



wwPDB EM Validation Summary Report ⓘ

May 4, 2026 – 05:21 PM JST

PDB ID : 9KDV / pdb_00009kdv
EMDB ID : EMD-62287
Title : Cryo-EM structure of 80S ribosome
Authors : Lu, Y.; Wang, X.; Qin, Y.; Cao, Y.
Deposited on : 2024-11-04
Resolution : 3.33 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

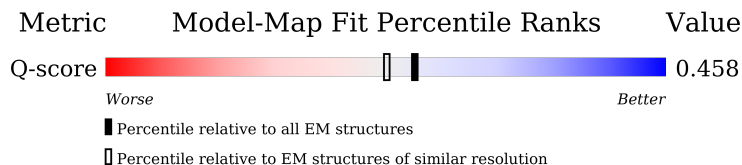
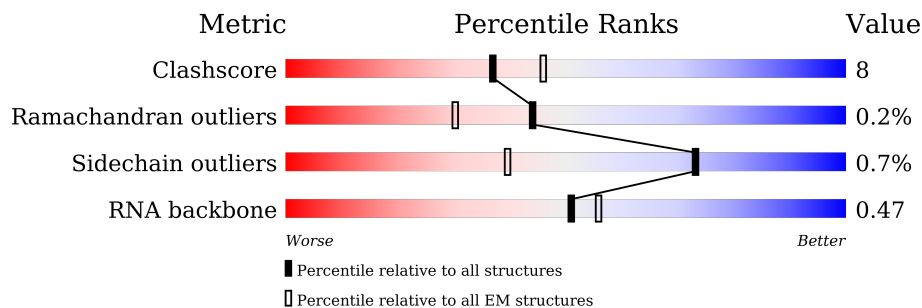
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.33 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.









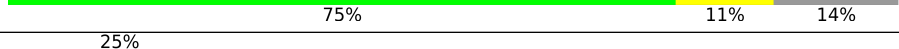
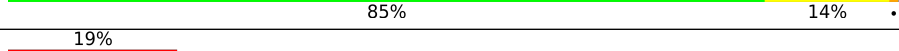
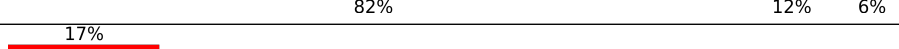
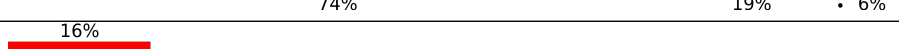


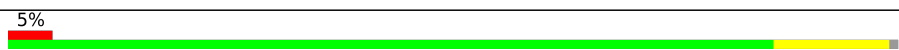

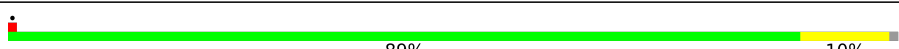






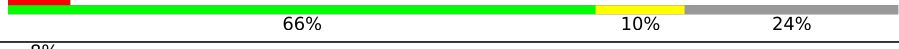



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14484 (2.83 - 3.83)

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	4731	
2	L7	120	
3	L8	158	

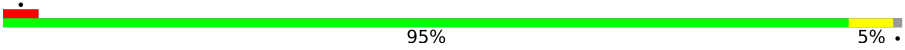





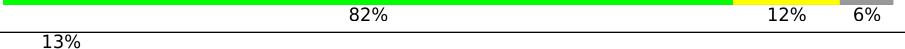
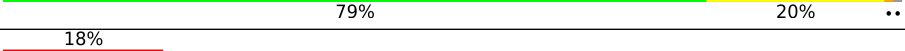
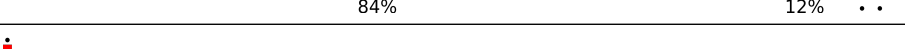

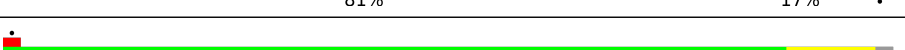

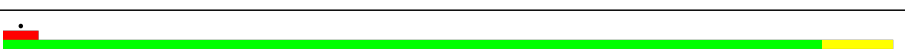

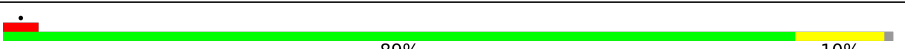

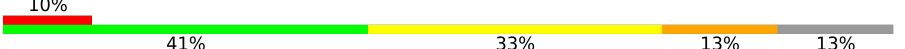



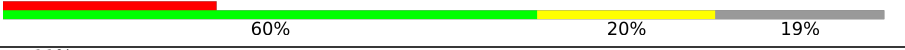
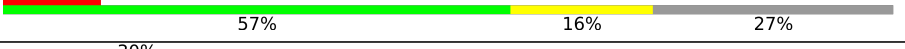



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Mol	Chain	Length	Quality of chain
4	LA	257	
5	LB	403	
6	LC	419	
7	LD	297	
8	LE	296	
9	LF	270	
10	LG	266	
11	LH	192	
12	LI	214	
13	LJ	178	
14	LL	211	
15	LM	217	
16	LN	204	
17	LO	203	
18	LP	184	
19	LQ	188	
20	LR	196	
21	LS	176	
22	LT	160	
23	LU	128	
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	160	
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	S2	1870	
47	S6	75	
47	S7	75	
48	SA	295	
49	SB	264	
50	SC	293	
51	SD	243	
52	SE	263	




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Mol	Chain	Length	Quality of chain
53	SF	204	
54	SG	249	
55	SH	194	
56	SI	208	
57	SJ	194	
58	SK	165	
59	SL	158	
60	SN	151	
61	SO	151	
62	SP	145	
63	SQ	146	
64	SR	135	
65	SS	152	
66	ST	145	
67	SU	119	
68	SV	83	
69	SW	130	
70	SX	143	
71	SY	133	
72	SZ	125	
73	Sa	115	
74	Sb	84	
75	Sc	69	
76	Sd	56	
77	Se	133	

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Mol	Chain	Length	Quality of chain
78	Sg	317	
79	Sx	10	
80	Z	8	

2 Entry composition

There are 82 unique types of molecules in this entry. The entry contains 204068 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 Mus musculus 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L5	3399	Total	C	N	O	P	0	0
			72884	32460	13325	23701	3398		

- Molecule 2 is a RNA chain called Mus musculus 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 Mus musculus 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L8	151	Total	C	N	O	P	0	0
			3210	1433	567	1060	150		

- Molecule 4 is a protein called Large ribosomal subunit protein uL2.

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 Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LB	397	Total	C	N	O	S	0	0
			3202	2039	603	546	14		

- Molecule 6 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LC	357	Total	C	N	O	S	0	0
			2857	1797	571	474	15		

- Molecule 7 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LD	293	Total	C	N	O	S	0	0
			2389	1509	441	425	14		

- Molecule 8 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LE	216	Total	C	N	O	S	0	0
			1743	1115	332	292	4		

- Molecule 9 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LF	214	Total	C	N	O	S	0	0
			1771	1139	337	287	8		

- Molecule 10 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LG	229	Total	C	N	O	S	0	0
			1848	1179	354	311	4		

- Molecule 11 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LH	190	Total	C	N	O	S	0	0
			1519	956	284	273	6		

- Molecule 12 is a protein called Large ribosomal subunit protein uL16-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LI	201	Total	C	N	O	S	0	0
			1631	1037	316	267	11		

- Molecule 13 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LJ	167	Total	C	N	O	S	0	0
			1340	848	250	236	6		

- Molecule 14 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LL	206	Total	C	N	O	S	0	0
			1667	1043	343	277	4		

- Molecule 15 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LM	136	Total	C	N	O	S	0	0
			1125	721	218	179	7		

- Molecule 16 is a protein called Large ribosomal subunit protein eL15.

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 Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LO	201	Total	C	N	O	S	0	0
			1640	1055	320	259	6		

- Molecule 18 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LP	154	Total	C	N	O	S	0	0
			1251	782	243	217	9		

- Molecule 19 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LQ	187	Total	C	N	O	S	0	0
			1515	948	314	249	4		

- Molecule 20 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LR	174	Total	C	N	O	S	0	0
			1457	901	316	231	9		

- Molecule 21 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LS	175	Total	C	N	O	S	0	0
			1451	924	283	234	10		

- Molecule 22 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LT	160	Total	C	N	O	S	0	0
			1307	829	253	218	7		

- Molecule 23 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LU	100	Total	C	N	O	S	0	0
			817	523	143	149	2		

- Molecule 24 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LV	130	Total	C	N	O	S	0	0
			973	615	183	170	5		

- Molecule 25 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LW	62	Total	C	N	O	S	0	0
			519	332	101	83	3		

- Molecule 26 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LX	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 27 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LY	132	Total	C	N	O	S	0	0
			1102	692	223	184	3		

- Molecule 28 is a protein called Large ribosomal subunit protein eL27.

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 Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	La	147	Total	C	N	O	S	0	0
			1164	736	239	185	4		

- Molecule 30 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Lb	99	Total	C	N	O	S	0	0
			807	505	174	124	4		

- Molecule 31 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Lc	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

- Molecule 32 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ld	108	Total	C	N	O	S	0	0
			896	566	172	156	2		

- Molecule 33 is a protein called Large ribosomal subunit protein eL32.

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 Large ribosomal subunit protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lf	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 35 is a protein called Large ribosomal subunit protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lg	110	Total	C	N	O	S	0	0
			873	546	180	141	6		

- Molecule 36 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lh	122	Total	C	N	O	S	0	0
			1015	643	204	167	1		

- Molecule 37 is a protein called Large ribosomal subunit protein eL36.

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 Large ribosomal subunit protein eL37.

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 Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lk	69	Total	C	N	O	S	0	0
			568	365	103	99	1		

- Molecule 40 is a protein called Large ribosomal subunit protein eL39-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Ll	50	Total	C	N	O	S	0	0
			438	279	93	64	2		

- Molecule 41 is a protein called Ubiquitin-ribosomal protein eL40 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lm	51	Total	C	N	O	S	0	0
			419	260	88	65	6		

- Molecule 42 is a protein called Small ribosomal subunit protein eS32.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ln	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 43 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lo	103	Total	C	N	O	S	0	0
			842	528	172	136	6		

- Molecule 44 is a protein called Large ribosomal subunit protein eL43.

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 Large ribosomal subunit protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lr	124	Total	C	N	O	S	0	0
			994	616	206	167	5		

- Molecule 46 is a RNA chain called Mus musculus 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	S2	1628	Total	C	N	O	P	0	0
			34749	15516	6241	11365	1627		

- Molecule 47 is a RNA chain called A*, P/E tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S6	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		
47	S7	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

- Molecule 48 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SA	207	Total	C	N	O	S	0	0
			1636	1042	288	298	8		

- Molecule 49 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SB	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 50 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SC	215	Total	C	N	O	S	0	0
			1665	1080	285	291	9		

- Molecule 51 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SD	209	Total	C	N	O	S	0	0
			1626	1036	296	287	7		

- Molecule 52 is a protein called Small ribosomal subunit protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SE	258	Total	C	N	O	S	0	0
			2050	1311	381	350	8		

- Molecule 53 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SF	179	Total	C	N	O	S	0	0
			1416	888	262	259	7		

- Molecule 54 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SG	204	Total	C	N	O	S	0	0
			1645	1029	330	280	6		

- Molecule 55 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SH	180	Total	C	N	O	S	0	0
			1449	924	266	258	1		

- Molecule 56 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SI	183	Total	C	N	O	S	0	0
			1499	943	293	258	5		

- Molecule 57 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SJ	138	Total	C	N	O	S	0	0
			1162	743	230	187	2		

- Molecule 58 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SK	90	Total	C	N	O	S	0	0
			760	495	135	124	6		

- Molecule 59 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SL	135	Total	C	N	O	S	0	0
			1110	708	207	189	6		

- Molecule 60 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 61 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SO	134	Total	C	N	O	S	0	0
			1002	612	197	187	6		

- Molecule 62 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SP	118	Total	C	N	O	S	0	0
			981	625	183	166	7		

- Molecule 63 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 64 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SR	131	Total	C	N	O	S	0	0
			1064	668	198	194	4		

- Molecule 65 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SS	140	Total	C	N	O	S	0	0
			1157	728	231	197	1		

- Molecule 66 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	ST	140	Total	C	N	O	S	0	0
			1090	681	212	195	2		

- Molecule 67 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SU	95	Total	C	N	O	S	0	0
			753	471	142	136	4		

- Molecule 68 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SV	81	Total	C	N	O	S	0	0
			619	379	116	119	5		

- Molecule 69 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 70 is a protein called Small ribosomal subunit protein uS12.

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

- Molecule 71 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SY	110	Total	C	N	O	S	0	0
			891	565	173	149	4		

- Molecule 72 is a protein called Small ribosomal subunit protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SZ	72	Total	C	N	O	S	0	0
			574	368	104	101	1		

- Molecule 73 is a protein called Small ribosomal subunit protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Sa	99	Total	C	N	O	S	0	0
			792	492	165	130	5		

- Molecule 74 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Sb	82	Total	C	N	O	S	0	0
			644	403	120	114	7		

- Molecule 75 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Sc	54	Total	C	N	O	S	0	0
			416	257	80	77	2		

- Molecule 76 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Sd	54	Total	C	N	O	S	0	0
			455	284	93	73	5		

- Molecule 77 is a protein called Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Se	48	Total	C	N	O	S	0	0
			384	234	86	63	1		

- Molecule 78 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Sg	276	Total	C	N	O	S	0	0
			2148	1357	378	401	12		

- Molecule 79 is a RNA chain called RNA (5'-R(P*AP*UP*CP*AP*UP*GP*AP*AP*GP*U)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Sx	10	Total	C	N	O	P	0	0
			214	96	39	69	10		

- Molecule 80 is a protein called Nascent peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
80	Z	8	Total	C	N	O	0	0
			39	23	8	8		

- Molecule 81 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
81	L5	93	Total	Mg	0
			93	93	
81	L7	1	Total	Mg	0
			1	1	
81	LN	1	Total	Mg	0
			1	1	
81	LP	1	Total	Mg	0
			1	1	
81	Le	1	Total	Mg	0
			1	1	

- Molecule 82 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
82	Lj	1	Total	Zn	0
			1	1	

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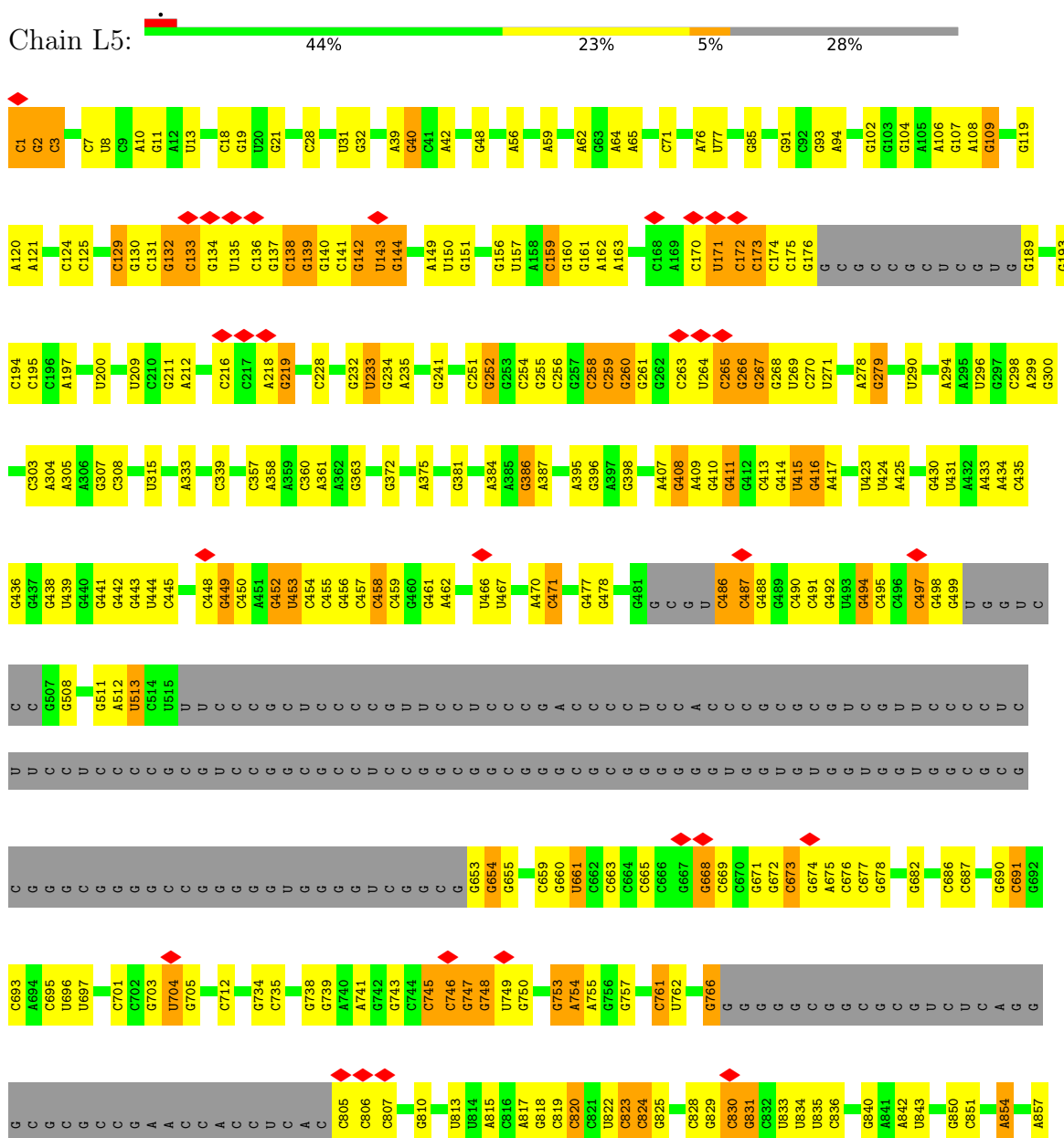
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Mol	Chain	Residues	Atoms		AltConf
82	Lm	1	Total 1	Zn 1	0
82	Lp	1	Total 1	Zn 1	0

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: Mus musculus 28S ribosomal RNA



