



wwPDB EM Validation Summary Report ⓘ

Aug 12, 2024 – 02:04 PM JST

PDB ID : 8Y0U
EMDB ID : EMD-37995
Title : dormant ribosome with STM1
Authors : Du, M.; Zeng, F.
Deposited on : 2024-01-23
Resolution : 3.59 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.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

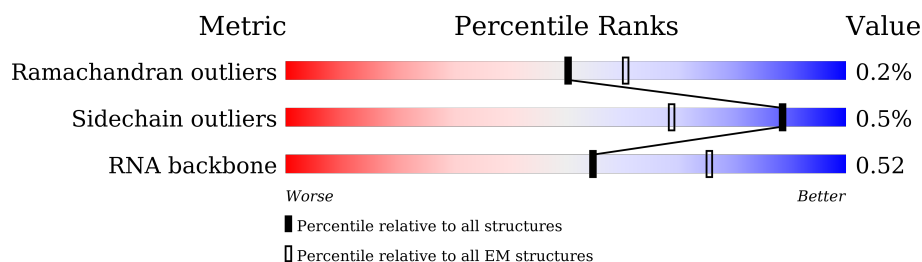
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.59 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.



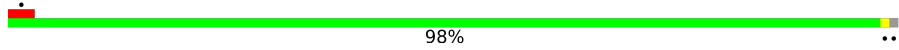
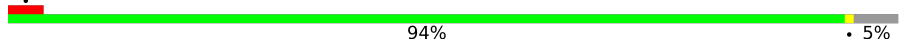
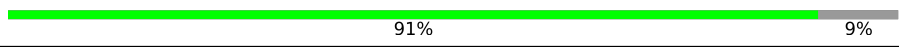
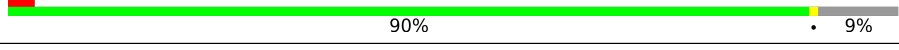
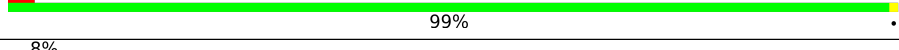
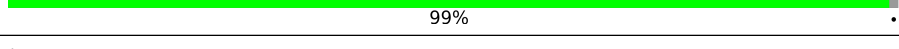
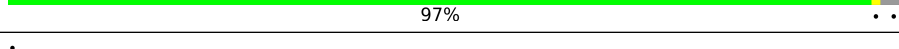
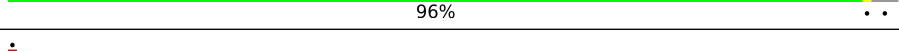
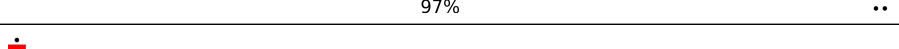
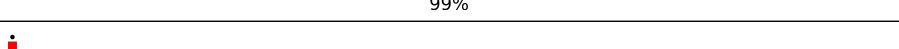
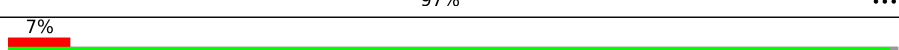
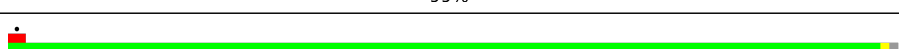
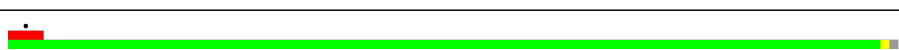
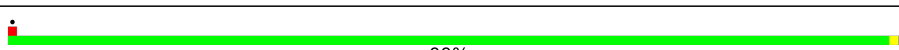
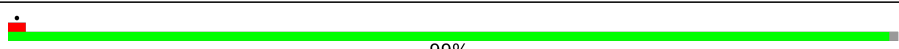

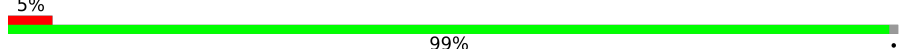


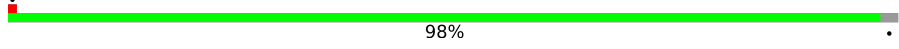
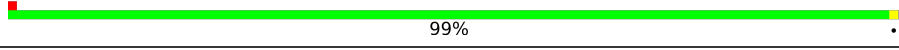
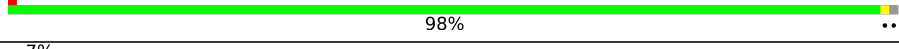
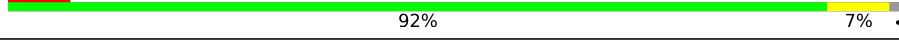


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	LA	254	 98%
2	SA	252	 82% 18%
3	LB	387	 99%
4	SB	255	 26% 87% 11%
5	C1	3396	 75% 20% 5%
6	C4	121	 86% 14%
7	C3	158	 81% 19%
8	LC	362	 99%

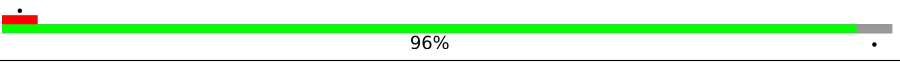
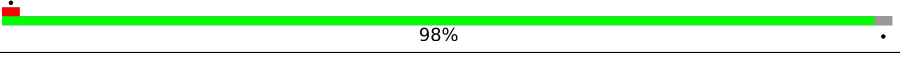
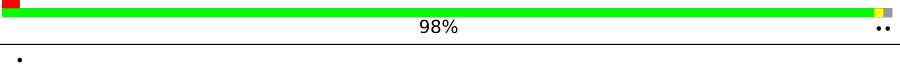
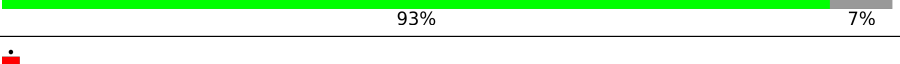
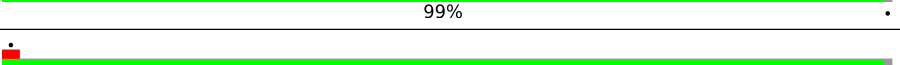
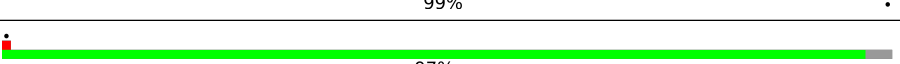
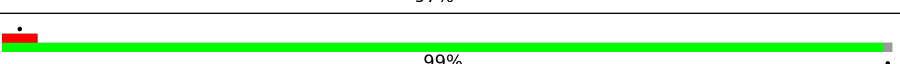
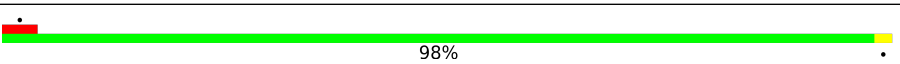

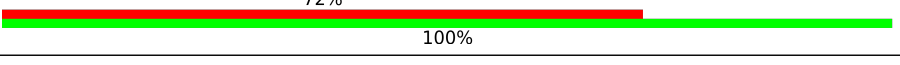
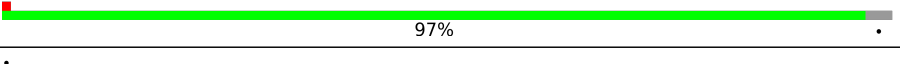
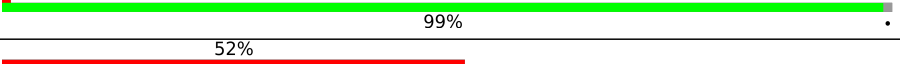

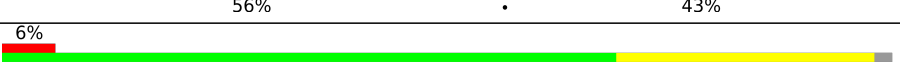
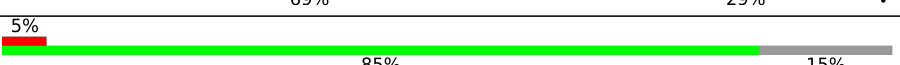
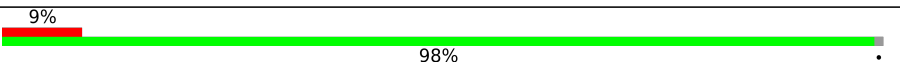
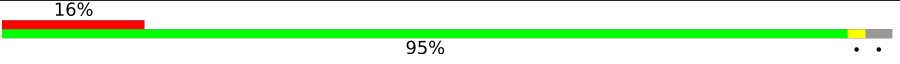
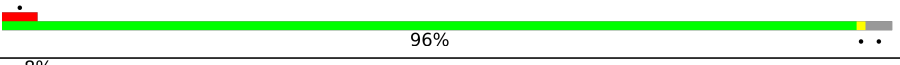
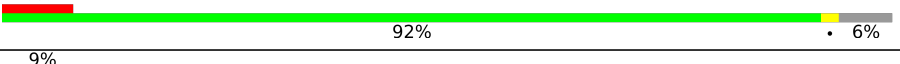
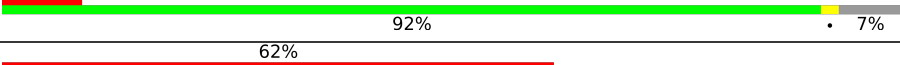

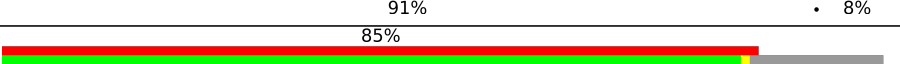



Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	LD	297	
10	LE	176	
11	LF	244	
12	LG	256	
13	LH	191	
14	LI	221	
15	LJ	174	
16	LL	199	
17	LM	138	
18	LN	204	
19	LO	199	
20	LP	184	
21	LQ	186	
22	LR	189	
23	LS	172	
24	LT	160	
25	LU	121	
26	LV	137	
27	LW	155	
28	LX	142	
29	LY	127	
30	LZ	136	
31	La	149	
32	Lb	59	
33	Lc	105	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	Ld	113	
35	Le	130	
36	Lf	107	
37	Lg	121	
38	Lh	120	
39	Li	100	
40	Lj	88	
41	Lk	78	
42	Ll	50	
43	Lm	128	
44	Ln	25	
45	Lo	106	
46	Lp	92	
47	P0	312	
48	P2	165	
49	C2	1800	
50	SC	254	
51	SE	261	
52	SG	236	
53	SH	190	
54	SI	200	
55	SJ	197	
56	SK	105	
57	SL	156	
58	SM	143	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
59	SN	151	
60	SO	138	
61	SV	87	
62	SW	130	
63	SX	145	
64	SY	135	
65	Sa	119	
66	Sb	82	
67	Se	63	
68	5	157	
69	Sf	152	
70	SP	142	
71	SZ	108	
72	ST	144	
73	SQ	143	
74	Sd	56	
75	SU	121	
76	Sc	67	
77	s	273	

2 Entry composition

There are 79 unique types of molecules in this entry. The entry contains 196269 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 protein called Large ribosomal subunit protein uL2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	LA	251	Total	C	N	O	S	0	0
			1899	1182	385	331	1		

- Molecule 2 is a protein called Small ribosomal subunit protein uS2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	SA	206	Total	C	N	O	S	0	0
			1603	1030	284	287	2		

- Molecule 3 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	LB	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 4 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SB	226	Total	C	N	O	S	0	0
			1798	1139	330	325	4		

- Molecule 5 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C1	3221	Total	C	N	O	P	0	0
			68888	30771	12409	22487	3221		

- Molecule 6 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C4	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 7 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C3	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 8 is a protein called Large ribosomal subunit protein uL4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LC	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 9 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LD	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		

- Molecule 10 is a protein called Large ribosomal subunit protein eL6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LE	167	Total	C	N	O		0	0
			1307	843	234	230			

- Molecule 11 is a protein called Large ribosomal subunit protein uL30A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LF	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 12 is a protein called Large ribosomal subunit protein eL8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LG	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 13 is a protein called Large ribosomal subunit protein uL6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LH	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		

- Molecule 14 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LI	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		

- Molecule 15 is a protein called Large ribosomal subunit protein uL5B.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LJ	169	Total	C	N	O	S	0	0
			1350	846	253	247	4		

- Molecule 16 is a protein called Large ribosomal subunit protein eL13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LL	193	Total	C	N	O	S	0	0
			1543	962	315	266			

- Molecule 17 is a protein called Large ribosomal subunit protein eL14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LM	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 18 is a protein called Large ribosomal subunit protein eL15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LN	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 19 is a protein called Large ribosomal subunit protein uL13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LO	197	Total	C	N	O	S	197	0
			1555	1003	289	262	1		

- Molecule 20 is a protein called Large ribosomal subunit protein uL22A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LP	183	Total	C	N	O	S	0	0
			1416	879	284	253			

- Molecule 21 is a protein called Large ribosomal subunit protein eL18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LQ	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 22 is a protein called Large ribosomal subunit protein eL19A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LR	188	Total	C	N	O	S	0	0
			1515	932	323	260			

- Molecule 23 is a protein called Large ribosomal subunit protein eL20A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LS	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 24 is a protein called Large ribosomal subunit protein eL21A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LT	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 25 is a protein called Large ribosomal subunit protein eL22A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LU	100	Total	C	N	O	S	0	0
			796	516	131	149			

- Molecule 26 is a protein called Large ribosomal subunit protein uL14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LV	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 27 is a protein called Large ribosomal subunit protein eL24A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LW	126	Total	C	N	O	S	0	0
			849	532	167	149	1		

- Molecule 28 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LX	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 29 is a protein called Large ribosomal subunit protein uL24A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LY	125	Total	C	N	O		0	0
			984	620	191	173			

- Molecule 30 is a protein called Large ribosomal subunit protein eL27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LZ	135	Total	C	N	O		0	0
			1092	710	202	180			

- Molecule 31 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	La	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 32 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Lb	58	Total	C	N	O		0	0
			462	289	100	73			

- Molecule 33 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lc	96	Total	C	N	O	S	0	0
			737	476	123	137	1		

- Molecule 34 is a protein called Large ribosomal subunit protein eL31A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Ld	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 35 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Le	127	Total	C	N	O	S	0	0
			1017	644	205	167	1		

- Molecule 36 is a protein called Large ribosomal subunit protein eL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lf	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 37 is a protein called Large ribosomal subunit protein eL34A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lg	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 38 is a protein called Large ribosomal subunit protein uL29A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lh	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 39 is a protein called Large ribosomal subunit protein eL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Li	99	Total	C	N	O	S	0	0
			766	478	154	132	2		

- Molecule 40 is a protein called Large ribosomal subunit protein eL37A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lj	85	Total	C	N	O	S	0	0
			670	408	146	111	5		

- Molecule 41 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	Lk	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 42 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ll	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 43 is a protein called Ubiquitin-ribosomal protein eL40A fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lm	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 44 is a protein called Large ribosomal subunit protein eL41A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Ln	25	Total	C	N	O	S	0	0
			229	139	62	27	1		

