



## wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 06:42 PM UTC

PDB ID : 9Y42 / pdb\_00009y42  
EMDB ID : EMD-72469  
Title : Structure of naked mole-rat ribosome with P/E tRNA and eEF2 (rotated)  
Authors : Gutierrez-Vargas, C.; De, S.; Maji, S.; Liu, Z.; Nieb, M.; Seluanov, A.; Gorbunova, V.; Frank, J.  
Deposited on : 2025-09-02  
Resolution : 5.00 Å (reported)  
Based on initial models : 4v6x, 707y

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>.

---

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

EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

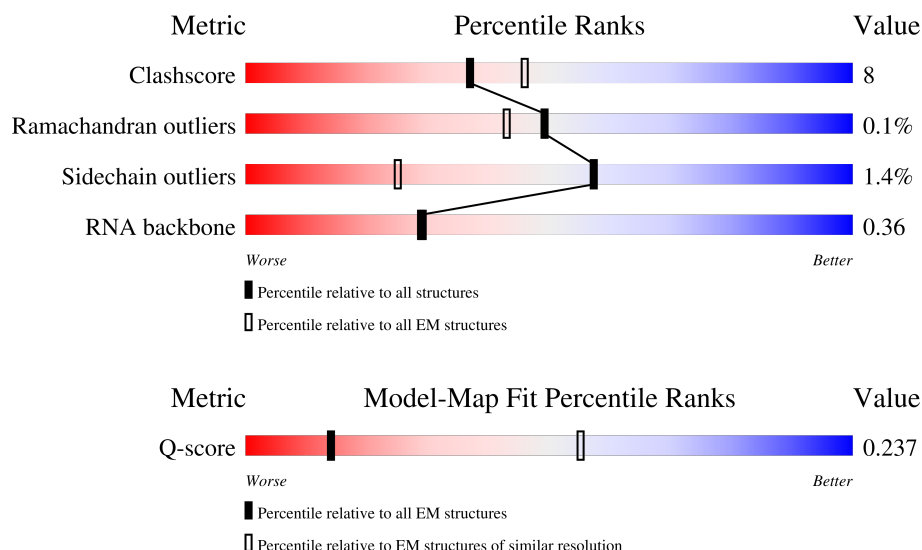
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 5.00 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.




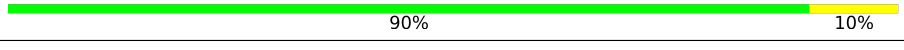
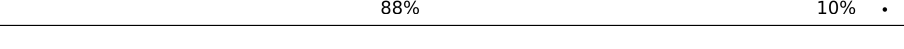
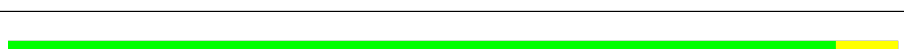



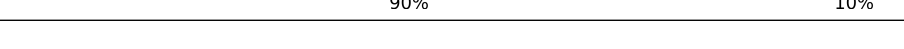
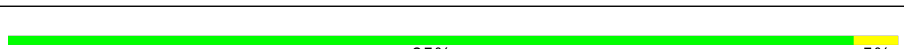

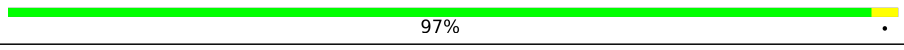
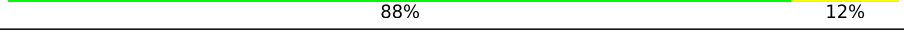
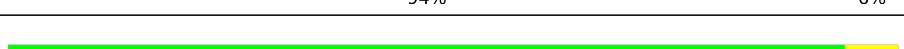
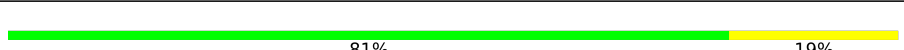

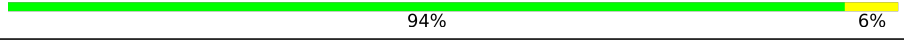
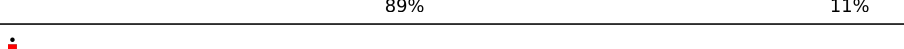



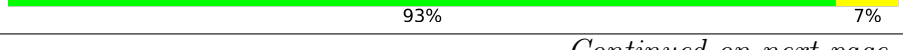



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	1057 ( 4.50 - 5.50 )

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  $\geq 3$ , 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	A	248	
2	B	398	
3	C	363	


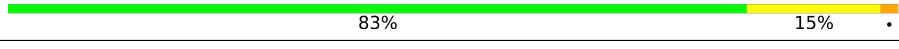
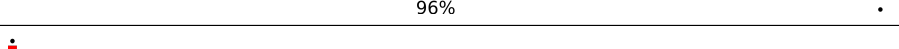
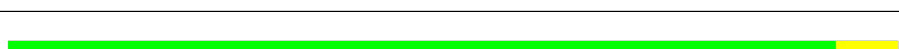
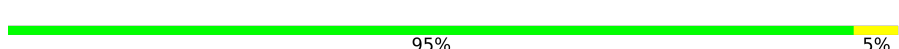
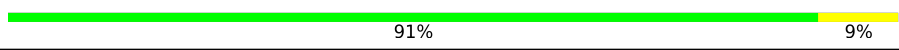
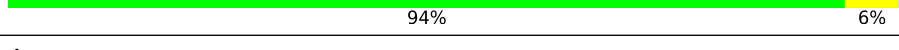
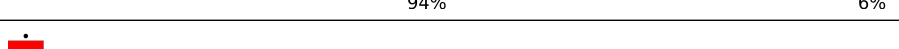
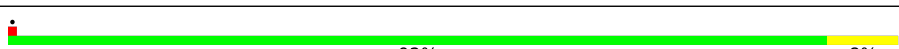

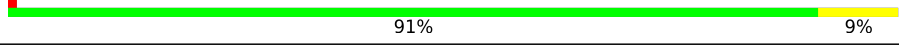
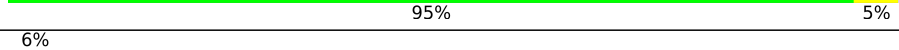

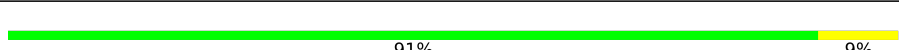
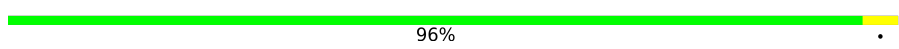

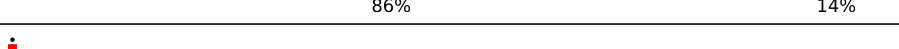



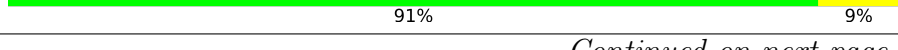



Continued on next page...

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
4	c	121	
5	D	293	
6	E	224	
7	F	225	
8	G	215	
9	H	190	
10	I	213	
11	J	170	
12	L	205	
13	M	136	
14	N	203	
15	O	199	
16	P	153	
17	Q	187	
18	S	176	
19	T	159	
20	U	99	
21	V	131	
22	W	180	
23	X	118	
24	Y	134	
25	Z	135	
26	a	147	
27	b	104	
28	d	107	



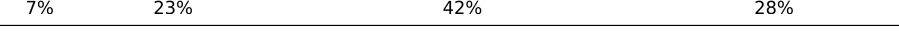
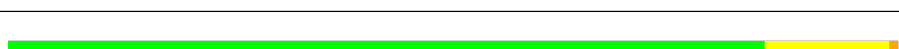
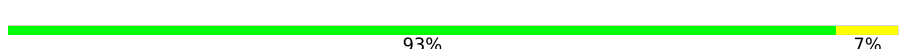

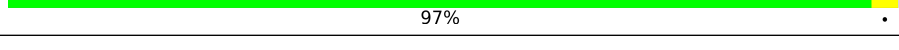
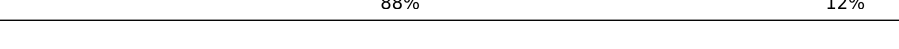

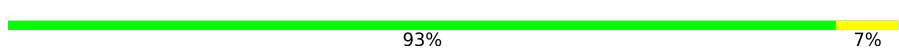

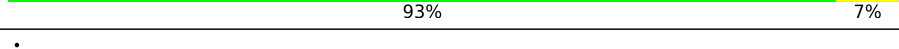

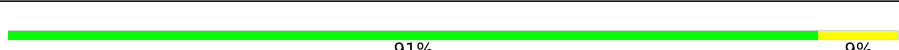
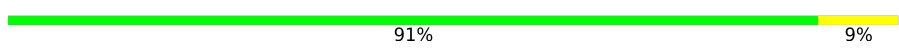
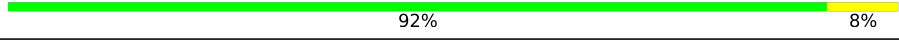
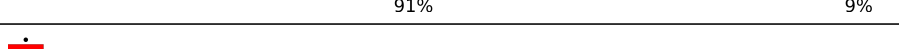







*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
29	e	128	
30	f	110	
31	g	110	
32	h	121	
33	i	102	
34	j	86	
35	k	69	
36	l	50	
37	m	51	
38	n	25	
39	o	105	
40	p	91	
41	r	127	
42	s	103	
43	t	156	
44	u	100	
45	bb	82	
46	ee	49	
47	aa	98	
48	CC	218	
49	EE	262	
50	GG	228	
51	HH	190	
52	II	206	
53	JJ	180	



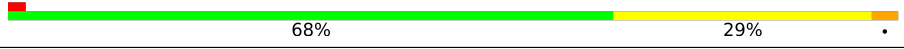



*Continued on next page...*

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	LL	149	
55	NN	149	
56	VV	83	
57	WW	129	
58	XX	141	
59	YY	125	
60	cc	61	
61	ff	67	
62	gg	313	
63	dd	55	
64	AA	214	
65	DD	225	
66	FF	189	
67	KK	96	
68	MM	124	
69	PP	118	
70	QQ	141	
71	SS	145	
72	TT	141	
73	UU	99	
74	ZZ	75	
75	EF	856	
76	Cc	77	
77	A5	1732	
78	A7	121	

Continued on next page...

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
79	A8	157	
80	B2	1837	
81	A6	2122	
82	BB	218	
83	OO	134	
84	RR	132	

## 2 Entry composition

There are 87 unique types of molecules in this entry. The entry contains 225388 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Large ribosomal subunit protein uL2.

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

- Molecule 2 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	398	Total	C	N	O	S	0	0
			3206	2042	605	546	13		

- Molecule 3 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	363	Total	C	N	O	S	0	0
			2895	1822	576	483	14		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	1	ACE	-	acetylation	UNP G5AN81
C	262	ASP	GLU	conflict	UNP G5AN81
C	352	GLU	ASP	conflict	UNP G5AN81

- Molecule 4 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	c	115	Total	C	N	O	S	0	0
			938	586	193	155	4		

- Molecule 5 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	293	Total	C	N	O	S	0	0
			2389	1511	437	427	14		

- Molecule 6 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	224	Total	C	N	O	S	0	0
			1789	1149	340	297	3		

- Molecule 7 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 8 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	215	Total	C	N	O	S	0	0
			1741	1111	333	293	4		

- Molecule 9 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 10 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	199	Total	C	N	O	S	0	0
			1620	1029	313	266	12		

- Molecule 11 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 12 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	205	Total	C	N	O	S	0	0
			1658	1037	346	271	4		

- Molecule 13 is a protein called Large ribosomal subunit protein eL14.



Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	136	Total	C	N	O	S	0	0
			1125	720	220	178	7		

- Molecule 14 is a protein called Ribosomal protein L15.

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

- Molecule 15 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 16 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 17 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	187	Total	C	N	O	S	0	0
			1512	946	313	249	4		

- Molecule 18 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	176	Total	C	N	O	S	0	0
			1461	930	284	236	11		

- Molecule 19 is a protein called Large ribosomal subunit protein eL21.

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

- Molecule 20 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	99	Total	C	N	O	S	0	0
			808	518	141	147	2		

- Molecule 21 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	131	Total	C	N	O	S	0	0
			973	612	184	172	5		

- Molecule 22 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 23 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 24 is a protein called 60S ribosomal protein L26.

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

- Molecule 25 is a protein called 60S ribosomal protein L27.

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

- Molecule 26 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	147	Total	C	N	O	S	0	0
			1163	734	239	186	4		

- Molecule 27 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	74	Total	C	N	O	S	0	0
			620	382	141	95	2		

- Molecule 28 is a protein called Large ribosomal subunit protein eL31.

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

- Molecule 29 is a protein called 60S ribosomal protein L32.

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

- Molecule 30 is a protein called Large ribosomal subunit protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	f	110	Total	C	N	O	S	0	0
			884	560	175	144	5		

- Molecule 31 is a protein called Large ribosomal subunit protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	g	110	Total	C	N	O	S	0	0
			873	547	180	140	6		

- Molecule 32 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	h	121	Total	C	N	O	S	0	0
			1011	640	204	166	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
h	119	TYR	PHE	conflict	UNP G5B6W3

- Molecule 33 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	i	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 34 is a protein called Ribosomal protein L37.

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

- Molecule 35 is a protein called Large ribosomal subunit protein eL38.

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

- Molecule 36 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	l	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 37 is a protein called Ubiquitin-ribosomal protein eL40 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	m	51	Total	C	N	O	S	0	0
			422	263	88	65	6		

- Molecule 38 is a protein called 60S ribosomal protein L41.

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

- Molecule 39 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	o	105	Total	C	N	O	S	0	0
			863	543	175	139	6		

- Molecule 40 is a protein called Large ribosomal subunit protein eL43.

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

- Molecule 41 is a protein called Large ribosomal subunit protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	r	127	Total	C	N	O	S	0	0
			1015	630	209	170	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
r	1	ACE	-	acetylation	UNP G5BVZ2

- Molecule 42 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	s	103	Total	C	N	O	S	0	0
			825	525	150	143	7		

- Molecule 43 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	t	156	Total	C	N	O	S	0	0
			1178	733	221	220	4		

- Molecule 44 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	u	88	Total	C	N	O	S	0	0
			672	425	116	125	6		

- Molecule 45 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	bb	82	Total	C	N	O	S	0	0
			640	402	118	113	7		

- Molecule 46 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	ee	49	Total	C	N	O	S	0	0
			398	243	90	64	1		

- Molecule 47 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	aa	98	Total	C	N	O	S	0	0
			781	486	161	129	5		

- Molecule 48 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	CC	218	Total	C	N	O	S	0	0
			1685	1092	288	296	9		

- Molecule 49 is a protein called 40S ribosomal protein S4, X isoform.

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

- Molecule 50 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	GG	228	Total	C	N	O	S	0	0
			1848	1155	368	318	7		

- Molecule 51 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	HH	184	Total	C	N	O	S	0	0
			1490	953	271	265	1		

- Molecule 52 is a protein called 40S ribosomal protein S8.

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

- Molecule 53 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	JJ	180	Total	C	N	O	S	0	0
			1499	955	300	242	2		

- Molecule 54 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	LL	141	Total	C	N	O	S	0	0
			1157	737	218	196	6		

- Molecule 55 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	NN	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 56 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	VV	83	Total	C	N	O	S	0	0
			637	392	117	123	5		

- Molecule 57 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 58 is a protein called Small ribosomal subunit protein uS12.

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

- Molecule 59 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	YY	125	Total	C	N	O	S	0	0
			1015	642	199	169	5		

- Molecule 60 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	cc	61	Total	C	N	O	S	0	0
			479	292	95	90	2		

- Molecule 61 is a protein called Ubiquitin-ribosomal protein eS31 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	ff	67	Total	C	N	O	S	0	0
			548	346	102	93	7		

- Molecule 62 is a protein called Small ribosomal subunit protein RACK1.

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

- Molecule 63 is a protein called Small ribosomal subunit protein uS14.

