



wwPDB EM Validation Summary Report ⓘ

Oct 8, 2022 – 07:49 pm BST

PDB ID : 7PAU
EMDB ID : EMD-13286
Title : free 50S in complex with ribosome recycling factor in untreated Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-07-30
Resolution : 8.30 Å (reported)
Based on initial models : 7OOD, 1EH1

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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

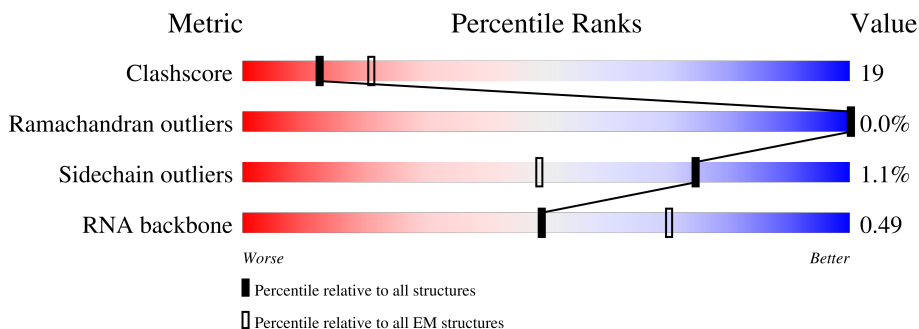
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 8.30 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	0	48	42% (green), 56% (yellow), . (grey)
2	1	59	76% (green), 24% (yellow)
3	2	37	54% (green), 46% (yellow)
4	7	184	39% (red), 57% (green), 41% (yellow), .. (grey)
5	a	287	. (red), 99% (green), . (grey)
6	b	287	. (red), 79% (green), . (grey), 20% (grey)
7	c	212	. (red), 99% (green), . (grey)

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Mol	Chain	Length	Quality of chain
8	d	180	9% 97% ..
9	e	184	8% 96% .
10	f	149	42% 97% ..
11	g	161	23% 72% 6% 22%
12	h	137	45% 93% 7%
13	i	146	98% ..
14	j	122	100%
15	k	151	98% .
16	l	139	98% .
17	m	124	95% ..
18	n	116	96% ..
19	o	119	97% .
20	p	127	90% 10%
21	q	100	97% ..
22	r	159	87% 13%
23	s	237	39% 61%
24	t	111	11% 100%
25	u	104	83% 17%
26	v	65	97% .
27	w	111	89% 10%
28	x	97	7% 45% 55%
29	y	57	91% 7% .
30	z	53	92% 6%
31	3	2907	27% 55% 16% .
32	4	108	38% 44% 16% .

2 Entry composition

There are 32 unique types of molecules in this entry. The entry contains 92803 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 protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	47	380	236	81	61	2	0	0

- Molecule 2 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	59	477	300	99	77	1	0	0

- Molecule 3 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	37	304	189	65	46	4	0	0

- Molecule 4 is a protein called Ribosome-recycling factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	7	182	1510	960	262	283	5	0	0

- Molecule 5 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	a	285	2225	1385	437	397	6	0	0

- Molecule 6 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	b	229	1762	1119	318	318	7	0	0

- Molecule 7 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	c	210	Total	C	N	O	S	0	0
			1644	1047	297	297	3		

- Molecule 8 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	d	175	Total	C	N	O	S	0	0
			1388	893	245	246	4		

- Molecule 9 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	e	176	Total	C	N	O	S	0	0
			1396	899	247	250			

- Molecule 10 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	f	145	Total	C	N	O	S	0	0
			1160	746	204	207	3		

- Molecule 11 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	g	126	Total	C	N	O	S	0	0
			960	612	167	178	3		

- Molecule 12 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	h	128	Total	C	N	O	S	0	0
			959	616	160	177	6		

- Molecule 13 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	i	144	Total	C	N	O	S	0	0
			1164	737	213	209	5		

- Molecule 14 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	j	122	944	595	178	167	4	0	0

- Molecule 15 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	k	148	1153	731	226	196		0	0

- Molecule 16 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	l	136	1079	694	196	182	7	0	0

- Molecule 17 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	m	119	958	609	175	171	3	0	0

- Molecule 18 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	n	112	889	557	175	155	2	0	0

- Molecule 19 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	o	115	938	592	180	165	1	0	0

- Molecule 20 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	p	114	947	603	188	154	2	0	0

- Molecule 21 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	q	99	811	525	148	134	4	0	0

- Molecule 22 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	r	139	1068	663	207	191	7	0	0

- Molecule 23 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	s	92	720	475	122	122	1	0	0

- Molecule 24 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	t	111	872	550	166	153	3	0	0

- Molecule 25 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	u	86	657	409	130	117	1	0	0

- Molecule 26 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	v	63	513	317	108	87	1	0	0

- Molecule 27 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
27	w	100	818	517	153	148	0	0

- Molecule 28 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	x	44	Total	C	N	O	S	0	0
			344	221	55	64	4		

- Molecule 29 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	y	56	Total	C	N	O	S	0	0
			452	274	98	75	5		

- Molecule 30 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	z	50	Total	C	N	O	S	0	0
			408	255	81	68	4		

- Molecule 31 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

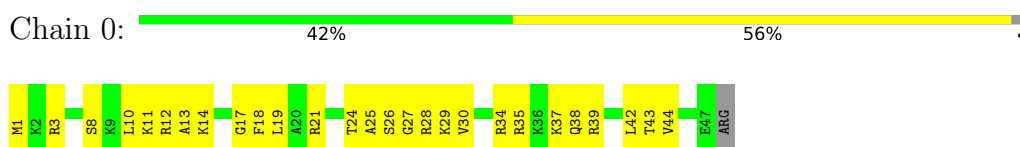
- Molecule 32 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

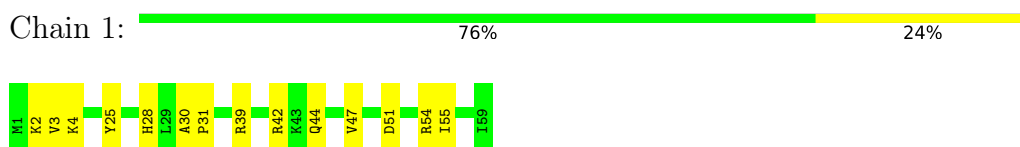
3 Residue-property plots [i](#)

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.

