



wwPDB EM Validation Summary Report ⓘ

May 20, 2026 – 10:27 PM JST

PDB ID : 9UZK / pdb_00009uzk
EMDB ID : EMD-64644
Title : EMCV IRES captured on mammalian 40S with initiator tRNA
Authors : Das, D.; Hussain, T.
Deposited on : 2025-05-16
Resolution : 4.60 Å(reported)
Based on initial models : 8OZ0, ., 6YAN

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

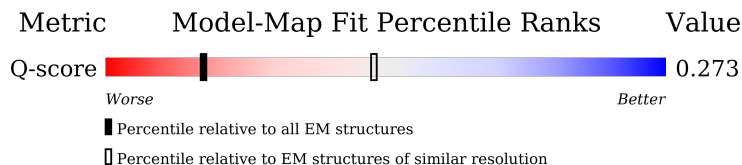
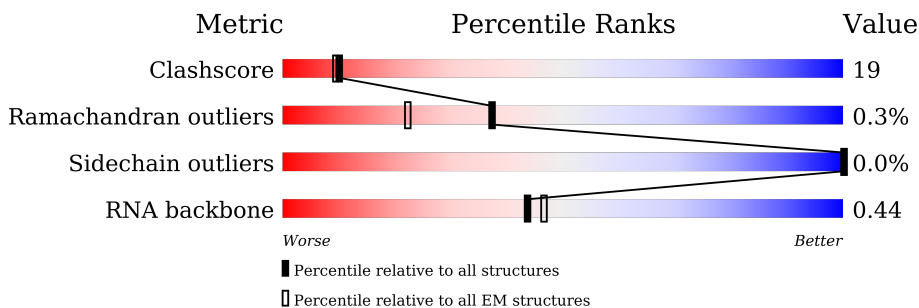
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.60 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.









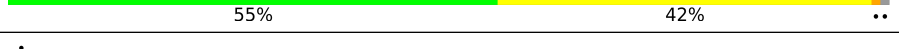
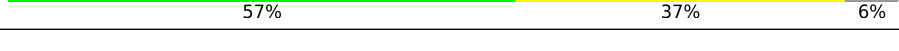
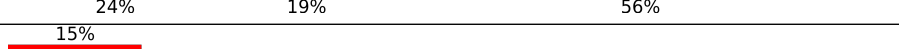
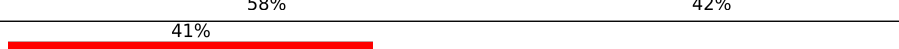
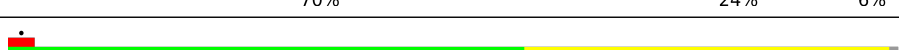

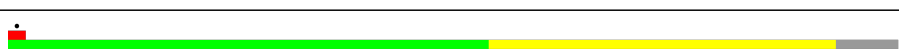

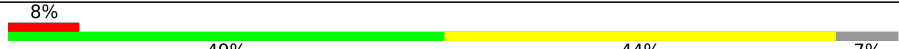





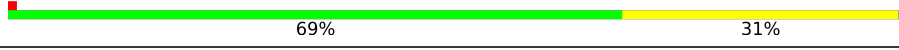
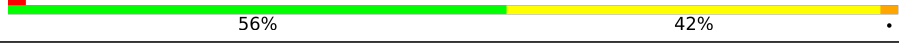



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	2407 (4.10 - 5.10)

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	C	295	
3	D	264	





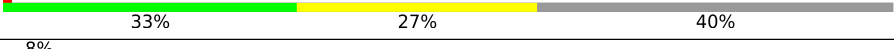


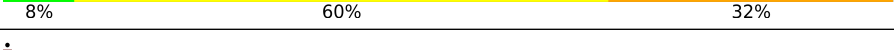
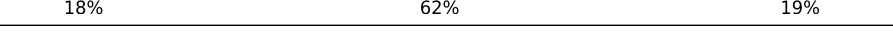
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Mol	Chain	Length	Quality of chain
4	E	226	
5	F	243	
6	G	263	
7	H	204	
8	I	249	
9	J	194	
10	K	208	
11	L	194	
12	M	225	
13	N	158	
14	O	132	
15	P	151	
16	Q	168	
17	R	145	
18	S	146	
19	T	135	
20	U	152	
21	V	141	
22	W	119	
23	X	83	
24	Y	130	
25	Z	143	
26	a	126	
27	b	115	
28	c	84	

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

2 Entry composition [i](#)

There are 37 unique types of molecules in this entry. The entry contains 80043 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
			37194	16608	6662	12184	1740		

- Molecule 2 is a protein called Small ribosomal subunit protein uS2.

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

- Molecule 3 is a protein called Small ribosomal subunit protein eS1.

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

- Molecule 4 is a protein called Small ribosomal subunit protein uS5.

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

- Molecule 5 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 6 is a protein called Small ribosomal subunit protein eS4.

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

- Molecule 7 is a protein called Small ribosomal subunit protein uS7.

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

- Molecule 8 is a protein called Small ribosomal subunit protein eS6.

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

- Molecule 9 is a protein called Small ribosomal subunit protein eS7.

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

- Molecule 10 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	206	Total	C	N	O	S	0	0
			1679	1054	329	291	5		

- Molecule 11 is a protein called Small ribosomal subunit protein uS4.

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

- Molecule 12 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	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 13 is a protein called Small ribosomal subunit protein uS17.

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

- Molecule 14 is a protein called Small ribosomal subunit protein eS12.

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

- Molecule 15 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 16 is a protein called Ribosomal protein S14.

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

- Molecule 17 is a protein called Small ribosomal subunit protein uS19.

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

- Molecule 18 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 19 is a protein called Small ribosomal subunit protein eS17.

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

- Molecule 20 is a protein called Small ribosomal subunit protein uS13.

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

- Molecule 21 is a protein called Small ribosomal subunit protein eS19.

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

- Molecule 22 is a protein called Small ribosomal subunit protein uS10.

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

- Molecule 23 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	82	Total	C	N	O	S	0	0
			619	378	117	119	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 24 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 25 is a protein called Small ribosomal subunit protein uS12.

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

- Molecule 26 is a protein called 40S ribosomal protein S24.

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

- Molecule 27 is a protein called Small ribosomal subunit protein eS26.

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

- Molecule 28 is a protein called Small ribosomal subunit protein eS27.

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

- Molecule 29 is a protein called Small ribosomal subunit protein eS28.

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

- Molecule 30 is a protein called Small ribosomal subunit protein uS14.

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

- Molecule 31 is a protein called Ubiquitin-ribosomal protein eS31 fusion protein.

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

- Molecule 32 is a protein called Small ribosomal subunit protein RACK1.

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

- Molecule 33 is a protein called Small ribosomal subunit protein eS25.

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

- Molecule 34 is a protein called Small ribosomal subunit protein eS30.

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

- Molecule 35 is a protein called Small ribosomal subunit protein eS32.

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

- Molecule 36 is a RNA chain called Initiator tRNA.

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

- Molecule 37 is a RNA chain called EMCV IRES.

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

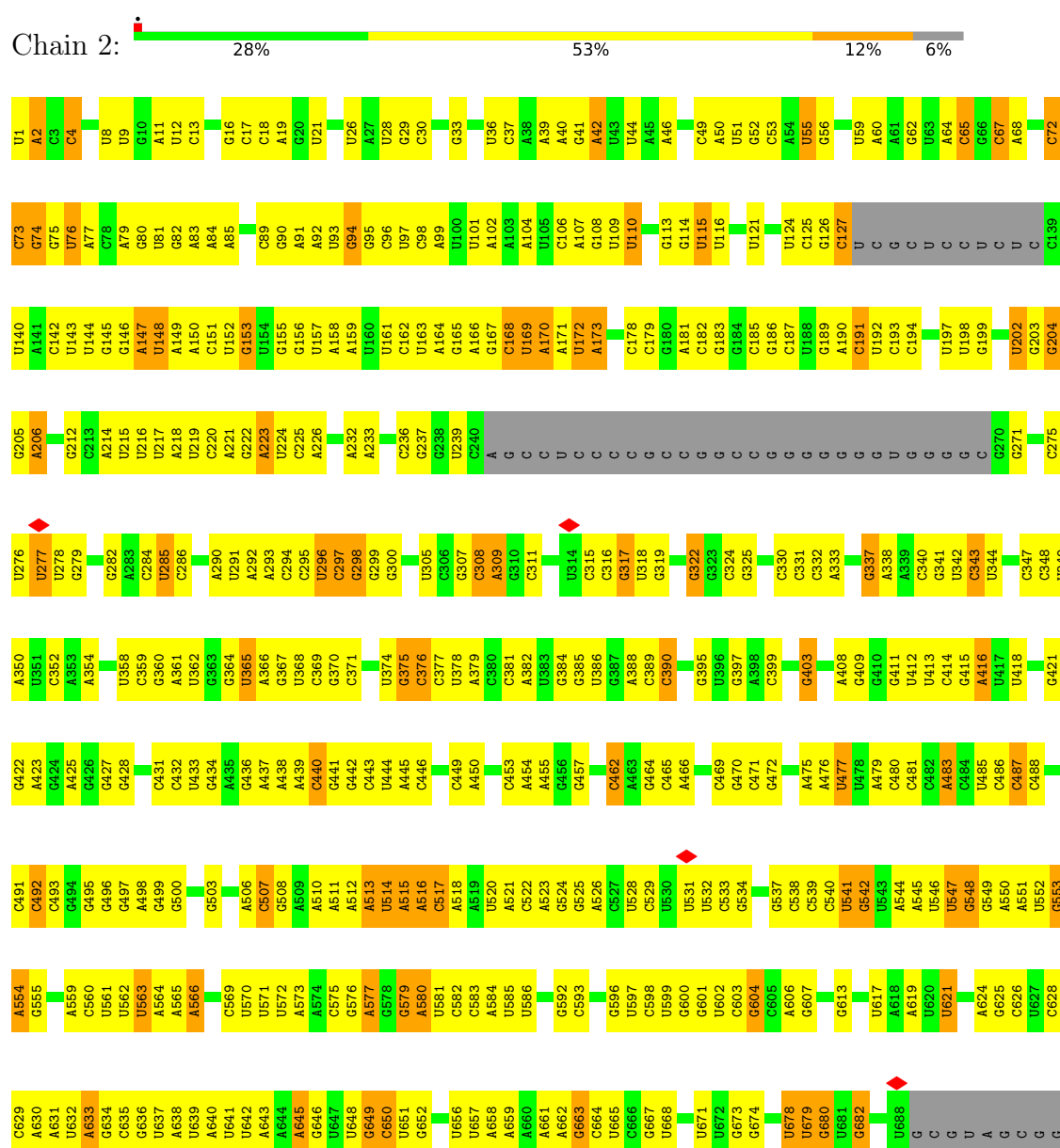
There are 8 discrepancies between the modelled and reference sequences:

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

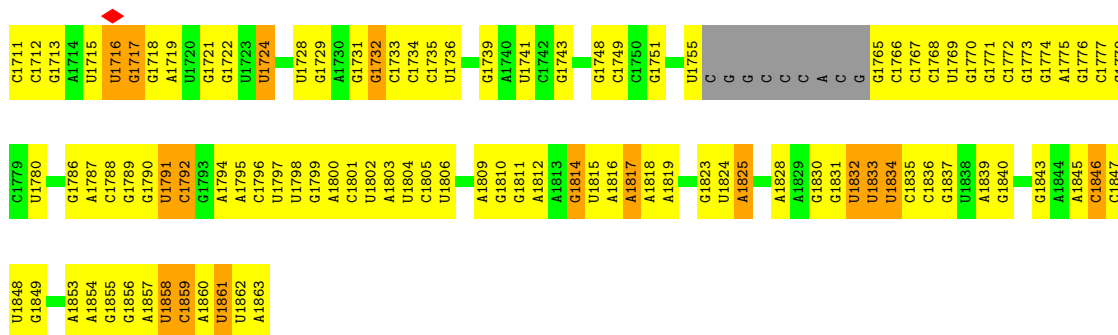
3 Residue-property plots

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.