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

- Molecule 64 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AA	205	Total	C	N	O	S	0	0
			1625	1035	283	299	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AA	1	ACE	-	acetylation	UNP A0A0P6K1L6

- Molecule 65 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	DD	225	Total	C	N	O	S	0	0
			1751	1116	315	313	7		

- Molecule 66 is a protein called Small ribosomal subunit protein uS7.



Mol	Chain	Residues	Atoms					AltConf	Trace
66	FF	186	Total	C	N	O	S	0	0
			1475	923	278	267	7		

- Molecule 67 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	KK	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 68 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	MM	124	Total	C	N	O	S	0	0
			958	600	170	179	9		

- Molecule 69 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	PP	118	Total	C	N	O	S	0	0
			979	621	185	166	7		

- Molecule 70 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	QQ	141	Total	C	N	O	S	0	0
			1124	715	212	194	3		

- Molecule 71 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SS	145	Total	C	N	O	S	0	0
			1193	748	241	203	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SS	1	ACE	-	acetylation	UNP G5BAZ4

- Molecule 72 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	TT	141	Total	C	N	O	S	0	0
			1097	687	211	196	3		

- Molecule 73 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	UU	99	Total	C	N	O	S	0	0
			790	495	151	140	4		

- Molecule 74 is a protein called 40S ribosomal protein S25.

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

- Molecule 75 is a protein called eEF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	EF	856	Total	C	N	O	S	0	0
			6669	4232	1147	1246	44		

- Molecule 76 is a RNA chain called P/E tRNA (77-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Cc	77	Total	C	N	O	P	0	0
			1644	732	298	537	77		

- Molecule 77 is a RNA chain called LSU alpha rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	A5	1732	Total	C	N	O	P	0	0
			36419	16179	6629	11880	1731		

- Molecule 78 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	A7	121	Total	C	N	O	P	0	0
			2578	1150	458	850	120		

- Molecule 79 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	A8	157	Total	C	N	O	P	0	0
			3334	1489	587	1102	156		

- Molecule 80 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	B2	1837	Total	C	N	O	P	0	0
			38185	17001	6745	12603	1836		

- Molecule 81 is a RNA chain called LSU beta rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	A6	2122	Total	C	N	O	P	0	0
			43819	19451	7789	14457	2122		

- Molecule 82 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	BB	218	Total	C	N	O	S	0	0
			1768	1120	320	314	14		

- Molecule 83 is a protein called 40S ribosomal protein S14.

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

- Molecule 84 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	RR	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 85 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
85	P	1	Total	Mg	0
			1	1	
85	a	1	Total	Mg	0
			1	1	
85	l	1	Total	Mg	0
			1	1	

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms		AltConf
85	A5	7	Total 7	Mg 7	0
85	A8	1	Total 1	Mg 1	0
85	B2	6	Total 6	Mg 6	0
85	A6	7	Total 7	Mg 7	0
85	BB	2	Total 2	Mg 2	0

- Molecule 86 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
86	g	1	Total 1	Zn 1	0
86	j	1	Total 1	Zn 1	0
86	m	1	Total 1	Zn 1	0
86	o	1	Total 1	Zn 1	0
86	p	1	Total 1	Zn 1	0
86	aa	1	Total 1	Zn 1	0
86	ff	1	Total 1	Zn 1	0
86	dd	1	Total 1	Zn 1	0

- Molecule 87 is water.

Mol	Chain	Residues	Atoms		AltConf
87	A6	1	Total 1	O 1	0

### 3 Residue-property plots

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

- Molecule 1: Large ribosomal subunit protein uL2

Chain A: 



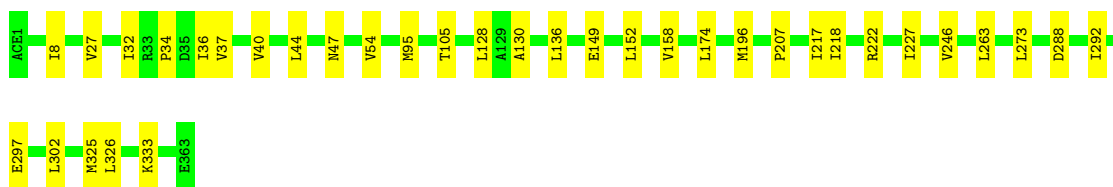
- Molecule 2: 60S ribosomal protein L3

Chain B: 




- Molecule 3: Large ribosomal subunit protein uL4

Chain C: 




- Molecule 4: Large ribosomal subunit protein eL24

Chain c: 

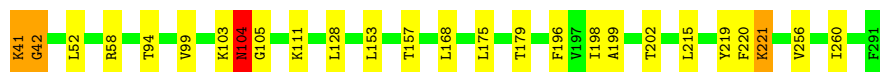
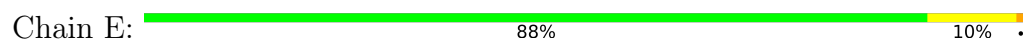


- Molecule 5: Large ribosomal subunit protein uL18

Chain D: 



- Molecule 6: 60S ribosomal protein L6



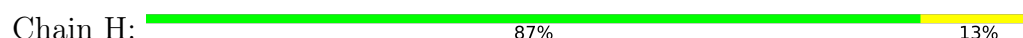
- Molecule 7: 60S ribosomal protein L7



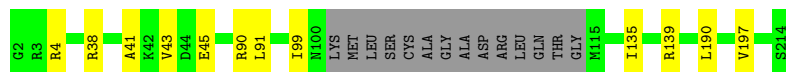
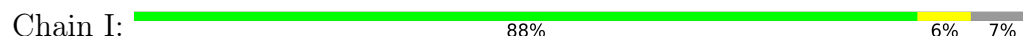
- Molecule 8: 60S ribosomal protein L7a



- Molecule 9: 60S ribosomal protein L9



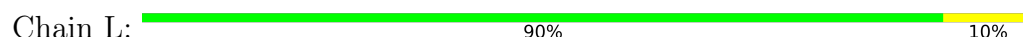
- Molecule 10: 60S ribosomal protein L10

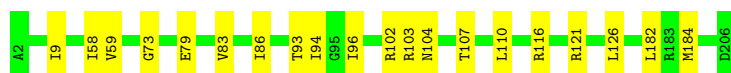


- Molecule 11: Large ribosomal subunit protein uL5

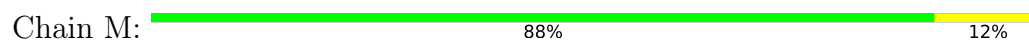


- Molecule 12: 60S ribosomal protein L13

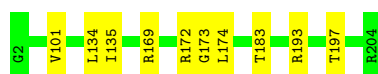




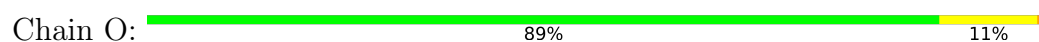
- Molecule 13: Large ribosomal subunit protein eL14



- Molecule 14: Ribosomal protein L15



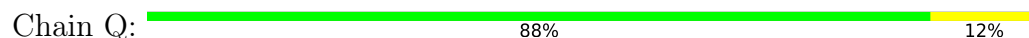
- Molecule 15: 60S ribosomal protein L13a



- Molecule 16: 60S ribosomal protein L17



- Molecule 17: 60S ribosomal protein L18

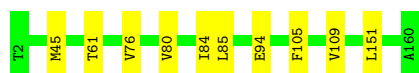


- Molecule 18: Large ribosomal subunit protein eL20



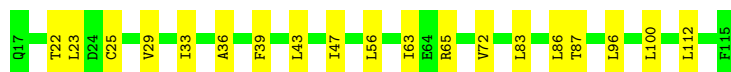
- Molecule 19: Large ribosomal subunit protein eL21





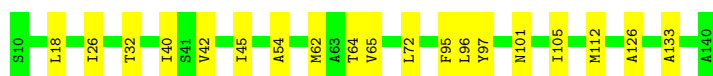
- Molecule 20: 60S ribosomal protein L22

Chain U: 81% 19%



- Molecule 21: Large ribosomal subunit protein uL14

Chain V: 85% 15%



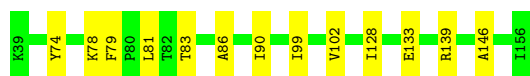
- Molecule 22: Ribosomal protein L19

Chain W: 94% 6%



- Molecule 23: Large ribosomal subunit protein uL23

Chain X: 89% 11%



- Molecule 24: 60S ribosomal protein L26

Chain Y: 89% 11%



- Molecule 25: 60S ribosomal protein L27

Chain Z: 88% 12%



- Molecule 26: 60S ribosomal protein L27a

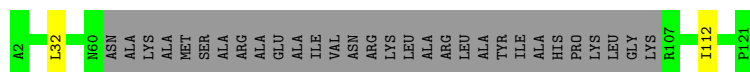
Chain a: 92% 8%





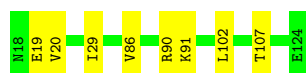
- Molecule 27: 60S ribosomal protein L29

Chain b: 69% 29%



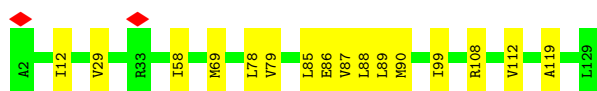
- Molecule 28: Large ribosomal subunit protein eL31

Chain d: 93% 7%



- Molecule 29: 60S ribosomal protein L32

Chain e: 88% 12%



- Molecule 30: Large ribosomal subunit protein eL33

Chain f: 83% 15%



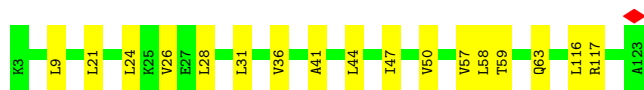
- Molecule 31: Large ribosomal subunit protein eL34

Chain g: 96%



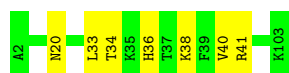
- Molecule 32: Large ribosomal subunit protein uL29

Chain h: 86% 14%



- Molecule 33: 60S ribosomal protein L36

Chain i: 93% 7%



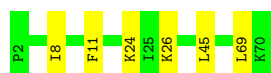
- Molecule 34: Ribosomal protein L37

Chain j: 95% 5%



- Molecule 35: Large ribosomal subunit protein eL38

Chain k: 91% 9%



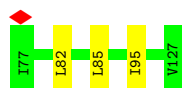
- Molecule 36: 60S ribosomal protein L39

Chain l: 94% 6%



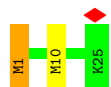
- Molecule 37: Ubiquitin-ribosomal protein eL40 fusion protein

Chain m: 94% 6%



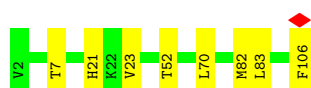
- Molecule 38: 60S ribosomal protein L41

Chain n: 92% 8%



- Molecule 39: 60S ribosomal protein L36a

Chain o: 92% 8%



- Molecule 40: Large ribosomal subunit protein eL43

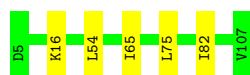
Chain p: 84% 16%



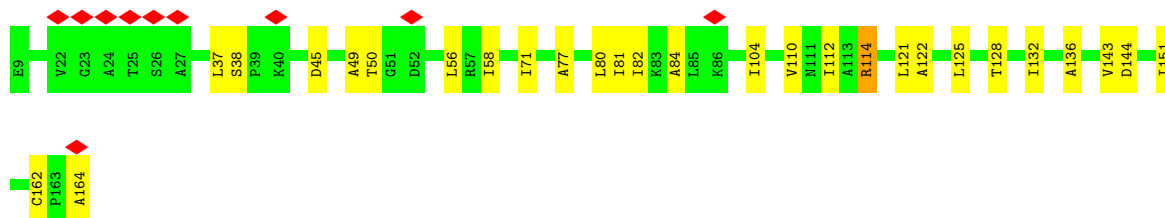
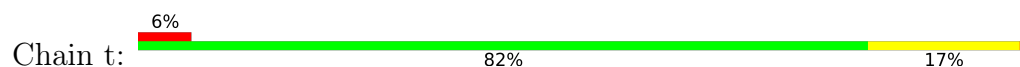
- Molecule 41: Large ribosomal subunit protein eL28



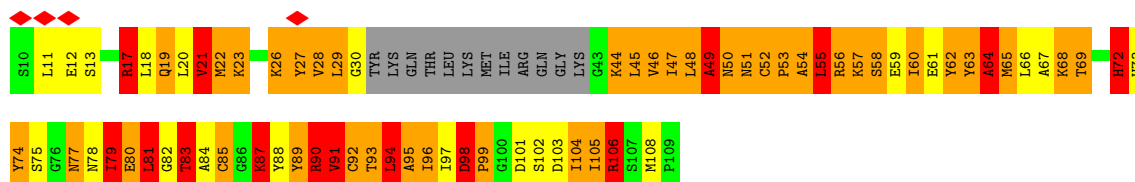
- Molecule 42: 60S acidic ribosomal protein P0



- Molecule 43: 60S ribosomal protein L12



- Molecule 44: Large ribosomal subunit protein eL30



- Molecule 45: 40S ribosomal protein S27



- Molecule 46: 40S ribosomal protein S30

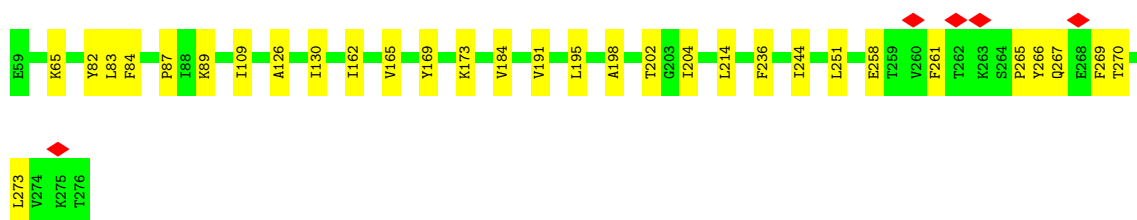
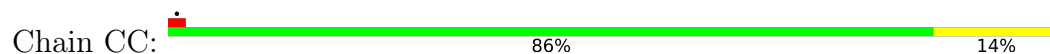




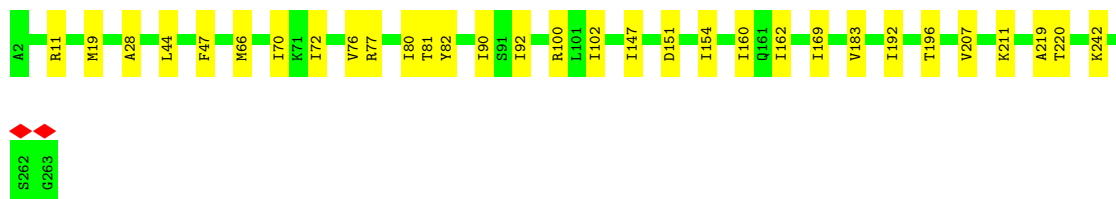
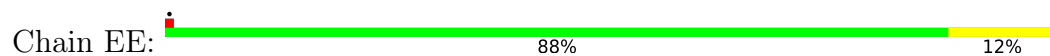
- Molecule 47: 40S ribosomal protein S26



- Molecule 48: 40S ribosomal protein S2



- Molecule 49: 40S ribosomal protein S4, X isoform



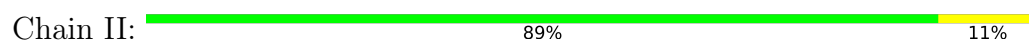
- Molecule 50: 40S ribosomal protein S6



- Molecule 51: 40S ribosomal protein S7



- Molecule 52: 40S ribosomal protein S8





- Molecule 53: Small ribosomal subunit protein uS4

Chain JJ: 91% 9%



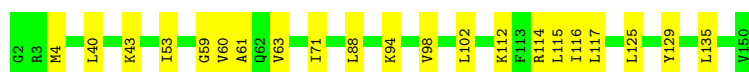
- Molecule 54: Small ribosomal subunit protein uS17

