



## wwPDB EM Validation Summary Report ⓘ

Dec 8, 2025 – 02:00 PM JST

PDB ID : 9KZX / pdb\_00009kzx  
EMDB ID : EMD-62679  
Title : Cryo-EM structure of the HCV IRES-dependently initiated CMV-stalled 80S ribosome (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 : 3.30 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.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

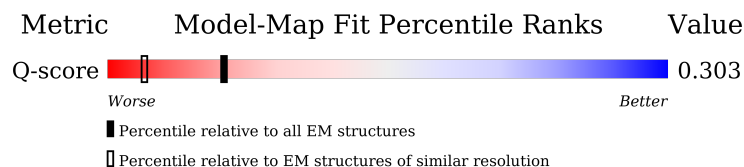
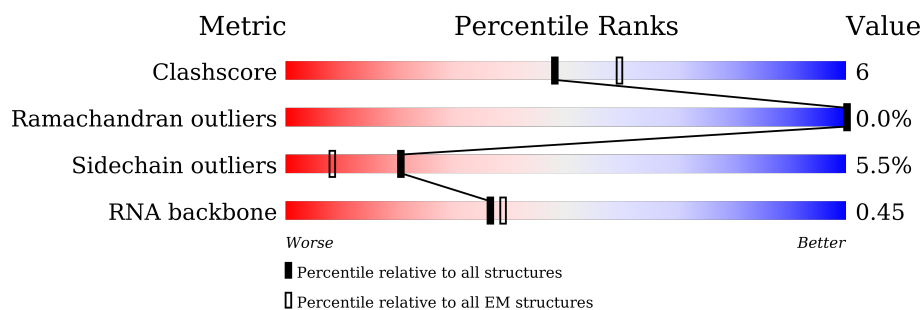
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.30 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.











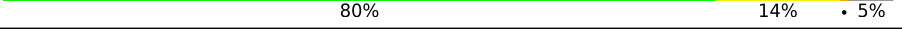

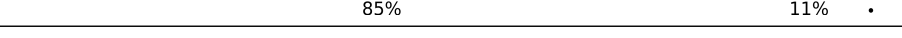
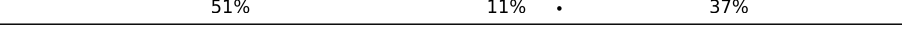

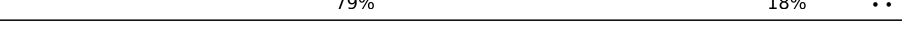


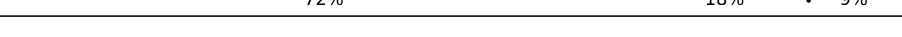

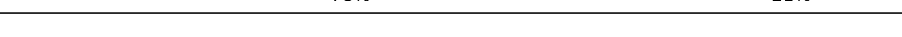






Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	15087 ( 2.80 - 3.80 )

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

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









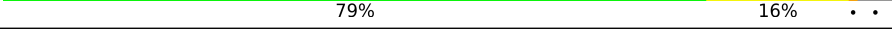

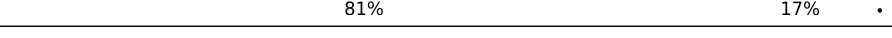
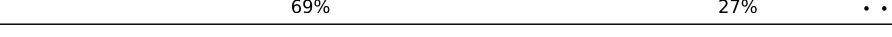

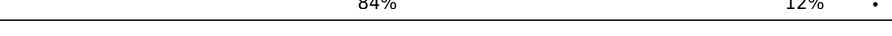


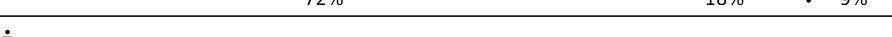

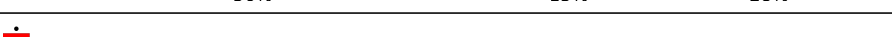






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Mol	Chain	Length	Quality of chain
4	LA	257	
5	LB	403	
6	LC	427	
7	LD	297	
8	LE	288	
9	LF	248	
10	LG	266	
11	LH	192	
12	LI	214	
13	LJ	178	
14	LL	211	
15	LM	215	
16	LN	204	
17	LO	203	
18	LP	184	
19	LQ	188	
20	LR	196	
21	LS	176	
22	LT	160	
23	LU	128	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



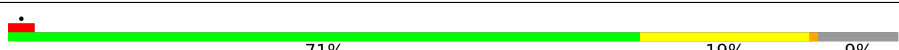
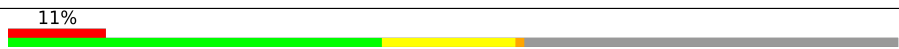
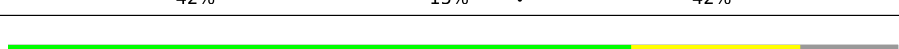
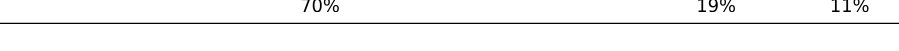
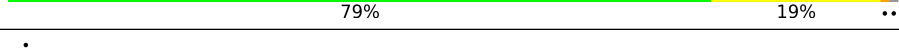





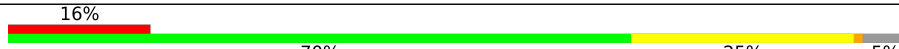


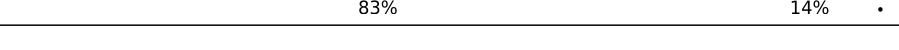



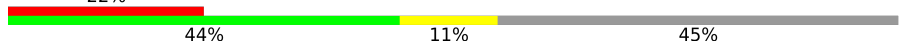




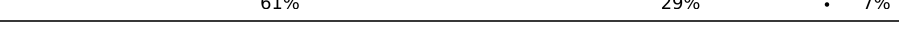
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Mol	Chain	Length	Quality of chain
29	La	148	
30	Lb	159	
31	Lc	115	
32	Ld	125	
33	Le	135	
34	Lf	110	
35	Lg	117	
36	Lh	123	
37	Li	105	
38	Lj	97	
39	Lk	70	
40	Ll	51	
41	Lm	128	
42	Ln	25	
43	Lo	106	
44	Lp	92	
45	Lr	137	
46	S2	1869	
47	SA	295	
48	SB	264	
49	SC	293	
50	SD	243	
51	SE	263	
52	SF	204	
53	SG	249	

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Mol	Chain	Length	Quality of chain
54	SH	194	
55	SI	208	
56	SJ	194	
57	SK	165	
58	SL	158	
59	SN	151	
60	SO	151	
61	SP	145	
62	SQ	146	
63	SR	135	
64	SS	152	
65	ST	145	
66	SU	119	
67	SV	83	
68	SW	130	
69	SX	143	
70	SY	133	
71	SZ	125	
72	Sa	115	
73	Sb	84	
74	Sc	69	
75	Sd	56	
76	Se	59	
77	Sf	132	
78	Sg	317	

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Mol	Chain	Length	Quality of chain
79	sh	156	
80	zu	75	
80	zy	75	
81	zv	19	
82	zx	31	
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 238047 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	3589	Total	C	N	O	P	0	0
			76925	34255	14066	25016	3588		

- 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
			1886	1183	386	311	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LB	393	Total	C	N	O	S	0	0
			3101	1979	583	525	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LC	365	Total	C	N	O	S	0	0
			2894	1819	578	482	15		

- 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
			2287	1455	426	392	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LE	220	Total	C	N	O	S	0	0
			1713	1104	326	279	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
			1844	1189	355	291	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LG	237	Total	C	N	O	S	0	0
			1797	1145	350	298	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LH	189	Total	C	N	O	S	0	0
			1439	910	273	250	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LI	203	Total	C	N	O	S	0	0
			1581	1007	306	254	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LJ	167	Total	C	N	O	S	0	0
			1226	780	228	212	6		

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



Mol	Chain	Residues	Atoms					AltConf	Trace
14	LL	204	Total	C	N	O	S	0	0
			1580	992	335	249	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LM	136	Total	C	N	O	S	0	0
			1097	705	211	174	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
			1693	1068	359	262	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
			1613	1042	318	248	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
			1203	754	238	202	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
			1493	931	311	246	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LR	178	Total	C	N	O	S	0	0
			1434	888	316	222	8		

- 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
			1436	915	281	230	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
			1268	805	249	209	5		

- 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
			768	497	136	133	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
			954	604	180	165	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LW	115	Total	C	N	O	S	0	0
			784	493	154	135	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LX	120	Total	C	N	O	S	0	0
			950	611	182	156	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
			1084	681	220	180	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
			1082	703	207	169	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	La	146	Total	C	N	O	S	0	0
			1145	726	233	183	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Lb	63	Total	C	N	O	S	0	0
			499	310	107	80	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Lc	93	Total	C	N	O	S	0	0
			716	456	125	129	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
			856	546	168	140	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Le	127	Total	C	N	O	S	0	0
			1045	661	215	164	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
			864	547	173	141	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lg	110	Total	C	N	O	S	0	0
			851	531	175	139	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lh	121	Total	C	N	O	S	0	0
			975	617	200	157	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Li	101	Total	C	N	O	S	0	0
			797	500	170	122	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
			701	431	154	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
			528	339	99	89	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
			440	278	97	64	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lm	50	Total	C	N	O	S	0	0
			393	244	82	61	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	98	Total	C	N	O	S	0	0
			774	488	159	121	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
			689	436	132	114	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
			982	609	205	164	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
46	S2	1691	Total	C	N	O	P	0	0
			35873	16003	6419	11761	1690		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SA	212	Total	C	N	O	S	0	0
			1575	1016	285	266	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
			1627	1041	296	277	13		

- Molecule 49 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SC	217	Total	C	N	O	S	0	0
			1590	1039	276	266	9		

- Molecule 50 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SD	212	Total	C	N	O	S	0	0
			1458	939	264	248	7		

- Molecule 51 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SE	257	Total	C	N	O	S	0	0
			1891	1218	358	307	8		

- Molecule 52 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SF	180	Total	C	N	O	S	0	0
			1365	861	261	237	6		

- Molecule 53 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SG	233	Total	C	N	O	S	0	0
			1740	1084	356	294	6		

- Molecule 54 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SH	178	Total	C	N	O	S	0	0
			1363	883	253	226	1		

- Molecule 55 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SI	202	Total	C	N	O	S	0	0
			1551	972	305	269	5		

- Molecule 56 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SJ	176	Total	C	N	O	S	0	0
			1407	899	280	226	2		

- Molecule 57 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SK	95	Total	C	N	O	S	0	0
			736	482	131	119	4		

- Molecule 58 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SL	140	Total	C	N	O	S	0	0
			1139	725	214	194	6		

- 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
			1199	766	229	203	1		

- Molecule 60 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SO	135	Total	C	N	O	S	0	0
			1003	615	198	184	6		

- Molecule 61 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SP	127	Total	C	N	O	S	0	0
			1001	636	188	170	7		

- Molecule 62 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SQ	141	Total	C	N	O	S	0	0
			1078	690	207	178	3		

- Molecule 63 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SR	125	Total	C	N	O	S	0	0
			879	551	166	159	3		

- Molecule 64 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SS	138	Total	C	N	O	S	0	0
			1080	684	220	175	1		

- Molecule 65 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	ST	138	Total	C	N	O	S	0	0
			975	612	192	169	2		

- Molecule 66 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SU	98	Total	C	N	O	S	0	0
			737	461	142	132	2		

- Molecule 67 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SV	83	Total	C	N	O	S	0	0
			589	369	111	104	5		

- Molecule 68 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SW	129	Total	C	N	O	S	0	0
			1027	655	192	174	6		

- Molecule 69 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SX	141	Total	C	N	O	S	0	0
			1048	663	206	176	3		

- Molecule 70 is a protein called 40S ribosomal protein S24.



Mol	Chain	Residues	Atoms					AltConf	Trace
70	SY	126	Total	C	N	O	S	0	0
			943	599	182	158	4		

- Molecule 71 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SZ	69	Total	C	N	O	S	0	0
			479	305	89	84	1		

- Molecule 72 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Sa	99	Total	C	N	O	S	0	0
			762	478	157	122	5		

- Molecule 73 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Sb	83	Total	C	N	O	S	0	0
			617	390	114	109	4		

- Molecule 74 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Sc	61	Total	C	N	O	S	0	0
			430	267	83	78	2		

- Molecule 75 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Sd	52	Total	C	N	O	S	0	0
			420	264	83	69	4		

- Molecule 76 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Se	51	Total	C	N	O	S	0	0
			386	240	83	62	1		

- Molecule 77 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Sf	78	Total	C	N	O	S	0	0
			483	307	90	82	4		

- Molecule 78 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Sg	282	Total	C	N	O	S	0	0
			1948	1241	340	358	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
79	sh	41	Total	C	N	O	S	0	0
			269	168	54	44	3		

- Molecule 80 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	zy	75	Total	C	N	O	P	0	0
			1599	713	284	528	74		
80	zu	72	Total	C	N	O	P	0	0
			1537	685	273	508	71		

- Molecule 81 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	zv	9	Total	C	N	O	P	0	0
			183	82	26	66	9		

- Molecule 82 is a protein called nascent chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
82	zx	20	Total	C	N	O	0	0
			111	71	20	20		

- Molecule 83 is a RNA chain called HCV IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	zz	211	Total	C	N	O	P	0	0
			4503	2005	801	1486	211		

- 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	646	Total	C	N	O	S	0	0
			4794	3015	876	876	27		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
89	3h	318	Total	C	N	O	S	0	0
			2520	1599	431	475	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
			4331	2805	714	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	52	Total	Mg	0
			52	52	
93	L7	1	Total	Mg	0
			1	1	
93	L8	3	Total	Mg	0
			3	3	
93	LV	1	Total	Mg	0
			1	1	
93	Le	1	Total	Mg	0
			1	1	
93	S2	8	Total	Mg	0
			8	8	

- 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	

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
94	Sd	1	1	1	0

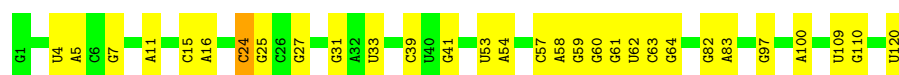








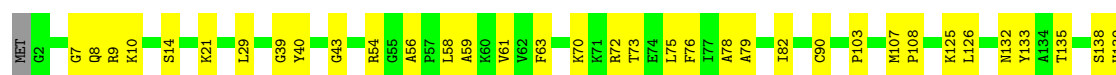




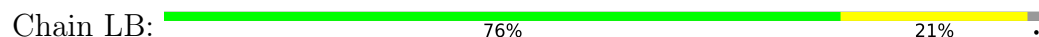
• Molecule 3: 5.8S\_ribosomal\_RNA



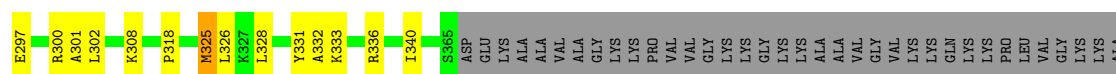
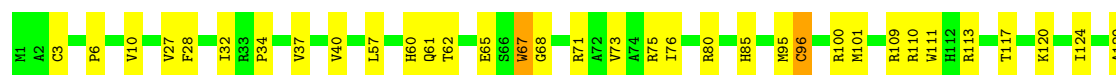
• Molecule 4: 60S ribosomal protein L8




• Molecule 5: 60S ribosomal protein L3

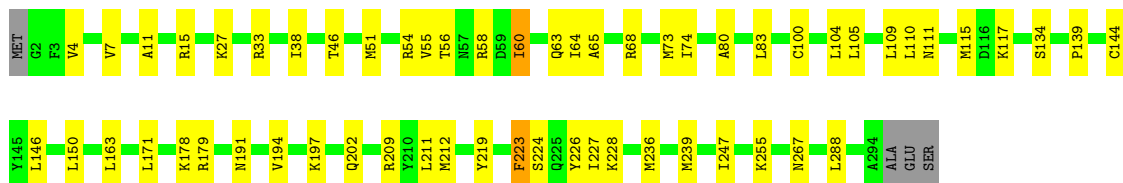


• Molecule 6: 60S ribosomal protein L4



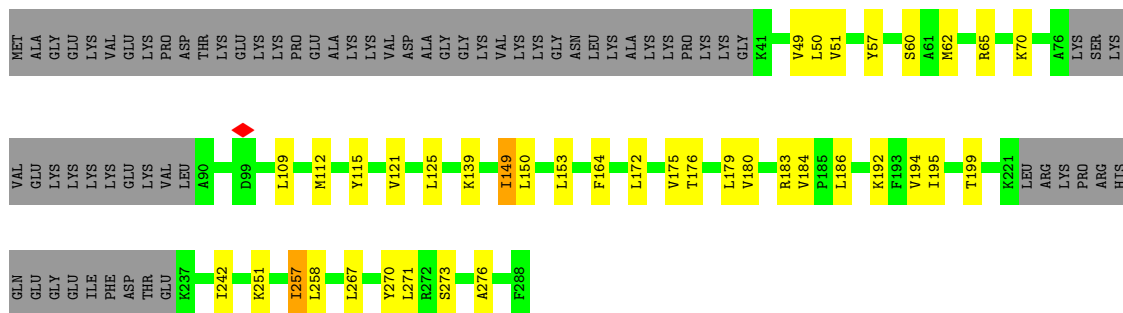
- Molecule 7: 60S ribosomal protein L5

Chain LD: 



