



wwPDB EM Validation Summary Report ⓘ

May 20, 2026 – 10:30 PM JST

PDB ID : 9UZL / pdb_00009uzl
EMDB ID : EMD-64645
Title : EMCV IRES captured on mammalian 40S ribosome with initiator tRNA and eIF2
Authors : Das, D.; Hussain, T.
Deposited on : 2025-05-16
Resolution : 5.01 Å (reported)
Based on initial models : ., 6YAN, 8OZ0

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.dev132
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

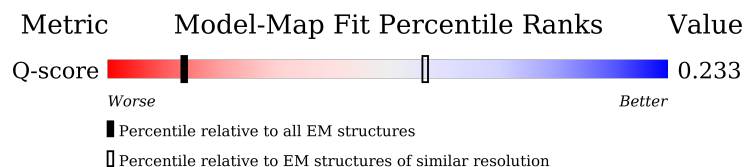
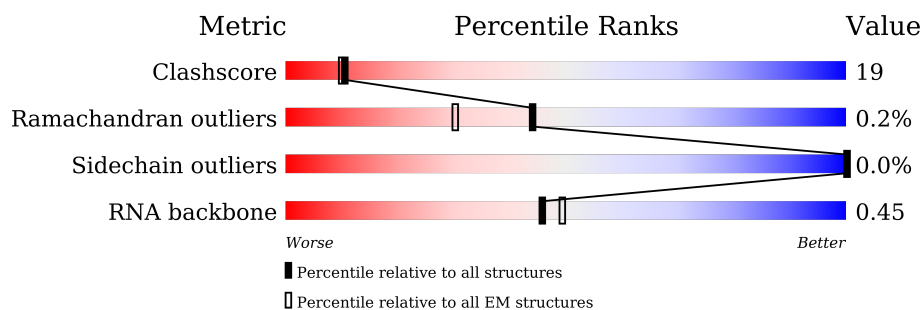
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.01 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.



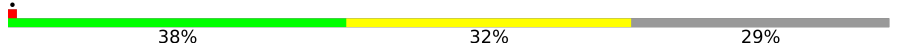

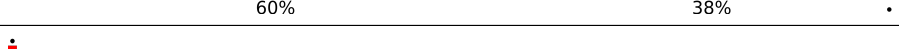
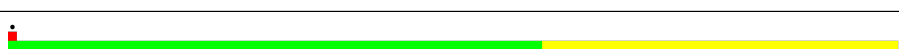



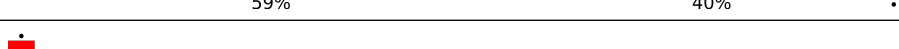





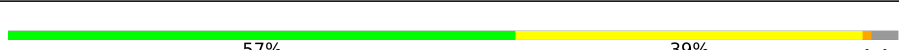


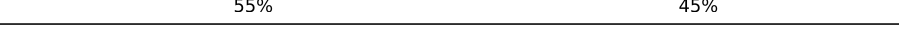







Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	859 (4.51 - 5.51)

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	2	1863	
2	A	315	
3	B	485	

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Mol	Chain	Length	Quality of chain
4	C	295	
5	D	264	
6	E	226	
7	F	243	
8	G	263	
9	H	204	
10	I	249	
11	J	194	
12	K	206	
13	L	194	
14	M	225	
15	N	158	
16	O	132	
17	P	151	
18	Q	168	
19	R	145	
20	S	146	
21	T	135	
22	U	152	
23	V	141	
24	W	119	
25	X	82	
26	Y	130	
27	Z	143	
28	a	126	

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Mol	Chain	Length	Quality of chain
29	b	115	
30	c	84	
31	d	64	
32	e	56	
33	f	156	
34	g	317	
35	h	125	
36	i	59	
37	l	25	
38	y	75	
39	z	93	

2 Entry composition [i](#)

There are 39 unique types of molecules in this entry. The entry contains 83705 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 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1744	Total	C	N	O	P	0	0
			37195	16608	6662	12185	1740		

- Molecule 2 is a protein called Eukaryotic translation initiation factor 2 subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	A	278	Total	C	N	O	0	0
			1378	822	278	278		

- Molecule 3 is a protein called Eukaryotic translation initiation factor 2 subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	B	464	Total	C	N	O	0	0
			2281	1352	464	465		

- Molecule 4 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	208	Total	C	N	O	S	0	0
			1642	1045	289	300	8		

- Molecule 5 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	215	Total	C	N	O	S	0	0
			1741	1107	309	310	15		

- Molecule 6 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	222	Total	C	N	O	S	0	0
			1721	1114	295	303	9		

- Molecule 7 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	227	Total	C	N	O	S	0	0
			1764	1124	317	315	8		

- Molecule 8 is a protein called Small ribosomal subunit protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	263	Total	C	N	O	S	0	0
			2083	1329	385	359	10		

- Molecule 9 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	191	Total	C	N	O	S	0	0
			1509	943	286	273	7		

- Molecule 10 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 11 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	190	Total	C	N	O	S	0	0
			1530	975	281	273	1		

- Molecule 12 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	206	Total	C	N	O	S	0	0
			1680	1054	329	292	5		

- Molecule 13 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	182	Total	C	N	O	S	0	0
			1498	952	300	244	2		

- Molecule 14 is a protein called Small ribosomal subunit protein eS10.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	-30	THR	ALA	conflict	UNP A0AAG1W9A6

- Molecule 15 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	158	Total	C	N	O	S	0	0
			1296	827	241	221	7		

- Molecule 16 is a protein called Small ribosomal subunit protein eS12.

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

- Molecule 17 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 18 is a protein called Ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 19 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	135	Total	C	N	O	S	0	0
			1111	704	211	189	7		

- Molecule 20 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	141	Total	C	N	O	S	0	0
			1123	715	212	193	3		

- Molecule 21 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	126	Total	C	N	O	S	0	0
			1019	639	188	187	5		

- Molecule 22 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	142	Total	C	N	O	S	0	0
			1172	733	239	199	1		

- Molecule 23 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	141	Total	C	N	O	S	0	0
			1113	701	213	196	3		

- Molecule 24 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	104	Total	C	N	O	S	0	0
			822	514	156	148	4		

- Molecule 25 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	82	Total	C	N	O	S	0	0
			620	378	117	120	5		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	3	SER	ASN	conflict	UNP G1TM82
X	4	ASN	ASP	conflict	UNP G1TM82
X	33	PRO	GLN	conflict	UNP G1TM82
X	50	SER	PHE	conflict	UNP G1TM82
X	76	HIS	ASP	conflict	UNP G1TM82

- Molecule 26 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 27 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	142	Total	C	N	O	S	0	0
			1106	698	220	184	4		

- Molecule 28 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	126	Total	C	N	O	S	0	0
			1022	645	198	174	5		

- Molecule 29 is a protein called Small ribosomal subunit protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	99	Total	C	N	O	S	0	0
			789	491	162	130	6		

- Molecule 30 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	84	Total	C	N	O	S	0	0
			659	413	122	116	8		

- Molecule 31 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	64	Total	C	N	O	S	0	0
			507	308	102	95	2		

- Molecule 32 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	53	Total	C	N	O	S	0	0
			445	278	90	72	5		

- Molecule 33 is a protein called Ubiquitin-ribosomal protein eS31 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	71	Total	C	N	O	S	0	0
			581	367	109	98	7		

- Molecule 34 is a protein called Small ribosomal subunit protein RACK1.

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

- Molecule 35 is a protein called Small ribosomal subunit protein eS25.

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

- Molecule 36 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	i	59	Total	C	N	O	S	0	0
			473	293	104	75	1		

- Molecule 37 is a protein called Small ribosomal subunit protein eS32.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	25	Total	C	N	O	S	0	0
			240	145	64	28	3		

- Molecule 38 is a RNA chain called Initiator tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	y	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

- Molecule 39 is a RNA chain called Encephalomyocarditis viral IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	z	93	Total	C	N	O	P	0	0
			1981	885	361	642	93		

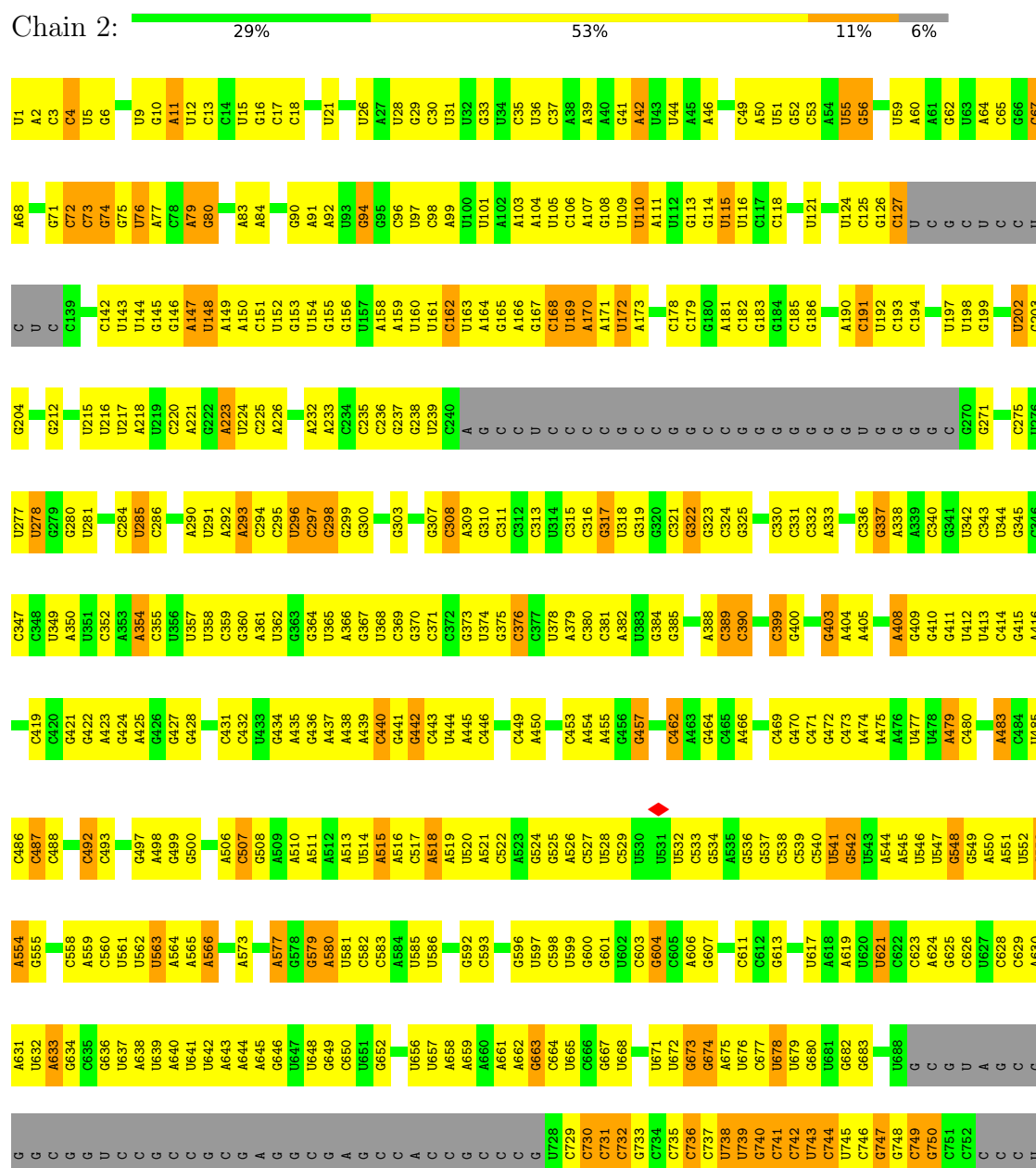
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
z	831	A	-	expression tag	GB 485965777
z	832	A	-	expression tag	GB 485965777
z	833	U	-	expression tag	GB 485965777
z	834	A	-	expression tag	GB 485965777
z	835	U	-	expression tag	GB 485965777
z	836	G	-	expression tag	GB 485965777
z	837	G	-	expression tag	GB 485965777
z	838	C	-	expression tag	GB 485965777

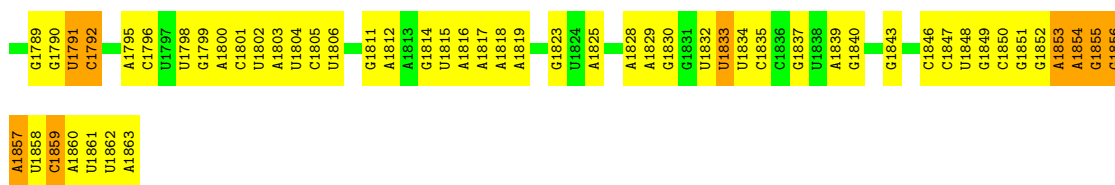
3 Residue-property plots

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.