Chain LL: 86% 9% 5%



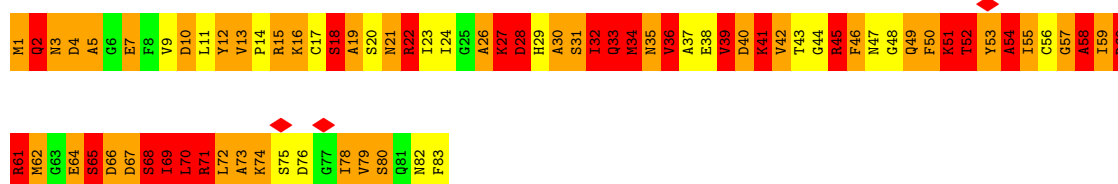
- Molecule 55: Small ribosomal subunit protein uS15

Chain NN: 86% 14%



- Molecule 56: 40S ribosomal protein S21

Chain VV: 7% 23% 42% 28%



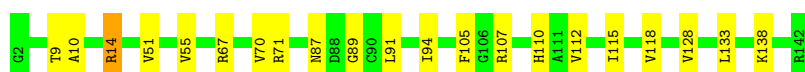
- Molecule 57: Small ribosomal subunit protein uS8

Chain WW: 81% 19%



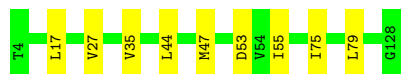
- Molecule 58: Small ribosomal subunit protein uS12

Chain XX: 85% 14%




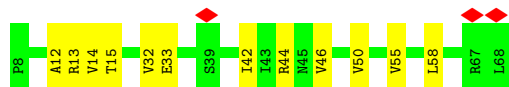
- Molecule 59: 40S ribosomal protein S24

Chain YY:  93% 7%



- Molecule 60: 40S ribosomal protein S28

Chain cc:  5% 80% 20%




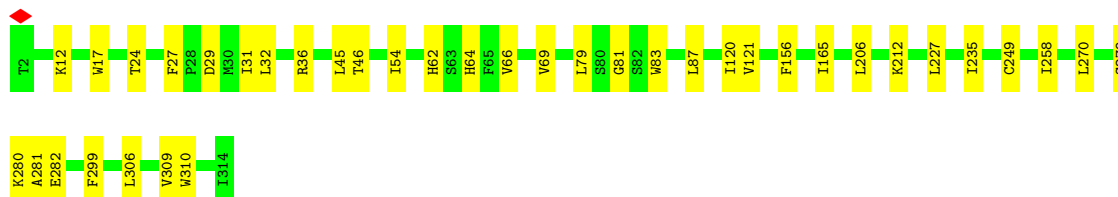
- Molecule 61: Ubiquitin-ribosomal protein eS31 fusion protein

Chain ff:  97% .



- Molecule 62: Small ribosomal subunit protein RACK1

Chain gg:  88% 12%



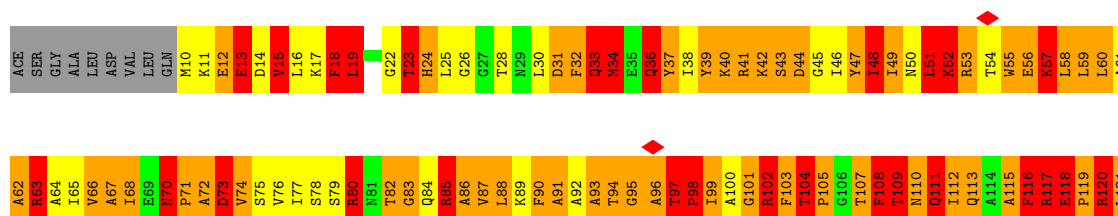
- Molecule 63: Small ribosomal subunit protein uS14

Chain dd:  91% 9%



- Molecule 64: Small ribosomal subunit protein uS2

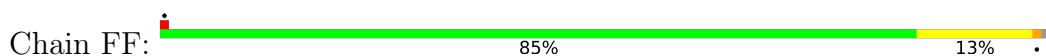
Chain AA:  6% 18% 45% 27% .



- Molecule 65: Small ribosomal subunit protein uS3



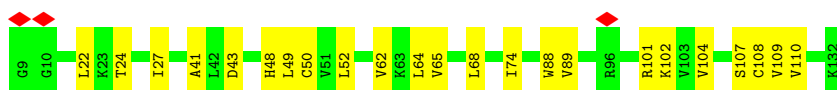
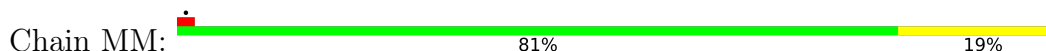
- Molecule 66: Small ribosomal subunit protein uS7



- Molecule 67: Small ribosomal subunit protein eS10



- Molecule 68: 40S ribosomal protein S12



- Molecule 69: 40S ribosomal protein S15

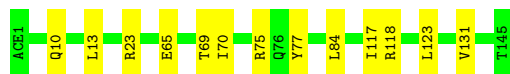


- Molecule 70: Small ribosomal subunit protein uS9



- Molecule 71: Small ribosomal subunit protein uS13

Chain SS:  91% 9%



- Molecule 72: Small ribosomal subunit protein eS19

Chain TT:  92% 8%



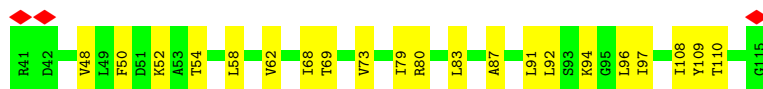
- Molecule 73: 40S ribosomal protein S20

Chain UU:  91% 9%




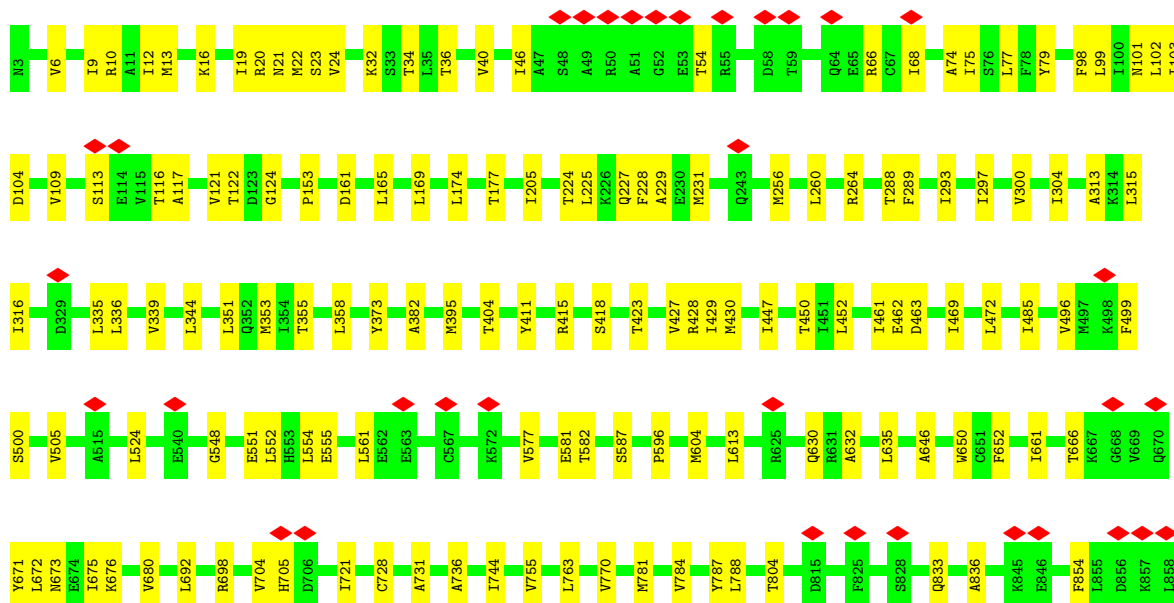
- Molecule 74: 40S ribosomal protein S25

Chain ZZ:  72% 28%



- Molecule 75: eEF2

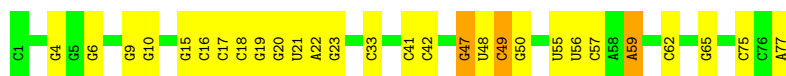
Chain EF:  83% 17%





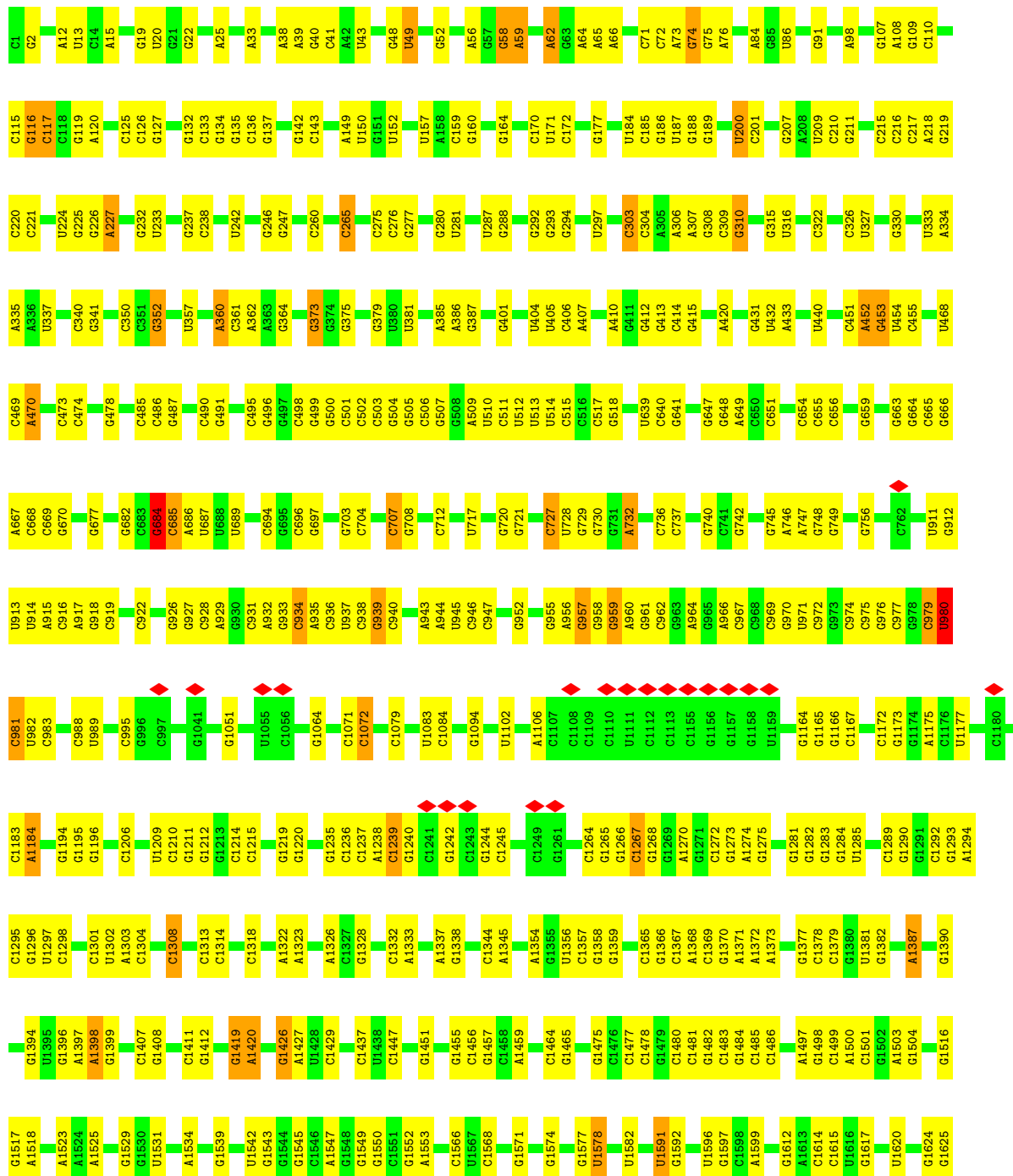
• Molecule 76: P/E tRNA (77-MER)

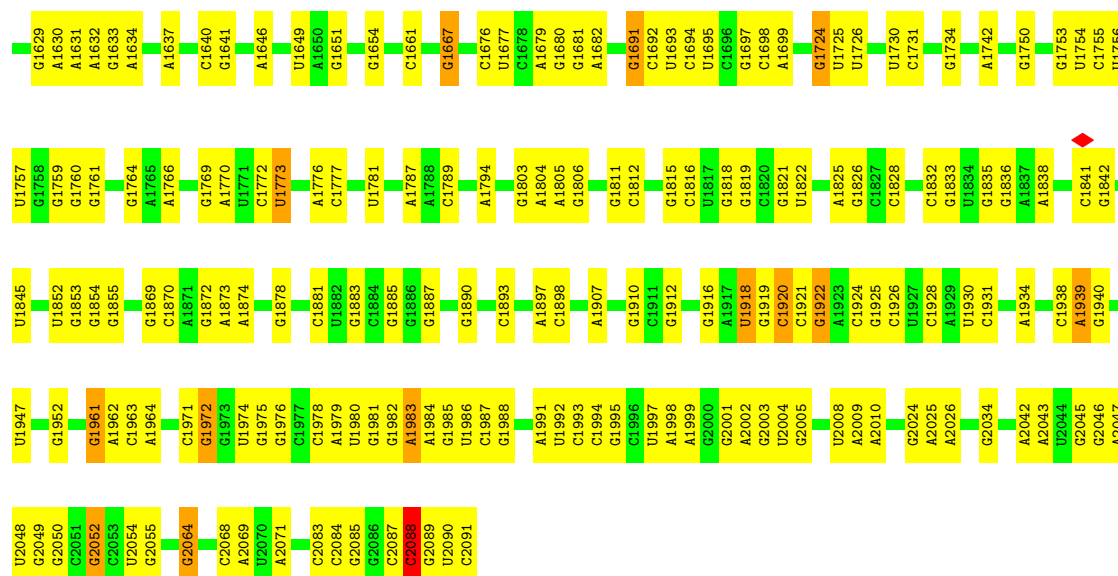
Chain Cc:  64% 32%



• Molecule 77: LSU alpha rRNA

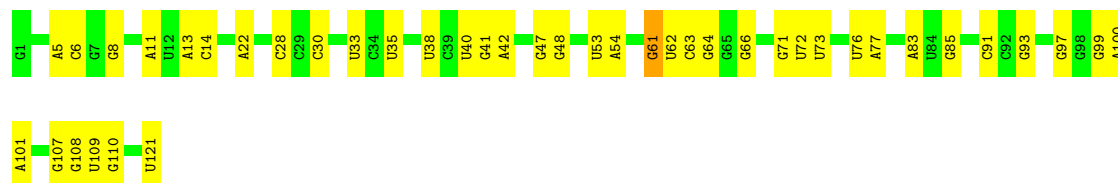
Chain A5:  62% 35%





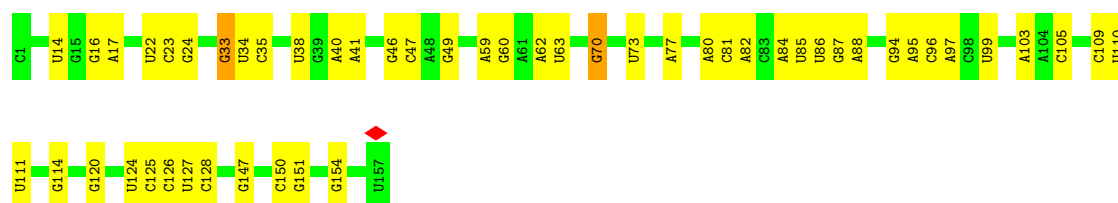
• Molecule 78: 5S ribosomal RNA

Chain A7: 65% 34% .



