



wwPDB EM Validation Summary Report ⓘ

Oct 1, 2025 – 03:04 PM JST

PDB ID : 9V21 / pdb_00009v21
EMDB ID : EMD-64713
Title : Cryo- EM structure of 75S ribosome with P- tRNA from Entamoeba histolytica
Authors : Sharma, S.; Mishra, S.; Gourinath, S.; Kaushal, P.S.
Deposited on : 2025-05-19
Resolution : 3.00 Å (reported)
Based on initial model : 6QZP

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev129
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.46

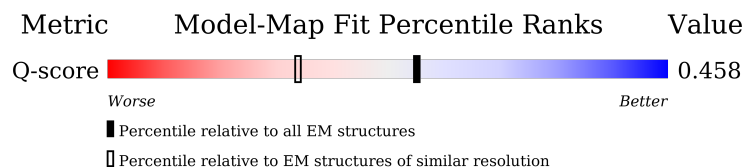
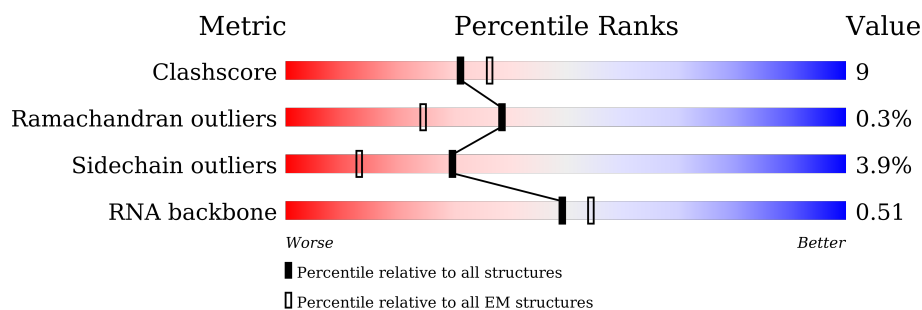
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.























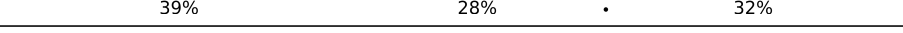




Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	14081 (2.50 - 3.50)

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

Mol	Chain	Length	Quality of chain
1	1A	3503	
2	1B	155	
3	1C	117	

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Mol	Chain	Length	Quality of chain
4	ID	246	
5	IE	402	
6	IF	431	
7	IG	286	
8	IH	203	
9	II	230	
10	IJ	286	
11	IK	197	
12	IL	210	
13	IM	174	
14	IN	291	
15	IO	204	
16	IP	135	
17	IQ	204	
18	IR	179	
19	IS	167	
20	IT	173	
21	IU	198	
22	IV	165	
23	IW	137	
24	IX	140	
25	IY	121	
26	IZ	163	
27	la	213	
28	lb	139	







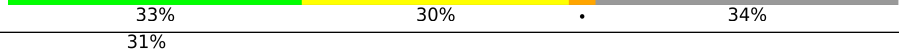
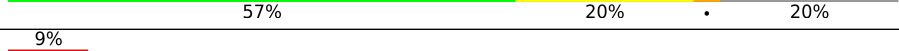
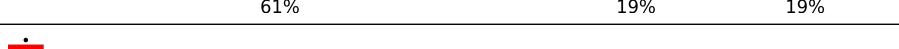
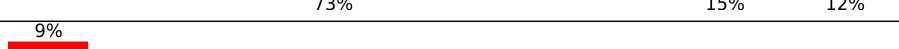
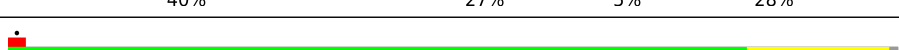

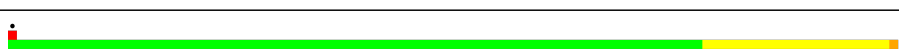

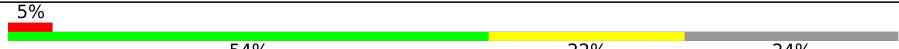





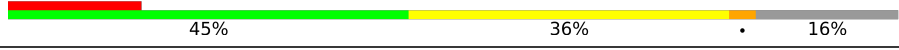
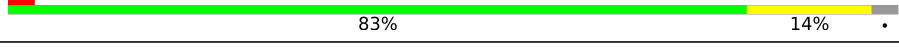



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Mol	Chain	Length	Quality of chain
29	lc	148	
30	ld	64	
31	le	109	
32	lf	150	
33	lg	134	
34	lh	137	
35	li	122	
36	lj	108	
37	lk	104	
38	ll	77	
39	lm	93	
40	ln	88	
41	lo	50	
42	lp	56	
43	lq	98	
44	ls	14	
45	sA	137	
46	sB	144	
47	sC	83	
48	sD	69	
49	sE	55	
50	sG	321	
51	sH	76	
52	sK	6	
53	sa	1947	

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Mol	Chain	Length	Quality of chain
54	sb	254	
55	sc	255	
56	sd	244	
57	se	256	
58	sf	326	
59	sg	206	
60	sh	266	
61	si	201	
62	sj	237	
63	sk	185	
64	sl	127	
65	sm	156	
66	sn	136	
67	so	150	
68	sp	146	
69	sq	144	
70	sr	129	
71	ss	157	
72	st	117	
73	su	155	
74	sv	155	
75	sw	118	
76	sx	86	
77	sy	141	
78	sz	140	

2 Entry composition

There are 78 unique types of molecules in this entry. The entry contains 191389 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 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1A	3180	Total	C	N	O	P	0	0
			67965	30470	12340	21975	3180		

- Molecule 2 is a RNA chain called 5.8S.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1B	145	Total	C	N	O	P	0	0
			3097	1390	560	1002	145		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1C	117	Total	C	N	O	P	0	0
			2477	1108	425	827	117		

- Molecule 4 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	1D	246	Total	C	N	O	S	0	0
			1881	1165	382	326	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	1E	388	Total	C	N	O	S	0	0
			3085	1961	579	530	15		

- Molecule 6 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	1F	420	Total	C	N	O	S	0	0
			3248	2070	617	547	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	lG	282	Total	C	N	O	S	0	0
			2245	1434	405	398	8		

- Molecule 8 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	lH	203	Total	C	N	O	S	0	0
			1608	1054	272	278	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	lI	210	Total	C	N	O	S	0	0
			1658	1067	301	282	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	lJ	209	Total	C	N	O	S	0	0
			1697	1097	310	285	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	lK	193	Total	C	N	O	S	0	0
			1538	974	279	279	6		

- Molecule 12 is a protein called Ribosomal protein L10, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	lL	201	Total	C	N	O	S	0	0
			1608	1023	306	265	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	lM	170	Total	C	N	O	S	0	0
			1350	857	243	245	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	lN	266	Total	C	N	O	S	0	0
			2121	1352	410	351	8		

- Molecule 15 is a protein called 60S ribosomal protein L13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	lO	204	Total	C	N	O	S	0	0
			1616	1030	302	275	9		

- Molecule 16 is a protein called 60S ribosomal protein L14, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	lP	130	Total	C	N	O	S	0	0
			1020	654	188	174	4		

- Molecule 17 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	lQ	204	Total	C	N	O	S	0	0
			1676	1051	356	264	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	lR	155	Total	C	N	O	S	0	0
			1211	765	234	207	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	lS	167	Total	C	N	O	S	0	0
			1321	835	258	219	9		

- Molecule 20 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	lT	173	Total	C	N	O	S	0	0
			1413	910	259	235	9		

- Molecule 21 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	IU	150	Total	C	N	O	S	0	0
			1235	787	246	197	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	IV	165	Total	C	N	O	S	0	0
			1320	846	254	217	3		

- Molecule 23 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	IW	93	Total	C	N	O	S	0	0
			763	493	132	133	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	IX	133	Total	C	N	O	S	0	0
			1015	629	196	182	8		

- Molecule 25 is a protein called Ribosomal protein L23A, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	IY	116	Total	C	N	O	S	0	0
			926	597	166	159	4		

- Molecule 26 is a protein called 60S ribosomal protein L24, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	IZ	57	Total	C	N	O	S	0	0
			481	318	88	73	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	la	210	Total	C	N	O	S	0	0
			1651	1055	304	285	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	lb	137	Total	C	N	O	S	0	0
			1094	707	196	187	4		

- Molecule 29 is a protein called Large ribosomal subunit protein uL15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	lc	148	Total	C	N	O	S	0	0
			1192	757	236	194	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	ld	60	Total	C	N	O	S	0	0
			478	297	97	82	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	le	103	Total	C	N	O	S	0	0
			768	486	131	149	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	lf	128	Total	C	N	O	S	0	0
			1039	671	193	169	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
33	lg	124	Total	C	N	O	S	0	0
			1019	649	202	163	5		

- Molecule 34 is a protein called 60S ribosomal protein L34, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	lh	105	Total	C	N	O	S	0	0
			820	512	169	133	6		

- Molecule 35 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	li	122	Total	C	N	O	S	0	0
			974	620	188	162	4		

- Molecule 36 is a protein called 60S ribosomal protein L35a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	lj	106	Total	C	N	O	S	0	0
			841	545	158	135	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	lk	89	Total	C	N	O	S	0	0
			712	447	144	116	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	ll	72	Total	C	N	O	S	0	0
			591	361	132	91	7		

- Molecule 39 is a protein called 60S ribosomal protein L37A, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	lm	90	Total	C	N	O	S	0	0
			688	428	135	119	6		

- Molecule 40 is a protein called 60S ribosomal protein L38, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	ln	73	Total	C	N	O	S	0	0
			584	378	104	100	2		

- Molecule 41 is a protein called Ribosomal protein L39, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	lo	50	Total	C	N	O	S	0	0
			432	275	91	63	3		

- Molecule 42 is a protein called 60S ribosomal protein L40, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	lp	53	Total	C	N	O	S	0	0
			420	259	86	69	6		

- Molecule 43 is a protein called 60S ribosomal protein L44, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	lq	92	Total	C	N	O	S	0	0
			756	480	148	122	6		

- Molecule 44 is a protein called nascent polypeptide (Unk).

Mol	Chain	Residues	Atoms					AltConf	Trace
44	ls	14	Total	C	N	O		0	0
			76	45	17	14			

- Molecule 45 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	sA	72	Total	C	N	O	S	0	0
			568	368	96	100	4		

- Molecule 46 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	sB	98	Total	C	N	O	S	0	0
			787	478	169	134	6		

- Molecule 47 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	sC	83	Total	C	N	O	S	0	0
			641	407	117	111	6		

- Molecule 48 is a protein called 40S ribosomal protein S28, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	sD	60	Total	C	N	O	S	0	0
			468	289	93	84	2		

- Molecule 49 is a protein called Ribosomal protein S29, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	sE	55	Total	C	N	O	S	0	0
			442	273	90	75	4		

- Molecule 50 is a protein called Guanine nucleotide-binding protein subunit beta 2-like 1, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	sG	305	Total	C	N	O	S	0	0
			2347	1488	398	448	13		

- Molecule 51 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	sH	74	Total	C	N	O	P	0	0
			1573	703	276	520	74		

- Molecule 52 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	sK	6	Total	C	N	O	P	0	0
			126	57	21	42	6		

- Molecule 53 is a RNA chain called 17S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	sa	1453	Total	C	N	O	P	0	0
			31080	13913	5653	10061	1453		

- Molecule 54 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	sb	205	Total	C	N	O	S	0	0
			1626	1029	286	296	15		

- Molecule 55 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	sc	215	Total	C	N	O	S	0	0
			1642	1052	291	291	8		

- Molecule 56 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	sd	221	Total	C	N	O	S	0	0
			1708	1080	312	305	11		

- Molecule 57 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	se	212	Total	C	N	O	S	0	0
			1717	1097	305	306	9		

- Molecule 58 is a protein called 40S ribosomal protein S4, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	sf	256	Total	C	N	O	S	0	0
			2031	1297	378	345	11		

- Molecule 59 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	sg	185	Total	C	N	O	S	0	0
			1473	930	267	265	11		

- Molecule 60 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	sh	176	Total	C	N	O	S	0	0
			1395	880	278	230	7		

- Molecule 61 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	si	160	Total	C	N	O	S	0	0
			1246	813	220	209	4		

- Molecule 62 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	sj	192	Total	C	N	O	S	0	0
			1536	970	285	276	5		

- Molecule 63 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	sk	162	Total	C	N	O	S	0	0
			1323	845	251	221	6		

- Molecule 64 is a protein called 40S ribosomal protein S10, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	sl	91	Total	C	N	O	S	0	0
			729	475	122	123	9		

- Molecule 65 is a protein called 40S ribosomal protein S11, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	sm	154	Total	C	N	O	S	0	0
			1263	796	243	217	7		

- Molecule 66 is a protein called 40S ribosomal protein S12, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	sn	53	Total	C	N	O	S	0	0
			428	277	77	72	2		

- Molecule 67 is a protein called 40S ribosomal protein S13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	so	150	Total	C	N	O	S	0	0
			1184	756	218	204	6		

- Molecule 68 is a protein called Ribosomal protein S14, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	sp	133	Total	C	N	O	S	0	0
			999	615	192	186	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
69	sq	109	Total	C	N	O	S	0	0
			873	561	155	152	5		

- Molecule 70 is a protein called 40S ribosomal protein S15a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	sr	129	Total	C	N	O	S	0	0
			1022	650	186	181	5		

- Molecule 71 is a protein called 40S ribosomal protein S16, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	ss	141	Total	C	N	O	S	0	0
			1104	713	198	189	4		

- Molecule 72 is a protein called 40S ribosomal protein S17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	st	111	Total	C	N	O	S	0	0
			907	573	169	162	3		

- Molecule 73 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	su	144	Total	C	N	O	S	0	0
			1163	722	233	202	6		

- Molecule 74 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	sv	155	Total	C	N	O	S	0	0
			1245	796	223	217	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
75	sw	99	Total	C	N	O	S	0	0
			774	490	135	144	5		

- Molecule 76 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	sx	83	Total	C	N	O	S	0	0
			651	412	117	119	3		

- Molecule 77 is a protein called 40S ribosomal protein S23, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	sy	130	Total	C	N	O	S	0	0
			1010	637	200	169	4		

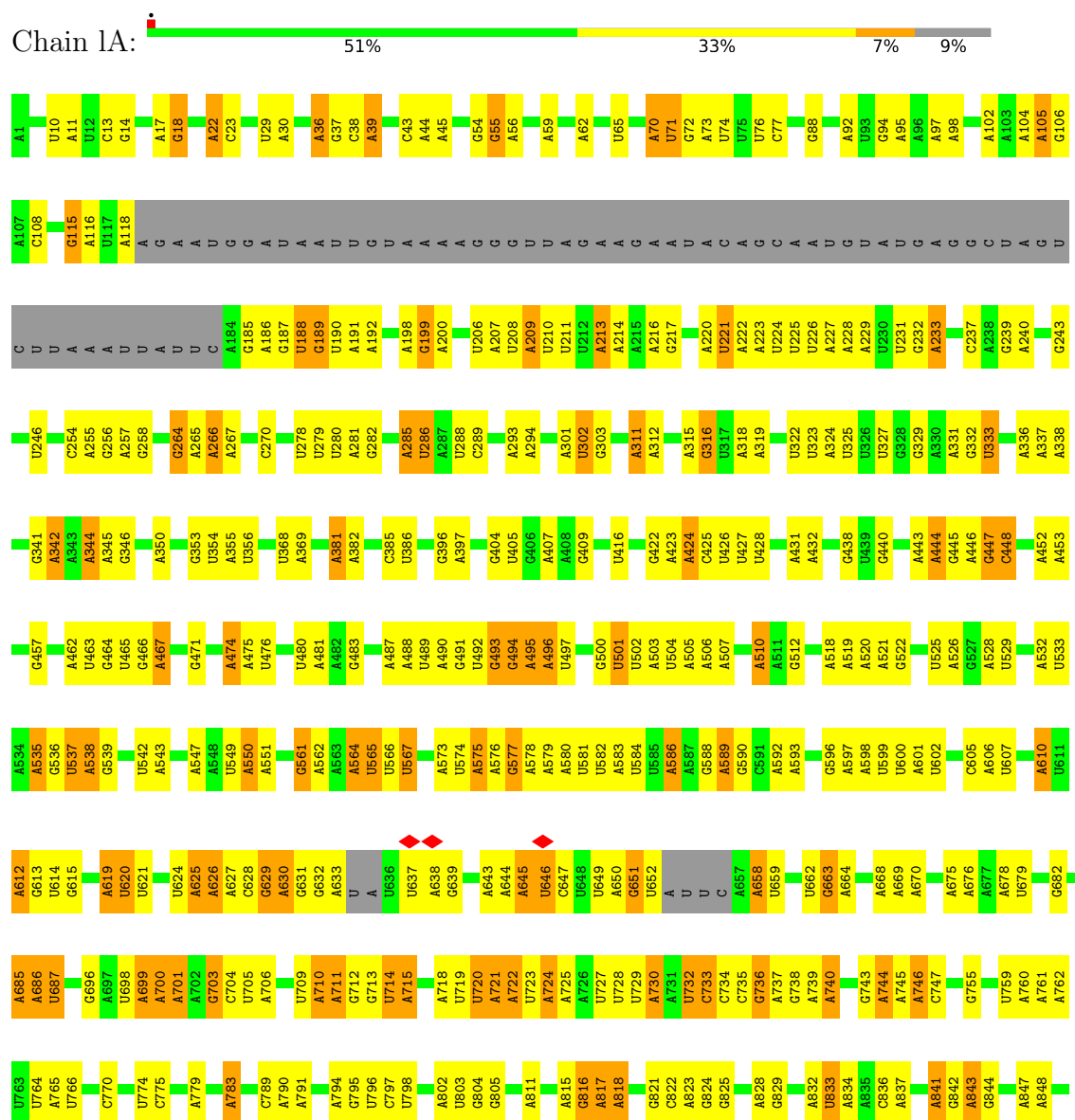
- Molecule 78 is a protein called 40S ribosomal protein S24, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	sz	76	Total	C	N	O	S	0	0
			598	394	103	99	2		