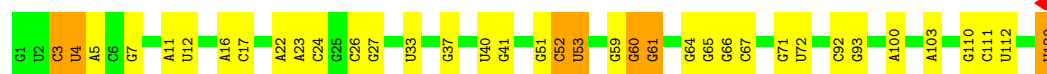




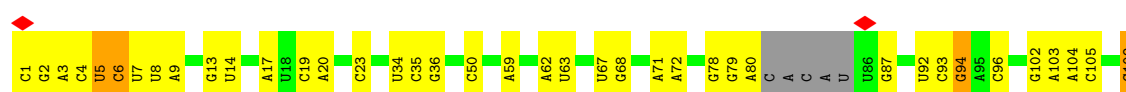
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C4606	U4528	C4393	G4300	G4198	U4076	C3941	C3824	G3748	C	G	G3531	A3431
U4607	G4529	A4394	A4301	A4201	G4077	C3944	U3827	A	C	U	A3534	A3432
G4608	G4530	A4395	G4305	G4202	G4078	G3944	G3828	G	G	G	G3535	G3433
G4609	U4531	C4396	G4309	U4208	C4087	G3950	G3836	C	C	A	G3536	G3434
C4612	C4532	A4397	U4309	C4213	U4088	G3958	G3837	C	C	U	G3537	A3441
A4613	U4533	G4399	C4323	G4216	U4089	C3967	G3838	G	C	A	G3538	A3442
A4614	G4537	U4402	C4324	U4217	U4090	C3967	U3842	A	C	A	C3544	U3443
A4615	A4538	G4403	A4325	A4217	U4095	G3975	U3843	G	G	U	G3547	G3449
A4616	A4539	G4404	U4326	G4220	C4097	A3976	A3844	G	G	G	A3548	A3452
C4617	A4540	G4408	G4331	G4224	U4101	A3977	U3846	G	C	G	U3549	U3453
A4618	C4541	C4411	G4332	U4225	G4105	A3978	U3847	C	C	A	C3553	U3459
A4619	U4546	C4412	A4333	U4228	U4110	G3982	G3848	U	C	G	G3554	U3462
U4620	G4549	C4413	A4334	G4231	U4111	C3983	G3849	C	C	G	A3558	G3463
U4621	C4550	C4414	G4341	U4232	C4112	C3984	A3856	G	C	C	G	G3466
U4624	A4551	G4415	U4342	U4233	U4113	C3985	C3868	C3767	G	C	A3563	G3467
A4627	C4552	U4419	G4343	U4234	U4114	A3989	G3869	U3768	U	C	G3564	G3468
C4628	G4553	G4425	A4344	G4235	U4115	C3990	C3872	U3769	A	G	C3566	G3469
A4630	A4554	C4426	C4345	C4236	A4117	G3991	A3872	C3770	A	G	C3567	U3471
U4633	G4557	C4427	A4346	U4237	U4118	A3992	G3878	G	A	C	C3568	A3474
U4636	A4558	C4428	U4352	A4238	C4119	A3992	U3878	G3773	U	G	U3569	U3475
U4637	G4559	G	A4353	G4239	U4120	G4008	U3882	A3778	C	C	U3572	G3476
U4638	C4560	C	A4354	G4240	U4121	G4009	U3885	A3779	C	C	G3573	G3477
U4639	G4561	C	C4357	U4241	U4122	G4010	A3886	C3780	A	G	A3574	G3480
C4640	A4562	C	A4358	A4242	U4123	U4011	G3888	G3786	C	C	C3575	C3491
U4641	C4563	C	C4359	A4243	U4124	U4012	U3889	U3787	A	C	U3577	C3492
U4645	C4564	C	G4360	U4244	U4125	U4013	G3891	C3788	C	C	U3578	U3495
U4652	G4565	C	U4361	G4245	U4126	G4021	A3892	C3789	U	C	U3584	G3496
C4653	C4566	C	C4362	U4246	U4127	G4022	G3893	C	C	G	A3585	U3497
U4654	U4567	C	C4363	U4247	C4128	U4025	C3896	C	C	U	G3586	C3500
U4655	C4568	C	G4364	A4255	C4129	C4155	C3905	C	C	C	C3587	U3501
U4659	G4569	C	C4365	G4259	U4165	U4156	A3906	U	C	C	C3588	A3502
C4661	C4570	C	U4370	A4263	A4166	A4030	G3907	G	C	G	C3594	U3505
A4662	U4571	C	C4373	G4271	A4171	A4031	A3908	C	C	U	G3595	A3506
G4663	C4572	C	G4376	U4272	C4172	A4032	A3909	C	C	G	C3597	U3508
A4665	G4573	C	A4377	U4273	G4173	A4033	A3910	C	C	U	G3598	A3513
U4669	C4579	C	G4378	G4278	U4174	C4040	C3911	G3803	G	G	G3601	G3516
U4671	A4580	C	G4379	U4279	A4175	A4047	C3912	G3804	G	G	A3602	A3517
C4672	G4581	C	U4380	U4280	G4176	U4059	U3913	G3805	U	U	A3603	A3518
A4673	C4582	C	A4381	U4281	A4177	G4060	C3914	G3806	C	C	A3604	A3606
U4675	U4583	C	A4382	G4282	C4178	U4061	G3917	G3807	G	G	U3607	A3519
C4676	C4584	C	G4383	U4283	G4181	U4062	G3917	C3808	G	G	G3608	A3524
U4677	G4585	C	G4384	G4284	U4182	A4068	A3924	G3809	G	G	A	C3527
U4678	A4586	C	C4385	U4287	C4190	G4071	G3925	A3810	C	C	G	A3528
G4681	C4587	C	A4386	A4288	G4191	U4192	A3926	C3811	A	A	G	A3529
A4682	G4588	C	A4387	U4289	U4192	C4193	A3926	C3812	C	C	G	
U4685	U4594	C	G4388	G4290	G4194	U4072	A3933	U3815	C	C	G	
	C4595	C	C4389			U4073		C3745				
	G4596	C	G4390			C4074		G3746				
	A4603	C	C4391									
	A4604	C										



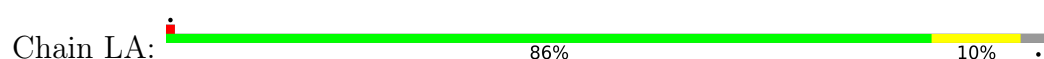
- Molecule 2: Mus musculus 5S ribosomal RNA



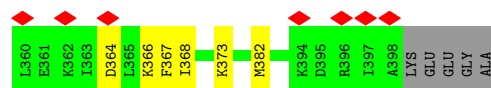
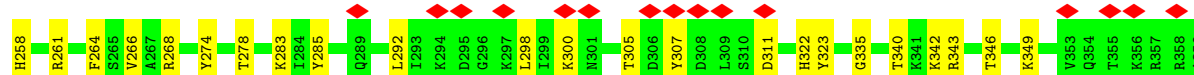
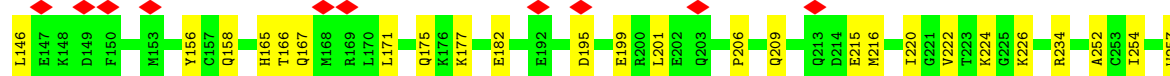
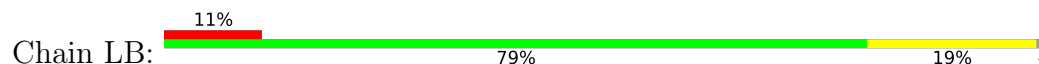
- Molecule 3: Mus musculus 5.8S ribosomal RNA



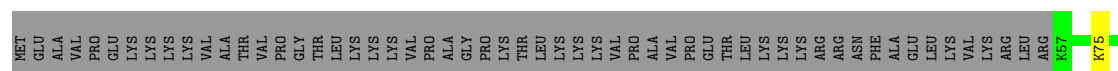
- Molecule 4: Large ribosomal subunit protein uL2



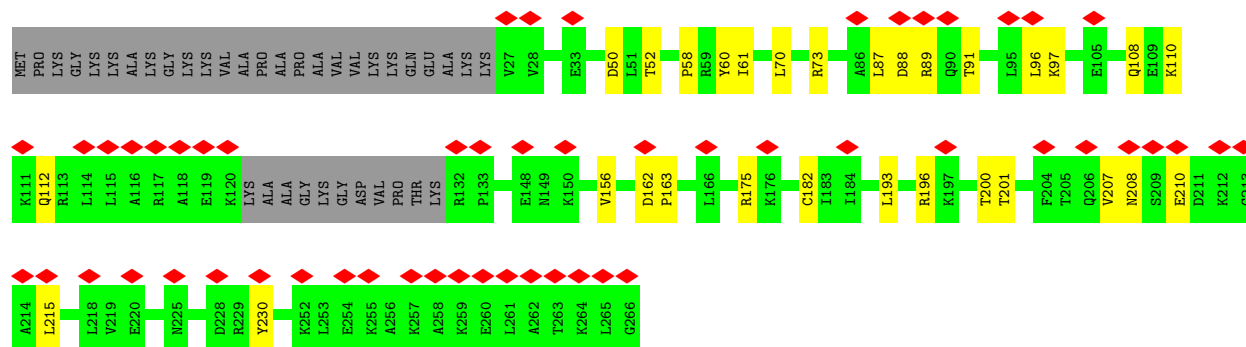
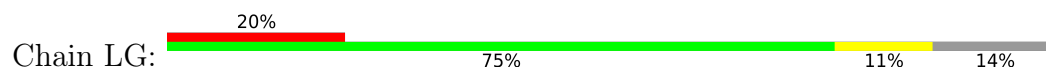
- Molecule 5: Large ribosomal subunit protein uL3



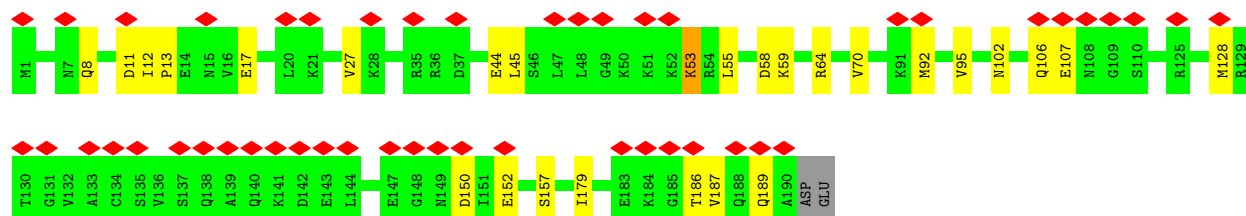
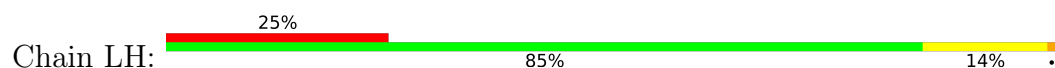
- Molecule 6: Large ribosomal subunit protein uL4



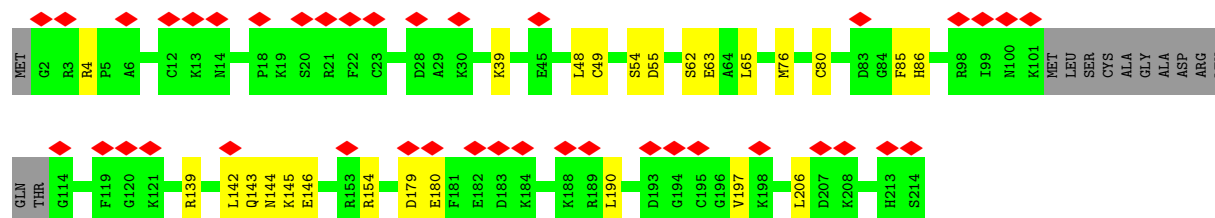
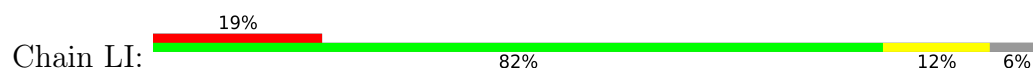
• Molecule 10: Large ribosomal subunit protein eL8



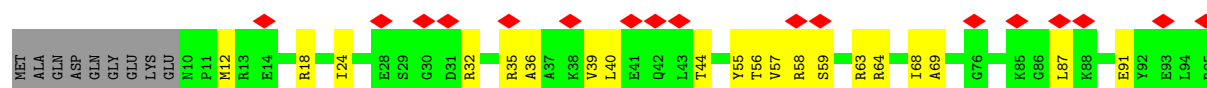
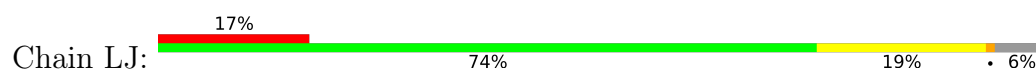
• Molecule 11: Large ribosomal subunit protein uL6

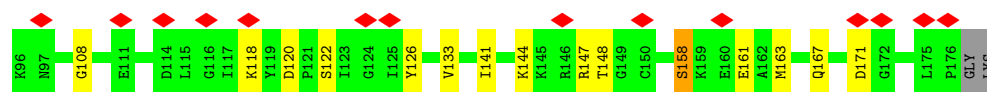


• Molecule 12: Large ribosomal subunit protein uL16-like

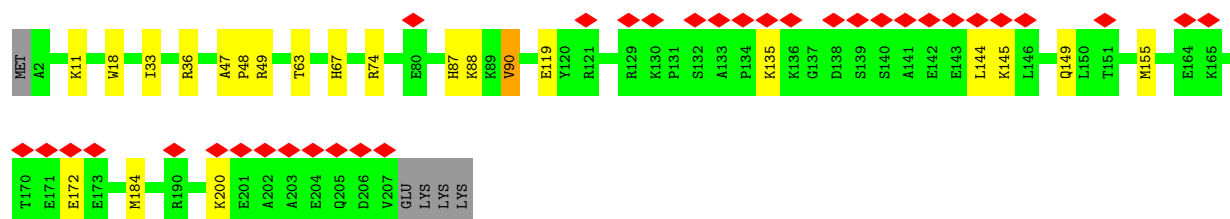
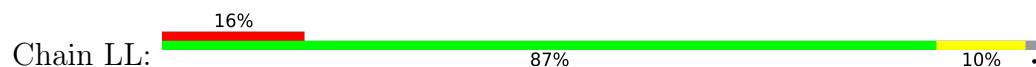


• Molecule 13: Large ribosomal subunit protein uL5

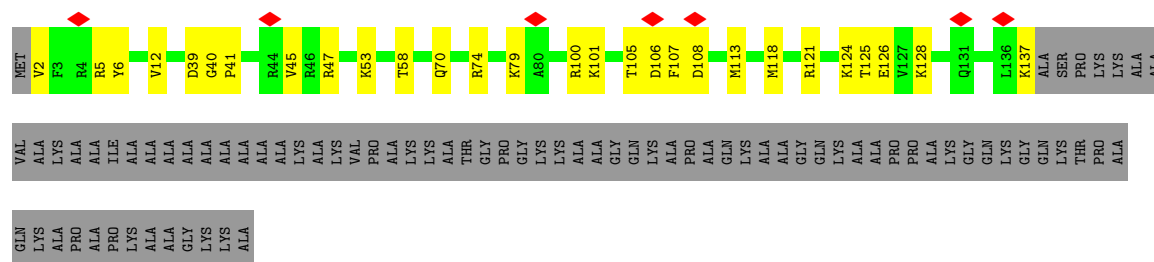




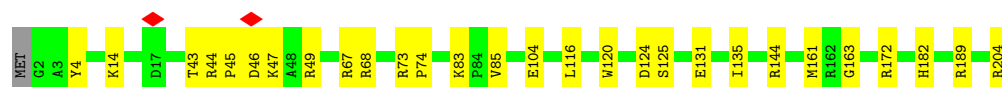
- Molecule 14: Large ribosomal subunit protein eL13



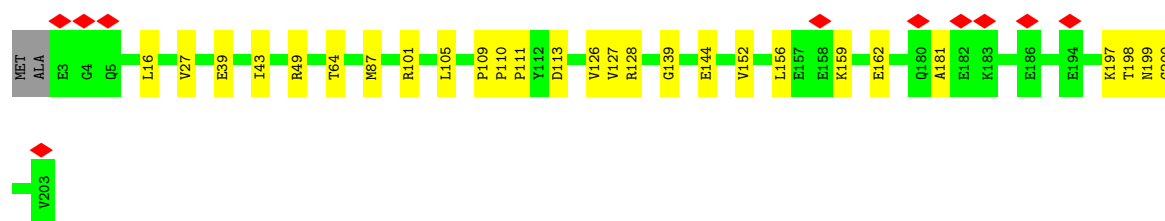
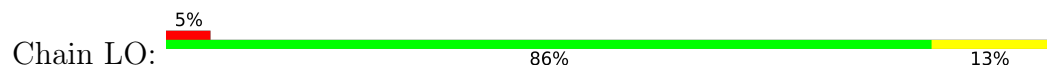
- Molecule 15: Large ribosomal subunit protein eL14



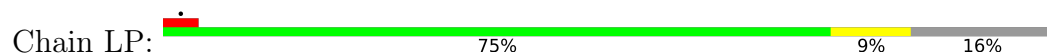
- Molecule 16: Large ribosomal subunit protein eL15

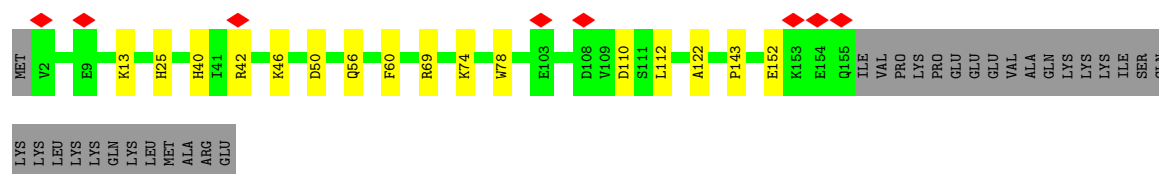


- Molecule 17: Large ribosomal subunit protein uL13

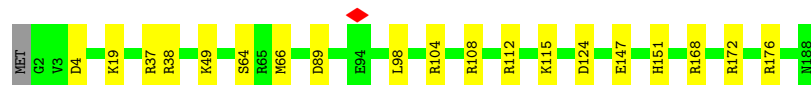
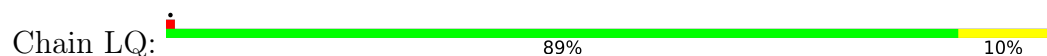


- Molecule 18: Large ribosomal subunit protein uL22

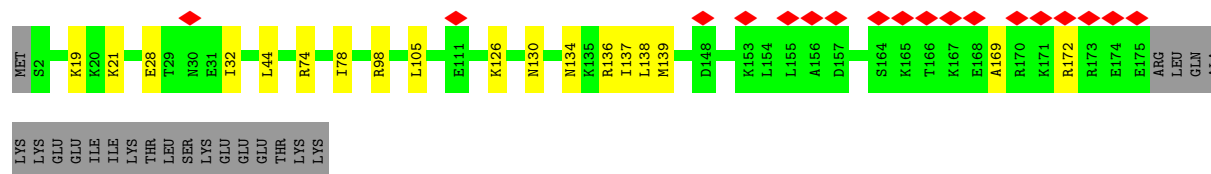
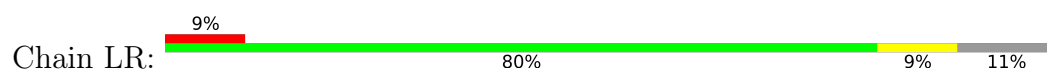




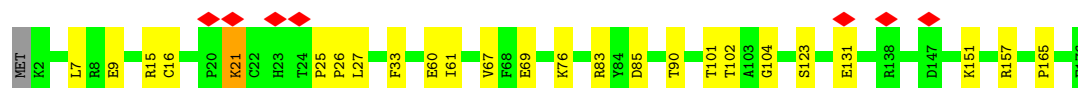
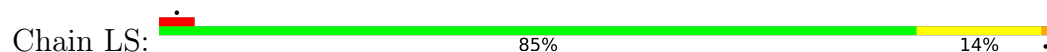
- Molecule 19: Large ribosomal subunit protein eL18



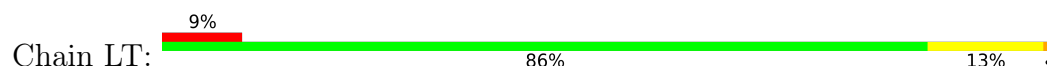
- Molecule 20: Large ribosomal subunit protein eL19



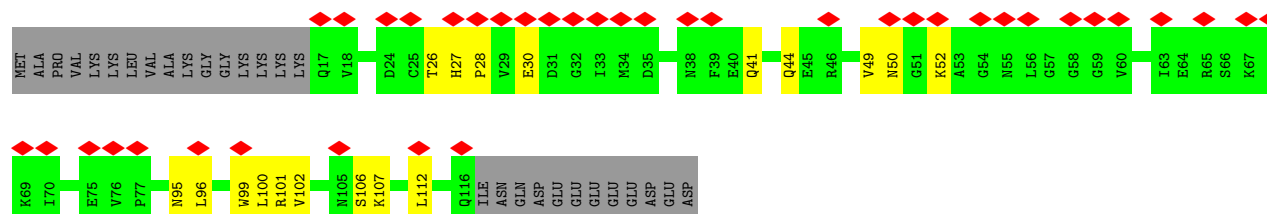
- Molecule 21: Large ribosomal subunit protein eL20



