



wwPDB EM Validation Summary Report ⓘ

May 4, 2026 – 05:20 PM JST

PDB ID : 9KDW / pdb_00009kdw
EMDB ID : EMD-62288
Title : Cryo-EM structure of 80S ribosome
Authors : Lu, Y.; Wang, X.; Qin, Y.; Cao, Y.
Deposited on : 2024-11-04
Resolution : 2.67 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

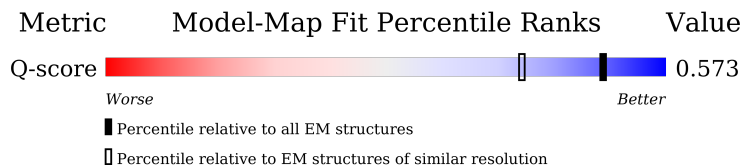
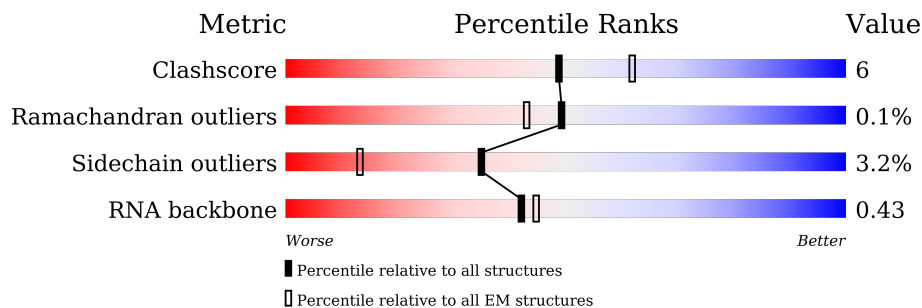
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.67 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.









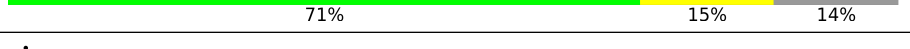
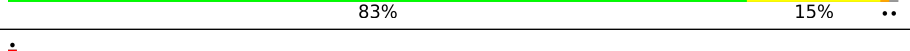
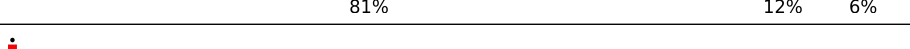
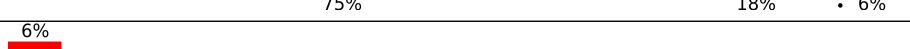


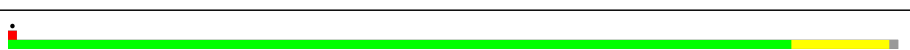

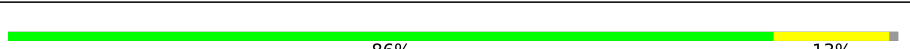






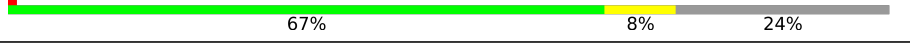



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	9182 (2.17 - 3.17)

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	







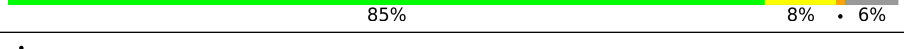
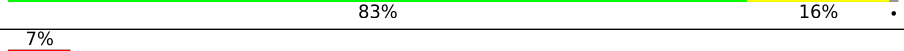
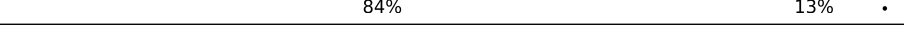
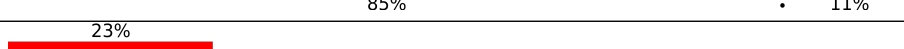
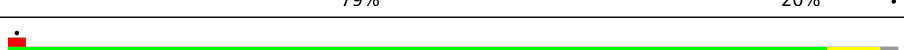
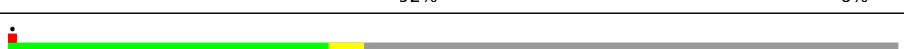
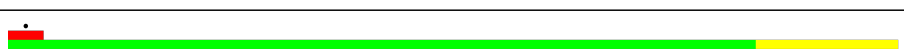



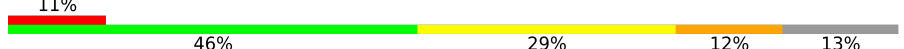

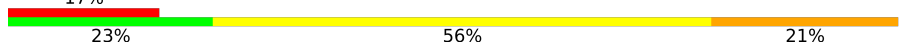

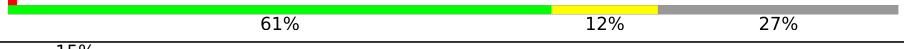



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Mol	Chain	Length	Quality of chain
4	LA	257	
5	LB	403	
6	LC	419	
7	LD	297	
8	LE	296	
9	LF	270	
10	LG	266	
11	LH	192	
12	LI	214	
13	LJ	178	
14	LL	211	
15	LM	217	
16	LN	204	
17	LO	203	
18	LP	184	
19	LQ	188	
20	LR	196	
21	LS	176	
22	LT	160	
23	LU	128	
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	

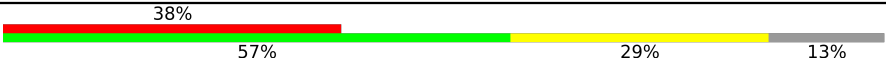
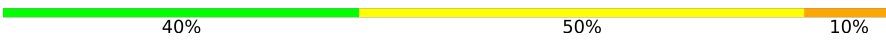
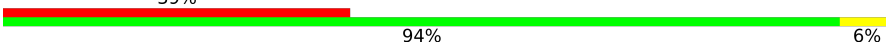
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Mol	Chain	Length	Quality of chain
53	SF	204	
54	SG	249	
55	SH	194	
56	SI	208	
57	SJ	194	
58	SK	165	
59	SL	158	
60	SN	151	
61	SO	151	
62	SP	145	
63	SQ	146	
64	SR	135	
65	SS	152	
66	ST	145	
67	SU	119	
68	SV	83	
69	SW	130	
70	SX	143	
71	SY	133	
72	SZ	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	18	

2 Entry composition

There are 82 unique types of molecules in this entry. The entry contains 204125 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, 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	83	Total	C	N	O	S	0	0
			651	408	121	115	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	18	Total	C	N	O	0	0
			89	53	18	18		

- 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	
82	Lm	1	Total	Zn	0
			1	1	

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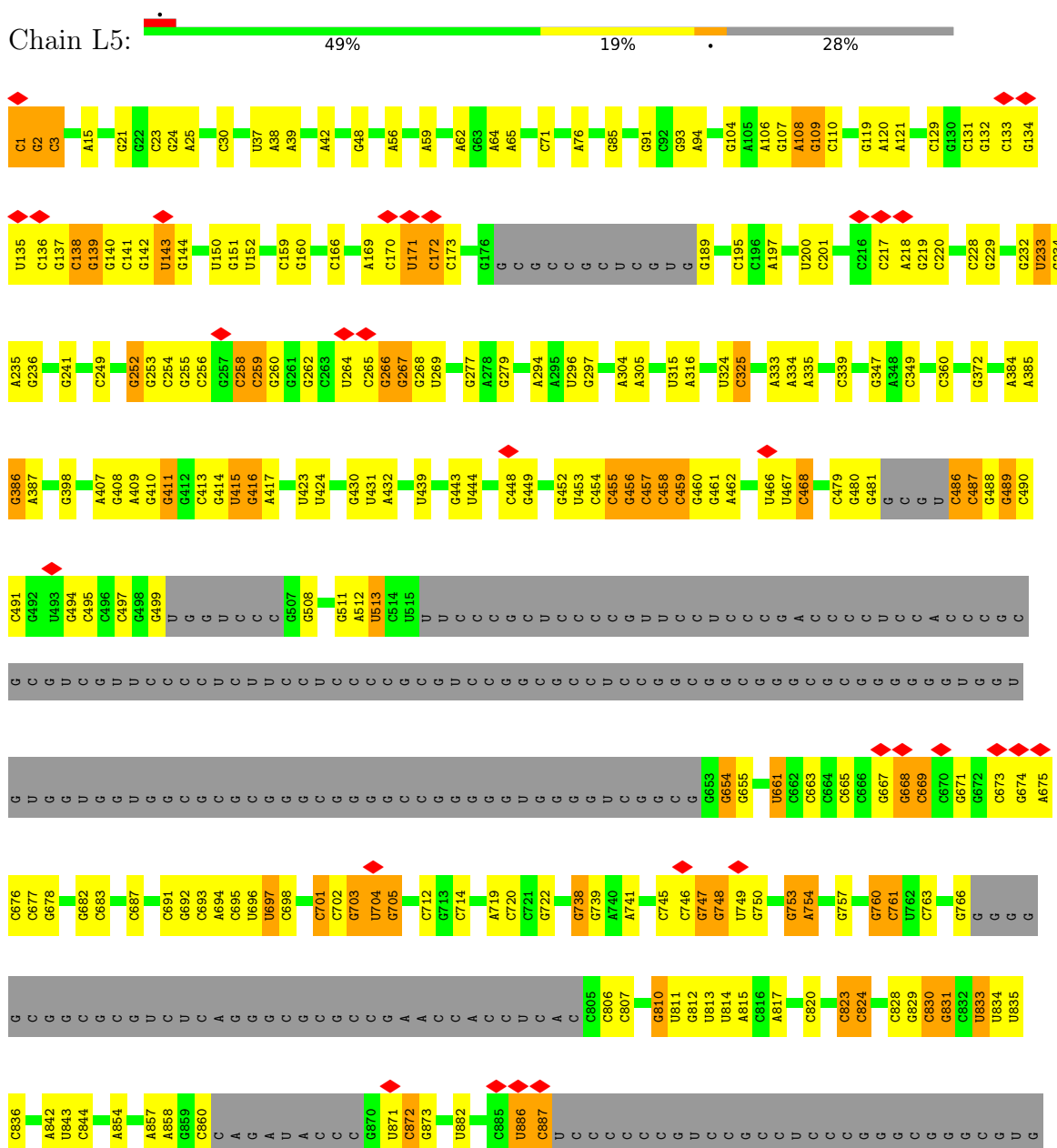
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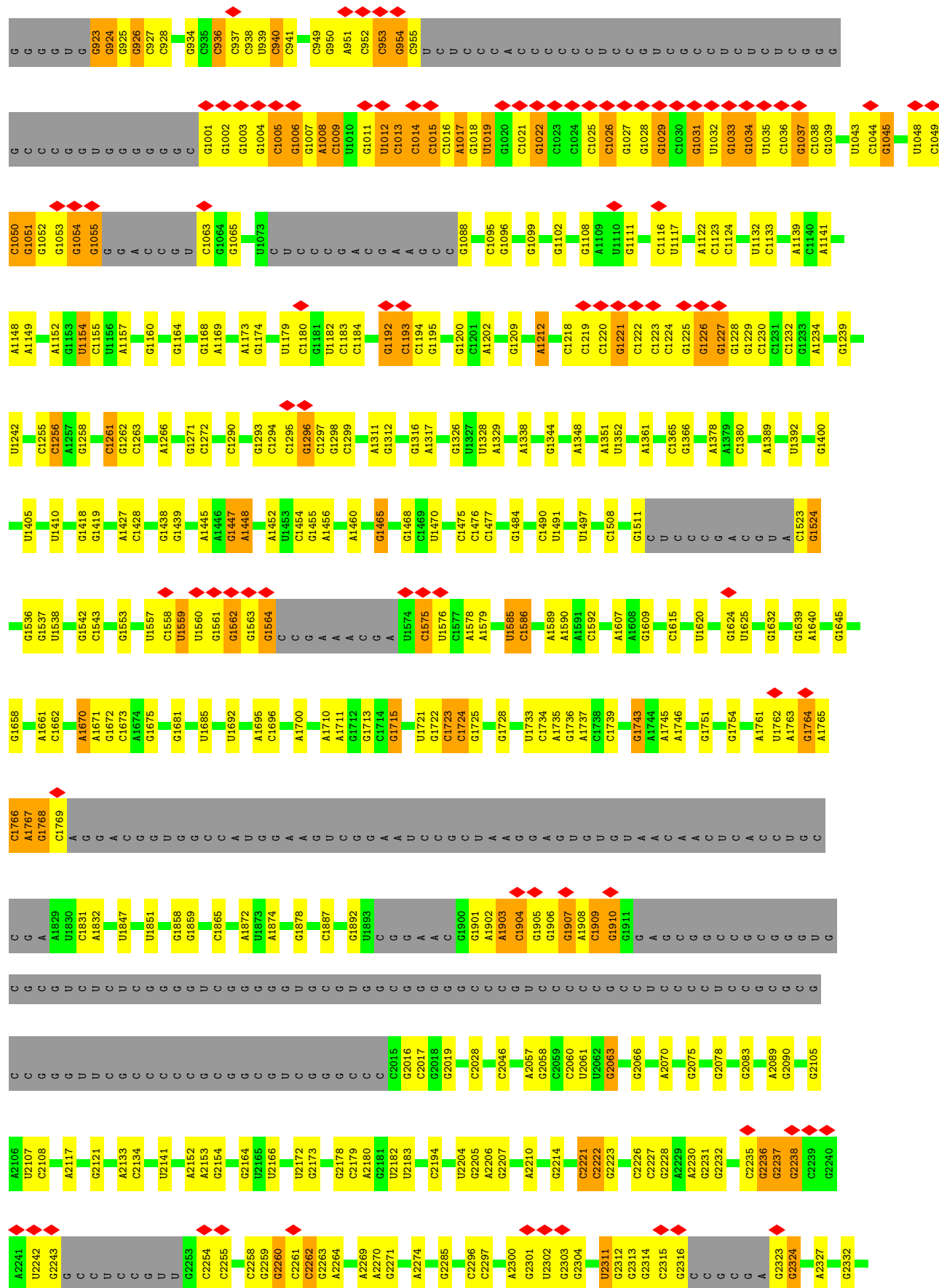
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
82	Lp	1	1	1	0

3 Residue-property plots

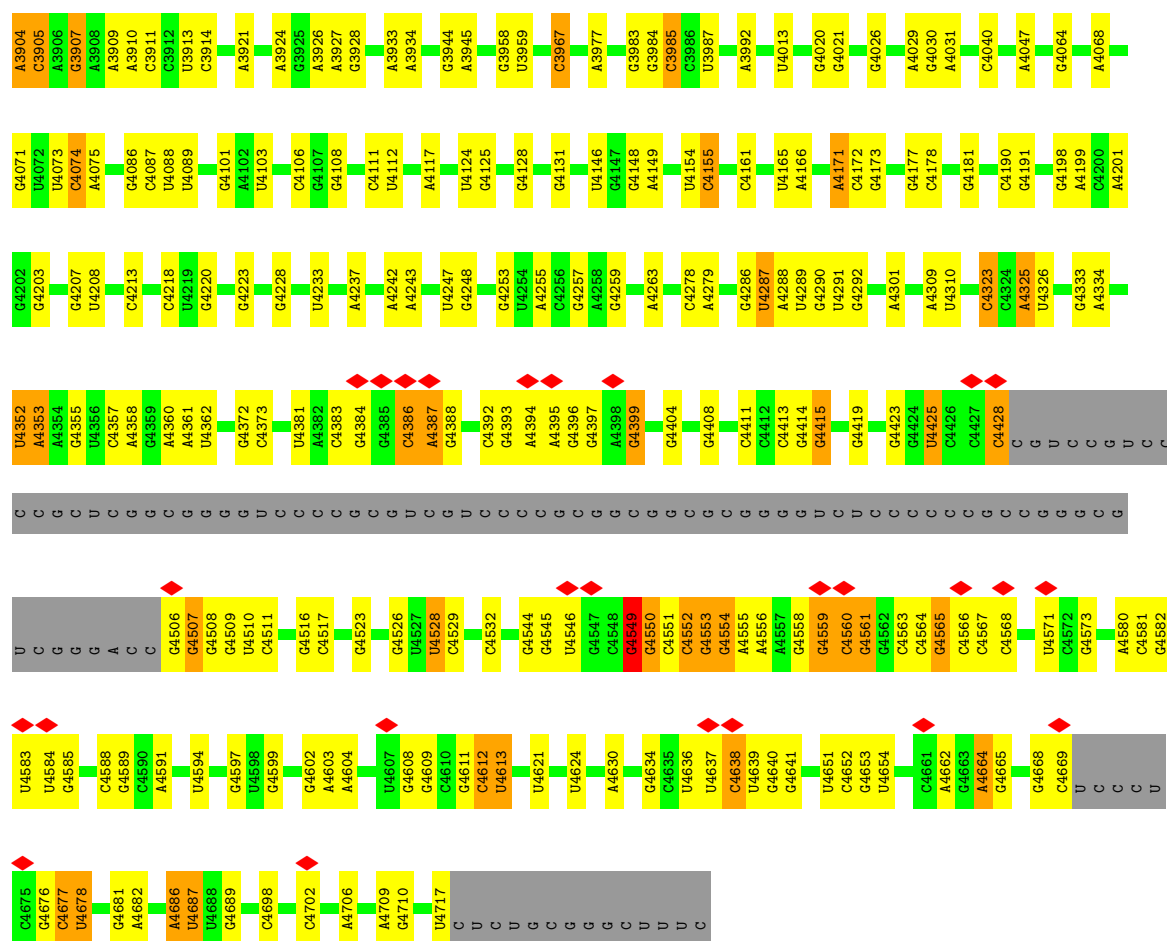
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