3 Residue-property plots

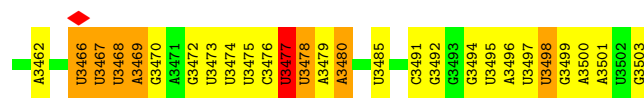
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 25S rRNA



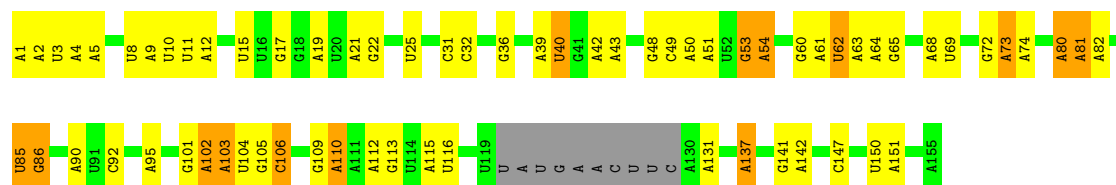
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G2061	G1975	A1887	A1630	A1516	G1430	G1358	G1252	A1155	G1086	C949	A852
A2062	A1988	A1888	A1631	C1517	A1431	U1359	A1255	C1156	G1087	A853	
G2063	C1980	G1892	A1632	A1520	U1433	G1360	G1256	A1157	G960	A854	
G2064	A1983	A1893	G1633	A1521	A1437	G1361	A1265	A1165	C968	A855	
A2067	U1982	A1894	U1635	G1522	A1437	C	G1270	A1166	A1091	A858	
A2075	A1983	A1897	U1636	U1523	A1440	A	G1276	A1167	A1092	G862	
A2079	A1984	A1736	U1639	G1524	A1441	A	A1275	C1168	G1093	A863	
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A2082	G1993	G1739	A1641	A1527	C1447	G	A1284	A1173	U1097	A868	
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A2085	C1905	A1744	U1652	A1535	A1452	G1370	A1290	A1181	U993	A871	
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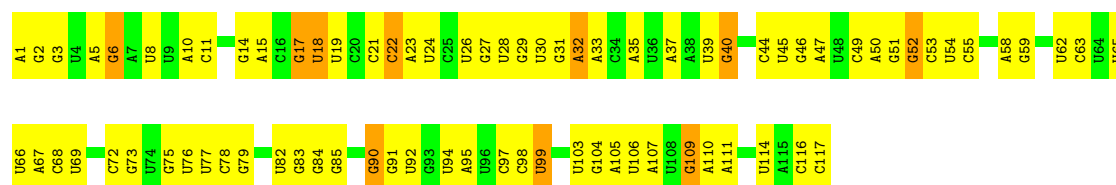
- Molecule 2: 5.8S

Chain 1B: 50% 34% 9% 6%



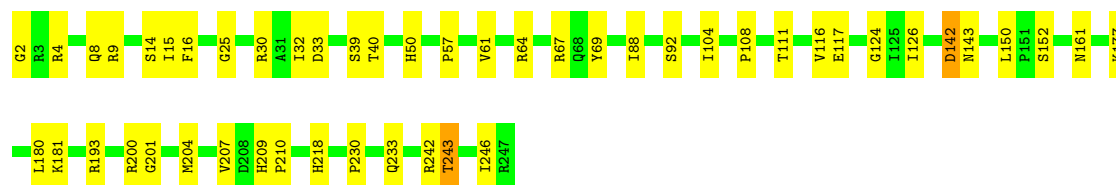
- Molecule 3: 5S rRNA

Chain 1C: 32% 59% 9%



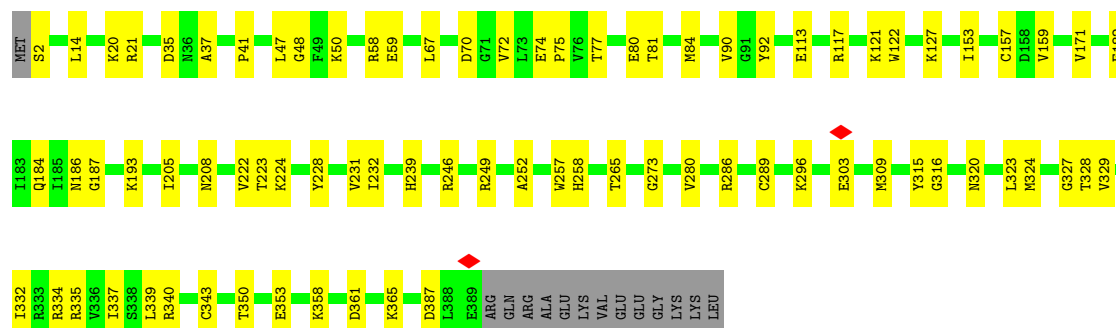
- Molecule 4: Large ribosomal subunit protein uL2

Chain 1D: 80% 19%




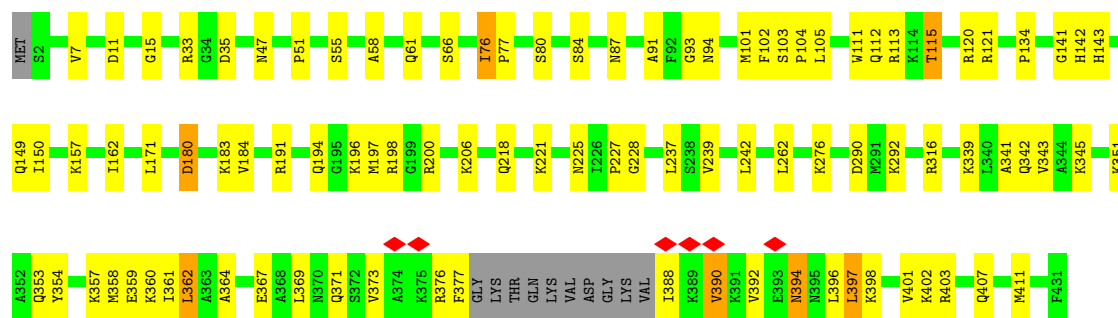
- Molecule 5: 60S ribosomal protein L3, putative

Chain 1E: 77% 20%




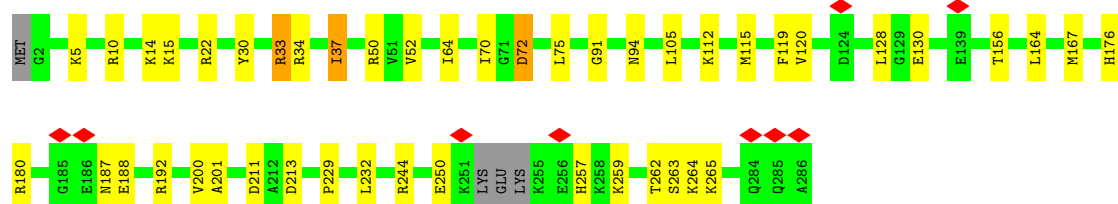
- Molecule 6: Large ribosomal subunit protein uL4

Chain 1F:  75% 20%




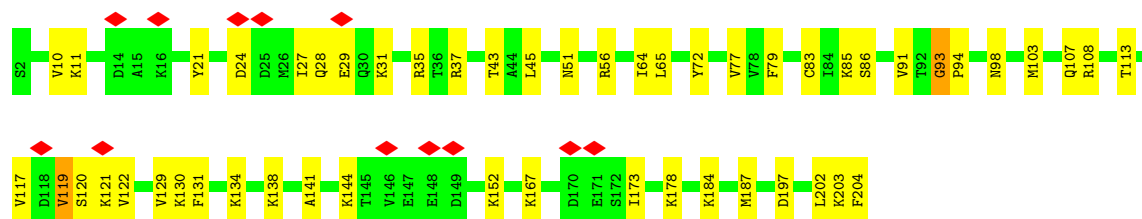
- Molecule 7: 60S ribosomal protein L5, putative

Chain 1G:  83% 15%




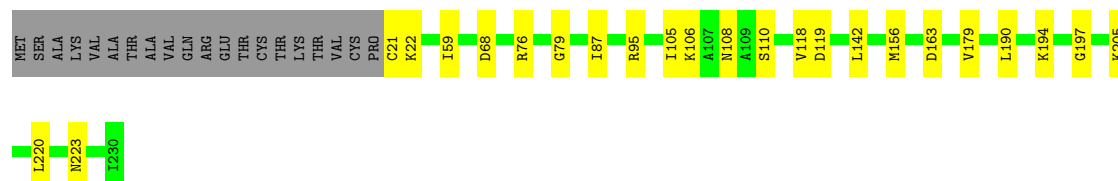
- Molecule 8: Large ribosomal subunit protein eL6

Chain 1H:  6% 74% 25%



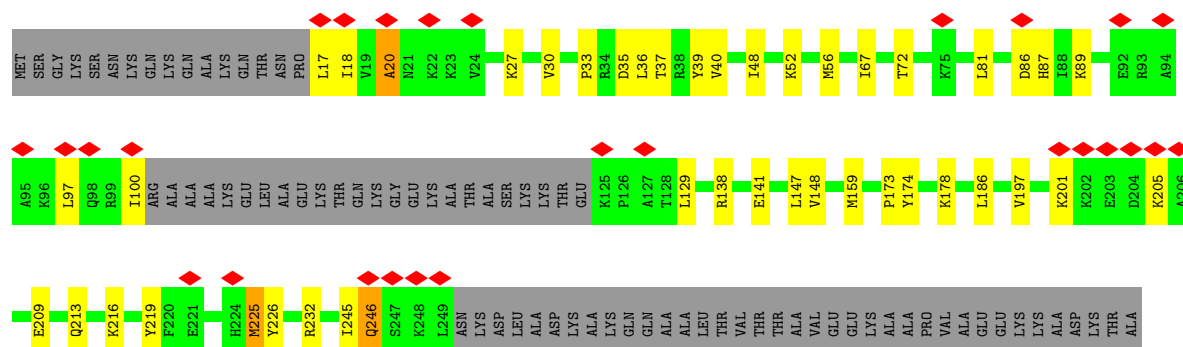
- Molecule 9: 60S ribosomal protein L7, putative

Chain 1I:  81% 10% 9%



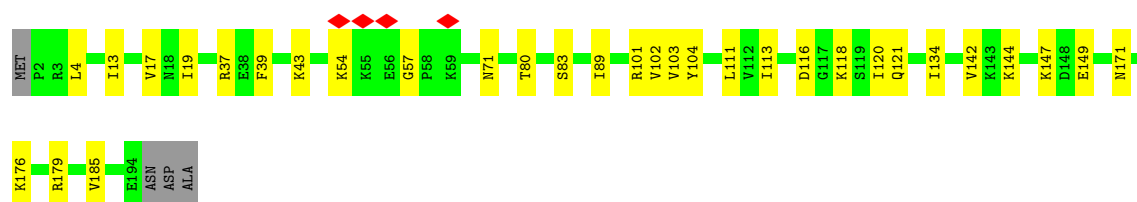
- Molecule 10: 60S ribosomal protein L7a

Chain 1J:  9% 58% 14% 27%



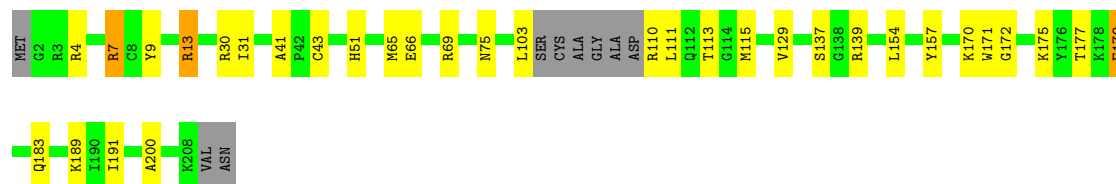
- Molecule 11: 60S ribosomal protein L9, putative

Chain IK: 82% 16% .



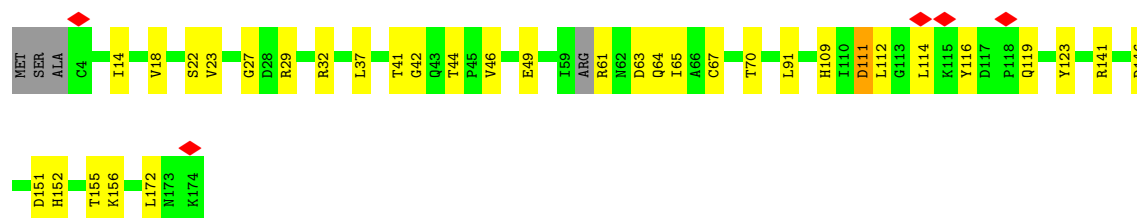
- Molecule 12: Ribosomal protein L10, putative

Chain IL: 80% 14% ..



- Molecule 13: 60S ribosomal protein L11, putative

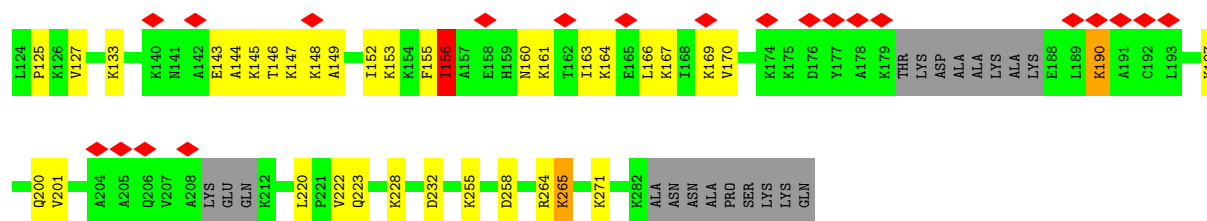
Chain IM: 78% 19% ..



- Molecule 14: 60S ribosomal protein L13, putative

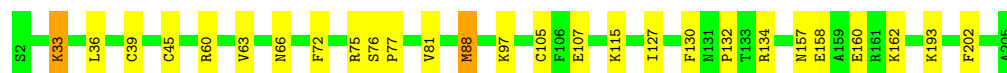
Chain IN: 8% 69% 21% 9%





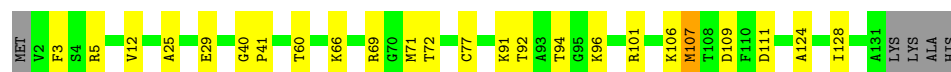
- Molecule 15: 60S ribosomal protein L13, putative

Chain IO: 87% 12%



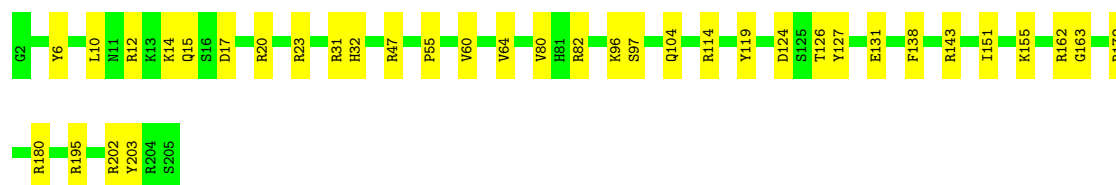
- Molecule 16: 60S ribosomal protein L14, putative

Chain IP: 79% 17%



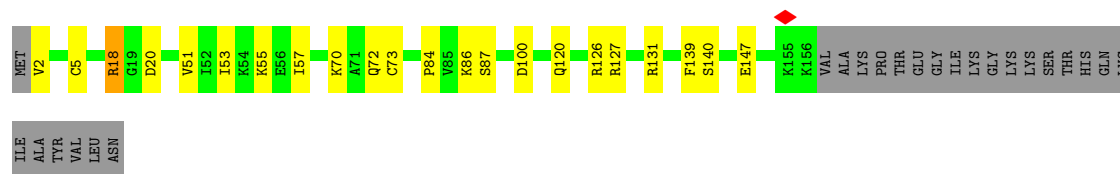
- Molecule 17: Ribosomal protein L15

Chain IQ: 82% 18%



- Molecule 18: 60S ribosomal protein L17, putative

Chain IR: 74% 12% 13%




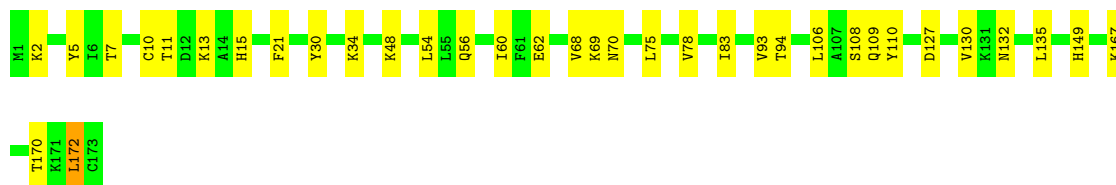
- Molecule 19: 60S ribosomal protein L18, putative

Chain IS: 87% 13%



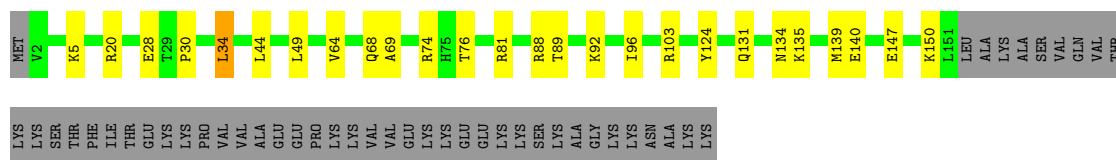
- Molecule 20: 60S ribosomal protein L18a

Chain IT:  80% 20% .




