



wwPDB EM Validation Summary Report ⓘ

Dec 8, 2025 – 02:05 PM JST

PDB ID : 9KZU / pdb_00009kzu
EMDB ID : EMD-62671
Title : Cryo-EM structure of the HCV IRES-dependently initiated CMV-stalled 80S ribosome (non-rotated state) in complexed with eIF3
Authors : Iwasaki, W.; Kashiwagi, K.; Sakamoto, A.; Nishimoto, M.; Takahashi, M.; Machida, K.; Imataka, H.; Matsumoto, A.; Shichino, Y.; Iwasaki, S.; Imami, K.; Ito, T.
Deposited on : 2024-12-11
Resolution : 3.00 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.dev129
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.47

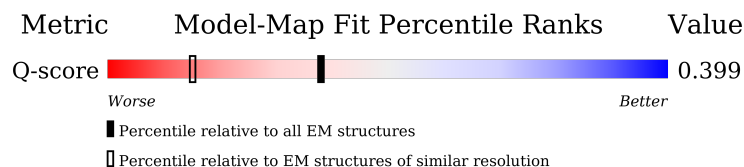
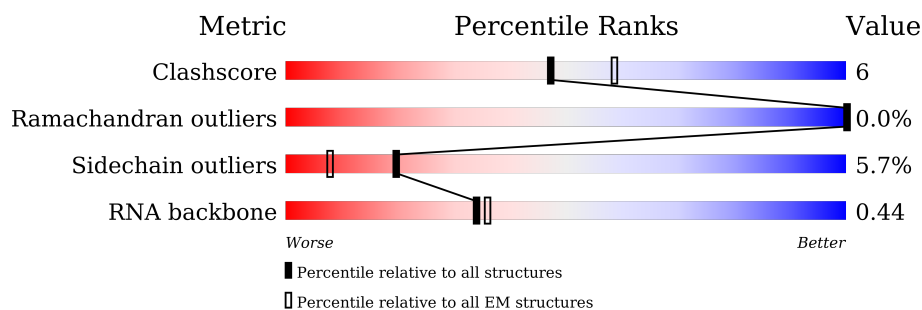
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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.











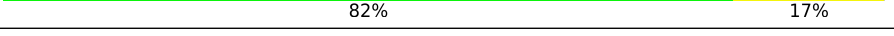

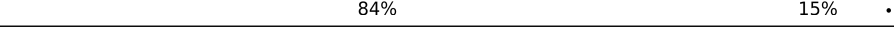
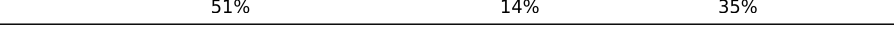

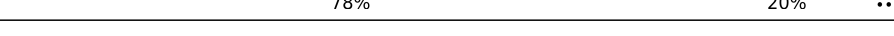


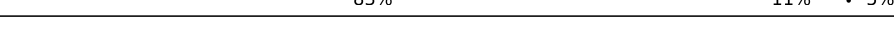

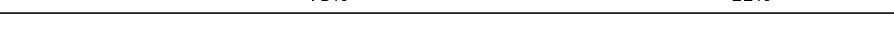






Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	14081 (2.50 - 3.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	L5	5070	
2	L7	120	
3	L8	156	


























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

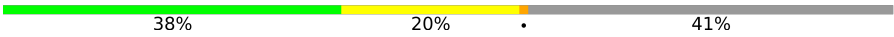









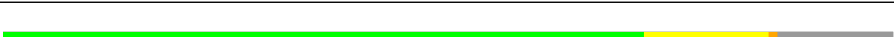


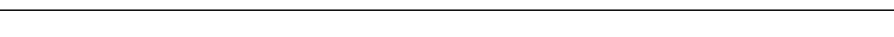
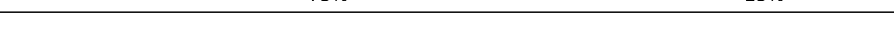
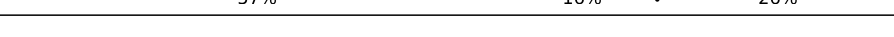



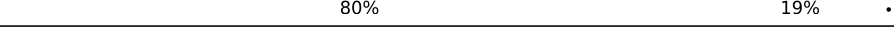





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Mol	Chain	Length	Quality of chain
29	La	148	
30	Lb	159	
31	Lc	115	
32	Ld	125	
33	Le	135	
34	Lf	110	
35	Lg	117	
36	Lh	123	
37	Li	105	
38	Lj	97	
39	Lk	70	
40	Ll	51	
41	Lm	128	
42	Ln	25	
43	Lo	106	
44	Lp	92	
45	Lr	137	
46	S2	1869	
47	SA	295	
48	SB	264	
49	SD	243	
50	SE	263	
51	SF	204	
52	SH	194	
53	SI	208	


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Mol	Chain	Length	Quality of chain
54	SK	165	
55	SL	158	
56	SP	145	
57	SQ	146	
58	SR	135	
59	SS	152	
60	ST	145	
61	SU	119	
62	SV	83	
63	SX	143	
64	Sa	115	
65	Sc	69	
66	Sd	56	
67	Sg	317	
68	SC	293	
69	SG	249	
70	SJ	194	
71	Sf	132	
72	SN	151	
73	SO	151	
74	SW	130	
75	SY	133	
76	SZ	125	
77	Sb	84	
78	Se	59	

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Mol	Chain	Length	Quality of chain
79	sh	156	
80	zv	19	
81	zx	31	
82	zy	75	
83	zz	332	
84	3m	374	
85	3f	357	
86	3a	1382	
87	3e	445	
88	3c	913	
89	3h	352	
90	3d	548	
91	3k	218	
92	3l	564	

2 Entry composition

There are 94 unique types of molecules in this entry. The entry contains 245916 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L5	3663	Total	C	N	O	P	0	0
			78531	34970	14374	25525	3662		

- Molecule 2 is a RNA chain called 5S_ribosomal_RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 3 is a RNA chain called 5.8S_ribosomal_RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 4 is a protein called 60S ribosomal protein L8.

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

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LB	399	Total	C	N	O	S	0	0
			3220	2050	605	551	14		

- Molecule 6 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LC	366	Total	C	N	O	S	0	0
			2914	1832	581	487	14		

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LD	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 8 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LE	226	Total	C	N	O	S	0	0
			1818	1169	345	300	4		

- Molecule 9 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LF	225	Total	C	N	O	S	0	0
			1866	1200	358	299	9		

- Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LG	239	Total	C	N	O	S	0	0
			1914	1220	369	321	4		

- Molecule 11 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LH	190	Total	C	N	O	S	0	0
			1510	952	282	270	6		

- Molecule 12 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LI	213	Total	C	N	O	S	0	0
			1711	1082	329	285	15		

- Molecule 13 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LJ	176	Total	C	N	O	S	0	0
			1410	888	263	253	6		

- Molecule 14 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LL	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 15 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 16 is a protein called 60S ribosomal protein L15.

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

- Molecule 17 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LO	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 18 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 19 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 20 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LR	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		

- Molecule 21 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 22 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LT	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 23 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LU	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 24 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LV	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 25 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LW	124	Total	C	N	O	S	0	0
			1015	634	207	170	4		

- Molecule 26 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LX	119	Total	C	N	O	S	0	0
			976	625	184	166	1		

- Molecule 27 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LY	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 28 is a protein called 60S ribosomal protein L27.

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

- Molecule 29 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	La	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Lb	109	Total	C	N	O	S	0	0
			876	546	189	137	4		

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Lc	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 32 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ld	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 33 is a protein called 60S ribosomal protein L32.

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

- Molecule 34 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lf	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 35 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lg	112	Total	C	N	O	S	0	0
			886	554	181	145	6		

- Molecule 36 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lh	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 37 is a protein called 60S ribosomal protein L36.

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

- Molecule 38 is a protein called 60S ribosomal protein L37.

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

- Molecule 39 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lk	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 40 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 41 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lm	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 42 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 43 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 44 is a protein called 60S ribosomal protein L37a.

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

- Molecule 45 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
46	S2	1741	Total	C	N	O	P	0	0
			36887	16454	6590	12103	1740		

- Molecule 47 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SA	222	Total	C	N	O	S	0	0
			1747	1109	306	324	8		

- Molecule 48 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SB	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 49 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SD	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 50 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 51 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SF	189	Total	C	N	O	S	0	0
			1483	926	282	268	7		

- Molecule 52 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SH	186	Total	C	N	O	S	0	0
			1494	953	273	267	1		

- Molecule 53 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SI	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 54 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 55 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SL	142	Total	C	N	O	S	0	0
			1162	740	218	198	6		

- Molecule 56 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SP	128	Total	C	N	O	S	0	0
			1050	666	198	179	7		

- Molecule 57 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SQ	146	Total	C	N	O	S	0	0
			1158	736	218	200	4		

- Molecule 58 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SR	132	Total	C	N	O	S	0	0
			1072	673	199	195	5		

- Molecule 59 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SS	145	Total	C	N	O	S	0	0
			1198	751	242	203	2		

- Molecule 60 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	ST	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

- Molecule 61 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SU	103	Total	C	N	O	S	0	0
			817	511	155	147	4		

- Molecule 62 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 64 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Sa	100	Total	C	N	O	S	0	0
			803	501	166	131	5		

- Molecule 65 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Sc	64	Total	C	N	O	S	0	0
			500	305	99	94	2		

- Molecule 66 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Sd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 67 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Sg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 68 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SC	217	Total	C	N	O	S	0	0
			1683	1090	288	295	10		

- Molecule 69 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SG	236	Total	C	N	O	S	0	0
			1915	1194	386	328	7		

- Molecule 70 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 71 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Sf	122	Total	C	N	O	S	0	0
			933	584	163	177	9		

- Molecule 72 is a protein called 40S ribosomal protein S13.

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

- Molecule 73 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SO	135	Total	C	N	O	S	0	0
			1010	618	198	188	6		

- Molecule 74 is a protein called 40S ribosomal protein S15a.

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

- Molecule 75 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SY	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		

- Molecule 76 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	SZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 77 is a protein called 40S ribosomal protein S27.

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

- Molecule 78 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Se	58	Total	C	N	O	S	0	0
			459	284	100	74	1		

- Molecule 79 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	sh	63	Total	C	N	O	S	0	0
			515	324	98	86	7		

- Molecule 80 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	zv	13	Total	C	N	O	P	0	0
			267	120	42	92	13		

- Molecule 81 is a protein called nascent peptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	zx	21	Total	C	N	O	S	0	0
			160	107	25	27	1		

- Molecule 82 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	zy	75	Total	C	N	O	P	0	0
			1599	713	284	528	74		

- Molecule 83 is a RNA chain called HCV IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	zz	210	Total	C	N	O	P	0	0
			4481	1995	796	1480	210		

- Molecule 84 is a protein called Eukaryotic translation initiation factor 3 subunit M.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	3m	363	Total	C	N	O	S	0	0
			2639	1666	450	511	12		

- Molecule 85 is a protein called Eukaryotic translation initiation factor 3 subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	3f	269	Total	C	N	O	S	0	0
			2063	1303	354	394	12		

- Molecule 86 is a protein called Eukaryotic translation initiation factor 3 subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	3a	592	Total	C	N	O	S	0	0
			4497	2849	805	822	21		

- Molecule 87 is a protein called Eukaryotic translation initiation factor 3 subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	3e	429	Total	C	N	O	S	0	0
			3218	2050	560	592	16		

- Molecule 88 is a protein called Eukaryotic translation initiation factor 3 subunit C.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	3c	652	Total	C	N	O	S	0	0
			4822	3030	881	885	26		

- Molecule 89 is a protein called Eukaryotic translation initiation factor 3 subunit H.

Mol	Chain	Residues	Atoms					AltConf	Trace
89	3h	315	Total	C	N	O	S	0	0
			2499	1585	427	472	15		

- Molecule 90 is a protein called Eukaryotic translation initiation factor 3 subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
90	3d	55	Total	C	N	O	S	0	0
			347	222	65	59	1		

- Molecule 91 is a protein called Eukaryotic translation initiation factor 3 subunit K.

Mol	Chain	Residues	Atoms					AltConf	Trace
91	3k	215	Total	C	N	O	S	0	0
			1475	932	251	282	10		

- Molecule 92 is a protein called Eukaryotic translation initiation factor 3 subunit L.

Mol	Chain	Residues	Atoms					AltConf	Trace
92	3l	520	Total	C	N	O	S	0	0
			4335	2808	715	793	19		

- Molecule 93 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
93	L5	70	Total	Mg	0
			70	70	
93	L8	1	Total	Mg	0
			1	1	
93	S2	10	Total	Mg	0
			10	10	

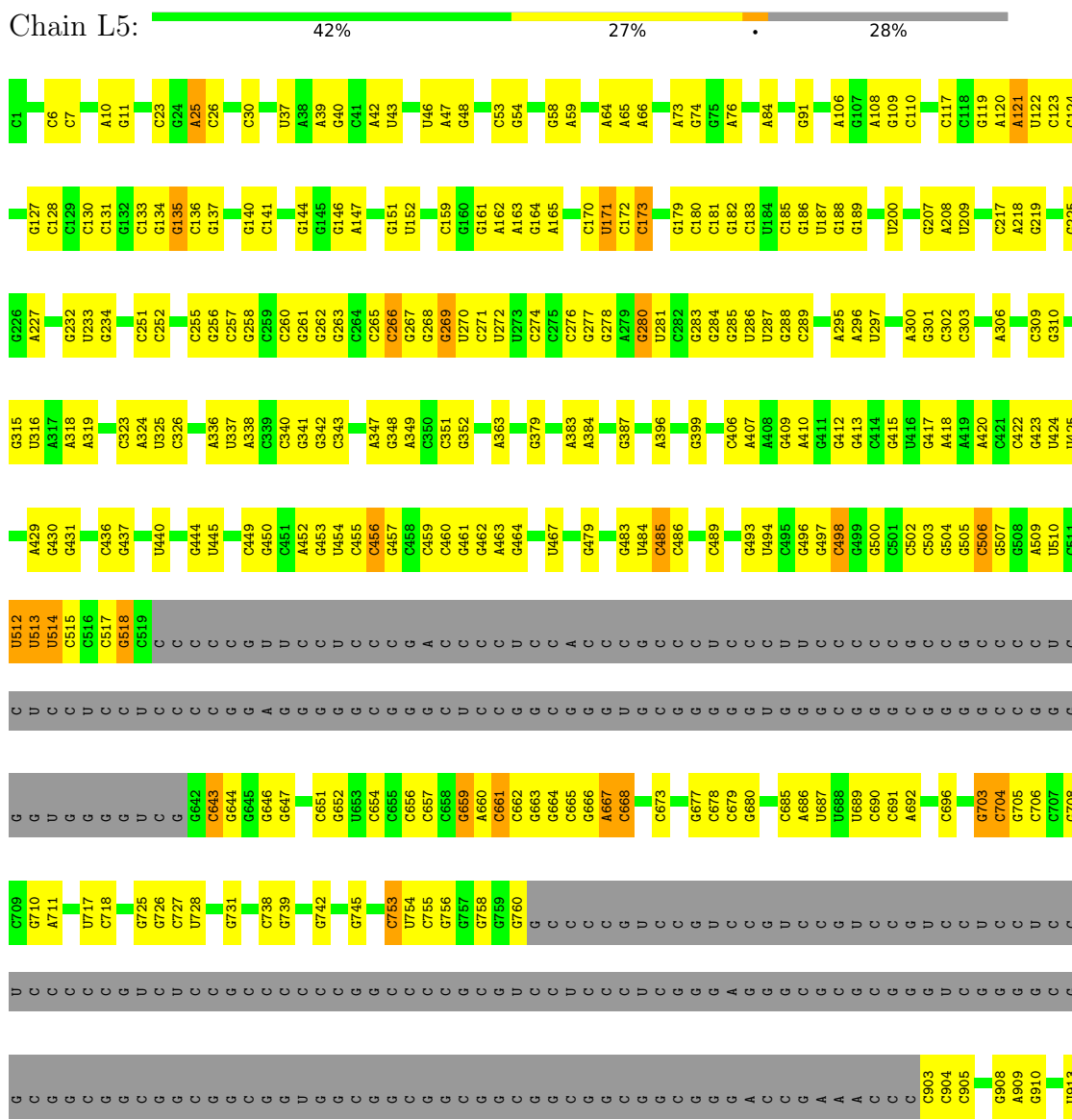
- Molecule 94 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