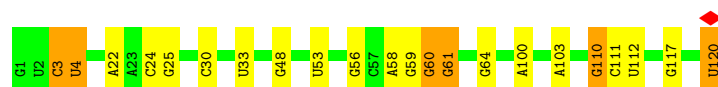
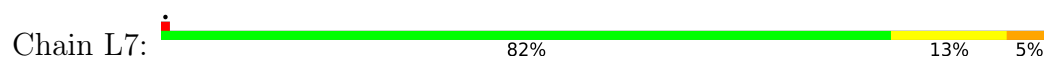




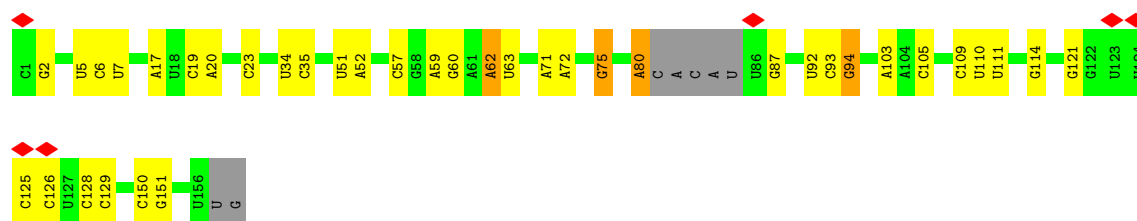




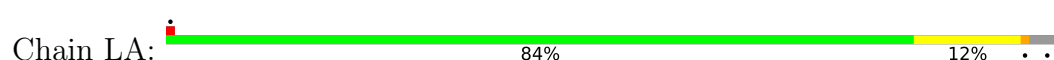
• Molecule 2: Mus musculus 5S ribosomal RNA



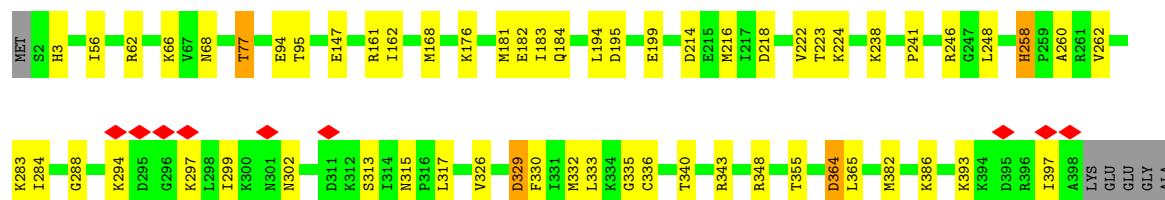
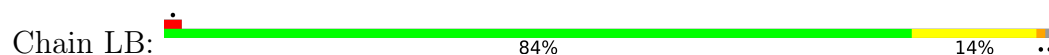
• Molecule 3: Mus musculus 5.8S ribosomal RNA



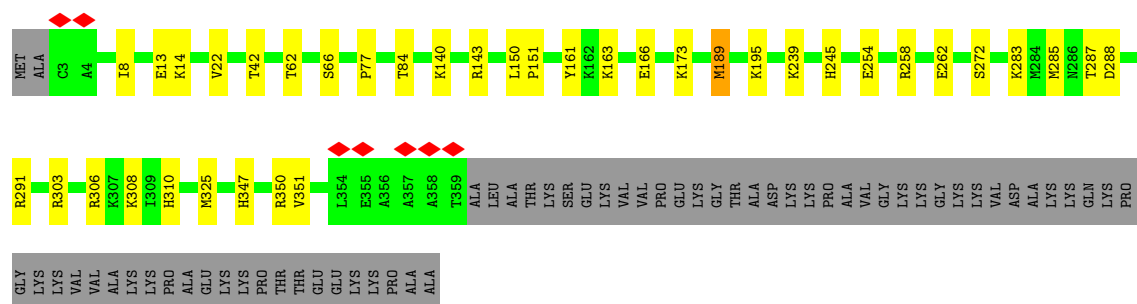
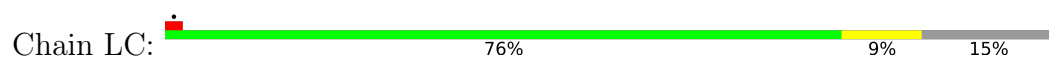
• Molecule 4: Large ribosomal subunit protein uL2



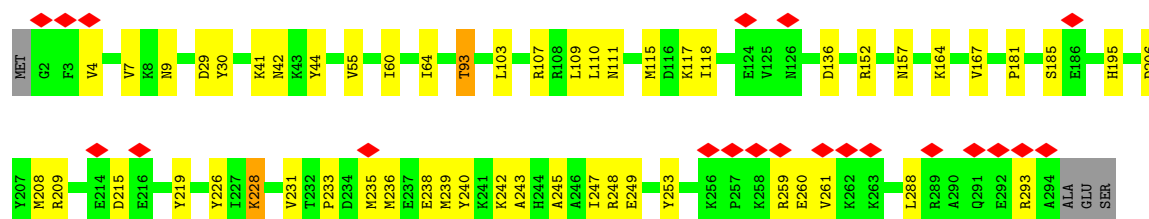
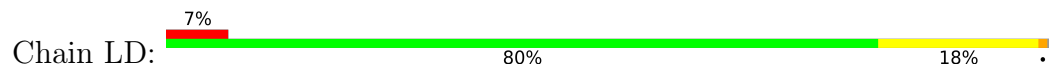
- Molecule 5: Large ribosomal subunit protein uL3



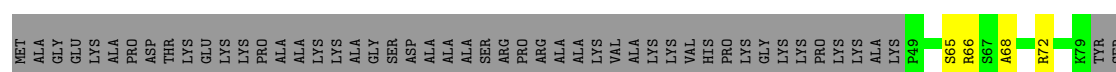
- Molecule 6: Large ribosomal subunit protein uL4

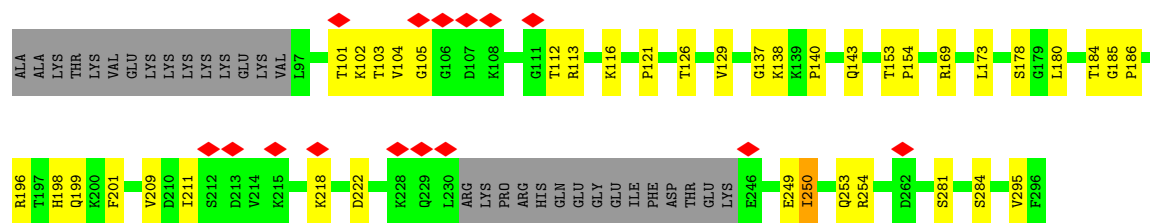


- Molecule 7: Large ribosomal subunit protein uL18



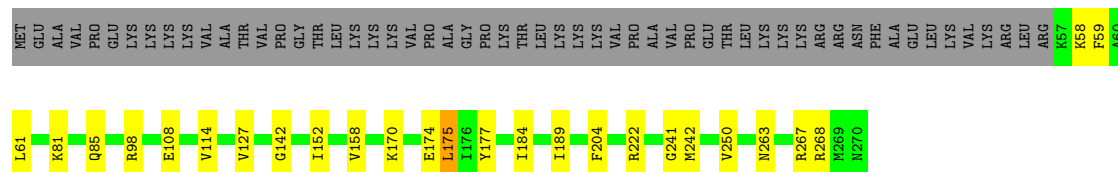
- Molecule 8: Large ribosomal subunit protein eL6





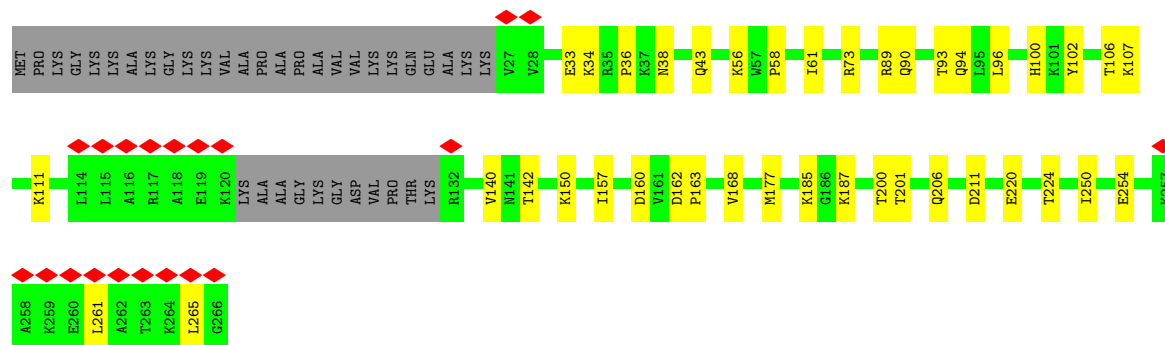
• Molecule 9: Large ribosomal subunit protein uL30

Chain LF: 70% 9% 21%



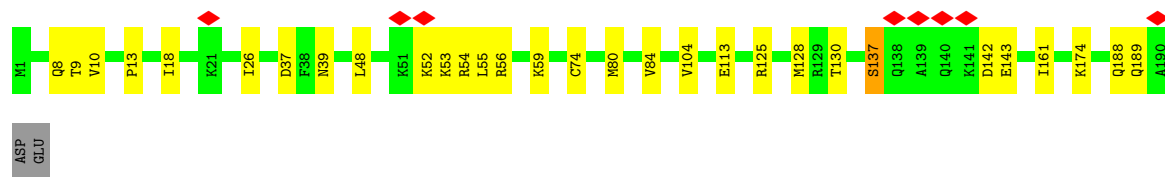
• Molecule 10: Large ribosomal subunit protein eL8

Chain LG: 8% 71% 15% 14%



• Molecule 11: Large ribosomal subunit protein uL6

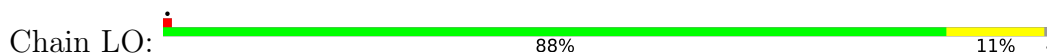
Chain LH: 83% 15% 2%



• Molecule 12: Large ribosomal subunit protein uL16-like

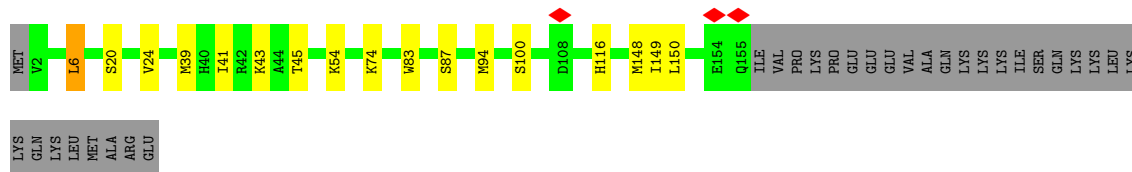
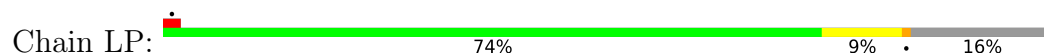
Chain LI: 81% 12% 6%



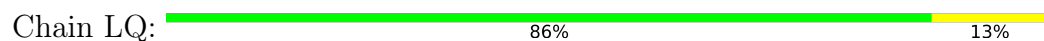




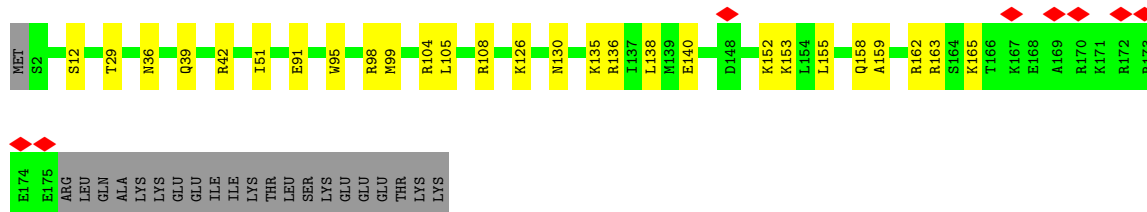
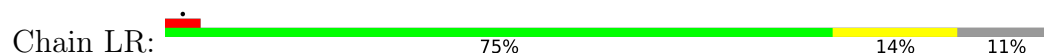
- Molecule 18: Large ribosomal subunit protein uL22



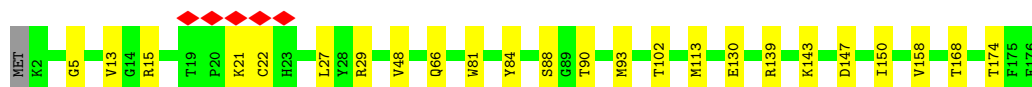
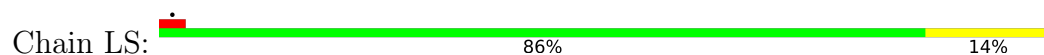
- Molecule 19: Large ribosomal subunit protein eL18



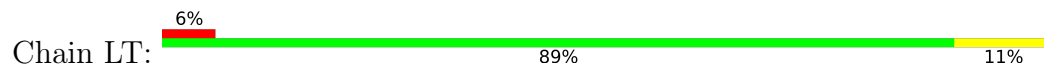
- Molecule 20: Large ribosomal subunit protein eL19



- Molecule 21: Large ribosomal subunit protein eL20

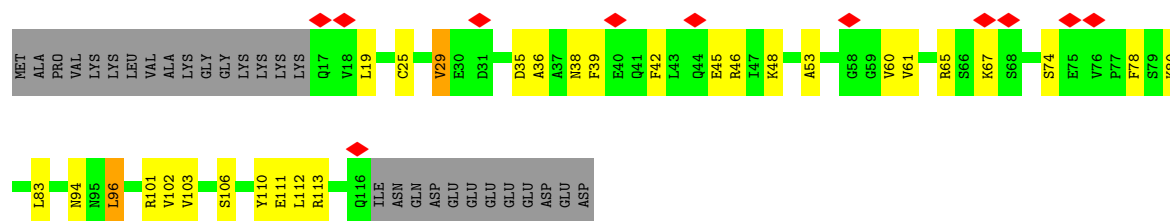


- Molecule 22: Large ribosomal subunit protein eL21



- Molecule 23: Large ribosomal subunit protein eL22





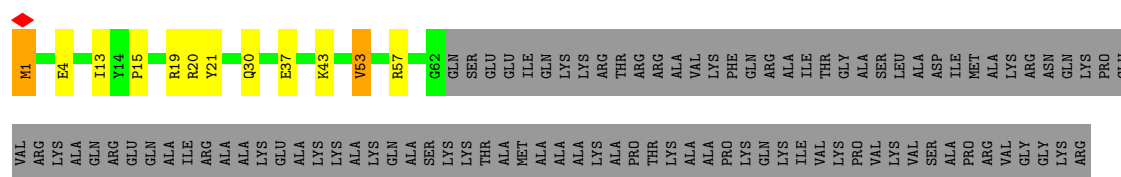
- Molecule 24: Large ribosomal subunit protein uL14

Chain LV: 82% 9% 7%



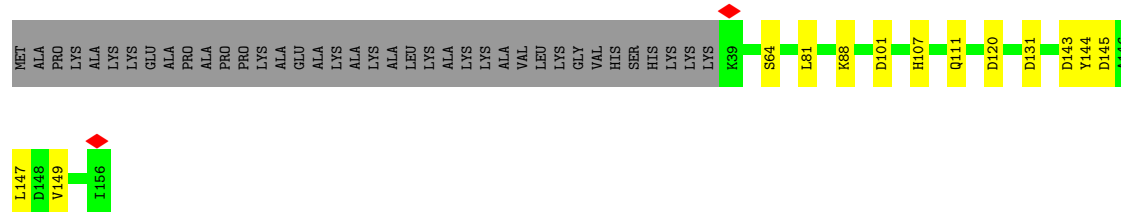
- Molecule 25: Large ribosomal subunit protein eL24

Chain LW: 32% 6% 61%



- Molecule 26: Large ribosomal subunit protein uL23

Chain LX: 67% 8% 24%



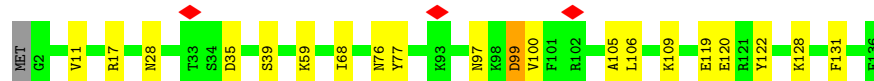
- Molecule 27: Large ribosomal subunit protein uL24

Chain LY: 80% 11% 9%




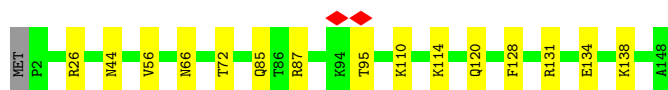
- Molecule 28: Large ribosomal subunit protein eL27

Chain LZ: 85% 14% ..



