



## wwPDB EM Validation Summary Report ⓘ

May 4, 2026 – 07:07 PM JST

PDB ID : 9KDT / pdb\_00009kdt  
EMDB ID : EMD-62285  
Title : Cryo-EM structure of 80S ribosome  
Authors : Lu, Y.; Wang, X.; Qin, Y.; Cao, Y.  
Deposited on : 2024-11-04  
Resolution : 2.63 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](mailto: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>.

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

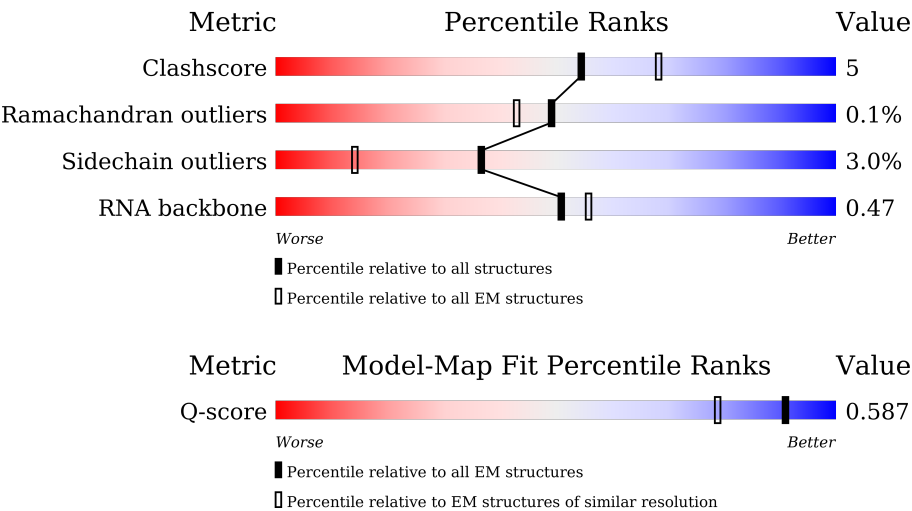
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : 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 2.63 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.



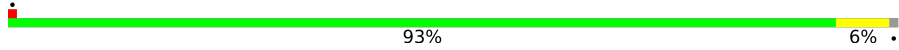

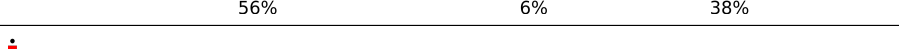
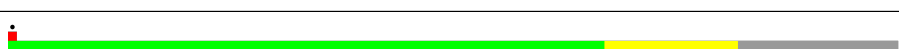



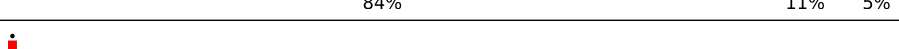



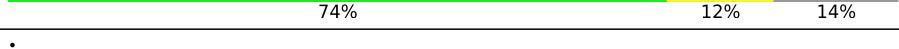

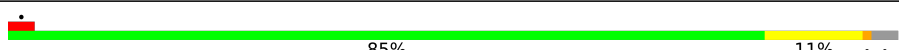


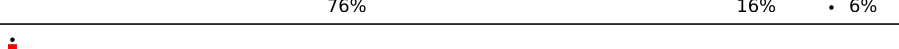







Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8888 ( 2.13 - 3.13 )

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  $\geq 3$ , 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	<div><div></div><div>49%18%5%28%</div></div>
2	L7	120	<div><div></div><div>82%14%</div></div>
3	L8	158	<div><div></div><div>63%28%</div></div>

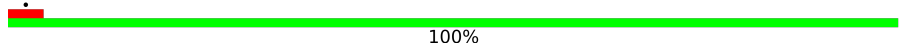
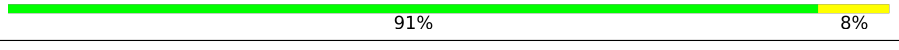
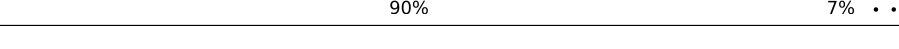
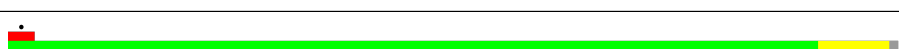

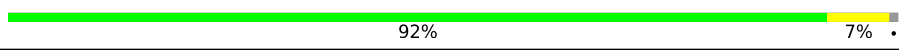

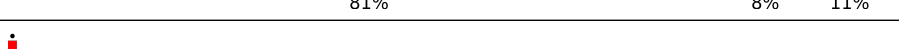



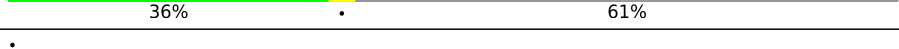

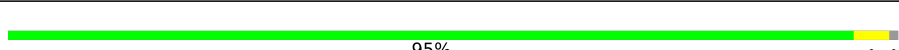


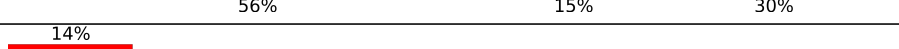







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Mol	Chain	Length	Quality of chain
4	La	148	
5	LA	257	
6	Lb	160	
7	LB	403	
8	Lc	115	
9	LC	419	
10	Ld	125	
11	LD	297	
12	Le	135	
13	LE	296	
14	Lf	110	
15	LF	270	
16	Lg	117	
17	LG	266	
18	Lh	123	
19	LH	190	
20	Li	105	
21	LI	214	
22	Lj	97	
23	LJ	178	
24	Lk	70	
25	Ll	51	
26	LL	211	
27	Lm	128	
28	LM	217	

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Mol	Chain	Length	Quality of chain
29	Ln	25	 100%
30	LN	204	 91% 8%
31	Lo	106	 90% 7% . .
32	LO	203	 89% 9% .
33	Lp	92	 91% 8% .
34	LP	184	 77% 6% . 16%
35	LQ	188	 92% 7% .
36	Lr	137	 82% 7% . 9%
37	LR	196	 81% 8% 11%
38	LS	176	 87% 13% .
39	LT	160	 87% 12% .
40	LU	128	 60% 17% . 22%
41	LV	140	 86% 7% 7%
42	LW	157	 36% . 61%
43	LX	156	 69% 6% . 24%
44	LY	145	 81% 10% 9%
45	LZ	136	 95% . .
46	S2	1870	 9% 44% 30% 12% . 13%
47	Sa	115	 75% 11% 14%
48	SA	295	 56% 15% 30%
49	Sb	84	 14% 82% 13% . .
50	SB	264	 72% 8% 19%
51	Sc	69	 6% 67% 12% 22%
52	SC	293	 64% 9% 27%
53	Sd	56	18% 68% 27% . .

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Mol	Chain	Length	Quality of chain
54	SD	243	
55	Se	133	
56	SE	263	
57	SF	204	
58	Sg	317	
59	SG	249	
60	SH	194	
61	SI	208	
62	SJ	194	
63	SK	165	
64	SL	158	
65	SN	151	
66	SO	151	
67	SP	145	
68	SQ	146	
69	SR	135	
70	SS	152	
71	ST	145	
72	SU	119	
73	SV	83	
74	SW	130	
75	Sx	10	
76	SX	143	
77	SY	133	
78	SZ	125	

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Mol	Chain	Length	Quality of chain
79	S6	75	<div><div><div></div><div></div><div></div></div><div>48%</div><div>43%</div><div>48%</div><div>9%</div></div>
79	S7	75	<div><div><div></div><div></div><div></div></div><div>40%</div><div>45%</div><div>15%</div></div>
80	Z	24	<div><div><div></div><div></div><div></div></div><div>79%</div><div>63%</div><div>38%</div></div>

## 2 Entry composition

There are 82 unique types of molecules in this entry. The entry contains 204155 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 uL15.

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

- Molecule 5 is a protein called Large ribosomal subunit protein uL2.

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

- Molecule 6 is a protein called Large ribosomal subunit protein eL29.

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

- Molecule 7 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 8 is a protein called Large ribosomal subunit protein eL30.

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

- Molecule 9 is a protein called Large ribosomal subunit protein uL4.

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

- Molecule 10 is a protein called Large ribosomal subunit protein eL31.

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

- Molecule 11 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 12 is a protein called Large ribosomal subunit protein eL32.

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

- Molecule 13 is a protein called Large ribosomal subunit protein eL6.

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

- Molecule 14 is a protein called Large ribosomal subunit protein eL33.



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

- Molecule 15 is a protein called Large ribosomal subunit protein uL30.

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

- Molecule 16 is a protein called Large ribosomal subunit protein eL34.

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

- Molecule 17 is a protein called Large ribosomal subunit protein eL8.

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

- Molecule 18 is a protein called Large ribosomal subunit protein uL29.

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

- Molecule 19 is a protein called Large ribosomal subunit protein uL6.

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

- Molecule 20 is a protein called Large ribosomal subunit protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 21 is a protein called Large ribosomal subunit protein uL16-like.

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

- Molecule 22 is a protein called Large ribosomal subunit protein eL37.

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

- Molecule 23 is a protein called Large ribosomal subunit protein uL5.

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

- Molecule 24 is a protein called Large ribosomal subunit protein eL38.

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

- Molecule 25 is a protein called Large ribosomal subunit protein eL39-like.

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

- Molecule 26 is a protein called Large ribosomal subunit protein eL13.

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

- Molecule 27 is a protein called Ubiquitin-ribosomal protein eL40 fusion protein.

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

- Molecule 28 is a protein called Large ribosomal subunit protein eL14.

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

- Molecule 29 is a protein called Small ribosomal subunit protein eS32.

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

- Molecule 30 is a protein called Large ribosomal subunit protein eL15.

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

- Molecule 31 is a protein called Large ribosomal subunit protein eL42.

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

- Molecule 32 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 33 is a protein called Large ribosomal subunit protein eL43.

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

- Molecule 34 is a protein called Large ribosomal subunit protein uL22.

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

- Molecule 35 is a protein called Large ribosomal subunit protein eL18.

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

- Molecule 36 is a protein called Large ribosomal subunit protein eL28.

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

- Molecule 37 is a protein called Large ribosomal subunit protein eL19.

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

- Molecule 38 is a protein called Large ribosomal subunit protein eL20.

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

- Molecule 39 is a protein called Large ribosomal subunit protein eL21.

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

- Molecule 40 is a protein called Large ribosomal subunit protein eL22.

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

- Molecule 41 is a protein called Large ribosomal subunit protein uL14.

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

- Molecule 42 is a protein called Large ribosomal subunit protein eL24.

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

- Molecule 43 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 44 is a protein called Large ribosomal subunit protein uL24.

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

- Molecule 45 is a protein called Large ribosomal subunit protein eL27.

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

- 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 protein called Small ribosomal subunit protein eS26.

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

- 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 eS27.

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

- Molecule 50 is a protein called Small ribosomal subunit protein eS1.

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

- Molecule 51 is a protein called Small ribosomal subunit protein eS28.

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

- Molecule 52 is a protein called Small ribosomal subunit protein uS5.

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

- Molecule 53 is a protein called Small ribosomal subunit protein uS14.

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

- Molecule 54 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 55 is a protein called Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein.

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

- Molecule 56 is a protein called Small ribosomal subunit protein eS4.

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

- Molecule 57 is a protein called Small ribosomal subunit protein uS7.

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

- Molecule 58 is a protein called Small ribosomal subunit protein RACK1.

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

- Molecule 59 is a protein called Small ribosomal subunit protein eS6.

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

- Molecule 60 is a protein called Small ribosomal subunit protein eS7.

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

- Molecule 61 is a protein called Small ribosomal subunit protein eS8.

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

- Molecule 62 is a protein called Small ribosomal subunit protein uS4.

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

- Molecule 63 is a protein called Small ribosomal subunit protein eS10.

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

- Molecule 64 is a protein called Small ribosomal subunit protein uS17.

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

- Molecule 65 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 66 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 67 is a protein called Small ribosomal subunit protein uS19.

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

- Molecule 68 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 69 is a protein called Small ribosomal subunit protein eS17.

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

- Molecule 70 is a protein called Small ribosomal subunit protein uS13.



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

- Molecule 71 is a protein called Small ribosomal subunit protein eS19.

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

- Molecule 72 is a protein called Small ribosomal subunit protein uS10.

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

- Molecule 73 is a protein called Small ribosomal subunit protein eS21.

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

- Molecule 74 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 75 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
75	Sx	10	Total	C	N	O	P	0	0
			214	96	39	69	10		

- Molecule 76 is a protein called Small ribosomal subunit protein uS12.

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

- Molecule 77 is a protein called Small ribosomal subunit protein eS24.

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

- Molecule 78 is a protein called Small ribosomal subunit protein eS25.

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

- Molecule 79 is a RNA chain called P/P, E/E tRNA.

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

- Molecule 80 is a protein called Nascent peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
80	Z	24	Total	C	N	O	0	0
			119	71	24	24		

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

Mol	Chain	Residues	Atoms		AltConf
81	L5	94	Total	Mg	0
			94	94	
81	L7	1	Total	Mg	0
			1	1	
81	LN	1	Total	Mg	0
			1	1	
81	LP	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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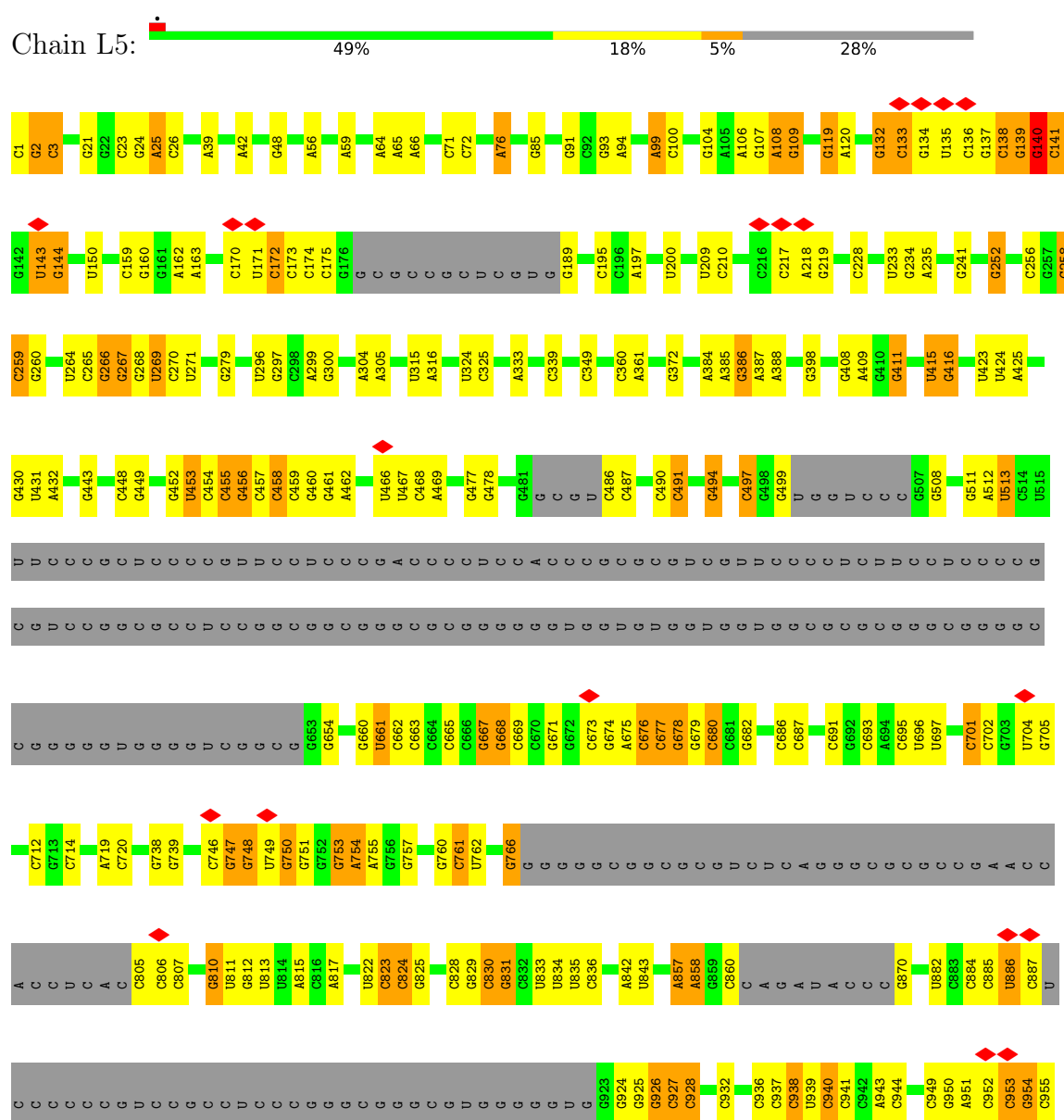
*Continued from previous page...*

