



wwPDB EM Validation Summary Report ⓘ

Jul 8, 2026 – 12:33 PM JST

PDB ID : 9KMU / pdb_00009kmu
EMDB ID : EMD-62445
Title : Bat SARSr-CoV RaTG15 Nsp1 bound to the Human 40S Ribosomal subunit-State2
Authors : Yuan, S.; Yan, R.; Wu, M.
Deposited on : 2024-11-18
Resolution : 2.87 Å(reported)

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

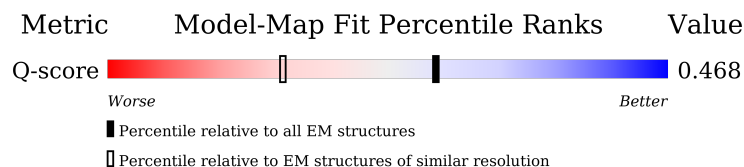
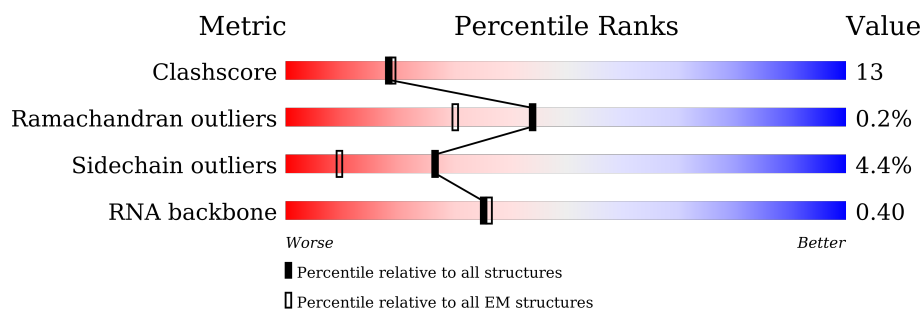
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

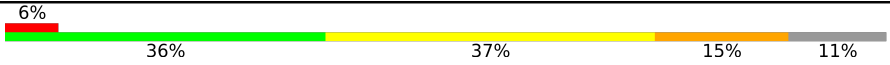
The reported resolution of this entry is 2.87 Å.

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.



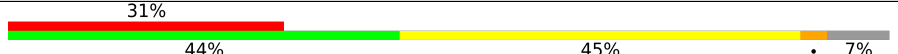
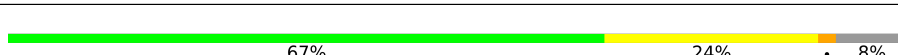
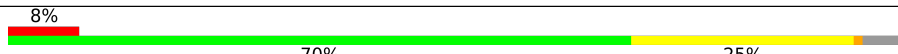
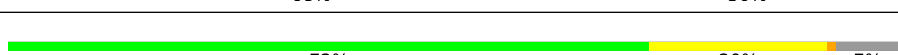
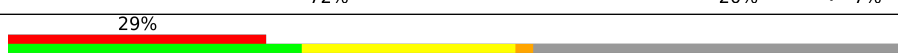
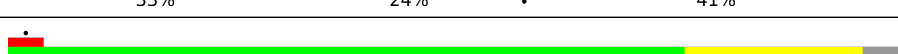
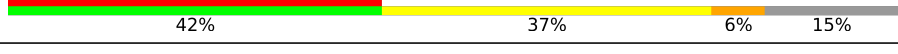
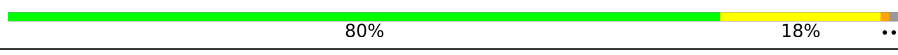
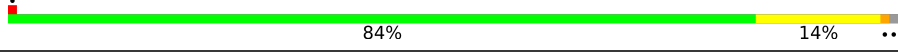
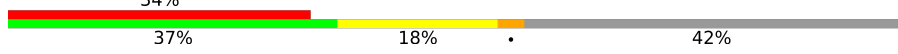
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12062 (2.37 - 3.37)

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	1869	
2	A	295	
3	B	264	

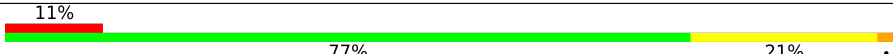
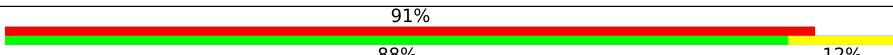
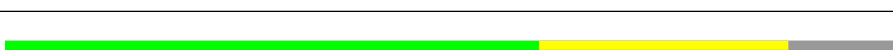
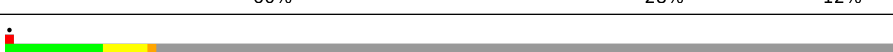
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Mol	Chain	Length	Quality of chain
4	C	293	
5	D	243	
6	E	263	
7	F	204	
8	G	249	
9	H	194	
10	I	208	
11	J	194	
12	K	165	
13	L	158	
14	M	132	
15	N	151	
16	O	151	
17	P	145	
18	Q	146	
19	R	135	
20	S	152	
21	T	145	
22	U	119	
23	V	83	
24	W	130	
25	X	143	
26	Y	130	
27	Z	125	
28	a	101	

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Mol	Chain	Length	Quality of chain
29	b	82	
30	c	62	
31	d	55	
32	e	56	
33	f	74	
34	g	315	
35	h	25	
36	n	180	

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 74574 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	1660	Total	C	N	O	P	0	0
			35423	15824	6374	11575	1650		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	213	Total	C	N	O	S	0	0
			1686	1072	295	311	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	218	Total	C	N	O	S	0	0
			1690	1094	289	297	10		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	225	Total	C	N	O	S	0	0
			1752	1117	315	313	7		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	230	Total	C	N	O	S	0	0
			1864	1164	373	320	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	221	ARG	LYS	variant	UNP P62753

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	186	Total	C	N	O	S	0	0
			1501	957	276	267	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	205	Total	C	N	O	S	0	0
			1682	1056	331	290	5		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	97	Total	C	N	O	S	0	0
			816	533	144	133	6		

- Molecule 13 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	151	Total	C	N	O	S	0	0
			1229	782	230	211	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	121	Total	C	N	O	S	0	0
			935	586	165	175	9		

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

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

- Molecule 16 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	135	Total	C	N	O	S	0	0
			1010	618	198	188	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	126	Total	C	N	O	S	0	0
			1037	659	196	175	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	138	Total	C	N	O	S	0	0
			1097	698	206	190	3		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	143	Total	C	N	O	S	0	0
			1184	743	240	200	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	144	Total	C	N	O	S	0	0
			1123	703	217	200	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	101	Total	C	N	O	S	0	0
			803	504	153	142	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	82	Total	C	N	O	S	0	0
			625	384	116	120	5		

- Molecule 24 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	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	X	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 26 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	124	Total	C	N	O	S	0	0
			1014	641	198	170	5		

- Molecule 27 is a protein called Small ribosomal subunit protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	72	Total	C	N	O	S	0	0
			574	368	104	101	1		

- Molecule 28 is a protein called Small ribosomal subunit protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	99	Total	C	N	O	S	0	0
			794	494	165	130	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	78	VAL	ALA	conflict	UNP P62854

- Molecule 29 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	82	Total	C	N	O	S	0	0
			641	402	118	114	7		

- Molecule 30 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	62	Total	C	N	O	S	0	0
			489	297	97	93	2		

- Molecule 31 is a protein called Small ribosomal subunit protein uS14.

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

- Molecule 32 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	56	Total	C	N	O	S	0	0
			442	273	96	72	1		

- Molecule 33 is a protein called Small ribosomal subunit protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	74	Total	C	N	O	S	0	0
			611	385	117	102	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	314	Total	C	N	O	S	0	0
			2441	1537	425	467	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	22	Total	C	N	O	S	0	0
			213	130	57	23	3		

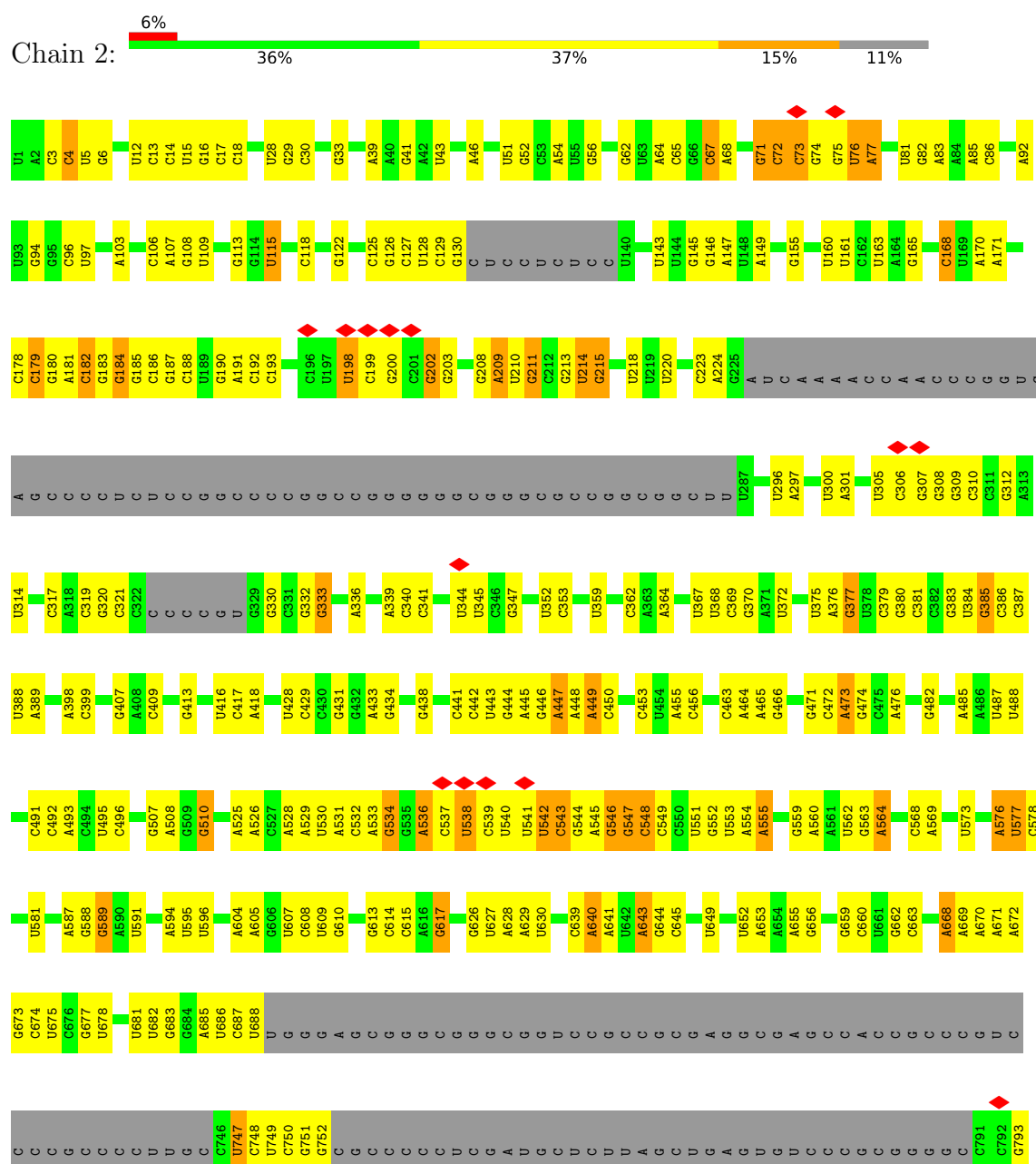
- Molecule 36 is a protein called ORF1ab polyprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	n	30	Total	C	N	O	S	0	0
			238	146	41	49	2		