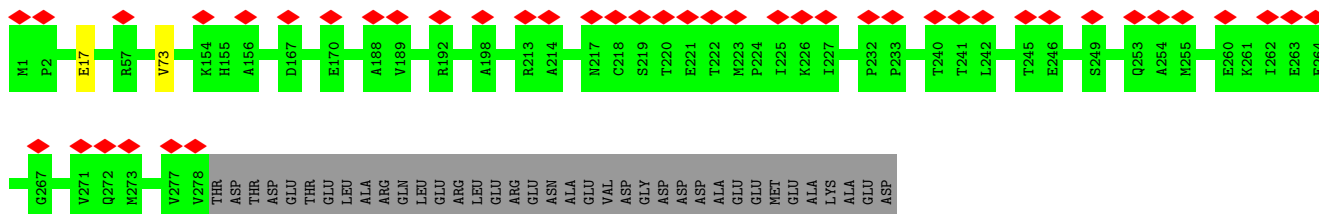
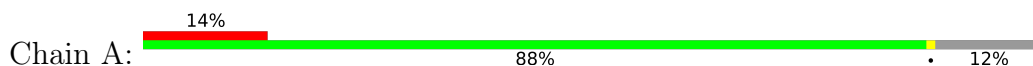
• Molecule 1: 18S ribosomal RNA



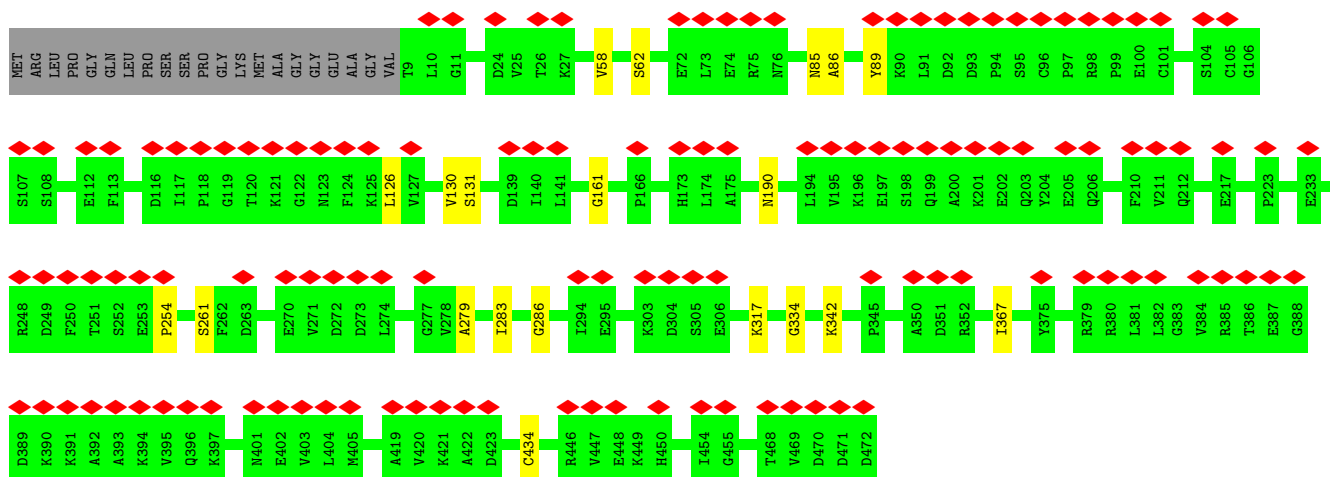
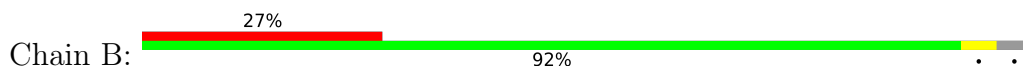
A1714	C1650	G1586	U1386	U1244	G1101	A1031	G955	U894	G827	C
U1715	G1651	C1587	C1367	C1245	C1102	A1032	U956	U895	G828	G
U1716	G1652	C1526	U1388	A1246	U1107	G1033	G957	U896	C829	A
G1717	G1653	C1527	A1451	A1247	U1108	C1034	A958	U897	G830	U
G1718	U1654	A1528	C1391	C1248	A1109	C1035	A959	G897	C831	G
C1655	G1655	G1531	U1392	A1249	U1110	U1041	A960	G898	G832	C
A1656	G1593	G1532	U1393	G1252	U1111	U1042	U963	A833	A833	U
U1720	U1594	C1533	G1394	G1253	U1112	U1043	U962	A834	G834	C
G1721	A1596	C1534	U1395	A1254	C1112	C1044	U964	C835	C835	U
U1724	C1597	U1534	U1396	A1255	C1113	A1045	U965	G836	G836	U
U1728	G1598	G1535	A1397	G1259	G1117	C1049	G966	C838	C838	G
U1663	G1662	U1536	A1398	U1259	A1118	G1050	G967	G905	C839	C
G1729	G1599	C1537	C1399	A1261	C1119	G1051	A968	U840	U840	U
G1664	G1600	U1538	U1400	C1260	U1190	U1051	A963	G841	G841	G
C1665	G1601	A1540	A1401	A1262	C1123	U1052	A976	G842	G842	A
G1732	G1666	C1540	G1402	C1262	C1124	C1053	A977	A843	A843	G
C1733	C1733	G1541	U1403	C1332	G1125	A1054	A978	U910	U910	U
C1734	U1667	C1542	U1404	C1333	G1126	G1055	A979	A845	A845	G
U1668	C1604	G1543	A1405	C1339	A1129	A1056	C980	A846	A846	U
G1669	G1605	U1544	C1406	U1339	U1057	U1057	A986	C847	C847	C
A1670	G1606	G1545	A1407	G1344	G1130	A1058	A987	C848	C848	C
U1671	U1607	U1546	U1408	G1345	C1131	C1059	G987	U915	U915	C
G1739	A1608	G1547	A1409	G1271	U1197	A1059	A988	C849	C849	C
U1740	C1673	U1472	U1473	A1272	G1199	C1060	G989	A916	A916	G
U1741	A1674	U1474	C1411	C1273	U1200	U1060	G989	G917	G917	C
C1742	G1675	G1475	C1412	A1274	C1201	C1063	A992	A918	U853	G
G1743	U1676	U1550	C1413	G1275	G1202	G1064	A993	G919	A854	G
U1677	C1613	A1551	G1414	C1281	G1203	U1065	A994	G920	G855	U
C1677	C1614	C1552	C1415	G1282	A1204	A1066	G995	A921	A858	C
C1749	A1615	C1553	C1416	U1283	C1214	C1075	C996	G922	U859	C
C1679	G1680	U1554	C1417	U1284	C1215	G1076	U1000	G923	A860	U
U1616	U1616	C1555	G1418	U1285	C1216	C1077	G1001	G924	U861	G
G1681	U1617	U1556	C1419	U1286	A1144	U1076	C1002	G925	U862	C
C1682	A1618	A1557	G1420	A1287	A1145	U1077	C1003	G926	G792	C
C1683	C1683	C1557	C1421	C1288	A1146	U1078	C1004	G927	G793	C
G1684	C1684	U1558	U1422	A1289	U1150	A1079	A1005	G928	G794	C
C1685	C1623	G1559	G1423	G1290	U1151	A1080	G1006	G929	U796	C
C1686	G1624	C1560	C1424	A1291	U1152	C1081	A1007	G930	U797	C
U1687	A1625	U1561	G1425	G1292	U1153	C1082	A1008	G931	A798	C
U1626	U1626	G1562	C1426	U1293	G1154	G1083	G869	G932	C799	C
G1627	G1627	C1563	G1427	A1294	G1155	U1084	G870	G933	U801	C
C1628	A1628	A1564	U1428	A1295	U1156	G1085	C871	G934	U801	C
A1692	C1630	C1567	C1429	U1296	G1157	C1086	C872	A940	A807	C
C1693	G1631	U1568	C1430	A1297	G1158	U1087	C873	U939	U807	C
C1695	A1632	C1569	C1431	G1298	G1159	C1088	C874	A941	U811	C
C1696	G1633	G1570	C1432	U1299	G1160	G1089	C875	U942	A882	C
G1697	G1634	U1571	C1433	A1300	G1161	U1090	C876	G943	G813	C
C1698	A1635	G1572	A1434	C1301	G1162	U1091	C877	C944	A814	C
C1699	U1636	U1573	C1435	C1302	G1163	G1092	C878	G945	G815	C
U1700	U1637	C1574	U1436	U1303	U1234	U1093	C879	C946	U818	C
G1701	U1638	A1575	U1437	U1304	U1235	C1094	C880	G947	U819	C
U1702	C1639	U1576	U1438	A1305	A1236	G1095	C881	C948	C820	C
G1703	C1640	G1577	C1439	U1306	A1237	C1096	C882	U949	A821	C
G1704	C1641	U1578	U1440	C1307	U1238	A1097	C883	U950	C822	C
U1707	G1642	G1579	A1441	C1380	U1239	U1098	C884	A951	A822	C
C1708	U1644	U1580	A1442	A1381	U1240	G1099	C885	A952	A823	C
U1709	A1645	U1581	C1443	A1382	U1241	G1100	C886	A953	U888	C
A1710	C1646	A1444	A1444	A1383	U1242	U1099	C887	A954	G890	C
C1711	G1647	G1445	G1446	A1384	U1243	G1100	C888	G954	U889	C
A1784	U1648	A1517	G1447	A1385	U1244	U1099	C889	U890	A824	C
A1785	C1712	U1648	G1447	C1385	U1245	G1100	C890	U891	G815	C
G1786	G1713	C1585	G1447	C1385	U1246	G1100	C891	U892	U811	C



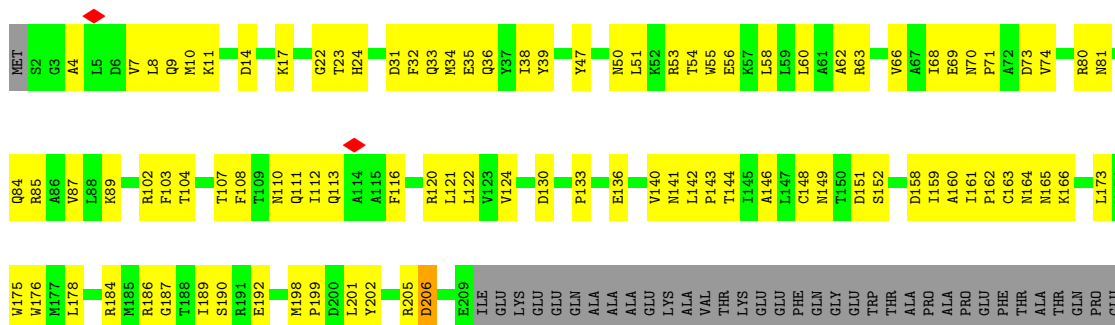
• Molecule 2: Eukaryotic translation initiation factor 2 subunit 1



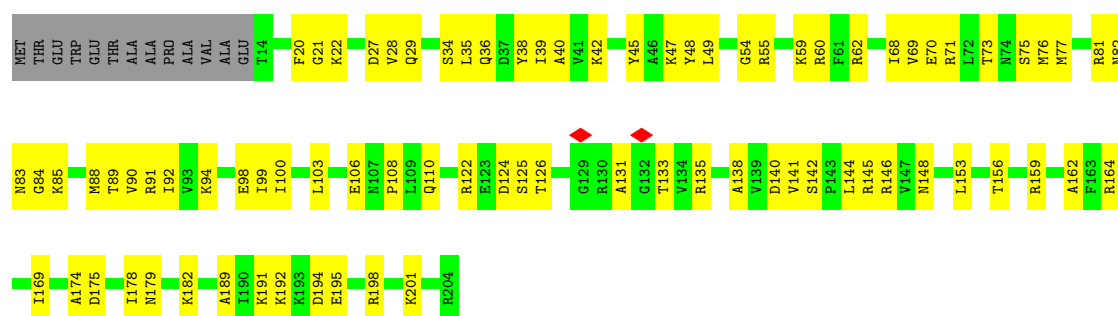
• Molecule 3: Eukaryotic translation initiation factor 2 subunit 3