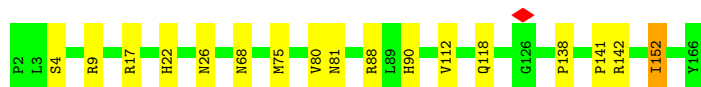
• Molecule 21: Ribosomal protein L19

Chain IU:  63% 13% 24% .



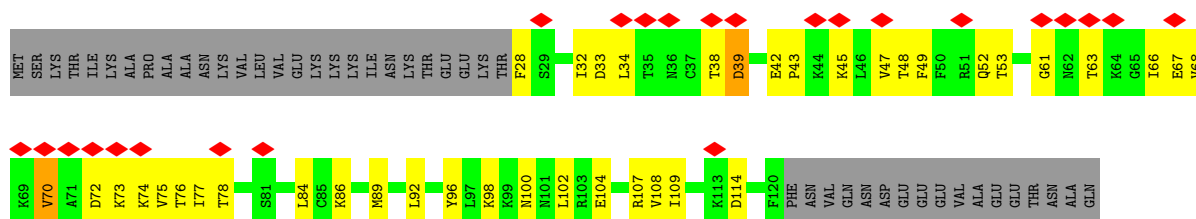
• Molecule 22: 60S ribosomal protein L21, putative

Chain IV:  90% 10% .



• Molecule 23: Large ribosomal subunit protein eL22

Chain IW:  18% 39% 28% 32% .




• Molecule 24: 60S ribosomal protein L23, putative

Chain IX:  76% 18% 5% .

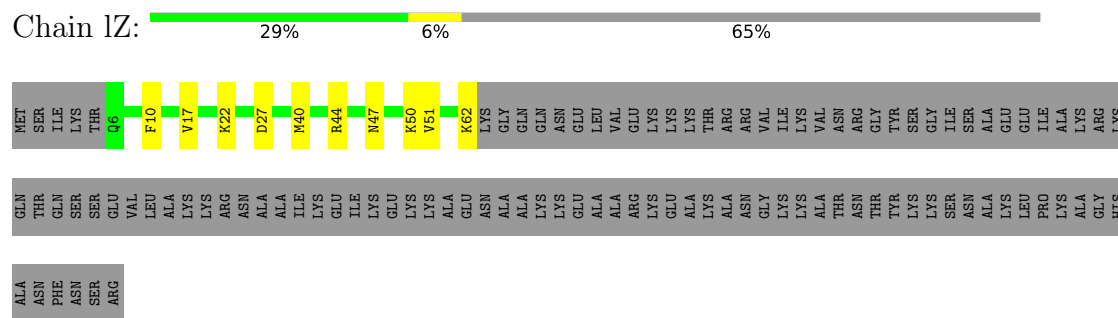


• Molecule 25: Ribosomal protein L23A, putative

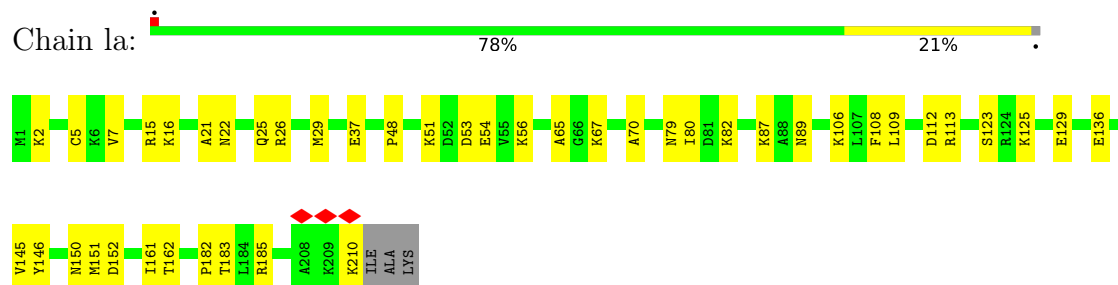
Chain IY:  81% 15% .



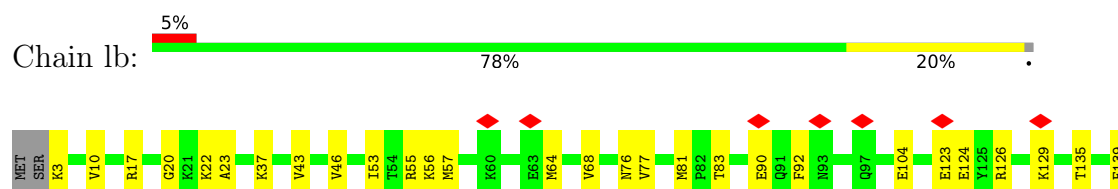
- Molecule 26: 60S ribosomal protein L24, putative



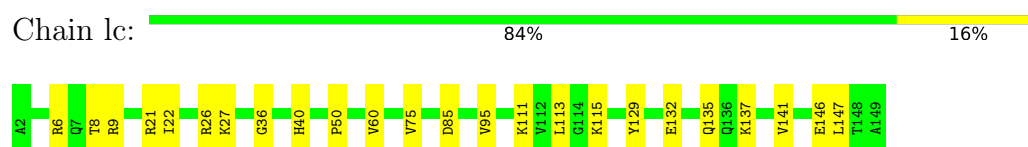
- Molecule 27: 60S ribosomal protein L26, putative



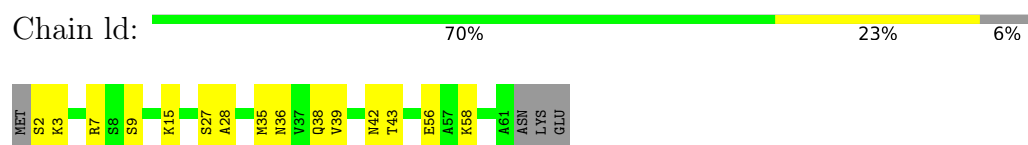
- Molecule 28: 60S ribosomal protein L27, putative



- Molecule 29: Large ribosomal subunit protein uL15A

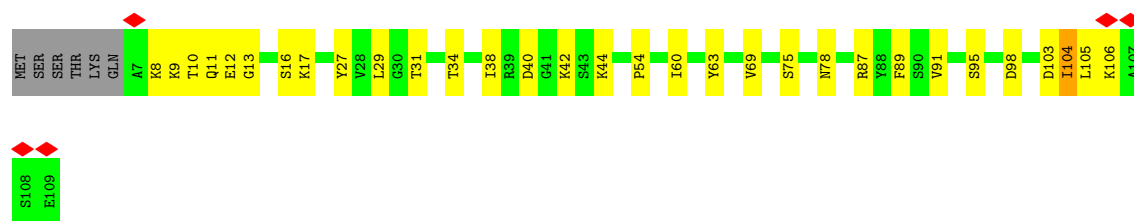


- Molecule 30: 60S ribosomal protein L29

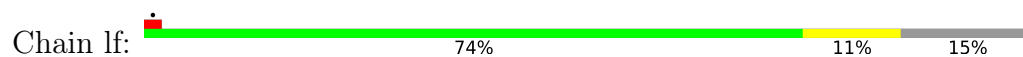


- Molecule 31: 60S ribosomal protein L30, putative

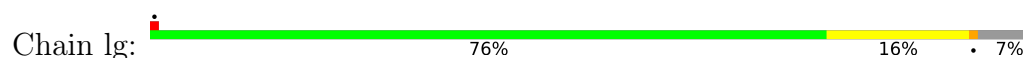




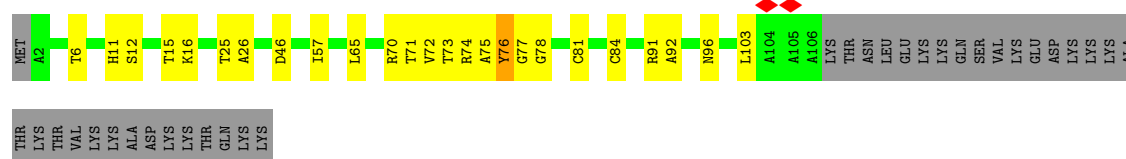
- Molecule 32: 60S ribosomal protein L31, putative



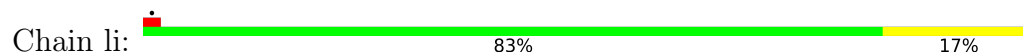
- Molecule 33: 60S ribosomal protein L32, putative



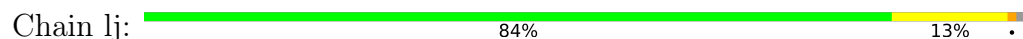
- Molecule 34: 60S ribosomal protein L34, putative



- Molecule 35: uL29



- Molecule 36: 60S ribosomal protein L35a, putative



- Molecule 37: 60S ribosomal protein L36, putative





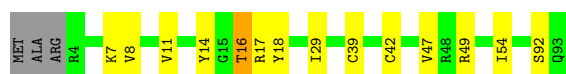
- Molecule 38: 60S ribosomal protein L37-A, putative

Chain ll: 70% 23% 6%



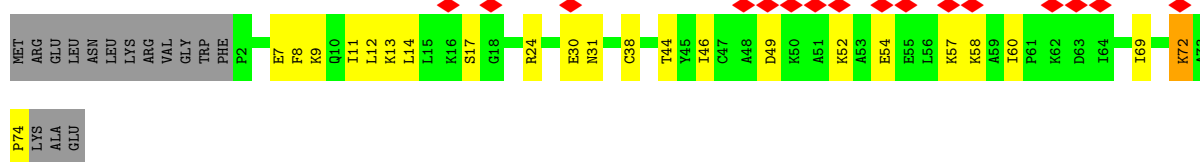
- Molecule 39: 60S ribosomal protein L37A, putative

Chain lm: 82% 14% ..



- Molecule 40: 60S ribosomal protein L38, putative

Chain ln: 18% 57% 25% 17%



- Molecule 41: Ribosomal protein L39, putative

Chain lo: 82% 16% .



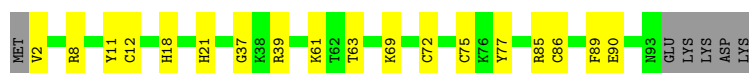
- Molecule 42: 60S ribosomal protein L40, putative

Chain lp: 73% 18% 5%



- Molecule 43: 60S ribosomal protein L44, putative

Chain lq: 76% 18% 6%

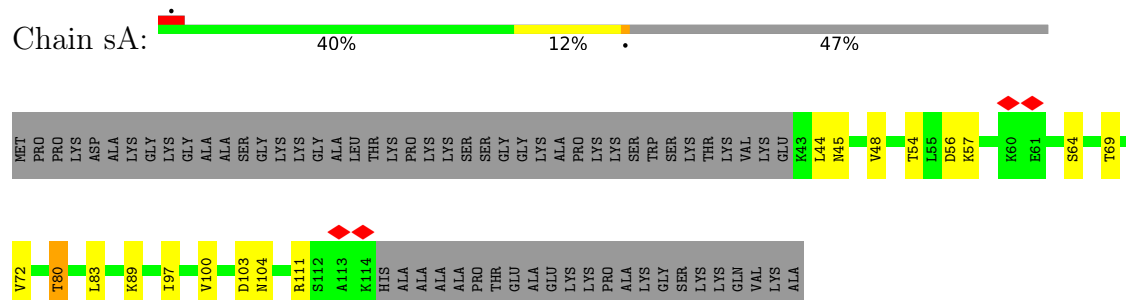


- Molecule 44: nascent polypeptide (Unk)

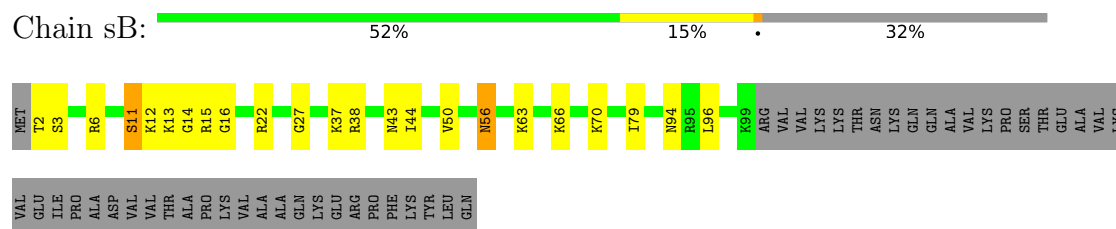
Chain ls:  100%

There are no outlier residues recorded for this chain.

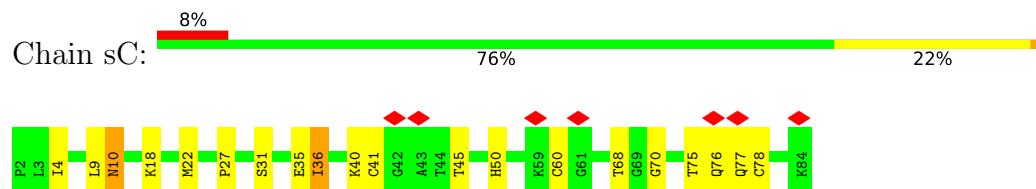
- Molecule 45: 40S ribosomal protein S25



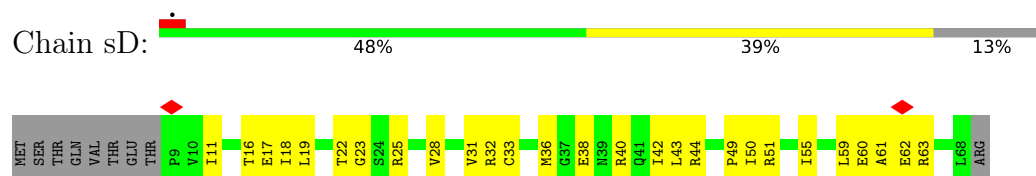
- Molecule 46: 40S ribosomal protein S26



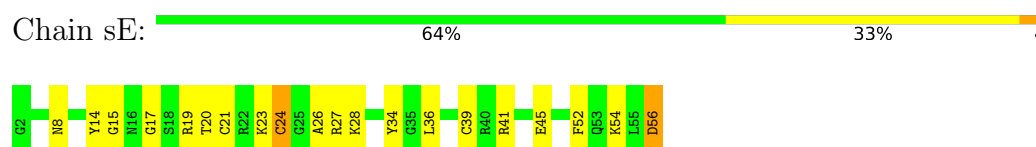
- Molecule 47: Small ribosomal subunit protein eS27



- Molecule 48: 40S ribosomal protein S28, putative

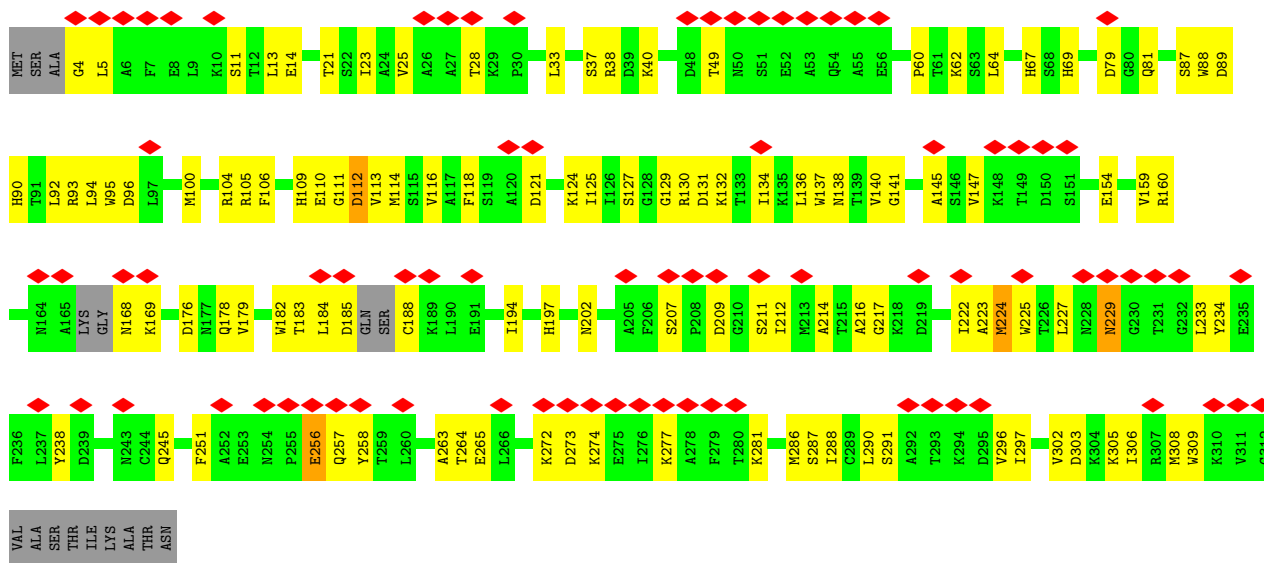


- Molecule 49: Ribosomal protein S29, putative

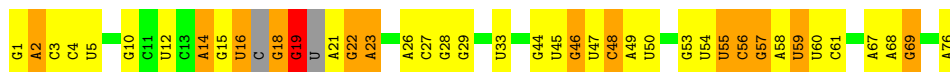


- Molecule 50: Guanine nucleotide-binding protein subunit beta 2-like 1, putative





