



wwPDB EM Validation Summary Report ⓘ

Nov 17, 2025 – 05:42 PM JST

PDB ID : 9KMW / pdb_00009kmw
EMDB ID : EMD-62447
Title : SARSr-MpCoV-GX Nsp1 bound to the Human 40S Ribosomal subunit-State2
Authors : Yuan, S.; Yan, R.; Wu, M.
Deposited on : 2024-11-18
Resolution : 2.73 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.dev129
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.46

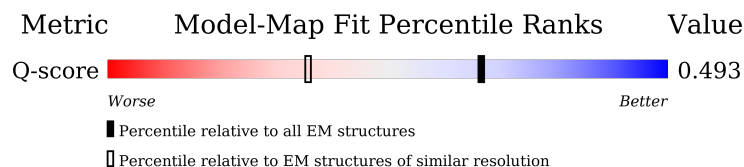
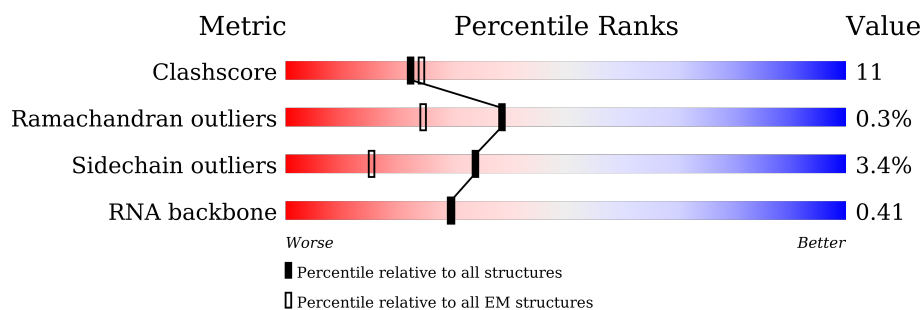
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.73 Å.

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




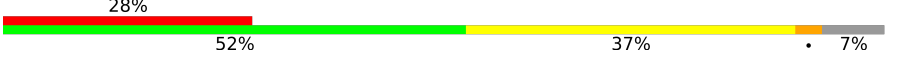



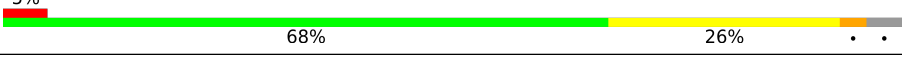

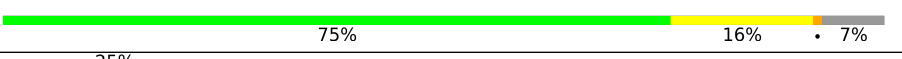
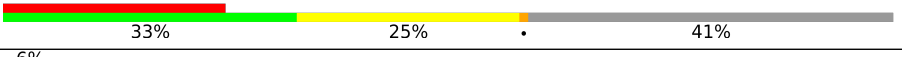


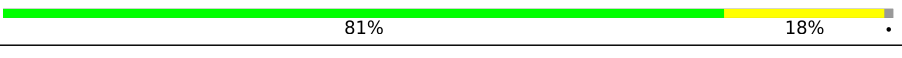







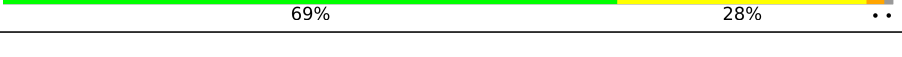
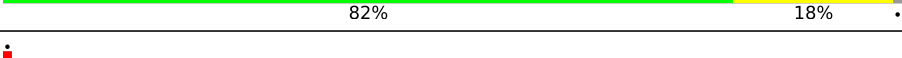
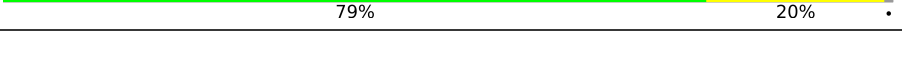

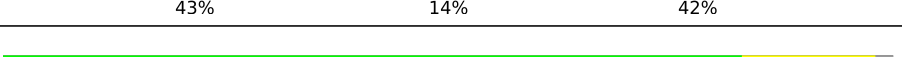

Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	10432 (2.23 - 3.23)

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	<div> <div>5%</div> <div>39%</div> <div>37%</div> <div>13%</div> <div>11%</div> </div>
2	A	295	<div> <div>54%</div> <div>18%</div> <div>28%</div> </div>
3	B	264	<div> <div>61%</div> <div>20%</div> <div>19%</div> </div>

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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 74798 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	1671	Total	C	N	O	P	0	0
			35647	15925	6406	11655	1661		

- 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		

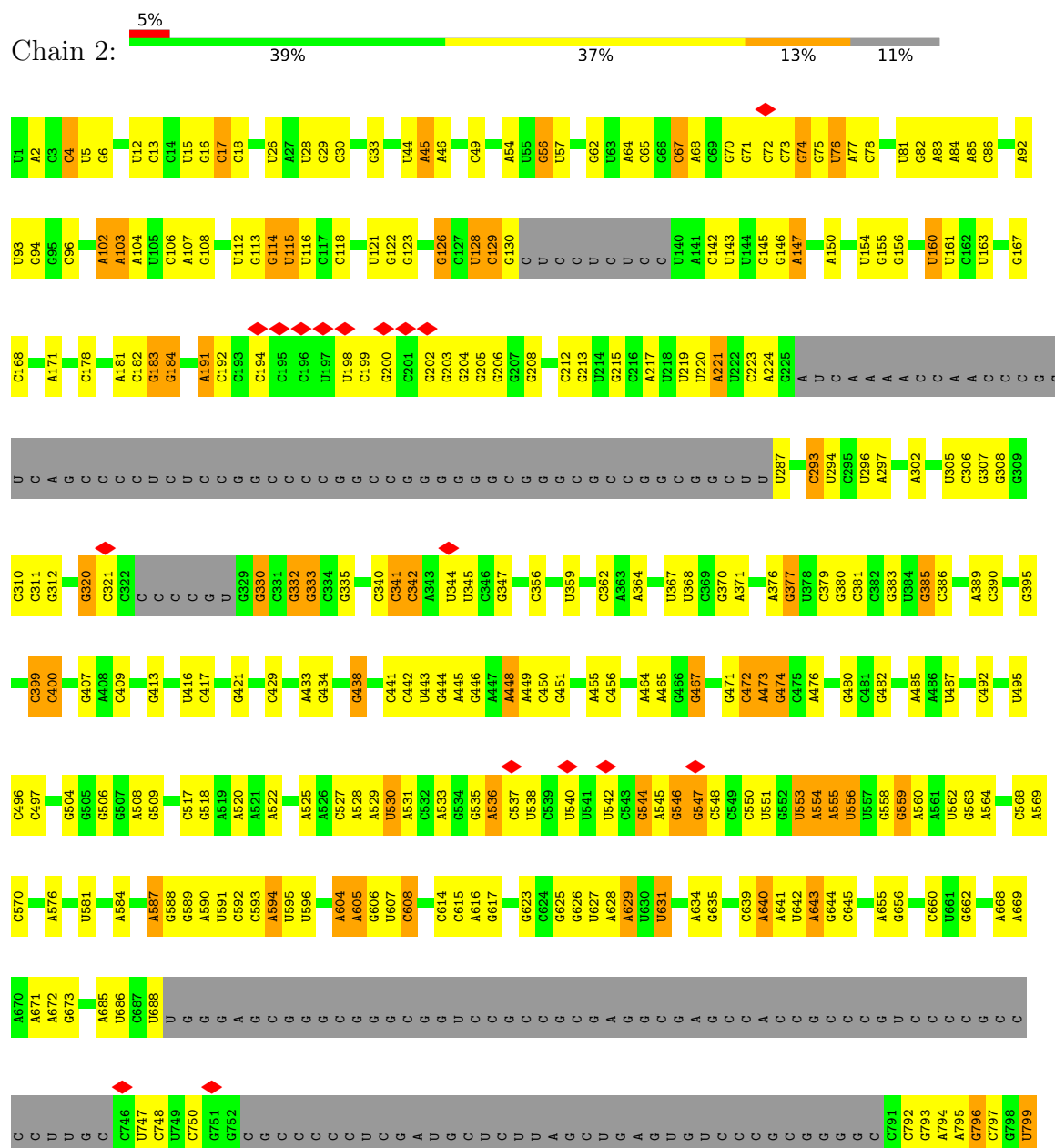
- Molecule 36 is a protein called ORF1ab polyprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	n	30	Total	C	N	O	S	0	0
			238	144	44	49	1		