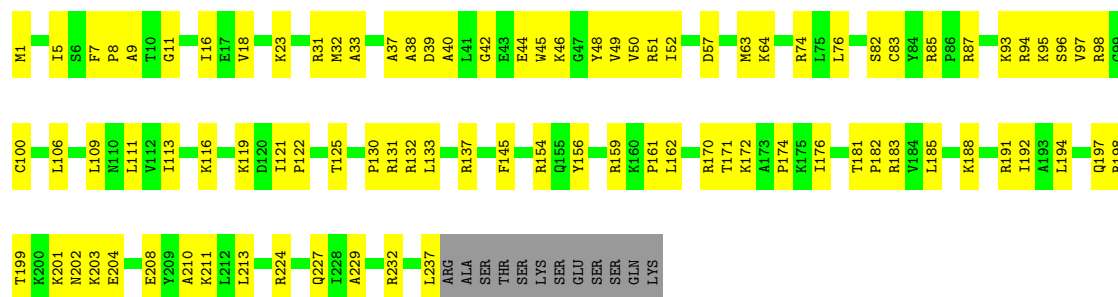
• Molecule 4: Small ribosomal subunit protein uS2



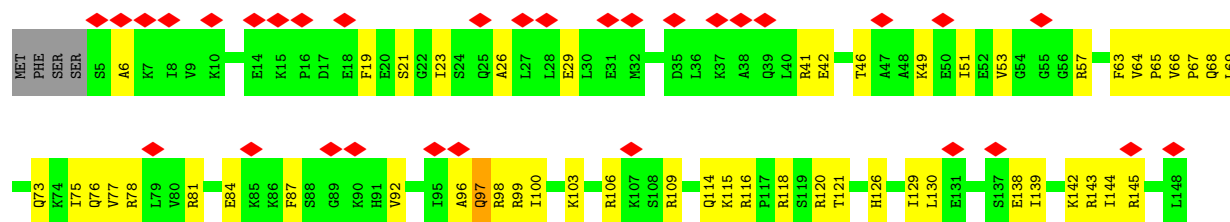
- Molecule 9: Small ribosomal subunit protein uS7

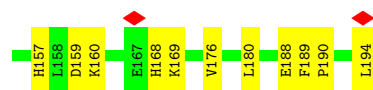


- Molecule 10: Small ribosomal subunit protein eS6



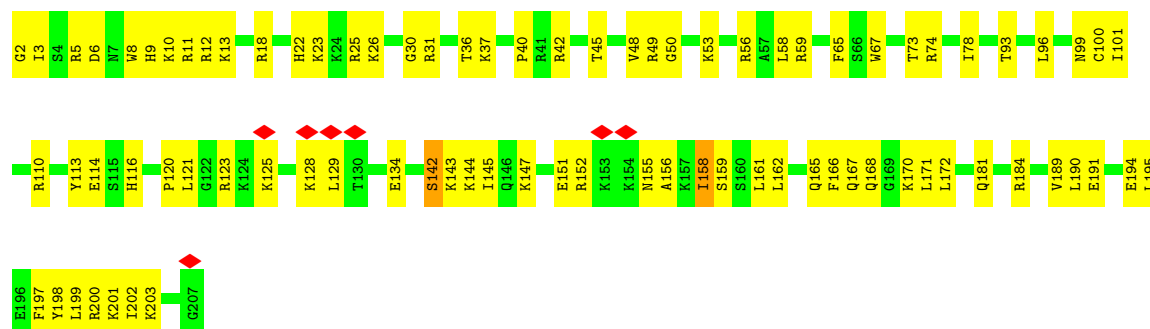
- Molecule 11: Small ribosomal subunit protein eS7





- Molecule 12: Small ribosomal subunit protein eS8

Chain K: 59% 40%



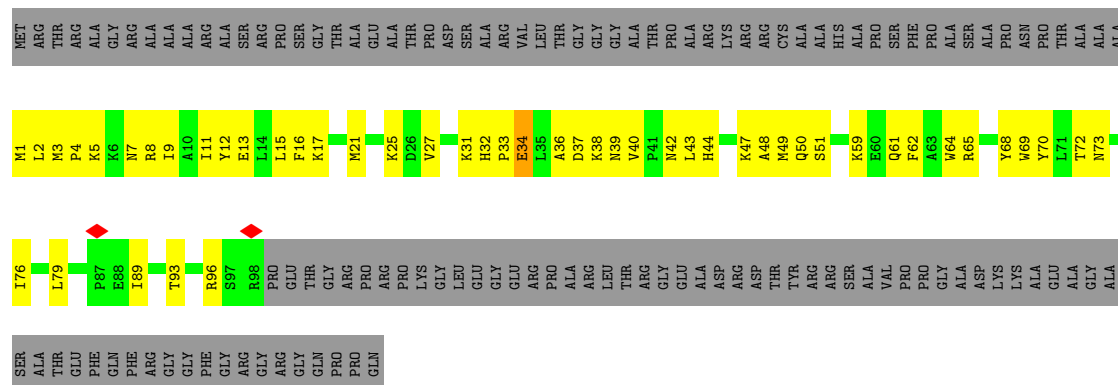
- Molecule 13: Small ribosomal subunit protein uS4

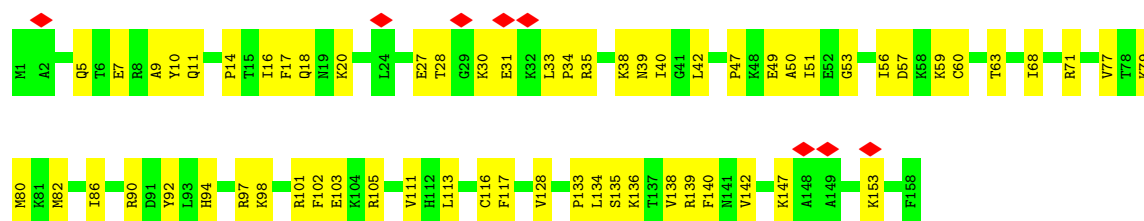
Chain L: 60% 33% 6%



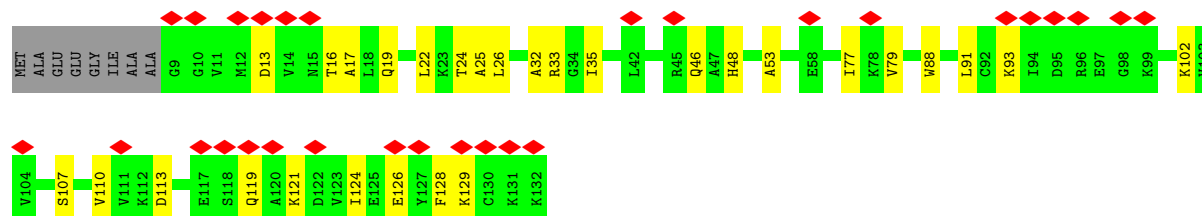
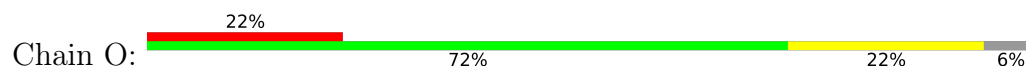
- Molecule 14: Small ribosomal subunit protein eS10

Chain M: 22% 21% 56%

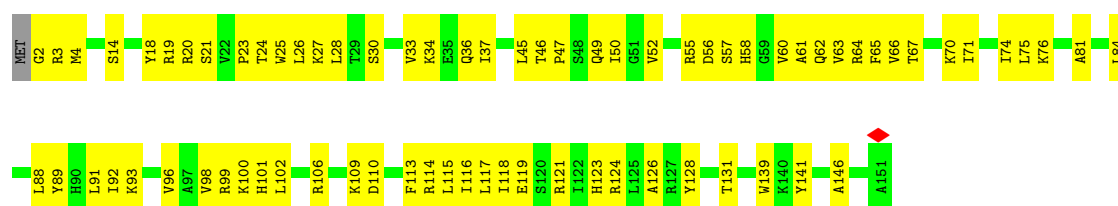




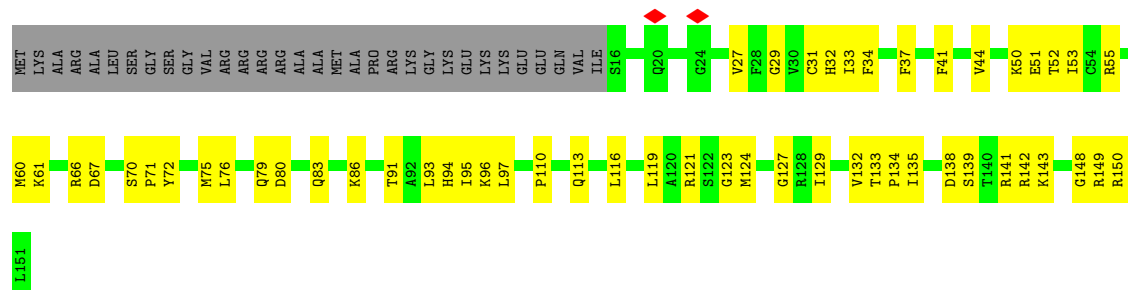
• Molecule 16: Small ribosomal subunit protein eS12



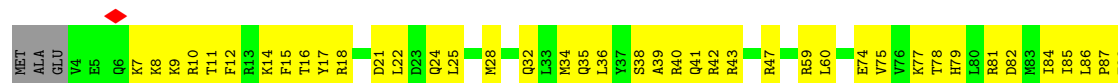
• Molecule 17: Small ribosomal subunit protein uS15



• Molecule 18: Ribosomal protein S14



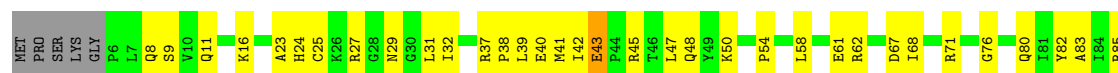
• Molecule 19: Small ribosomal subunit protein uS19





- Molecule 20: Small ribosomal subunit protein uS9

Chain S: 57% 39%



- Molecule 21: Small ribosomal subunit protein eS17

Chain T: 55% 39% 7%



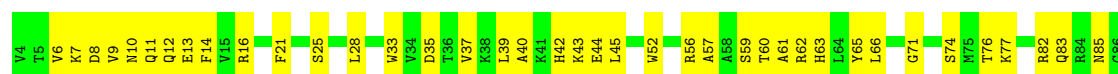
- Molecule 22: Small ribosomal subunit protein uS13

Chain U: 59% 34% 7%



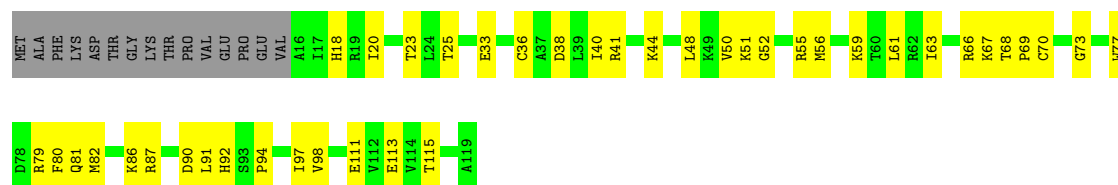
- Molecule 23: Small ribosomal subunit protein eS19

Chain V: 55% 45%



- Molecule 24: Small ribosomal subunit protein uS10

Chain W: 53% 34% 13%



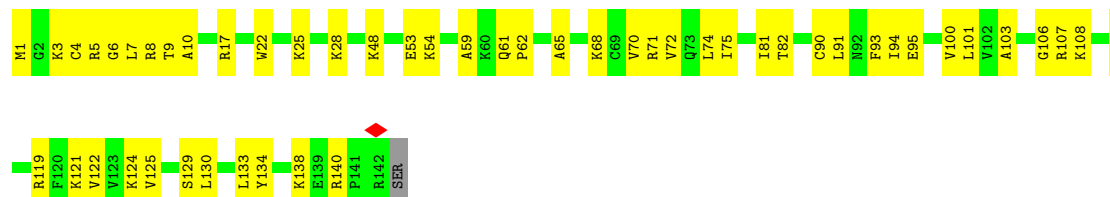
- Molecule 25: Small ribosomal subunit protein eS21