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

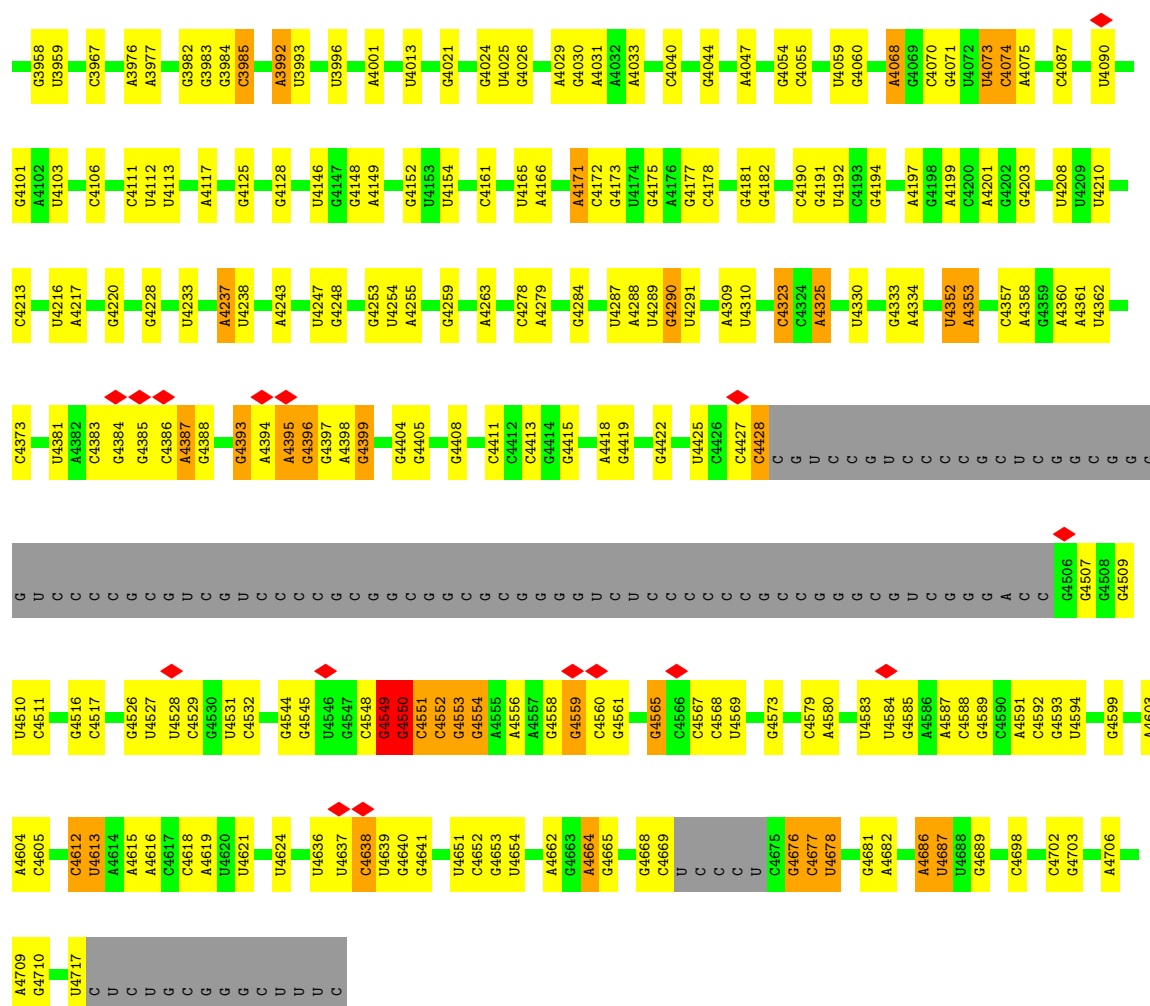
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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

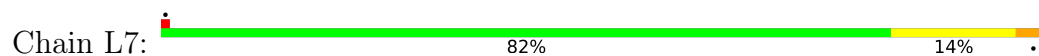




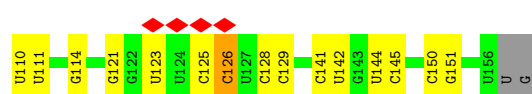
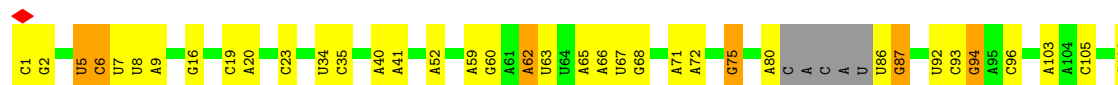




- Molecule 2: Mus musculus 5S ribosomal RNA

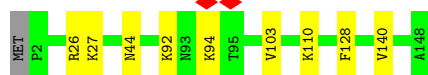


- Molecule 3: Mus musculus 5.8S ribosomal RNA



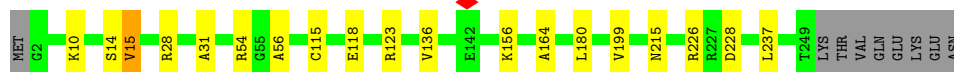
- Molecule 4: Large ribosomal subunit protein uL15

Chain La:  93% 6% .



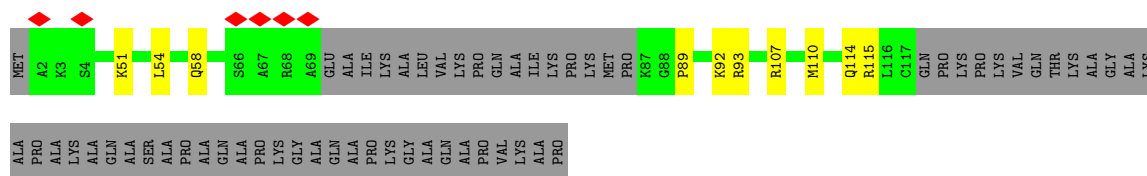
- Molecule 5: Large ribosomal subunit protein uL2

Chain LA:  89% 7% .



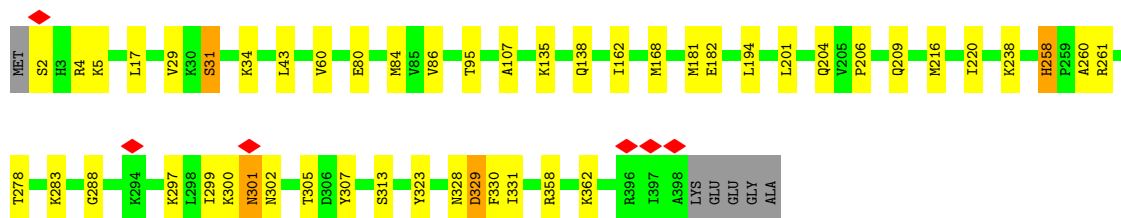
- Molecule 6: Large ribosomal subunit protein eL29

Chain Lb:  56% 6% 38%



- Molecule 7: Large ribosomal subunit protein uL3

Chain LB:  86% 11% ..




- Molecule 8: Large ribosomal subunit protein eL30

Chain Lc:  67% 15% 18%

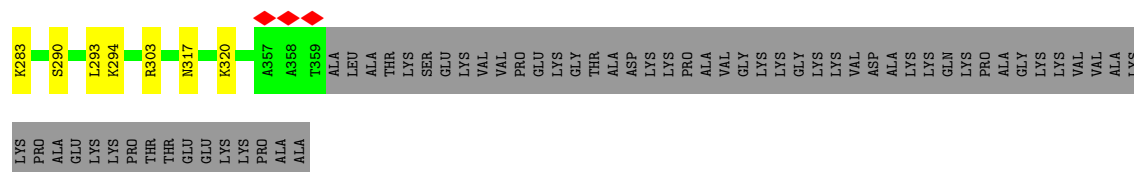


- Molecule 9: Large ribosomal subunit protein uL4

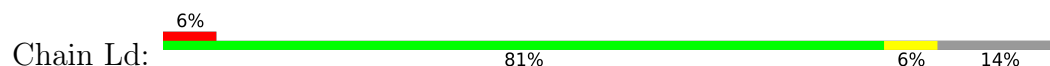
Chain LC:  76% 9% 15%



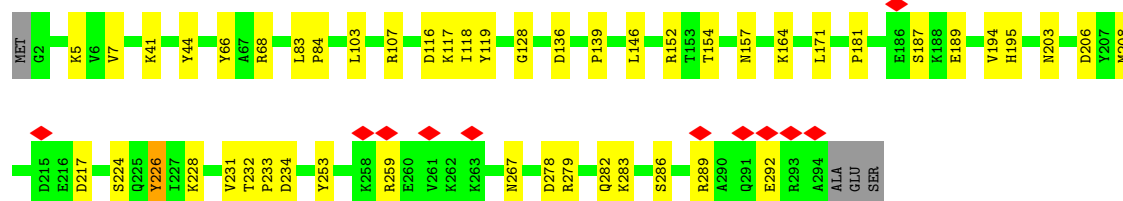
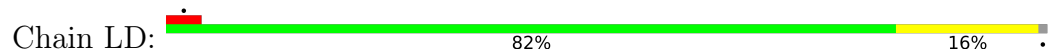




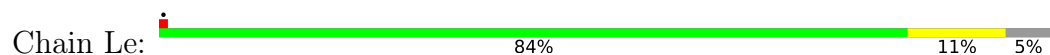
- Molecule 10: Large ribosomal subunit protein eL31



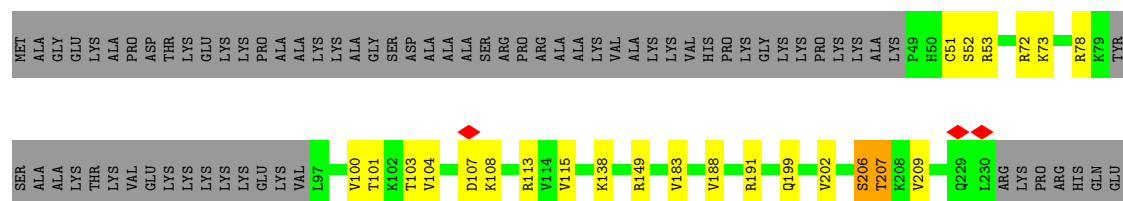
- Molecule 11: Large ribosomal subunit protein uL18



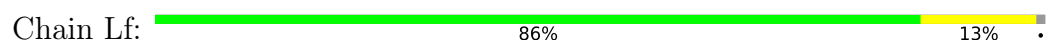
- Molecule 12: Large ribosomal subunit protein eL32



- Molecule 13: Large ribosomal subunit protein eL6



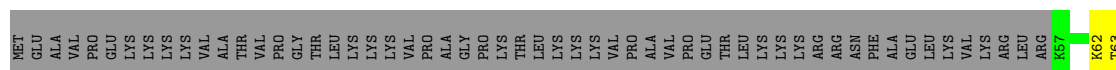
- Molecule 14: Large ribosomal subunit protein eL33





- Molecule 15: Large ribosomal subunit protein uL30

Chain LF: 70% 9% 21%



- Molecule 16: Large ribosomal subunit protein eL34

Chain Lg: 89% 5% 6%



- Molecule 17: Large ribosomal subunit protein eL8

Chain LG: 9% 74% 12% 14%



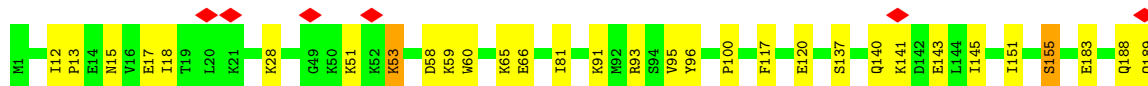
- Molecule 18: Large ribosomal subunit protein uL29

Chain Lh: 85% 14% 1%




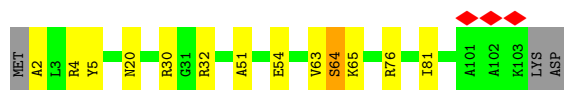
- Molecule 19: Large ribosomal subunit protein uL6

Chain LH: 84% 15% 1%




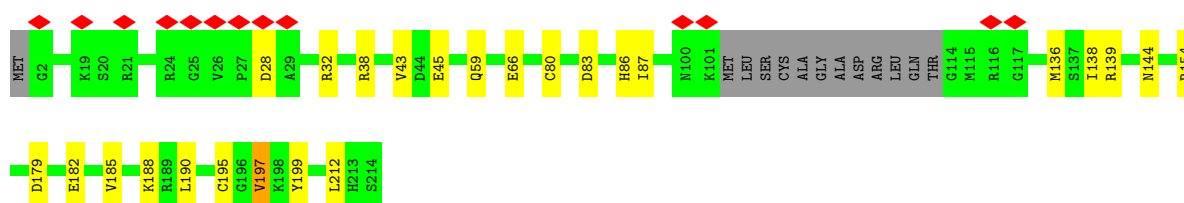
- Molecule 20: Large ribosomal subunit protein eL36

Chain Li:  85% 11% ..




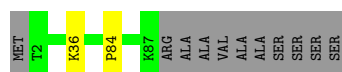
- Molecule 21: Large ribosomal subunit protein uL16-like

Chain LI:  6% 82% 11% 6%




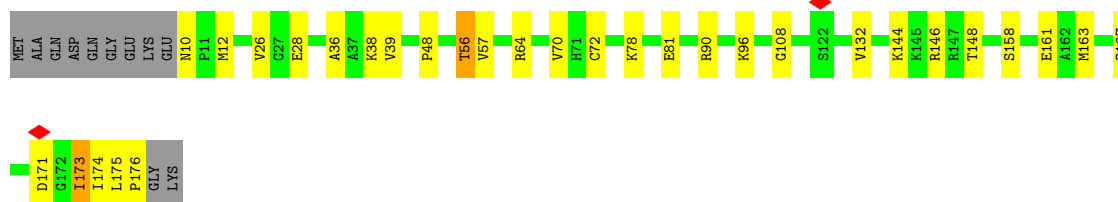
- Molecule 22: Large ribosomal subunit protein eL37

Chain Lj:  87% 11%




- Molecule 23: Large ribosomal subunit protein uL5

Chain LJ:  76% 16% 6%



- Molecule 24: Large ribosomal subunit protein eL38

Chain Lk:  86% 10% ..

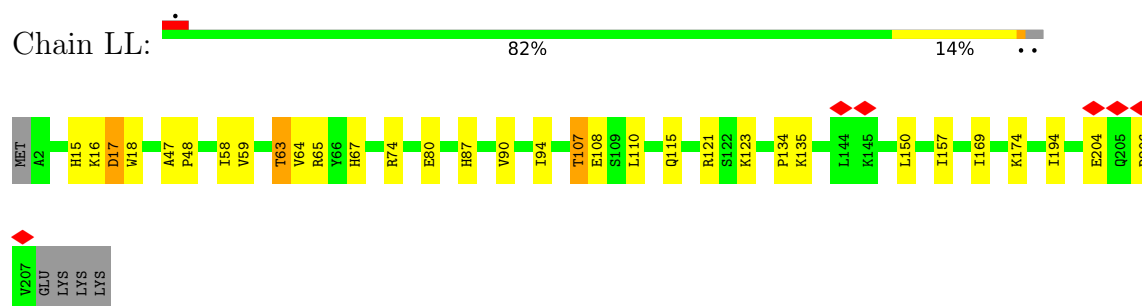


- Molecule 25: Large ribosomal subunit protein eL39-like

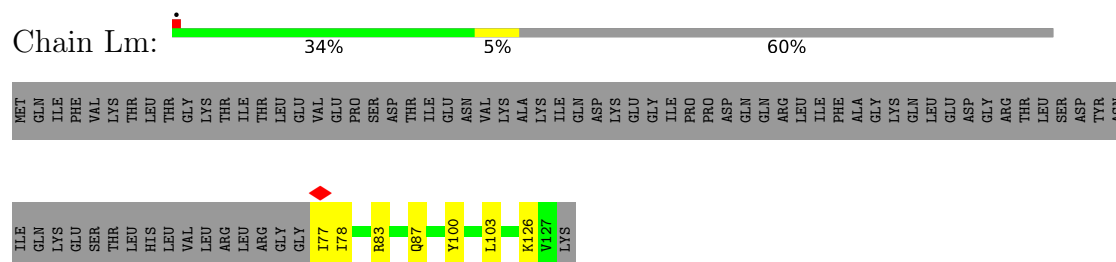
Chain Ll:  94% ..