- Molecule 45 is a protein called Large ribosomal subunit protein eL42A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lo	103	Total	C	N	O	S	0	0
			824	517	167	135	5		

- Molecule 46 is a protein called Large ribosomal subunit protein eL43A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lp	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 47 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	P0	189	Total	C	N	O	S	0	0
			1473	942	257	270	4		

- Molecule 48 is a protein called Large ribosomal subunit protein uL11A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	P2	94	Total	C	N	O	S	0	0
			723	448	138	135	2		

- Molecule 49 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	C2	1771	Total	C	N	O	P	0	0
			37604	16807	6624	12402	1771		

- Molecule 50 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SC	216	Total	C	N	O	S	0	0
			1626	1042	287	295	2		

- Molecule 51 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SE	258	Total	C	N	O	S	0	0
			2056	1308	387	358	3		

- Molecule 52 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SG	228	Total	C	N	O	S	0	0
			1815	1138	351	323	3		

- Molecule 53 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	SH	184	Total	C	N	O	0	0
			1473	946	263	264		

- Molecule 54 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SI	187	Total	C	N	O	S	0	0
			1476	916	295	263	2		

- Molecule 55 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SJ	184	Total	C	N	O	S	0	0
			1479	935	285	258	1		

- Molecule 56 is a protein called Small ribosomal subunit protein eS10A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SK	92	Total	C	N	O	S	0	0
			752	487	122	141	2		

- Molecule 57 is a protein called Small ribosomal subunit protein uS17A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SL	144	Total	C	N	O	S	0	0
			1159	742	219	195	3		

- Molecule 58 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SM	121	Total	C	N	O	S	0	0
			875	551	153	169	2		

- Molecule 59 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SN	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 60 is a protein called Small ribosomal subunit protein uS11B.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SO	127	Total	C	N	O	S	0	0
			926	569	185	169	3		

- Molecule 61 is a protein called Small ribosomal subunit protein eS21A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SV	87	Total	C	N	O	S	0	0
			673	415	125	131	2		

- Molecule 62 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SW	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 63 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SX	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 64 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SY	134	Total	C	N	O	S	0	0
			1073	676	208	189			

- Molecule 65 is a protein called Small ribosomal subunit protein eS26B.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Sa	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 66 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Sb	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 67 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Se	60	Total	C	N	O	S	0	0
			472	298	97	76	1		

- Molecule 68 is a protein called Eukaryotic translation initiation factor 5A-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	5	152	Total	C	N	O	S	0	0
			1118	693	189	227	9		

- Molecule 69 is a protein called Ubiquitin-ribosomal protein eS31 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Sf	73	Total	C	N	O	S	0	0
			556	352	105	95	4		

- Molecule 70 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SP	117	Total	C	N	O	S	0	0
			916	583	171	155	7		

- Molecule 71 is a protein called Small ribosomal subunit protein eS25A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SZ	100	Total	C	N	O	S	0	0
			771	491	147	133			

- Molecule 72 is a protein called Small ribosomal subunit protein eS19A.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	ST	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 73 is a protein called Small ribosomal subunit protein uS9A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SQ	139	Total	C	N	O	S	0	0
			1082	693	198	191			

- Molecule 74 is a protein called Small ribosomal subunit protein uS14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Sd	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 75 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SU	100	Total	C	N	O	S	0	0
			797	506	144	146	1		

- Molecule 76 is a protein called Small ribosomal subunit protein eS28A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Sc	63	Total	C	N	O	S	0	0
			491	303	96	91	1		

- Molecule 77 is a protein called Suppressor protein STM1.

Mol	Chain	Residues	Atoms				AltConf	Trace
77	s	42	Total	C	N	O	0	0
			261	153	58	50		

- Molecule 78 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
78	LA	2	Total	Mg	0
			2	2	
78	C1	187	Total	Mg	0
			187	187	
78	C4	1	Total	Mg	0
			1	1	
78	C3	1	Total	Mg	0
			1	1	
78	LN	2	Total	Mg	0
			2	2	
78	LP	1	Total	Mg	0
			1	1	
78	LV	1	Total	Mg	0
			1	1	
78	Le	1	Total	Mg	0
			1	1	
78	C2	78	Total	Mg	0
			78	78	
78	SC	1	Total	Mg	0
			1	1	
78	SE	1	Total	Mg	0
			1	1	
78	Sa	1	Total	Mg	0
			1	1	
78	ST	2	Total	Mg	0
			2	2	
78	SQ	2	Total	Mg	0
			2	2	

- Molecule 79 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
79	Lg	1	Total	Zn	0
			1	1	
79	Lj	1	Total	Zn	0
			1	1	

Continued on next page...

Continued from previous page...

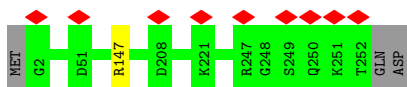
Mol	Chain	Residues	Atoms		AltConf
79	Lm	1	Total 1	Zn 1	0
79	Lo	1	Total 1	Zn 1	0
79	Lp	1	Total 1	Zn 1	0
79	Sf	1	Total 1	Zn 1	0
79	Sd	1	Total 1	Zn 1	0

3 Residue-property plots [i](#)


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.

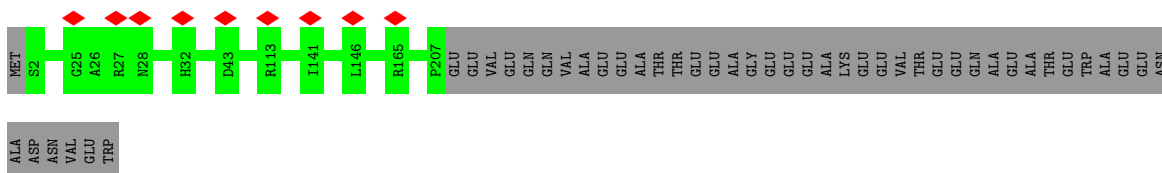
- Molecule 1: Large ribosomal subunit protein uL2A

Chain LA:  98%



- Molecule 2: Small ribosomal subunit protein uS2A

Chain SA:  82% 18%




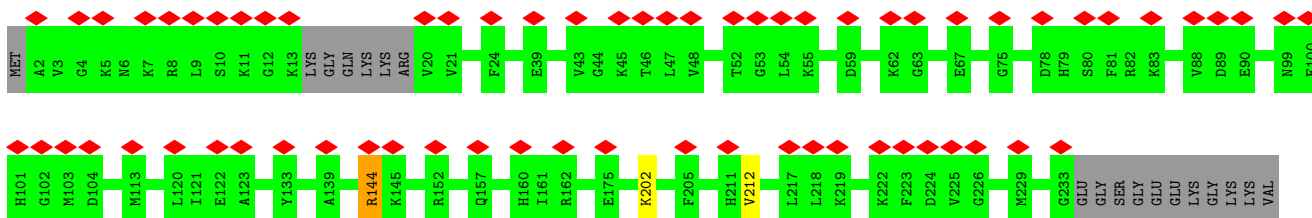
- Molecule 3: Large ribosomal subunit protein uL3

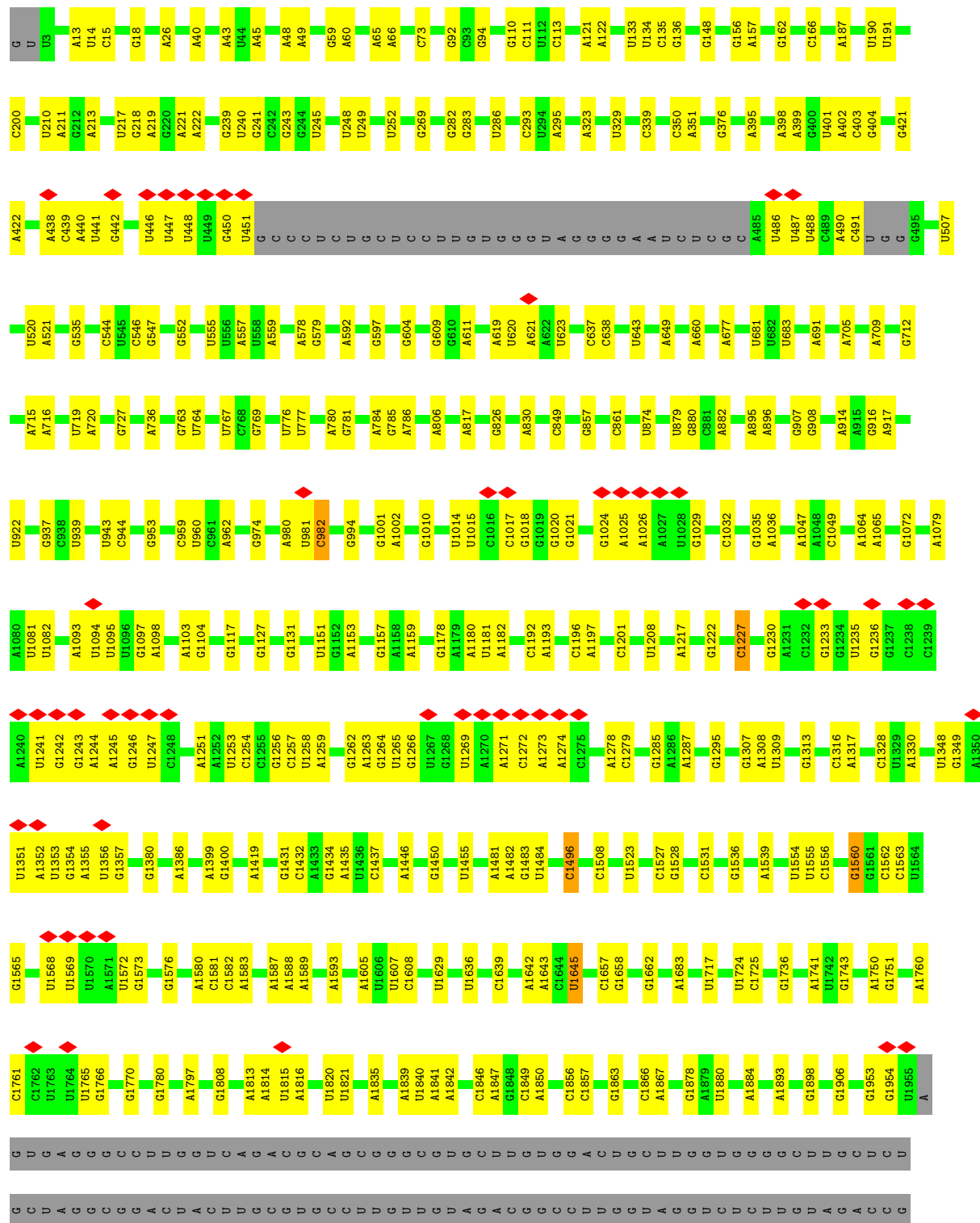
Chain LB:  99%



- Molecule 4: 40S ribosomal protein S1-A

Chain SB:  26% 87% 11%



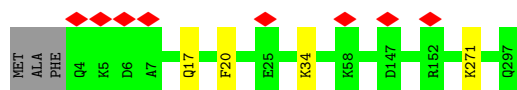


Chain LC:  99%



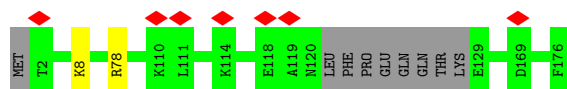
- Molecule 9: Large ribosomal subunit protein uL18

Chain LD:  98%



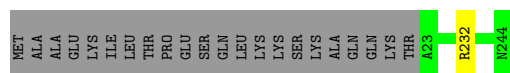
- Molecule 10: Large ribosomal subunit protein eL6B

Chain LE:  94%



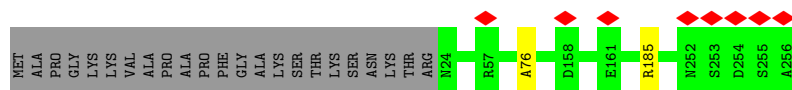
- Molecule 11: Large ribosomal subunit protein uL30A

Chain LF:  91%



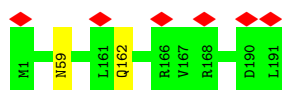
- Molecule 12: Large ribosomal subunit protein eL8A

Chain LG:  90%



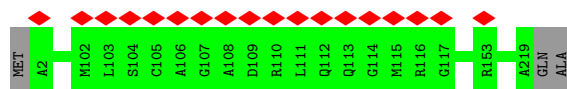
- Molecule 13: Large ribosomal subunit protein uL6A

Chain LH:  99%



- Molecule 14: Large ribosomal subunit protein uL16

Chain LI:  8%



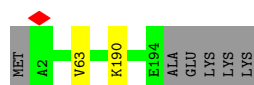
- Molecule 15: Large ribosomal subunit protein uL5B

Chain LJ:  97%



- Molecule 16: Large ribosomal subunit protein eL13A

Chain LL:  96%



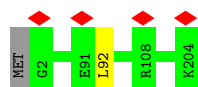
- Molecule 17: Large ribosomal subunit protein eL14A

Chain LM:  97%



- Molecule 18: Large ribosomal subunit protein eL15A

Chain LN:  99%



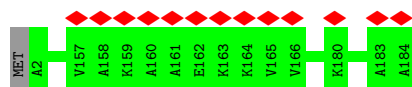
- Molecule 19: Large ribosomal subunit protein uL13A

Chain LO:  97%



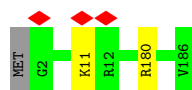
- Molecule 20: Large ribosomal subunit protein uL22A

Chain LP:  7% 99%



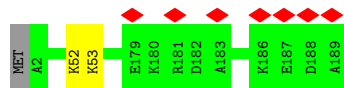
- Molecule 21: Large ribosomal subunit protein eL18A

Chain LQ:  98%



- Molecule 22: Large ribosomal subunit protein eL19A

Chain LR: 98%



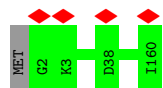
- Molecule 23: Large ribosomal subunit protein eL20A

Chain LS: 99%



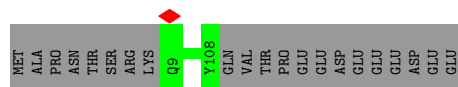
- Molecule 24: Large ribosomal subunit protein eL21A

Chain LT: 99%



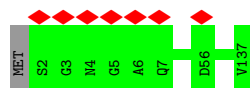
- Molecule 25: Large ribosomal subunit protein eL22A

Chain LU: 83% 17%



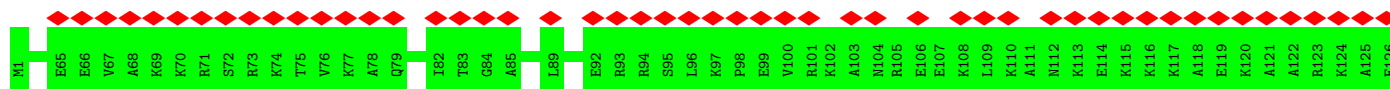
- Molecule 26: Large ribosomal subunit protein uL14A