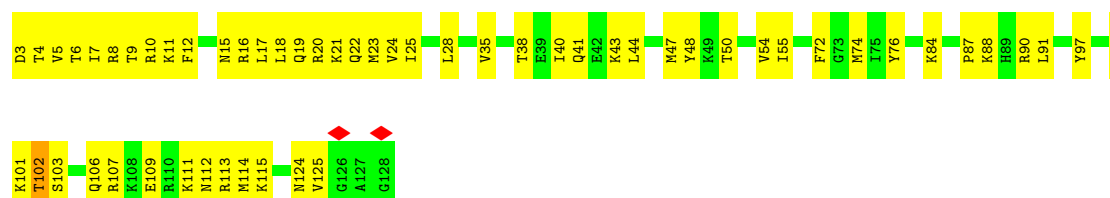
- Molecule 26: Small ribosomal subunit protein uS8



- Molecule 27: Small ribosomal subunit protein uS12

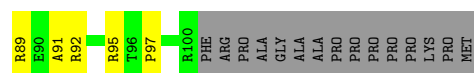


- Molecule 28: 40S ribosomal protein S24

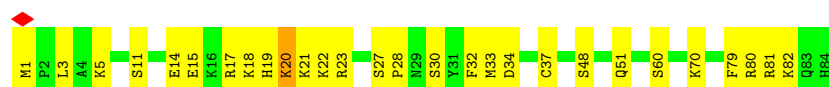


- Molecule 29: Small ribosomal subunit protein eS26





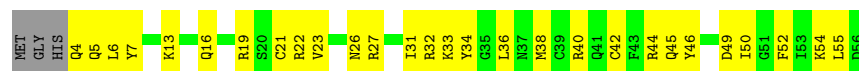
- Chain c: 67% 32%

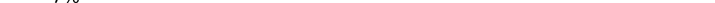


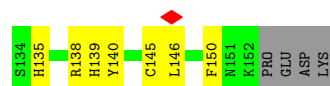
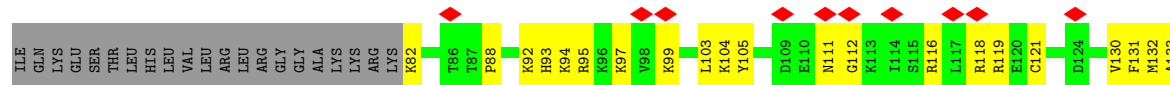
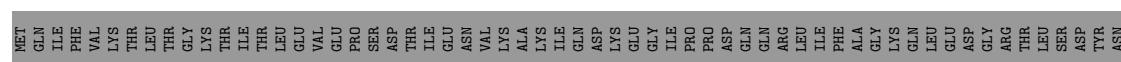
- Chain d:  59% 41%



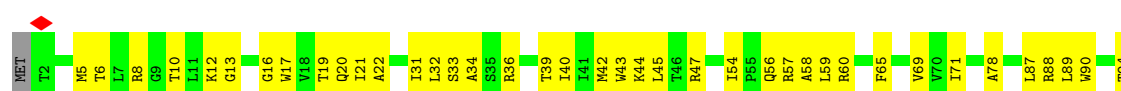
- Chain e: 45% 50% 5%

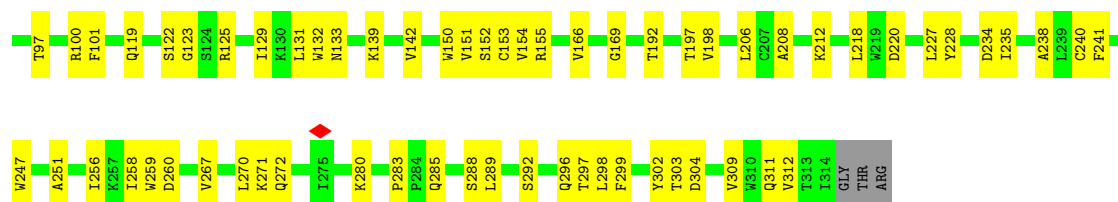


- Chain f:  7% 28% 18% 47%



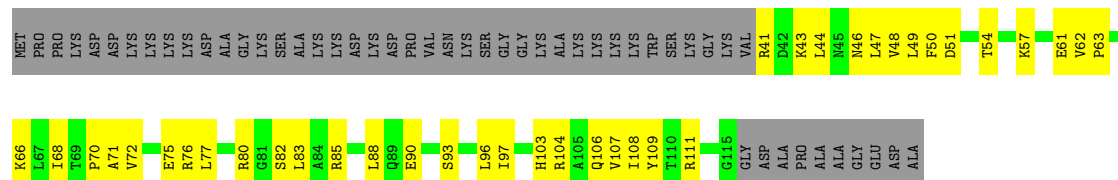
- Chain g:  67% 32%





• Molecule 35: Small ribosomal subunit protein eS25

Chain h: 30% 30% 40%



• Molecule 36: Small ribosomal subunit protein eS30

Chain i: 7% 66% 32%



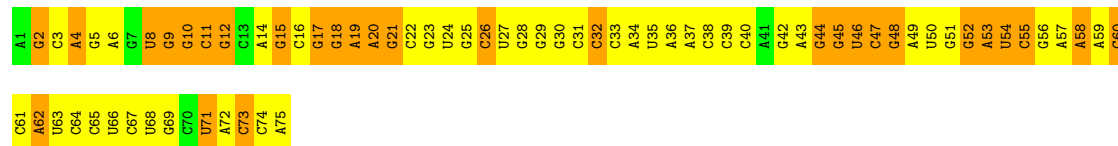
• Molecule 37: Small ribosomal subunit protein eS32

Chain l: 32% 68%



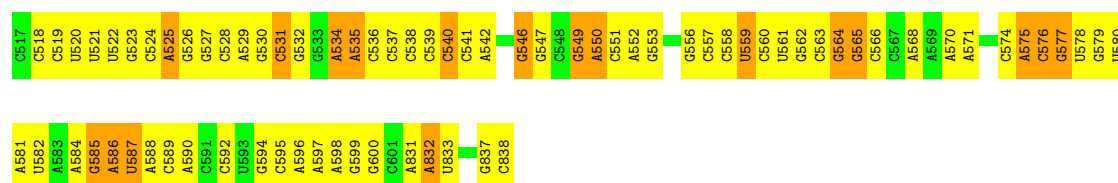
• Molecule 38: Initiator tRNA

Chain y: 7% 55% 39%



• Molecule 39: Encephalomyocarditis viral IRES

Chain z: 20% 60% 19%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	28439	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	55	Depositor
Minimum defocus (nm)	1250	Depositor
Maximum defocus (nm)	2750	Depositor
Magnification	36000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.554	Depositor
Minimum map value	-0.216	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.0618	Depositor
Map size (\AA)	467.99997, 467.99997, 467.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.17, 1.17, 1.17	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	2	0.11	0/41588	0.28	0/64818
2	A	0.13	0/1377	0.36	0/1919
3	B	0.10	0/2280	0.31	0/3165
4	C	0.15	0/1679	0.42	0/2283
5	D	0.16	0/1769	0.48	0/2367
6	E	0.21	0/1757	0.50	0/2371
7	F	0.17	0/1792	0.48	2/2412 (0.1%)
8	G	0.14	0/2125	0.37	0/2856
9	H	0.16	0/1531	0.44	0/2059
10	I	0.16	0/1946	0.43	0/2590
11	J	0.16	0/1553	0.44	0/2079
12	K	0.14	0/1709	0.53	2/2278 (0.1%)
13	L	0.13	0/1522	0.38	0/2031
14	M	0.16	0/851	0.60	2/1147 (0.2%)
15	N	0.14	0/1319	0.42	0/1761
16	O	0.11	0/968	0.34	0/1296
17	P	0.17	0/1232	0.41	0/1656
18	Q	0.14	0/1029	0.40	0/1380
19	R	0.16	0/1132	0.52	0/1510
20	S	0.14	0/1141	0.46	0/1528
21	T	0.13	0/1031	0.45	0/1383
22	U	0.15	0/1190	0.49	0/1592
23	V	0.16	0/1133	0.41	0/1517
24	W	0.13	0/832	0.38	0/1117
25	X	0.12	0/627	0.41	0/839
26	Y	0.18	0/1051	0.50	0/1406
27	Z	0.16	0/1124	0.42	0/1500
28	a	0.15	0/1039	0.54	2/1380 (0.1%)
29	b	0.20	0/802	0.45	0/1076
30	c	0.19	0/673	0.63	4/902 (0.4%)
31	d	0.16	0/509	0.45	0/680
32	e	0.18	0/455	0.46	0/603
33	f	0.13	0/593	0.36	0/786
34	g	0.12	0/2493	0.38	0/3394

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	h	0.15	0/604	0.36	0/810
36	i	0.19	0/478	0.62	2/628 (0.3%)
37	l	0.17	0/241	0.49	0/305
38	y	0.13	0/1795	0.29	0/2798
39	z	0.11	0/2213	0.25	0/3442
All	All	0.13	0/89183	0.36	14/129664 (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
11	J	0	1
20	S	0	1
All	All	0	2

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	K	142	SER	CA-C-N	11.15	141.77	121.70
12	K	142	SER	C-N-CA	11.15	141.77	121.70
14	M	1	MET	CA-C-N	8.95	137.81	121.70
14	M	1	MET	C-N-CA	8.95	137.81	121.70
28	a	102	THR	CA-C-N	8.60	137.18	121.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
11	J	66	VAL	Peptide
20	S	43	GLU	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	2	37195	0	18794	1205	0
2	A	1378	0	611	1	0
3	B	2281	0	1035	10	0
4	C	1642	0	1646	88	0
5	D	1741	0	1815	84	0
6	E	1721	0	1812	84	0
7	F	1764	0	1863	67	0
8	G	2083	0	2189	99	0
9	H	1509	0	1563	72	0
10	I	1923	0	2089	74	0
11	J	1530	0	1627	61	0
12	K	1680	0	1762	87	0
13	L	1498	0	1608	58	0
14	M	827	0	854	46	0
15	N	1296	0	1374	60	0
16	O	958	0	993	22	0
17	P	1208	0	1294	69	0
18	Q	1016	0	1039	53	0
19	R	1111	0	1168	68	0
20	S	1123	0	1193	51	0
21	T	1019	0	1075	48	0
22	U	1172	0	1226	55	0
23	V	1113	0	1149	53	0
24	W	822	0	887	40	0
25	X	620	0	622	34	0
26	Y	1034	0	1080	57	0
27	Z	1106	0	1179	56	0
28	a	1022	0	1085	50	0
29	b	789	0	839	46	0
30	c	659	0	683	24	0
31	d	507	0	536	26	0
32	e	445	0	442	38	0
33	f	581	0	599	35	0
34	g	2436	0	2393	77	0
35	h	598	0	656	37	0
36	i	473	0	524	20	0
37	l	240	0	289	18	0
38	y	1604	0	816	79	0
39	z	1981	0	1011	71	0
All	All	83705	0	63420	2712	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 19.

