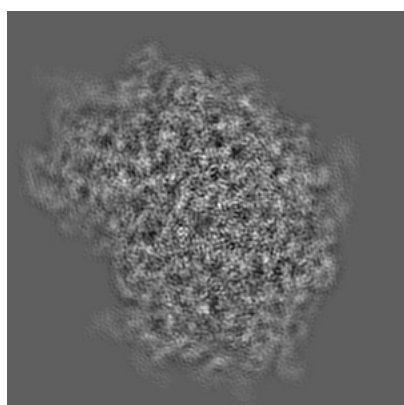
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2938. These allow visual inspection of the internal detail of the map and identification of artifacts.

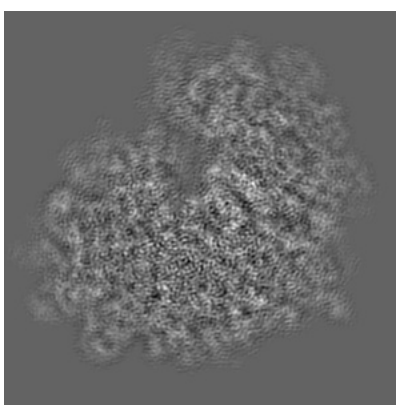
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

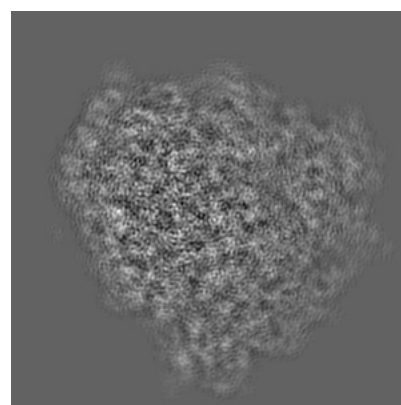
6.1.1 Primary map



X



Y

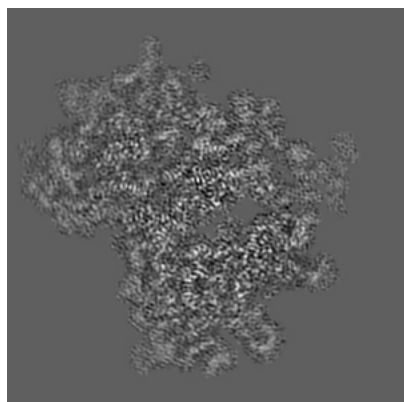


Z

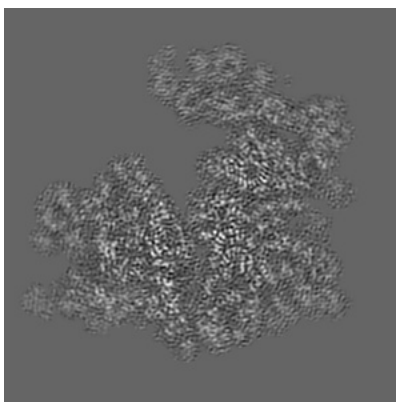
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

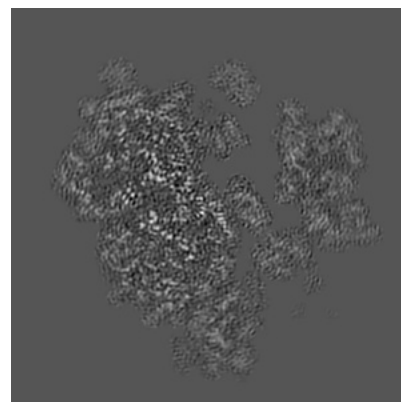
6.2.1 Primary map



X Index: 150



Y Index: 150

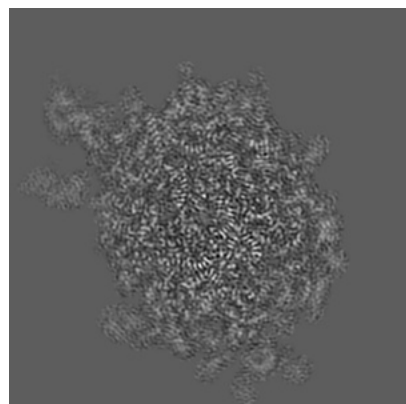


Z Index: 150

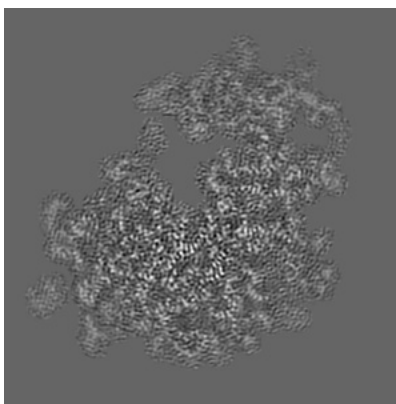
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