Chain LV: 5% 99%




- Molecule 27: Large ribosomal subunit protein eL24A

Chain LW: 33% 81% 19%



LYS
ALA
LYS
SER
SER
ALA
GLY
THR
GLN
SER
SER
LYS
SER
ALA
LYS
PHE
SER
LYS
GLN
GLN
ALA
LYS
GLY
ALA
PHE
GLN
LYS
VAL
ALA
ALA
THR
SER
ARG

- Molecule 28: Large ribosomal subunit protein uL23

Chain LX:  83% 15%

MET
ALA
PRO
SER
SER
ALA
LYS
THR
GLN
SER
LYS
LYS
VAL
VAL
LYS
GLY
THR
ASN
GLY
LYS
K22
A23
L24
K25
A43
P44
T142

- Molecule 29: Large ribosomal subunit protein uL24A

Chain LY:  98%

MET
A2
D7
L126
GLU

- Molecule 30: Large ribosomal subunit protein eL27A

Chain LZ:  99%

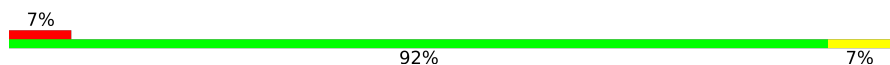
MET
A2
K3
R135
F136

- Molecule 31: Large ribosomal subunit protein uL15

Chain La:  98%

MET
F2
H40
L78
A149

- Molecule 32: Large ribosomal subunit protein eL29

Chain Lb:  7% 92% 7%

MET
A2
K3
S4
K5
N11
P24
K33
H48
K59

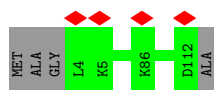
- Molecule 33: Large ribosomal subunit protein eL30

Chain Lc:  91% 9%

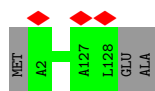
MET
ALA
PRO
VAL
LYS
SER
GLN
GLU
S9
L104
ALA

- Molecule 34: Large ribosomal subunit protein eL31A

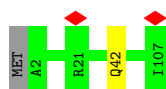
Chain Ld:  96%



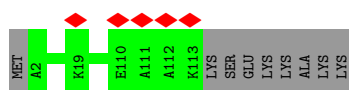
- Molecule 35: Large ribosomal subunit protein eL32



- Molecule 36: Large ribosomal subunit protein eL33A



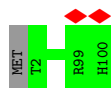
- Molecule 37: Large ribosomal subunit protein eL34A



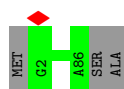
- Molecule 38: Large ribosomal subunit protein uL29A



- Molecule 39: Large ribosomal subunit protein eL36A

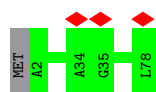


- Molecule 40: Large ribosomal subunit protein eL37A



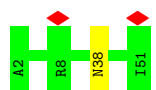
- Molecule 41: Large ribosomal subunit protein eL38

Chain Lk:  99%




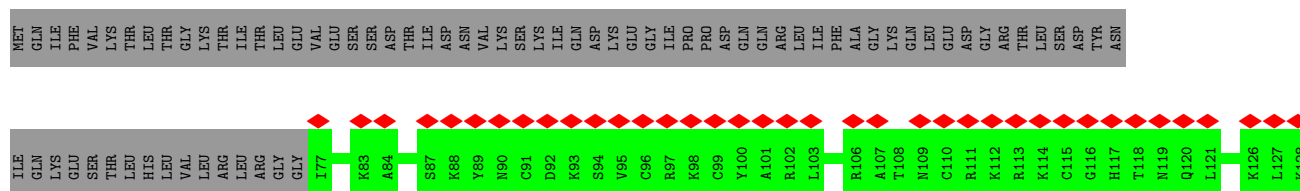
- Molecule 42: Large ribosomal subunit protein eL39

Chain Ll:  98%




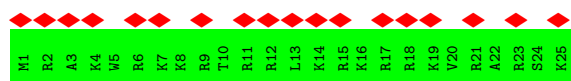
- Molecule 43: Ubiquitin-ribosomal protein eL40A fusion protein

Chain Lm:  30% 41% 59%



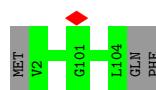
- Molecule 44: Large ribosomal subunit protein eL41A

Chain Ln:  72% 100%



- Molecule 45: Large ribosomal subunit protein eL42A

Chain Lo:  97%



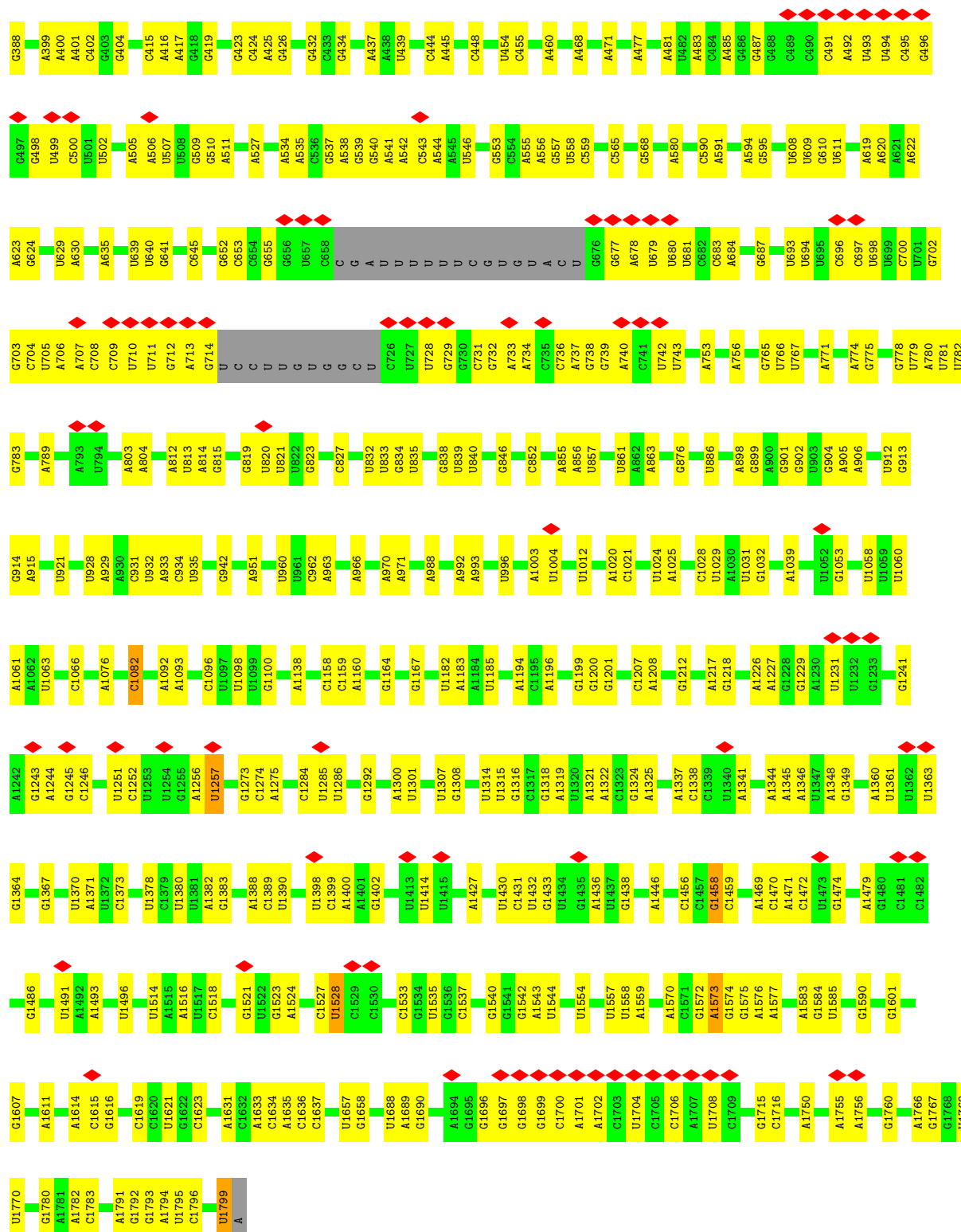
- Molecule 46: Large ribosomal subunit protein eL43A

Chain Lp:  99%

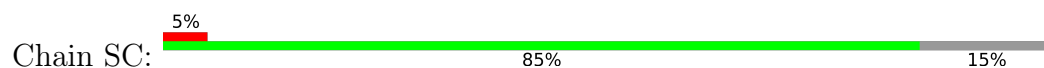


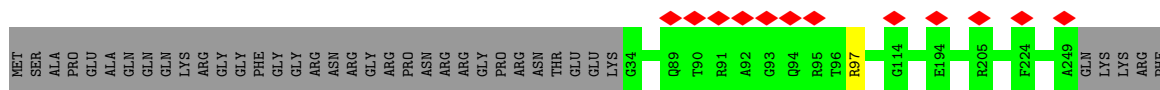
- Molecule 47: Large ribosomal subunit protein uL10

Chain P0:  52% 60% 39%

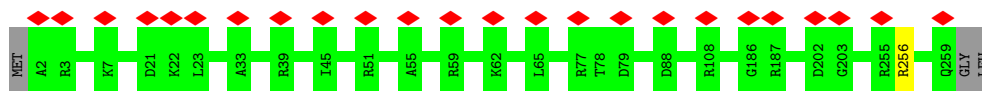


• Molecule 50: 40S ribosomal protein S2

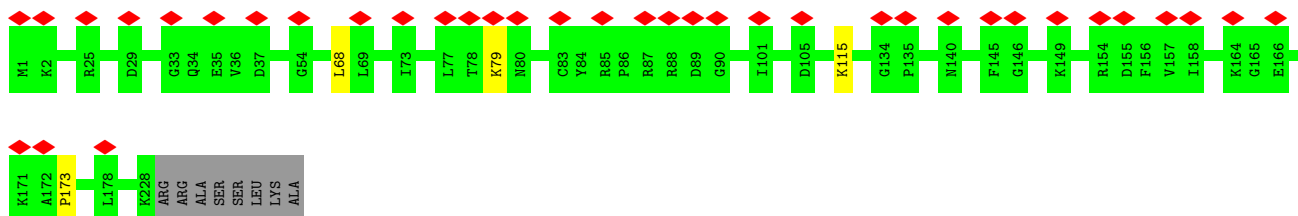




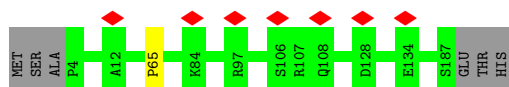
- Molecule 51: 40S ribosomal protein S4-A



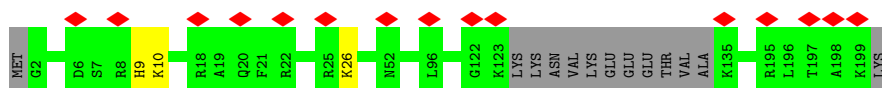
- Molecule 52: 40S ribosomal protein S6-A



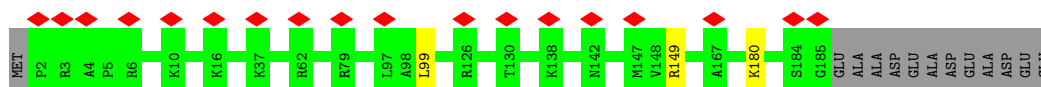
- Molecule 53: 40S ribosomal protein S7-A



- Molecule 54: 40S ribosomal protein S8-A

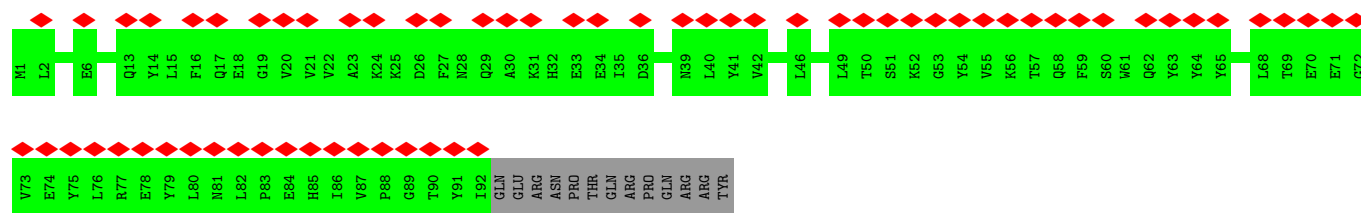


- Molecule 55: 40S ribosomal protein S9-A

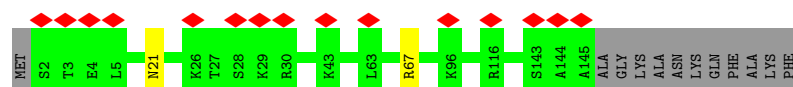
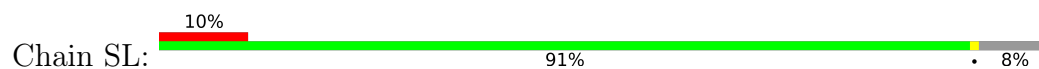


- Molecule 56: Small ribosomal subunit protein eS10A

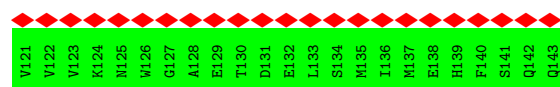
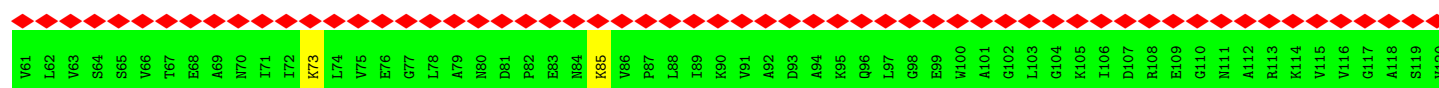
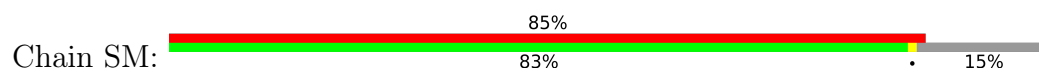




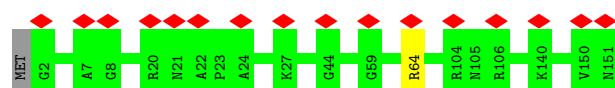
- Molecule 57: Small ribosomal subunit protein uS17A



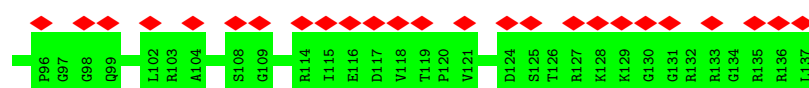
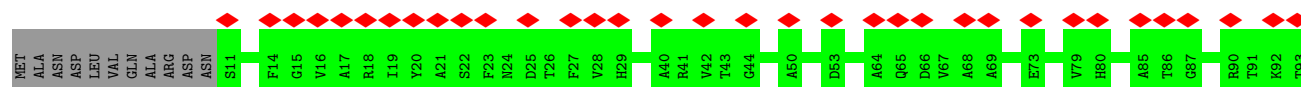
- Molecule 58: Small ribosomal subunit protein eS12



