



wwPDB EM Validation Summary Report ⓘ

Jun 30, 2026 – 01:15 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 : ., 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.dev133
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) : 2.50

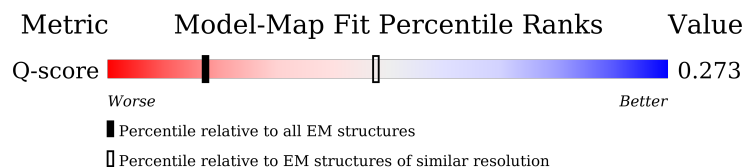
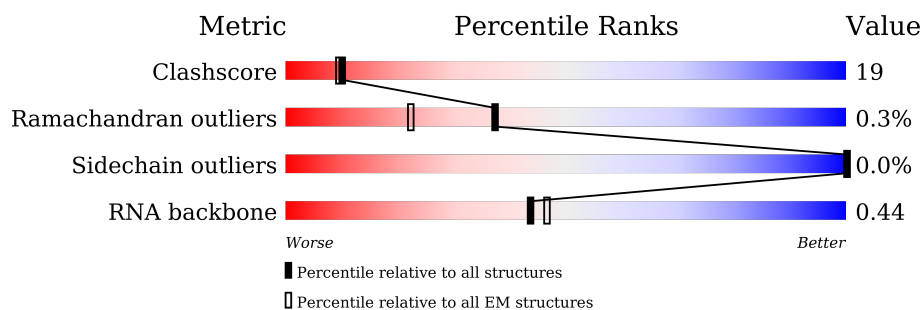
1 Overall quality at a glance

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.



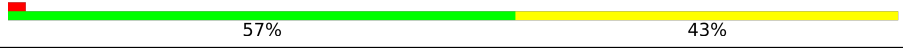
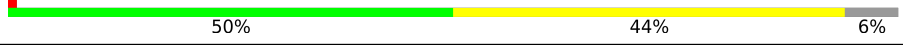
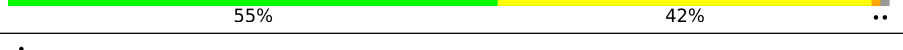
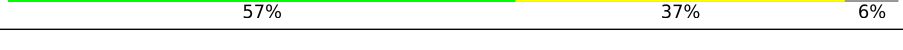
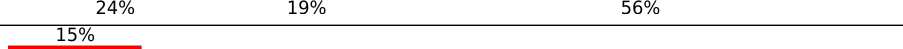
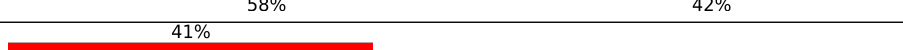
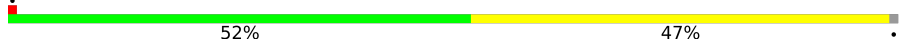
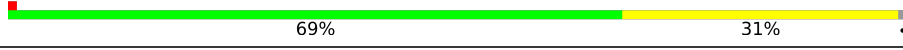
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	2407 (4.10 - 5.10)

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	

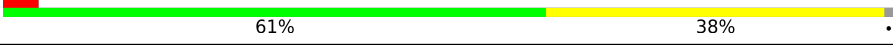
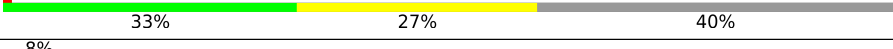
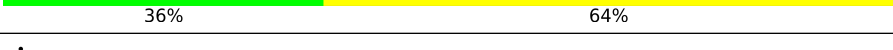
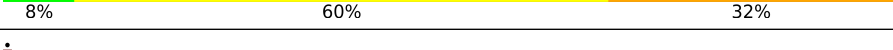
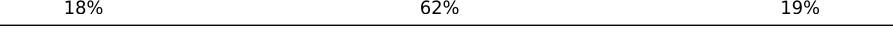
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Mol	Chain	Length	Quality of chain
4	E	226	
5	F	243	
6	G	263	
7	H	204	
8	I	249	
9	J	194	
10	K	208	
11	L	194	
12	M	225	
13	N	158	
14	O	132	
15	P	151	
16	Q	168	
17	R	145	
18	S	146	
19	T	135	
20	U	152	
21	V	141	
22	W	119	
23	X	83	
24	Y	130	
25	Z	143	
26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

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		

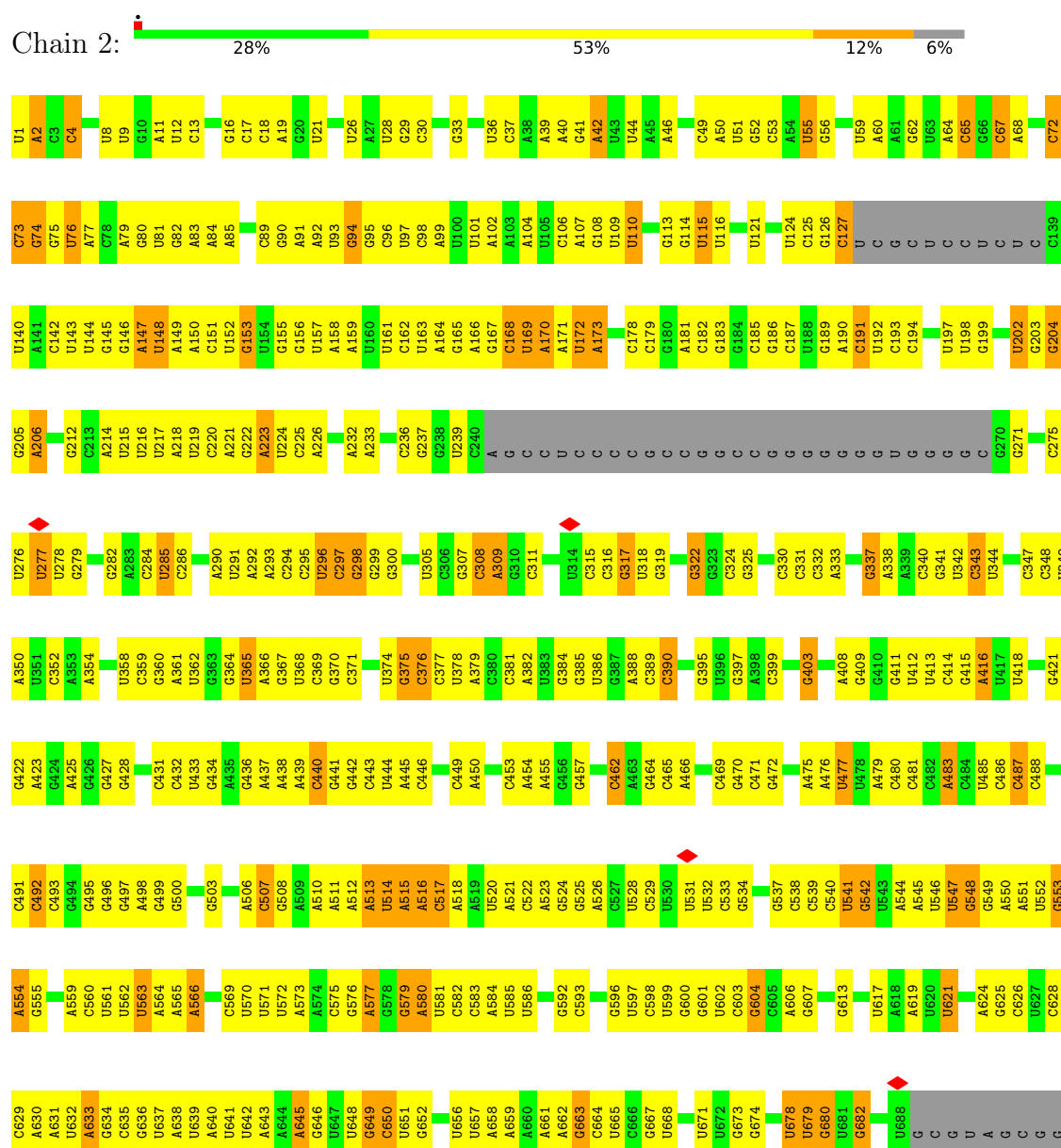
There are 8 discrepancies between the modelled and reference sequences:

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

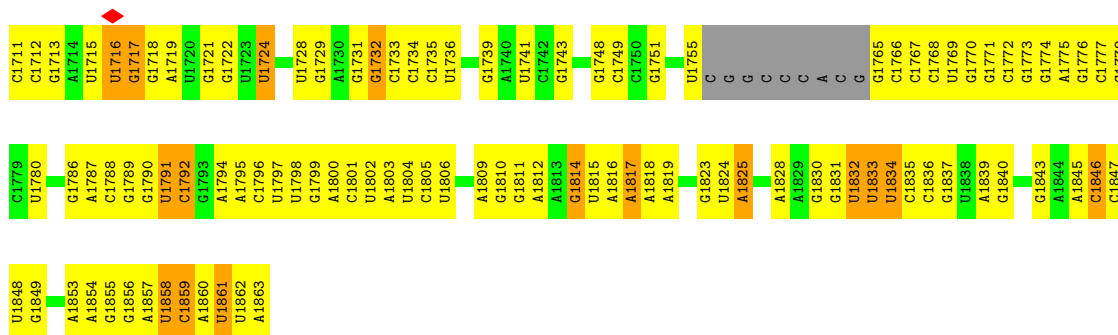
3 Residue-property plots

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.