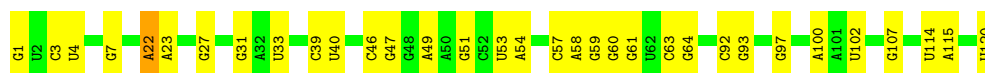
• Molecule 1: 28S ribosomal RNA







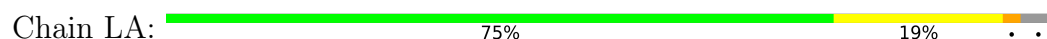
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U4989	U4986	G4889	G	A4762	G4686	A4583	G4494	U4354	C4252	G4140	A	U3932	U3932	C3855
U4989	U4986	G4887	G	U4763	A4687	A4584	G4495	U4354	C4253	G4142	C	G3933	G3933	A3856
U4989	U4986	U4688	C	G4764	C4688	G4585	A4496	C4365	G4254	C4142	C	G3934	U3934	U3856
U4989	U4986	U4689	G	G4765	U4689	G4586	G4497	C4366	A4255	C4143	C	C3937	G3938	A3861
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U4989	U4986	A4691	G	U4769	A4691	A4590	U4500	A4378	A4257	C4145	C	G3939	G3939	A3867
U4989	U4986	U4770	A	U4770	U4770	A4591	U4501	A4379	C4258	G4151	A	G3944	G3944	C3868
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U4989	U4986	C4772	G	C4772	C4695	A4593	A4508	A4381	U4261	C4151	G	G3946	G3946	C3870
U4989	U4986	C4773	G	C4773	U4594	A4594	U4509	C4387	C4262	C4152	G	G3947	G3947	A3871
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U4989	U4986	C4775	G	C4775	A4599	A4599	A4511	A4389	G4264	U4163	C	A3949	A3949	G3873
U4989	U4986	C4776	G	C4776	G4600	G4600	A4512	A4390	A4273	G4168	C	U3950	U3950	G3874
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U4989	U4986	C4778	C	C4778	G4617	G4617	C4514	A4392	G4275	A4170	G	A3952	A3952	A3877
U4989	U4986	C4779	C	C4779	U4626	U4626	A4518	A4393	A4280	G4173	G	A3953	A3953	C3878
U4989	U4986	C4780	C	C4780	U4627	U4627	A4519	U4394	A4281	G4174	G	G3953	G3953	G3879
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U4989	U4986	C4782	C	C4782	U4629	U4629	A4521	U4396	A4283	G4179	C	G3954	G3954	G3881
U4989	U4986	C4783	C	C4783	U4630	U4630	U4532	A4397	A4284	G4180	C	G3955	G3955	G3882
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U4989	U4986	C4788	C	C4788	U4635	U4635	U4537	U4402	A4289	G4185	C	G3960	G3960	A3887
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U4989	U4986	C4799	C	C4799	U4646	U4646	U4548	U4413	U4300	G4196	C	C3909	C3909	C3910
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U4989	U4986	C4804	C	C4804	U4651	U4651	U4553	U4418	U4305	G4201	C	U3921	U3921	U3921
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U4989	U4986	C4807	C	C4807	U4654	U4654	U4556	U4421	U4308	G4204	C	U3930	U3930	U3930
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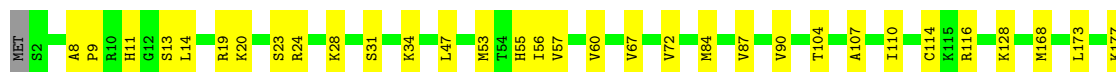
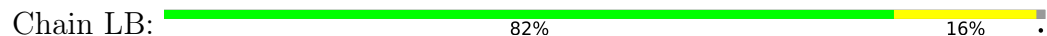
• Molecule 3: 5.8S_ribosomal_RNA



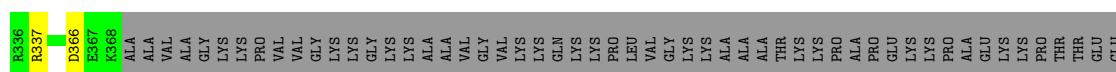
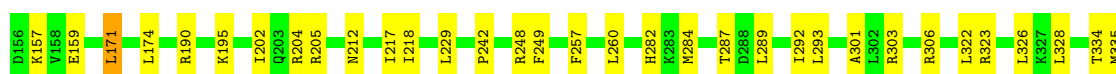
• Molecule 4: 60S ribosomal protein L8



• Molecule 5: 60S ribosomal protein L3




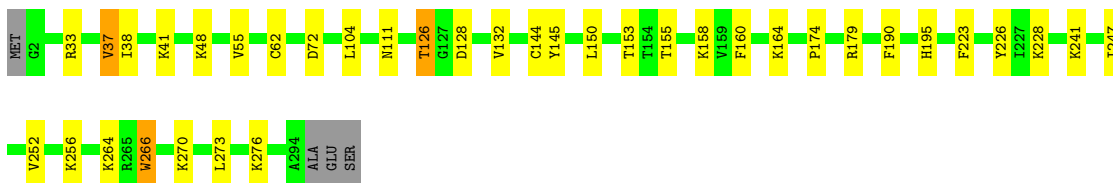
• Molecule 6: 60S ribosomal protein L4



LYS
LYS
PRO
ALA
ALA

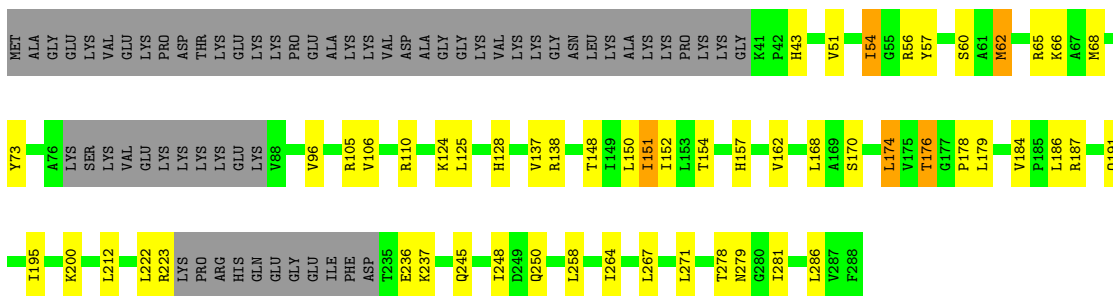
• Molecule 7: 60S ribosomal protein L5

Chain LD:  86% 11% ..



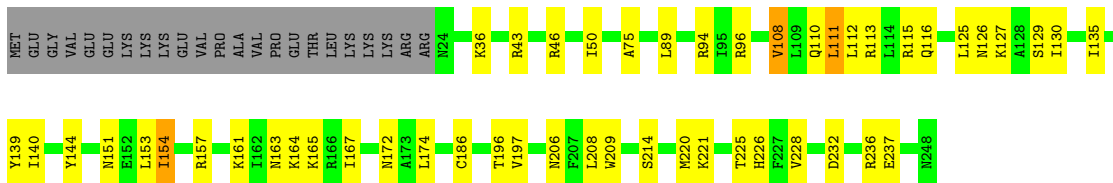
• Molecule 8: 60S ribosomal protein L6

Chain LE:  59% 17% • 22%



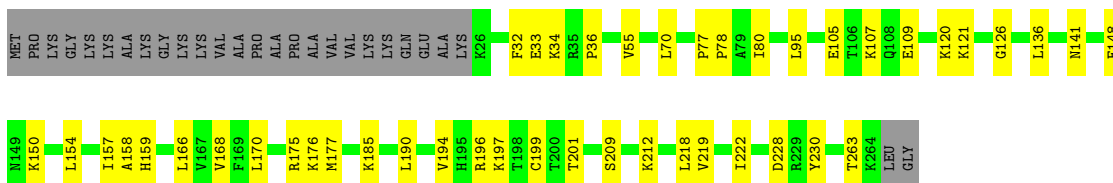
• Molecule 9: 60S ribosomal protein L7

Chain LF:  71% 19% • 9%




• Molecule 10: 60S ribosomal protein L7a

Chain LG:  73% 17% 10%



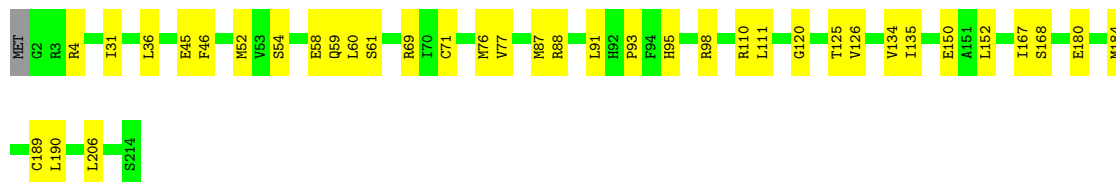
• Molecule 11: 60S ribosomal protein L9

Chain LH:  80% 18% ..



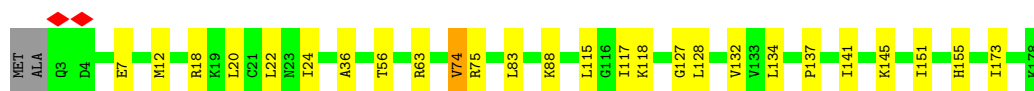
- Molecule 12: 60S ribosomal protein L10-like

Chain LI: 82% 17%



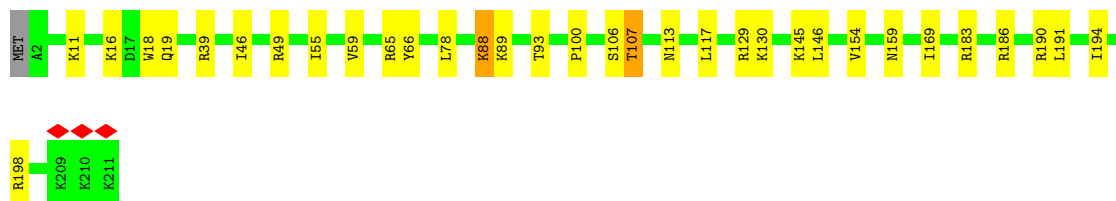
- Molecule 13: 60S ribosomal protein L11

Chain LJ: 84% 14% ..



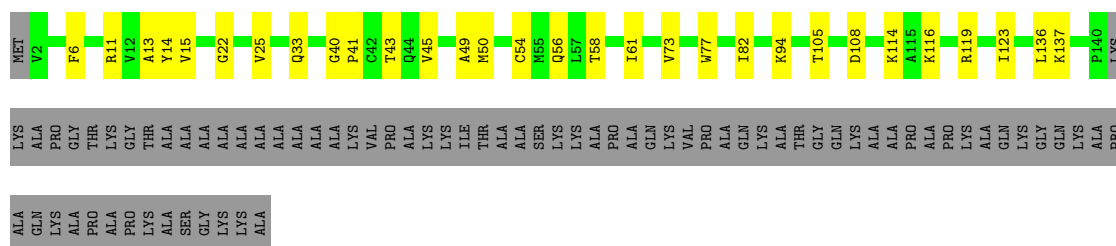
- Molecule 14: 60S ribosomal protein L13

Chain LL: 84% 15% .



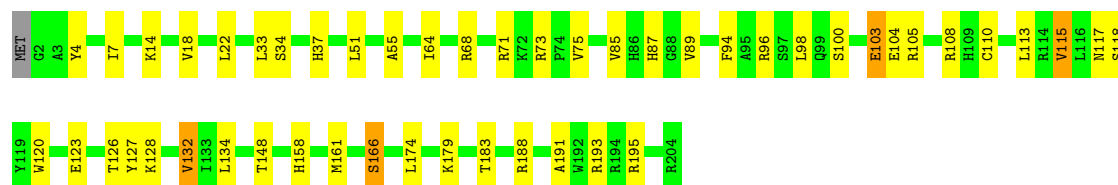
- Molecule 15: 60S ribosomal protein L14

Chain LM: 51% 14% 35%



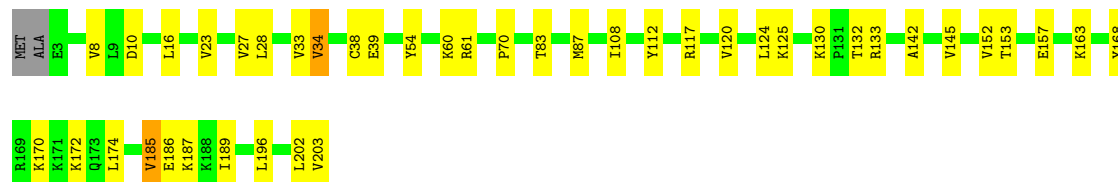
- Molecule 16: 60S ribosomal protein L15

Chain LN: 75% 22% .



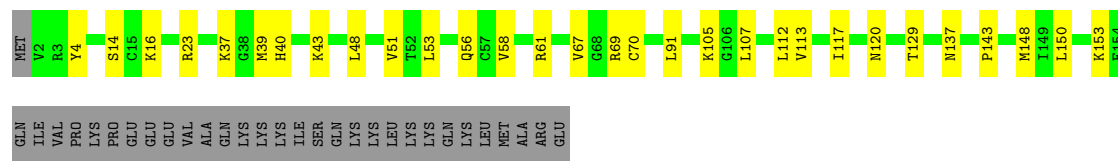
- Molecule 17: 60S ribosomal protein L13a

Chain LO: 78% 20% ..



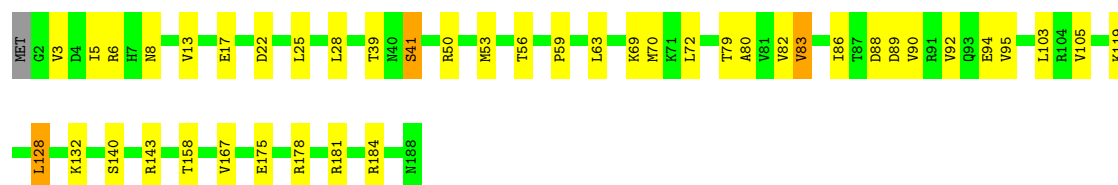
- Molecule 18: 60S ribosomal protein L17

Chain LP: 67% 16% 17%



- Molecule 19: 60S ribosomal protein L18

Chain LQ: 77% 21% ..



- Molecule 20: 60S ribosomal protein L19

Chain LR: 83% 11% 5%



- Molecule 21: 60S ribosomal protein L18a

Chain LS: 72% 27% ..





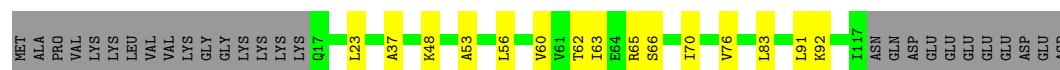
- Molecule 22: 60S ribosomal protein L21

Chain LT: 73% 22% . .



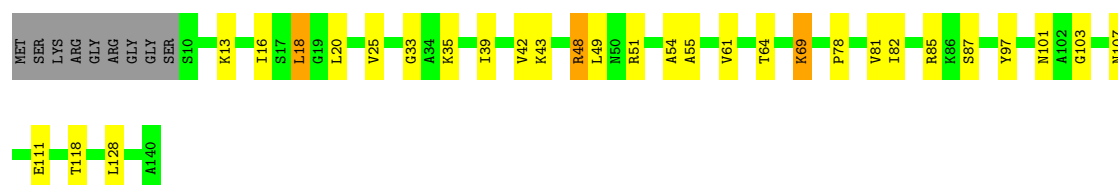
- Molecule 23: 60S ribosomal protein L22

Chain LU: 67% 12% 21%



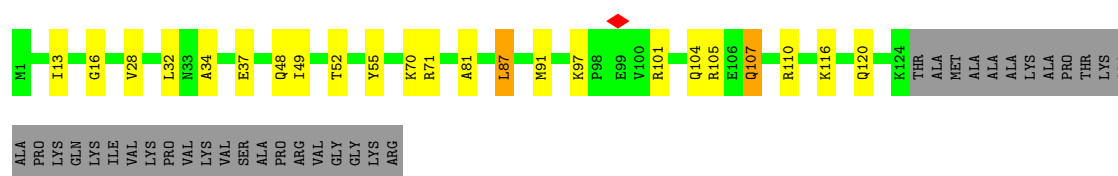
- Molecule 24: 60S ribosomal protein L23

Chain LV: 72% 19% 6%



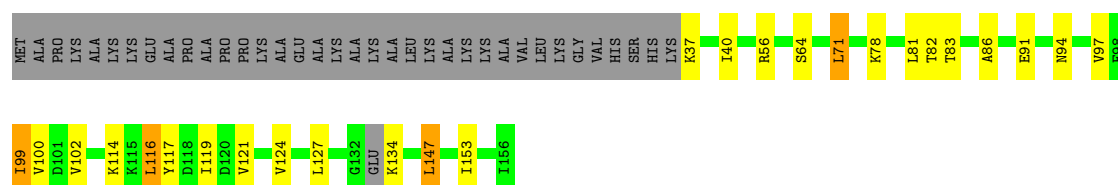
- Molecule 25: 60S ribosomal protein L24

Chain LW: 64% 13% 21%



- Molecule 26: 60S ribosomal protein L23a

Chain LX: 60% 14% 24%





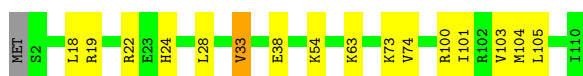
- Molecule 33: 60S ribosomal protein L32

Chain Le: 81% 13% 5%



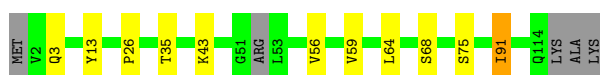
- Molecule 34: 60S ribosomal protein L35a

Chain Lf: 85% 14% ..



- Molecule 35: 60S ribosomal protein L34

Chain Lg: 86% 9% ..



- Molecule 36: 60S ribosomal protein L35

Chain Lh: 85% 13% ..



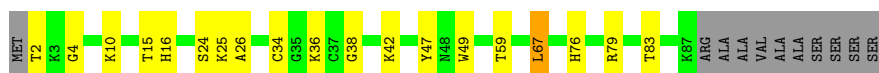
- Molecule 37: 60S ribosomal protein L36

Chain Li: 79% 18% .



- Molecule 38: 60S ribosomal protein L37

Chain Lj: 69% 19% . 11%

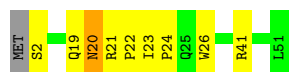
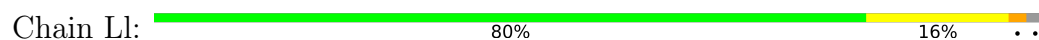


- Molecule 39: 60S ribosomal protein L38

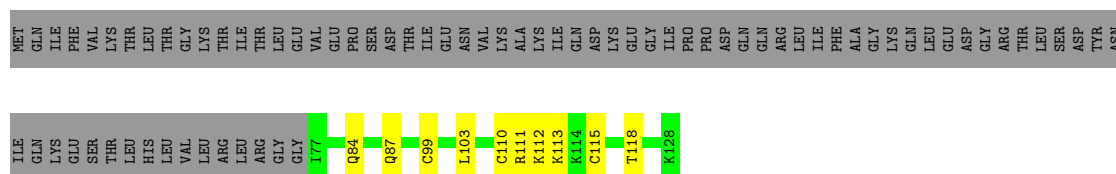
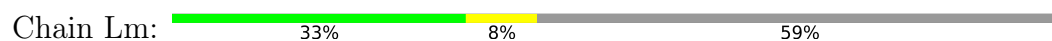
Chain Lk: 77% 17% ..