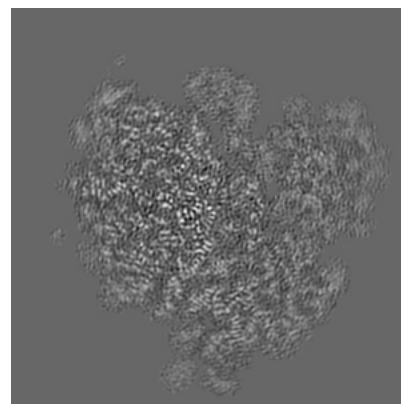
6.3.1 Primary map



X Index: 123



Y Index: 162

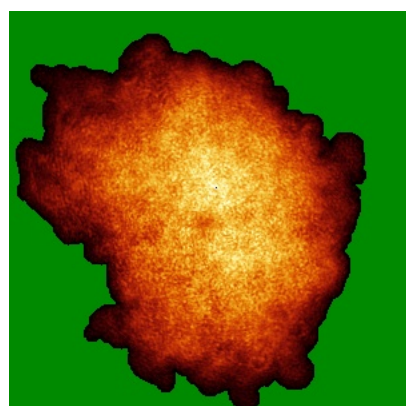


Z Index: 172

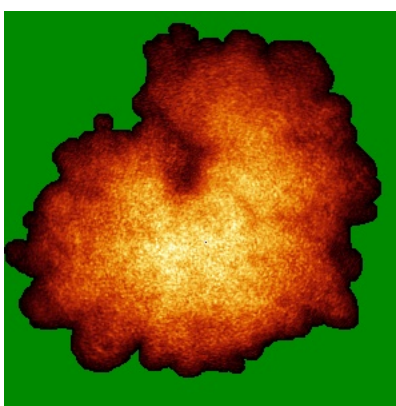
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