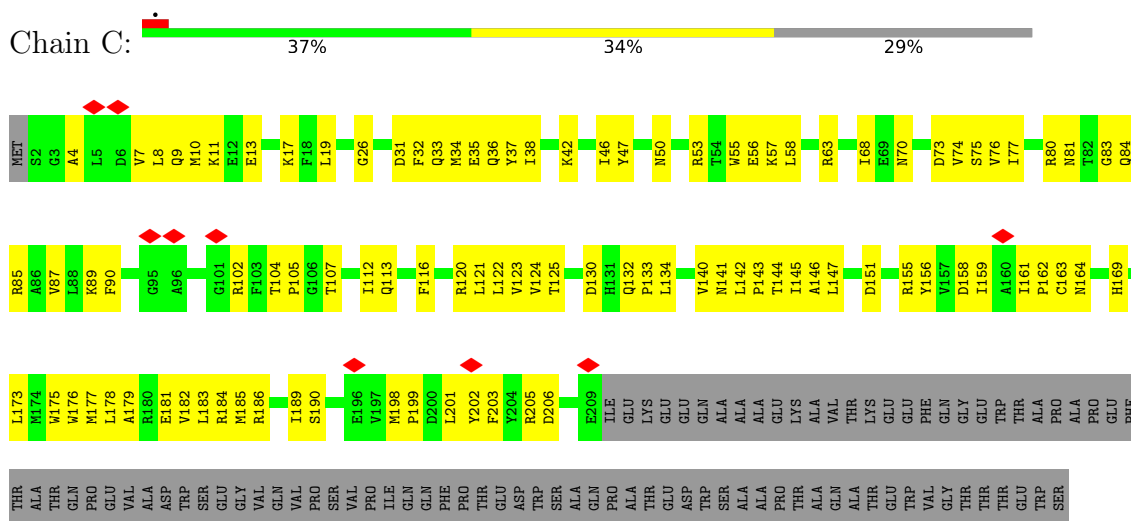
• Molecule 1: 18S ribosomal RNA



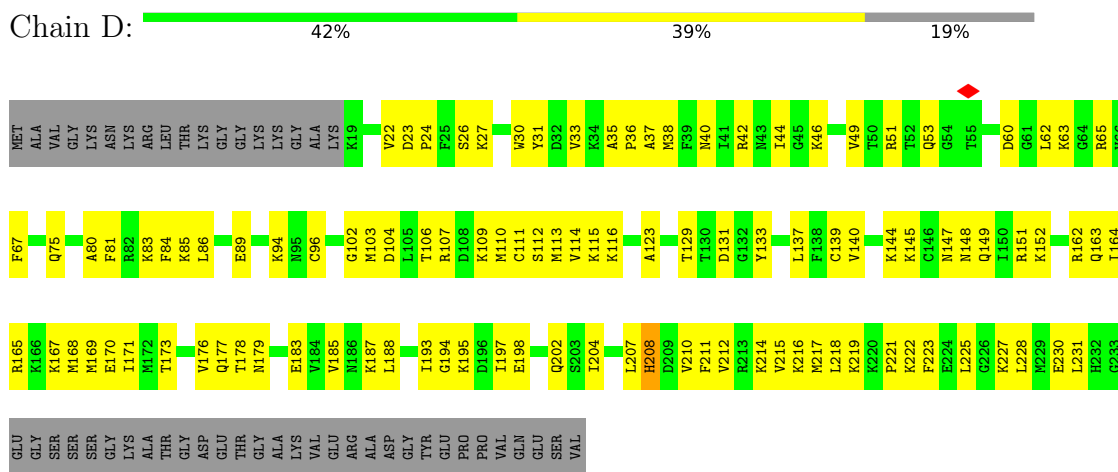
A1636	G1668	U1501	U1437	G1371	C1299	U1169	G1100	A1031	U961	C896	G828	G
U1637	C1669	A1502	U1438	A1372	U1300	A1169	G1101	A1032	U965	G897	C829	C
U1638	G1570	G1503	C1439	U1373	C1301	U1173	C1102	G1033	G966	G898	C830	G
C1639	G1571	U1440	U1440	U1374	U1304	U1174	C1103	G1034	C899	A899	C831	G
C1640	G1572	U1441	U1305	A1375	U1239	G1175	C1104	C1035	G967	U900	G832	U
G1641	U1573	A1442	U1306	C1376	U1240	C1176	C1105	U1041	A968	C901	A833	C
A1642	G1443	U1307	U1306	G1377	G1241	A1177	G1106	U1042	C969	U902	G834	C
G1643	A1444	C1308	G1307	U1382	U1244	A1178	U1107	U1043	C970	G903	C835	G
U1575	G1445	G1510	G1446	A1383	C1245	A1179	U1108	C1043	G971	A904	C836	U
C1576	G1447	G1512	G1447	A1384	A1246	G1180	U1109	G1044	G972	G905	C837	C
U1580	U1514	C1513	U1449	U1385	A1247	C1181	U1111	A1045	A976	C907	C838	G
G1581	U1514	U1386	U1314	U1386	G1248	C1182	U1112	C1049	A977	C908	C839	U
A1582	U1515	C1387	U1315	C1387	A1249	G1183	C1113	G1050	G978	U909	U840	G
C1583	C1516	U1388	G1317	U1388	G1250	A1184	U1108	A1051	C979	G910	G841	A
U1584	C1517	G1389	G1316	A1517	G1251	A1185	U1109	U1052	A979	G911	G842	G
C1585	C1518	G1390	G1318	G1390	G1252	A1186	U1110	C1053	G980	U912	A843	U
G1586	G1519	C1391	U1319	C1391	G1253	C1187	U1111	G1054	G981	A913	G844	G
U1587	U1520	A1392	G1320	U1392	A1254	U1188	C1120	C1055	C984	U914	A845	U
C1588	U1521	U1393	G1321	U1393	A1255	U1189	C1121	A1056	C985	A915	C846	C
A1589	C1522	C1394	G1322	A1394	A1256	U1190	G1122	U1057	G987	G917	C847	G
U1590	C1523	G1395	G1323	C1395	C1257	A1191	C1123	C1058	A988	A918	U853	C
C1591	C1524	U1396	G1324	U1396	C1258	A1192	C1124	C1059	C989	G919	A854	C
G1592	U1525	G1397	U1325	A1397	U1259	G1193	G1125	C1060	G920	G925	G855	C
U1593	C1526	A1398	G1326	A1398	C1260	G1194	G1126	G1061	U1000	C926	G856	G
C1594	U1527	C1399	A1328	C1399	A1261	A1195	G1127	U1062	G1001	C927	G784	C
A1595	C1528	U1400	G1331	U1400	G1262	A1196	C1128	C1063	U1009	G928	G789	C
U1596	C1529	A1401	C1332	G1401	C1267	A1197	C1129	G1064	C1002	G929	G792	C
G1597	U1530	G1402	C1333	U1402	C1268	U1198	G1130	U1065	U999	G924	G793	C
C1598	C1531	U1403	U1338	U1403	C1269	A1200	C1131	A1066	U1000	C925	G794	C
U1599	U1532	A1404	U1339	A1404	G1270	C1201	G1134	U1068	G1001	C926	G795	C
C1600	C1533	U1405	U1340	U1405	C1271	G1202	C1135	U1069	C1002	G927	U796	C
G1601	U1534	A1406	C1341	A1406	G1272	A1203	G1136	C1070	U1009	G928	U797	C
A1602	C1535	U1407	U1342	U1407	A1273	G1204	G1137	C1071	C1003	G929	A798	C
U1603	U1536	G1408	U1343	G1408	C1274	A1205	G1138	G1072	A1006	U999	C733	C
C1604	C1537	A1409	G1344	A1409	C1275	G1206	A1139	A1073	G1006	G930	C734	C
U1605	U1538	U1410	U1345	U1410	G1276	A1211	A1140	U1076	G1007	C937	C735	C
G1606	C1539	C1411	G1346	C1411	G1277	C1212	A1141	A1079	U1008	U939	C736	C
U1607	U1540	C1412	U1347	C1412	A1278	G1213	C1142	A1080	U1009	A940	C737	C
A1608	C1541	C1413	C1482	C1413	C1279	A1214	C1143	U1011	G1010	U941	U738	C
U1609	U1542	C1414	U1350	U1414	C1280	C1215	A1144	G1081	U1012	U942	U739	C
C1610	C1543	G1418	G1352	G1418	G1281	C1216	A1145	G1082	U1013	G943	C740	C
U1611	U1544	C1419	U1353	C1419	G1282	A1216	A1146	A1083	U1014	C944	C741	C
G1612	U1545	G1420	U1354	G1420	U1283	G1217	U1150	C1086	C1015	C946	C742	C
C1613	C1546	C1421	U1355	C1421	U1284	U1221	U1151	C1087	A1016	G947	C743	C
U1614	U1547	G1422	U1356	G1422	U1285	G1222	G1152	U1088	U1017	G948	C744	C
A1615	C1548	C1423	U1357	C1423	U1286	U1223	G1153	A1089	U1018	U949	U745	C
U1616	U1549	U1424	U1358	U1424	A1287	G1224	G1154	C1090	A1019	C950	U746	C
C1617	C1550	G1425	C1359	G1425	U1288	U1225	U1155	U1091	U1020	U951	G747	C
A1618	U1551	G1426	U1360	G1426	A1289	G1226	G1160	G1092	U1021	G952	G748	C
U1619	C1552	C1427	G1361	C1427	G1290	A1224	G1161	G1093	C1022	A953	C749	C
C1620	C1553	U1428	C1362	U1428	A1291	G1226	G1162	C1094	A1023	G954	G750	C
G1621	U1554	U1429	U1363	U1429	G1294	U1227	G1163	G1095	U1026	G955	C751	C
C1622	C1555	C1430	A1365	C1430	A1295	G1228	G1164	A1096	A1027	U956	C752	C
U1623	U1556	C1431	U1367	C1431	U1296	G1229	G1165	U1097	C1028	A958	C825	C
A1624	C1557	C1432	C1368	C1432	U1297	G1232	G1166	G1098	U1029	A959	G824	C
C1625	G1558	C1433	U1369	C1433	C1436	G1233	G1167	C1099	A1030	U960	G825	C
U1626	U1559	U1436	U1370	U1436	U1436	G1233	U1168	U1099	U961	G827	C826	C
G1627	C1560	C1437	C1370	C1437	U1437	G1234	U1169	U1100	U962	G828	C827	C
U1628	U1561	U1438	U1371	U1438	U1438	G1235	U1170	U1101	U963	G829	C828	C
C1629	G1562	C1439	A1366	C1439	A1296	G1236	U1171	U1102	U964	G830	C829	C
U1630	C1563	C1440	U1372	C1440	U1297	G1237	U1172	U1103	U965	G831	C830	C
G1631	A1564	C1441	U1373	C1441	U1298	G1238	U1173	U1104	U966	G832	C831	C
U1632	U1565	C1442	C1374	C1442	U1299	G1239	U1174	U1105	U967	G833	C832	C
C1633	G1566	C1443	U1375	C1443	U1300	G1240	U1175	U1106	U968	G834	C833	C
A1634	C1567	U1444	U1376	U1444	U1301	U1176	U1176	U1107	C969	G835	C834	C
U1635	U1568	U1445	U1377	U1445	U1302	A1177	U1177	U1108	C970	C836	C835	C
C1636	U1569	G1446	U1378	G1446	U1303	A1178	U1178	U1109	G971	A904	C837	G
A1637	G1570	A1447	C1439	A1447	A1309	A1179	U1179	U1110	G972	G905	C838	C
U1638	U1571	U1448	U1340	U1448	U1310	C1180	U1180	A1045	A976	C907	C839	U
C1639	C1572	U1449	U1341	U1449	U1311	C1181	U1181	C1049	A977	C908	U840	G
G1640	U1573	U1450	U1342	U1450	U1312	C1182	U1182	G1050	G978	U909	G841	A
U1641	C1574	A1451	U1343	A1451	A1249	G1183	U1183	U1052	A979	G910	G842	G
C1642	C1575	G1452	G1317	G1452	G1251	A1184	U1184	C1053	G980	U912	A843	U
A1643	U1574	U1453	G1318	U1453	G1252	A1185	U1185	G1054	G981	A913	G844	G
U1644	G1575	G1454	U1319	G1454	G1253	C1186	U1186	C1055	C984	U914	A845	U
C1645	U1576	U1455	U1320	U1455	A1254	U1187	C1187	A1056	C985	A915	C846	C
A1646	U1577	U1456	G1321	U1456	A1255	U1188	U1188	U1057	G987	G917	C847	G
U1647	C1578	U1457	G1322	U1457	A1256	U1189	U1189	C1058	A988	A918	U853	C
C1648	U1579	U1458	U1323	U1458	C1257	A1190	U1190	G1060	C989	G919	A854	C
G1649	U1580	U1459	U1324	U1459	C1258	A1191	C1191	C1061	G920	G925	G855	C
U1650	U1581	U1460	U1325	U1460	C1259	A1192	C1192	U1062	G921	C926	G856	G
C1651	C1580	U1461	U1326	U1461	A1260	A1193	G1193	U1063	A994	A922	G789	C
U1652	U1581	U1462	U1327	U1462	C1261	A1194	G1194	C1064	G995	A923	G792	C
G1653	U1582	U1463	U1328	U1463	C1262	A1195	G1195	U1065	U999	G924	G793	C
U1654	C1582	U1464	A1328	U1464	A1262	A1196	G1196	U1066	G1000	C925	G794	C
C1655	U1583	U1465	G1331	U1465	C1267	A1197	C1197	U1068	G1001	C926	G795	C
A1656	C1583	U1466	C1332	U1466	C1268	A1198	G1198	U1069	C1002	G927	U796	C
U1657	U1584	U1467	U1333	U1467	C1269	U1199	C1199	C1070	U1009	G928	U797	C
C1658	C1585	U1468	U1334	U1468	G1270	A1200	C1201	G1071	C1003	G929	A798	C
U1659	U1586	U1469	C1335	U1469	C1271	A1201	G1202	U1072	A1006	U999	C733	C
G1660	C1587	U1470	U1336	U1470	C1272	A1202	G1203	A1073	G1006	G930	C734	C
U1661	U1588	U1471	U1337	U1471	C1273	A1203	G1204	U1076	G1007	C937	C735	C
C1662	C1589	U1472	U1338	U1472	C1274	A1204	G1205	A1079	U1008	U939	C736	C
U1663	U1590	U1473	U1339	U1473	C1275	A1205	G1206	A1080	U1009	A940	C737	C
A1664	C1591	U1474	U1340	U1474	C1276	A1206	G1207	A1081	U1010	U941	U738	C
U1665	U1592	U1475	U1341	U1475	C1277	A1207	G1208	A1082	U1011	U942	U739	C
C1666	C1593	U1476	U1342	U1476	C1278	A1208	G1209	G1083	U1012	G943	C740	C
U1667	U1594	U1477	U1343	U1477	C1279	A1209	G1210	A1084	U1013	C944	C741	C
G1668	C1595	U1478	U1344	U1478	C1280	A1210	G1211	C1086	C1015	C946	C742	C
U1669	U1596	U1479	U1345	U1479	C1281	A1211	G1212	C1087	A1016	G947	C743	C
C1670	C1597	U1480	U1346	U1480	C1282	A1212	G1213	U1088	U1017	G948	C744	C
U1671	U1598	U1481	U1347	U1481	C1283	A1213	G1214	A1089	U1018	U949	U745	C
A1672	C1599	U1482	U1348	U1482	C1284	A1214	G1215	C1090	A1019	C950	G746	C
U1												



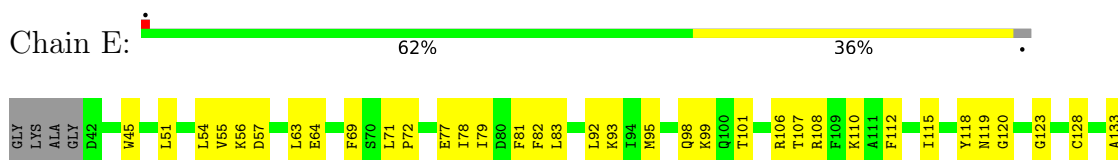
• Molecule 2: Small ribosomal subunit protein uS2