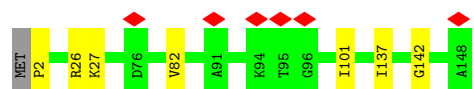
- Molecule 22: Large ribosomal subunit protein eL21



- Molecule 23: Large ribosomal subunit protein eL22

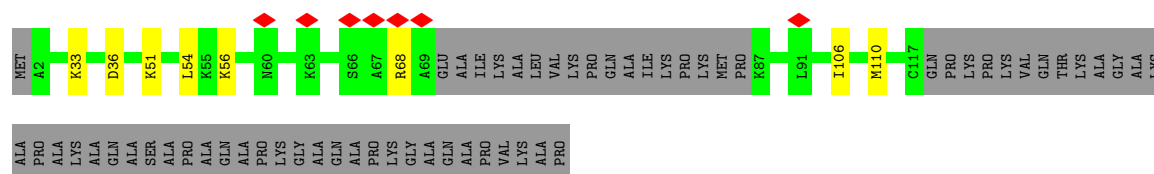


Chain La:  95% 5%



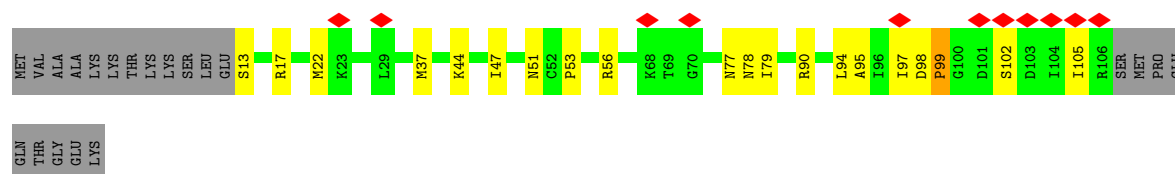
- Molecule 30: Large ribosomal subunit protein eL29

Chain Lb:  57% 5% 38%




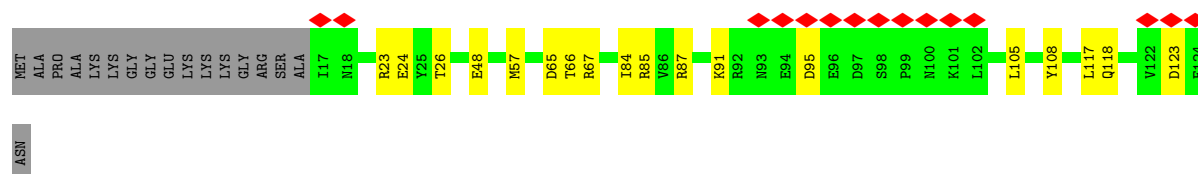
- Molecule 31: Large ribosomal subunit protein eL30

Chain Lc:  10% 64% 17% 18%




- Molecule 32: Large ribosomal subunit protein eL31

Chain Ld:  12% 72% 14% 14%




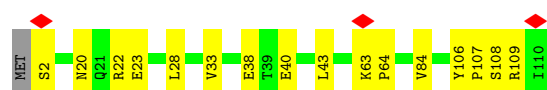
- Molecule 33: Large ribosomal subunit protein eL32

Chain Le:  81% 14% 5%

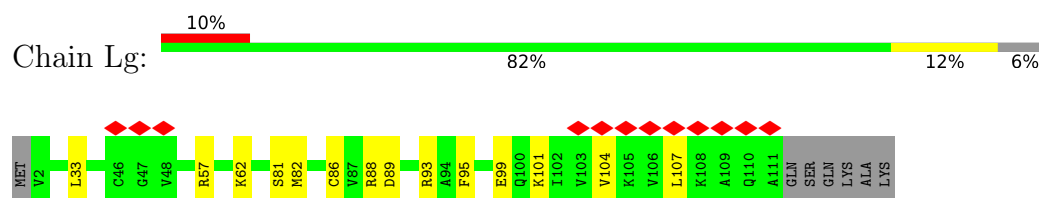


- Molecule 34: Large ribosomal subunit protein eL33

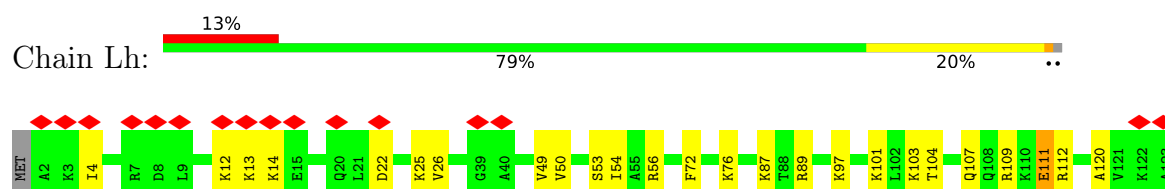
Chain Lf:  85% 15%



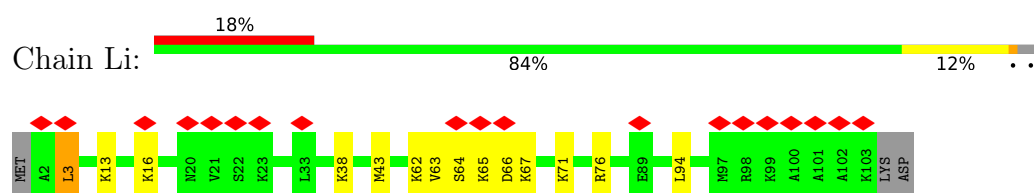
- Molecule 35: Large ribosomal subunit protein eL34



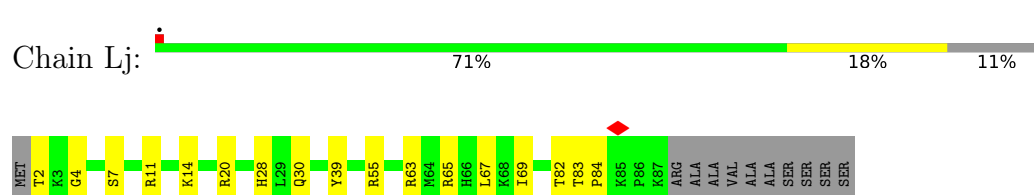
- Molecule 36: Large ribosomal subunit protein uL29



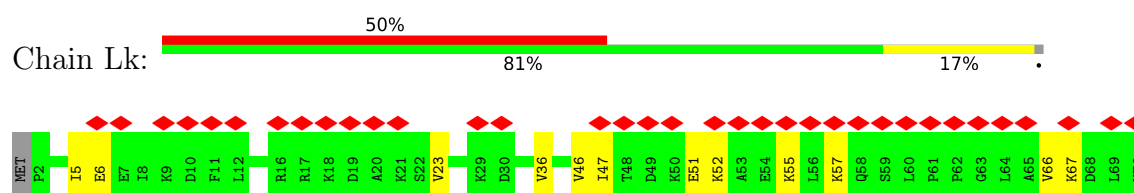
- Molecule 37: Large ribosomal subunit protein eL36



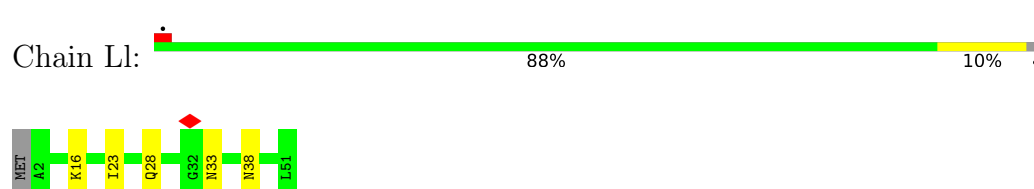
- Molecule 38: Large ribosomal subunit protein eL37



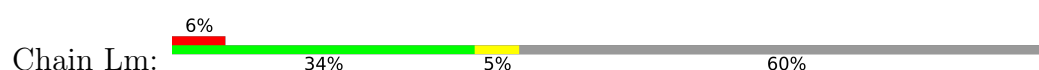
- Molecule 39: Large ribosomal subunit protein eL38



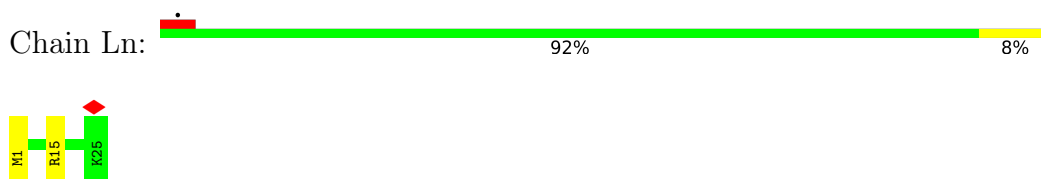
- Molecule 40: Large ribosomal subunit protein eL39-like



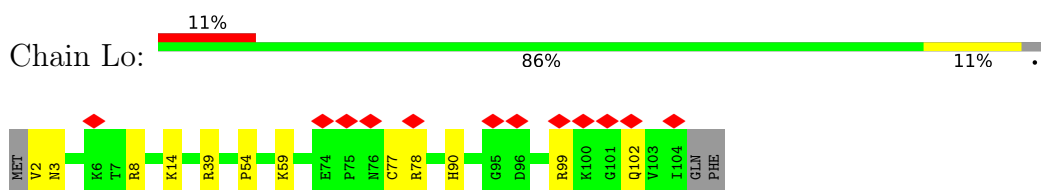
- Molecule 41: Ubiquitin-ribosomal protein eL40 fusion protein



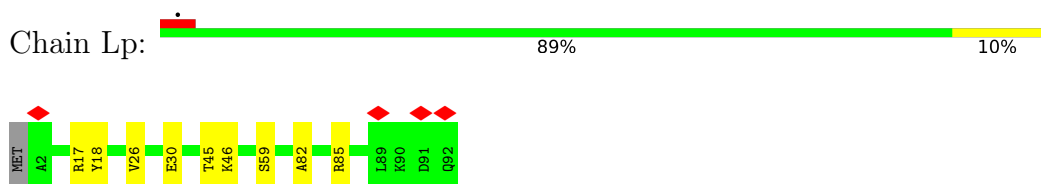
- Molecule 42: Small ribosomal subunit protein eS32



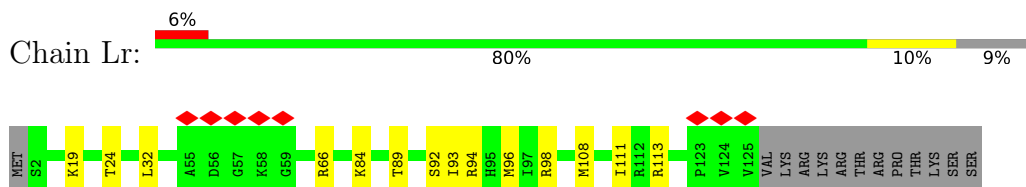
- Molecule 43: Large ribosomal subunit protein eL42



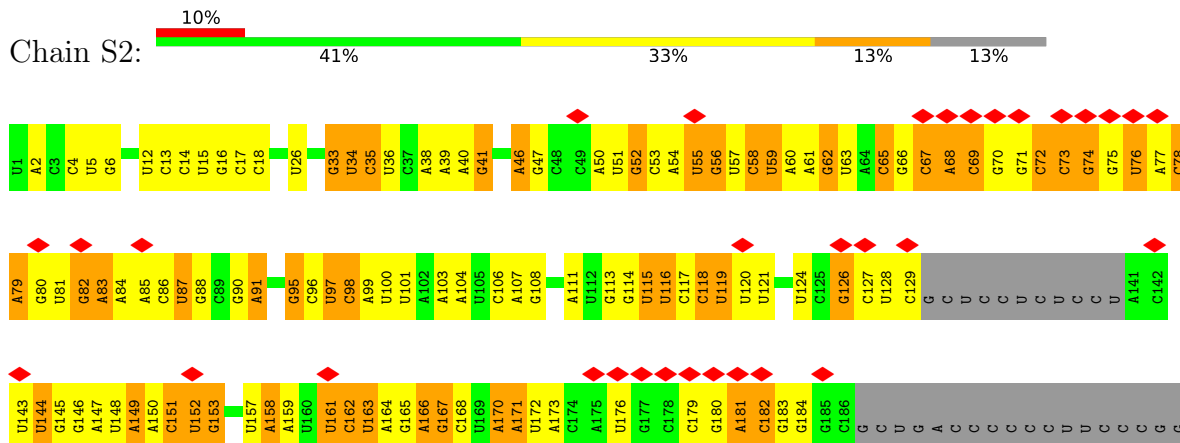
- Molecule 44: Large ribosomal subunit protein eL43

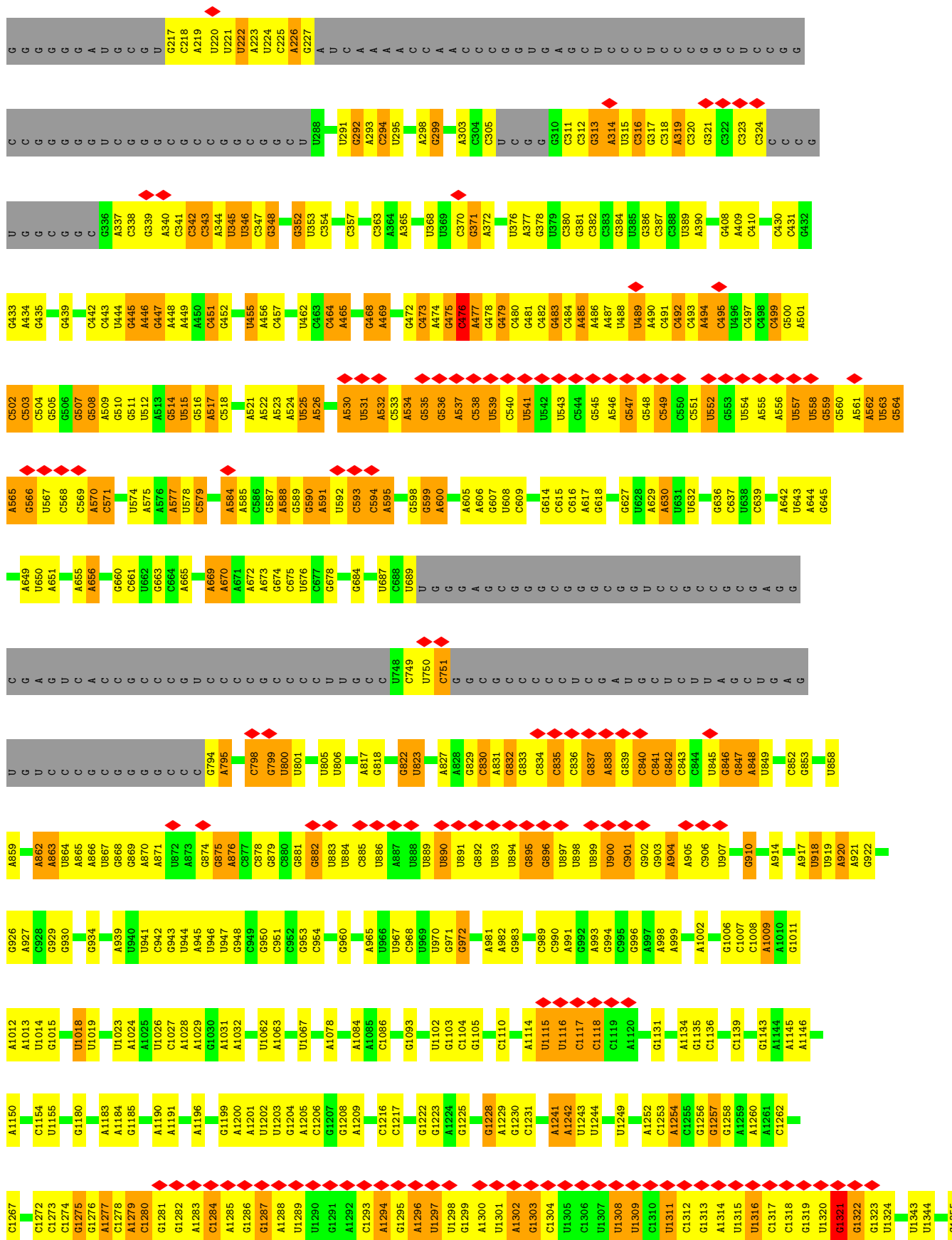


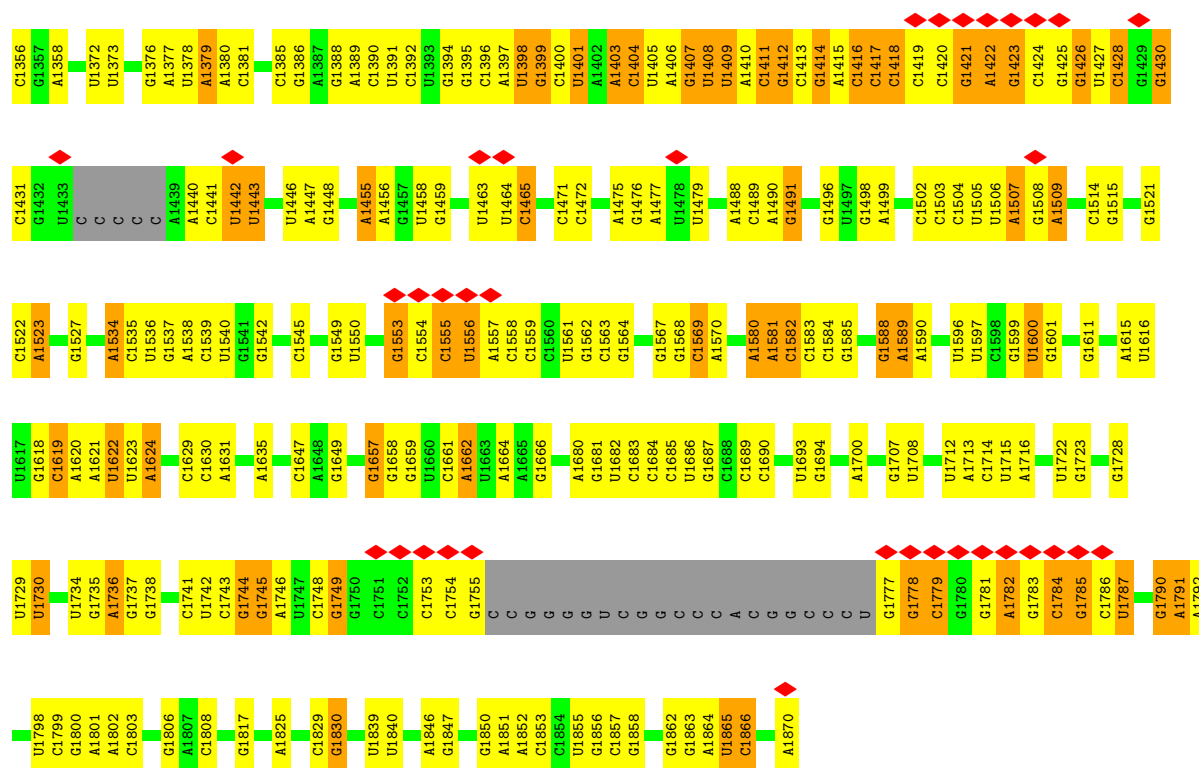
- Molecule 45: Large ribosomal subunit protein eL28