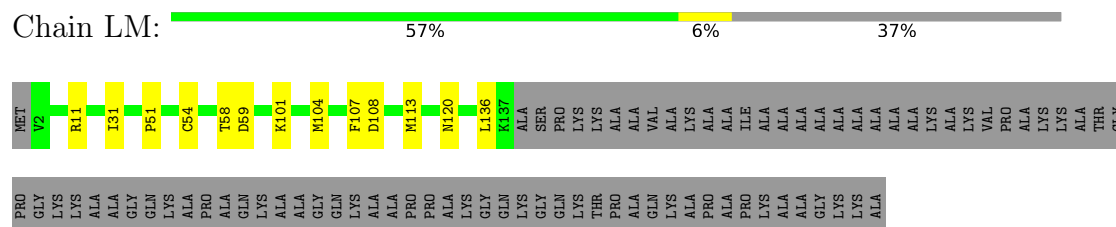
- Molecule 26: Large ribosomal subunit protein eL13



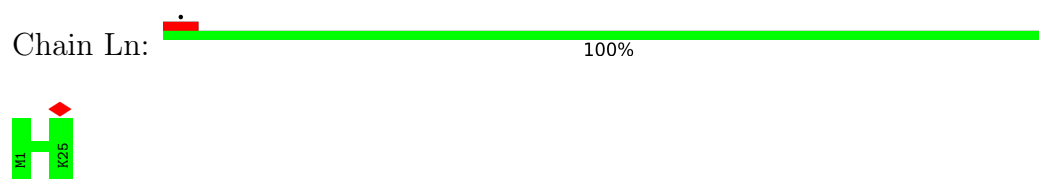
- Molecule 27: Ubiquitin-ribosomal protein eL40 fusion protein



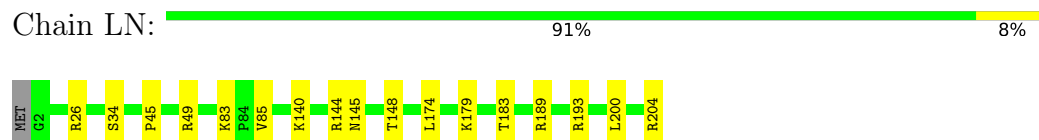
- Molecule 28: Large ribosomal subunit protein eL14



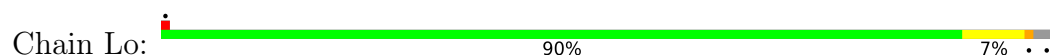
- Molecule 29: Small ribosomal subunit protein eS32

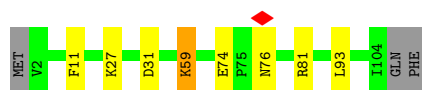


- Molecule 30: Large ribosomal subunit protein eL15



- Molecule 31: Large ribosomal subunit protein eL42





- Molecule 32: Large ribosomal subunit protein uL13

Chain LO: 89% 9%



- Molecule 33: Large ribosomal subunit protein eL43

Chain Lp: 91% 8%



- Molecule 34: Large ribosomal subunit protein uL22

Chain LP: 77% 6% 16%



- Molecule 35: Large ribosomal subunit protein eL18

Chain LQ: 92% 7%



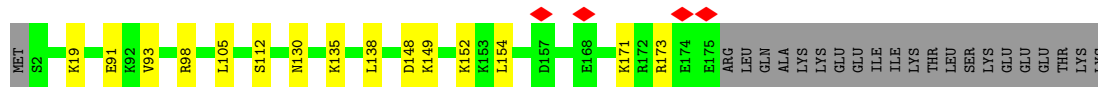
- Molecule 36: Large ribosomal subunit protein eL28

Chain Lr: 82% 7% 9%



- Molecule 37: Large ribosomal subunit protein eL19

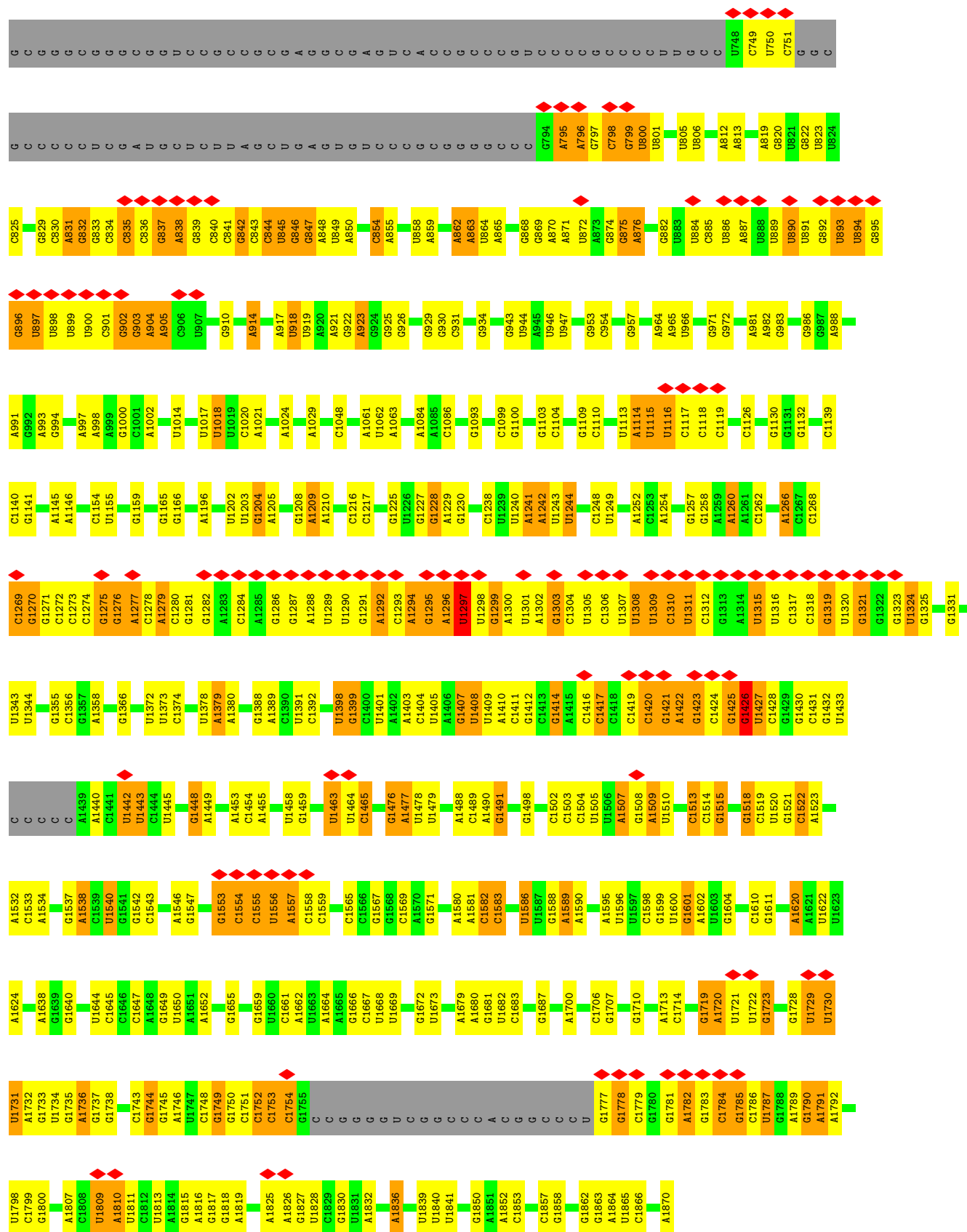
Chain LR: 81% 8% 11%



- Molecule 38: Large ribosomal subunit protein eL20

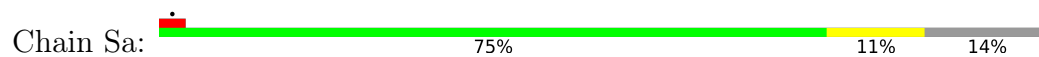




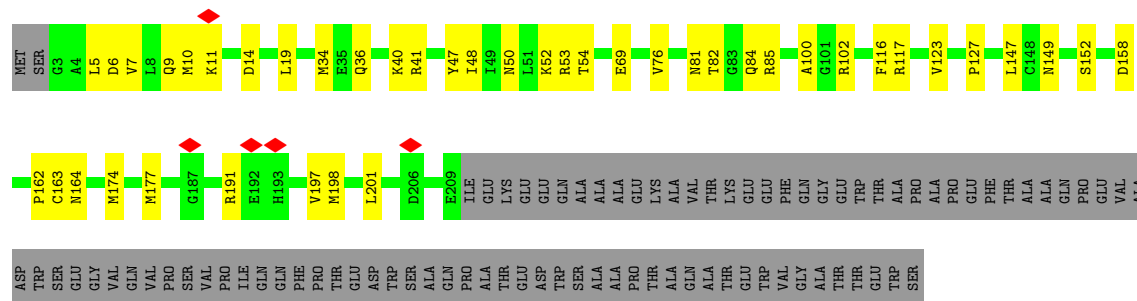


- Molecule 47: Small ribosomal subunit protein eS26

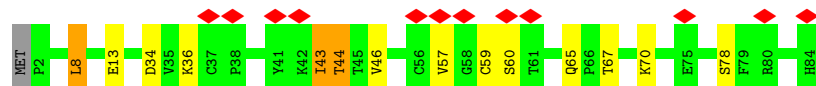
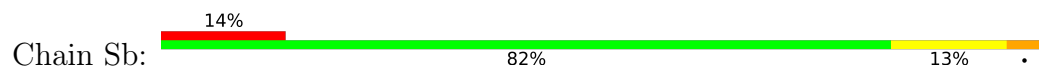




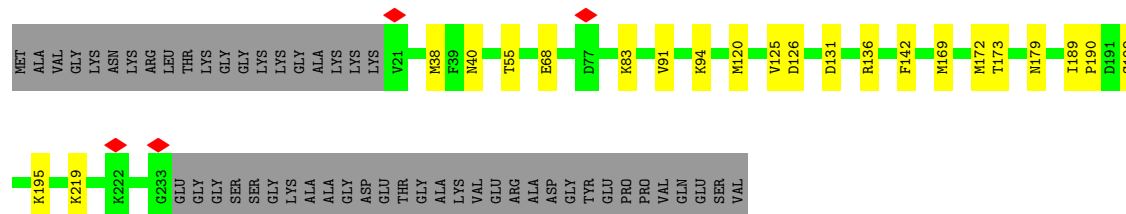
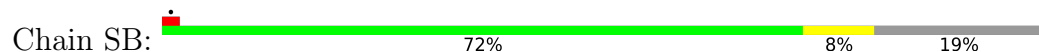
• Molecule 48: Small ribosomal subunit protein uS2



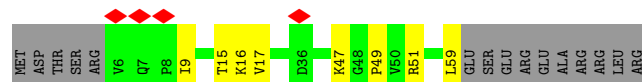
• Molecule 49: Small ribosomal subunit protein eS27



• Molecule 50: Small ribosomal subunit protein eS1



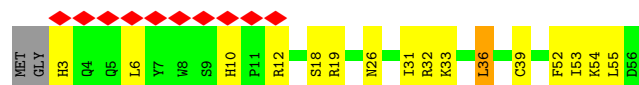
• Molecule 51: Small ribosomal subunit protein eS28



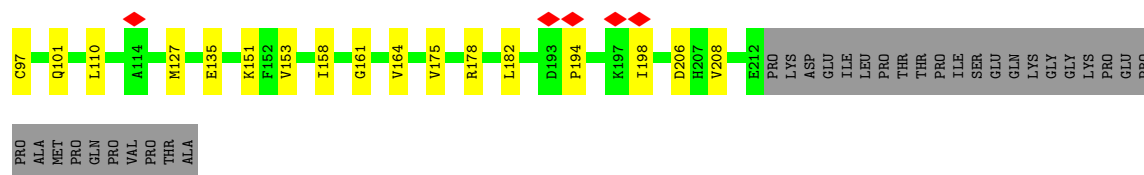
• Molecule 52: Small ribosomal subunit protein uS5



- Molecule 53: Small ribosomal subunit protein uS14



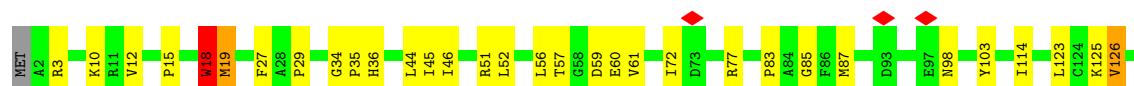
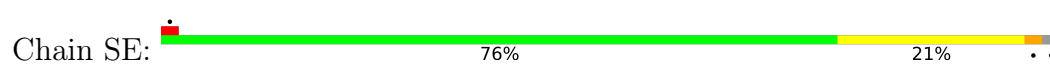
- Molecule 54: Small ribosomal subunit protein uS3




- Molecule 55: Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein

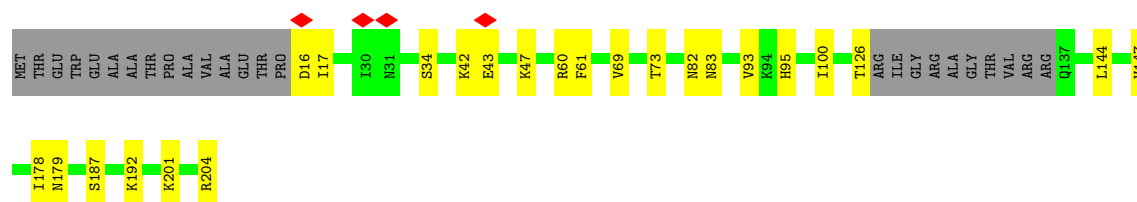


- Molecule 56: Small ribosomal subunit protein eS4



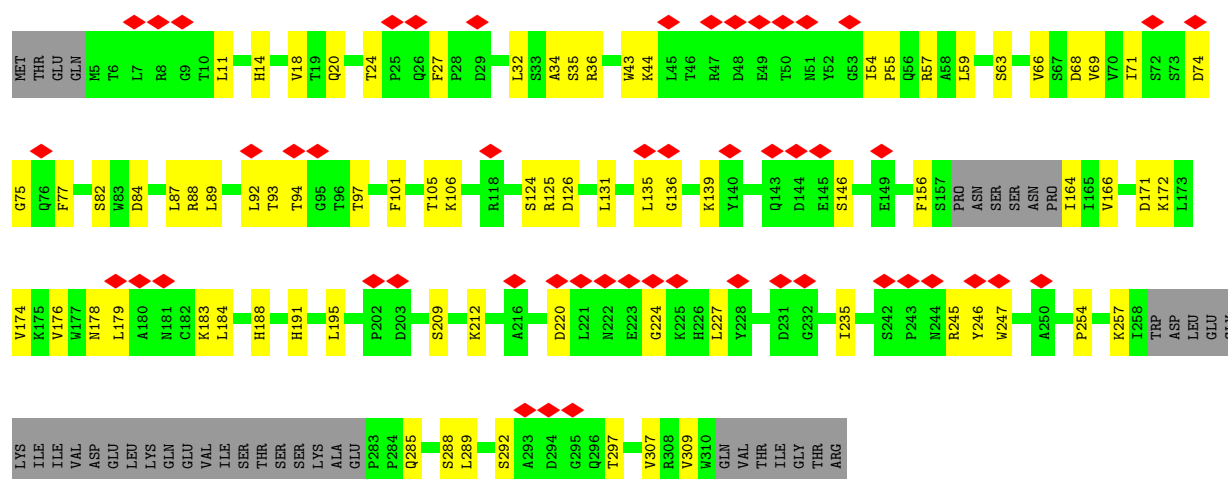
- Molecule 57: Small ribosomal subunit protein uS7

Chain SF: 



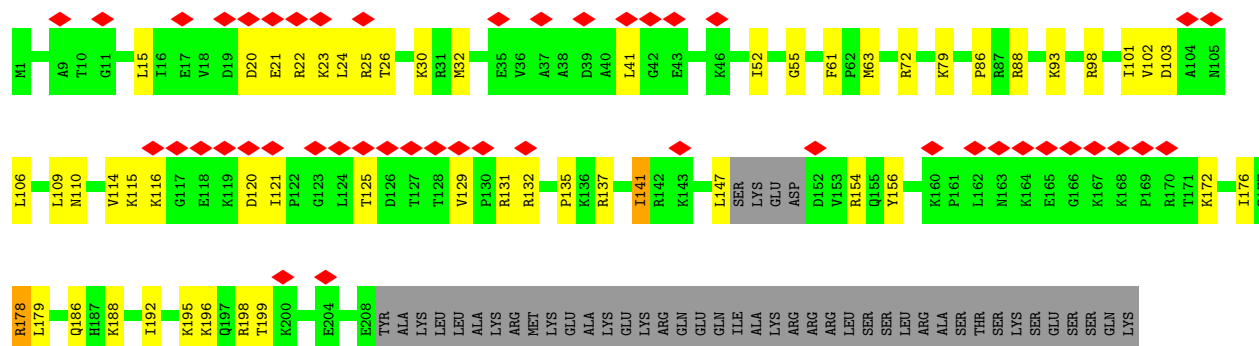
- Molecule 58: Small ribosomal subunit protein RACK1