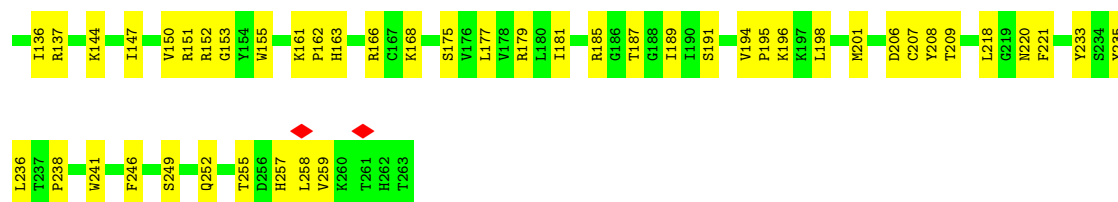


• Molecule 3: Small ribosomal subunit protein eS1

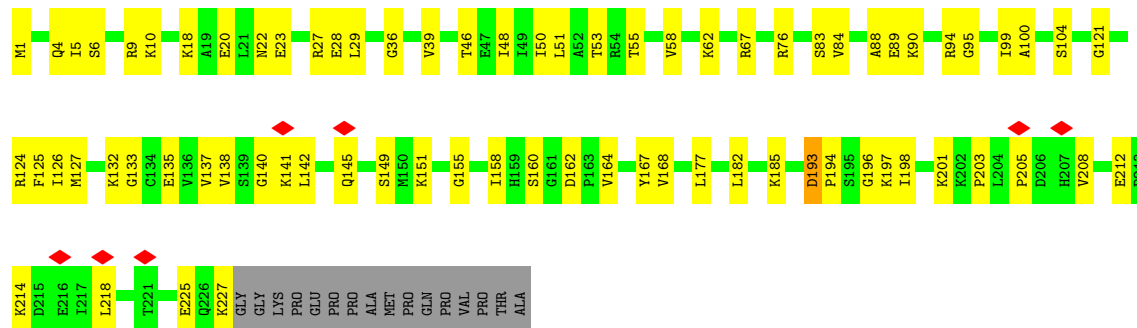


• Molecule 4: Small ribosomal subunit protein uS5

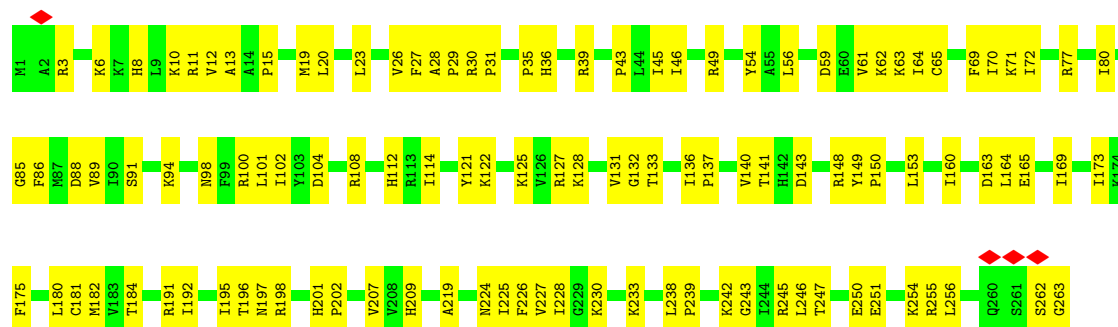




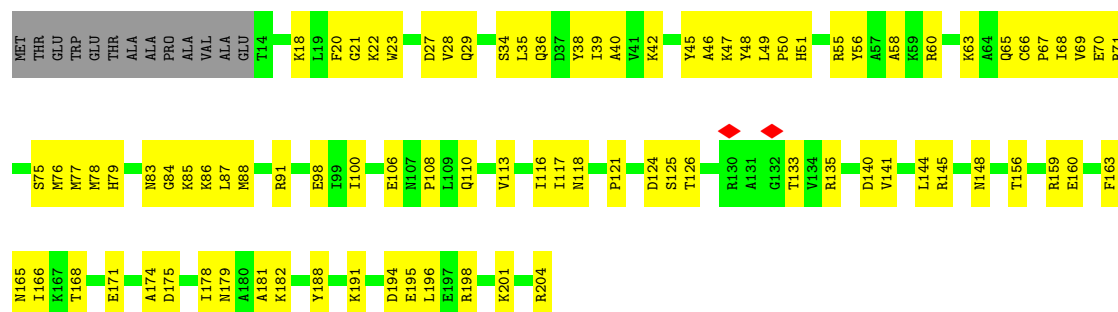
• Molecule 5: Small ribosomal subunit protein uS3



• Molecule 6: Small ribosomal subunit protein eS4

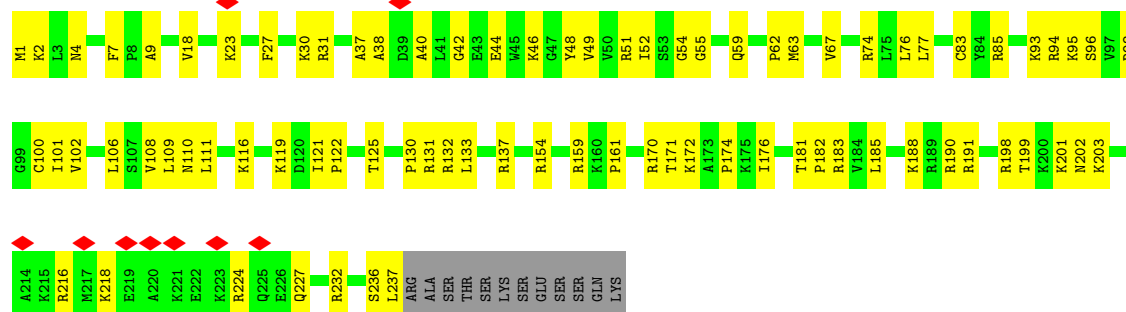


• Molecule 7: Small ribosomal subunit protein uS7



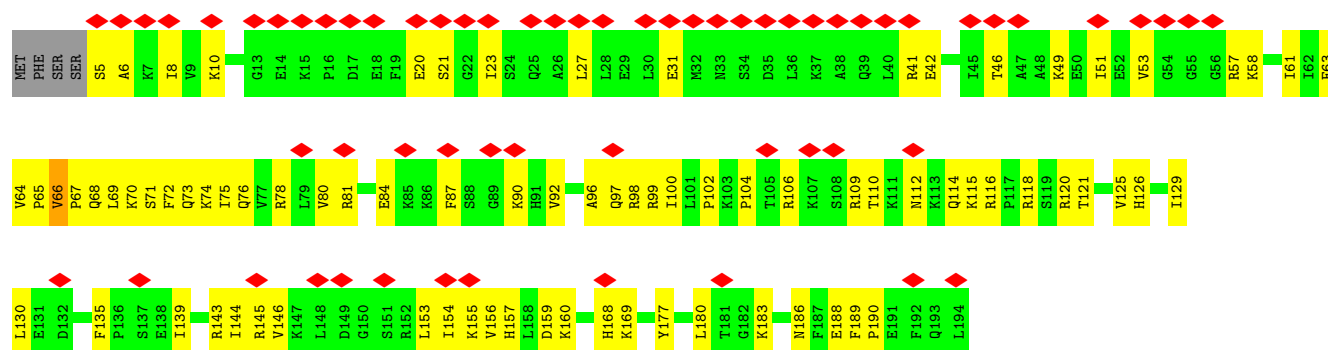
• Molecule 8: Small ribosomal subunit protein eS6

Chain I: 



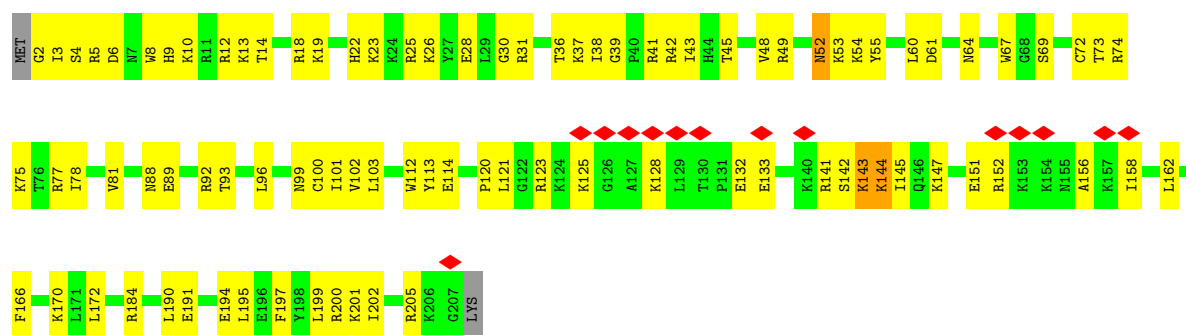
• Molecule 9: Small ribosomal subunit protein eS7

Chain J: 



• Molecule 10: Small ribosomal subunit protein eS8

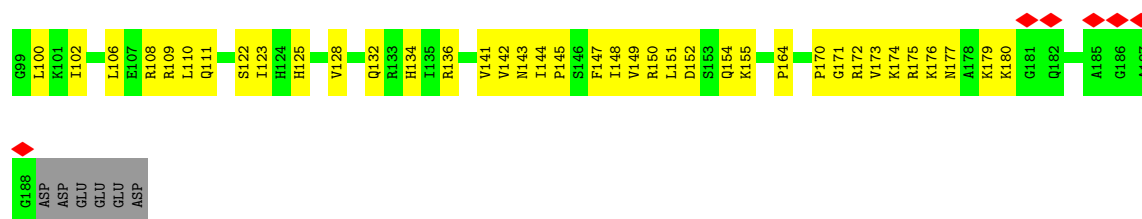
Chain K: 



• Molecule 11: Small ribosomal subunit protein uS4

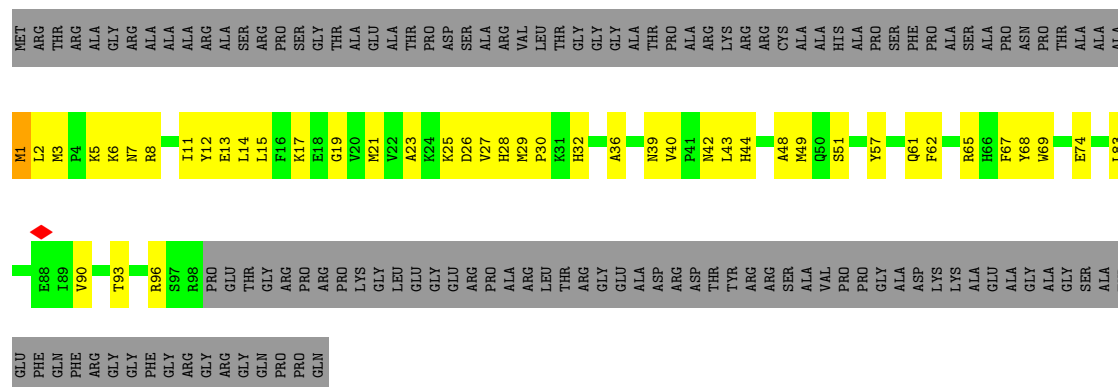
Chain L: 





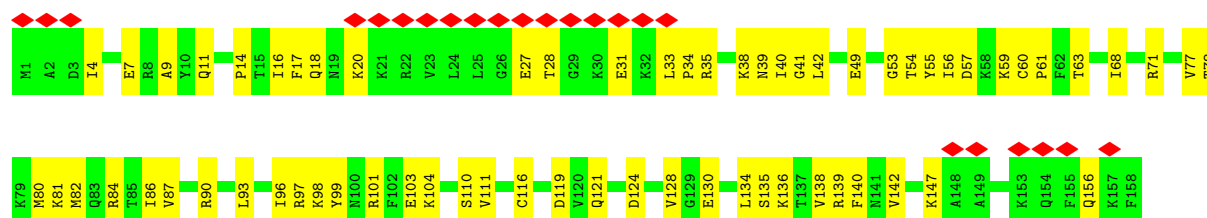
• Molecule 12: Small ribosomal subunit protein eS10

Chain M: 24% 19% 56%



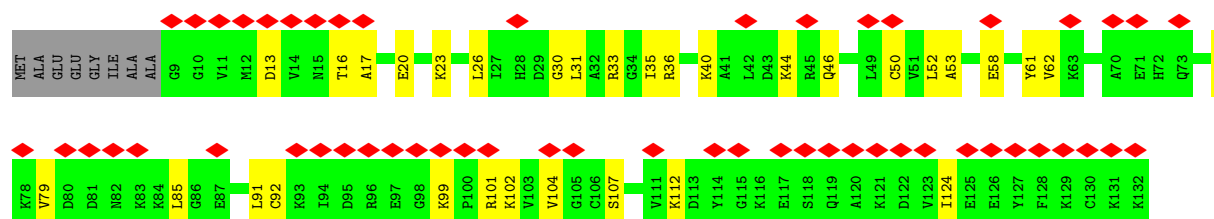
• Molecule 13: Small ribosomal subunit protein uS17

Chain N: 15% 58% 42%



• Molecule 14: Small ribosomal subunit protein eS12

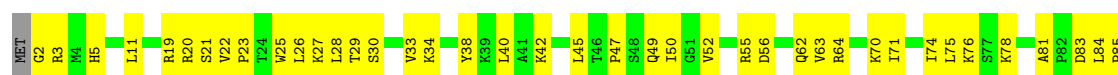
Chain O: 41% 70% 24% 6%



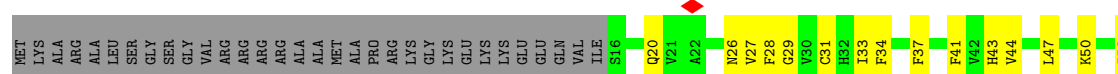
• Molecule 15: Small ribosomal subunit protein uS15