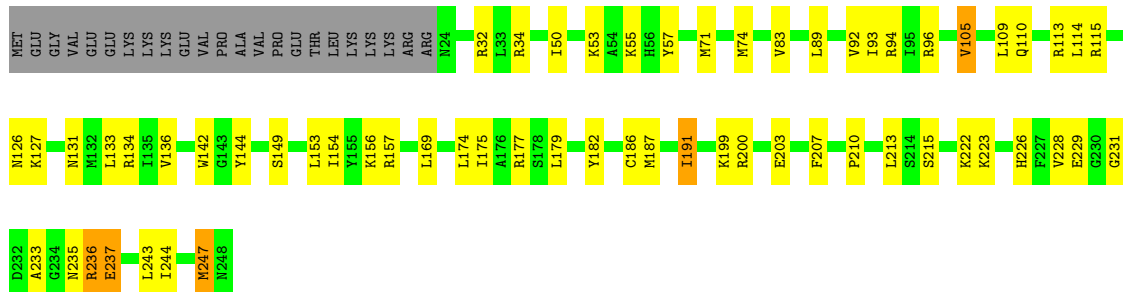
- Molecule 8: 60S ribosomal protein L6

Chain LE: 



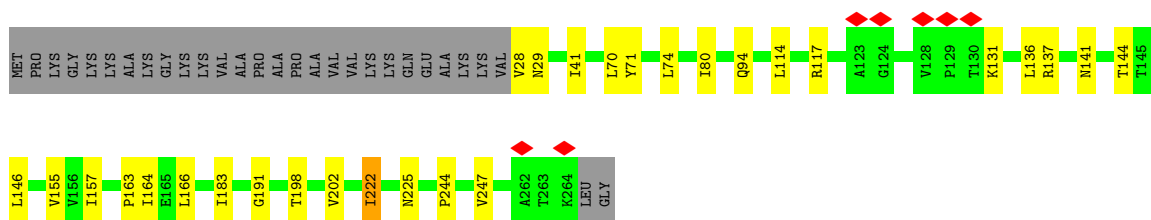
- Molecule 9: 60S ribosomal protein L7

Chain LF:  66% 23% 9%

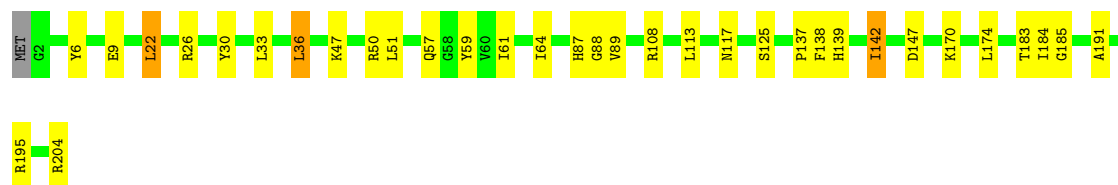


- Molecule 10: 60S ribosomal protein L7a

Chain LG: 

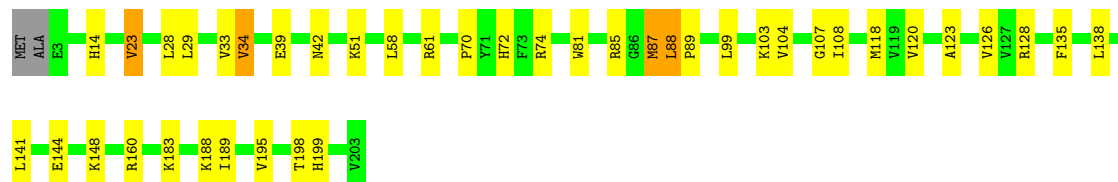






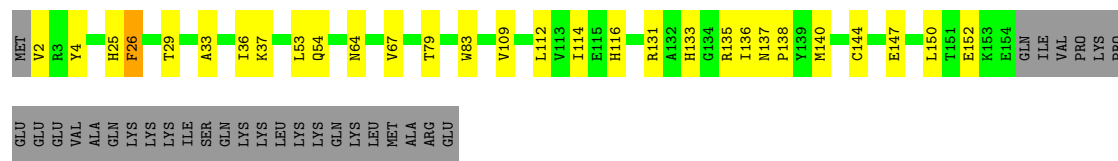
- Molecule 17: 60S ribosomal protein L13a

Chain LO: 79% 18% ..



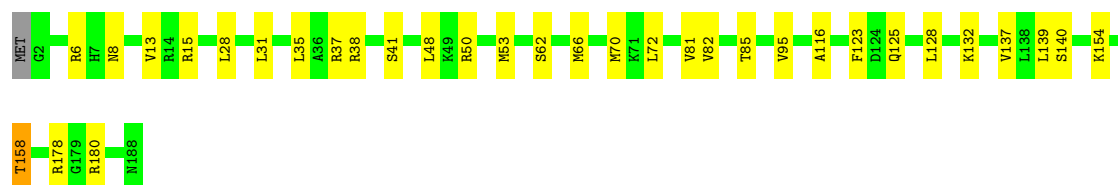
- Molecule 18: 60S ribosomal protein L17

Chain LP: 67% 15% 17%



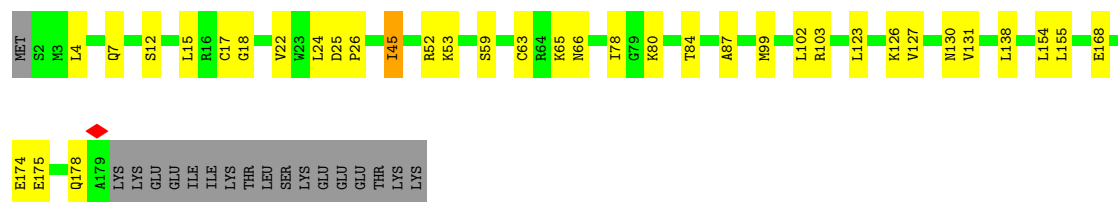
- Molecule 19: 60S ribosomal protein L18

Chain LQ: 82% 17% ..



- Molecule 20: 60S ribosomal protein L19

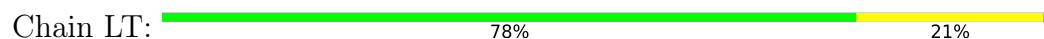
Chain LR: 72% 18% 9%



- Molecule 21: 60S ribosomal protein L18a

Chain LS: 73% 24% ..

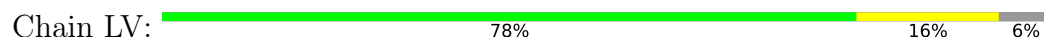
- Molecule 22: 60S ribosomal protein L21



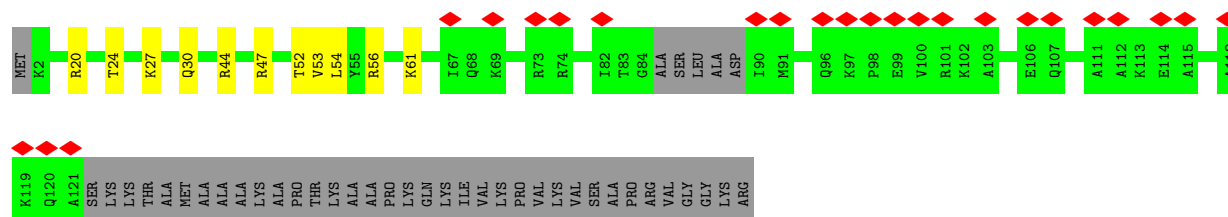
- Molecule 23: 60S ribosomal protein L22



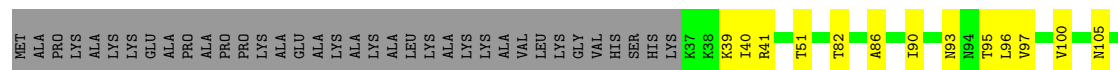
- Molecule 24: 60S ribosomal protein L23



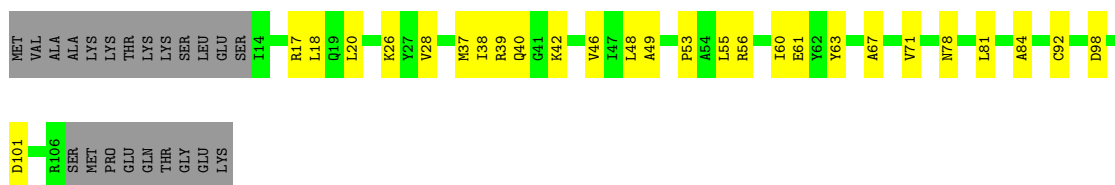
- Molecule 25: 60S ribosomal protein L24



- Molecule 26: 60S ribosomal protein L23a

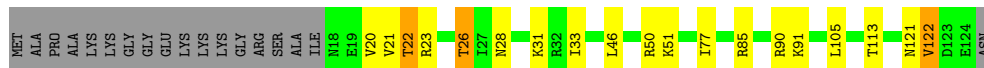






- Molecule 32: 60S ribosomal protein L31

Chain Ld: 70% 13% 14%



- Molecule 33: 60S ribosomal protein L32

Chain Le: 79% 15% 6%



- Molecule 34: 60S ribosomal protein L35a

Chain Lf: 86% 13% 1%



- Molecule 35: 60S ribosomal protein L34

Chain Lg: 72% 21% 6%



- Molecule 36: 60S ribosomal protein L35

Chain Lh: 82% 16% 2%




- Molecule 37: 60S ribosomal protein L36

Chain Li: 79% 16% 5%




- Molecule 38: 60S ribosomal protein L37



Chain Lj:  79% 9% 11%



- Molecule 39: 60S ribosomal protein L38

Chain Lk:  81% 17%



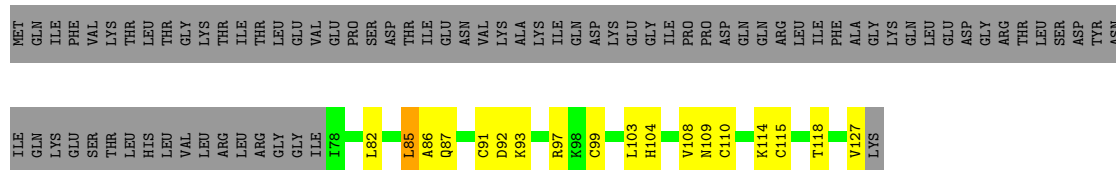
- Molecule 40: 60S ribosomal protein L39

Chain Ll:  69% 27%




- Molecule 41: Ubiquitin-60S ribosomal protein L40

Chain Lm:  25% 13% 61%




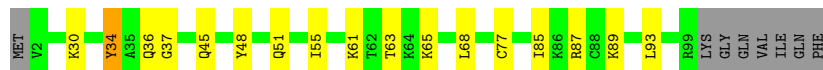
- Molecule 42: 60S ribosomal protein L41

Chain Ln:  84% 12%




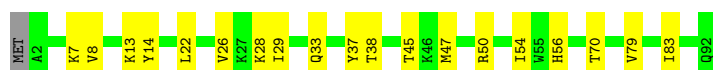
- Molecule 43: 60S ribosomal protein L36a

Chain Lo:  76% 15% 8%



- Molecule 44: 60S ribosomal protein L37a

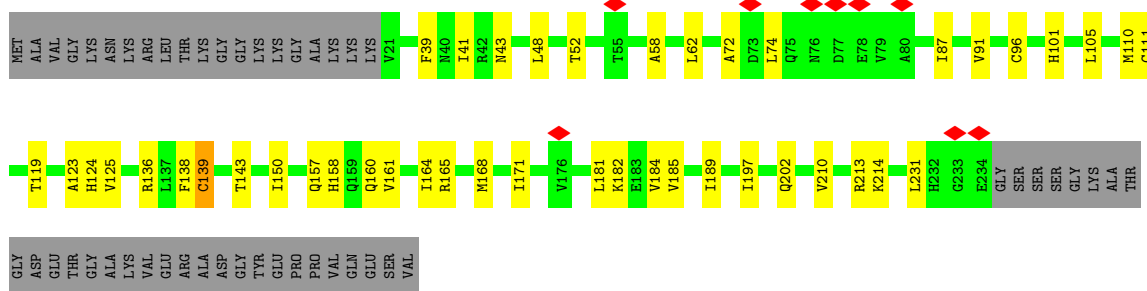
Chain Lp:  78% 21%



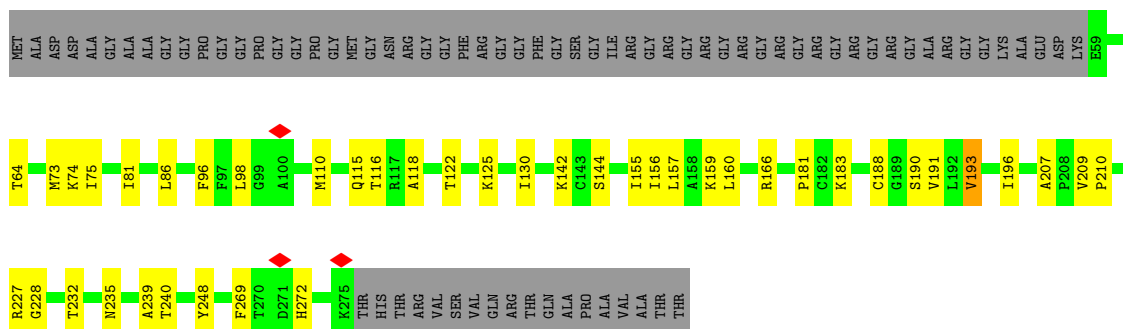
- [illegible]



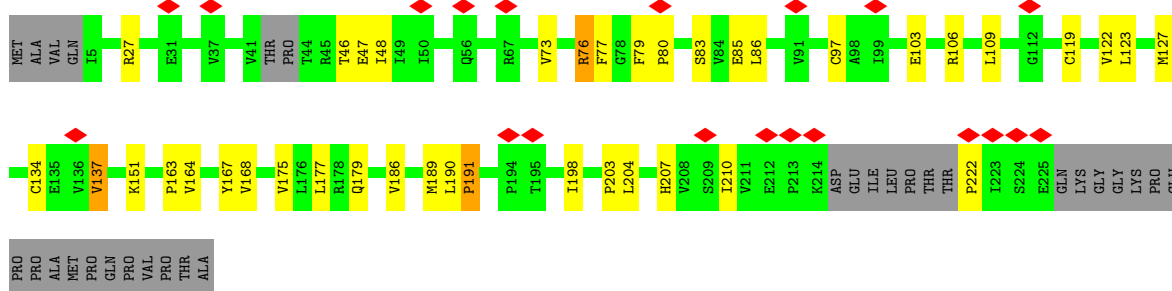
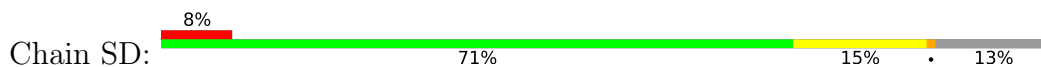
- Molecule 48: 40S ribosomal protein S3a



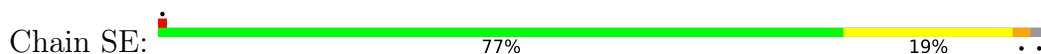
- Molecule 49: 40S ribosomal protein S2

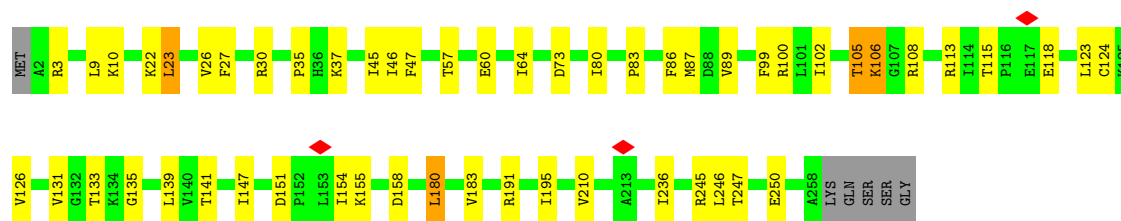


- Molecule 50: 40S ribosomal protein S3

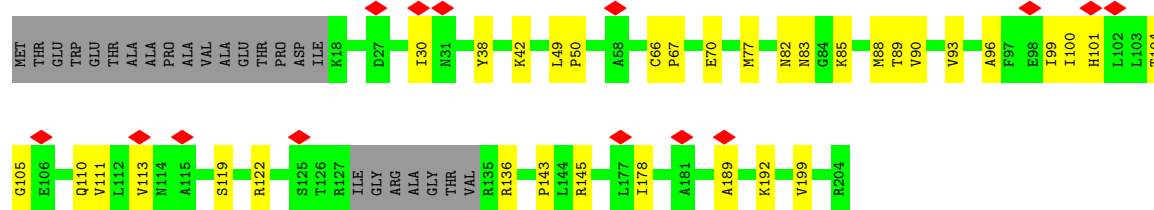
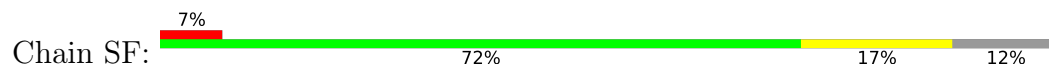