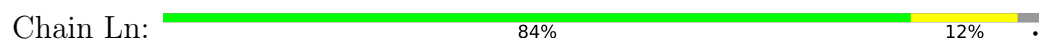
- Molecule 40: 60S ribosomal protein L39



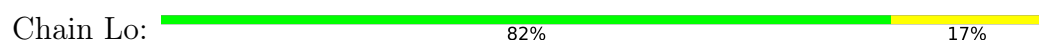
- Molecule 41: Ubiquitin-60S ribosomal protein L40



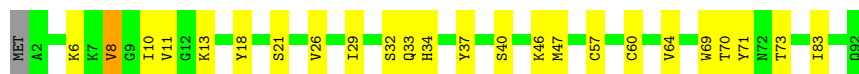
- Molecule 42: 60S ribosomal protein L41



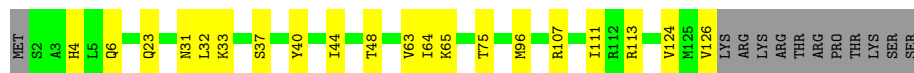
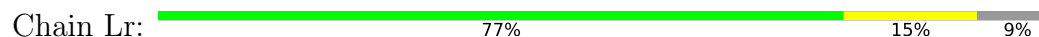
- Molecule 43: 60S ribosomal protein L36a



- Molecule 44: 60S ribosomal protein L37a



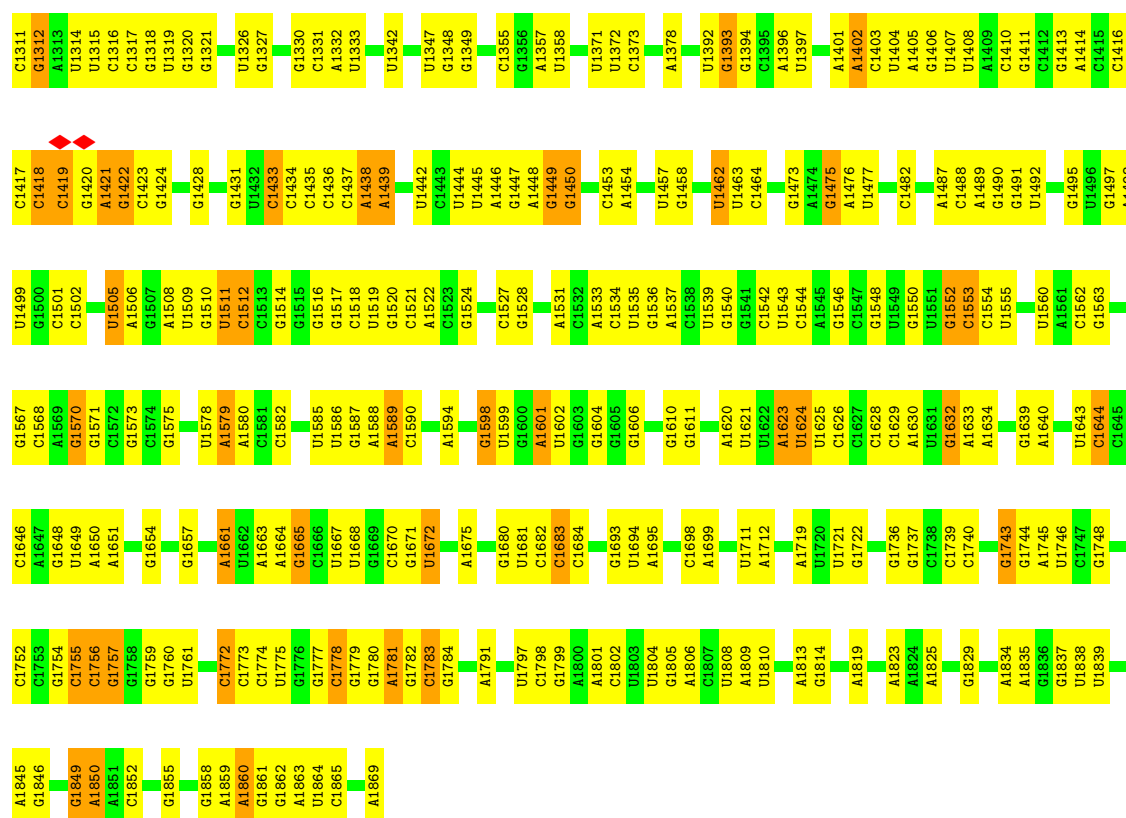
- Molecule 45: 60S ribosomal protein L28



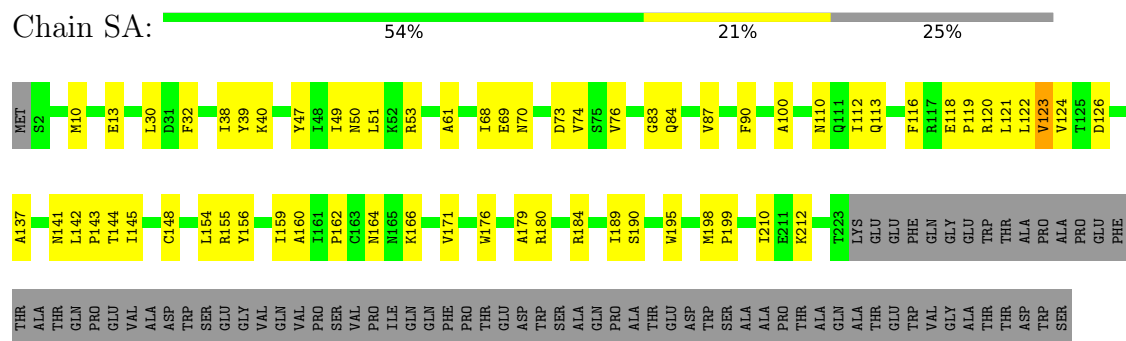
- Molecule 46: 18S ribosomal RNA

Response	Percentage
Yes	49%
No	37%
Don't know	7%
No answer	7%

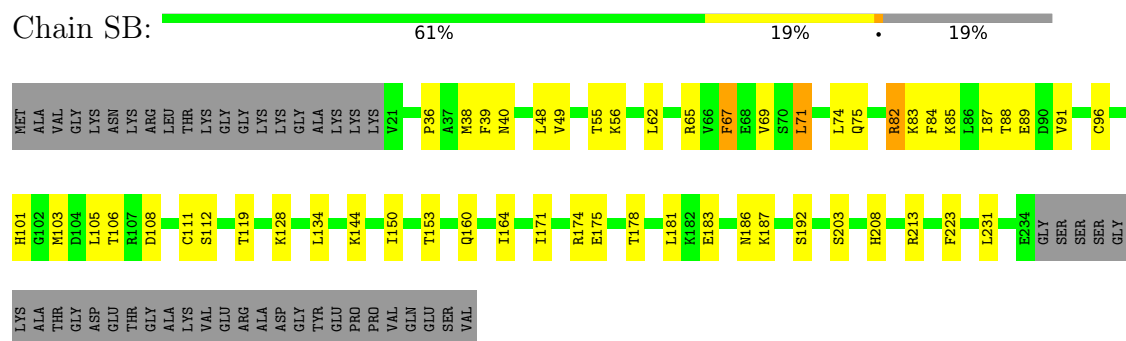





- Molecule 47: Small ribosomal subunit protein uS2

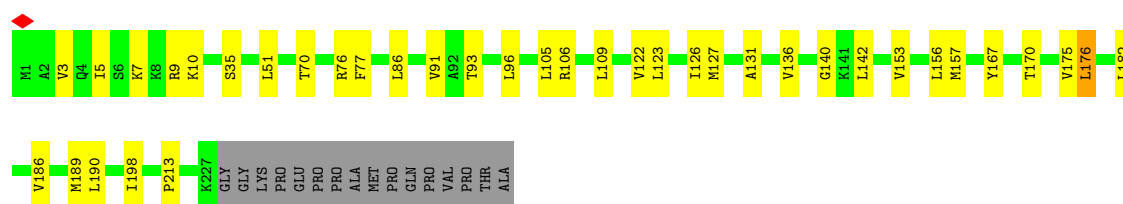


- Molecule 48: 40S ribosomal protein S3a




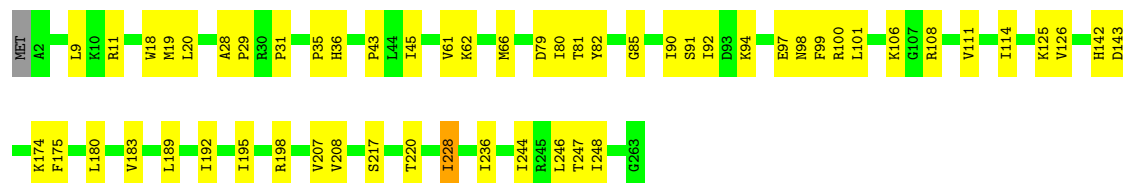
- Molecule 49: 40S ribosomal protein S3

Chain SD:  78% 15% 7%



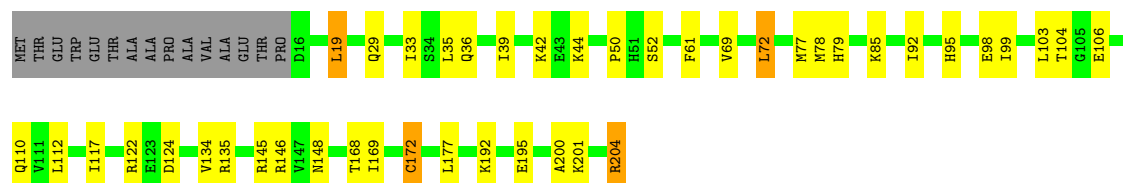
- Molecule 50: 40S ribosomal protein S4, X isoform

Chain SE:  79% 21%




- Molecule 51: 40S ribosomal protein S5

Chain SF:  72% 19% 7%



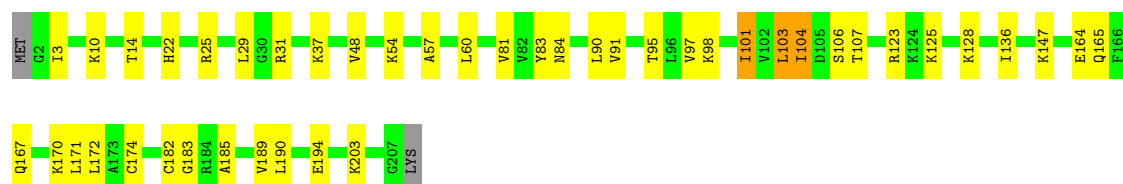
- Molecule 52: 40S ribosomal protein S7

Chain SH:  76% 20% 4%

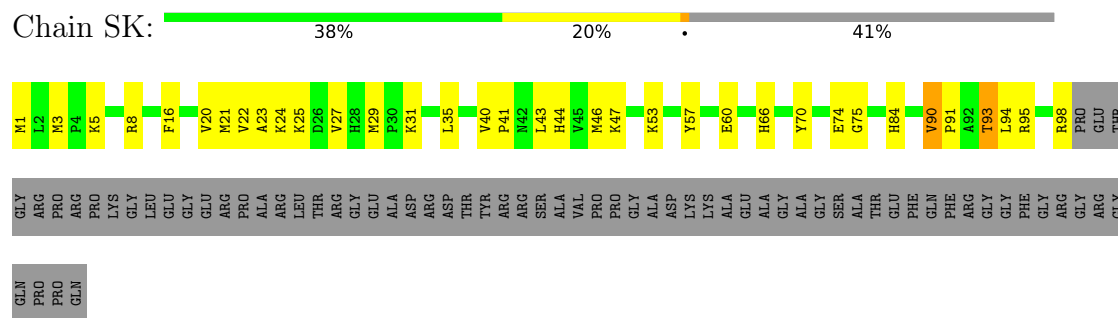


- Molecule 53: 40S ribosomal protein S8

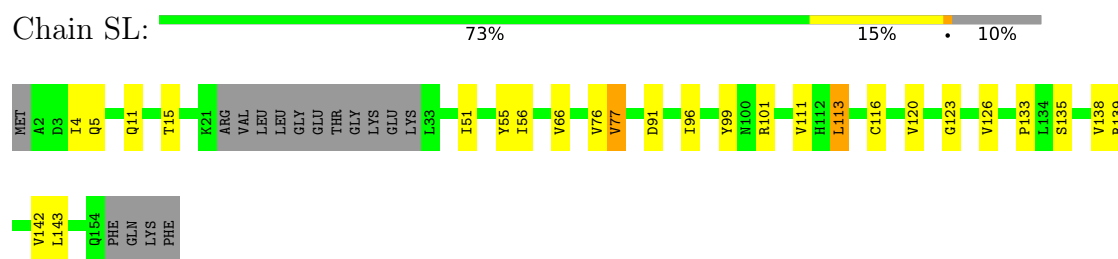
Chain SI:  78% 20% 2%



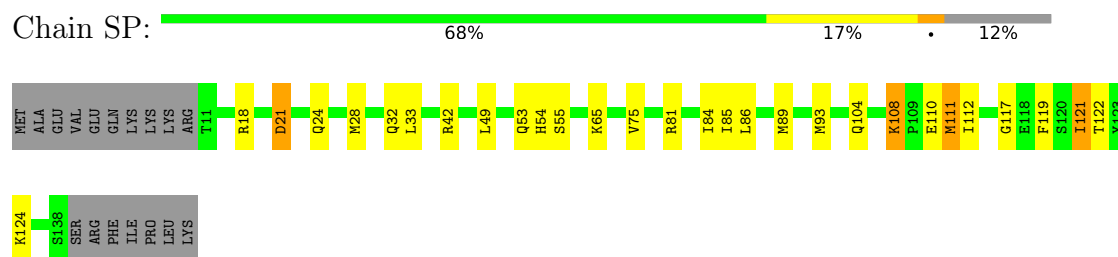
- Molecule 54: 40S ribosomal protein S10



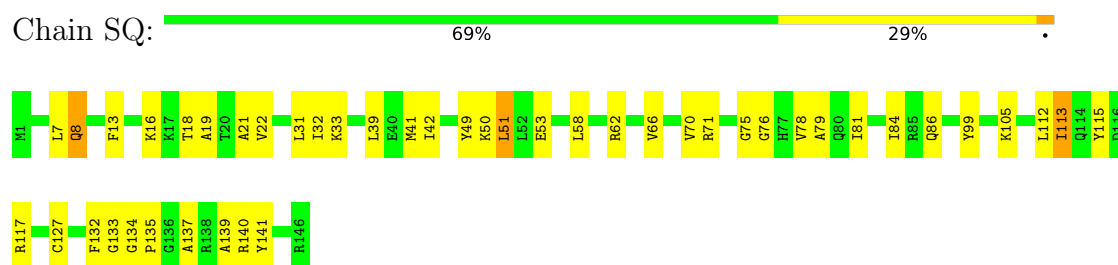
- Molecule 55: 40S ribosomal protein S11



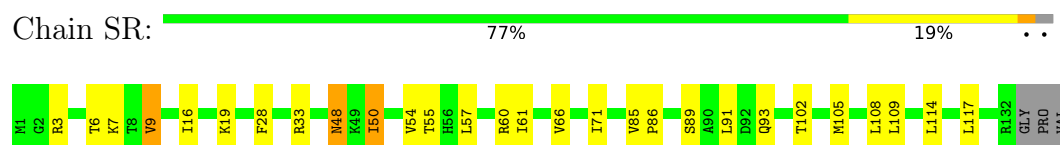
- Molecule 56: 40S ribosomal protein S15



- Molecule 57: 40S ribosomal protein S16

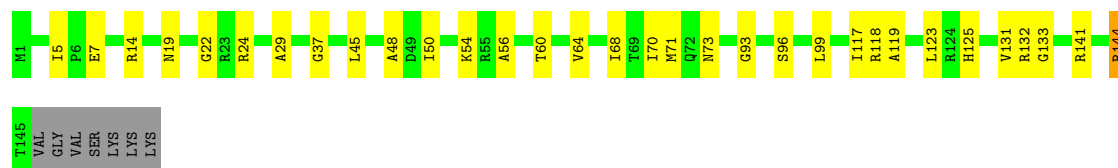


- Molecule 58: 40S ribosomal protein S17




- Molecule 59: 40S ribosomal protein S18

Chain SS:  74% 20% 5%



- Molecule 60: 40S ribosomal protein S19

Chain ST:  83% 14% ..




- Molecule 61: 40S ribosomal protein S20

Chain SU:  68% 18% 13%




- Molecule 62: 40S ribosomal protein S21

Chain SV:  76% 24%



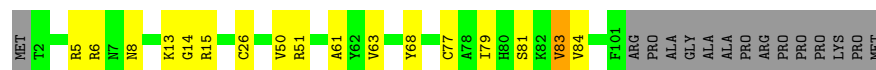
- Molecule 63: 40S ribosomal protein S23

Chain SX:  81% 17% ..