Chain P: 58% 41%





• Molecule 16: Ribosomal protein S14



• Molecule 17: Small ribosomal subunit protein uS19



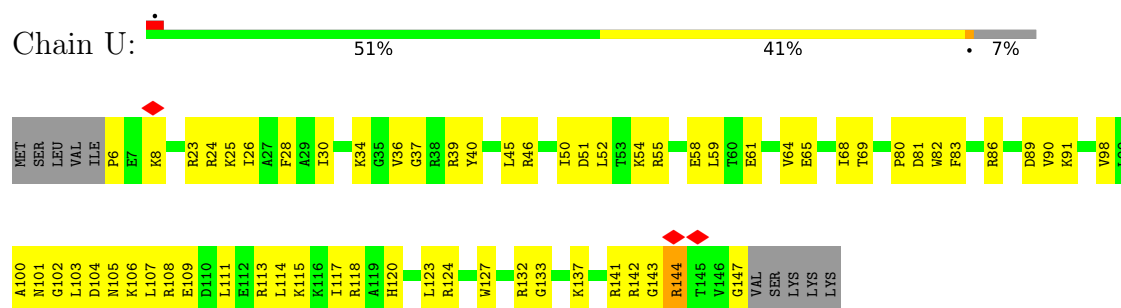
• Molecule 18: Small ribosomal subunit protein uS9



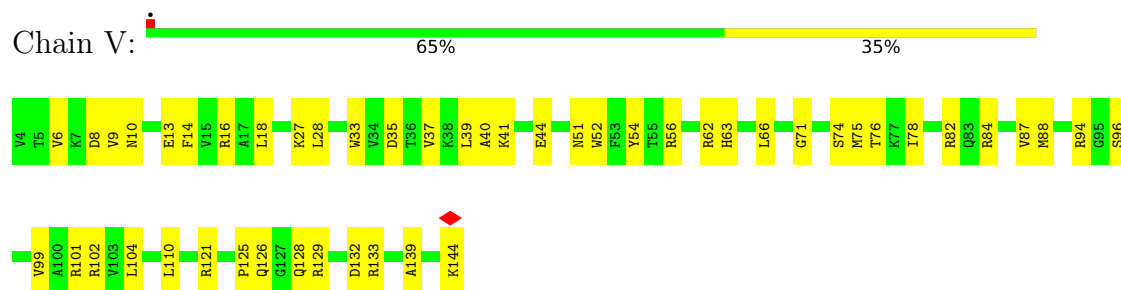
• Molecule 19: Small ribosomal subunit protein eS17



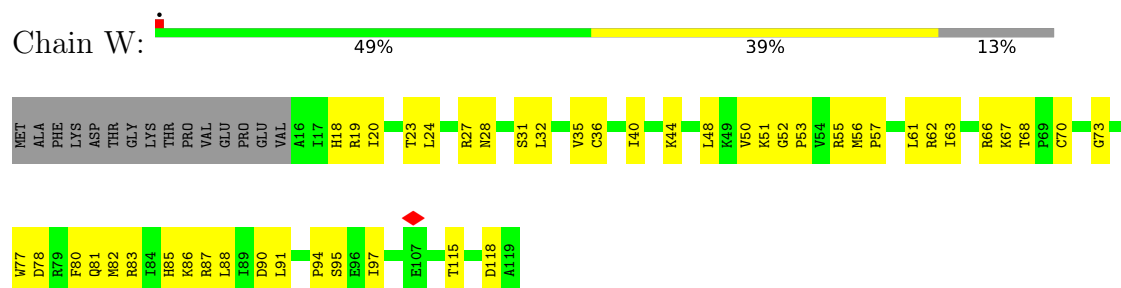
- Molecule 20: Small ribosomal subunit protein uS13



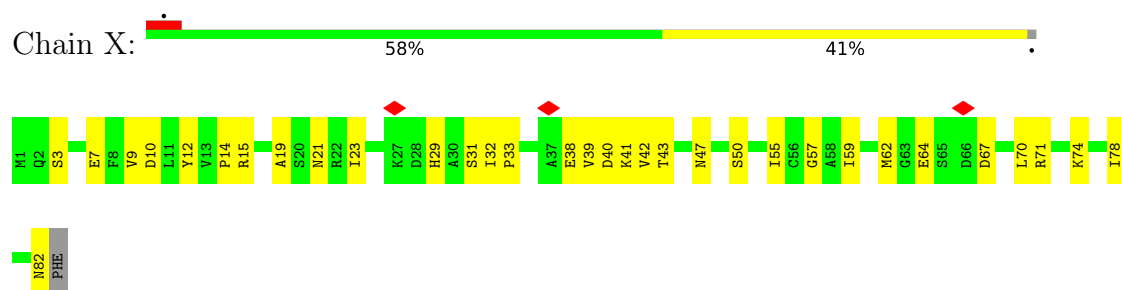
- Molecule 21: Small ribosomal subunit protein eS19



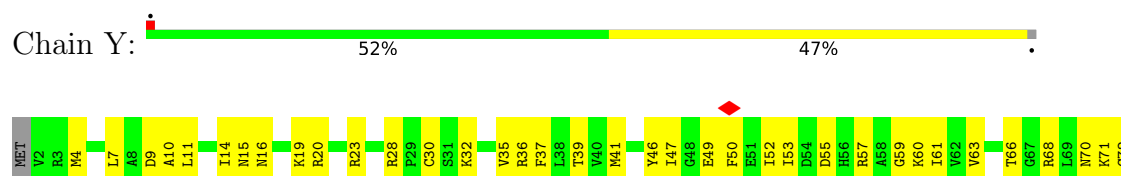
- Molecule 22: Small ribosomal subunit protein uS10



- Molecule 23: Small ribosomal subunit protein eS21

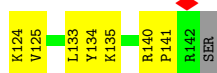
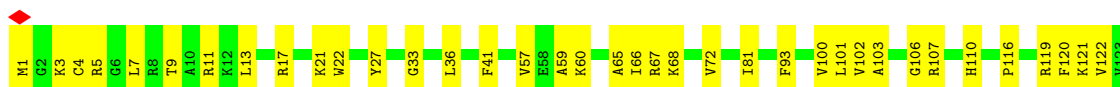


- Molecule 24: Small ribosomal subunit protein uS8

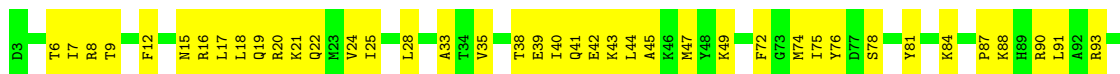




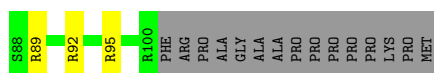
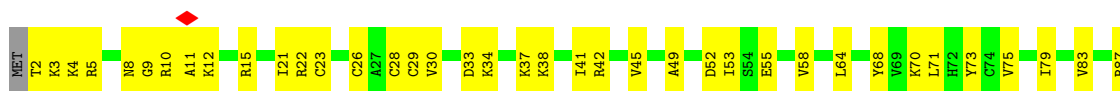
- Molecule 25: Small ribosomal subunit protein uS12



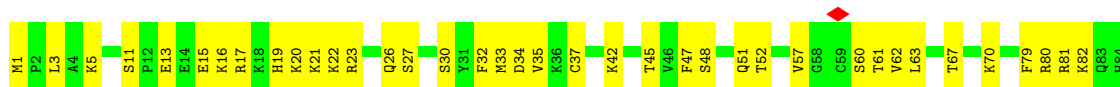
- Molecule 26: 40S ribosomal protein S24



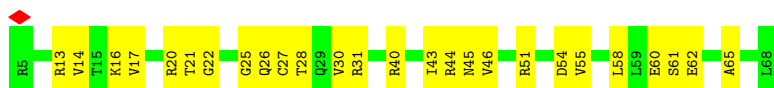
- Molecule 27: Small ribosomal subunit protein eS26



- Molecule 28: Small ribosomal subunit protein eS27

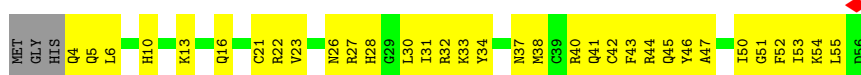


- Molecule 29: Small ribosomal subunit protein eS28



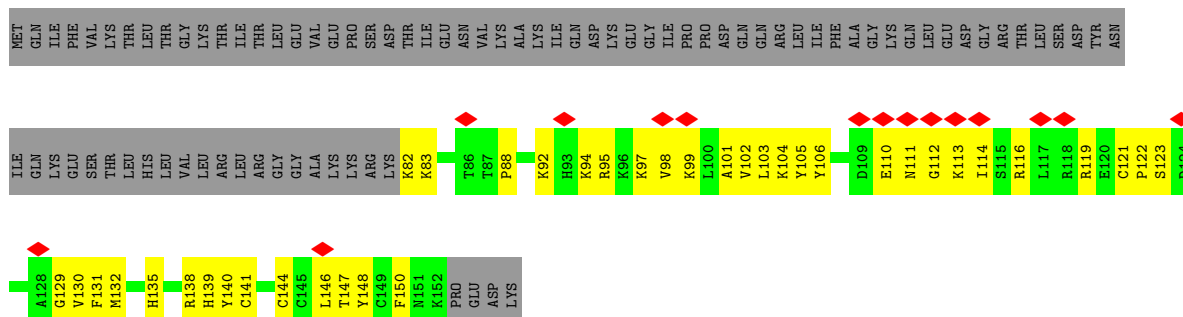
- Molecule 30: Small ribosomal subunit protein uS14

Chain e: 



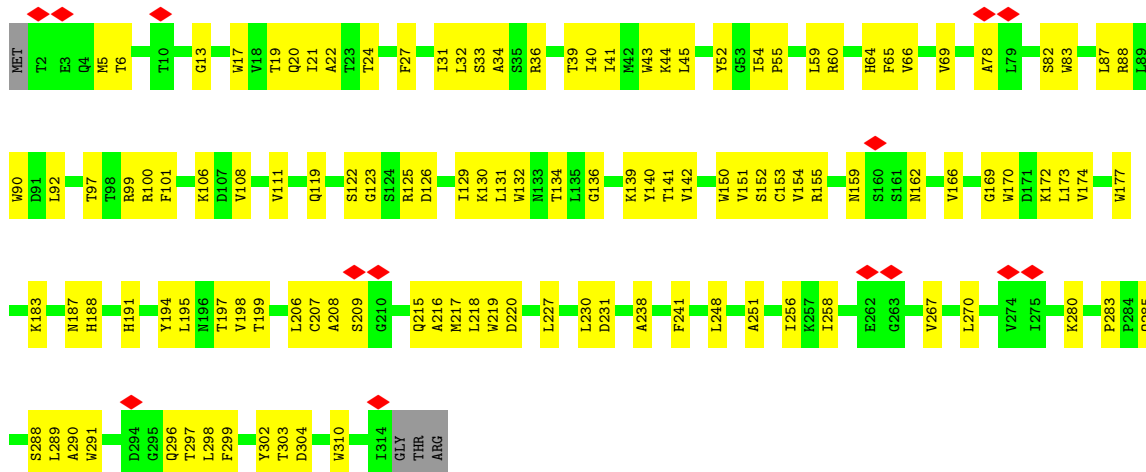
- Molecule 31: Ubiquitin-ribosomal protein eS31 fusion protein

Chain f: 

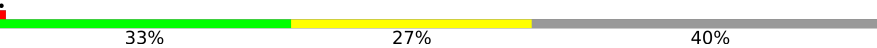


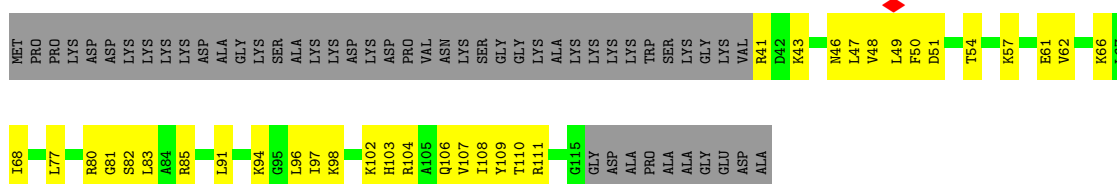
- Molecule 32: Small ribosomal subunit protein RACK1

Chain g: 

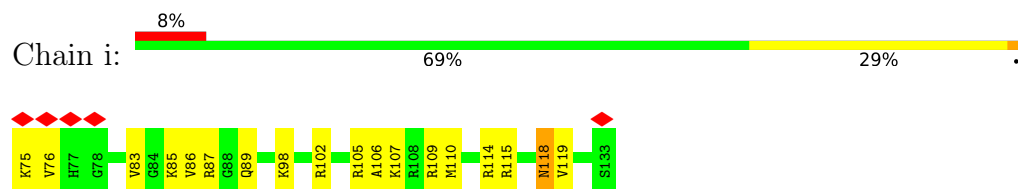


- Molecule 33: Small ribosomal subunit protein eS25

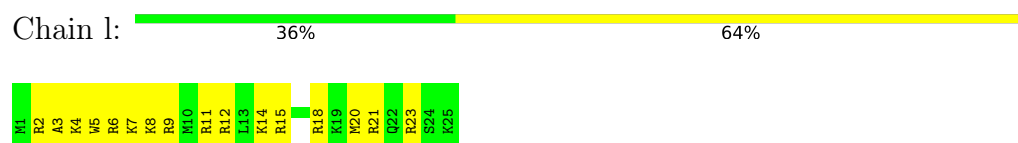
Chain h: 



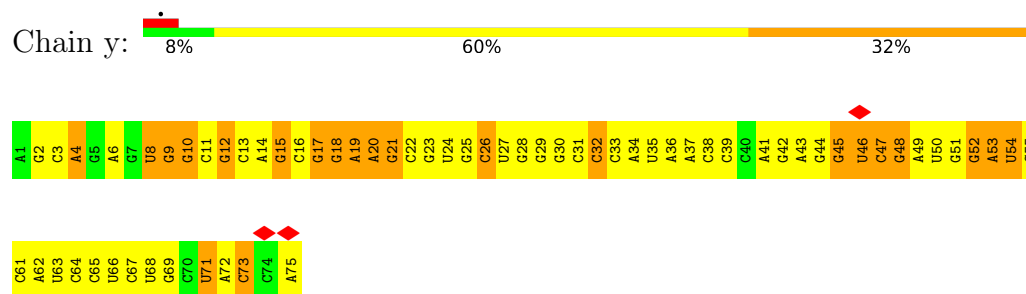
- Molecule 34: Small ribosomal subunit protein eS30