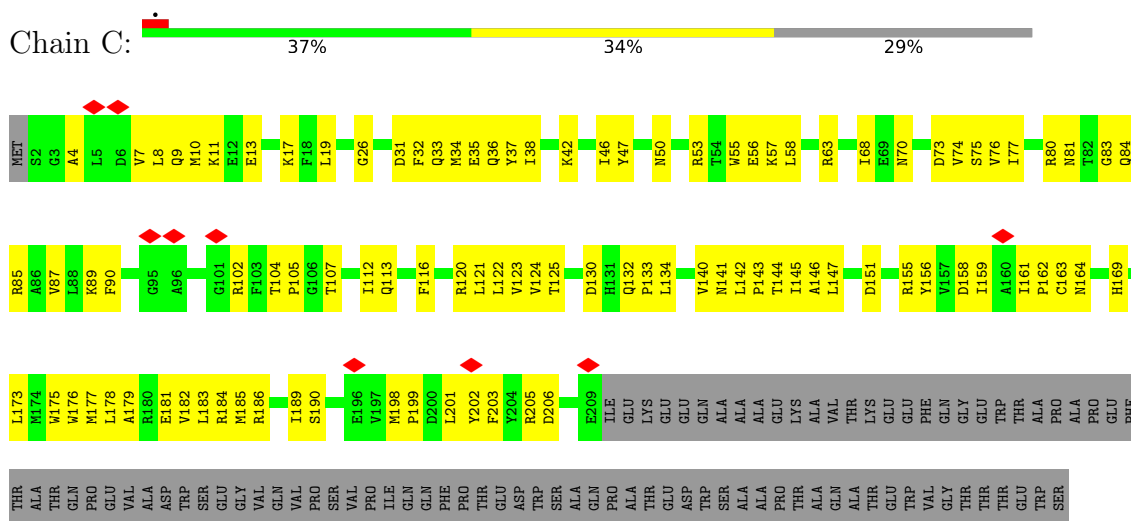
• Molecule 1: 18S ribosomal RNA



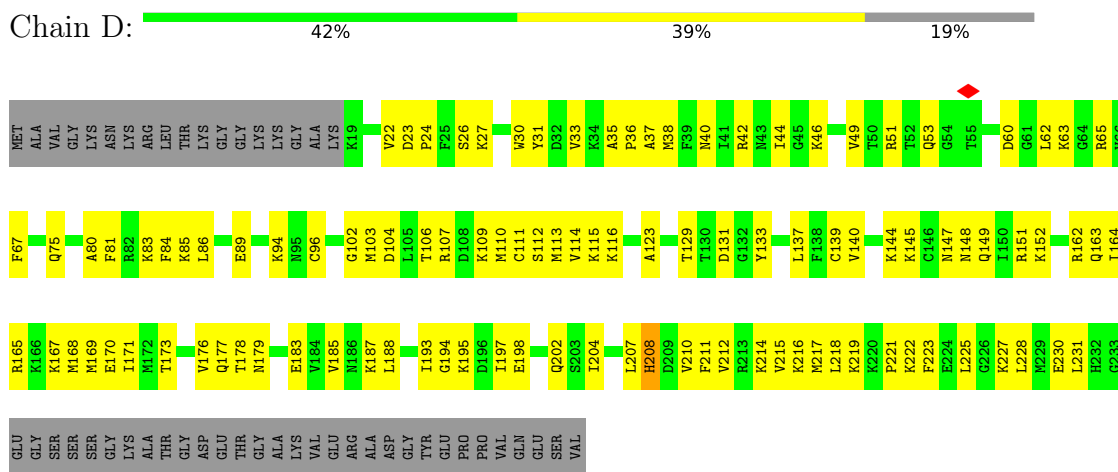
A1636	G1668	U1501	U1437	G1371	C1299	U1169	G1100	A1031	U961	C896	G828	G
U1637	C1669	A1502	U1438	A1372	U1300	A1169	G1101	A1032	U965	G897	C829	C
U1638	G1570	G1503	C1439	U1373	C1301	U1173	C1102	G1033	G966	G898	C830	G
C1639	G1571	U1440	U1440	U1374	U1304	U1174	C1103	A1033	U967	A899	C831	G
C1640	G1572	U1441	U1305	A1375	C1305	G1175	C1104	C1035	A968	A900	G832	U
G1641	U1507	A1442	U1443	C1376	U1249	C1176	C1105	U1041	C969	C901	A833	C
A1642	C1508	G1443	U1306	G1377	G1241	A1177	G1106	U1042	U970	U902	G834	C
G1643	G1509	A1444	C1307	U1382	U1244	A1178	U1107	G1043	C971	G903	C835	G
U1575	G1510	G1445	G1308	A1383	C1245	G1179	U1108	C1043	G972	A904	C836	U
C1576	G1511	G1446	A1309	A1384	A1246	G1180	U1109	G1044	G973	G905	C837	C
U1580	G1512	G1447	U1314	U1385	A1247	C1181	U1110	A1045	A976	C907	G838	G
G1581	C1513	A1448	U1315	U1386	G1248	C1182	U1111	C1049	A977	C908	C839	U
U1648	G1514	U1449	U1316	C1387	A1249	G1183	C1112	G1050	G978	U909	U840	G
A1583	G1515	A1450	U1317	U1388	G1250	A1184	C1113	A1051	C979	G910	G841	A
C1584	C1516	A1451	G1316	U1389	G1251	A1185	U1052	C1053	C980	U911	G842	G
G1585	A1517	G1452	G1317	A1390	G1252	C1186	U1053	A1054	G981	A912	G843	U
C1586	C1518	U1453	U1318	G1391	G1253	C1187	C1118	C1054	C982	U913	U844	G
G1587	G1519	G1454	G1319	A1392	A1254	U1188	C1119	G1055	C983	U914	A845	A
C1588	U1520	U1455	G1320	U1393	G1255	U1189	C1120	A1056	C984	U915	C846	C
A1589	G1521	U1456	G1321	U1394	A1256	U1190	C1121	C1057	C985	A916	C847	G
U1590	C1522	C1466	C1322	U1395	C1257	A1191	C1122	A1058	C987	G917	G848	C
C1591	G1523	G1467	U1323	U1396	G1258	A1192	C1123	C1059	A988	A918	U853	C
G1592	C1524	C1468	G1324	U1397	U1259	G1193	C1124	C1060	C989	G919	A854	C
U1593	U1525	A1469	U1325	A1398	C1260	G1194	G1125	G1061	G920	G921	G855	C
C1594	G1526	U1470	G1326	U1400	A1261	A1195	G1126	U1062	A922	A923	G856	G
A1595	C1527	C1471	C1327	U1401	G1262	A1196	G1127	C1063	G924	G925	A857	C
U1596	G1528	G1472	U1328	G1402	C1263	U1197	C1128	A1064	A924	G926	G858	C
C1597	C1529	A1473	G1329	U1403	C1264	U1198	C1129	C1065	A925	G927	U792	C
G1598	U1530	G1474	U1330	U1404	C1265	U1199	C1130	A1066	U999	C928	G793	C
A1601	G1531	C1475	U1331	U1405	C1266	A1200	C1131	G1067	U1000	C929	G794	C
C1602	C1532	A1476	C1332	A1406	G1267	C1201	G1134	U1068	G1001	G930	U795	C
U1603	U1533	G1477	U1333	U1407	C1268	G1202	C1135	U1069	C1002	U939	U796	C
G1604	G1534	C1478	G1334	U1408	G1269	A1203	G1136	C1070	C1003	A940	U797	C
U1609	C1535	U1479	U1335	U1409	C1270	G1204	G1137	C1071	A1004	U941	A807	C
A1610	U1536	A1480	C1336	U1410	A1271	A1205	G1138	G1072	A1005	U942	A808	C
U1611	G1537	C1479	G1337	C1411	C1272	G1206	U1139	A1073	G1006	G943	A809	C
C1612	C1538	U1481	U1338	C1412	G1273	U1207	A1140	A1076	A1007	C944	U811	C
G1613	U1539	A1482	C1339	C1413	G1274	C1211	A1141	A1077	U1008	C945	A812	C
A1614	G1540	C1483	U1340	C1414	C1275	A1212	C1142	A1079	U1009	U950	A813	C
U1615	C1541	U1484	G1341	C1415	C1276	A1213	C1143	A1080	G1010	C946	A814	C
G1616	U1542	C1485	C1342	U1416	G1277	A1214	A1144	G1081	U1011	C947	U739	C
A1617	G1543	A1486	U1343	U1417	C1278	C1215	A1145	G1082	U1012	G948	G740	C
U1618	C1544	G1487	U1344	C1418	G1279	A1216	A1146	A1083	U1013	U949	U741	C
C1619	U1545	U1488	C1345	G1419	U1280	G1217	U1150	A1086	C1014	C950	U742	C
U1620	G1546	U1489	U1346	G1420	A1281	A1218	U1151	C1087	U1015	C951	U743	C
G1621	C1547	G1490	G1360	C1421	U1282	A1219	U1152	G1088	A1016	U952	U744	C
A1622	U1548	A1491	C1361	U1422	U1283	G1220	U1153	C1089	U1017	G953	U745	C
C1623	C1549	U1492	U1362	U1423	U1284	G1221	G1154	A1090	U1018	C954	G815	C
U1624	U1550	G1493	G1363	G1424	U1285	G1222	G1155	C1091	A1019	U955	U818	C
A1625	G1551	C1494	U1364	C1425	U1286	A1223	G1156	G1092	U1020	G956	U819	C
C1626	C1552	U1495	C1365	G1426	U1287	G1224	U1157	G1093	U1021	A957	C820	C
G1627	U1553	G1496	U1366	U1427	U1288	A1225	U1158	C1094	C1022	G958	A821	C
U1628	C1554	A1497	U1367	C1428	U1289	G1226	G1160	G1095	A1023	U959	A822	C
C1629	U1555	C1498	C1368	U1429	U1290	G1227	G1161	A1096	U1024	U960	A823	C
G1704	G1556	U1499	U1369	A1430	A1291	U1228	G1162	C1097	A1026	U966	G824	C
U1707	C1557	G1500	C1370	C1431	G1294	G1229	G1163	A1098	A1027	G967	C825	C
C1708	U1558	U1501	U1500	C1432	A1295	U1296	G1164	A1099	C1028	U968	G826	C
U1709	G1559	C1566	C1371	C1433	U1297	G1232	G1165	G1098	G1029	A959	A826	C
A1710	C1560	C1567	C1372	C1436	U1298	G1233	G1167	C1099	A1030	A960	G827	C



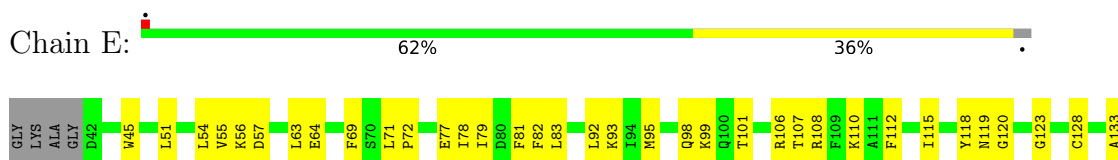
• Molecule 2: Small ribosomal subunit protein uS2