- Molecule 64: 40S ribosomal protein S26


Chain Sa:  72% 14% 13%

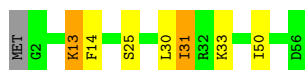


- Molecule 65: 40S ribosomal protein S28

Chain Sc:  72% 19% 7%

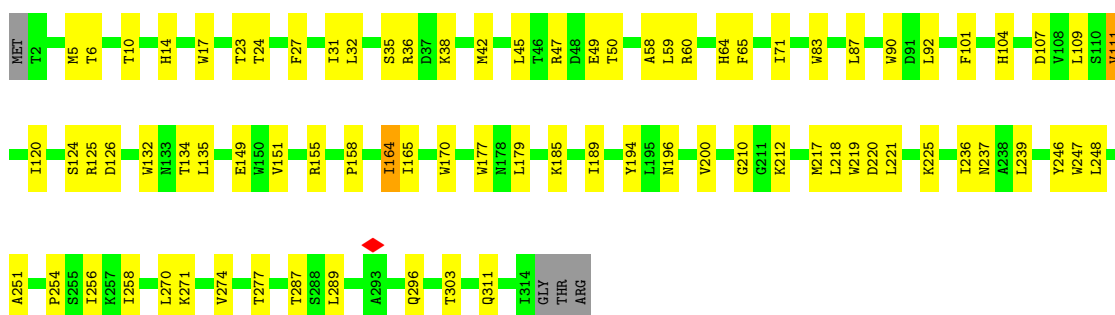
- Molecule 66: 40S ribosomal protein S29

Chain Sd:  86% 9% .



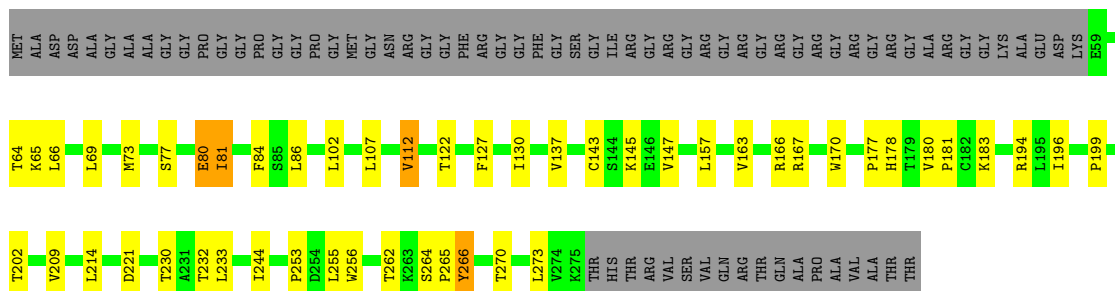
- Molecule 67: Receptor of activated protein C kinase 1

Chain Sg:  73% 25% ..

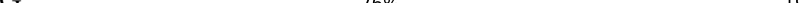


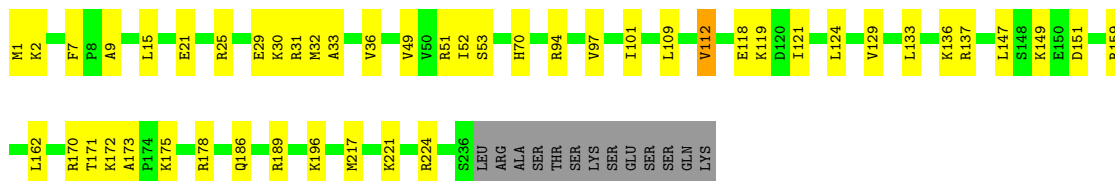
- Molecule 68: 40S ribosomal protein S2

Chain SC:  57% 16% 26%



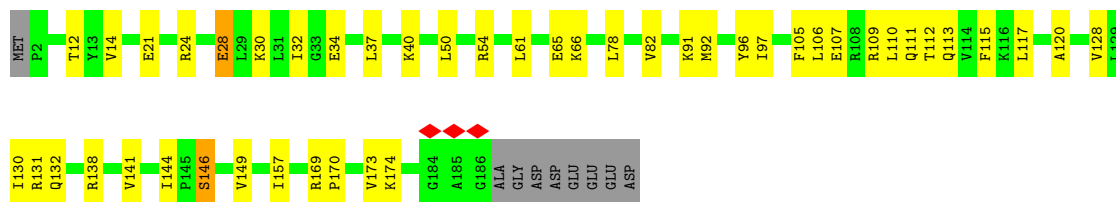
- Molecule 69: 40S ribosomal protein S6

Chain SG:  76% 19% 5%



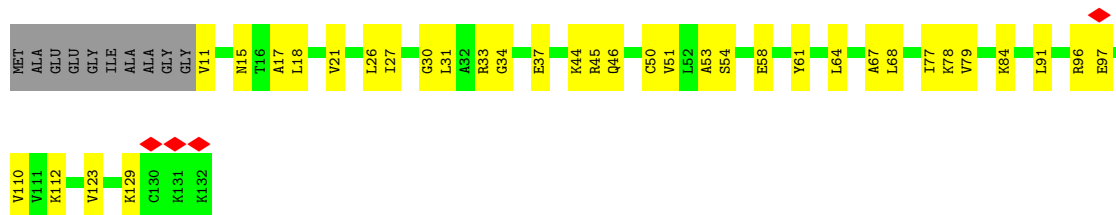
- Molecule 70: 40S ribosomal protein S9

Chain SJ:  72% 23% 5%




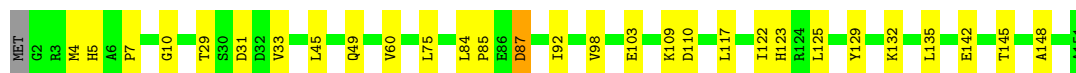
- Molecule 71: 40S ribosomal protein S12

Chain Sf:  66% 27% 8%



- Molecule 72: 40S ribosomal protein S13

Chain SN:  80% 19% ..




- Molecule 73: 40S ribosomal protein S14

Chain SO:  68% 19% 11%




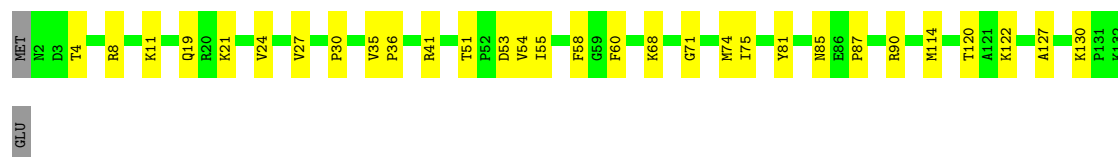
- Molecule 74: 40S ribosomal protein S15a

Chain SW:  76% 21% ..

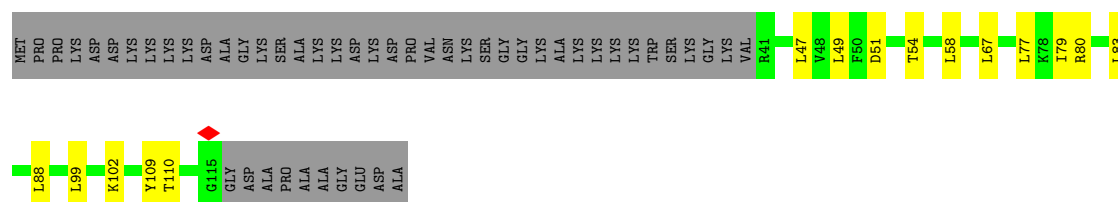


- Molecule 75: 40S ribosomal protein S24

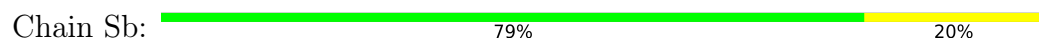
Chain SY:  76% 23% .



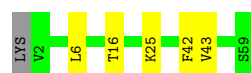
- Molecule 76: 40S ribosomal protein S25



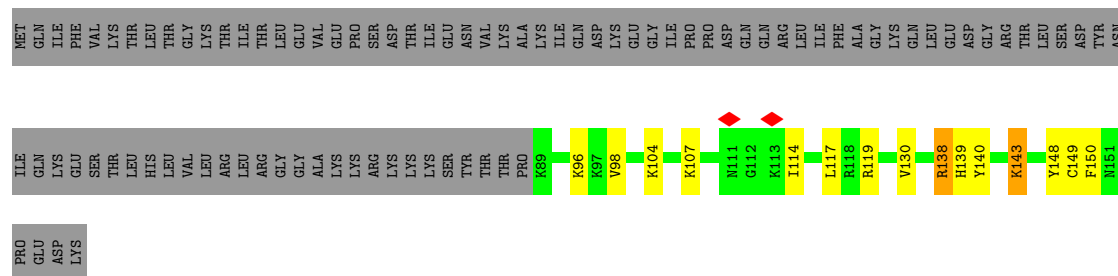
- Molecule 77: 40S ribosomal protein S27



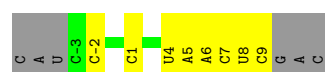
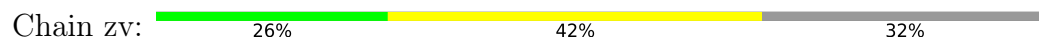
- Molecule 78: 40S ribosomal protein S30



- Molecule 79: Ubiquitin-40S ribosomal protein S27a



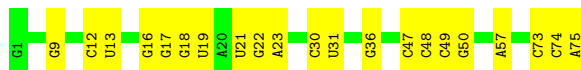
- Molecule 80: mRNA



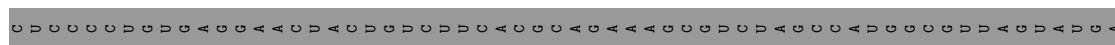
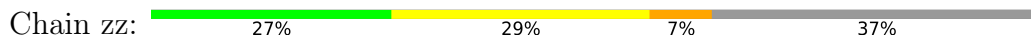
- Molecule 81: nascent peptide



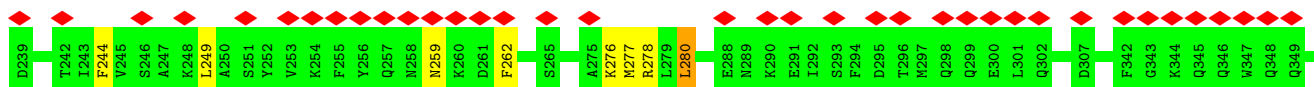
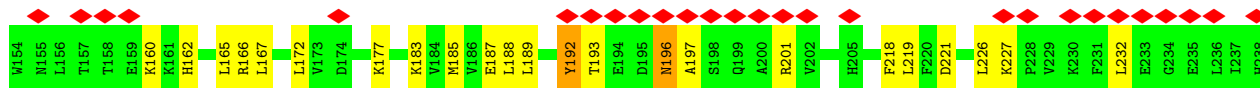
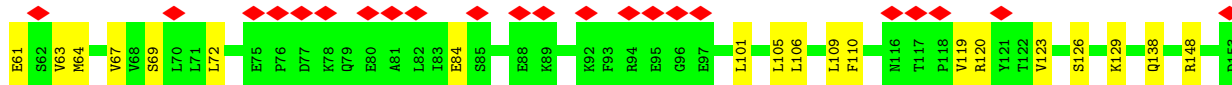
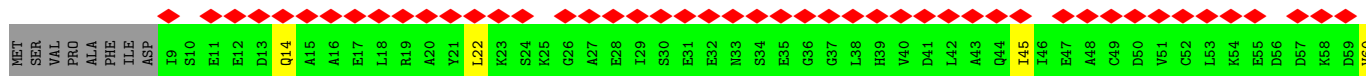
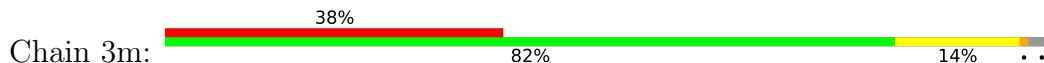
- Molecule 82: P-site tRNA



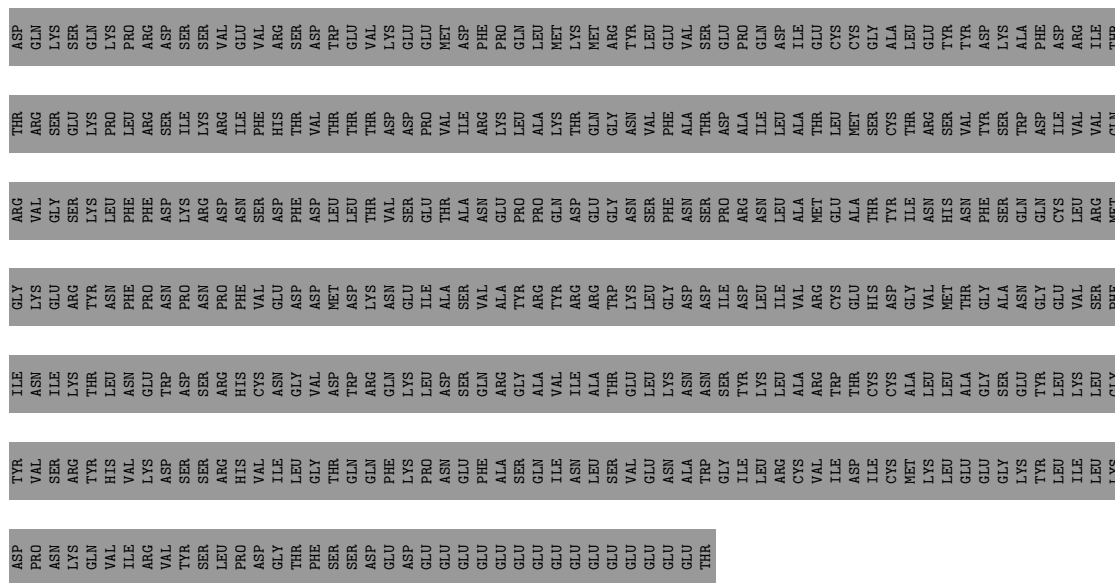
- Molecule 83: HCV IRES



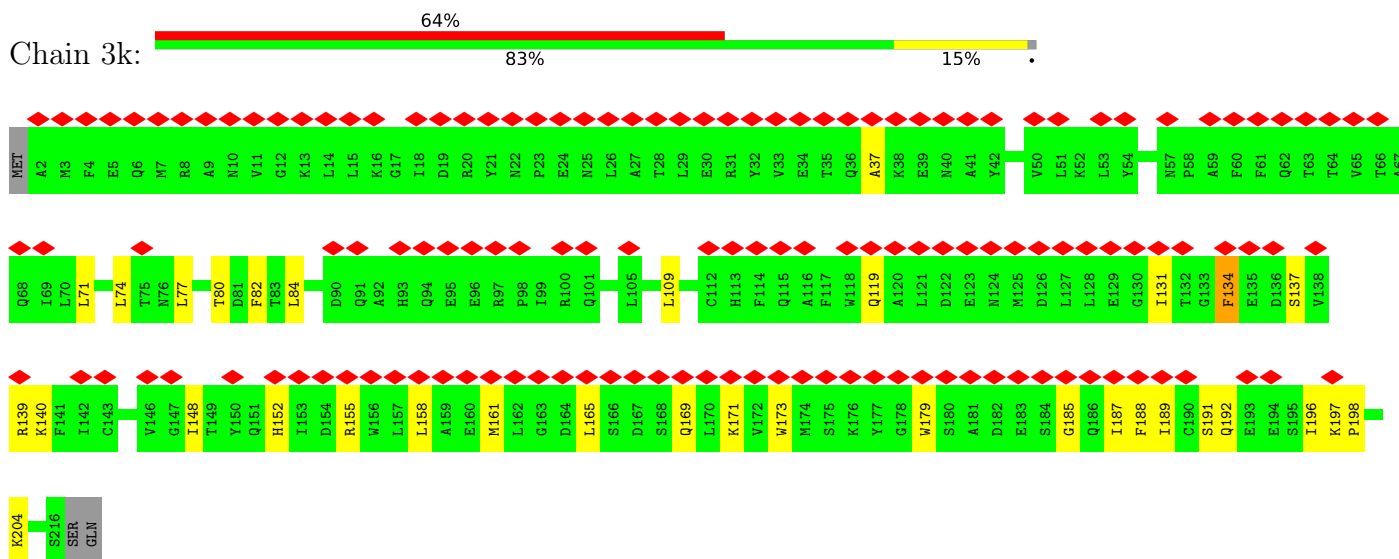
- Molecule 84: Eukaryotic translation initiation factor 3 subunit M