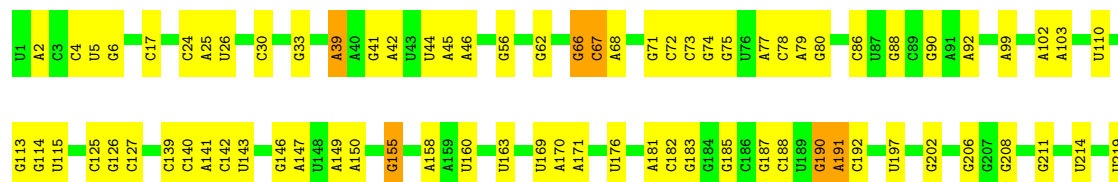
• Molecule 79: 5.8S ribosomal RNA

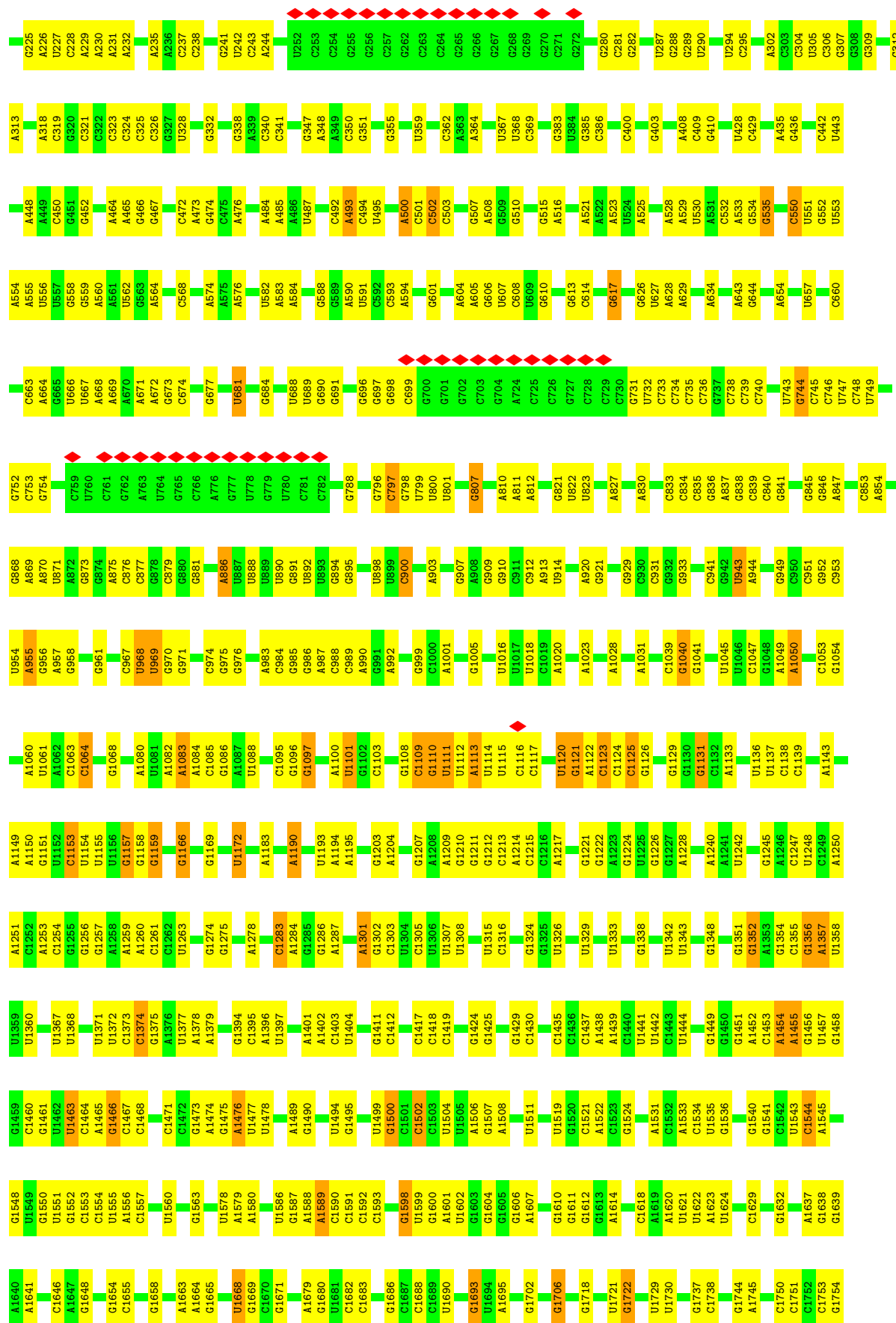
Chain A8: 68% 31% .

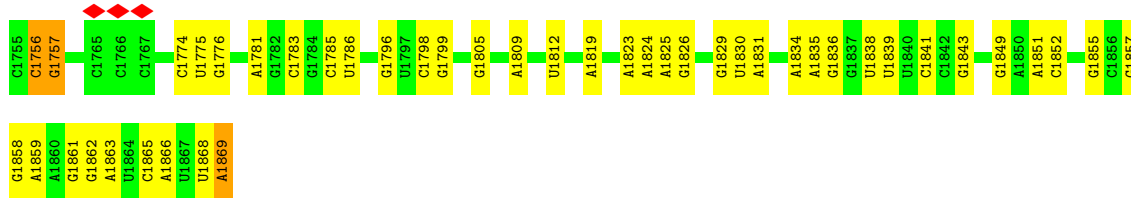


• Molecule 80: 18S ribosomal RNA

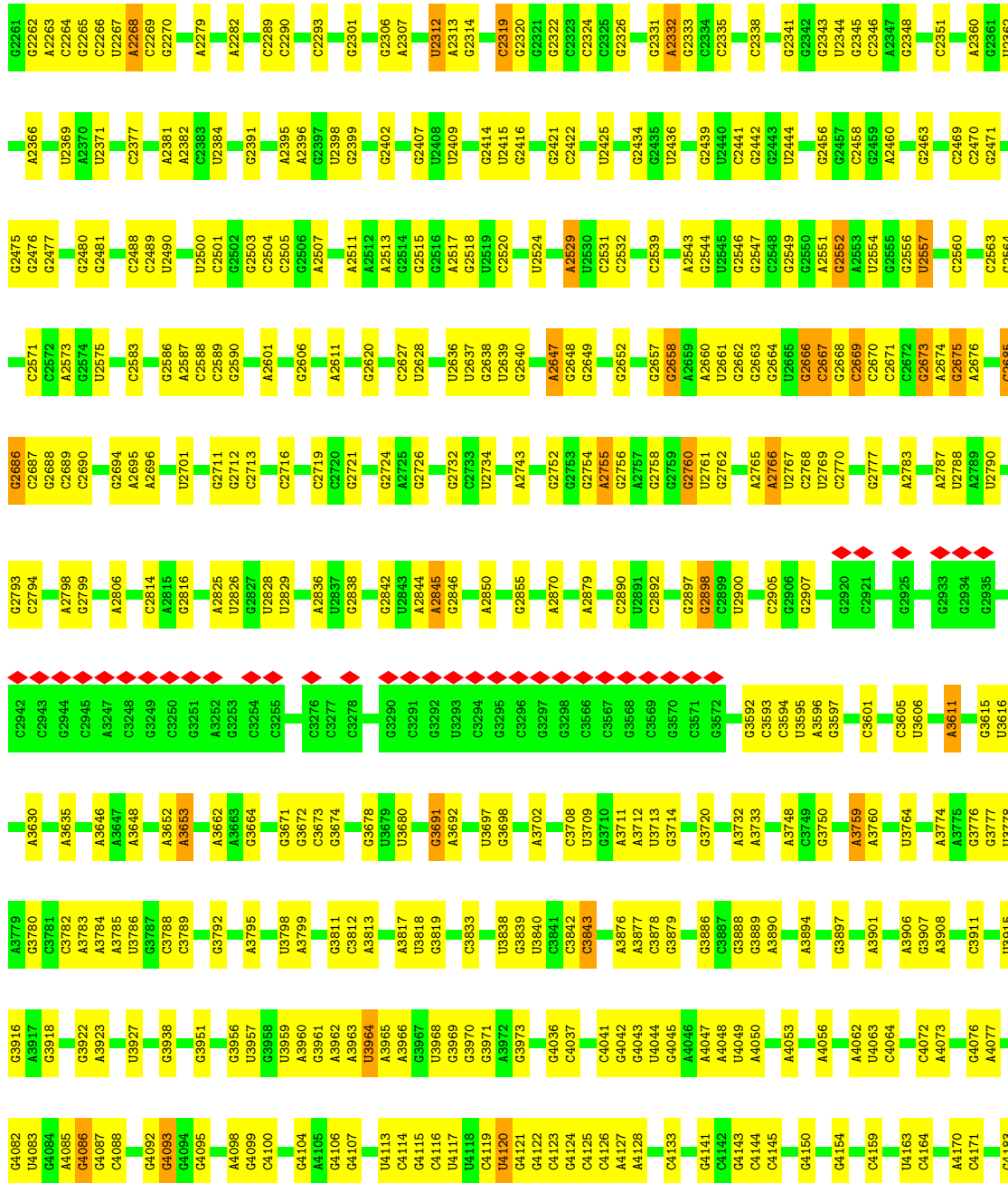
Chain B2: 62% 35% .

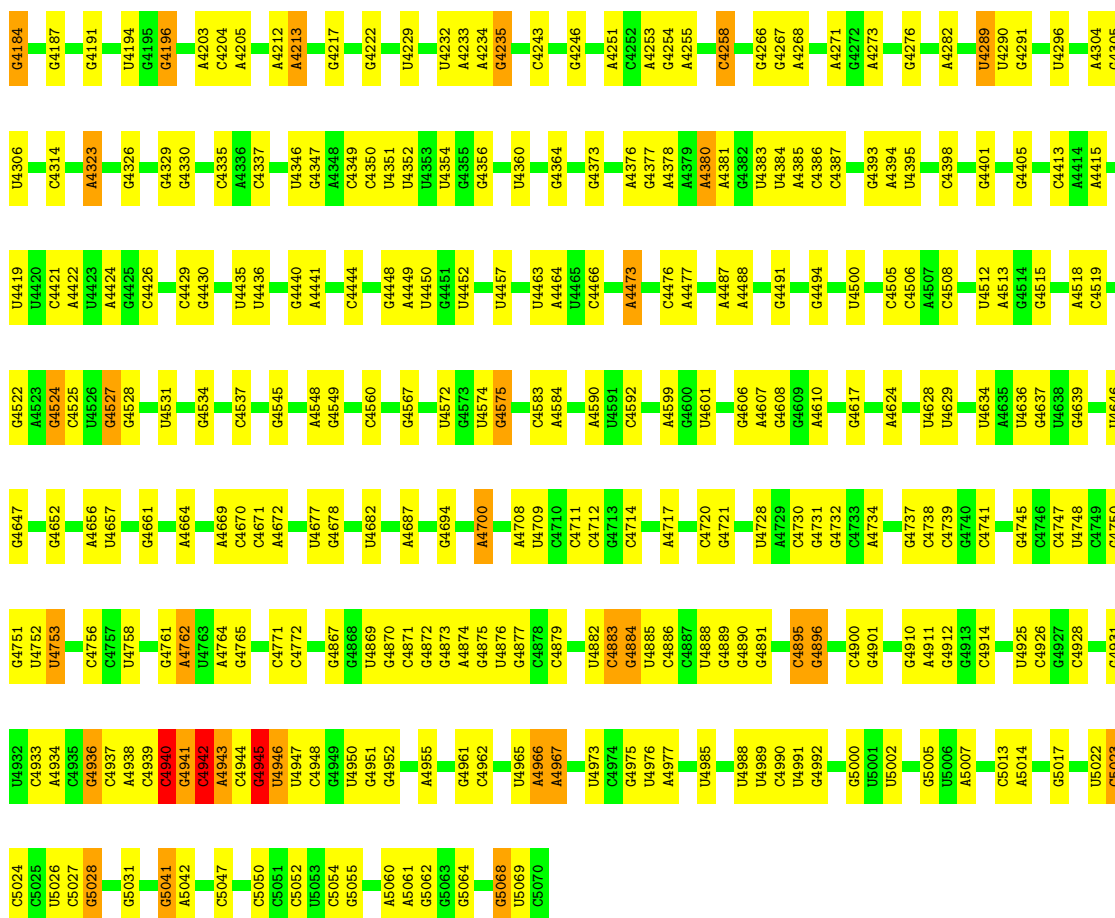






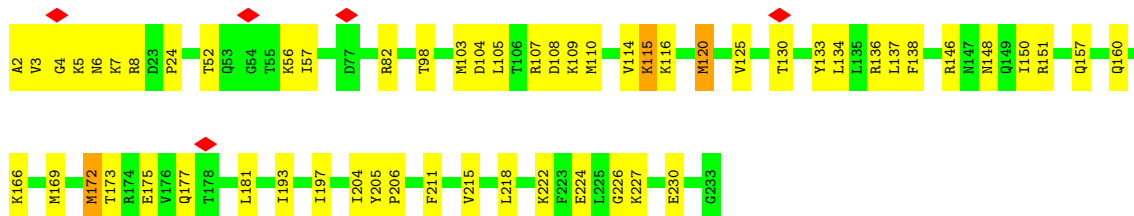
• Molecule 81: LSU beta rRNA





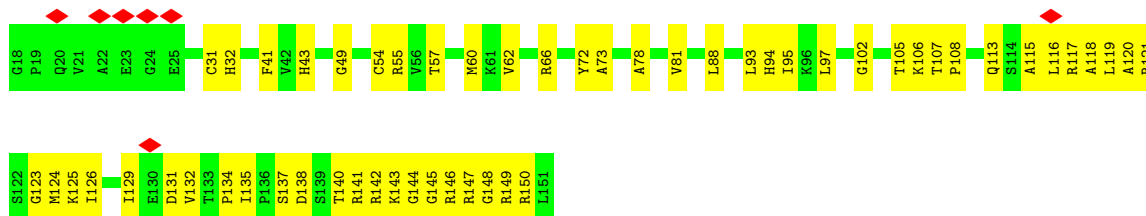
• Molecule 82: 40S ribosomal protein S3a

Chain BB: 74% 25%

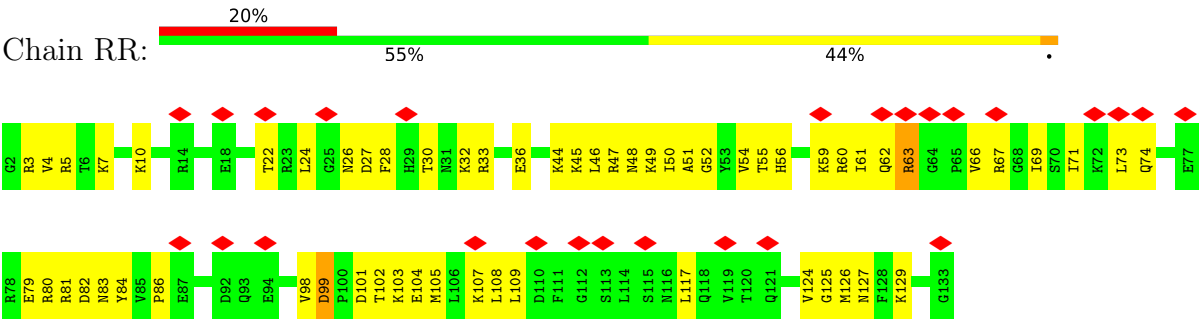


• Molecule 83: 40S ribosomal protein S14

Chain OO: 5% 59% 41%



• Molecule 84: Small ribosomal subunit protein eS17



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	Not provided	
Resolution determination method	Not provided	
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.059	Depositor
Minimum map value	-0.020	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	459.8, 459.8, 459.8	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HIC, MG, ACE, M3L, V5N, NMM, MLZ, 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	A	0.22	0/1936	0.48	0/2596
2	B	0.20	0/3261	0.47	0/4364
3	C	0.21	0/2948	0.45	0/3959
4	c	0.24	0/952	0.50	0/1262
5	D	0.21	0/2435	0.47	0/3261
6	E	2.87	8/1822 (0.4%)	1.05	11/2442 (0.5%)
7	F	0.22	0/1911	0.51	0/2549
8	G	0.22	0/1772	0.49	0/2387
9	H	0.22	0/1535	0.45	0/2063
10	I	0.20	0/1658	0.45	0/2214
11	J	0.20	0/1385	0.47	0/1852
12	L	0.20	0/1689	0.46	0/2261
13	M	0.20	0/1146	0.43	0/1531
14	N	0.21	0/1746	0.46	0/2338
15	O	0.24	0/1662	0.52	1/2222 (0.0%)
16	P	0.23	0/1268	0.51	0/1700
17	Q	0.19	0/1537	0.46	0/2052
18	S	0.20	0/1501	0.44	0/2013
19	T	0.22	0/1326	0.50	0/1770
20	U	0.21	0/822	0.51	0/1103
21	V	0.24	0/986	0.58	1/1323 (0.1%)
22	W	0.26	0/1524	0.61	0/2013
23	X	0.20	0/984	0.41	0/1323
24	Y	0.25	0/1132	0.50	0/1504
25	Z	0.18	0/1130	0.41	0/1507
26	a	0.17	0/1179	0.41	0/1572
27	b	0.21	0/619	0.50	0/814
28	d	0.22	0/903	0.47	0/1216
29	e	0.21	0/1071	0.47	0/1429
30	f	2.83	4/903 (0.4%)	1.02	6/1208 (0.5%)
31	g	0.19	0/883	0.45	0/1177
32	h	0.22	0/1019	0.51	0/1344