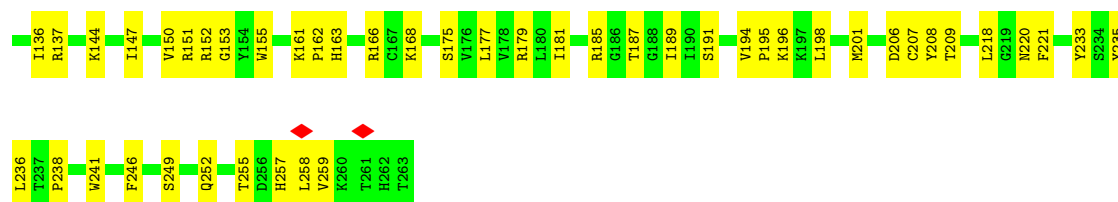


• Molecule 3: Small ribosomal subunit protein eS1

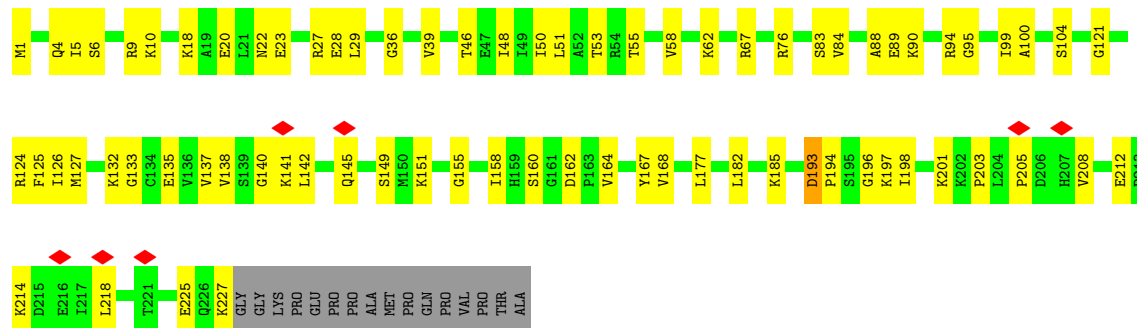


• Molecule 4: Small ribosomal subunit protein uS5

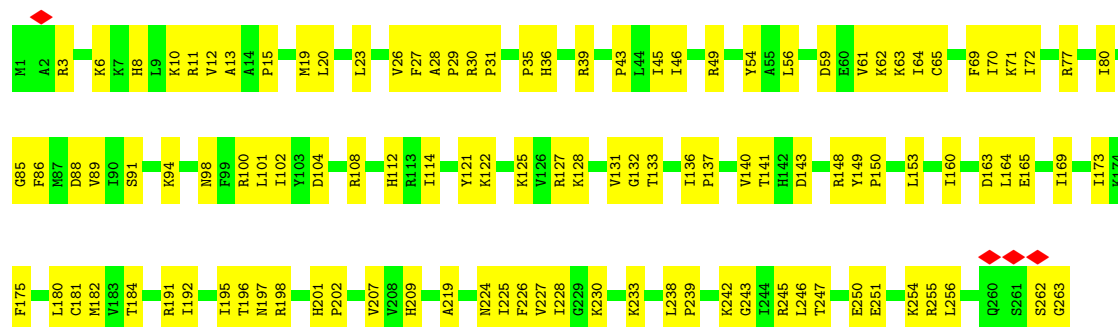




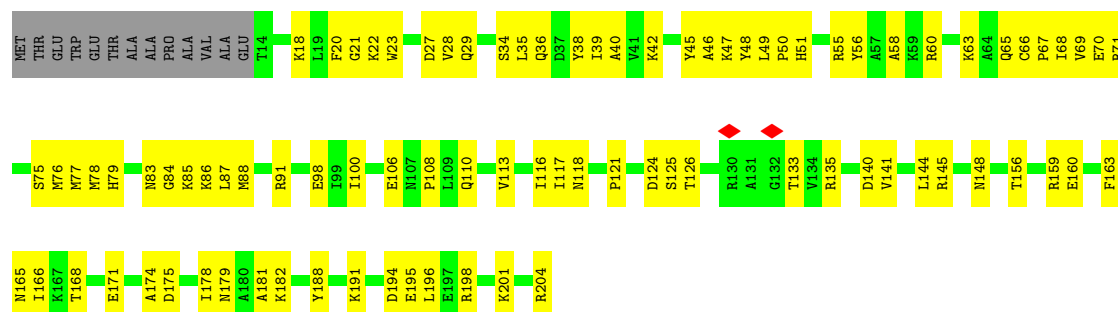
• Molecule 5: Small ribosomal subunit protein uS3



• Molecule 6: Small ribosomal subunit protein eS4

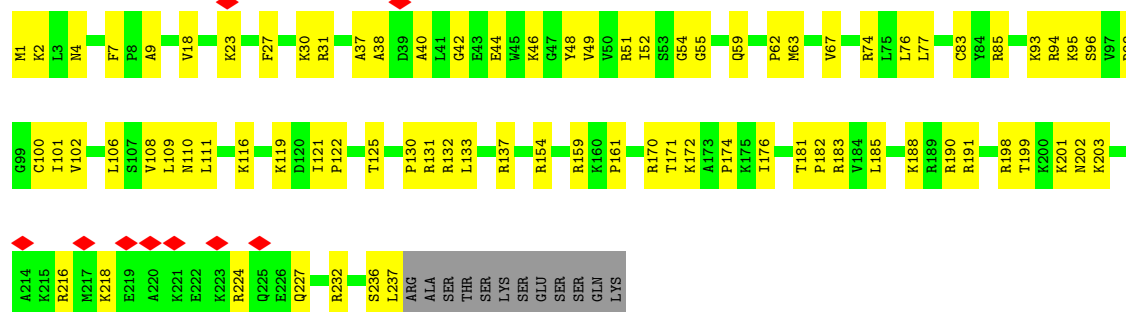


• Molecule 7: Small ribosomal subunit protein uS7



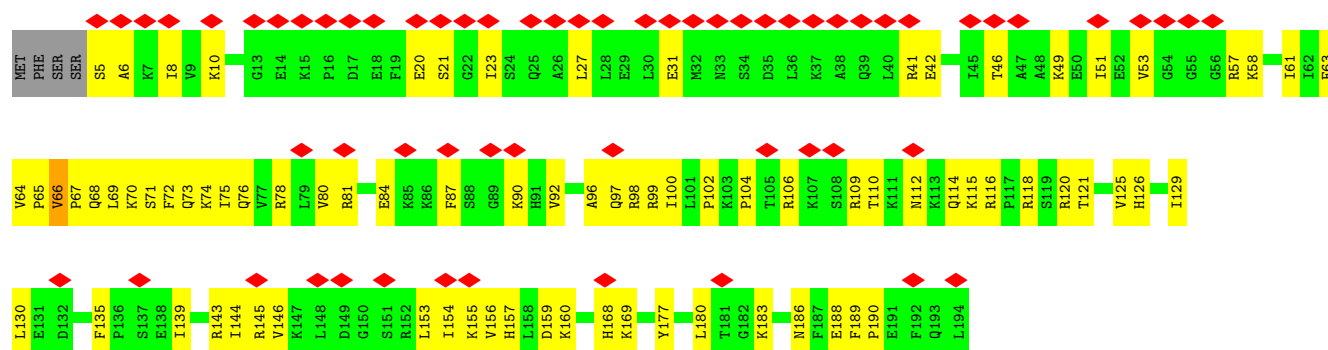
• Molecule 8: Small ribosomal subunit protein eS6

Chain I: 



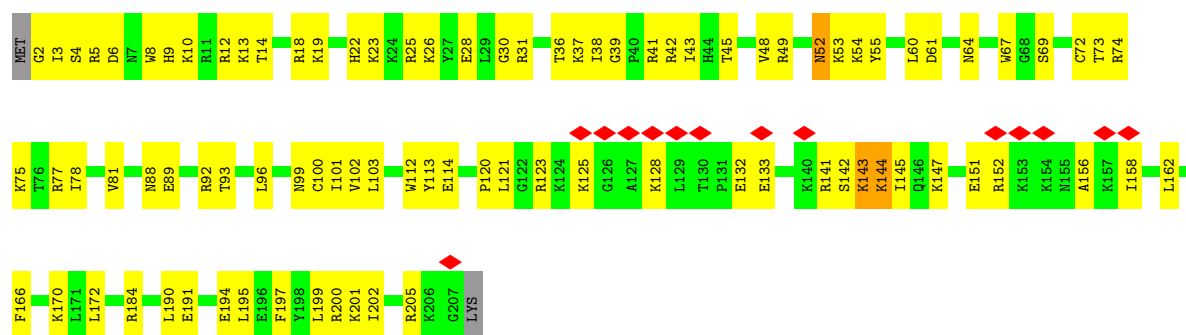
• Molecule 9: Small ribosomal subunit protein eS7

Chain J: 



• Molecule 10: Small ribosomal subunit protein eS8

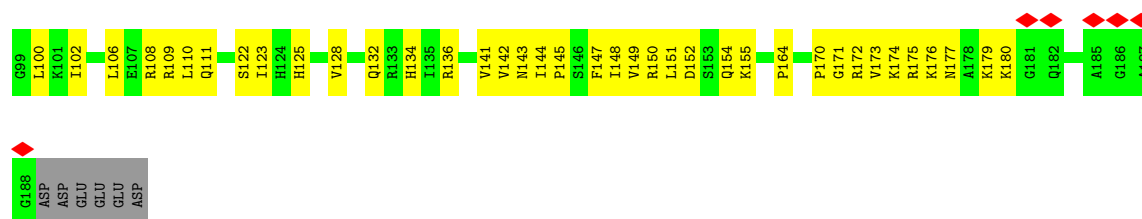
Chain K: 



• Molecule 11: Small ribosomal subunit protein uS4

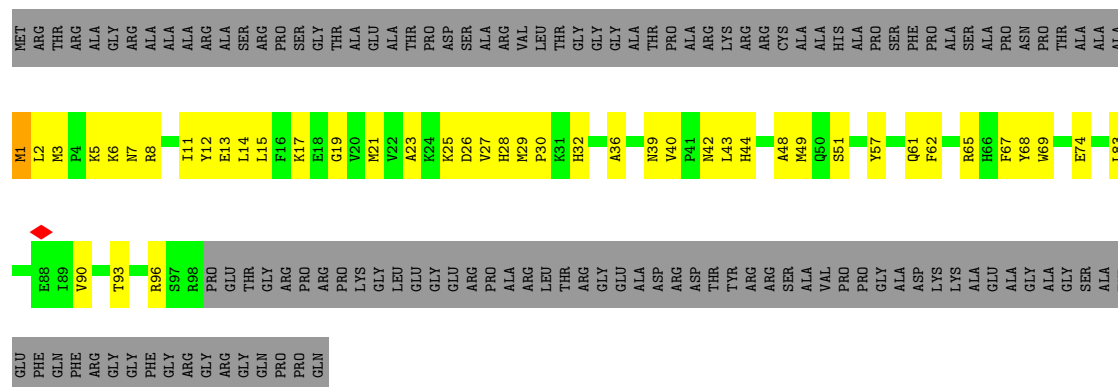
Chain L: 





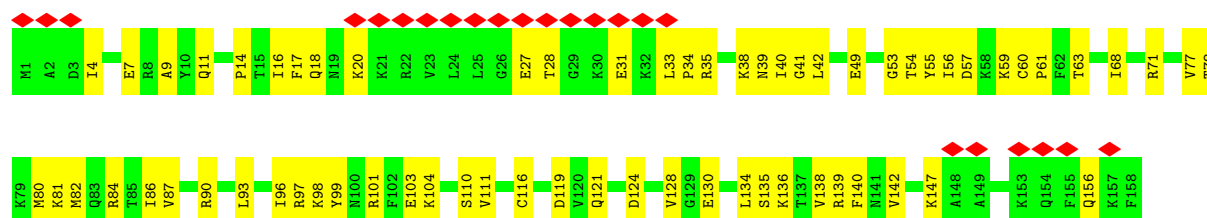
• Molecule 12: Small ribosomal subunit protein eS10

Chain M: 24% 19% 56%



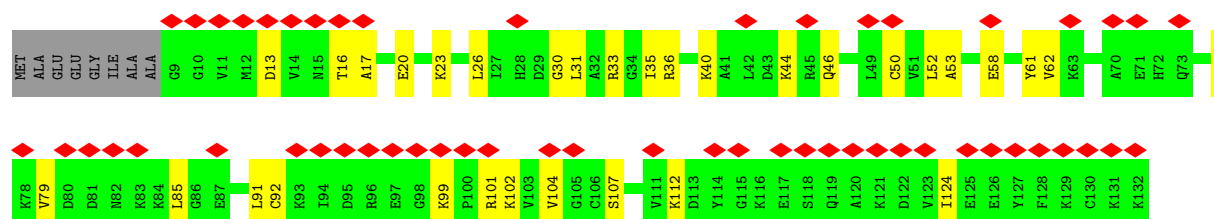
• Molecule 13: Small ribosomal subunit protein uS17

Chain N: 15% 58% 42%



• Molecule 14: Small ribosomal subunit protein eS12

Chain O: 41% 70% 24% 6%



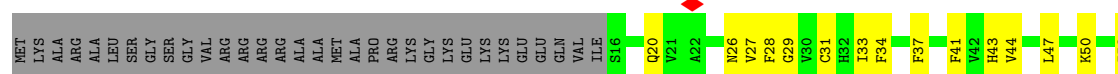
• Molecule 15: Small ribosomal subunit protein uS15