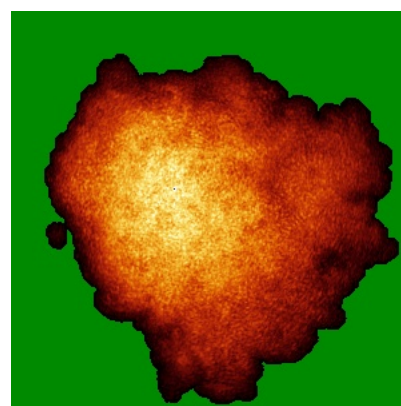
6.4.1 Primary map



X



Y

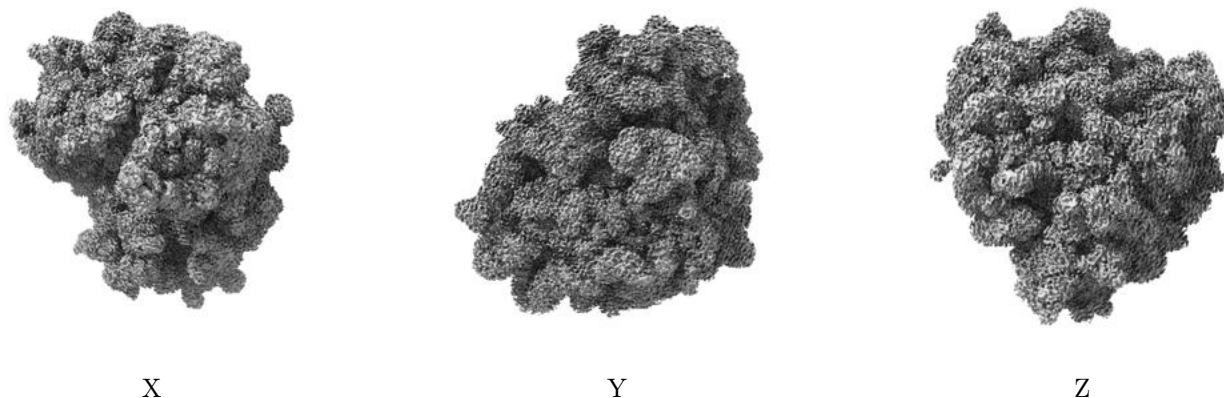


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

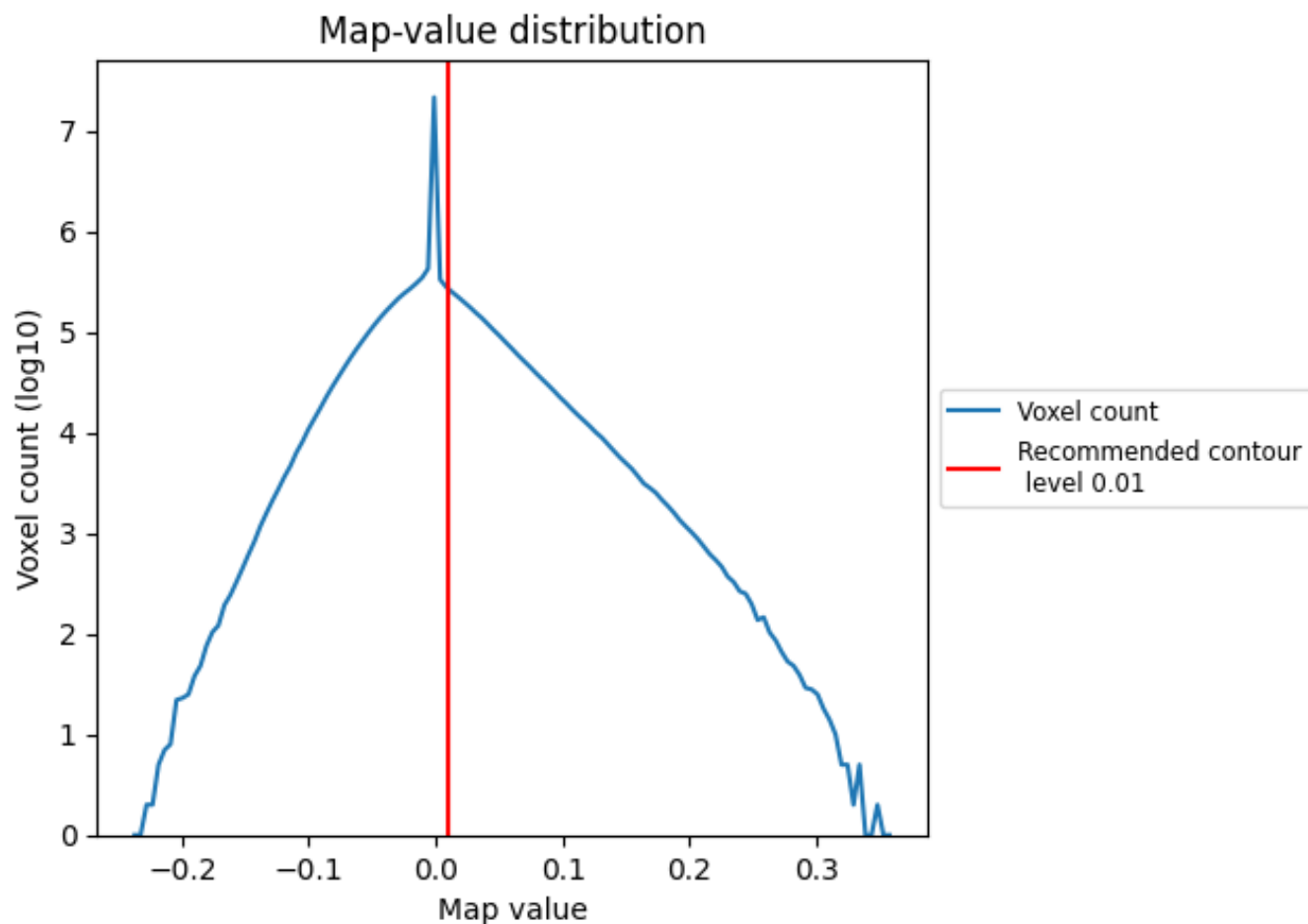
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