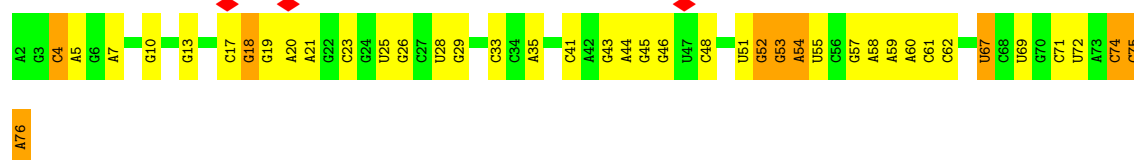
- Molecule 46: *Mus musculus* 18S ribosomal RNA



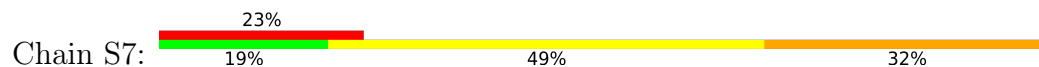




• Molecule 47: A*, P/E tRNA

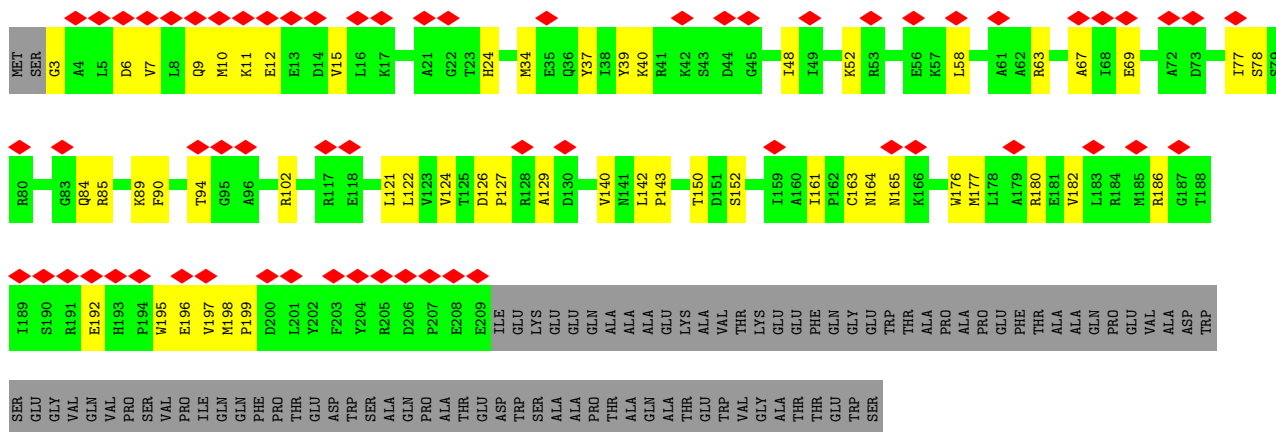


• Molecule 47: A*, P/E tRNA

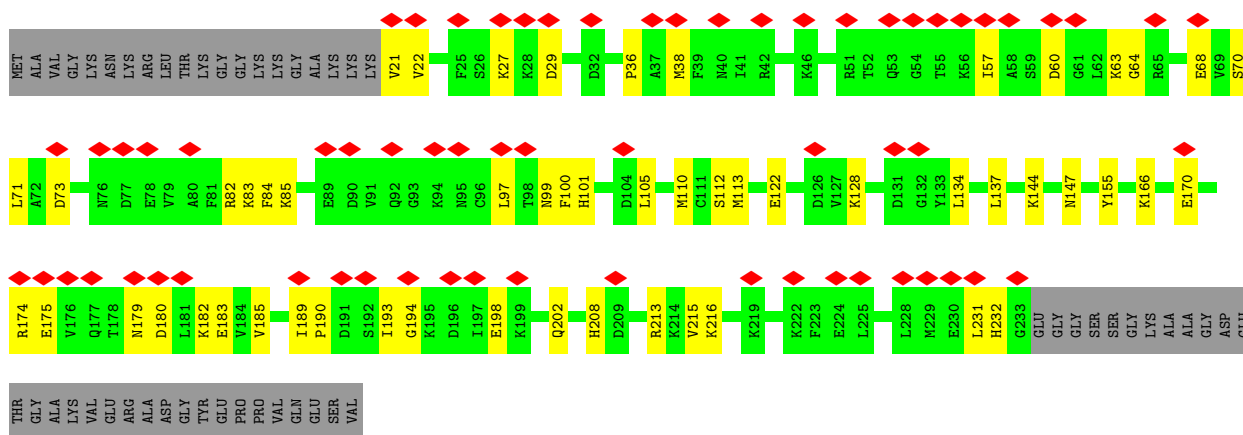


• Molecule 48: Small ribosomal subunit protein uS2

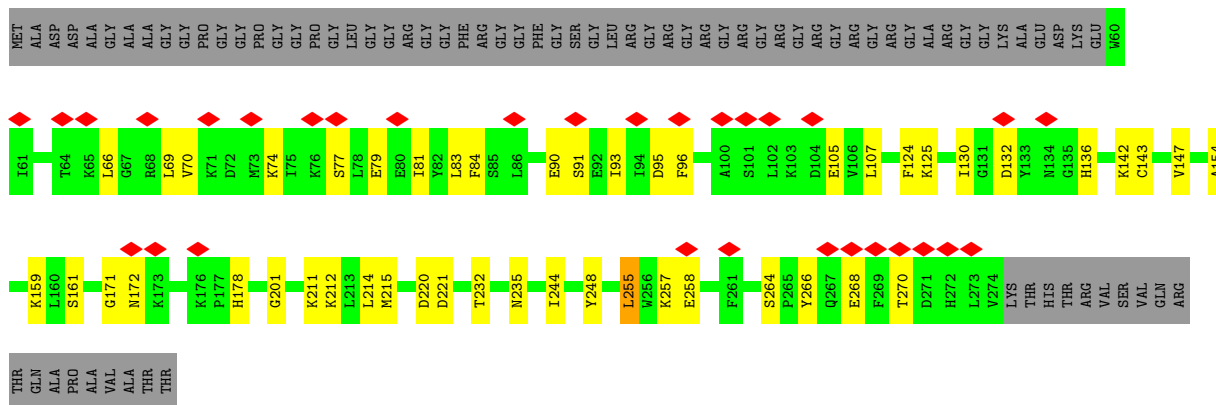




• Molecule 49: Small ribosomal subunit protein eS1

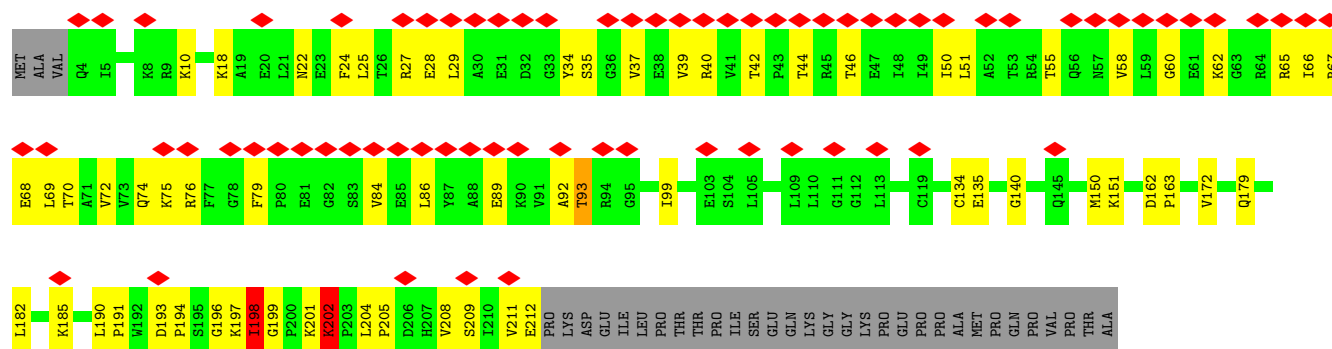


• Molecule 50: Small ribosomal subunit protein uS5

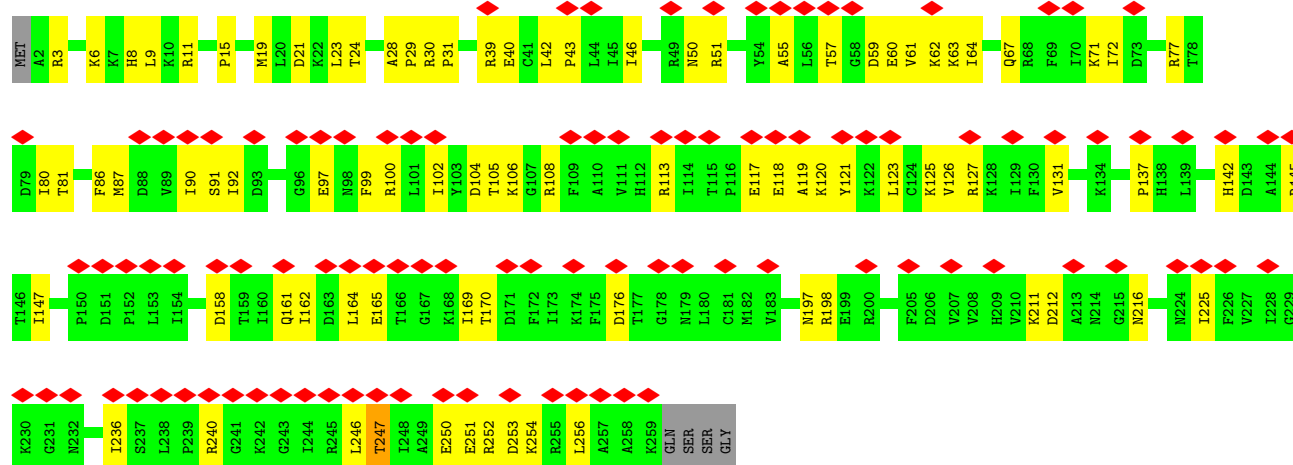
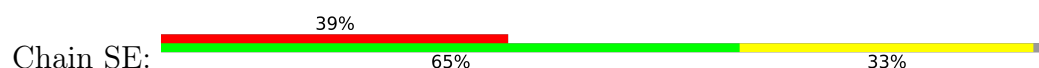


• Molecule 51: Small ribosomal subunit protein uS3

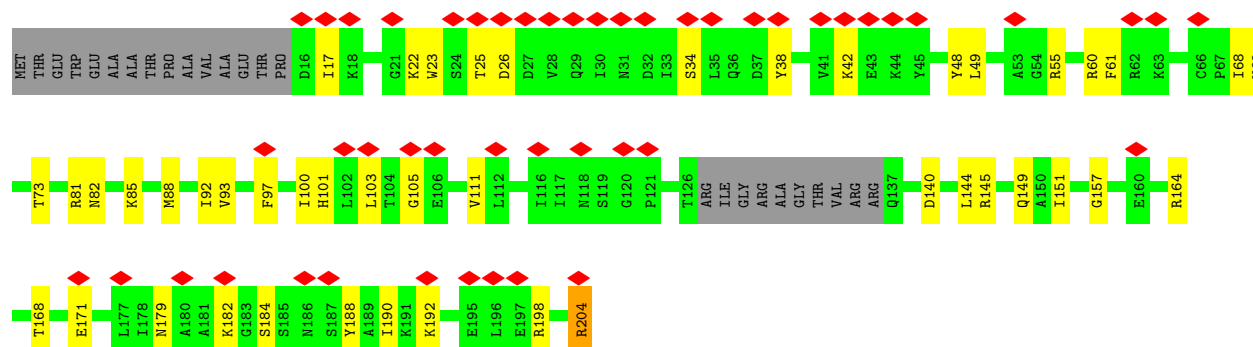




• Molecule 52: Small ribosomal subunit protein eS4

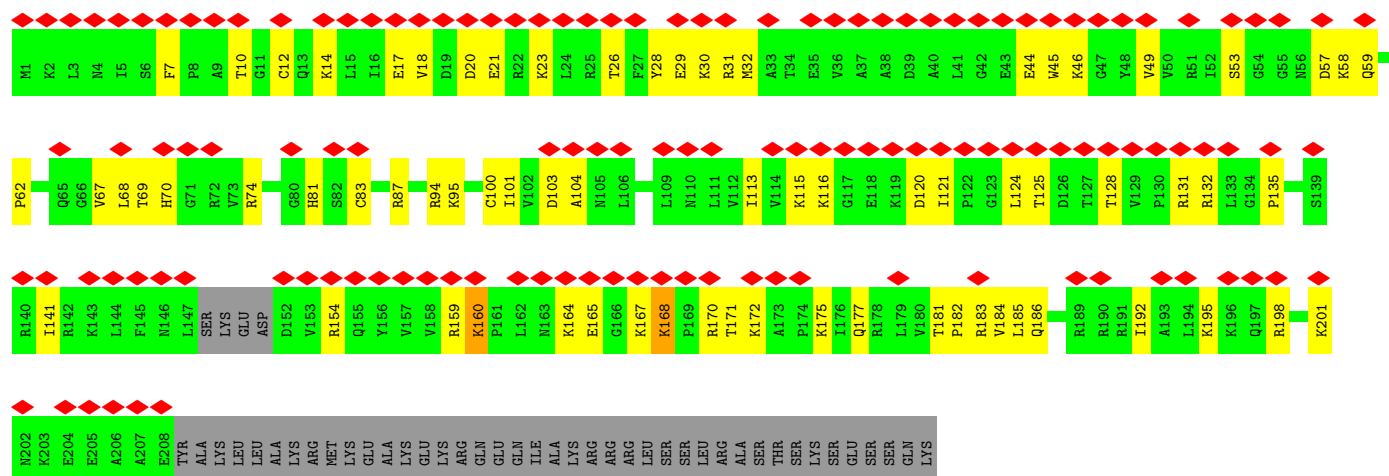


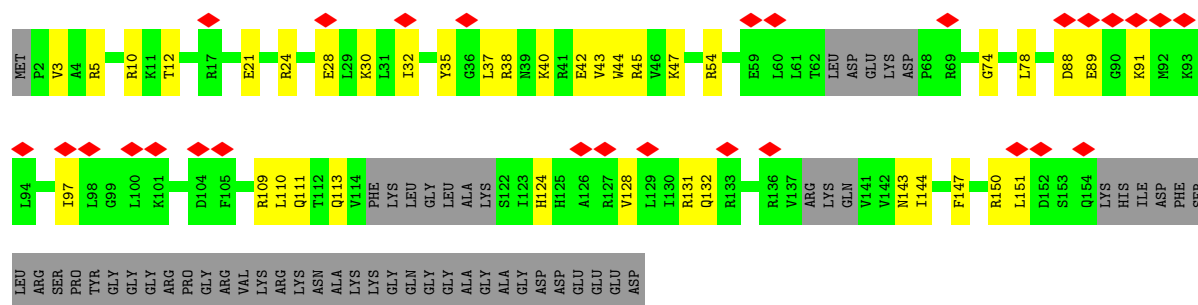
• Molecule 53: Small ribosomal subunit protein uS7



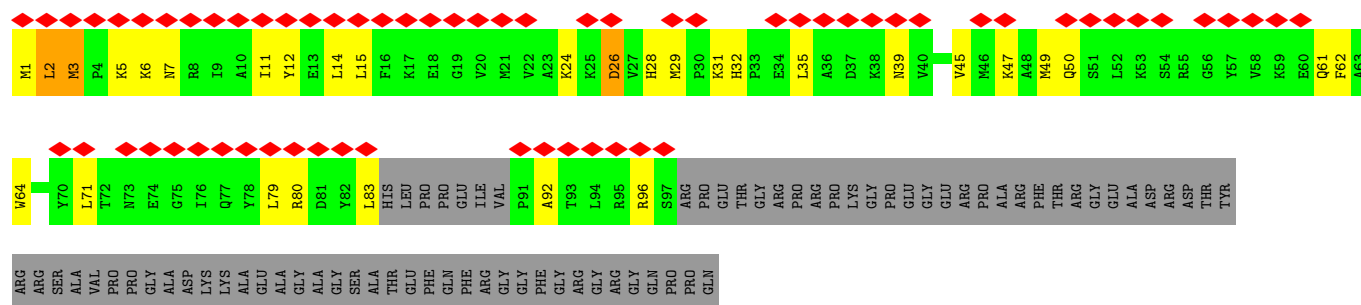
• Molecule 54: Small ribosomal subunit protein eS6



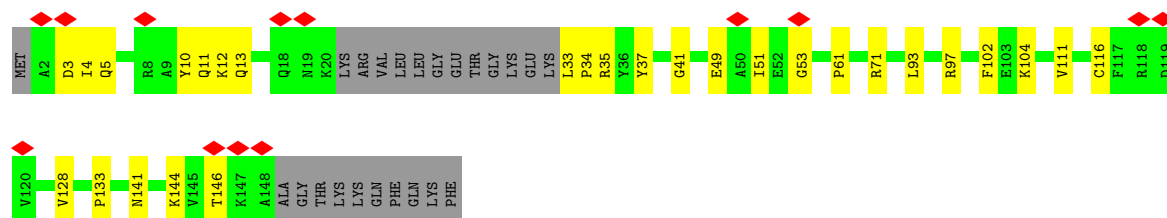




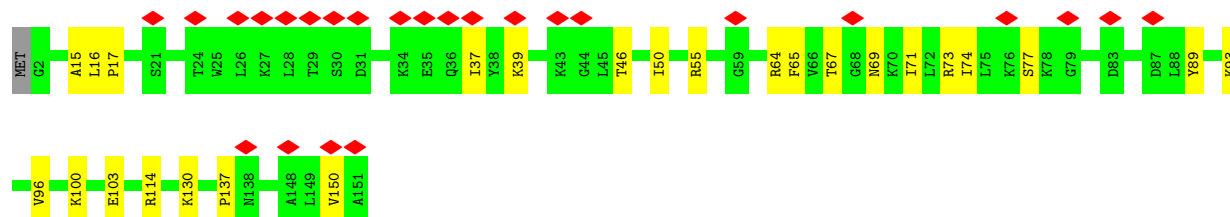
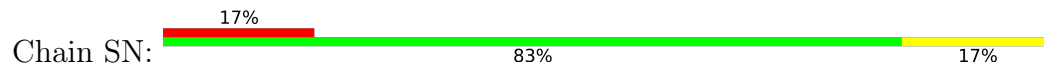
- Molecule 58: Small ribosomal subunit protein eS10



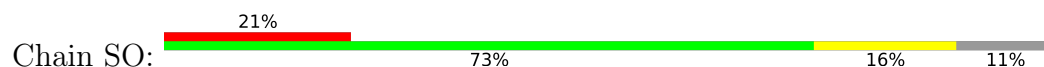
- Molecule 59: Small ribosomal subunit protein uS17