- Molecule 59: 40S ribosomal protein S13

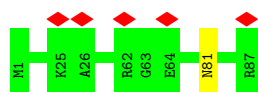


- Molecule 60: Small ribosomal subunit protein uS11B



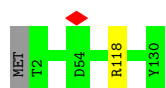
- Molecule 61: Small ribosomal subunit protein eS21A

Chain SV:  6% 99%



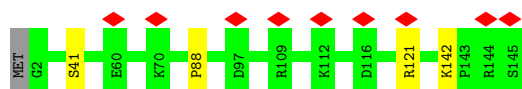
- Molecule 62: 40S ribosomal protein S22-A

Chain SW:  98%



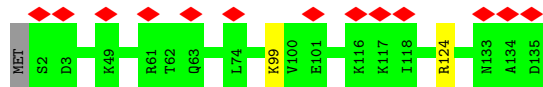
- Molecule 63: 40S ribosomal protein S23-A

Chain SX:  6% 97%




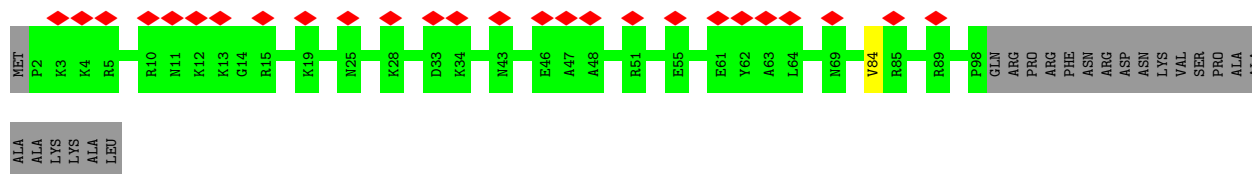
- Molecule 64: 40S ribosomal protein S24-A

Chain SY:  10% 98%



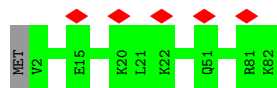
- Molecule 65: Small ribosomal subunit protein eS26B

Chain Sa:  22% 81% 18%



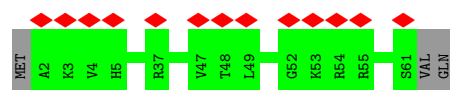
- Molecule 66: 40S ribosomal protein S27-A

Chain Sb:  6% 99%

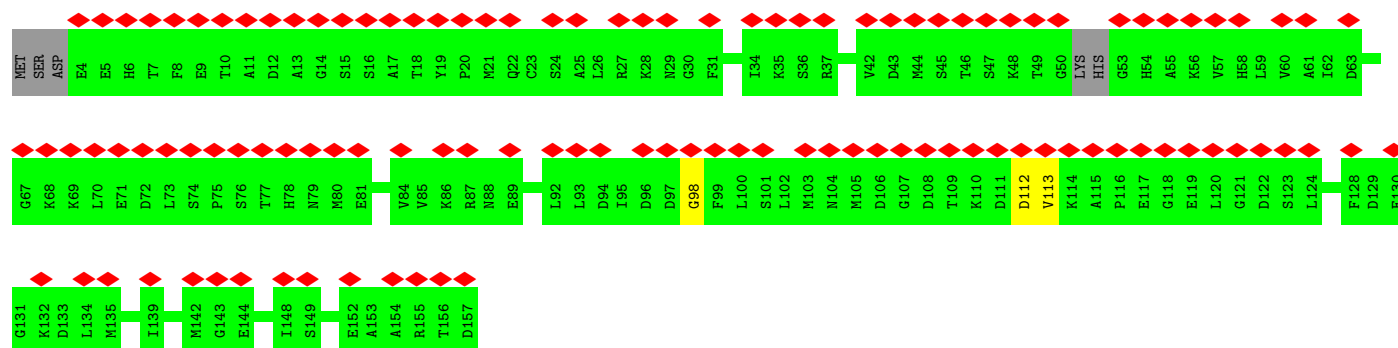


- Molecule 67: 40S ribosomal protein S30-A

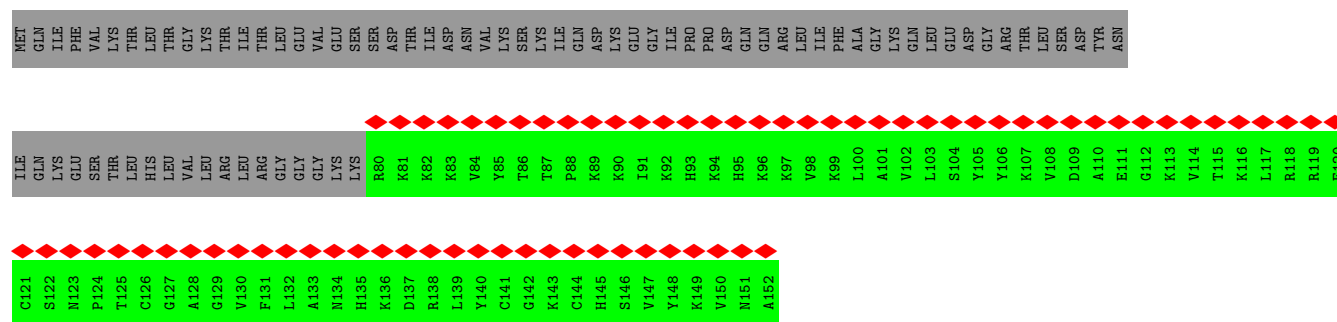
Chain Se:  21% 95% 5%



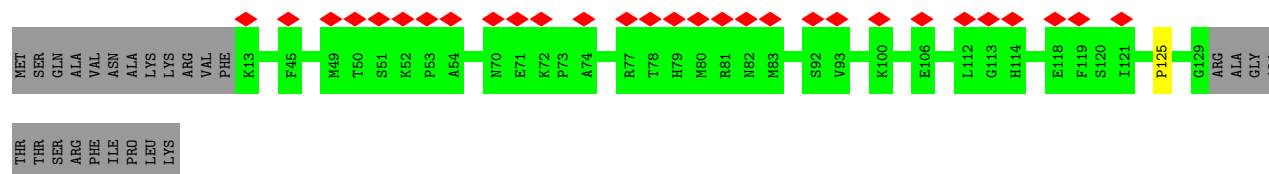
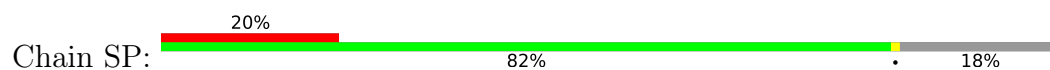
- Molecule 68: Eukaryotic translation initiation factor 5A-1



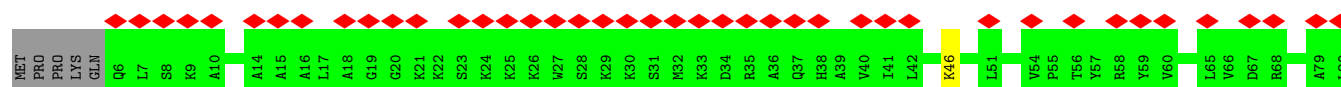
- Molecule 69: Ubiquitin-ribosomal protein eS31 fusion protein

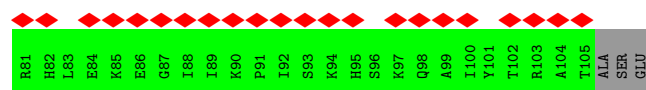


- Molecule 70: Small ribosomal subunit protein uS19

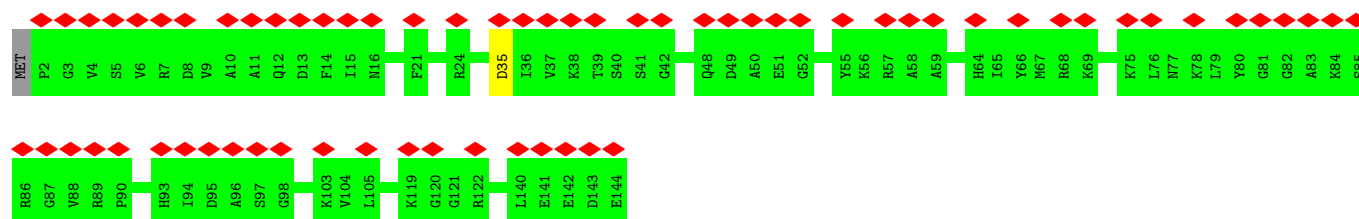


- Molecule 71: Small ribosomal subunit protein eS25A

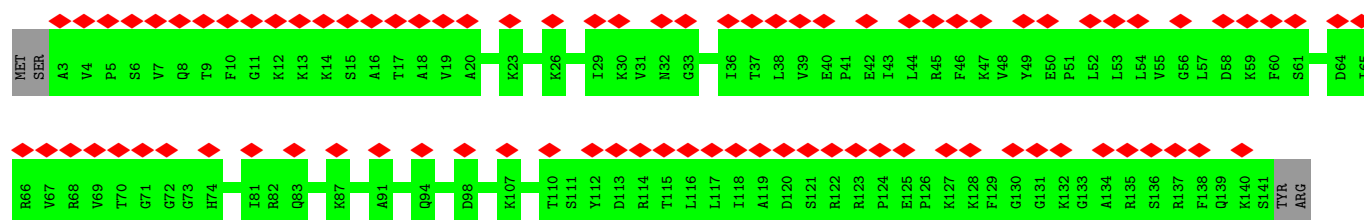




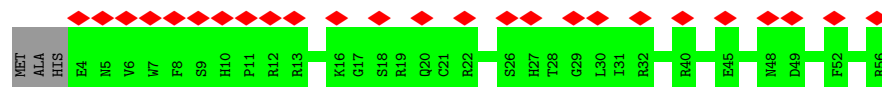
- Molecule 72: Small ribosomal subunit protein eS19A



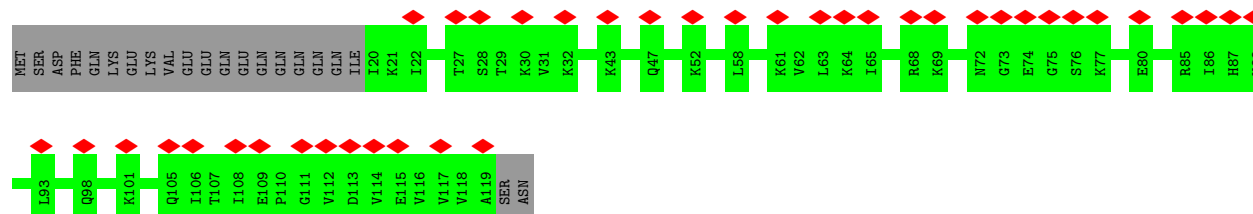
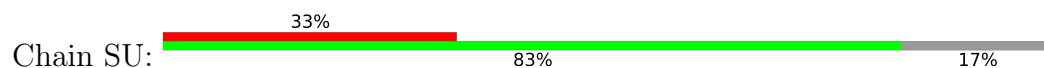
- Molecule 73: Small ribosomal subunit protein uS9A



- Molecule 74: Small ribosomal subunit protein uS14A



- Molecule 75: Small ribosomal subunit protein uS10



- Molecule 76: Small ribosomal subunit protein eS28A





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	80383	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.035	Depositor
Minimum map value	-0.021	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	484.15363, 484.15363, 484.15363	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0807, 1.0807, 1.0807	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	LA	0.48	0/1933	0.58	0/2598
2	SA	0.36	0/1644	0.54	0/2249
3	LB	0.48	0/3146	0.57	0/4228
4	SB	0.31	0/1823	0.64	1/2447 (0.0%)
5	C1	0.88	1/77108 (0.0%)	0.92	44/120216 (0.0%)
6	C4	0.82	0/2883	0.85	1/4491 (0.0%)
7	C3	0.91	0/3746	0.90	3/5832 (0.1%)
8	LC	0.47	0/2800	0.55	0/3790
9	LD	0.45	0/2400	0.57	2/3239 (0.1%)
10	LE	0.43	0/1329	0.56	0/1794
11	LF	0.51	0/1821	0.53	0/2451
12	LG	0.45	0/1836	0.57	1/2481 (0.0%)
13	LH	0.44	0/1529	0.60	0/2060
14	LI	0.43	0/1801	0.54	0/2416
15	LJ	0.40	0/1371	0.64	0/1838
16	LL	0.47	0/1568	0.59	0/2106
17	LM	0.46	1/1068 (0.1%)	0.54	0/1438
18	LN	0.53	0/1757	0.55	1/2354 (0.0%)
19	LO	0.50	0/1585	0.54	0/2128
20	LP	0.47	0/1439	0.55	0/1938
21	LQ	0.48	0/1465	0.56	0/1965
22	LR	0.43	0/1532	0.55	0/2043
23	LS	0.49	0/1473	0.54	0/1980
24	LT	0.48	0/1300	0.52	0/1743
25	LU	0.45	0/812	0.56	0/1099
26	LV	0.47	0/1018	0.54	0/1369
27	LW	0.41	0/863	0.53	0/1169
28	LX	0.49	0/979	0.57	0/1321
29	LY	0.45	0/995	0.54	0/1329
30	LZ	0.45	0/1118	0.53	0/1497
31	La	0.47	0/1204	0.56	0/1612
32	Lb	0.39	0/473	0.55	0/629

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Lc	0.47	0/745	0.54	0/1001
34	Ld	0.46	0/890	0.58	0/1196
35	Le	0.48	0/1038	0.56	0/1390
36	Lf	0.53	0/868	0.54	0/1168
37	Lg	0.47	0/890	0.54	0/1189
38	Lh	0.44	0/978	0.59	0/1301
39	Li	0.39	0/772	0.57	0/1026
40	Lj	0.48	0/685	0.54	0/908
41	Lk	0.39	0/618	0.58	0/826
42	Ll	0.46	0/443	0.59	0/588
43	Lm	0.31	0/423	0.52	0/562
44	Ln	0.30	0/230	0.45	0/296
45	Lo	0.48	0/836	0.53	0/1104
46	Lp	0.49	0/701	0.62	0/934
47	P0	0.28	0/1498	0.56	1/2025 (0.0%)
48	P2	0.25	0/728	0.54	0/975
49	C2	0.58	0/42053	0.87	24/65522 (0.0%)
50	SC	0.39	0/1656	0.61	0/2251
51	SE	0.37	0/2097	0.54	0/2823
52	SG	0.32	0/1839	0.57	0/2460
53	SH	0.35	0/1498	0.61	0/2019
54	SI	0.36	0/1501	0.58	0/2006
55	SJ	0.37	0/1504	0.58	0/2016
56	SK	0.29	0/769	0.55	0/1039
57	SL	0.43	0/1185	0.55	0/1598
58	SM	0.26	0/883	0.58	0/1199
59	SN	0.37	0/1215	0.57	0/1638
60	SO	0.32	0/937	0.58	0/1261
61	SV	0.40	0/682	0.63	0/921
62	SW	0.44	0/1038	0.63	0/1395
63	SX	0.39	0/1139	0.57	0/1518
64	SY	0.35	0/1087	0.62	0/1449
65	Sa	0.33	0/782	0.58	0/1047
66	Sb	0.32	0/620	0.53	0/838
67	Se	0.33	0/480	0.59	0/639
68	5	0.28	0/1131	0.58	0/1522
69	Sf	0.27	0/567	0.57	0/764
70	SP	0.32	0/936	0.57	1/1259 (0.1%)
71	SZ	0.28	0/781	0.52	0/1045
72	ST	0.30	0/1130	0.56	1/1517 (0.1%)
73	SQ	0.32	0/1101	0.54	0/1478
74	Sd	0.33	0/452	0.49	0/600
75	SU	0.31	0/807	0.60	0/1091