• Molecule 51: P-tRNA

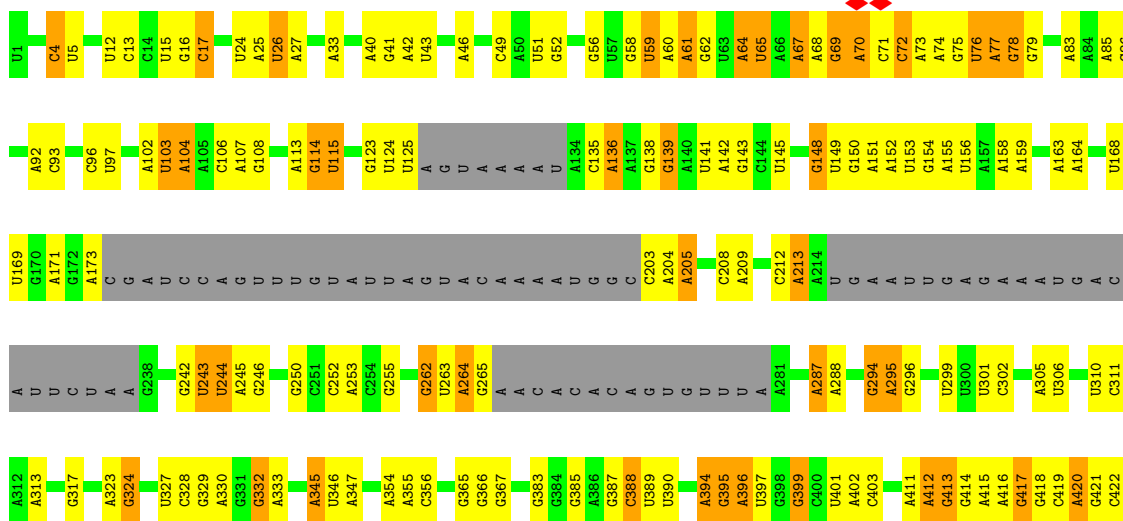


• Molecule 52: mRNA

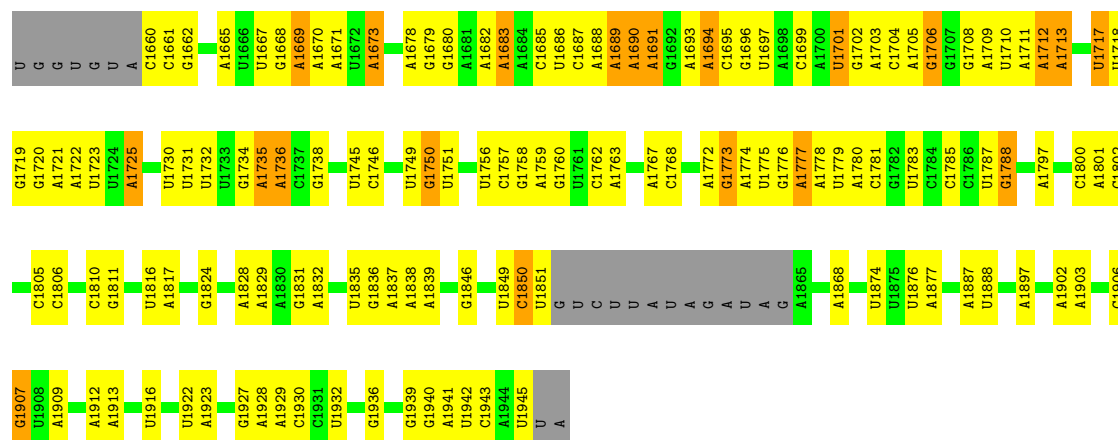


There are no outlier residues recorded for this chain.

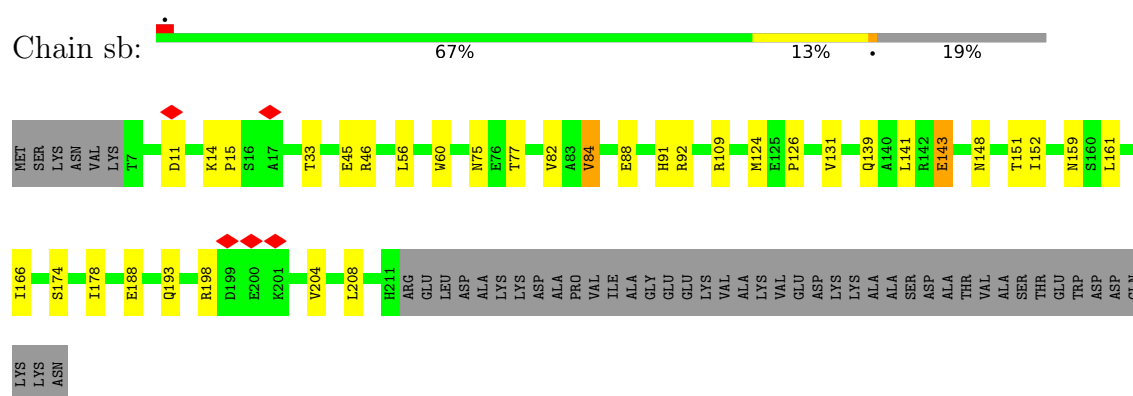
• Molecule 53: 17S rRNA



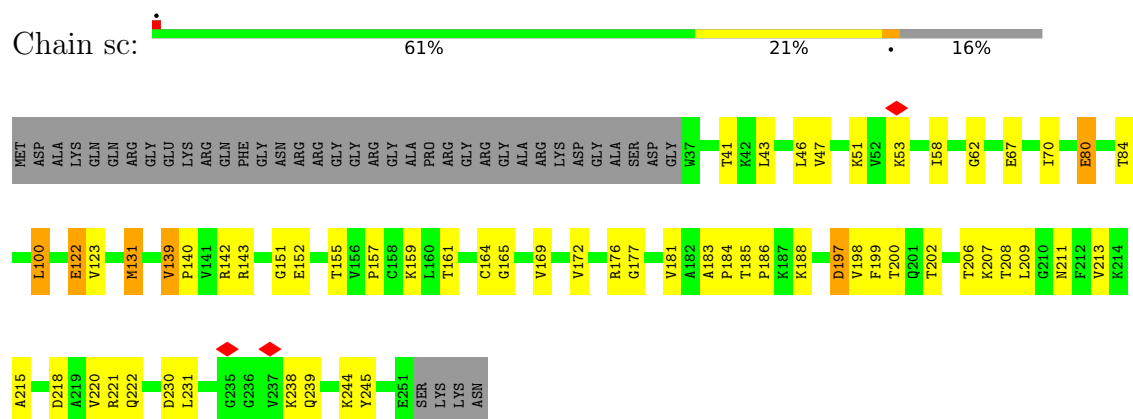
[illegible]



- Molecule 54: Small ribosomal subunit protein uS2

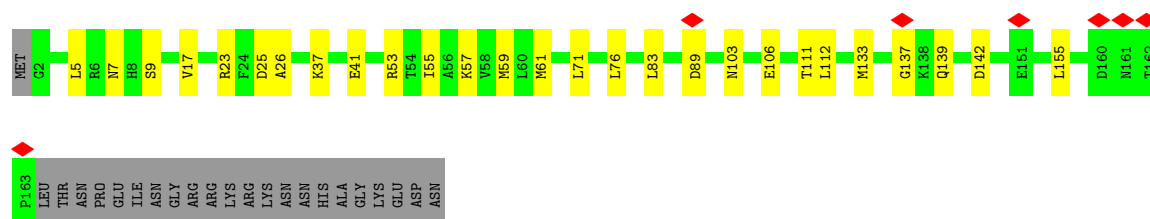


- Molecule 55: Small ribosomal subunit protein uS5

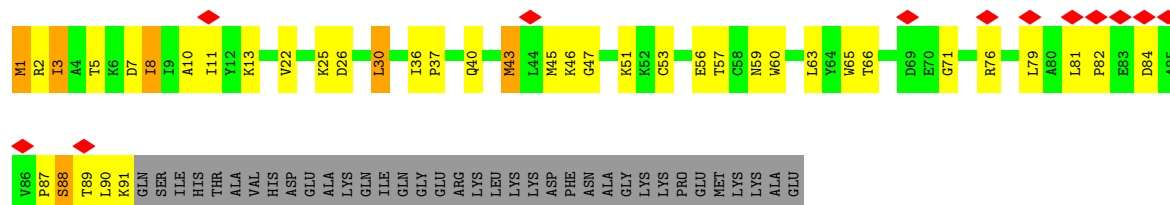
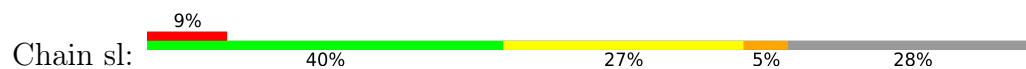


- Molecule 56: 40S ribosomal protein S3

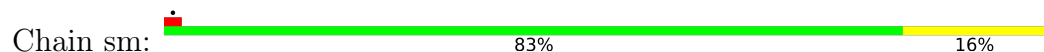




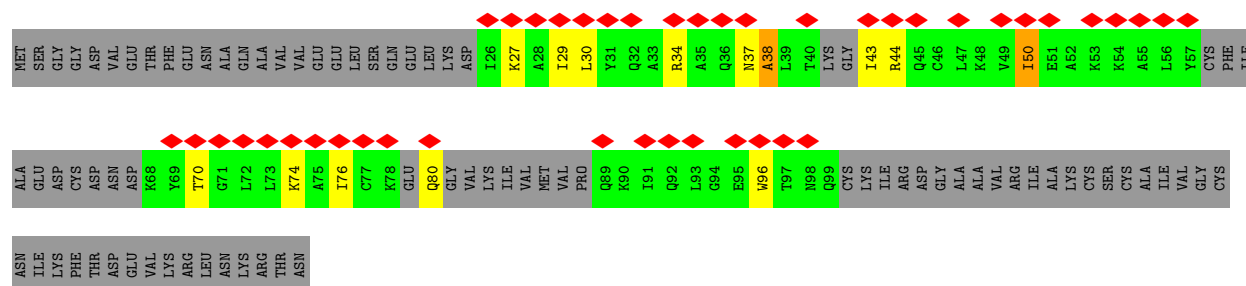
- Molecule 64: 40S ribosomal protein S10, putative



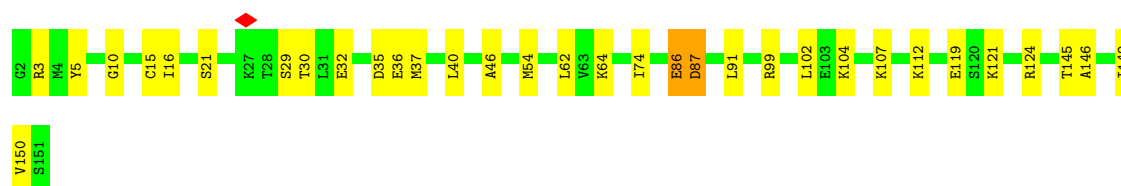
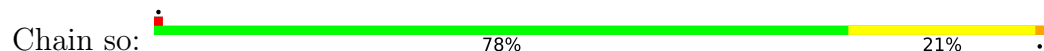
- Molecule 65: 40S ribosomal protein S11, putative



- Molecule 66: 40S ribosomal protein S12, putative

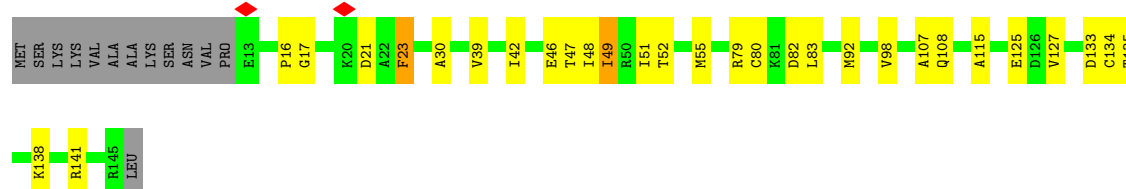


- Molecule 67: 40S ribosomal protein S13, putative



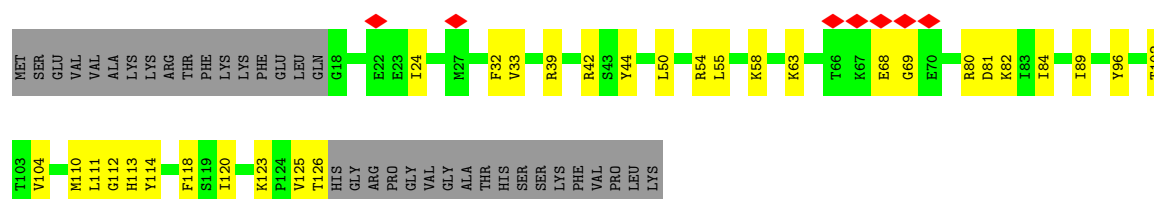
- Molecule 68: Ribosomal protein S14, putative

Chain sp: 




- Molecule 69: 40S ribosomal protein S15, putative

Chain sq: 



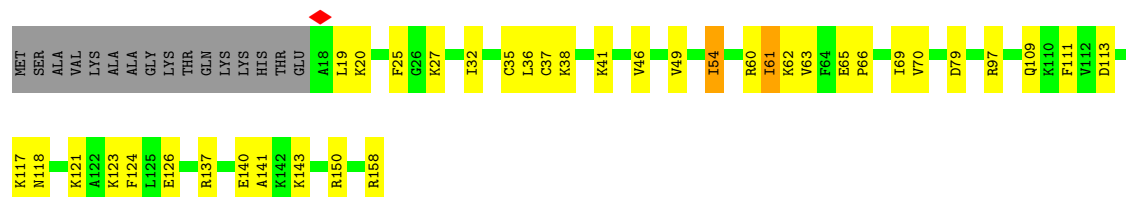
- Molecule 70: 40S ribosomal protein S15a, putative

Chain sr: 



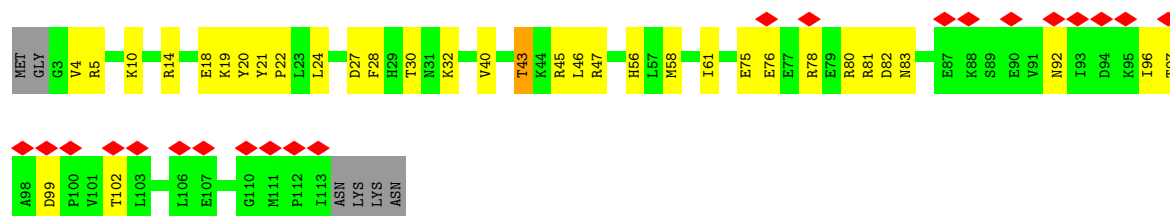
- Molecule 71: 40S ribosomal protein S16, putative

Chain ss: 

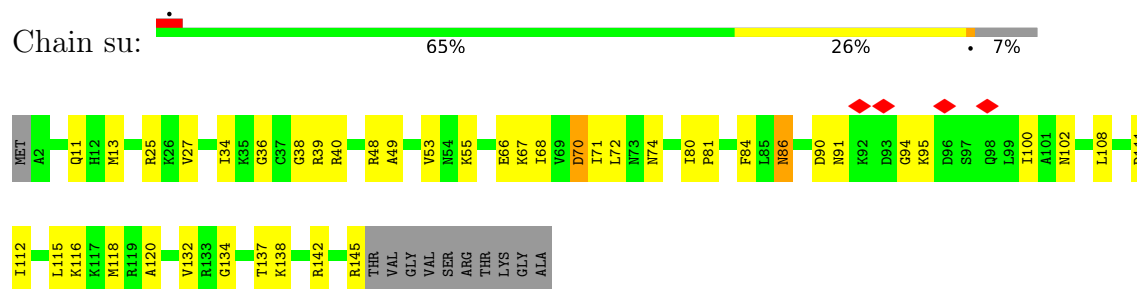


- Molecule 72: 40S ribosomal protein S17, putative

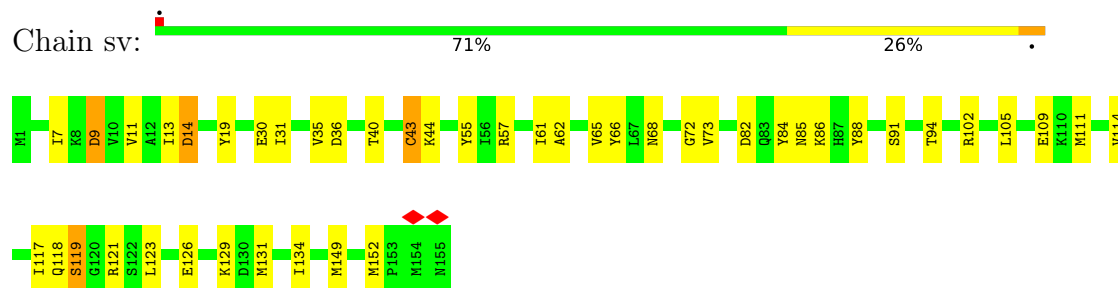
Chain st: 



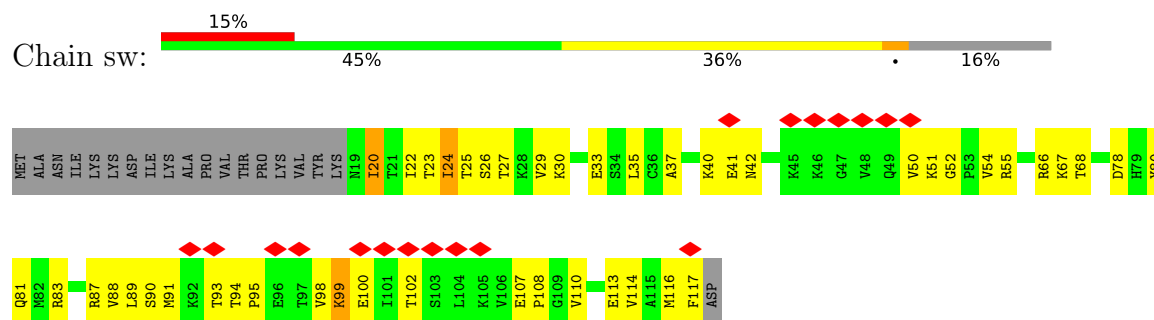
- Molecule 73: Small ribosomal subunit protein uS13