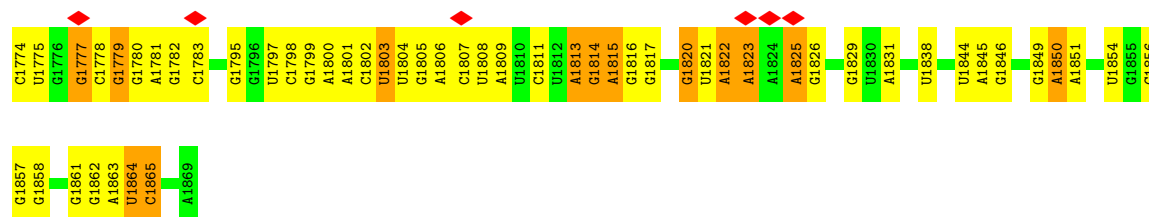
3 Residue-property plots

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

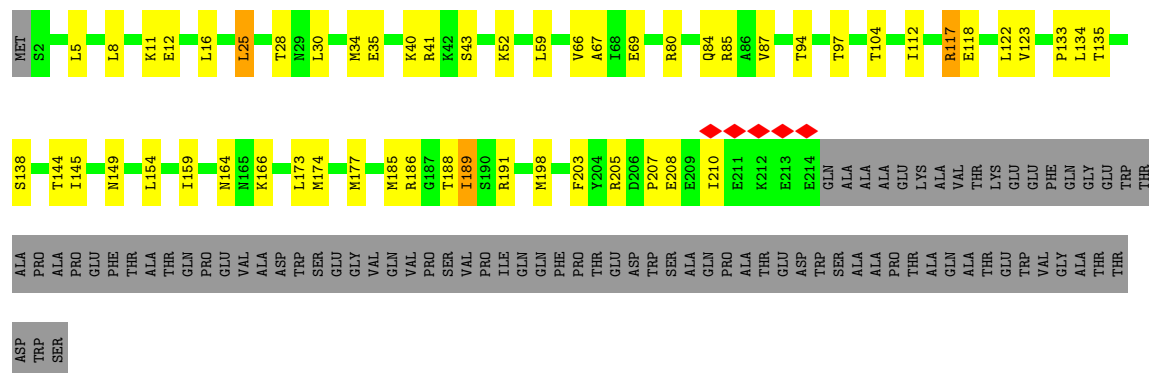


U800	G881	U954	A1060	G1157	U1243	C1303	U1377	U1441	U1509	C1572	G1635	C1698
U804	U882	A955	U1061	G1164	U1244	U1304	A1378	U1442	U1510	G1573	G1636	C1699
U805	C883	G956	A1062	G1165	G1245	C1305	A1379	U1443	U1511	G1574	A1637	C1703
A809	U885	G961	C1063	G1171	C1246	U1306	G1381	U1444	C1512	G1575	G1638	C1704
A810	U886	A962	C1078	G1172	C1247	U1307	A1382	U1445	C1513	G1576	G1639	C1705
A811	U887	A963	C1079	U1173	C1248	U1308	C1383	G1447	G1514	G1577	A1641	G1706
U814	U888	A964	A1080	U1174	A1250	C1309	C1384	A1448	G1515	U1578	U1642	U1711
U820	U889	U965	A1083	U1175	A1251	U1310	G1385	U1449	G1516	A1579	U1643	A1712
U821	G891	G970	A1084	G1176	A1252	C1311	A1386	G1450	G1517	A1580	U1644	A1713
U822	U892	G971	A1085	U1177	A1253	G1312	G1387	G1451	U1518	C1581	C1644	A1714
G824	U893	G894	C1085	U1178	A1254	A1313	A1388	A1452	U1519	C1582	C1645	U1715
A830	G895	A981	C1091	U1179	G1255	U1314	C1389	A1453	G1520	C1583	C1646	U1716
G831	U896	G982	C1098	A1181	G1256	C1315	U1390	A1454	C1521	U1586	A1647	C1717
C834	U897	G982	C1098	A1182	G1257	C1316	C1391	U1457	C1523	G1587	G1648	G1718
C	U898	G985	C1099	A1183	A1258	C1317	C1392	G1458	G1524	A1588	U1649	G1719
G	U899	G986	A1100	A1189	A1260	G1318	C1395	U1462	C1525	A1589	A1650	U1720
A	G901	A987	U1101	A1190	C1261	U1319	A1396	U1463	G1526	C1590	A1651	U1721
G	G902	U988	G1102	A1194	C1262	G1320	U1397	A1464	C1527	C1591	U1652	G1722
A	G903	C989	C1103	A1195	C1264	U1321	A1401	A1465	G1528	C1592	U1653	G1723
C	A904	C990	G1104	A1199	A1265	U1322	A1402	A1466	U1529	C1593	C1654	A1724
C	G905	A992	C1109	A1199	C1266	G1323	C1403	U1477	U1530	U1594	G1655	U1725
C	U906	A996	A1113	A1200	C1267	G1324	A1404	C1470	A1531	C1597	G1656	U1726
G841	G907	A997	U1114	U1201	C1268	G1325	A1405	C1471	C1532	G1598	U1667	U1727
A847	A908	U998	U1115	U1202	G1269	U1326	A1406	G1472	C1534	U1599	U1668	U1729
U848	G909	G999	U1116	G1207	G1270	G1327	U1407	G1473	U1535	G1600	A1661	U1730
A849	C912	U1002	C1117	C1215	G1271	G1328	U1408	U1474	U1536	A1601	U1662	A1731
A913	U914	G1005	U1118	C1216	C1272	U1329	A1409	G1475	U1537	U1602	A1663	G1732
C851	U918	C1006	U1119	C1217	C1273	U1330	C1410	U1476	U1538	G1604	A1664	U1733
G852	A919	G1010	U1120	A1217	C1274	G1331	G1413	U1477	G1540	G1605	C1666	U1734
U857	A920	A1011	U1121	C1218	G1275	U1332	A1414	A1480	G1541	G1606	U1667	C1739
G859	G921	U1012	U1122	C1219	C1276	U1333	C1415	U1481	C1542	U1607	U1668	C1740
G860	A922	U1013	U1123	C1220	C1277	G1334	C1416	G1482	U1543	C1608	G1669	A1745
A861	G925	U1016	C1124	A1220	C1278	G1335	C	A1483	U1544	A1483	C1670	A1746
U862	G926	U1017	G1130	G1221	C1279	U1336	C	U1485	A1545	U1485	G1671	U1747
U863	G928	A1023	A1133	G1222	C1280	C1337	C	U1486	G1548	U1486	U1672	U1748
A864	C930	A1024	C1138	G1223	G1281	U1338	A	U1489	U1549	G1489	U1673	C1753
U865	G933	U1025	C1139	G1224	C1282	U1339	C	G1490	U1550	G1490	G1674	G1754
G867	G934	C1026	G1140	G1225	A1283	U1340	C	G1491	U1551	U1551	A1675	G1755
U868	G935	A1030	U1141	G1226	C1284	C1341	C	U1492	C1552	U1616	U1676	C1756
A869	U940	A1031	G1142	G1227	A1285	U1342	G1424	G1493	C1553	G1617	A1677	G1757
U870	C941	A1032	A1143	A1228	G1286	U1343	G1425	U1494	C1554	C1618	A1678	G1758
A871	G942	C1032	A1144	G1229	G1287	A1344	U1426	G1495	U1555	A1619	G1680	G1759
G873	U943	G1033	C1146	G1230	C1288	U1345	G1427	U1496	U1556	A1620	U1681	G1760
G874	A944	U1037	C1147	G1231	C1289	G1348	G1428	U1497	A1557	U1621	C1682	U1761
A875	U945	G1047	A1148	C1232	U1289	U1349	G1429	U1498	C1558	U1622	C1683	C
C877	U946	G1048	A1149	C1237	G1290	G1354	C1430	U1499	U1559	A1623	C1684	G
G878	G952	U1050	A1150	U1239	C1291	U1357	U1432	G1500	U1560	U1624	U1685	G
C879	C953	C1047	C1153	A1240	C1292	A1357	C	C1501	C1561	U1625	C1686	C
G880		G1047	U1154	A1241	G1293	U1358	C	C1502	G1562	C1626	C1687	C
				U1242	C1294	G1365	C	U1504	G1563	C1627	C1688	A
					A1295	G1366	C	U1505	G1567	C1628	U1689	C
					U1296	U1371	A1438	U1506	C1568	C1629	U1692	G
					U1297	U1372	A1439	A1507	A1569	A1630	G1693	G1771
					U1298	C1373	C	G1507	G1570	U1633	U1694	C1772
					G1299	G1374	A1439			A1634	A1695	C1773
					U1300	A1376	C					
					A1301							
					G1302							



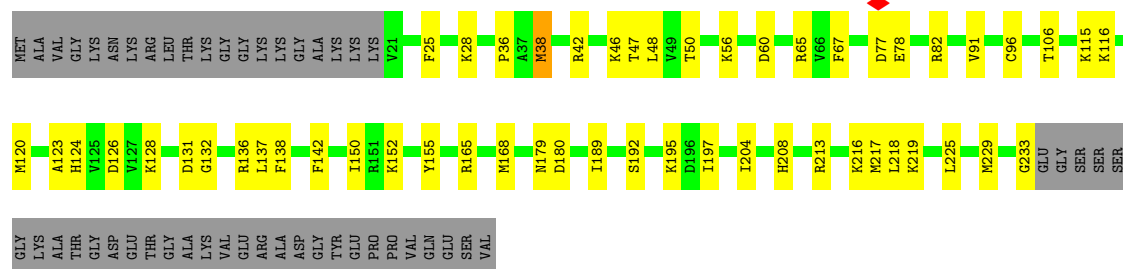
• Molecule 2: Small ribosomal subunit protein uS2

Chain A: 54% 18% 28%



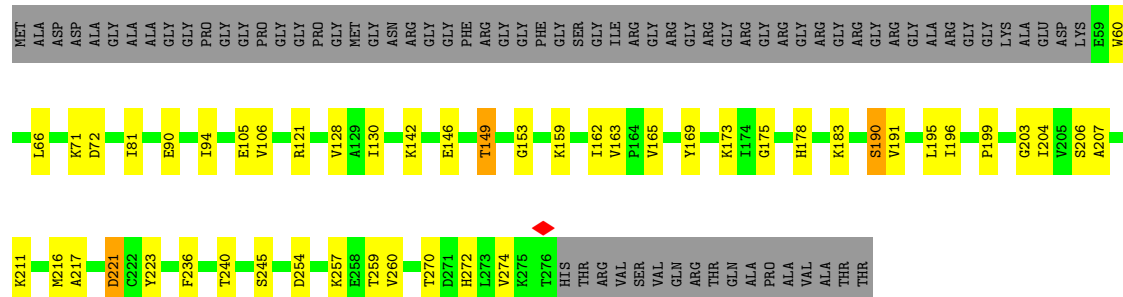
• Molecule 3: Small ribosomal subunit protein eS1

Chain B: 61% 20% 19%

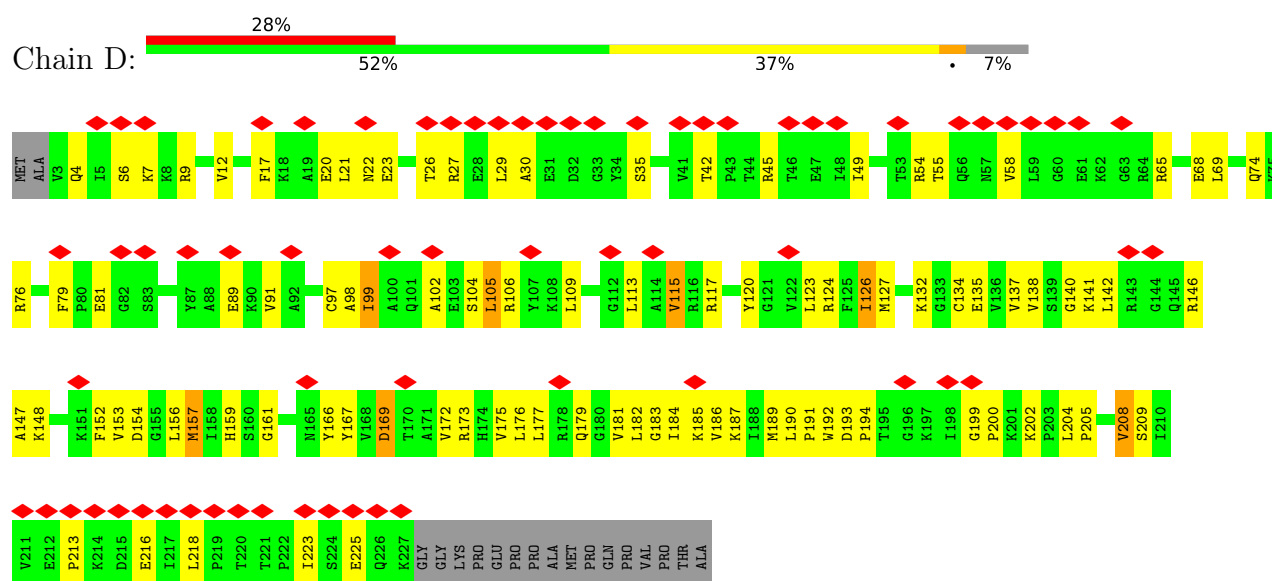


• Molecule 4: Small ribosomal subunit protein uS5

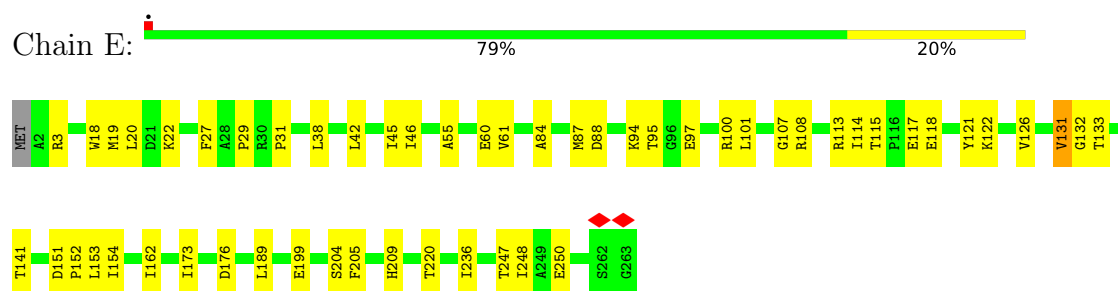
Chain C: 58% 16% 26%



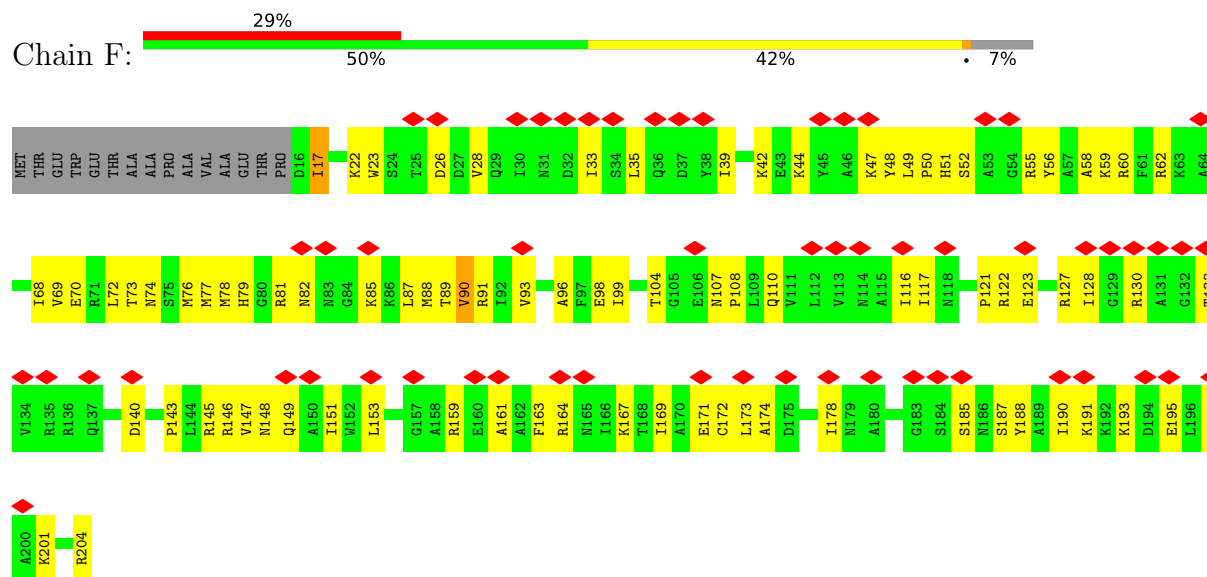
• Molecule 5: Small ribosomal subunit protein uS3



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

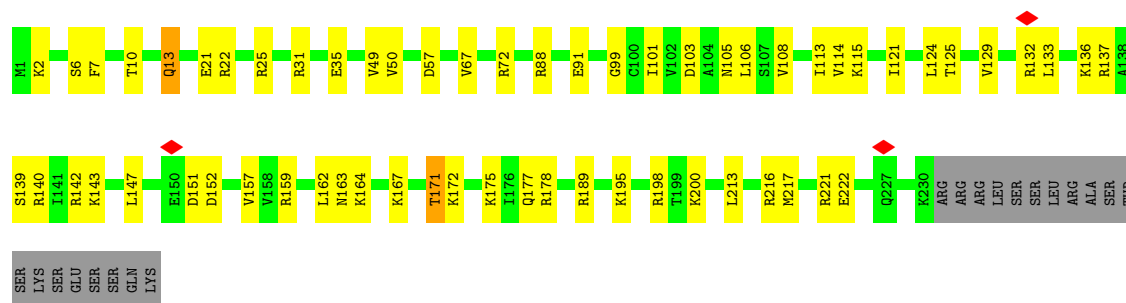


- Molecule 7: Small ribosomal subunit protein uS7

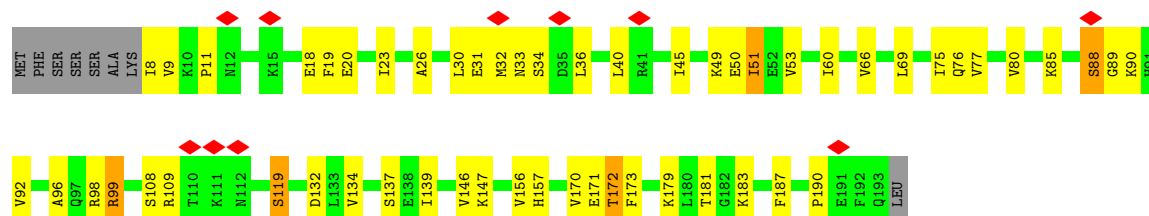


- Molecule 8: Small ribosomal subunit protein eS6

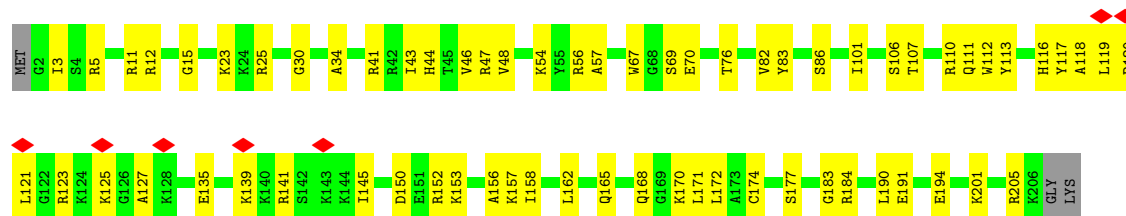




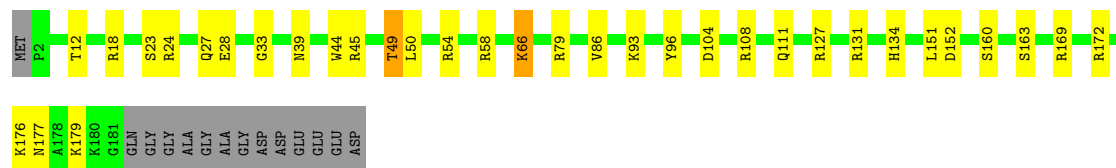
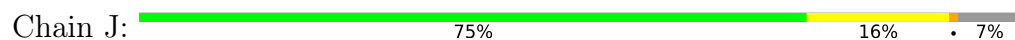
- Molecule 9: Small ribosomal subunit protein eS7