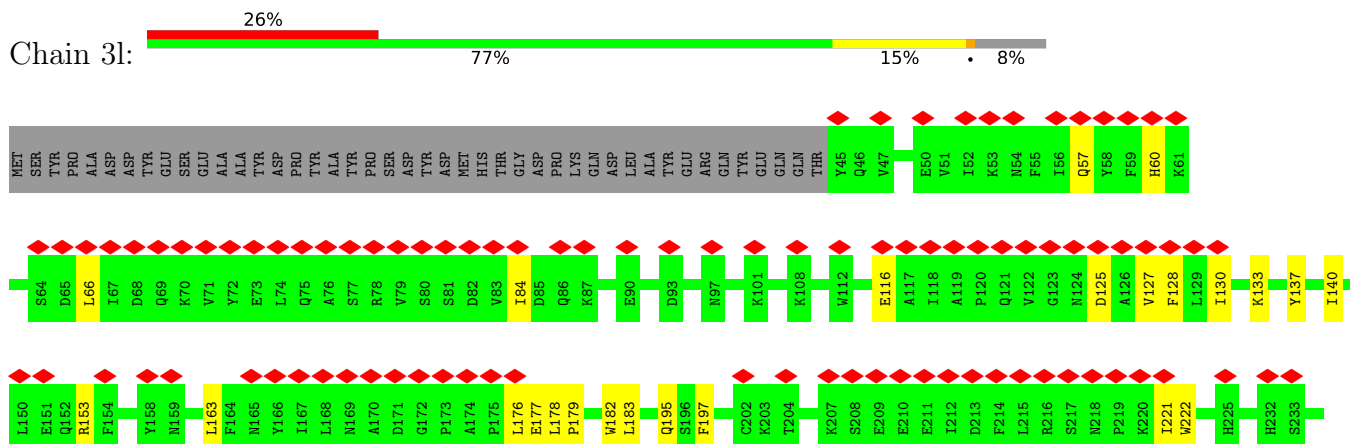




- Molecule 91: Eukaryotic translation initiation factor 3 subunit K



- Molecule 92: Eukaryotic translation initiation factor 3 subunit L





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	63366	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	56.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.174	Depositor
Minimum map value	-0.042	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.01	Depositor
Map size (\AA)	742.0, 742.0, 742.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.484, 1.484, 1.484	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	L5	0.26	0/87848	0.34	0/137041
2	L7	0.24	0/2858	0.30	0/4455
3	L8	0.26	0/3701	0.34	0/5766
4	LA	0.29	0/1936	0.49	0/2596
5	LB	0.25	0/3288	0.42	0/4400
6	LC	0.27	0/2968	0.49	0/3985
7	LD	0.21	0/2428	0.42	0/3252
8	LE	0.24	0/1852	0.52	1/2484 (0.0%)
9	LF	0.27	0/1901	0.43	0/2534
10	LG	0.23	0/1947	0.46	0/2621
11	LH	0.24	0/1529	0.48	0/2056
12	LI	0.26	0/1751	0.50	0/2340
13	LJ	0.20	0/1433	0.42	0/1915
14	LL	0.22	0/1732	0.39	0/2315
15	LM	0.21	0/1161	0.38	0/1554
16	LN	0.30	0/1746	0.46	0/2338
17	LO	0.27	0/1682	0.41	0/2250
18	LP	0.28	0/1268	0.50	0/1701
19	LQ	0.27	0/1537	0.50	1/2052 (0.0%)
20	LR	0.23	0/1582	0.45	0/2091
21	LS	0.28	0/1493	0.50	0/2003
22	LT	0.26	0/1326	0.46	0/1770
23	LU	0.26	0/839	0.67	2/1126 (0.2%)
24	LV	0.27	0/993	0.56	1/1332 (0.1%)
25	LW	0.23	0/1030	0.48	0/1364
26	LX	0.25	0/992	0.53	0/1330
27	LY	0.24	0/1132	0.45	0/1504
28	LZ	0.24	0/1130	0.49	1/1507 (0.1%)
29	La	0.28	0/1191	0.45	0/1591
30	Lb	0.21	0/889	0.41	0/1175
31	Lc	0.26	0/774	0.48	0/1038
32	Ld	0.24	0/903	0.44	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.25	0/1071	0.42	0/1429
34	Lf	0.28	0/895	0.48	0/1198
35	Lg	0.25	0/895	0.41	0/1192
36	Lh	0.23	0/1023	0.47	0/1351
37	Li	0.20	0/843	0.41	0/1115
38	Lj	0.27	0/720	0.47	0/952
39	Lk	0.24	0/575	0.56	0/761
40	Ll	0.27	0/454	0.48	0/599
41	Lm	0.26	0/435	0.56	0/575
42	Ln	0.21	0/231	0.34	0/294
43	Lo	0.25	0/876	0.47	0/1156
44	Lp	0.27	0/718	0.43	0/953
45	Lr	0.24	0/1017	0.44	0/1364
46	S2	0.23	0/41229	0.34	0/64235
47	SA	0.26	0/1784	0.51	0/2424
48	SB	0.24	0/1765	0.54	0/2362
49	SD	0.19	0/1793	0.46	0/2414
50	SE	0.21	0/2118	0.44	0/2849
51	SF	0.22	0/1504	0.48	0/2024
52	SH	0.20	0/1516	0.51	2/2030 (0.1%)
53	SI	0.25	0/1715	0.48	0/2287
54	SK	0.26	0/851	0.56	0/1147
55	SL	0.25	0/1182	0.46	0/1581
56	SP	0.21	0/1071	0.54	0/1432
57	SQ	0.22	0/1177	0.54	0/1575
58	SR	0.23	0/1086	0.57	0/1457
59	SS	0.21	0/1216	0.53	0/1628
60	ST	0.18	0/1131	0.44	0/1515
61	SU	0.19	0/827	0.48	0/1110
62	SV	0.23	0/643	0.48	0/860
63	SX	0.25	0/1116	0.55	1/1490 (0.1%)
64	Sa	0.26	0/817	0.47	0/1095
65	Sc	0.20	0/502	0.55	0/673
66	Sd	0.27	0/470	0.67	1/623 (0.2%)
67	Sg	0.17	0/2493	0.41	0/3394
68	SC	0.26	0/1719	0.47	0/2322
69	SG	0.18	0/1938	0.43	0/2579
70	SJ	0.22	0/1550	0.51	0/2069
71	Sf	0.16	0/943	0.52	0/1267
72	SN	0.24	0/1232	0.49	0/1656
73	SO	0.27	0/1023	0.51	0/1372
74	SW	0.29	0/1051	0.60	0/1406
75	SY	0.21	0/1083	0.52	0/1438

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SZ	0.23	0/604	0.44	0/810
77	Sb	0.22	0/665	0.51	0/891
78	Se	0.17	0/465	0.41	0/612
79	sh	0.16	0/525	0.46	0/695
80	zv	0.19	0/295	0.45	0/455
81	zx	0.21	0/163	0.68	0/221
82	zy	0.18	0/1786	0.28	0/2784
83	zz	0.14	0/5005	0.29	0/7803
84	3m	0.13	0/2676	0.37	0/3635
85	3f	0.11	0/2099	0.32	0/2856
86	3a	0.12	0/4583	0.34	0/6237
87	3e	0.10	0/3282	0.29	0/4467
88	3c	0.12	0/4900	0.35	1/6641 (0.0%)
89	3h	0.12	0/2550	0.35	0/3456
90	3d	0.10	0/358	0.29	0/493
91	3k	0.21	0/1502	0.52	0/2052
92	3l	0.11	0/4446	0.32	0/6013
All	All	0.24	0/263042	0.39	11/384076 (0.0%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	SH	65	PRO	CA-C-N	6.95	124.62	120.24
52	SH	65	PRO	C-N-CA	6.95	124.62	120.24
24	LV	111	GLU	CA-CB-CG	6.75	127.60	114.10
8	LE	279	ASN	N-CA-CB	-6.07	107.25	114.17
19	LQ	94	GLU	CA-CB-CG	5.72	125.53	114.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	78531	0	39682	651	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	L7	2558	0	1296	13	0
3	L8	3314	0	1683	35	0
4	LA	1898	0	1993	30	0
5	LB	3220	0	3362	35	0
6	LC	2914	0	3087	43	0
7	LD	2382	0	2410	22	0
8	LE	1818	0	1979	31	0
9	LF	1866	0	1992	28	0
10	LG	1914	0	2060	25	0
11	LH	1510	0	1589	19	0
12	LI	1711	0	1749	20	0
13	LJ	1410	0	1441	16	0
14	LL	1701	0	1818	22	0
15	LM	1138	0	1204	16	0
16	LN	1701	0	1749	27	0
17	LO	1650	0	1794	23	0
18	LP	1242	0	1269	16	0
19	LQ	1513	0	1628	24	0
20	LR	1566	0	1729	14	0
21	LS	1453	0	1490	29	0
22	LT	1298	0	1366	29	0
23	LU	825	0	850	6	0
24	LV	979	0	1039	13	0
25	LW	1015	0	1079	17	0
26	LX	976	0	1059	13	0
27	LY	1115	0	1205	15	0
28	LZ	1107	0	1182	19	0
29	La	1162	0	1213	27	0
30	Lb	876	0	948	12	0
31	Lc	764	0	804	20	0
32	Ld	888	0	930	9	0
33	Le	1053	0	1147	11	0
34	Lf	876	0	912	7	0
35	Lg	886	0	971	6	0
36	Lh	1015	0	1148	11	0
37	Li	832	0	917	12	0
38	Lj	705	0	737	12	0
39	Lk	569	0	637	6	0
40	Ll	444	0	483	6	0
41	Lm	429	0	465	6	0
42	Ln	230	0	276	3	0
43	Lo	862	0	930	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	Lp	708	0	757	15	0
45	Lr	1002	0	1068	9	0
46	S2	36887	0	18594	362	0
47	SA	1747	0	1751	34	0
48	SB	1738	0	1809	25	0
49	SD	1765	0	1865	19	0
50	SE	2076	0	2177	28	0
51	SF	1483	0	1523	27	0
52	SH	1494	0	1582	22	0
53	SI	1686	0	1772	22	0
54	SK	827	0	854	21	0
55	SL	1162	0	1227	12	0
56	SP	1050	0	1094	22	0
57	SQ	1158	0	1232	28	0
58	SR	1072	0	1130	14	0
59	SS	1198	0	1261	19	0
60	ST	1112	0	1146	13	0
61	SU	817	0	882	14	0
62	SV	636	0	637	15	0
63	SX	1098	0	1167	11	0
64	Sa	803	0	850	9	0
65	Sc	500	0	525	6	0
66	Sd	459	0	452	7	0
67	Sg	2436	0	2393	46	0
68	SC	1683	0	1770	31	0
69	SG	1915	0	2078	34	0
70	SJ	1525	0	1640	24	0
71	Sf	933	0	945	20	0
72	SN	1208	0	1294	18	0
73	SO	1010	0	1034	20	0
74	SW	1034	0	1080	14	0
75	SY	1065	0	1142	16	0
76	SZ	598	0	656	9	0
77	Sb	651	0	672	3	0
78	Se	459	0	503	2	0
79	sh	515	0	522	9	0
80	zv	267	0	141	0	0
81	zx	160	0	183	6	0
82	zy	1599	0	810	5	0
83	zz	4481	0	2267	53	0
84	3m	2639	0	2442	40	0
85	3f	2063	0	2054	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	3a	4497	0	4224	42	0
87	3e	3218	0	2920	31	0
88	3c	4822	0	4415	52	0
89	3h	2499	0	2418	34	0
90	3d	347	0	259	1	0
91	3k	1475	0	1239	21	0
92	3l	4335	0	4272	52	0
93	L5	70	0	0	0	0
93	L8	1	0	0	0	0
93	S2	10	0	0	0	0
94	Lg	1	0	0	0	0
94	Lj	1	0	0	0	0
94	Lm	1	0	0	0	0
94	Lo	1	0	0	0	0
94	Lp	1	0	0	0	0
94	Sa	1	0	0	0	0
94	sh	1	0	0	0	0
All	All	245916	0	186030	2513	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 2513 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:1302:G:O6	46:S2:1307:U:C4	2.18	0.97
1:L5:1177:U:H3	1:L5:1183:C:N4	1.64	0.95
1:L5:2845:A:H61	1:L5:3843:C:N4	1.63	0.95
83:zz:145:G:H1	83:zz:248:U:H3	1.10	0.94
1:L5:2845:A:N6	1:L5:3843:C:H42	1.65	0.93

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%)	224 (91%)	22 (9%)	0	100	100
5	LB	397/403 (98%)	366 (92%)	30 (8%)	1 (0%)	37	70
6	LC	364/427 (85%)	345 (95%)	19 (5%)	0	100	100
7	LD	291/297 (98%)	259 (89%)	31 (11%)	1 (0%)	37	70
8	LE	220/288 (76%)	191 (87%)	29 (13%)	0	100	100
9	LF	223/248 (90%)	215 (96%)	8 (4%)	0	100	100
10	LG	237/266 (89%)	218 (92%)	19 (8%)	0	100	100
11	LH	188/192 (98%)	171 (91%)	17 (9%)	0	100	100
12	LI	211/214 (99%)	192 (91%)	19 (9%)	0	100	100
13	LJ	174/178 (98%)	166 (95%)	8 (5%)	0	100	100
14	LL	208/211 (99%)	194 (93%)	14 (7%)	0	100	100
15	LM	137/215 (64%)	131 (96%)	6 (4%)	0	100	100
16	LN	201/204 (98%)	189 (94%)	12 (6%)	0	100	100
17	LO	199/203 (98%)	196 (98%)	3 (2%)	0	100	100
18	LP	151/184 (82%)	142 (94%)	9 (6%)	0	100	100
19	LQ	185/188 (98%)	177 (96%)	8 (4%)	0	100	100
20	LR	185/196 (94%)	183 (99%)	2 (1%)	0	100	100
21	LS	173/176 (98%)	157 (91%)	16 (9%)	0	100	100
22	LT	157/160 (98%)	143 (91%)	14 (9%)	0	100	100
23	LU	99/128 (77%)	89 (90%)	10 (10%)	0	100	100
24	LV	129/140 (92%)	120 (93%)	9 (7%)	0	100	100
25	LW	122/157 (78%)	117 (96%)	5 (4%)	0	100	100
26	LX	115/156 (74%)	110 (96%)	5 (4%)	0	100	100
27	LY	132/145 (91%)	127 (96%)	5 (4%)	0	100	100
28	LZ	133/136 (98%)	123 (92%)	10 (8%)	0	100	100
29	La	145/148 (98%)	136 (94%)	9 (6%)	0	100	100
30	Lb	105/159 (66%)	96 (91%)	9 (9%)	0	100	100
31	Lc	96/115 (84%)	93 (97%)	3 (3%)	0	100	100
32	Ld	105/125 (84%)	99 (94%)	6 (6%)	0	100	100
33	Le	126/135 (93%)	122 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	Lf	107/110 (97%)	99 (92%)	8 (8%)	0	100	100
35	Lg	108/117 (92%)	101 (94%)	7 (6%)	0	100	100
36	Lh	120/123 (98%)	112 (93%)	8 (7%)	0	100	100
37	Li	100/105 (95%)	98 (98%)	2 (2%)	0	100	100
38	Lj	84/97 (87%)	77 (92%)	7 (8%)	0	100	100
39	Lk	67/70 (96%)	61 (91%)	6 (9%)	0	100	100
40	Ll	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
41	Lm	50/128 (39%)	47 (94%)	3 (6%)	0	100	100
42	Ln	22/25 (88%)	22 (100%)	0	0	100	100
43	Lo	103/106 (97%)	94 (91%)	9 (9%)	0	100	100
44	Lp	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
45	Lr	123/137 (90%)	112 (91%)	11 (9%)	0	100	100
47	SA	220/295 (75%)	210 (96%)	10 (4%)	0	100	100
48	SB	212/264 (80%)	199 (94%)	13 (6%)	0	100	100
49	SD	225/243 (93%)	222 (99%)	3 (1%)	0	100	100
50	SE	260/263 (99%)	243 (94%)	17 (6%)	0	100	100
51	SF	187/204 (92%)	177 (95%)	10 (5%)	0	100	100
52	SH	182/194 (94%)	170 (93%)	12 (7%)	0	100	100
53	SI	204/208 (98%)	191 (94%)	13 (6%)	0	100	100
54	SK	96/165 (58%)	91 (95%)	5 (5%)	0	100	100
55	SL	138/158 (87%)	127 (92%)	11 (8%)	0	100	100
56	SP	126/145 (87%)	120 (95%)	6 (5%)	0	100	100
57	SQ	144/146 (99%)	129 (90%)	14 (10%)	1 (1%)	19	54
58	SR	130/135 (96%)	125 (96%)	5 (4%)	0	100	100
59	SS	143/152 (94%)	132 (92%)	11 (8%)	0	100	100
60	ST	141/145 (97%)	139 (99%)	2 (1%)	0	100	100
61	SU	101/119 (85%)	96 (95%)	5 (5%)	0	100	100
62	SV	81/83 (98%)	72 (89%)	9 (11%)	0	100	100
63	SX	139/143 (97%)	125 (90%)	14 (10%)	0	100	100
64	Sa	98/115 (85%)	93 (95%)	4 (4%)	1 (1%)	13	46
65	Sc	62/69 (90%)	53 (86%)	9 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
66	Sd	53/56 (95%)	47 (89%)	6 (11%)	0	100	100
67	Sg	311/317 (98%)	292 (94%)	19 (6%)	0	100	100
68	SC	215/293 (73%)	199 (93%)	16 (7%)	0	100	100
69	SG	234/249 (94%)	228 (97%)	6 (3%)	0	100	100
70	SJ	183/194 (94%)	171 (93%)	12 (7%)	0	100	100
71	Sf	120/132 (91%)	108 (90%)	12 (10%)	0	100	100
72	SN	148/151 (98%)	141 (95%)	7 (5%)	0	100	100
73	SO	133/151 (88%)	121 (91%)	12 (9%)	0	100	100
74	SW	127/130 (98%)	117 (92%)	10 (8%)	0	100	100
75	SY	129/133 (97%)	124 (96%)	5 (4%)	0	100	100
76	SZ	73/125 (58%)	68 (93%)	5 (7%)	0	100	100
77	Sb	81/84 (96%)	75 (93%)	6 (7%)	0	100	100
78	Se	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
79	sh	61/156 (39%)	55 (90%)	5 (8%)	1 (2%)	8	34
81	zx	19/31 (61%)	12 (63%)	7 (37%)	0	100	100
84	3m	361/374 (96%)	350 (97%)	11 (3%)	0	100	100
85	3f	267/357 (75%)	263 (98%)	4 (2%)	0	100	100
86	3a	590/1382 (43%)	578 (98%)	12 (2%)	0	100	100
87	3e	427/445 (96%)	417 (98%)	10 (2%)	0	100	100
88	3c	644/913 (70%)	633 (98%)	11 (2%)	0	100	100
89	3h	313/352 (89%)	305 (97%)	8 (3%)	0	100	100
90	3d	53/548 (10%)	53 (100%)	0	0	100	100
91	3k	213/218 (98%)	204 (96%)	9 (4%)	0	100	100
92	3l	518/564 (92%)	507 (98%)	11 (2%)	0	100	100
All	All	14693/17872 (82%)	13878 (94%)	810 (6%)	5 (0%)	100	100