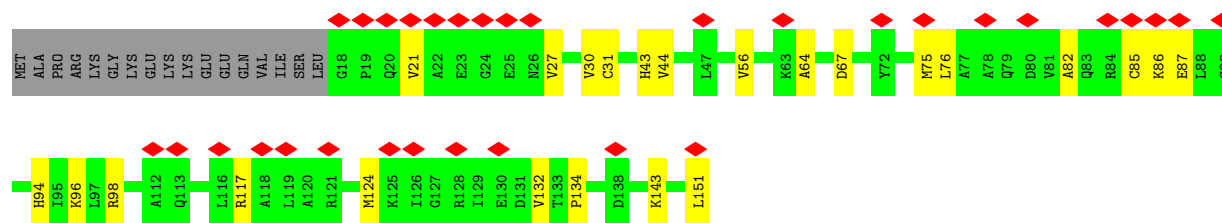


- Molecule 60: Small ribosomal subunit protein uS15



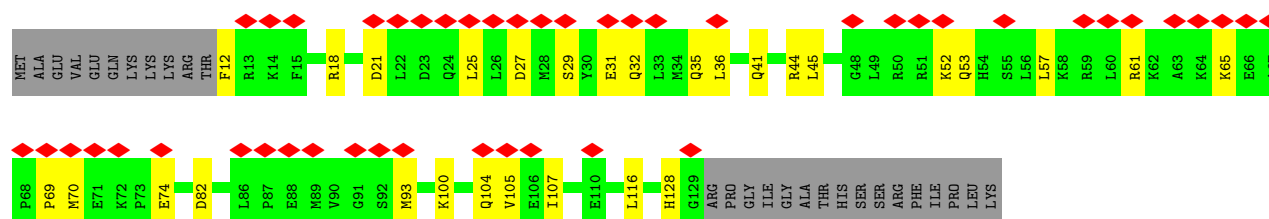
- Molecule 61: Small ribosomal subunit protein uS11





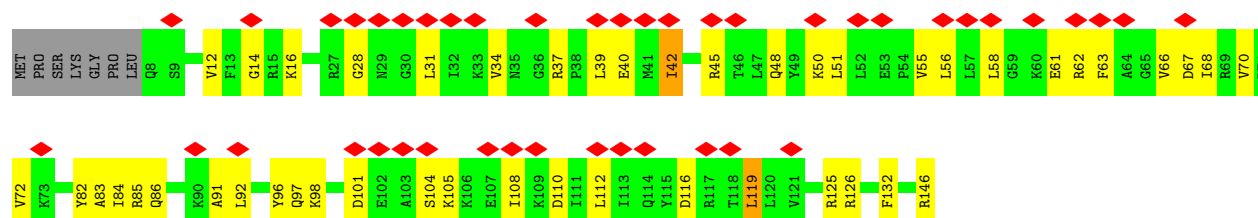
- Molecule 62: Small ribosomal subunit protein uS19

Chain SP:



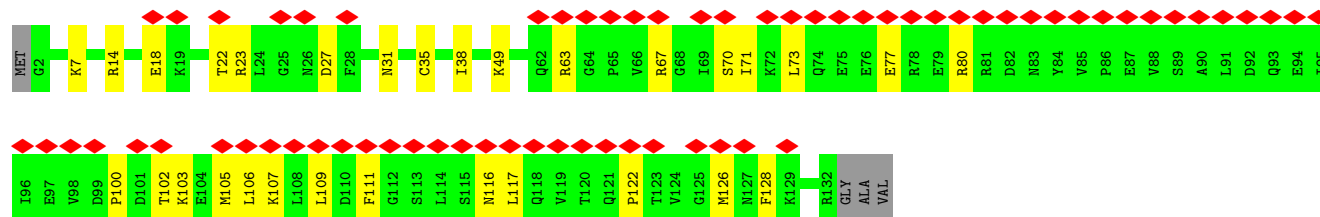
- Molecule 63: Small ribosomal subunit protein uS9

Chain SQ:



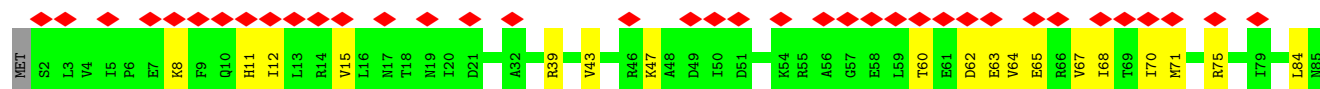
- Molecule 64: Small ribosomal subunit protein eS17

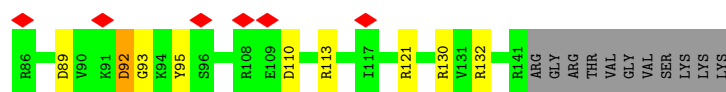
Chain SR:



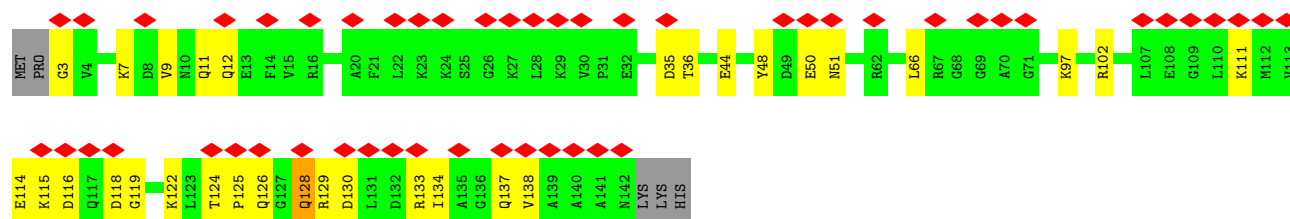
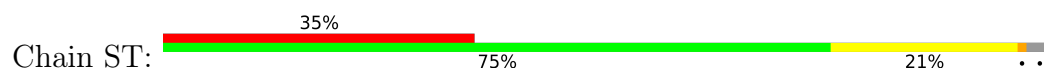
- Molecule 65: Small ribosomal subunit protein uS13

Chain SS:

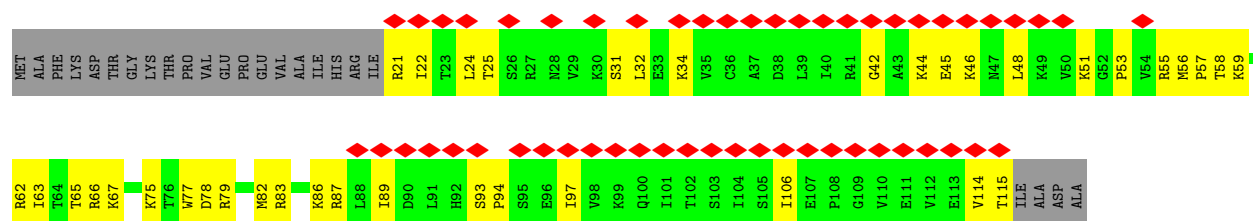




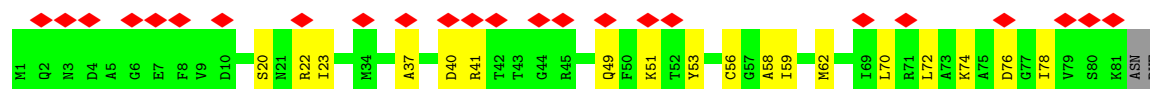
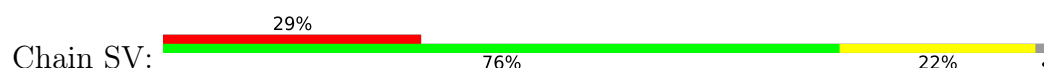
- Molecule 66: Small ribosomal subunit protein eS19



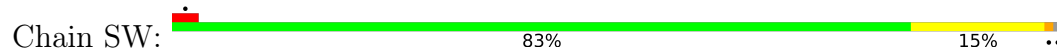
- Molecule 67: Small ribosomal subunit protein uS10



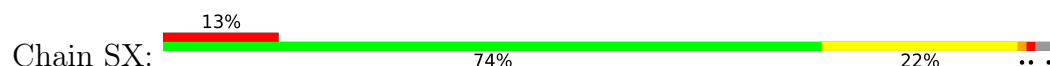
- Molecule 68: Small ribosomal subunit protein eS21

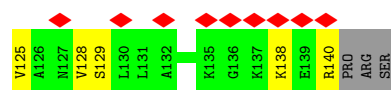


- Molecule 69: Small ribosomal subunit protein uS8

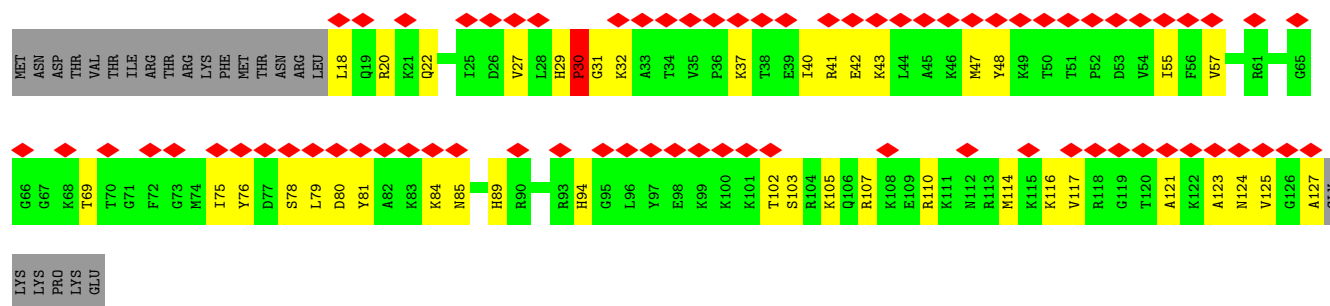


- Molecule 70: Small ribosomal subunit protein uS12

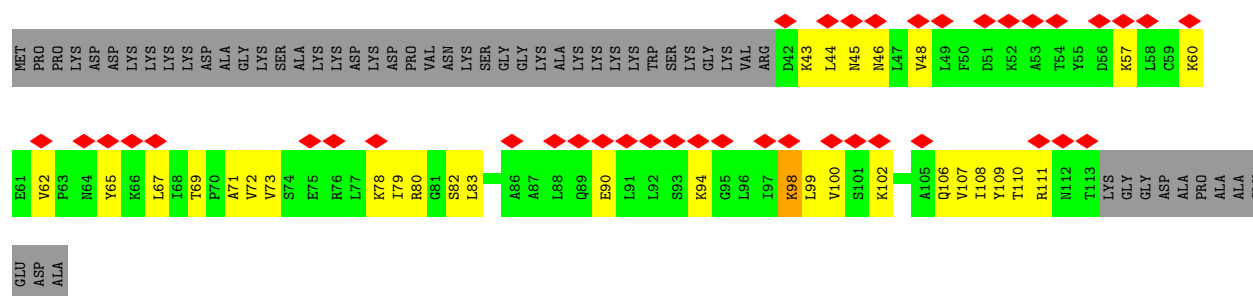
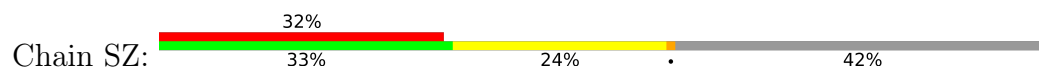




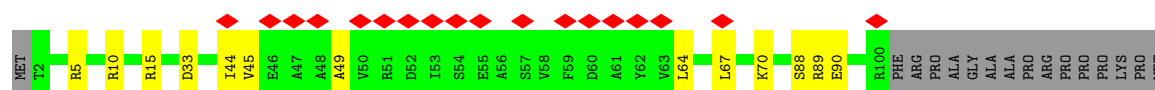
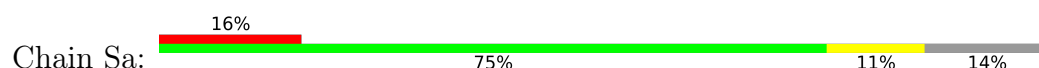
- Molecule 71: Small ribosomal subunit protein eS24



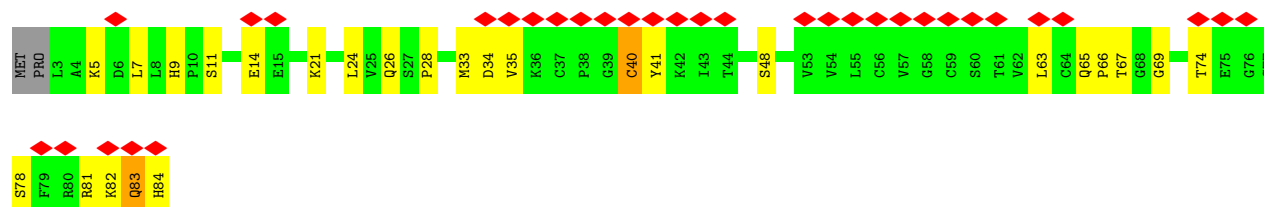
- Molecule 72: Small ribosomal subunit protein eS25



- Molecule 73: Small ribosomal subunit protein eS26



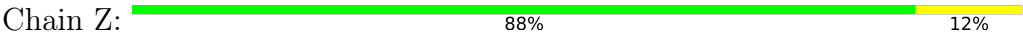
- Molecule 74: Small ribosomal subunit protein eS27



- Molecule 75: Small ribosomal subunit protein eS28



● Molecule 80: Nascent peptide



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	7458	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.513	Depositor
Minimum map value	-0.466	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.073	Depositor
Recommended contour level	0.38	Depositor
Map size (Å)	616.0, 616.0, 616.0	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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	0.17	0/81527	0.31	8/127149 (0.0%)
2	L7	0.15	0/2858	0.29	0/4455
3	L8	0.15	0/3584	0.29	0/5582
4	LA	0.17	0/1936	0.36	0/2596
5	LB	0.16	0/3269	0.35	0/4375
6	LC	0.16	0/2911	0.36	0/3907
7	LD	0.16	0/2435	0.39	0/3260
8	LE	0.15	0/1775	0.39	0/2381
9	LF	0.18	0/1805	0.37	0/2408
10	LG	0.14	0/1880	0.34	0/2531
11	LH	0.17	0/1537	0.43	0/2065
12	LI	0.15	0/1669	0.38	0/2227
13	LJ	0.14	0/1363	0.33	0/1824
14	LL	0.15	0/1698	0.32	0/2274
15	LM	0.14	0/1146	0.34	0/1531
16	LN	0.16	0/1746	0.31	0/2338
17	LO	0.16	0/1670	0.33	0/2232
18	LP	0.15	0/1277	0.34	0/1712
19	LQ	0.17	0/1539	0.34	0/2053
20	LR	0.13	0/1473	0.30	0/1947
21	LS	0.25	0/1491	0.41	0/2000
22	LT	0.15	0/1335	0.34	1/1781 (0.1%)
23	LU	0.18	0/831	0.49	0/1115
24	LV	0.15	0/987	0.35	0/1324
25	LW	0.14	0/532	0.32	0/708
26	LX	0.16	0/984	0.35	0/1323
27	LY	0.14	0/1119	0.33	0/1488
28	LZ	0.15	0/1130	0.35	0/1507
29	La	0.15	0/1193	0.32	0/1593
30	Lb	0.13	0/821	0.30	0/1082
31	Lc	0.16	0/742	0.38	0/996
32	Ld	0.15	0/911	0.32	0/1227

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.16	0/1071	0.32	0/1429
34	Lf	0.17	0/895	0.41	0/1198
35	Lg	0.14	0/883	0.34	0/1178
36	Lh	0.17	0/1023	0.34	0/1350
37	Li	0.13	0/843	0.36	0/1115
38	Lj	0.16	0/720	0.32	0/952
39	Lk	0.18	0/574	0.45	0/760
40	Ll	0.16	0/448	0.30	0/592
41	Lm	0.14	0/425	0.38	0/564
42	Ln	0.13	0/240	0.26	0/305
43	Lo	0.16	0/855	0.36	0/1128
44	Lp	0.15	0/718	0.27	0/953
45	Lr	0.15	0/1009	0.31	0/1353
46	S2	0.17	0/38859	0.33	5/60556 (0.0%)
47	S6	0.12	0/1795	0.27	0/2798
47	S7	0.17	0/1795	0.38	0/2798
48	SA	0.15	0/1673	0.45	2/2275 (0.1%)
49	SB	0.15	0/1756	0.41	0/2350
50	SC	0.26	0/1701	0.48	0/2300
51	SD	0.37	0/1651	0.60	0/2219
52	SE	0.15	0/2092	0.44	0/2816
53	SF	0.15	0/1436	0.38	0/1930
54	SG	0.28	0/1666	0.53	0/2222
55	SH	0.16	0/1470	0.43	0/1968
56	SI	0.13	0/1526	0.36	0/2038
57	SJ	0.12	0/1178	0.33	0/1574
58	SK	0.30	0/780	0.50	0/1046
59	SL	0.14	0/1130	0.37	0/1514
60	SN	0.13	0/1232	0.30	0/1656
61	SO	0.16	0/1015	0.40	0/1361
62	SP	0.16	0/1000	0.43	0/1335
63	SQ	0.22	0/1126	0.47	1/1506 (0.1%)
64	SR	0.27	0/1078	0.45	0/1447
65	SS	0.14	0/1175	0.37	0/1575
66	ST	0.15	0/1108	0.36	0/1486
67	SU	0.16	0/762	0.48	0/1023
68	SV	0.17	0/625	0.50	1/836 (0.1%)
69	SW	0.15	0/1051	0.34	0/1406
70	SX	0.20	0/1097	0.52	3/1464 (0.2%)
71	SY	0.20	0/907	0.54	1/1204 (0.1%)
72	SZ	0.16	0/580	0.46	0/780
73	Sa	0.14	0/805	0.35	0/1079
74	Sb	0.35	0/657	0.61	0/880

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	Sc	0.15	0/418	0.42	0/562
76	Sd	0.27	1/466 (0.2%)	0.33	0/618
77	Se	0.15	0/386	0.38	0/504
78	Sg	0.22	0/2199	0.49	0/2989
79	Sx	0.13	0/239	0.33	0/370
All	All	0.17	1/219312 (0.0%)	0.35	22/322353 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
76	Sd	8	TRP	CA-CB	5.01	1.58	1.52

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	S2	476	C	C4'-C3'-O3'	12.17	131.25	113.00
46	S2	477	A	C2'-C3'-O3'	-9.21	99.88	113.70
1	L5	458	C	C2'-C3'-O3'	8.85	126.97	113.70
1	L5	4549	G	C3'-C2'-C1'	-8.63	92.87	101.50
48	SA	197	VAL	CA-C-N	8.54	133.66	120.68

There are no chirality outliers.

There are no planarity outliers.