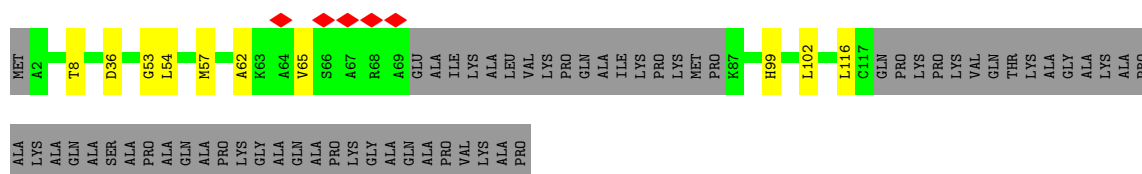
- Molecule 29: Large ribosomal subunit protein uL15

Chain La:  89% 10%



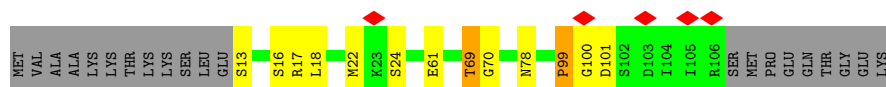
- Molecule 30: Large ribosomal subunit protein eL29

Chain Lb:  56% 6% 38%




- Molecule 31: Large ribosomal subunit protein eL30

Chain Lc:  70% 10% 18%




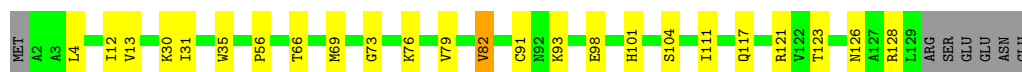
- Molecule 32: Large ribosomal subunit protein eL31

Chain Ld:  7% 77% 10% 14%




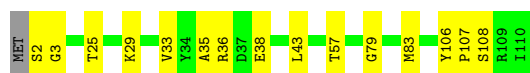
- Molecule 33: Large ribosomal subunit protein eL32

Chain Le:  77% 17% 5%




- Molecule 34: Large ribosomal subunit protein eL33

Chain Lf:  85% 14%

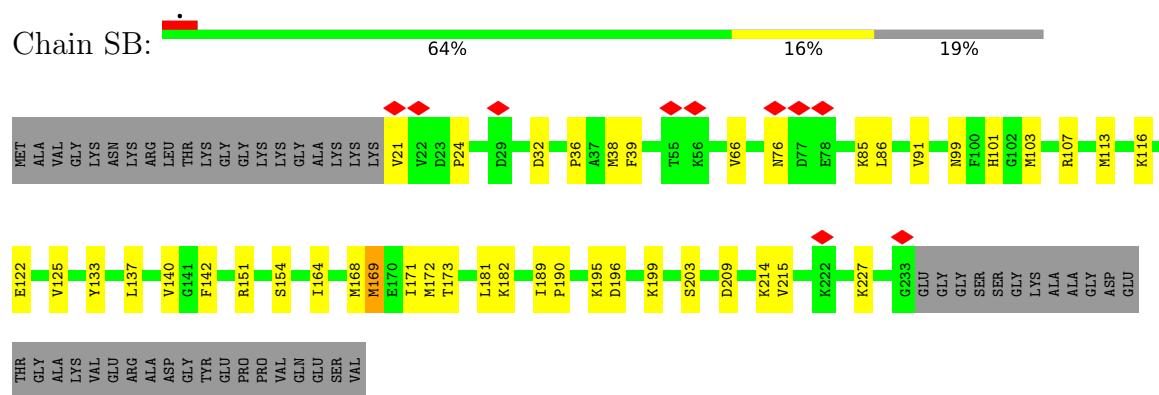


- Molecule 35: Large ribosomal subunit protein eL34

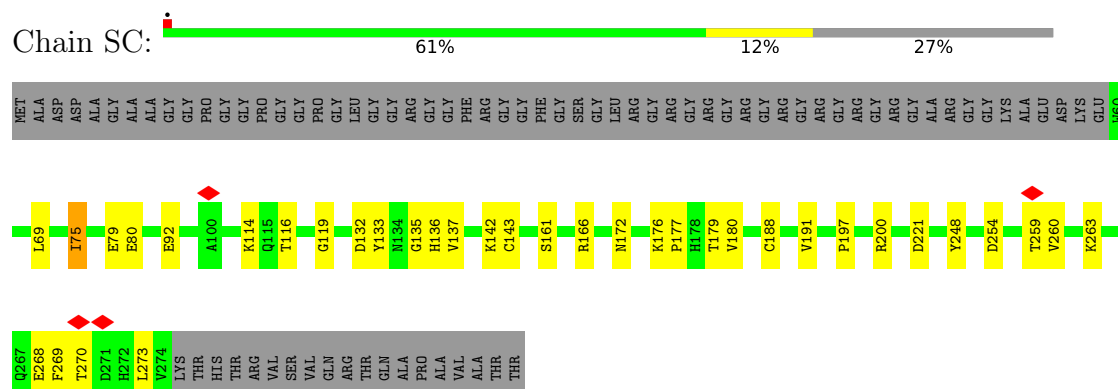
Chain Lg:  6% 85% 8% 6%

- [illegible]

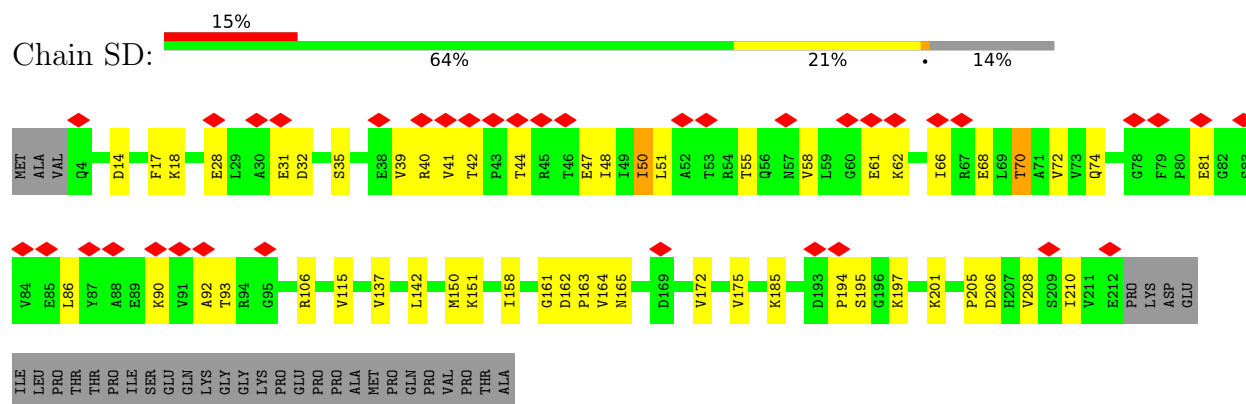




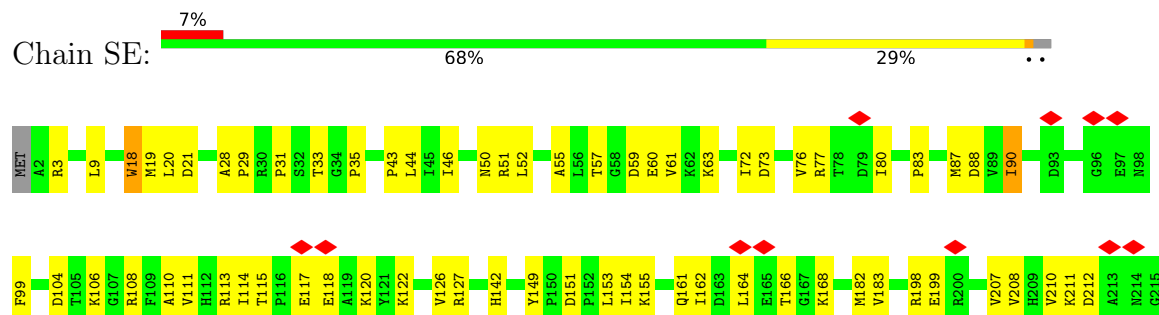
- Molecule 50: Small ribosomal subunit protein uS5

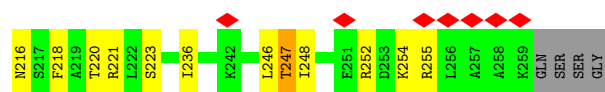


- Molecule 51: Small ribosomal subunit protein uS3

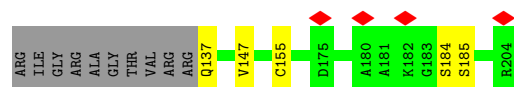
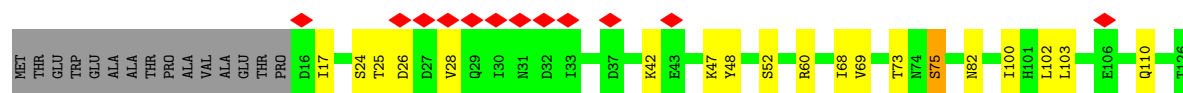
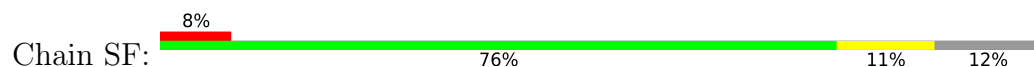


- Molecule 52: Small ribosomal subunit protein eS4

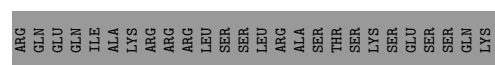
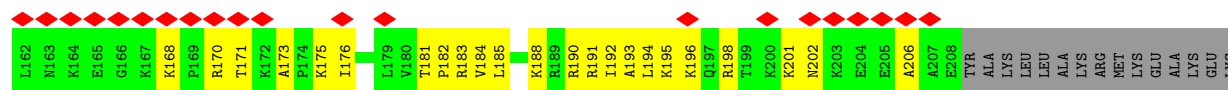
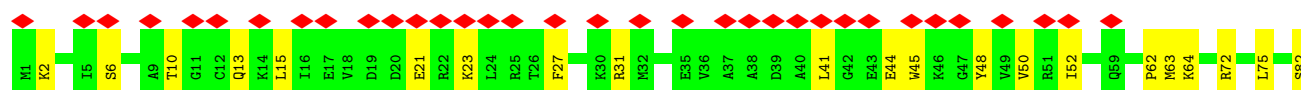




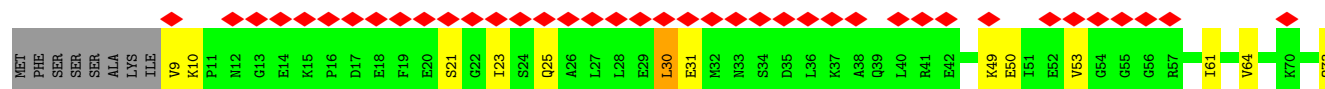
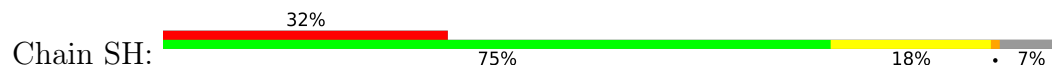
- Molecule 53: Small ribosomal subunit protein uS7



- Molecule 54: Small ribosomal subunit protein eS6



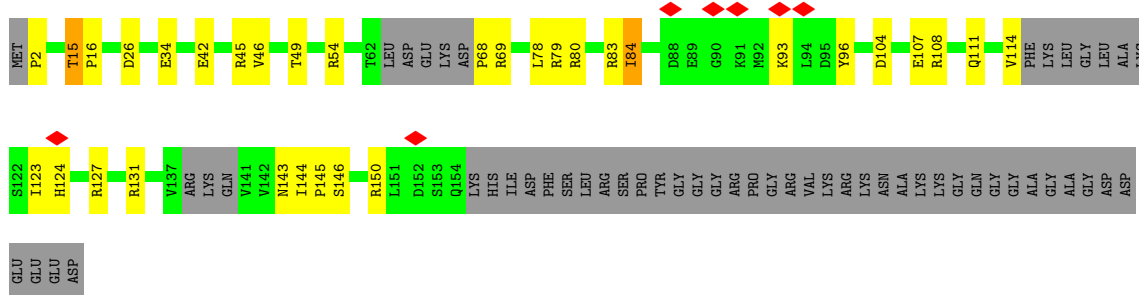
- Molecule 55: Small ribosomal subunit protein eS7



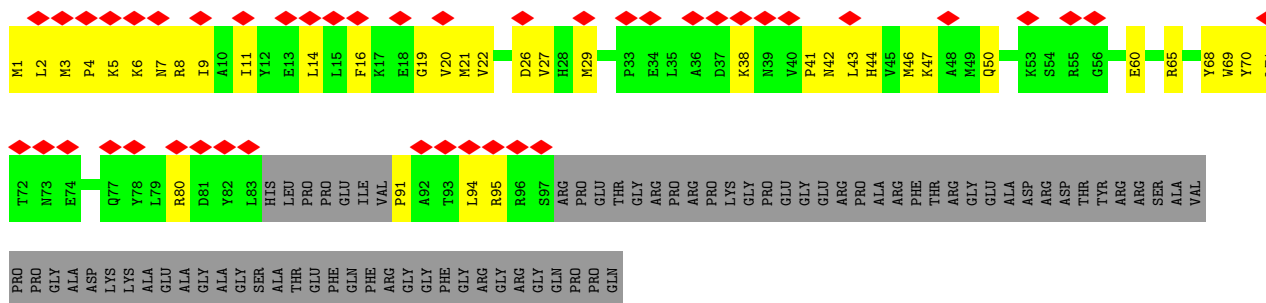
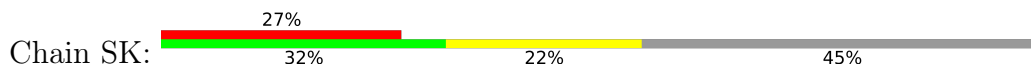
- Molecule 56: Small ribosomal subunit protein eS8



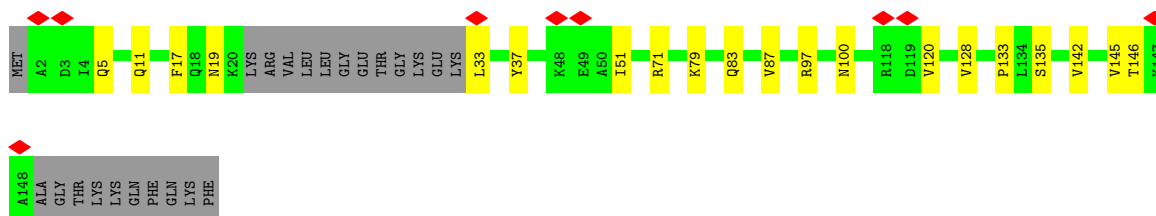
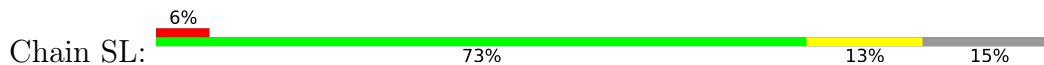
- Molecule 57: Small ribosomal subunit protein uS4