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	i	0.20	0/841	0.51	0/1112
34	j	0.21	0/720	0.50	0/952
35	k	0.20	0/575	0.42	0/761
36	l	0.21	0/459	0.50	0/608
37	m	0.23	0/416	0.55	0/553
38	n	0.28	0/240	0.58	0/305
39	o	0.19	0/866	0.43	0/1141
40	p	0.23	0/718	0.51	0/953
41	r	0.25	0/1028	0.54	0/1377
42	s	0.22	0/837	0.50	0/1121
43	t	0.28	0/1193	0.57	0/1609
44	u	1.58	12/681 (1.8%)	2.72	69/916 (7.5%)
45	bb	0.17	0/653	0.42	0/876
46	ee	0.22	0/399	0.55	0/520
47	aa	0.26	0/794	0.58	0/1065
48	CC	0.23	0/1721	0.46	0/2328
49	EE	0.19	0/2118	0.42	0/2849
50	GG	0.20	0/1871	0.46	0/2492
51	HH	0.19	0/1511	0.40	0/2023
52	II	0.18	0/1715	0.41	0/2287
53	JJ	0.18	0/1524	0.40	0/2035
54	LL	0.28	0/1177	0.52	0/1575
55	NN	0.22	0/1226	0.45	0/1649
56	VV	1.68	16/644 (2.5%)	3.01	88/862 (10.2%)
57	WW	0.21	0/1051	0.50	0/1406
58	XX	0.23	0/1115	0.51	0/1486
59	YY	0.18	0/1032	0.45	0/1371
60	cc	0.23	0/481	0.53	0/643
61	ff	0.22	0/560	0.52	0/745
62	gg	0.20	0/2493	0.48	0/3394
63	dd	0.27	0/470	0.62	0/623
64	AA	1.64	29/1662 (1.7%)	3.25	271/2259 (12.0%)
65	DD	0.20	0/1779	0.43	0/2395
66	FF	0.21	0/1495	0.50	0/2008
67	KK	0.28	0/834	0.57	0/1125
68	MM	0.22	0/968	0.52	1/1296 (0.1%)
69	PP	0.21	0/997	0.46	0/1330
70	QQ	0.21	0/1142	0.50	0/1528
71	SS	0.21	0/1209	0.47	0/1620
72	TT	0.21	0/1102	0.49	0/1476
73	UU	0.20	0/800	0.51	0/1074
74	ZZ	0.31	0/604	0.59	0/810
75	EF	0.24	0/6800	0.55	0/9184

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	Cc	0.17	0/1836	0.37	0/2859
77	A5	0.78	11/40680 (0.0%)	0.45	9/63377 (0.0%)
78	A7	0.18	0/2880	0.37	0/4489
79	A8	0.18	0/3723	0.41	0/5800
80	B2	0.18	0/42627	0.42	0/66334
81	A6	0.75	13/48903 (0.0%)	0.42	3/76100 (0.0%)
82	BB	1.60	2/1794 (0.1%)	0.74	4/2396 (0.2%)
83	OO	0.22	0/1015	0.53	0/1361
84	RR	0.28	0/1082	0.63	0/1452
All	All	0.62	95/241706 (0.0%)	0.57	464/354279 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	C	0	1
4	c	0	2
6	E	0	1
12	L	0	2
23	X	0	1
26	a	0	2
30	f	0	1
38	n	0	1
43	t	0	1
44	u	0	4
47	aa	0	2
50	GG	0	1
56	VV	0	14
58	XX	0	1
63	dd	0	1
64	AA	0	19
66	FF	0	1
75	EF	0	1
81	A6	1	0
All	All	1	56

The worst 5 of 95 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	E	104	ASN	CA-C	105.00	2.49	1.53

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	f	58	VAL	CA-CB	82.92	2.67	1.54
82	BB	115	LYS	CA-CB	66.18	2.48	1.53
77	A5	684	G	O4'-C1'	61.83	2.65	1.41
77	A5	980	U	C4'-O4'	59.57	2.64	1.45

The worst 5 of 464 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
64	AA	152	SER	N-CA-C	18.92	125.25	108.22
6	E	104	ASN	O-C-N	-18.12	102.81	122.38
6	E	221	LYS	N-CA-C	-17.89	80.51	108.96
64	AA	182	VAL	N-CA-C	-17.12	93.16	110.62
6	E	104	ASN	N-CA-CB	-16.86	84.43	110.39

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
81	A6	4942	C	C1'

5 of 56 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	95	MET	Peptide
6	E	104	ASN	Peptide
12	L	102	ARG	Peptide
4	c	1	MET	Peptide
4	c	94	ARG	Sidechain

## 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	A	1898	0	1993	15	0
2	B	3206	0	3353	23	0
3	C	2895	0	3064	25	0
4	c	938	0	990	12	0
5	D	2389	0	2423	23	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	E	1789	0	1941	89	0
7	F	1875	0	1995	17	0
8	G	1741	0	1861	10	0
9	H	1516	0	1597	20	0
10	I	1620	0	1663	10	0
11	J	1362	0	1399	17	0
12	L	1658	0	1766	14	0
13	M	1125	0	1198	15	0
14	N	1701	0	1749	8	0
15	O	1630	0	1778	21	0
16	P	1242	0	1274	4	0
17	Q	1512	0	1629	19	0
18	S	1461	0	1502	9	0
19	T	1298	0	1366	6	0
20	U	808	0	831	16	0
21	V	973	0	1032	16	0
22	W	1508	0	1664	10	0
23	X	967	0	1040	11	0
24	Y	1115	0	1205	11	0
25	Z	1107	0	1182	11	0
26	a	1163	0	1202	12	0
27	b	620	0	665	3	0
28	d	888	0	930	5	0
29	e	1053	0	1147	13	0
30	f	884	0	924	47	0
31	g	873	0	964	6	0
32	h	1011	0	1150	14	0
33	i	830	0	916	8	0
34	j	705	0	737	5	0
35	k	569	0	637	4	0
36	l	447	0	480	3	0
37	m	422	0	458	3	0
38	n	239	0	289	2	0
39	o	863	0	929	8	0
40	p	708	0	756	21	0
41	r	1015	0	1085	9	0
42	s	825	0	866	4	0
43	t	1178	0	1235	18	0
44	u	672	0	689	138	0
45	bb	640	0	665	6	0
46	ee	398	0	443	3	0
47	aa	781	0	821	288	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
48	CC	1685	0	1768	53	0
49	EE	2076	0	2177	24	0
50	GG	1848	0	2000	14	0
51	HH	1490	0	1583	10	0
52	II	1686	0	1772	15	0
53	JJ	1499	0	1618	11	0
54	LL	1157	0	1223	13	0
55	NN	1202	0	1289	16	0
56	VV	637	0	630	231	0
57	WW	1034	0	1080	19	0
58	XX	1098	0	1167	19	0
59	YY	1015	0	1086	6	0
60	cc	479	0	507	7	0
61	ff	548	0	552	2	0
62	gg	2436	0	2392	108	0
63	dd	459	0	448	4	0
64	AA	1625	0	1609	572	0
65	DD	1751	0	1846	10	0
66	FF	1475	0	1527	17	0
67	KK	810	0	836	6	0
68	MM	958	0	993	16	0
69	PP	979	0	1029	4	0
70	QQ	1124	0	1193	8	0
71	SS	1193	0	1253	11	0
72	TT	1097	0	1125	7	0
73	UU	790	0	857	6	0
74	ZZ	598	0	656	16	0
75	EF	6669	0	6742	99	0
76	Cc	1644	0	837	5	0
77	A5	36419	0	18340	161	0
78	A7	2578	0	1306	10	0
79	A8	3334	0	1693	11	0
80	B2	38185	0	19135	634	0
81	A6	43819	0	21847	237	0
82	BB	1768	0	1837	277	0
83	OO	1002	0	1009	360	0
84	RR	1068	0	1093	467	0
85	A5	7	0	0	0	0
85	A6	7	0	0	0	0
85	A8	1	0	0	0	0
85	B2	6	0	0	0	0
85	BB	2	0	0	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
85	P	1	0	0	0	0
85	a	1	0	0	0	0
85	l	1	0	0	0	0
86	aa	1	0	0	0	0
86	dd	1	0	0	0	0
86	ff	1	0	0	0	0
86	g	1	0	0	0	0
86	j	1	0	0	0	0
86	m	1	0	0	0	0
86	o	1	0	0	0	0
86	p	1	0	0	0	0
87	A6	1	0	0	0	0
All	All	225388	0	167538	2943	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 8.

The worst 5 of 2943 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)
64:AA:180:ARG:HD2	64:AA:195:TRP:CH2	1.27	1.69
47:aa:29:CYS:SG	83:OO:146:ARG:HA	1.34	1.61
47:aa:67:LEU:HD13	83:OO:108:PRO:CD	1.18	1.59
47:aa:69:VAL:CG2	83:OO:107:THR:H	1.08	1.59
47:aa:67:LEU:HD13	83:OO:108:PRO:CG	1.28	1.58

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	
1	A	246/248 (99%)	228 (93%)	18 (7%)	0	100	100
2	B	395/398 (99%)	361 (91%)	34 (9%)	0	100	100
3	C	361/363 (99%)	348 (96%)	13 (4%)	0	100	100
4	c	111/121 (92%)	104 (94%)	6 (5%)	1 (1%)	14	50
5	D	291/293 (99%)	271 (93%)	20 (7%)	0	100	100
6	E	217/224 (97%)	197 (91%)	20 (9%)	0	100	100
7	F	223/225 (99%)	208 (93%)	15 (7%)	0	100	100
8	G	211/215 (98%)	201 (95%)	10 (5%)	0	100	100
9	H	188/190 (99%)	177 (94%)	11 (6%)	0	100	100
10	I	195/213 (92%)	186 (95%)	9 (5%)	0	100	100
11	J	168/170 (99%)	154 (92%)	14 (8%)	0	100	100
12	L	203/205 (99%)	192 (95%)	11 (5%)	0	100	100
13	M	134/136 (98%)	128 (96%)	6 (4%)	0	100	100
14	N	201/203 (99%)	185 (92%)	16 (8%)	0	100	100
15	O	197/199 (99%)	189 (96%)	8 (4%)	0	100	100
16	P	151/153 (99%)	145 (96%)	6 (4%)	0	100	100
17	Q	185/187 (99%)	171 (92%)	14 (8%)	0	100	100
18	S	174/176 (99%)	165 (95%)	9 (5%)	0	100	100
19	T	157/159 (99%)	148 (94%)	9 (6%)	0	100	100
20	U	97/99 (98%)	95 (98%)	2 (2%)	0	100	100
21	V	129/131 (98%)	115 (89%)	14 (11%)	0	100	100
22	W	178/180 (99%)	173 (97%)	5 (3%)	0	100	100
23	X	116/118 (98%)	107 (92%)	9 (8%)	0	100	100
24	Y	132/134 (98%)	127 (96%)	5 (4%)	0	100	100
25	Z	133/135 (98%)	124 (93%)	9 (7%)	0	100	100
26	a	144/147 (98%)	138 (96%)	6 (4%)	0	100	100
27	b	69/104 (66%)	67 (97%)	2 (3%)	0	100	100
28	d	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
29	e	126/128 (98%)	119 (94%)	7 (6%)	0	100	100
30	f	108/110 (98%)	99 (92%)	9 (8%)	0	100	100
31	g	108/110 (98%)	101 (94%)	7 (6%)	0	100	100
32	h	119/121 (98%)	115 (97%)	4 (3%)	0	100	100

Continued on next page...

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	i	100/102 (98%)	95 (95%)	5 (5%)	0	100	100
34	j	84/86 (98%)	79 (94%)	5 (6%)	0	100	100
35	k	67/69 (97%)	67 (100%)	0	0	100	100
36	l	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
37	m	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
38	n	23/25 (92%)	23 (100%)	0	0	100	100
39	o	102/105 (97%)	93 (91%)	9 (9%)	0	100	100
40	p	89/91 (98%)	82 (92%)	7 (8%)	0	100	100
41	r	125/127 (98%)	116 (93%)	9 (7%)	0	100	100
42	s	101/103 (98%)	94 (93%)	7 (7%)	0	100	100
43	t	154/156 (99%)	140 (91%)	14 (9%)	0	100	100
44	u	84/100 (84%)	81 (96%)	2 (2%)	1 (1%)	10	42
45	bb	80/82 (98%)	75 (94%)	5 (6%)	0	100	100
46	ee	45/49 (92%)	43 (96%)	2 (4%)	0	100	100
47	aa	96/98 (98%)	79 (82%)	17 (18%)	0	100	100
48	CC	216/218 (99%)	199 (92%)	17 (8%)	0	100	100
49	EE	260/262 (99%)	249 (96%)	11 (4%)	0	100	100
50	GG	226/228 (99%)	212 (94%)	14 (6%)	0	100	100
51	HH	178/190 (94%)	167 (94%)	11 (6%)	0	100	100
52	II	204/206 (99%)	199 (98%)	5 (2%)	0	100	100
53	JJ	178/180 (99%)	173 (97%)	5 (3%)	0	100	100
54	LL	137/149 (92%)	131 (96%)	6 (4%)	0	100	100
55	NN	147/149 (99%)	140 (95%)	7 (5%)	0	100	100
56	VV	81/83 (98%)	68 (84%)	11 (14%)	2 (2%)	4	25
57	WW	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
58	XX	137/141 (97%)	125 (91%)	11 (8%)	1 (1%)	18	55
59	YY	123/125 (98%)	117 (95%)	6 (5%)	0	100	100
60	cc	59/61 (97%)	53 (90%)	6 (10%)	0	100	100
61	ff	65/67 (97%)	60 (92%)	5 (8%)	0	100	100
62	gg	311/313 (99%)	276 (89%)	35 (11%)	0	100	100
63	dd	53/55 (96%)	51 (96%)	2 (4%)	0	100	100

*Continued on next page...*



Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
64	AA	203/214 (95%)	179 (88%)	17 (8%)	7 (3%)	3	20
65	DD	223/225 (99%)	211 (95%)	12 (5%)	0	100	100
66	FF	182/189 (96%)	175 (96%)	7 (4%)	0	100	100
67	KK	94/96 (98%)	87 (93%)	7 (7%)	0	100	100
68	MM	122/124 (98%)	111 (91%)	11 (9%)	0	100	100
69	PP	116/118 (98%)	107 (92%)	9 (8%)	0	100	100
70	QQ	139/141 (99%)	124 (89%)	15 (11%)	0	100	100
71	SS	143/145 (99%)	131 (92%)	12 (8%)	0	100	100
72	TT	138/141 (98%)	131 (95%)	6 (4%)	1 (1%)	18	55
73	UU	97/99 (98%)	95 (98%)	2 (2%)	0	100	100
74	ZZ	73/75 (97%)	69 (94%)	4 (6%)	0	100	100
75	EF	854/856 (100%)	743 (87%)	109 (13%)	2 (0%)	43	77
82	BB	214/218 (98%)	204 (95%)	10 (5%)	0	100	100
83	OO	132/134 (98%)	122 (92%)	10 (8%)	0	100	100
84	RR	130/132 (98%)	124 (95%)	6 (5%)	0	100	100
All	All	12180/12459 (98%)	11346 (93%)	819 (7%)	15 (0%)	49	83

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
64	AA	98	PRO
64	AA	155	ARG
64	AA	162	PRO
64	AA	198	MET
56	VV	80	SER

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	190/190 (100%)	190 (100%)	0	100	100

Continued on next page...