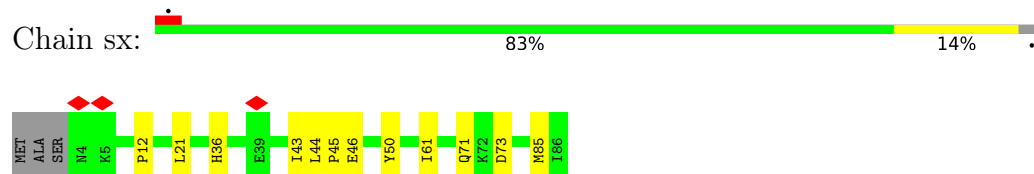
- Molecule 74: Small ribosomal subunit protein eS19



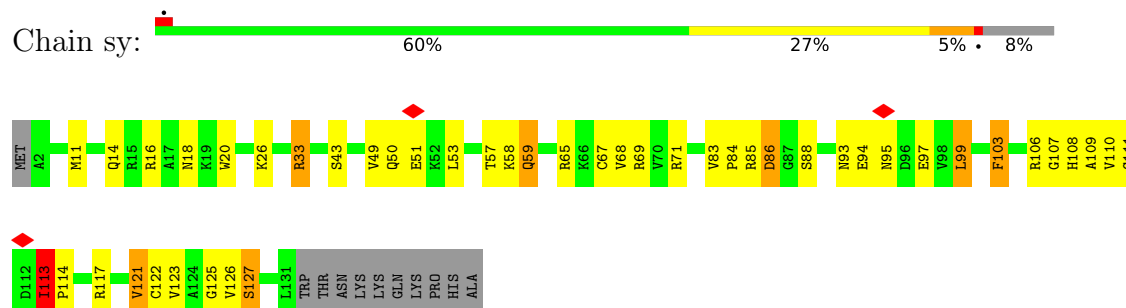
- Molecule 75: Small ribosomal subunit protein uS10



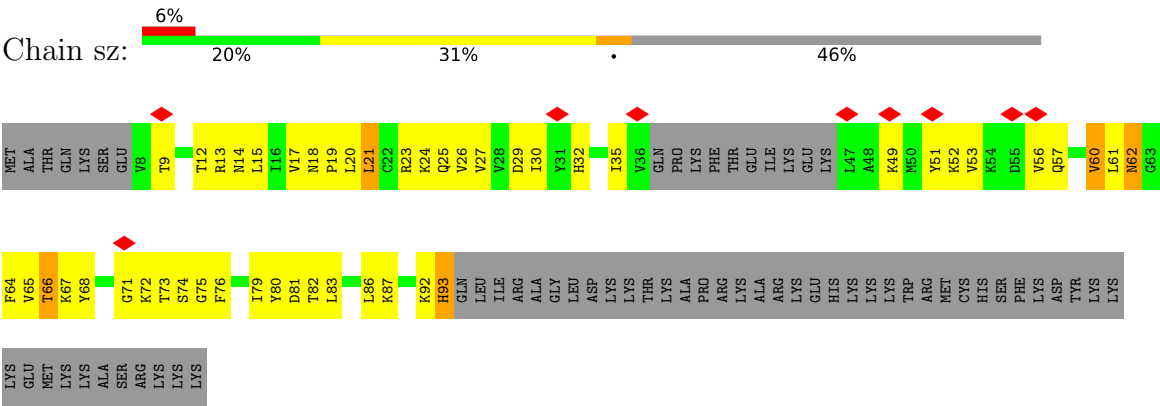
- Molecule 76: 40S ribosomal protein S21



- Molecule 77: 40S ribosomal protein S23, putative



● Molecule 78: 40S ribosomal protein S24, putative



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	53764	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.106	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	17.312	Depositor
Minimum map value	-5.684	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2.5	Depositor
Map size (Å)	428.00003, 428.00003, 428.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	1A	0.20	1/76160 (0.0%)	0.31	1/118640 (0.0%)
2	1B	0.18	0/3470	0.29	0/5401
3	1C	0.21	0/2765	0.38	2/4303 (0.0%)
4	1D	0.18	0/1920	0.29	0/2582
5	1E	0.16	0/3149	0.28	0/4228
6	1F	0.18	0/3306	0.36	1/4437 (0.0%)
7	1G	0.15	0/2284	0.31	0/3059
8	1H	0.14	0/1640	0.30	0/2204
9	1I	0.15	0/1680	0.24	0/2252
10	1J	0.12	0/1727	0.29	0/2320
11	1K	0.14	0/1562	0.24	0/2103
12	1L	0.14	0/1644	0.25	0/2198
13	1M	0.14	0/1369	0.30	0/1834
14	1N	0.15	0/2149	0.29	0/2864
15	1O	0.16	0/1646	0.24	0/2209
16	1P	0.15	0/1032	0.23	0/1388
17	1Q	0.18	0/1707	0.25	0/2276
18	1R	0.16	0/1230	0.23	0/1647
19	1S	0.16	0/1342	0.25	0/1796
20	1T	0.16	0/1445	0.24	0/1946
21	1U	0.16	0/1253	0.22	0/1666
22	1V	0.16	0/1351	0.26	0/1819
23	1W	0.17	0/774	0.38	0/1031
24	1X	0.18	0/1030	0.29	0/1384
25	1Y	0.13	0/941	0.22	0/1262
26	1Z	0.17	0/492	0.25	0/656
27	1a	0.13	0/1673	0.24	0/2236
28	1b	0.14	0/1112	0.25	0/1489
29	1c	0.18	0/1223	0.24	0/1636
30	1d	0.16	0/485	0.24	0/639
31	1e	0.17	0/776	0.38	0/1044
32	1f	0.15	0/1058	0.24	0/1413
33	1g	0.16	0/1036	0.23	0/1381
34	1h	0.16	0/833	0.32	0/1115

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	li	0.12	0/984	0.21	0/1310
36	lj	0.19	0/862	0.29	0/1163
37	lk	0.12	0/721	0.19	0/955
38	ll	0.20	0/602	0.32	0/797
39	lm	0.20	0/696	0.34	0/928
40	ln	0.14	0/592	0.27	0/789
41	lo	0.18	0/444	0.22	0/587
42	lp	0.17	0/425	0.44	2/563 (0.4%)
43	lq	0.16	0/770	0.23	0/1019
44	ls	0.09	0/10	0.27	0/11
45	sA	0.15	0/575	0.39	0/775
46	sB	0.17	0/797	0.30	0/1062
47	sC	0.13	0/654	0.29	0/879
48	sD	0.15	0/470	0.44	0/630
49	sE	0.17	0/449	0.40	0/595
50	sG	0.11	0/2395	0.29	0/3248
51	sH	0.24	0/1755	0.48	3/2727 (0.1%)
52	sK	0.13	0/140	0.17	0/215
53	sa	0.18	0/34809	0.31	7/54226 (0.0%)
54	sb	0.13	0/1659	0.25	0/2243
55	sc	0.15	0/1673	0.29	0/2257
56	sd	0.12	0/1729	0.30	0/2316
57	se	0.15	0/1741	0.28	0/2328
58	sf	0.14	0/2072	0.29	0/2792
59	sg	0.12	0/1495	0.27	0/2009
60	sh	0.19	0/1411	0.50	0/1875
61	si	0.13	0/1265	0.36	0/1698
62	sj	0.16	0/1560	0.28	0/2083
63	sk	0.13	0/1344	0.26	0/1800
64	sl	0.12	0/745	0.32	0/1007
65	sm	0.15	0/1291	0.27	0/1725
66	sn	0.09	0/428	0.39	0/566
67	so	0.14	0/1204	0.26	0/1613
68	sp	0.14	0/1013	0.30	0/1361
69	sq	0.12	0/888	0.35	0/1186
70	sr	0.16	0/1040	0.30	0/1404
71	ss	0.14	0/1121	0.30	0/1503
72	st	0.12	0/919	0.28	0/1234
73	su	0.14	0/1181	0.32	0/1584
74	sv	0.12	0/1271	0.25	0/1708
75	sw	0.13	0/784	0.37	0/1055
76	sx	0.14	0/663	0.26	0/898
77	sy	0.24	0/1027	0.75	1/1376 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	sz	0.25	0/608	0.76	0/820
All	All	0.18	1/205546 (0.0%)	0.31	17/301378 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
5	lE	0	1
8	lH	0	1
34	lh	0	1
38	ll	0	1
49	sE	0	1
70	sr	0	1
77	sy	0	1
All	All	0	7

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	lA	3473	U	O3'-P	-5.31	1.53	1.61

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	lC	62	U	OP1-P-O3'	-8.78	81.66	108.00
3	lC	62	U	OP2-P-O3'	-8.72	81.83	108.00
53	sa	1396	A	C1'-C2'-O2'	-8.07	96.30	108.40
1	lA	3477	U	C2'-C3'-O3'	-7.42	98.36	109.50
53	sa	1425	A	C4'-C3'-O3'	-6.86	102.71	113.00

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	lE	258	HIS	Peptide
8	lH	93	GLY	Peptide
34	lh	76	TYR	Peptide
38	ll	39	TYR	Peptide
49	sE	15	GLY	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1A	67965	0	34095	930	0
2	1B	3097	0	1552	47	0
3	1C	2477	0	1252	86	0
4	1D	1881	0	1928	32	0
5	1E	3085	0	3215	51	0
6	1F	3248	0	3472	65	0
7	1G	2245	0	2325	32	0
8	1H	1608	0	1728	32	0
9	1I	1658	0	1802	17	0
10	1J	1697	0	1820	25	0
11	1K	1538	0	1598	21	0
12	1L	1608	0	1667	25	0
13	1M	1350	0	1390	22	0
14	1N	2121	0	2325	52	0
15	1O	1616	0	1700	20	0
16	1P	1020	0	1107	20	0
17	1Q	1676	0	1777	24	0
18	1R	1211	0	1280	17	0
19	1S	1321	0	1427	19	0
20	1T	1413	0	1479	22	0
21	1U	1235	0	1369	17	0
22	1V	1320	0	1406	12	0
23	1W	763	0	818	28	0
24	1X	1015	0	1054	17	0
25	1Y	926	0	997	13	0
26	1Z	481	0	518	4	0
27	1a	1651	0	1822	29	0
28	1b	1094	0	1174	20	0
29	1c	1192	0	1205	18	0
30	1d	478	0	507	10	0
31	1e	768	0	810	21	0
32	1f	1039	0	1121	11	0
33	1g	1019	0	1104	17	0
34	1h	820	0	864	15	0
35	1i	974	0	1093	13	0
36	1j	841	0	878	11	0
37	1k	712	0	755	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	ll	591	0	617	10	0
39	lm	688	0	728	14	0
40	ln	584	0	643	16	0
41	lo	432	0	444	8	0
42	lp	420	0	450	10	0
43	lq	756	0	821	12	0
44	ls	76	0	34	0	0
45	sA	568	0	627	14	0
46	sB	787	0	831	19	0
47	sC	641	0	681	14	0
48	sD	468	0	500	20	0
49	sE	442	0	443	19	0
50	sG	2347	0	2325	73	0
51	sH	1573	0	797	31	0
52	sK	126	0	64	0	0
53	sa	31080	0	15618	475	0
54	sb	1626	0	1627	23	0
55	sc	1642	0	1721	38	0
56	sd	1708	0	1809	43	0
57	se	1717	0	1822	26	0
58	sf	2031	0	2145	51	0
59	sg	1473	0	1533	38	0
60	sh	1395	0	1518	82	0
61	si	1246	0	1370	30	0
62	sj	1536	0	1588	37	0
63	sk	1323	0	1420	17	0
64	sl	729	0	760	28	0
65	sm	1263	0	1279	16	0
66	sn	428	0	466	7	0
67	so	1184	0	1272	22	0
68	sp	999	0	1024	22	0
69	sq	873	0	942	18	0
70	sr	1022	0	1051	17	0
71	ss	1104	0	1185	29	0
72	st	907	0	962	24	0
73	su	1163	0	1202	30	0
74	sv	1245	0	1285	36	0
75	sw	774	0	835	31	0
76	sx	651	0	668	8	0
77	sy	1010	0	1067	35	0
78	sz	598	0	650	39	0
All	All	191389	0	143258	2840	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 9.

The worst 5 of 2840 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)
1:lA:3454:G:N1	1:lA:3501:A:C2	2.19	1.11
1:lA:3454:G:N1	1:lA:3501:A:H2	1.49	1.08
3:lC:27:G:H1	3:lC:50:A:N6	1.60	0.98
53:sa:1441:C:HO2'	53:sa:1442:A:H8	0.97	0.97
1:lA:631:G:H1	1:lA:659:U:H3	0.96	0.95

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	ID	244/246 (99%)	232 (95%)	11 (4%)	1 (0%)	30	66
5	IE	386/402 (96%)	370 (96%)	16 (4%)	0	100	100
6	IF	416/431 (96%)	391 (94%)	25 (6%)	0	100	100
7	IG	278/286 (97%)	255 (92%)	22 (8%)	1 (0%)	30	66
8	IH	201/203 (99%)	183 (91%)	17 (8%)	1 (0%)	25	61
9	II	208/230 (90%)	198 (95%)	9 (4%)	1 (0%)	25	61
10	IJ	205/286 (72%)	191 (93%)	12 (6%)	2 (1%)	13	46
11	IK	191/197 (97%)	182 (95%)	8 (4%)	1 (0%)	25	61
12	IL	197/210 (94%)	190 (96%)	7 (4%)	0	100	100
13	IM	166/174 (95%)	161 (97%)	4 (2%)	1 (1%)	22	57
14	IN	260/291 (89%)	247 (95%)	12 (5%)	1 (0%)	30	66
15	IO	202/204 (99%)	196 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	lP	128/135 (95%)	126 (98%)	2 (2%)	0	100	100
17	lQ	202/204 (99%)	194 (96%)	8 (4%)	0	100	100
18	lR	153/179 (86%)	152 (99%)	1 (1%)	0	100	100
19	lS	165/167 (99%)	153 (93%)	12 (7%)	0	100	100
20	lT	171/173 (99%)	162 (95%)	9 (5%)	0	100	100
21	lU	148/198 (75%)	146 (99%)	2 (1%)	0	100	100
22	lV	163/165 (99%)	160 (98%)	3 (2%)	0	100	100
23	lW	91/137 (66%)	87 (96%)	4 (4%)	0	100	100
24	lX	131/140 (94%)	125 (95%)	6 (5%)	0	100	100
25	lY	114/121 (94%)	112 (98%)	2 (2%)	0	100	100
26	lZ	55/163 (34%)	53 (96%)	2 (4%)	0	100	100
27	la	208/213 (98%)	202 (97%)	6 (3%)	0	100	100
28	lb	135/139 (97%)	133 (98%)	2 (2%)	0	100	100
29	lc	146/148 (99%)	138 (94%)	8 (6%)	0	100	100
30	ld	58/64 (91%)	56 (97%)	2 (3%)	0	100	100
31	le	101/109 (93%)	94 (93%)	7 (7%)	0	100	100
32	lf	124/150 (83%)	123 (99%)	1 (1%)	0	100	100
33	lg	122/134 (91%)	119 (98%)	3 (2%)	0	100	100
34	lh	103/137 (75%)	96 (93%)	6 (6%)	1 (1%)	13	46
35	li	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
36	lj	104/108 (96%)	102 (98%)	2 (2%)	0	100	100
37	lk	83/104 (80%)	83 (100%)	0	0	100	100
38	ll	70/77 (91%)	65 (93%)	4 (6%)	1 (1%)	9	37
39	lm	88/93 (95%)	81 (92%)	7 (8%)	0	100	100
40	ln	71/88 (81%)	69 (97%)	2 (3%)	0	100	100
41	lo	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
42	lp	51/56 (91%)	51 (100%)	0	0	100	100
43	lq	90/98 (92%)	87 (97%)	3 (3%)	0	100	100
44	ls	1/14 (7%)	1 (100%)	0	0	100	100
45	sA	70/137 (51%)	65 (93%)	4 (6%)	1 (1%)	9	37
46	sB	96/144 (67%)	89 (93%)	6 (6%)	1 (1%)	13	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
47	sC	81/83 (98%)	77 (95%)	4 (5%)	0	100	100
48	sD	58/69 (84%)	54 (93%)	4 (7%)	0	100	100
49	sE	53/55 (96%)	45 (85%)	8 (15%)	0	100	100
50	sG	299/321 (93%)	280 (94%)	19 (6%)	0	100	100
54	sb	203/254 (80%)	199 (98%)	4 (2%)	0	100	100
55	sc	213/255 (84%)	203 (95%)	9 (4%)	1 (0%)	25	61
56	sd	219/244 (90%)	195 (89%)	23 (10%)	1 (0%)	25	61
57	se	210/256 (82%)	203 (97%)	7 (3%)	0	100	100
58	sf	254/326 (78%)	239 (94%)	14 (6%)	1 (0%)	30	66
59	sg	181/206 (88%)	171 (94%)	10 (6%)	0	100	100
60	sh	170/266 (64%)	144 (85%)	21 (12%)	5 (3%)	3	20
61	si	154/201 (77%)	141 (92%)	10 (6%)	3 (2%)	6	31
62	sj	188/237 (79%)	181 (96%)	7 (4%)	0	100	100
63	sk	160/185 (86%)	157 (98%)	3 (2%)	0	100	100
64	sl	89/127 (70%)	81 (91%)	7 (8%)	1 (1%)	12	44
65	sm	152/156 (97%)	145 (95%)	7 (5%)	0	100	100
66	sn	44/136 (32%)	36 (82%)	7 (16%)	1 (2%)	5	26
67	so	148/150 (99%)	144 (97%)	4 (3%)	0	100	100
68	sp	131/146 (90%)	124 (95%)	7 (5%)	0	100	100
69	sq	107/144 (74%)	97 (91%)	9 (8%)	1 (1%)	14	49
70	sr	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
71	ss	139/157 (88%)	132 (95%)	7 (5%)	0	100	100
72	st	109/117 (93%)	104 (95%)	3 (3%)	2 (2%)	7	32
73	su	142/155 (92%)	131 (92%)	11 (8%)	0	100	100
74	sv	153/155 (99%)	148 (97%)	5 (3%)	0	100	100
75	sw	97/118 (82%)	90 (93%)	6 (6%)	1 (1%)	13	46
76	sx	81/86 (94%)	79 (98%)	2 (2%)	0	100	100
77	sy	128/141 (91%)	100 (78%)	25 (20%)	3 (2%)	5	26
78	sz	72/140 (51%)	52 (72%)	18 (25%)	2 (3%)	4	21
All	All	10526/12142 (87%)	9954 (95%)	537 (5%)	35 (0%)	38	70