3 Residue-property plots

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

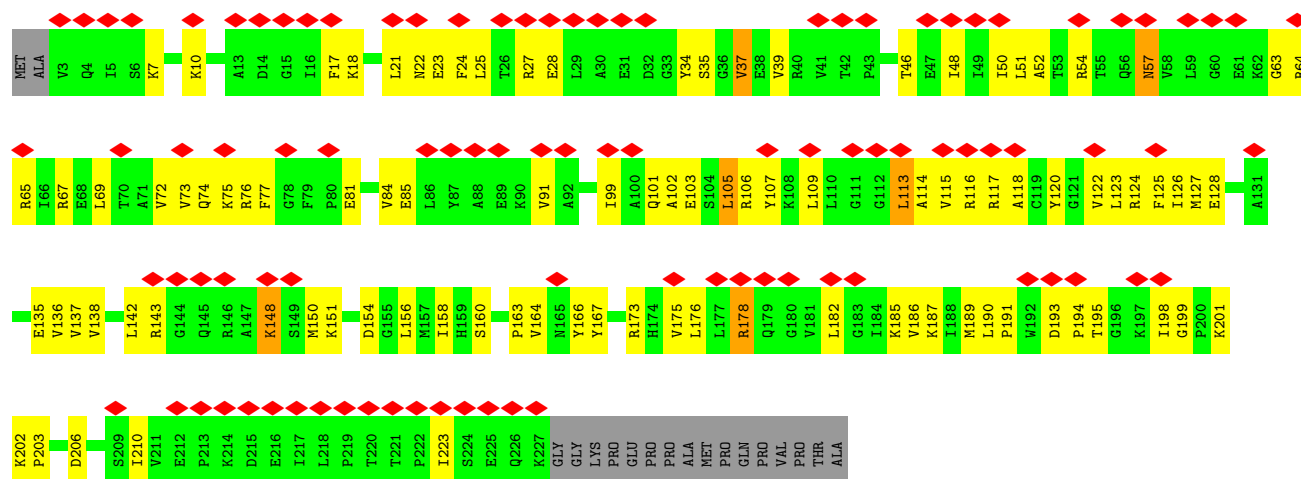
• Molecule 1: 18S ribosomal RNA



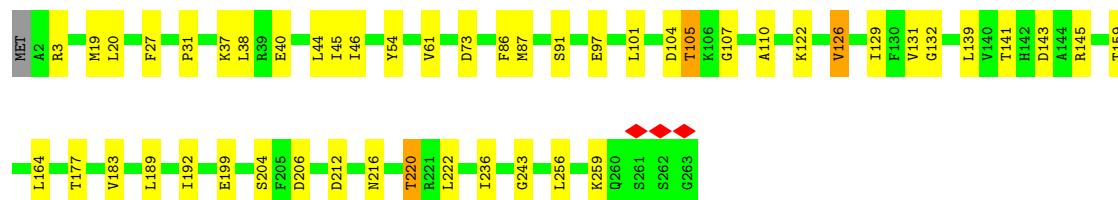
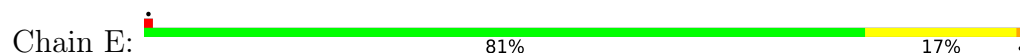
U1672	U1485	G1546	G1610	A1485	A1357	C1292	U1232	A1143	G1043	C953	U	A794
A1675	A1486	C1547	G1611	G	A1357	A1293	G1233	A1143	G1043	U954	U	A795
U1676	A1487	U1548	G1612	C	U1358	G1294	C1234	A1144	G1044	A955	C	A796
U1677	C1488	U1549	G1613	G1424	U1359	G1295	G1235	A1145	U1045	G956	U	C797
A1678	A1489	U1550	A1614	G1425	G1360	A1295	G1236	G1425	U1046	A957	A886	A886
A1679	U1490	U1551	U	U1426	U1361	U1296	C1237	A1148	C1047	G958	U887	U799
C1680	G1491	G1552	G1616	C1427	U1362	U1297	U1238	A1149	C1053	G959	U888	
C1683	U1492	C1553	G1617	G1428	C1363	G1298	U1239	C1153	A1058	U960	U889	U804
C1684	C1493	U1554	C1618	G1429	G1364	A1299	U1240	U1154	A1059	G961	U890	U805
A1685	U1494	U1555	A1619	C1430	G1365	U1300	A1241	G1059	A962	A963	G891	A809
G1686	G1495	A1556	A1620	G1431	G1366	U1301	U1242	U1060	A1060	A964	U892	A810
C1687	U1496	C1557	U1621	U1432	U1367	A1302	U1243	G1157	U1061	U965	G893	A811
C1688	G1497	C	U1622	C	U1371	G1303	U1244	U1160	A1062	G895	G895	A812
A1695	U1500	C	U1623	C	U1372	C1304	G1245	G1164	A1070	G971	U896	
A1699	A1561	C	U1624	C	C1373	U1304	G1246	G1165	G1071	G978	U897	G817
G1702	C1562	C	U1625	C	G1374	C1305	A1247	G1170	U1072	G979	U898	G821
C1703	G1563	A1438	C1627	A1439	G1375	U1306	C1247	A1170	U1073	A980	U899	U822
C1704	U1504	U1441	C1628	U1440	U1376	U1307	U1248	G1171	A1080	A981	C900	U823
C1705	U1505	U1442	U1631	U1443	U1377	U1308	A1250	A1172	A1083	A982	G901	C824
G1706	A1506	C1443	U1632	U1444	U1378	C1311	A1251	G1175	A1084	A983	A903	A830
G1709	G1507	U1444	U1633	U1445	G1381	G1312	A1252	G1176	C1085	A984	A904	G831
C1710	A1508	A1446	A1634	A1446	C1384	A1313	C1254	A1183	G1086	C989	U906	C834
C1711	U1509	A1447	C1635	A1447	G1385	U1314	G1255	A1188	A1087	A990	G907	C
U1711	G1510	A1448	G1636	A1448	A1386	U1315	G1256	A1189	U1088	G991	A908	G
U1712	U1511	G1449	G1637	A1449	G1387	C1316	A1258	A1189	G1089	A992	G909	A
C1713	C1512	G1450	G1638	G1450	A1388	C1317	A1259	A1190	C1090	G910	G910	C
U1714	G1513	G1451	G1639	G1451	C1389	U1318	C1261	A1194	G1091	A996	C911	C
C1715	C1514	A1452	U1640	A1452	U1390	U1319	C1262	A1195	G1092	A997	A913	C
C1716	A1571	U1454	U1641	U1454	C1391	G1320	U1263	G1203	G1093	A998	U914	G841
C1717	G1572	A1455	U1642	A1455	C1395	G1321	A1265	G1205	G1095	G999	U917	G846
G1718	G1573	G1456	U1643	A1456	A1396	G1322	G1266	G1206	G1096	U1002	A847	
A1719	U1574	U1457	C1644	U1457	U1397	U1323	C1267	G1207	G1097	C1007	A920	G852
U1720	G1584	G1458	U1645	G1458	G1398	G1324	C1268	A1100	C1098	A1008	G921	
U1721	G1587	U1462	U1646	U1462	C1399	U1325	G1269	A1109	A1009	U857	A922	U857
G1722	A1588	U1463	U1647	U1463	U1400	U1326	G1270	G1211	G1010	G858	G925	G859
A1724	C1523	G1466	U1648	G1466	A1401	G1327	C1271	G1212	A1012	G860	G928	A861
U1725	C1524	C1467	U1649	C1467	A1402	U1328	C1272	C1109	U1013	A862	G929	A862
G1726	G1525	A1468	A1650	A1468	C1403	U1329	C1273	A1113	U1016	G868	G930	G868
C1727	C1526	C1469	A1651	C1469	U1404	G1330	G1274	U1114	G933	A869	U940	A870
U1728	G1527	A1470	U1652	A1470	U1405	C1331	G1275	U1115	C941	U871	G942	A872
G1729	C1528	C1471	U1653	C1471	G1406	A1332	A1276	C1116	U1024	G873	G943	G874
U1730	U1530	C1472	C1654	C1472	U1407	U1333	G1277	A1220	A1027	A875	A944	A875
A1731	A1531	G1473	U1655	G1473	U1408	G1334	A1278	G1221	A1028	C876	U945	C876
C1732	C1532	U1474	G1656	U1474	C1409	U1335	C1279	G1222	G1033	C877	G947	C877
U1733	A1533	G1475	U1657	G1475	C1410	G1338	G1280	A1119	A1034	G878	C948	G878
G1734	C1534	A1476	U1658	A1476	G1411	U1339	G1281	U1223	A1035	C879	G949	G880
A1735	U1535	U1477	U1659	U1477	G1412	U1340	U1224	A1225	A1036	G881	G952	
G1736	G1536	U1478	U1660	U1478	A1414	U1341	G1282	G1226	G1037			
C1737	A1537	G1479	U1661	G1479	C1415	C1342	A1282	G1227				
C1738	C1538	A1480	U1662	A1480	C1416	U1343	C1283	A1228				
C1739	U1539	U1483	U1663	U1483	C	U1344	A1284	G1229				
C1740	G1540	A1483	U1664	A1483	C	A1344	G1285	C1230				
U1741	U1606	U1484	U1665	U1484	C	U1347	G1286	C1231				
	A	U	U1666	U	G	G1348	A1287					
	C	A1484	U1667	A1484		G1349	U1288					
			U1668			U1350	U1289					
			U1669			G1351	G1290					
						G1352	A1291					
						A1353						
						G1354						



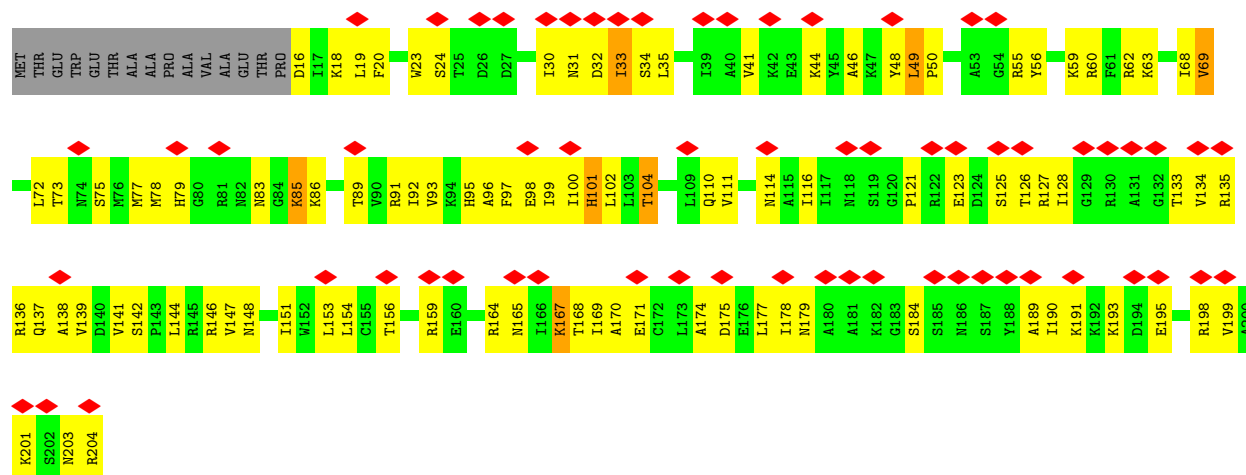
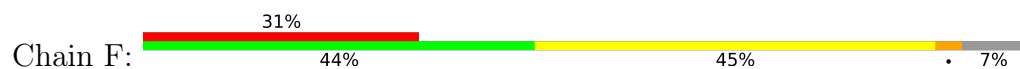
• Molecule 5: Small ribosomal subunit protein uS3



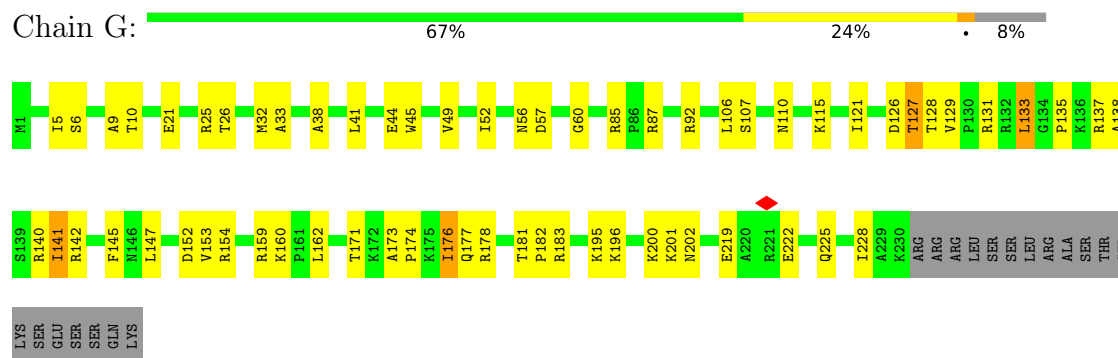
• Molecule 6: Small ribosomal subunit protein eS4, X isoform



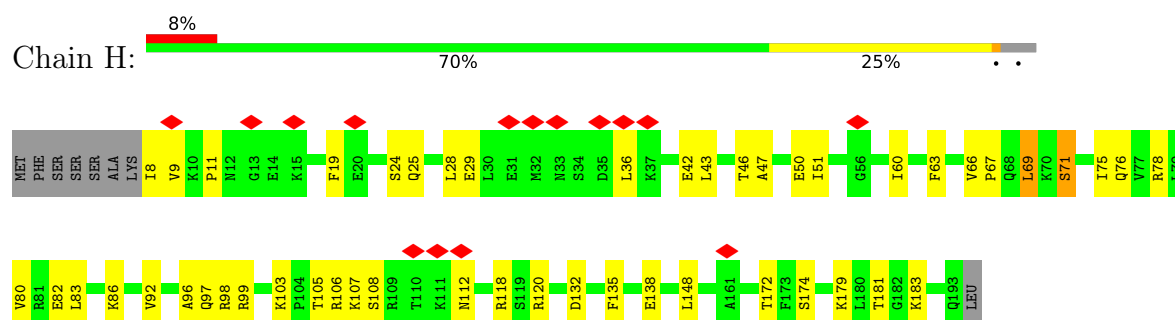
• Molecule 7: Small ribosomal subunit protein uS7