Chain Sg: 



- Molecule 59: Small ribosomal subunit protein eS6

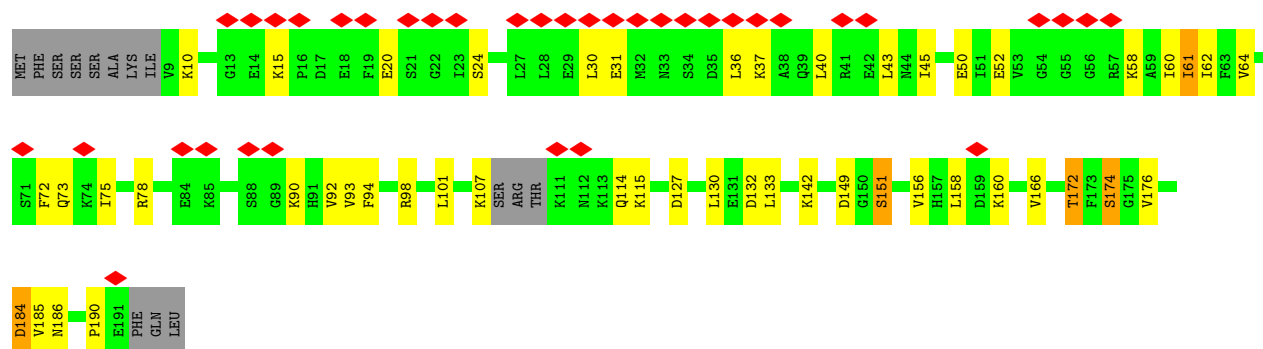
Chain SG: 



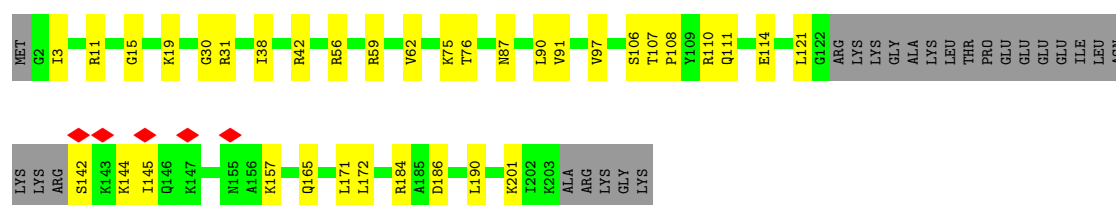
- Molecule 60: Small ribosomal subunit protein eS7

Chain SH: 

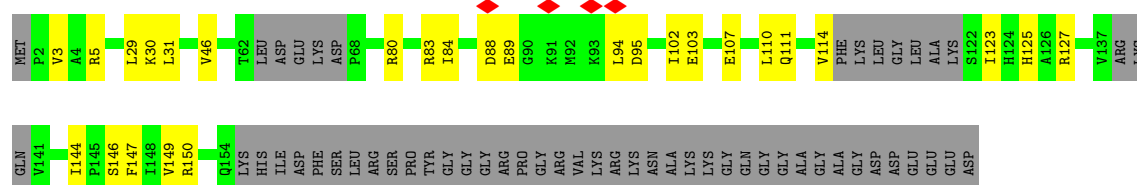




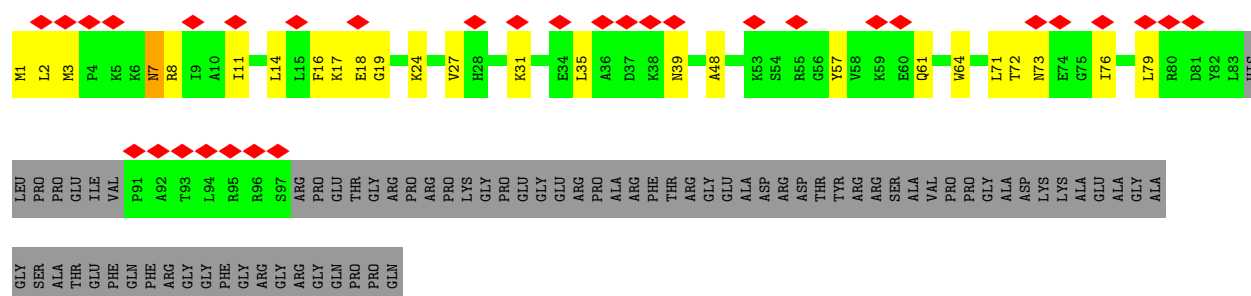
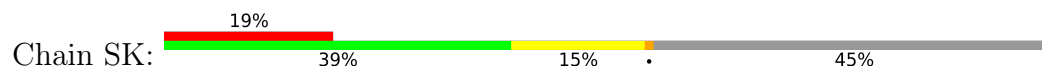
- Molecule 61: Small ribosomal subunit protein eS8



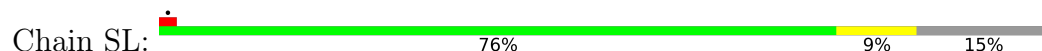
- Molecule 62: Small ribosomal subunit protein uS4



- Molecule 63: Small ribosomal subunit protein eS10

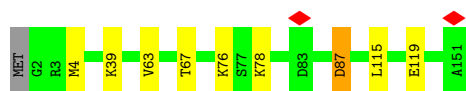


- Molecule 64: Small ribosomal subunit protein uS17

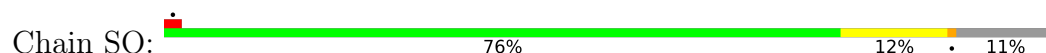




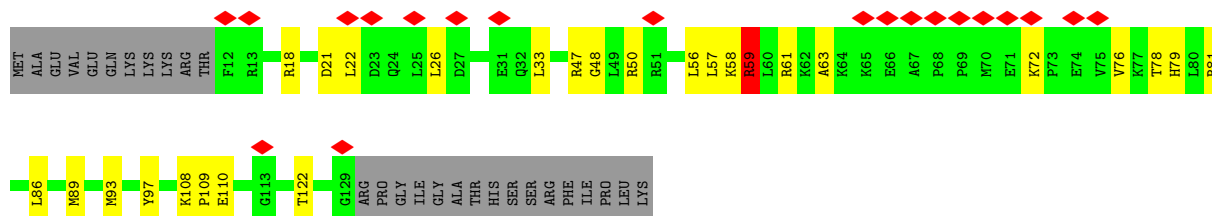
- Molecule 65: Small ribosomal subunit protein uS15



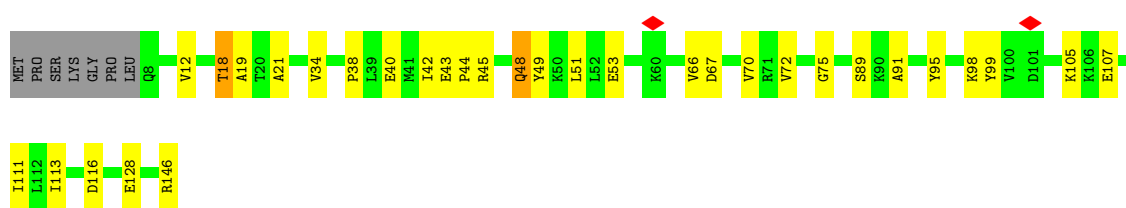
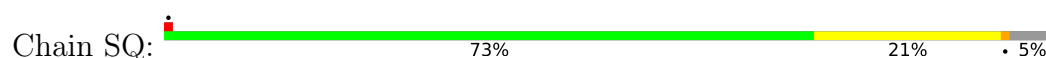
- Molecule 66: Small ribosomal subunit protein uS11



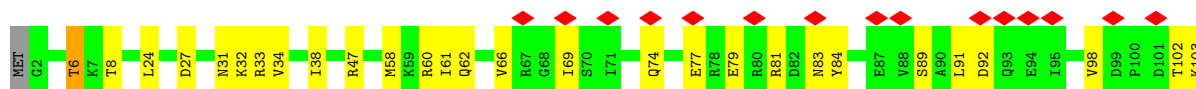
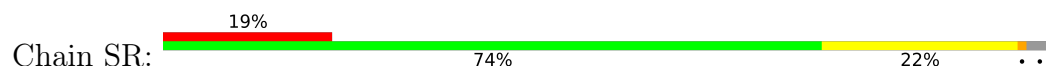
- Molecule 67: Small ribosomal subunit protein uS19

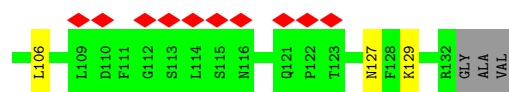


- Molecule 68: Small ribosomal subunit protein uS9

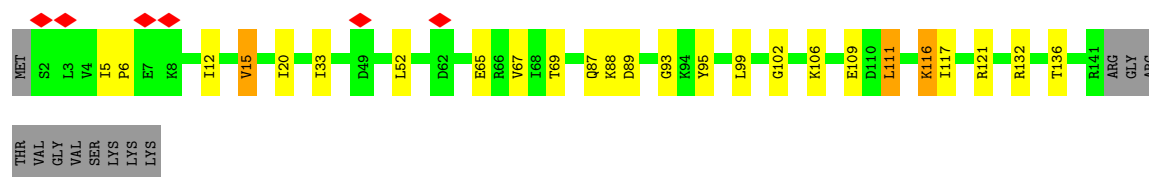
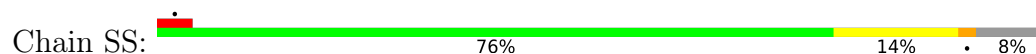


- Molecule 69: Small ribosomal subunit protein eS17

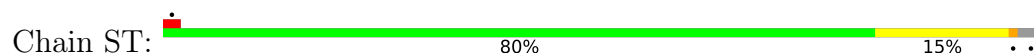




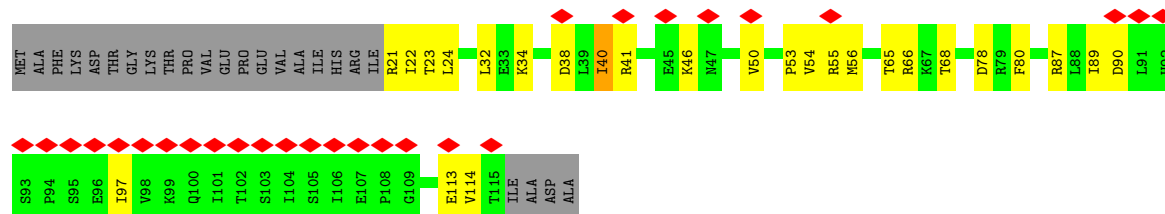
- Molecule 70: Small ribosomal subunit protein uS13



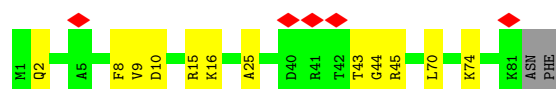
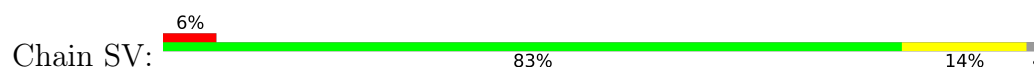
- Molecule 71: Small ribosomal subunit protein eS19



- Molecule 72: Small ribosomal subunit protein uS10



- Molecule 73: Small ribosomal subunit protein eS21

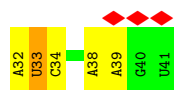


- Molecule 74: Small ribosomal subunit protein uS8

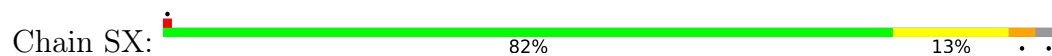


- Molecule 75: RNA (5'-R(P\*AP\*UP\*CP\*AP\*UP\*GP\*AP\*AP\*GP\*U)-3')

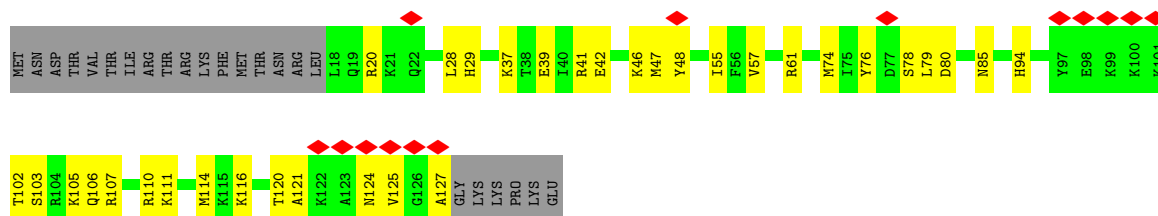




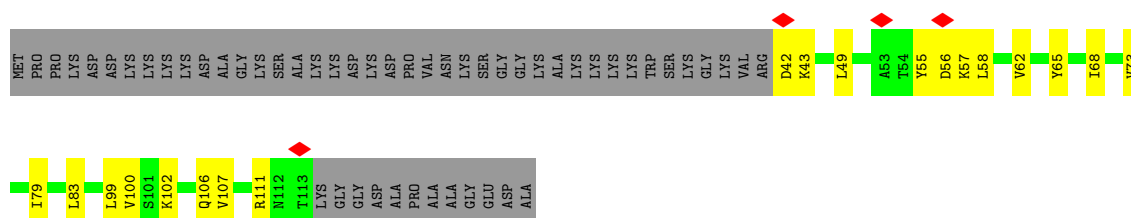
- Molecule 76: Small ribosomal subunit protein uS12



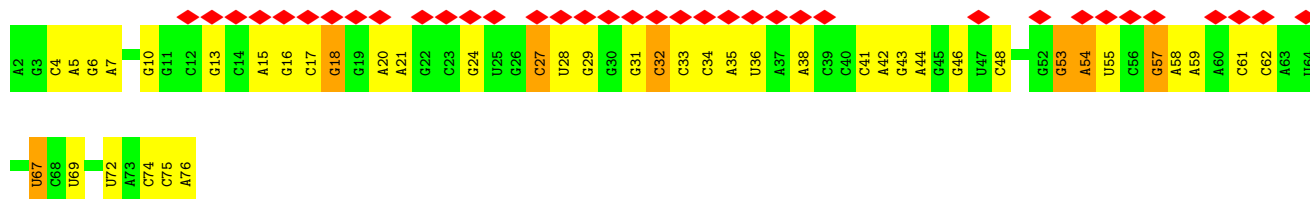
- Molecule 77: Small ribosomal subunit protein eS24



- Molecule 78: Small ribosomal subunit protein eS25

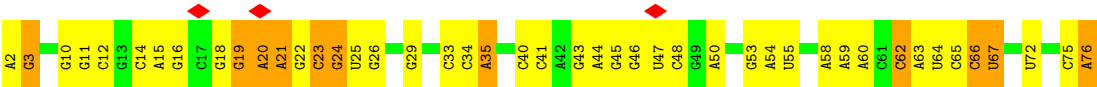


- Molecule 79: P/P, E/E tRNA

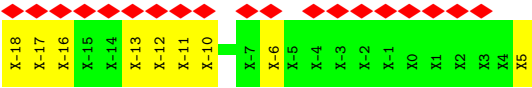
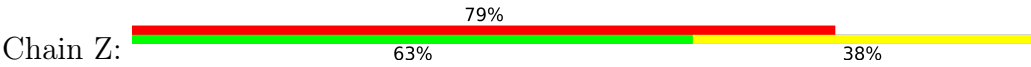