Chain P: 58% 41%

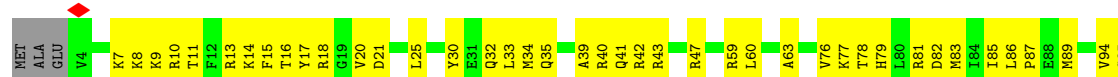




• Molecule 16: Ribosomal protein S14



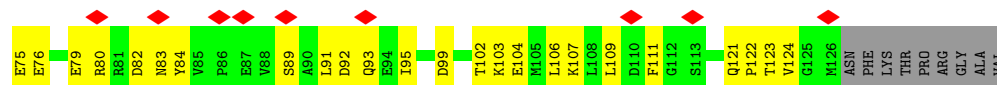
• Molecule 17: Small ribosomal subunit protein uS19



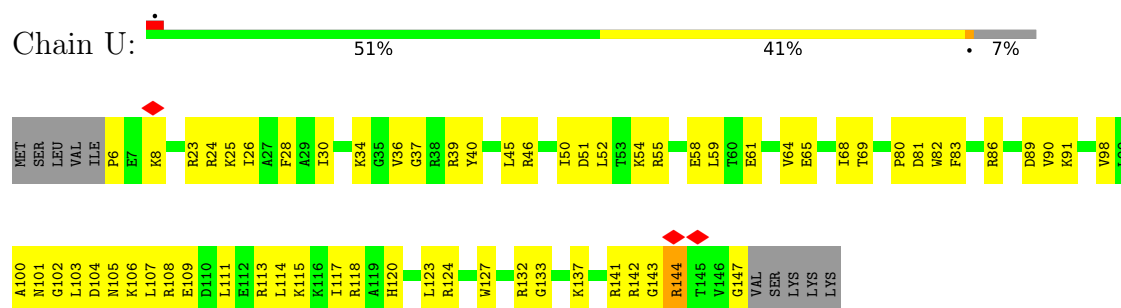
• Molecule 18: Small ribosomal subunit protein uS9



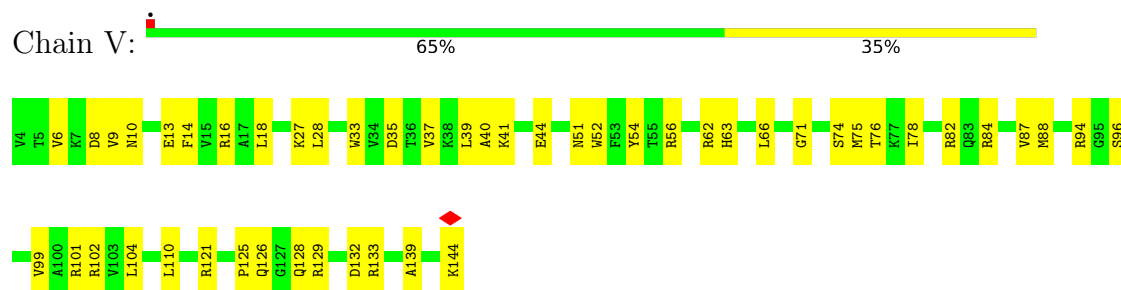
• Molecule 19: Small ribosomal subunit protein eS17



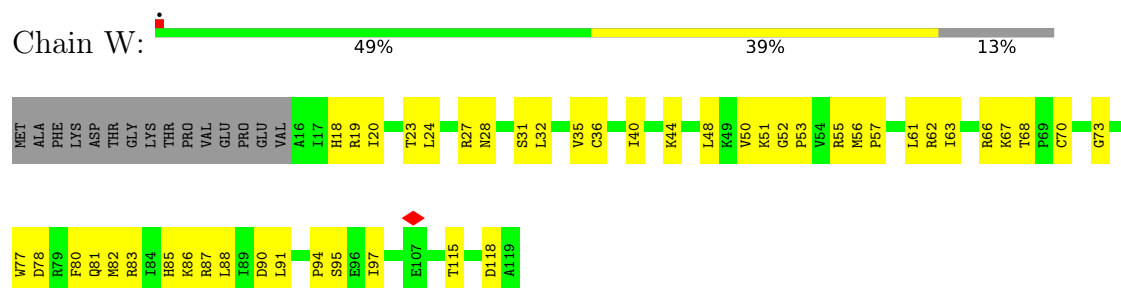
- Molecule 20: Small ribosomal subunit protein uS13



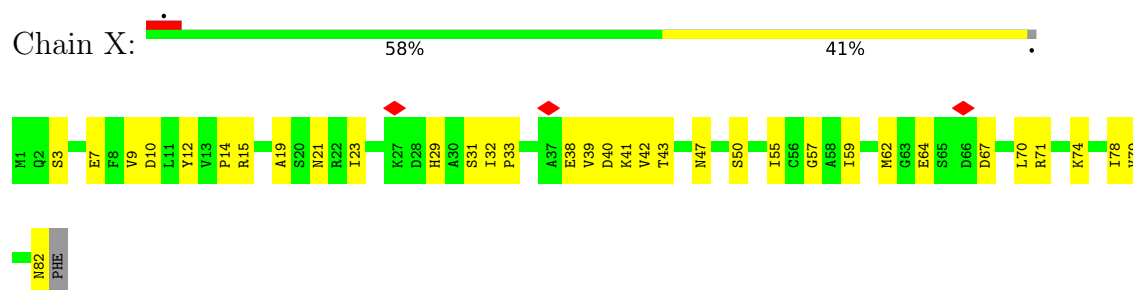
- Molecule 21: Small ribosomal subunit protein eS19



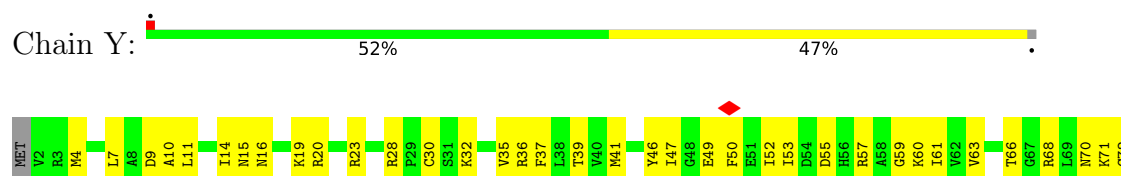
- Molecule 22: Small ribosomal subunit protein uS10



- Molecule 23: Small ribosomal subunit protein eS21



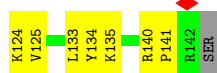
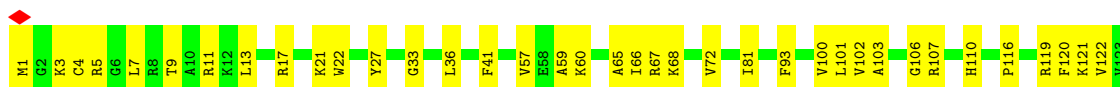
- Molecule 24: Small ribosomal subunit protein uS8





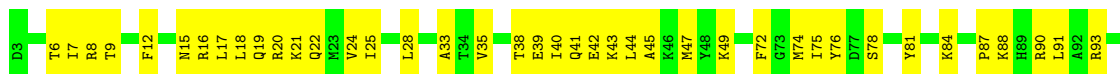
- Molecule 25: Small ribosomal subunit protein uS12

Chain Z: 69% 31%



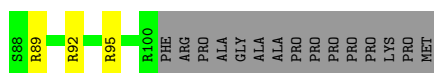
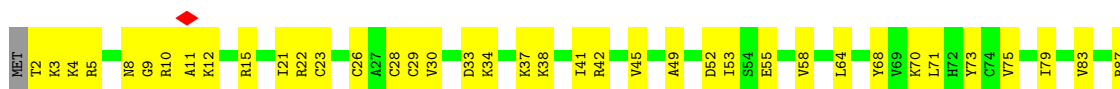
- Molecule 26: 40S ribosomal protein S24

Chain a: 56% 42%



- Molecule 27: Small ribosomal subunit protein eS26

Chain b: 50% 36% 14%



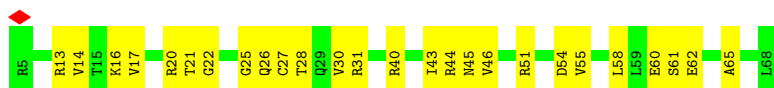
- Molecule 28: Small ribosomal subunit protein eS27

Chain c: 55% 45%



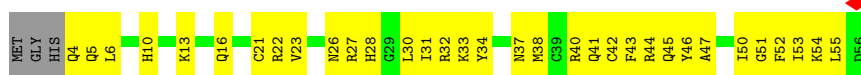
- Molecule 29: Small ribosomal subunit protein eS28

Chain d: 59% 41%



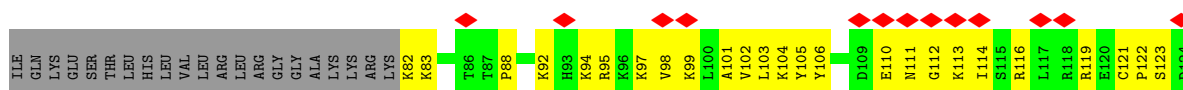
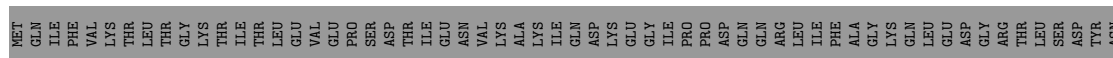
- Molecule 30: Small ribosomal subunit protein uS14

Chain e: 



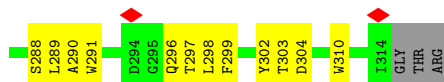
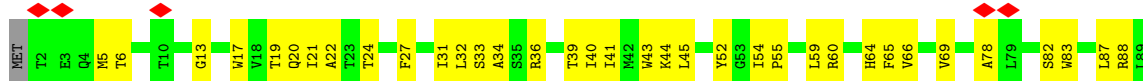
- Molecule 31: Ubiquitin-ribosomal protein eS31 fusion protein

Chain f: 

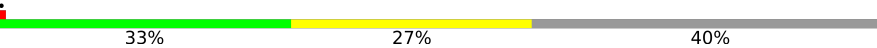


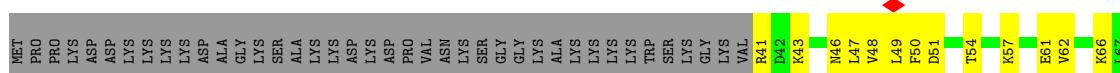
- Molecule 32: Small ribosomal subunit protein RACK1

Chain g: 

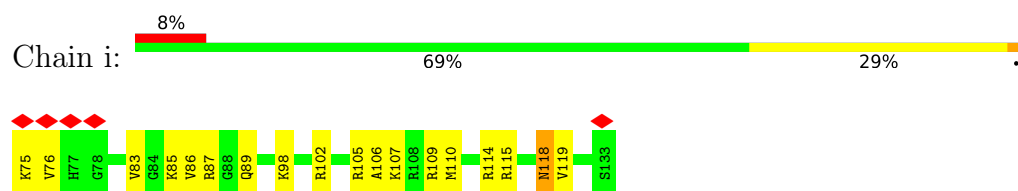


- Molecule 33: Small ribosomal subunit protein eS25

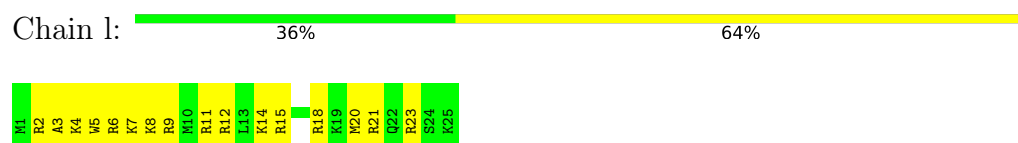
Chain h: 