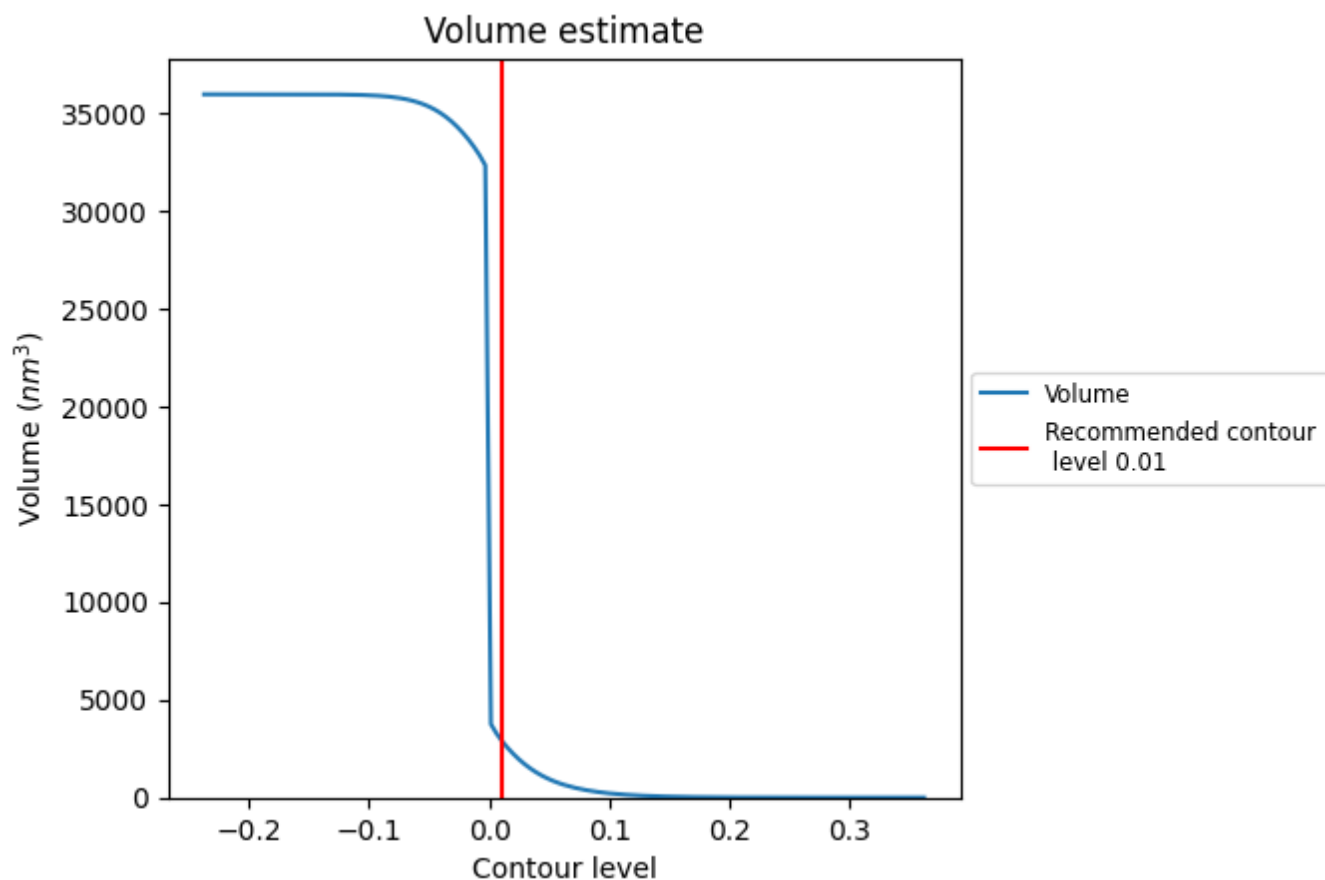
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