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Sc	0.30	0/493	0.60	0/663
77	s	0.29	0/261	0.57	0/351
All	All	0.67	2/210786 (0.0%)	0.80	80/310268 (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
3	LB	0	1
4	SB	0	1
8	LC	0	1
11	LF	0	1
12	LG	0	1
17	LM	0	1
19	LO	0	1
28	LX	0	1
52	SG	0	1
54	SI	0	1
63	SX	0	1
65	Sa	0	1
68	5	0	1
77	s	0	1
All	All	0	14

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C1	2149	A	N9-C4	-5.48	1.34	1.37
17	LM	65	LEU	C-N	-5.40	1.21	1.34

The worst 5 of 80 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	C2	1389	C	C2-N1-C1'	8.19	127.81	118.80
49	C2	553	G	N1-C6-O6	-7.52	115.39	119.90
5	C1	1857	C	C2-N1-C1'	7.48	127.03	118.80
5	C1	1857	C	N1-C2-O2	7.13	123.18	118.90
5	C1	3278	C	N1-C2-O2	7.03	123.12	118.90

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	LB	255	TRP	Peptide
8	LC	13	GLY	Peptide
11	LF	232	ARG	Peptide
12	LG	76	ALA	Peptide
4	SB	144	ARG	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	
1	LA	249/254 (98%)	221 (89%)	28 (11%)	0	100	100
2	SA	204/252 (81%)	180 (88%)	24 (12%)	0	100	100
3	LB	384/387 (99%)	339 (88%)	45 (12%)	0	100	100
4	SB	222/255 (87%)	185 (83%)	36 (16%)	1 (0%)	29	68
8	LC	359/362 (99%)	318 (89%)	39 (11%)	2 (1%)	25	64
9	LD	292/297 (98%)	266 (91%)	25 (9%)	1 (0%)	41	75
10	LE	163/176 (93%)	140 (86%)	23 (14%)	0	100	100
11	LF	220/244 (90%)	205 (93%)	15 (7%)	0	100	100
12	LG	231/256 (90%)	216 (94%)	15 (6%)	0	100	100
13	LH	189/191 (99%)	170 (90%)	19 (10%)	0	100	100
14	LI	216/221 (98%)	203 (94%)	13 (6%)	0	100	100
15	LJ	167/174 (96%)	144 (86%)	23 (14%)	0	100	100
16	LL	191/199 (96%)	168 (88%)	22 (12%)	1 (0%)	29	68
17	LM	134/138 (97%)	124 (92%)	10 (8%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	LN	201/204 (98%)	180 (90%)	21 (10%)	0	100	100
19	LO	195/199 (98%)	186 (95%)	7 (4%)	2 (1%)	15	55
20	LP	181/184 (98%)	165 (91%)	16 (9%)	0	100	100
21	LQ	183/186 (98%)	170 (93%)	13 (7%)	0	100	100
22	LR	186/189 (98%)	178 (96%)	6 (3%)	2 (1%)	14	53
23	LS	169/172 (98%)	160 (95%)	9 (5%)	0	100	100
24	LT	157/160 (98%)	147 (94%)	10 (6%)	0	100	100
25	LU	98/121 (81%)	86 (88%)	12 (12%)	0	100	100
26	LV	134/137 (98%)	127 (95%)	7 (5%)	0	100	100
27	LW	124/155 (80%)	111 (90%)	13 (10%)	0	100	100
28	LX	119/142 (84%)	111 (93%)	7 (6%)	1 (1%)	19	59
29	LY	123/127 (97%)	114 (93%)	9 (7%)	0	100	100
30	LZ	133/136 (98%)	121 (91%)	12 (9%)	0	100	100
31	La	146/149 (98%)	126 (86%)	18 (12%)	2 (1%)	11	48
32	Lb	56/59 (95%)	50 (89%)	5 (9%)	1 (2%)	8	43
33	Lc	94/105 (90%)	88 (94%)	6 (6%)	0	100	100
34	Ld	107/113 (95%)	96 (90%)	11 (10%)	0	100	100
35	Le	125/130 (96%)	116 (93%)	9 (7%)	0	100	100
36	Lf	104/107 (97%)	95 (91%)	9 (9%)	0	100	100
37	Lg	110/121 (91%)	105 (96%)	5 (4%)	0	100	100
38	Lh	117/120 (98%)	111 (95%)	6 (5%)	0	100	100
39	Li	97/100 (97%)	88 (91%)	9 (9%)	0	100	100
40	Lj	83/88 (94%)	78 (94%)	5 (6%)	0	100	100
41	Lk	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
42	Ll	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
43	Lm	50/128 (39%)	46 (92%)	4 (8%)	0	100	100
44	Ln	23/25 (92%)	23 (100%)	0	0	100	100
45	Lo	101/106 (95%)	94 (93%)	7 (7%)	0	100	100
46	Lp	89/92 (97%)	80 (90%)	9 (10%)	0	100	100
47	P0	187/312 (60%)	164 (88%)	23 (12%)	0	100	100
48	P2	92/165 (56%)	76 (83%)	16 (17%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	SC	214/254 (84%)	201 (94%)	13 (6%)	0	100	100
51	SE	256/261 (98%)	229 (90%)	27 (10%)	0	100	100
52	SG	226/236 (96%)	202 (89%)	23 (10%)	1 (0%)	34	71
53	SH	182/190 (96%)	159 (87%)	22 (12%)	1 (0%)	29	68
54	SI	183/200 (92%)	156 (85%)	26 (14%)	1 (0%)	29	68
55	SJ	182/197 (92%)	160 (88%)	21 (12%)	1 (0%)	29	68
56	SK	90/105 (86%)	81 (90%)	9 (10%)	0	100	100
57	SL	142/156 (91%)	122 (86%)	20 (14%)	0	100	100
58	SM	119/143 (83%)	84 (71%)	35 (29%)	0	100	100
59	SN	148/151 (98%)	131 (88%)	17 (12%)	0	100	100
60	SO	125/138 (91%)	112 (90%)	13 (10%)	0	100	100
61	SV	85/87 (98%)	67 (79%)	17 (20%)	1 (1%)	13	51
62	SW	127/130 (98%)	116 (91%)	11 (9%)	0	100	100
63	SX	142/145 (98%)	123 (87%)	18 (13%)	1 (1%)	22	61
64	SY	132/135 (98%)	121 (92%)	11 (8%)	0	100	100
65	Sa	95/119 (80%)	79 (83%)	16 (17%)	0	100	100
66	Sb	79/82 (96%)	67 (85%)	12 (15%)	0	100	100
67	Se	58/63 (92%)	51 (88%)	7 (12%)	0	100	100
68	5	148/157 (94%)	124 (84%)	22 (15%)	2 (1%)	11	48
69	Sf	71/152 (47%)	42 (59%)	29 (41%)	0	100	100
70	SP	115/142 (81%)	104 (90%)	11 (10%)	0	100	100
71	SZ	98/108 (91%)	83 (85%)	15 (15%)	0	100	100
72	ST	141/144 (98%)	130 (92%)	11 (8%)	0	100	100
73	SQ	137/143 (96%)	127 (93%)	10 (7%)	0	100	100
74	Sd	51/56 (91%)	50 (98%)	1 (2%)	0	100	100
75	SU	98/121 (81%)	91 (93%)	7 (7%)	0	100	100
76	Sc	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
77	s	38/273 (14%)	31 (82%)	6 (16%)	1 (3%)	5	35
All	All	10471/11721 (89%)	9388 (90%)	1061 (10%)	22 (0%)	50	79

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
31	La	78	LEU
54	SI	10	LYS
68	5	113	VAL
19	LO	111[A]	PRO
28	LX	44	PRO

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	
1	LA	190/196 (97%)	189 (100%)	1 (0%)	88	95
2	SA	170/210 (81%)	170 (100%)	0	100	100
3	LB	319/323 (99%)	318 (100%)	1 (0%)	92	97
4	SB	200/224 (89%)	199 (100%)	1 (0%)	88	95
8	LC	288/289 (100%)	288 (100%)	0	100	100
9	LD	241/245 (98%)	240 (100%)	1 (0%)	91	97
10	LE	139/155 (90%)	137 (99%)	2 (1%)	67	85
11	LF	186/205 (91%)	186 (100%)	0	100	100
12	LG	187/208 (90%)	187 (100%)	0	100	100
13	LH	168/171 (98%)	166 (99%)	2 (1%)	71	87
14	LI	185/187 (99%)	185 (100%)	0	100	100
15	LJ	146/151 (97%)	145 (99%)	1 (1%)	84	93
16	LL	154/159 (97%)	153 (99%)	1 (1%)	86	94
17	LM	107/109 (98%)	107 (100%)	0	100	100
18	LN	175/176 (99%)	175 (100%)	0	100	100
19	LO	160/162 (99%)	159 (99%)	1 (1%)	86	94
20	LP	138/146 (94%)	138 (100%)	0	100	100
21	LQ	150/151 (99%)	148 (99%)	2 (1%)	69	86
22	LR	152/154 (99%)	152 (100%)	0	100	100
23	LS	155/156 (99%)	154 (99%)	1 (1%)	86	94

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	LT	136/137 (99%)	136 (100%)	0	100	100
25	LU	87/107 (81%)	87 (100%)	0	100	100
26	LV	104/105 (99%)	104 (100%)	0	100	100
27	LW	60/129 (46%)	60 (100%)	0	100	100
28	LX	104/118 (88%)	103 (99%)	1 (1%)	76	88
29	LY	108/110 (98%)	108 (100%)	0	100	100
30	LZ	115/116 (99%)	114 (99%)	1 (1%)	78	90
31	La	118/119 (99%)	118 (100%)	0	100	100
32	Lb	46/47 (98%)	43 (94%)	3 (6%)	17	51
33	Lc	81/88 (92%)	81 (100%)	0	100	100
34	Ld	92/97 (95%)	92 (100%)	0	100	100
35	Le	108/111 (97%)	108 (100%)	0	100	100
36	Lf	90/91 (99%)	89 (99%)	1 (1%)	73	88
37	Lg	95/103 (92%)	95 (100%)	0	100	100
38	Lh	104/105 (99%)	104 (100%)	0	100	100
39	Li	80/82 (98%)	80 (100%)	0	100	100
40	Lj	69/71 (97%)	69 (100%)	0	100	100
41	Lk	68/69 (99%)	68 (100%)	0	100	100
42	Ll	45/45 (100%)	44 (98%)	1 (2%)	52	77
43	Lm	47/116 (40%)	47 (100%)	0	100	100
44	Ln	22/23 (96%)	22 (100%)	0	100	100
45	Lo	87/91 (96%)	87 (100%)	0	100	100
46	Lp	71/72 (99%)	71 (100%)	0	100	100
47	P0	160/254 (63%)	158 (99%)	2 (1%)	69	86
48	P2	81/136 (60%)	80 (99%)	1 (1%)	71	87
50	SC	175/205 (85%)	174 (99%)	1 (1%)	86	94
51	SE	220/222 (99%)	219 (100%)	1 (0%)	88	95
52	SG	189/201 (94%)	187 (99%)	2 (1%)	73	88
53	SH	163/170 (96%)	163 (100%)	0	100	100
54	SI	148/161 (92%)	147 (99%)	1 (1%)	84	93
55	SJ	156/166 (94%)	154 (99%)	2 (1%)	69	86

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
56	SK	77/98 (79%)	77 (100%)	0	100	100
57	SL	129/137 (94%)	127 (98%)	2 (2%)	62	83
58	SM	88/119 (74%)	86 (98%)	2 (2%)	50	76
59	SN	127/128 (99%)	126 (99%)	1 (1%)	81	91
60	SO	91/105 (87%)	91 (100%)	0	100	100
61	SV	71/74 (96%)	71 (100%)	0	100	100
62	SW	110/111 (99%)	109 (99%)	1 (1%)	78	90
63	SX	119/120 (99%)	117 (98%)	2 (2%)	60	82
64	SY	112/113 (99%)	110 (98%)	2 (2%)	59	81
65	Sa	83/100 (83%)	83 (100%)	0	100	100
66	Sb	70/71 (99%)	70 (100%)	0	100	100
67	Se	50/54 (93%)	50 (100%)	0	100	100
68	5	117/133 (88%)	117 (100%)	0	100	100
69	Sf	56/135 (42%)	56 (100%)	0	100	100
70	SP	95/118 (80%)	95 (100%)	0	100	100
71	SZ	77/89 (86%)	76 (99%)	1 (1%)	69	86
72	ST	115/116 (99%)	115 (100%)	0	100	100
73	SQ	115/119 (97%)	115 (100%)	0	100	100
74	Sd	47/49 (96%)	47 (100%)	0	100	100
75	SU	93/114 (82%)	93 (100%)	0	100	100
76	Sc	55/60 (92%)	55 (100%)	0	100	100
77	s	15/228 (7%)	15 (100%)	0	100	100
All	All	8751/9835 (89%)	8709 (100%)	42 (0%)	89	95

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
54	SI	26	LYS
59	SN	64	ARG
55	SJ	149	ARG
57	SL	67	ARG
63	SX	121	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 54 such sidechains are listed below:

Mol	Chain	Res	Type
35	Le	20	HIS
47	P0	83	ASN
62	SW	113	HIS
35	Le	88	HIS
37	Lg	18	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
49	C2	1768/1800 (98%)	501 (28%)	46 (2%)
5	C1	3217/3396 (94%)	637 (19%)	43 (1%)
6	C4	120/121 (99%)	15 (12%)	1 (0%)
7	C3	157/158 (99%)	28 (17%)	1 (0%)
All	All	5262/5475 (96%)	1181 (22%)	91 (1%)

5 of 1181 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	C1	13	A
5	C1	14	U
5	C1	15	C
5	C1	18	G
5	C1	26	A

5 of 91 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
49	C2	541	A
49	C2	1226	A
49	C2	609	U
49	C2	711	U
49	C2	1274	C

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 288 ligands modelled in this entry, 288 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

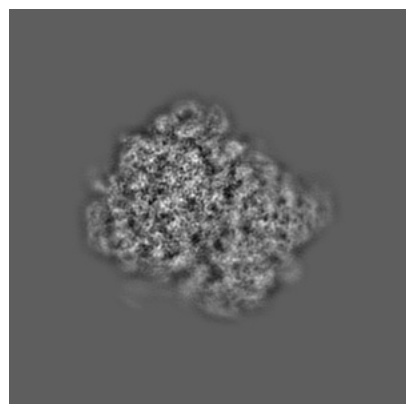
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37995. These allow visual inspection of the internal detail of the map and identification of artifacts.