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	72884	0	36802	685	0
2	L7	2558	0	1296	26	0
3	L8	3210	0	1630	38	0
4	LA	1898	0	1993	19	0
5	LB	3202	0	3347	53	0
6	LC	2857	0	3030	23	0
7	LD	2389	0	2420	32	0
8	LE	1743	0	1880	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	LF	1771	0	1886	23	0
10	LG	1848	0	1981	22	0
11	LH	1519	0	1603	18	0
12	LI	1631	0	1682	17	0
13	LJ	1340	0	1377	24	0
14	LL	1667	0	1771	18	0
15	LM	1125	0	1202	22	0
16	LN	1701	0	1749	18	0
17	LO	1640	0	1792	20	0
18	LP	1251	0	1282	11	0
19	LQ	1515	0	1639	16	0
20	LR	1457	0	1601	15	0
21	LS	1451	0	1488	15	0
22	LT	1307	0	1380	17	0
23	LU	817	0	839	12	0
24	LV	973	0	1034	13	0
25	LW	519	0	533	4	0
26	LX	967	0	1040	10	0
27	LY	1102	0	1189	9	0
28	LZ	1107	0	1182	21	0
29	La	1164	0	1213	5	0
30	Lb	807	0	875	6	0
31	Lc	732	0	769	13	0
32	Ld	896	0	941	13	0
33	Le	1053	0	1147	11	0
34	Lf	876	0	912	12	0
35	Lg	873	0	961	11	0
36	Lh	1015	0	1156	21	0
37	Li	832	0	917	12	0
38	Lj	705	0	737	15	0
39	Lk	568	0	635	9	0
40	Ll	438	0	474	3	0
41	Lm	419	0	452	6	0
42	Ln	239	0	289	1	0
43	Lo	842	0	916	9	0
44	Lp	708	0	756	6	0
45	Lr	994	0	1057	10	0
46	S2	34749	0	17548	611	0
47	S6	1604	0	816	20	0
47	S7	1604	0	816	35	0
48	SA	1636	0	1641	35	0
49	SB	1729	0	1803	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	SC	1665	0	1753	32	0
51	SD	1626	0	1714	38	0
52	SE	2050	0	2156	66	0
53	SF	1416	0	1458	39	0
54	SG	1645	0	1780	57	0
55	SH	1449	0	1539	35	0
56	SI	1499	0	1561	44	0
57	SJ	1162	0	1252	33	0
58	SK	760	0	783	22	0
59	SL	1110	0	1165	19	0
60	SN	1208	0	1294	18	0
61	SO	1002	0	1023	17	0
62	SP	981	0	1026	24	0
63	SQ	1109	0	1174	39	0
64	SR	1064	0	1118	20	0
65	SS	1157	0	1213	21	0
66	ST	1090	0	1116	29	0
67	SU	753	0	815	30	0
68	SV	619	0	620	12	0
69	SW	1034	0	1080	19	0
70	SX	1080	0	1147	26	0
71	SY	891	0	948	38	0
72	SZ	574	0	627	24	0
73	Sa	792	0	845	13	0
74	Sb	644	0	664	17	0
75	Sc	416	0	445	18	0
76	Sd	455	0	449	15	0
77	Se	384	0	422	13	0
78	Sg	2148	0	2108	71	0
79	Sx	214	0	108	3	0
80	Z	39	0	13	1	0
81	L5	93	0	0	0	0
81	L7	1	0	0	0	0
81	LN	1	0	0	0	0
81	LP	1	0	0	0	0
81	Le	1	0	0	0	0
82	Lj	1	0	0	0	0
82	Lm	1	0	0	0	0
82	Lp	1	0	0	0	0
All	All	204068	0	150895	2646	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 8.

The worst 5 of 2646 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)
1:L5:1910:G:C3'	1:L5:1911:G:H5'	1.61	1.28
1:L5:1910:G:H3'	1:L5:1911:G:C5'	1.64	1.26
1:L5:1910:G:N3	1:L5:1911:G:H5''	1.76	1.00
49:SB:189:ILE:HG23	49:SB:190:PRO:HD3	1.56	0.87
12:LI:80:CYS:SG	12:LI:144:ASN:ND2	2.47	0.87

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	LA	246/257 (96%)	230 (94%)	16 (6%)	0	100	100
5	LB	395/403 (98%)	367 (93%)	28 (7%)	0	100	100
6	LC	355/419 (85%)	331 (93%)	24 (7%)	0	100	100
7	LD	291/297 (98%)	269 (92%)	21 (7%)	1 (0%)	36	65
8	LE	210/296 (71%)	196 (93%)	14 (7%)	0	100	100
9	LF	212/270 (78%)	201 (95%)	11 (5%)	0	100	100
10	LG	225/266 (85%)	215 (96%)	10 (4%)	0	100	100
11	LH	188/192 (98%)	178 (95%)	7 (4%)	3 (2%)	7	32
12	LI	197/214 (92%)	187 (95%)	10 (5%)	0	100	100
13	LJ	165/178 (93%)	159 (96%)	6 (4%)	0	100	100
14	LL	204/211 (97%)	195 (96%)	9 (4%)	0	100	100
15	LM	134/217 (62%)	126 (94%)	8 (6%)	0	100	100
16	LN	201/204 (98%)	193 (96%)	8 (4%)	0	100	100
17	LO	199/203 (98%)	191 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	LP	152/184 (83%)	150 (99%)	2 (1%)	0	100	100
19	LQ	185/188 (98%)	181 (98%)	4 (2%)	0	100	100
20	LR	172/196 (88%)	169 (98%)	3 (2%)	0	100	100
21	LS	173/176 (98%)	162 (94%)	10 (6%)	1 (1%)	21	51
22	LT	158/160 (99%)	155 (98%)	3 (2%)	0	100	100
23	LU	98/128 (77%)	89 (91%)	9 (9%)	0	100	100
24	LV	128/140 (91%)	125 (98%)	3 (2%)	0	100	100
25	LW	60/157 (38%)	60 (100%)	0	0	100	100
26	LX	116/156 (74%)	112 (97%)	4 (3%)	0	100	100
27	LY	130/145 (90%)	129 (99%)	1 (1%)	0	100	100
28	LZ	133/136 (98%)	127 (96%)	6 (4%)	0	100	100
29	La	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
30	Lb	95/160 (59%)	93 (98%)	2 (2%)	0	100	100
31	Lc	92/115 (80%)	91 (99%)	0	1 (1%)	11	40
32	Ld	106/125 (85%)	104 (98%)	2 (2%)	0	100	100
33	Le	126/135 (93%)	117 (93%)	9 (7%)	0	100	100
34	Lf	107/110 (97%)	106 (99%)	1 (1%)	0	100	100
35	Lg	108/117 (92%)	105 (97%)	3 (3%)	0	100	100
36	Lh	120/123 (98%)	119 (99%)	1 (1%)	0	100	100
37	Li	100/105 (95%)	92 (92%)	8 (8%)	0	100	100
38	Lj	84/97 (87%)	81 (96%)	3 (4%)	0	100	100
39	Lk	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
40	Ll	48/51 (94%)	48 (100%)	0	0	100	100
41	Lm	49/128 (38%)	49 (100%)	0	0	100	100
42	Ln	23/25 (92%)	23 (100%)	0	0	100	100
43	Lo	101/106 (95%)	95 (94%)	5 (5%)	1 (1%)	12	41
44	Lp	89/92 (97%)	86 (97%)	3 (3%)	0	100	100
45	Lr	122/137 (89%)	117 (96%)	5 (4%)	0	100	100
48	SA	205/295 (70%)	189 (92%)	16 (8%)	0	100	100
49	SB	211/264 (80%)	202 (96%)	9 (4%)	0	100	100
50	SC	213/293 (73%)	206 (97%)	6 (3%)	1 (0%)	24	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	SD	207/243 (85%)	192 (93%)	10 (5%)	5 (2%)	4	24
52	SE	256/263 (97%)	240 (94%)	15 (6%)	1 (0%)	30	59
53	SF	175/204 (86%)	165 (94%)	10 (6%)	0	100	100
54	SG	200/249 (80%)	185 (92%)	14 (7%)	1 (0%)	24	55
55	SH	176/194 (91%)	160 (91%)	16 (9%)	0	100	100
56	SI	179/208 (86%)	168 (94%)	11 (6%)	0	100	100
57	SJ	130/194 (67%)	119 (92%)	11 (8%)	0	100	100
58	SK	86/165 (52%)	75 (87%)	11 (13%)	0	100	100
59	SL	131/158 (83%)	127 (97%)	4 (3%)	0	100	100
60	SN	148/151 (98%)	145 (98%)	3 (2%)	0	100	100
61	SO	132/151 (87%)	121 (92%)	11 (8%)	0	100	100
62	SP	116/145 (80%)	112 (97%)	4 (3%)	0	100	100
63	SQ	137/146 (94%)	123 (90%)	14 (10%)	0	100	100
64	SR	129/135 (96%)	116 (90%)	11 (8%)	2 (2%)	7	32
65	SS	138/152 (91%)	131 (95%)	7 (5%)	0	100	100
66	ST	138/145 (95%)	134 (97%)	4 (3%)	0	100	100
67	SU	93/119 (78%)	90 (97%)	3 (3%)	0	100	100
68	SV	79/83 (95%)	74 (94%)	5 (6%)	0	100	100
69	SW	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
70	SX	137/143 (96%)	126 (92%)	10 (7%)	1 (1%)	18	49
71	SY	108/133 (81%)	99 (92%)	8 (7%)	1 (1%)	14	43
72	SZ	70/125 (56%)	62 (89%)	8 (11%)	0	100	100
73	Sa	97/115 (84%)	89 (92%)	8 (8%)	0	100	100
74	Sb	80/84 (95%)	74 (92%)	5 (6%)	1 (1%)	9	35
75	Sc	52/69 (75%)	43 (83%)	9 (17%)	0	100	100
76	Sd	52/56 (93%)	52 (100%)	0	0	100	100
77	Se	44/133 (33%)	38 (86%)	6 (14%)	0	100	100
78	Sg	270/317 (85%)	233 (86%)	37 (14%)	0	100	100
All	All	10625/12499 (85%)	10037 (94%)	568 (5%)	20 (0%)	44	71

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
31	Lc	99	PRO
70	SX	61	GLN
21	LS	165	PRO
50	SC	172	ASN
64	SR	67	ARG

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%)	190 (100%)	0	100	100
5	LB	344/348 (99%)	344 (100%)	0	100	100
6	LC	301/348 (86%)	300 (100%)	1 (0%)	86	85
7	LD	246/249 (99%)	246 (100%)	0	100	100
8	LE	194/256 (76%)	193 (100%)	1 (0%)	81	82
9	LF	185/234 (79%)	185 (100%)	0	100	100
10	LG	197/223 (88%)	197 (100%)	0	100	100
11	LH	169/171 (99%)	169 (100%)	0	100	100
12	LI	170/180 (94%)	169 (99%)	1 (1%)	78	81
13	LJ	141/149 (95%)	140 (99%)	1 (1%)	76	79
14	LL	173/178 (97%)	171 (99%)	2 (1%)	63	74
15	LM	116/157 (74%)	116 (100%)	0	100	100
16	LN	171/172 (99%)	171 (100%)	0	100	100
17	LO	172/173 (99%)	171 (99%)	1 (1%)	78	81
18	LP	135/163 (83%)	135 (100%)	0	100	100
19	LQ	164/165 (99%)	164 (100%)	0	100	100
20	LR	154/175 (88%)	154 (100%)	0	100	100
21	LS	155/156 (99%)	154 (99%)	1 (1%)	78	81
22	LT	140/140 (100%)	140 (100%)	0	100	100
23	LU	90/114 (79%)	90 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	LV	100/107 (94%)	100 (100%)	0	100	100
25	LW	54/126 (43%)	54 (100%)	0	100	100
26	LX	106/133 (80%)	104 (98%)	2 (2%)	50	68
27	LY	123/135 (91%)	123 (100%)	0	100	100
28	LZ	117/118 (99%)	116 (99%)	1 (1%)	70	77
29	La	120/121 (99%)	120 (100%)	0	100	100
30	Lb	83/124 (67%)	83 (100%)	0	100	100
31	Lc	79/97 (81%)	79 (100%)	0	100	100
32	Ld	99/110 (90%)	99 (100%)	0	100	100
33	Le	114/121 (94%)	114 (100%)	0	100	100
34	Lf	88/89 (99%)	88 (100%)	0	100	100
35	Lg	94/100 (94%)	94 (100%)	0	100	100
36	Lh	109/110 (99%)	108 (99%)	1 (1%)	70	77
37	Li	86/89 (97%)	85 (99%)	1 (1%)	63	74
38	Lj	73/80 (91%)	73 (100%)	0	100	100
39	Lk	64/65 (98%)	64 (100%)	0	100	100
40	Ll	46/47 (98%)	46 (100%)	0	100	100
41	Lm	47/116 (40%)	47 (100%)	0	100	100
42	Ln	24/24 (100%)	23 (96%)	1 (4%)	26	55
43	Lo	91/94 (97%)	91 (100%)	0	100	100
44	Lp	74/75 (99%)	74 (100%)	0	100	100
45	Lr	108/121 (89%)	108 (100%)	0	100	100
48	SA	173/242 (72%)	173 (100%)	0	100	100
49	SB	194/229 (85%)	194 (100%)	0	100	100
50	SC	181/224 (81%)	177 (98%)	4 (2%)	45	65
51	SD	173/202 (86%)	162 (94%)	11 (6%)	16	44
52	SE	221/225 (98%)	221 (100%)	0	100	100
53	SF	152/170 (89%)	151 (99%)	1 (1%)	76	79
54	SG	178/218 (82%)	172 (97%)	6 (3%)	32	59
55	SH	161/174 (92%)	159 (99%)	2 (1%)	63	74
56	SI	159/180 (88%)	159 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	SJ	126/168 (75%)	126 (100%)	0	100	100
58	SK	81/136 (60%)	75 (93%)	6 (7%)	13	39
59	SL	123/142 (87%)	123 (100%)	0	100	100
60	SN	130/131 (99%)	128 (98%)	2 (2%)	57	71
61	SO	104/119 (87%)	103 (99%)	1 (1%)	68	75
62	SP	107/130 (82%)	105 (98%)	2 (2%)	50	68
63	SQ	115/121 (95%)	113 (98%)	2 (2%)	53	70
64	SR	119/121 (98%)	118 (99%)	1 (1%)	73	78
65	SS	122/132 (92%)	121 (99%)	1 (1%)	73	78
66	ST	110/115 (96%)	109 (99%)	1 (1%)	70	77
67	SU	88/107 (82%)	88 (100%)	0	100	100
68	SV	65/67 (97%)	65 (100%)	0	100	100
69	SW	112/113 (99%)	111 (99%)	1 (1%)	70	77
70	SX	111/115 (96%)	111 (100%)	0	100	100
71	SY	93/115 (81%)	91 (98%)	2 (2%)	45	65
72	SZ	64/103 (62%)	63 (98%)	1 (2%)	55	71
73	Sa	86/98 (88%)	86 (100%)	0	100	100
74	Sb	74/76 (97%)	71 (96%)	3 (4%)	27	55
75	Sc	48/62 (77%)	46 (96%)	2 (4%)	26	55
76	Sd	48/49 (98%)	48 (100%)	0	100	100
77	Se	39/106 (37%)	39 (100%)	0	100	100
78	Sg	237/275 (86%)	235 (99%)	2 (1%)	73	78
All	All	9300/10617 (88%)	9235 (99%)	65 (1%)	73	79

5 of 65 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
72	SZ	98	LYS
74	Sb	40	CYS
51	SD	204	LEU
51	SD	202	LYS
74	Sb	83	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 83 such sidechains are listed below:

Mol	Chain	Res	Type
51	SD	159	HIS
63	SQ	86	GLN
52	SE	209	HIS
55	SH	97	GLN
66	ST	42	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3378/4731 (71%)	710 (21%)	34 (1%)
2	L7	119/120 (99%)	16 (13%)	3 (2%)
3	L8	149/158 (94%)	27 (18%)	1 (0%)
46	S2	1619/1870 (86%)	472 (29%)	25 (1%)
47	S6	74/75 (98%)	22 (29%)	2 (2%)
47	S7	74/75 (98%)	40 (54%)	2 (2%)
79	Sx	9/10 (90%)	1 (11%)	0
All	All	5422/7039 (77%)	1288 (23%)	67 (1%)

5 of 1288 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	2	G
1	L5	3	C
1	L5	13	U
1	L5	21	G
1	L5	39	A

5 of 67 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
46	S2	1343	U
46	S2	1416	C
47	S7	29	G
1	L5	3715	C
1	L5	3417	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 100 ligands modelled in this entry, 100 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](#)

There are no chain breaks in this entry.

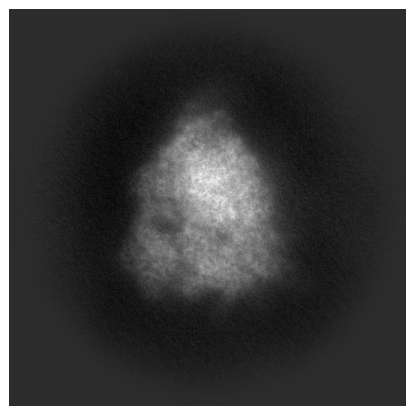
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62287. These allow visual inspection of the internal detail of the map and identification of artifacts.

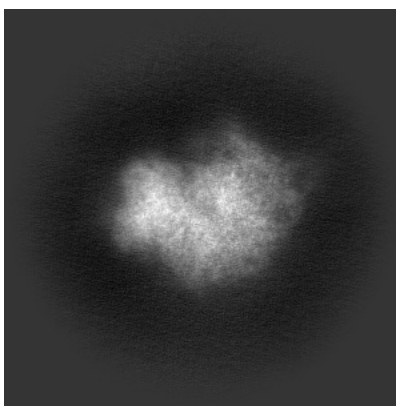
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

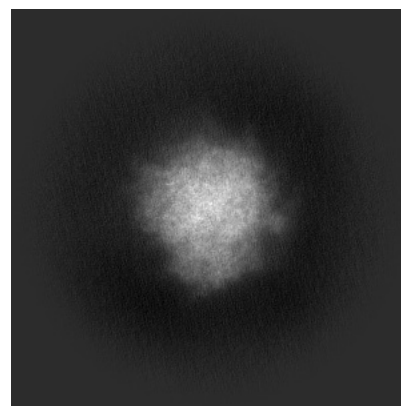
6.1.1 Primary map



X

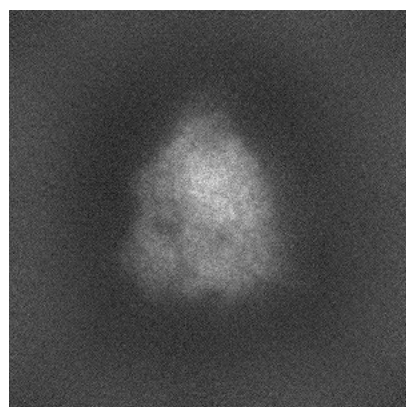


Y

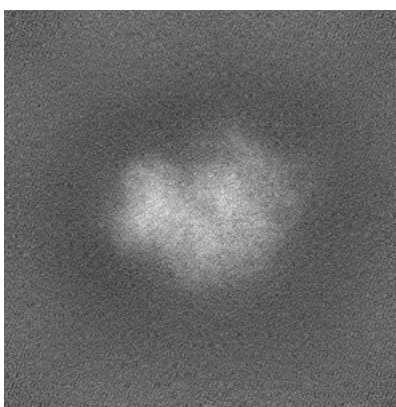


Z

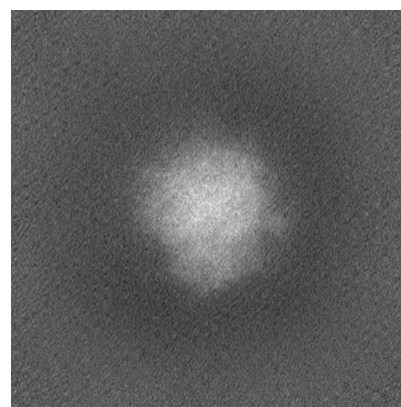
6.1.2 Raw map



X



Y

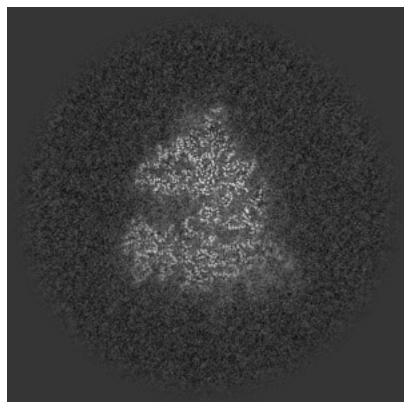


Z

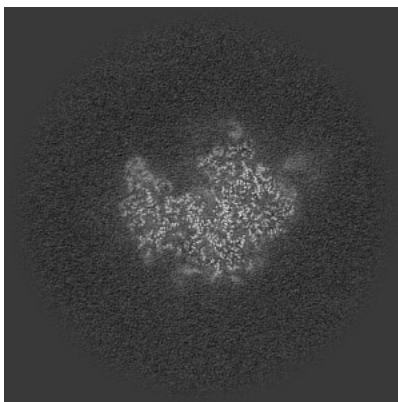
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