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	LB	303	ALA
7	LD	126	THR
64	Sa	61	ALA
79	sh	138	ARG
57	SQ	42	ILE

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%)	169 (89%)	21 (11%)	5	21
5	LB	347/349 (99%)	329 (95%)	18 (5%)	19	52
6	LC	305/348 (88%)	292 (96%)	13 (4%)	25	58
7	LD	246/250 (98%)	237 (96%)	9 (4%)	29	63
8	LE	200/252 (79%)	188 (94%)	12 (6%)	16	47
9	LF	193/215 (90%)	179 (93%)	14 (7%)	11	39
10	LG	202/223 (91%)	192 (95%)	10 (5%)	20	53
11	LH	167/171 (98%)	162 (97%)	5 (3%)	36	69
12	LI	180/181 (99%)	168 (93%)	12 (7%)	13	43
13	LJ	148/149 (99%)	141 (95%)	7 (5%)	22	56
14	LL	176/177 (99%)	166 (94%)	10 (6%)	17	49
15	LM	118/161 (73%)	110 (93%)	8 (7%)	13	42
16	LN	171/172 (99%)	156 (91%)	15 (9%)	8	31
17	LO	173/174 (99%)	160 (92%)	13 (8%)	11	38
18	LP	134/163 (82%)	126 (94%)	8 (6%)	16	47
19	LQ	164/165 (99%)	151 (92%)	13 (8%)	10	35
20	LR	166/175 (95%)	156 (94%)	10 (6%)	16	47
21	LS	156/157 (99%)	141 (90%)	15 (10%)	7	27
22	LT	139/140 (99%)	119 (86%)	20 (14%)	2	13
23	LU	91/115 (79%)	85 (93%)	6 (7%)	14	43
24	LV	101/107 (94%)	90 (89%)	11 (11%)	5	22
25	LW	103/126 (82%)	100 (97%)	3 (3%)	37	70
26	LX	107/133 (80%)	96 (90%)	11 (10%)	6	24
27	LY	124/135 (92%)	117 (94%)	7 (6%)	17	49
28	LZ	117/118 (99%)	112 (96%)	5 (4%)	25	58
29	La	120/121 (99%)	113 (94%)	7 (6%)	17	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	Lb	88/126 (70%)	87 (99%)	1 (1%)	70	87
31	Lc	83/97 (86%)	72 (87%)	11 (13%)	3	15
32	Ld	98/110 (89%)	94 (96%)	4 (4%)	26	60
33	Le	114/121 (94%)	109 (96%)	5 (4%)	24	58
34	Lf	88/89 (99%)	81 (92%)	7 (8%)	10	35
35	Lg	96/100 (96%)	90 (94%)	6 (6%)	15	45
36	Lh	109/110 (99%)	102 (94%)	7 (6%)	14	44
37	Li	86/89 (97%)	82 (95%)	4 (5%)	22	56
38	Lj	73/80 (91%)	69 (94%)	4 (6%)	18	50
39	Lk	64/65 (98%)	56 (88%)	8 (12%)	3	17
40	Ll	47/48 (98%)	44 (94%)	3 (6%)	14	44
41	Lm	48/116 (41%)	47 (98%)	1 (2%)	48	77
42	Ln	23/24 (96%)	23 (100%)	0	100	100
43	Lo	93/94 (99%)	83 (89%)	10 (11%)	5	22
44	Lp	74/75 (99%)	64 (86%)	10 (14%)	3	14
45	Lr	109/121 (90%)	105 (96%)	4 (4%)	29	63
47	SA	184/243 (76%)	173 (94%)	11 (6%)	16	47
48	SB	195/231 (84%)	179 (92%)	16 (8%)	9	34
49	SD	190/202 (94%)	180 (95%)	10 (5%)	19	51
50	SE	224/225 (100%)	210 (94%)	14 (6%)	15	45
51	SF	156/170 (92%)	149 (96%)	7 (4%)	23	57
52	SH	166/174 (95%)	159 (96%)	7 (4%)	25	59
53	SI	178/180 (99%)	164 (92%)	14 (8%)	10	35
54	SK	89/136 (65%)	83 (93%)	6 (7%)	13	43
55	SL	128/142 (90%)	116 (91%)	12 (9%)	7	28
56	SP	114/130 (88%)	105 (92%)	9 (8%)	10	35
57	SQ	121/121 (100%)	109 (90%)	12 (10%)	6	26
58	SR	120/122 (98%)	108 (90%)	12 (10%)	6	25
59	SS	126/132 (96%)	122 (97%)	4 (3%)	34	67
60	ST	113/115 (98%)	108 (96%)	5 (4%)	24	58
61	SU	94/107 (88%)	89 (95%)	5 (5%)	19	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
62	SV	67/67 (100%)	64 (96%)	3 (4%)	23	57
63	SX	113/115 (98%)	103 (91%)	10 (9%)	8	31
64	Sa	87/98 (89%)	82 (94%)	5 (6%)	17	49
65	Sc	56/62 (90%)	47 (84%)	9 (16%)	2	10
66	Sd	48/49 (98%)	45 (94%)	3 (6%)	15	45
67	Sg	272/275 (99%)	257 (94%)	15 (6%)	18	50
68	SC	183/225 (81%)	170 (93%)	13 (7%)	12	40
69	SG	206/218 (94%)	200 (97%)	6 (3%)	37	70
70	SJ	161/168 (96%)	150 (93%)	11 (7%)	13	42
71	Sf	100/108 (93%)	95 (95%)	5 (5%)	20	53
72	SN	130/131 (99%)	121 (93%)	9 (7%)	13	42
73	SO	105/119 (88%)	95 (90%)	10 (10%)	7	28
74	SW	112/113 (99%)	101 (90%)	11 (10%)	6	26
75	SY	113/115 (98%)	110 (97%)	3 (3%)	40	71
76	SZ	66/103 (64%)	63 (96%)	3 (4%)	23	57
77	Sb	75/76 (99%)	62 (83%)	13 (17%)	1	8
78	Se	47/48 (98%)	44 (94%)	3 (6%)	14	44
79	sh	56/140 (40%)	51 (91%)	5 (9%)	8	31
81	zx	20/29 (69%)	19 (95%)	1 (5%)	20	53
84	3m	252/335 (75%)	245 (97%)	7 (3%)	38	70
85	3f	229/289 (79%)	221 (96%)	8 (4%)	31	65
86	3a	439/1259 (35%)	431 (98%)	8 (2%)	54	80
87	3e	301/406 (74%)	297 (99%)	4 (1%)	65	85
88	3c	442/811 (54%)	433 (98%)	9 (2%)	50	78
89	3h	270/310 (87%)	263 (97%)	7 (3%)	41	72
90	3d	20/494 (4%)	20 (100%)	0	100	100
91	3k	121/193 (63%)	117 (97%)	4 (3%)	33	67
92	3l	475/515 (92%)	467 (98%)	8 (2%)	56	81
All	All	12395/15442 (80%)	11690 (94%)	705 (6%)	20	49

5 of 705 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
55	SL	126	VAL
69	SG	109	LEU
57	SQ	18	THR
55	SL	120	VAL
63	SX	94	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 121 such sidechains are listed below:

Mol	Chain	Res	Type
55	SL	154	GLN
92	3l	180	ASN
68	SC	178	HIS
92	3l	92	GLN
92	3l	495	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3652/5070 (72%)	876 (23%)	19 (0%)
2	L7	119/120 (99%)	17 (14%)	0
3	L8	155/156 (99%)	31 (20%)	2 (1%)
46	S2	1714/1869 (91%)	496 (28%)	8 (0%)
80	zv	12/19 (63%)	8 (66%)	0
82	zy	74/75 (98%)	13 (17%)	0
83	zz	209/332 (62%)	76 (36%)	0
All	All	5935/7641 (77%)	1517 (25%)	29 (0%)

5 of 1517 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	23	C
1	L5	25	A
1	L5	30	C
1	L5	39	A
1	L5	42	A

5 of 29 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	4452	U
46	S2	1849	G

Continued on next page...

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Mol	Chain	Res	Type
1	L5	4731	G
46	S2	604	A
1	L5	4699	U

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 88 ligands modelled in this entry, 88 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.

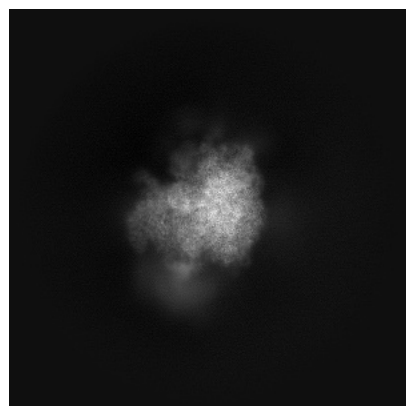
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62671. These allow visual inspection of the internal detail of the map and identification of artifacts.

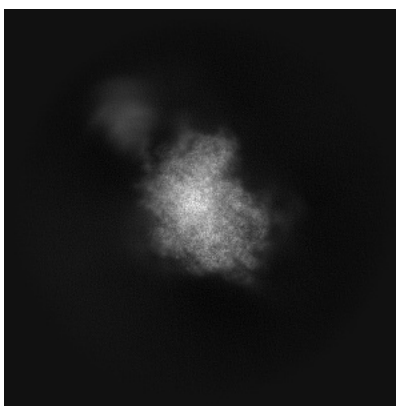
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

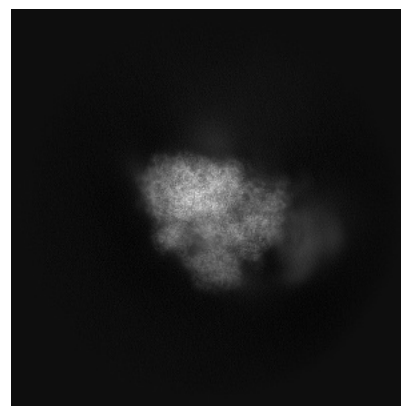
6.1.1 Primary map



X

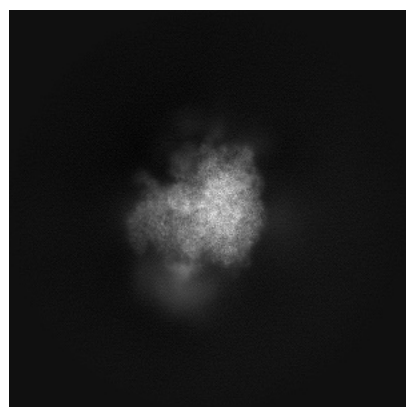


Y

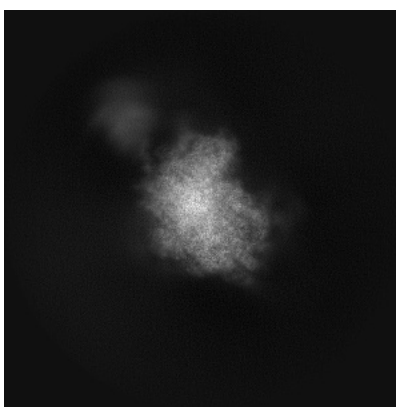


Z

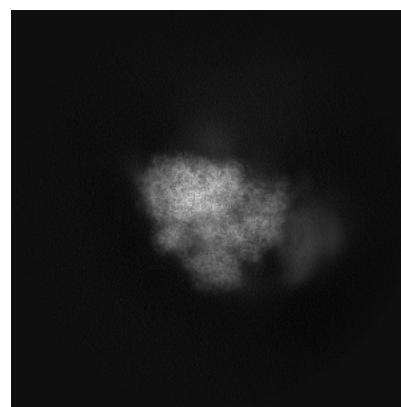
6.1.2 Raw map



X



Y

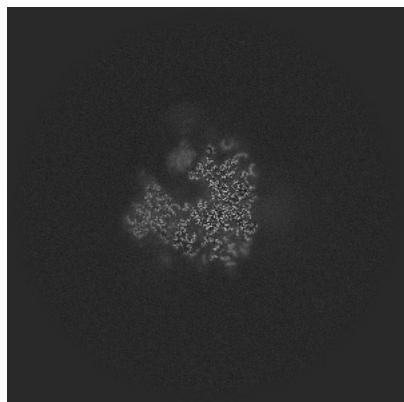


Z

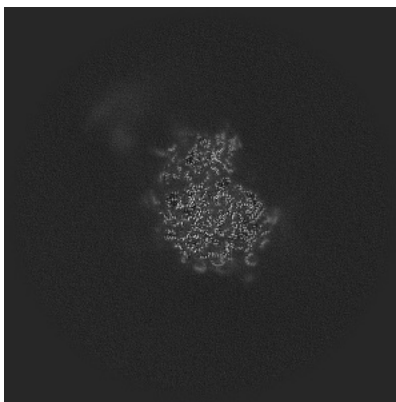
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

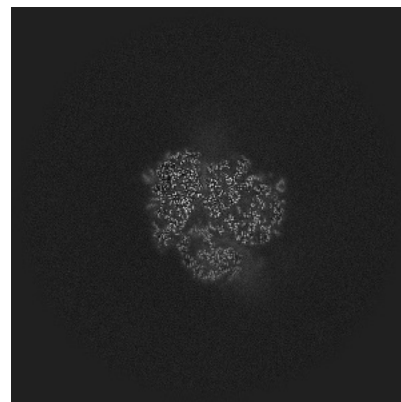
6.2.1 Primary map



X Index: 250

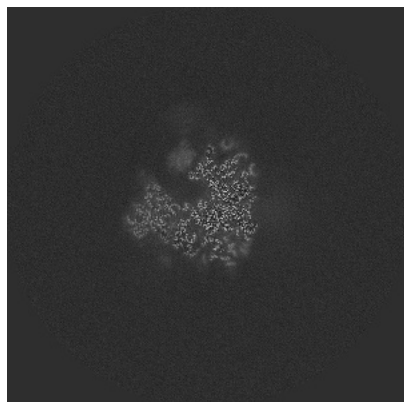


Y Index: 250

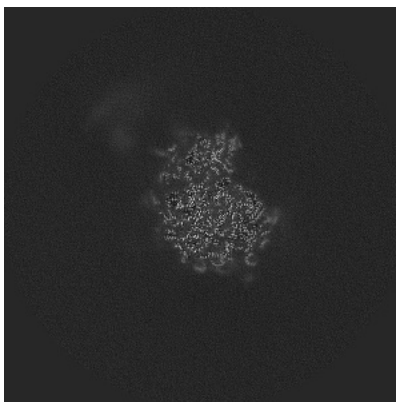


Z Index: 250

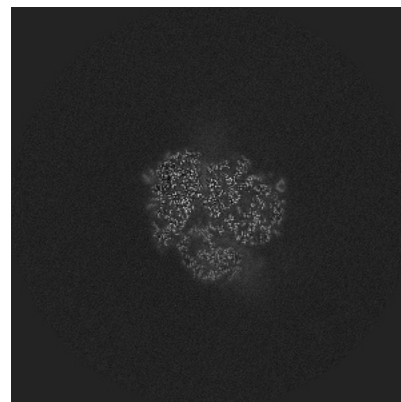
6.2.2 Raw map



X Index: 250



Y Index: 250

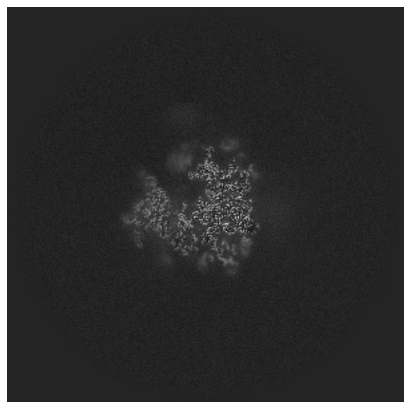


Z Index: 250

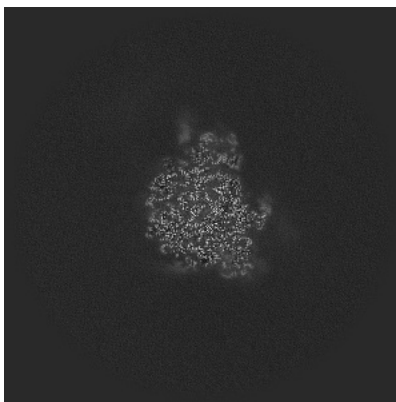
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

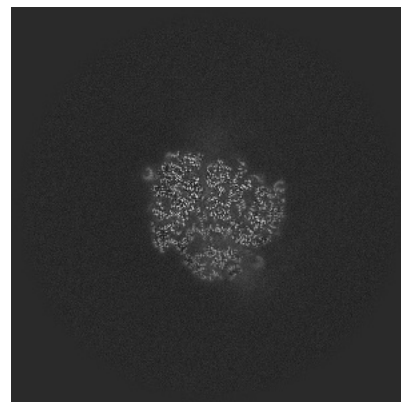
6.3.1 Primary map



X Index: 253

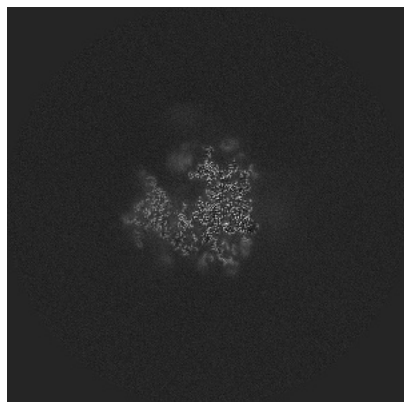


Y Index: 271

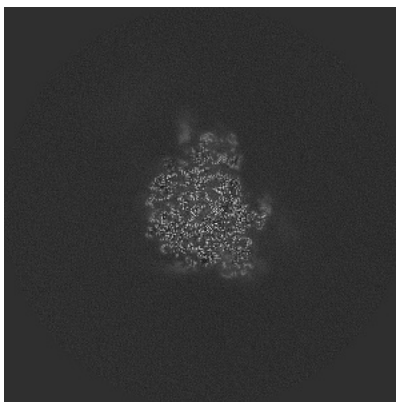


Z Index: 253

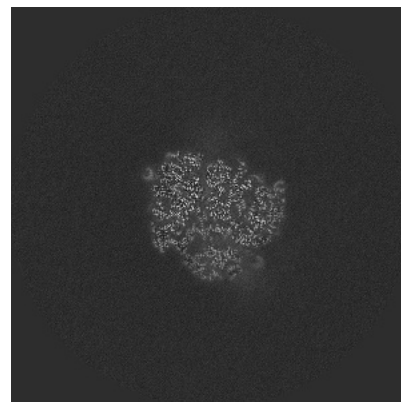
6.3.2 Raw map



X Index: 253



Y Index: 271

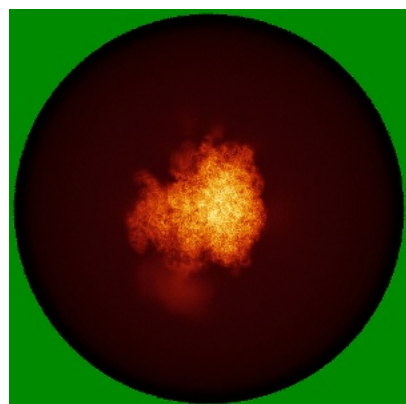


Z Index: 253

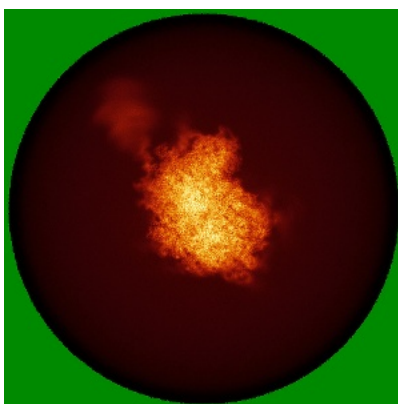
The images above show the largest variance slices of the map in three orthogonal directions.