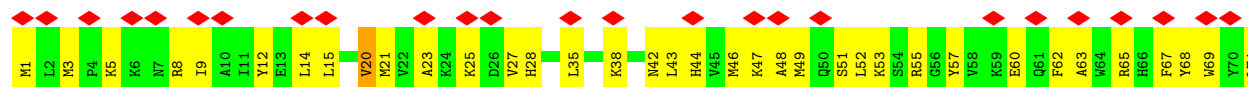
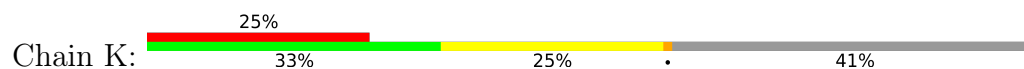
- Molecule 10: Small ribosomal subunit protein eS8

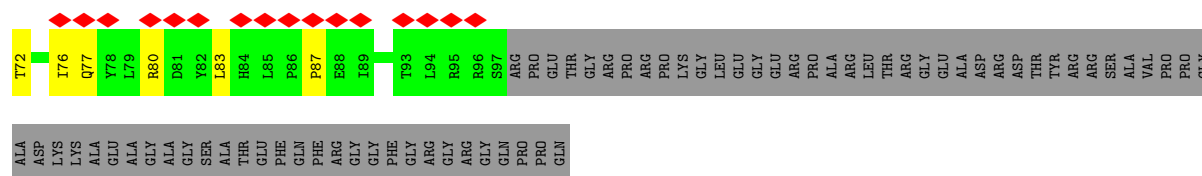


- Molecule 11: Small ribosomal subunit protein uS4

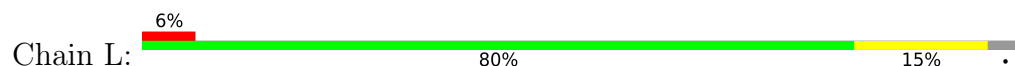


- Molecule 12: Small ribosomal subunit protein eS10

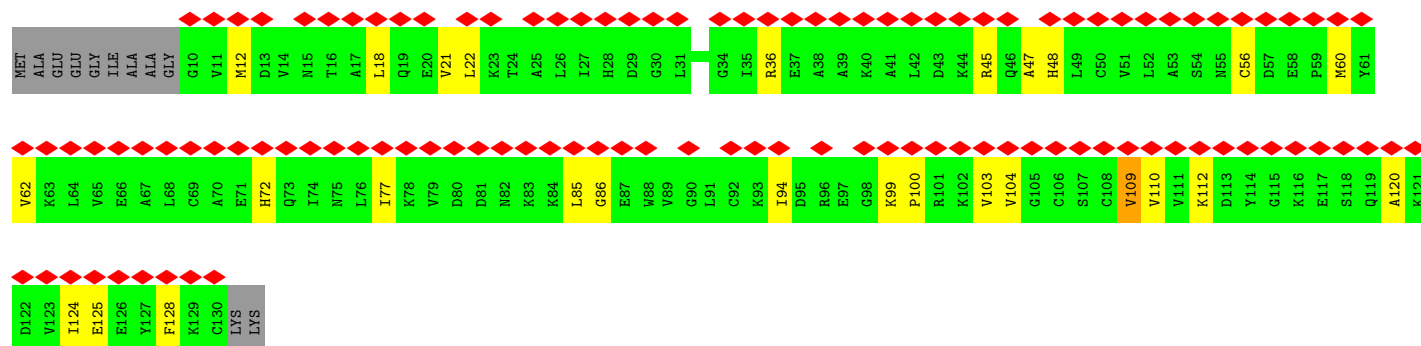
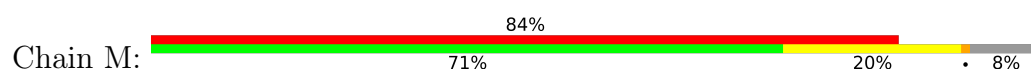




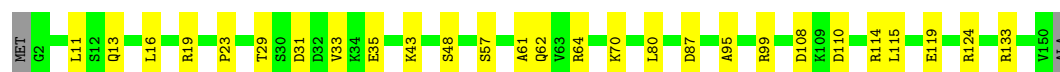
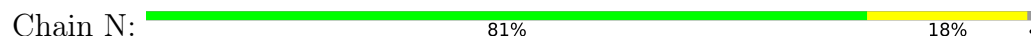
- Molecule 13: Small ribosomal subunit protein uS17



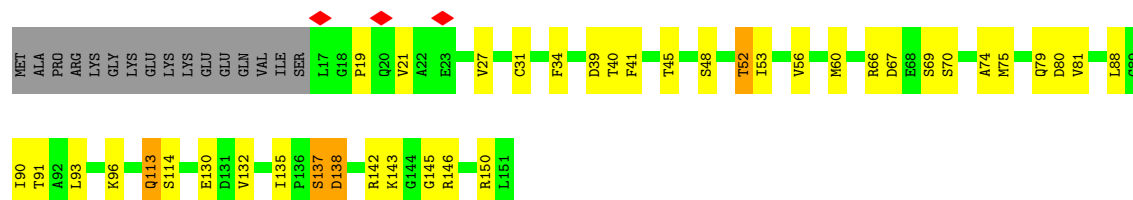
- Molecule 14: Small ribosomal subunit protein eS12



- Molecule 15: Small ribosomal subunit protein uS15

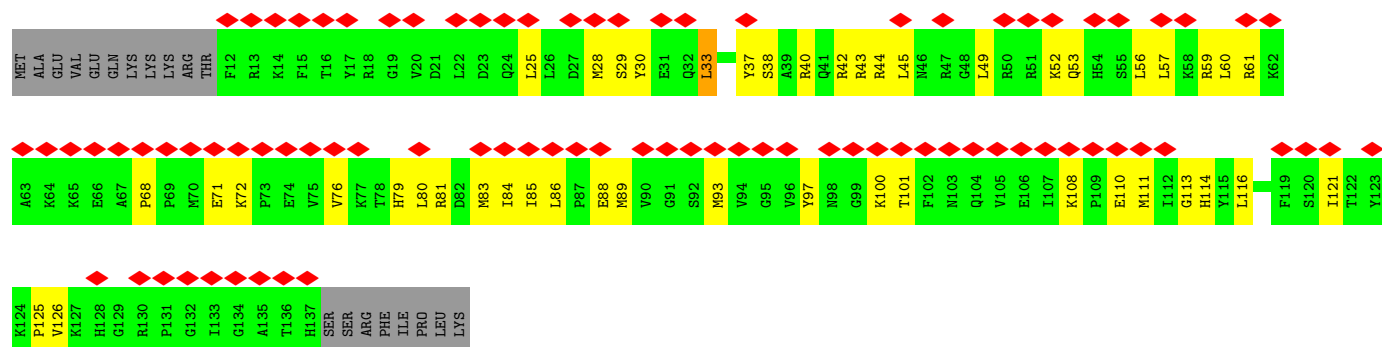


- Molecule 16: Small ribosomal subunit protein uS11

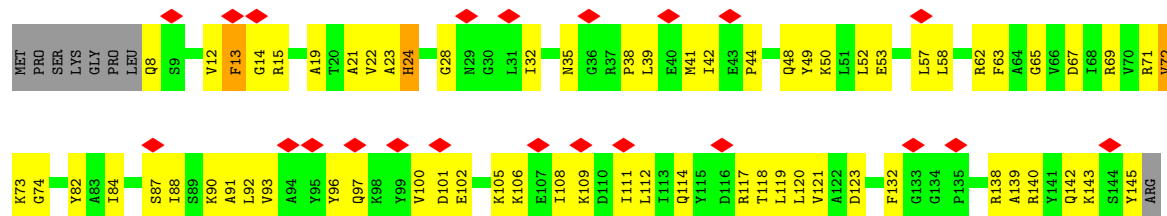


- Molecule 17: Small ribosomal subunit protein uS19

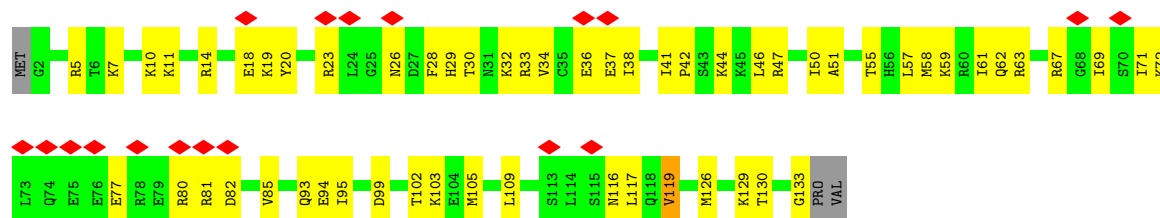




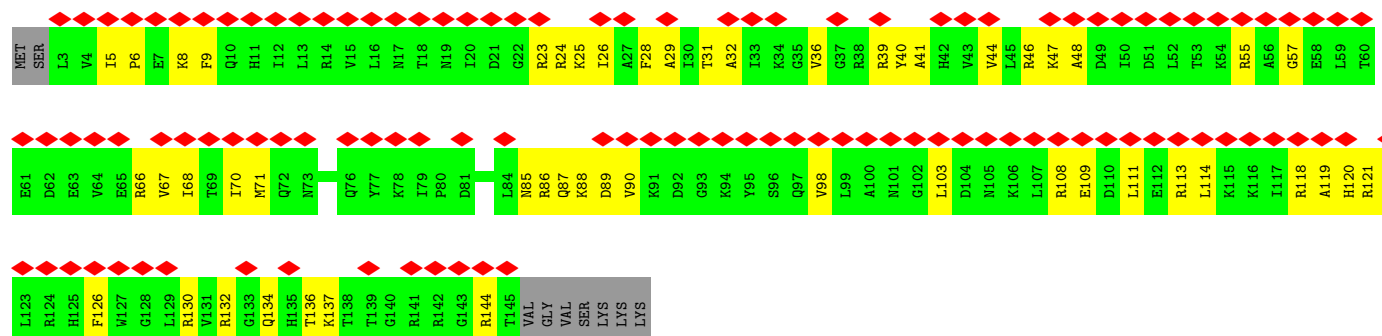
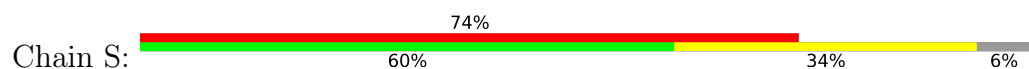
- Molecule 18: Small ribosomal subunit protein uS9



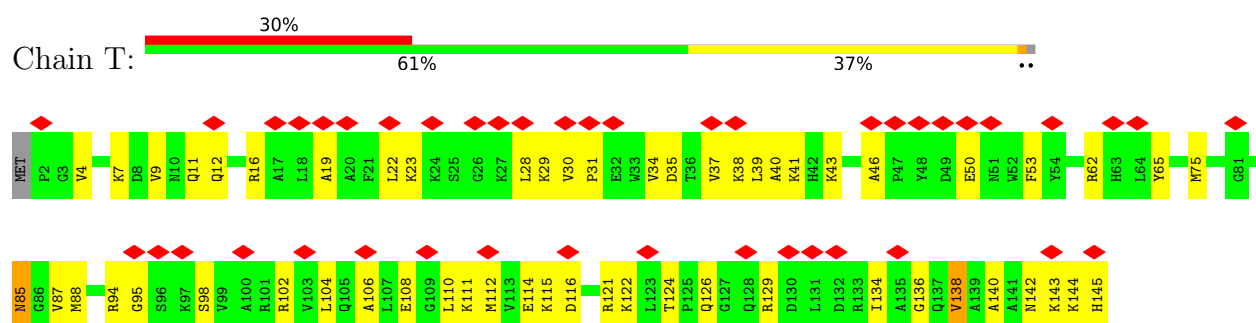
- Molecule 19: Small ribosomal subunit protein eS17



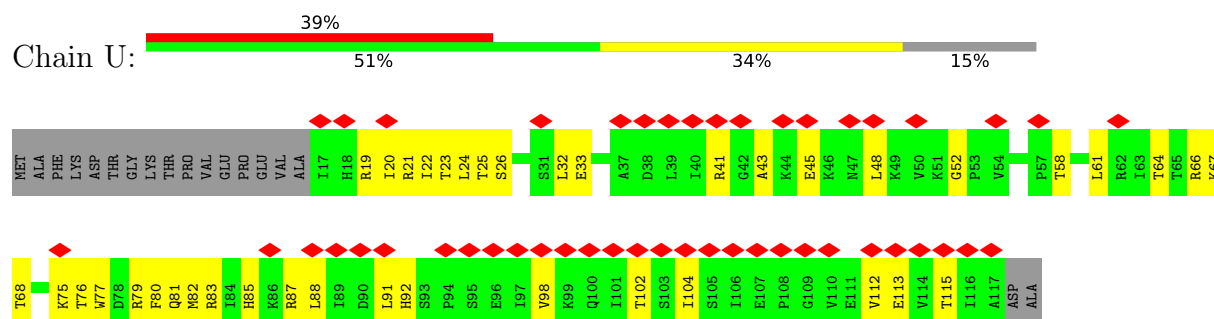
- Molecule 20: Small ribosomal subunit protein uS13