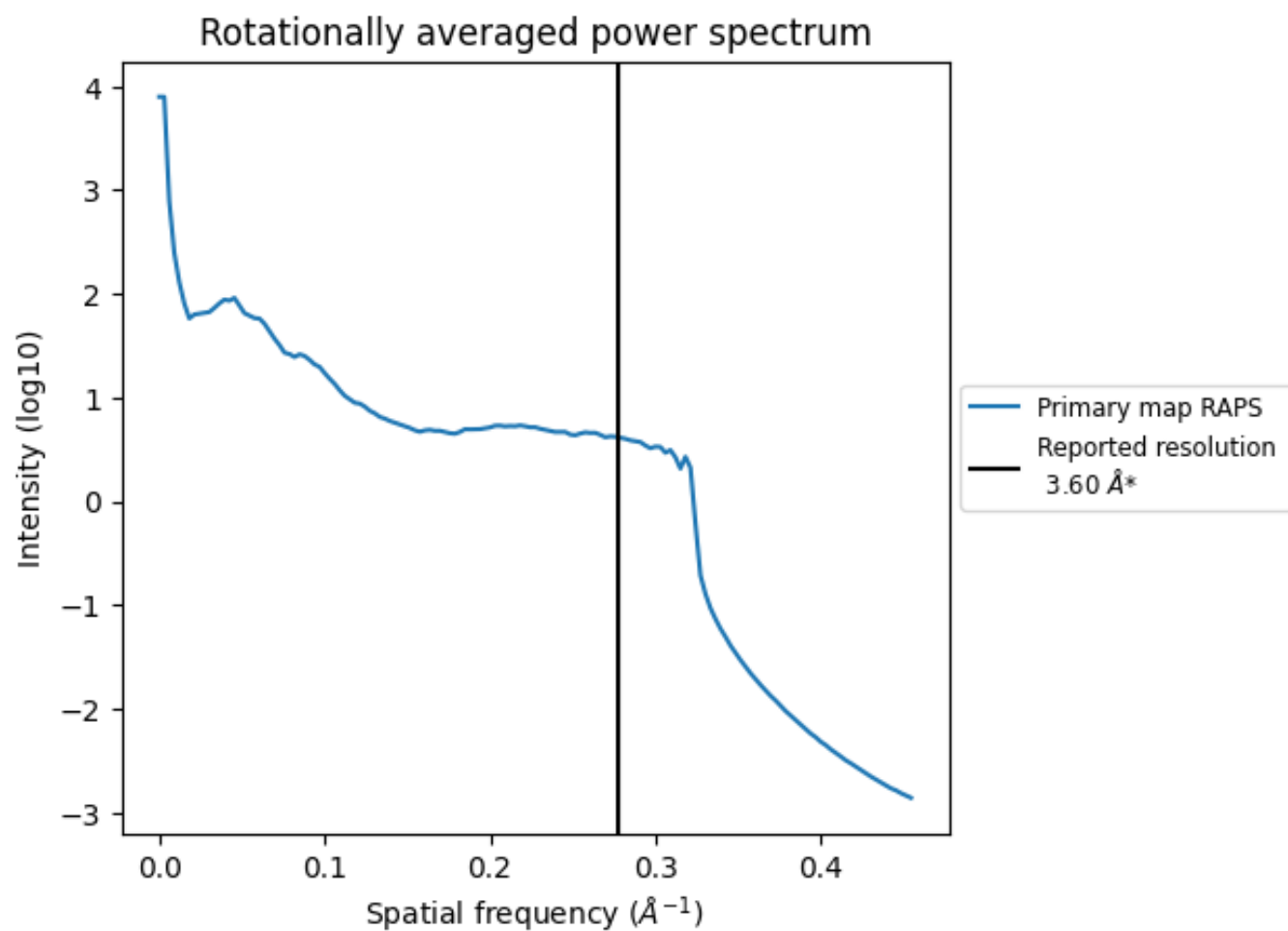
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2951 nm³; this corresponds to an approximate mass of 2666 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