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	344/344 (100%)	344 (100%)	0	100	100
3	C	303/303 (100%)	303 (100%)	0	100	100
4	c	94/100 (94%)	94 (100%)	0	100	100
5	D	247/247 (100%)	247 (100%)	0	100	100
6	E	197/197 (100%)	197 (100%)	0	100	100
7	F	196/196 (100%)	196 (100%)	0	100	100
8	G	187/187 (100%)	187 (100%)	0	100	100
9	H	169/169 (100%)	169 (100%)	0	100	100
10	I	170/180 (94%)	170 (100%)	0	100	100
11	J	143/143 (100%)	143 (100%)	0	100	100
12	L	170/170 (100%)	170 (100%)	0	100	100
13	M	116/116 (100%)	116 (100%)	0	100	100
14	N	171/171 (100%)	171 (100%)	0	100	100
15	O	171/171 (100%)	171 (100%)	0	100	100
16	P	134/134 (100%)	134 (100%)	0	100	100
17	Q	164/164 (100%)	164 (100%)	0	100	100
18	S	157/157 (100%)	157 (100%)	0	100	100
19	T	139/139 (100%)	139 (100%)	0	100	100
20	U	89/89 (100%)	89 (100%)	0	100	100
21	V	100/101 (99%)	100 (100%)	0	100	100
22	W	159/159 (100%)	159 (100%)	0	100	100
23	X	106/106 (100%)	106 (100%)	0	100	100
24	Y	124/124 (100%)	124 (100%)	0	100	100
25	Z	117/117 (100%)	117 (100%)	0	100	100
26	a	118/118 (100%)	118 (100%)	0	100	100
27	b	63/84 (75%)	63 (100%)	0	100	100
28	d	98/98 (100%)	98 (100%)	0	100	100
29	e	114/114 (100%)	114 (100%)	0	100	100
30	f	89/89 (100%)	89 (100%)	0	100	100
31	g	94/94 (100%)	94 (100%)	0	100	100
32	h	109/109 (100%)	109 (100%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	i	86/86 (100%)	86 (100%)	0	100	100
34	j	73/73 (100%)	73 (100%)	0	100	100
35	k	64/64 (100%)	64 (100%)	0	100	100
36	l	47/47 (100%)	47 (100%)	0	100	100
37	m	46/46 (100%)	46 (100%)	0	100	100
38	n	24/24 (100%)	24 (100%)	0	100	100
39	o	92/92 (100%)	92 (100%)	0	100	100
40	p	74/74 (100%)	74 (100%)	0	100	100
41	r	110/110 (100%)	110 (100%)	0	100	100
42	s	90/90 (100%)	90 (100%)	0	100	100
43	t	128/128 (100%)	128 (100%)	0	100	100
44	u	74/85 (87%)	39 (53%)	35 (47%)	0	0
45	bb	74/74 (100%)	74 (100%)	0	100	100
46	ee	41/41 (100%)	41 (100%)	0	100	100
47	aa	85/85 (100%)	85 (100%)	0	100	100
48	CC	182/183 (100%)	182 (100%)	0	100	100
49	EE	224/224 (100%)	224 (100%)	0	100	100
50	GG	199/199 (100%)	199 (100%)	0	100	100
51	HH	167/170 (98%)	167 (100%)	0	100	100
52	II	178/178 (100%)	178 (100%)	0	100	100
53	JJ	160/160 (100%)	160 (100%)	0	100	100
54	LL	128/134 (96%)	128 (100%)	0	100	100
55	NN	130/130 (100%)	130 (100%)	0	100	100
56	VV	68/68 (100%)	45 (66%)	23 (34%)	0	2
57	WW	112/112 (100%)	112 (100%)	0	100	100
58	XX	113/113 (100%)	113 (100%)	0	100	100
59	YY	107/107 (100%)	107 (100%)	0	100	100
60	cc	54/54 (100%)	54 (100%)	0	100	100
61	ff	60/60 (100%)	60 (100%)	0	100	100
62	gg	272/272 (100%)	272 (100%)	0	100	100
63	dd	48/48 (100%)	48 (100%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
64	AA	172/179 (96%)	96 (56%)	76 (44%)	0	0
65	DD	189/189 (100%)	189 (100%)	0	100	100
66	FF	158/159 (99%)	158 (100%)	0	100	100
67	KK	87/87 (100%)	87 (100%)	0	100	100
68	MM	104/104 (100%)	104 (100%)	0	100	100
69	PP	107/107 (100%)	107 (100%)	0	100	100
70	QQ	117/117 (100%)	117 (100%)	0	100	100
71	SS	125/125 (100%)	125 (100%)	0	100	100
72	TT	110/110 (100%)	110 (100%)	0	100	100
73	UU	92/92 (100%)	92 (100%)	0	100	100
74	ZZ	66/66 (100%)	66 (100%)	0	100	100
75	EF	727/728 (100%)	727 (100%)	0	100	100
82	BB	197/197 (100%)	192 (98%)	5 (2%)	42	62
83	OO	104/104 (100%)	102 (98%)	2 (2%)	50	66
84	RR	119/119 (100%)	115 (97%)	4 (3%)	32	54
All	All	10626/10694 (99%)	10481 (99%)	145 (1%)	57	72

5 of 145 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
64	AA	169	HIS
84	RR	99	ASP
64	AA	178	LEU
64	AA	209	GLU
56	VV	45	ARG

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

Mol	Chain	Res	Type
52	II	88	ASN
56	VV	81	GLN
82	BB	158	HIS
52	II	165	GLN
56	VV	21	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
76	Cc	76/77 (98%)	25 (32%)	0
77	A5	1668/1732 (96%)	582 (34%)	82 (4%)
78	A7	120/121 (99%)	29 (24%)	1 (0%)
79	A8	156/157 (99%)	46 (29%)	5 (3%)
80	B2	1756/1837 (95%)	581 (33%)	53 (3%)
81	A6	1995/2122 (94%)	607 (30%)	56 (2%)
All	All	5771/6046 (95%)	1870 (32%)	197 (3%)

5 of 1870 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
76	Cc	4	G
76	Cc	6	G
76	Cc	9	G
76	Cc	10	G
76	Cc	16	C

5 of 197 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
80	B2	869	A
81	A6	2266	C
80	B2	1283	C
80	B2	1556	A
81	A6	2517	A

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

6 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
39	MLZ	o	53	39	8,9,10	0.77	0	4,9,11	0.52	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
27	MLZ	b	5	27	8,9,10	0.79	0	4,9,11	0.62	0
72	NMM	TT	67	72	8,11,12	0.76	0	7,12,14	1.21	1 (14%)
37	M3L	m	98	37	10,11,12	0.40	0	9,14,16	0.32	0
26	V5N	a	39	26	8,11,12	0.57	0	8,14,16	1.00	0
2	HIC	B	245	2	10,11,12	0.52	0	9,14,16	0.61	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	MLZ	o	53	39	-	2/7/8/10	-
27	MLZ	b	5	27	-	2/7/8/10	-
72	NMM	TT	67	72	-	0/9/11/13	-
37	M3L	m	98	37	-	0/9/10/12	-
26	V5N	a	39	26	-	4/9/10/12	0/1/1/1
2	HIC	B	245	2	-	0/5/6/8	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
72	TT	67	NMM	NE-CZ-NH1	2.09	124.10	120.26

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
39	o	53	MLZ	CD-CE-NZ-CM
26	a	39	V5N	O-C-CA-CB
26	a	39	V5N	C-CA-CB-CG
26	a	39	V5N	C-CA-CB-O2
27	b	5	MLZ	N-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 34 ligands modelled in this entry, 34 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
77	A5	9
81	A6	4
6	E	3
80	B2	3
82	BB	1
8	G	1
46	ee	1
58	XX	1

The worst 5 of 23 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A5	1703:C	O3'	1720:C	P	20.34
1	E	78:ALA	C	90:LYS	N	20.05
1	BB	8:ARG	C	23:ASP	N	19.98
1	B2	704:G	O3'	724:A	P	19.89
1	B2	766:C	O3'	776:A	P	18.72

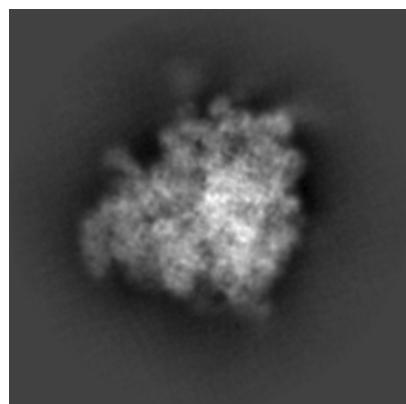
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72469. These allow visual inspection of the internal detail of the map and identification of artifacts.

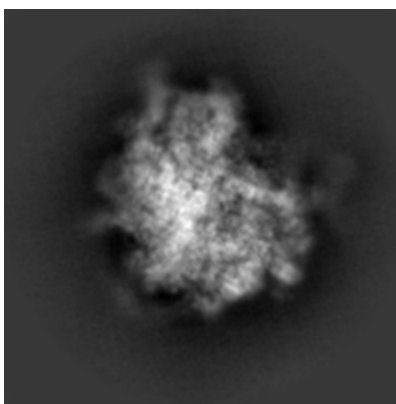
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

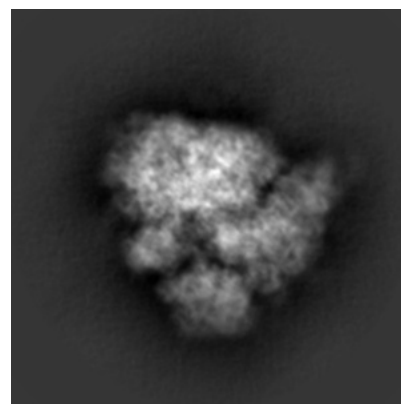
#### 6.1.1 Primary map



X

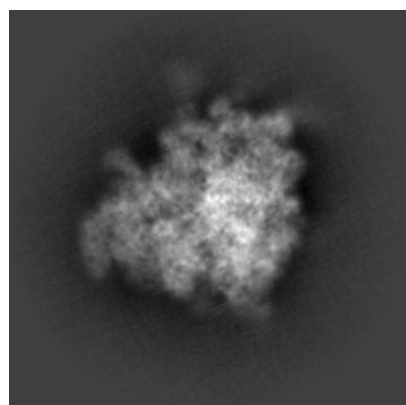


Y

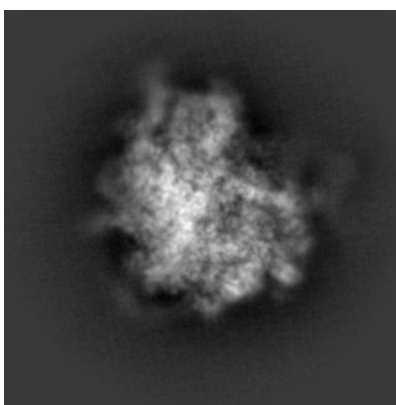


Z

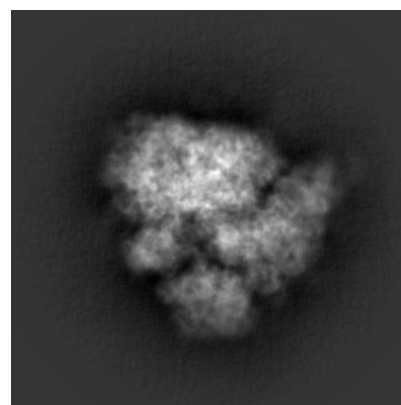
#### 6.1.2 Raw map



X



Y



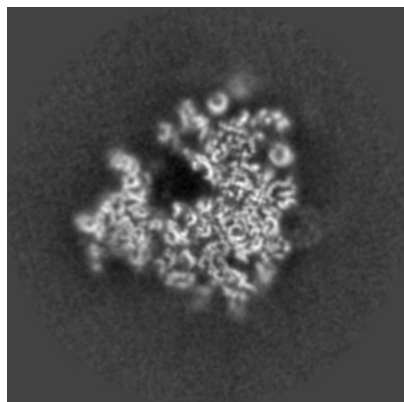
Z

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

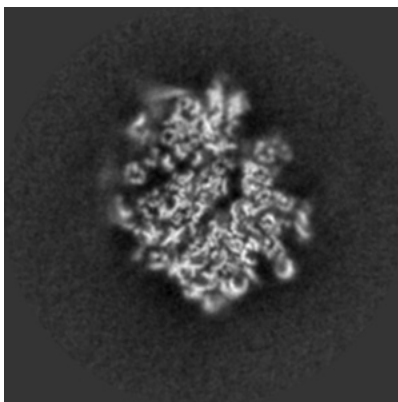


## 6.2 Central slices [i](#)

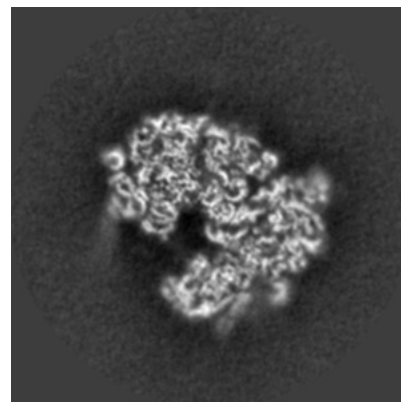
### 6.2.1 Primary map



X Index: 220

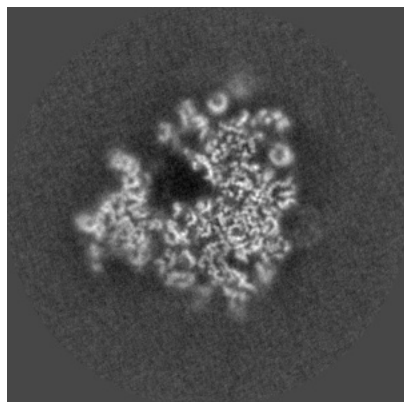


Y Index: 220

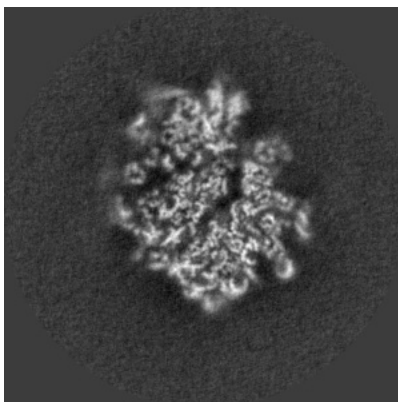


Z Index: 220

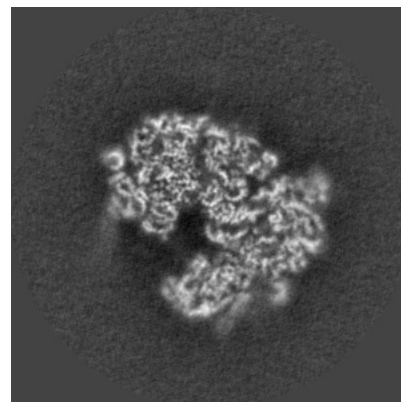
### 6.2.2 Raw map



X Index: 220



Y Index: 220

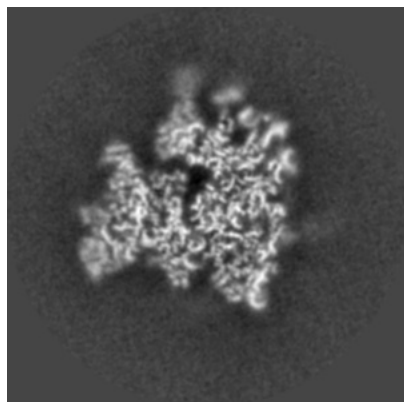


Z Index: 220

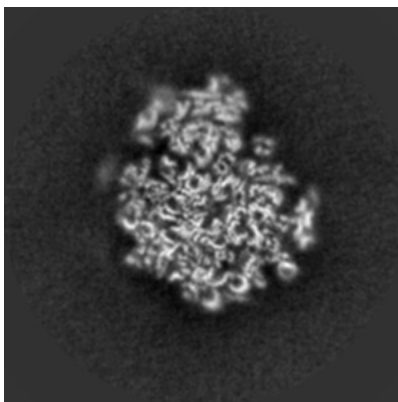
The images above show central slices of the map in three orthogonal directions.