- Molecule 79: P/P, E/E tRNA





● 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	217714	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	9.612	Depositor
Minimum map value	-4.282	Depositor
Average map value	-0.006	Depositor
Map value standard deviation	0.230	Depositor
Recommended contour level	0.8	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	0.15	0/81527	0.34	21/127149 (0.0%)
2	L7	0.11	0/2858	0.28	0/4455
3	L8	0.12	0/3584	0.29	0/5582
4	La	0.19	0/1193	0.39	0/1593
5	LA	0.15	0/1936	0.42	0/2596
6	Lb	0.24	0/821	0.41	0/1082
7	LB	0.21	1/3269 (0.0%)	0.44	0/4375
8	Lc	0.30	0/742	0.53	0/996
9	LC	0.22	0/2911	0.42	0/3907
10	Ld	0.19	0/911	0.41	0/1227
11	LD	0.23	0/2435	0.46	0/3260
12	Le	0.20	0/1071	0.38	0/1429
13	LE	0.18	0/1775	0.39	0/2381
14	Lf	0.17	0/895	0.39	0/1198
15	LF	0.26	0/1805	0.44	0/2408
16	Lg	0.18	0/883	0.36	0/1178
17	LG	0.30	0/1880	0.48	0/2531
18	Lh	0.31	0/1023	0.44	0/1350
19	LH	0.22	0/1537	0.44	0/2065
20	Li	0.25	0/843	0.42	0/1115
21	LI	0.25	0/1669	0.43	0/2227
22	Lj	0.19	0/720	0.38	0/952
23	LJ	0.25	0/1363	0.49	2/1824 (0.1%)
24	Lk	0.22	0/574	0.43	0/760
25	Ll	0.19	0/448	0.33	0/592
26	LL	0.38	2/1698 (0.1%)	0.62	3/2274 (0.1%)
27	Lm	0.21	0/425	0.41	0/564
28	LM	0.29	0/1146	0.51	0/1531
29	Ln	0.34	0/240	0.45	0/305
30	LN	0.21	0/1746	0.44	0/2338
31	Lo	0.18	0/855	0.40	0/1128
32	LO	0.36	0/1670	0.59	2/2232 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	Lp	0.23	0/718	0.41	0/953
34	LP	0.25	0/1277	0.46	0/1712
35	LQ	0.21	0/1539	0.40	0/2053
36	Lr	0.34	0/1009	0.56	3/1353 (0.2%)
37	LR	0.31	0/1473	0.47	0/1947
38	LS	0.47	4/1491 (0.3%)	0.58	0/2000
39	LT	0.16	0/1335	0.37	0/1781
40	LU	0.25	0/831	0.52	0/1115
41	LV	0.14	0/987	0.38	0/1324
42	LW	0.20	0/532	0.42	0/708
43	LX	0.19	0/984	0.40	0/1323
44	LY	0.23	0/1119	0.41	0/1488
45	LZ	0.20	0/1130	0.39	0/1507
46	S2	0.21	2/38859 (0.0%)	0.45	55/60556 (0.1%)
47	Sa	0.64	2/805 (0.2%)	0.63	2/1079 (0.2%)
48	SA	0.24	0/1673	0.48	0/2275
49	Sb	0.15	0/665	0.42	0/891
50	SB	0.20	0/1756	0.41	0/2350
51	Sc	0.18	0/418	0.47	0/562
52	SC	0.21	0/1701	0.46	0/2300
53	Sd	0.18	0/466	0.36	0/618
54	SD	0.27	0/1651	0.53	0/2219
55	Se	0.17	0/386	0.41	0/504
56	SE	0.20	0/2092	0.48	0/2816
57	SF	0.27	0/1436	0.47	0/1930
58	Sg	0.19	0/2199	0.52	0/2989
59	SG	0.21	0/1666	0.40	0/2222
60	SH	0.23	0/1470	0.47	0/1968
61	SI	0.18	0/1526	0.41	0/2038
62	SJ	0.24	0/1178	0.45	0/1574
63	SK	0.19	0/780	0.43	0/1046
64	SL	0.13	0/1130	0.34	0/1514
65	SN	0.32	0/1232	0.43	0/1656
66	SO	0.23	0/1015	0.46	0/1361
67	SP	0.33	0/1000	0.69	5/1335 (0.4%)
68	SQ	0.22	0/1126	0.49	0/1506
69	SR	0.26	0/1078	0.49	0/1447
70	SS	0.18	0/1175	0.34	0/1575
71	ST	0.25	0/1108	0.41	0/1486
72	SU	0.25	0/762	0.51	0/1023
73	SV	0.18	0/625	0.40	0/836
74	SW	0.24	0/1051	0.44	0/1406
75	Sx	0.09	0/239	0.25	0/370

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	SX	0.21	0/1097	0.46	0/1464
77	SY	0.27	0/907	0.57	0/1204
78	SZ	0.22	0/580	0.48	0/780
79	S6	0.19	0/1795	0.39	1/2798 (0.0%)
79	S7	0.13	0/1795	0.31	0/2798
All	All	0.20	11/219320 (0.0%)	0.41	94/322364 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
56	SE	0	1
60	SH	0	1
All	All	0	2

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	Sa	98	PRO	CA-C	15.29	1.60	1.51
38	LS	167	PHE	C-O	-7.07	1.15	1.24
47	Sa	97	PRO	CA-C	6.83	1.56	1.52
38	LS	164	LYS	C-O	-6.57	1.17	1.24
46	S2	485	A	O3'-P	-6.55	1.51	1.61

The worst 5 of 94 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	S2	593	C	C4'-C3'-O3'	13.58	133.37	113.00
46	S2	482	C	C2'-C3'-O3'	-13.56	93.36	113.70
26	LL	16	LYS	CB-CA-C	-12.30	92.19	111.74
46	S2	492	C	C4'-C3'-O3'	12.02	131.03	113.00
47	Sa	98	PRO	O-C-N	11.96	126.81	121.31

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
56	SE	18	TRP	Peptide
60	SH	15	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	72884	0	36803	455	0
2	L7	2558	0	1296	13	0
3	L8	3210	0	1630	25	0
4	La	1164	0	1213	5	0
5	LA	1898	0	1993	11	0
6	Lb	807	0	875	7	0
7	LB	3202	0	3347	32	0
8	Lc	732	0	769	9	0
9	LC	2857	0	3030	29	0
10	Ld	896	0	941	2	0
11	LD	2389	0	2420	28	0
12	Le	1053	0	1147	7	0
13	LE	1743	0	1880	16	0
14	Lf	876	0	912	9	0
15	LF	1771	0	1886	16	0
16	Lg	873	0	961	4	0
17	LG	1848	0	1981	21	0
18	Lh	1015	0	1156	11	0
19	LH	1519	0	1603	17	0
20	Li	832	0	917	9	0
21	LI	1631	0	1682	13	0
22	Lj	705	0	737	2	0
23	LJ	1340	0	1377	15	0
24	Lk	568	0	635	6	0
25	Ll	438	0	474	1	0
26	LL	1667	0	1771	15	0
27	Lm	419	0	452	4	0
28	LM	1125	0	1202	8	0
29	Ln	239	0	289	0	0
30	LN	1701	0	1749	10	0
31	Lo	842	0	916	6	0
32	LO	1640	0	1792	13	0
33	Lp	708	0	756	3	0
34	LP	1251	0	1282	7	0
35	LQ	1515	0	1639	10	0
36	Lr	994	0	1057	5	0
37	LR	1457	0	1601	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	LS	1451	0	1488	7	0
39	LT	1307	0	1380	15	0
40	LU	817	0	839	14	0
41	LV	973	0	1034	7	0
42	LW	519	0	533	4	0
43	LX	967	0	1040	6	0
44	LY	1102	0	1189	8	0
45	LZ	1107	0	1182	4	0
46	S2	34749	0	17548	459	0
47	Sa	792	0	845	7	0
48	SA	1636	0	1641	27	0
49	Sb	651	0	672	5	0
50	SB	1729	0	1803	13	0
51	Sc	416	0	445	5	0
52	SC	1665	0	1753	17	0
53	Sd	455	0	449	12	0
54	SD	1626	0	1714	26	0
55	Se	384	0	422	6	0
56	SE	2050	0	2156	38	0
57	SF	1416	0	1458	20	0
58	Sg	2148	0	2108	47	0
59	SG	1645	0	1780	39	0
60	SH	1449	0	1539	29	0
61	SI	1499	0	1561	19	0
62	SJ	1162	0	1252	22	0
63	SK	760	0	783	18	0
64	SL	1110	0	1165	9	0
65	SN	1208	0	1294	6	0
66	SO	1002	0	1023	10	0
67	SP	981	0	1026	19	0
68	SQ	1109	0	1174	16	0
69	SR	1064	0	1118	21	0
70	SS	1157	0	1213	14	0
71	ST	1090	0	1116	16	0
72	SU	753	0	815	21	0
73	SV	619	0	620	7	0
74	SW	1034	0	1080	11	0
75	Sx	214	0	108	5	0
76	SX	1080	0	1147	16	0
77	SY	891	0	948	28	0
78	SZ	574	0	627	19	0
79	S6	1604	0	816	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
79	S7	1604	0	816	20	0
80	Z	119	0	36	9	0
81	L5	94	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
82	Lj	1	0	0	0	0
82	Lm	1	0	0	0	0
82	Lp	1	0	0	0	0
All	All	204155	0	150927	1780	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 5.

The worst 5 of 1780 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)
46:S2:1720:A:H62	46:S2:1815:G:N2	1.36	1.22
46:S2:1720:A:N6	46:S2:1815:G:H21	1.41	1.17
46:S2:159:A:C2	46:S2:468:G:N2	2.26	1.01
79:S7:76:A:O3'	80:Z:5:UNK:C	2.08	1.01
46:S2:1744:G:H21	46:S2:1792:A:H62	1.15	0.94

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	145/148 (98%)	136 (94%)	9 (6%)	0	100	100
5	LA	246/257 (96%)	228 (93%)	18 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	Lb	95/160 (59%)	93 (98%)	2 (2%)	0	100	100
7	LB	395/403 (98%)	372 (94%)	23 (6%)	0	100	100
8	Lc	92/115 (80%)	90 (98%)	1 (1%)	1 (1%)	11	16
9	LC	355/419 (85%)	335 (94%)	20 (6%)	0	100	100
10	Ld	106/125 (85%)	103 (97%)	3 (3%)	0	100	100
11	LD	291/297 (98%)	263 (90%)	28 (10%)	0	100	100
12	Le	126/135 (93%)	119 (94%)	7 (6%)	0	100	100
13	LE	210/296 (71%)	200 (95%)	10 (5%)	0	100	100
14	Lf	107/110 (97%)	104 (97%)	3 (3%)	0	100	100
15	LF	212/270 (78%)	201 (95%)	11 (5%)	0	100	100
16	Lg	108/117 (92%)	107 (99%)	1 (1%)	0	100	100
17	LG	225/266 (85%)	215 (96%)	10 (4%)	0	100	100
18	Lh	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
19	LH	188/190 (99%)	175 (93%)	10 (5%)	3 (2%)	7	10
20	Li	100/105 (95%)	93 (93%)	7 (7%)	0	100	100
21	LI	197/214 (92%)	194 (98%)	3 (2%)	0	100	100
22	Lj	84/97 (87%)	81 (96%)	3 (4%)	0	100	100
23	LJ	165/178 (93%)	158 (96%)	7 (4%)	0	100	100
24	Lk	67/70 (96%)	64 (96%)	3 (4%)	0	100	100
25	Ll	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
26	LL	204/211 (97%)	191 (94%)	13 (6%)	0	100	100
27	Lm	49/128 (38%)	49 (100%)	0	0	100	100
28	LM	134/217 (62%)	129 (96%)	5 (4%)	0	100	100
29	Ln	23/25 (92%)	23 (100%)	0	0	100	100
30	LN	201/204 (98%)	193 (96%)	8 (4%)	0	100	100
31	Lo	101/106 (95%)	95 (94%)	5 (5%)	1 (1%)	12	18
32	LO	199/203 (98%)	188 (94%)	10 (5%)	1 (0%)	24	36
33	Lp	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
34	LP	152/184 (83%)	148 (97%)	4 (3%)	0	100	100
35	LQ	185/188 (98%)	178 (96%)	7 (4%)	0	100	100
36	Lr	122/137 (89%)	113 (93%)	8 (7%)	1 (1%)	16	24

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	LR	172/196 (88%)	169 (98%)	3 (2%)	0	100	100
38	LS	173/176 (98%)	165 (95%)	8 (5%)	0	100	100
39	LT	158/160 (99%)	154 (98%)	4 (2%)	0	100	100
40	LU	98/128 (77%)	87 (89%)	11 (11%)	0	100	100
41	LV	128/140 (91%)	125 (98%)	3 (2%)	0	100	100
42	LW	60/157 (38%)	59 (98%)	1 (2%)	0	100	100
43	LX	116/156 (74%)	113 (97%)	3 (3%)	0	100	100
44	LY	130/145 (90%)	129 (99%)	1 (1%)	0	100	100
45	LZ	133/136 (98%)	128 (96%)	5 (4%)	0	100	100
47	Sa	97/115 (84%)	91 (94%)	6 (6%)	0	100	100
48	SA	205/295 (70%)	189 (92%)	16 (8%)	0	100	100
49	Sb	81/84 (96%)	73 (90%)	8 (10%)	0	100	100
50	SB	211/264 (80%)	197 (93%)	14 (7%)	0	100	100
51	Sc	52/69 (75%)	46 (88%)	5 (10%)	1 (2%)	6	8
52	SC	213/293 (73%)	206 (97%)	7 (3%)	0	100	100
53	Sd	52/56 (93%)	50 (96%)	2 (4%)	0	100	100
54	SD	207/243 (85%)	193 (93%)	13 (6%)	1 (0%)	24	36
55	Se	44/133 (33%)	39 (89%)	5 (11%)	0	100	100
56	SE	256/263 (97%)	242 (94%)	13 (5%)	1 (0%)	30	42
57	SF	175/204 (86%)	165 (94%)	10 (6%)	0	100	100
58	Sg	270/317 (85%)	244 (90%)	26 (10%)	0	100	100
59	SG	200/249 (80%)	191 (96%)	9 (4%)	0	100	100
60	SH	176/194 (91%)	162 (92%)	14 (8%)	0	100	100
61	SI	179/208 (86%)	173 (97%)	6 (3%)	0	100	100
62	SJ	130/194 (67%)	123 (95%)	7 (5%)	0	100	100
63	SK	86/165 (52%)	75 (87%)	11 (13%)	0	100	100
64	SL	131/158 (83%)	126 (96%)	5 (4%)	0	100	100
65	SN	148/151 (98%)	147 (99%)	1 (1%)	0	100	100
66	SO	132/151 (87%)	123 (93%)	9 (7%)	0	100	100
67	SP	116/145 (80%)	111 (96%)	5 (4%)	0	100	100
68	SQ	137/146 (94%)	125 (91%)	12 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	SR	129/135 (96%)	116 (90%)	13 (10%)	0	100	100
70	SS	138/152 (91%)	128 (93%)	10 (7%)	0	100	100
71	ST	138/145 (95%)	130 (94%)	8 (6%)	0	100	100
72	SU	93/119 (78%)	86 (92%)	7 (8%)	0	100	100
73	SV	79/83 (95%)	74 (94%)	5 (6%)	0	100	100
74	SW	127/130 (98%)	120 (94%)	7 (6%)	0	100	100
76	SX	137/143 (96%)	126 (92%)	10 (7%)	1 (1%)	18	27
77	SY	108/133 (81%)	102 (94%)	6 (6%)	0	100	100
78	SZ	70/125 (56%)	62 (89%)	8 (11%)	0	100	100
All	All	10626/12497 (85%)	10050 (95%)	565 (5%)	11 (0%)	49	64