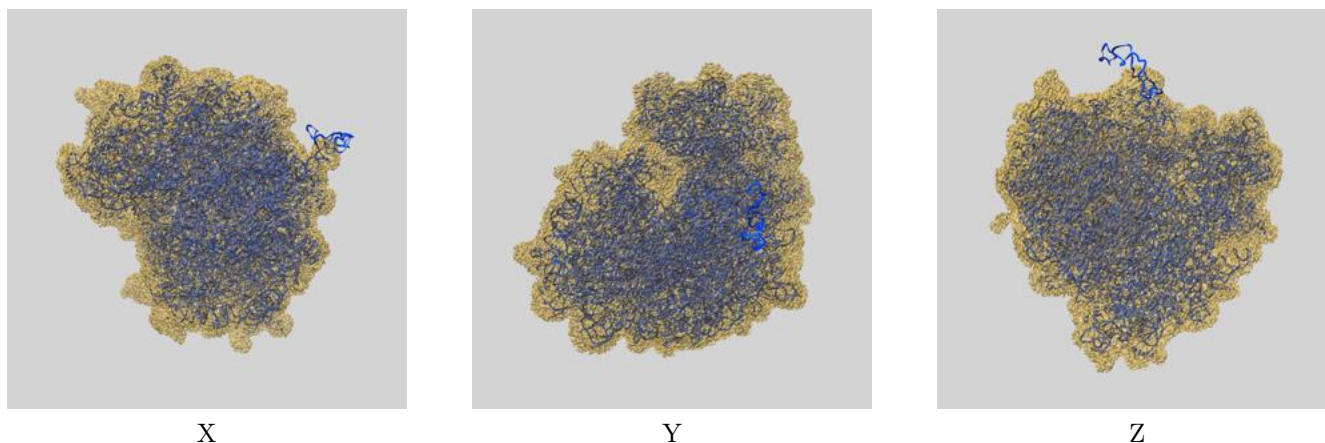
8 Fourier-Shell correlation

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

9 Map-model fit ⓘ

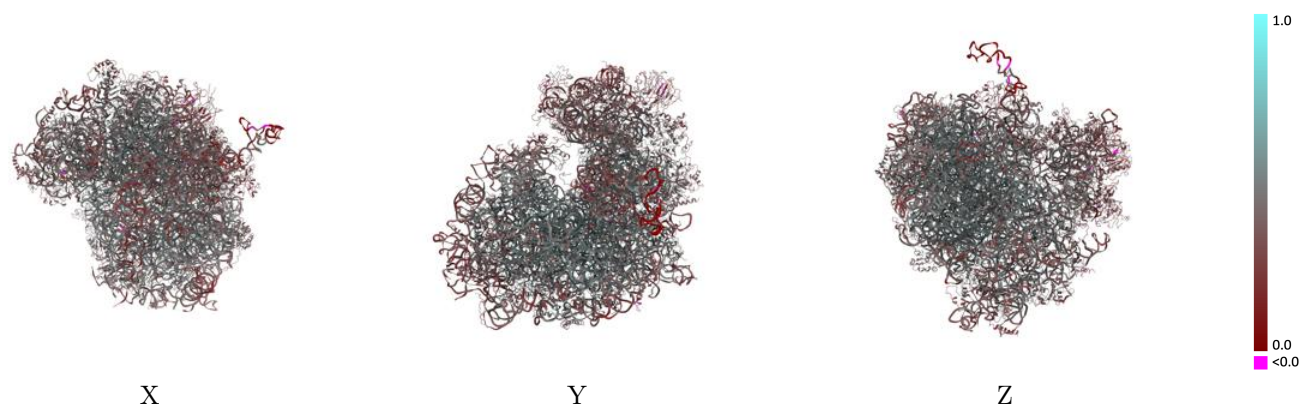
This section contains information regarding the fit between EMDB map EMD-2938 and PDB model 4UG0. Per-residue inclusion information can be found in section 3 on page 20.