5 of 35 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	lJ	246	GLN
34	lh	77	GLY
38	ll	40	PRO
60	sh	222	THR
60	sh	227	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	ID	195/195 (100%)	188 (96%)	7 (4%)	30	64
5	IE	331/343 (96%)	320 (97%)	11 (3%)	33	67
6	IF	336/345 (97%)	323 (96%)	13 (4%)	27	61
7	IG	227/231 (98%)	221 (97%)	6 (3%)	41	72
8	IH	172/172 (100%)	168 (98%)	4 (2%)	45	75
9	II	178/195 (91%)	176 (99%)	2 (1%)	70	87
10	IJ	184/242 (76%)	177 (96%)	7 (4%)	28	62
11	IK	171/174 (98%)	167 (98%)	4 (2%)	45	75
12	IL	170/176 (97%)	165 (97%)	5 (3%)	37	70
13	IM	144/147 (98%)	141 (98%)	3 (2%)	48	77
14	IN	223/243 (92%)	217 (97%)	6 (3%)	40	71
15	IO	167/167 (100%)	164 (98%)	3 (2%)	54	80
16	IP	113/117 (97%)	111 (98%)	2 (2%)	54	80
17	IQ	171/171 (100%)	169 (99%)	2 (1%)	67	86
18	IR	127/147 (86%)	124 (98%)	3 (2%)	44	74
19	IS	142/142 (100%)	142 (100%)	0	100	100
20	IT	156/156 (100%)	151 (97%)	5 (3%)	34	67
21	IU	132/174 (76%)	128 (97%)	4 (3%)	36	69
22	IV	144/144 (100%)	141 (98%)	3 (2%)	48	77
23	IW	86/125 (69%)	79 (92%)	7 (8%)	9	34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	lX	109/113 (96%)	104 (95%)	5 (5%)	23	56
25	lY	99/102 (97%)	97 (98%)	2 (2%)	50	78
26	lZ	52/137 (38%)	49 (94%)	3 (6%)	17	48
27	la	177/179 (99%)	171 (97%)	6 (3%)	32	66
28	lb	121/123 (98%)	119 (98%)	2 (2%)	56	81
29	lc	120/120 (100%)	118 (98%)	2 (2%)	56	81
30	ld	50/54 (93%)	48 (96%)	2 (4%)	27	61
31	le	86/92 (94%)	83 (96%)	3 (4%)	31	65
32	lf	110/128 (86%)	107 (97%)	3 (3%)	40	71
33	lg	108/116 (93%)	106 (98%)	2 (2%)	52	79
34	lh	86/116 (74%)	82 (95%)	4 (5%)	22	56
35	li	103/103 (100%)	102 (99%)	1 (1%)	73	88
36	lj	89/91 (98%)	86 (97%)	3 (3%)	32	66
37	lk	71/82 (87%)	70 (99%)	1 (1%)	62	83
38	ll	60/64 (94%)	57 (95%)	3 (5%)	20	53
39	lm	72/74 (97%)	71 (99%)	1 (1%)	62	83
40	ln	63/76 (83%)	60 (95%)	3 (5%)	21	55
41	lo	44/44 (100%)	42 (96%)	2 (4%)	23	57
42	lp	45/48 (94%)	44 (98%)	1 (2%)	47	76
43	lq	85/91 (93%)	85 (100%)	0	100	100
44	ls	1/1 (100%)	1 (100%)	0	100	100
45	sA	66/112 (59%)	64 (97%)	2 (3%)	36	69
46	sB	87/127 (68%)	84 (97%)	3 (3%)	32	66
47	sC	72/72 (100%)	67 (93%)	5 (7%)	13	42
48	sD	50/59 (85%)	47 (94%)	3 (6%)	16	47
49	sE	45/45 (100%)	41 (91%)	4 (9%)	8	31
50	sG	260/272 (96%)	243 (94%)	17 (6%)	14	43
54	sb	178/218 (82%)	173 (97%)	5 (3%)	38	70
55	sc	172/199 (86%)	160 (93%)	12 (7%)	12	41
56	sd	184/206 (89%)	168 (91%)	16 (9%)	8	32
57	se	193/227 (85%)	188 (97%)	5 (3%)	41	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	sf	223/283 (79%)	211 (95%)	12 (5%)	18	50
59	sg	165/178 (93%)	161 (98%)	4 (2%)	44	74
60	sh	146/220 (66%)	137 (94%)	9 (6%)	15	45
61	si	136/167 (81%)	127 (93%)	9 (7%)	14	43
62	sj	163/205 (80%)	160 (98%)	3 (2%)	54	80
63	sk	144/164 (88%)	139 (96%)	5 (4%)	31	65
64	sl	81/111 (73%)	71 (88%)	10 (12%)	4	18
65	sm	136/138 (99%)	134 (98%)	2 (2%)	60	83
66	sn	44/114 (39%)	40 (91%)	4 (9%)	7	30
67	so	128/128 (100%)	123 (96%)	5 (4%)	27	61
68	sp	103/114 (90%)	99 (96%)	4 (4%)	27	61
69	sq	97/127 (76%)	89 (92%)	8 (8%)	9	34
70	sr	112/112 (100%)	107 (96%)	5 (4%)	23	57
71	ss	114/126 (90%)	110 (96%)	4 (4%)	31	65
72	st	101/106 (95%)	98 (97%)	3 (3%)	36	69
73	su	122/130 (94%)	112 (92%)	10 (8%)	9	34
74	sv	132/132 (100%)	124 (94%)	8 (6%)	15	46
75	sw	90/107 (84%)	81 (90%)	9 (10%)	6	25
76	sx	75/77 (97%)	74 (99%)	1 (1%)	65	85
77	sy	104/114 (91%)	94 (90%)	10 (10%)	7	27
78	sz	67/125 (54%)	56 (84%)	11 (16%)	2	9
All	All	9110/10275 (89%)	8756 (96%)	354 (4%)	30	61

5 of 354 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
59	sg	33	ILE
69	sq	89	ILE
60	sh	222	THR
64	sl	1	MET
71	ss	61	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 78 such sidechains are listed below:

Mol	Chain	Res	Type
58	sf	15	HIS
70	sr	24	GLN
59	sg	80	GLN
65	sm	10	GLN
74	sv	69	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	lA	3165/3503 (90%)	588 (18%)	0
2	lB	143/155 (92%)	32 (22%)	0
3	lC	116/117 (99%)	21 (18%)	0
51	sH	72/76 (94%)	22 (30%)	0
52	sK	5/6 (83%)	0	0
53	sa	1440/1947 (73%)	314 (21%)	0
All	All	4941/5804 (85%)	977 (19%)	0

5 of 977 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	lA	18	G
1	lA	22	A
1	lA	29	U
1	lA	30	A
1	lA	36	A

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

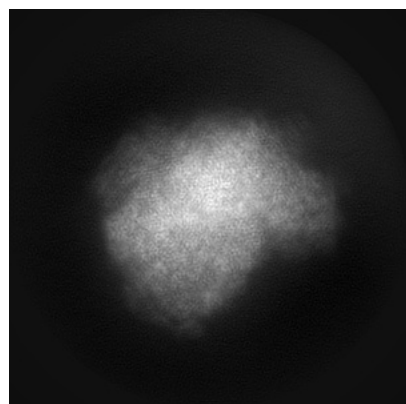
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64713. These allow visual inspection of the internal detail of the map and identification of artifacts.

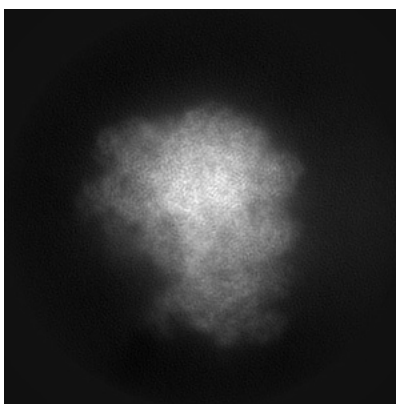
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

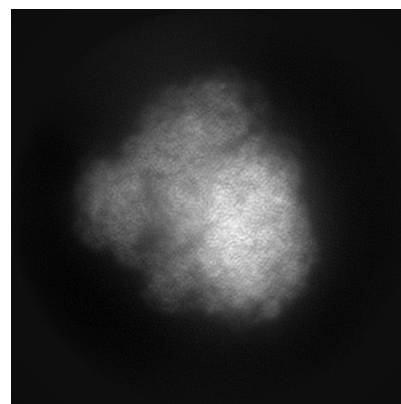
6.1.1 Primary map



X

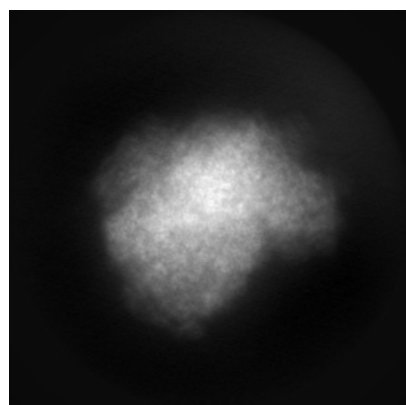


Y

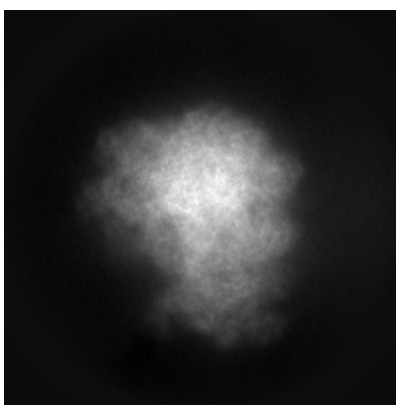


Z

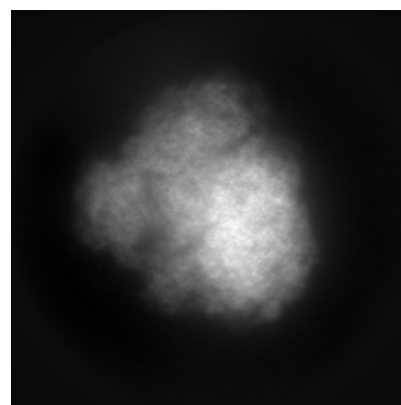
6.1.2 Raw map



X



Y

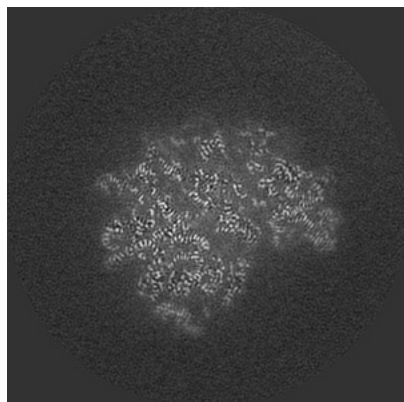


Z

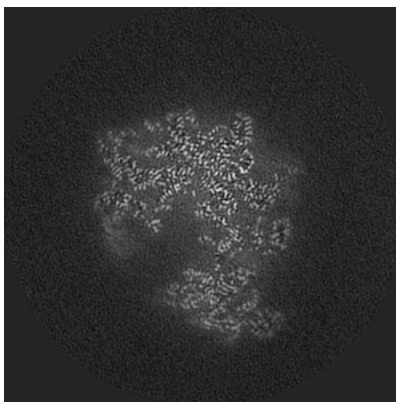
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

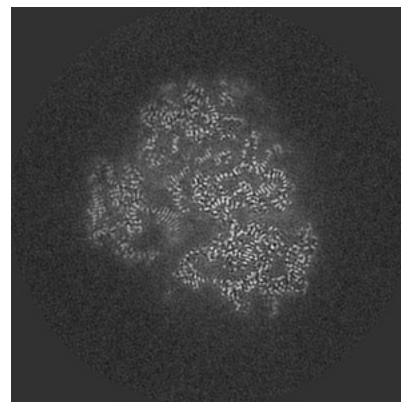
6.2.1 Primary map



X Index: 200

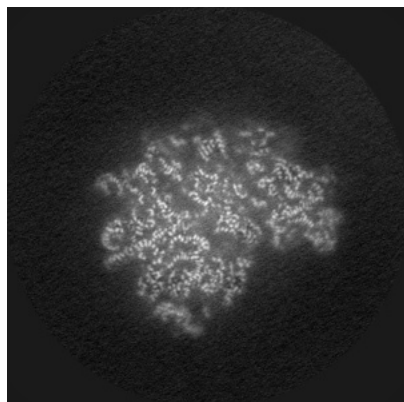


Y Index: 200

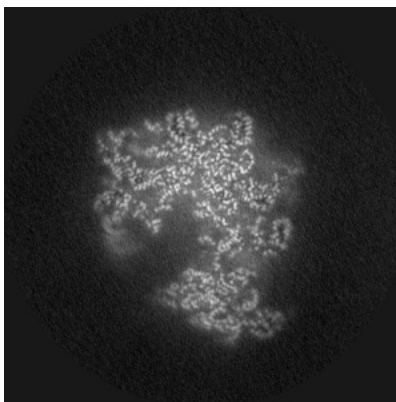


Z Index: 200

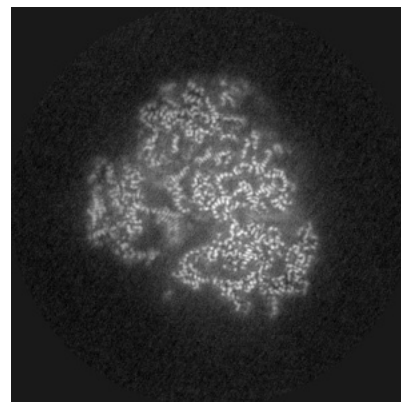
6.2.2 Raw map



X Index: 200



Y Index: 200

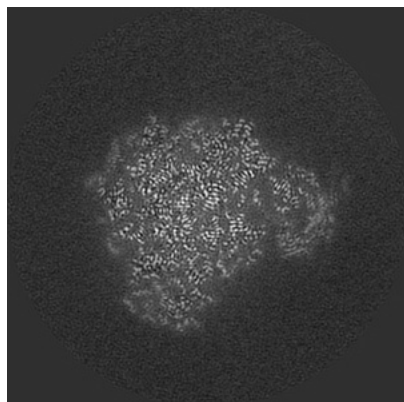


Z Index: 200

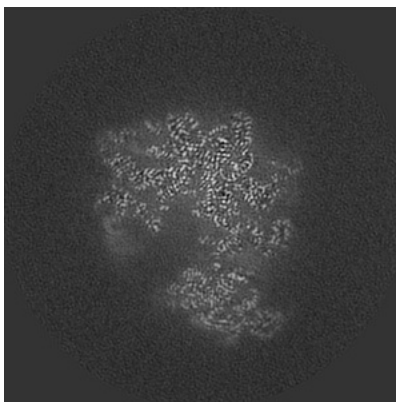
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

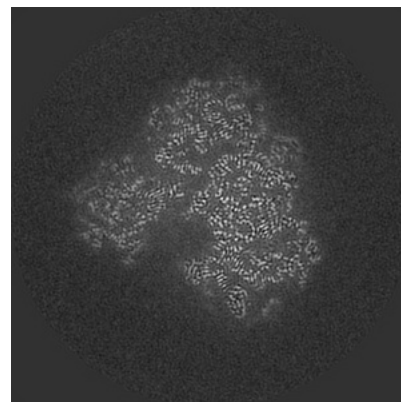
6.3.1 Primary map



X Index: 221

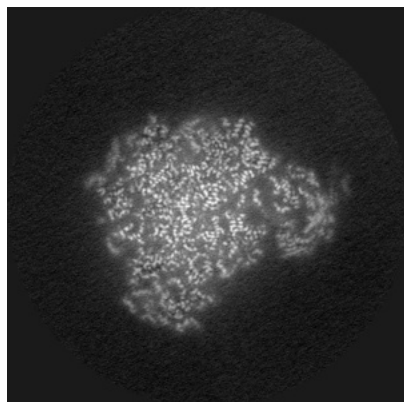


Y Index: 201

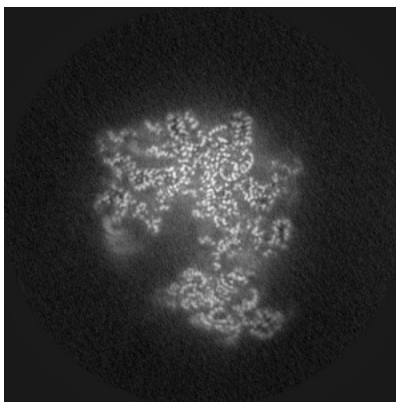


Z Index: 212

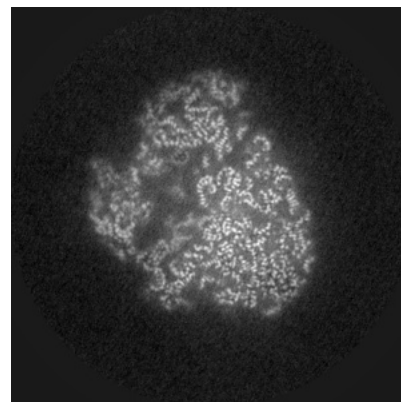
6.3.2 Raw map



X Index: 221



Y Index: 201

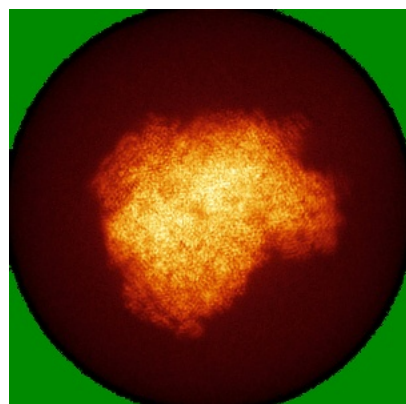


Z Index: 191

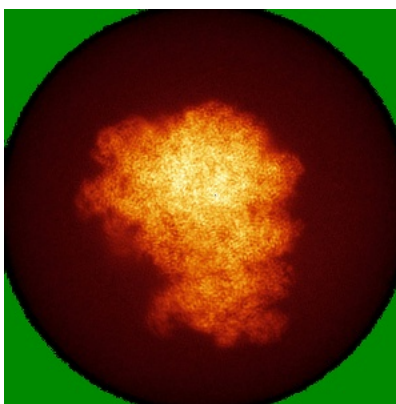
The images above show the largest variance slices of the map in three orthogonal directions.