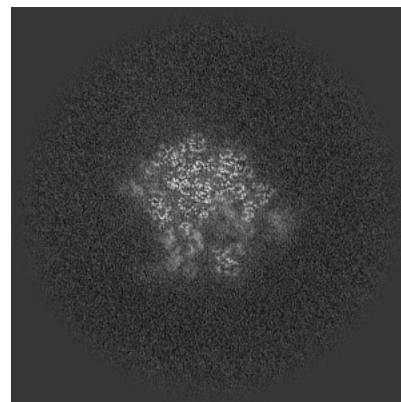
6.2.1 Primary map



X Index: 280

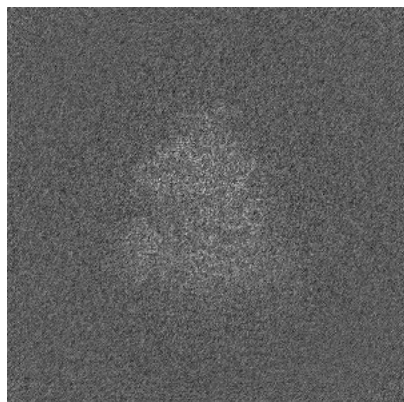


Y Index: 280

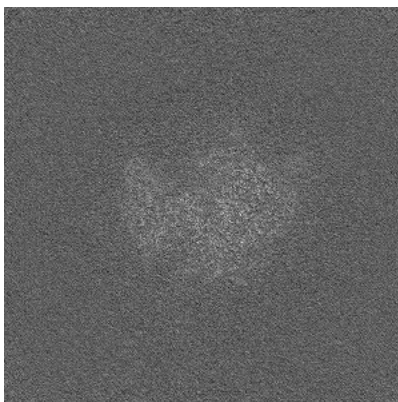


Z Index: 280

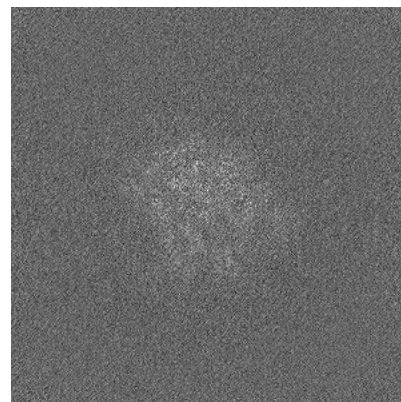
6.2.2 Raw map



X Index: 280



Y Index: 280

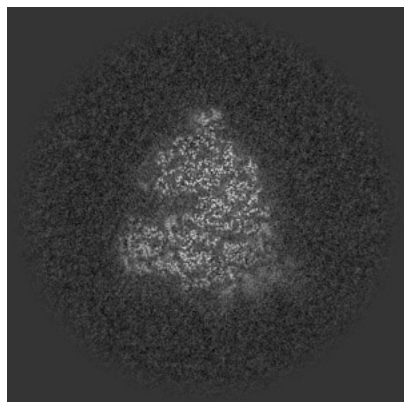


Z Index: 280

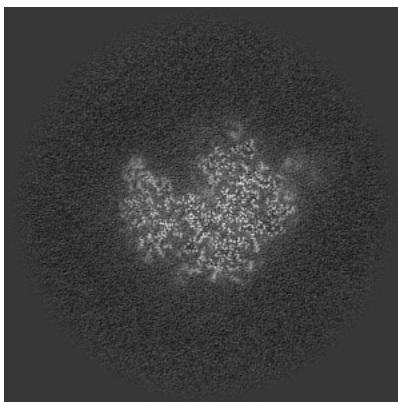
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

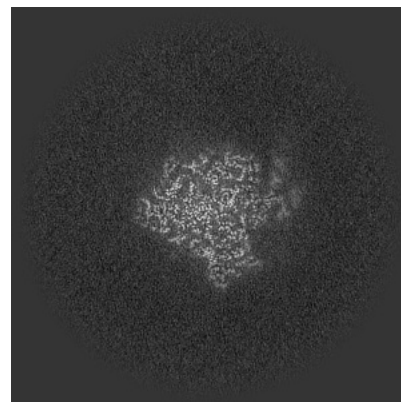
6.3.1 Primary map



X Index: 272

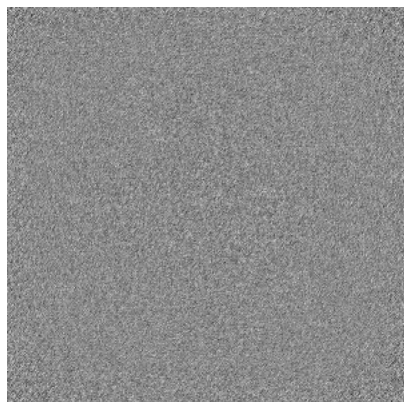


Y Index: 278

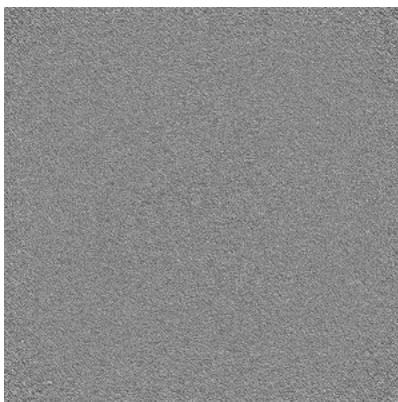


Z Index: 317

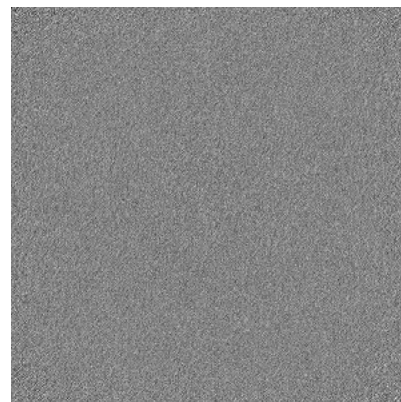
6.3.2 Raw map



X Index: 0



Y Index: 0

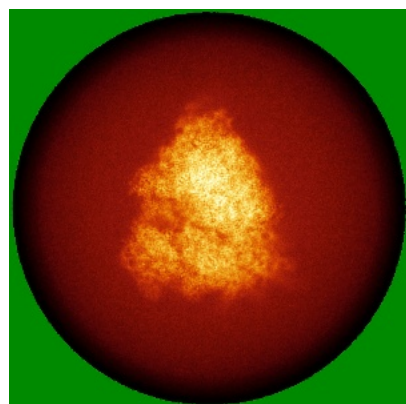


Z Index: 0

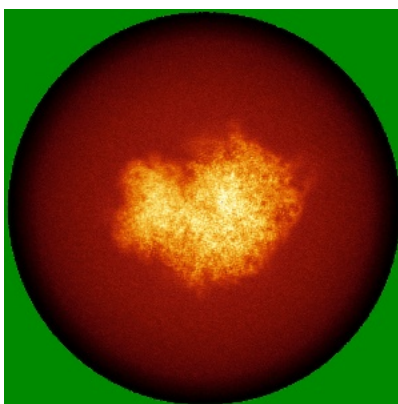
The images above show the largest variance slices of the map in three orthogonal directions.

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

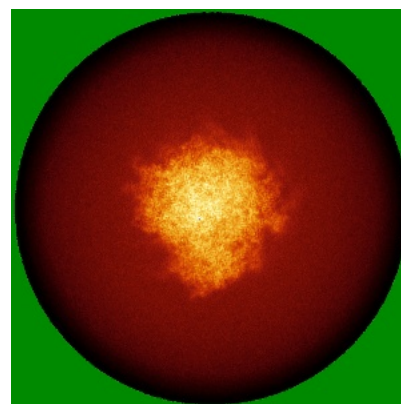
6.4.1 Primary map



X

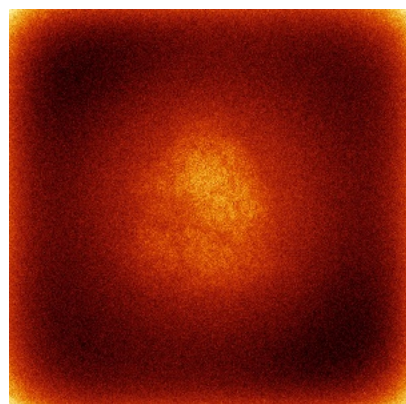


Y

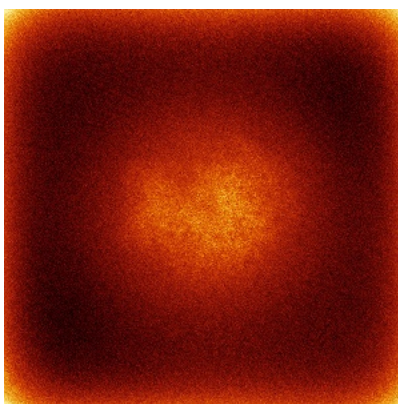


Z

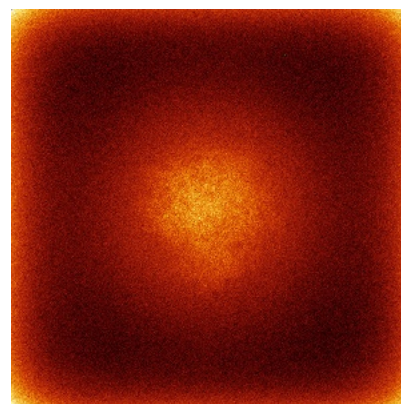
6.4.2 Raw map



X



Y

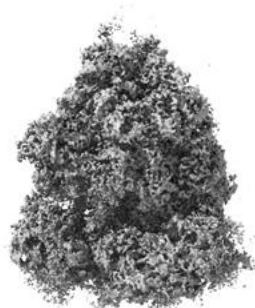


Z

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



X



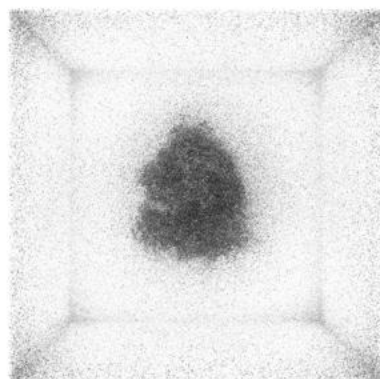
Y



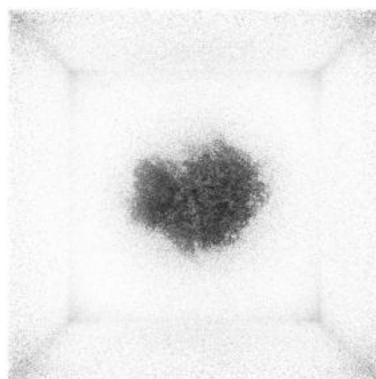
Z

The images above show the 3D surface view of the map at the recommended contour level 0.38. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

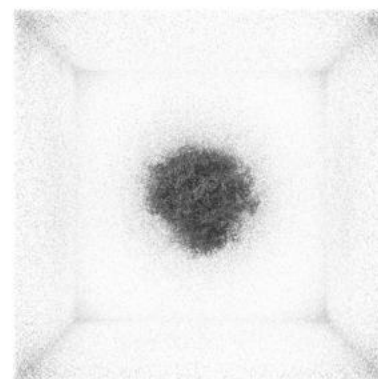
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

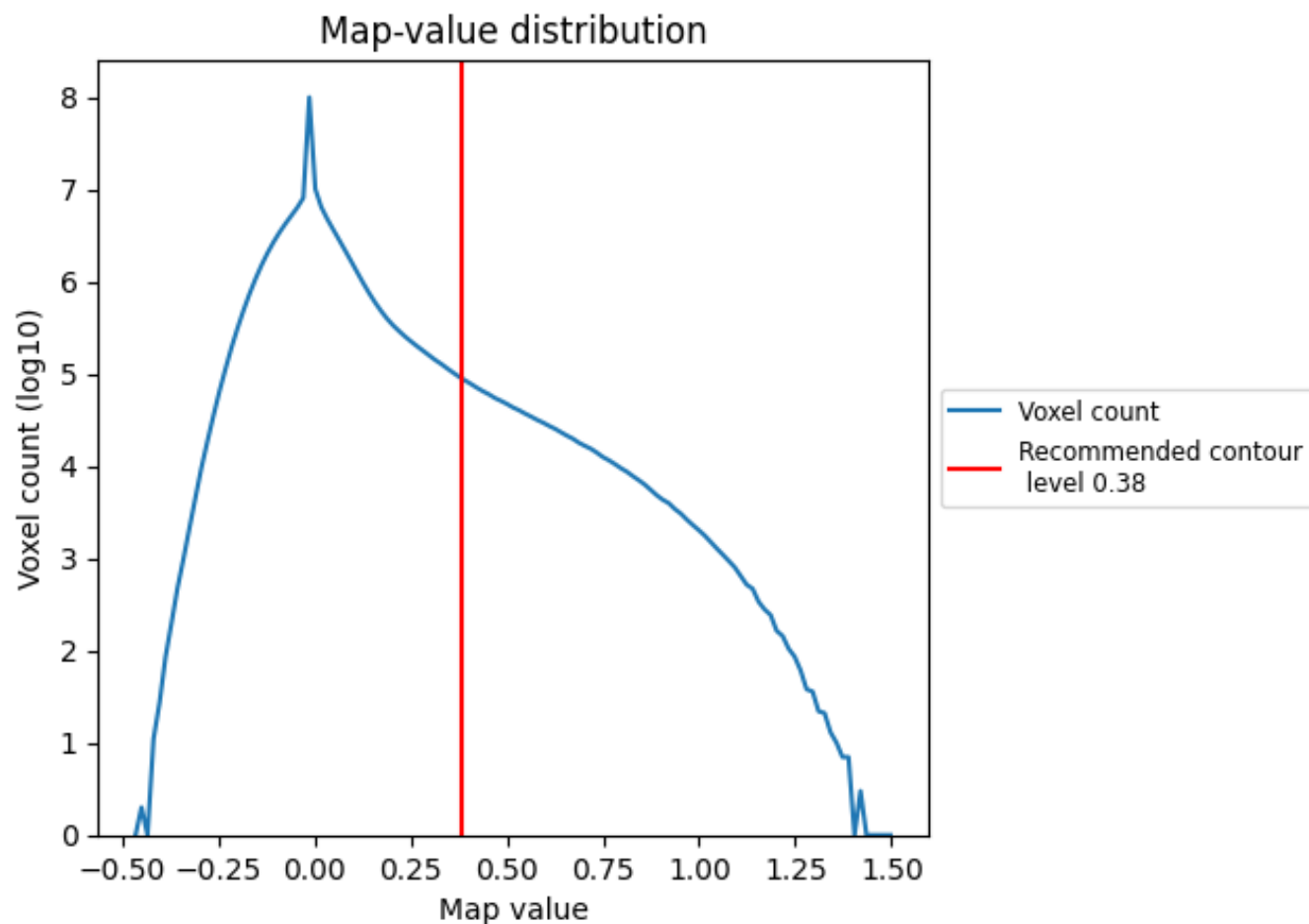
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

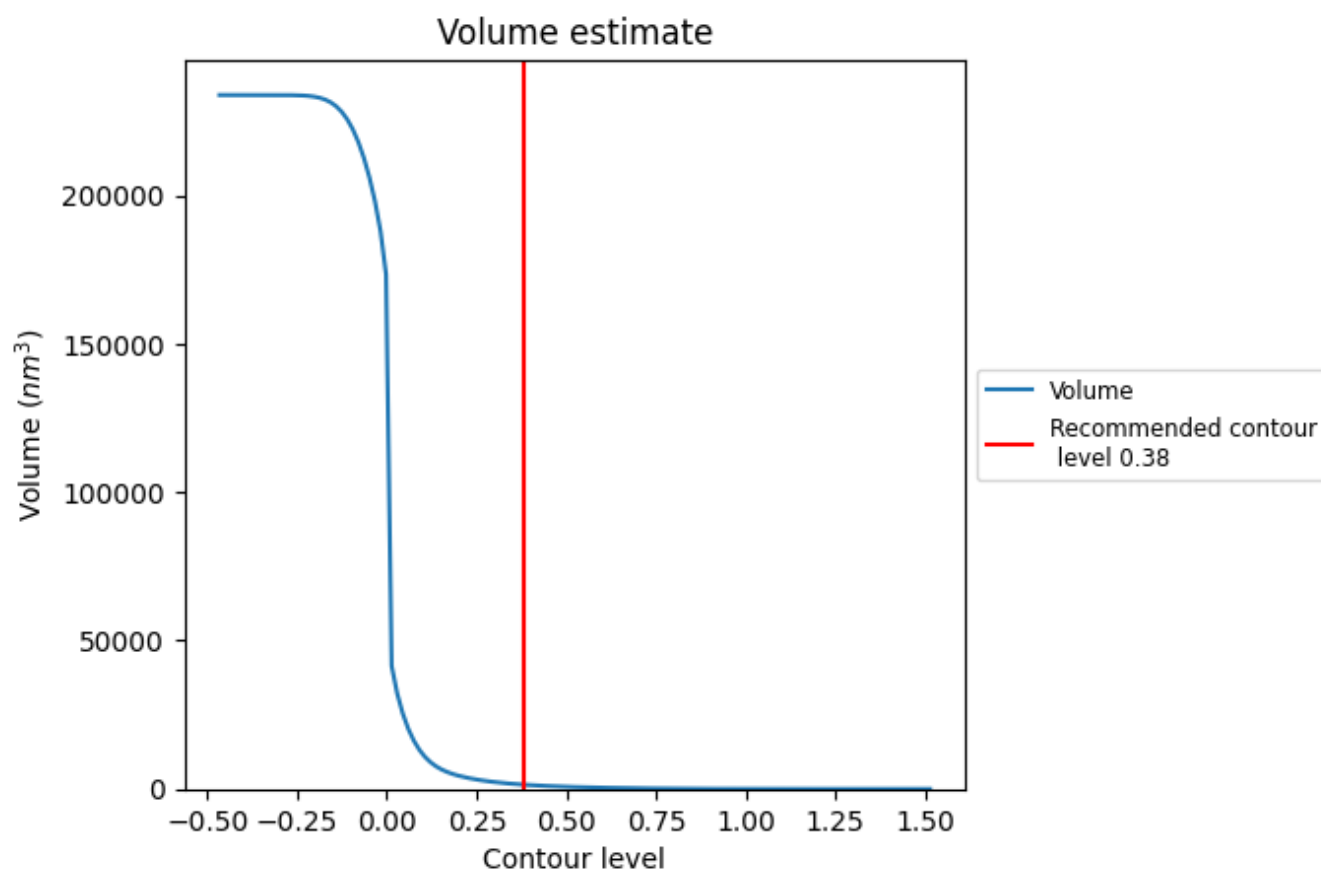
This section contains the results of statistical analysis of the map.

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.