9.1 Map-model overlay ⓘ



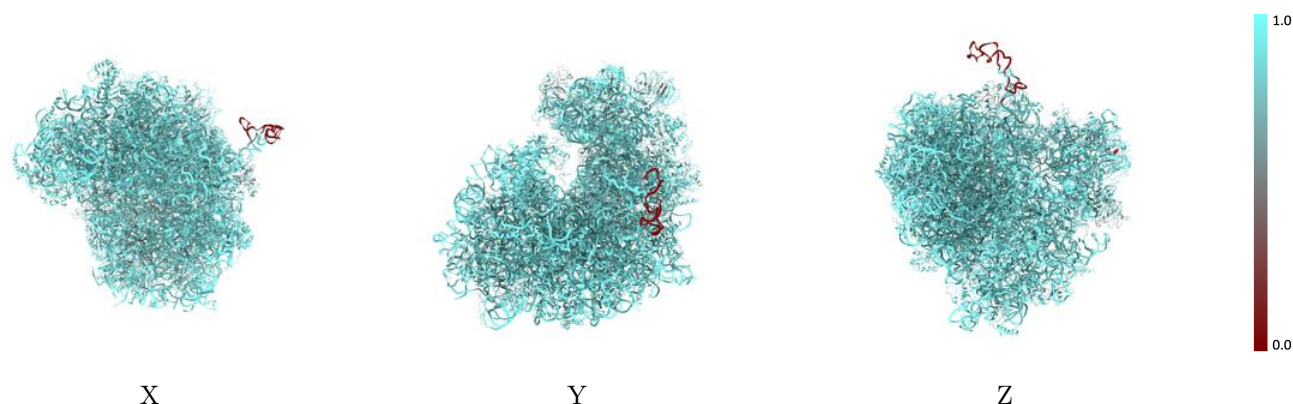
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



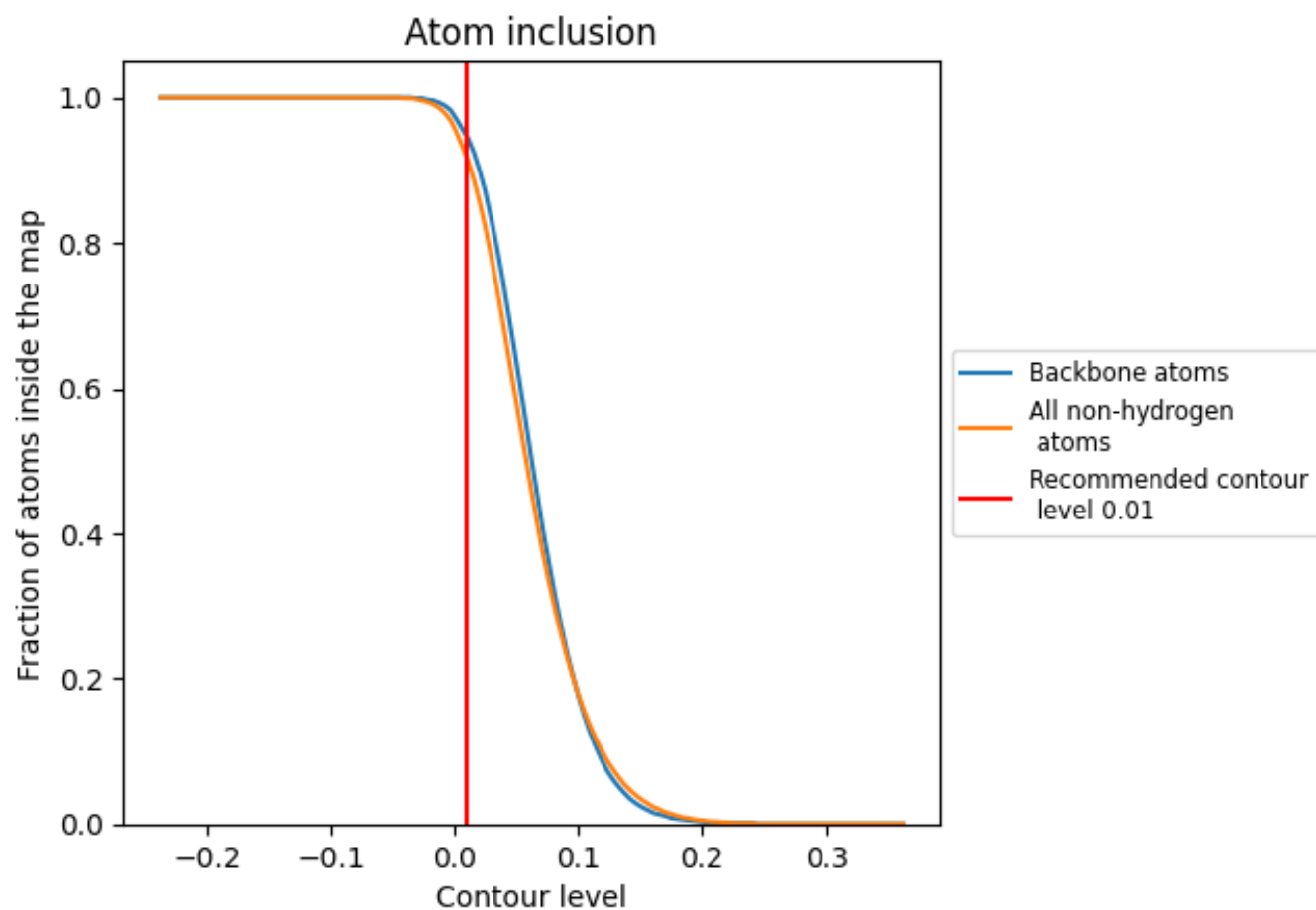
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9180	 0.4400
L5	 0.9450	 0.4620
L7	 0.9730	 0.4890
L8	 0.9590	 0.4900
LA	 0.9160	 0.5040
LB	 0.9120	 0.4670
LC	 0.9040	 0.4700
LD	 0.8970	 0.4170
LE	 0.8790	 0.4070
LF	 0.8920	 0.4770
LG	 0.8960	 0.4090
LH	 0.9030	 0.4300
LI	 0.8930	 0.4370
LJ	 0.8880	 0.3890
LL	 0.9250	 0.4550
LM	 0.9090	 0.4410
LN	 0.8950	 0.5010
LO	 0.9180	 0.4750
LP	 0.9070	 0.4790
LQ	 0.9000	 0.4750
LR	 0.9110	 0.4530
LS	 0.9130	 0.4730
LT	 0.9090	 0.4680
LU	 0.9110	 0.4010
LV	 0.9250	 0.4790
LW	 0.8720	 0.3930
LX	 0.8910	 0.4510
LY	 0.9130	 0.4350
LZ	 0.9020	 0.4380
La	 0.9190	 0.4960
Lb	 0.8800	 0.4310
Lc	 0.9140	 0.4480
Ld	 0.9220	 0.4620
Le	 0.9050	 0.4980
Lf	 0.9240	 0.5010