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	Lc	99	PRO
19	LH	13	PRO
32	LO	187	LYS
36	Lr	123	PRO
51	Sc	51	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	120/121 (99%)	117 (98%)	3 (2%)	42	63
5	LA	190/199 (96%)	187 (98%)	3 (2%)	55	73
6	Lb	83/124 (67%)	82 (99%)	1 (1%)	63	78
7	LB	344/348 (99%)	334 (97%)	10 (3%)	37	57
8	Lc	79/97 (81%)	78 (99%)	1 (1%)	61	76
9	LC	301/348 (86%)	297 (99%)	4 (1%)	61	76
10	Ld	99/110 (90%)	96 (97%)	3 (3%)	36	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	LD	246/249 (99%)	236 (96%)	10 (4%)	27	44
12	Le	114/121 (94%)	110 (96%)	4 (4%)	32	51
13	LE	194/256 (76%)	187 (96%)	7 (4%)	31	50
14	Lf	88/89 (99%)	87 (99%)	1 (1%)	65	79
15	LF	185/234 (79%)	182 (98%)	3 (2%)	55	73
16	Lg	94/100 (94%)	93 (99%)	1 (1%)	65	79
17	LG	197/223 (88%)	189 (96%)	8 (4%)	27	44
18	Lh	109/110 (99%)	108 (99%)	1 (1%)	70	82
19	LH	169/169 (100%)	162 (96%)	7 (4%)	27	44
20	Li	86/89 (97%)	85 (99%)	1 (1%)	63	78
21	LI	170/180 (94%)	165 (97%)	5 (3%)	37	57
22	Lj	73/80 (91%)	73 (100%)	0	100	100
23	LJ	141/149 (95%)	133 (94%)	8 (6%)	18	31
24	Lk	64/65 (98%)	62 (97%)	2 (3%)	35	55
25	Ll	46/47 (98%)	45 (98%)	1 (2%)	45	66
26	LL	173/178 (97%)	164 (95%)	9 (5%)	21	34
27	Lm	47/116 (40%)	45 (96%)	2 (4%)	26	42
28	LM	116/157 (74%)	114 (98%)	2 (2%)	53	72
29	Ln	24/24 (100%)	24 (100%)	0	100	100
30	LN	171/172 (99%)	170 (99%)	1 (1%)	78	87
31	Lo	91/94 (97%)	91 (100%)	0	100	100
32	LO	172/173 (99%)	168 (98%)	4 (2%)	44	65
33	Lp	74/75 (99%)	71 (96%)	3 (4%)	27	44
34	LP	135/163 (83%)	132 (98%)	3 (2%)	45	66
35	LQ	164/165 (99%)	163 (99%)	1 (1%)	78	87
36	Lr	108/121 (89%)	105 (97%)	3 (3%)	38	58
37	LR	154/175 (88%)	149 (97%)	5 (3%)	34	54
38	LS	155/156 (99%)	149 (96%)	6 (4%)	28	47
39	LT	140/140 (100%)	137 (98%)	3 (2%)	47	67
40	LU	90/114 (79%)	88 (98%)	2 (2%)	45	66
41	LV	100/107 (94%)	97 (97%)	3 (3%)	36	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	LW	54/126 (43%)	54 (100%)	0	100	100
43	LX	106/133 (80%)	103 (97%)	3 (3%)	38	58
44	LY	123/135 (91%)	122 (99%)	1 (1%)	73	84
45	LZ	117/118 (99%)	117 (100%)	0	100	100
47	Sa	86/98 (88%)	81 (94%)	5 (6%)	18	30
48	SA	173/242 (72%)	170 (98%)	3 (2%)	53	72
49	Sb	75/76 (99%)	67 (89%)	8 (11%)	6	9
50	SB	194/229 (85%)	191 (98%)	3 (2%)	57	74
51	Sc	48/62 (77%)	46 (96%)	2 (4%)	26	44
52	SC	181/224 (81%)	176 (97%)	5 (3%)	38	58
53	Sd	48/49 (98%)	45 (94%)	3 (6%)	16	27
54	SD	173/202 (86%)	166 (96%)	7 (4%)	28	45
55	Se	39/106 (37%)	38 (97%)	1 (3%)	40	61
56	SE	221/225 (98%)	207 (94%)	14 (6%)	16	27
57	SF	152/170 (89%)	149 (98%)	3 (2%)	48	68
58	Sg	237/275 (86%)	231 (98%)	6 (2%)	42	63
59	SG	178/218 (82%)	172 (97%)	6 (3%)	32	52
60	SH	161/174 (92%)	150 (93%)	11 (7%)	14	23
61	SI	159/180 (88%)	154 (97%)	5 (3%)	35	55
62	SJ	126/168 (75%)	123 (98%)	3 (2%)	43	64
63	SK	81/136 (60%)	80 (99%)	1 (1%)	63	78
64	SL	123/142 (87%)	120 (98%)	3 (2%)	43	64
65	SN	130/131 (99%)	127 (98%)	3 (2%)	44	65
66	SO	104/119 (87%)	101 (97%)	3 (3%)	37	57
67	SP	107/130 (82%)	101 (94%)	6 (6%)	19	31
68	SQ	115/121 (95%)	108 (94%)	7 (6%)	17	29
69	SR	119/121 (98%)	116 (98%)	3 (2%)	42	63
70	SS	122/132 (92%)	113 (93%)	9 (7%)	13	20
71	ST	110/115 (96%)	104 (94%)	6 (6%)	19	32
72	SU	88/107 (82%)	86 (98%)	2 (2%)	44	65
73	SV	65/67 (97%)	62 (95%)	3 (5%)	24	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
74	SW	112/113 (99%)	106 (95%)	6 (5%)	20	33
76	SX	111/115 (96%)	104 (94%)	7 (6%)	16	27
77	SY	93/115 (81%)	93 (100%)	0	100	100
78	SZ	64/103 (62%)	63 (98%)	1 (2%)	55	73
All	All	9301/10615 (88%)	9021 (97%)	280 (3%)	37	56

5 of 280 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
67	SP	57	LEU
68	SQ	48	GLN
71	ST	113	VAL
30	LN	34	SER
27	Lm	126	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 90 such sidechains are listed below:

Mol	Chain	Res	Type
53	Sd	37	ASN
64	SL	100	ASN
55	Se	132	ASN
60	SH	165	ASN
67	SP	32	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3377/4731 (71%)	685 (20%)	33 (0%)
2	L7	119/120 (99%)	10 (8%)	3 (2%)
3	L8	149/158 (94%)	28 (18%)	1 (0%)
46	S2	1618/1870 (86%)	508 (31%)	35 (2%)
75	Sx	9/10 (90%)	1 (11%)	0
79	S6	74/75 (98%)	23 (31%)	3 (4%)
79	S7	74/75 (98%)	27 (36%)	1 (1%)
All	All	5420/7039 (76%)	1282 (23%)	76 (1%)

5 of 1282 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	2	G
1	L5	3	C
1	L5	21	G
1	L5	25	A
1	L5	39	A

5 of 76 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
46	S2	629	A
46	S2	1784	C
46	S2	862	A
46	S2	1408	U
79	S7	53	G

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

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

## 5.5 Carbohydrates [i](#)

There are no 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 ⓘ

There are no chain breaks in this entry.

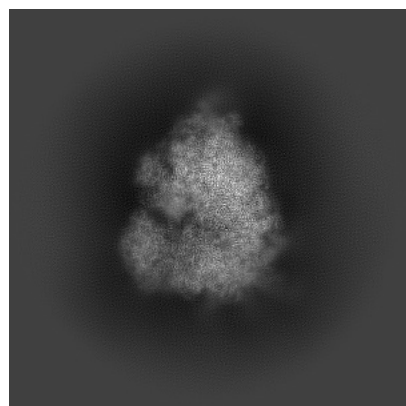
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62285. These allow visual inspection of the internal detail of the map and identification of artifacts.

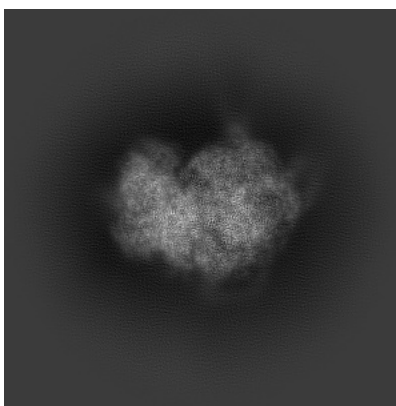
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

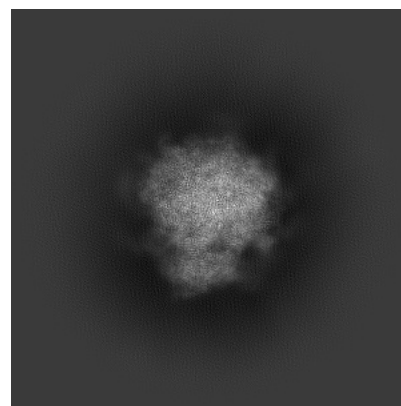
#### 6.1.1 Primary map



X

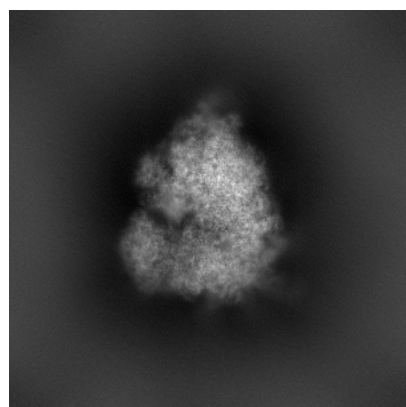


Y

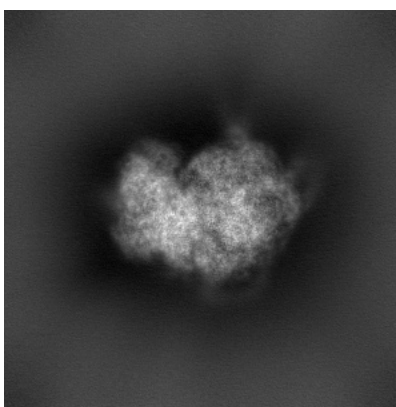


Z

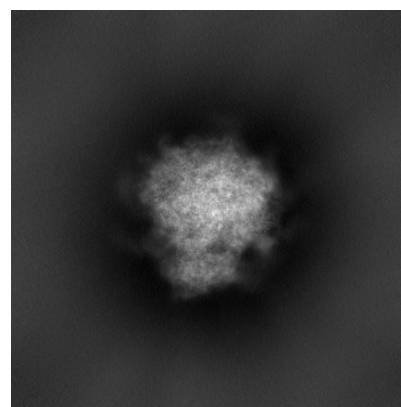
#### 6.1.2 Raw map



X



Y



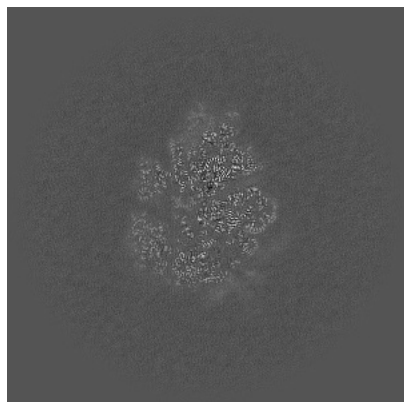
Z

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

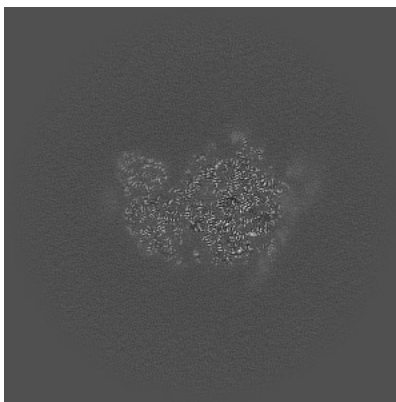


## 6.2 Central slices [i](#)

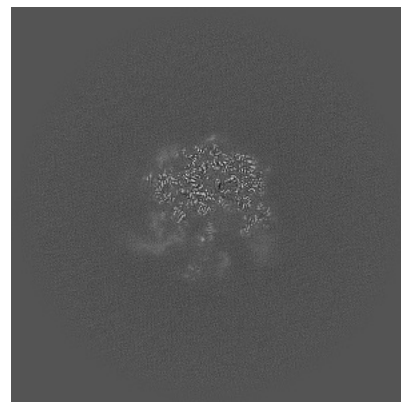
### 6.2.1 Primary map



X Index: 280

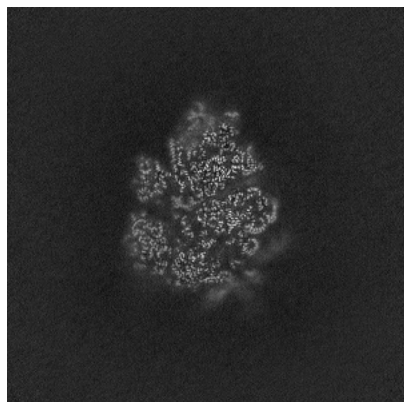


Y Index: 280

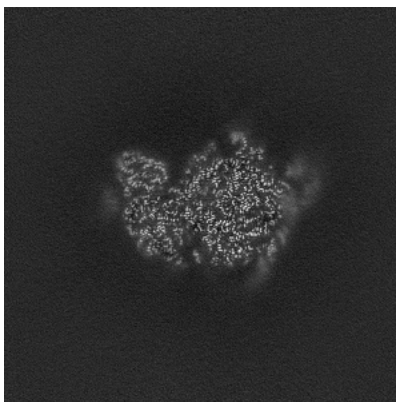


Z Index: 280

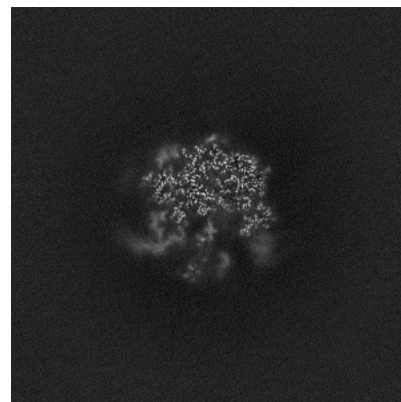
### 6.2.2 Raw map



X Index: 280



Y Index: 280

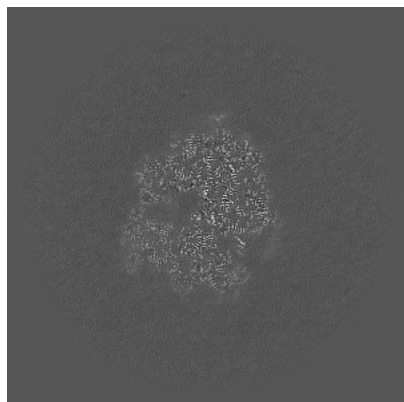


Z Index: 280

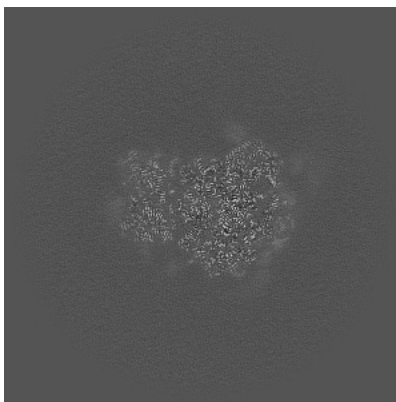
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

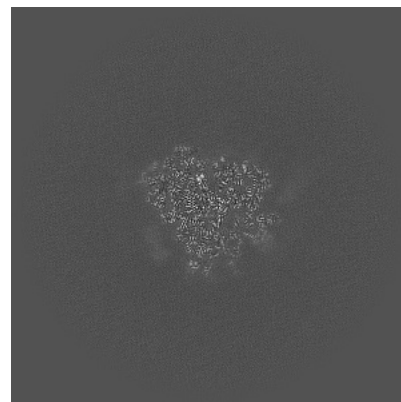
### 6.3.1 Primary map



X Index: 260

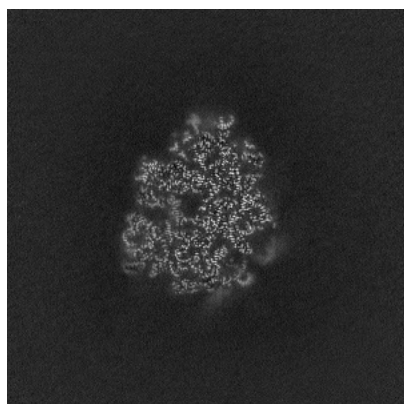


Y Index: 292

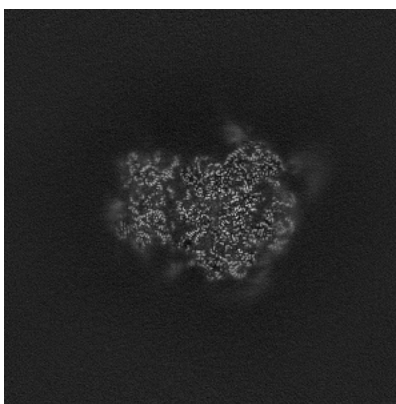


Z Index: 312

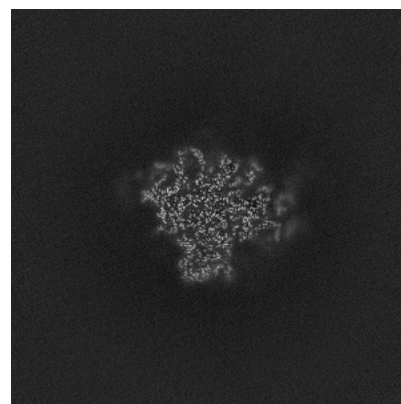
### 6.3.2 Raw map



X Index: 268



Y Index: 294

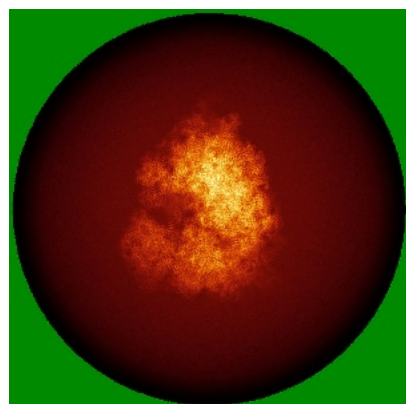


Z Index: 325

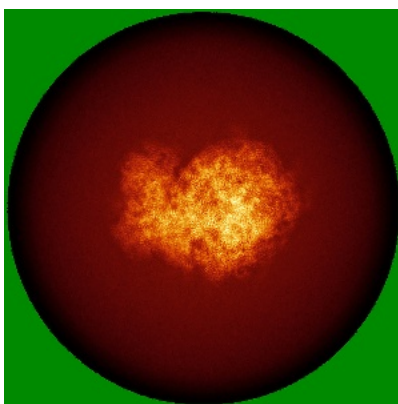
The images above show the largest variance slices of the map in three orthogonal directions.