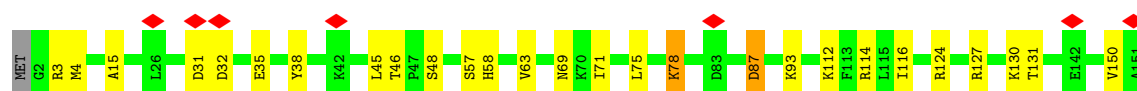
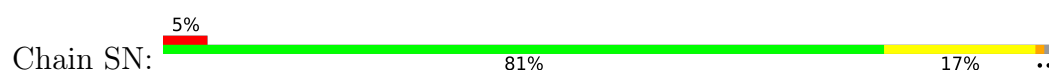
- Molecule 58: Small ribosomal subunit protein eS10



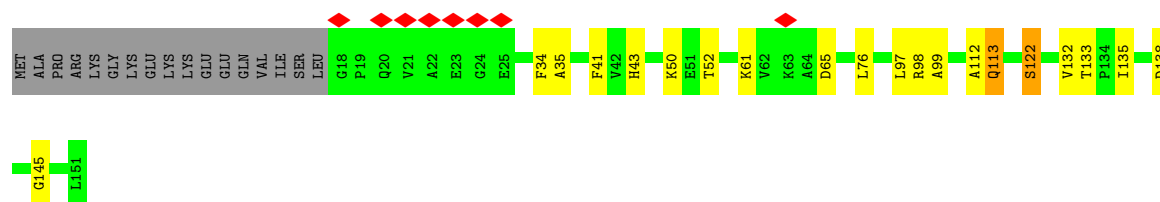
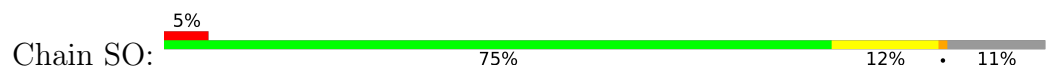
- Molecule 59: Small ribosomal subunit protein uS17



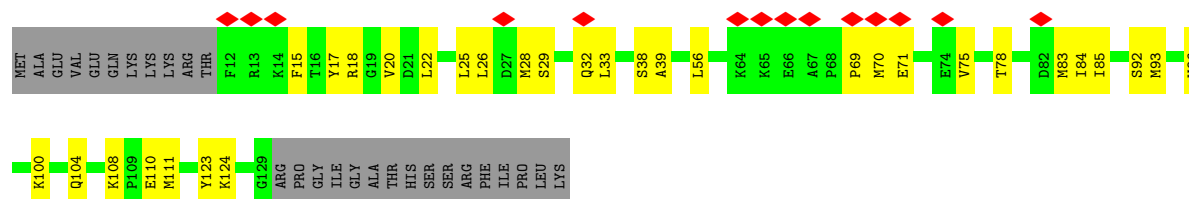
- Molecule 60: Small ribosomal subunit protein uS15



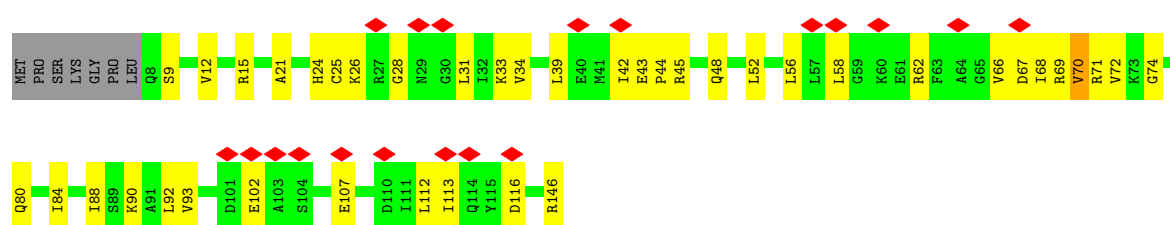
- Molecule 61: Small ribosomal subunit protein uS11



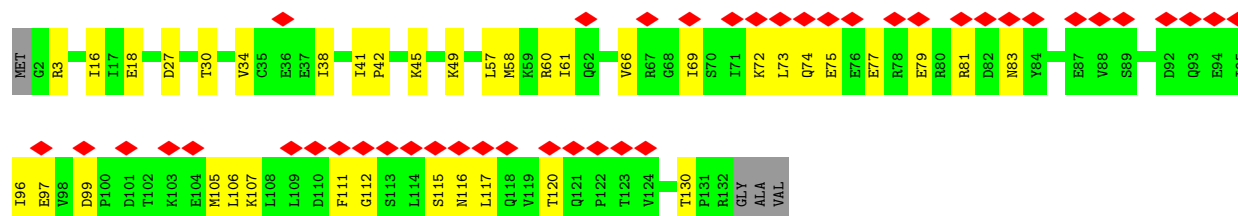
- Molecule 62: Small ribosomal subunit protein uS19



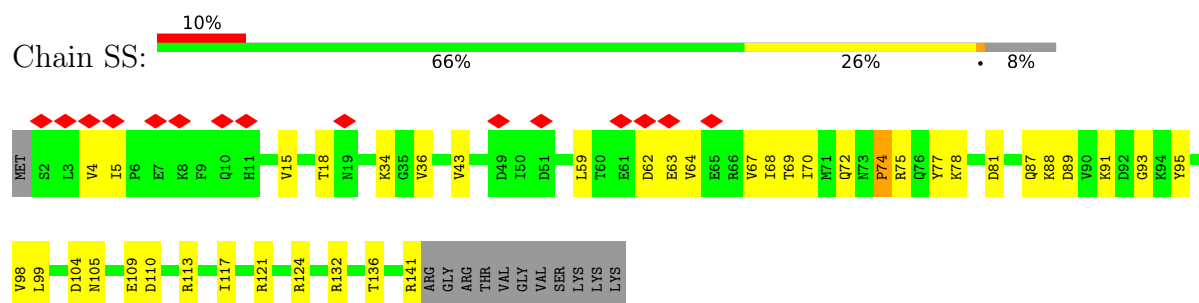
- Molecule 63: Small ribosomal subunit protein uS9



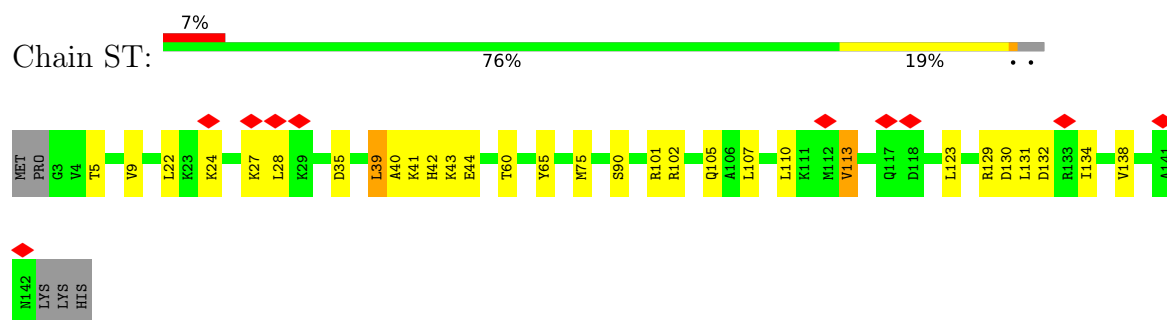
- Molecule 64: Small ribosomal subunit protein eS17



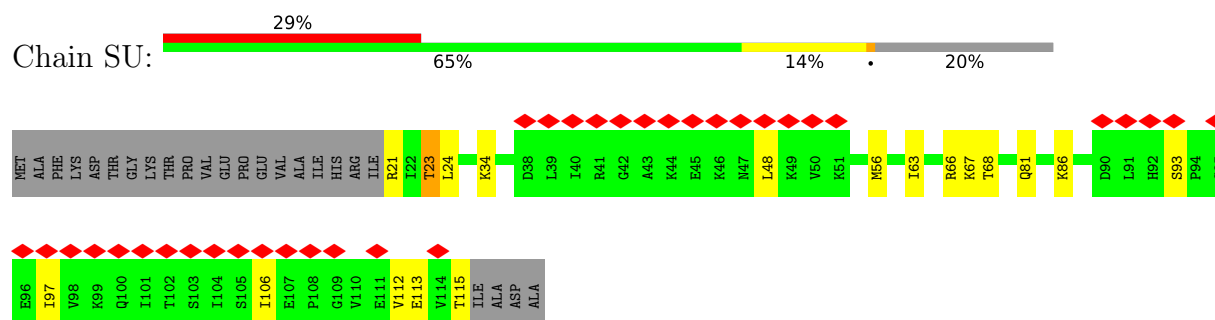
- Molecule 65: Small ribosomal subunit protein uS13



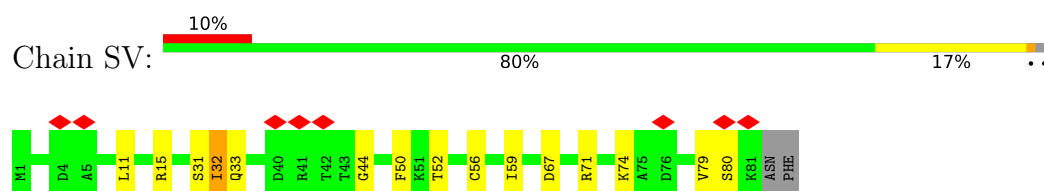
- Molecule 66: Small ribosomal subunit protein eS19



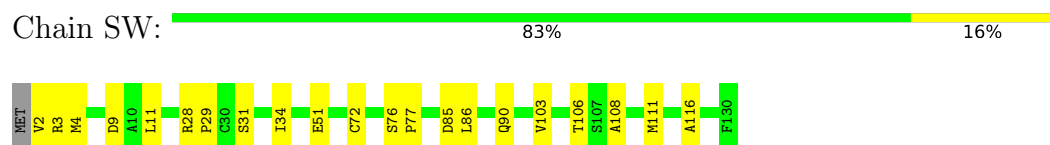
- Molecule 67: Small ribosomal subunit protein uS10



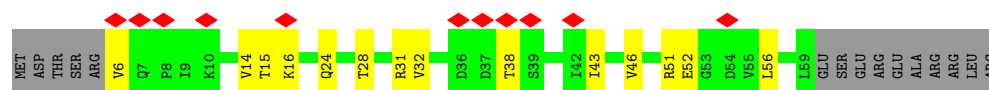
- Molecule 68: Small ribosomal subunit protein eS21



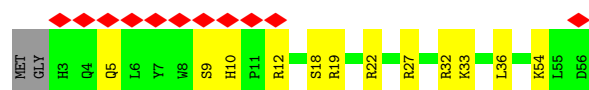
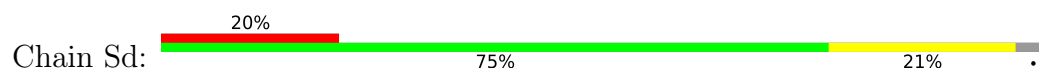
- Molecule 69: Small ribosomal subunit protein uS8



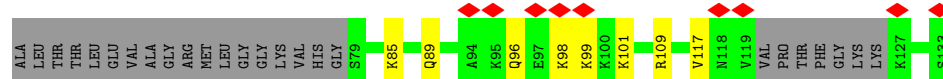
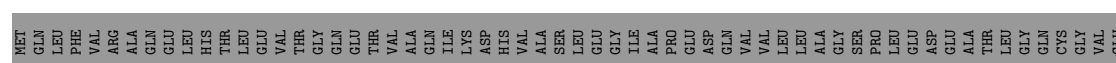
- Molecule 70: Small ribosomal subunit protein uS12



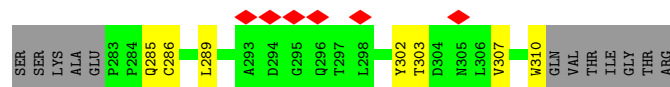
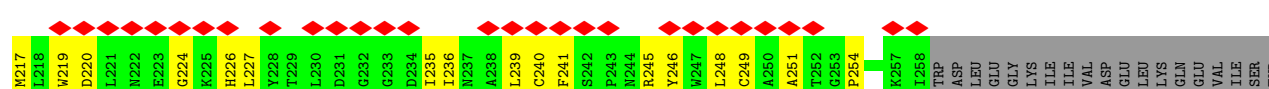
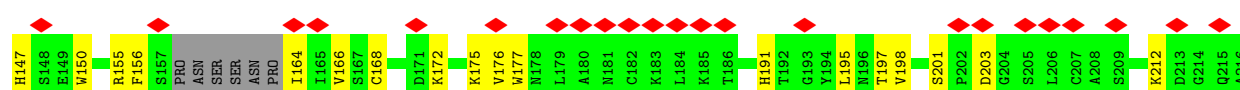
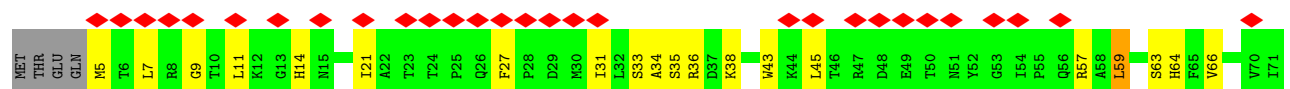
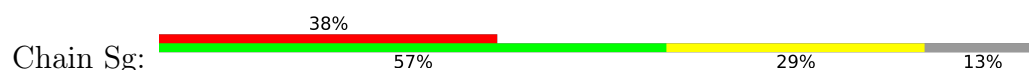
- Molecule 76: Small ribosomal subunit protein uS14



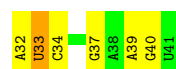
- Molecule 77: Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein



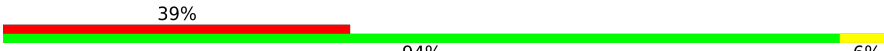
- Molecule 78: Small ribosomal subunit protein RACK1

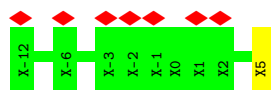


- Molecule 79: RNA (5'-R(P*AP*UP*CP*AP*UP*GP*AP*AP*GP*U)-3')



- Molecule 80: Nascent peptide

Chain Z:  39% 94% 6%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	97838	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	4.233	Depositor
Minimum map value	-2.071	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.102	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: ZN, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	L5	0.25	0/81527	0.36	1/127149 (0.0%)
2	L7	0.23	0/2858	0.38	2/4455 (0.0%)
3	L8	0.24	0/3584	0.34	0/5582
4	LA	0.24	0/1936	0.47	0/2596
5	LB	0.22	0/3269	0.45	0/4375
6	LC	0.24	0/2911	0.45	0/3907
7	LD	0.23	0/2435	0.46	1/3260 (0.0%)
8	LE	0.21	0/1775	0.46	0/2381
9	LF	0.24	0/1805	0.40	0/2408
10	LG	0.21	0/1880	0.45	0/2531
11	LH	0.20	0/1537	0.44	0/2065
12	LI	0.19	0/1669	0.40	0/2227
13	LJ	0.28	1/1363 (0.1%)	0.61	3/1824 (0.2%)
14	LL	0.22	0/1698	0.44	0/2274
15	LM	0.23	0/1146	0.44	0/1531
16	LN	0.25	0/1746	0.45	0/2338
17	LO	0.23	0/1670	0.45	0/2232
18	LP	0.23	0/1277	0.42	0/1712
19	LQ	0.24	0/1539	0.44	0/2053
20	LR	0.21	0/1473	0.39	0/1947
21	LS	0.22	0/1491	0.42	0/2000
22	LT	0.21	0/1335	0.40	0/1781
23	LU	0.20	0/831	0.49	0/1115
24	LV	0.20	0/987	0.39	0/1324
25	LW	0.22	0/532	0.42	0/708
26	LX	0.20	0/984	0.41	0/1323
27	LY	0.21	0/1119	0.41	0/1488
28	LZ	0.20	0/1130	0.41	1/1507 (0.1%)
29	La	0.24	0/1193	0.39	0/1593
30	Lb	0.21	0/821	0.46	0/1082
31	Lc	0.21	0/742	0.41	0/996
32	Ld	0.22	0/911	0.40	0/1227