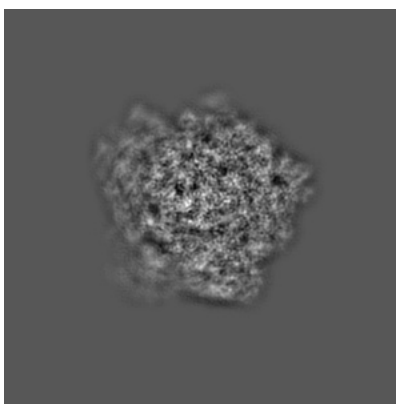
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

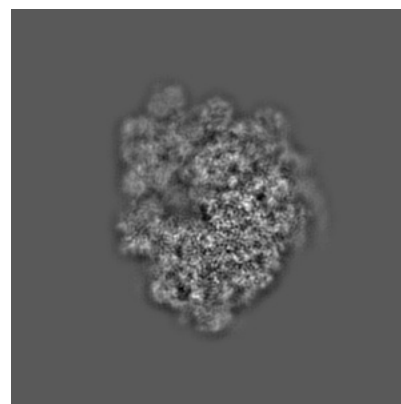
6.1.1 Primary map



X

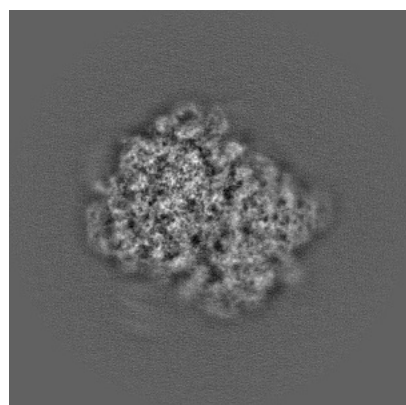


Y

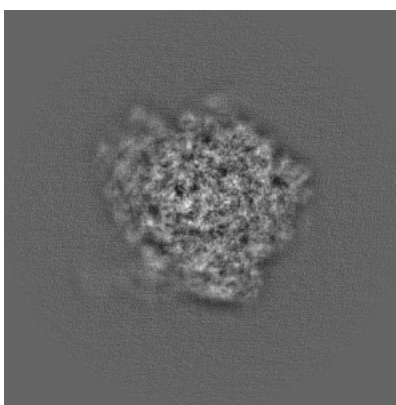


Z

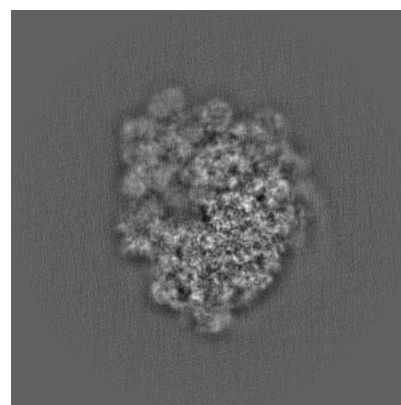
6.1.2 Raw map



X



Y

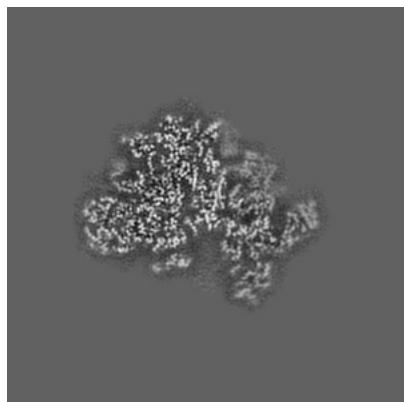


Z

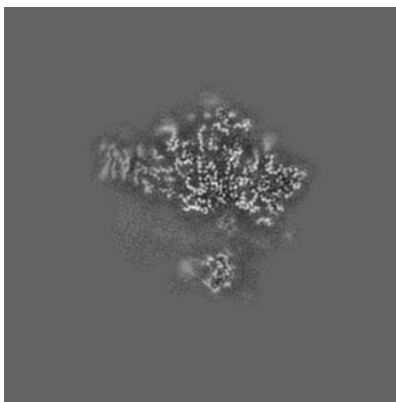
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

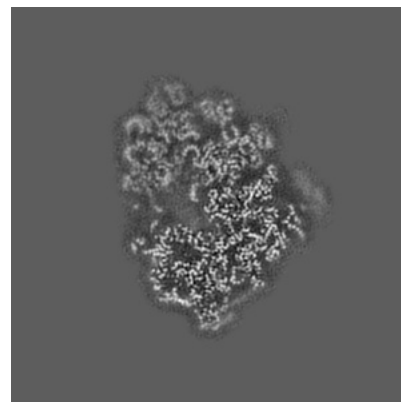
6.2.1 Primary map



X Index: 224

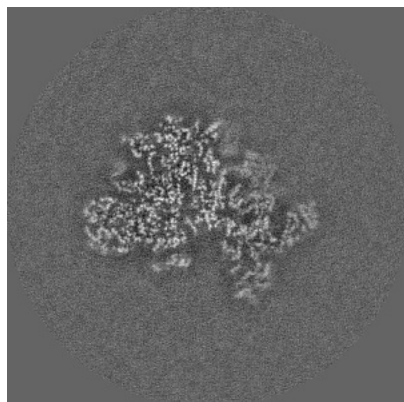


Y Index: 224

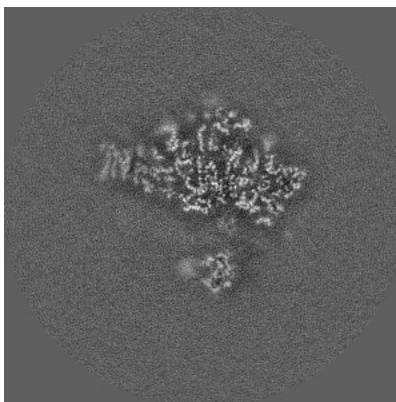


Z Index: 224

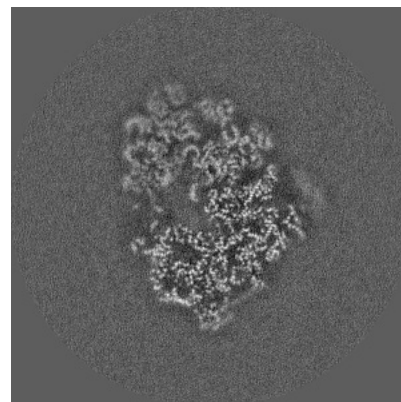
6.2.2 Raw map



X Index: 224



Y Index: 224

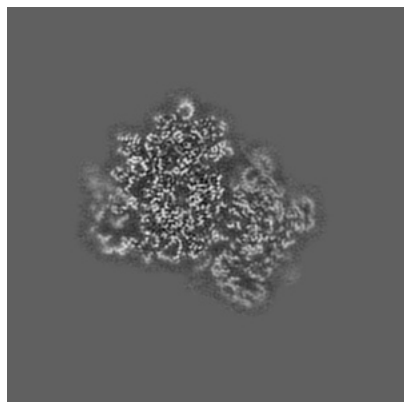


Z Index: 224

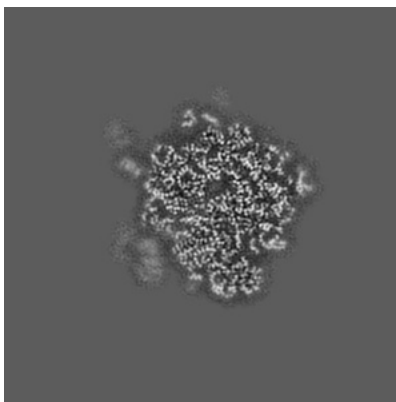
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

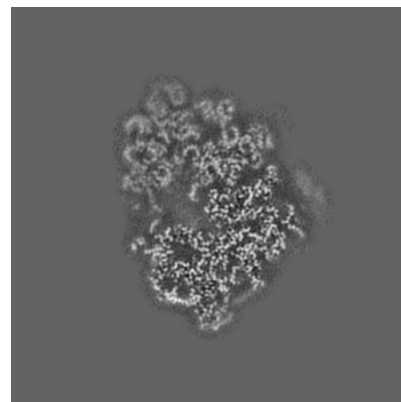
6.3.1 Primary map



X Index: 240

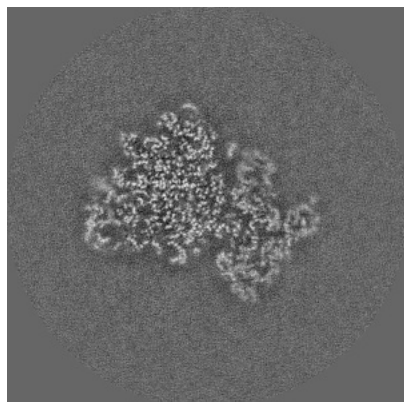


Y Index: 191

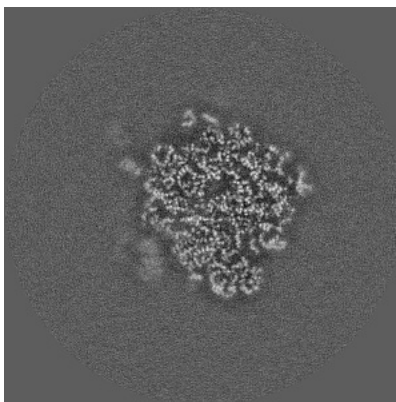


Z Index: 223

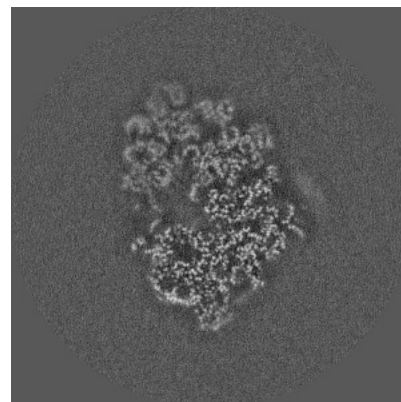
6.3.2 Raw map



X Index: 232



Y Index: 191

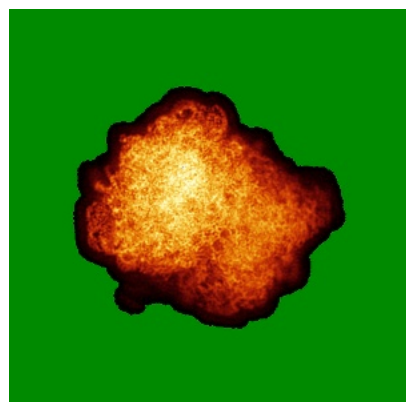


Z Index: 223

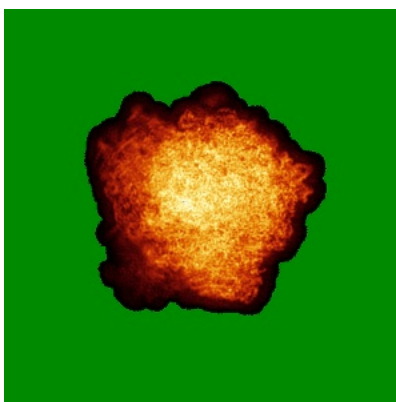
The images above show the largest variance slices of the map in three orthogonal directions.

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

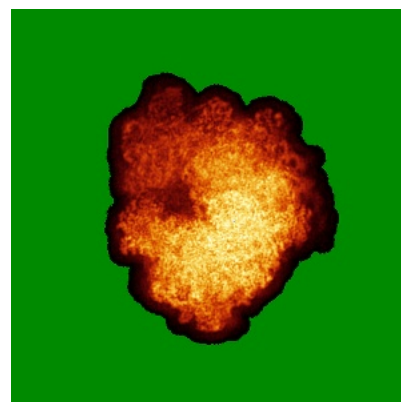
6.4.1 Primary map



X

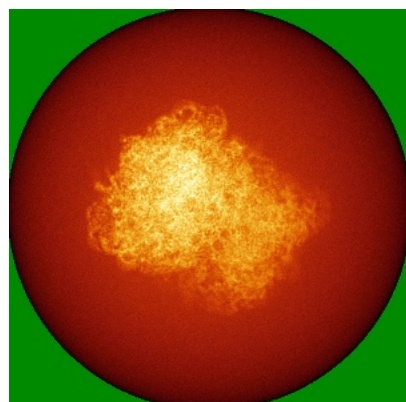


Y

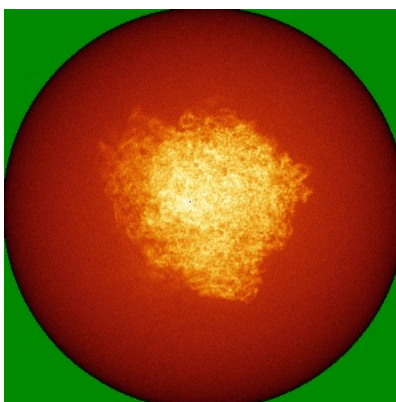


Z

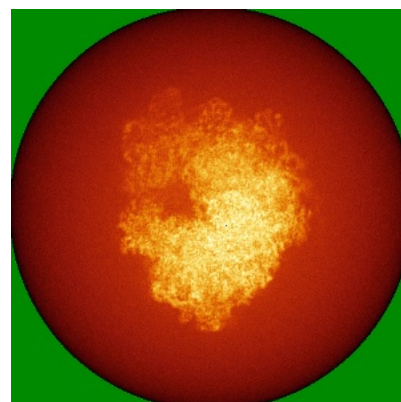
6.4.2 Raw map



X



Y

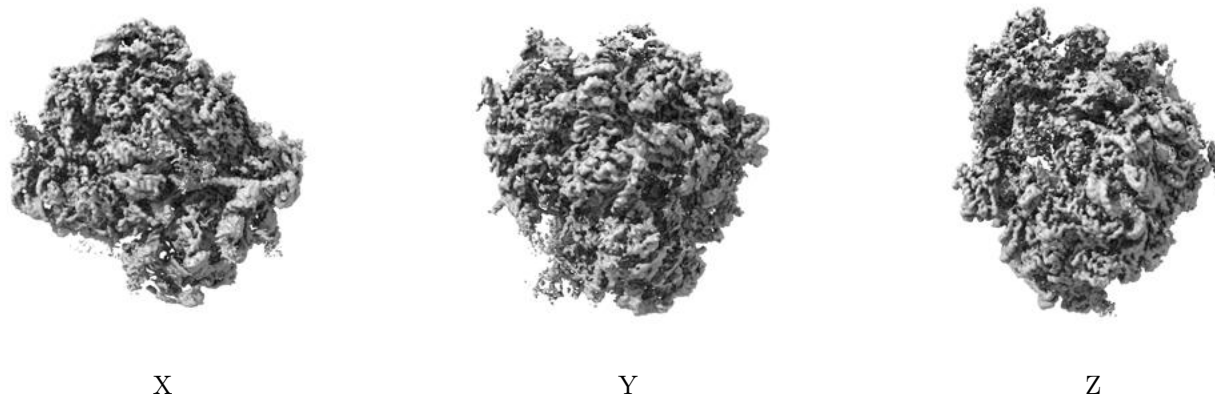


Z

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.