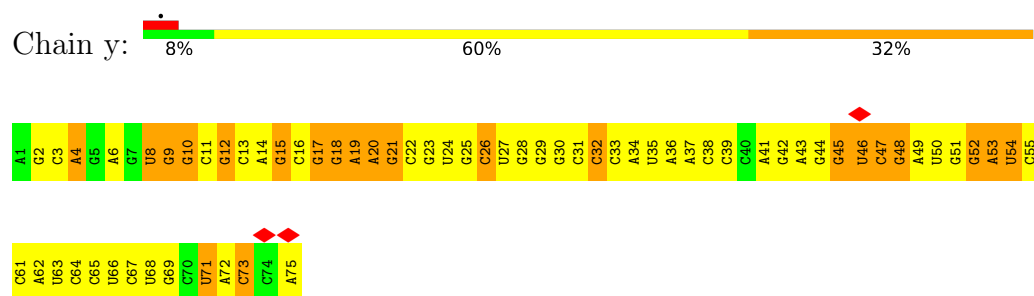
- Molecule 34: Small ribosomal subunit protein eS30



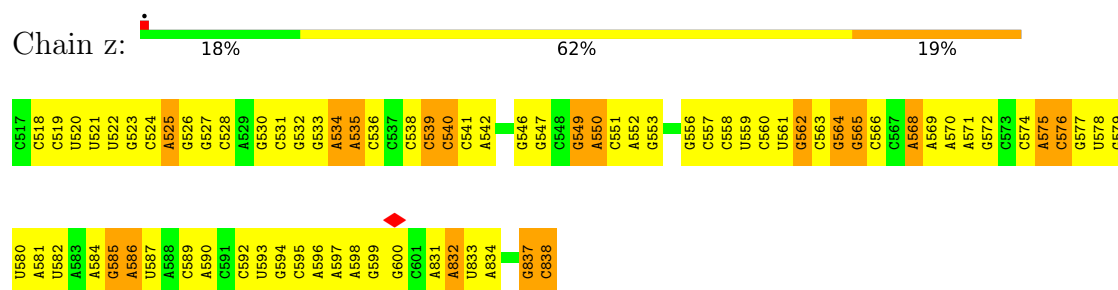
- Molecule 35: Small ribosomal subunit protein eS32



- 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 (Å)	467.99997, 467.99997, 467.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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

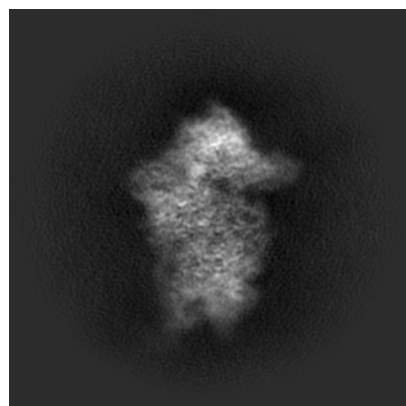
6 Map visualisation [i](#)

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.

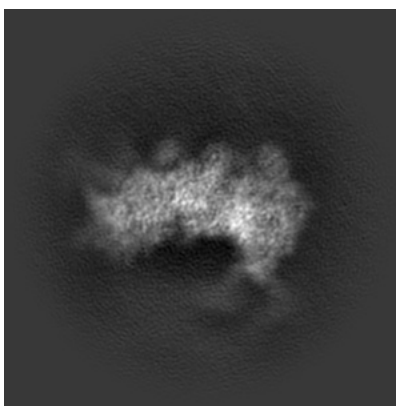
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

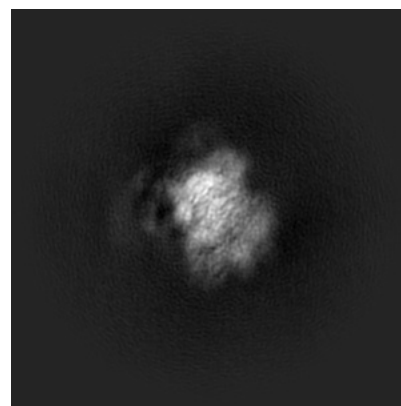
6.1.1 Primary map



X

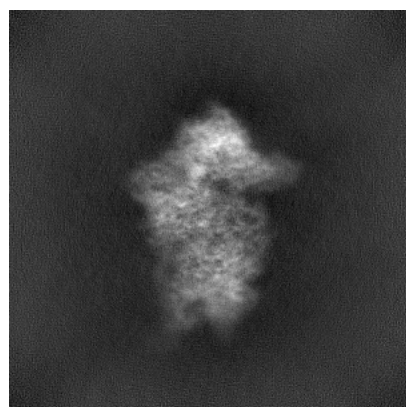


Y

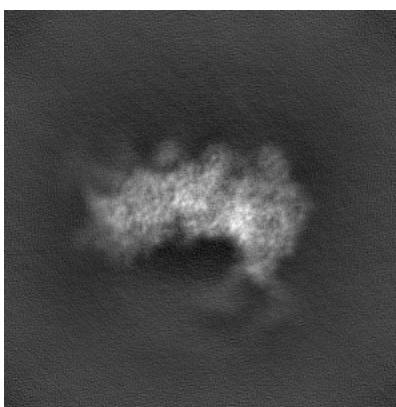


Z

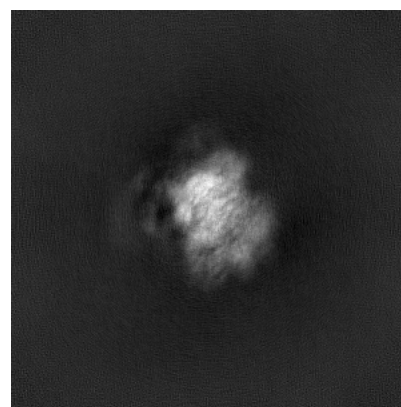
6.1.2 Raw map



X



Y

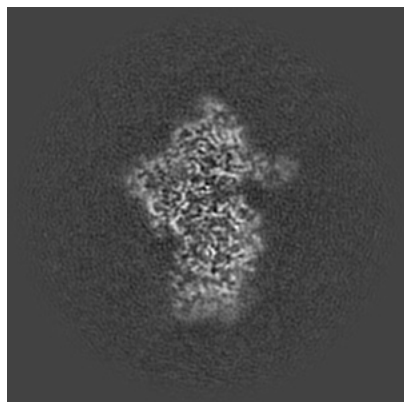


Z

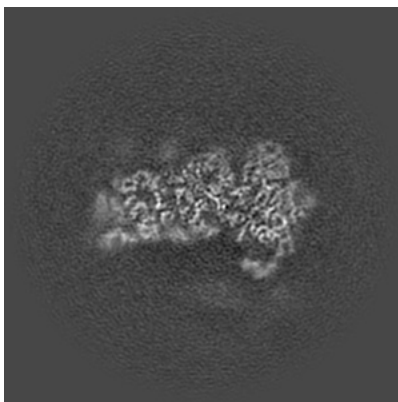
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

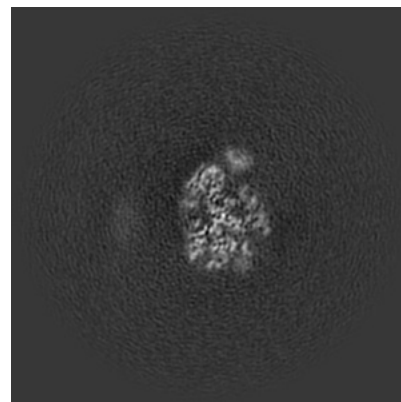
6.2.1 Primary map



X Index: 200

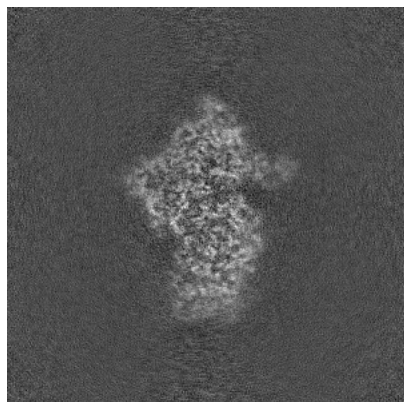


Y Index: 200

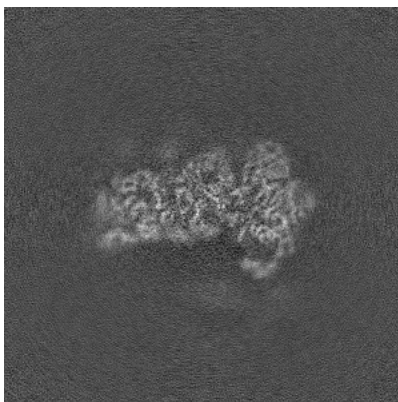


Z Index: 200

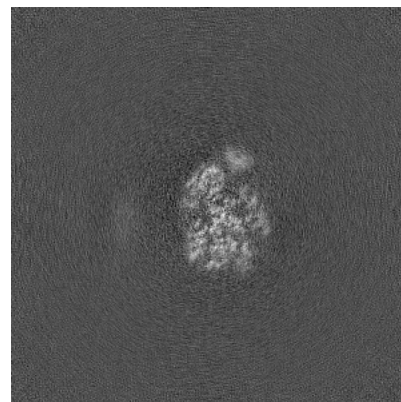
6.2.2 Raw map



X Index: 200



Y Index: 200

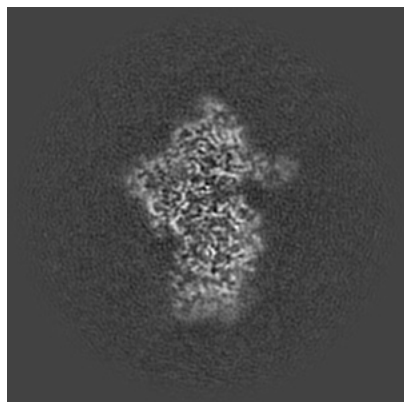


Z Index: 200

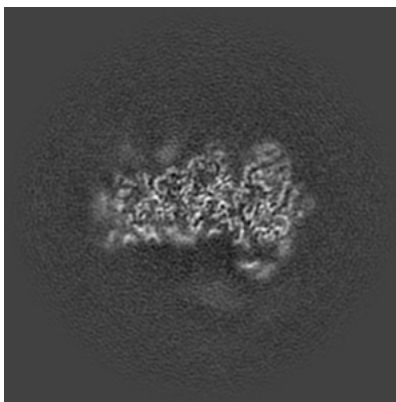
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