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.23	0/1071	0.37	0/1429
34	Lf	0.24	0/895	0.42	0/1198
35	Lg	0.21	0/883	0.42	0/1178
36	Lh	0.22	0/1023	0.42	0/1350
37	Li	0.20	0/843	0.46	0/1115
38	Lj	0.25	0/720	0.42	0/952
39	Lk	0.20	0/574	0.43	0/760
40	Ll	0.24	0/448	0.34	0/592
41	Lm	0.20	0/425	0.39	0/564
42	Ln	0.23	0/240	0.40	0/305
43	Lo	0.30	0/855	0.58	1/1128 (0.1%)
44	Lp	0.22	0/718	0.44	0/953
45	Lr	0.22	0/1009	0.41	0/1353
46	S2	0.20	0/38859	0.34	0/60556
47	S6	0.16	0/1795	0.30	0/2798
47	S7	0.14	0/1795	0.33	0/2798
48	SA	0.20	0/1673	0.43	0/2275
49	SB	0.20	0/1756	0.45	1/2350 (0.0%)
50	SC	0.20	0/1701	0.41	0/2300
51	SD	0.19	0/1651	0.44	0/2219
52	SE	0.18	0/2092	0.48	0/2816
53	SF	0.18	0/1436	0.41	0/1930
54	SG	0.17	0/1666	0.42	0/2222
55	SH	0.19	0/1470	0.48	0/1968
56	SI	0.20	0/1526	0.42	0/2038
57	SJ	0.19	0/1178	0.47	0/1574
58	SK	0.19	0/780	0.47	0/1046
59	SL	0.19	0/1130	0.43	0/1514
60	SN	0.20	0/1232	0.39	0/1656
61	SO	0.21	0/1015	0.47	0/1361
62	SP	0.18	0/1000	0.37	0/1335
63	SQ	0.19	0/1126	0.45	0/1506
64	SR	0.19	0/1078	0.45	0/1447
65	SS	0.21	0/1175	0.46	2/1575 (0.1%)
66	ST	0.19	0/1108	0.42	0/1486
67	SU	0.20	0/762	0.43	0/1023
68	SV	0.17	0/625	0.35	0/836
69	SW	0.20	0/1051	0.39	0/1406
70	SX	0.20	0/1097	0.50	0/1464
71	SY	0.20	0/907	0.55	0/1204
72	SZ	0.18	0/580	0.51	0/780
73	Sa	0.25	0/805	0.45	0/1079
74	Sb	0.19	0/665	0.43	0/891

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	Sc	0.20	0/418	0.44	0/562
76	Sd	0.18	0/466	0.40	0/618
77	Se	0.19	0/386	0.44	0/504
78	Sg	0.18	0/2199	0.48	0/2989
79	Sx	0.21	0/239	0.34	0/370
All	All	0.23	1/219320 (0.0%)	0.39	12/322364 (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
8	LE	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	LJ	176	PRO	CG-CD	-7.10	1.26	1.50

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	LJ	176	PRO	N-CD-CG	-12.51	84.43	103.20
43	Lo	75	PRO	CA-N-CD	-11.21	96.31	112.00
13	LJ	176	PRO	CA-N-CD	-9.78	98.30	112.00
2	L7	48	G	OP1-P-O3'	-9.29	80.14	108.00
7	LD	233	PRO	CA-N-CD	-7.93	100.90	112.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	LE	137	GLY	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	36804	388	0
2	L7	2558	0	1296	10	0
3	L8	3210	0	1630	9	0
4	LA	1898	0	1993	16	0
5	LB	3202	0	3347	37	0
6	LC	2857	0	3030	21	0
7	LD	2389	0	2420	39	0
8	LE	1743	0	1880	27	0
9	LF	1771	0	1886	15	0
10	LG	1848	0	1981	24	0
11	LH	1519	0	1603	14	0
12	LI	1631	0	1682	14	0
13	LJ	1340	0	1377	17	0
14	LL	1667	0	1771	20	0
15	LM	1125	0	1202	20	0
16	LN	1701	0	1749	17	0
17	LO	1640	0	1792	17	0
18	LP	1251	0	1282	8	0
19	LQ	1515	0	1639	16	0
20	LR	1457	0	1601	13	0
21	LS	1451	0	1488	14	0
22	LT	1307	0	1380	13	0
23	LU	817	0	839	19	0
24	LV	973	0	1034	13	0
25	LW	519	0	533	9	0
26	LX	967	0	1040	6	0
27	LY	1102	0	1189	12	0
28	LZ	1107	0	1182	12	0
29	La	1164	0	1213	10	0
30	Lb	807	0	875	4	0
31	Lc	732	0	769	6	0
32	Ld	896	0	941	5	0
33	Le	1053	0	1147	15	0
34	Lf	876	0	912	10	0
35	Lg	873	0	961	7	0
36	Lh	1015	0	1156	14	0
37	Li	832	0	917	11	0
38	Lj	705	0	737	3	0
39	Lk	568	0	635	9	0
40	Ll	438	0	474	2	0
41	Lm	419	0	452	3	0
42	Ln	239	0	289	4	0
43	Lo	842	0	916	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	Lp	708	0	756	6	0
45	Lr	994	0	1057	10	0
46	S2	34749	0	17548	472	0
47	S6	1604	0	816	17	0
47	S7	1604	0	816	29	0
48	SA	1636	0	1641	30	0
49	SB	1729	0	1803	25	0
50	SC	1665	0	1753	20	0
51	SD	1626	0	1714	37	0
52	SE	2050	0	2156	50	0
53	SF	1416	0	1458	13	0
54	SG	1645	0	1780	54	0
55	SH	1449	0	1539	23	0
56	SI	1499	0	1561	35	0
57	SJ	1162	0	1252	26	0
58	SK	760	0	783	30	0
59	SL	1110	0	1165	15	0
60	SN	1208	0	1294	14	0
61	SO	1002	0	1023	15	0
62	SP	981	0	1026	22	0
63	SQ	1109	0	1174	34	0
64	SR	1064	0	1118	25	0
65	SS	1157	0	1213	27	0
66	ST	1090	0	1116	18	0
67	SU	753	0	815	8	0
68	SV	619	0	620	12	0
69	SW	1034	0	1080	15	0
70	SX	1080	0	1147	22	0
71	SY	891	0	948	37	0
72	SZ	574	0	627	17	0
73	Sa	792	0	845	13	0
74	Sb	651	0	672	13	0
75	Sc	416	0	445	8	0
76	Sd	455	0	449	9	0
77	Se	384	0	422	11	0
78	Sg	2148	0	2108	67	0
79	Sx	214	0	108	6	0
80	Z	89	0	26	1	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
82	Lj	1	0	0	0	0
82	Lm	1	0	0	0	0
82	Lp	1	0	0	0	0
All	All	204125	0	150918	2005	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 6.

The worst 5 of 2005 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)
47:S7:76:A:O3'	80:Z:5:UNK:C	2.06	1.03
46:S2:160:U:H3	46:S2:469:A:HO2'	1.10	0.96
46:S2:516:G:H5''	46:S2:517:A:H5'	1.53	0.91
46:S2:889:U:H4'	46:S2:890:U:H5'	1.55	0.89
46:S2:1506:U:H4'	46:S2:1509:A:H1'	1.53	0.88

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%)	228 (93%)	18 (7%)	0	100	100
5	LB	395/403 (98%)	370 (94%)	25 (6%)	0	100	100
6	LC	355/419 (85%)	337 (95%)	18 (5%)	0	100	100
7	LD	291/297 (98%)	268 (92%)	23 (8%)	0	100	100
8	LE	210/296 (71%)	197 (94%)	13 (6%)	0	100	100
9	LF	212/270 (78%)	201 (95%)	11 (5%)	0	100	100
10	LG	225/266 (85%)	217 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	LH	188/192 (98%)	175 (93%)	10 (5%)	3 (2%)	7	18
12	LI	197/214 (92%)	194 (98%)	3 (2%)	0	100	100
13	LJ	165/178 (93%)	159 (96%)	5 (3%)	1 (1%)	21	41
14	LL	204/211 (97%)	193 (95%)	11 (5%)	0	100	100
15	LM	134/217 (62%)	125 (93%)	9 (7%)	0	100	100
16	LN	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
17	LO	199/203 (98%)	189 (95%)	10 (5%)	0	100	100
18	LP	152/184 (83%)	148 (97%)	4 (3%)	0	100	100
19	LQ	185/188 (98%)	181 (98%)	4 (2%)	0	100	100
20	LR	172/196 (88%)	170 (99%)	2 (1%)	0	100	100
21	LS	173/176 (98%)	168 (97%)	5 (3%)	0	100	100
22	LT	158/160 (99%)	154 (98%)	4 (2%)	0	100	100
23	LU	98/128 (77%)	85 (87%)	13 (13%)	0	100	100
24	LV	128/140 (91%)	124 (97%)	4 (3%)	0	100	100
25	LW	60/157 (38%)	59 (98%)	1 (2%)	0	100	100
26	LX	116/156 (74%)	115 (99%)	1 (1%)	0	100	100
27	LY	130/145 (90%)	130 (100%)	0	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	26
32	Ld	106/125 (85%)	102 (96%)	4 (4%)	0	100	100
33	Le	126/135 (93%)	117 (93%)	9 (7%)	0	100	100
34	Lf	107/110 (97%)	103 (96%)	4 (4%)	0	100	100
35	Lg	108/117 (92%)	107 (99%)	1 (1%)	0	100	100
36	Lh	120/123 (98%)	119 (99%)	1 (1%)	0	100	100
37	Li	100/105 (95%)	91 (91%)	9 (9%)	0	100	100
38	Lj	84/97 (87%)	80 (95%)	4 (5%)	0	100	100
39	Lk	67/70 (96%)	64 (96%)	3 (4%)	0	100	100
40	Ll	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
41	Lm	49/128 (38%)	48 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	Ln	23/25 (92%)	23 (100%)	0	0	100	100
43	Lo	101/106 (95%)	95 (94%)	5 (5%)	1 (1%)	12	28
44	Lp	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
45	Lr	122/137 (89%)	112 (92%)	10 (8%)	0	100	100
48	SA	205/295 (70%)	191 (93%)	14 (7%)	0	100	100
49	SB	211/264 (80%)	201 (95%)	10 (5%)	0	100	100
50	SC	213/293 (73%)	206 (97%)	6 (3%)	1 (0%)	24	45
51	SD	207/243 (85%)	195 (94%)	12 (6%)	0	100	100
52	SE	256/263 (97%)	233 (91%)	22 (9%)	1 (0%)	30	51
53	SF	175/204 (86%)	164 (94%)	11 (6%)	0	100	100
54	SG	200/249 (80%)	188 (94%)	12 (6%)	0	100	100
55	SH	176/194 (91%)	161 (92%)	15 (8%)	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%)	128 (98%)	3 (2%)	0	100	100
60	SN	148/151 (98%)	146 (99%)	2 (1%)	0	100	100
61	SO	132/151 (87%)	121 (92%)	11 (8%)	0	100	100
62	SP	116/145 (80%)	113 (97%)	3 (3%)	0	100	100
63	SQ	137/146 (94%)	122 (89%)	15 (11%)	0	100	100
64	SR	129/135 (96%)	120 (93%)	9 (7%)	0	100	100
65	SS	138/152 (91%)	127 (92%)	11 (8%)	0	100	100
66	ST	138/145 (95%)	132 (96%)	6 (4%)	0	100	100
67	SU	93/119 (78%)	89 (96%)	4 (4%)	0	100	100
68	SV	79/83 (95%)	75 (95%)	4 (5%)	0	100	100
69	SW	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
70	SX	137/143 (96%)	127 (93%)	9 (7%)	1 (1%)	18	37
71	SY	108/133 (81%)	98 (91%)	10 (9%)	0	100	100
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	81/84 (96%)	74 (91%)	7 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
75	Sc	52/69 (75%)	44 (85%)	7 (14%)	1 (2%)	6	15
76	Sd	52/56 (93%)	51 (98%)	1 (2%)	0	100	100
77	Se	44/133 (33%)	39 (89%)	5 (11%)	0	100	100
78	Sg	270/317 (85%)	229 (85%)	41 (15%)	0	100	100
All	All	10626/12499 (85%)	10031 (94%)	585 (6%)	10 (0%)	49	71

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	LH	13	PRO
31	Lc	99	PRO
70	SX	61	GLN
75	Sc	51	ARG
11	LH	189	GLN

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%)	180 (95%)	10 (5%)	20	43
5	LB	344/348 (99%)	332 (96%)	12 (4%)	32	58
6	LC	301/348 (86%)	294 (98%)	7 (2%)	44	71
7	LD	246/249 (99%)	238 (97%)	8 (3%)	33	60
8	LE	194/256 (76%)	189 (97%)	5 (3%)	40	68
9	LF	185/234 (79%)	181 (98%)	4 (2%)	45	72
10	LG	197/223 (88%)	191 (97%)	6 (3%)	36	63
11	LH	169/171 (99%)	164 (97%)	5 (3%)	36	63
12	LI	170/180 (94%)	163 (96%)	7 (4%)	27	52
13	LJ	141/149 (95%)	136 (96%)	5 (4%)	32	58
14	LL	173/178 (97%)	171 (99%)	2 (1%)	63	82
15	LM	116/157 (74%)	116 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	LN	171/172 (99%)	169 (99%)	2 (1%)	63	82
17	LO	172/173 (99%)	170 (99%)	2 (1%)	63	82
18	LP	135/163 (83%)	129 (96%)	6 (4%)	25	50
19	LQ	164/165 (99%)	159 (97%)	5 (3%)	36	63
20	LR	154/175 (88%)	148 (96%)	6 (4%)	28	54
21	LS	155/156 (99%)	147 (95%)	8 (5%)	21	43
22	LT	140/140 (100%)	137 (98%)	3 (2%)	47	73
23	LU	90/114 (79%)	86 (96%)	4 (4%)	25	50
24	LV	100/107 (94%)	96 (96%)	4 (4%)	28	53
25	LW	54/126 (43%)	52 (96%)	2 (4%)	30	56
26	LX	106/133 (80%)	102 (96%)	4 (4%)	29	55
27	LY	123/135 (91%)	122 (99%)	1 (1%)	73	87
28	LZ	117/118 (99%)	113 (97%)	4 (3%)	32	59
29	La	120/121 (99%)	117 (98%)	3 (2%)	42	69
30	Lb	83/124 (67%)	80 (96%)	3 (4%)	31	57
31	Lc	79/97 (81%)	75 (95%)	4 (5%)	21	44
32	Ld	99/110 (90%)	97 (98%)	2 (2%)	48	74
33	Le	114/121 (94%)	110 (96%)	4 (4%)	32	58
34	Lf	88/89 (99%)	86 (98%)	2 (2%)	44	71
35	Lg	94/100 (94%)	91 (97%)	3 (3%)	34	61
36	Lh	109/110 (99%)	107 (98%)	2 (2%)	51	76
37	Li	86/89 (97%)	85 (99%)	1 (1%)	63	82
38	Lj	73/80 (91%)	73 (100%)	0	100	100
39	Lk	64/65 (98%)	61 (95%)	3 (5%)	23	47
40	Ll	46/47 (98%)	45 (98%)	1 (2%)	45	72
41	Lm	47/116 (40%)	47 (100%)	0	100	100
42	Ln	24/24 (100%)	24 (100%)	0	100	100
43	Lo	91/94 (97%)	89 (98%)	2 (2%)	45	72
44	Lp	74/75 (99%)	72 (97%)	2 (3%)	39	67
45	Lr	108/121 (89%)	105 (97%)	3 (3%)	38	65
48	SA	173/242 (72%)	163 (94%)	10 (6%)	18	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	SB	194/229 (85%)	188 (97%)	6 (3%)	35	62
50	SC	181/224 (81%)	177 (98%)	4 (2%)	45	72
51	SD	173/202 (86%)	166 (96%)	7 (4%)	28	53
52	SE	221/225 (98%)	205 (93%)	16 (7%)	13	29
53	SF	152/170 (89%)	144 (95%)	8 (5%)	20	43
54	SG	178/218 (82%)	174 (98%)	4 (2%)	45	72
55	SH	161/174 (92%)	159 (99%)	2 (1%)	63	82
56	SI	159/180 (88%)	156 (98%)	3 (2%)	50	75
57	SJ	126/168 (75%)	121 (96%)	5 (4%)	28	53
58	SK	81/136 (60%)	80 (99%)	1 (1%)	63	82
59	SL	123/142 (87%)	120 (98%)	3 (2%)	43	70
60	SN	130/131 (99%)	123 (95%)	7 (5%)	20	42
61	SO	104/119 (87%)	101 (97%)	3 (3%)	37	64
62	SP	107/130 (82%)	104 (97%)	3 (3%)	38	65
63	SQ	115/121 (95%)	111 (96%)	4 (4%)	32	58
64	SR	119/121 (98%)	116 (98%)	3 (2%)	42	69
65	SS	122/132 (92%)	114 (93%)	8 (7%)	15	33
66	ST	110/115 (96%)	104 (94%)	6 (6%)	19	41
67	SU	88/107 (82%)	82 (93%)	6 (7%)	14	32
68	SV	65/67 (97%)	63 (97%)	2 (3%)	35	62
69	SW	112/113 (99%)	110 (98%)	2 (2%)	51	76
70	SX	111/115 (96%)	107 (96%)	4 (4%)	31	57
71	SY	93/115 (81%)	89 (96%)	4 (4%)	26	51
72	SZ	64/103 (62%)	56 (88%)	8 (12%)	4	10
73	Sa	86/98 (88%)	84 (98%)	2 (2%)	44	71
74	Sb	75/76 (99%)	69 (92%)	6 (8%)	11	25
75	Sc	48/62 (77%)	46 (96%)	2 (4%)	26	52
76	Sd	48/49 (98%)	47 (98%)	1 (2%)	47	73
77	Se	39/106 (37%)	38 (97%)	1 (3%)	40	68
78	Sg	237/275 (86%)	233 (98%)	4 (2%)	53	77
All	All	9301/10617 (88%)	8999 (97%)	302 (3%)	35	61