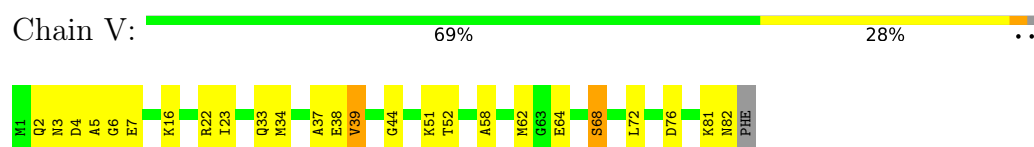
- Molecule 21: Small ribosomal subunit protein eS19



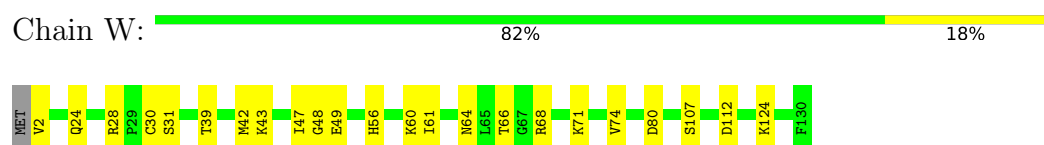
- Molecule 22: Small ribosomal subunit protein uS10



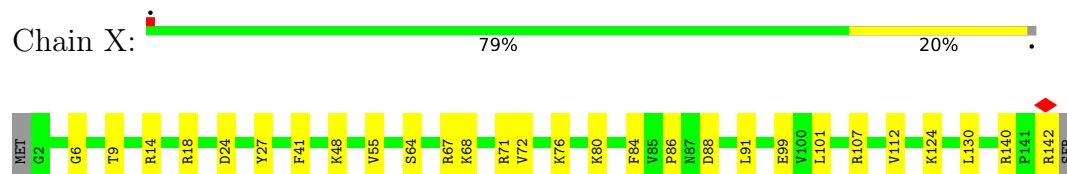
- Molecule 23: Small ribosomal subunit protein eS21



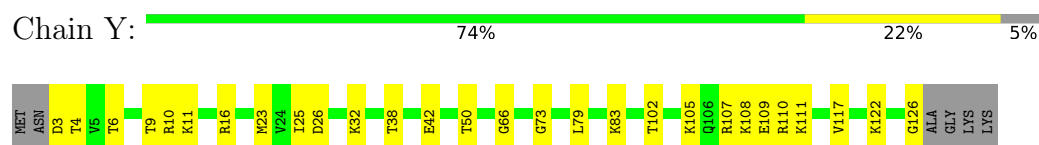
- Molecule 24: Small ribosomal subunit protein uS8



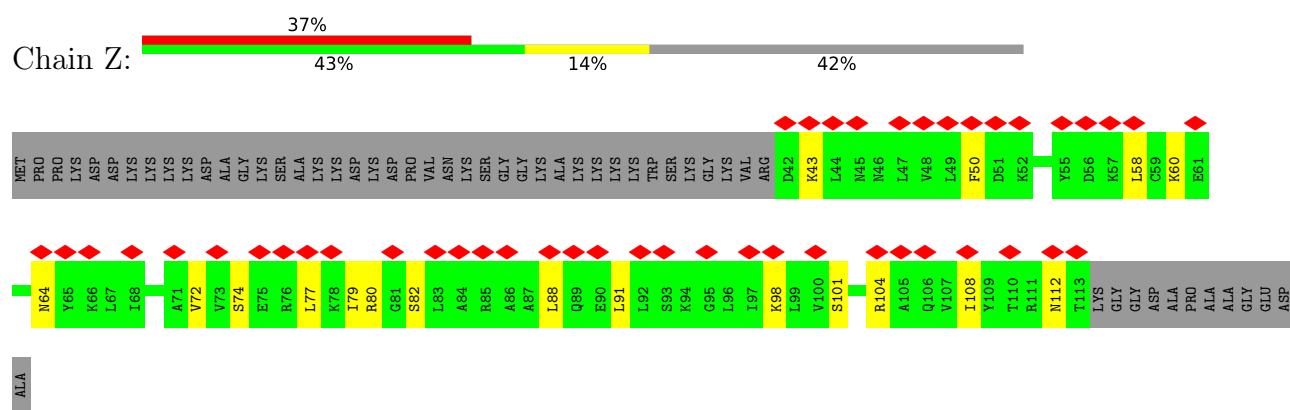
- Molecule 25: Small ribosomal subunit protein uS12



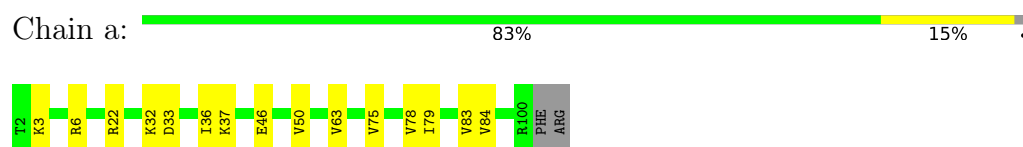
- Molecule 26: Small ribosomal subunit protein eS24



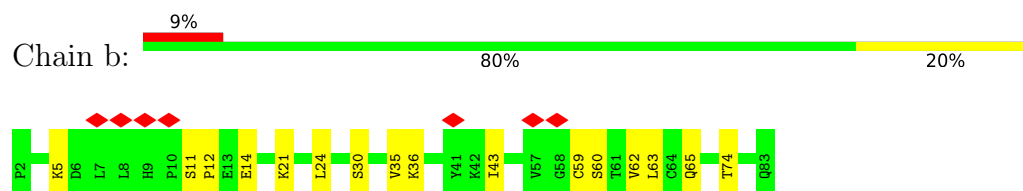
- Molecule 27: Small ribosomal subunit protein eS25



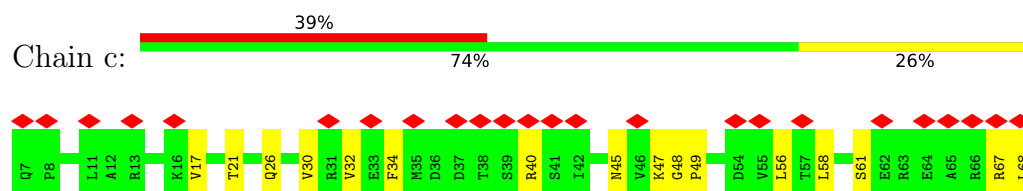
- Molecule 28: Small ribosomal subunit protein eS26



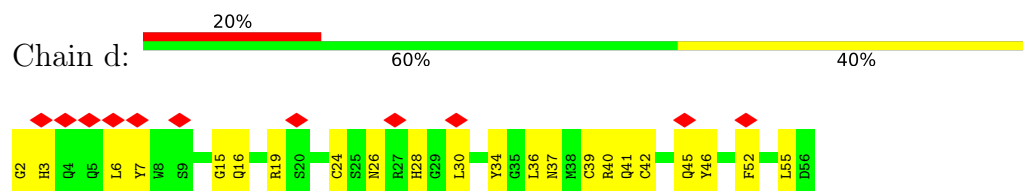
- Molecule 29: Small ribosomal subunit protein eS27



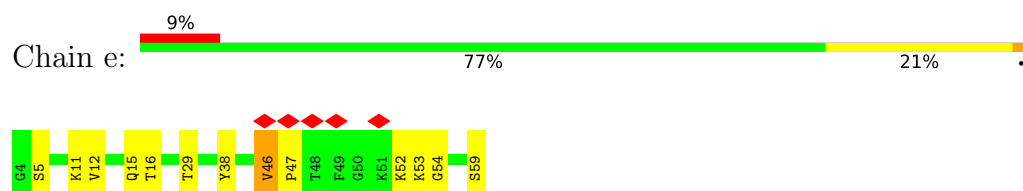
- Molecule 30: Small ribosomal subunit protein eS28



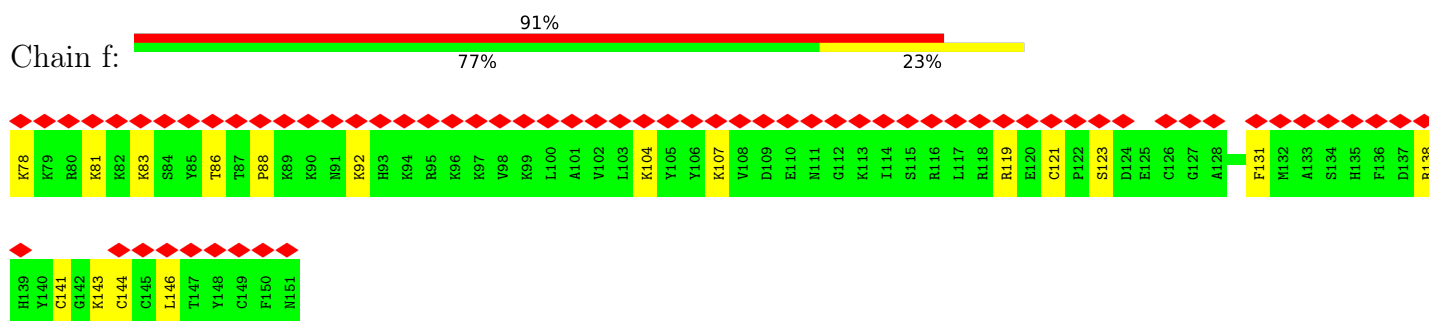
- Molecule 31: Small ribosomal subunit protein uS14



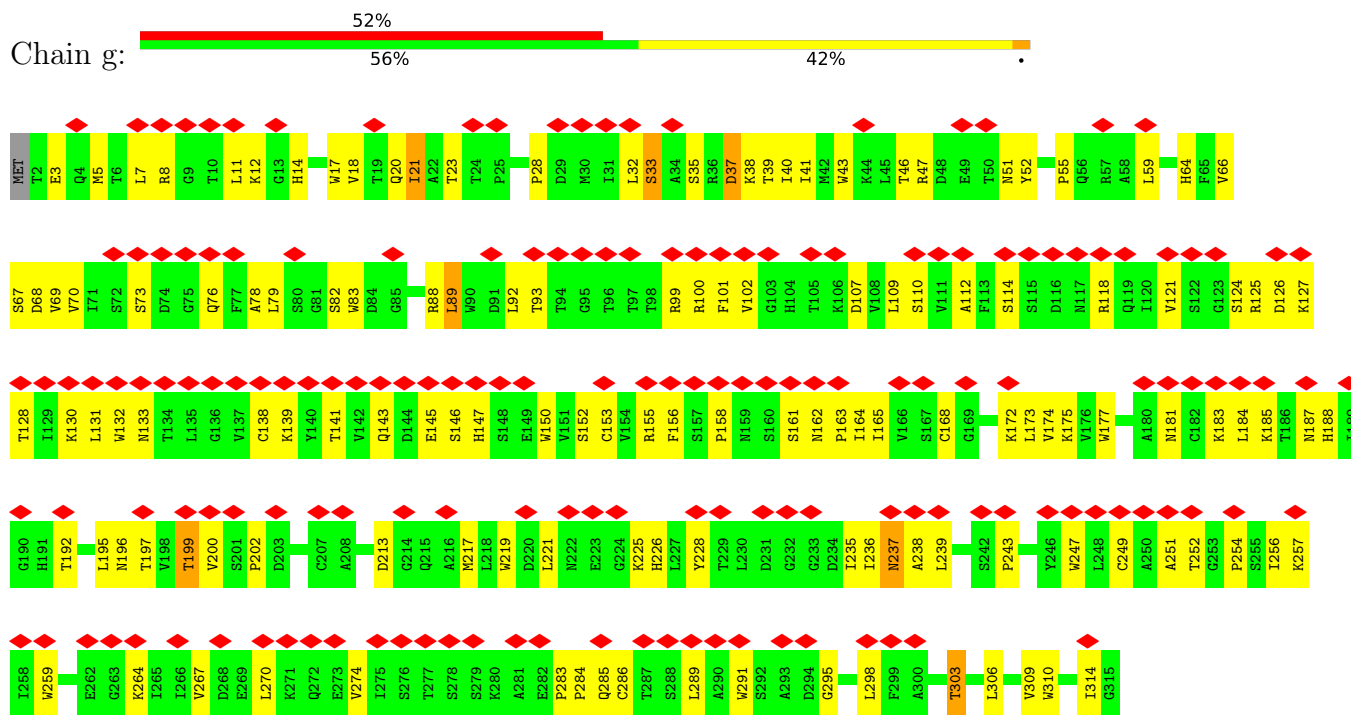
- Molecule 32: Small ribosomal subunit protein eS30



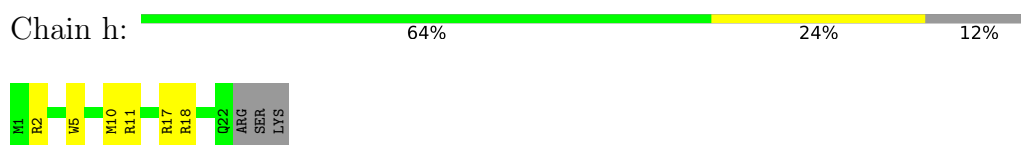
- Molecule 33: Small ribosomal subunit protein eS31