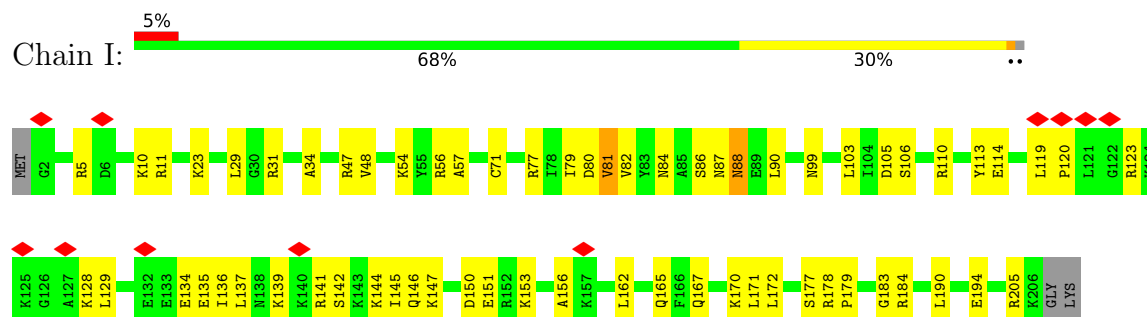
- Molecule 8: Small ribosomal subunit protein eS6



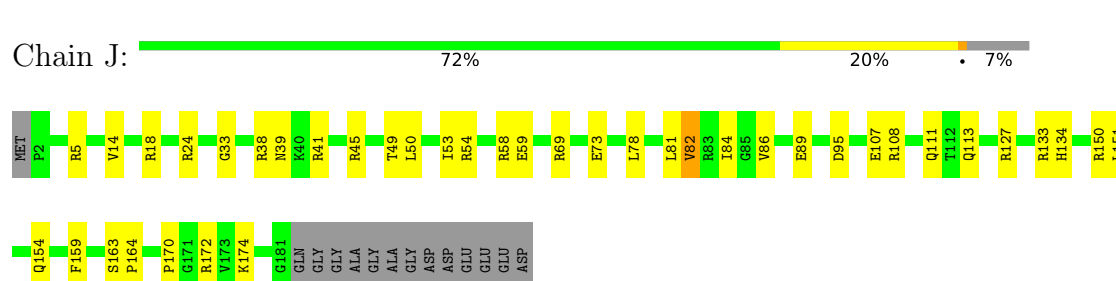
- Molecule 9: Small ribosomal subunit protein eS7



- Molecule 10: Small ribosomal subunit protein eS8



- Molecule 11: Small ribosomal subunit protein uS4

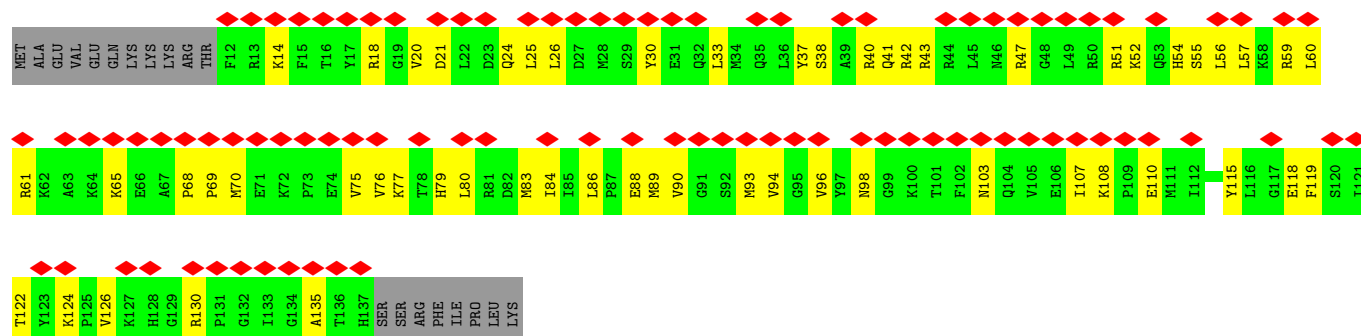


- Molecule 12: Small ribosomal subunit protein eS10

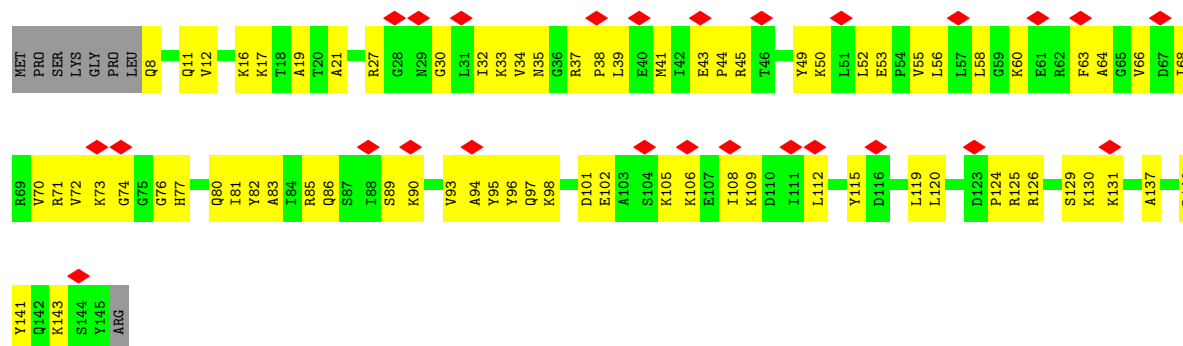
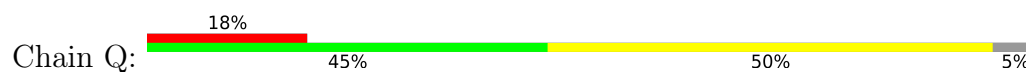




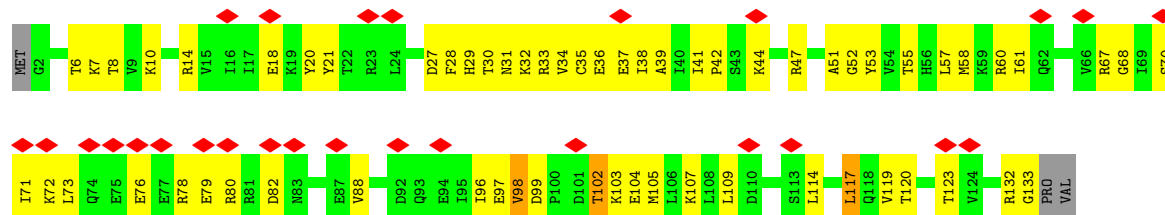
• Molecule 17: Small ribosomal subunit protein uS19



• Molecule 18: Small ribosomal subunit protein uS9

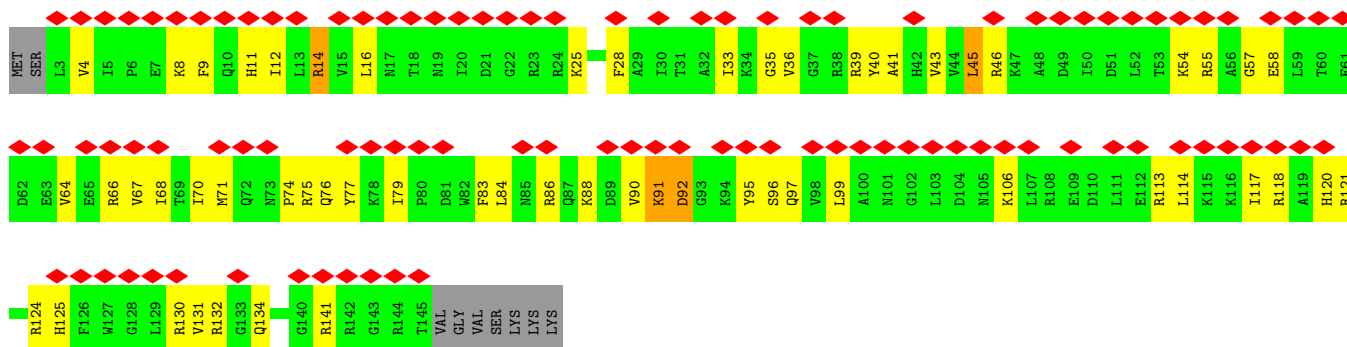


• Molecule 19: Small ribosomal subunit protein eS17

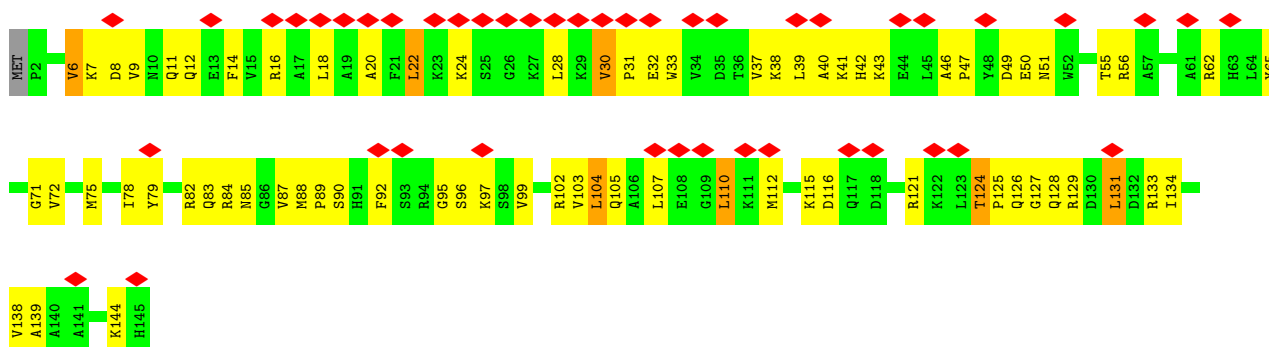


• Molecule 20: Small ribosomal subunit protein uS13

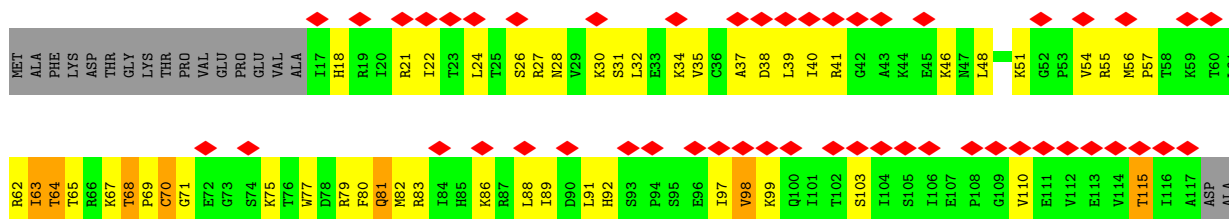




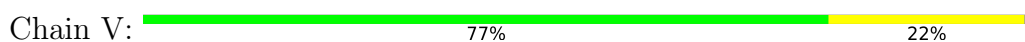
- Molecule 21: Small ribosomal subunit protein eS19



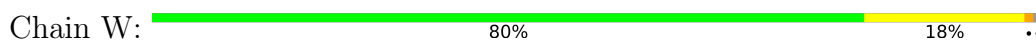
- Molecule 22: Small ribosomal subunit protein uS10



- Molecule 23: Small ribosomal subunit protein eS21

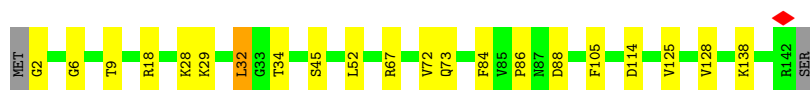


- Molecule 24: Small ribosomal subunit protein uS8



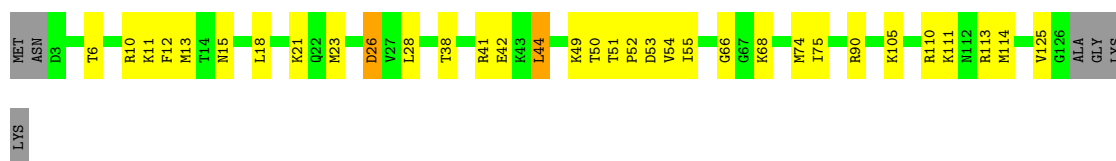
- Molecule 25: Small ribosomal subunit protein uS12

Chain X:  84% 14% ..