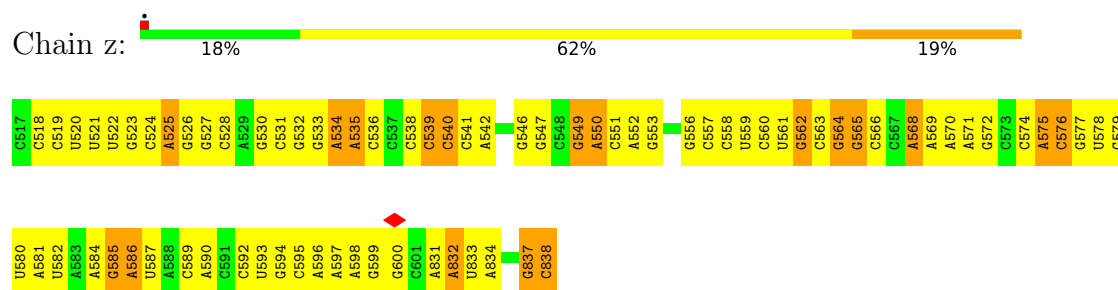
- Molecule 35: Small ribosomal subunit protein eS32



- Molecule 36: Initiator tRNA



- Molecule 37: EMCV IRES



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	55231	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	0.621	Depositor
Minimum map value	-0.247	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.0811	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	0.12	0/41584	0.29	0/64804
2	C	0.18	0/1679	0.47	0/2283
3	D	0.16	0/1769	0.46	0/2367
4	E	0.19	0/1757	0.43	0/2371
5	F	0.14	0/1792	0.44	2/2412 (0.1%)
6	G	0.15	0/2125	0.39	0/2856
7	H	0.16	0/1531	0.39	0/2059
8	I	0.11	0/1945	0.35	0/2587
9	J	0.17	0/1553	0.45	0/2079
10	K	0.14	0/1708	0.46	2/2278 (0.1%)
11	L	0.15	0/1522	0.41	0/2031
12	M	0.16	0/851	0.50	2/1147 (0.2%)
13	N	0.16	0/1319	0.41	0/1761
14	O	0.09	0/968	0.32	0/1296
15	P	0.13	0/1232	0.39	0/1656
16	Q	0.14	0/1029	0.42	0/1380
17	R	0.14	0/1132	0.46	0/1510
18	S	0.13	0/1141	0.38	0/1528
19	T	0.15	0/1031	0.46	0/1383
20	U	0.15	0/1190	0.47	0/1592
21	V	0.13	0/1133	0.35	0/1517
22	W	0.12	0/832	0.33	0/1117
23	X	0.13	0/626	0.42	0/839
24	Y	0.19	0/1051	0.45	0/1406
25	Z	0.14	0/1124	0.41	0/1500
26	a	0.20	0/1038	0.57	4/1377 (0.3%)
27	b	0.21	0/802	0.44	0/1076
28	c	0.22	0/673	0.50	2/902 (0.2%)
29	d	0.14	0/509	0.41	0/680
30	e	0.15	0/455	0.46	0/603
31	f	0.13	0/593	0.41	0/786
32	g	0.11	0/2493	0.34	0/3394
33	h	0.15	0/604	0.34	0/810
34	i	0.12	0/478	0.57	2/628 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	l	0.14	0/241	0.41	0/305
36	y	0.13	0/1795	0.30	0/2798
37	z	0.11	0/2213	0.27	0/3442
All	All	0.13	0/85518	0.35	14/124560 (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
3	D	0	1
9	J	0	1
18	S	0	1
26	a	0	2
All	All	0	5

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	M	1	MET	CA-C-N	8.63	137.23	121.70
12	M	1	MET	C-N-CA	8.63	137.23	121.70
5	F	197	LYS	CA-C-N	7.29	134.83	121.70
5	F	197	LYS	C-N-CA	7.29	134.83	121.70
34	i	118	ASN	CA-C-N	6.48	133.36	121.70

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	D	208	HIS	Peptide
9	J	66	VAL	Peptide
18	S	43	GLU	Peptide
26	a	102	THR	Peptide
26	a	103	SER	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	37194	0	18795	1207	0
2	C	1642	0	1646	97	0
3	D	1741	0	1815	82	0
4	E	1721	0	1812	69	0
5	F	1764	0	1863	58	0
6	G	2083	0	2189	98	0
7	H	1509	0	1563	75	0
8	I	1923	0	2088	63	0
9	J	1530	0	1627	83	0
10	K	1679	0	1760	77	0
11	L	1498	0	1608	72	0
12	M	827	0	854	35	0
13	N	1296	0	1374	59	0
14	O	958	0	993	26	0
15	P	1208	0	1294	58	0
16	Q	1016	0	1039	47	0
17	R	1111	0	1168	67	0
18	S	1123	0	1193	60	0
19	T	1019	0	1075	56	0
20	U	1172	0	1226	67	0
21	V	1113	0	1149	37	0
22	W	822	0	887	43	0
23	X	619	0	622	35	0
24	Y	1034	0	1080	70	0
25	Z	1106	0	1179	41	0
26	a	1022	0	1084	54	0
27	b	789	0	839	45	0
28	c	659	0	683	32	0
29	d	507	0	536	21	0
30	e	445	0	442	36	0
31	f	581	0	599	39	0
32	g	2436	0	2393	95	0
33	h	598	0	656	30	0
34	i	473	0	524	17	0
35	l	240	0	289	17	0
36	y	1604	0	816	61	0
37	z	1981	0	1011	74	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	80043	0	61771	2688	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 2688 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)
1:2:124:U:H3	1:2:330:C:N4	1.55	1.02
1:2:1704:G:H1	1:2:1818:A:H61	1.00	1.00
1:2:1751:G:H1	1:2:1769:U:H3	1.07	0.97
1:2:432:C:N4	1:2:439:A:H62	1.62	0.96
1:2:432:C:H42	1:2:439:A:N6	1.64	0.94

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	C	206/295 (70%)	176 (85%)	29 (14%)	1 (0%)	24	63
3	D	213/264 (81%)	188 (88%)	24 (11%)	1 (0%)	24	63
4	E	220/226 (97%)	210 (96%)	9 (4%)	1 (0%)	24	63
5	F	225/243 (93%)	211 (94%)	13 (6%)	1 (0%)	30	67
6	G	261/263 (99%)	240 (92%)	21 (8%)	0	100	100
7	H	189/204 (93%)	172 (91%)	17 (9%)	0	100	100
8	I	233/249 (94%)	223 (96%)	10 (4%)	0	100	100
9	J	188/194 (97%)	174 (93%)	14 (7%)	0	100	100
10	K	204/208 (98%)	177 (87%)	23 (11%)	4 (2%)	6	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	L	180/194 (93%)	173 (96%)	6 (3%)	1 (1%)	21	58
12	M	96/225 (43%)	83 (86%)	13 (14%)	0	100	100
13	N	156/158 (99%)	149 (96%)	7 (4%)	0	100	100
14	O	122/132 (92%)	109 (89%)	13 (11%)	0	100	100
15	P	148/151 (98%)	144 (97%)	4 (3%)	0	100	100
16	Q	134/168 (80%)	115 (86%)	19 (14%)	0	100	100
17	R	133/145 (92%)	115 (86%)	18 (14%)	0	100	100
18	S	139/146 (95%)	133 (96%)	6 (4%)	0	100	100
19	T	124/135 (92%)	116 (94%)	8 (6%)	0	100	100
20	U	140/152 (92%)	123 (88%)	16 (11%)	1 (1%)	18	55
21	V	139/141 (99%)	127 (91%)	11 (8%)	1 (1%)	18	55
22	W	102/119 (86%)	97 (95%)	5 (5%)	0	100	100
23	X	80/83 (96%)	71 (89%)	9 (11%)	0	100	100
24	Y	127/130 (98%)	117 (92%)	10 (8%)	0	100	100
25	Z	140/143 (98%)	132 (94%)	8 (6%)	0	100	100
26	a	122/126 (97%)	111 (91%)	9 (7%)	2 (2%)	7	37
27	b	97/115 (84%)	88 (91%)	9 (9%)	0	100	100
28	c	82/84 (98%)	74 (90%)	8 (10%)	0	100	100
29	d	62/64 (97%)	60 (97%)	2 (3%)	0	100	100
30	e	51/56 (91%)	41 (80%)	10 (20%)	0	100	100
31	f	69/156 (44%)	58 (84%)	11 (16%)	0	100	100
32	g	311/317 (98%)	285 (92%)	26 (8%)	0	100	100
33	h	73/125 (58%)	70 (96%)	3 (4%)	0	100	100
34	i	57/59 (97%)	52 (91%)	5 (9%)	0	100	100
35	l	23/25 (92%)	23 (100%)	0	0	100	100
All	All	4846/5495 (88%)	4437 (92%)	396 (8%)	13 (0%)	37	71

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
20	U	144	ARG
5	F	193	ASP
10	K	156	ALA

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Mol	Chain	Res	Type
26	a	103	SER
10	K	144	LYS

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	
2	C	174/244 (71%)	174 (100%)	0	100	100
3	D	196/231 (85%)	196 (100%)	0	100	100
4	E	186/187 (100%)	186 (100%)	0	100	100
5	F	190/202 (94%)	190 (100%)	0	100	100
6	G	225/225 (100%)	225 (100%)	0	100	100
7	H	161/170 (95%)	161 (100%)	0	100	100
8	I	207/218 (95%)	207 (100%)	0	100	100
9	J	170/174 (98%)	170 (100%)	0	100	100
10	K	177/180 (98%)	177 (100%)	0	100	100
11	L	157/168 (94%)	157 (100%)	0	100	100
12	M	89/173 (51%)	89 (100%)	0	100	100
13	N	142/142 (100%)	142 (100%)	0	100	100
14	O	104/108 (96%)	104 (100%)	0	100	100
15	P	130/131 (99%)	130 (100%)	0	100	100
16	Q	106/130 (82%)	106 (100%)	0	100	100
17	R	121/130 (93%)	120 (99%)	1 (1%)	73	77
18	S	117/121 (97%)	117 (100%)	0	100	100
19	T	114/121 (94%)	114 (100%)	0	100	100
20	U	122/132 (92%)	122 (100%)	0	100	100
21	V	113/113 (100%)	113 (100%)	0	100	100
22	W	94/107 (88%)	94 (100%)	0	100	100
23	X	67/68 (98%)	67 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	Y	112/113 (99%)	112 (100%)	0	100	100
25	Z	114/115 (99%)	114 (100%)	0	100	100
26	a	108/108 (100%)	108 (100%)	0	100	100
27	b	87/99 (88%)	87 (100%)	0	100	100
28	c	76/76 (100%)	76 (100%)	0	100	100
29	d	57/57 (100%)	57 (100%)	0	100	100
30	e	47/49 (96%)	47 (100%)	0	100	100
31	f	64/140 (46%)	64 (100%)	0	100	100
32	g	272/275 (99%)	272 (100%)	0	100	100
33	h	66/103 (64%)	66 (100%)	0	100	100
34	i	49/49 (100%)	49 (100%)	0	100	100
35	l	24/24 (100%)	24 (100%)	0	100	100
All	All	4238/4683 (90%)	4237 (100%)	1 (0%)	100	100

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

Mol	Chain	Res	Type
17	R	104	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
13	N	94	HIS
17	R	35	GLN
33	h	106	GLN
13	N	121	GLN
15	P	5	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1733/1863 (93%)	383 (22%)	7 (0%)
36	y	74/75 (98%)	33 (44%)	0
37	z	91/93 (97%)	31 (34%)	0
All	All	1898/2031 (93%)	447 (23%)	7 (0%)

5 of 447 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	26	U
1	2	33	G
1	2	39	A

5 of 7 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	747	G
1	2	914	U
1	2	1431	C
1	2	1338	U
1	2	740	G

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
1	2	2

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Mol	Chain	Number of breaks
37	z	1
8	I	1
26	a	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	113.27
1	2	730:C	O3'	731:C	P	8.43
1	2	363:G	O3'	364:G	P	3.41
1	I	217:MET	C	218:LYS	N	3.36
1	a	9:THR	C	10:ARG	N	3.13

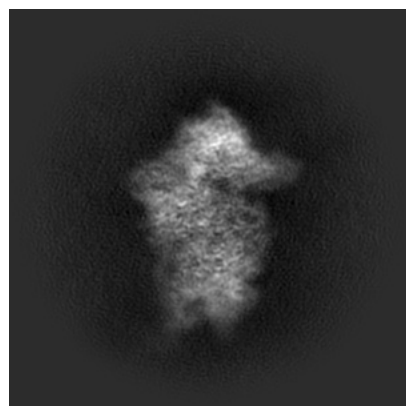
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64644. These allow visual inspection of the internal detail of the map and identification of artifacts.