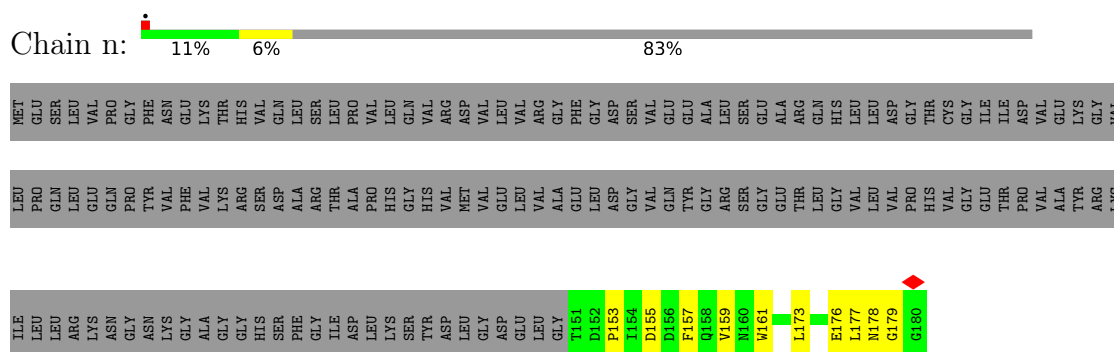
• Molecule 34: Small ribosomal subunit protein RACK1



• Molecule 35: Small ribosomal subunit protein eS32



• Molecule 36: ORF1ab polypeptide



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	57459	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	2.348	Depositor
Minimum map value	-0.994	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.053	Depositor
Recommended contour level	0.158	Depositor
Map size (Å)	486.4, 486.4, 486.4	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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	0.21	0/39865	0.30	2/62134 (0.0%)
2	A	0.19	0/1723	0.30	0/2341
3	B	0.18	0/1756	0.33	0/2350
4	C	0.22	0/1726	0.37	0/2332
5	D	0.16	0/1780	0.42	0/2397
6	E	0.22	0/2118	0.33	0/2849
7	F	0.18	0/1516	0.50	0/2037
8	G	0.18	0/1887	0.35	0/2513
9	H	0.17	0/1524	0.36	0/2042
10	I	0.19	0/1711	0.38	0/2282
11	J	0.21	0/1524	0.29	0/2035
12	K	0.13	0/840	0.39	0/1133
13	L	0.22	0/1250	0.33	0/1673
14	M	0.11	0/945	0.34	0/1269
15	N	0.18	0/1226	0.28	0/1649
16	O	0.19	0/1023	0.32	0/1372
17	P	0.15	0/1058	0.40	0/1414
18	Q	0.14	0/1114	0.40	0/1492
19	R	0.14	0/1082	0.34	0/1452
20	S	0.12	0/1202	0.40	0/1610
21	T	0.17	0/1143	0.41	0/1530
22	U	0.12	0/813	0.35	0/1092
23	V	0.18	0/631	0.32	0/844
24	W	0.23	0/1051	0.32	0/1406
25	X	0.21	0/1116	0.32	0/1490
26	Y	0.21	0/1031	0.35	0/1370
27	Z	0.12	0/580	0.38	0/780
28	a	0.20	0/807	0.35	0/1082
29	b	0.22	0/654	0.46	1/876 (0.1%)
30	c	0.13	0/491	0.36	0/656
31	d	0.12	0/470	0.39	0/623
32	e	0.19	0/447	0.47	0/587
33	f	0.11	0/623	0.32	0/822
34	g	0.13	0/2498	0.38	1/3399 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	h	0.16	0/214	0.32	0/272
36	n	0.21	0/242	0.36	0/325
All	All	0.20	0/79681	0.33	4/115530 (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
16	O	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1501	C	OP1-P-O3'	6.31	126.92	108.00
29	b	12	PRO	CA-N-CD	-5.53	104.26	112.00
1	2	1244	U	OP2-P-O3'	5.15	123.44	108.00
34	g	37	ASP	N-CA-C	-5.07	107.59	112.97

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
16	O	137	SER	Peptide

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	35647	0	18022	611	0
2	A	1686	0	1688	37	0
3	B	1729	0	1803	35	0
4	C	1690	0	1777	30	0
5	D	1752	0	1848	77	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	E	2076	0	2177	32	0
7	F	1495	0	1549	86	0
8	G	1864	0	2018	43	0
9	H	1501	0	1593	34	0
10	I	1682	0	1769	58	0
11	J	1499	0	1618	24	0
12	K	816	0	841	40	0
13	L	1229	0	1302	18	0
14	M	935	0	964	15	0
15	N	1202	0	1289	17	0
16	O	1010	0	1034	29	0
17	P	1037	0	1082	47	0
18	Q	1097	0	1161	54	0
19	R	1068	0	1121	39	0
20	S	1184	0	1244	42	0
21	T	1123	0	1153	49	0
22	U	803	0	873	31	0
23	V	625	0	628	16	0
24	W	1034	0	1080	17	0
25	X	1098	0	1167	18	0
26	Y	1014	0	1082	18	0
27	Z	574	0	627	13	0
28	a	794	0	849	14	0
29	b	641	0	665	8	0
30	c	489	0	514	15	0
31	d	459	0	452	25	0
32	e	442	0	487	11	0
33	f	611	0	638	14	0
34	g	2441	0	2396	99	0
35	h	213	0	258	8	0
36	n	238	0	219	6	0
All	All	74798	0	58988	1452	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 11.

The worst 5 of 1452 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)
1:2:191:A:H62	1:2:208:G:N2	1.61	0.98
1:2:1656:G:H1	1:2:1668:U:H3	1.00	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1091:C:HO2'	24:W:2:VAL:N	1.61	0.97
1:2:1033:G:H1	1:2:1080:A:HO2'	1.15	0.94
1:2:1290:G:H1	1:2:1301:A:HO2'	1.05	0.93

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A	211/295 (72%)	205 (97%)	5 (2%)	1 (0%)	25	41
3	B	211/264 (80%)	204 (97%)	7 (3%)	0	100	100
4	C	216/293 (74%)	211 (98%)	5 (2%)	0	100	100
5	D	223/243 (92%)	220 (99%)	3 (1%)	0	100	100
6	E	260/263 (99%)	251 (96%)	9 (4%)	0	100	100
7	F	187/204 (92%)	170 (91%)	16 (9%)	1 (0%)	25	41
8	G	228/249 (92%)	221 (97%)	7 (3%)	0	100	100
9	H	184/194 (95%)	174 (95%)	8 (4%)	2 (1%)	12	21
10	I	203/208 (98%)	194 (96%)	9 (4%)	0	100	100
11	J	178/194 (92%)	172 (97%)	5 (3%)	1 (1%)	22	37
12	K	95/165 (58%)	90 (95%)	5 (5%)	0	100	100
13	L	149/158 (94%)	142 (95%)	6 (4%)	1 (1%)	19	33
14	M	119/132 (90%)	110 (92%)	6 (5%)	3 (2%)	4	7
15	N	147/151 (97%)	145 (99%)	2 (1%)	0	100	100
16	O	133/151 (88%)	128 (96%)	5 (4%)	0	100	100
17	P	124/145 (86%)	112 (90%)	12 (10%)	0	100	100
18	Q	136/146 (93%)	127 (93%)	8 (6%)	1 (1%)	19	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	R	130/135 (96%)	127 (98%)	3 (2%)	0	100	100
20	S	141/152 (93%)	124 (88%)	17 (12%)	0	100	100
21	T	142/145 (98%)	136 (96%)	6 (4%)	0	100	100
22	U	99/119 (83%)	94 (95%)	5 (5%)	0	100	100
23	V	80/83 (96%)	80 (100%)	0	0	100	100
24	W	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
25	X	139/143 (97%)	137 (99%)	2 (1%)	0	100	100
26	Y	122/130 (94%)	121 (99%)	1 (1%)	0	100	100
27	Z	70/125 (56%)	64 (91%)	6 (9%)	0	100	100
28	a	97/101 (96%)	95 (98%)	1 (1%)	1 (1%)	13	23
29	b	80/82 (98%)	75 (94%)	5 (6%)	0	100	100
30	c	60/62 (97%)	57 (95%)	3 (5%)	0	100	100
31	d	53/55 (96%)	48 (91%)	5 (9%)	0	100	100
32	e	54/56 (96%)	53 (98%)	1 (2%)	0	100	100
33	f	72/74 (97%)	60 (83%)	12 (17%)	0	100	100
34	g	312/315 (99%)	278 (89%)	32 (10%)	2 (1%)	22	37
35	h	20/25 (80%)	20 (100%)	0	0	100	100
36	n	28/180 (16%)	28 (100%)	0	0	100	100
All	All	4830/5567 (87%)	4595 (95%)	222 (5%)	13 (0%)	38	55

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	189	ILE
9	H	171	GLU
28	a	63	VAL
14	M	110	VAL
9	H	88	SER

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%)	169 (94%)	10 (6%)	17	32
3	B	194/231 (84%)	186 (96%)	8 (4%)	26	45
4	C	184/225 (82%)	177 (96%)	7 (4%)	28	48
5	D	189/202 (94%)	176 (93%)	13 (7%)	13	23
6	E	224/225 (100%)	215 (96%)	9 (4%)	27	46
7	F	159/170 (94%)	155 (98%)	4 (2%)	42	63
8	G	200/218 (92%)	192 (96%)	8 (4%)	27	46
9	H	167/174 (96%)	158 (95%)	9 (5%)	18	33
10	I	178/180 (99%)	177 (99%)	1 (1%)	84	90
11	J	160/168 (95%)	158 (99%)	2 (1%)	65	80
12	K	88/136 (65%)	85 (97%)	3 (3%)	32	53
13	L	135/142 (95%)	134 (99%)	1 (1%)	81	89
14	M	102/108 (94%)	100 (98%)	2 (2%)	50	69
15	N	130/131 (99%)	126 (97%)	4 (3%)	35	56
16	O	105/119 (88%)	98 (93%)	7 (7%)	13	24
17	P	112/130 (86%)	110 (98%)	2 (2%)	54	72
18	Q	114/121 (94%)	109 (96%)	5 (4%)	24	42
19	R	119/122 (98%)	112 (94%)	7 (6%)	16	29
20	S	124/132 (94%)	122 (98%)	2 (2%)	58	75
21	T	114/115 (99%)	111 (97%)	3 (3%)	41	62
22	U	93/107 (87%)	92 (99%)	1 (1%)	70	83
23	V	66/67 (98%)	63 (96%)	3 (4%)	23	41
24	W	112/113 (99%)	111 (99%)	1 (1%)	75	86
25	X	113/115 (98%)	110 (97%)	3 (3%)	40	60
26	Y	108/112 (96%)	105 (97%)	3 (3%)	38	59
27	Z	64/103 (62%)	63 (98%)	1 (2%)	58	75
28	a	87/89 (98%)	86 (99%)	1 (1%)	70	83
29	b	74/74 (100%)	73 (99%)	1 (1%)	62	78
30	c	55/55 (100%)	54 (98%)	1 (2%)	54	72
31	d	48/48 (100%)	47 (98%)	1 (2%)	48	69
32	e	45/45 (100%)	42 (93%)	3 (7%)	13	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	f	67/67 (100%)	65 (97%)	2 (3%)	36	57
34	g	272/273 (100%)	257 (94%)	15 (6%)	18	32
35	h	21/24 (88%)	21 (100%)	0	100	100
36	n	26/150 (17%)	26 (100%)	0	100	100
All	All	4228/4734 (89%)	4085 (97%)	143 (3%)	34	53

5 of 143 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
26	Y	4	THR
28	a	3	LYS
34	g	23	THR
7	F	90	VAL
7	F	17	ILE

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

Mol	Chain	Res	Type
19	R	116	ASN
30	c	45	ASN
20	S	105	ASN
26	Y	15	ASN
31	d	26	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1661/1869 (88%)	511 (30%)	23 (1%)

5 of 511 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	17	C
1	2	26	U
1	2	33	G

5 of 23 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	1409	A
1	2	1464	C
1	2	1428	G
1	2	1517	G
1	2	559	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](#)

There are no chain breaks in this entry.

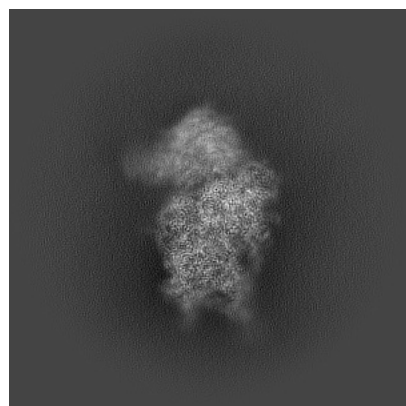
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62447. These allow visual inspection of the internal detail of the map and identification of artifacts.