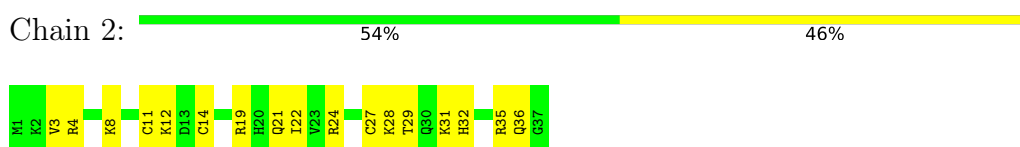
- Molecule 1: 50S ribosomal protein L34



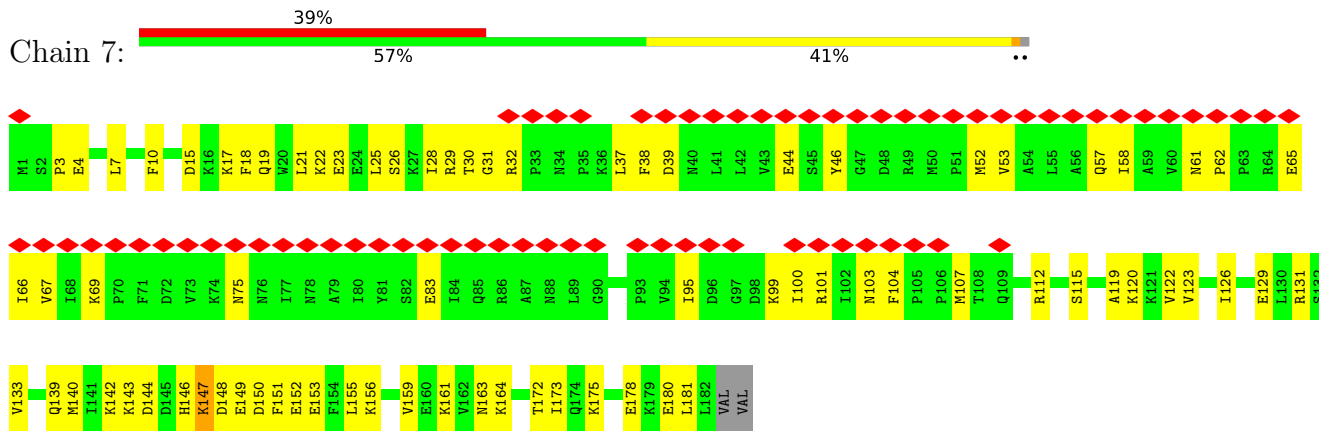
- Molecule 2: 50S ribosomal protein L35



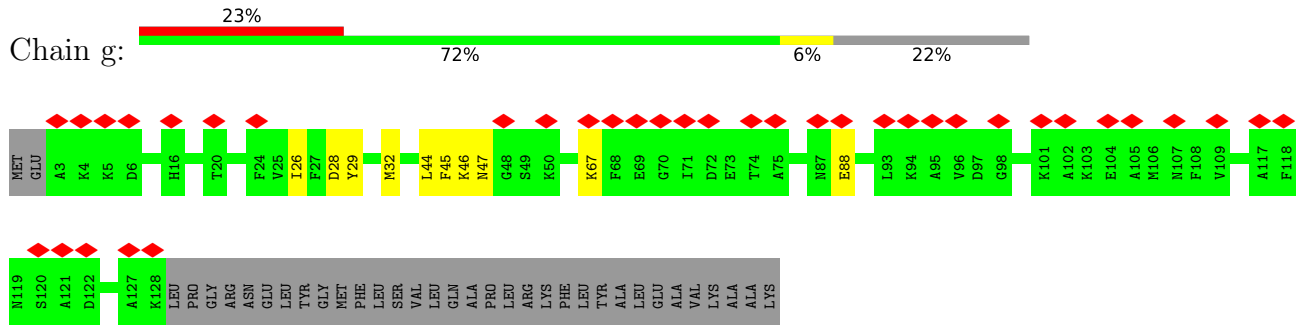
- Molecule 3: 50S ribosomal protein L36



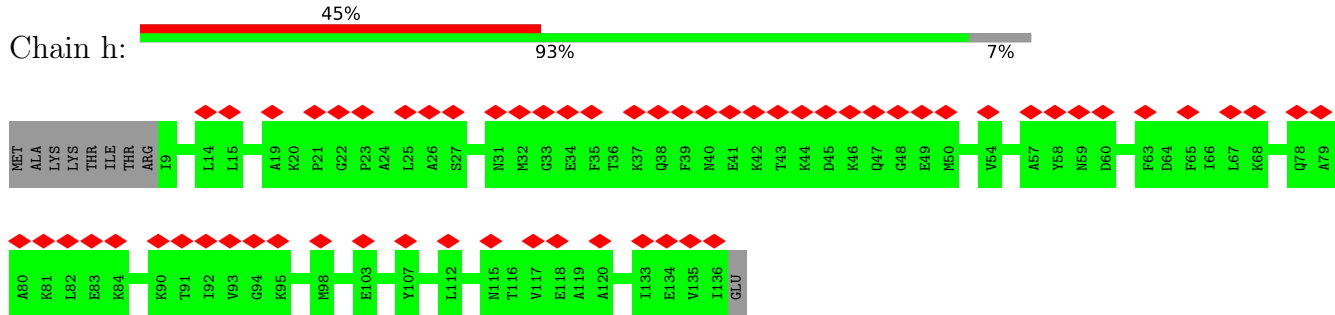
- Molecule 4: Ribosome-recycling factor



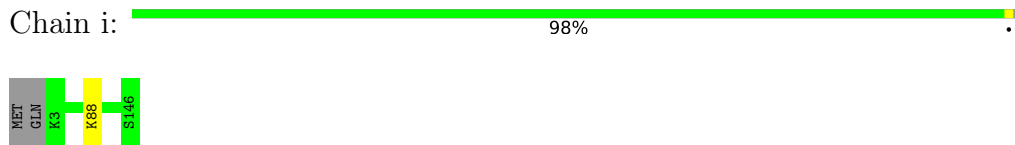
- Molecule 5: 50S ribosomal protein L2



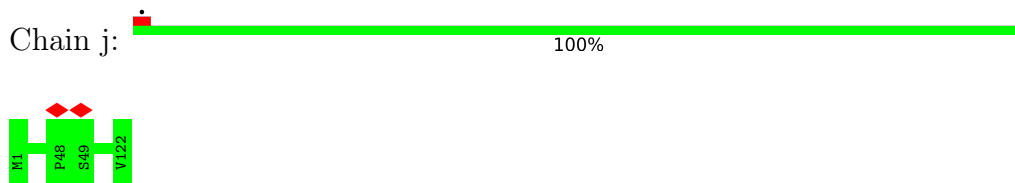
- Molecule 12: 50S ribosomal protein L11



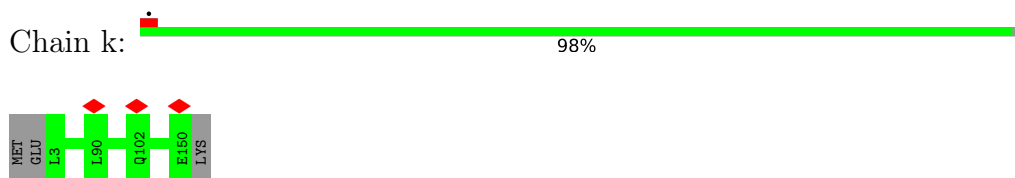
- Molecule 13: 50S ribosomal protein L13