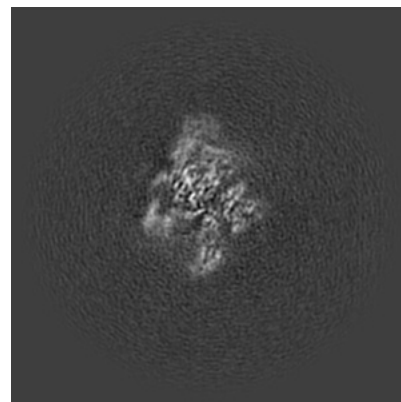
6.3.1 Primary map



X Index: 200

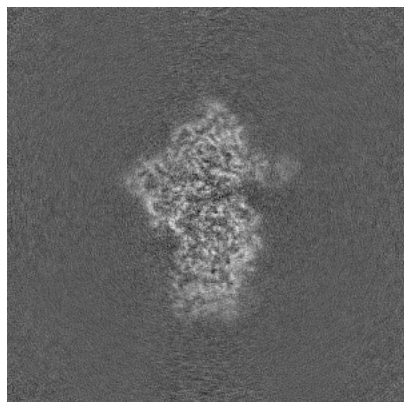


Y Index: 196

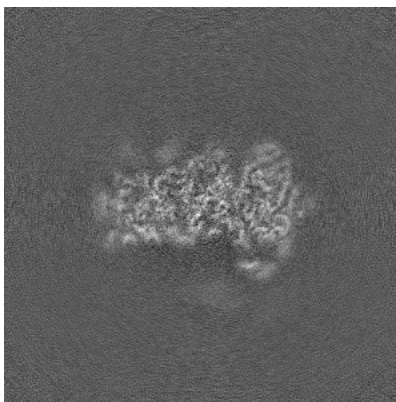


Z Index: 243

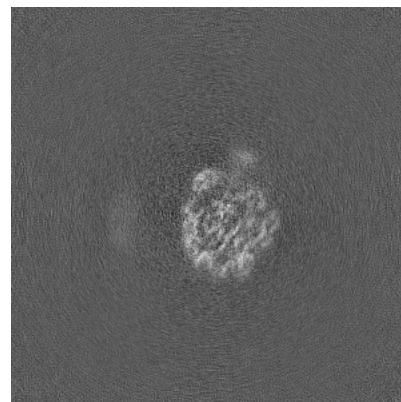
6.3.2 Raw map



X Index: 199



Y Index: 196

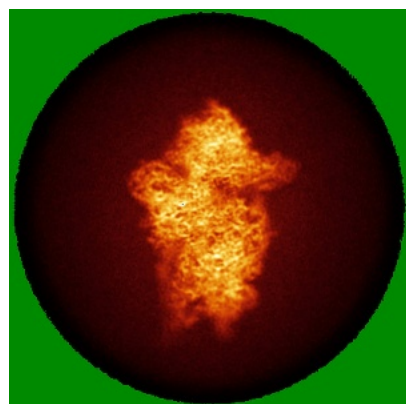


Z Index: 208

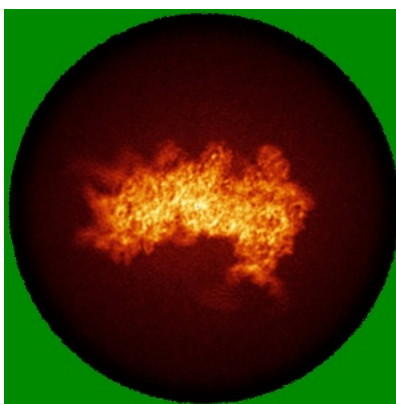
The images above show the largest variance slices of the map in three orthogonal directions.

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

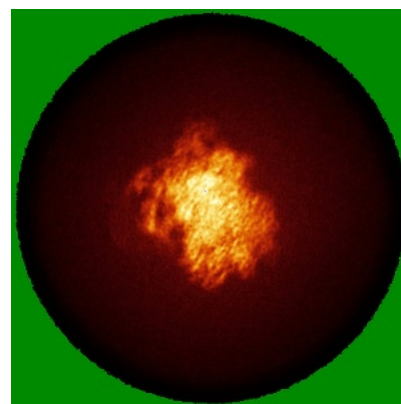
6.4.1 Primary map



X

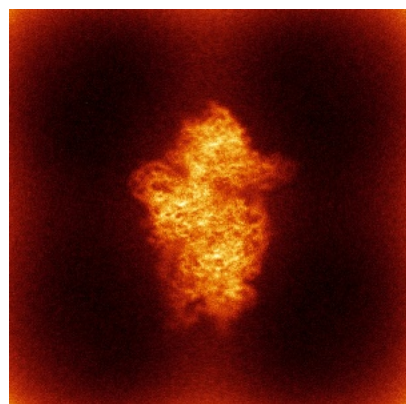


Y

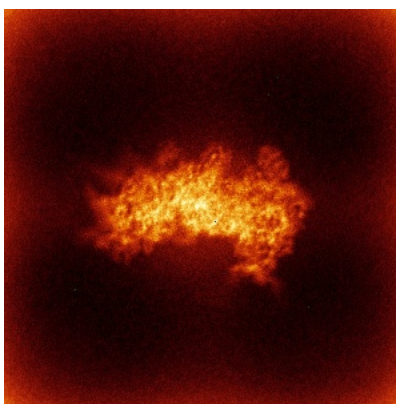


Z

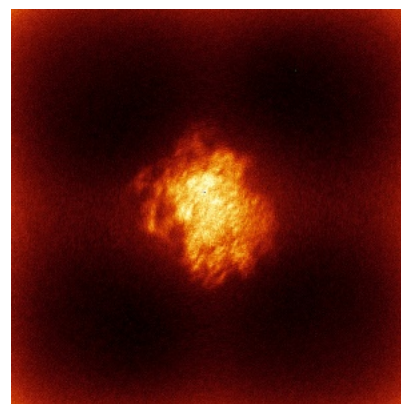
6.4.2 Raw map



X



Y

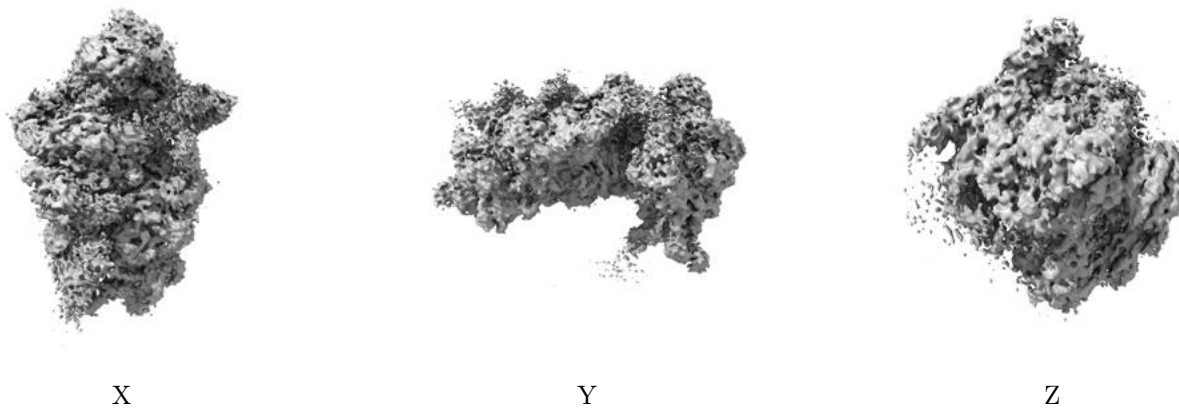


Z

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.

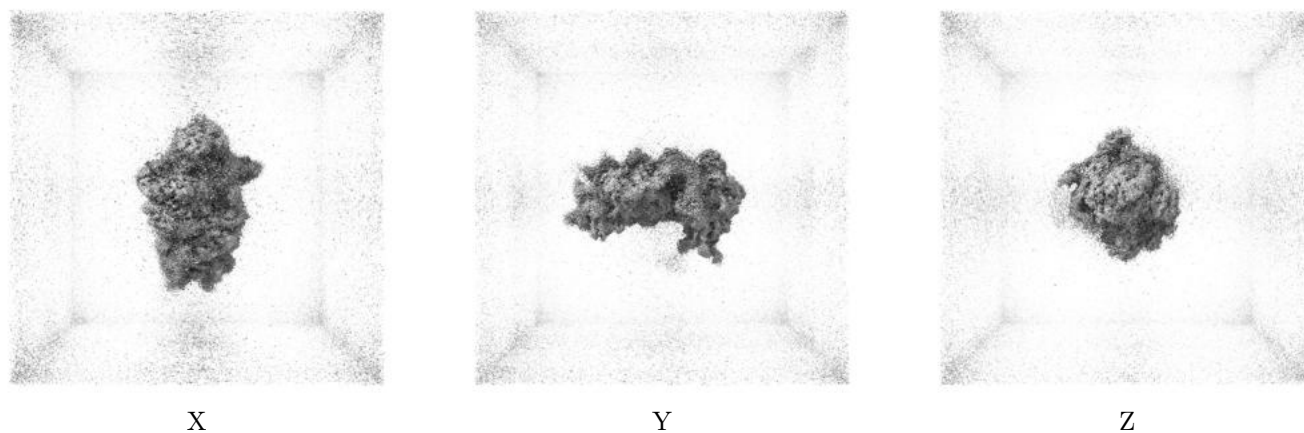
6.5 Orthogonal surface views [i](#)

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.

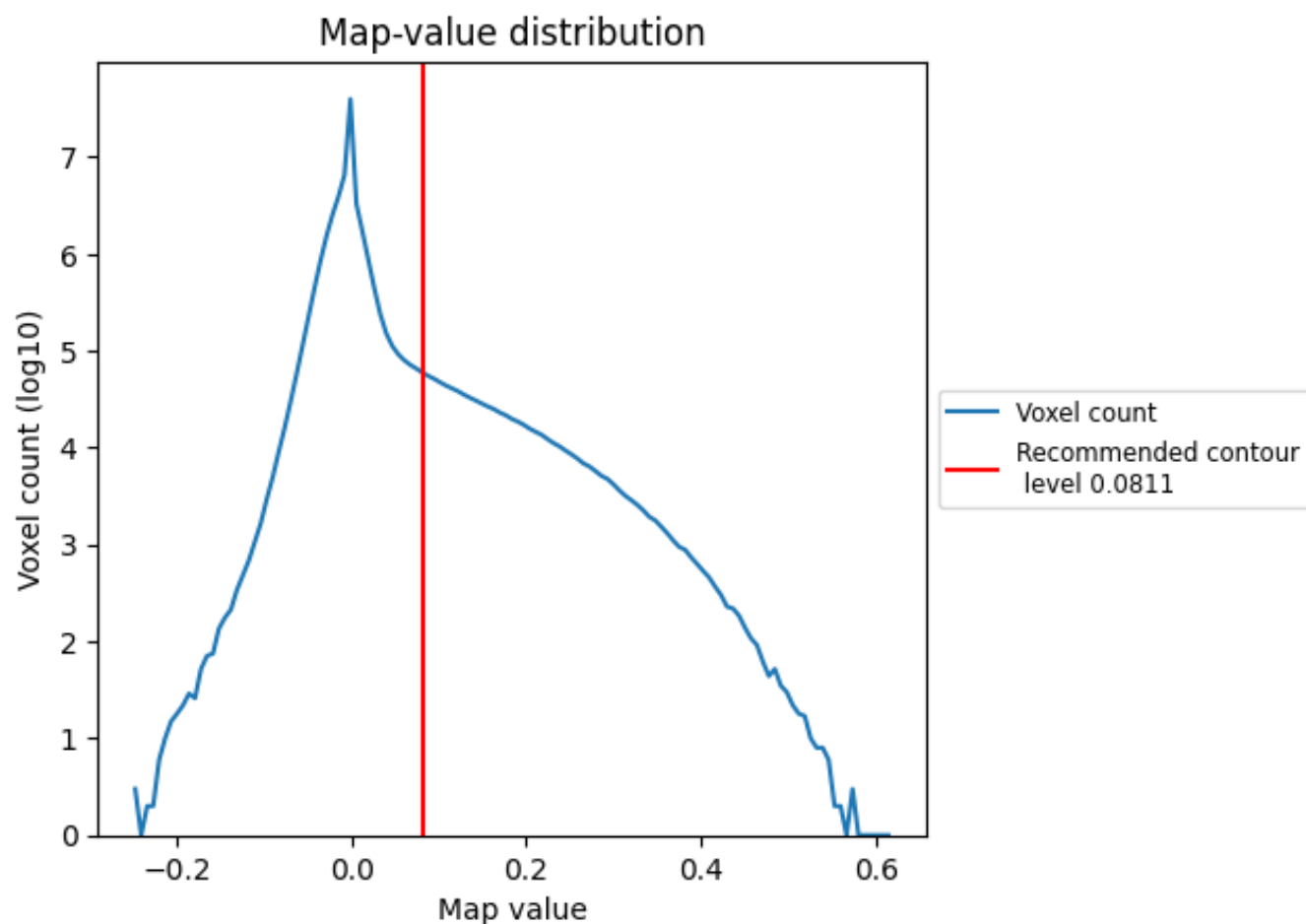
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