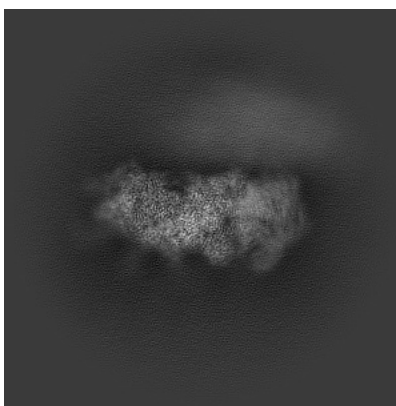
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

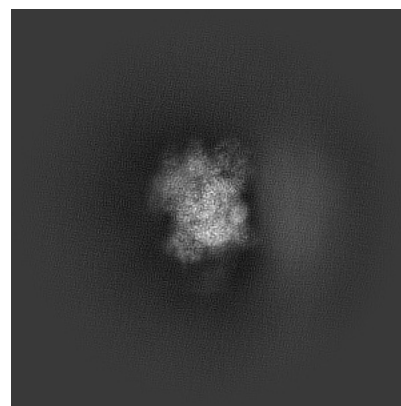
6.1.1 Primary map



X

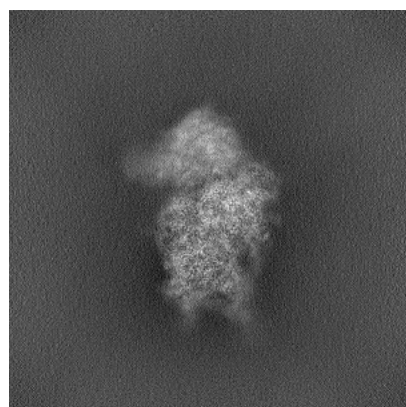


Y

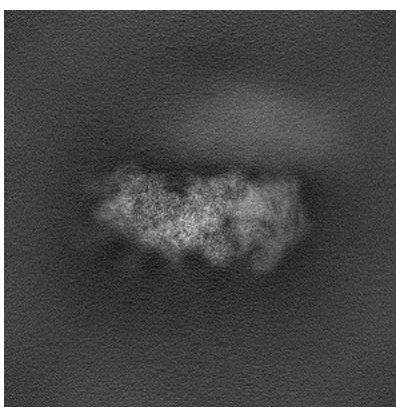


Z

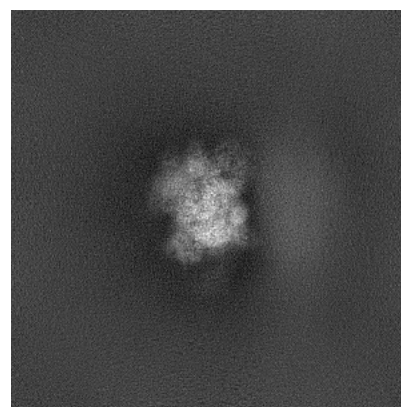
6.1.2 Raw map



X



Y

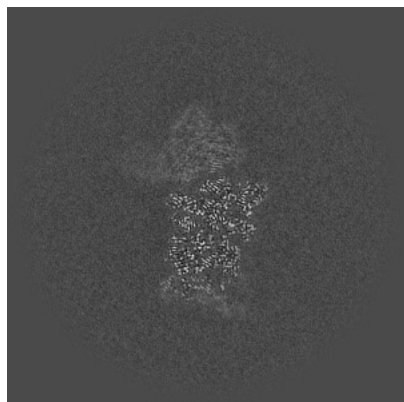


Z

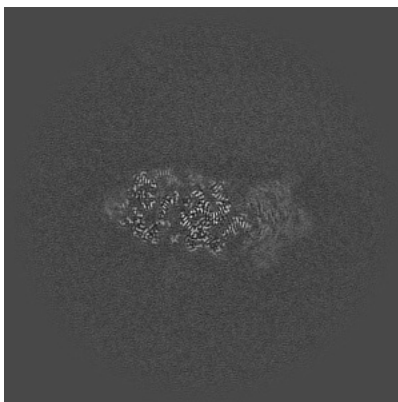
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

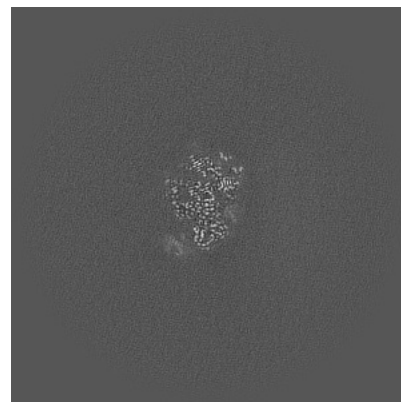
6.2.1 Primary map



X Index: 256

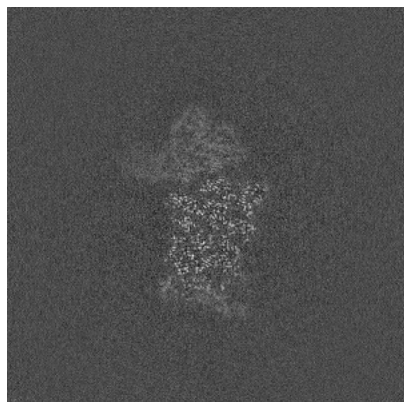


Y Index: 256

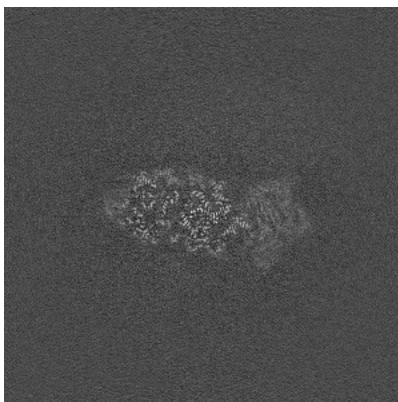


Z Index: 256

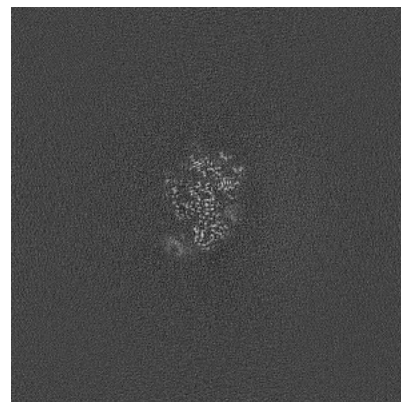
6.2.2 Raw map



X Index: 256



Y Index: 256

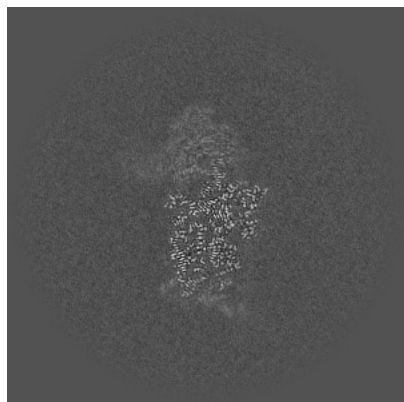


Z Index: 256

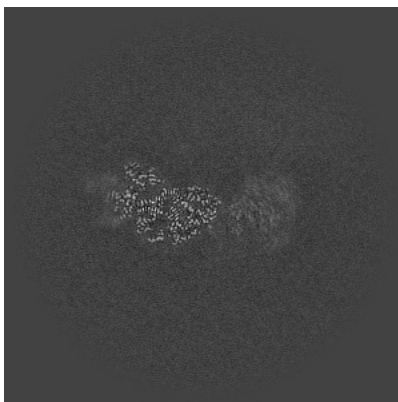
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

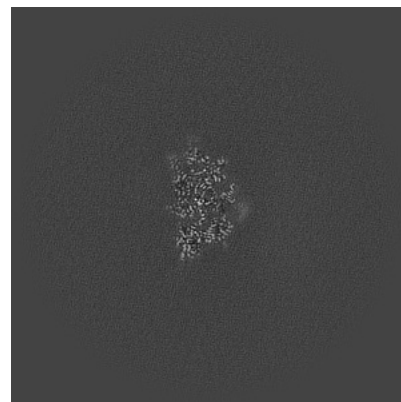
6.3.1 Primary map



X Index: 252

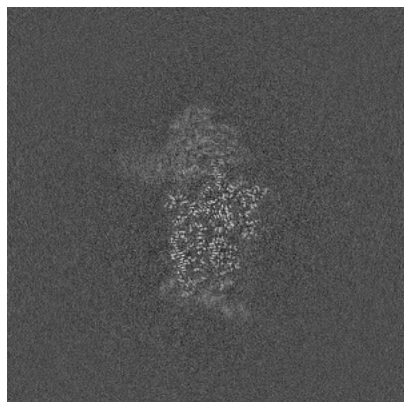


Y Index: 224

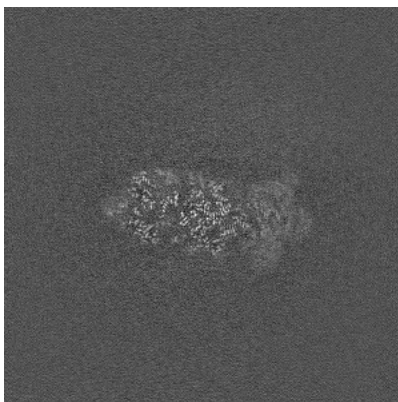


Z Index: 237

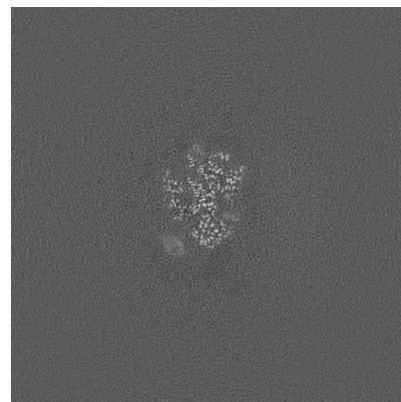
6.3.2 Raw map



X Index: 252



Y Index: 257

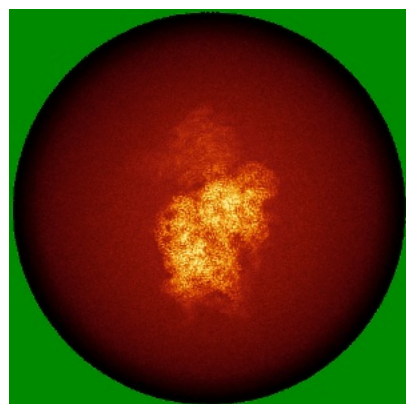


Z Index: 260

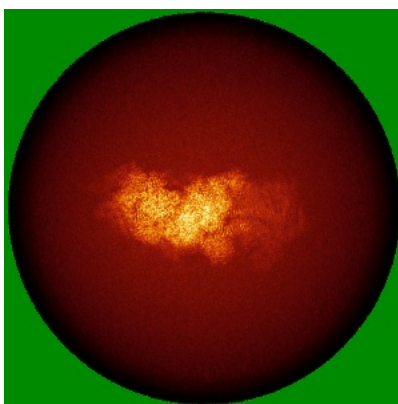
The images above show the largest variance slices of the map in three orthogonal directions.

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

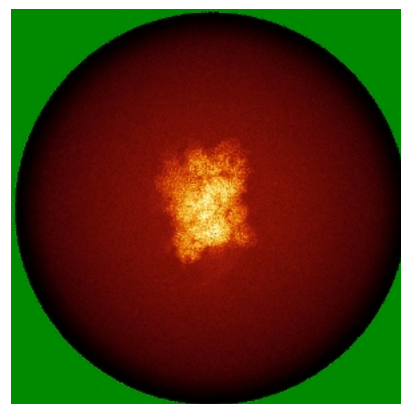
6.4.1 Primary map



X

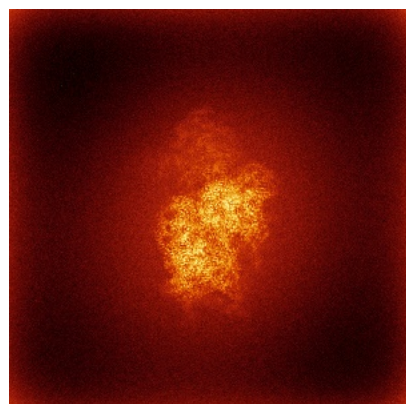


Y

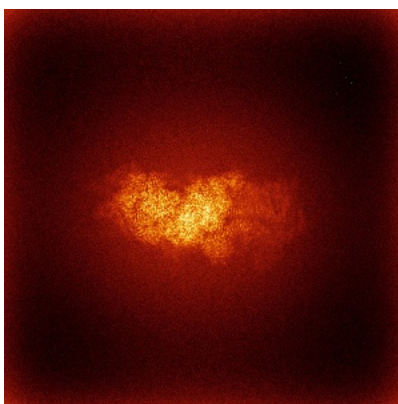


Z

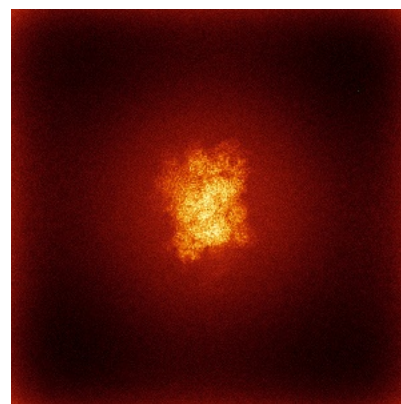
6.4.2 Raw map



X



Y

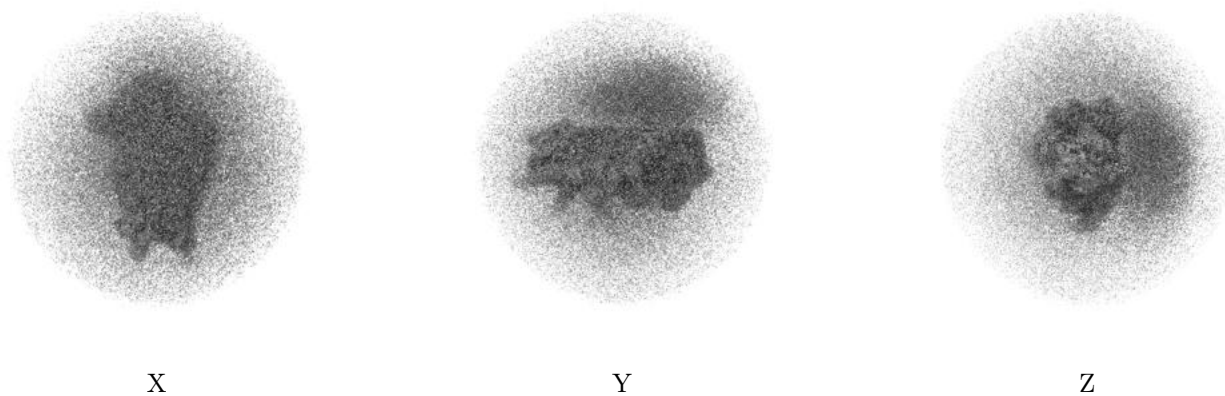


Z

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.