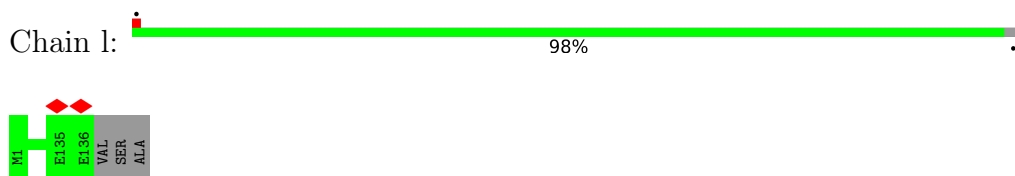
- Molecule 14: 50S ribosomal protein L14



- Molecule 15: 50S ribosomal protein L15

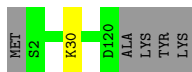


- Molecule 16: 50S ribosomal protein L16



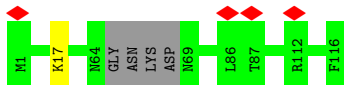
- Molecule 17: 50S ribosomal protein L17

Chain m:  95%



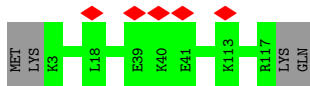
- Molecule 18: 50S ribosomal protein L18

Chain n:  96%




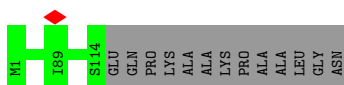
- Molecule 19: 50S ribosomal protein L19

Chain o:  97%



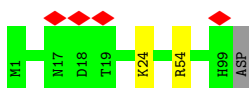
- Molecule 20: 50S ribosomal protein L20

Chain p:  90% 10%




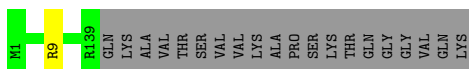
- Molecule 21: 50S ribosomal protein L21

Chain q:  97%



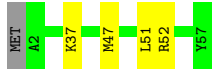
- Molecule 22: 50S ribosomal protein L22

Chain r:  87% 13%



- Molecule 23: 50S ribosomal protein L23

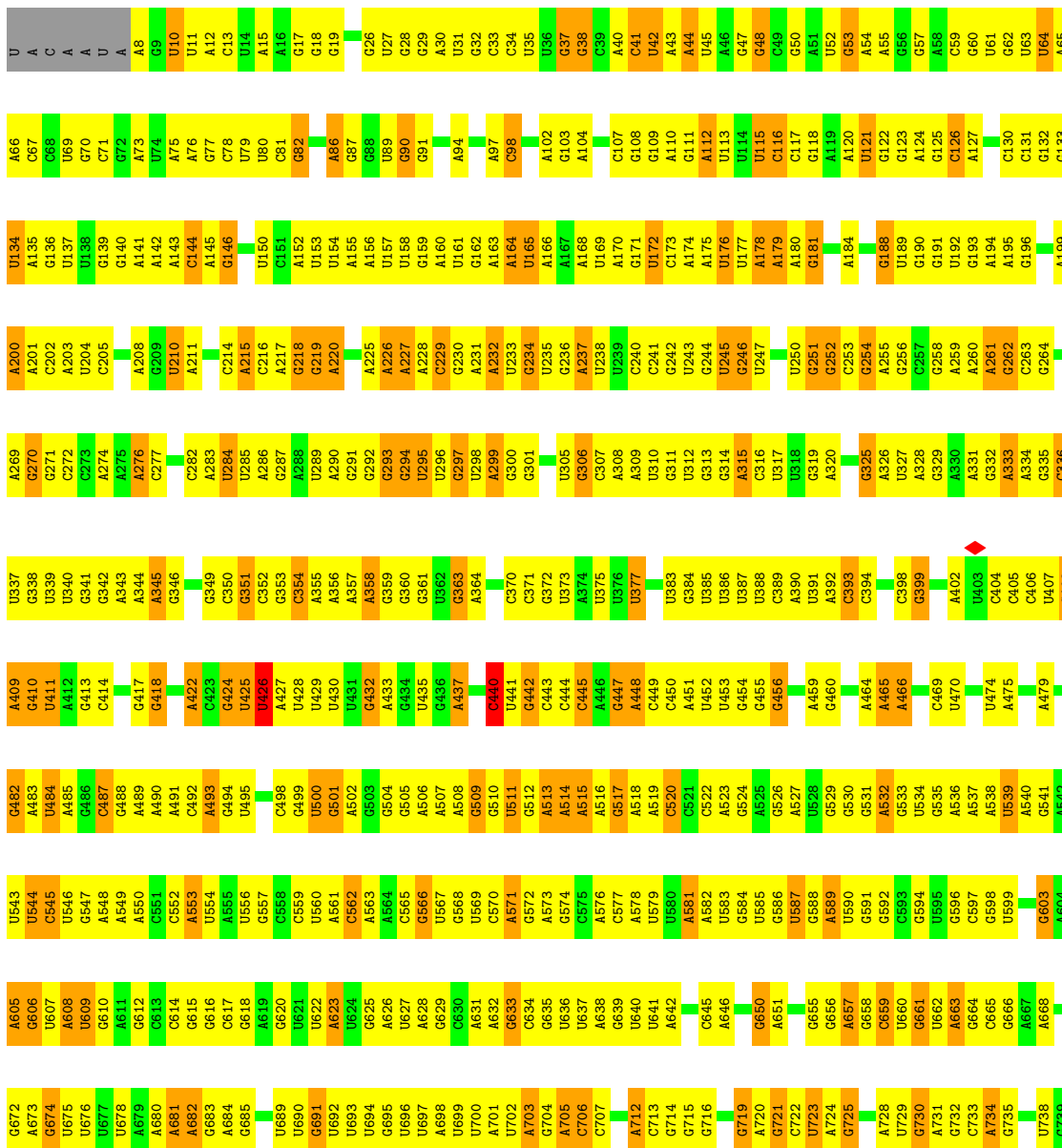
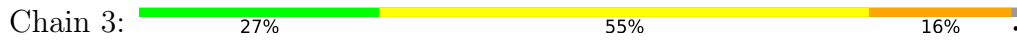
Chain s:  39% 61%