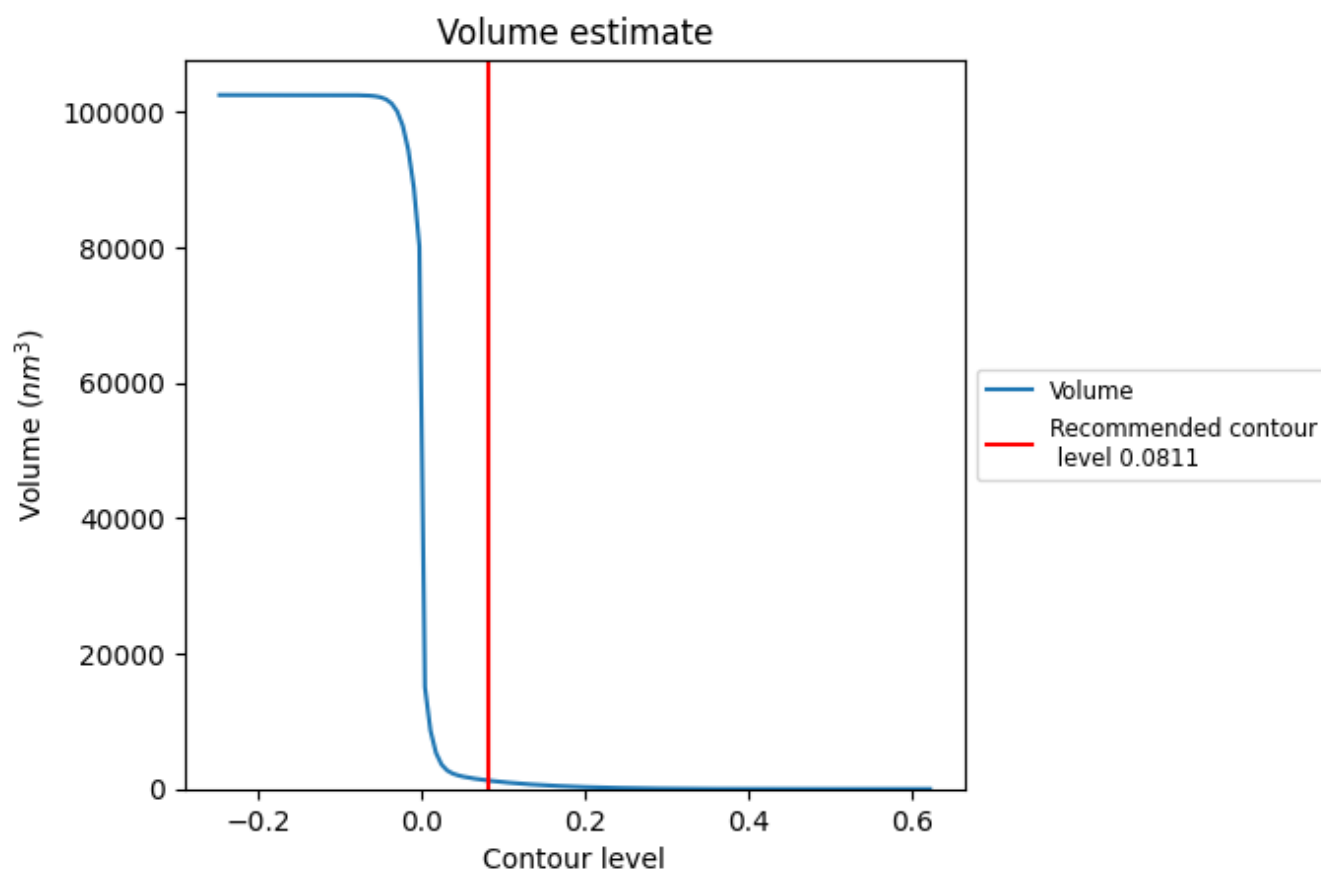
This section contains the results of statistical analysis of the map.

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.

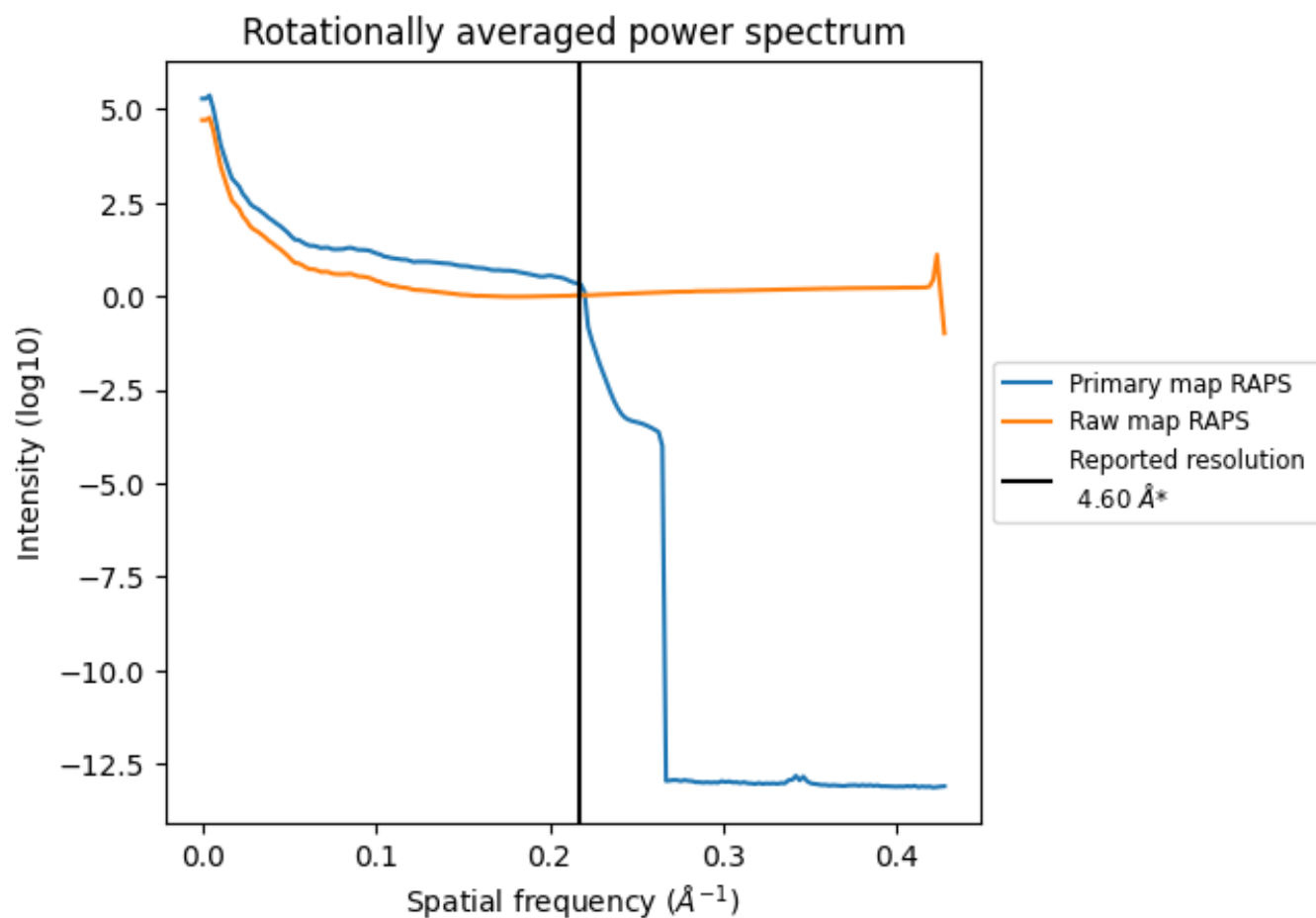
7.2 Volume estimate [i](#)