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

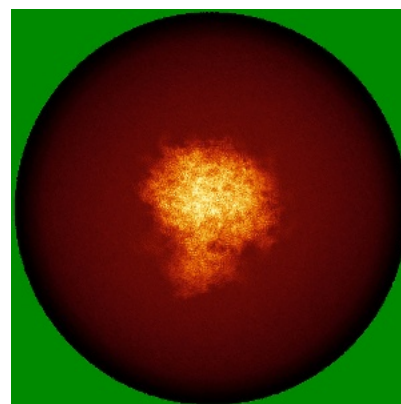
### 6.4.1 Primary map



X

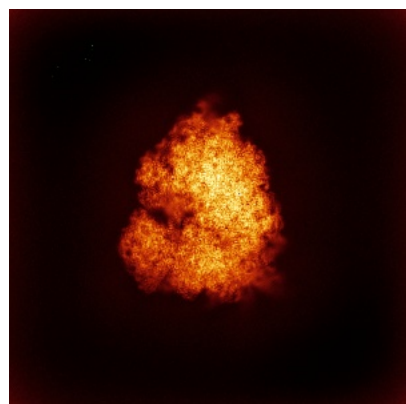


Y

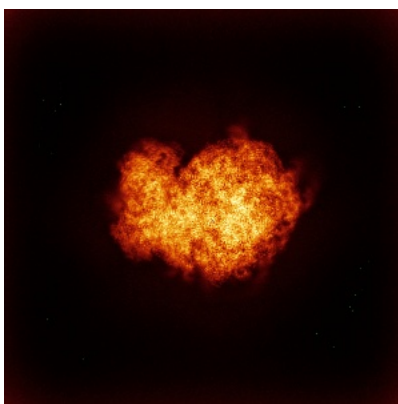


Z

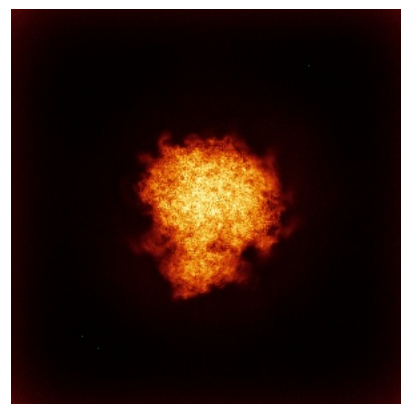
### 6.4.2 Raw map



X



Y

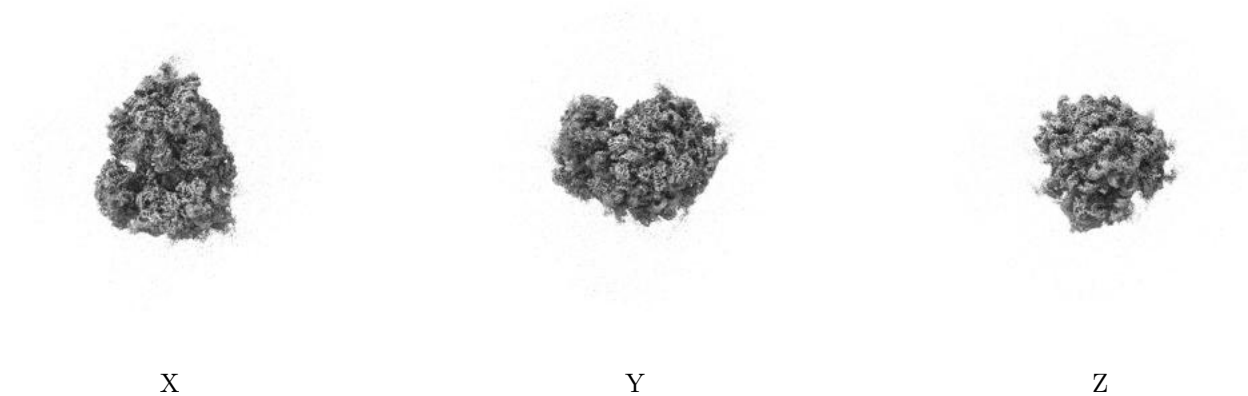


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.8. 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



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.

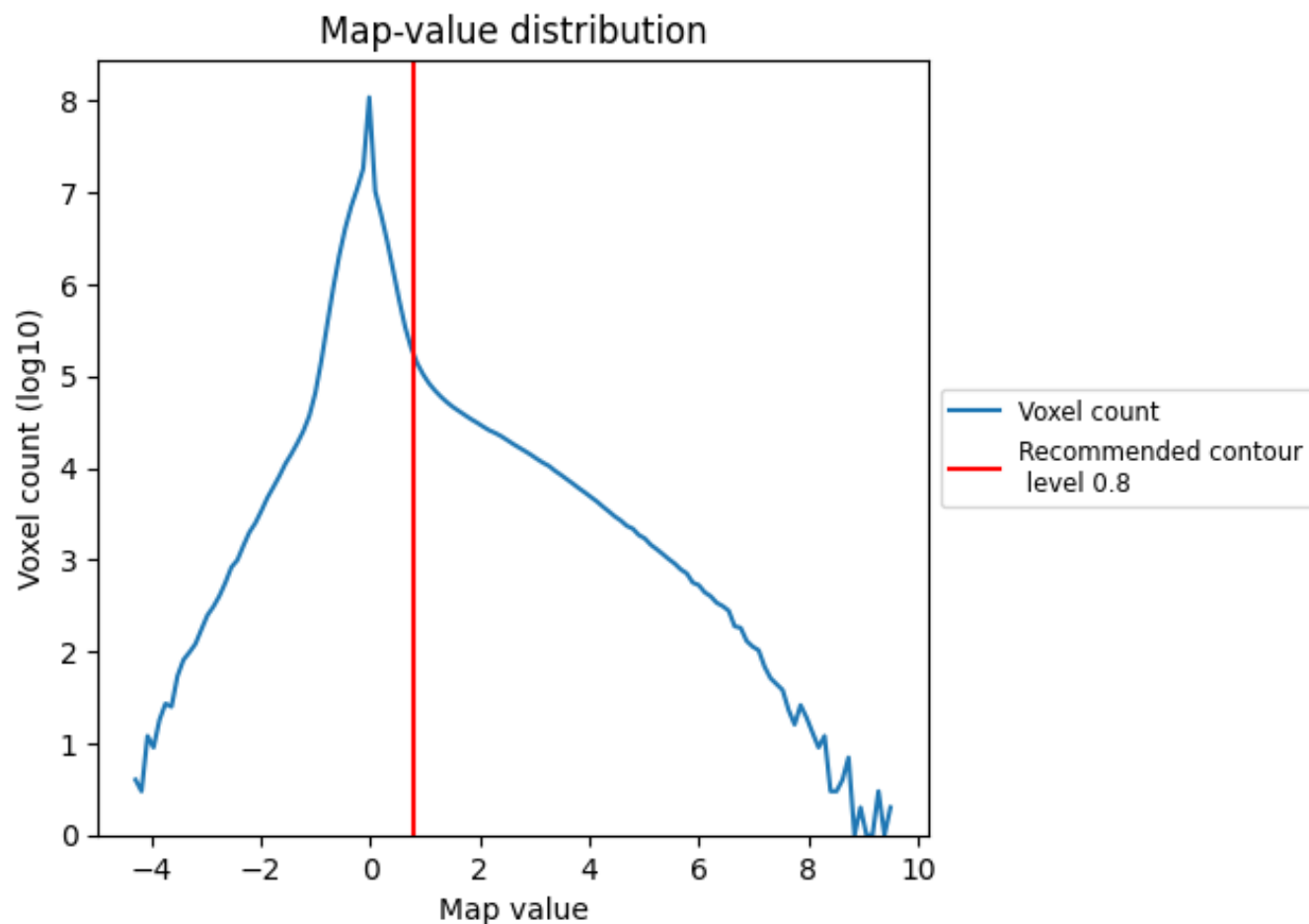
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

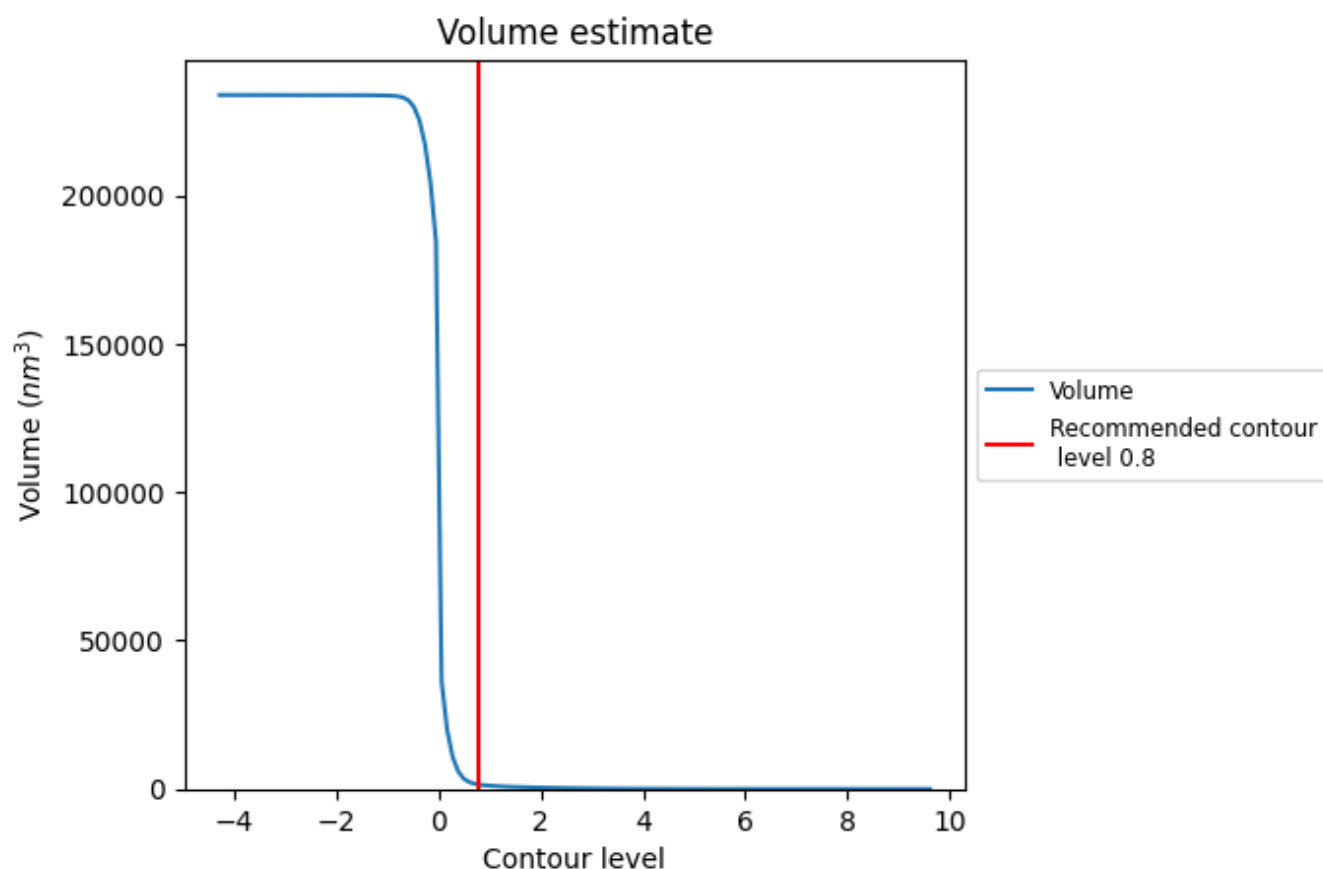
This section contains the results of statistical analysis of the map.

### 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.

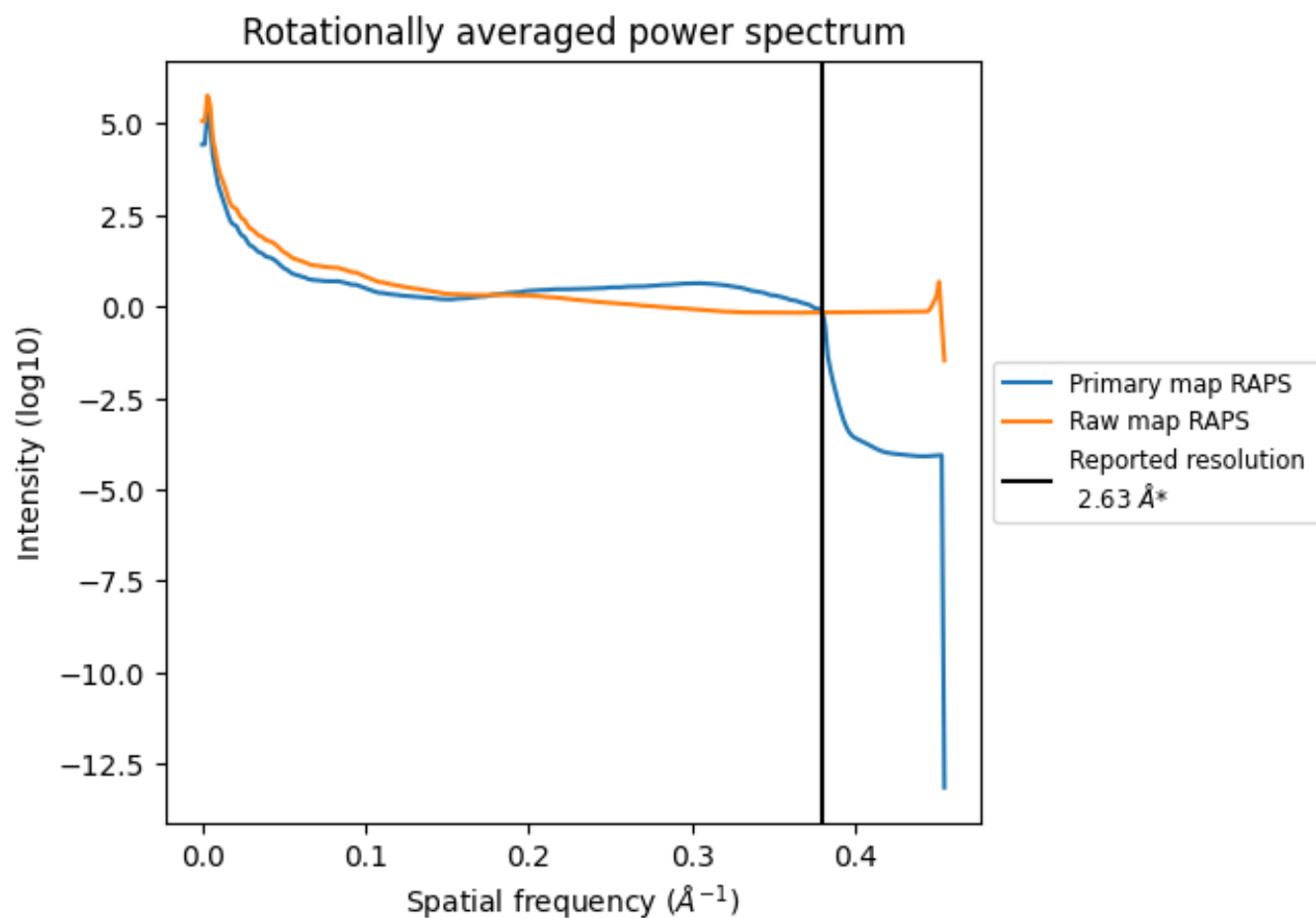
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1473  $\text{nm}^3$ ; this corresponds to an approximate mass of 1331 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 ⓘ