- Molecule 51: 40S ribosomal protein S4, X isoform

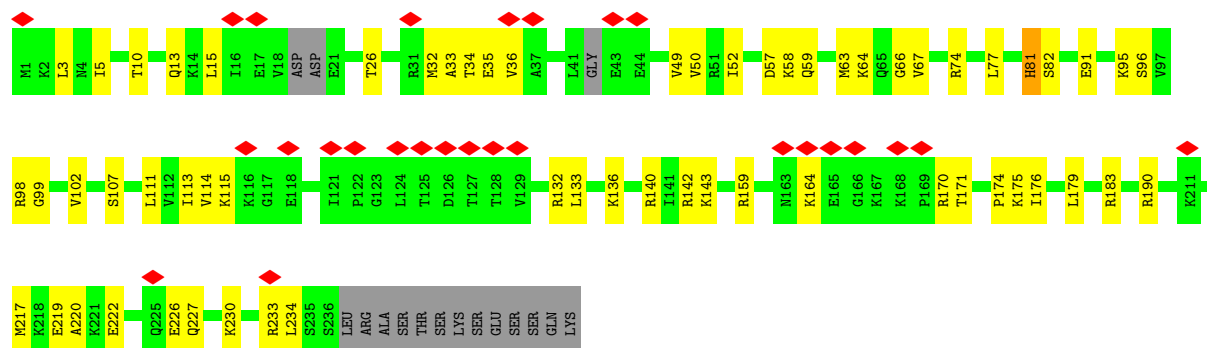




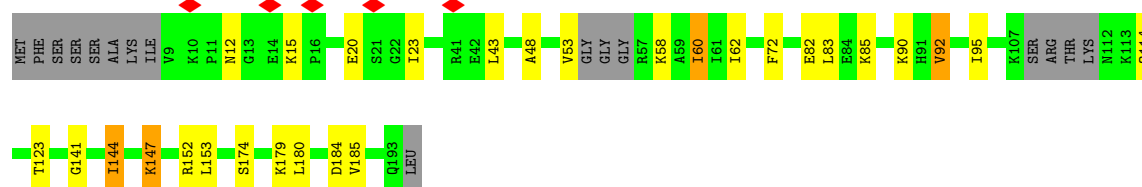
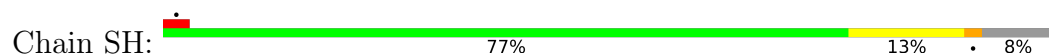
- Molecule 52: 40S ribosomal protein S5



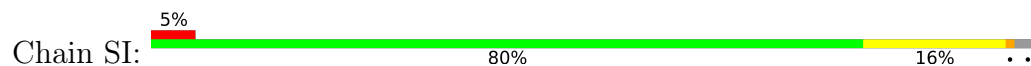
- Molecule 53: 40S ribosomal protein S6

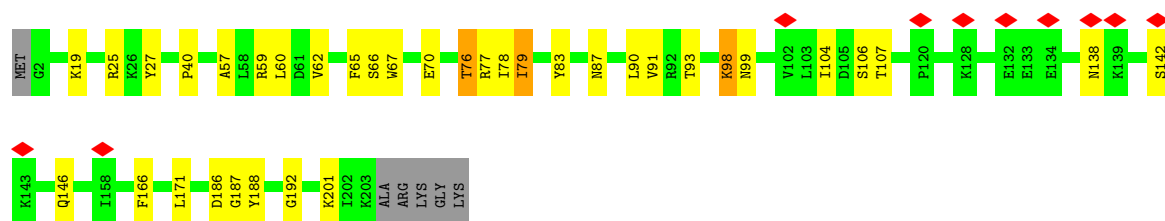


- Molecule 54: 40S ribosomal protein S7

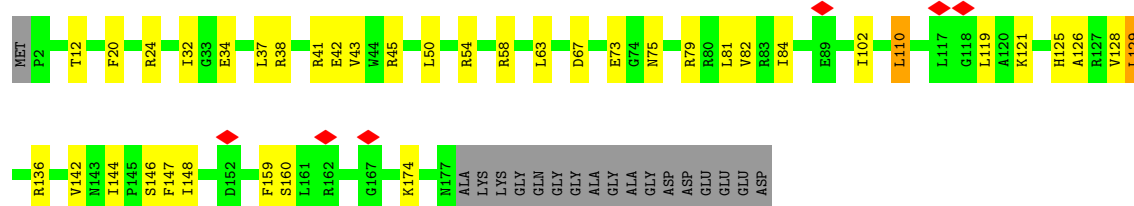


- Molecule 55: 40S ribosomal protein S8

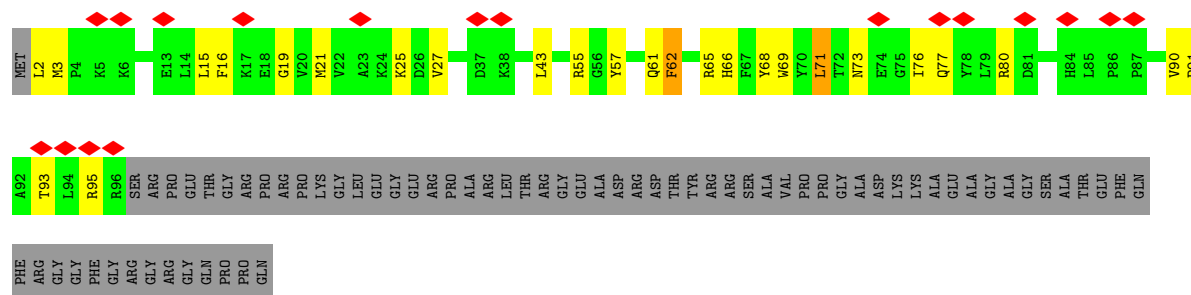
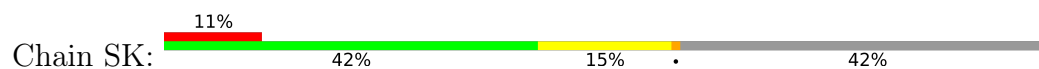




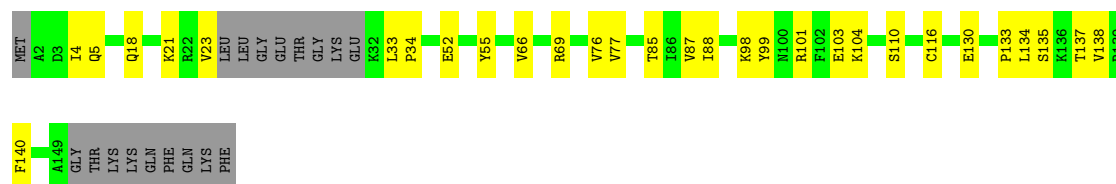
- Molecule 56: 40S ribosomal protein S9



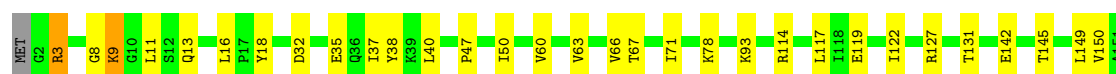
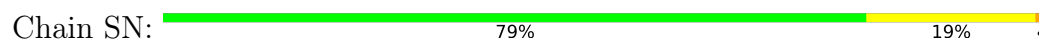
- Molecule 57: 40S ribosomal protein S10



- Molecule 58: 40S ribosomal protein S11



- Molecule 59: 40S ribosomal protein S13




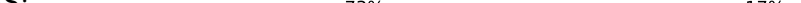
- Molecule 60: 40S ribosomal protein S14

The chart displays the distribution of amino acid types across 1000 residues. The top section (residues 1-1000) is divided into two groups: 'Non-polar' (residues 1-1000) and 'Polar' (residues 1001-2000). The 'Non-polar' group includes residues MET, ALA, PRO, ARG, LYS, GLY, LYS, GLU, LYS, GLU, GLN, VAL, ILE, SER, L17, G18, P19, Q20, V21, A22, E23, G24, V27, F28, G29, V30, C31, H32, T40, F41, V42, H43, V44, I53, V56, H60, K63, R66, V81, K86, G89, I90, T91, A92, L93, and A99. The 'Polar' group includes residues G101, M124, K125, R128, I129, T133, P134, I135, and L151. The chart uses a color-coded system: green for non-polar, yellow for polar, and orange for charged. Red diamonds indicate specific residues of interest.

- Chain SP: 

- Chain SQ: 

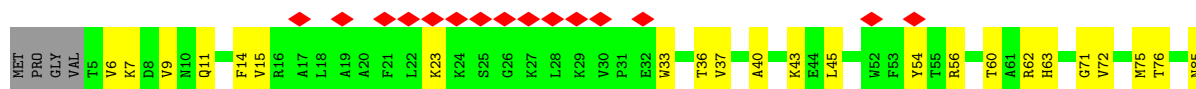
- Chain SR: 

- Chain SS: 

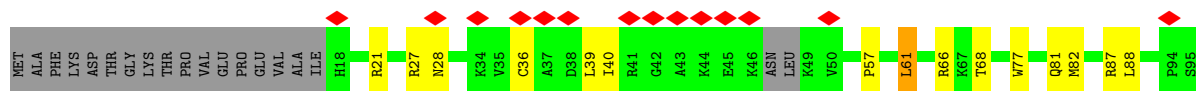
MET	SEU	LEU	VAL
I5	P6	E7	K8
H11			
I12			
L13			
R14			
V15			
L16			
N17			
T18			
N19			
I20			
R23			
R24			
K25			
T31			
Y40			
V44			
K47			
A48			
D49			
I50			
D51			
L52			
T60			
E61			
D62			
F63			
V64			
E65			
R66			
V67			
I68			
M71			
Q72			
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K78			
I79			
P80			
D81			
W82			
F83			



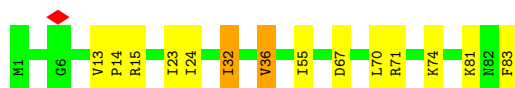
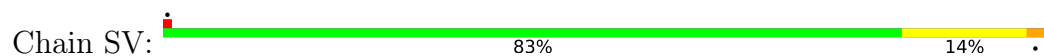
- Molecule 65: 40S ribosomal protein S19



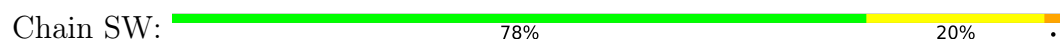
- Molecule 66: 40S ribosomal protein S20



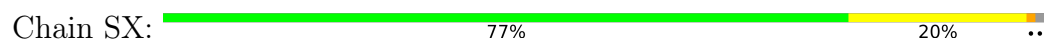
- Molecule 67: 40S ribosomal protein S21



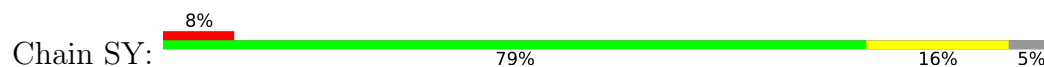
- Molecule 68: 40S ribosomal protein S15a



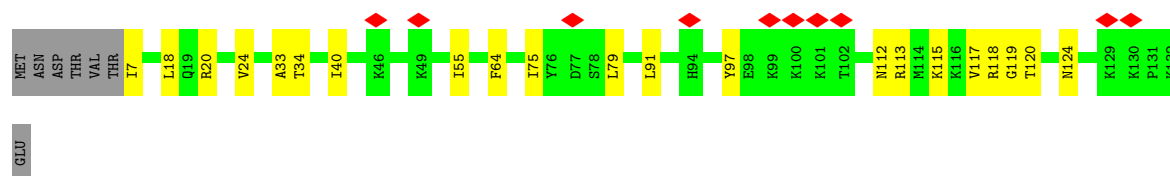
- Molecule 69: 40S ribosomal protein S23



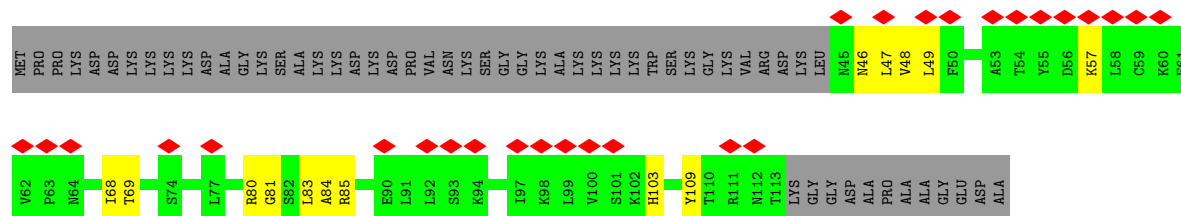
- Molecule 70: 40S ribosomal protein S24







- Molecule 71: 40S ribosomal protein S25



- Molecule 72: 40S ribosomal protein S26



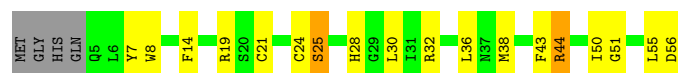
- Molecule 73: 40S ribosomal protein S27



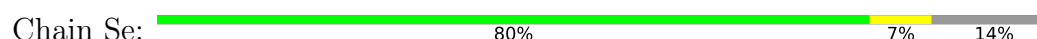
- Molecule 74: 40S ribosomal protein S28



- Molecule 75: 40S ribosomal protein S29



- Molecule 76: 40S ribosomal protein S30

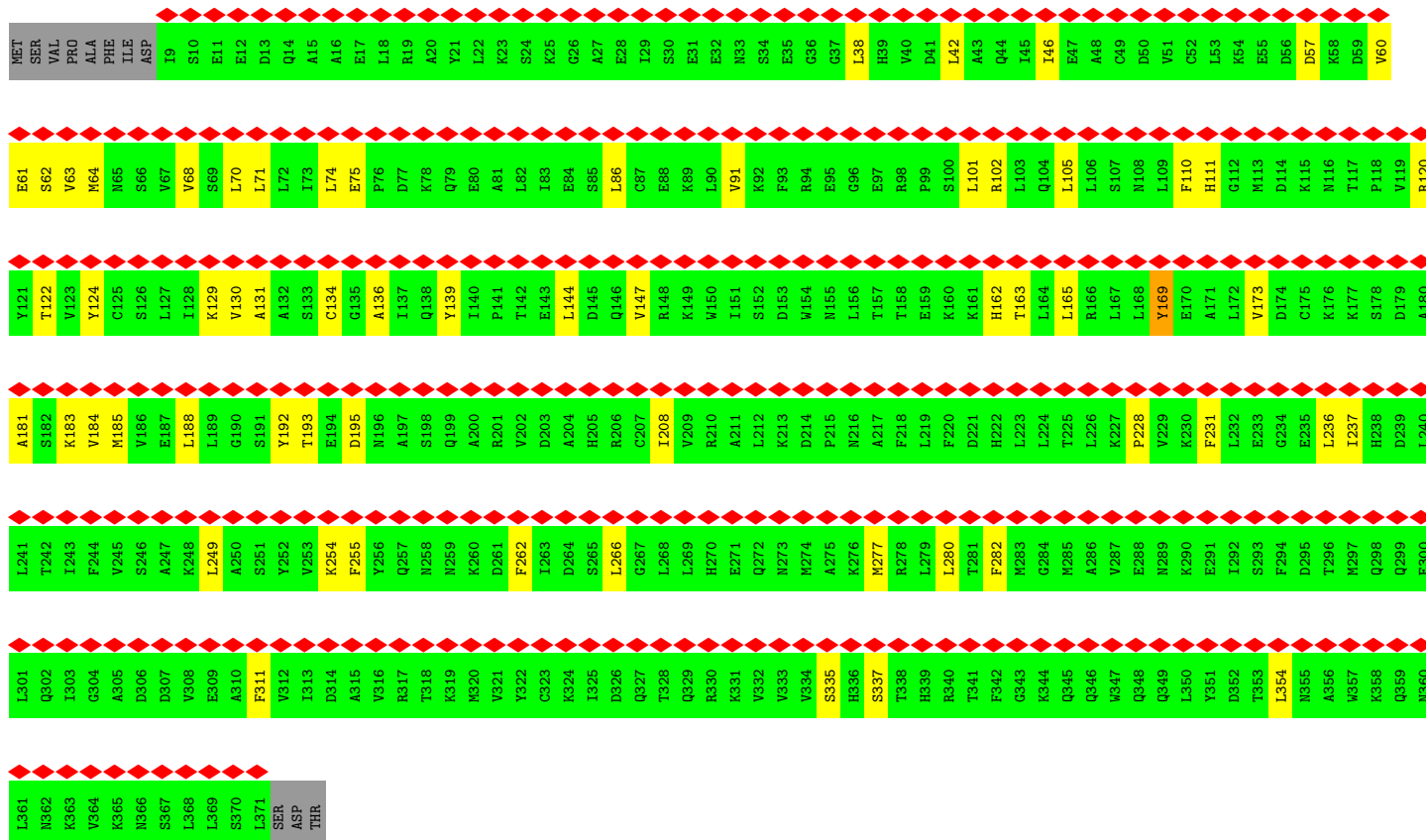
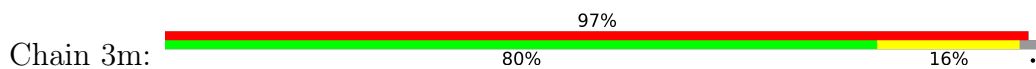