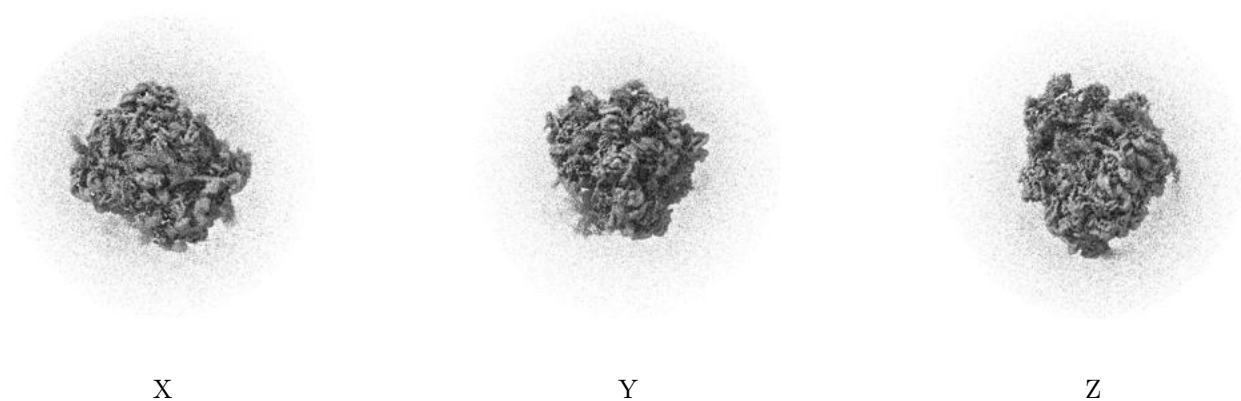
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.005. 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.

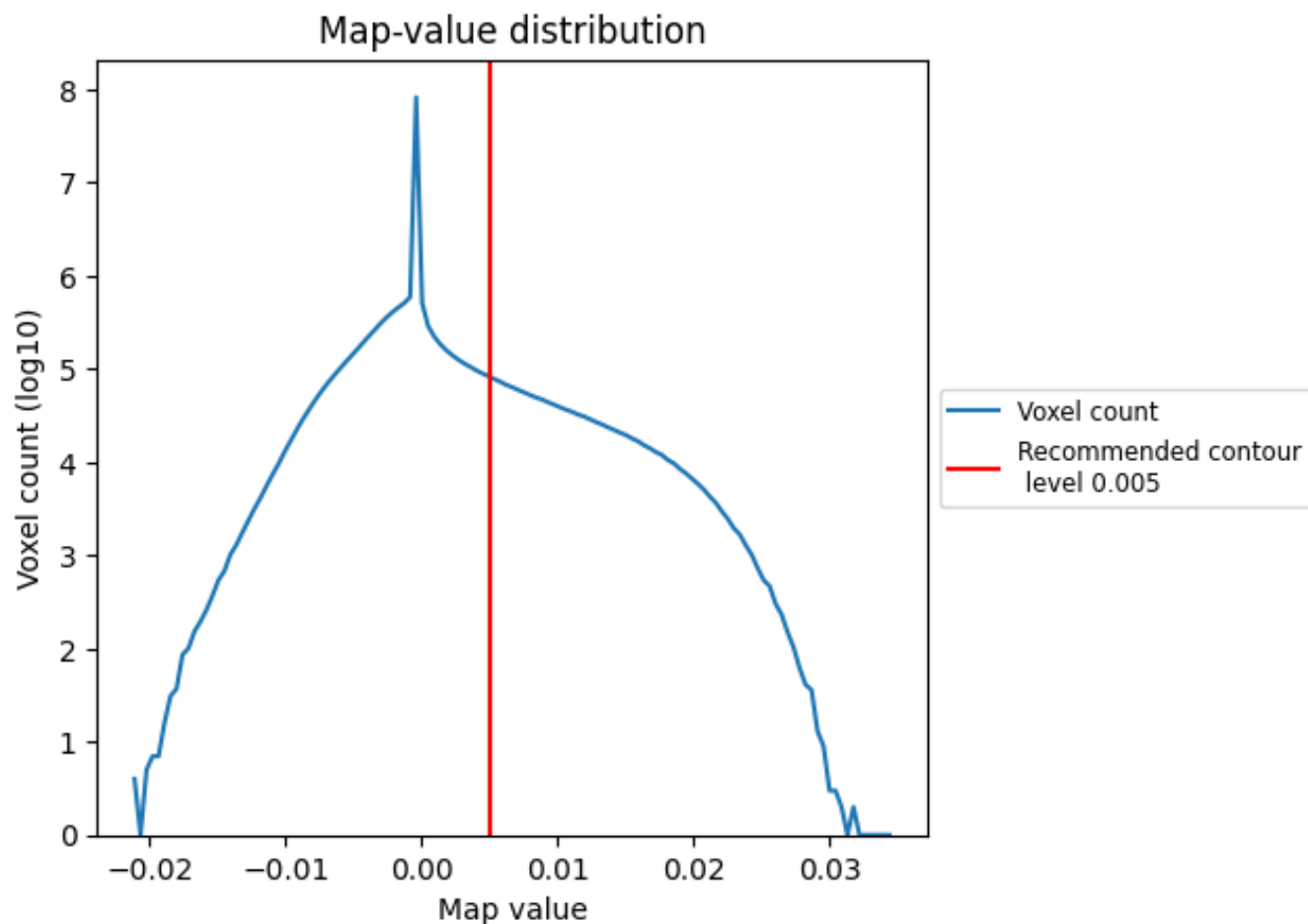
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

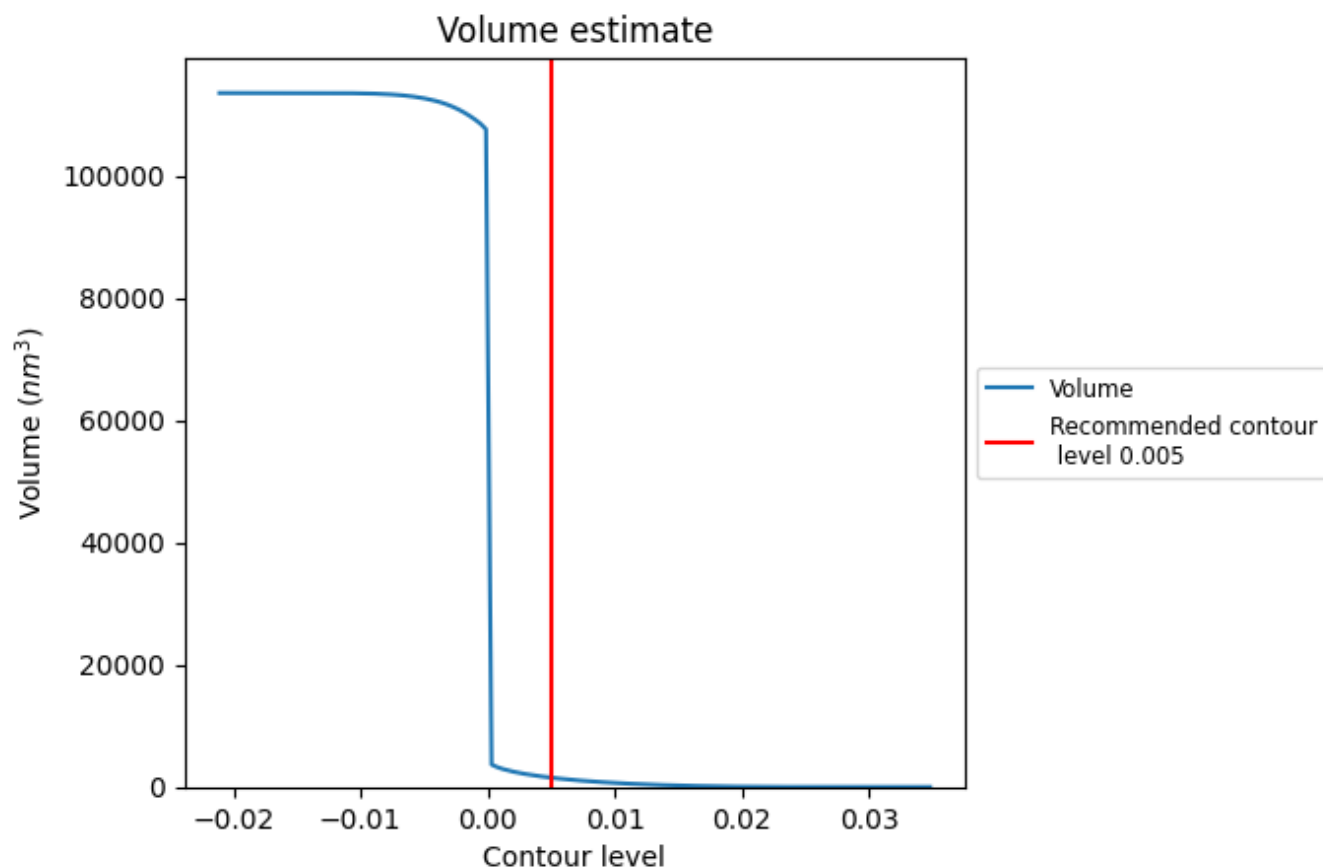
This section contains the results of statistical analysis of the map.

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.

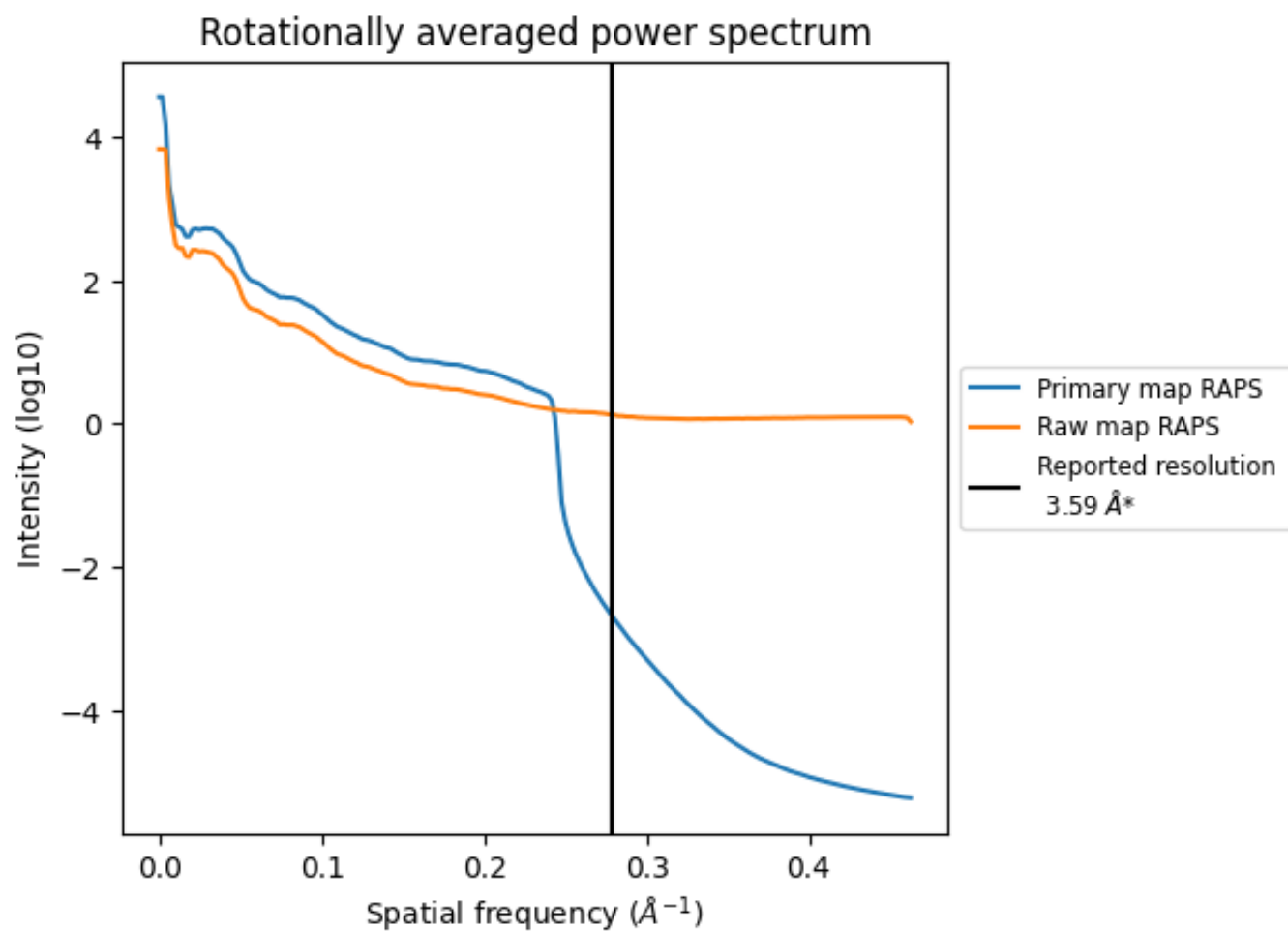
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1519 nm^3 ; this corresponds to an approximate mass of 1372 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 ⓘ