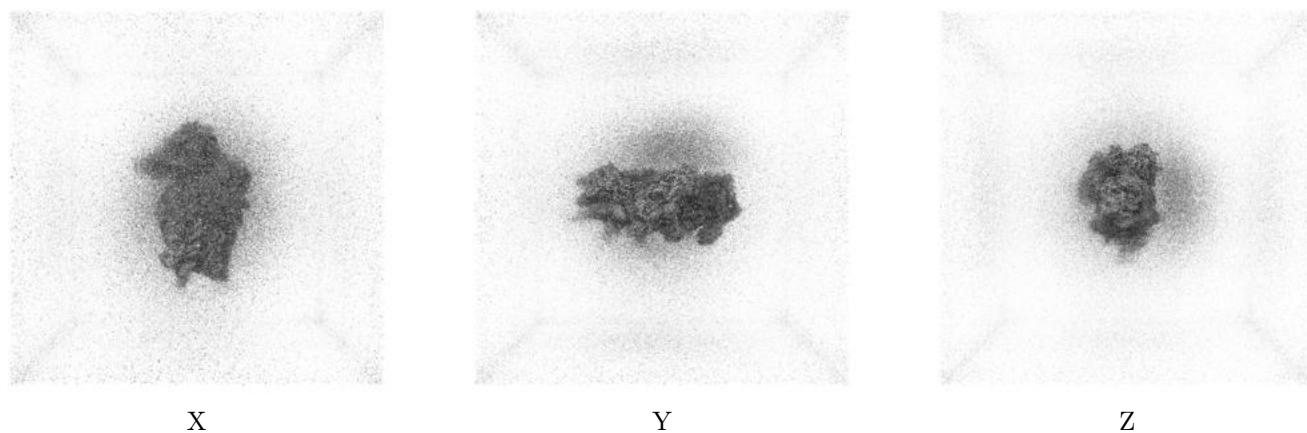
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.158. 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.

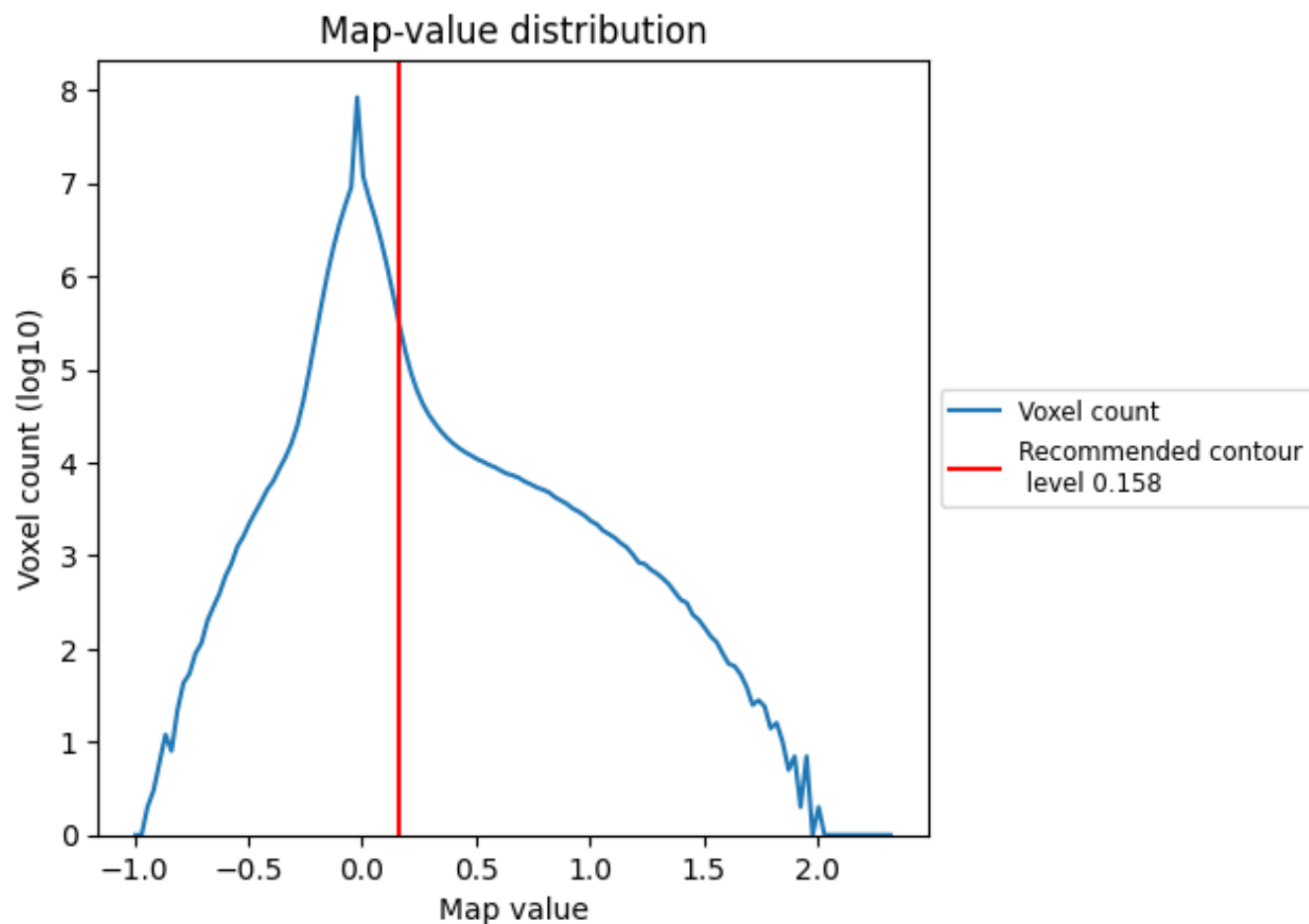
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

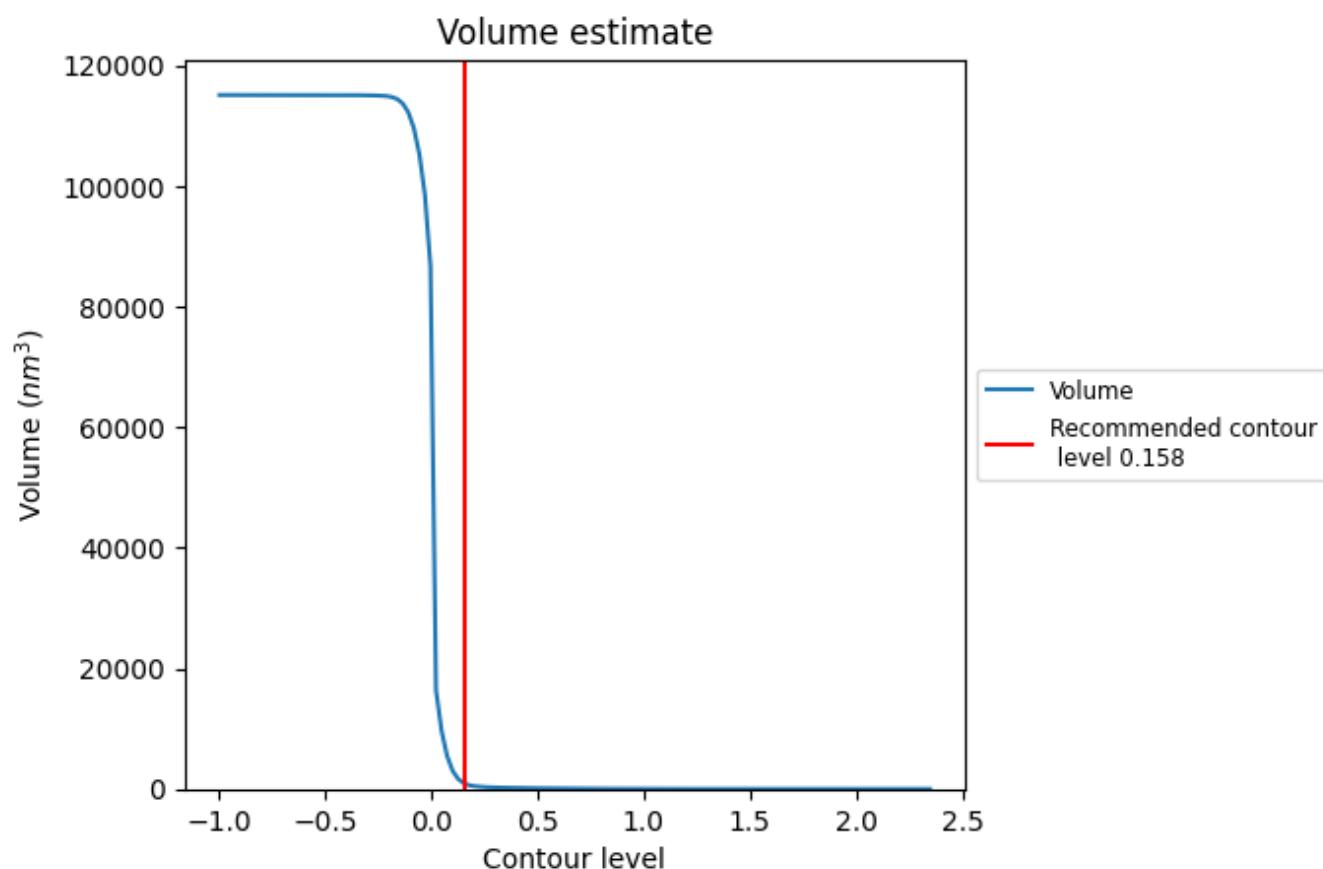
This section contains the results of statistical analysis of the map.

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.

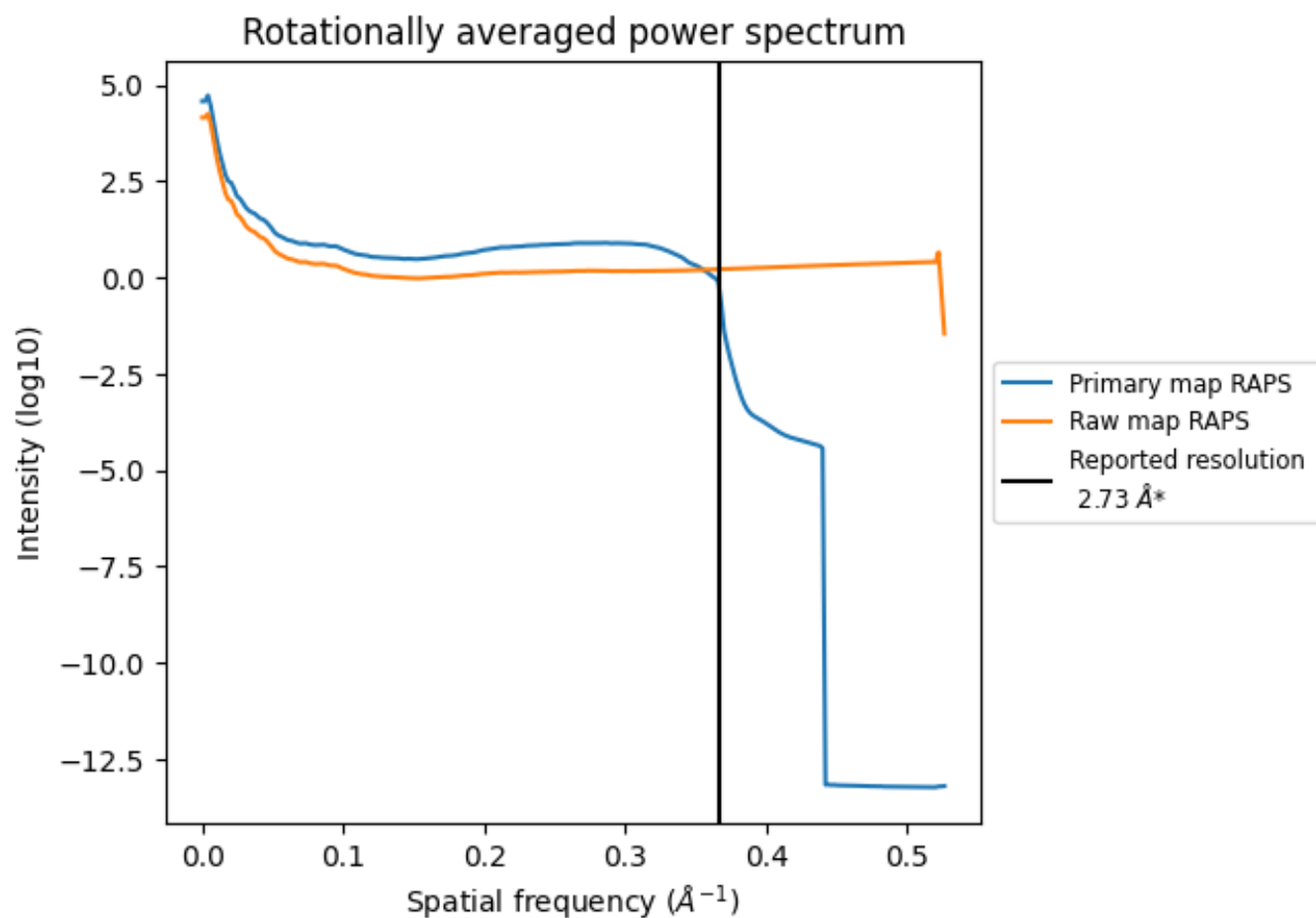
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 919 nm^3 ; this corresponds to an approximate mass of 831 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 ⓘ