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 ⓘ

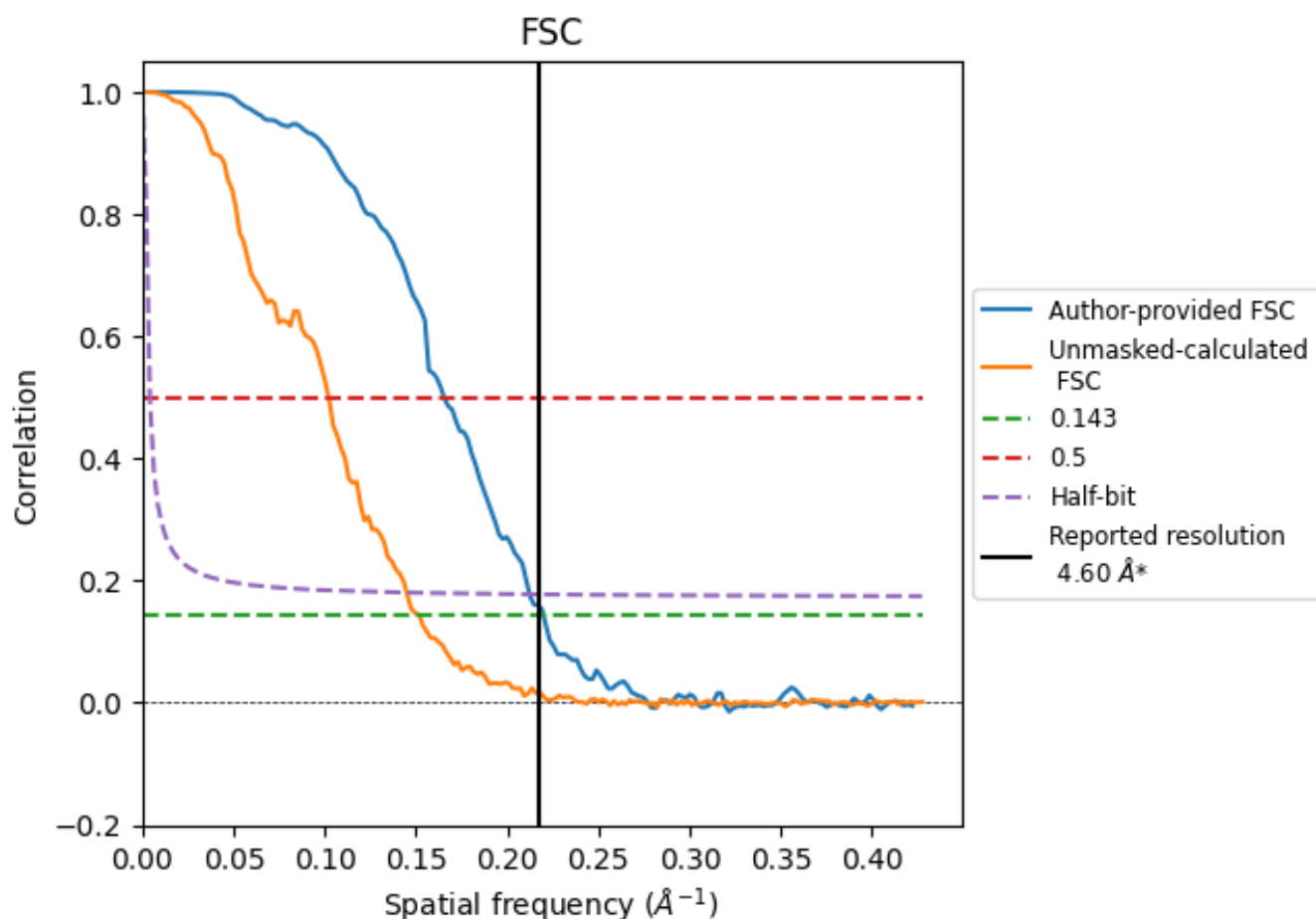


*Reported resolution corresponds to spatial frequency of 0.217 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

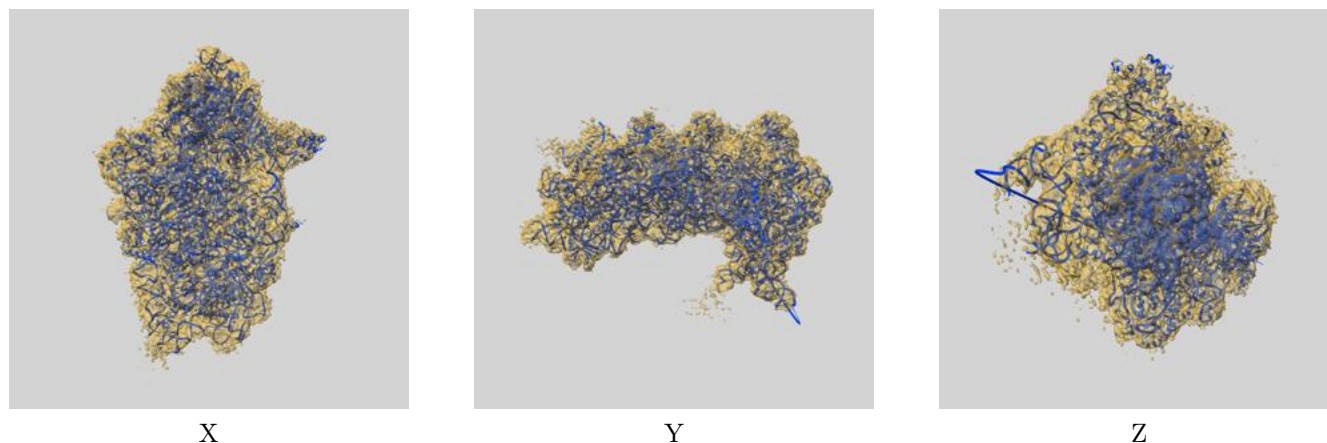
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.60	-	-
Author-provided FSC curve	4.55	6.05	4.71
Unmasked-calculated*	6.58	9.79	6.90

*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](#)

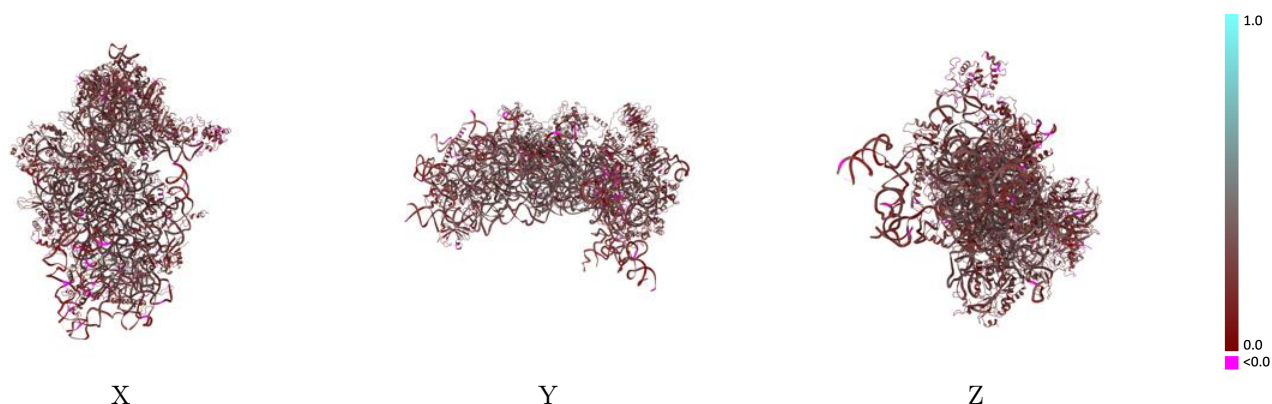
This section contains information regarding the fit between EMDB map EMD-64644 and PDB model 9UZK. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



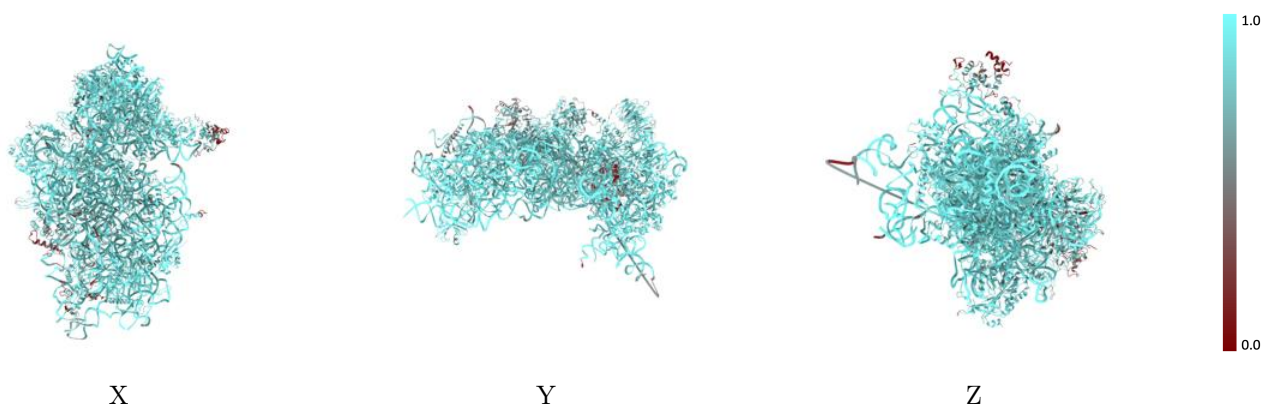
The images above show the 3D surface view of the map at the recommended contour level 0.0811 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



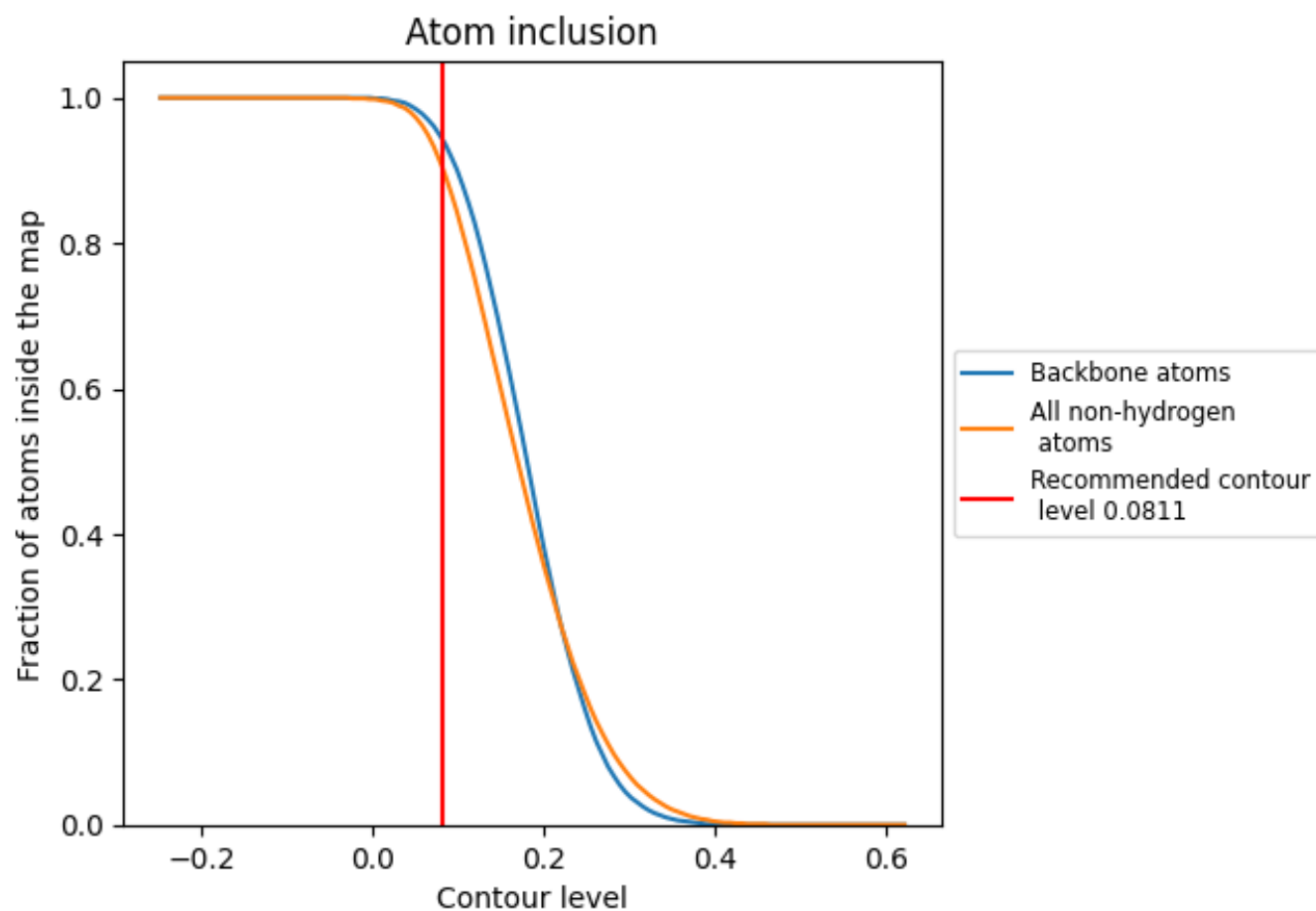
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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