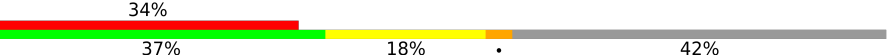


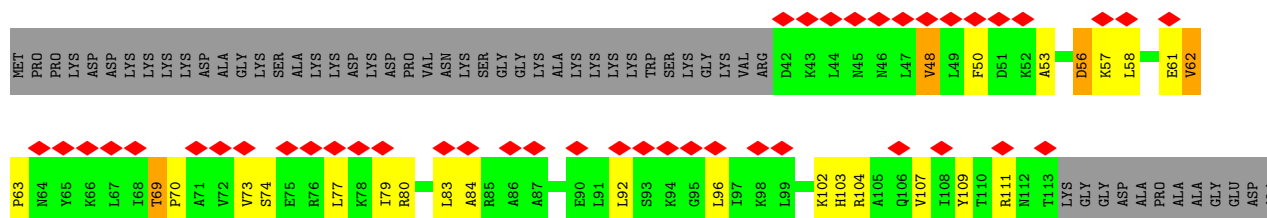
- Molecule 26: Small ribosomal subunit protein eS24

Chain Y:  70% 24% • 5%



- Molecule 27: Small ribosomal subunit protein eS25

Chain Z:  34% 37% 18% • 42%



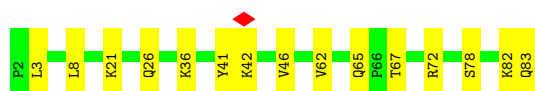
- Molecule 28: Small ribosomal subunit protein eS26

Chain a:  65% 30% • ..



- Molecule 29: Small ribosomal subunit protein eS27

Chain b:  82% 18%

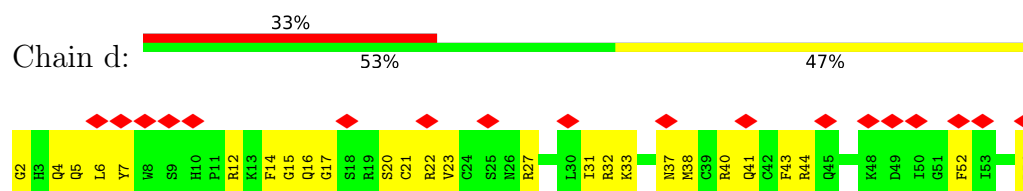


- Molecule 30: Small ribosomal subunit protein eS28

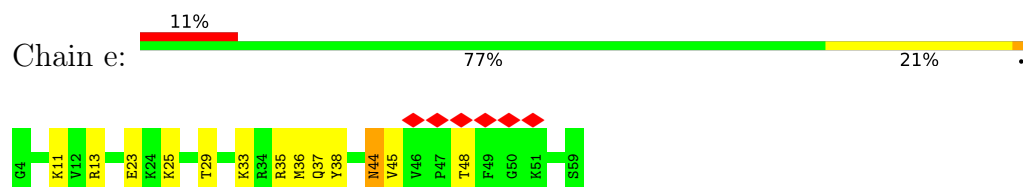
Chain c:  44% 66% 32% •



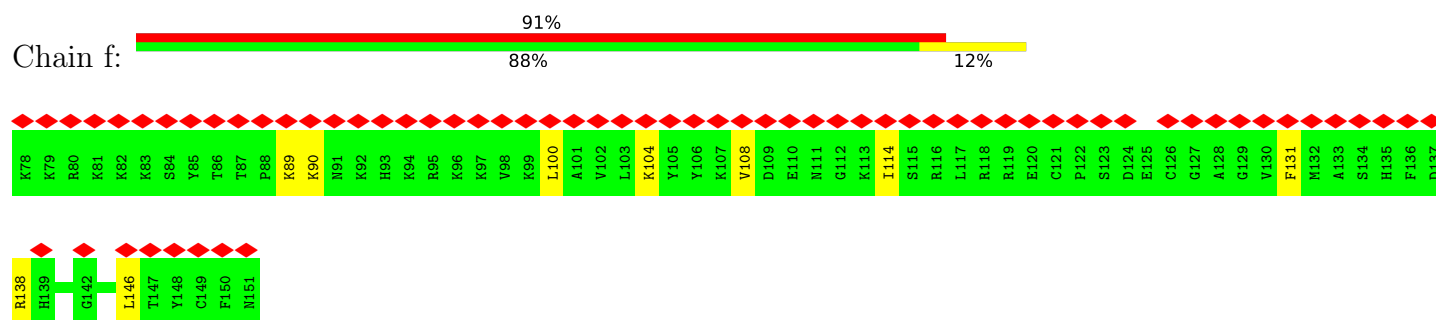
- Molecule 31: Small ribosomal subunit protein uS14



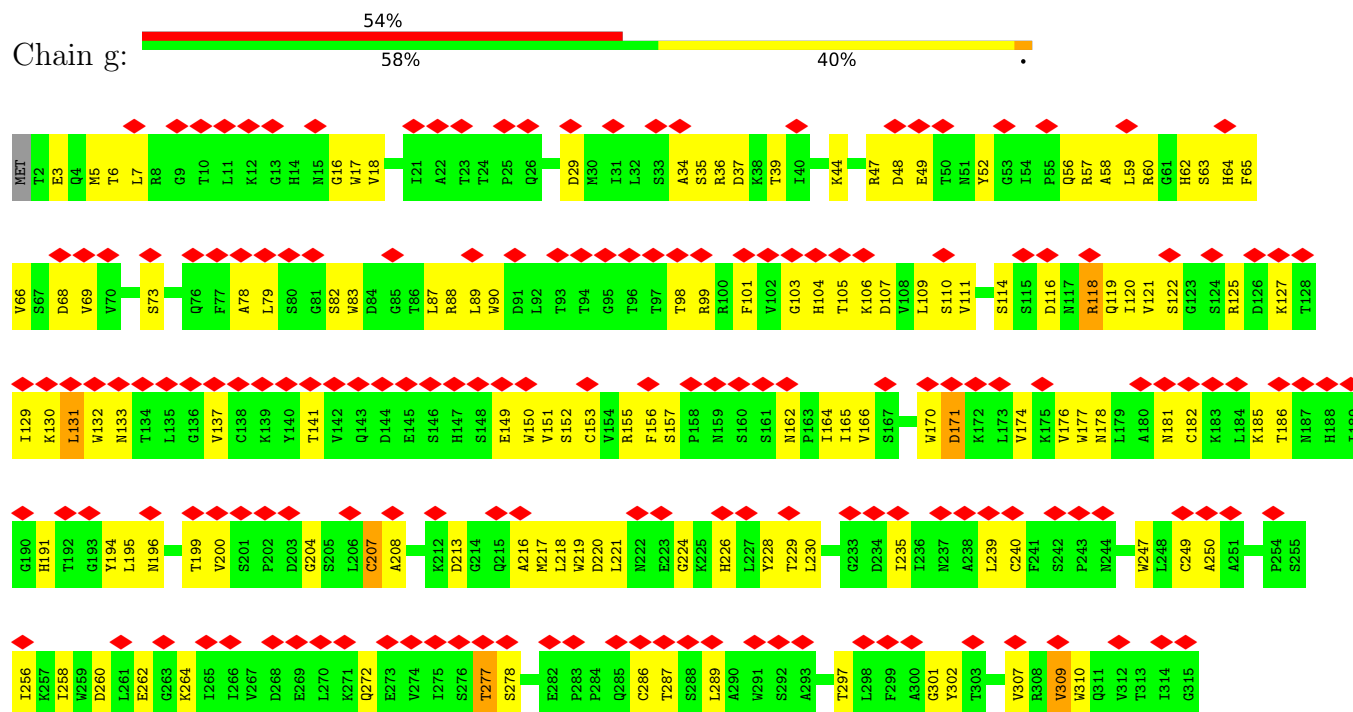
- Molecule 32: Small ribosomal subunit protein eS30



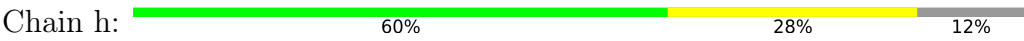
- Molecule 33: Small ribosomal subunit protein eS31



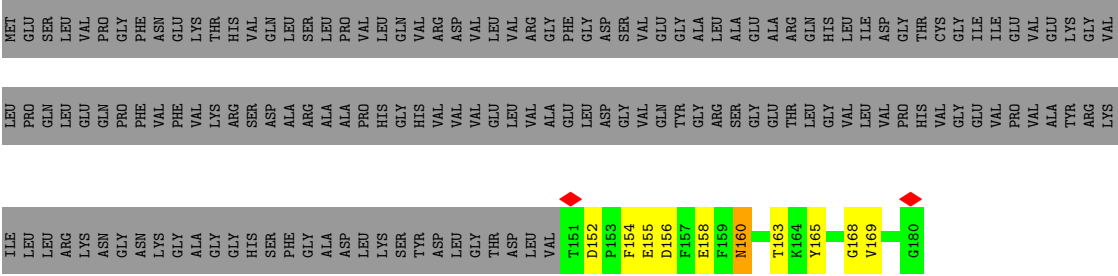
- Molecule 34: Small ribosomal subunit protein RACK1



- Molecule 35: Small ribosomal subunit protein eS32



● Molecule 36: ORF1ab polyprotein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	51346	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.635	Depositor
Minimum map value	-0.792	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.046	Depositor
Recommended contour level	0.15	Depositor
Map size ($\text{\AA}$)	486.4, 486.4, 486.4	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.95, 0.95, 0.95	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.24	1/39611 (0.0%)	0.31	0/61726
2	A	0.21	0/1723	0.33	0/2341
3	B	0.22	0/1756	0.34	0/2350
4	C	0.24	0/1726	0.36	0/2332
5	D	0.20	0/1780	0.50	1/2397 (0.0%)
6	E	0.25	0/2118	0.32	0/2849
7	F	0.21	0/1516	0.50	0/2037
8	G	0.19	0/1887	0.31	0/2513
9	H	0.17	0/1524	0.38	0/2042
10	I	0.21	0/1711	0.34	0/2282
11	J	0.25	0/1524	0.30	0/2035
12	K	0.14	0/840	0.38	0/1133
13	L	0.26	0/1250	0.37	0/1673
14	M	0.12	0/945	0.38	0/1269
15	N	0.20	0/1226	0.29	0/1649
16	O	0.22	0/1023	0.37	0/1372
17	P	0.15	0/1058	0.45	0/1414
18	Q	0.17	0/1114	0.49	0/1492
19	R	0.17	0/1082	0.47	0/1452
20	S	0.14	0/1202	0.43	0/1610
21	T	0.24	0/1143	0.51	1/1530 (0.1%)
22	U	0.14	0/813	0.39	0/1092
23	V	0.21	0/631	0.30	0/844
24	W	0.27	0/1051	0.35	0/1406
25	X	0.25	0/1116	0.37	0/1490
26	Y	0.24	0/1031	0.31	0/1370
27	Z	0.13	0/580	0.42	0/780
28	a	0.22	0/807	0.35	0/1082
29	b	0.21	0/654	0.42	0/876
30	c	0.13	0/491	0.36	0/656
31	d	0.14	0/470	0.43	0/623
32	e	0.20	0/447	0.34	0/587
33	f	0.11	0/623	0.33	0/822
34	g	0.14	0/2498	0.40	0/3399

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	h	0.19	0/214	0.28	0/272
36	n	0.23	0/242	0.38	0/324
All	All	0.22	1/79427 (0.0%)	0.35	2/115121 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	510	G	C1'-N9	-6.03	1.39	1.48

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	198	ILE	N-CA-C	-5.91	106.73	111.81
21	T	110	LEU	N-CA-C	-5.05	106.71	112.92

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	35423	0	17912	703	0
2	A	1686	0	1688	44	0
3	B	1729	0	1803	54	0
4	C	1690	0	1777	51	0
5	D	1752	0	1848	87	0
6	E	2076	0	2177	27	0
7	F	1495	0	1549	75	0
8	G	1864	0	2018	49	0
9	H	1501	0	1593	36	0
10	I	1682	0	1769	50	0
11	J	1499	0	1618	29	0
12	K	816	0	841	40	0
13	L	1229	0	1302	21	0
14	M	935	0	964	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	N	1202	0	1289	18	0
16	O	1010	0	1034	53	0
17	P	1037	0	1082	51	0
18	Q	1097	0	1161	58	0
19	R	1068	0	1121	58	0
20	S	1184	0	1244	55	0
21	T	1123	0	1153	65	0
22	U	803	0	873	44	0
23	V	625	0	628	14	0
24	W	1034	0	1080	17	0
25	X	1098	0	1167	15	0
26	Y	1014	0	1082	25	0
27	Z	574	0	627	25	0
28	a	794	0	849	28	0
29	b	641	0	665	15	0
30	c	489	0	514	14	0
31	d	459	0	452	37	0
32	e	442	0	487	12	0
33	f	611	0	638	6	0
34	g	2441	0	2396	102	0
35	h	213	0	258	8	0
36	n	238	0	214	8	0
All	All	74574	0	58873	1718	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 13.