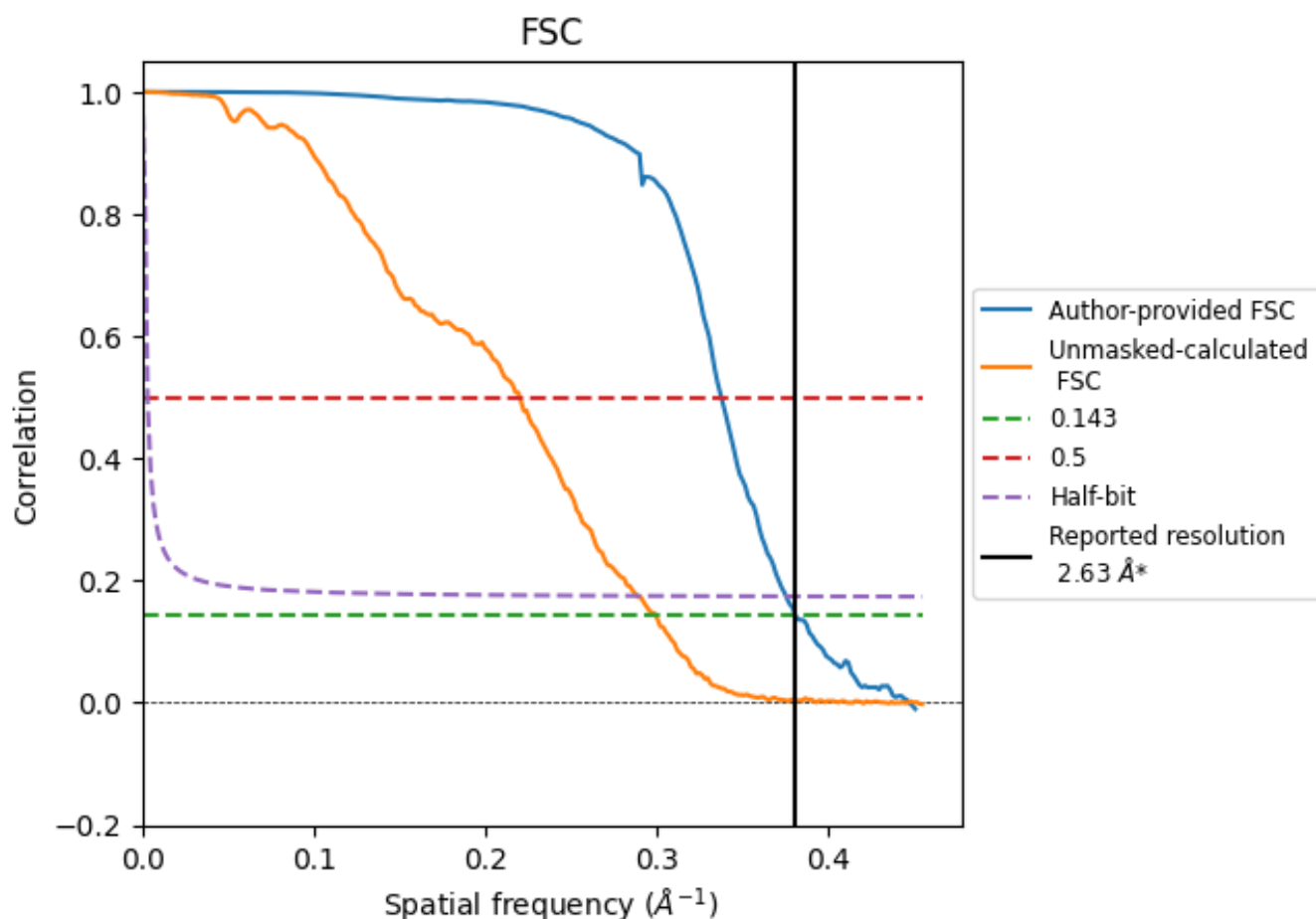
\*Reported resolution corresponds to spatial frequency of 0.380 Å<sup>-1</sup>



## 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  $0.380 \text{ \AA}^{-1}$



## 8.2 Resolution estimates [i](#)

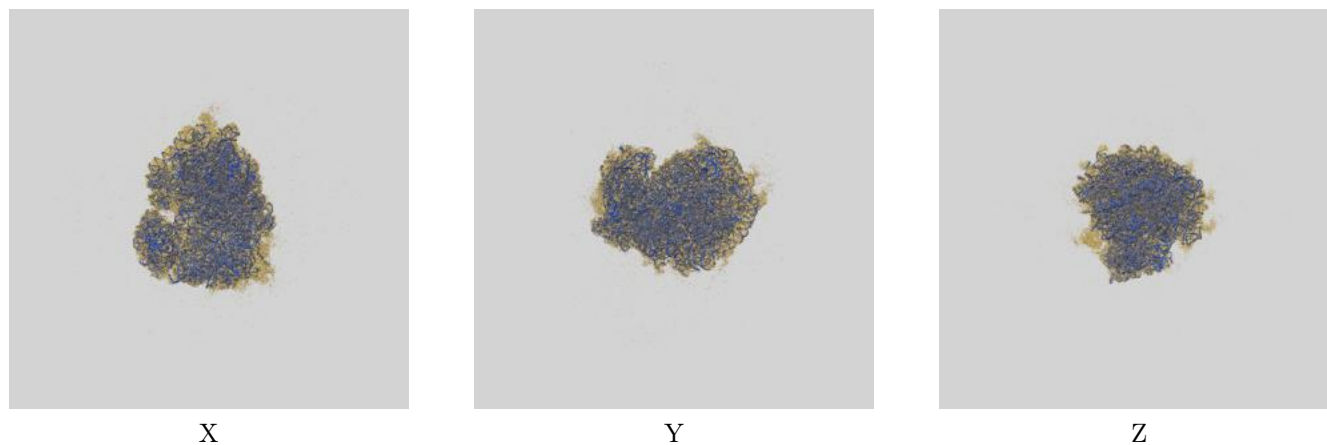
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.63	-	-
Author-provided FSC curve	2.63	2.96	2.67
Unmasked-calculated*	3.34	4.55	3.47

\*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 3.34 differs from the reported value 2.63 by more than 10 %

## 9 Map-model fit [i](#)

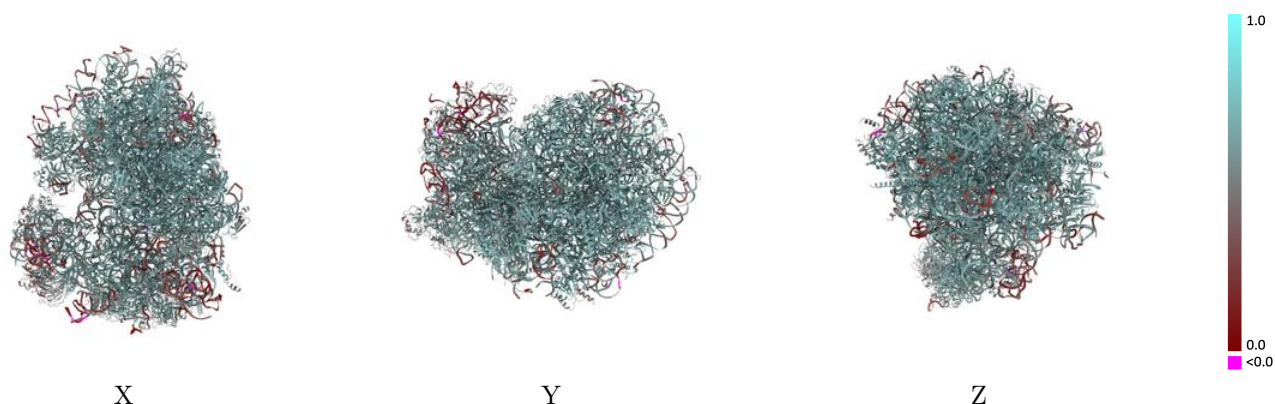
This section contains information regarding the fit between EMDB map EMD-62285 and PDB model 9KDT. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

### 9.1 Map-model overlay [i](#)



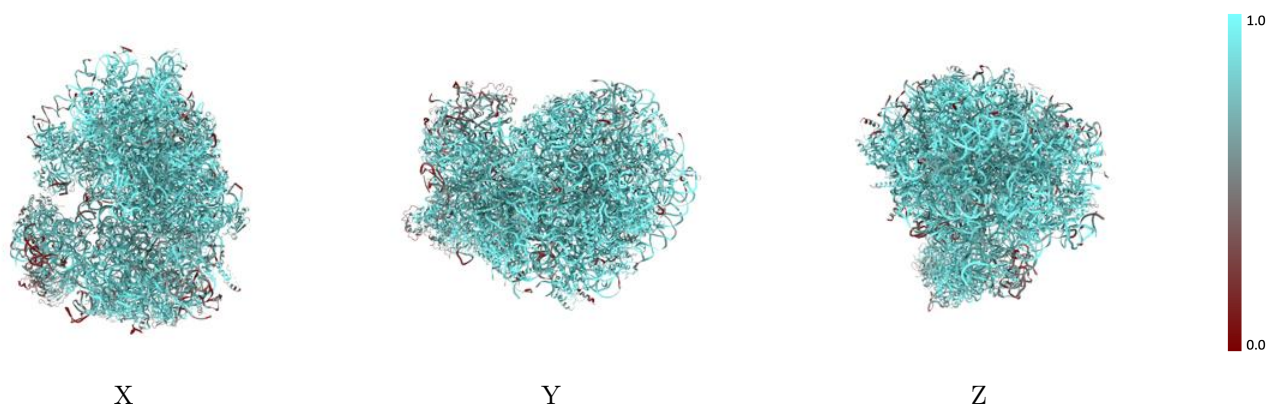
The images above show the 3D surface view of the map at the recommended contour level 0.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



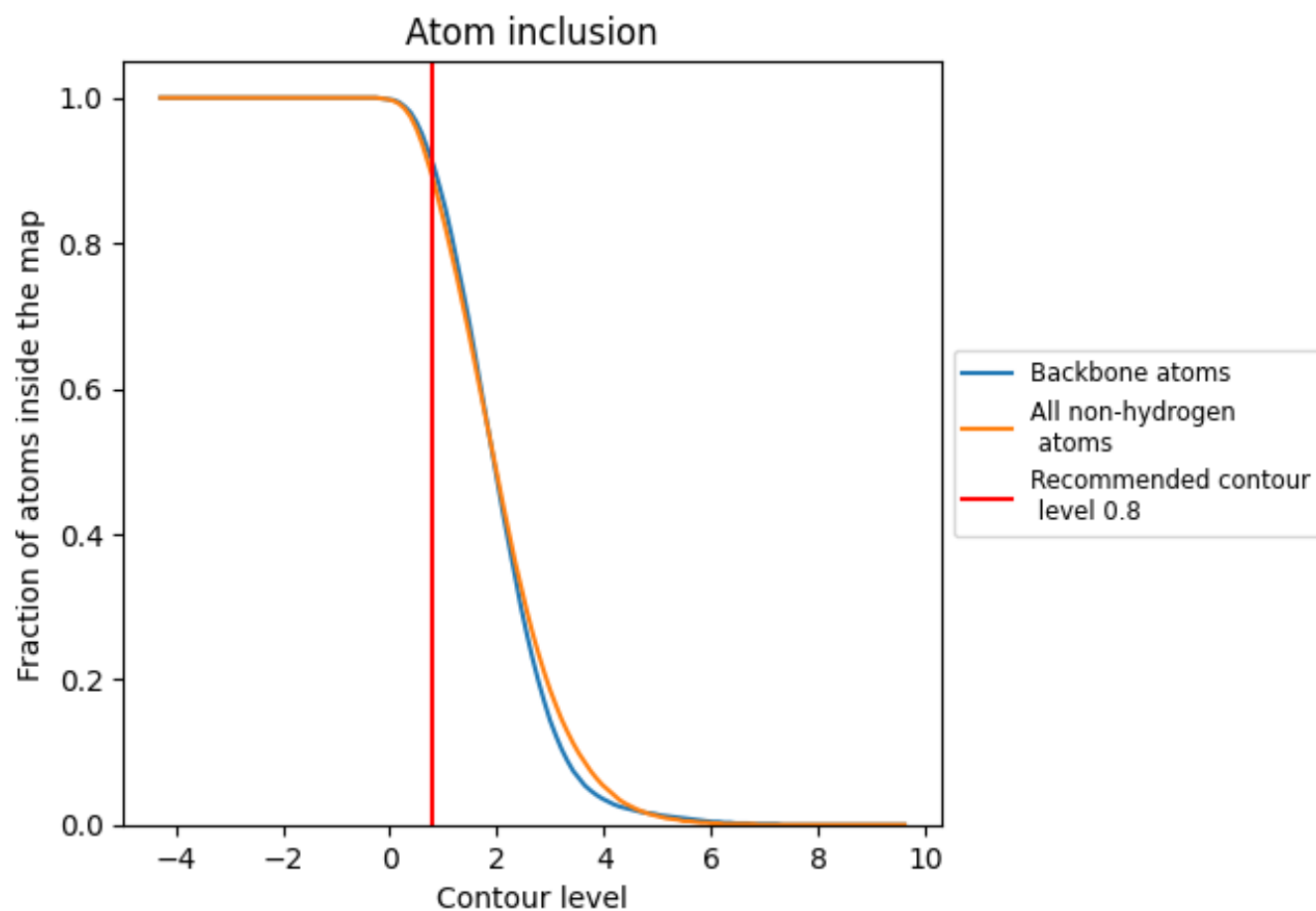
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.8).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 89% 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 (0.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8900	 0.5870
L5	 0.9350	 0.6010
L7	 0.9850	 0.6320
L8	 0.9570	 0.6200
LA	 0.9630	 0.6540
LB	 0.9260	 0.6360
LC	 0.9570	 0.6470
LD	 0.8890	 0.5990
LE	 0.9070	 0.6080
LF	 0.9670	 0.6540
LG	 0.8370	 0.5950
LH	 0.8910	 0.6110
LI	 0.8170	 0.5950
LJ	 0.8650	 0.5960
LL	 0.9110	 0.6300
LM	 0.9360	 0.6320
LN	 0.9870	 0.6690
LO	 0.9570	 0.6490
LP	 0.9490	 0.6480
LQ	 0.9730	 0.6660
LR	 0.9090	 0.6310
LS	 0.9570	 0.6490
LT	 0.9030	 0.6310
LU	 0.8140	 0.5640
LV	 0.9430	 0.6480
LW	 0.9400	 0.6400
LX	 0.9270	 0.6430
LY	 0.9240	 0.6310
LZ	 0.9280	 0.6350
La	 0.9650	 0.6620
Lb	 0.8730	 0.5950
Lc	 0.9400	 0.6350
Ld	 0.8870	 0.6150
Le	 0.9710	 0.6600
Lf	 0.9730	 0.6600













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Chain	Atom inclusion	Q-score
Lg	 0.9380	 0.6440
Lh	 0.9160	 0.6360
Li	 0.8920	 0.6210
Lj	 0.9760	 0.6600
Lk	 0.7970	 0.5870
Ll	 0.9720	 0.6510
Lm	 0.9380	 0.6310
Ln	 0.9310	 0.6480
Lo	 0.9290	 0.6390
Lp	 0.9200	 0.6420
Lr	 0.9720	 0.6540
S2	 0.8490	 0.5280
S6	 0.4630	 0.2770
S7	 0.8640	 0.5610
SA	 0.8780	 0.6040
SB	 0.8540	 0.6010
SC	 0.9060	 0.6160
SD	 0.7170	 0.5250
SE	 0.8800	 0.5820
SF	 0.8500	 0.5770
SG	 0.6310	 0.4860
SH	 0.6690	 0.5110
SI	 0.8960	 0.6000
SJ	 0.9000	 0.5850
SK	 0.5200	 0.4220
SL	 0.9310	 0.6370
SN	 0.9150	 0.6250
SO	 0.8900	 0.6140
SP	 0.6670	 0.4970
SQ	 0.8420	 0.5630
SR	 0.6850	 0.5170
SS	 0.7910	 0.5540
ST	 0.8240	 0.5550
SU	 0.6130	 0.4760
SV	 0.8340	 0.5770
SW	 0.9440	 0.6310
SX	 0.9050	 0.6150
SY	 0.7000	 0.4570
SZ	 0.7520	 0.5140
Sa	 0.9030	 0.6100
Sb	 0.7570	 0.5450
Sc	 0.7870	 0.5560

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Chain	Atom inclusion	Q-score
Sd	 0.7350	 0.5090
Se	 0.7700	 0.5480
Sg	 0.6290	 0.4660
Sx	 0.5890	 0.3720
Z	 0.3530	 0.3540