The worst 5 of 2712 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)
1:2:1284:U:H3	1:2:1307:C:N4	1.45	1.14
1:2:432:C:N4	1:2:439:A:H62	1.51	1.08
1:2:957:G:C2	39:z:831:A:N1	2.24	1.05
1:2:432:C:H42	1:2:439:A:N6	1.53	1.04
1:2:149:A:N6	1:2:169:U:C2	2.26	1.03

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	
2	A	276/315 (88%)	267 (97%)	9 (3%)	0	100	100
3	B	462/485 (95%)	453 (98%)	9 (2%)	0	100	100
4	C	206/295 (70%)	179 (87%)	26 (13%)	1 (0%)	24	63
5	D	213/264 (81%)	195 (92%)	17 (8%)	1 (0%)	24	63
6	E	220/226 (97%)	203 (92%)	16 (7%)	1 (0%)	24	63
7	F	225/243 (93%)	212 (94%)	12 (5%)	1 (0%)	30	67
8	G	261/263 (99%)	242 (93%)	19 (7%)	0	100	100
9	H	189/204 (93%)	174 (92%)	15 (8%)	0	100	100
10	I	235/249 (94%)	224 (95%)	11 (5%)	0	100	100
11	J	188/194 (97%)	172 (92%)	16 (8%)	0	100	100
12	K	204/206 (99%)	185 (91%)	17 (8%)	2 (1%)	12	47
13	L	180/194 (93%)	172 (96%)	7 (4%)	1 (1%)	21	58
14	M	96/225 (43%)	79 (82%)	16 (17%)	1 (1%)	12	47
15	N	156/158 (99%)	148 (95%)	8 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	O	122/132 (92%)	108 (88%)	14 (12%)	0	100	100
17	P	148/151 (98%)	144 (97%)	4 (3%)	0	100	100
18	Q	134/168 (80%)	117 (87%)	17 (13%)	0	100	100
19	R	133/145 (92%)	115 (86%)	18 (14%)	0	100	100
20	S	139/146 (95%)	127 (91%)	12 (9%)	0	100	100
21	T	124/135 (92%)	121 (98%)	3 (2%)	0	100	100
22	U	140/152 (92%)	124 (89%)	15 (11%)	1 (1%)	18	55
23	V	139/141 (99%)	126 (91%)	12 (9%)	1 (1%)	18	55
24	W	102/119 (86%)	96 (94%)	6 (6%)	0	100	100
25	X	80/82 (98%)	72 (90%)	8 (10%)	0	100	100
26	Y	127/130 (98%)	119 (94%)	8 (6%)	0	100	100
27	Z	140/143 (98%)	132 (94%)	8 (6%)	0	100	100
28	a	124/126 (98%)	117 (94%)	7 (6%)	0	100	100
29	b	97/115 (84%)	91 (94%)	6 (6%)	0	100	100
30	c	82/84 (98%)	72 (88%)	10 (12%)	0	100	100
31	d	62/64 (97%)	59 (95%)	3 (5%)	0	100	100
32	e	51/56 (91%)	42 (82%)	9 (18%)	0	100	100
33	f	69/156 (44%)	59 (86%)	10 (14%)	0	100	100
34	g	311/317 (98%)	286 (92%)	25 (8%)	0	100	100
35	h	73/125 (58%)	71 (97%)	2 (3%)	0	100	100
36	i	57/59 (97%)	51 (90%)	6 (10%)	0	100	100
37	l	23/25 (92%)	23 (100%)	0	0	100	100
All	All	5588/6292 (89%)	5177 (93%)	401 (7%)	10 (0%)	44	77

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	M	34	GLU
22	U	144	ARG
7	F	193	ASP
12	K	156	ALA
12	K	158	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	C	174/244 (71%)	174 (100%)	0	100	100
5	D	196/231 (85%)	196 (100%)	0	100	100
6	E	186/187 (100%)	186 (100%)	0	100	100
7	F	190/202 (94%)	190 (100%)	0	100	100
8	G	225/225 (100%)	225 (100%)	0	100	100
9	H	161/170 (95%)	161 (100%)	0	100	100
10	I	207/218 (95%)	207 (100%)	0	100	100
11	J	170/174 (98%)	169 (99%)	1 (1%)	78	81
12	K	177/177 (100%)	177 (100%)	0	100	100
13	L	157/168 (94%)	157 (100%)	0	100	100
14	M	89/173 (51%)	89 (100%)	0	100	100
15	N	142/142 (100%)	142 (100%)	0	100	100
16	O	104/108 (96%)	104 (100%)	0	100	100
17	P	130/131 (99%)	130 (100%)	0	100	100
18	Q	106/130 (82%)	106 (100%)	0	100	100
19	R	121/130 (93%)	121 (100%)	0	100	100
20	S	117/121 (97%)	117 (100%)	0	100	100
21	T	114/121 (94%)	114 (100%)	0	100	100
22	U	122/132 (92%)	122 (100%)	0	100	100
23	V	113/113 (100%)	113 (100%)	0	100	100
24	W	94/107 (88%)	94 (100%)	0	100	100
25	X	67/67 (100%)	67 (100%)	0	100	100
26	Y	112/113 (99%)	112 (100%)	0	100	100
27	Z	114/115 (99%)	114 (100%)	0	100	100
28	a	108/108 (100%)	108 (100%)	0	100	100
29	b	87/99 (88%)	87 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	c	76/76 (100%)	76 (100%)	0	100	100
31	d	57/57 (100%)	57 (100%)	0	100	100
32	e	47/49 (96%)	47 (100%)	0	100	100
33	f	64/140 (46%)	64 (100%)	0	100	100
34	g	272/275 (99%)	272 (100%)	0	100	100
35	h	66/103 (64%)	66 (100%)	0	100	100
36	i	49/49 (100%)	49 (100%)	0	100	100
37	l	24/24 (100%)	24 (100%)	0	100	100
All	All	4238/4679 (91%)	4237 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	J	97	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 51 such sidechains are listed below:

Mol	Chain	Res	Type
19	R	6	GLN
24	W	92	HIS
35	h	106	GLN
19	R	35	GLN
22	U	19	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1736/1863 (93%)	362 (20%)	4 (0%)
38	y	74/75 (98%)	35 (47%)	0
39	z	91/93 (97%)	32 (35%)	0
All	All	1901/2031 (93%)	429 (22%)	4 (0%)

5 of 429 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	4	C
1	2	11	A

Continued on next page...

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Mol	Chain	Res	Type
1	2	26	U
1	2	33	G
1	2	39	A

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	740	G
1	2	747	G
1	2	792	G
1	2	914	U

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
39	z	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	z	601:C	O3'	831:A	P	113.25

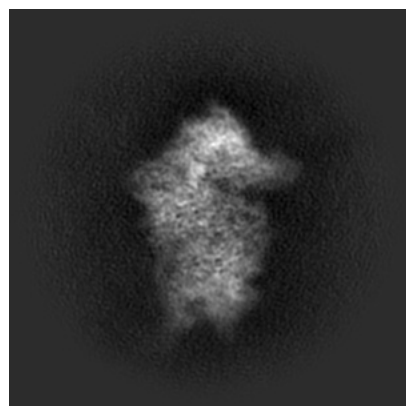
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64645. These allow visual inspection of the internal detail of the map and identification of artifacts.

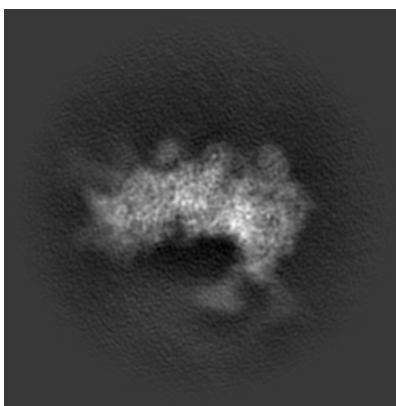
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

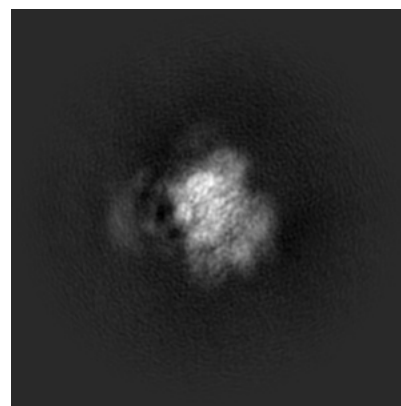
6.1.1 Primary map



X

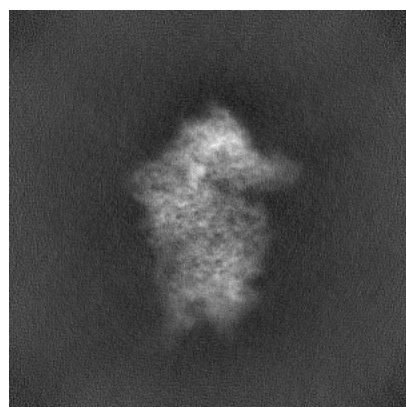


Y

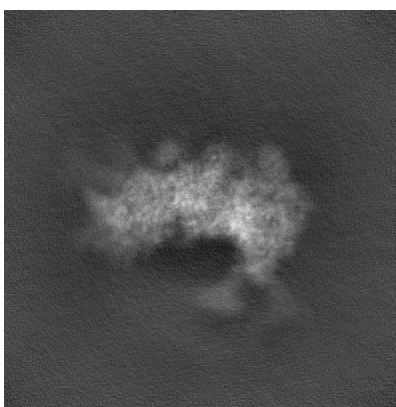


Z

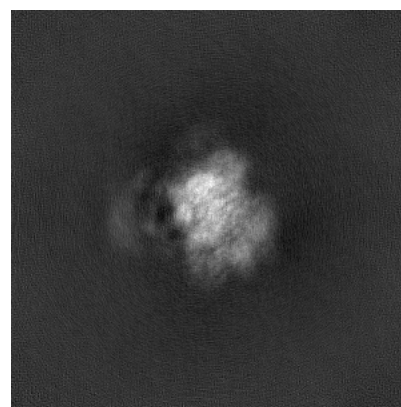
6.1.2 Raw map



X



Y

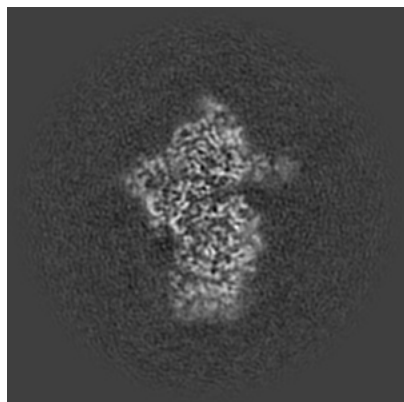


Z

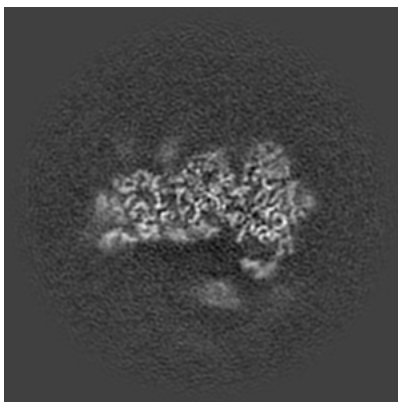
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

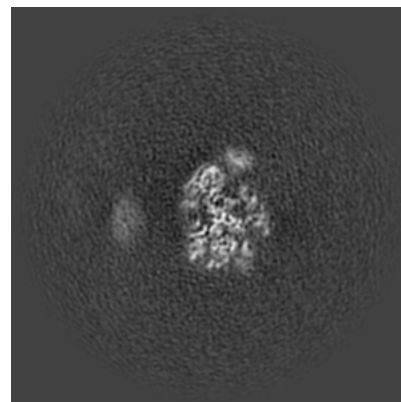
6.2.1 Primary map



X Index: 200

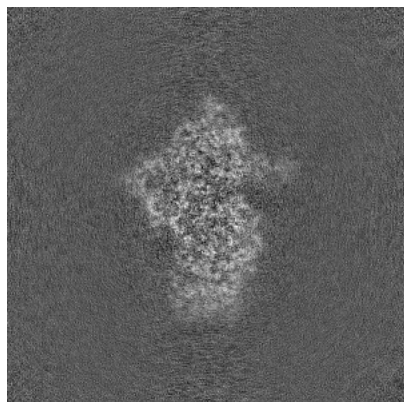


Y Index: 200

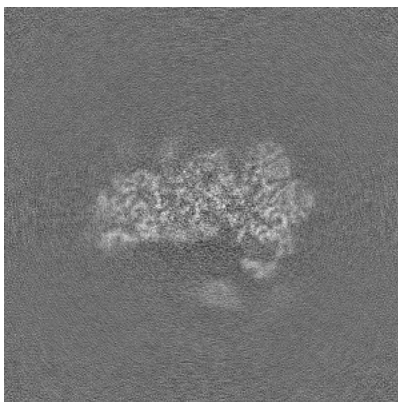


Z Index: 200

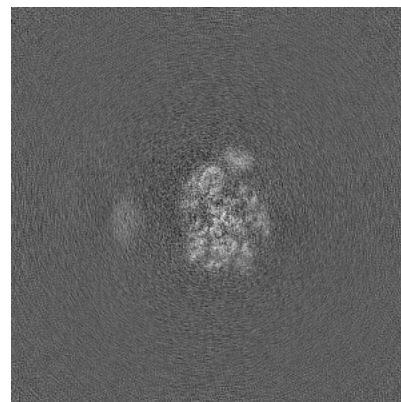
6.2.2 Raw map



X Index: 200



Y Index: 200

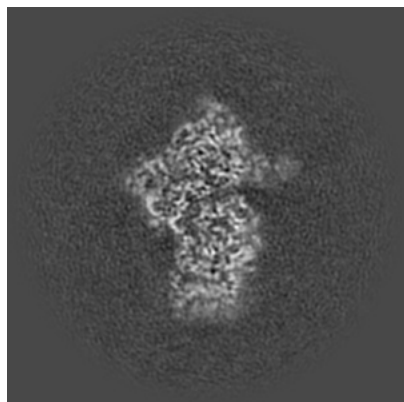


Z Index: 200

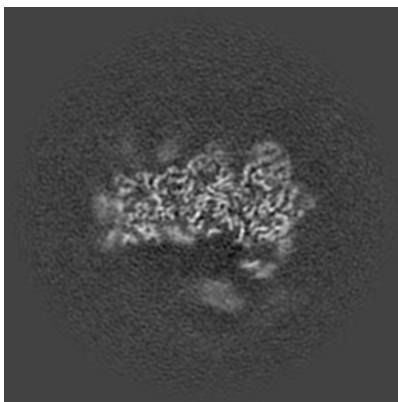
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