The worst 5 of 1718 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)
5:D:195:THR:CG2	5:D:199:GLY:O	1.66	1.44
5:D:195:THR:HG23	5:D:199:GLY:CA	1.46	1.44
5:D:195:THR:HG23	5:D:199:GLY:C	1.57	1.26
5:D:195:THR:HG21	5:D:199:GLY:O	1.21	1.25
1:2:1172:U:H3	1:2:1188:A:N6	1.32	1.23

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A	211/295 (72%)	206 (98%)	4 (2%)	1 (0%)	24	51
3	B	211/264 (80%)	206 (98%)	5 (2%)	0	100	100
4	C	216/293 (74%)	206 (95%)	10 (5%)	0	100	100
5	D	223/243 (92%)	206 (92%)	17 (8%)	0	100	100
6	E	260/263 (99%)	250 (96%)	10 (4%)	0	100	100
7	F	187/204 (92%)	167 (89%)	19 (10%)	1 (0%)	24	51
8	G	228/249 (92%)	221 (97%)	7 (3%)	0	100	100
9	H	184/194 (95%)	177 (96%)	7 (4%)	0	100	100
10	I	203/208 (98%)	189 (93%)	14 (7%)	0	100	100
11	J	178/194 (92%)	168 (94%)	10 (6%)	0	100	100
12	K	95/165 (58%)	86 (90%)	9 (10%)	0	100	100
13	L	149/158 (94%)	144 (97%)	4 (3%)	1 (1%)	18	44
14	M	119/132 (90%)	107 (90%)	10 (8%)	2 (2%)	7	23
15	N	147/151 (97%)	146 (99%)	1 (1%)	0	100	100
16	O	133/151 (88%)	128 (96%)	5 (4%)	0	100	100
17	P	124/145 (86%)	109 (88%)	15 (12%)	0	100	100
18	Q	136/146 (93%)	123 (90%)	13 (10%)	0	100	100
19	R	130/135 (96%)	129 (99%)	1 (1%)	0	100	100
20	S	141/152 (93%)	123 (87%)	17 (12%)	1 (1%)	18	44
21	T	142/145 (98%)	131 (92%)	11 (8%)	0	100	100
22	U	99/119 (83%)	88 (89%)	11 (11%)	0	100	100
23	V	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
24	W	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
25	X	139/143 (97%)	135 (97%)	4 (3%)	0	100	100
26	Y	122/130 (94%)	119 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	Z	70/125 (56%)	61 (87%)	9 (13%)	0	100	100
28	a	97/101 (96%)	93 (96%)	3 (3%)	1 (1%)	12	35
29	b	80/82 (98%)	77 (96%)	3 (4%)	0	100	100
30	c	60/62 (97%)	55 (92%)	5 (8%)	0	100	100
31	d	53/55 (96%)	46 (87%)	7 (13%)	0	100	100
32	e	54/56 (96%)	50 (93%)	4 (7%)	0	100	100
33	f	72/74 (97%)	61 (85%)	10 (14%)	1 (1%)	9	28
34	g	312/315 (99%)	285 (91%)	26 (8%)	1 (0%)	36	62
35	h	20/25 (80%)	20 (100%)	0	0	100	100
36	n	28/180 (16%)	25 (89%)	3 (11%)	0	100	100
All	All	4830/5567 (87%)	4534 (94%)	287 (6%)	9 (0%)	44	70

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	189	ILE
7	F	33	ILE
14	M	109	VAL
14	M	110	VAL
28	a	63	VAL

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	A	179/243 (74%)	175 (98%)	4 (2%)	45	75
3	B	194/231 (84%)	188 (97%)	6 (3%)	35	66
4	C	184/225 (82%)	178 (97%)	6 (3%)	33	65
5	D	189/202 (94%)	177 (94%)	12 (6%)	16	42
6	E	224/225 (100%)	213 (95%)	11 (5%)	22	51
7	F	159/170 (94%)	146 (92%)	13 (8%)	10	30

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	G	200/218 (92%)	193 (96%)	7 (4%)	32	63
9	H	167/174 (96%)	161 (96%)	6 (4%)	31	63
10	I	178/180 (99%)	170 (96%)	8 (4%)	24	55
11	J	160/168 (95%)	155 (97%)	5 (3%)	35	66
12	K	88/136 (65%)	84 (96%)	4 (4%)	24	55
13	L	135/142 (95%)	135 (100%)	0	100	100
14	M	102/108 (94%)	98 (96%)	4 (4%)	28	60
15	N	130/131 (99%)	120 (92%)	10 (8%)	12	33
16	O	105/119 (88%)	99 (94%)	6 (6%)	18	47
17	P	112/130 (86%)	108 (96%)	4 (4%)	31	63
18	Q	114/121 (94%)	112 (98%)	2 (2%)	51	78
19	R	119/122 (98%)	114 (96%)	5 (4%)	26	58
20	S	124/132 (94%)	118 (95%)	6 (5%)	23	53
21	T	114/115 (99%)	106 (93%)	8 (7%)	14	37
22	U	93/107 (87%)	86 (92%)	7 (8%)	12	34
23	V	66/67 (98%)	64 (97%)	2 (3%)	36	67
24	W	112/113 (99%)	106 (95%)	6 (5%)	20	49
25	X	113/115 (98%)	109 (96%)	4 (4%)	32	63
26	Y	108/112 (96%)	106 (98%)	2 (2%)	50	77
27	Z	64/103 (62%)	59 (92%)	5 (8%)	11	32
28	a	87/89 (98%)	82 (94%)	5 (6%)	18	47
29	b	74/74 (100%)	72 (97%)	2 (3%)	39	70
30	c	55/55 (100%)	52 (94%)	3 (6%)	19	48
31	d	48/48 (100%)	48 (100%)	0	100	100
32	e	45/45 (100%)	42 (93%)	3 (7%)	15	39
33	f	67/67 (100%)	66 (98%)	1 (2%)	57	82
34	g	272/273 (100%)	256 (94%)	16 (6%)	18	45
35	h	21/24 (88%)	21 (100%)	0	100	100
36	n	26/147 (18%)	24 (92%)	2 (8%)	12	33
All	All	4228/4731 (89%)	4043 (96%)	185 (4%)	27	56

5 of 185 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
20	S	28	PHE
25	X	72	VAL
21	T	6	VAL
22	U	70	CYS
27	Z	62	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
21	T	126	GLN
26	Y	85	ASN
22	U	81	GLN
25	X	31	HIS
32	e	15	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1645/1869 (88%)	549 (33%)	22 (1%)

5 of 549 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	4	C
1	2	33	G
1	2	41	G
1	2	46	A
1	2	56	G

5 of 22 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	1612	G
1	2	1666	C
1	2	1649	U
1	2	1709	G
1	2	1329	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

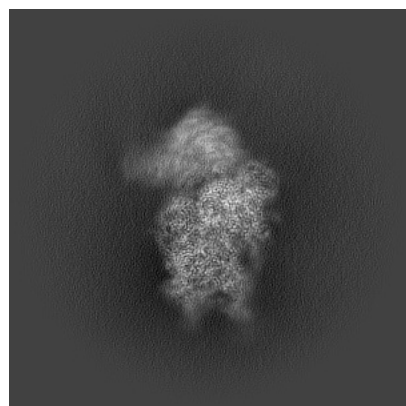
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62445. These allow visual inspection of the internal detail of the map and identification of artifacts.

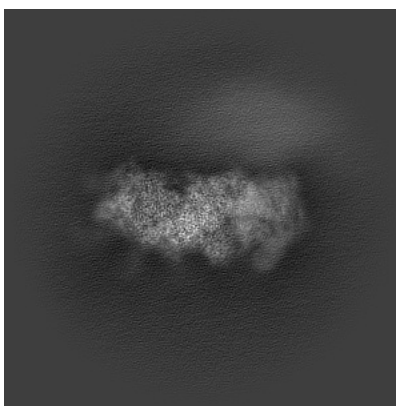
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

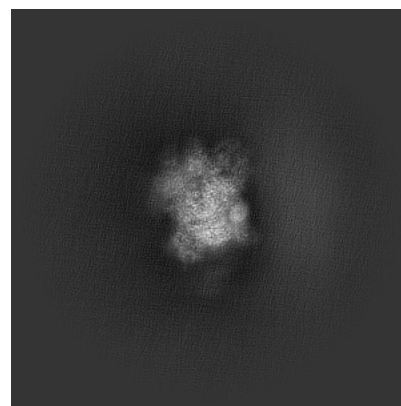
6.1.1 Primary map



X

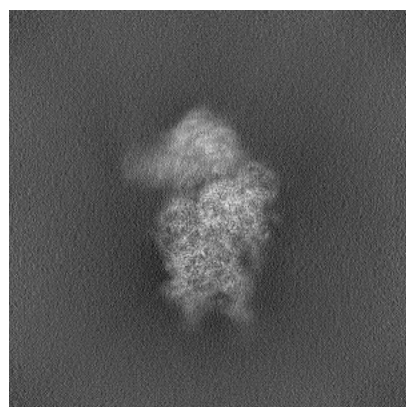


Y

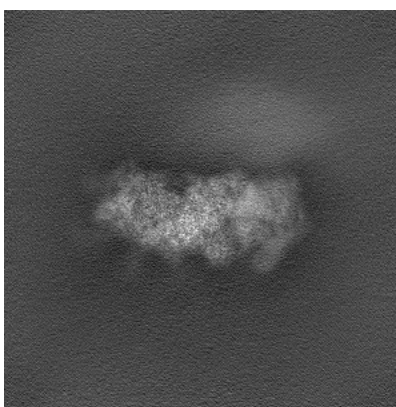


Z

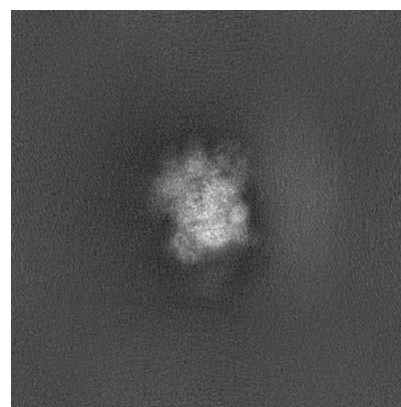
6.1.2 Raw map



X



Y

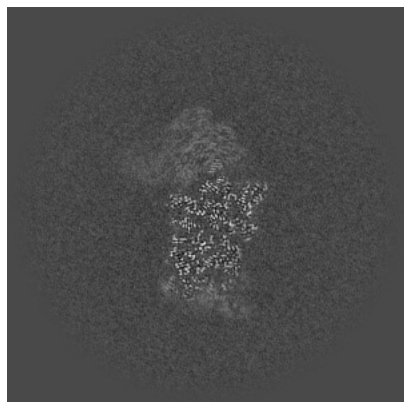


Z

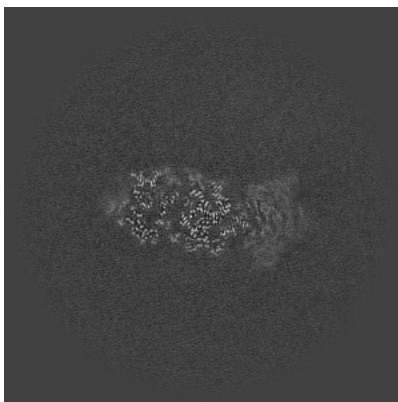
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