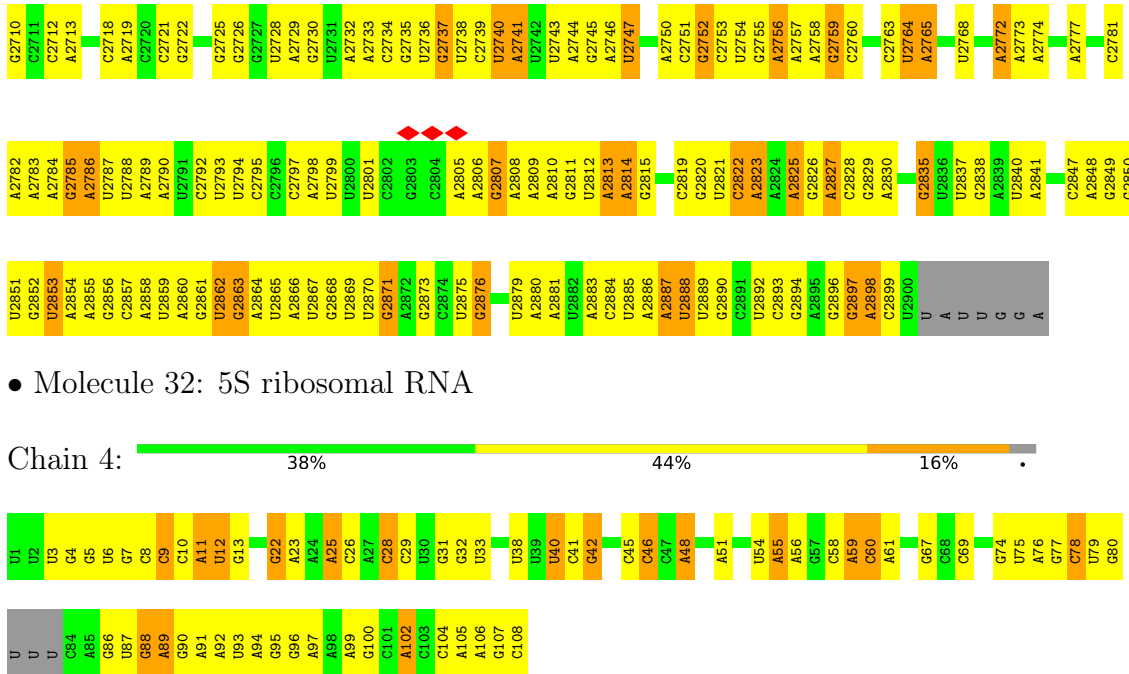
- Molecule 30: 50S ribosomal protein L33 1



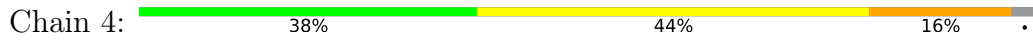
- Molecule 31: 23S ribosomal RNA



U1691	U1692	U1693	U1694	U1695	U1696	U1697	U1698	U1699	U1700	U1701	U1702	U1703	U1704	U1707	U1708	U1709	U1710	U1711	U1712	U1715	U1716	U1721	U1722	U1723	U1724	U1728	U1729	U1730	U1731	U1732	U1733	U1734	U1735	U1736	U1737	U1738	U1739	U1743	U1744	U1745	U1746	U1747	U1748	U1751	U1752	U1753	U1754	U1755	U1756	U1757	U1758	U1759	C1690																							
C1622	U1623	G1624	G1625	G1628	U1629	U1630	U1631	C1632	C1633	U1634	U1635	U1636	U1637	C1638	U1639	U1640	U1641	U1642	U1643	U1644	U1645	U1646	U1647	U1648	U1649	U1650	U1651	U1652	U1653	U1654	U1655	C1659	U1659	U1660	U1661	U1662	U1663	U1664	U1665	U1666	U1667	U1668	U1669	U1670	U1671	U1672	U1673	U1674	U1675	U1676	U1677	U1678	U1679	U1680	U1681	U1682	U1683	U1684	U1685	U1686	U1687	U1688	U1689	U1690												
A	G	U	U	U	U	C	A	A	U1570	G1571	U1572	A1573	C1574	C1575	U1576	A1577	C1578	U1579	U1580	U1581	U1582	U1583	U1584	U1585	U1586	U1587	U1588	U1589	U1590	C1591	U1592	U1593	U1594	C1595	U1596	U1597	U1598	U1599	A1600	U1601	U1602	U1603	U1604	U1605	U1606	U1607	U1608	U1609	U1610	U1611	U1612	U1613	U1614	U1615	U1616	U1617	U1618	U1619	U1620	U1621																
A1495	A1496	U1497	U1498	U1499	U1500	U1501	A1502	A1503	U1504	U1505	U1506	U1507	U1508	U1509	U1510	C1511	U1512	U1513	U1514	C1518	C1523	U1524	U1525	U1526	U1527	U1528	U1529	U1530	U1531	U1532	U1533	U1534	U1535	U1536	U1537	U1538	U1539	U1540	U1541	U1542	U1543	U1544	U1545	U1546	U1547	U1548	U1549	U1550	U1551	U1552	U1553	U1554	U1555	U1556	U1557	U1558	U1559	U	G																	
U1428	G1429	U1430	U1431	U1432	U1433	U1434	U1435	U1436	U1439	U1440	U1441	U1442	U1443	U1444	U1445	U1446	U1449	U1450	U1451	U1452	U1453	U1454	U1455	U1456	U1457	U1458	U1459	U1460	U1461	U1462	U1463	U1464	U1465	U1466	U1467	C1473	C1474	C1475	U1476	U1477	U1478	U1479	U1480	U1481	U1482	U1483	U1486	U1487	U1488	U1489	U1490	U1491	U1492	U1493	U1494																					
C1355	G1356	U1357	C1358	C1359	U1360	U1361	C1362	C1363	A1364	U1369	U1370	U1371	U1372	G1376	U1380	A1381	C1382	C1383	C1384	U1385	U1386	A1387	U1388	U1389	C1390	A1393	A1394	C1397	C1398	C1399	U1400	A1401	G1402	U1406	U1407	U1408	U1409	U1410	C1411	U1412	U1413	U1414	U1415	U1416	U1417	U1418	U1419	U1420	U1421	U1422	U1423	U1424	U1425	C1427																						
U1284	U1285	G1286	U1287	A1288	U1292	U1293	U1294	U1295	U1296	U1297	U1298	U1299	C1300	U1301	U1302	U1303	U1304	U1305	U1306	U1307	U1308	U1309	U1310	U1311	U1314	U1315	U1316	U1317	U1318	A1322	C1325	C1326	C1327	U1328	U1329	U1330	C1331	A1332	C1333	U1334	U1335	U1336	U1337	U1338	U1341	C1342	U1343	U1344	U1345	A1350	U1353	U1354	U1355																							
G1218	U1219	A1220	G1221	A1222	U1228	U1229	U1230	U1231	U1232	U1233	U1234	U1235	U1236	U1237	U1238	U1239	U1240	U1241	U1242	U1243	A1244	G1245	U1246	C1247	U1248	U1249	A1250	U1251	C1252	U1253	U1254	U1255	U1256	U1257	U1258	U1259	U1260	U1261	U1262	U1263	U1264	U1265	U1266	U1267	U1268	U1269	U1270	A1271	U1274	C1275	U1278	U1279	U1280	U1281	U1282	U1283	A1283																			
U1151	U1154	G1155	C1156	U1157	U1158	C1159	U1160	U1161	U1162	U1163	U1164	U1165	U1166	U1167	U1168	U1169	U1170	U1171	C1175	U1176	C1177	U1178	U1179	U1183	U1186	C1187	U1188	U1189	A1190	U1191	U1192	U1193	U1194	U1196	U1197	U1198	U1199	U1200	A1201	U1202	U1203	U1204	U1205	U1206	U1209	A1210	U1211	U1212	U1213	U1214	U1215	U1216	U1217																							
G1076	G1077	C1078	A1081	U1082	U1083	C1084	U1085	C1086	U1087	U1088	U1089	U1090	U1091	U1092	U1093	U1094	U1095	U1096	U1097	U1098	C1099	U1100	U1101	U1102	U1103	U1104	U1105	U1106	C1111	U1112	U1113	U1114	U1115	U1116	U1123	U1124	U1125	U1126	A1131	C1132	U1136	U1137	U1138	C1139	U1140	U1141	U1142	U1143	U1144	U1145	U1146	U1147	U1148	U1149	U1150																					
A1009	G1010	U1011	G1012	G1013	A1016	A1019	G1020	G1021	G1022	G1023	A1024	G1025	A1026	U1027	G1028	U1029	U1030	U1031	A1032	U1033	U1034	U1035	A1037	U1038	U1039	U1040	U1045	A1046	A1047	A1048	U1049	A1050	U1051	A1052	U1053	U1054	A1055	A1056	G1057	U1058	A1061	A1062	A1063	A1064	U1065	U1066	U1067	U1068	U1069	U1070	U1071	A1072	U1073	A1074	G1075																					
U944	U945	U946	A947	U948	C949	U950	C951	U952	U953	U954	U955	U956	U957	C958	U963	U964	U965	U966	U967	U970	U971	C972	U973	U974	U975	U976	U977	U978	U979	U980	U981	U982	U983	U984	U985	U986	U989	U994	U995	U996	U997	U998	U999	U1000	U1001	U1002	U1003	U1004	U1005	U1006	U1007	A1008																								
C880	A881	C882	A883	U884	U885	U886	A887	U888	U889	U890	U891	U892	U893	U894	U895	U896	U897	U898	U899	U900	C901	U902	U903	U904	U905	U906	U907	U908	U909	U910	U911	U912	U913	U914	U915	U916	U917	U918	C922	A	C	C	U	A	G928	G929	U930	C930	U931	U932	U933	U934	U935	U936	U937	U938	U939	U940																		
U813	A816	U817	U818	U819	U820	C821	U822	A823	U824	U825	U826	C827	U828	A829	U830	U831	C832	U833	U834	U835	U836	U837	U840	U841	U842	U843	U844	U847	U848	U849	U850	U851	U852	U853	U854	U855	U856	U862	U863	U864	U865	U866	U867	U868	U869	U870	U871	U872	U873	U874	U875	U876	U877	U878	U879	U880	U881	U882	U883	U884	U885	U886	U887	U888	U889	U890	U891	U892	U893	U894	U895	U896	U897	U898	U899	U900
A740	A741	G742	U745	G746	A747	G748	C752	A753	U754	C755	U756	A757	U758	U759	G760	G761	A762	G763	G764	A765	C766	C767	G768	A774	C775	U781	U782	G783	A784	G788	U789	U790	U791	G792	C793	G794	U797	A799	C800	U801	U802	U803	U804	G805	U806	U807	G810	G811	G812																											