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

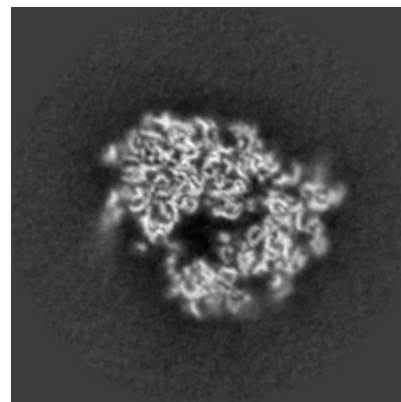
### 6.3.1 Primary map



X Index: 236

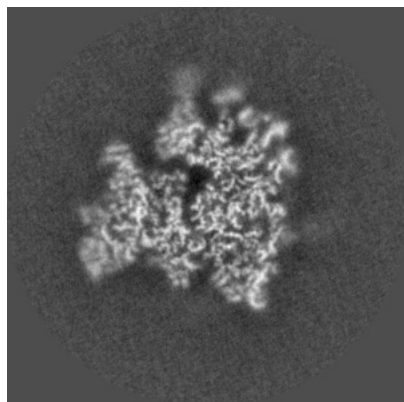


Y Index: 228

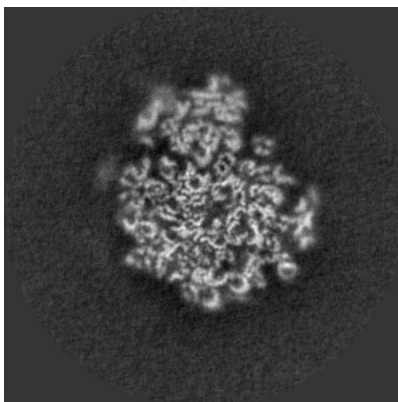


Z Index: 229

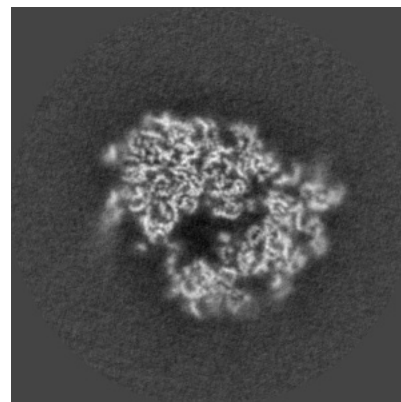
### 6.3.2 Raw map



X Index: 236



Y Index: 229

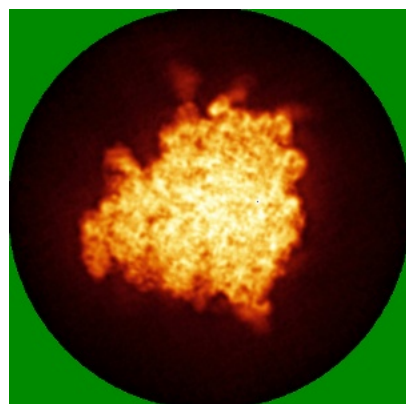


Z Index: 229

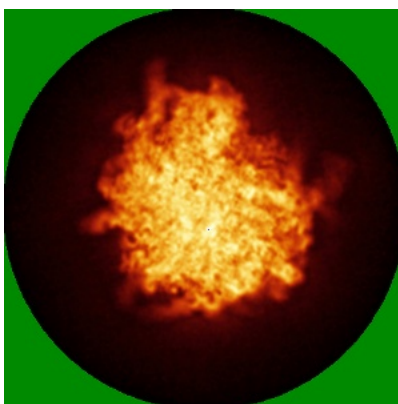
The images above show the largest variance slices of the map in three orthogonal directions.

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

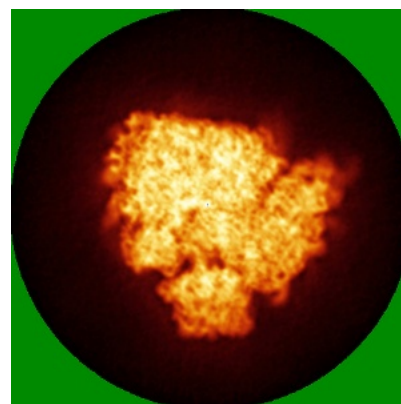
### 6.4.1 Primary map



X

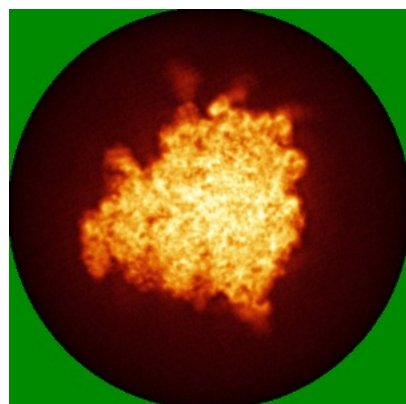


Y

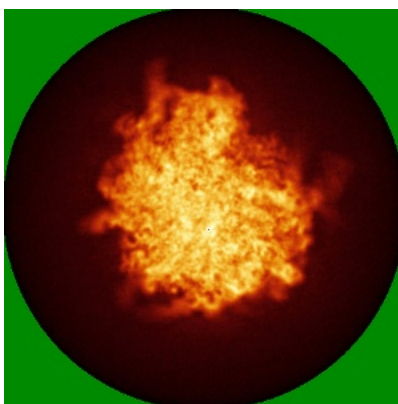


Z

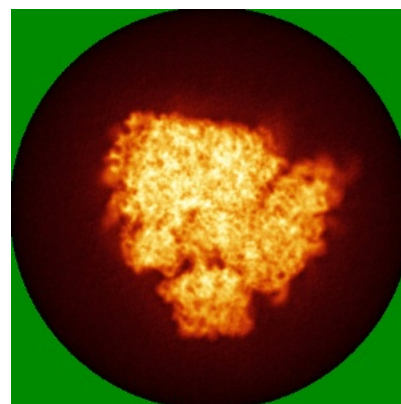
### 6.4.2 Raw map



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.

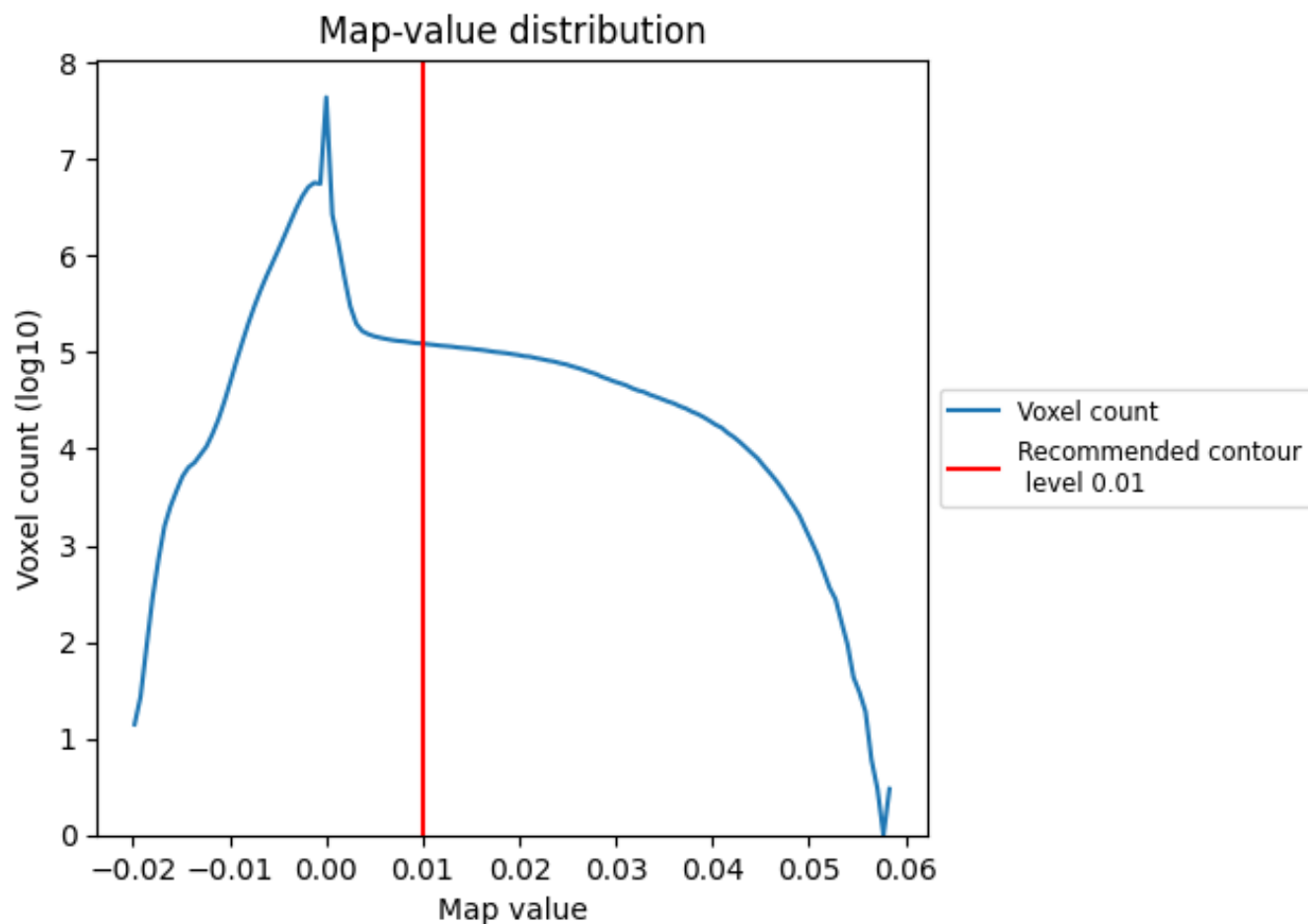
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

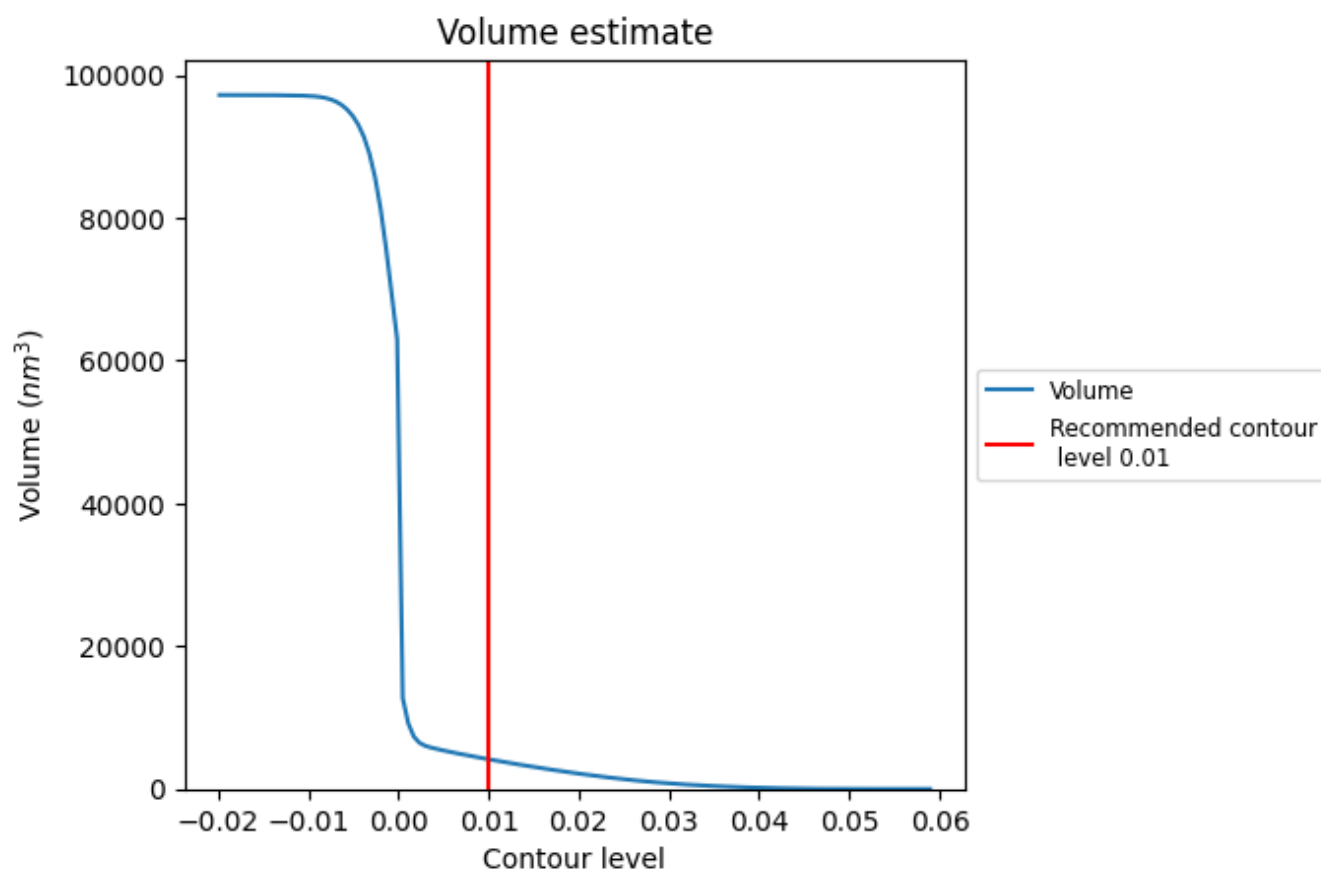
This section contains the results of statistical analysis of the map.