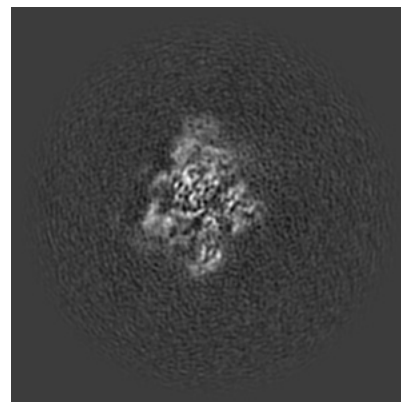
6.3.1 Primary map



X Index: 199

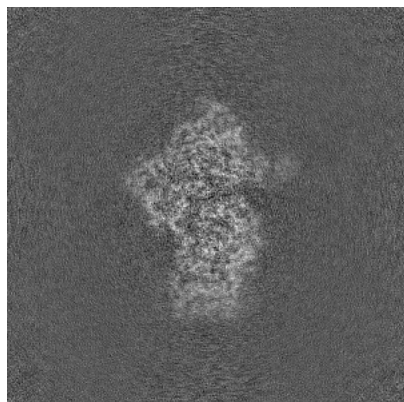


Y Index: 197

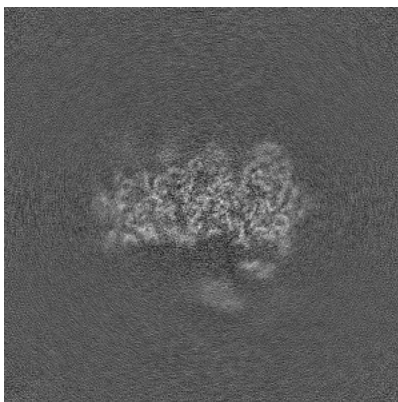


Z Index: 243

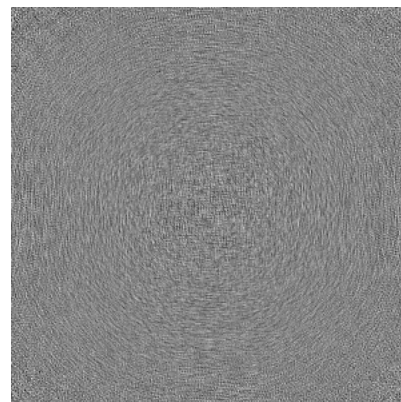
6.3.2 Raw map



X Index: 199



Y Index: 196

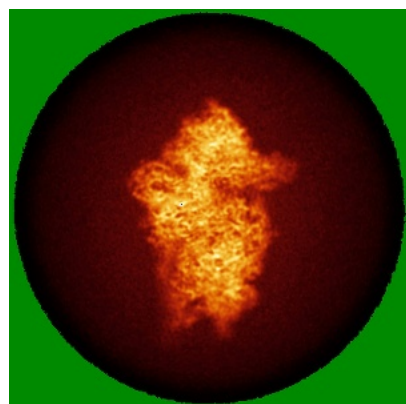


Z Index: 0

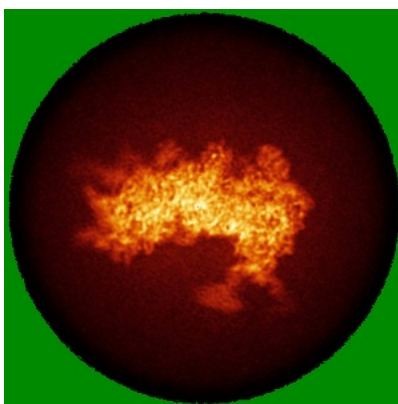
The images above show the largest variance slices of the map in three orthogonal directions.

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

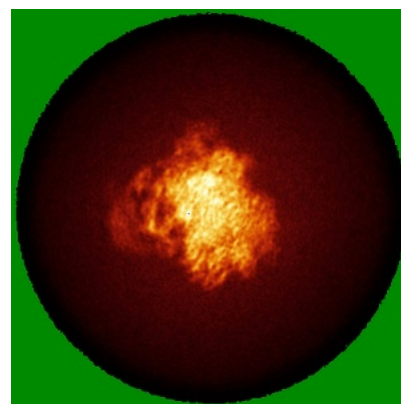
6.4.1 Primary map



X

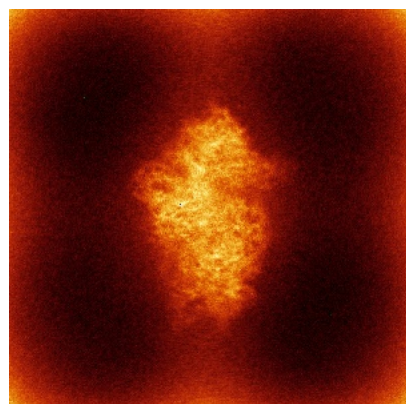


Y

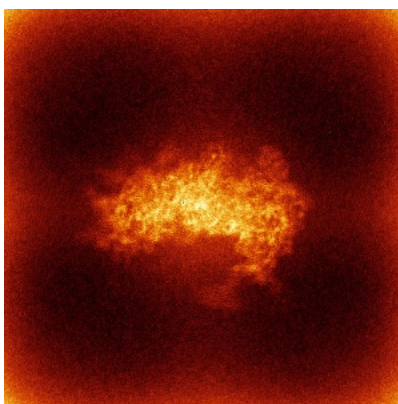


Z

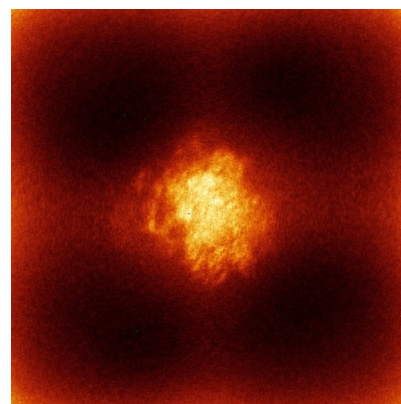
6.4.2 Raw map



X



Y

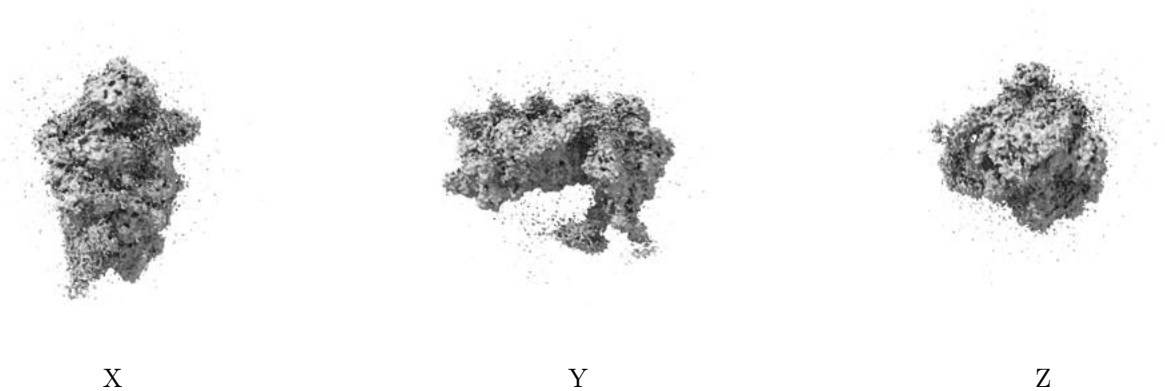


Z

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.

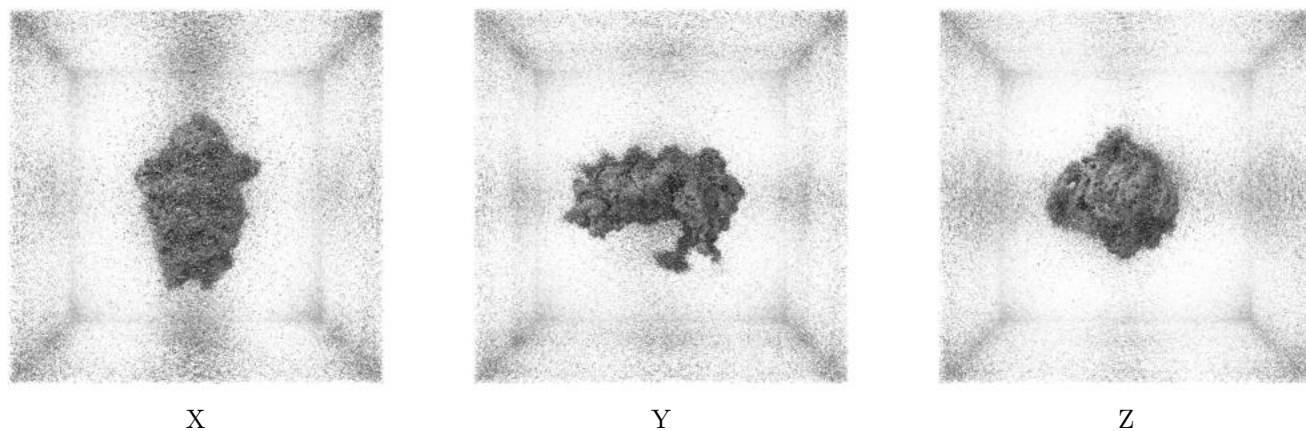
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0618. 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.