• Molecule 32: 5S ribosomal RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	8203	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	3.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.619	Depositor
Minimum map value	-0.546	Depositor
Average map value	0.016	Depositor
Map value standard deviation	0.104	Depositor
Recommended contour level	0.46	Depositor
Map size (Å)	480.00003, 480.00003, 480.00003	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.4, 2.4, 2.4	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	0	0.22	0/383	0.43	0/504
2	1	0.23	0/484	0.41	0/637
3	2	0.23	0/306	0.46	0/401
4	7	0.26	0/1535	0.43	0/2061
5	a	0.24	0/2267	0.45	0/3044
6	b	0.25	0/1795	0.47	0/2412
7	c	0.25	0/1671	0.47	0/2246
8	d	0.24	0/1409	0.45	0/1894
9	e	0.25	0/1420	0.47	0/1912
10	f	0.24	0/1183	0.47	0/1587
11	g	0.38	0/969	0.57	0/1295
12	h	0.24	0/968	0.46	0/1298
13	i	0.24	0/1186	0.43	0/1592
14	j	0.25	0/953	0.46	0/1275
15	k	0.23	0/1170	0.43	0/1559
16	l	0.24	0/1104	0.44	0/1481
17	m	0.23	0/973	0.43	0/1309
18	n	0.23	0/897	0.44	0/1198
19	o	0.24	0/948	0.46	0/1262
20	p	0.23	0/961	0.39	0/1278
21	q	0.25	0/828	0.46	0/1111
22	r	0.25	0/1077	0.46	0/1441
23	s	0.24	0/732	0.46	0/988
24	t	0.24	0/879	0.44	0/1165
25	u	0.25	0/665	0.47	0/884
26	v	0.22	0/519	0.49	0/695
27	w	0.22	0/826	0.40	0/1104
28	x	0.25	0/353	0.45	0/474
29	y	0.29	0/457	0.54	0/601
30	z	0.23	0/412	0.43	0/547
31	3	0.19	0/69073	0.78	31/107710 (0.0%)
32	4	0.18	0/2505	0.77	0/3902
All	All	0.21	0/100908	0.71	31/150867 (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
10	f	0	1

There are no bond length outliers.

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	3	545	C	N1-C2-O2	8.87	124.22	118.90
31	3	440	C	N1-C2-O2	8.73	124.14	118.90
31	3	440	C	C2-N1-C1'	8.04	127.65	118.80
31	3	1341	U	C2-N1-C1'	7.91	127.19	117.70
31	3	1786	U	C2-N1-C1'	7.66	126.90	117.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	f	11	ASN	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	0	380	0	429	25	0
2	1	477	0	530	12	0
3	2	304	0	350	18	0
4	7	1510	0	1553	60	0
5	a	2225	0	2301	0	0
6	b	1762	0	1808	0	0
7	c	1644	0	1731	0	0
8	d	1388	0	1469	0	0
9	e	1396	0	1481	0	0
10	f	1160	0	1172	0	0
11	g	960	0	1014	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	h	959	0	1039	0	0
13	i	1164	0	1192	0	0
14	j	944	0	1019	0	0
15	k	1153	0	1256	0	0
16	l	1079	0	1134	0	0
17	m	958	0	1011	0	0
18	n	889	0	952	0	0
19	o	938	0	1008	0	0
20	p	947	0	1028	0	0
21	q	811	0	858	0	0
22	r	1068	0	1150	0	0
23	s	720	0	803	0	0
24	t	872	0	972	0	0
25	u	657	0	695	0	0
26	v	513	0	560	0	0
27	w	818	0	870	0	0
28	x	344	0	333	0	0
29	y	452	0	472	0	0
30	z	408	0	440	0	0
31	3	61664	0	30954	1703	0
32	4	2239	0	1137	52	0
All	All	92803	0	62721	1839	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 19.