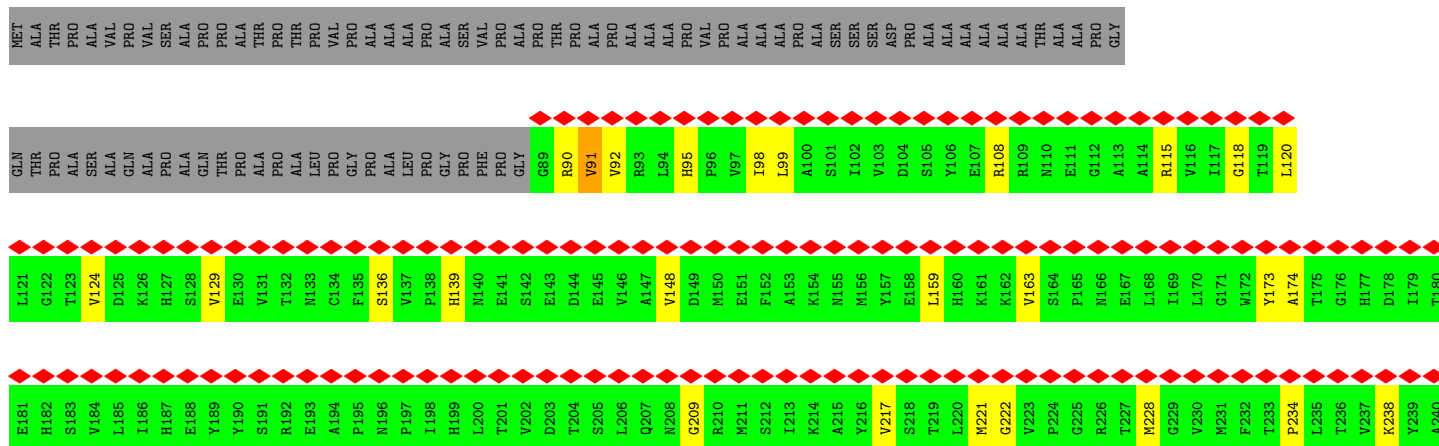
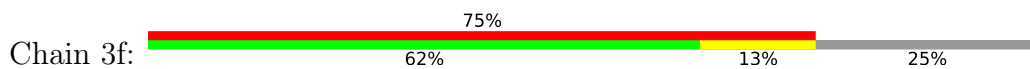


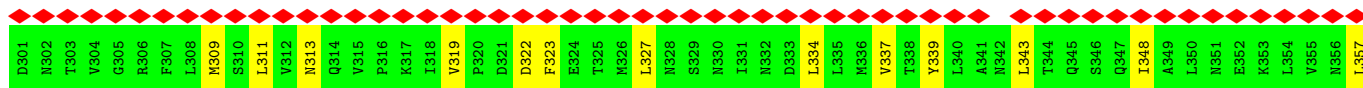
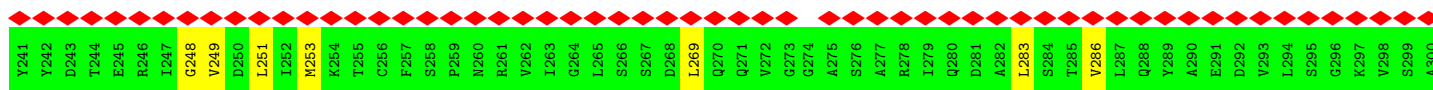


• Molecule 84: Eukaryotic translation initiation factor 3 subunit M

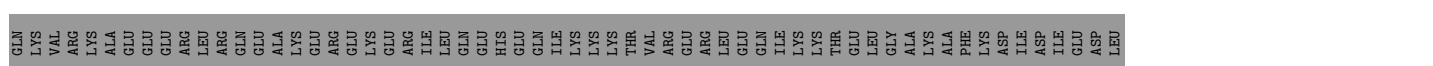
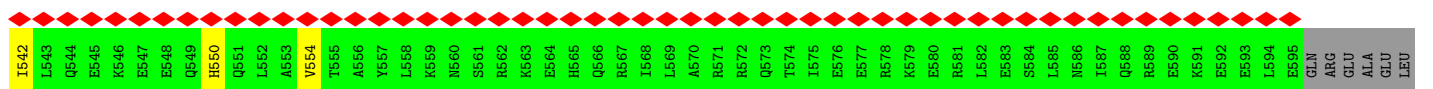
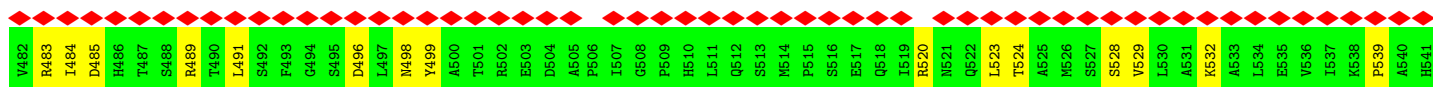
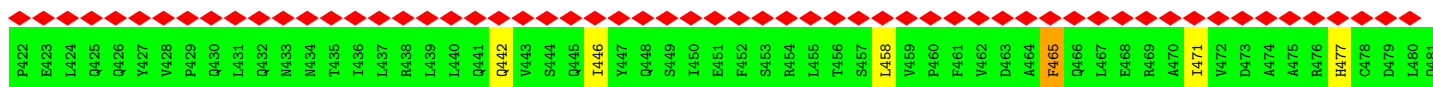
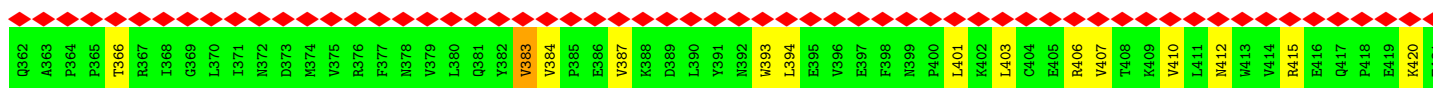
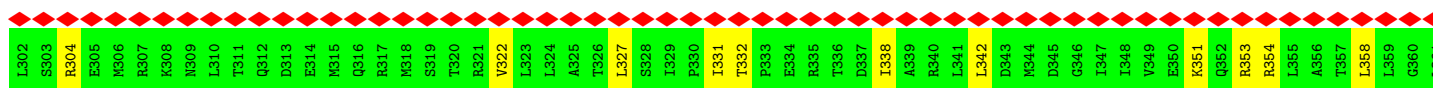
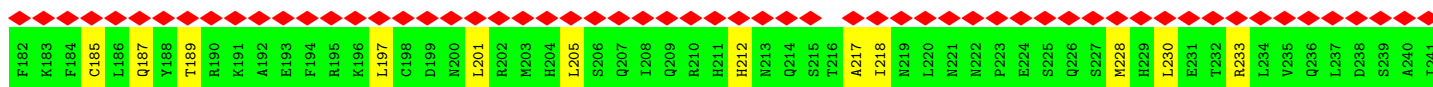
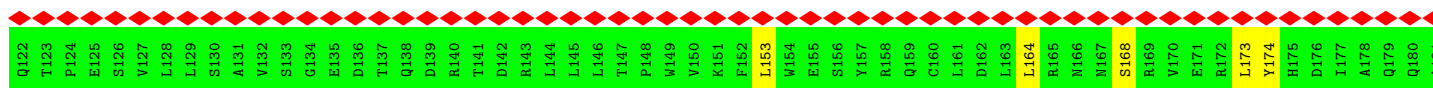
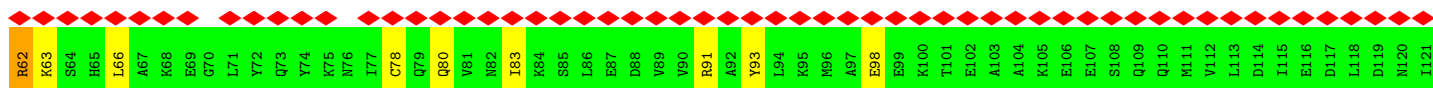
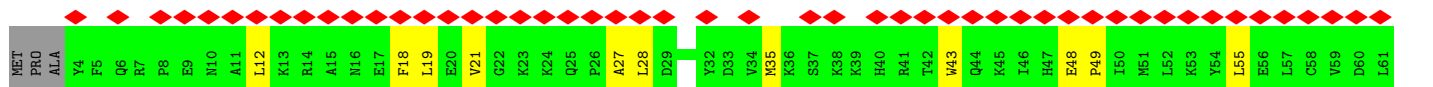
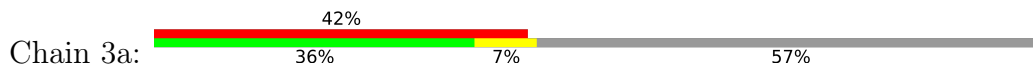


• Molecule 85: Eukaryotic translation initiation factor 3 subunit F



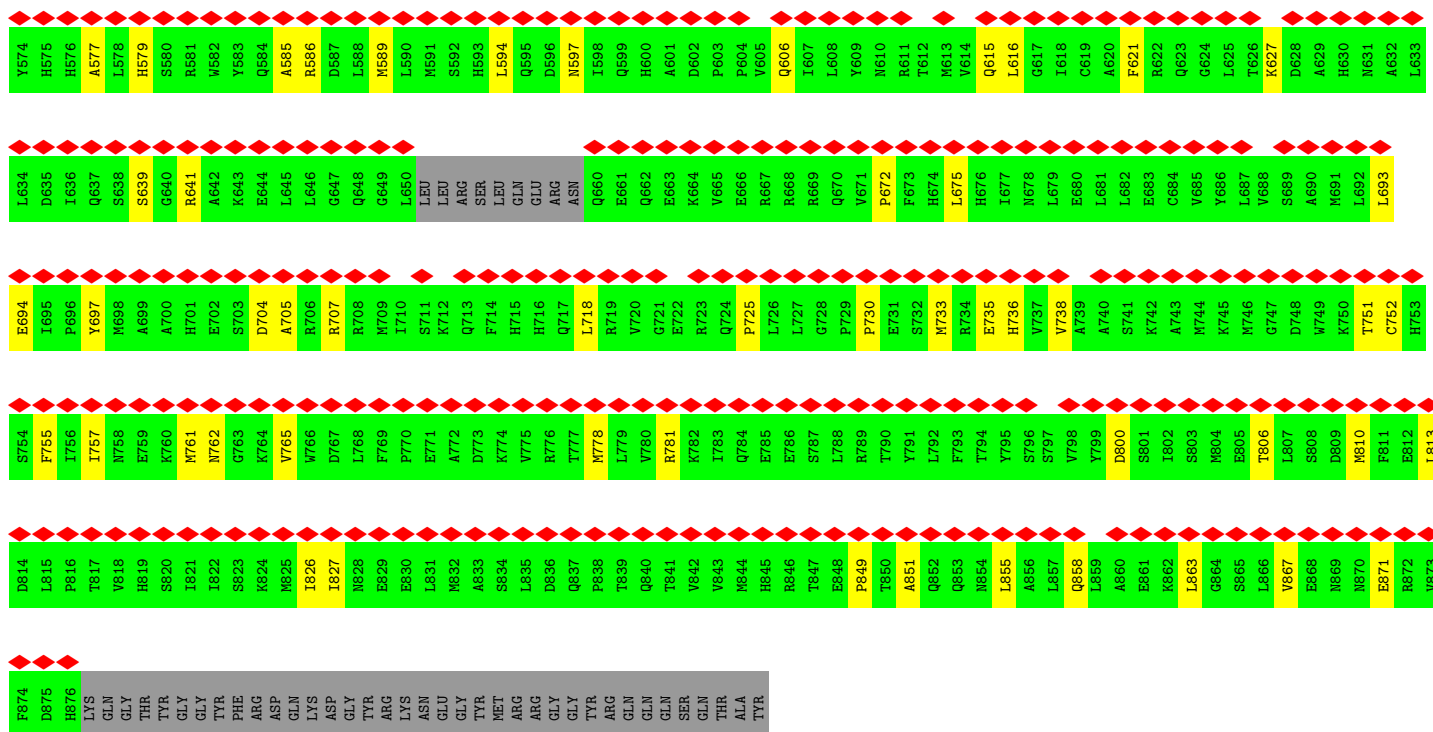


• Molecule 86: Eukaryotic translation initiation factor 3 subunit A

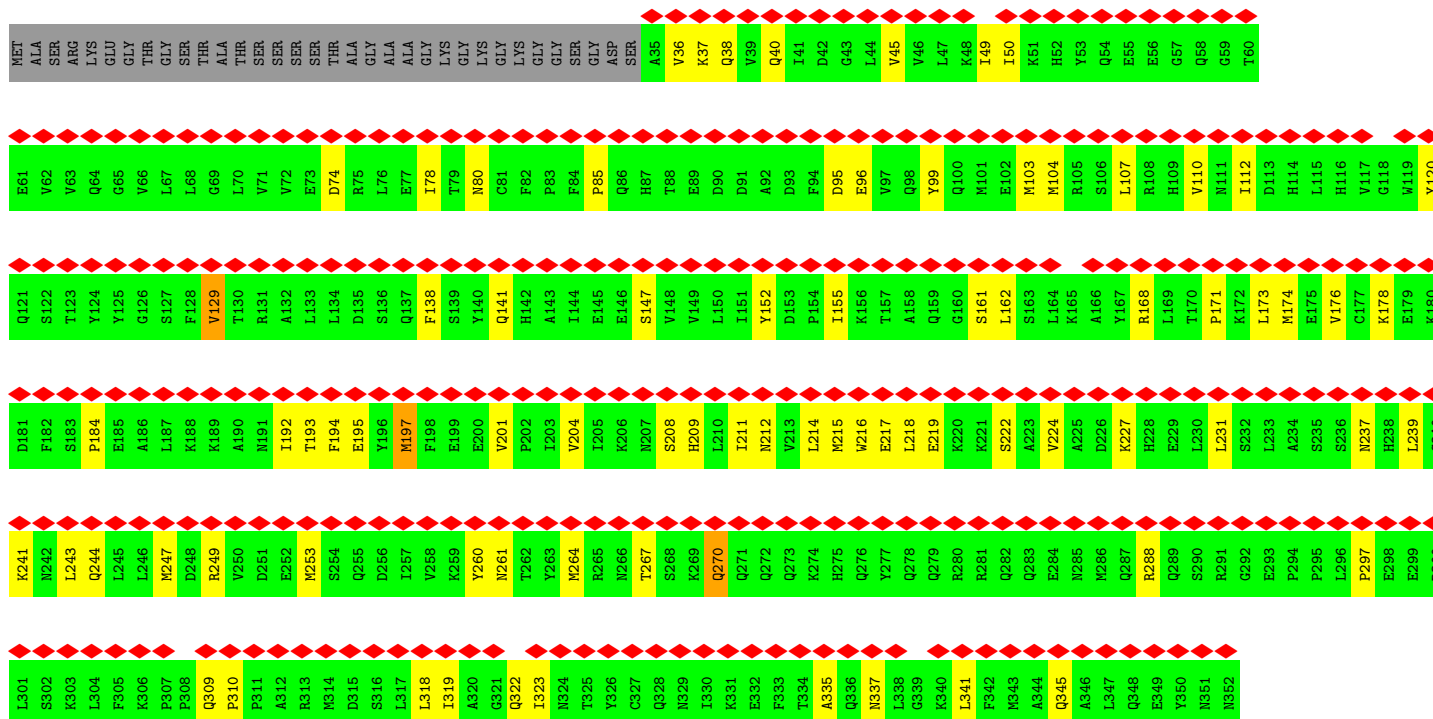








• Molecule 89: Eukaryotic translation initiation factor 3 subunit H



• Molecule 90: Eukaryotic translation initiation factor 3 subunit D









## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	13805	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	0.136	Depositor
Minimum map value	-0.027	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.015	Depositor
Map size ( $\text{\AA}$ )	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 ( $\text{\AA}$ )	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: ZN, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	L5	0.19	0/86040	0.33	0/134204
2	L7	0.18	0/2858	0.30	0/4455
3	L8	0.19	0/3701	0.32	0/5766
4	LA	0.21	0/1924	0.51	0/2581
5	LB	0.19	0/3168	0.44	0/4253
6	LC	0.22	0/2948	0.46	0/3960
7	LD	0.17	0/2333	0.44	0/3139
8	LE	0.19	0/1747	0.46	0/2354
9	LF	0.23	0/1879	0.55	1/2507 (0.0%)
10	LG	0.18	0/1830	0.45	0/2484
11	LH	0.20	0/1458	0.50	0/1973
12	LI	0.19	0/1619	0.47	1/2170 (0.0%)
13	LJ	0.20	0/1249	0.49	0/1690
14	LL	0.18	0/1611	0.39	0/2167
15	LM	0.21	0/1119	0.51	0/1501
16	LN	0.23	0/1738	0.45	0/2328
17	LO	0.22	0/1645	0.50	0/2205
18	LP	0.21	0/1229	0.49	0/1655
19	LQ	0.20	0/1517	0.45	0/2030
20	LR	0.21	0/1450	0.52	0/1927
21	LS	0.22	0/1476	0.50	2/1983 (0.1%)
22	LT	0.20	0/1296	0.48	0/1734
23	LU	0.20	0/782	0.56	0/1057
24	LV	0.22	0/968	0.55	0/1303
25	LW	0.19	0/798	0.51	0/1081
26	LX	0.23	0/967	0.58	0/1304
27	LY	0.19	0/1101	0.44	0/1469
28	LZ	0.23	0/1105	0.45	0/1475
29	La	0.22	0/1173	0.47	0/1568
30	Lb	0.22	0/509	0.58	0/675
31	Lc	0.20	0/726	0.48	0/977
32	Ld	0.20	0/871	0.46	0/1176