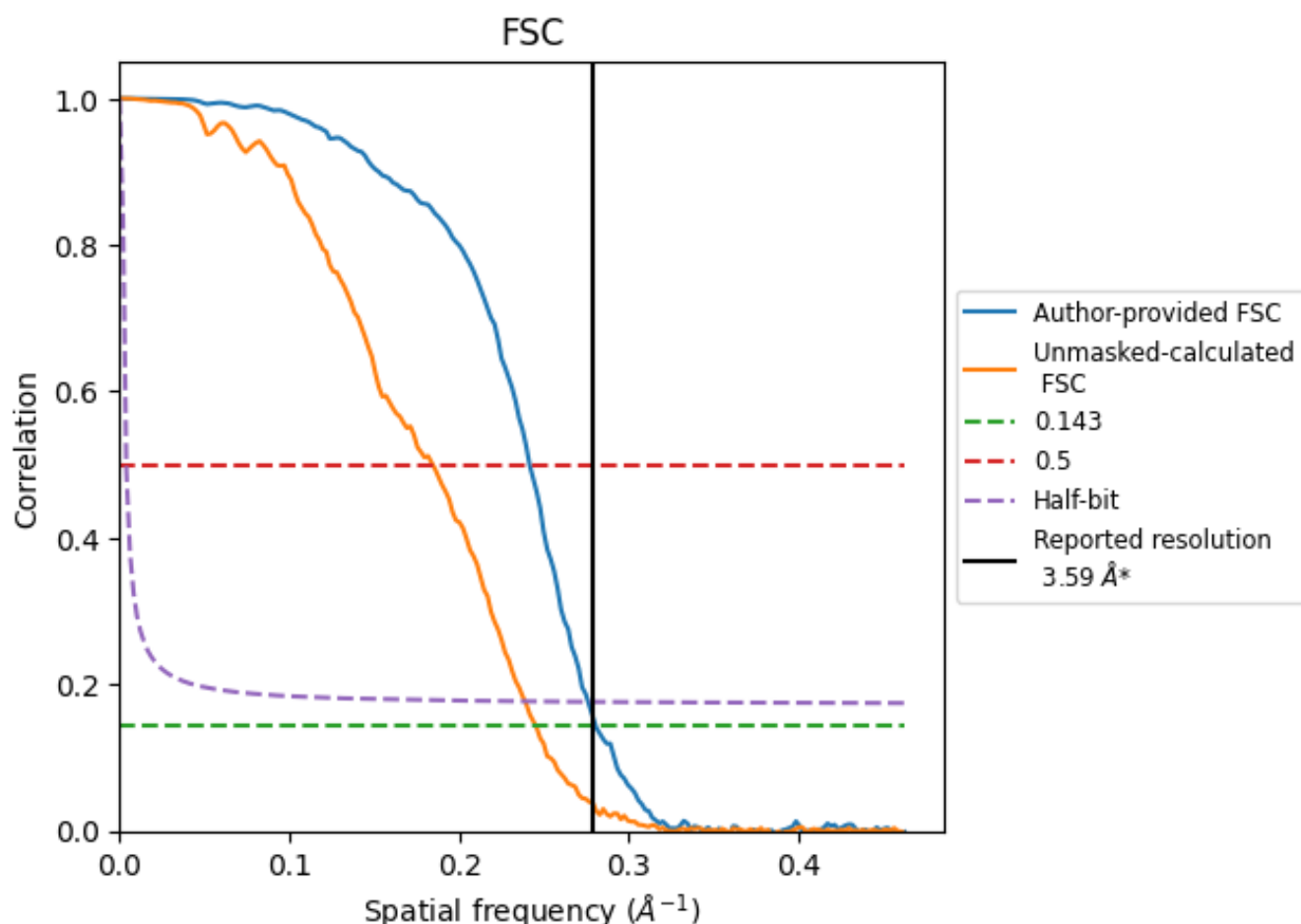


*Reported resolution corresponds to spatial frequency of 0.279 Å⁻¹

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 0.279 \AA^{-1}

8.2 Resolution estimates [i](#)

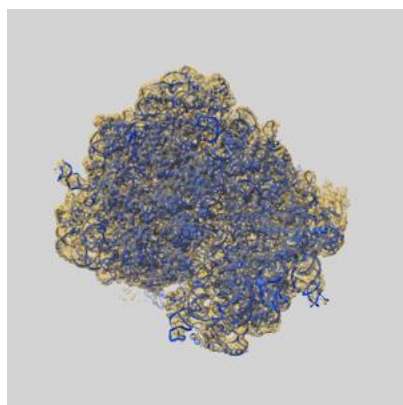
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.59	-	-
Author-provided FSC curve	3.56	4.14	3.62
Unmasked-calculated*	4.08	5.42	4.18

*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 4.08 differs from the reported value 3.59 by more than 10 %

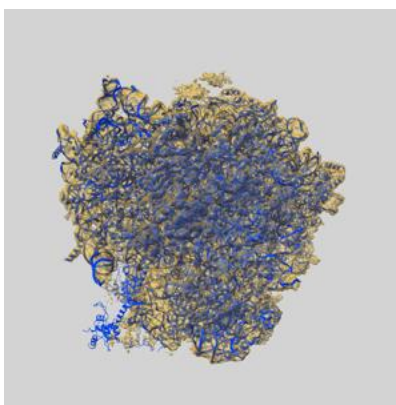
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37995 and PDB model 8Y0U. Per-residue inclusion information can be found in section [3](#) on page [19](#).

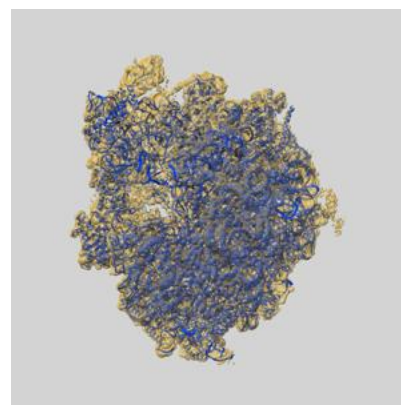
9.1 Map-model overlay [i](#)



X



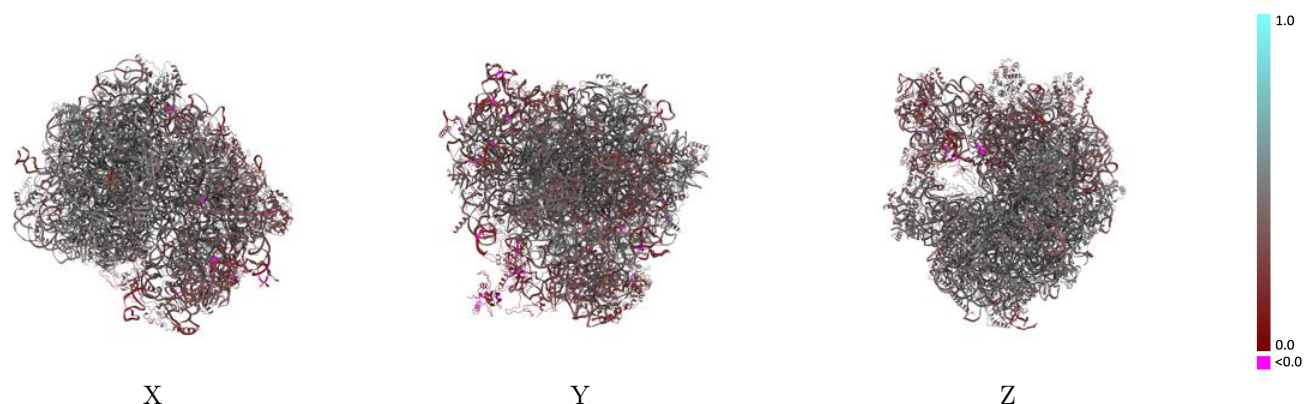
Y



Z

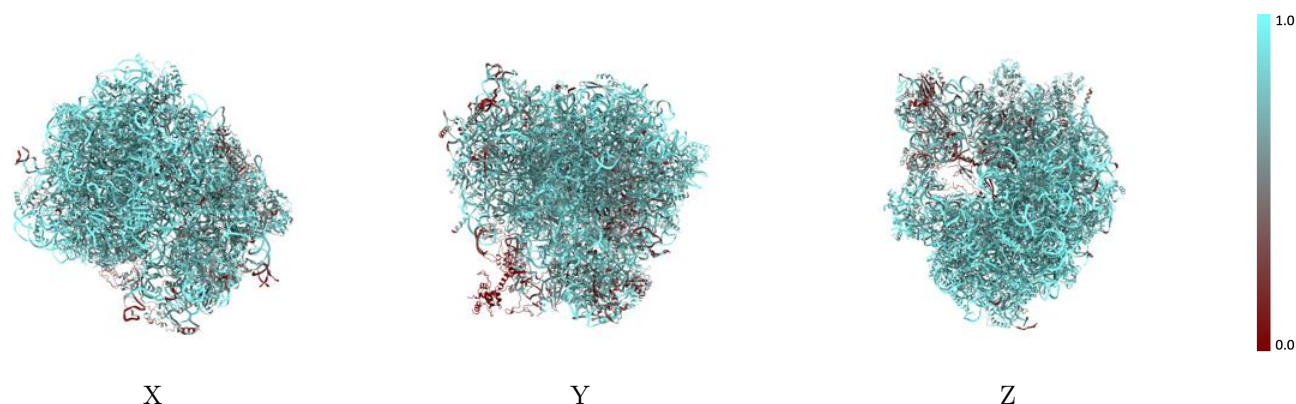
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



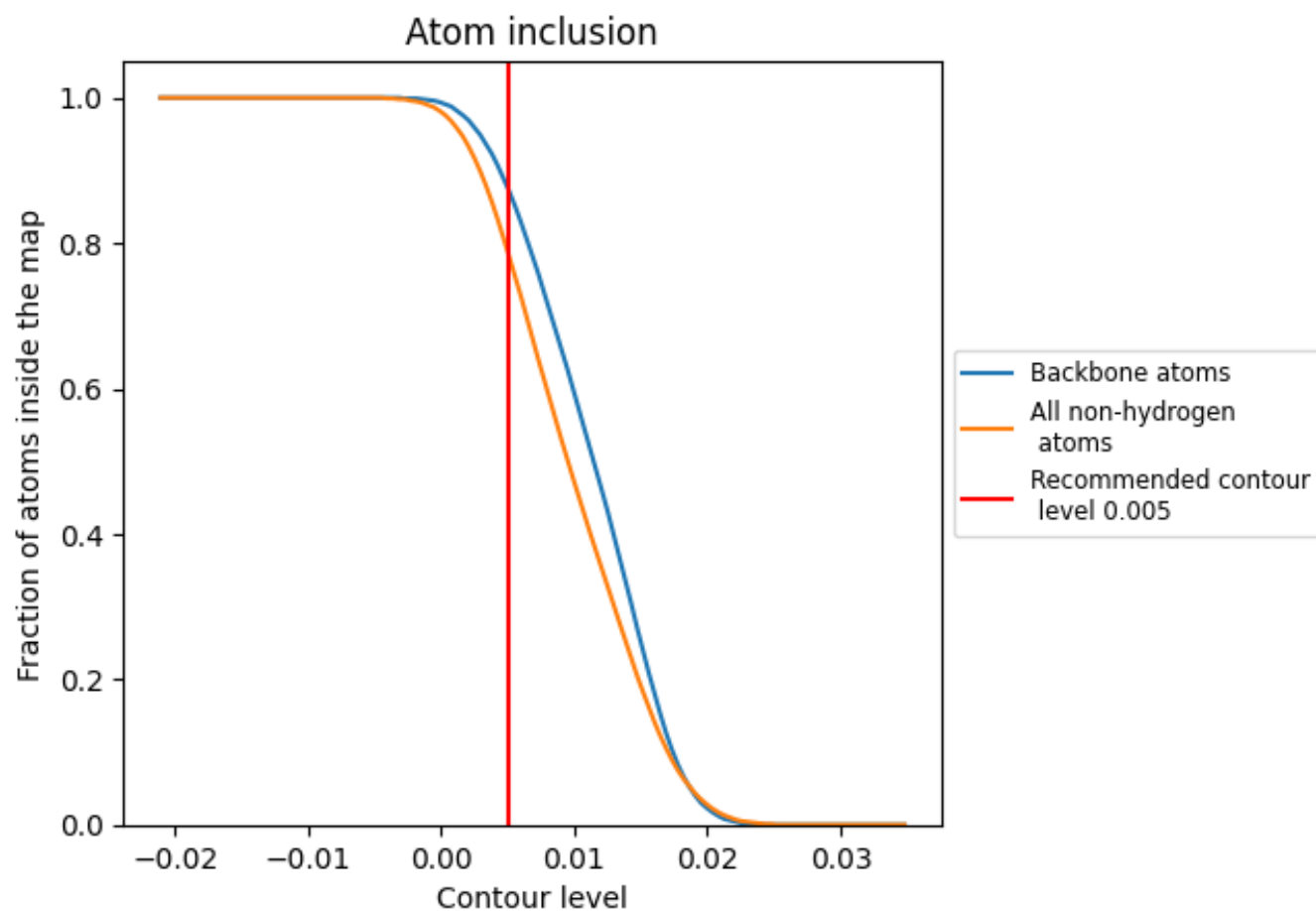
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 79% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7880	 0.4110
5	 0.2420	 0.3670
C1	 0.8980	 0.4270
C2	 0.8110	 0.3730
C3	 0.9280	 0.4480
C4	 0.9560	 0.4460
LA	 0.7400	 0.4880
LB	 0.8010	 0.4780
LC	 0.8220	 0.4760
LD	 0.7950	 0.4230
LE	 0.7670	 0.4340
LF	 0.8040	 0.4610
LG	 0.8090	 0.4440
LH	 0.7960	 0.4540
LI	 0.7460	 0.4440
LJ	 0.7760	 0.4310
LL	 0.8200	 0.4620
LM	 0.8230	 0.4560
LN	 0.7200	 0.4840
LO	 0.7940	 0.4640
LP	 0.7610	 0.4640
LQ	 0.7760	 0.4750
LR	 0.7830	 0.4320
LS	 0.7850	 0.4790
LT	 0.7790	 0.4740
LU	 0.8260	 0.4290
LV	 0.7260	 0.4890
LW	 0.5730	 0.3620
LX	 0.7740	 0.4770
LY	 0.8130	 0.4760
LZ	 0.7900	 0.4570
La	 0.7930	 0.4800
Lb	 0.7040	 0.4560
Lc	 0.8510	 0.4550
Ld	 0.7980	 0.4600





Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Le	 0.7540	 0.4870
Lf	 0.7350	 0.4880
Lg	 0.6980	 0.4680
Lh	 0.8090	 0.4520
Li	 0.8000	 0.4420
Lj	 0.8060	 0.4970
Lk	 0.7810	 0.4470
Ll	 0.7210	 0.4730
Lm	 0.2750	 0.4310
Ln	 0.3560	 0.4310
Lo	 0.7820	 0.4810
Lp	 0.7920	 0.4600
P0	 0.1530	 0.1650
P2	 0.0730	 0.1360
SA	 0.7220	 0.3850
SB	 0.5460	 0.3300
SC	 0.7080	 0.4180
SE	 0.6590	 0.4180
SG	 0.6140	 0.3470
SH	 0.7180	 0.3580
SI	 0.6750	 0.4150
SJ	 0.6370	 0.3700
SK	 0.2900	 0.1880
SL	 0.6750	 0.4370
SM	 0.0170	 0.0980
SN	 0.6600	 0.3880
SO	 0.4500	 0.3290
SP	 0.5510	 0.3310
SQ	 0.3470	 0.3190
ST	 0.4380	 0.3160
SU	 0.4760	 0.3010
SV	 0.7640	 0.4060
SW	 0.6690	 0.4360
SX	 0.6590	 0.4420
SY	 0.6560	 0.3610
SZ	 0.3080	 0.2110
Sa	 0.5570	 0.3840
Sb	 0.7260	 0.3930
Sc	 0.3430	 0.2750
Sd	 0.4010	 0.3410
Se	 0.5530	 0.3700
Sf	 0.0420	 0.1600

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
s	 0.4590	 0.2750