The worst 5 of 1839 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)
31:3:900:G:N2	31:3:903:A:H61	1.58	1.01
31:3:1807:C:H42	31:3:1824:G:N2	1.57	1.01
31:3:2299:U:H3	31:3:2349:G:H1	1.03	1.00
31:3:1746:U:H3	31:3:1753:G:H1	1.04	1.00
31:3:1807:C:N4	31:3:1824:G:H22	1.59	0.99

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	
1	0	45/48 (94%)	44 (98%)	1 (2%)	0	100	100
2	1	57/59 (97%)	55 (96%)	2 (4%)	0	100	100
3	2	35/37 (95%)	32 (91%)	3 (9%)	0	100	100
4	7	180/184 (98%)	168 (93%)	12 (7%)	0	100	100
5	a	283/287 (99%)	266 (94%)	17 (6%)	0	100	100
6	b	227/287 (79%)	209 (92%)	18 (8%)	0	100	100
7	c	208/212 (98%)	196 (94%)	12 (6%)	0	100	100
8	d	173/180 (96%)	163 (94%)	10 (6%)	0	100	100
9	e	174/184 (95%)	167 (96%)	7 (4%)	0	100	100
10	f	143/149 (96%)	130 (91%)	13 (9%)	0	100	100
11	g	124/161 (77%)	109 (88%)	14 (11%)	1 (1%)	19	60
12	h	126/137 (92%)	118 (94%)	8 (6%)	0	100	100
13	i	142/146 (97%)	135 (95%)	7 (5%)	0	100	100
14	j	120/122 (98%)	118 (98%)	2 (2%)	0	100	100
15	k	146/151 (97%)	137 (94%)	9 (6%)	0	100	100
16	l	134/139 (96%)	126 (94%)	8 (6%)	0	100	100
17	m	117/124 (94%)	109 (93%)	8 (7%)	0	100	100
18	n	108/116 (93%)	98 (91%)	10 (9%)	0	100	100
19	o	113/119 (95%)	102 (90%)	11 (10%)	0	100	100
20	p	112/127 (88%)	109 (97%)	3 (3%)	0	100	100
21	q	97/100 (97%)	86 (89%)	11 (11%)	0	100	100
22	r	137/159 (86%)	126 (92%)	11 (8%)	0	100	100
23	s	90/237 (38%)	84 (93%)	6 (7%)	0	100	100
24	t	109/111 (98%)	102 (94%)	7 (6%)	0	100	100
25	u	84/104 (81%)	79 (94%)	5 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	v	61/65 (94%)	57 (93%)	4 (7%)	0	100	100
27	w	96/111 (86%)	92 (96%)	4 (4%)	0	100	100
28	x	42/97 (43%)	34 (81%)	8 (19%)	0	100	100
29	y	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
30	z	48/53 (91%)	47 (98%)	1 (2%)	0	100	100
All	All	3585/4063 (88%)	3347 (93%)	237 (7%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	g	45	PHE

5.3.2 Protein sidechains [i](#)

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	
1	0	40/41 (98%)	40 (100%)	0	100	100
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	35 (100%)	0	100	100
4	7	170/172 (99%)	164 (96%)	6 (4%)	36	59
5	a	241/243 (99%)	240 (100%)	1 (0%)	91	94
6	b	186/233 (80%)	183 (98%)	3 (2%)	62	79
7	c	182/184 (99%)	181 (100%)	1 (0%)	88	93
8	d	150/154 (97%)	149 (99%)	1 (1%)	84	90
9	e	153/159 (96%)	153 (100%)	0	100	100
10	f	123/134 (92%)	123 (100%)	0	100	100
11	g	101/129 (78%)	92 (91%)	9 (9%)	9	30
12	h	102/110 (93%)	102 (100%)	0	100	100
13	i	126/128 (98%)	125 (99%)	1 (1%)	81	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	j	103/103 (100%)	103 (100%)	0	100	100
15	k	123/126 (98%)	123 (100%)	0	100	100
16	l	113/115 (98%)	113 (100%)	0	100	100
17	m	105/109 (96%)	104 (99%)	1 (1%)	76	86
18	n	96/99 (97%)	95 (99%)	1 (1%)	76	86
19	o	101/105 (96%)	101 (100%)	0	100	100
20	p	100/108 (93%)	100 (100%)	0	100	100
21	q	90/91 (99%)	88 (98%)	2 (2%)	52	71
22	r	116/132 (88%)	115 (99%)	1 (1%)	78	87
23	s	82/208 (39%)	82 (100%)	0	100	100
24	t	96/96 (100%)	96 (100%)	0	100	100
25	u	69/85 (81%)	69 (100%)	0	100	100
26	v	58/60 (97%)	58 (100%)	0	100	100
27	w	87/98 (89%)	86 (99%)	1 (1%)	73	84
28	x	41/86 (48%)	41 (100%)	0	100	100
29	y	48/49 (98%)	44 (92%)	4 (8%)	11	34
30	z	47/50 (94%)	46 (98%)	1 (2%)	53	72
All	All	3135/3493 (90%)	3102 (99%)	33 (1%)	74	84

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	y	37	LYS
29	y	47	MET
30	z	23	LYS
11	g	26	ILE
8	d	80	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
7	c	177	ASN
17	m	81	HIS
25	u	26	ASN
18	n	37	ASN

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Mol	Chain	Res	Type
7	c	156	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
31	3	2875/2907 (98%)	790 (27%)	28 (0%)
32	4	103/108 (95%)	25 (24%)	4 (3%)
All	All	2978/3015 (98%)	815 (27%)	32 (1%)

5 of 815 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
31	3	10	U
31	3	15	A
31	3	28	G
31	3	37	G
31	3	38	G

5 of 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
32	4	10	C
32	4	54	U
31	3	1216	U
31	3	1209	U
32	4	59	A

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 monosaccharides 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.

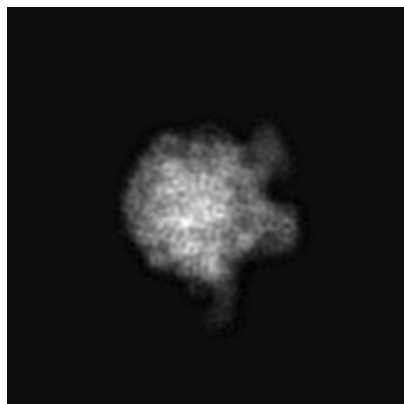
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13286. These allow visual inspection of the internal detail of the map and identification of artifacts.