5 of 302 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
60	SN	78	LYS
73	Sa	71	LEU
62	SP	96	VAL
67	SU	21	ARG
78	Sg	113	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 87 such sidechains are listed below:

Mol	Chain	Res	Type
52	SE	214	ASN
58	SK	32	HIS
52	SE	224	ASN
55	SH	39	GLN
65	SS	73	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3378/4731 (71%)	767 (22%)	29 (0%)
2	L7	119/120 (99%)	13 (10%)	2 (1%)
3	L8	149/158 (94%)	30 (20%)	1 (0%)
46	S2	1618/1870 (86%)	495 (30%)	26 (1%)
47	S6	74/75 (98%)	26 (35%)	2 (2%)
47	S7	74/75 (98%)	40 (54%)	2 (2%)
79	Sx	9/10 (90%)	1 (11%)	0
All	All	5421/7039 (77%)	1372 (25%)	62 (1%)

5 of 1372 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	2	G
1	L5	3	C
1	L5	15	A
1	L5	21	G
1	L5	25	A

5 of 62 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	4686	A
46	S2	1555	C
46	S2	96	C
46	S2	1476	G
47	S6	54	A

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

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

5.5 Carbohydrates [i](#)

There are no 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.

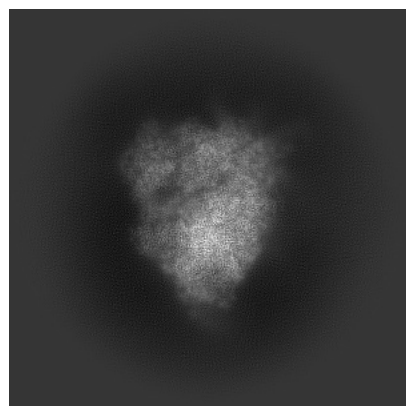
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62288. These allow visual inspection of the internal detail of the map and identification of artifacts.

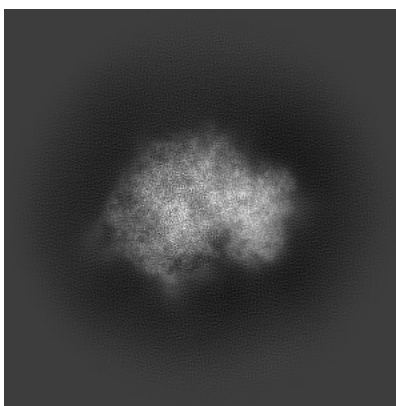
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

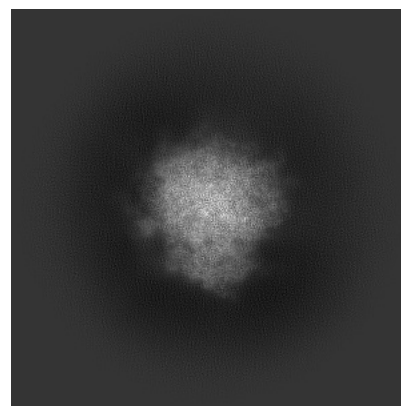
6.1.1 Primary map



X

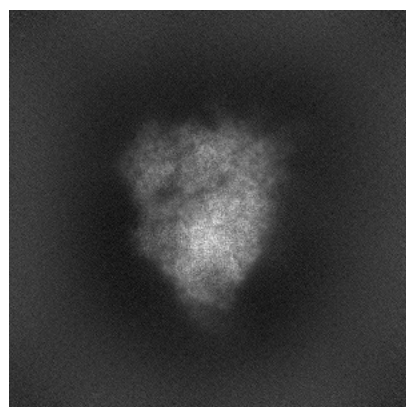


Y

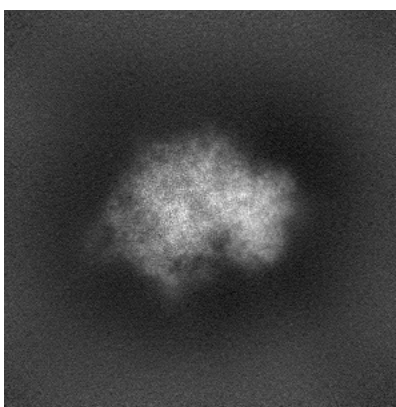


Z

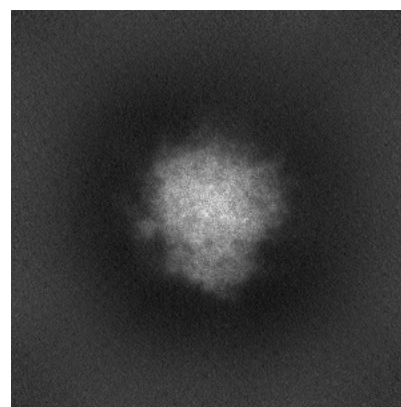
6.1.2 Raw map



X



Y

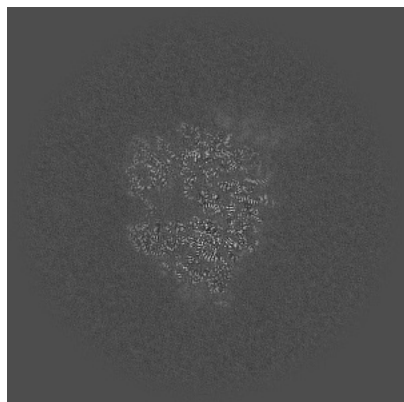


Z

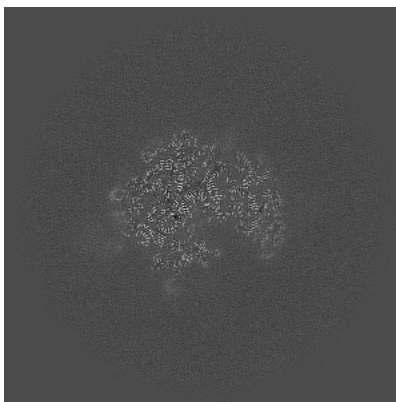
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

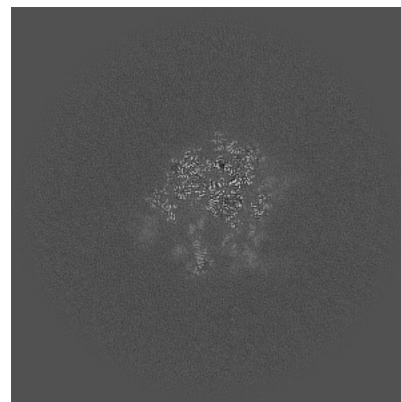
6.2.1 Primary map



X Index: 280

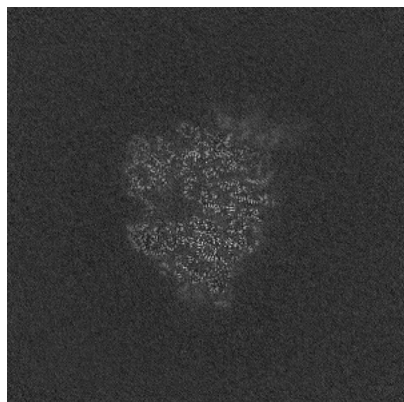


Y Index: 280

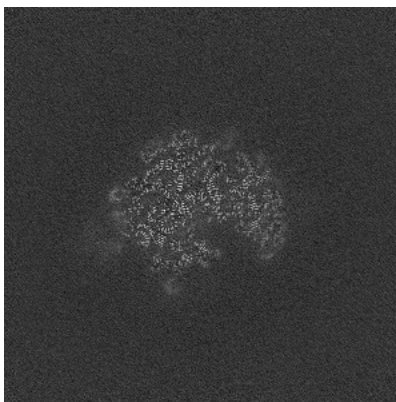


Z Index: 280

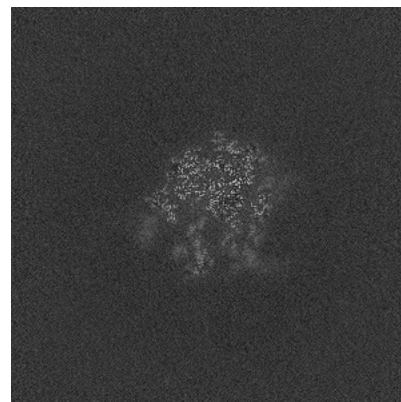
6.2.2 Raw map



X Index: 280



Y Index: 280

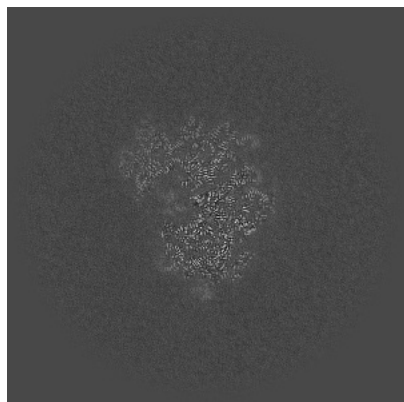


Z Index: 280

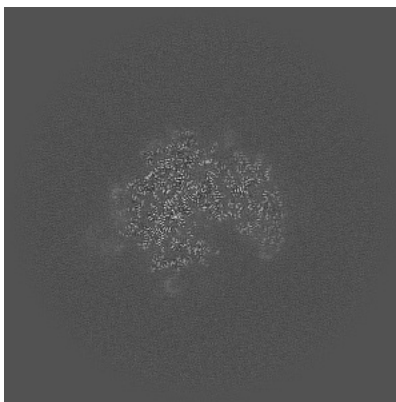
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

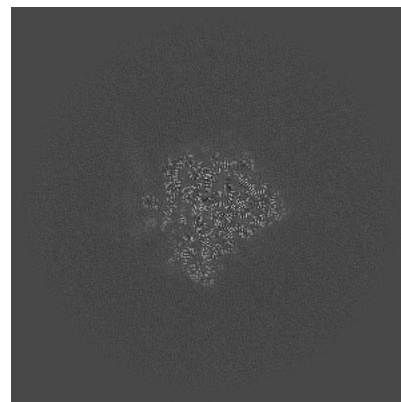
6.3.1 Primary map



X Index: 303

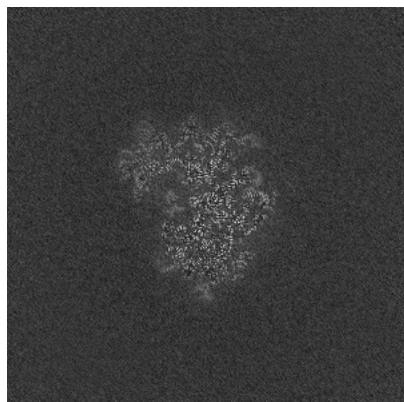


Y Index: 278

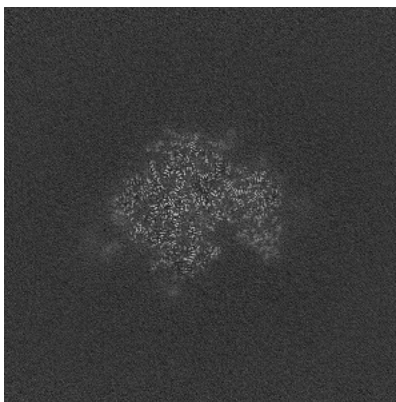


Z Index: 246

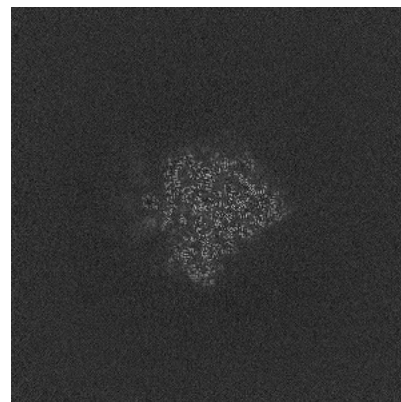
6.3.2 Raw map



X Index: 302



Y Index: 287

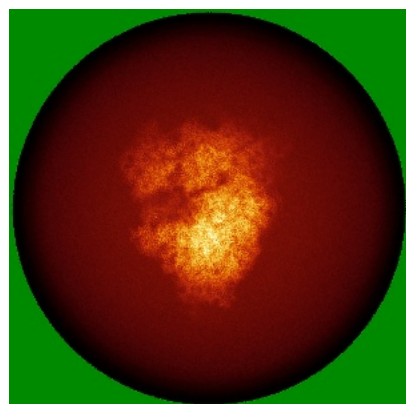


Z Index: 246

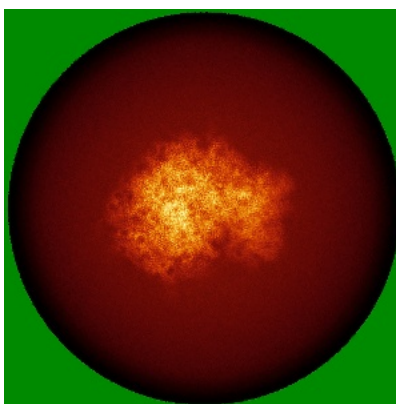
The images above show the largest variance slices of the map in three orthogonal directions.