### 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.

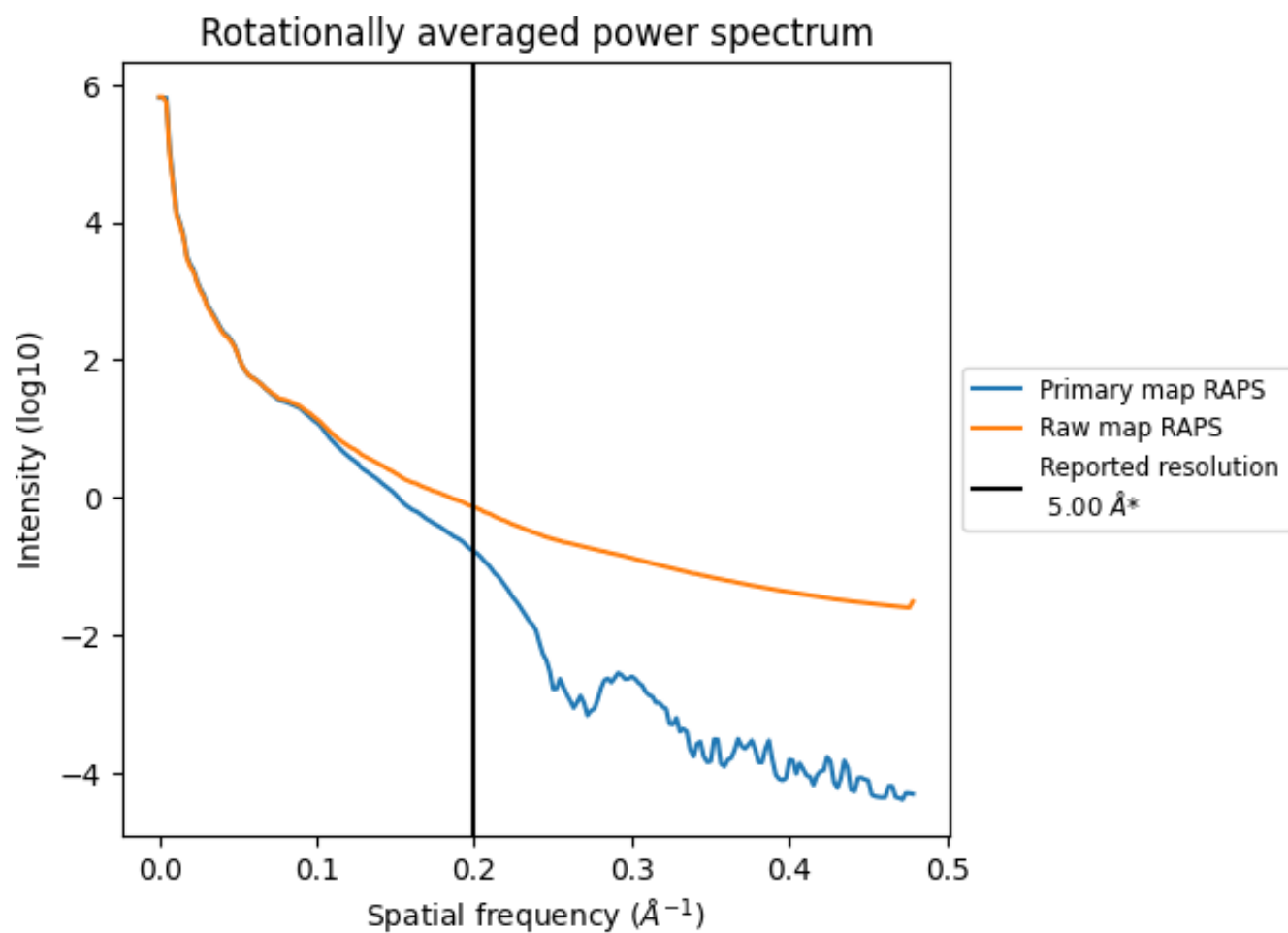
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4156  $\text{nm}^3$ ; this corresponds to an approximate mass of 3755 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 ⓘ

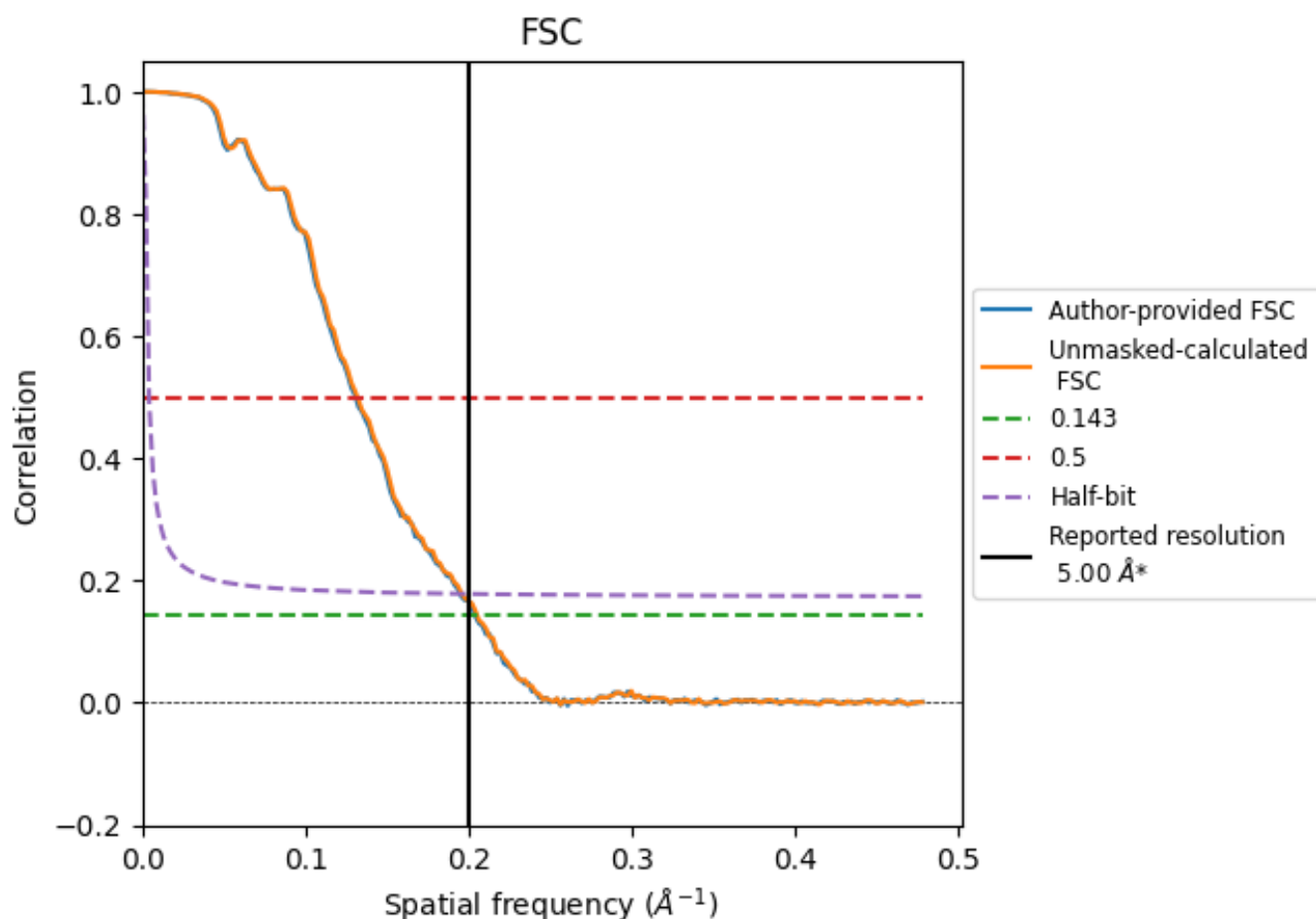


\*Reported resolution corresponds to spatial frequency of 0.200  $\text{\AA}^{-1}$

## 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 0.200 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	-	-	-
Author-provided FSC curve	4.90	7.64	5.13
Unmasked-calculated*	4.87	7.58	5.10

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

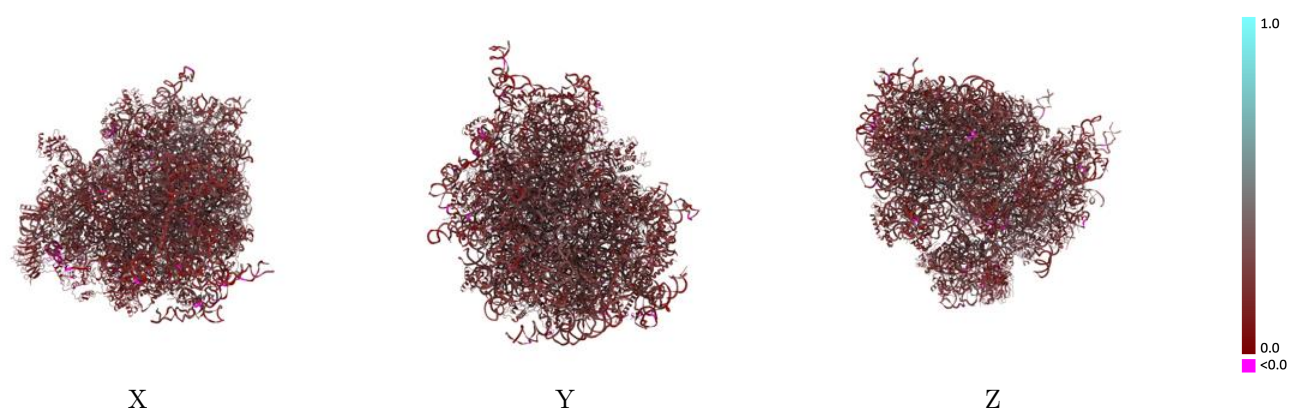
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-72469 and PDB model 9Y42. Per-residue inclusion information can be found in section 3 on page 21.

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

This section was not generated.

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

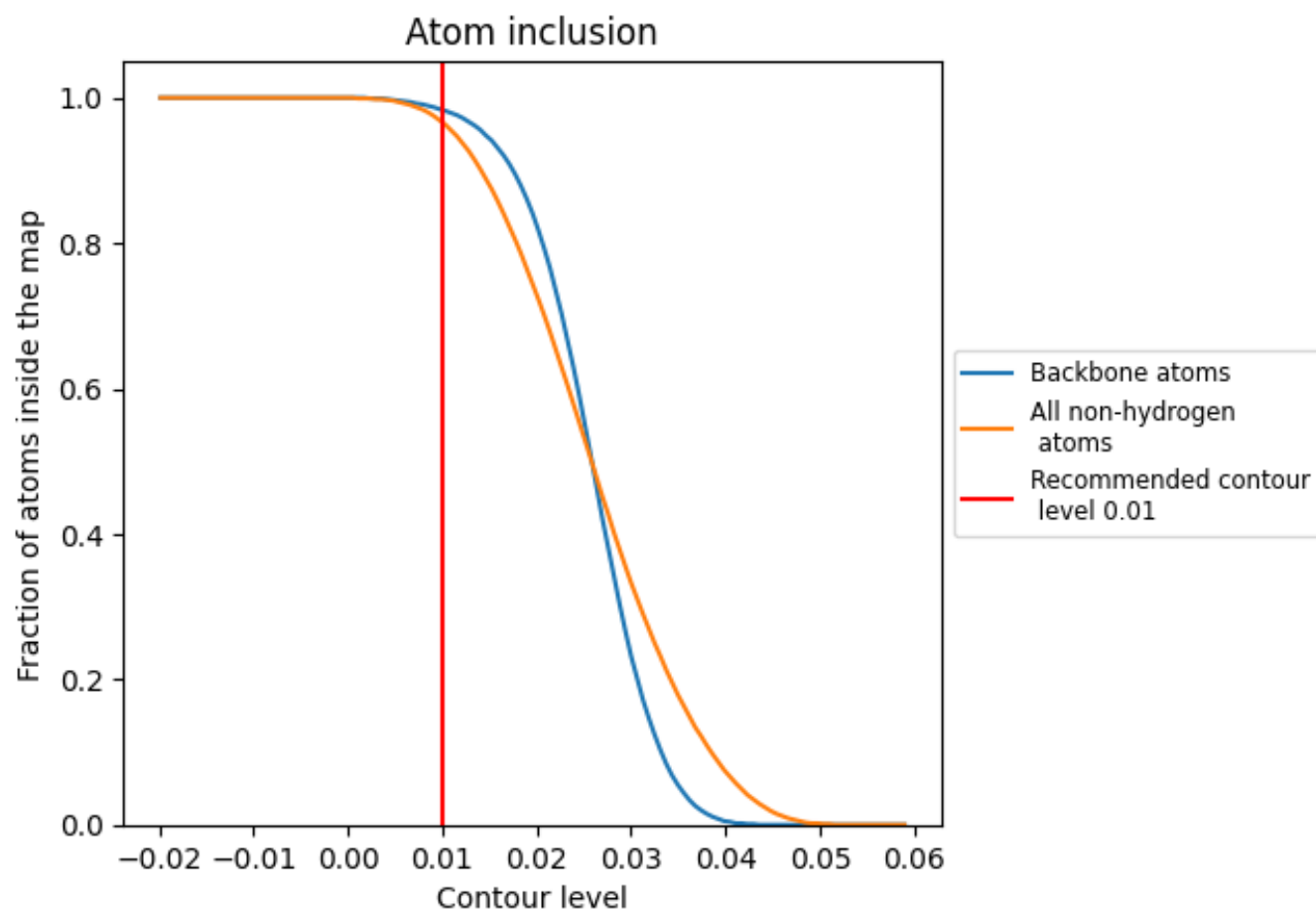


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 97% 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	 0.9660	 0.2370
A	 0.9140	 0.2370
A5	 0.9870	 0.2570
A6	 0.9900	 0.2680
A7	 0.9980	 0.2760
A8	 0.9930	 0.2580
AA	 0.8950	 0.1840
B	 0.9490	 0.2330
B2	 0.9850	 0.2500
BB	 0.9060	 0.1380
C	 0.9520	 0.2360
CC	 0.9100	 0.2210
Cc	 0.9880	 0.2470
D	 0.9840	 0.2080
DD	 0.9430	 0.2260
E	 0.9720	 0.2280
EE	 0.9680	 0.2120
EF	 0.8390	 0.1890
F	 0.9370	 0.2220
FF	 0.9610	 0.1810
G	 0.9590	 0.2130
GG	 0.9660	 0.1780
H	 0.9400	 0.2250
HH	 0.9170	 0.2060
I	 0.9440	 0.2460
II	 0.9560	 0.1950
J	 0.9800	 0.2030
JJ	 0.9720	 0.2010
KK	 0.9920	 0.1980
L	 0.9590	 0.2350
LL	 0.9180	 0.2350
M	 0.9750	 0.2270
MM	 0.9490	 0.1840
N	 0.9620	 0.2160
NN	 0.9260	 0.2010



















*Continued on next page...*

*Continued from previous page...*

Chain	Atom inclusion	Q-score
O	 0.9240	 0.2250
OO	 0.8970	 0.1160
P	 0.9500	 0.2260
PP	 0.9760	 0.1940
Q	 0.9280	 0.2400
QQ	 0.9810	 0.1790
RR	 0.7460	 0.0790
S	 0.9680	 0.2360
SS	 0.9700	 0.1830
T	 0.9490	 0.2450
TT	 0.9900	 0.1770
U	 0.9810	 0.2110
UU	 0.9790	 0.2010
V	 0.8730	 0.2370
VV	 0.8590	 0.2030
W	 0.9420	 0.2020
WW	 0.9250	 0.2210
X	 0.9700	 0.2310
XX	 0.9380	 0.2500
Y	 0.9680	 0.2200
YY	 0.9830	 0.1850
Z	 0.9800	 0.2130
ZZ	 0.9500	 0.1580
a	 0.9690	 0.2450
aa	 0.9270	 0.1880
b	 0.9580	 0.1830
bb	 0.9670	 0.2210
c	 0.9380	 0.1830
cc	 0.9330	 0.2010
d	 0.9640	 0.2340
dd	 0.9750	 0.1860
e	 0.9280	 0.2540
ee	 0.9820	 0.2050
f	 0.9460	 0.2380
ff	 0.9790	 0.1870
g	 0.9510	 0.2210
gg	 0.9790	 0.1900
h	 0.9640	 0.2100
i	 0.9490	 0.2170
j	 0.9760	 0.2110
k	 0.9570	 0.2020
l	 0.9700	 0.2290

*Continued on next page...*

*Continued from previous page...*

Chain	Atom inclusion	Q-score
m	 0.9440	 0.2290
n	 0.8670	 0.1580
o	 0.9390	 0.2250
p	 0.8850	 0.2290
r	 0.9360	 0.2500
s	 0.9800	 0.1910
t	 0.8940	 0.1390
u	 0.8560	 0.2190