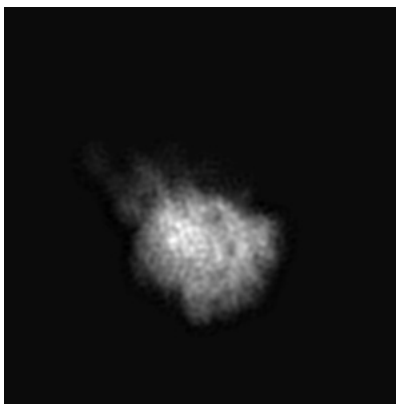
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

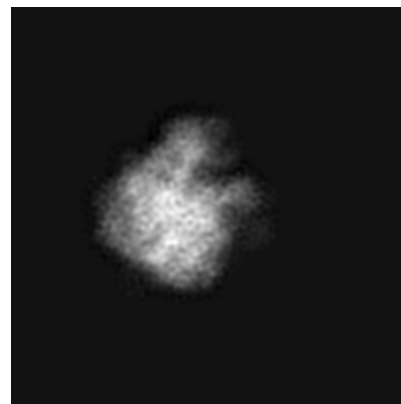
6.1.1 Primary map



X

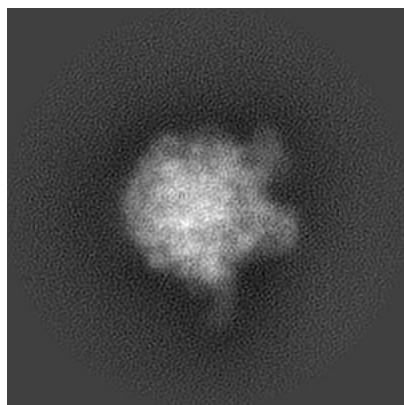


Y

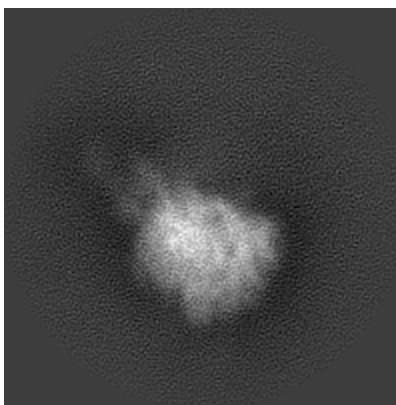


Z

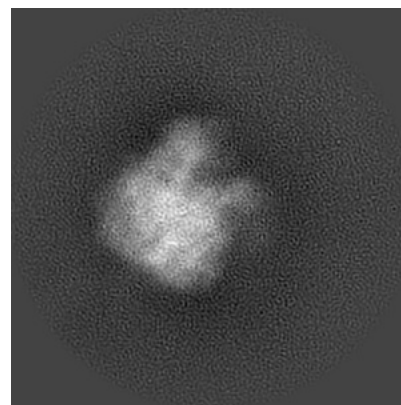
6.1.2 Raw map



X



Y

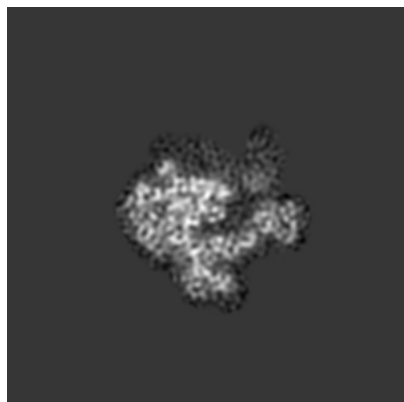


Z

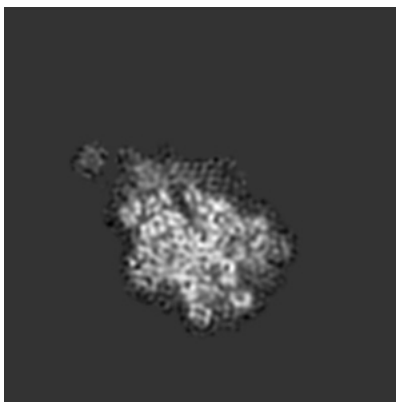
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

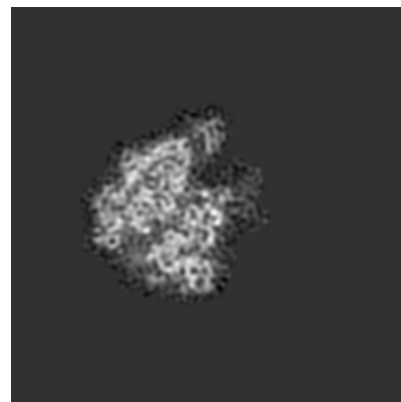
6.2.1 Primary map



X Index: 100

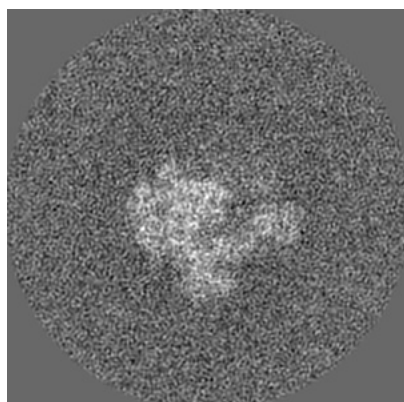


Y Index: 100

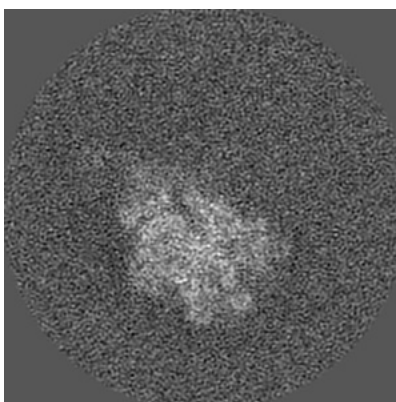


Z Index: 100

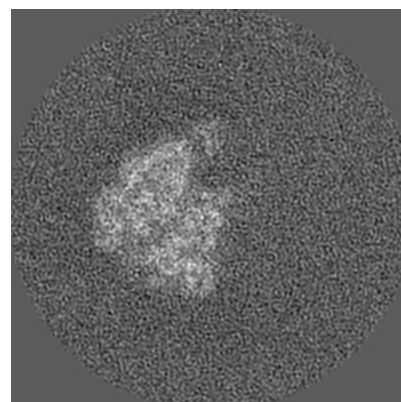
6.2.2 Raw map



X Index: 100



Y Index: 100



Z Index: 100

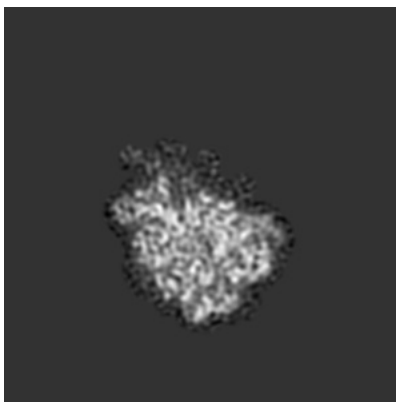
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