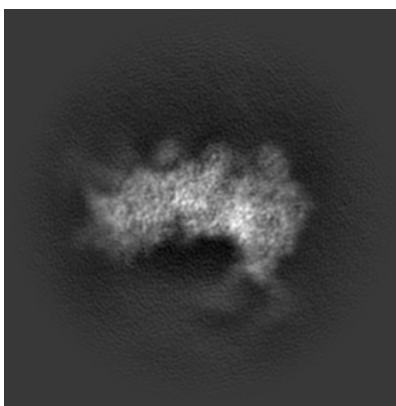
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

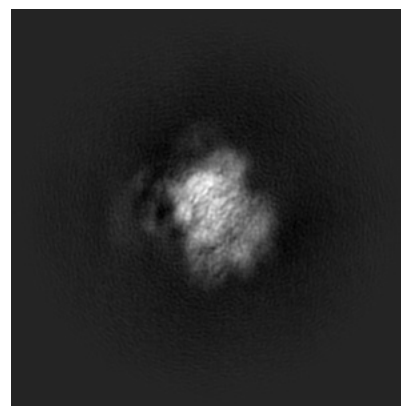
6.1.1 Primary map



X

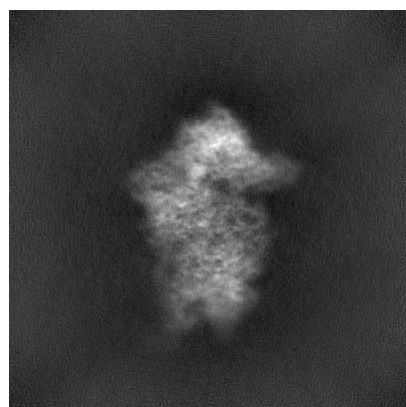


Y

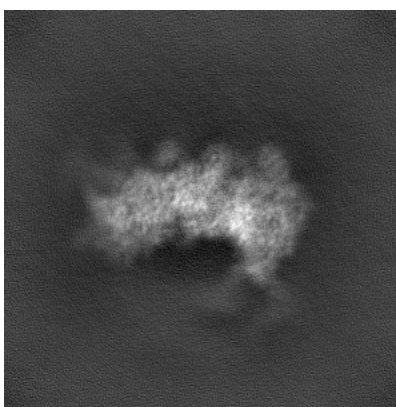


Z

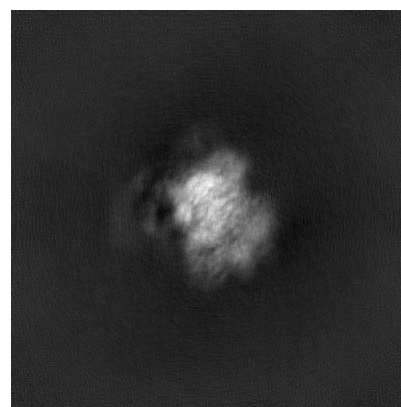
6.1.2 Raw map



X



Y

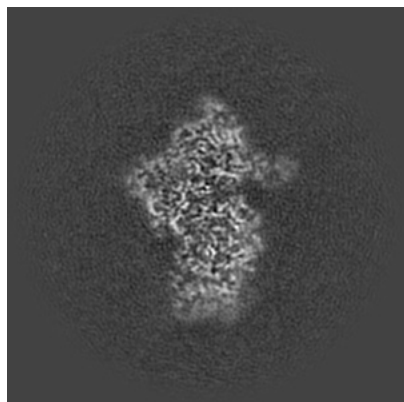


Z

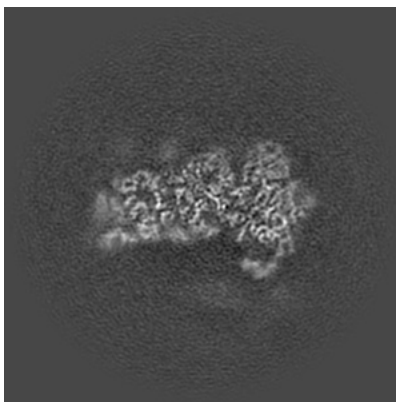
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

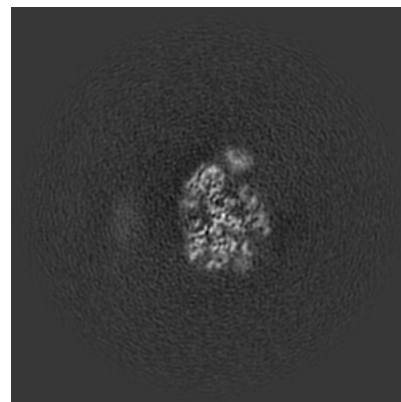
6.2.1 Primary map



X Index: 200

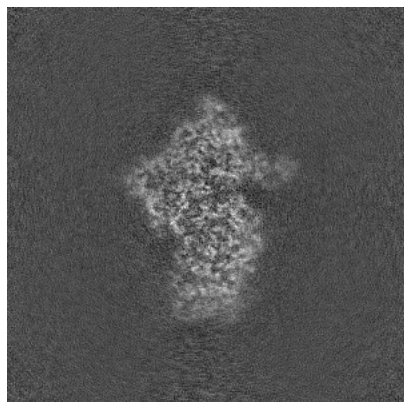


Y Index: 200

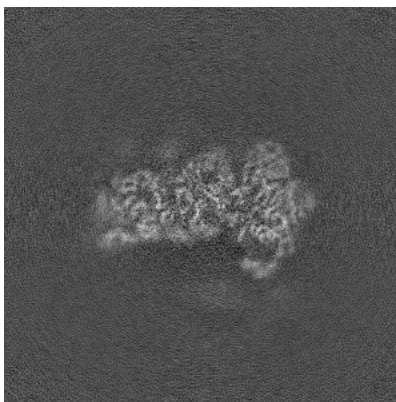


Z Index: 200

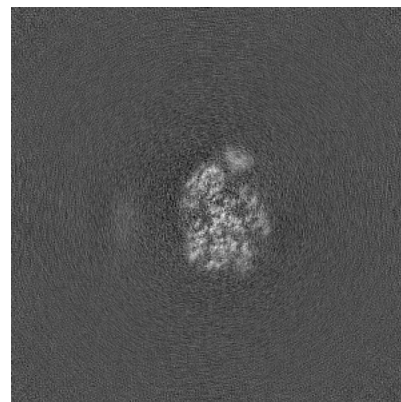
6.2.2 Raw map



X Index: 200



Y Index: 200

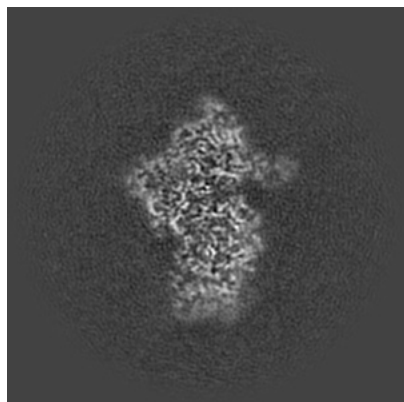


Z Index: 200

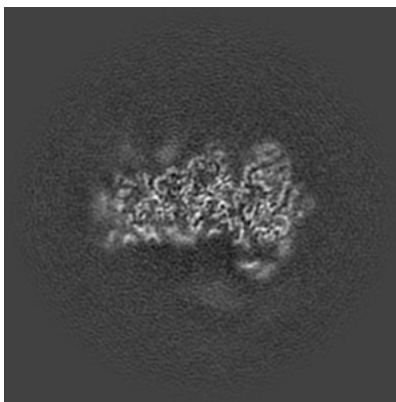
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

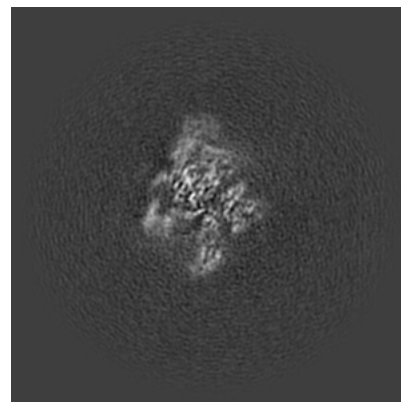
6.3.1 Primary map



X Index: 200

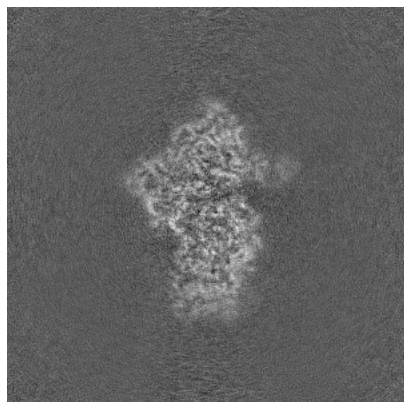


Y Index: 196

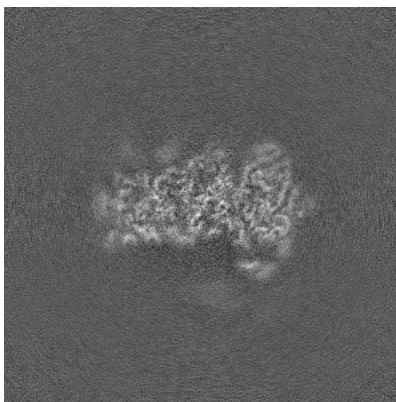


Z Index: 243

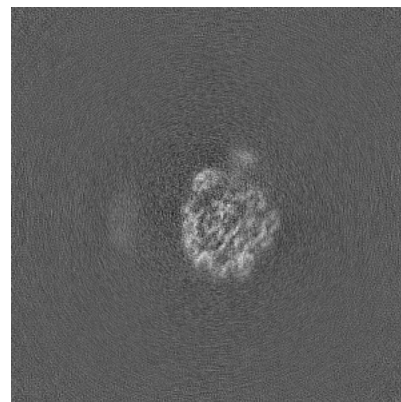
6.3.2 Raw map



X Index: 199



Y Index: 196

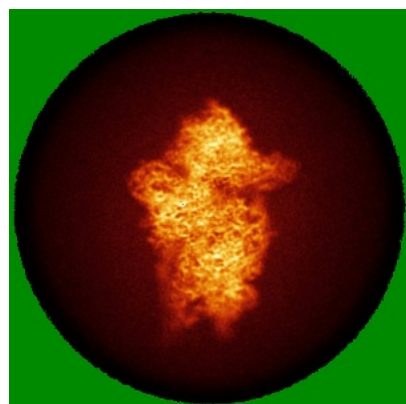


Z Index: 208

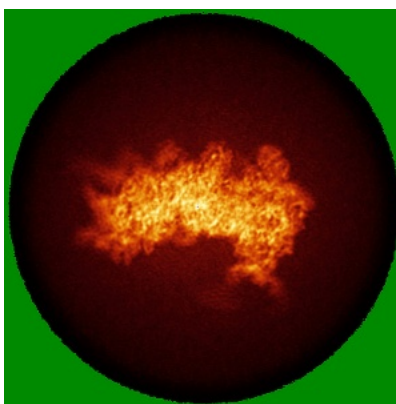
The images above show the largest variance slices of the map in three orthogonal directions.

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

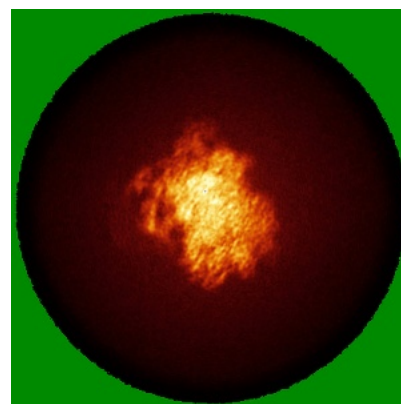
6.4.1 Primary map



X

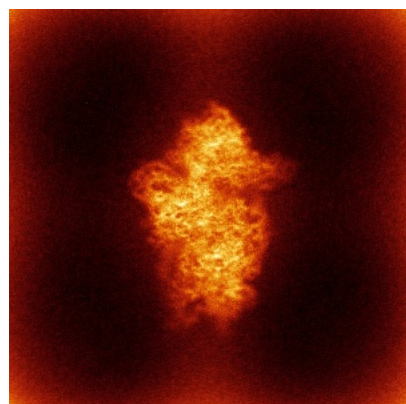


Y

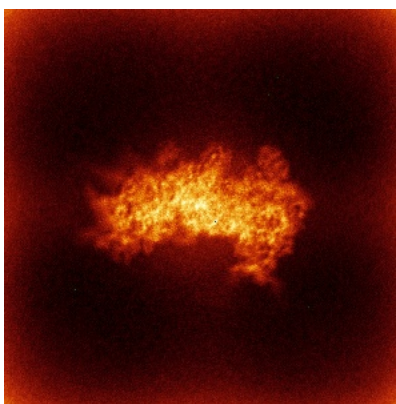


Z

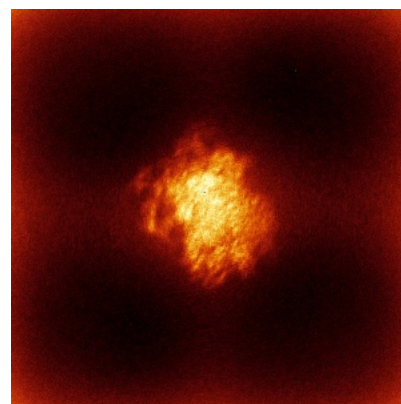
6.4.2 Raw map



X



Y

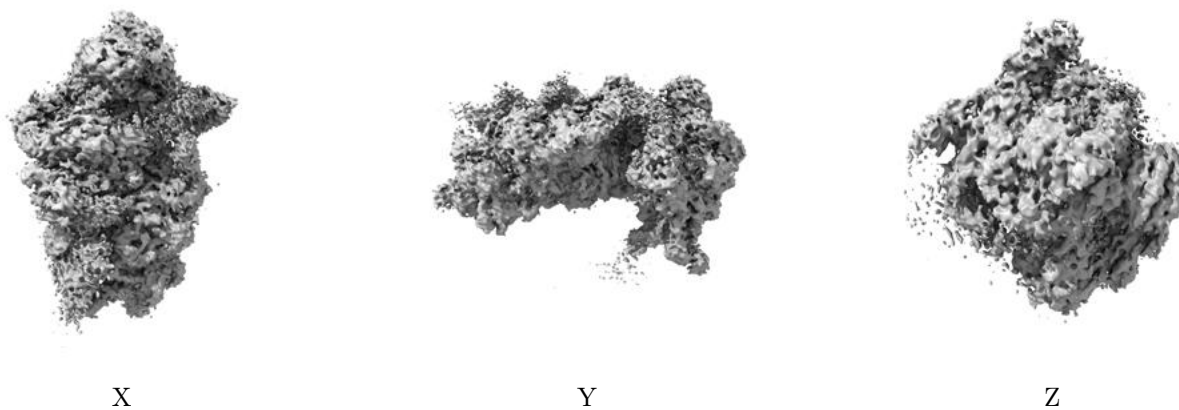


Z

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.