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

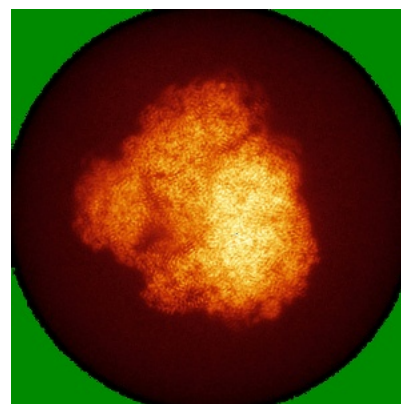
6.4.1 Primary map



X

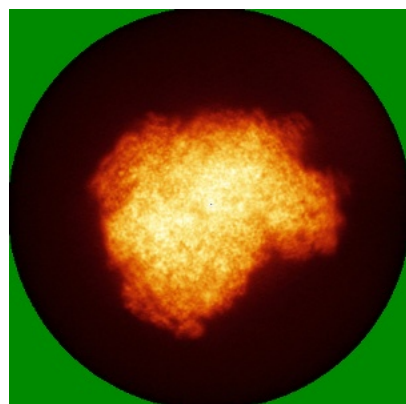


Y

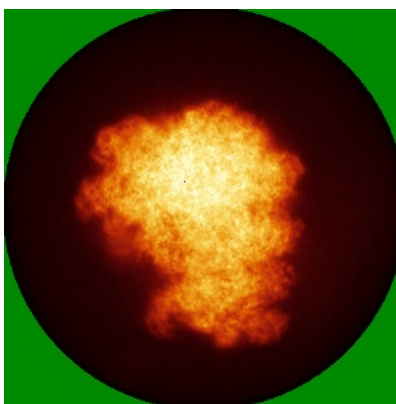


Z

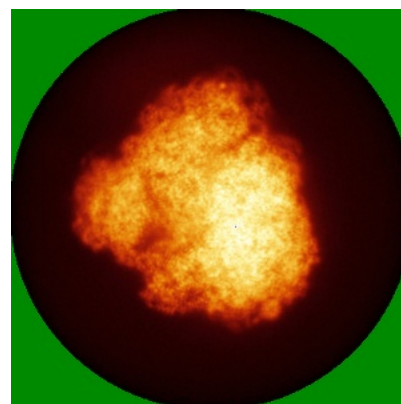
6.4.2 Raw map



X



Y

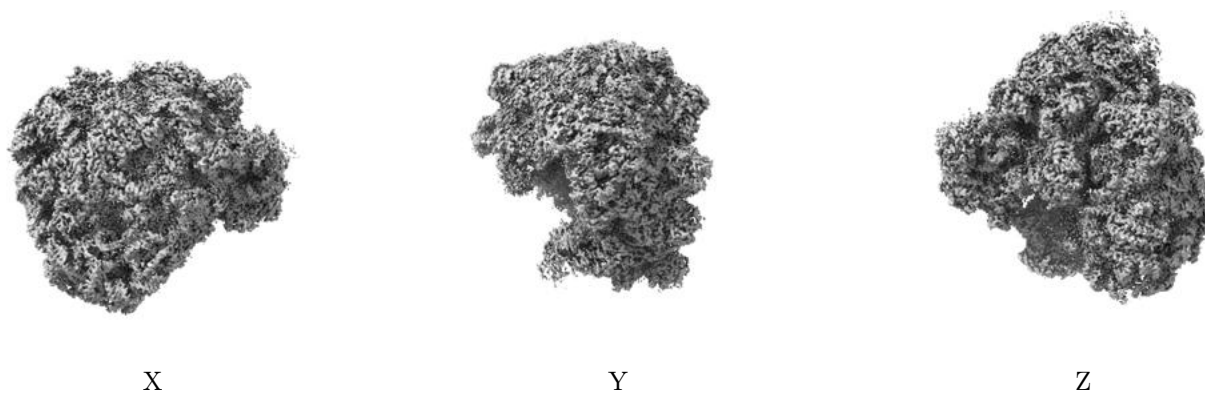


Z

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.

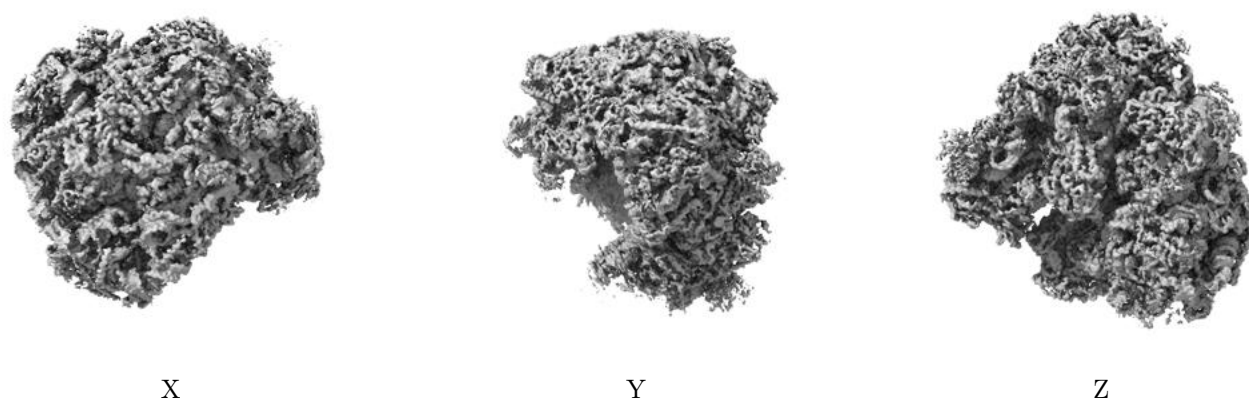
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.5. 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.

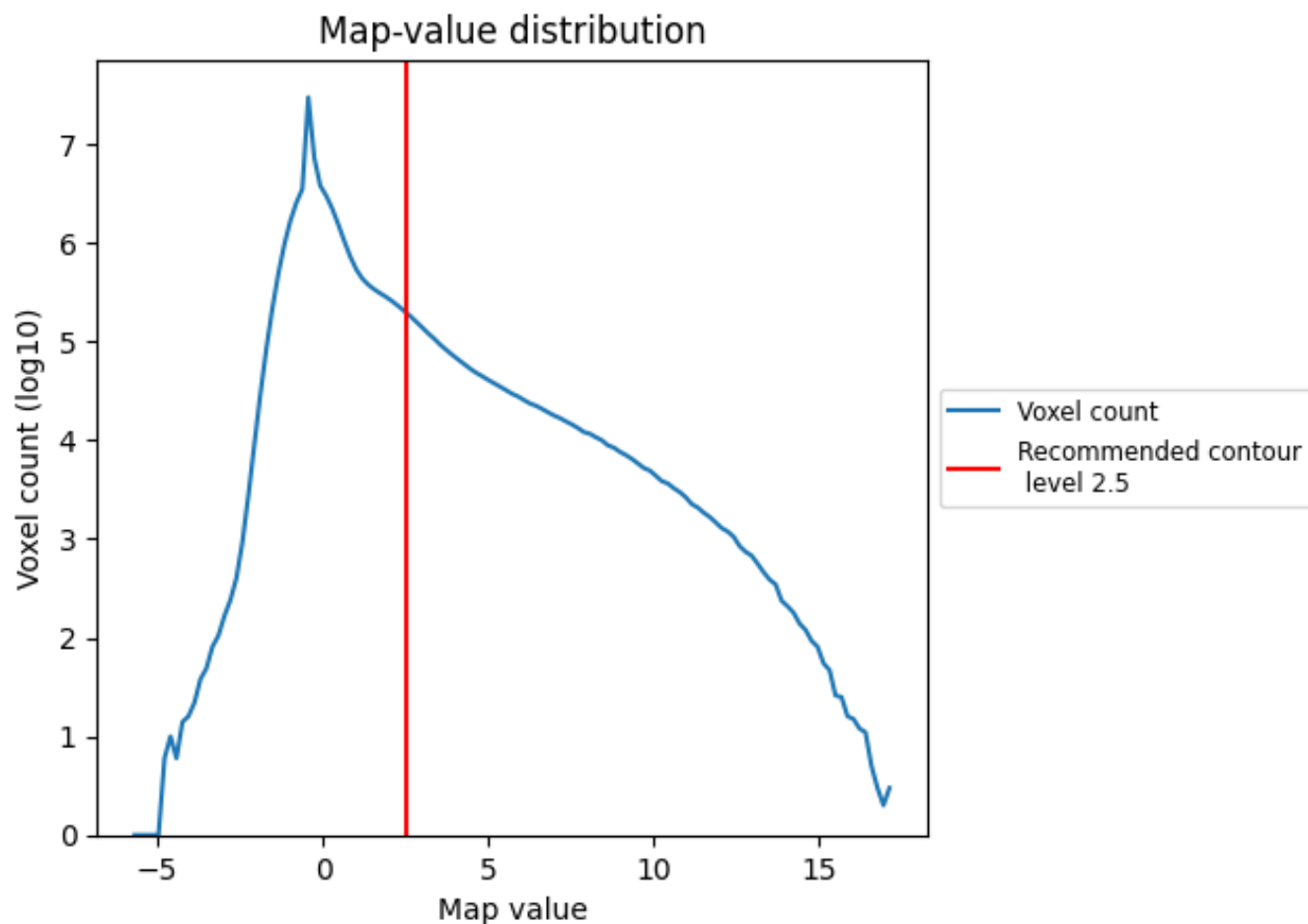
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

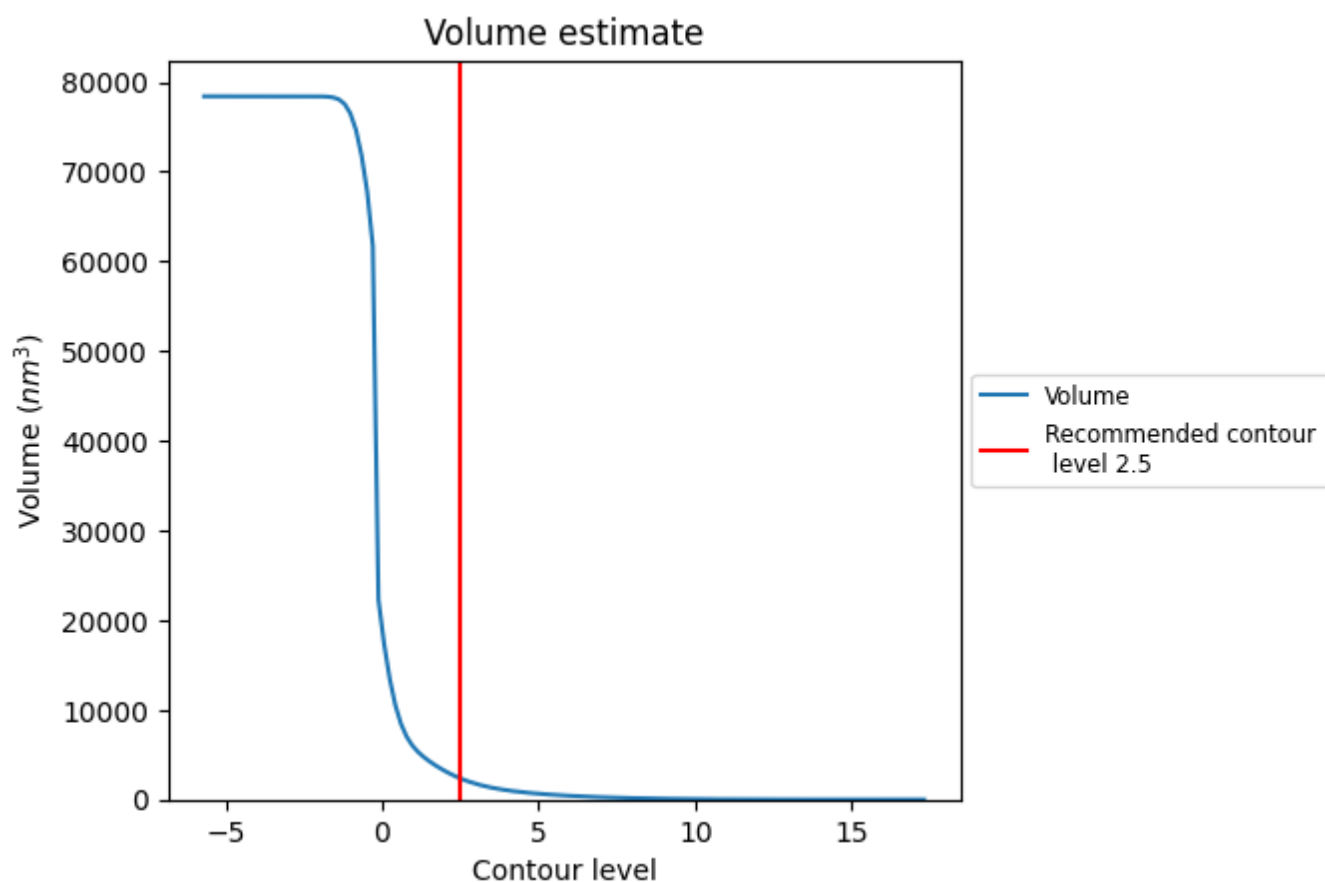
This section contains the results of statistical analysis of the map.

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.