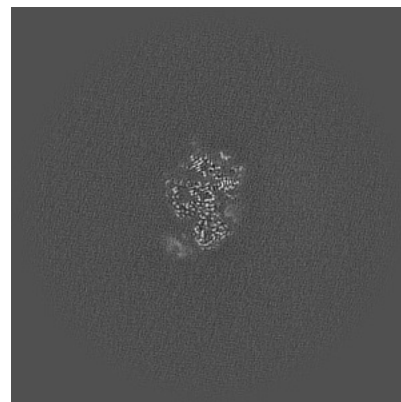
6.2.1 Primary map



X Index: 256

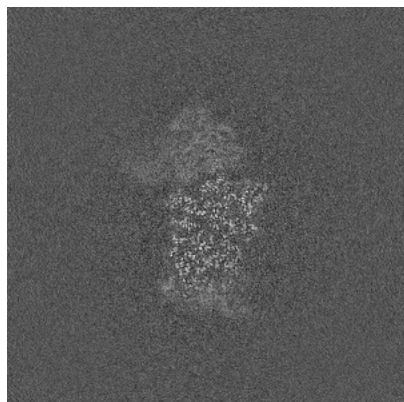


Y Index: 256

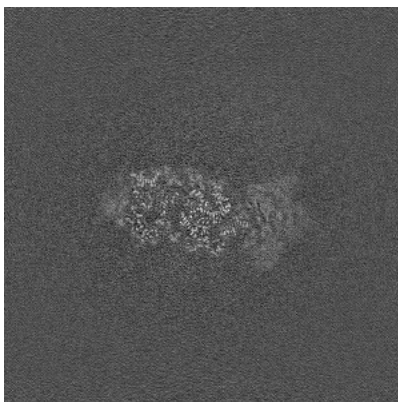


Z Index: 256

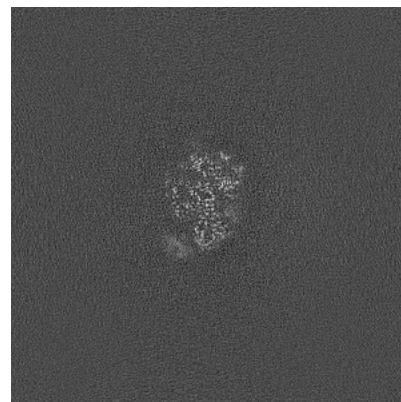
6.2.2 Raw map



X Index: 256



Y Index: 256

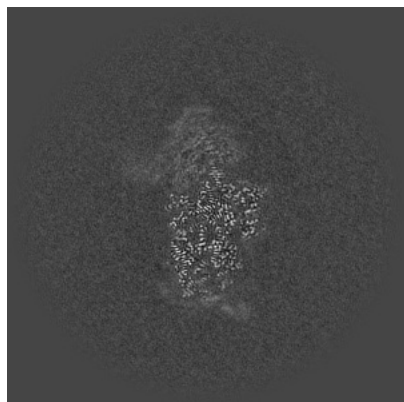


Z Index: 256

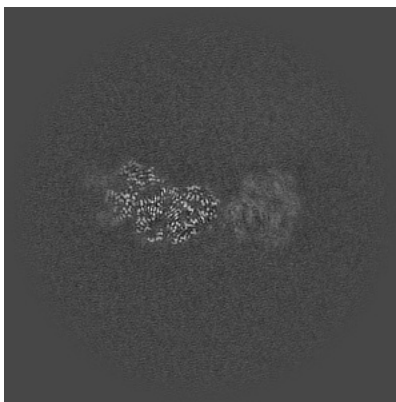
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

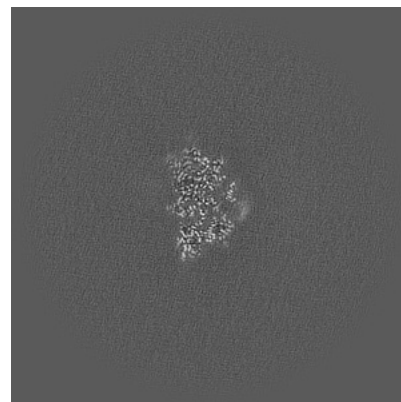
6.3.1 Primary map



X Index: 251

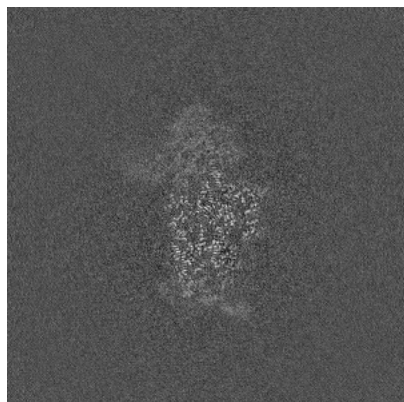


Y Index: 225

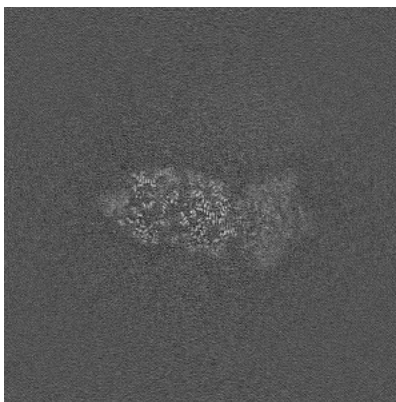


Z Index: 236

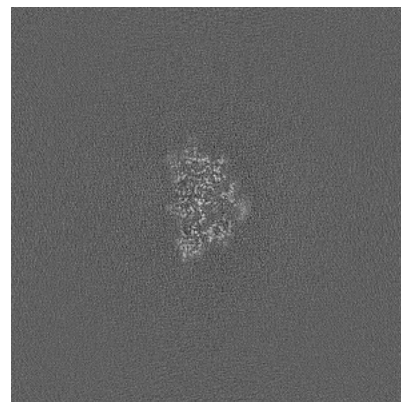
6.3.2 Raw map



X Index: 251



Y Index: 257

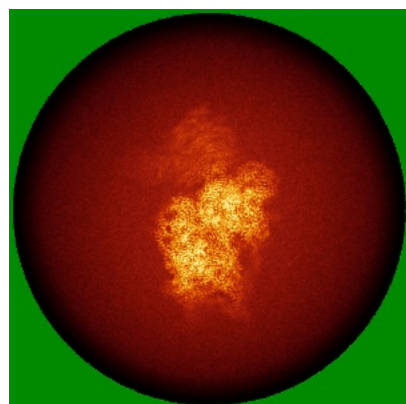


Z Index: 237

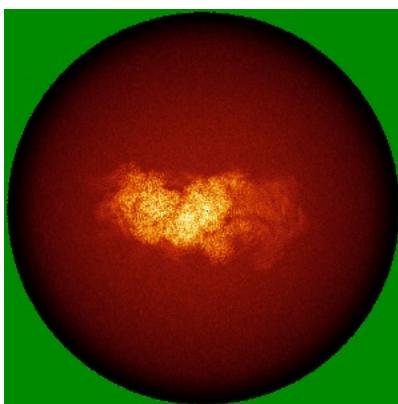
The images above show the largest variance slices of the map in three orthogonal directions.

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

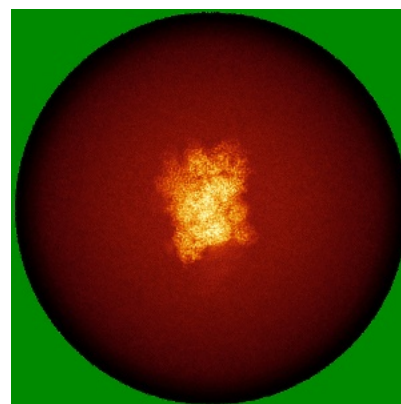
6.4.1 Primary map



X

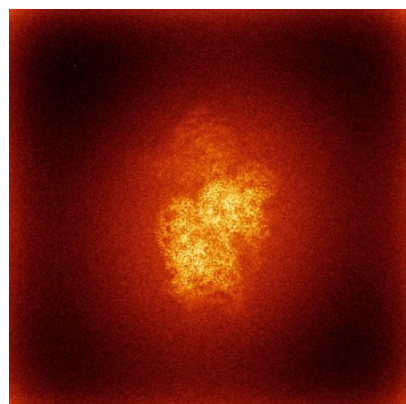


Y

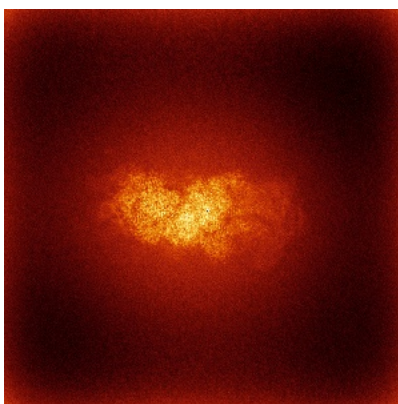


Z

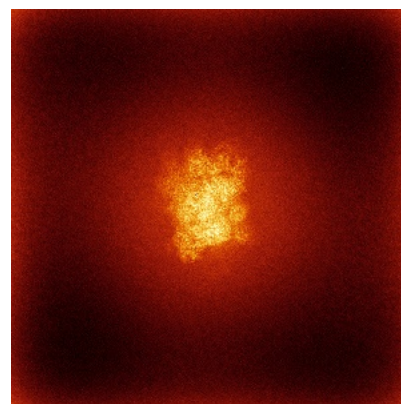
6.4.2 Raw map



X



Y

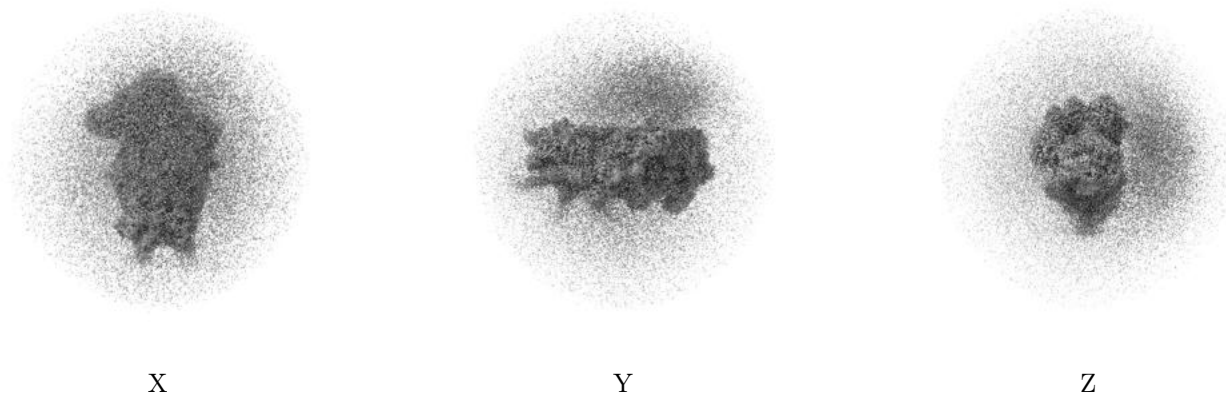


Z

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.

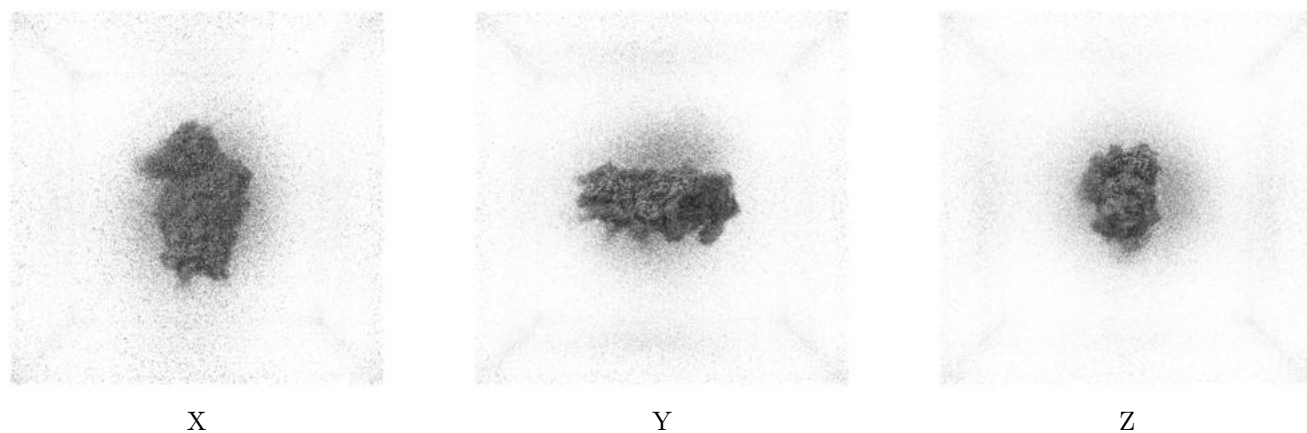
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. 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.