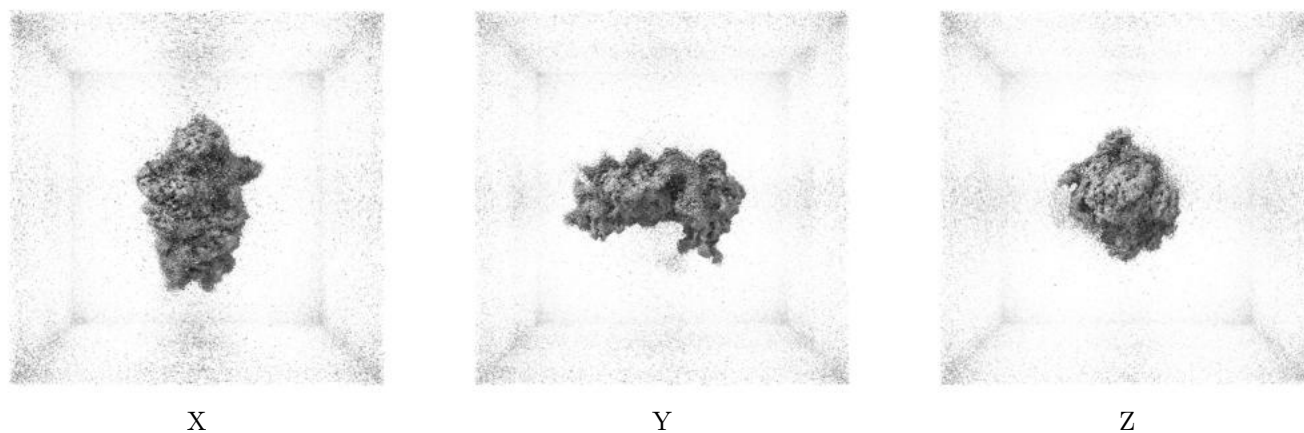
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0811. 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.

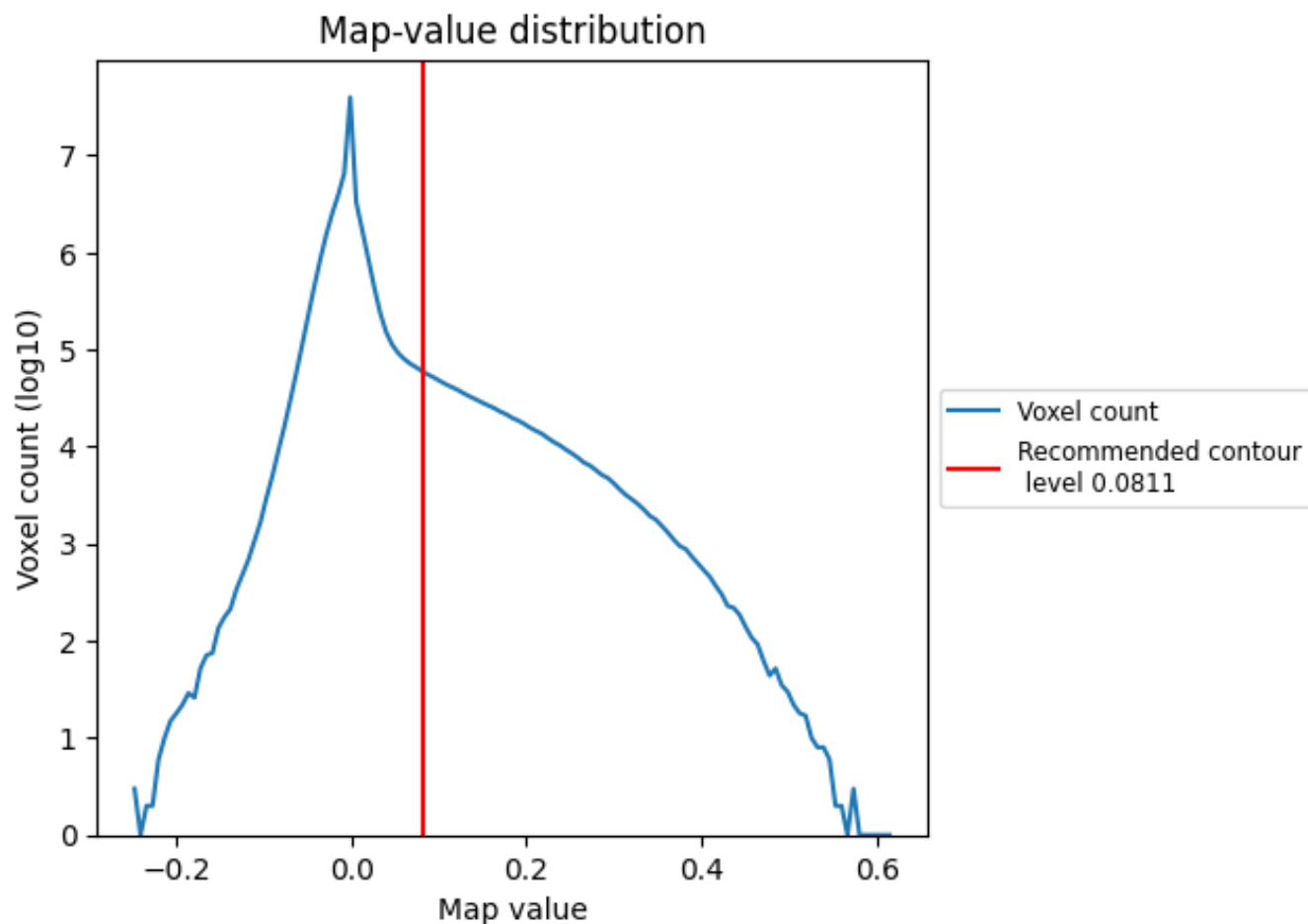
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

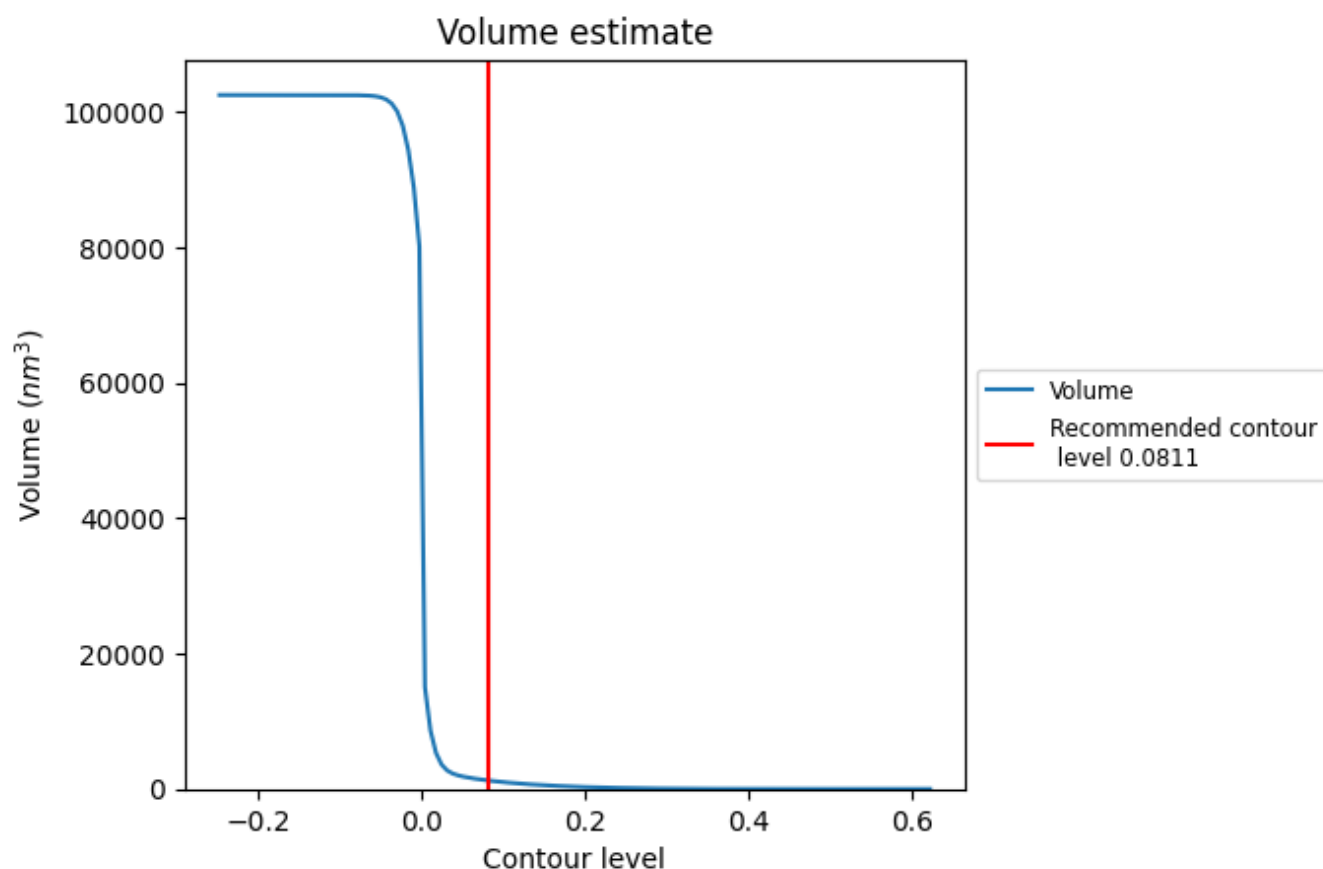
This section contains the results of statistical analysis of the map.

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.

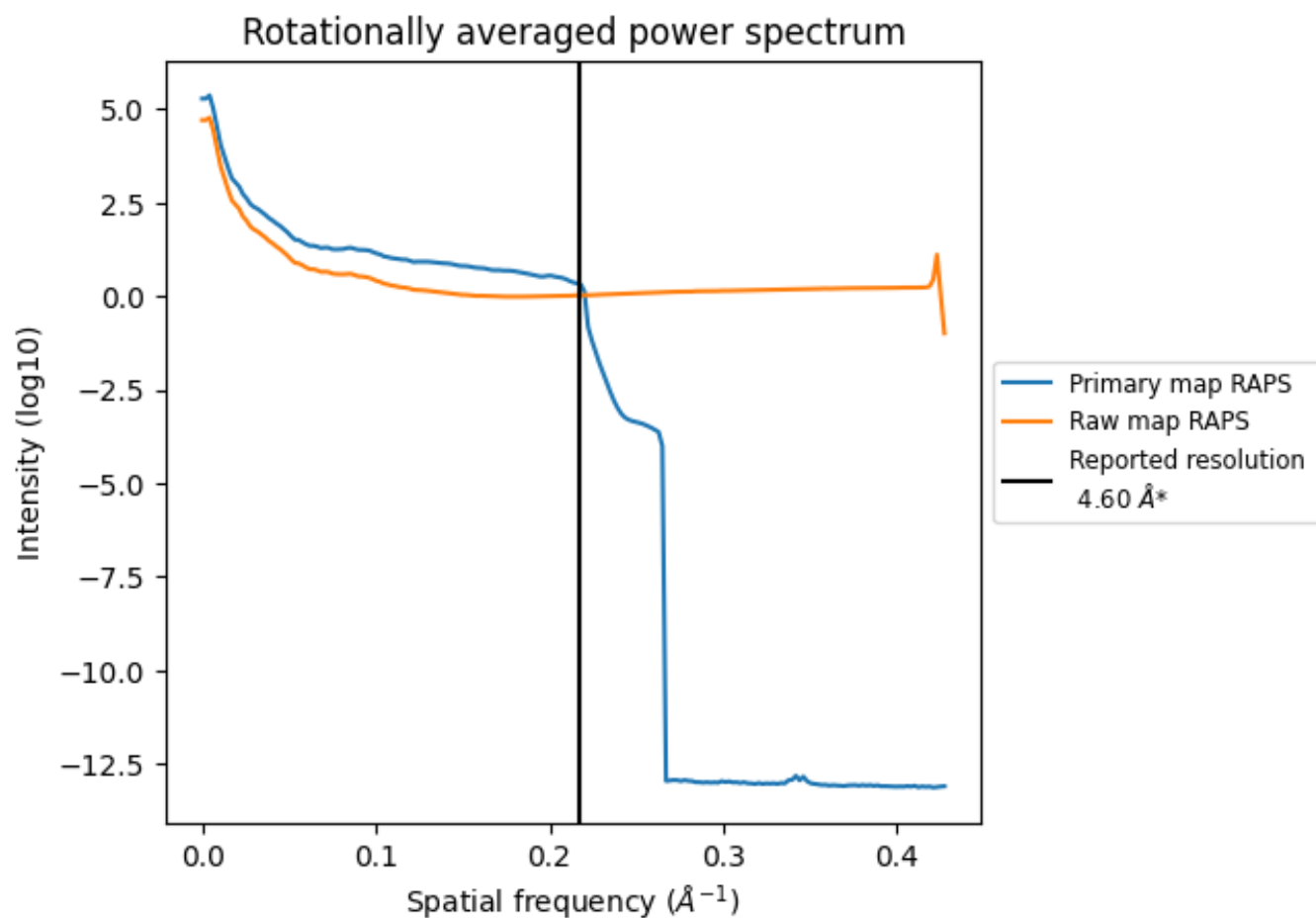
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1251 nm^3 ; this corresponds to an approximate mass of 1130 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 ⓘ