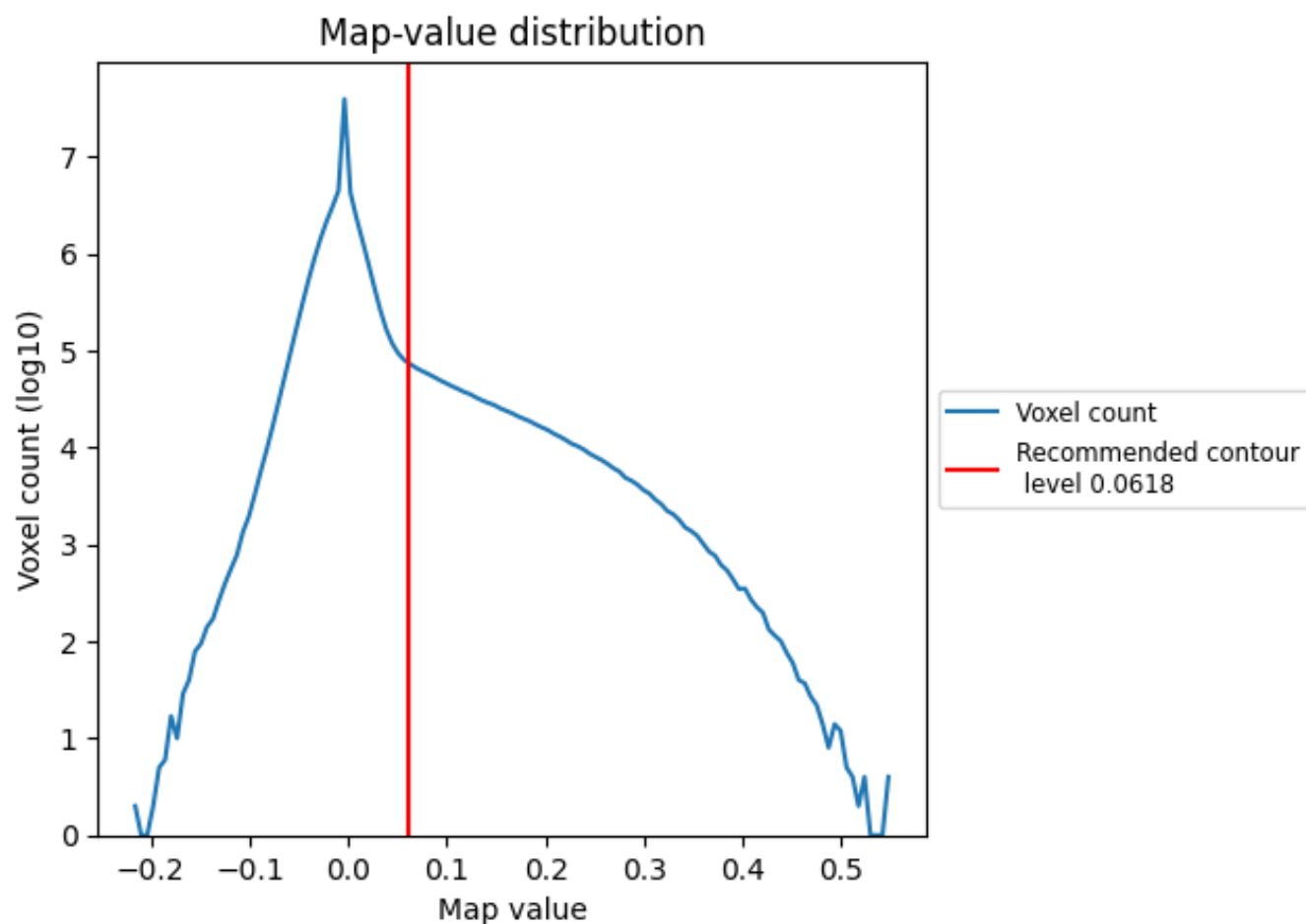
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

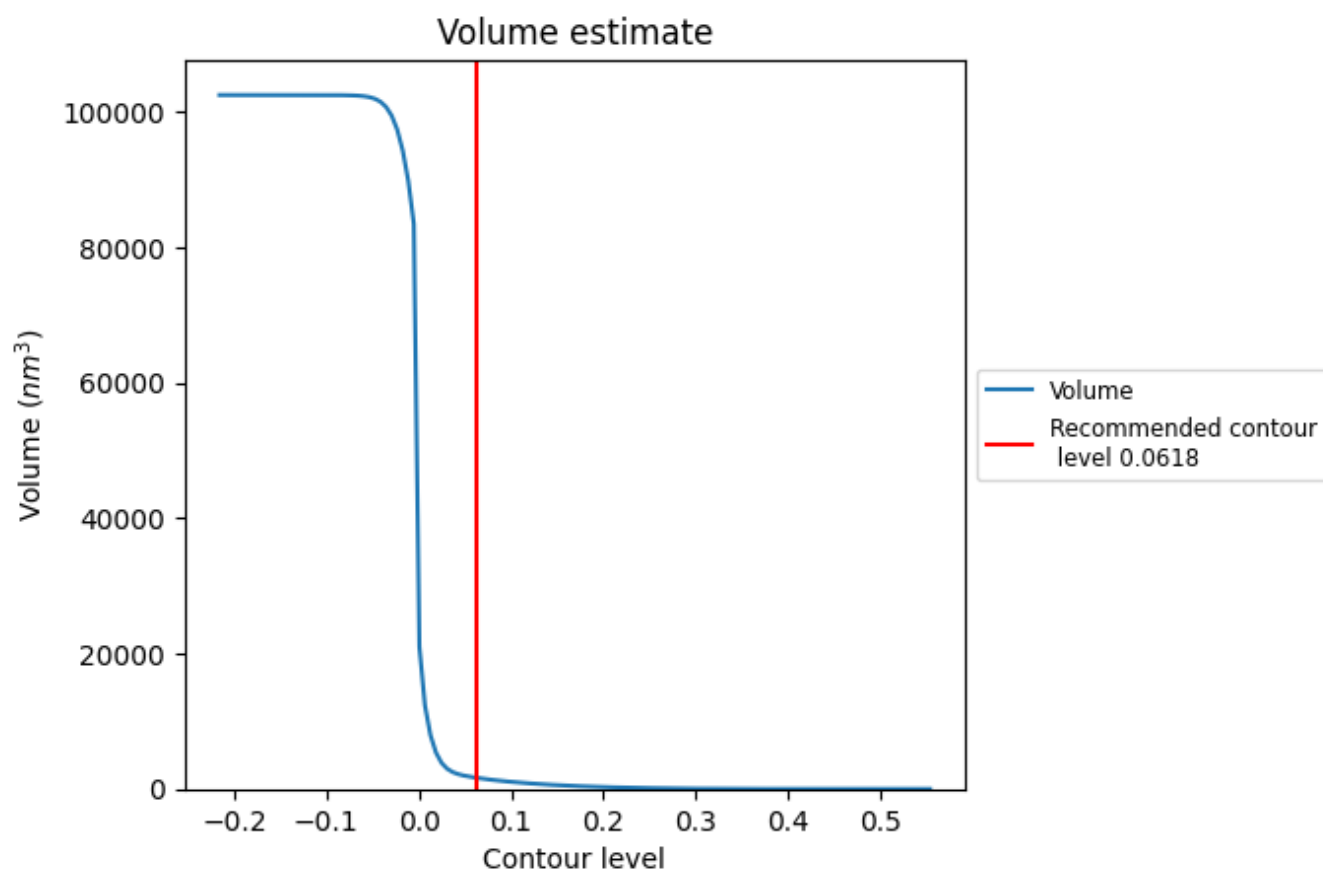
This section contains the results of statistical analysis of the map.

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.

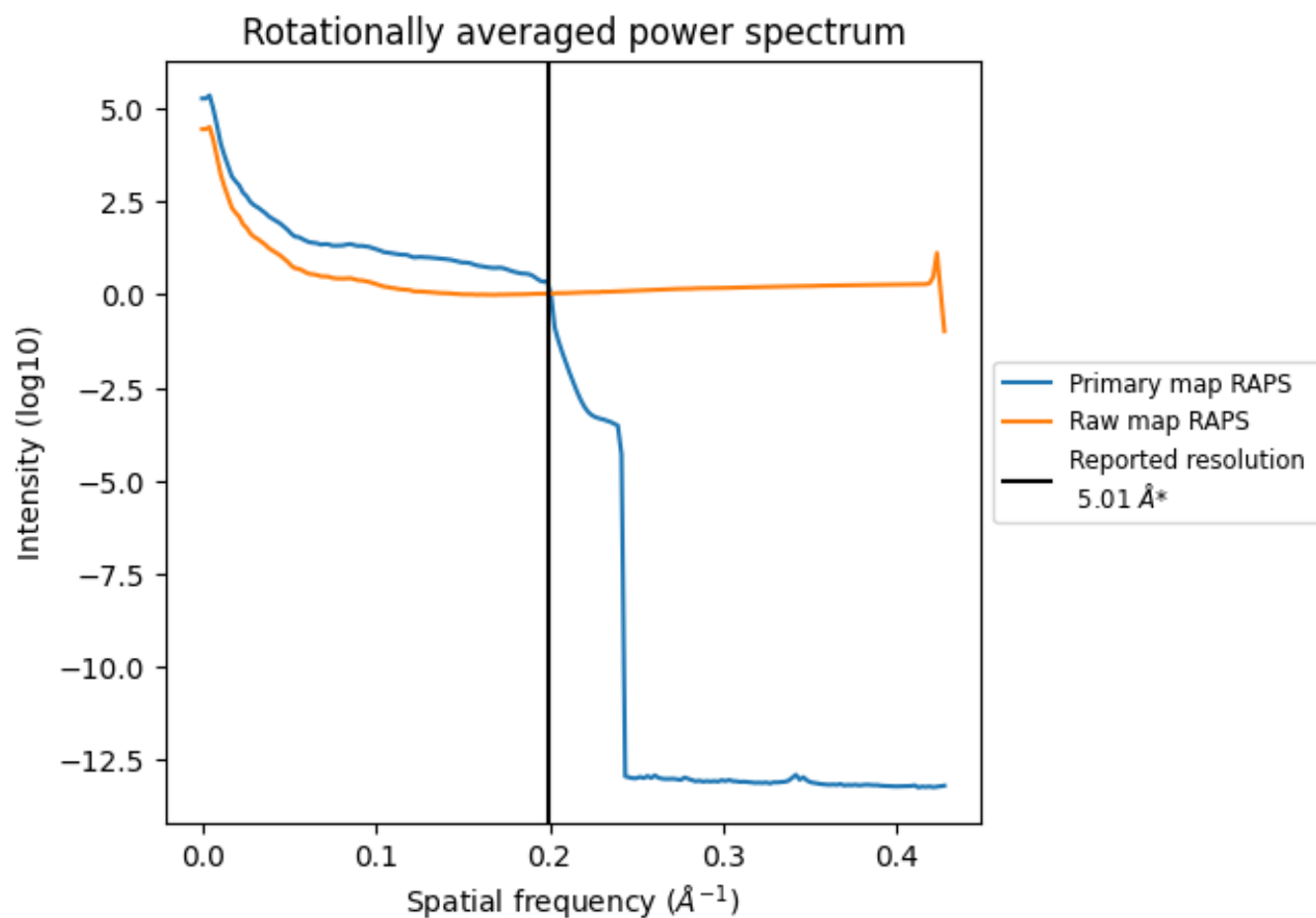
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1660 nm^3 ; this corresponds to an approximate mass of 1500 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 ⓘ

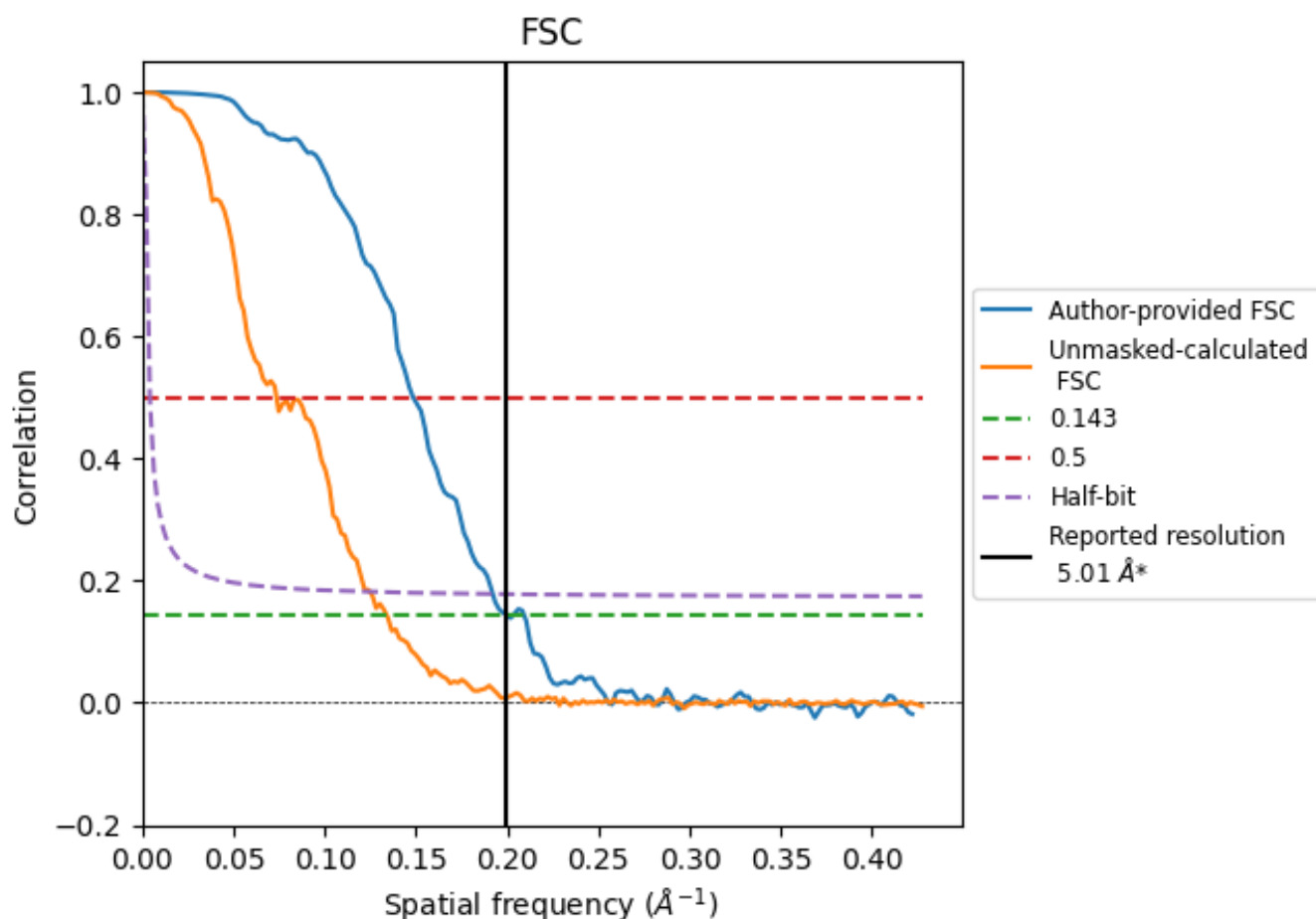


*Reported resolution corresponds to spatial frequency of 0.200 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