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

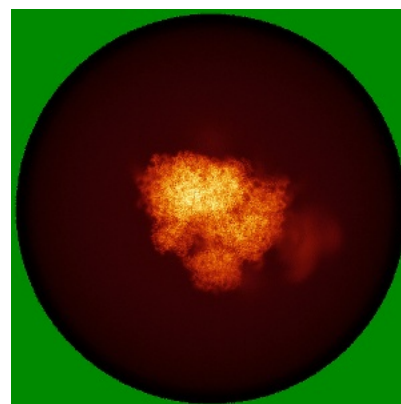
6.4.1 Primary map



X

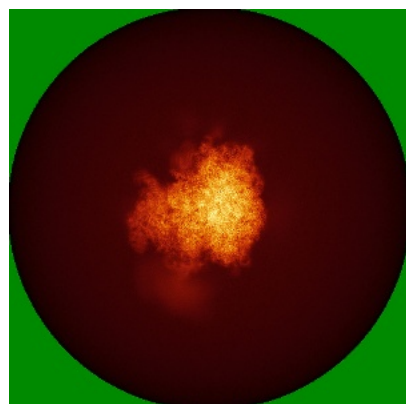


Y

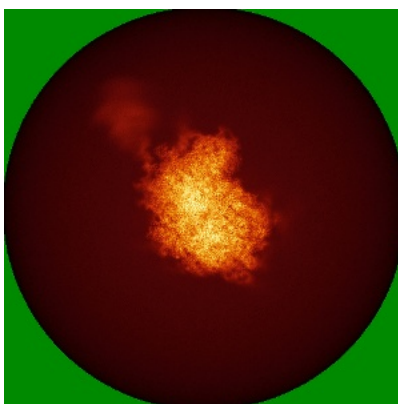


Z

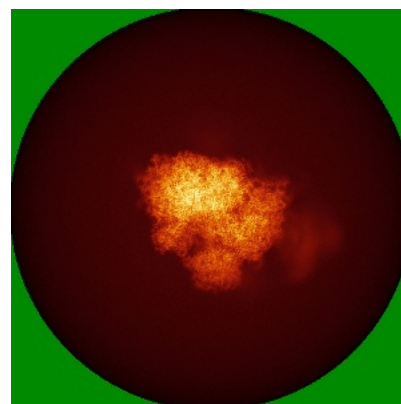
6.4.2 Raw map



X



Y

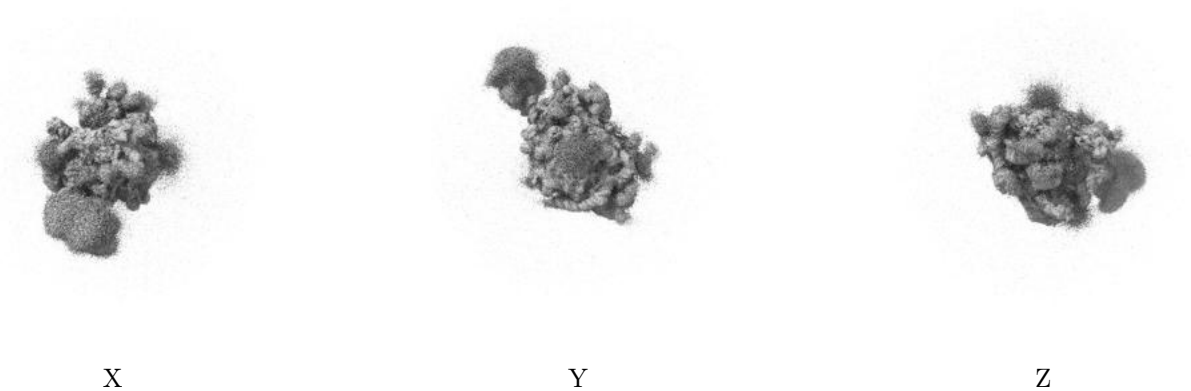


Z

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.

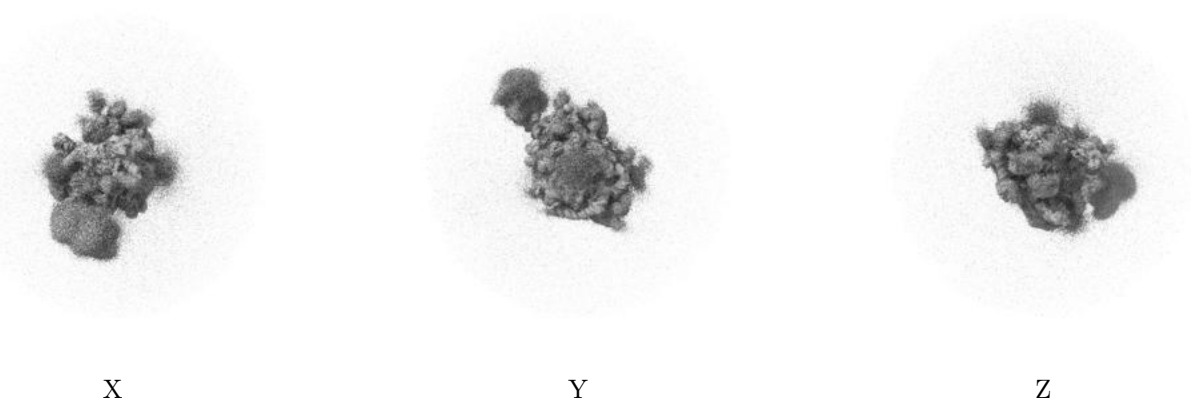
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. 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.

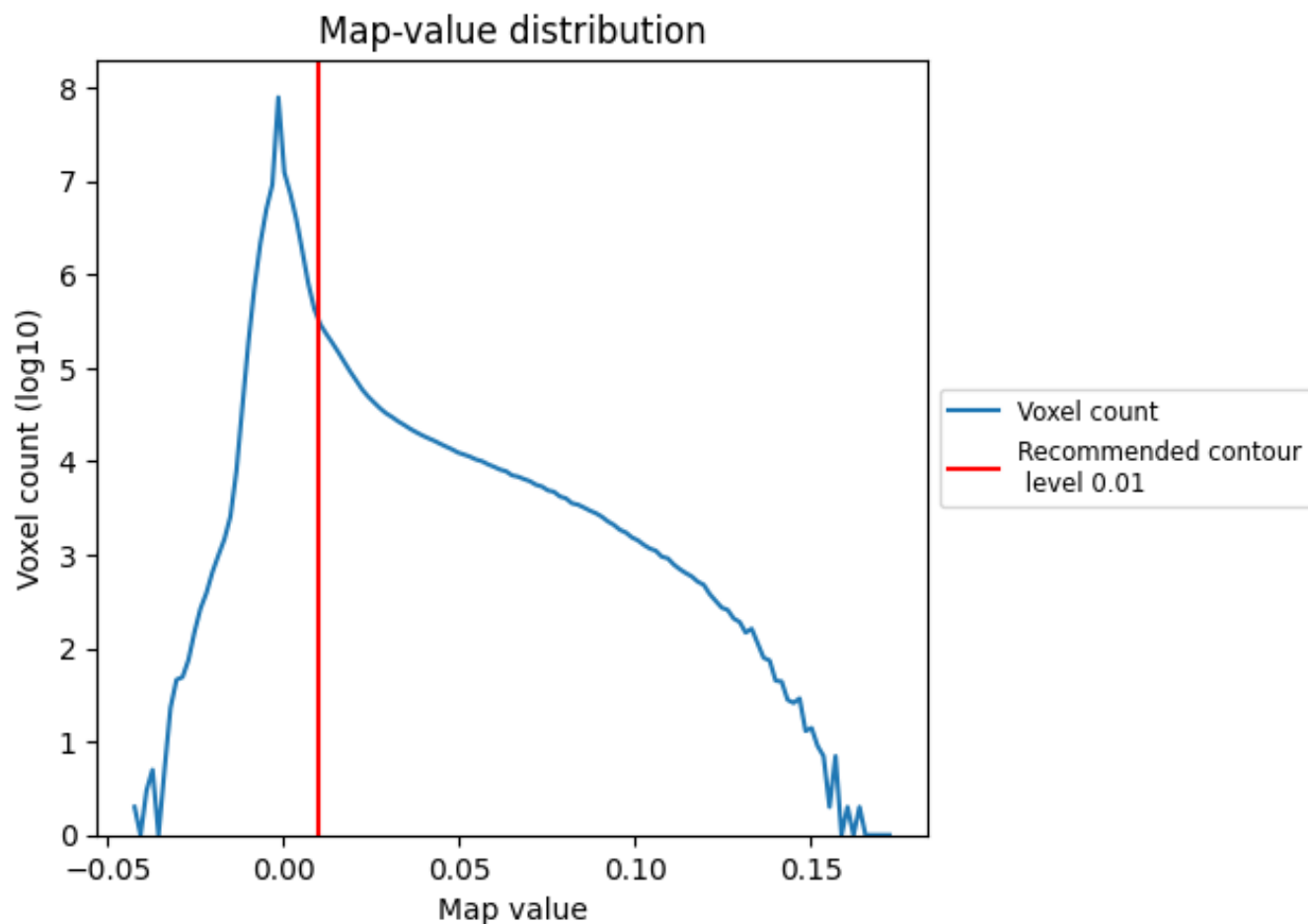
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

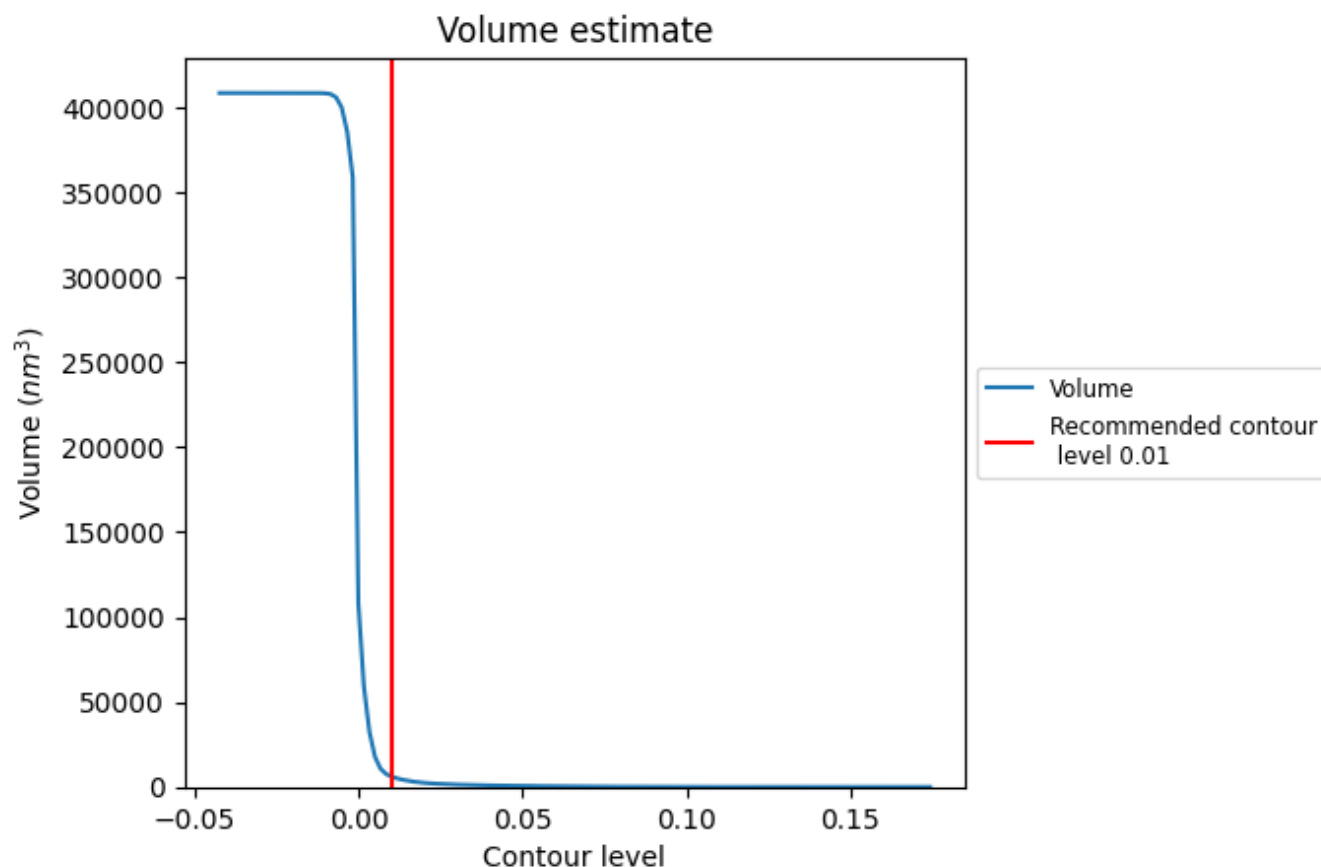
This section contains the results of statistical analysis of the map.

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.

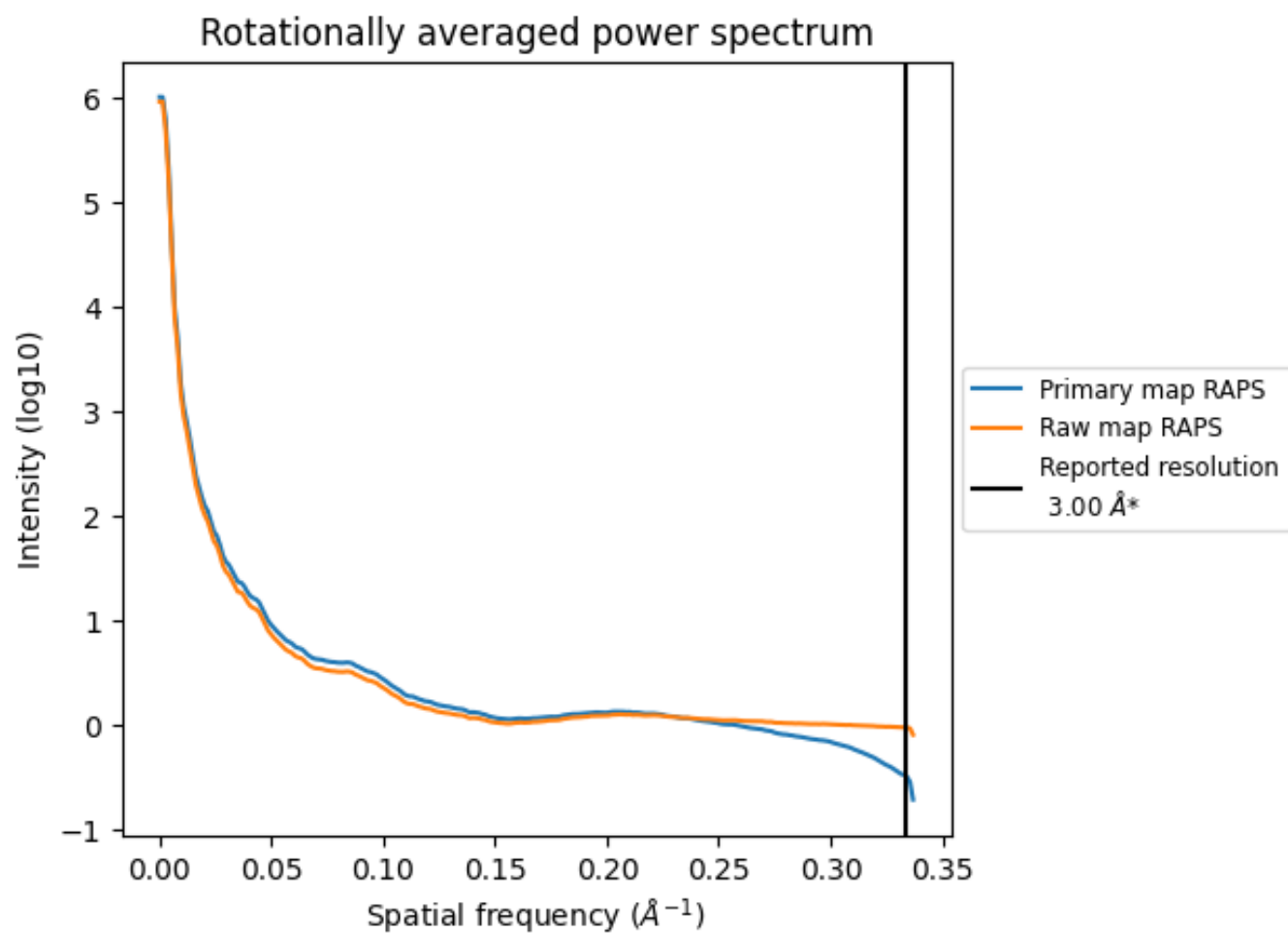
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 6223 nm³; this corresponds to an approximate mass of 5622 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 ⓘ