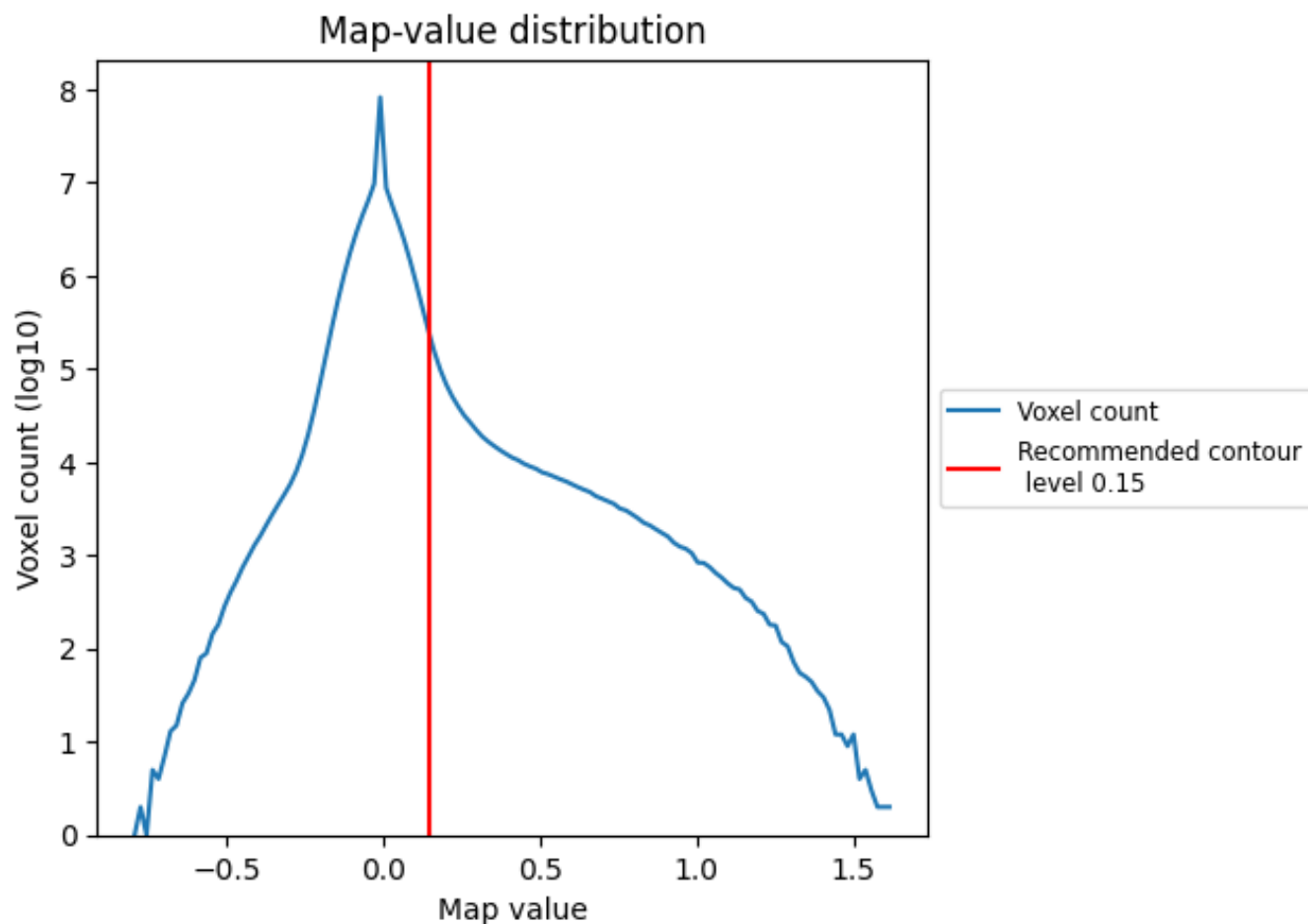
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

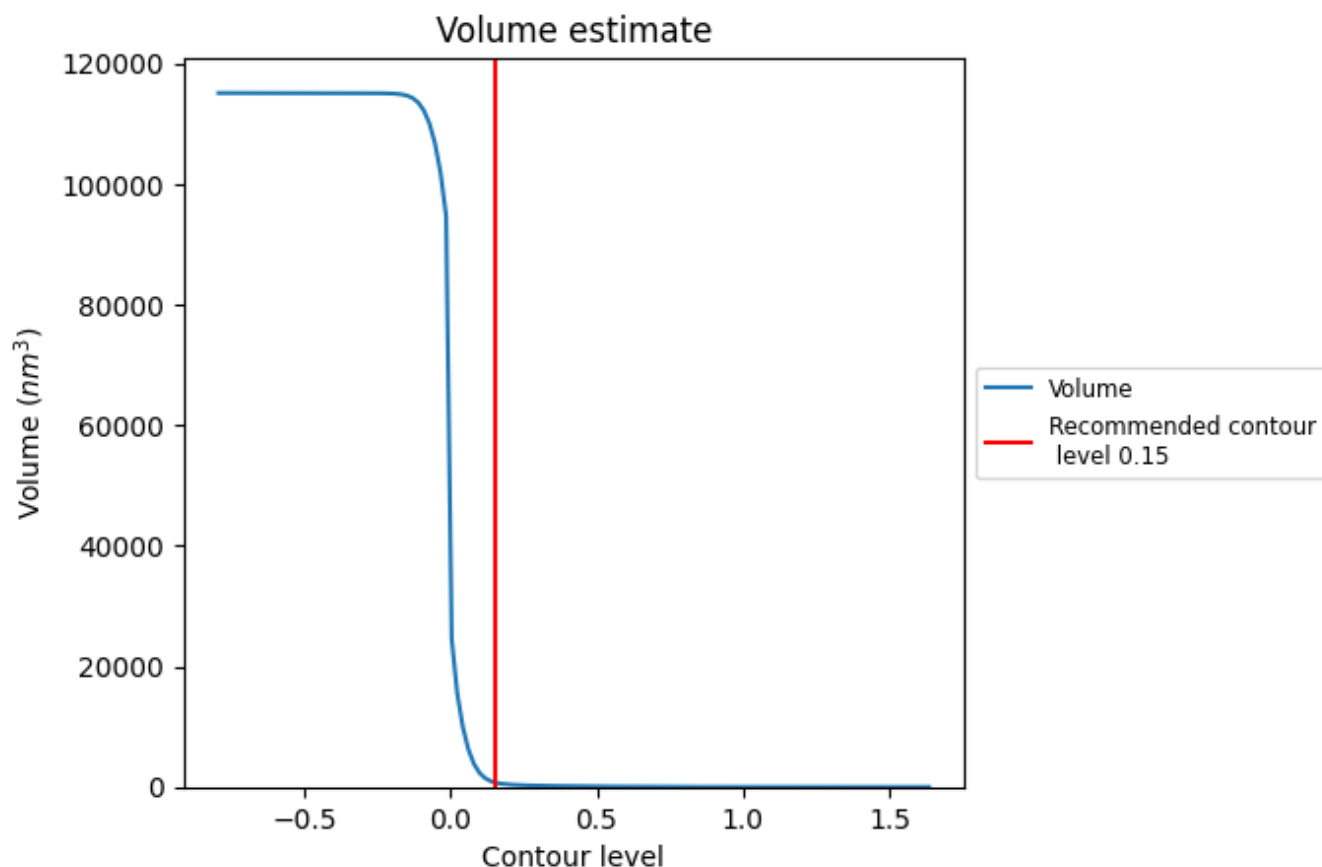
This section contains the results of statistical analysis of the map.

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.

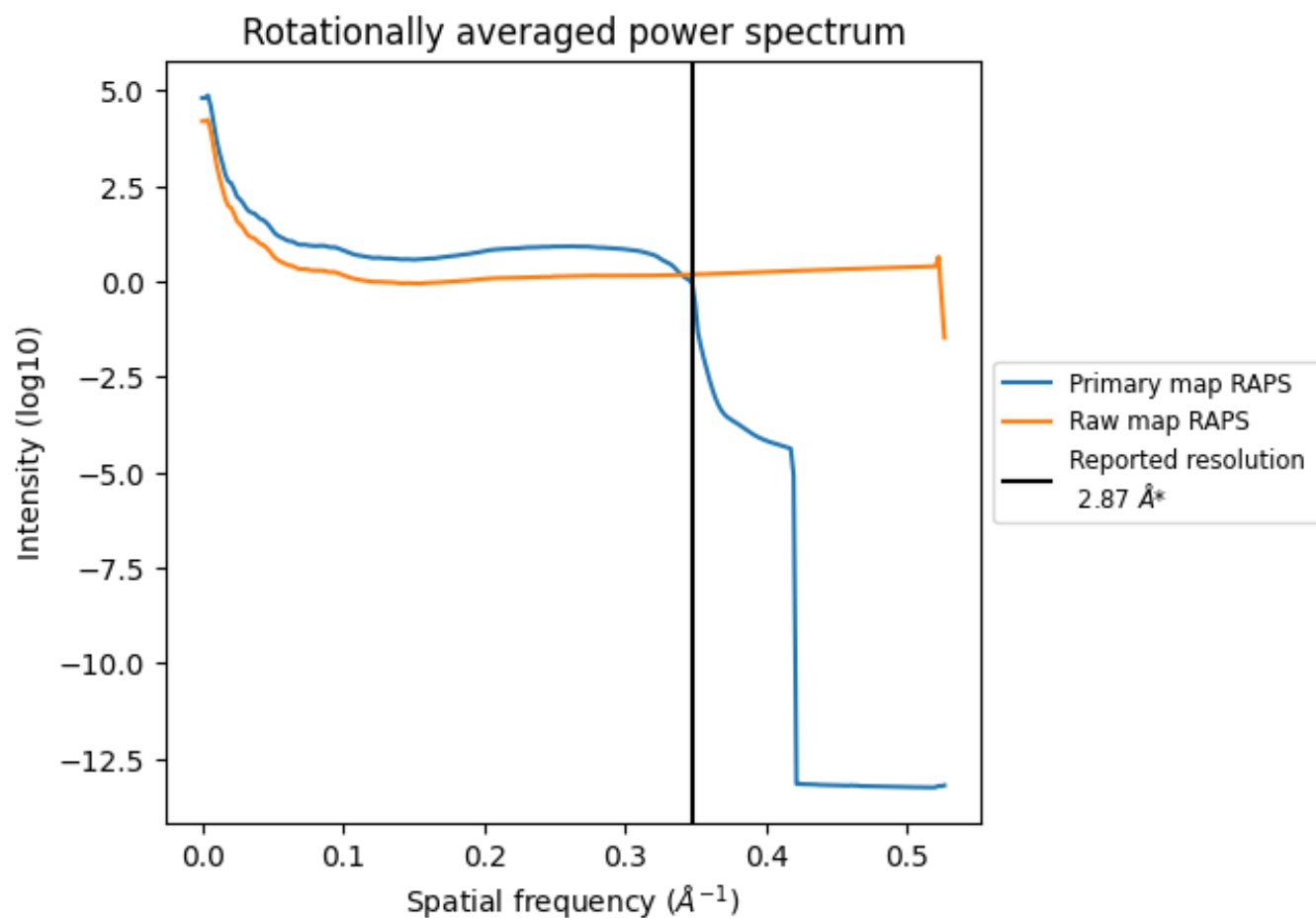
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 789 nm³; this corresponds to an approximate mass of 712 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 ⓘ