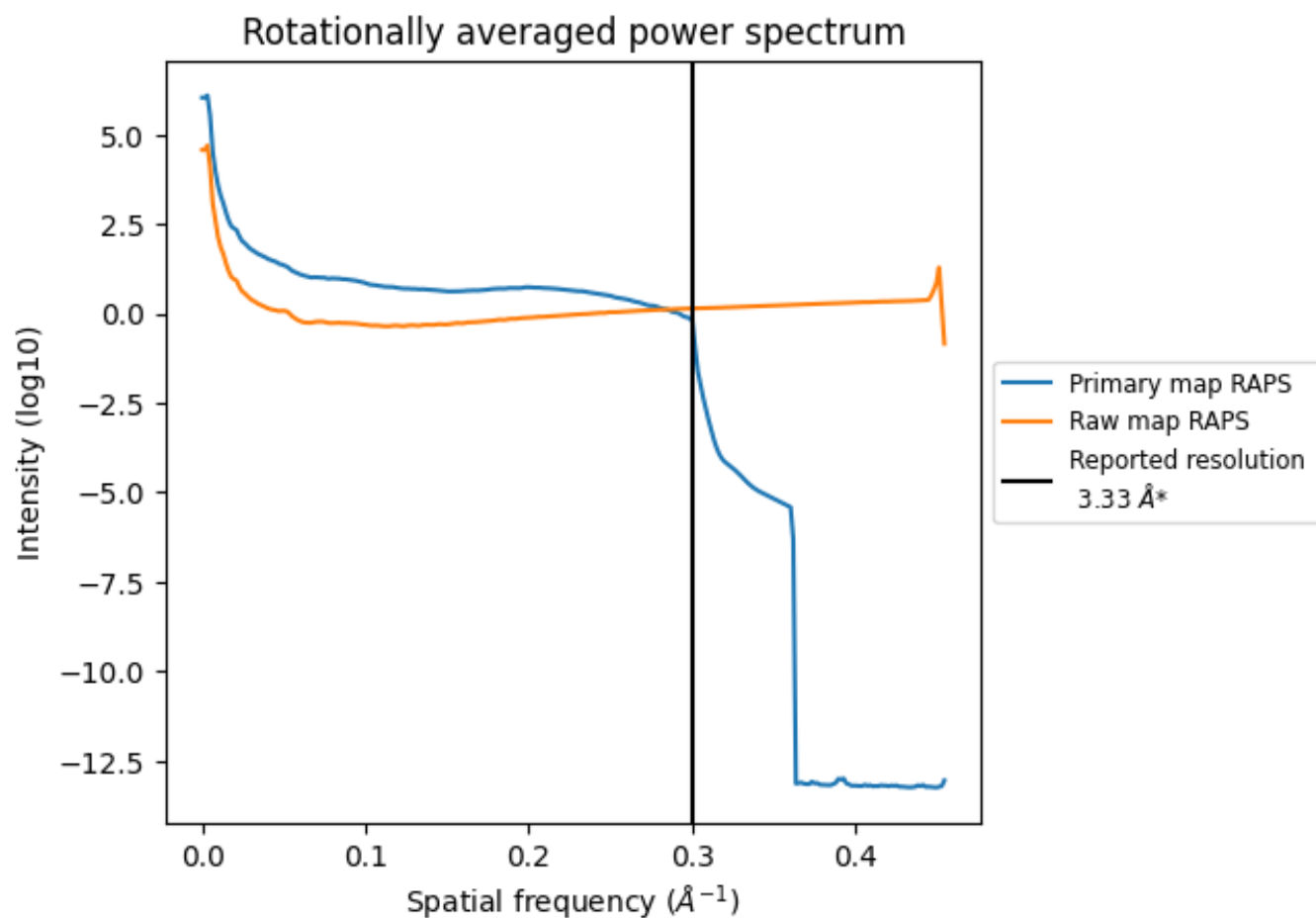
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1455 nm³; this corresponds to an approximate mass of 1314 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 ⓘ

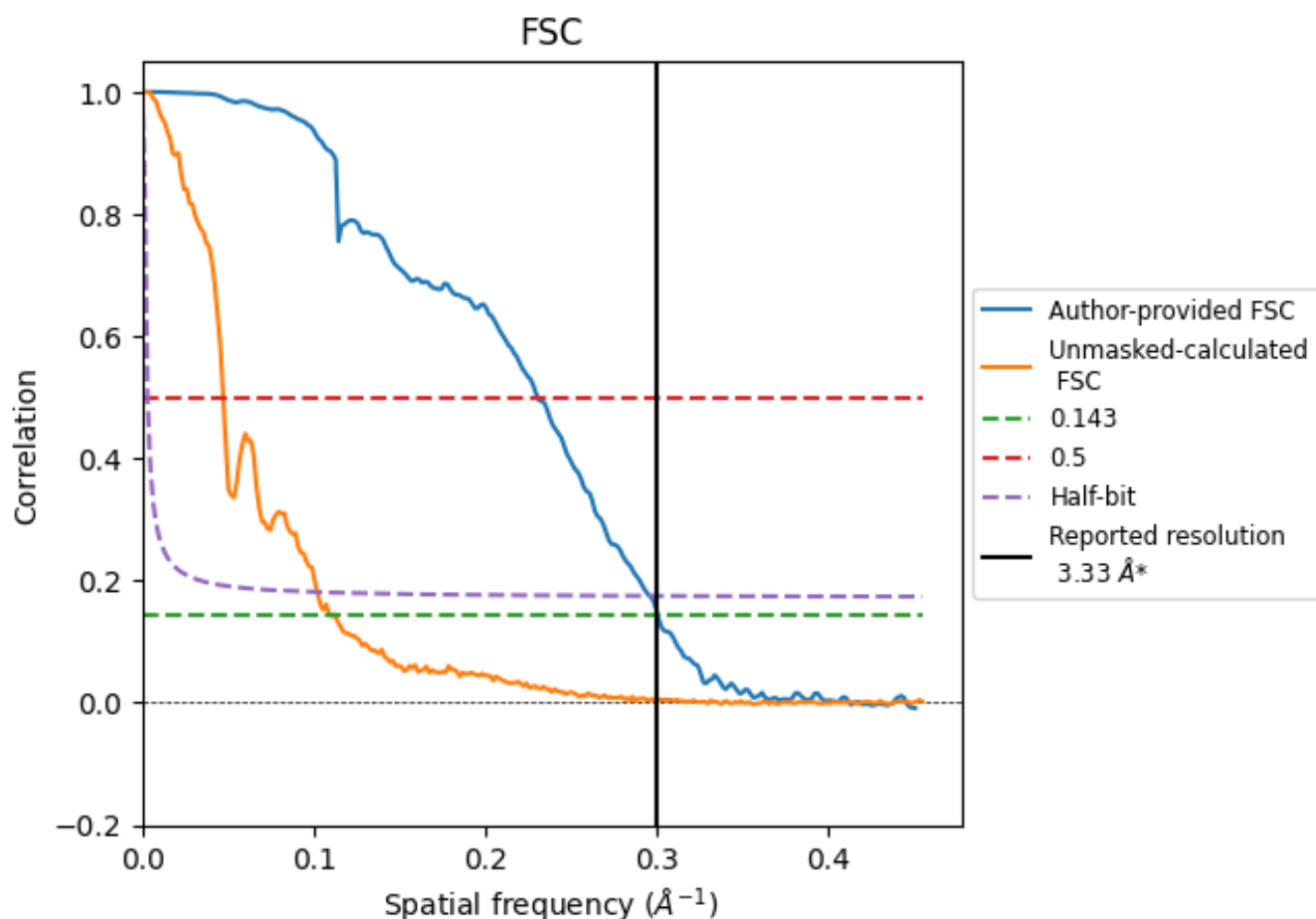


*Reported resolution corresponds to spatial frequency of 0.300 \AA^{-1}

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.300 \AA^{-1}

8.2 Resolution estimates [i](#)

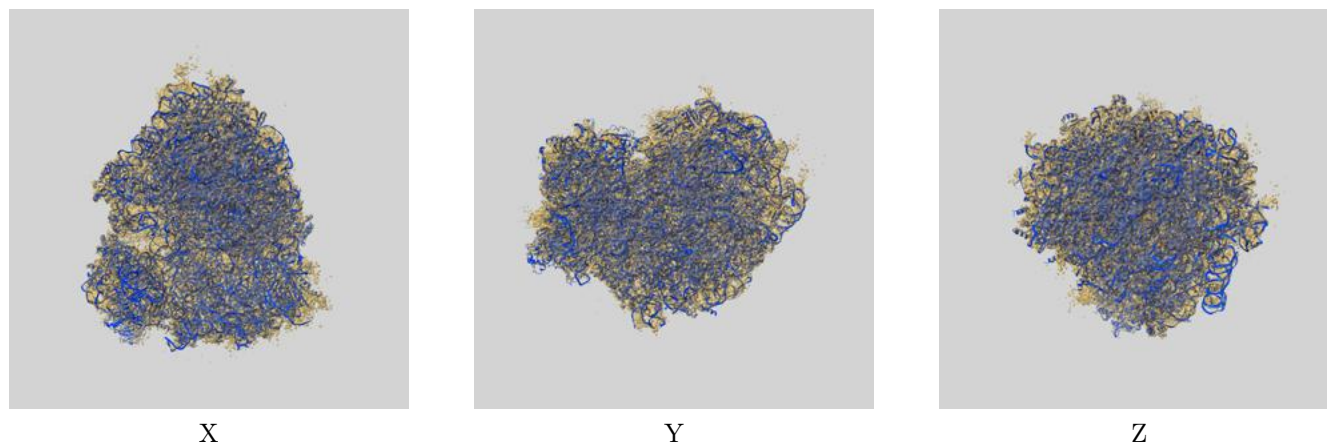
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.33	-	-
Author-provided FSC curve	3.33	4.34	3.38
Unmasked-calculated*	9.10	21.19	9.79

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 9.10 differs from the reported value 3.33 by more than 10 %

9 Map-model fit [i](#)

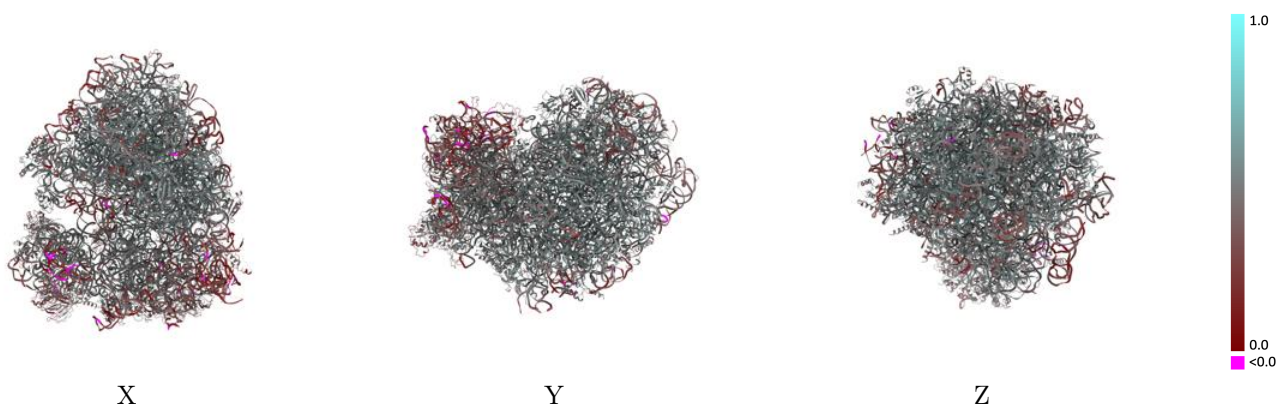
This section contains information regarding the fit between EMDB map EMD-62287 and PDB model 9KDV. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

9.1 Map-model overlay [i](#)



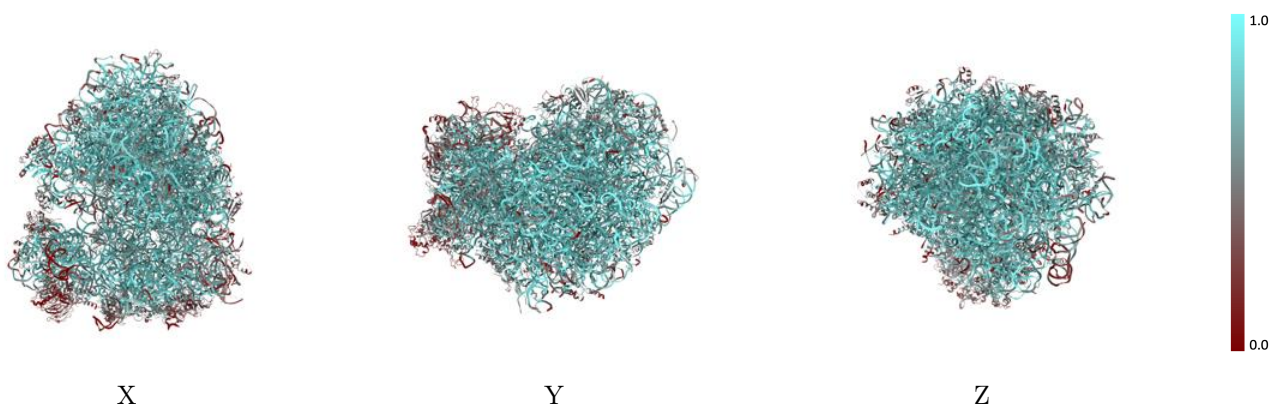
The images above show the 3D surface view of the map at the recommended contour level 0.38 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



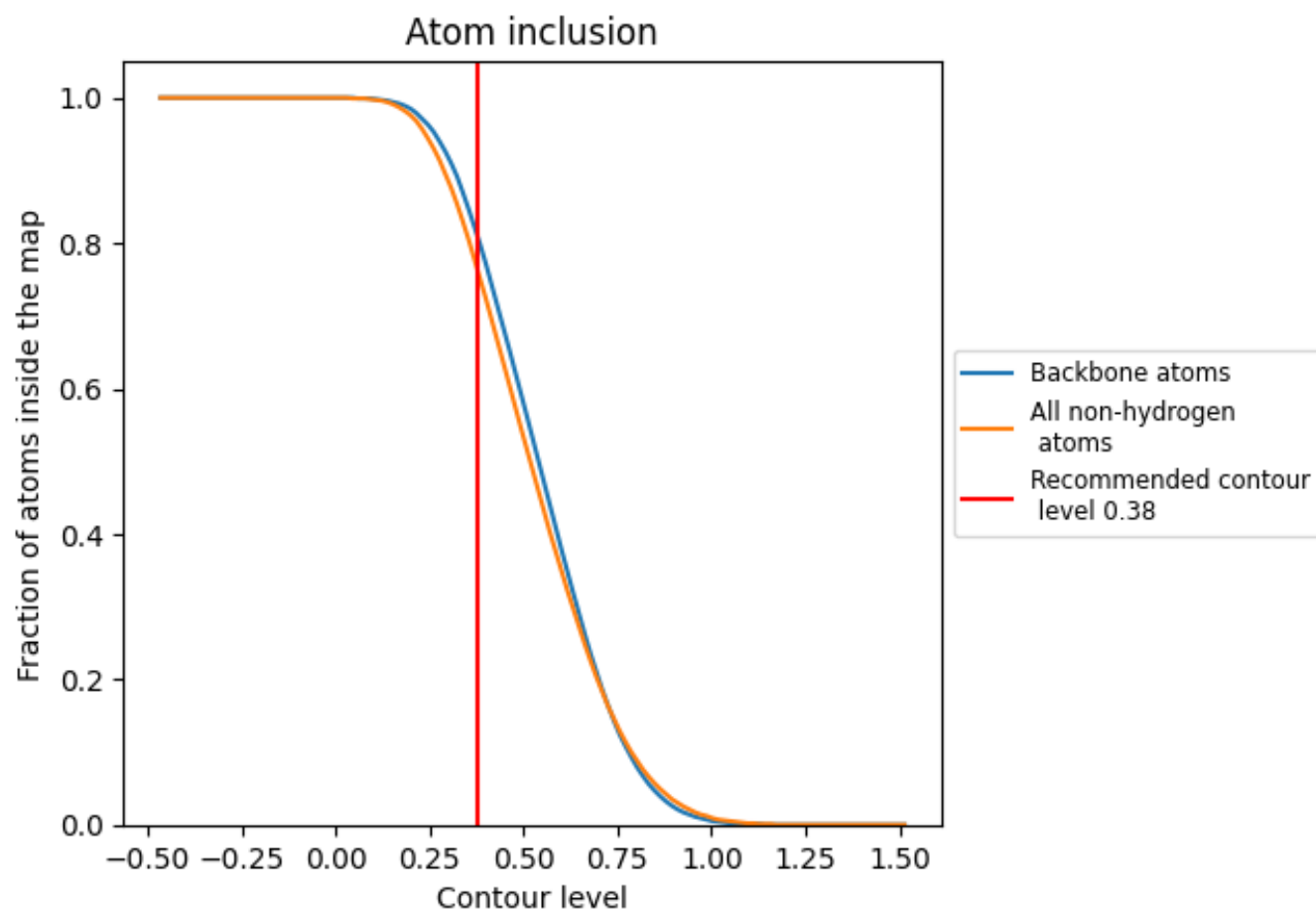
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.38).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 76% 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 (0.38) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7590	 0.4580
L5	 0.8780	 0.4720
L7	 0.9200	 0.4970
L8	 0.9040	 0.4820
LA	 0.8490	 0.5370
LB	 0.7010	 0.5050
LC	 0.8040	 0.5240
LD	 0.5970	 0.4740
LE	 0.6360	 0.4770
LF	 0.8460	 0.5240
LG	 0.5780	 0.4800
LH	 0.5500	 0.4850
LI	 0.6020	 0.4680
LJ	 0.6030	 0.4740
LL	 0.6880	 0.4880
LM	 0.7090	 0.5060
LN	 0.8800	 0.5400
LO	 0.7520	 0.5180
LP	 0.7960	 0.5200
LQ	 0.8280	 0.5340
LR	 0.7390	 0.4920
LS	 0.7710	 0.5220
LT	 0.7550	 0.5010
LU	 0.4740	 0.4290
LV	 0.7780	 0.5260
LW	 0.7840	 0.5070
LX	 0.6840	 0.4980
LY	 0.7160	 0.5120
LZ	 0.6270	 0.4920
La	 0.8360	 0.5380
Lb	 0.7420	 0.4930
Lc	 0.6660	 0.4830
Ld	 0.6880	 0.4900
Le	 0.8380	 0.5300
Lf	 0.8410	 0.5260













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Chain	Atom inclusion	Q-score
Lg	 0.7550	 0.5050
Lh	 0.6900	 0.4910
Li	 0.6140	 0.4840
Lj	 0.9020	 0.5320
Lk	 0.4440	 0.4500
Ll	 0.8670	 0.5170
Lm	 0.7170	 0.4970
Ln	 0.8300	 0.5180
Lo	 0.7340	 0.5070
Lp	 0.8100	 0.5100
Lr	 0.7520	 0.5210
S2	 0.8040	 0.4070
S6	 0.7970	 0.3570
S7	 0.5660	 0.2480
SA	 0.5220	 0.4670
SB	 0.5310	 0.4640
SC	 0.6500	 0.4690
SD	 0.4620	 0.4030
SE	 0.4940	 0.3820
SF	 0.5420	 0.4400
SG	 0.3070	 0.3360
SH	 0.3330	 0.3900
SI	 0.5840	 0.4140
SJ	 0.5890	 0.4100
SK	 0.2780	 0.3630
SL	 0.6820	 0.4750
SN	 0.6300	 0.4810
SO	 0.6070	 0.4660
SP	 0.4950	 0.4480
SQ	 0.5430	 0.4350
SR	 0.3900	 0.4060
SS	 0.5390	 0.4460
ST	 0.5080	 0.4270
SU	 0.3800	 0.3840
SV	 0.5270	 0.4720
SW	 0.7110	 0.4960
SX	 0.6710	 0.4630
SY	 0.3020	 0.3230
SZ	 0.4050	 0.4260
Sa	 0.6870	 0.4830
Sb	 0.4510	 0.4370
Sc	 0.4180	 0.4230

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Chain	Atom inclusion	Q-score
Sd	 0.6410	 0.4160
Se	 0.4820	 0.3890
Sg	 0.2090	 0.3480
Sx	 0.8650	 0.4210
Z	 0.9490	 0.4250