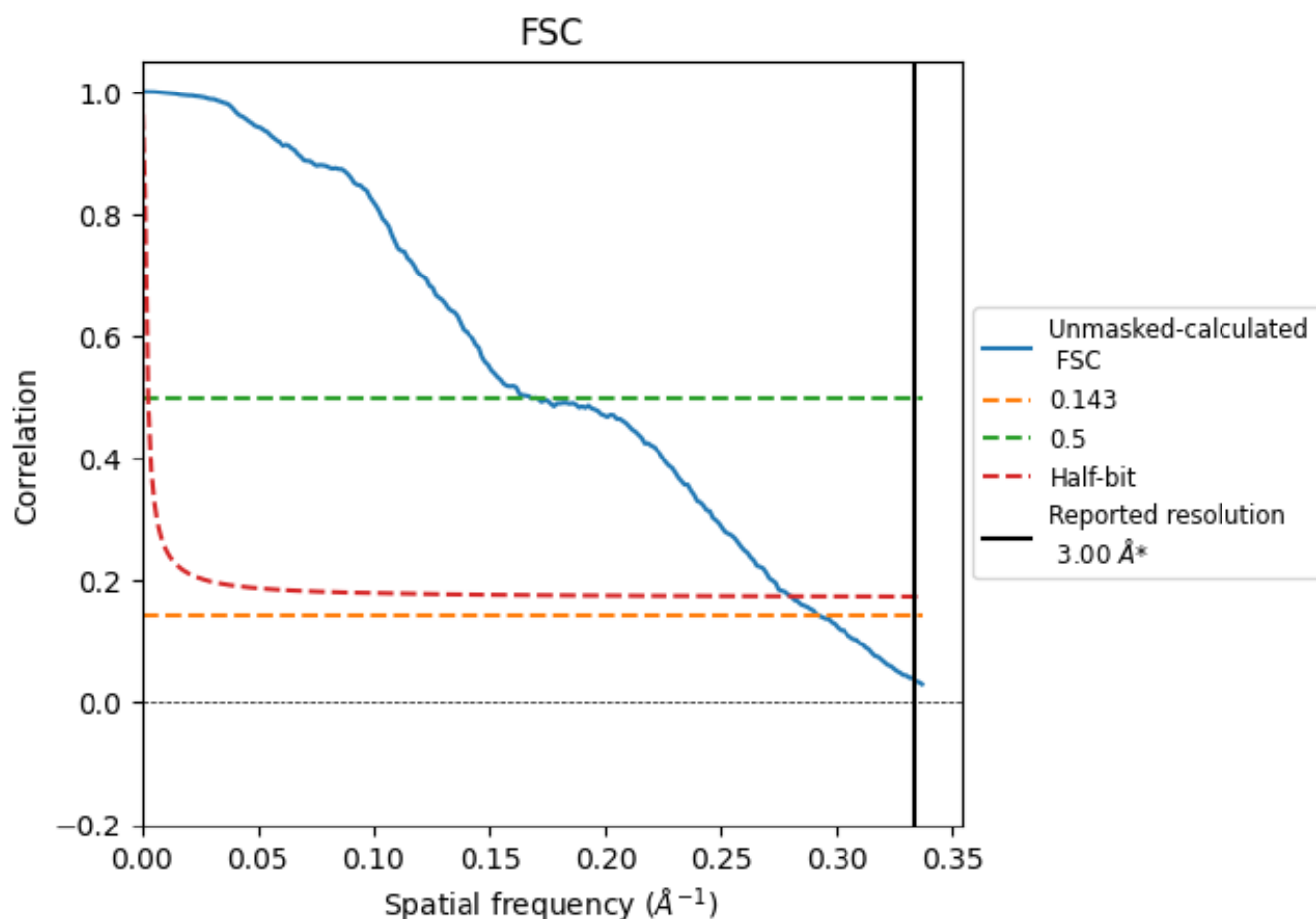


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

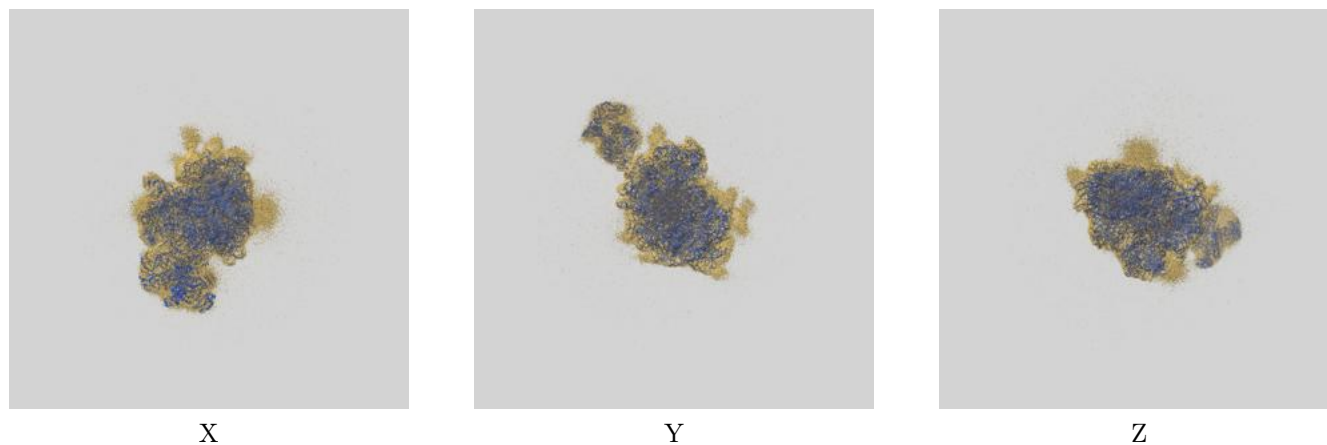
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.42	5.96	3.57

*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 3.42 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

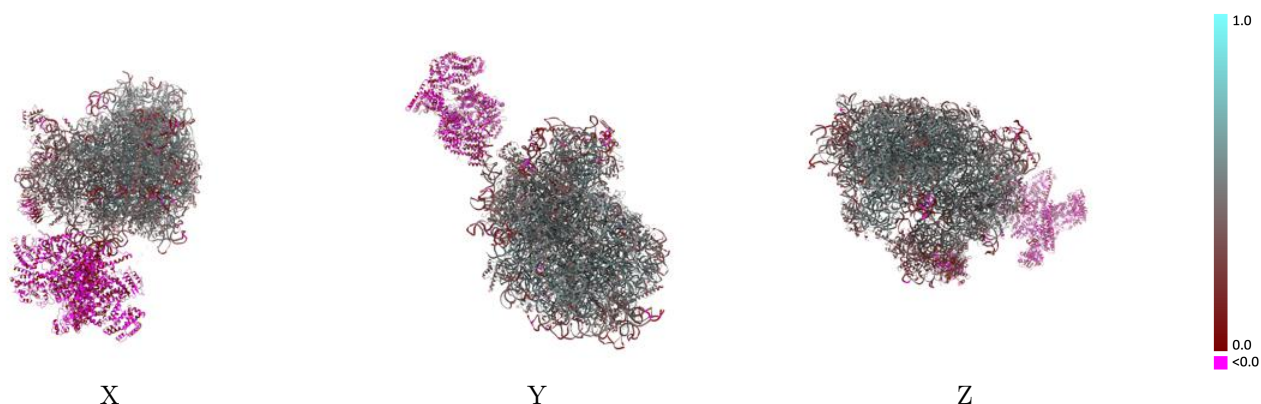
This section contains information regarding the fit between EMDB map EMD-62671 and PDB model 9KZU. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



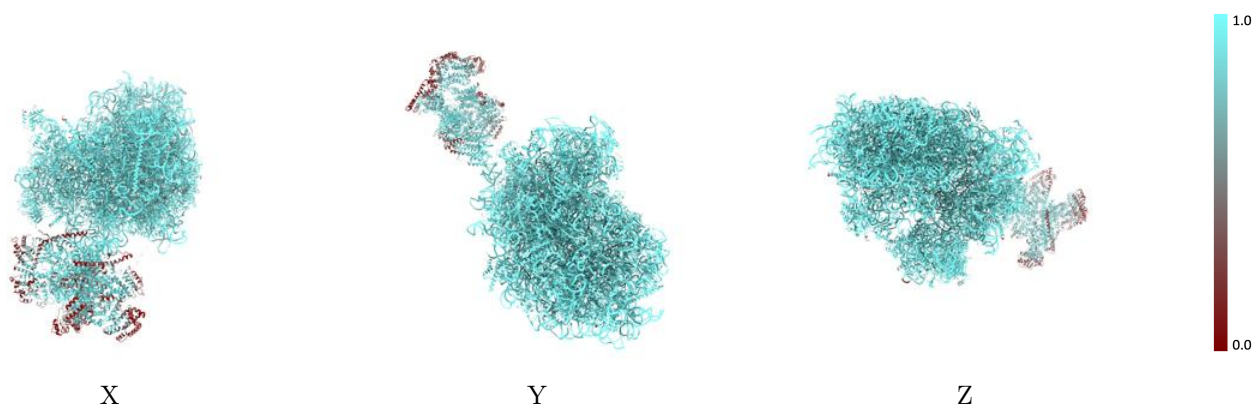
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



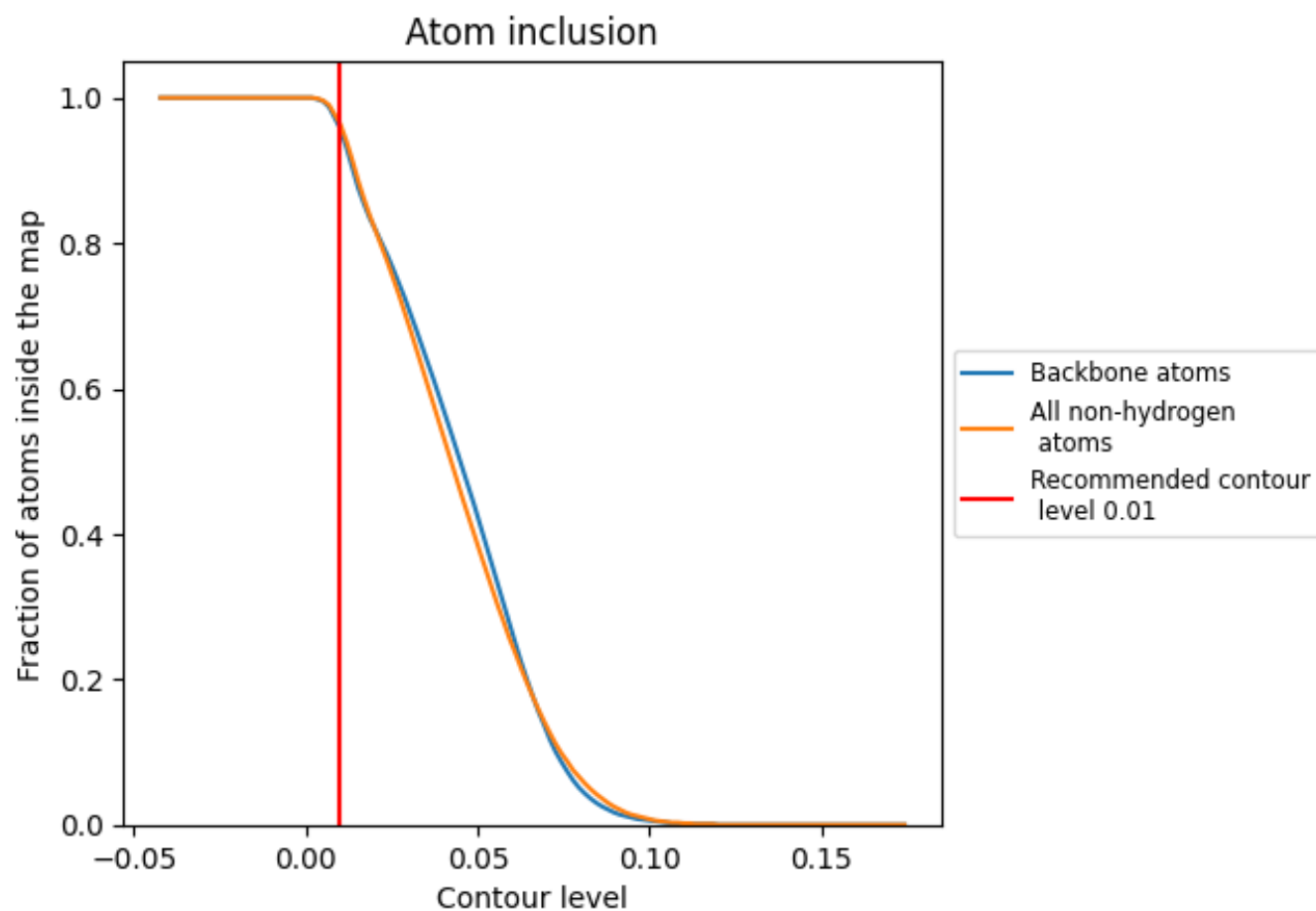
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 96% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































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

Chain	Atom inclusion	Q-score
All	 0.9640	 0.3990
3a	 0.8530	 0.0400
3c	 0.8570	 0.0900
3d	 0.6770	 0.0280
3e	 0.6950	 0.0250
3f	 0.8210	 0.0330
3h	 0.8250	 0.0060
3k	 0.3450	 0.0190
3l	 0.6430	 0.0240
3m	 0.5320	 0.0400
L5	 0.9980	 0.4730
L7	 1.0000	 0.5110
L8	 0.9940	 0.4930
LA	 0.9970	 0.5170
LB	 0.9920	 0.4940
LC	 0.9940	 0.4860
LD	 0.9810	 0.4320
LE	 0.9900	 0.4290
LF	 0.9970	 0.5030
LG	 0.9800	 0.4330
LH	 0.9920	 0.4630
LI	 0.9950	 0.4900
LJ	 0.9760	 0.4370
LL	 0.9700	 0.4760
LM	 0.9970	 0.5020
LN	 0.9990	 0.5360
LO	 0.9940	 0.5020
LP	 0.9900	 0.4730
LQ	 0.9980	 0.5060
LR	 0.9910	 0.4550
LS	 0.9960	 0.5170
LT	 0.9950	 0.4730
LU	 0.9550	 0.3270
LV	 0.9950	 0.5010
LW	 0.9810	 0.3640



































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Chain	Atom inclusion	Q-score
LX	 0.9870	 0.4660
LY	 0.9910	 0.4600
LZ	 0.9880	 0.4110
La	 0.9900	 0.4860
Lb	 0.9680	 0.4120
Lc	 0.9870	 0.4700
Ld	 0.9810	 0.4470
Le	 0.9980	 0.5280
Lf	 0.9950	 0.5310
Lg	 0.9950	 0.4840
Lh	 0.9910	 0.4720
Li	 0.9940	 0.4780
Lj	 1.0000	 0.5160
Lk	 0.9620	 0.3710
Ll	 1.0000	 0.4880
Lm	 0.9900	 0.4820
Ln	 1.0000	 0.5030
Lo	 0.9950	 0.5140
Lp	 0.9970	 0.5100
Lr	 0.9960	 0.4800
S2	 0.9970	 0.4260
SA	 0.9680	 0.3950
SB	 0.9920	 0.4380
SC	 0.9740	 0.3830
SD	 0.9780	 0.3520
SE	 0.9880	 0.4460
SF	 0.9830	 0.2980
SG	 0.9940	 0.4010
SH	 0.9770	 0.3910
SI	 0.9930	 0.4570
SJ	 0.9750	 0.4350
SK	 0.9740	 0.3000
SL	 0.9960	 0.4900
SN	 0.9970	 0.4850
SO	 0.9900	 0.4570
SP	 0.9750	 0.3510
SQ	 0.9830	 0.2580
SR	 0.9750	 0.3600
SS	 0.9790	 0.3460
ST	 0.9660	 0.2460
SU	 0.9850	 0.3290
SV	 0.9660	 0.3550

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Chain	Atom inclusion	Q-score
SW	 0.9860	 0.4020
SX	 0.9940	 0.4600
SY	 0.9870	 0.4210
SZ	 0.9620	 0.2610
Sa	 0.9970	 0.4720
Sb	 0.9830	 0.4130
Sc	 0.9940	 0.3920
Sd	 0.9980	 0.3720
Se	 0.9960	 0.3880
Sf	 0.8840	 0.2150
Sg	 0.9440	 0.1500
sh	 0.9460	 0.2260
zv	 1.0000	 0.3530
zx	 1.0000	 0.2170
zy	 1.0000	 0.4800
zz	 0.9760	 0.2000