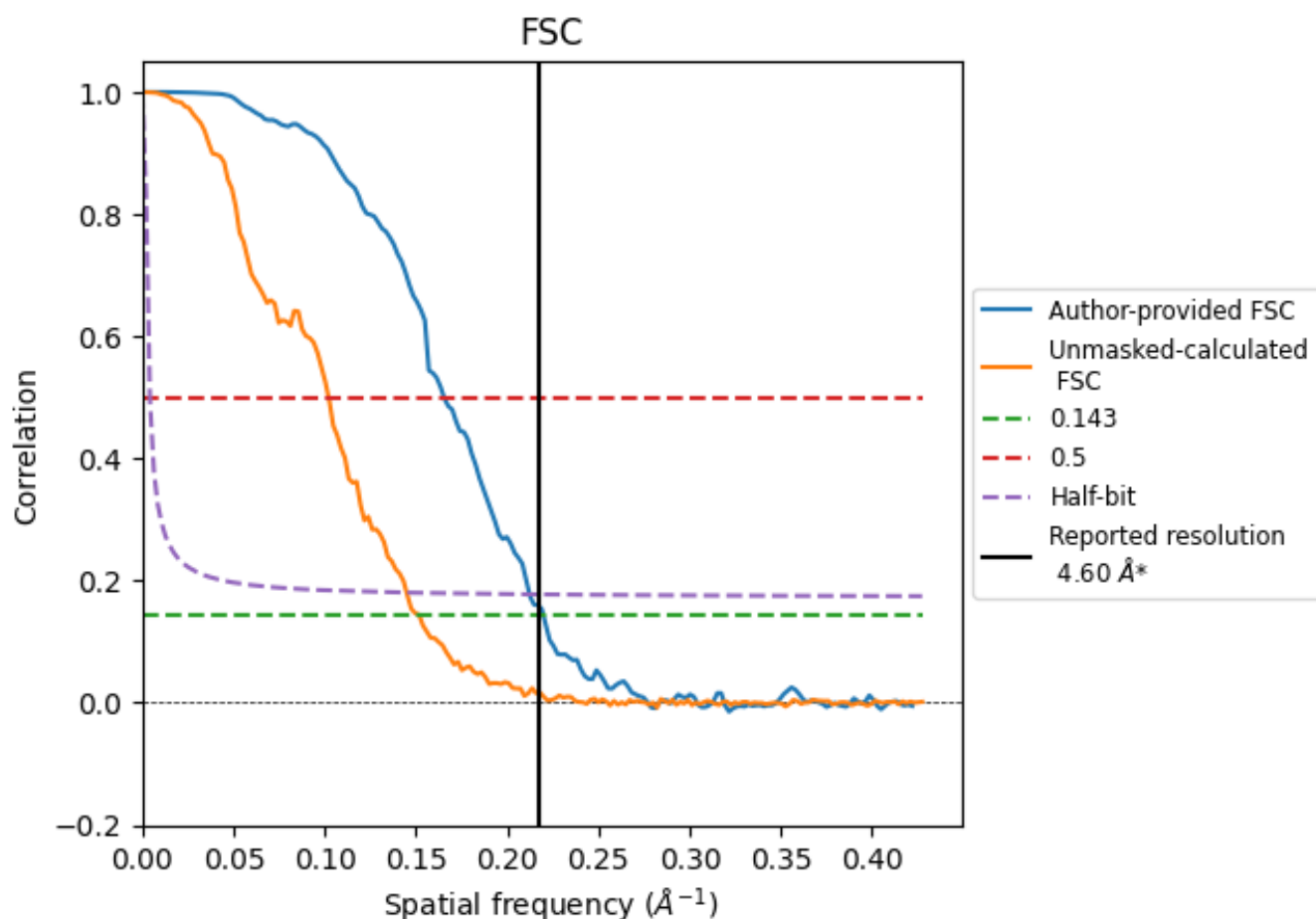


*Reported resolution corresponds to spatial frequency of 0.217 Å⁻¹

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 0.217 Å⁻¹

8.2 Resolution estimates [i](#)

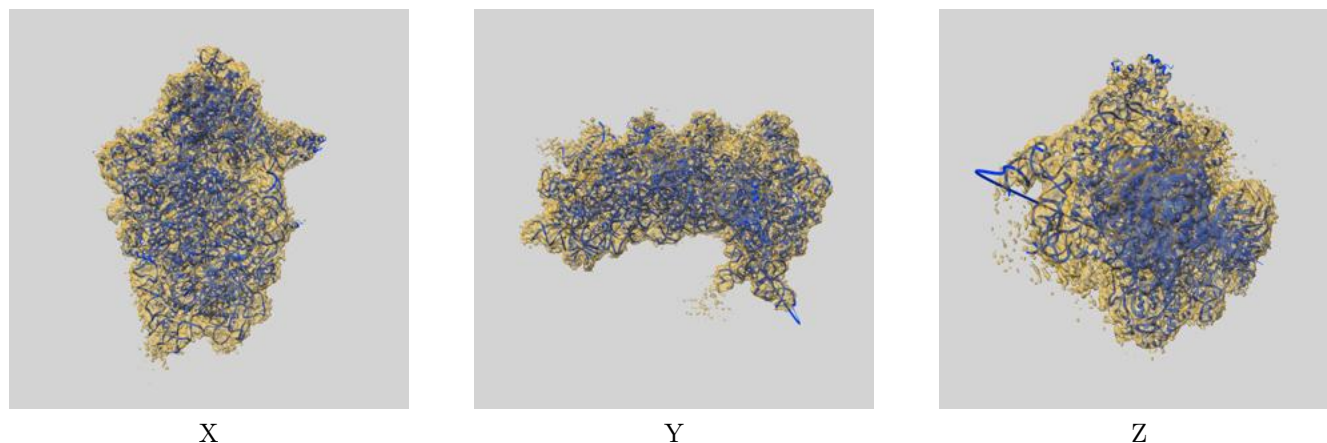
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.60	-	-
Author-provided FSC curve	4.55	6.05	4.71
Unmasked-calculated*	6.58	9.79	6.90

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.58 differs from the reported value 4.6 by more than 10 %

9 Map-model fit [i](#)

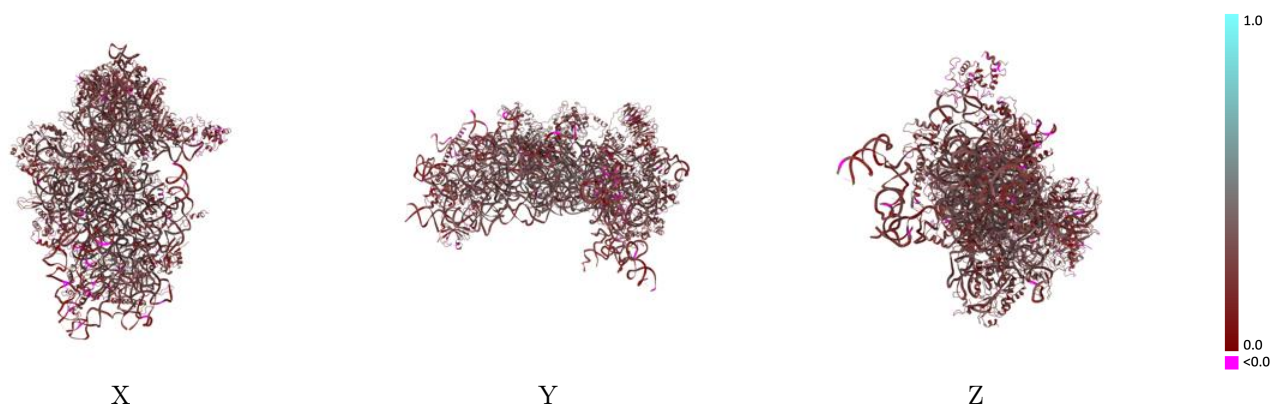
This section contains information regarding the fit between EMDB map EMD-64644 and PDB model 9UZK. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



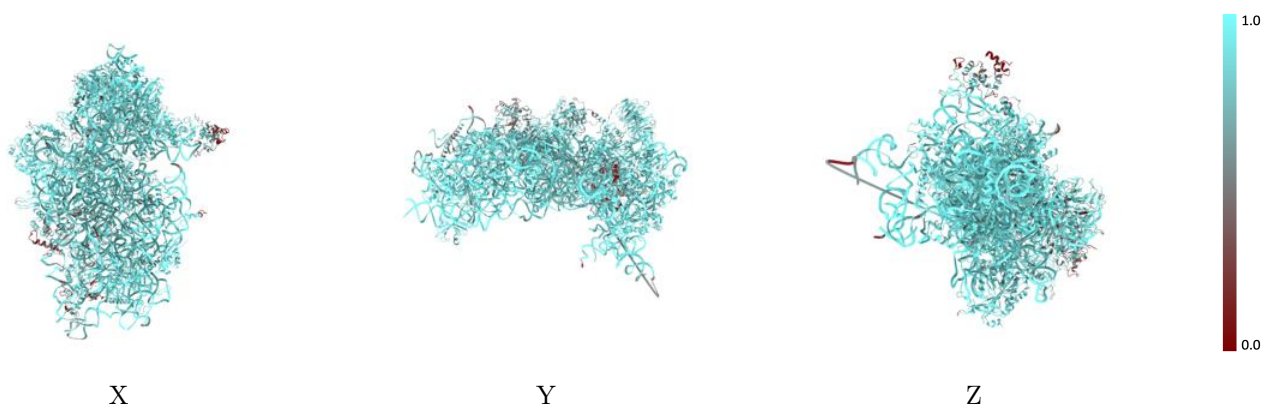
The images above show the 3D surface view of the map at the recommended contour level 0.0811 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



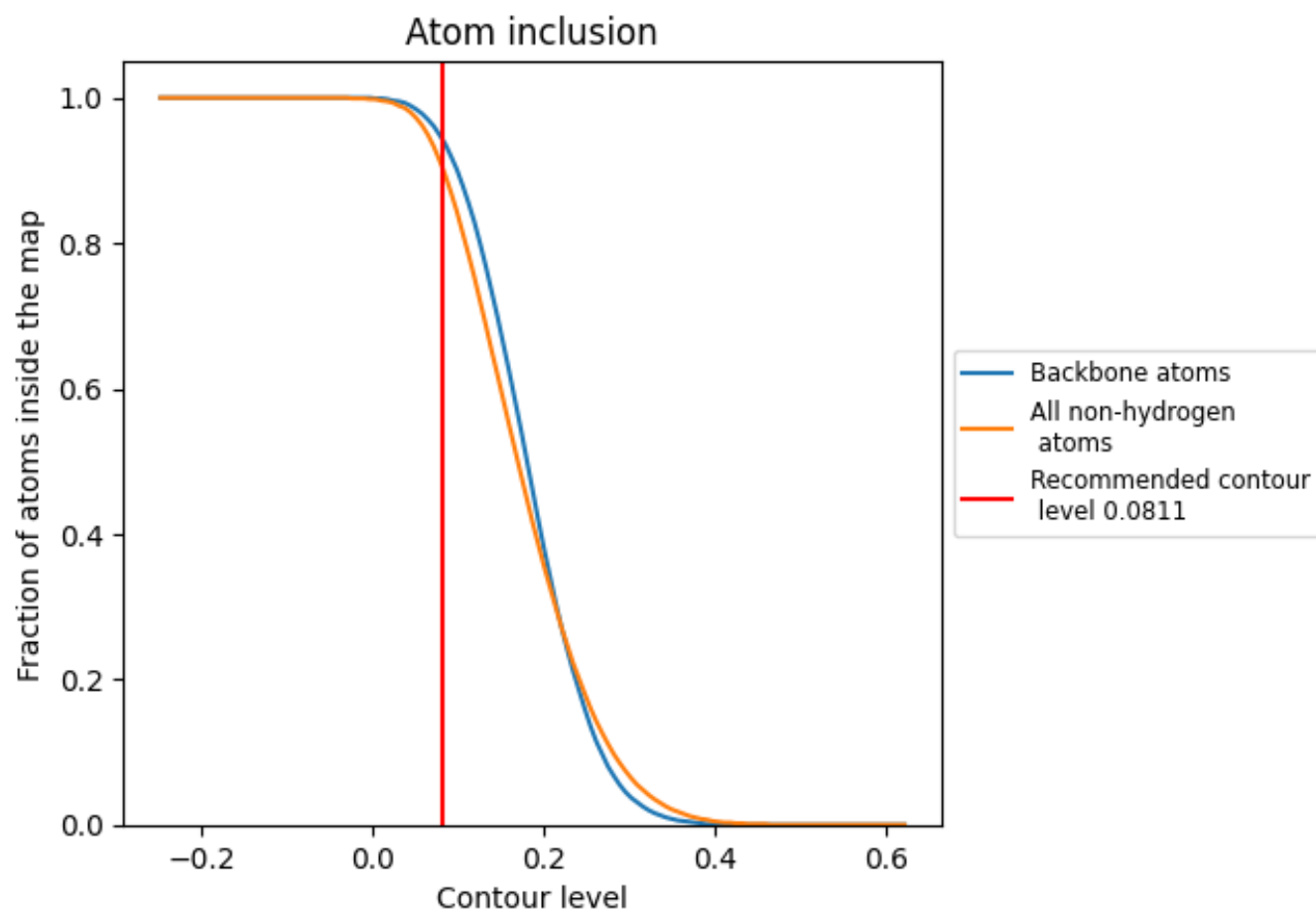
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0811).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 94% 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 (0.0811) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9060	 0.2730
2	 0.9640	 0.2880
C	 0.7970	 0.2600
D	 0.8920	 0.2580
E	 0.8620	 0.2970
F	 0.8480	 0.2630
G	 0.9100	 0.2880
H	 0.8900	 0.2790
I	 0.8790	 0.2400
J	 0.5590	 0.2290
K	 0.8290	 0.2540
L	 0.8730	 0.2790
M	 0.8990	 0.2530
N	 0.7630	 0.2890
O	 0.4810	 0.1680
P	 0.8830	 0.2890
Q	 0.8950	 0.2720
R	 0.9110	 0.2520
S	 0.9080	 0.2680
T	 0.7870	 0.2640
U	 0.9090	 0.2640
V	 0.9550	 0.2640
W	 0.8950	 0.2520
X	 0.8550	 0.2810
Y	 0.8290	 0.3140
Z	 0.9090	 0.3280
a	 0.9520	 0.2630
b	 0.9070	 0.3160
c	 0.8280	 0.2800
d	 0.9120	 0.2950
e	 0.8900	 0.2670
f	 0.6310	 0.1620
g	 0.8720	 0.2360
h	 0.8730	 0.2330
i	 0.8180	 0.2430



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Chain	Atom inclusion	Q-score
l	 0.9310	 0.2970
y	 0.9450	 0.2150
z	 0.9160	 0.1990