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

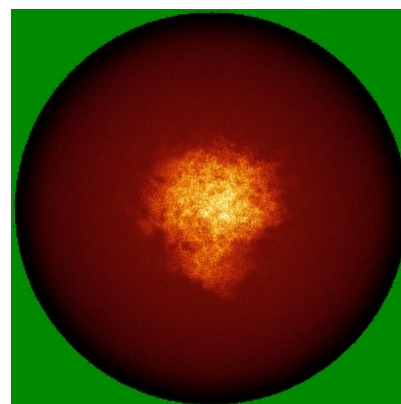
6.4.1 Primary map



X

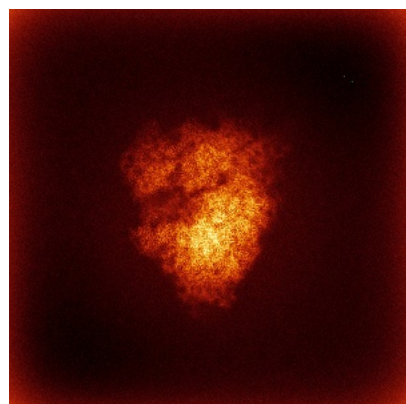


Y

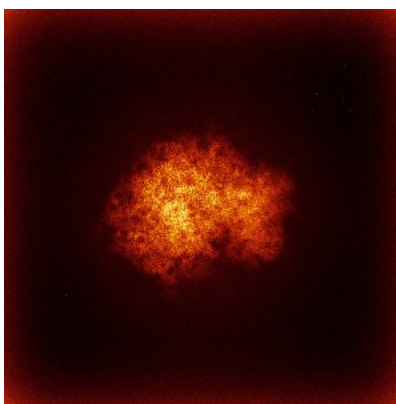


Z

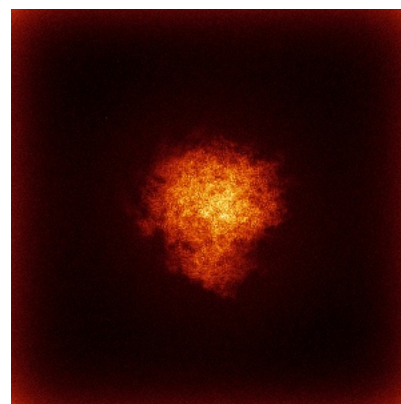
6.4.2 Raw map



X



Y

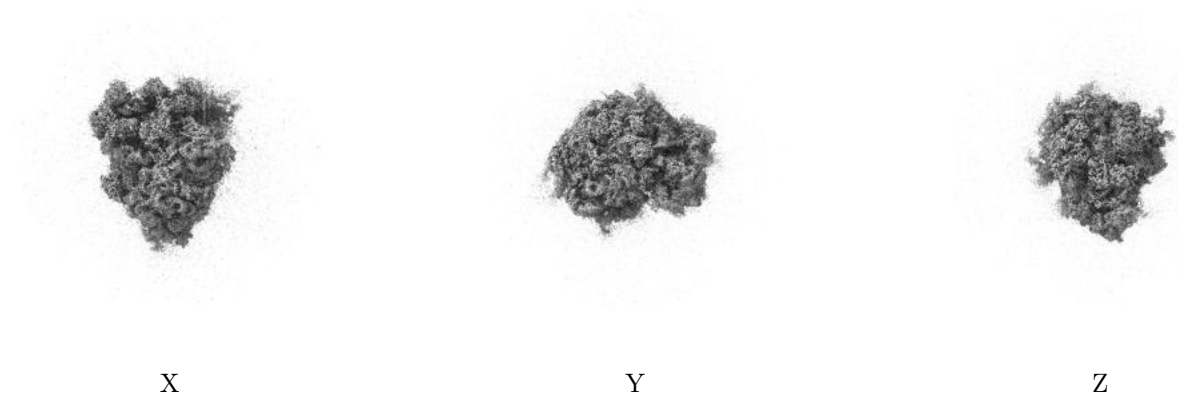


Z

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.

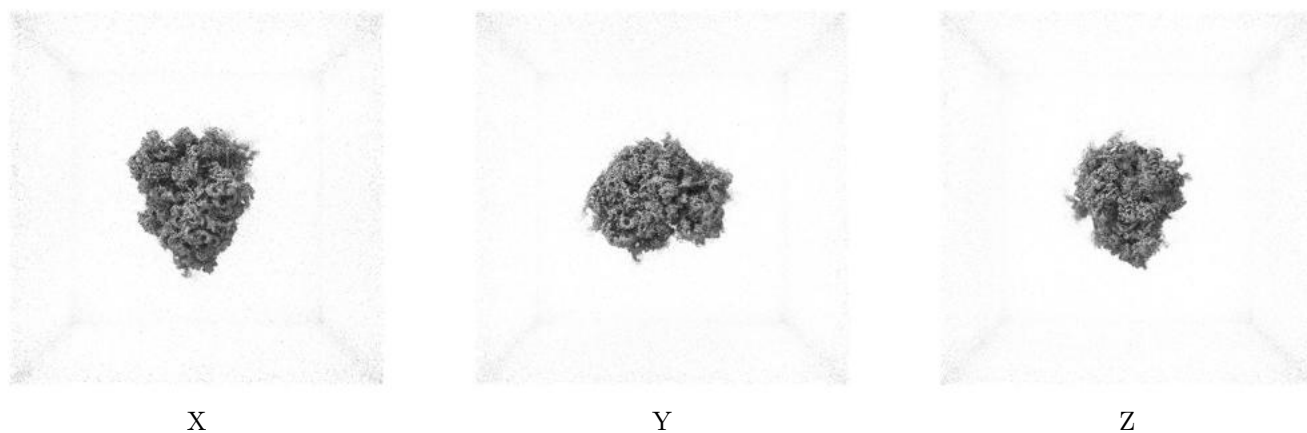
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.38. 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



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.

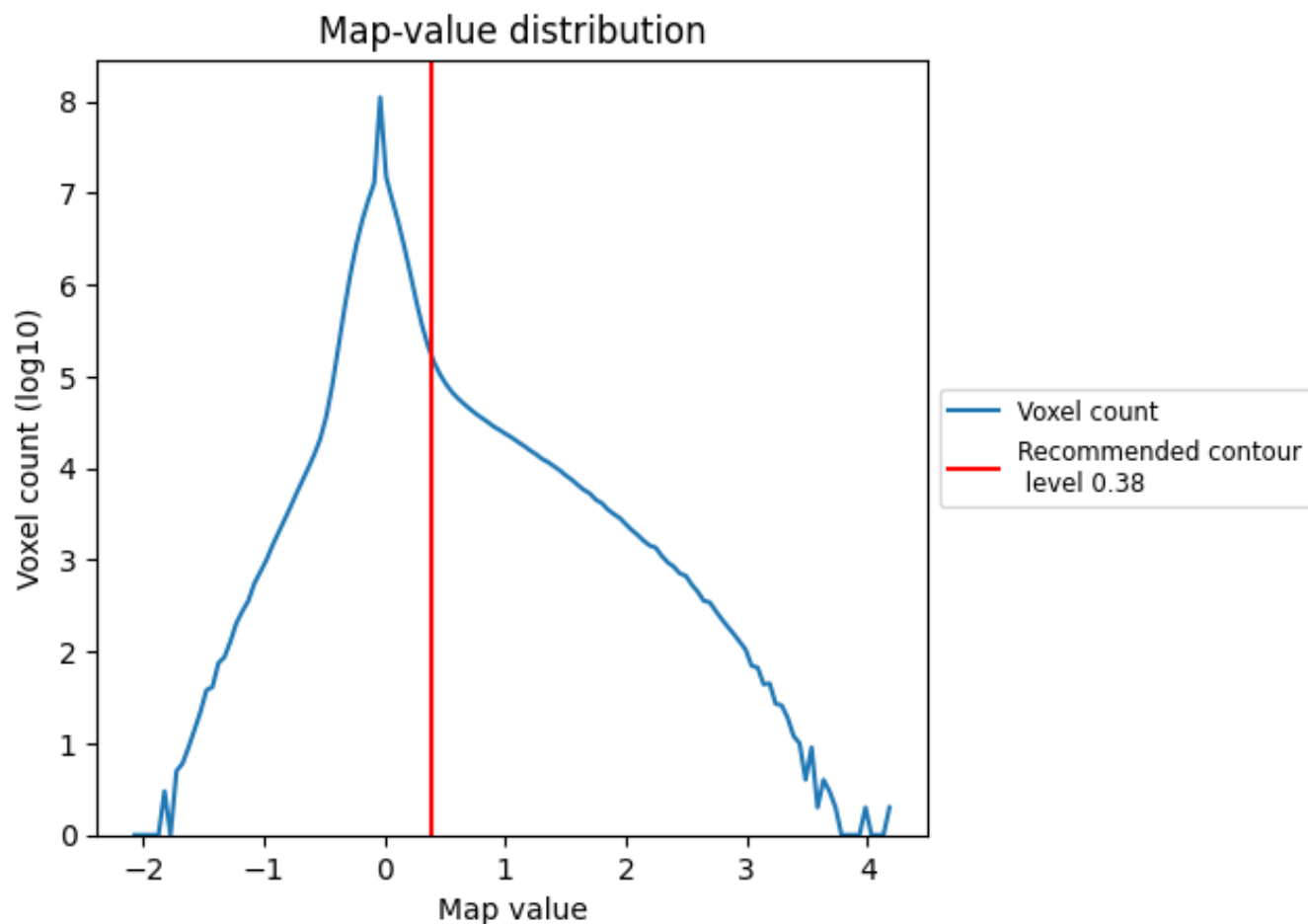
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

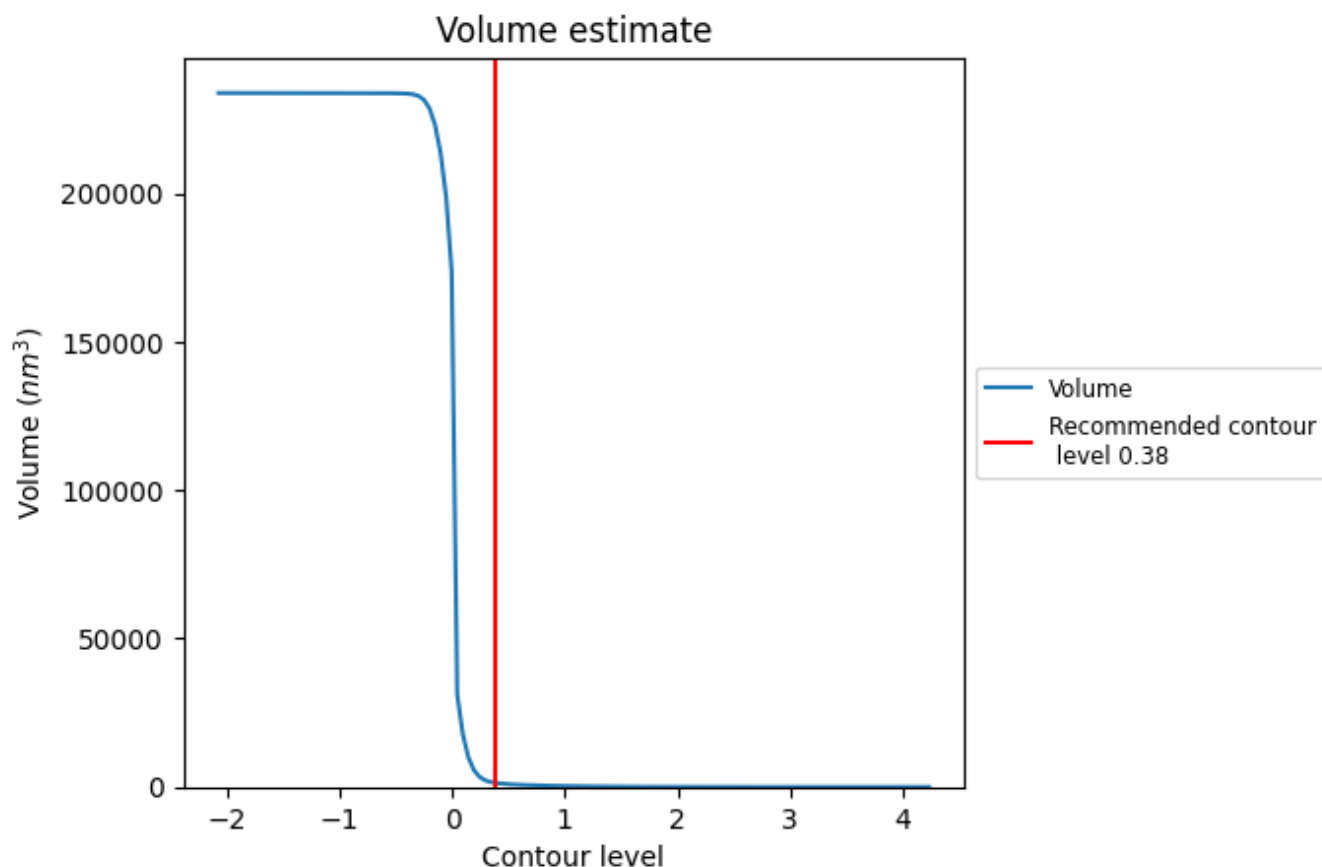
This section contains the results of statistical analysis of the map.

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.

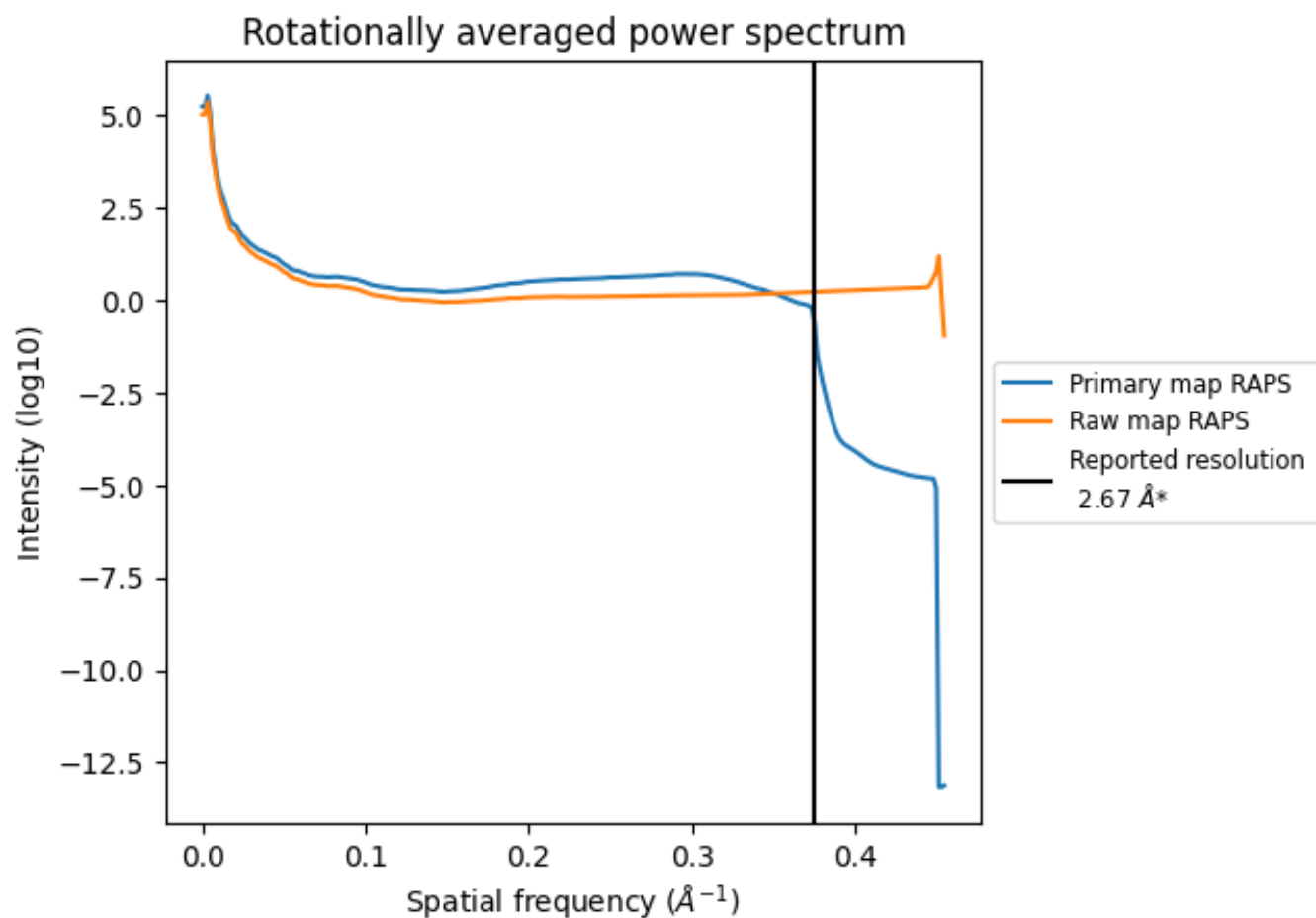
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1414 nm³; this corresponds to an approximate mass of 1278 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 ⓘ