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	Le	0.21	0/1063	0.45	0/1418
34	Lf	0.23	0/883	0.59	0/1185
35	Lg	0.21	0/861	0.51	0/1153
36	Lh	0.17	0/983	0.41	0/1304
37	Li	0.20	0/808	0.51	0/1074
38	Lj	0.20	0/716	0.40	0/948
39	Lk	0.20	0/534	0.52	0/712
40	Ll	0.22	0/450	0.44	0/595
41	Lm	0.23	0/399	0.74	2/532 (0.4%)
42	Ln	0.22	0/231	0.58	0/294
43	Lo	0.20	0/787	0.46	0/1042
44	Lp	0.17	0/699	0.45	0/931
45	Lr	0.23	0/997	0.59	0/1341
46	S2	0.16	0/40097	0.33	0/62465
47	SA	0.20	0/1612	0.56	0/2203
48	SB	0.17	0/1654	0.45	0/2227
49	SC	0.20	0/1626	0.53	0/2211
50	SD	0.18	0/1482	0.50	0/2018
51	SE	0.15	0/1933	0.41	0/2623
52	SF	0.18	0/1385	0.49	0/1870
53	SG	0.17	0/1761	0.51	0/2362
54	SH	0.20	0/1384	0.54	0/1862
55	SI	0.19	0/1580	0.46	0/2131
56	SJ	0.19	0/1432	0.53	1/1926 (0.1%)
57	SK	0.20	0/759	0.61	0/1036
58	SL	0.20	0/1159	0.50	0/1555
59	SN	0.19	0/1223	0.53	0/1644
60	SO	0.18	0/1016	0.51	0/1363
61	SP	0.21	0/1020	0.55	0/1369
62	SQ	0.19	0/1096	0.51	0/1473
63	SR	0.23	0/890	0.64	0/1207
64	SS	0.18	0/1098	0.49	0/1480
65	ST	0.20	0/993	0.53	0/1345
66	SU	0.20	0/746	0.53	0/1007
67	SV	0.20	0/596	0.54	0/800
68	SW	0.20	0/1044	0.51	0/1398
69	SX	0.21	0/1066	0.58	0/1434
70	SY	0.18	0/960	0.52	0/1287
71	SZ	0.18	0/485	0.53	0/661
72	Sa	0.18	0/775	0.47	0/1042
73	Sb	0.19	0/631	0.54	0/853
74	Sc	0.20	0/432	0.62	0/582
75	Sd	0.21	0/430	0.52	0/573

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	Se	0.16	0/390	0.40	0/515
77	Sf	0.11	0/485	0.36	0/661
78	Sg	0.14	0/1989	0.41	0/2725
79	sh	0.09	0/270	0.27	0/359
80	zu	0.12	0/1717	0.28	0/2677
80	zy	0.12	0/1786	0.26	0/2784
81	zv	0.18	0/201	0.47	0/309
82	zx	0.25	0/113	0.64	0/158
83	zz	0.12	0/5030	0.29	0/7842
84	3m	0.15	0/2676	0.40	0/3635
85	3f	0.15	0/2099	0.38	0/2856
86	3a	0.16	0/4583	0.40	0/6237
87	3e	0.14	0/3282	0.37	0/4467
88	3c	0.15	0/4872	0.40	2/6599 (0.0%)
89	3h	0.16	0/2571	0.41	1/3484 (0.0%)
90	3d	0.14	0/358	0.35	0/493
91	3k	0.17	0/1502	0.48	1/2052 (0.0%)
92	3l	0.17	0/4442	0.42	0/6009
All	All	0.18	0/254977	0.39	11/373549 (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(°)
41	Lm	86	ALA	CA-C-N	-6.57	110.49	122.38
41	Lm	86	ALA	C-N-CA	-6.57	110.49	122.38
56	SJ	129	LEU	CA-CB-CG	5.88	136.86	116.30
12	LI	30	LYS	CA-CB-CG	5.64	125.37	114.10
91	3k	148	ILE	N-CA-C	-5.48	107.01	113.42

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L5	76925	0	38887	570	0
2	L7	2558	0	1296	10	0
3	L8	3314	0	1683	26	0
4	LA	1886	0	1973	37	0
5	LB	3101	0	3177	44	0
6	LC	2894	0	3061	50	0
7	LD	2287	0	2254	32	0
8	LE	1713	0	1812	18	0
9	LF	1844	0	1961	35	0
10	LG	1797	0	1833	14	0
11	LH	1439	0	1469	15	0
12	LI	1581	0	1574	15	0
13	LJ	1226	0	1168	11	0
14	LL	1580	0	1646	12	0
15	LM	1097	0	1142	13	0
16	LN	1693	0	1741	25	0
17	LO	1613	0	1737	29	0
18	LP	1203	0	1210	12	0
19	LQ	1493	0	1587	17	0
20	LR	1434	0	1539	20	0
21	LS	1436	0	1457	27	0
22	LT	1268	0	1309	18	0
23	LU	768	0	762	3	0
24	LV	954	0	994	9	0
25	LW	784	0	662	8	0
26	LX	950	0	1010	12	0
27	LY	1084	0	1143	15	0
28	LZ	1082	0	1152	25	0
29	La	1145	0	1178	23	0
30	Lb	499	0	506	7	0
31	Lc	716	0	742	14	0
32	Ld	856	0	890	12	0
33	Le	1045	0	1133	8	0
34	Lf	864	0	888	8	0
35	Lg	851	0	908	13	0
36	Lh	975	0	1081	10	0
37	Li	797	0	859	11	0
38	Lj	701	0	726	5	0
39	Lk	528	0	554	7	0
40	Ll	440	0	472	10	0
41	Lm	393	0	410	11	0
42	Ln	230	0	276	1	0
43	Lo	774	0	819	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	Lp	689	0	731	9	0
45	Lr	982	0	1026	16	0
46	S2	35873	0	18084	360	0
47	SA	1575	0	1533	25	0
48	SB	1627	0	1616	26	0
49	SC	1590	0	1606	24	0
50	SD	1458	0	1379	22	0
51	SE	1891	0	1867	30	0
52	SF	1365	0	1367	21	0
53	SG	1740	0	1737	40	0
54	SH	1363	0	1405	12	0
55	SI	1551	0	1515	22	0
56	SJ	1407	0	1450	23	0
57	SK	736	0	691	17	0
58	SL	1139	0	1185	18	0
59	SN	1199	0	1274	18	0
60	SO	1003	0	1028	16	0
61	SP	1001	0	1011	23	0
62	SQ	1078	0	1124	27	0
63	SR	879	0	816	11	0
64	SS	1080	0	1092	15	0
65	ST	975	0	908	25	0
66	SU	737	0	750	12	0
67	SV	589	0	566	12	0
68	SW	1027	0	1067	15	0
69	SX	1048	0	1065	18	0
70	SY	943	0	933	13	0
71	SZ	479	0	442	8	0
72	Sa	762	0	800	10	0
73	Sb	617	0	602	7	0
74	Sc	430	0	425	9	0
75	Sd	420	0	397	10	0
76	Se	386	0	411	4	0
77	Sf	483	0	399	5	0
78	Sg	1948	0	1654	26	0
79	sh	269	0	221	6	0
80	zu	1537	0	777	13	0
80	zy	1599	0	810	14	0
81	zv	183	0	97	1	0
82	zx	111	0	74	3	0
83	zz	4503	0	2278	33	0
84	3m	2639	0	2442	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
85	3f	2063	0	2054	38	0
86	3a	4497	0	4224	63	0
87	3e	3218	0	2920	34	0
88	3c	4794	0	4416	46	0
89	3h	2520	0	2445	55	0
90	3d	347	0	259	1	0
91	3k	1475	0	1239	16	0
92	3l	4331	0	4261	70	0
93	L5	52	0	0	0	0
93	L7	1	0	0	0	0
93	L8	3	0	0	0	0
93	LV	1	0	0	0	0
93	Le	1	0	0	0	0
93	S2	8	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	Sd	1	0	0	0	0
All	All	238047	0	175154	2358	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 2358 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)
80:zu:10:G:H1	80:zu:24:U:H3	1.04	0.99
1:L5:493:G:N1	1:L5:660:A:C2	2.31	0.99
1:L5:493:G:N1	1:L5:660:A:H2	1.61	0.98
46:S2:1656:G:H1	46:S2:1668:U:H3	1.08	0.98
1:L5:2557:G:H1	1:L5:2570:U:H3	1.08	0.98

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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%)	213 (87%)	33 (13%)	0	100	100
5	LB	389/403 (96%)	353 (91%)	36 (9%)	0	100	100
6	LC	363/427 (85%)	336 (93%)	27 (7%)	0	100	100
7	LD	291/297 (98%)	277 (95%)	14 (5%)	0	100	100
8	LE	214/288 (74%)	199 (93%)	15 (7%)	0	100	100
9	LF	223/248 (90%)	212 (95%)	11 (5%)	0	100	100
10	LG	235/266 (88%)	218 (93%)	17 (7%)	0	100	100
11	LH	187/192 (97%)	174 (93%)	13 (7%)	0	100	100
12	LI	199/214 (93%)	187 (94%)	12 (6%)	0	100	100
13	LJ	165/178 (93%)	155 (94%)	10 (6%)	0	100	100
14	LL	202/211 (96%)	186 (92%)	16 (8%)	0	100	100
15	LM	134/215 (62%)	127 (95%)	7 (5%)	0	100	100
16	LN	201/204 (98%)	190 (94%)	11 (6%)	0	100	100
17	LO	199/203 (98%)	192 (96%)	7 (4%)	0	100	100
18	LP	151/184 (82%)	140 (93%)	11 (7%)	0	100	100
19	LQ	185/188 (98%)	180 (97%)	5 (3%)	0	100	100
20	LR	176/196 (90%)	175 (99%)	1 (1%)	0	100	100
21	LS	173/176 (98%)	160 (92%)	12 (7%)	1 (1%)	22	53
22	LT	157/160 (98%)	142 (90%)	15 (10%)	0	100	100
23	LU	99/128 (77%)	92 (93%)	7 (7%)	0	100	100
24	LV	129/140 (92%)	117 (91%)	12 (9%)	0	100	100
25	LW	111/157 (71%)	104 (94%)	7 (6%)	0	100	100
26	LX	118/156 (76%)	107 (91%)	11 (9%)	0	100	100
27	LY	132/145 (91%)	122 (92%)	10 (8%)	0	100	100
28	LZ	133/136 (98%)	128 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	La	142/148 (96%)	132 (93%)	10 (7%)	0	100	100
30	Lb	61/159 (38%)	58 (95%)	3 (5%)	0	100	100
31	Lc	91/115 (79%)	90 (99%)	1 (1%)	0	100	100
32	Ld	105/125 (84%)	99 (94%)	6 (6%)	0	100	100
33	Le	125/135 (93%)	117 (94%)	8 (6%)	0	100	100
34	Lf	107/110 (97%)	95 (89%)	12 (11%)	0	100	100
35	Lg	108/117 (92%)	102 (94%)	6 (6%)	0	100	100
36	Lh	119/123 (97%)	117 (98%)	2 (2%)	0	100	100
37	Li	99/105 (94%)	97 (98%)	2 (2%)	0	100	100
38	Lj	84/97 (87%)	81 (96%)	3 (4%)	0	100	100
39	Lk	67/70 (96%)	60 (90%)	7 (10%)	0	100	100
40	Ll	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
41	Lm	48/128 (38%)	48 (100%)	0	0	100	100
42	Ln	22/25 (88%)	22 (100%)	0	0	100	100
43	Lo	96/106 (91%)	91 (95%)	5 (5%)	0	100	100
44	Lp	89/92 (97%)	86 (97%)	3 (3%)	0	100	100
45	Lr	123/137 (90%)	114 (93%)	9 (7%)	0	100	100
47	SA	210/295 (71%)	195 (93%)	15 (7%)	0	100	100
48	SB	212/264 (80%)	203 (96%)	9 (4%)	0	100	100
49	SC	215/293 (73%)	201 (94%)	14 (6%)	0	100	100
50	SD	206/243 (85%)	188 (91%)	17 (8%)	1 (0%)	25	56
51	SE	255/263 (97%)	235 (92%)	20 (8%)	0	100	100
52	SF	176/204 (86%)	166 (94%)	10 (6%)	0	100	100
53	SG	227/249 (91%)	205 (90%)	21 (9%)	1 (0%)	30	61
54	SH	172/194 (89%)	155 (90%)	17 (10%)	0	100	100
55	SI	200/208 (96%)	179 (90%)	21 (10%)	0	100	100
56	SJ	174/194 (90%)	165 (95%)	8 (5%)	1 (1%)	22	53
57	SK	93/165 (56%)	85 (91%)	8 (9%)	0	100	100
58	SL	136/158 (86%)	126 (93%)	10 (7%)	0	100	100
59	SN	148/151 (98%)	136 (92%)	12 (8%)	0	100	100
60	SO	133/151 (88%)	118 (89%)	15 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
61	SP	123/145 (85%)	111 (90%)	11 (9%)	1 (1%)	16	46
62	SQ	139/146 (95%)	129 (93%)	10 (7%)	0	100	100
63	SR	123/135 (91%)	106 (86%)	17 (14%)	0	100	100
64	SS	136/152 (90%)	124 (91%)	12 (9%)	0	100	100
65	ST	136/145 (94%)	126 (93%)	10 (7%)	0	100	100
66	SU	94/119 (79%)	89 (95%)	5 (5%)	0	100	100
67	SV	81/83 (98%)	77 (95%)	4 (5%)	0	100	100
68	SW	127/130 (98%)	117 (92%)	10 (8%)	0	100	100
69	SX	139/143 (97%)	119 (86%)	20 (14%)	0	100	100
70	SY	124/133 (93%)	119 (96%)	5 (4%)	0	100	100
71	SZ	67/125 (54%)	61 (91%)	6 (9%)	0	100	100
72	Sa	97/115 (84%)	91 (94%)	6 (6%)	0	100	100
73	Sb	81/84 (96%)	66 (82%)	15 (18%)	0	100	100
74	Sc	59/69 (86%)	49 (83%)	10 (17%)	0	100	100
75	Sd	50/56 (89%)	50 (100%)	0	0	100	100
76	Se	47/59 (80%)	43 (92%)	4 (8%)	0	100	100
77	Sf	68/132 (52%)	60 (88%)	8 (12%)	0	100	100
78	Sg	258/317 (81%)	228 (88%)	30 (12%)	0	100	100
79	sh	35/156 (22%)	31 (89%)	4 (11%)	0	100	100
82	zx	18/31 (58%)	11 (61%)	7 (39%)	0	100	100
84	3m	361/374 (96%)	346 (96%)	15 (4%)	0	100	100
85	3f	267/357 (75%)	263 (98%)	4 (2%)	0	100	100
86	3a	590/1382 (43%)	573 (97%)	17 (3%)	0	100	100
87	3e	427/445 (96%)	407 (95%)	20 (5%)	0	100	100
88	3c	638/913 (70%)	618 (97%)	20 (3%)	0	100	100
89	3h	316/352 (90%)	311 (98%)	5 (2%)	0	100	100
90	3d	53/548 (10%)	47 (89%)	6 (11%)	0	100	100
91	3k	213/218 (98%)	202 (95%)	11 (5%)	0	100	100
92	3l	518/564 (92%)	504 (97%)	14 (3%)	0	100	100
All	All	14288/17872 (80%)	13376 (94%)	907 (6%)	5 (0%)	100	100