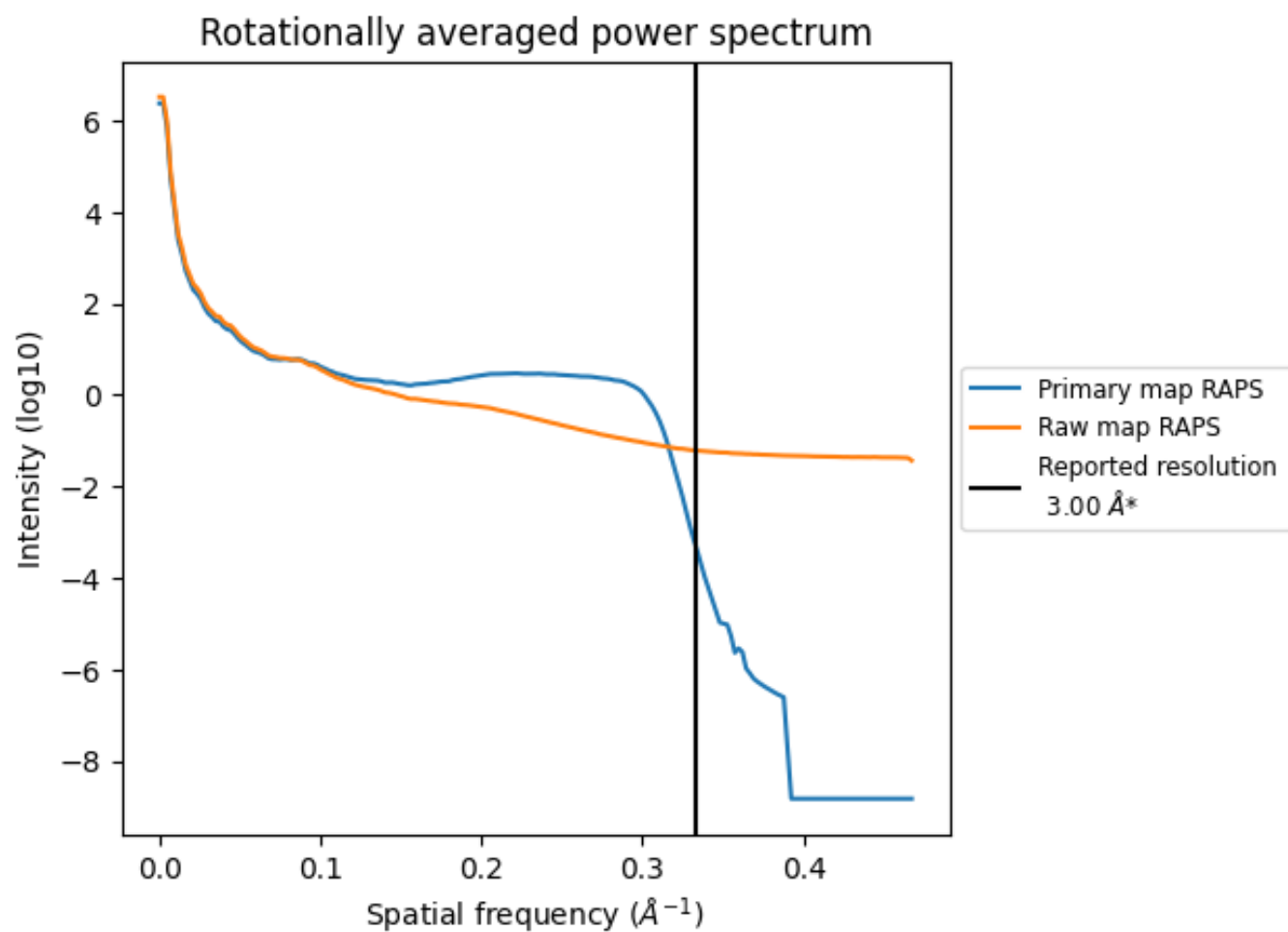
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2367 nm³; this corresponds to an approximate mass of 2138 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

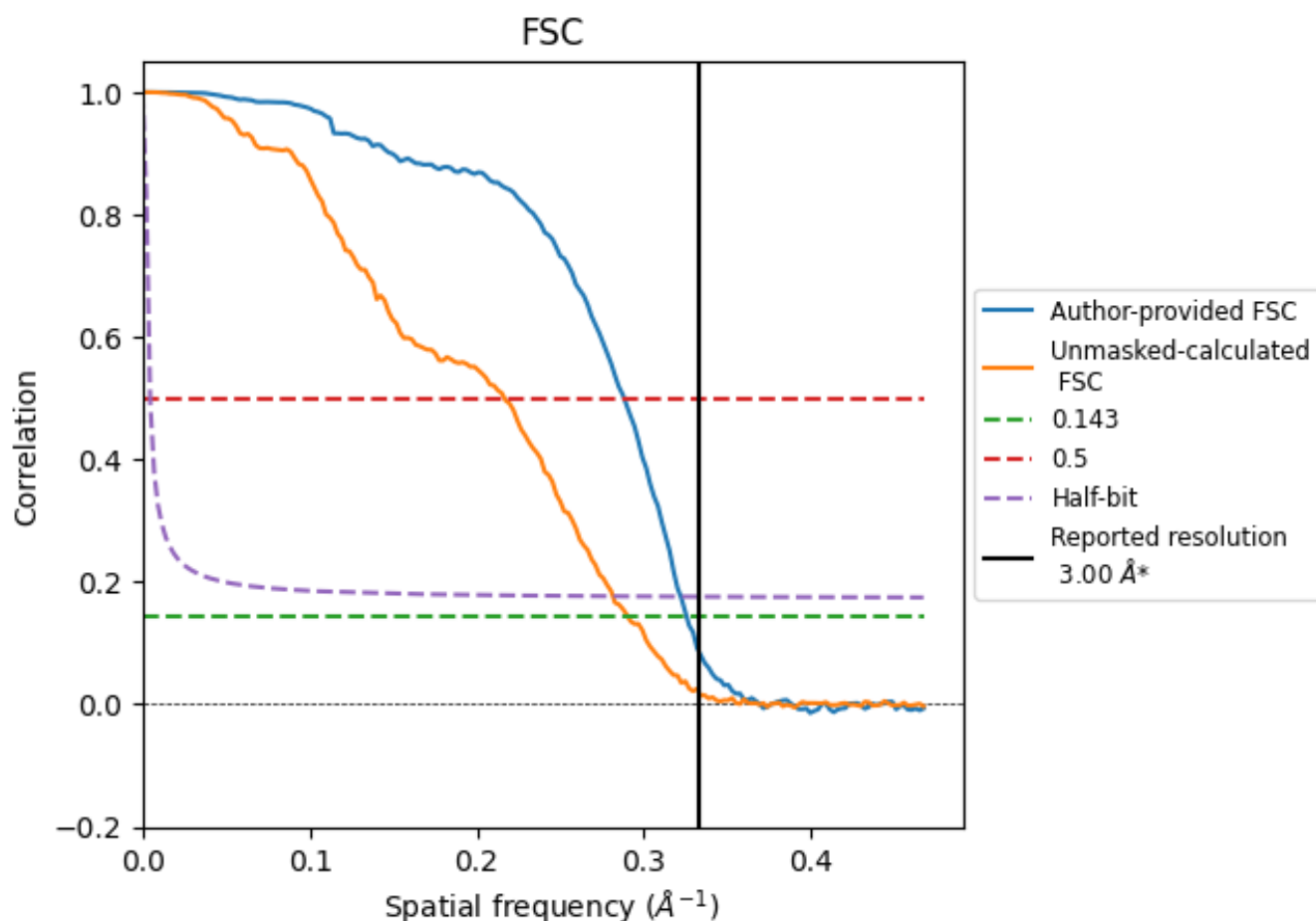


*Reported resolution corresponds to spatial frequency of 0.333 \AA^{-1}

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 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

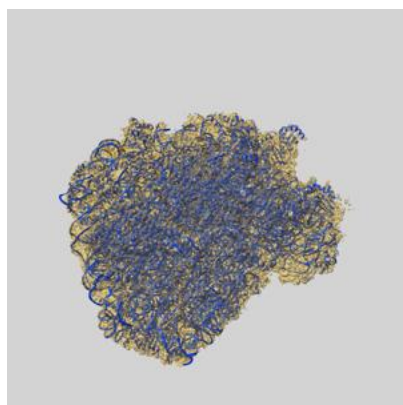
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.07	3.47	3.10
Unmasked-calculated*	3.44	4.62	3.55

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.44 differs from the reported value 3.0 by more than 10 %

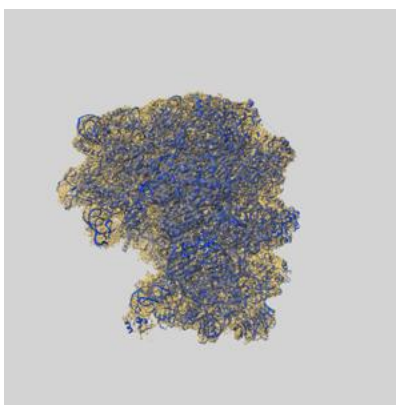
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-64713 and PDB model 9V21. Per-residue inclusion information can be found in [section 3](#) on [page 18](#).

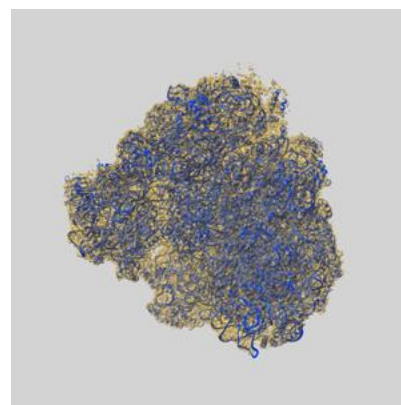
9.1 Map-model overlay [i](#)



X



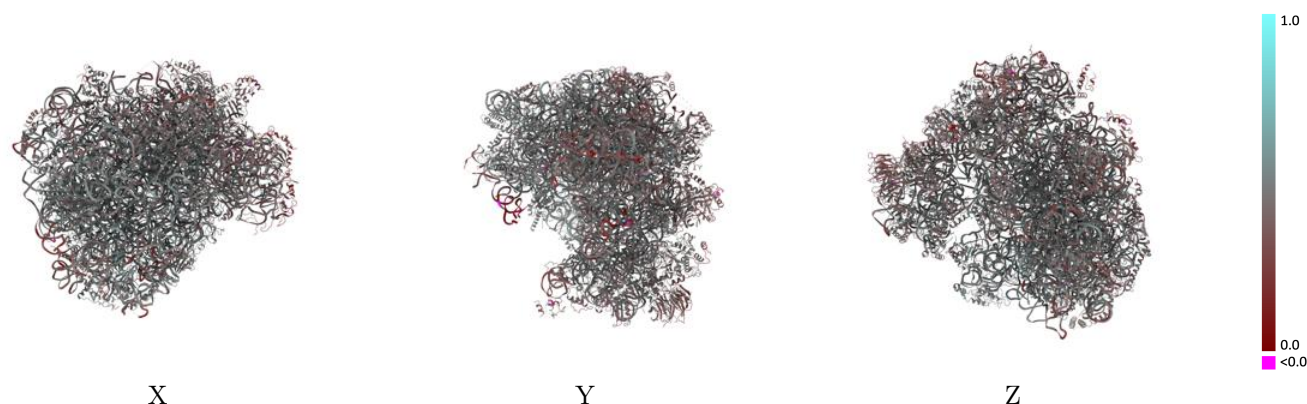
Y



Z

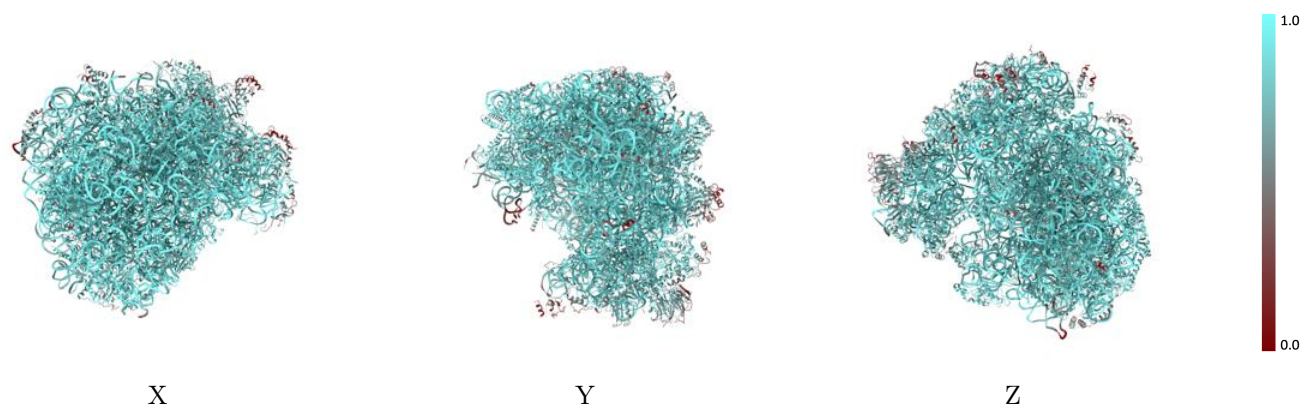
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



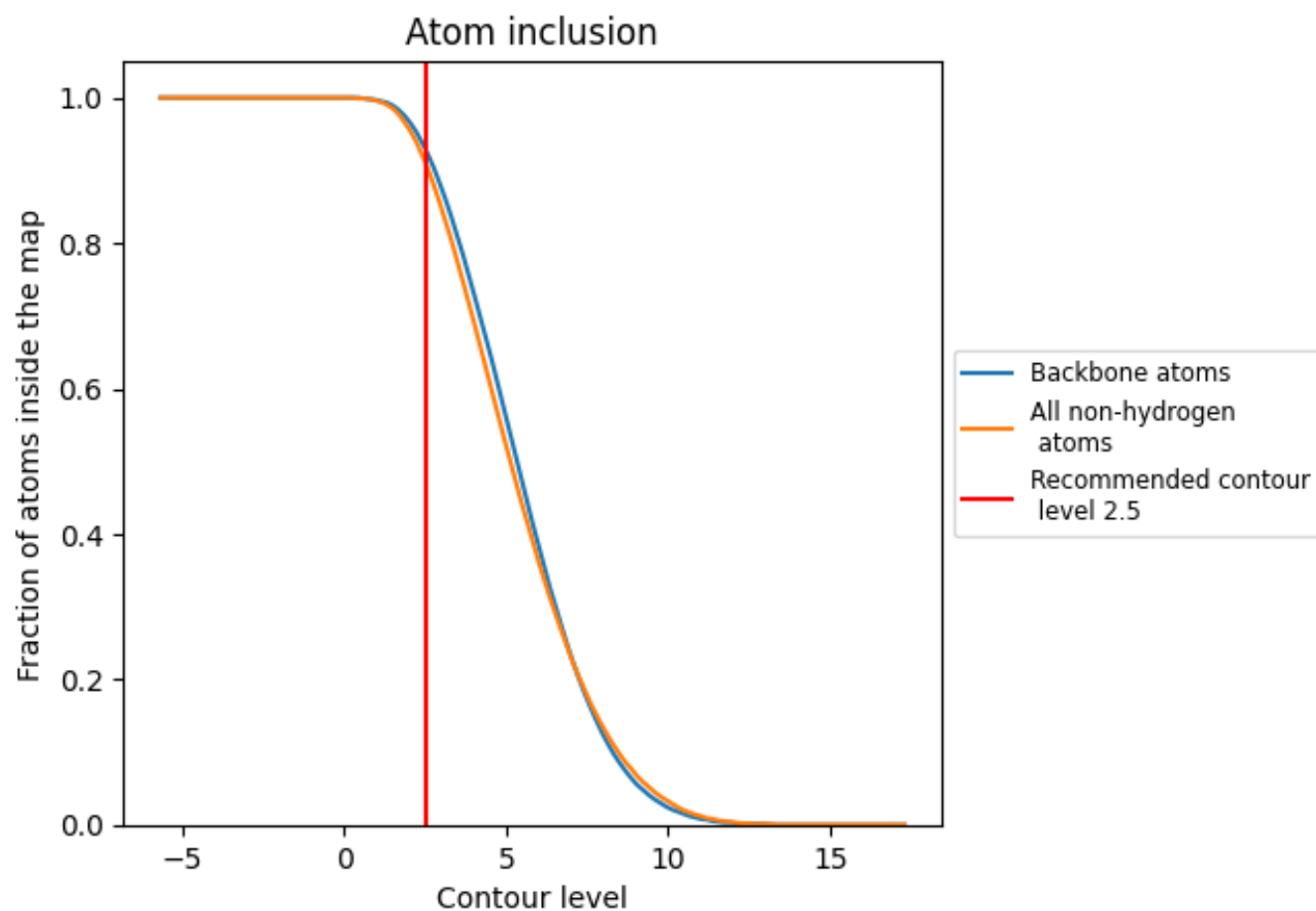
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.5).































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 91% 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 (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9110	 0.4580
1A	 0.9560	 0.4660
1B	 0.9730	 0.4670
1C	 0.9780	 0.4740
1D	 0.9680	 0.4800
1E	 0.9350	 0.4840
1F	 0.9140	 0.4890
1G	 0.8720	 0.5020
1H	 0.7950	 0.4520
1I	 0.9500	 0.5050
1J	 0.7410	 0.4250
1K	 0.8660	 0.4730
1L	 0.9630	 0.4890
1M	 0.8610	 0.4670
1N	 0.7900	 0.4470
1O	 0.9370	 0.4960
1P	 0.9130	 0.5010
1Q	 0.9730	 0.4920
1R	 0.9540	 0.4730
1S	 0.9710	 0.5040
1T	 0.9640	 0.5110
1U	 0.9190	 0.4440
1V	 0.9510	 0.5150
1W	 0.5700	 0.3230
1X	 0.9630	 0.4730
1Y	 0.8680	 0.4300
1Z	 0.9440	 0.4680
1a	 0.8720	 0.4580
1b	 0.7650	 0.4120
1c	 0.9580	 0.5120
1d	 0.9700	 0.5060
1e	 0.8160	 0.4350
1f	 0.8770	 0.4480
1g	 0.9560	 0.4880
1h	 0.9310	 0.4420







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Chain	Atom inclusion	Q-score
li	 0.8660	 0.4390
lj	 0.9560	 0.5040
lk	 0.9050	 0.4760
ll	 0.9910	 0.4900
lm	 0.9610	 0.4620
ln	 0.6570	 0.3740
lo	 0.9860	 0.4740
lp	 0.9360	 0.4900
lq	 0.9650	 0.5010
ls	 1.0000	 0.4080
sA	 0.7400	 0.4520
sB	 0.9300	 0.4760
sC	 0.7760	 0.4200
sD	 0.8350	 0.4170
sE	 0.9260	 0.4610
sG	 0.5630	 0.3670
sH	 0.9890	 0.4410
sK	 1.0000	 0.4930
sa	 0.9630	 0.4520
sb	 0.8280	 0.4380
sc	 0.8810	 0.4680
sd	 0.7700	 0.4310
se	 0.8440	 0.4410
sf	 0.8050	 0.4300
sg	 0.8650	 0.4610
sh	 0.6160	 0.3070
si	 0.4910	 0.3530
sj	 0.7700	 0.3930
sk	 0.8070	 0.4430
sl	 0.6620	 0.4140
sm	 0.8940	 0.4400
sn	 0.2170	 0.3190
so	 0.8680	 0.4270
sp	 0.9170	 0.4720
sq	 0.7640	 0.4360
sr	 0.9160	 0.4570
ss	 0.8530	 0.4680
st	 0.6810	 0.3580
su	 0.8500	 0.4500
sv	 0.8230	 0.4580
sw	 0.6830	 0.4090
sx	 0.8150	 0.4440

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Chain	Atom inclusion	Q-score
sy	 0.8520	 0.4310
sz	 0.6220	 0.3850