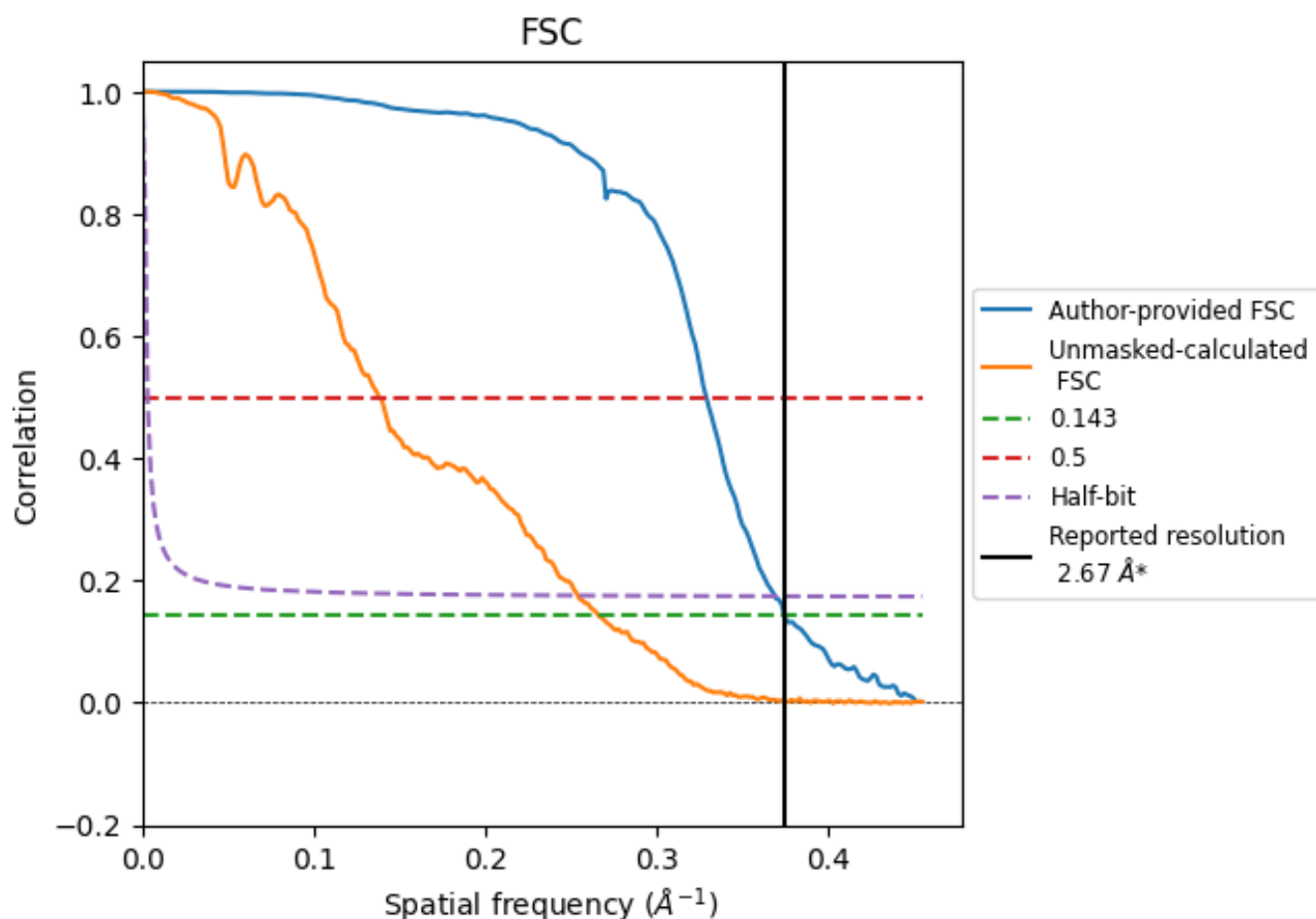


*Reported resolution corresponds to spatial frequency of 0.375 Å⁻¹

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 0.375 Å⁻¹

8.2 Resolution estimates [i](#)

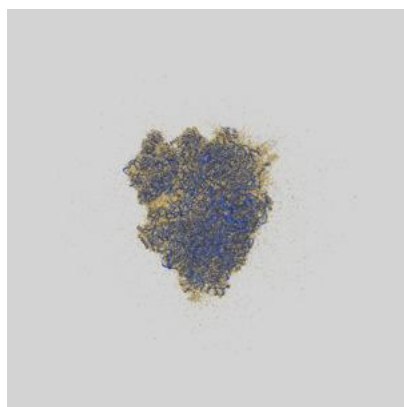
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.67	-	-
Author-provided FSC curve	2.67	3.04	2.71
Unmasked-calculated*	3.76	7.25	3.94

*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 3.76 differs from the reported value 2.67 by more than 10 %

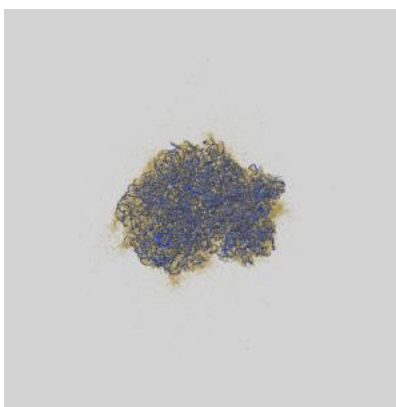
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-62288 and PDB model 9KDW. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

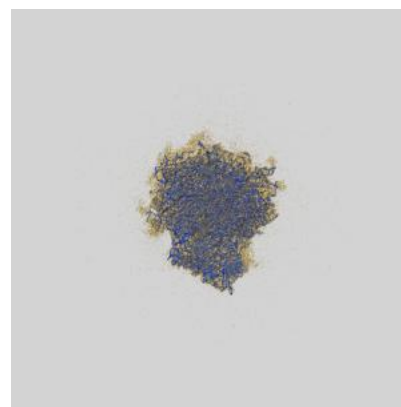
9.1 Map-model overlay [i](#)



X



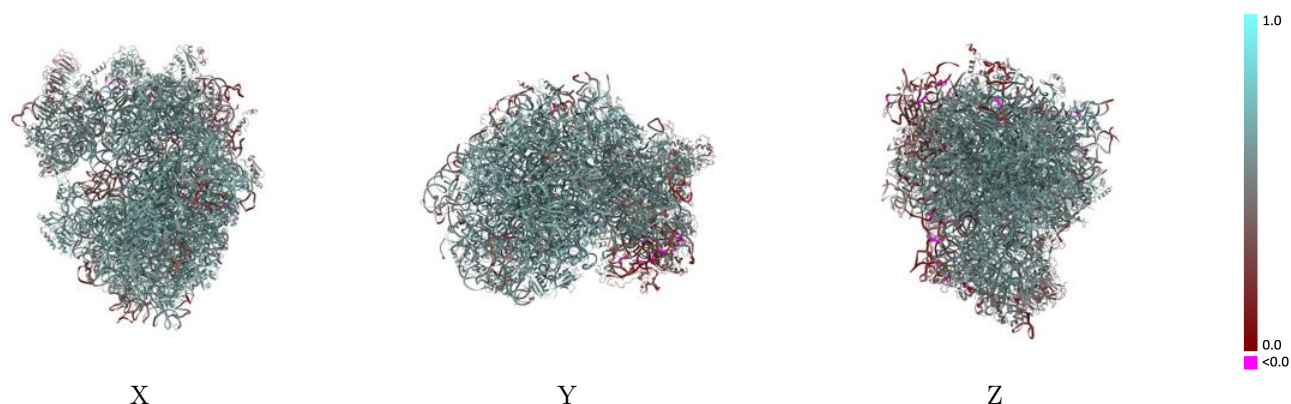
Y



Z

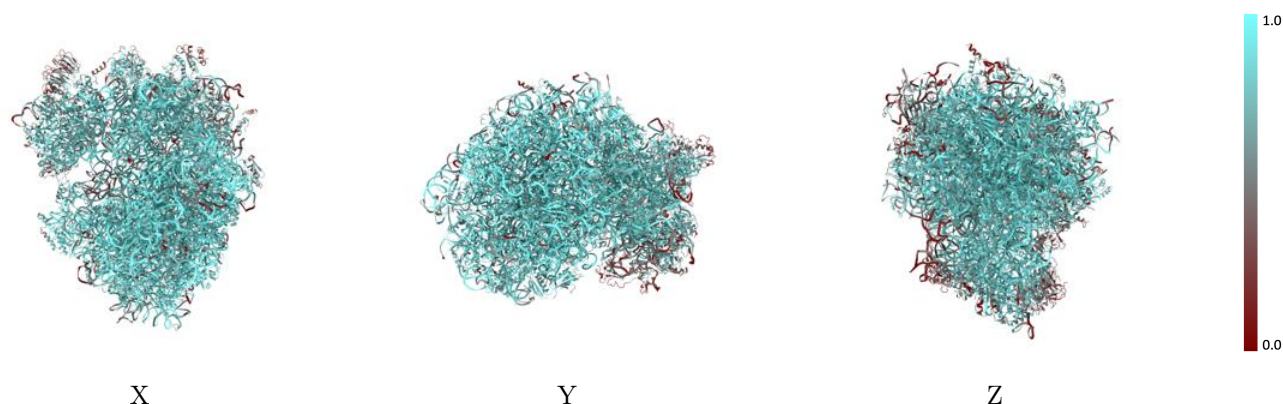
The images above show the 3D surface view of the map at the recommended contour level 0.38 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



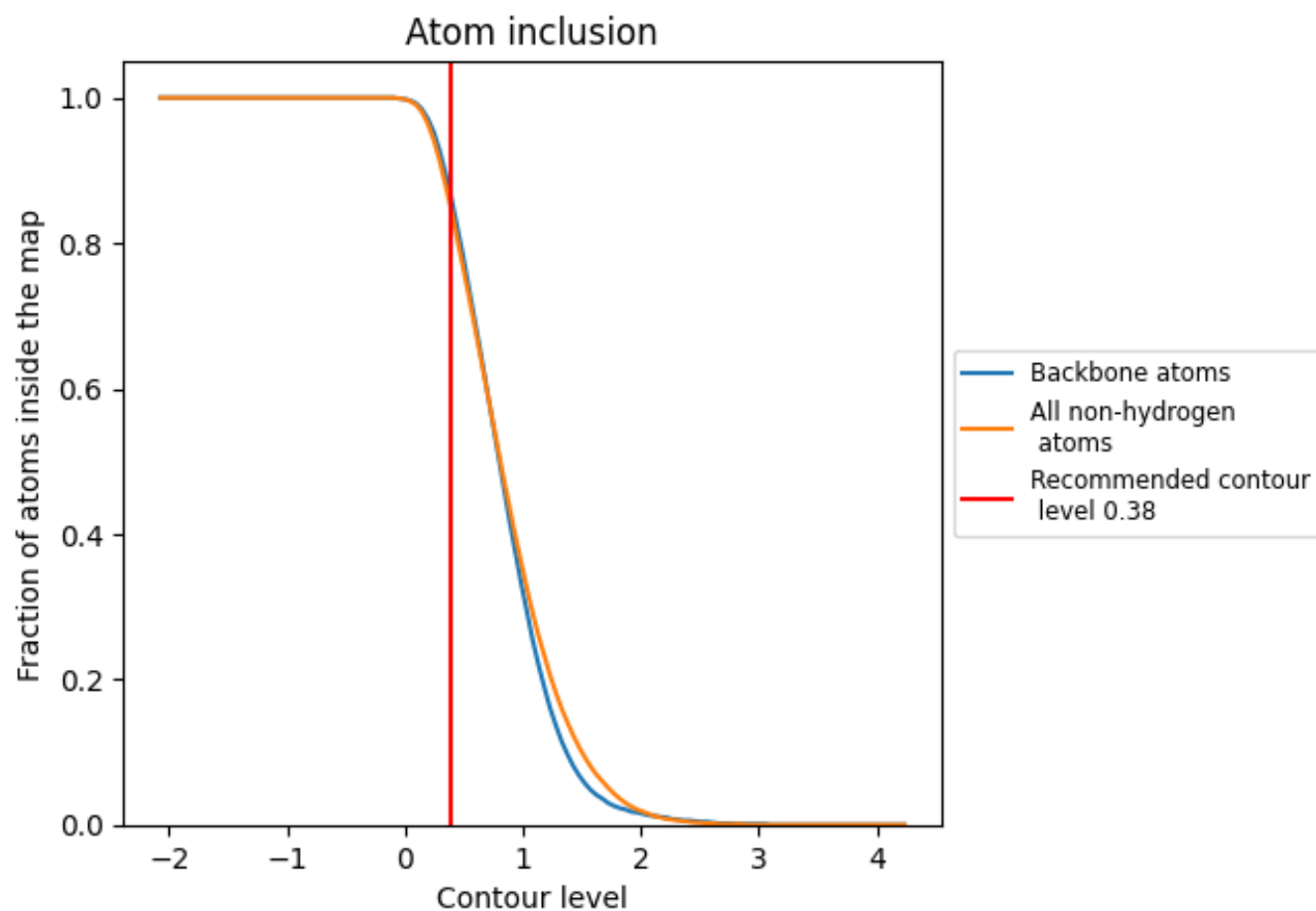
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 87% of all backbone atoms, 86% 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	 0.8550	 0.5730
L5	 0.9140	 0.5940
L7	 0.9850	 0.6360
L8	 0.9420	 0.6120
LA	 0.9500	 0.6440
LB	 0.8990	 0.6270
LC	 0.9310	 0.6310
LD	 0.8190	 0.5830
LE	 0.8370	 0.5900
LF	 0.9550	 0.6410
LG	 0.8060	 0.5750
LH	 0.8450	 0.5980
LI	 0.8870	 0.6140
LJ	 0.8290	 0.5990
LL	 0.8580	 0.6070
LM	 0.9110	 0.6180
LN	 0.9750	 0.6550
LO	 0.9250	 0.6360
LP	 0.9270	 0.6350
LQ	 0.9430	 0.6430
LR	 0.8610	 0.5950
LS	 0.9330	 0.6310
LT	 0.8850	 0.6080
LU	 0.6950	 0.5150
LV	 0.9150	 0.6300
LW	 0.9240	 0.6380
LX	 0.8790	 0.6140
LY	 0.8830	 0.6140
LZ	 0.8580	 0.6050
La	 0.9400	 0.6440
Lb	 0.8440	 0.5850
Lc	 0.8630	 0.6050
Ld	 0.8450	 0.5980
Le	 0.9560	 0.6480
Lf	 0.9640	 0.6490













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Chain	Atom inclusion	Q-score
Lg	 0.8950	 0.6160
Lh	 0.8590	 0.6070
Li	 0.8180	 0.5930
Lj	 0.9700	 0.6480
Lk	 0.6850	 0.5490
Ll	 0.9530	 0.6300
Lm	 0.9110	 0.6290
Ln	 0.8940	 0.6160
Lo	 0.8900	 0.6210
Lp	 0.9160	 0.6330
Lr	 0.9360	 0.6290
S2	 0.8280	 0.5180
S6	 0.7820	 0.4740
S7	 0.6480	 0.4140
SA	 0.7960	 0.5780
SB	 0.7940	 0.5810
SC	 0.8380	 0.5850
SD	 0.6570	 0.5130
SE	 0.7190	 0.5120
SF	 0.7350	 0.5430
SG	 0.4740	 0.3840
SH	 0.5440	 0.4740
SI	 0.7550	 0.5240
SJ	 0.7770	 0.5410
SK	 0.4610	 0.4290
SL	 0.8750	 0.5910
SN	 0.8350	 0.5930
SO	 0.8140	 0.5800
SP	 0.7210	 0.5310
SQ	 0.7460	 0.5380
SR	 0.5860	 0.4890
SS	 0.7570	 0.5620
ST	 0.7550	 0.5480
SU	 0.5560	 0.4570
SV	 0.7740	 0.5690
SW	 0.9170	 0.6130
SX	 0.8460	 0.5840
SY	 0.4760	 0.3790
SZ	 0.6200	 0.4990
Sa	 0.8200	 0.5860
Sb	 0.6290	 0.5000
Sc	 0.6260	 0.4880

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Chain	Atom inclusion	Q-score
Sd	 0.7280	 0.4900
Se	 0.6530	 0.4680
Sg	 0.4370	 0.4130
Sx	 0.8740	 0.5500
Z	 0.5390	 0.4090