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
21	LS	164	LYS
53	SG	132	ARG
61	SP	73	PRO
56	SJ	110	LEU
50	SD	191	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	
4	LA	187/199 (94%)	178 (95%)	9 (5%)	21	50
5	LB	324/349 (93%)	299 (92%)	25 (8%)	10	33
6	LC	301/348 (86%)	285 (95%)	16 (5%)	19	47
7	LD	218/250 (87%)	205 (94%)	13 (6%)	16	42
8	LE	179/252 (71%)	165 (92%)	14 (8%)	10	33
9	LF	187/215 (87%)	173 (92%)	14 (8%)	11	34
10	LG	173/223 (78%)	164 (95%)	9 (5%)	19	47
11	LH	150/171 (88%)	138 (92%)	12 (8%)	10	32
12	LI	156/181 (86%)	145 (93%)	11 (7%)	12	37
13	LJ	113/149 (76%)	103 (91%)	10 (9%)	8	28
14	LL	152/177 (86%)	145 (95%)	7 (5%)	23	52
15	LM	110/161 (68%)	102 (93%)	8 (7%)	11	35
16	LN	169/172 (98%)	161 (95%)	8 (5%)	22	51
17	LO	163/174 (94%)	154 (94%)	9 (6%)	18	45
18	LP	124/163 (76%)	116 (94%)	8 (6%)	14	40
19	LQ	159/165 (96%)	148 (93%)	11 (7%)	13	38
20	LR	143/175 (82%)	132 (92%)	11 (8%)	10	33
21	LS	151/157 (96%)	139 (92%)	12 (8%)	10	32
22	LT	130/140 (93%)	119 (92%)	11 (8%)	8	30
23	LU	77/115 (67%)	67 (87%)	10 (13%)	3	14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	LV	94/107 (88%)	86 (92%)	8 (8%)	8	30
25	LW	54/126 (43%)	50 (93%)	4 (7%)	11	34
26	LX	98/133 (74%)	94 (96%)	4 (4%)	26	54
27	LY	116/135 (86%)	106 (91%)	10 (9%)	8	30
28	LZ	109/118 (92%)	100 (92%)	9 (8%)	9	31
29	La	116/121 (96%)	109 (94%)	7 (6%)	16	42
30	Lb	49/126 (39%)	45 (92%)	4 (8%)	9	31
31	Lc	76/97 (78%)	73 (96%)	3 (4%)	27	55
32	Ld	88/110 (80%)	83 (94%)	5 (6%)	17	44
33	Le	113/121 (93%)	107 (95%)	6 (5%)	19	47
34	Lf	85/89 (96%)	83 (98%)	2 (2%)	44	68
35	Lg	88/100 (88%)	78 (89%)	10 (11%)	4	18
36	Lh	100/110 (91%)	92 (92%)	8 (8%)	10	32
37	Li	79/89 (89%)	74 (94%)	5 (6%)	15	41
38	Lj	72/80 (90%)	69 (96%)	3 (4%)	25	53
39	Lk	52/65 (80%)	50 (96%)	2 (4%)	28	56
40	Ll	46/48 (96%)	43 (94%)	3 (6%)	14	40
41	Lm	42/116 (36%)	39 (93%)	3 (7%)	12	37
42	Ln	23/24 (96%)	21 (91%)	2 (9%)	8	29
43	Lo	79/94 (84%)	73 (92%)	6 (8%)	11	34
44	Lp	70/75 (93%)	64 (91%)	6 (9%)	8	30
45	Lr	103/121 (85%)	96 (93%)	7 (7%)	13	38
47	SA	147/243 (60%)	135 (92%)	12 (8%)	9	31
48	SB	162/231 (70%)	157 (97%)	5 (3%)	35	61
49	SC	155/225 (69%)	148 (96%)	7 (4%)	23	52
50	SD	125/202 (62%)	118 (94%)	7 (6%)	17	45
51	SE	176/225 (78%)	165 (94%)	11 (6%)	15	41
52	SF	133/170 (78%)	132 (99%)	1 (1%)	79	87
53	SG	160/218 (73%)	153 (96%)	7 (4%)	24	52
54	SH	137/174 (79%)	126 (92%)	11 (8%)	10	32
55	SI	149/180 (83%)	142 (95%)	7 (5%)	22	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
56	SJ	140/168 (83%)	135 (96%)	5 (4%)	30	57
57	SK	68/136 (50%)	65 (96%)	3 (4%)	24	52
58	SL	124/142 (87%)	119 (96%)	5 (4%)	27	55
59	SN	127/131 (97%)	122 (96%)	5 (4%)	27	55
60	SO	103/119 (87%)	96 (93%)	7 (7%)	13	38
61	SP	103/130 (79%)	96 (93%)	7 (7%)	13	38
62	SQ	105/121 (87%)	101 (96%)	4 (4%)	28	56
63	SR	77/122 (63%)	74 (96%)	3 (4%)	27	55
64	SS	103/132 (78%)	96 (93%)	7 (7%)	13	38
65	ST	80/115 (70%)	72 (90%)	8 (10%)	6	23
66	SU	77/107 (72%)	72 (94%)	5 (6%)	14	40
67	SV	53/67 (79%)	50 (94%)	3 (6%)	17	44
68	SW	110/113 (97%)	99 (90%)	11 (10%)	6	23
69	SX	101/115 (88%)	92 (91%)	9 (9%)	8	28
70	SY	87/115 (76%)	84 (97%)	3 (3%)	32	59
71	SZ	39/103 (38%)	36 (92%)	3 (8%)	10	33
72	Sa	79/98 (81%)	74 (94%)	5 (6%)	15	41
73	Sb	64/76 (84%)	58 (91%)	6 (9%)	7	25
74	Sc	41/62 (66%)	35 (85%)	6 (15%)	2	12
75	Sd	42/49 (86%)	33 (79%)	9 (21%)	1	4
76	Se	37/48 (77%)	36 (97%)	1 (3%)	40	65
77	Sf	30/108 (28%)	27 (90%)	3 (10%)	6	23
78	Sg	167/275 (61%)	151 (90%)	16 (10%)	7	25
79	sh	17/140 (12%)	17 (100%)	0	100	100
82	zx	5/29 (17%)	5 (100%)	0	100	100
84	3m	252/335 (75%)	245 (97%)	7 (3%)	38	64
85	3f	229/289 (79%)	226 (99%)	3 (1%)	65	79
86	3a	439/1259 (35%)	426 (97%)	13 (3%)	36	62
87	3e	301/406 (74%)	295 (98%)	6 (2%)	50	71
88	3c	442/811 (54%)	430 (97%)	12 (3%)	40	65
89	3h	272/310 (88%)	264 (97%)	8 (3%)	37	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
90	3d	20/494 (4%)	19 (95%)	1 (5%)	20	48
91	3k	121/193 (63%)	115 (95%)	6 (5%)	20	48
92	3l	474/515 (92%)	467 (98%)	7 (2%)	60	77
All	All	10991/15442 (71%)	10381 (94%)	610 (6%)	20	45

5 of 610 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
65	ST	87	VAL
87	3e	326	VAL
68	SW	16	ASN
65	ST	63	HIS
75	Sd	14	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 107 such sidechains are listed below:

Mol	Chain	Res	Type
50	SD	159	HIS
70	SY	124	ASN
89	3h	261	ASN
55	SI	165	GLN
62	SQ	35	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3572/5070 (70%)	798 (22%)	14 (0%)
2	L7	119/120 (99%)	17 (14%)	1 (0%)
3	L8	155/156 (99%)	36 (23%)	2 (1%)
46	S2	1662/1869 (88%)	480 (28%)	13 (0%)
80	zu	71/75 (94%)	20 (28%)	0
80	zy	74/75 (98%)	16 (21%)	0
81	zv	8/19 (42%)	5 (62%)	0
83	zz	210/332 (63%)	73 (34%)	0
All	All	5871/7716 (76%)	1445 (24%)	30 (0%)

5 of 1445 RNA backbone outliers are listed below:



Mol	Chain	Res	Type
1	L5	17	A
1	L5	21	G
1	L5	25	A
1	L5	26	C
1	L5	30	C

5 of 30 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	L7	109	U
46	S2	1788	A
46	S2	129	C
46	S2	1860	A
46	S2	1585	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 73 ligands modelled in this entry, 73 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

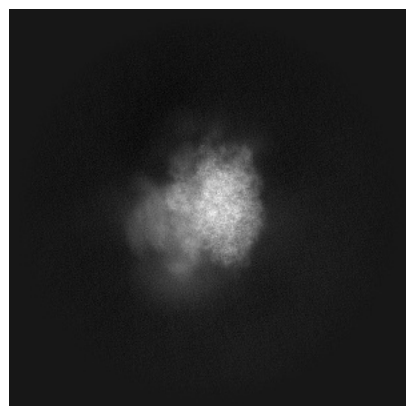
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62679. These allow visual inspection of the internal detail of the map and identification of artifacts.

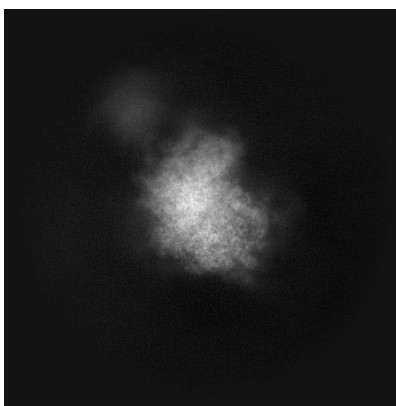
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

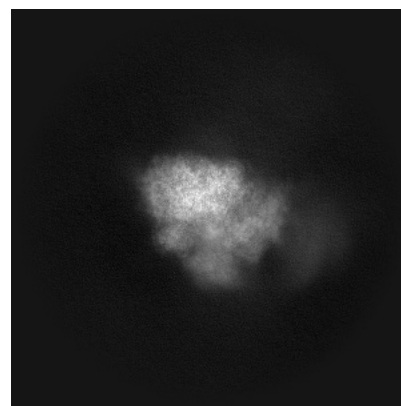
#### 6.1.1 Primary map



X

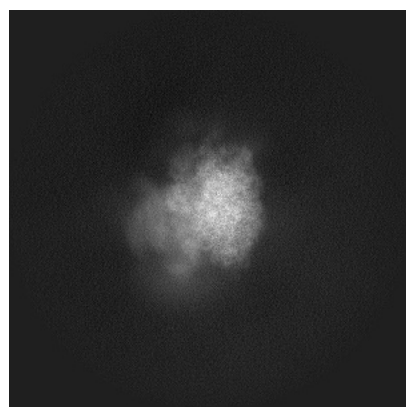


Y

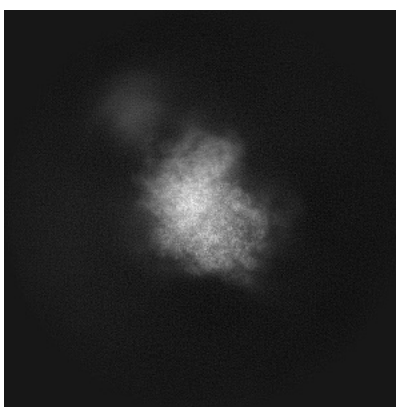


Z

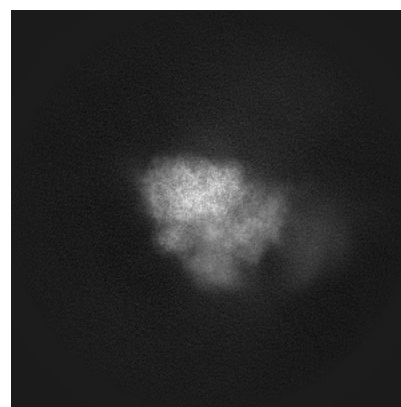
#### 6.1.2 Raw map



X



Y

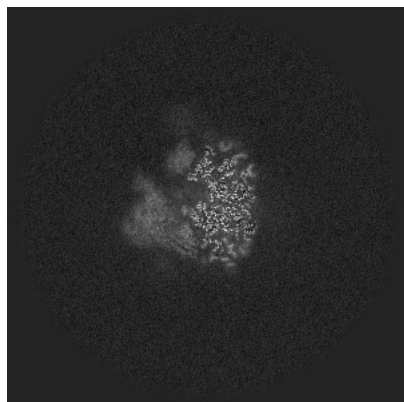


Z

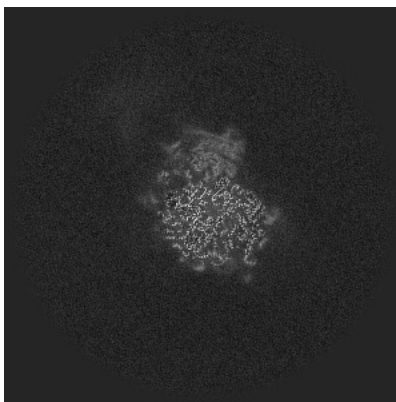
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

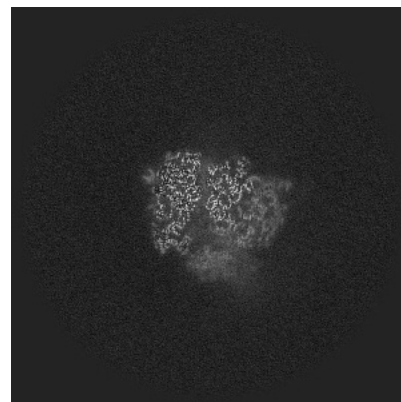
### 6.2.1 Primary map



X Index: 250

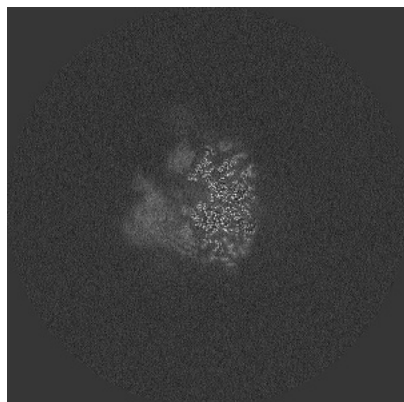


Y Index: 250

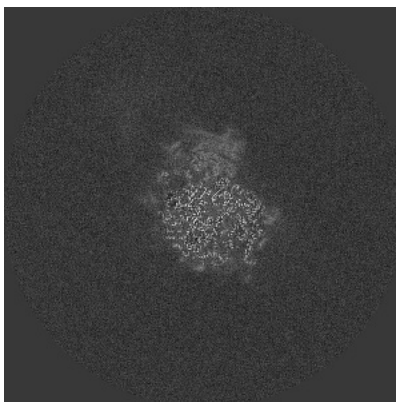


Z Index: 250

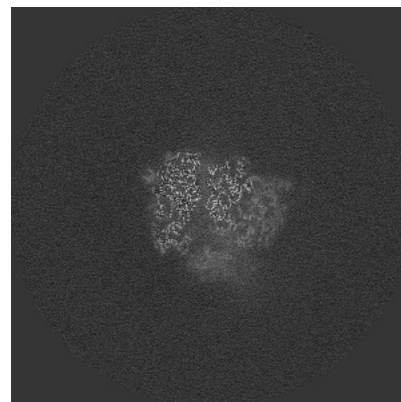
### 6.2.2 Raw map



X Index: 250



Y Index: 250

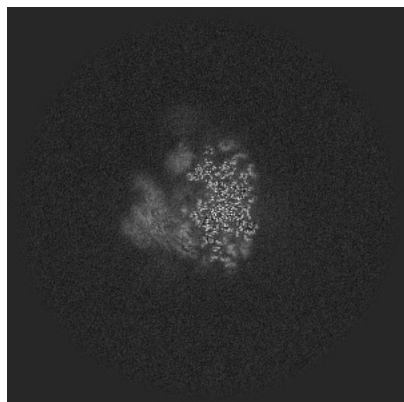


Z Index: 250

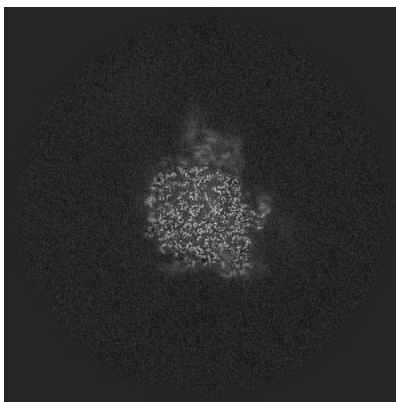
The images above show central slices of the map in three orthogonal directions.