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Chain	Atom inclusion	Q-score
Lg	 0.9000	 0.4660
Lh	 0.9030	 0.4350
Li	 0.9060	 0.4380
Lj	 0.9150	 0.4900
Lk	 0.9140	 0.4010
Ll	 0.9010	 0.4850
Lm	 0.9090	 0.4620
Ln	 0.9330	 0.5140
Lo	 0.9200	 0.4800
Lp	 0.9240	 0.4920
Lr	 0.9210	 0.4730
Lz	 0.7030	 0.2650
S2	 0.9430	 0.4350
S6	 0.8860	 0.3390
SA	 0.8920	 0.4110
SB	 0.9040	 0.4260
SC	 0.8890	 0.4200
SD	 0.8440	 0.3480
SE	 0.8780	 0.4290
SF	 0.8400	 0.3670
SG	 0.8730	 0.3710
SH	 0.8900	 0.3800
SI	 0.8870	 0.4320
SJ	 0.8800	 0.4030
SK	 0.8210	 0.3020
SL	 0.8940	 0.4650
SM	 0.6630	 0.2750
SN	 0.8920	 0.4370
SO	 0.8870	 0.4430
SP	 0.8590	 0.3280
SQ	 0.8210	 0.3530
SR	 0.8620	 0.3650
SS	 0.8560	 0.3290
ST	 0.8360	 0.3470
SU	 0.8340	 0.3320
SV	 0.9020	 0.4270
SW	 0.8770	 0.4560
SX	 0.8890	 0.4620
SY	 0.8820	 0.3870
SZ	 0.8830	 0.3340
Sa	 0.9070	 0.4620
Sb	 0.9220	 0.4170

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Chain	Atom inclusion	Q-score
Sc	 0.8750	 0.3650
Sd	 0.7940	 0.3770
Se	 0.8060	 0.3560
Sf	 0.5800	 0.2210
Sg	 0.8160	 0.3010