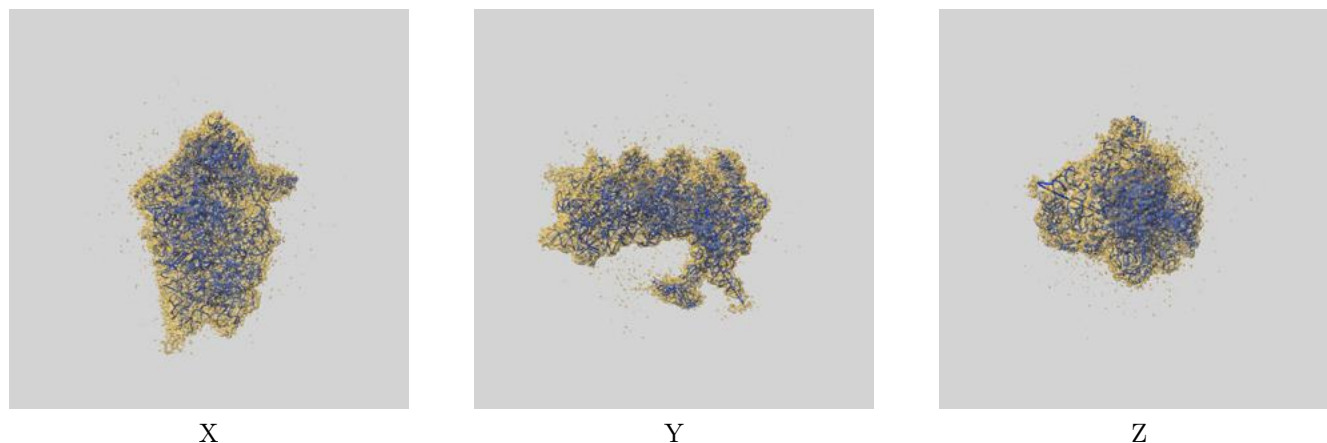
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.01	-	-
Author-provided FSC curve	5.01	6.73	5.21
Unmasked-calculated*	7.46	13.59	8.02

*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 7.46 differs from the reported value 5.01 by more than 10 %

9 Map-model fit [i](#)

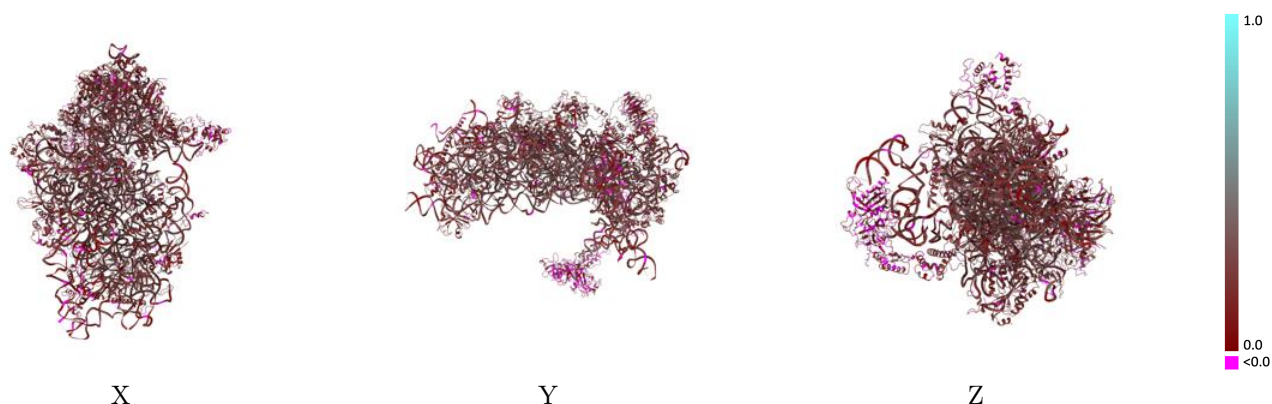
This section contains information regarding the fit between EMDB map EMD-64645 and PDB model 9UZL. Per-residue inclusion information can be found in section [3](#) on page [12](#).

9.1 Map-model overlay [i](#)



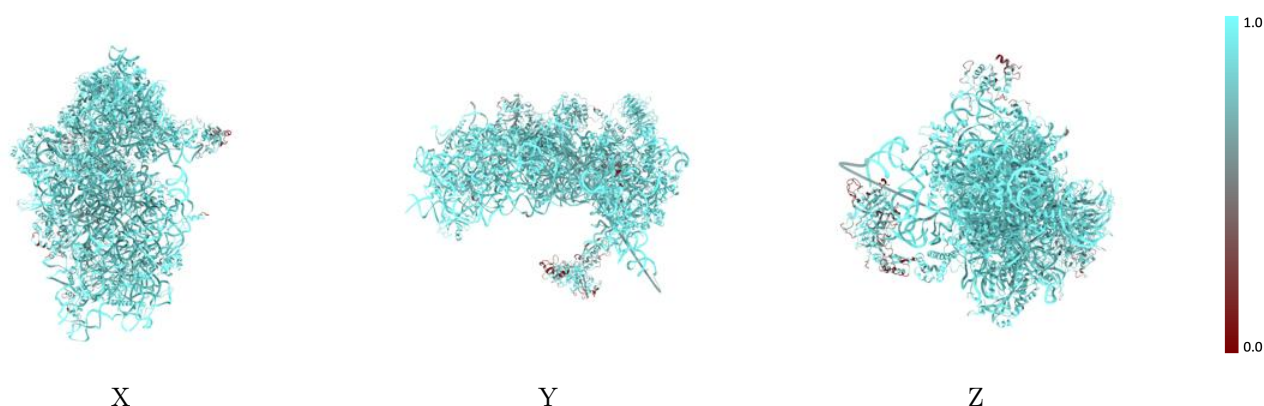
The images above show the 3D surface view of the map at the recommended contour level 0.0618 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



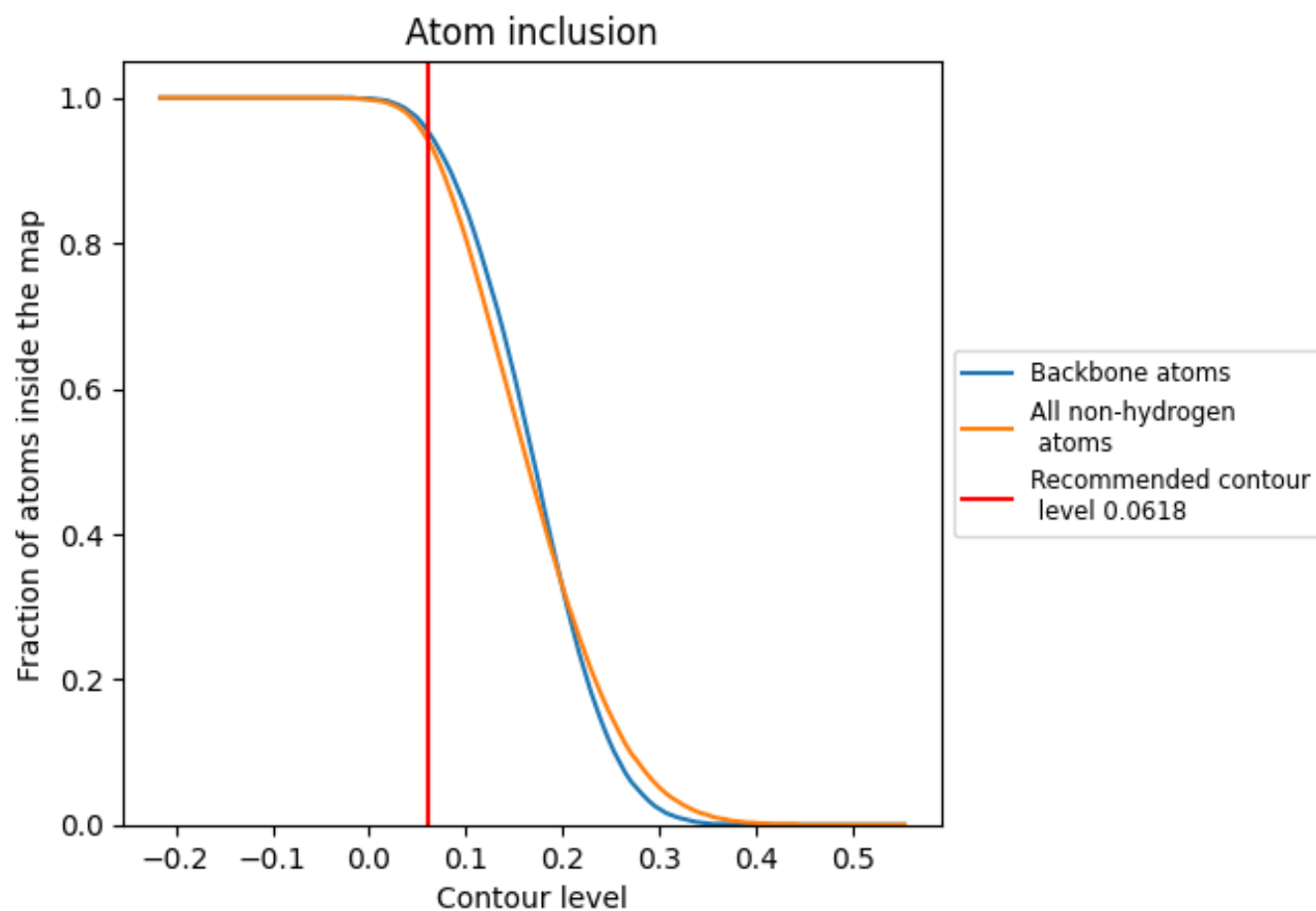
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0618).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 94% 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 (0.0618) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9390	 0.2330
2	 0.9860	 0.2600
A	 0.8150	 0.1880
B	 0.7000	 0.1000
C	 0.8910	 0.2400
D	 0.9240	 0.2150
E	 0.9080	 0.2490
F	 0.9110	 0.2150
G	 0.9510	 0.2460
H	 0.9370	 0.2310
I	 0.9570	 0.1950
J	 0.7160	 0.1760
K	 0.9080	 0.2050
L	 0.9280	 0.2270
M	 0.9440	 0.2080
N	 0.8590	 0.2400
O	 0.6610	 0.1140
P	 0.9350	 0.2320
Q	 0.9310	 0.2080
R	 0.9560	 0.2150
S	 0.9380	 0.2270
T	 0.8650	 0.2280
U	 0.9420	 0.2230
V	 0.9670	 0.2240
W	 0.9480	 0.2100
X	 0.9290	 0.2390
Y	 0.8600	 0.2530
Z	 0.9370	 0.2650
a	 0.9630	 0.2130
b	 0.9430	 0.2720
c	 0.9180	 0.2380
d	 0.9690	 0.2480
e	 0.9560	 0.2330
f	 0.7390	 0.1330
g	 0.9390	 0.2030



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Chain	Atom inclusion	Q-score
h	 0.9470	 0.1970
i	 0.8880	 0.1830
l	 0.9680	 0.2520
y	 0.9780	 0.2060
z	 0.9670	 0.1930