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

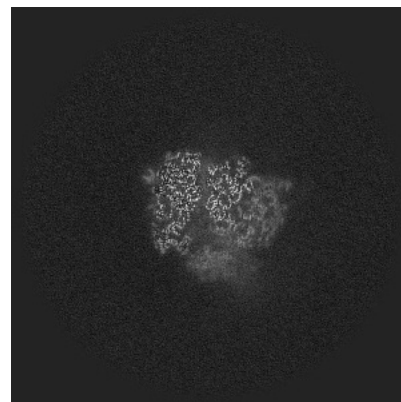
### 6.3.1 Primary map



X Index: 251

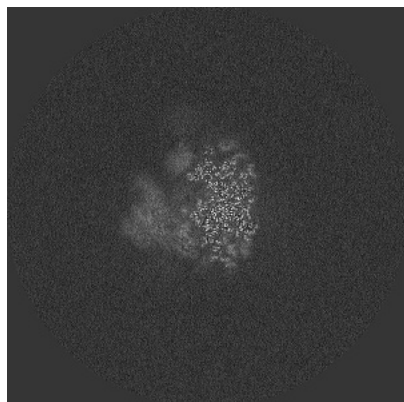


Y Index: 270

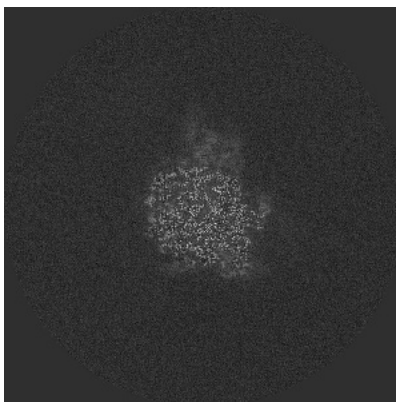


Z Index: 250

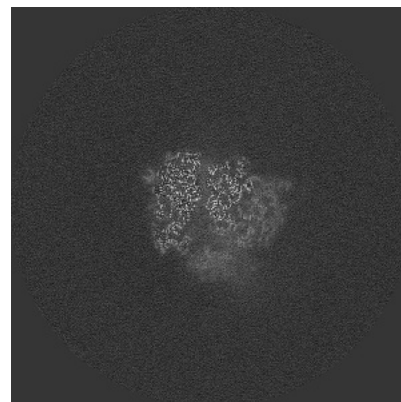
### 6.3.2 Raw map



X Index: 251



Y Index: 270



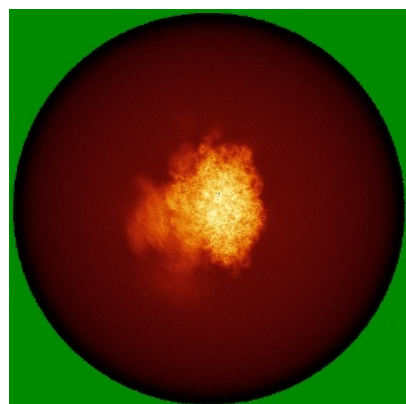
Z Index: 250

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

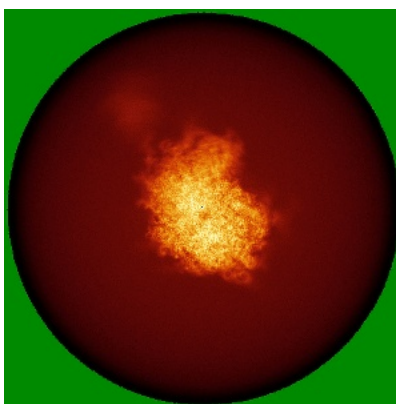


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

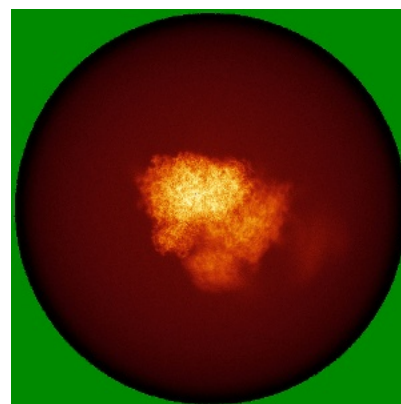
### 6.4.1 Primary map



X

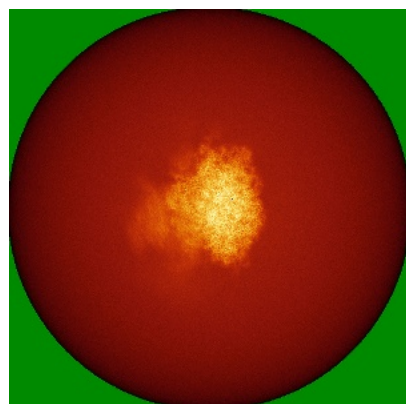


Y

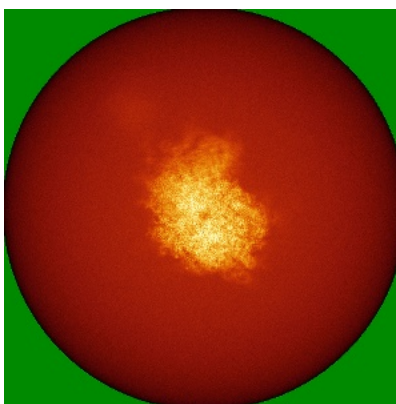


Z

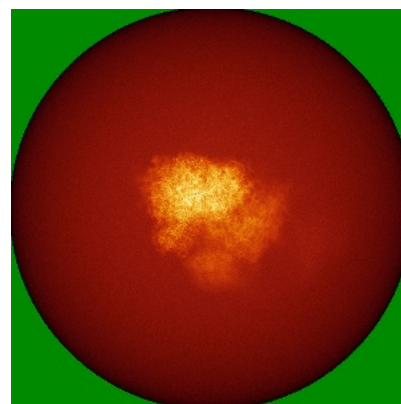
### 6.4.2 Raw map



X



Y

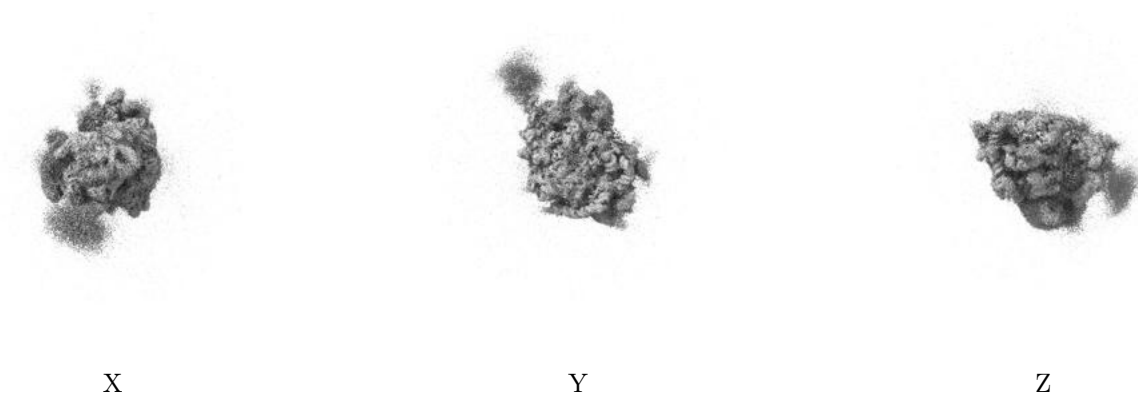


Z

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.

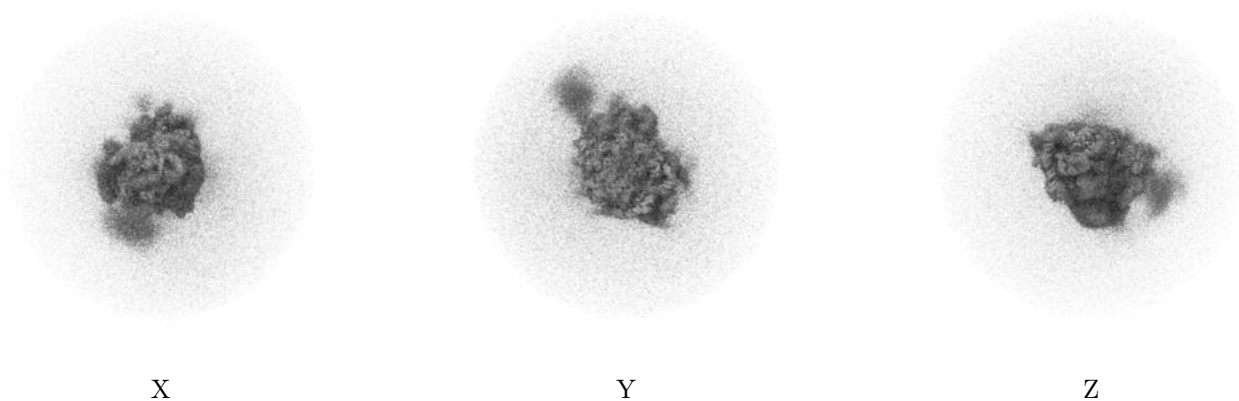
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.015. 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.

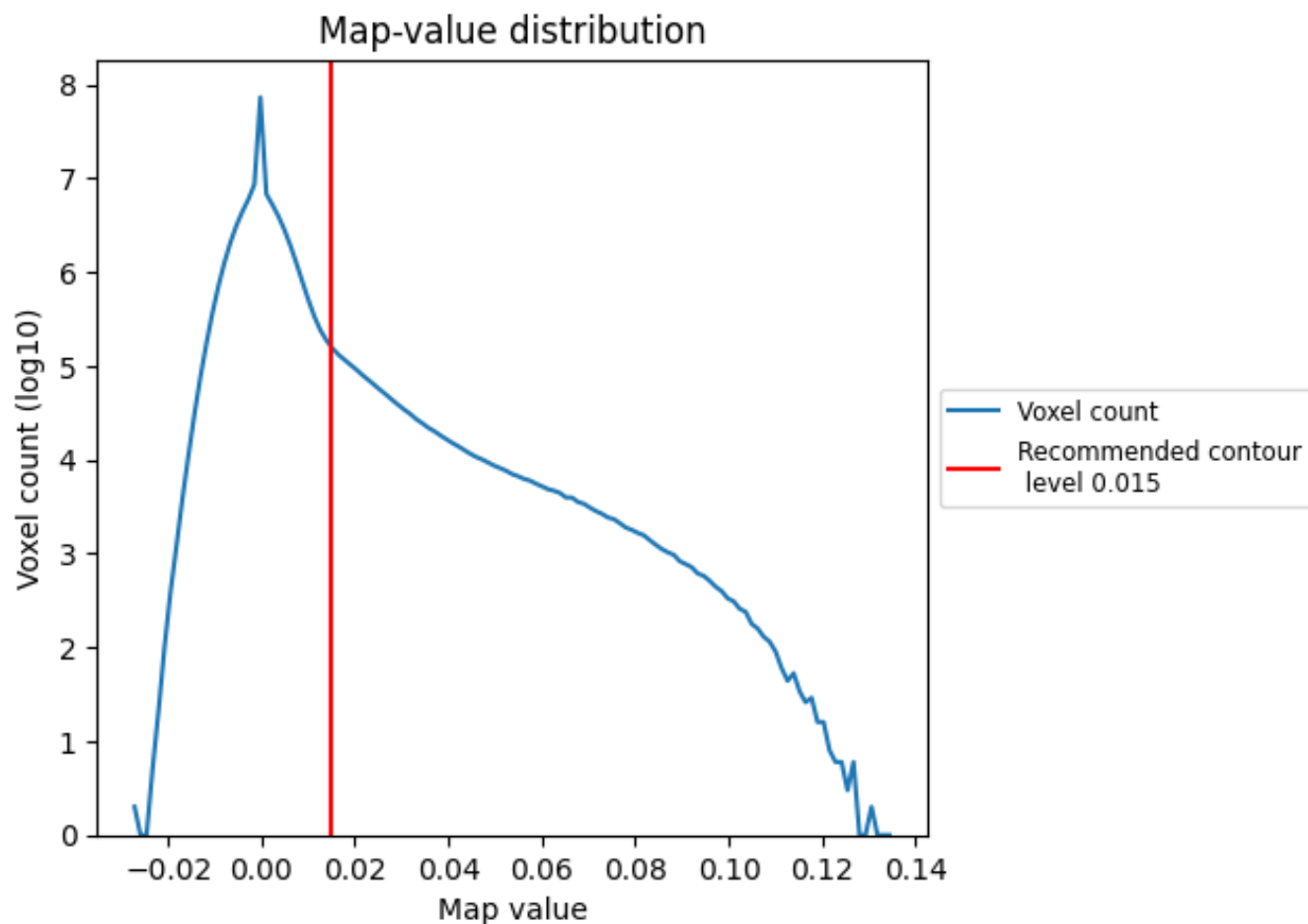
## 6.6 Mask visualisation [i](#)

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.

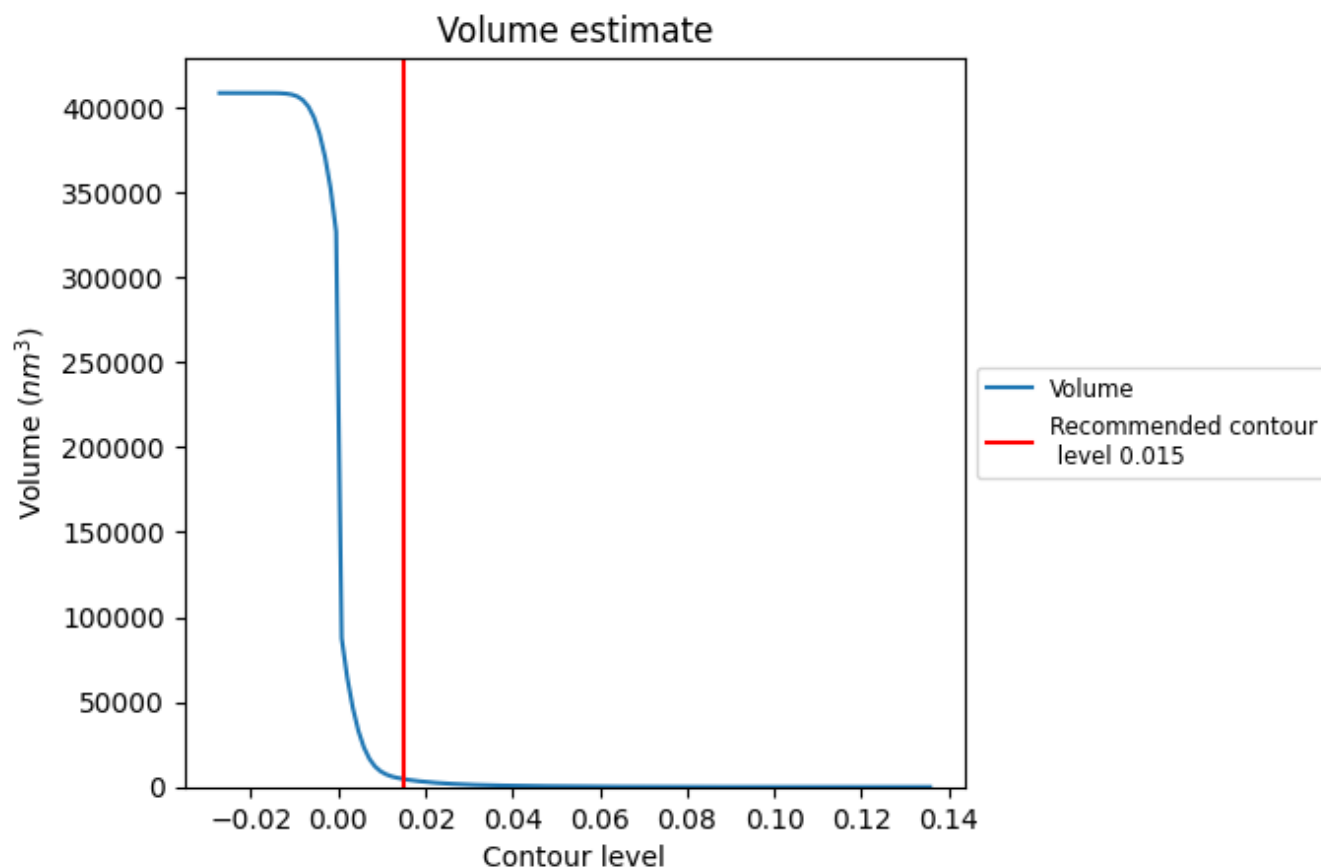
### 7.1 Map-value distribution [i](#)



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.



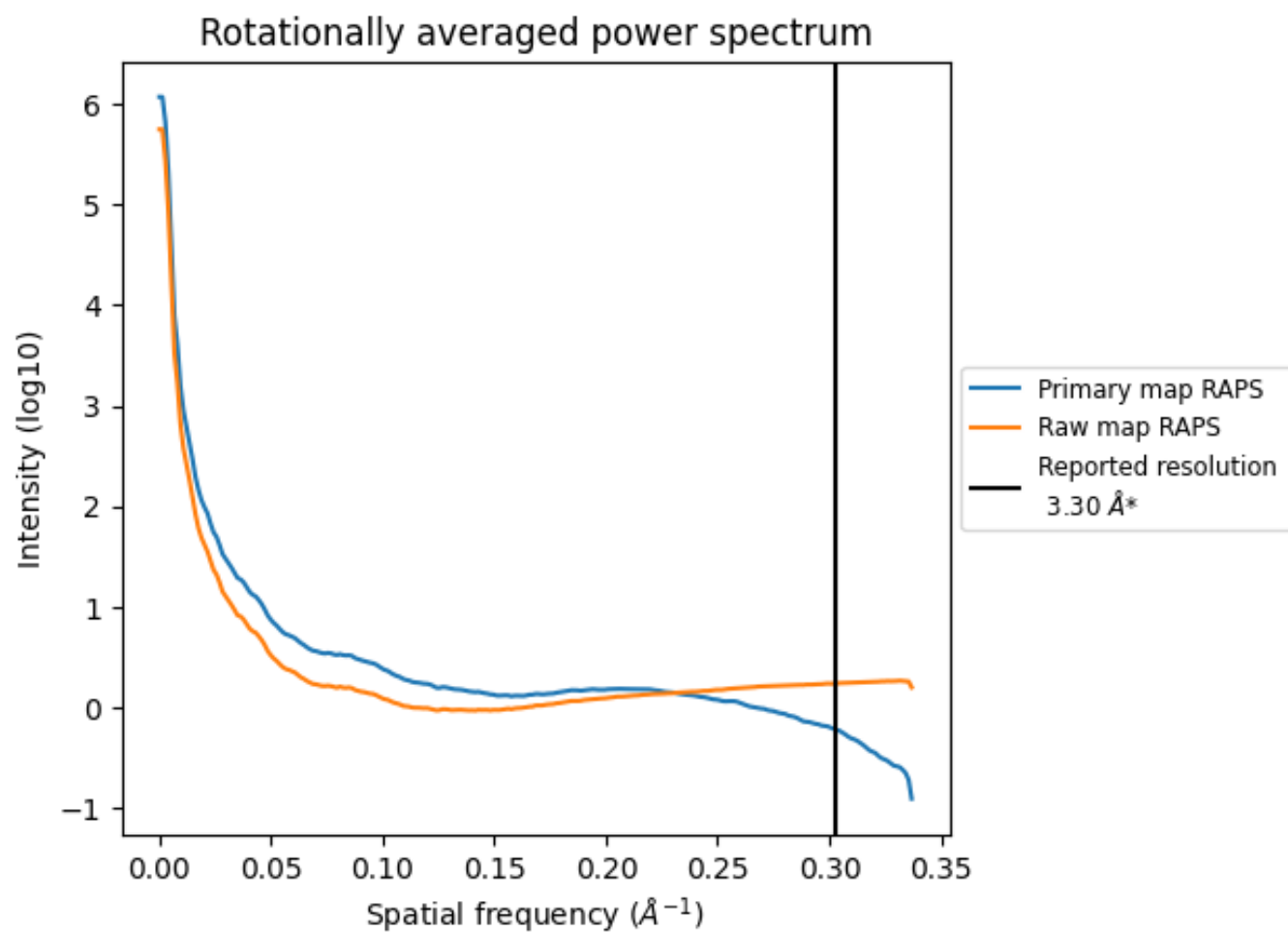
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4651 nm<sup>3</sup>; this corresponds to an approximate mass of 4201 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 ⓘ