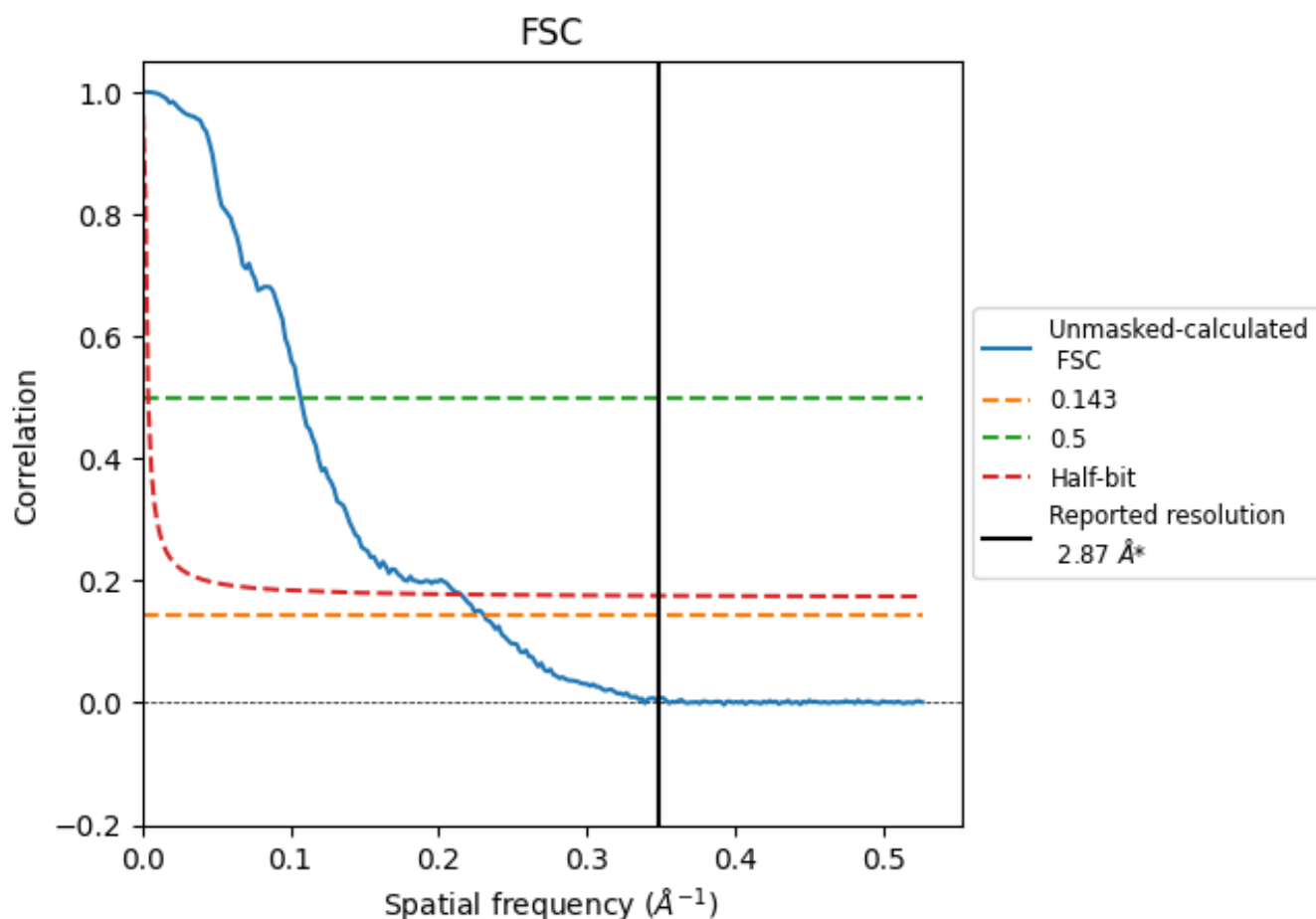


*Reported resolution corresponds to spatial frequency of 0.348 Å⁻¹

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 0.348 Å⁻¹

8.2 Resolution estimates [i](#)

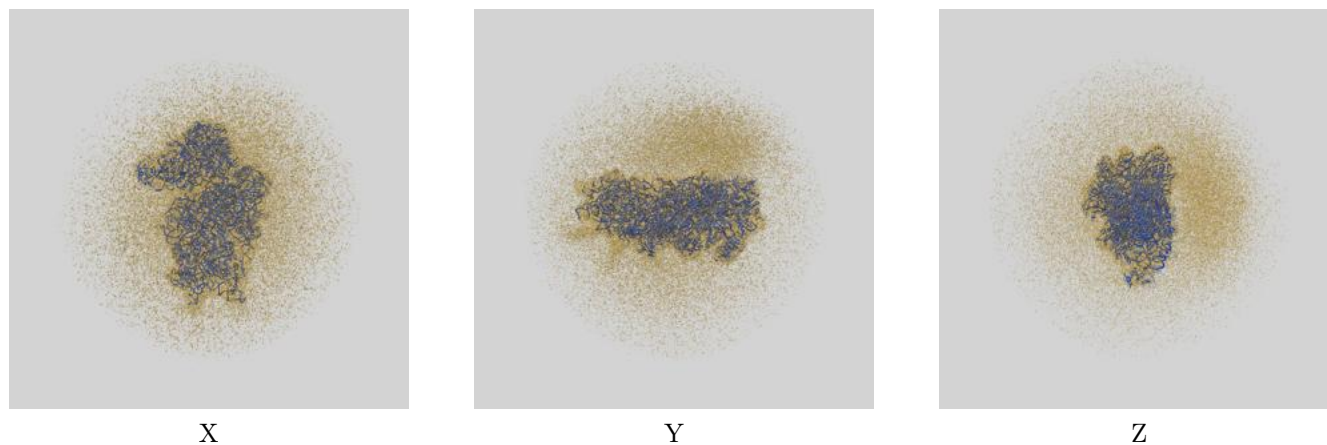
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.87	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.34	9.36	4.65

*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 4.34 differs from the reported value 2.87 by more than 10 %

9 Map-model fit [i](#)

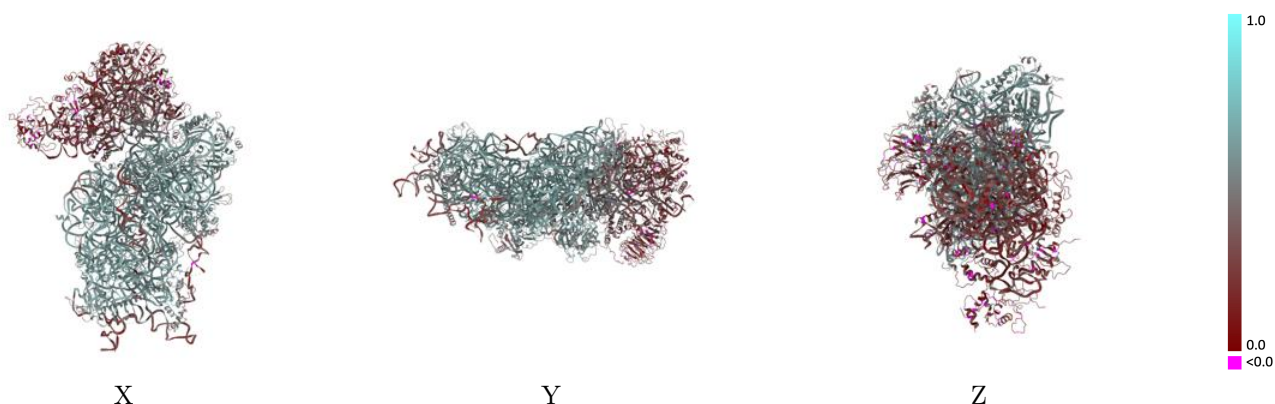
This section contains information regarding the fit between EMDB map EMD-62445 and PDB model 9KMU. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



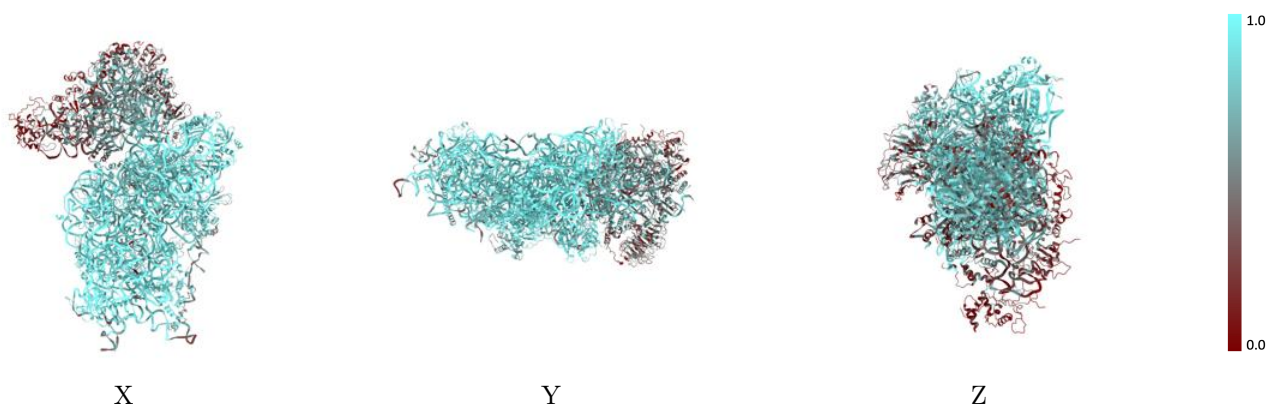
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



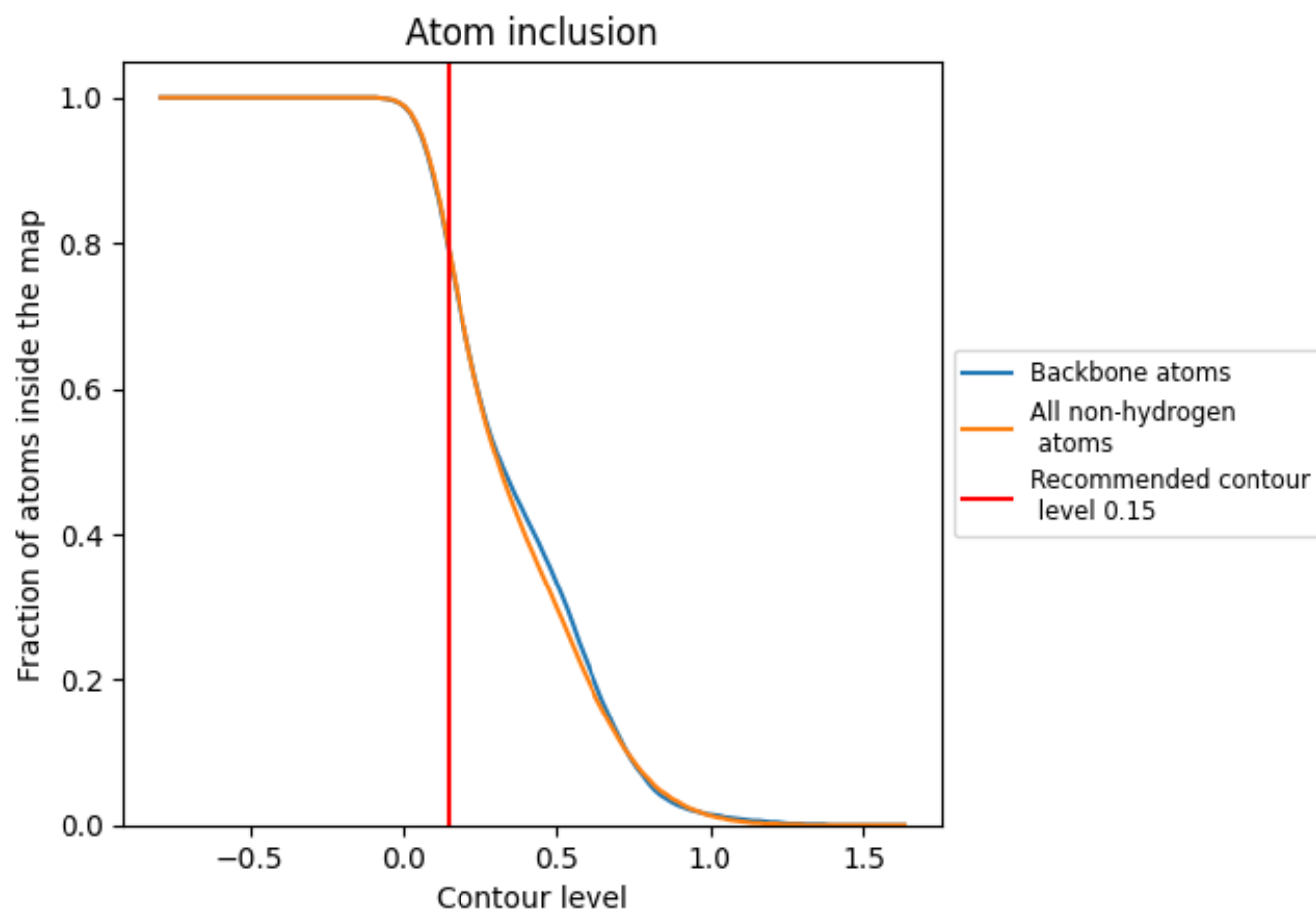
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 79% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7880	 0.4680
2	 0.8650	 0.4840
A	 0.9250	 0.5710
B	 0.9180	 0.5660
C	 0.9360	 0.5890
D	 0.4620	 0.2810
E	 0.9600	 0.6080
F	 0.5200	 0.2980
G	 0.9150	 0.5400
H	 0.7850	 0.4920
I	 0.8730	 0.5390
J	 0.9700	 0.6040
K	 0.4080	 0.2480
L	 0.9200	 0.5810
M	 0.1630	 0.2130
N	 0.9530	 0.5810
O	 0.9060	 0.5630
P	 0.2580	 0.2430
Q	 0.6060	 0.3260
R	 0.6420	 0.3980
S	 0.2970	 0.2790
T	 0.5430	 0.2790
U	 0.4090	 0.2850
V	 0.9570	 0.5890
W	 0.9570	 0.6070
X	 0.9630	 0.5980
Y	 0.9630	 0.5990
Z	 0.3300	 0.2530
a	 0.9300	 0.5780
b	 0.8790	 0.5420
c	 0.4690	 0.3100
d	 0.5120	 0.2700
e	 0.8600	 0.5500
f	 0.1280	 0.2490
g	 0.3920	 0.2590



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Chain	Atom inclusion	Q-score
h	 0.8870	 0.5560
n	 0.8500	 0.5430