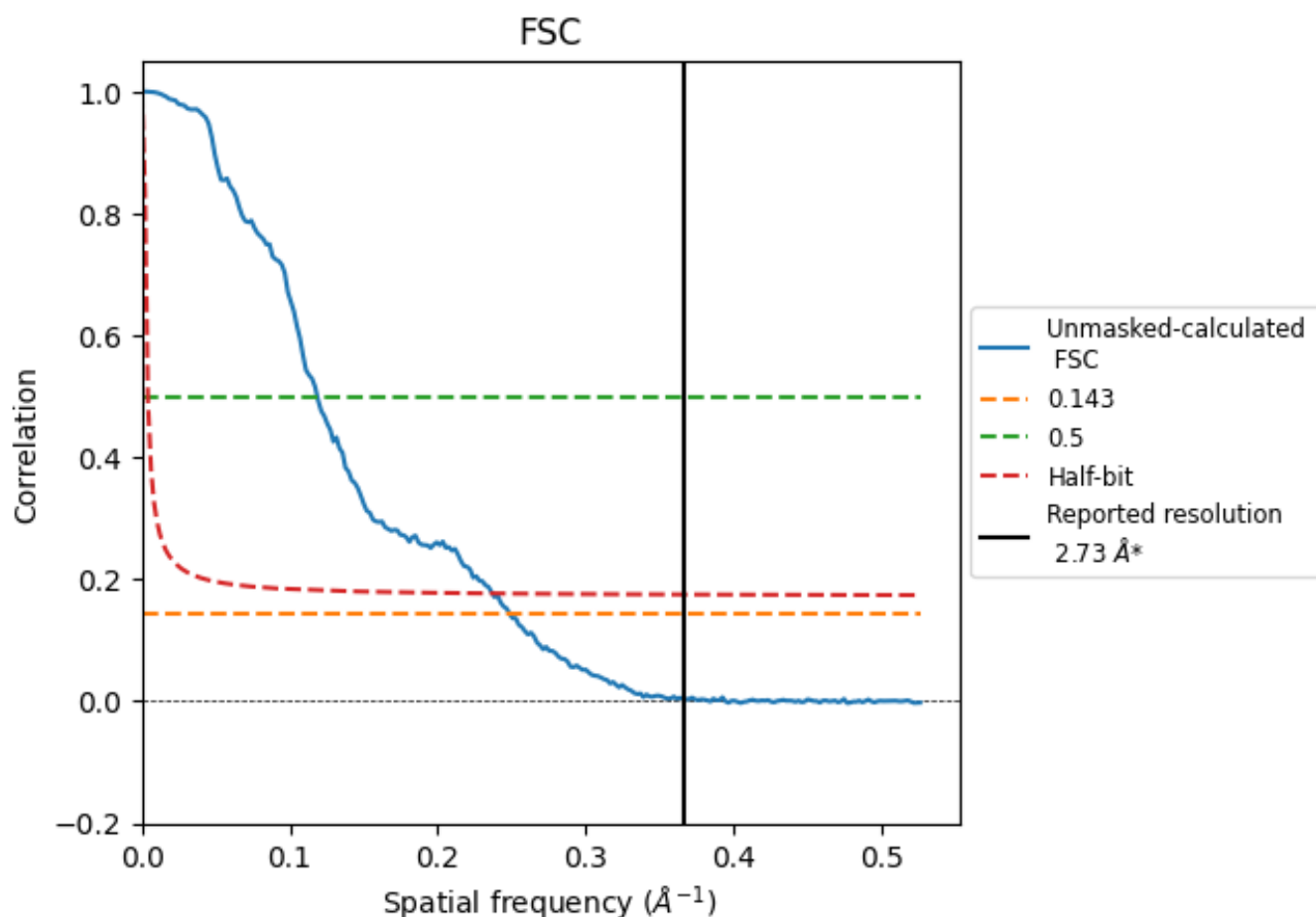


*Reported resolution corresponds to spatial frequency of 0.366 \AA^{-1}

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 0.366 Å⁻¹

8.2 Resolution estimates [i](#)

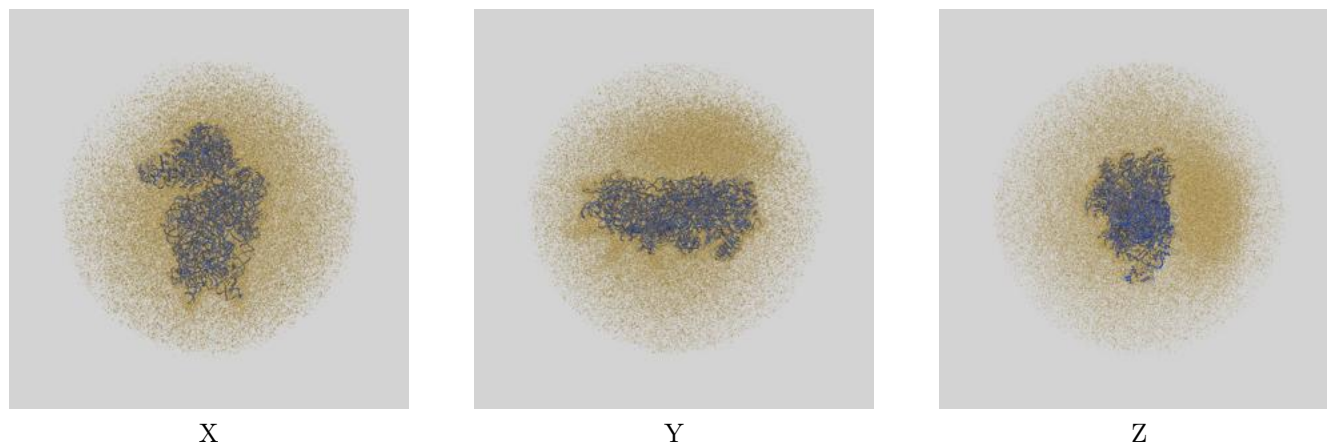
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.73	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.02	8.43	4.22

*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 4.02 differs from the reported value 2.73 by more than 10 %

9 Map-model fit [i](#)

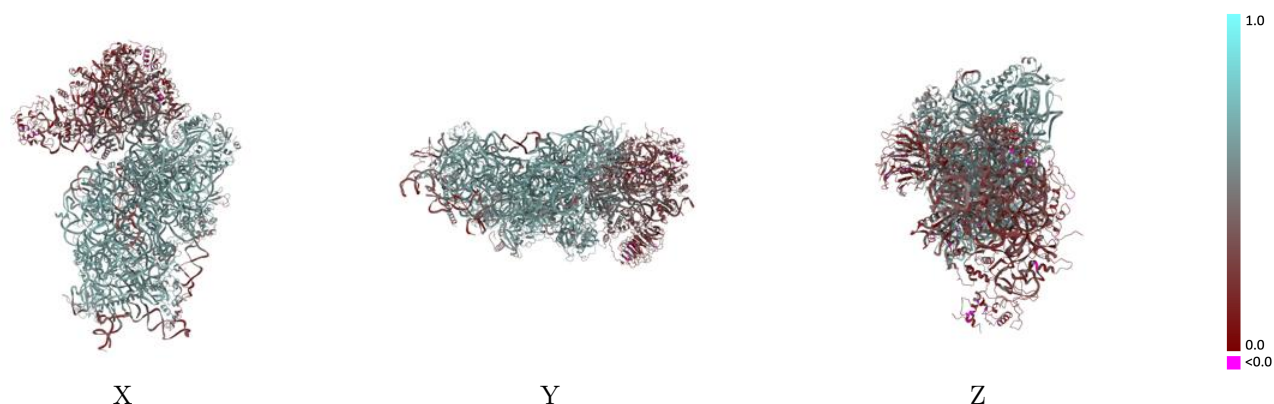
This section contains information regarding the fit between EMDB map EMD-62447 and PDB model 9KMW. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

9.1 Map-model overlay [i](#)



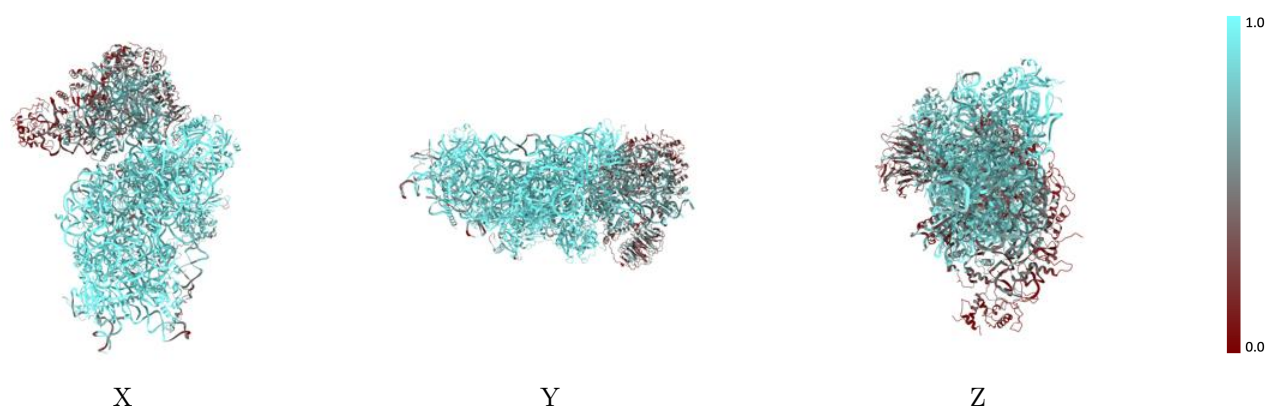
The images above show the 3D surface view of the map at the recommended contour level 0.158 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



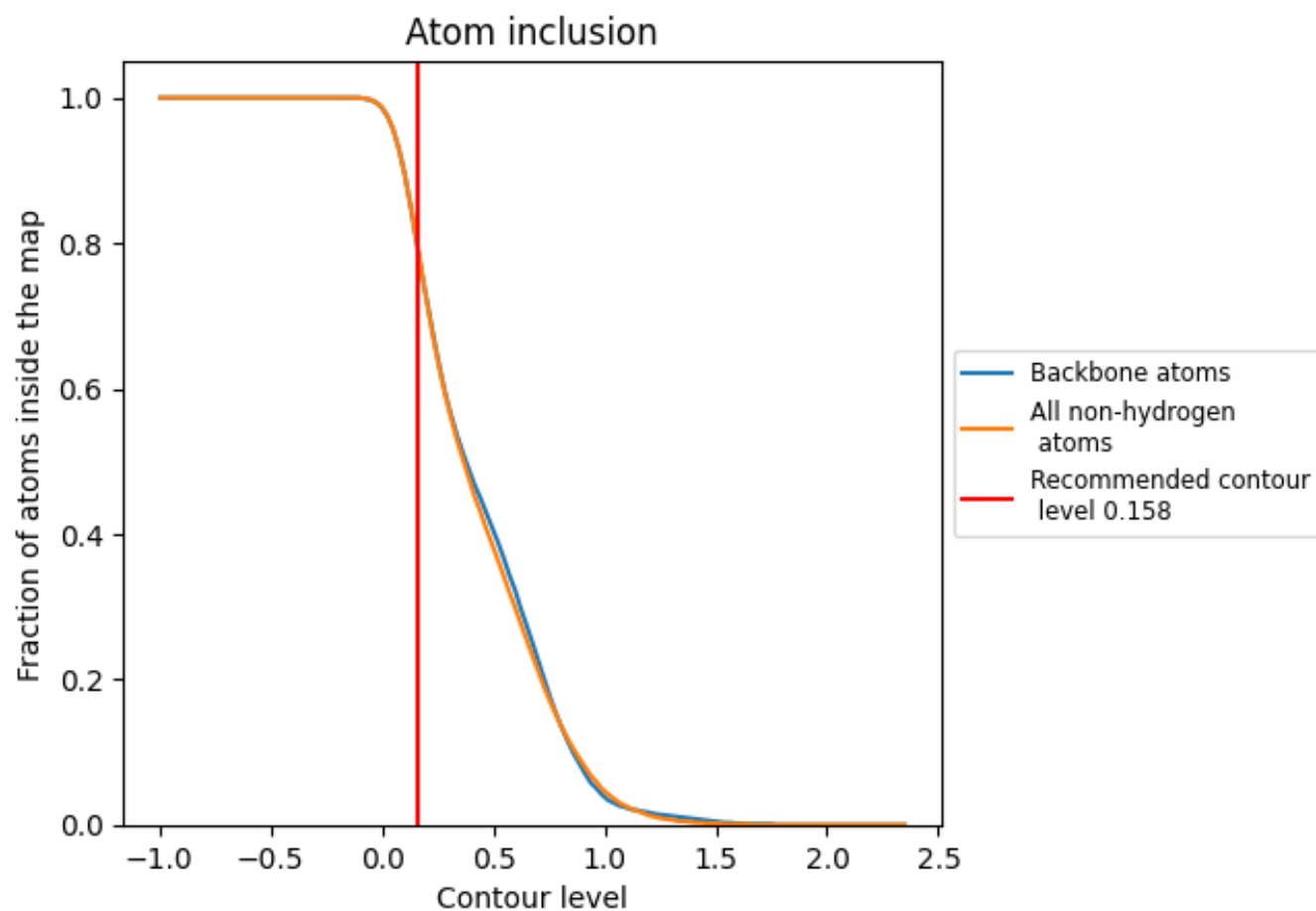
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.158).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 80% 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 (0.158) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8000	 0.4930
2	 0.8670	 0.5090
A	 0.9360	 0.5980
B	 0.9390	 0.5900
C	 0.9610	 0.6200
D	 0.5520	 0.3530
E	 0.9690	 0.6260
F	 0.5310	 0.3090
G	 0.9230	 0.5630
H	 0.8100	 0.5160
I	 0.9000	 0.5730
J	 0.9760	 0.6250
K	 0.4660	 0.2880
L	 0.9150	 0.6030
M	 0.1540	 0.2340
N	 0.9570	 0.6060
O	 0.9360	 0.5910
P	 0.2900	 0.2600
Q	 0.6570	 0.3620
R	 0.7000	 0.4510
S	 0.2470	 0.2750
T	 0.5420	 0.3040
U	 0.4580	 0.3320
V	 0.9660	 0.6140
W	 0.9800	 0.6360
X	 0.9700	 0.6260
Y	 0.9670	 0.6210
Z	 0.3300	 0.2550
a	 0.9520	 0.6080
b	 0.8320	 0.5120
c	 0.5120	 0.3460
d	 0.6240	 0.3390
e	 0.8810	 0.5820
f	 0.1430	 0.2520
g	 0.4170	 0.2720



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Chain	Atom inclusion	Q-score
h	 0.9120	 0.5910
n	 0.9060	 0.5990