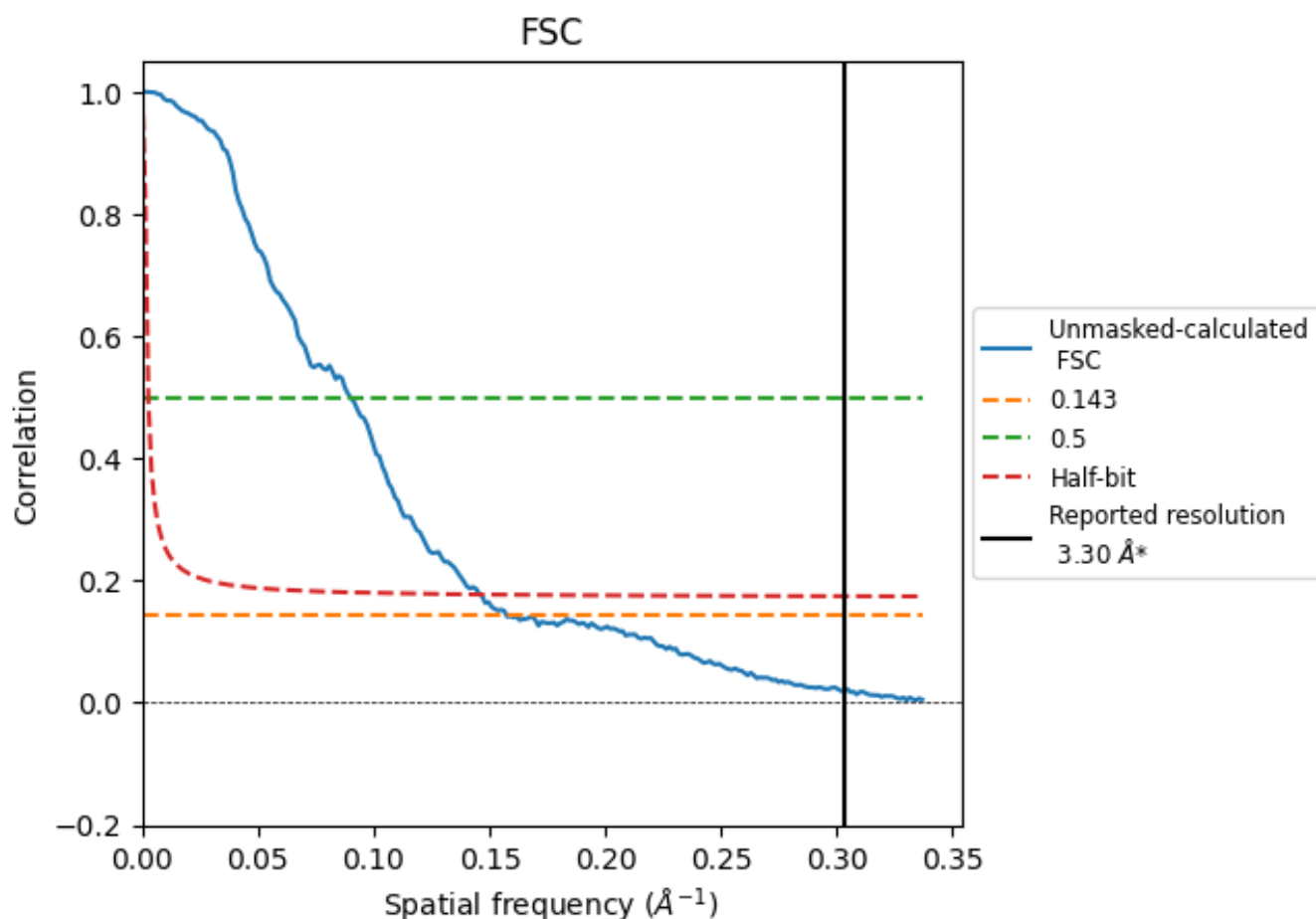


\*Reported resolution corresponds to spatial frequency of 0.303 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.303 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

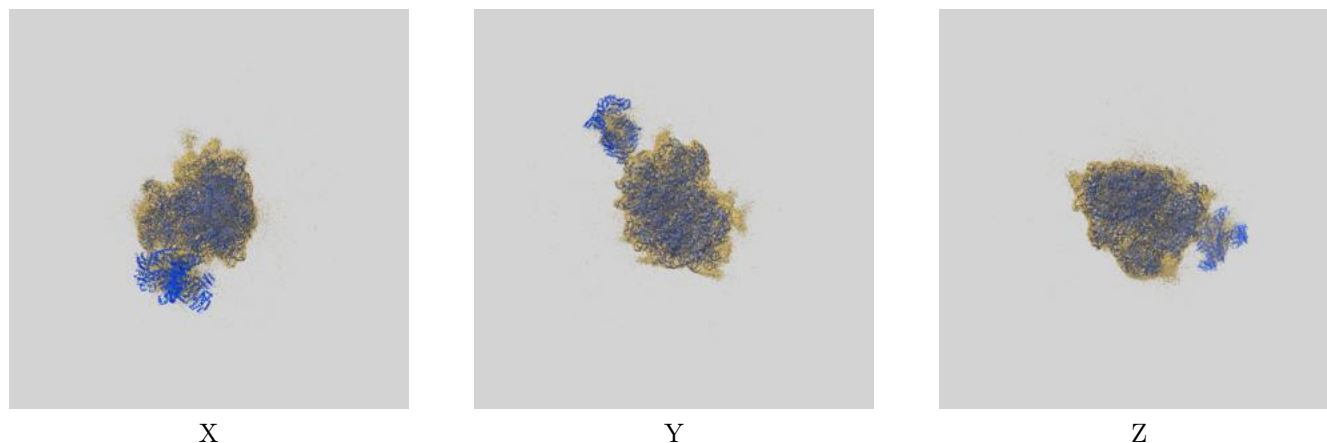
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.35	11.12	6.85

\*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 6.35 differs from the reported value 3.3 by more than 10 %

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

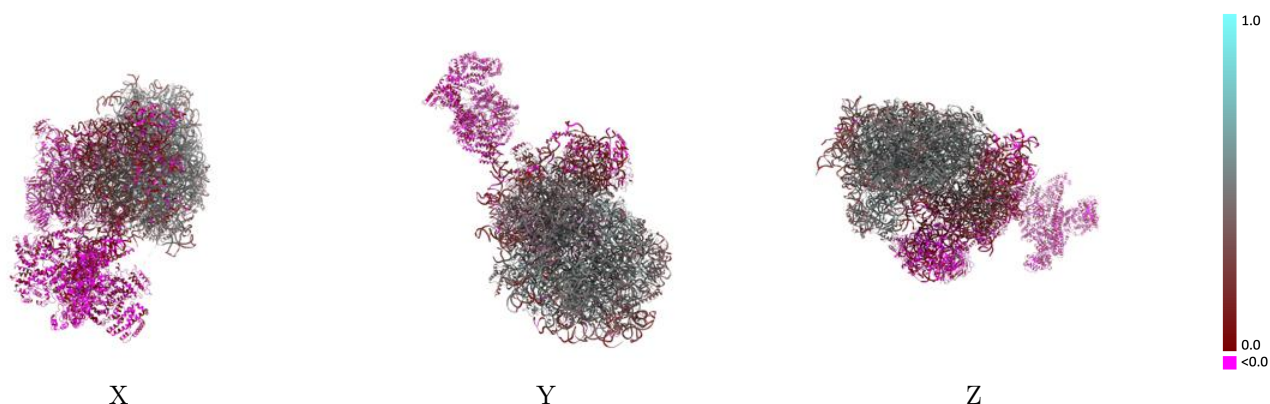
This section contains information regarding the fit between EMDB map EMD-62679 and PDB model 9KZX. Per-residue inclusion information can be found in section [3](#) on page [22](#).

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



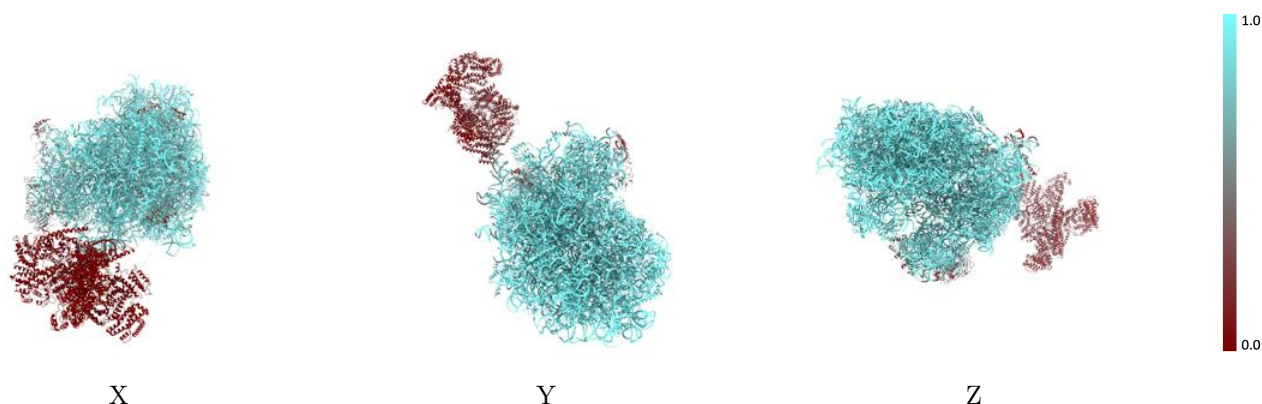
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



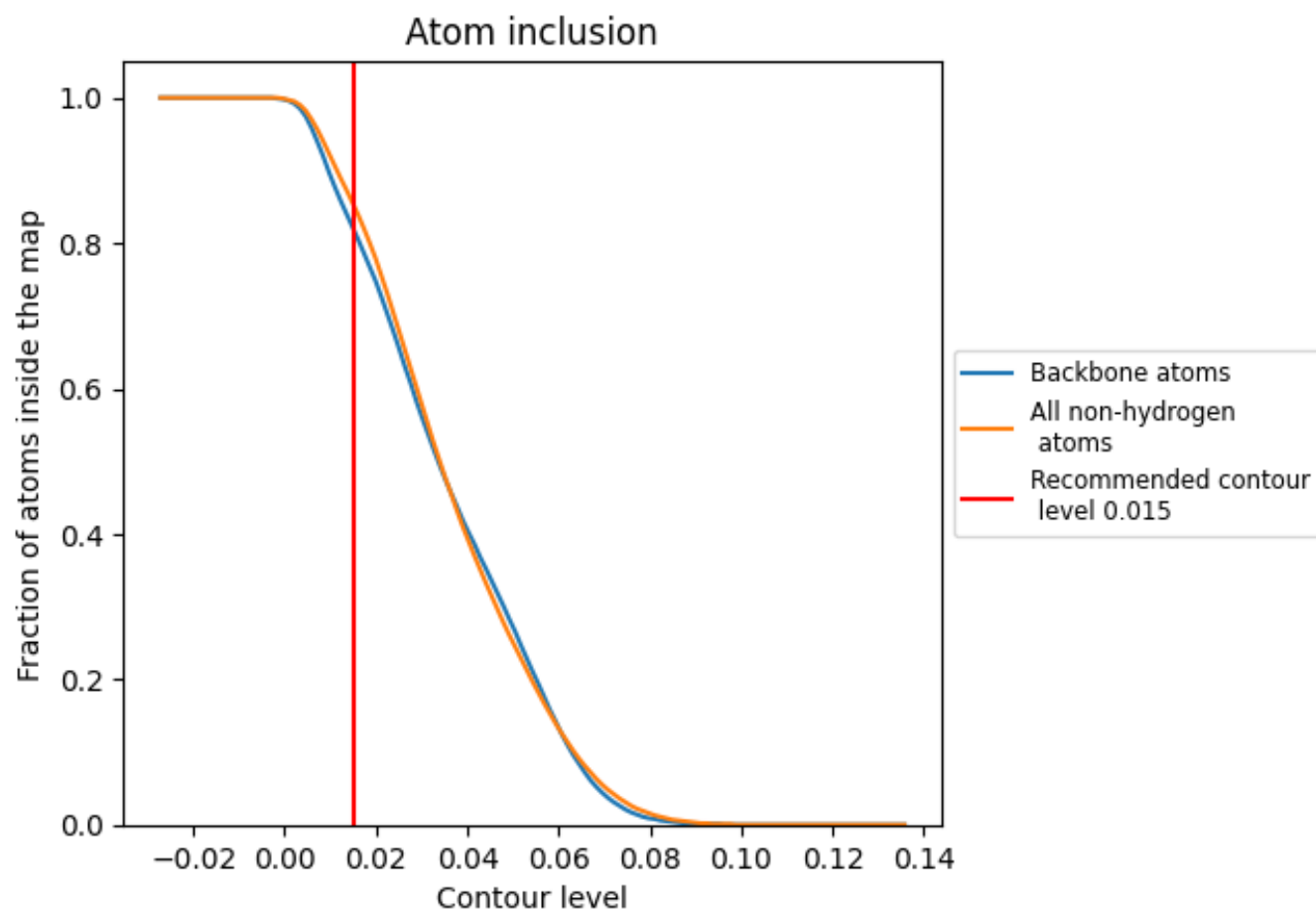
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.015).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 85% 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 (0.015) and Q-score for the entire model and for each chain.





















































































Chain	Atom inclusion	Q-score
All	 0.8540	 0.3030
3a	 0.0720	 0.0320
3c	 0.1340	 0.0740
3d	 0.0350	 0.0220
3e	 0.0220	 0.0120
3f	 0.0370	 0.0300
3h	 0.0680	 0.0240
3k	 0.0030	 0.0030
3l	 0.0120	 0.0280
3m	 0.0080	 0.0160
L5	 0.9920	 0.4470
L7	 0.9970	 0.4960
L8	 0.9870	 0.4470
LA	 0.9860	 0.4760
LB	 0.9860	 0.4820
LC	 0.9810	 0.4580
LD	 0.9680	 0.4410
LE	 0.9690	 0.4020
LF	 0.9930	 0.4700
LG	 0.9500	 0.4070
LH	 0.9810	 0.4600
LI	 0.9870	 0.4640
LJ	 0.9750	 0.4190
LL	 0.9830	 0.4670
LM	 0.9780	 0.4520
LN	 0.9960	 0.5210
LO	 0.9900	 0.4830
LP	 0.9920	 0.4790
LQ	 0.9880	 0.4810
LR	 0.9800	 0.4360
LS	 0.9880	 0.4900
LT	 0.9920	 0.4760
LU	 0.9520	 0.4230
LV	 0.9860	 0.4660
LW	 0.8200	 0.3240



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
































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Chain	Atom inclusion	Q-score
LX	 0.9770	 0.4390
LY	 0.9740	 0.4430
LZ	 0.9630	 0.4130
La	 0.9770	 0.4530
Lb	 0.9980	 0.4630
Lc	 0.9640	 0.4180
Ld	 0.9770	 0.4570
Le	 0.9920	 0.4750
Lf	 0.9930	 0.4850
Lg	 0.9840	 0.4370
Lh	 0.9810	 0.4530
Li	 0.9780	 0.4470
Lj	 0.9990	 0.4990
Lk	 0.9440	 0.4150
Ll	 0.9950	 0.4710
Lm	 0.9870	 0.4570
Ln	 1.0000	 0.3860
Lo	 0.9960	 0.4870
Lp	 0.9870	 0.4760
Lr	 0.9870	 0.4540
S2	 0.9710	 0.1730
SA	 0.8540	 0.1460
SB	 0.8490	 0.1170
SC	 0.9200	 0.1780
SD	 0.8080	 0.0260
SE	 0.9420	 0.1600
SF	 0.8310	 0.0140
SG	 0.8420	 0.1160
SH	 0.8830	 0.2120
SI	 0.9080	 0.1390
SJ	 0.9280	 0.1310
SK	 0.7290	 0.0010
SL	 0.9830	 0.2650
SN	 0.9620	 0.2890
SO	 0.9120	 0.0760
SP	 0.8370	 0.0840
SQ	 0.7710	 0.0070
SR	 0.7510	 0.0560
SS	 0.7690	 0.0510
ST	 0.7760	 0.0150
SU	 0.7530	 0.0320
SV	 0.8840	 0.2360

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Chain	Atom inclusion	Q-score
SW	 0.9690	 0.3350
SX	 0.9800	 0.2540
SY	 0.8850	 0.1080
SZ	 0.5920	 0.0140
Sa	 0.9610	 0.1460
Sb	 0.9360	 0.2050
Sc	 0.8790	 0.0030
Sd	 0.9800	 0.0110
Se	 0.9250	 0.0920
Sf	 0.3510	 0.0500
Sg	 0.5700	 0.0160
sh	 0.6690	 0.0640
zu	 0.9370	 0.1280
zv	 1.0000	 0.1440
zx	 1.0000	 0.2020
zy	 0.6500	 0.0660
zz	 0.6200	 0.0620