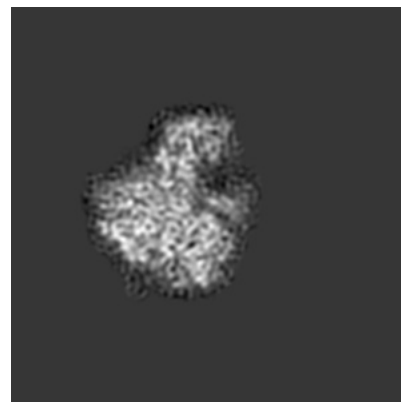
6.3.1 Primary map



X Index: 83

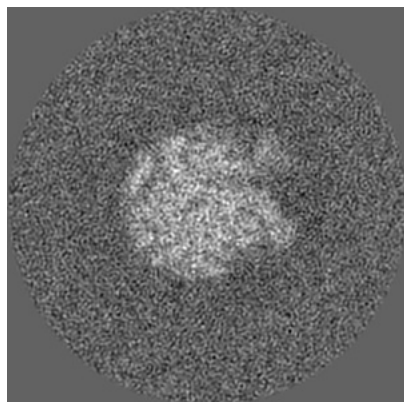


Y Index: 93

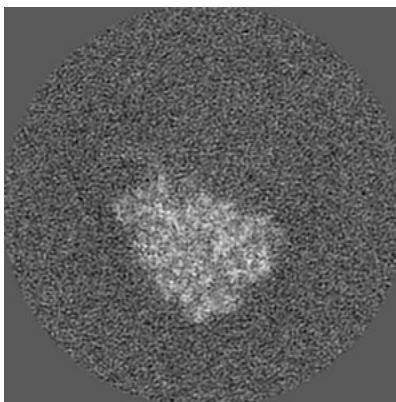


Z Index: 93

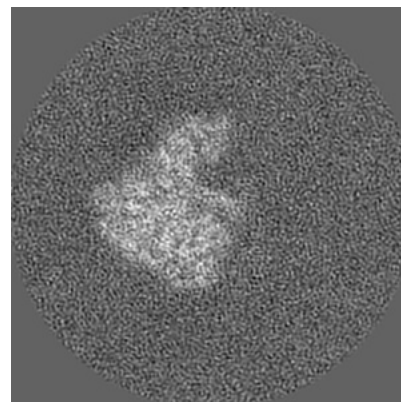
6.3.2 Raw map



X Index: 80



Y Index: 93

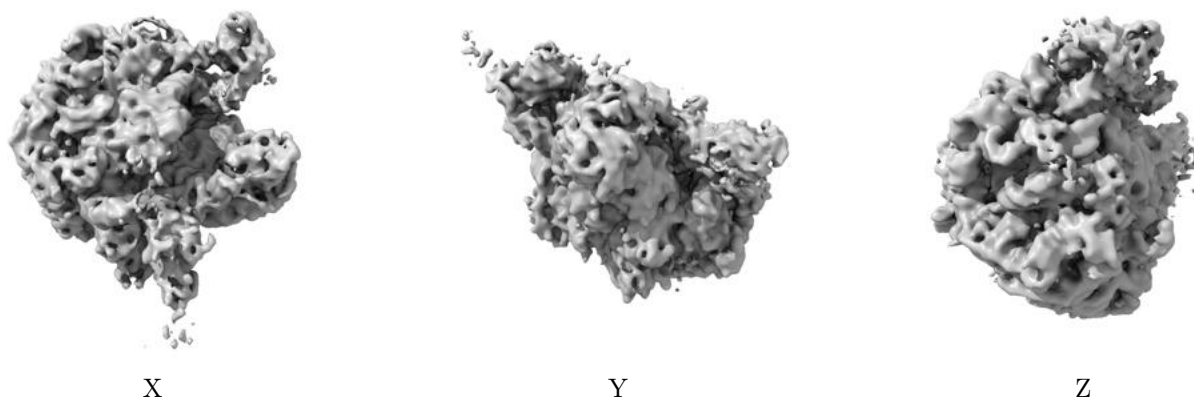


Z Index: 94

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

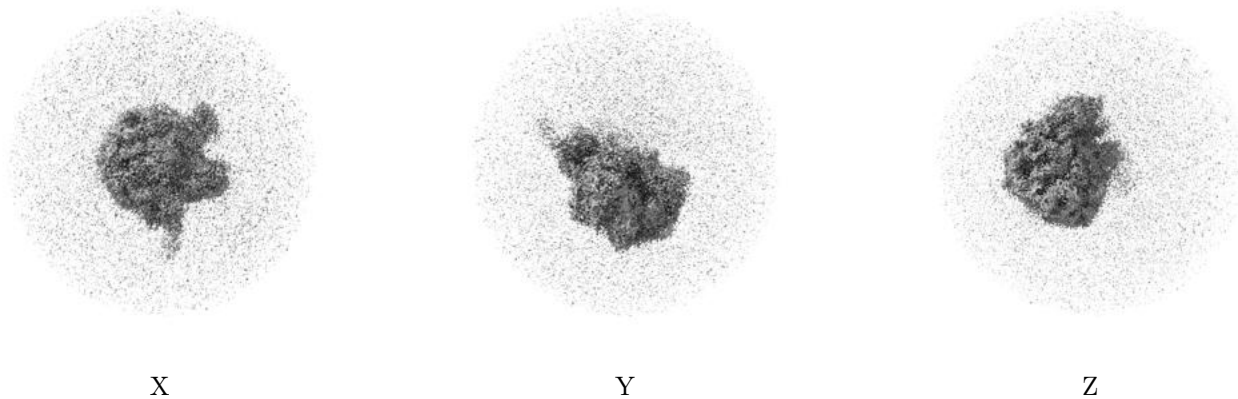
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.46. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

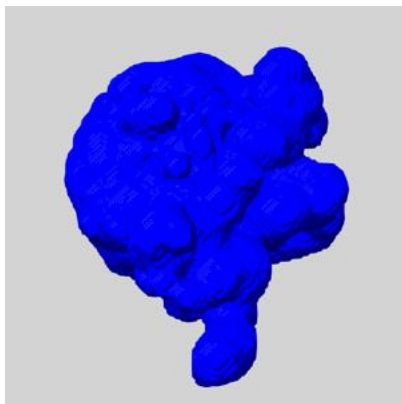
6.5 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

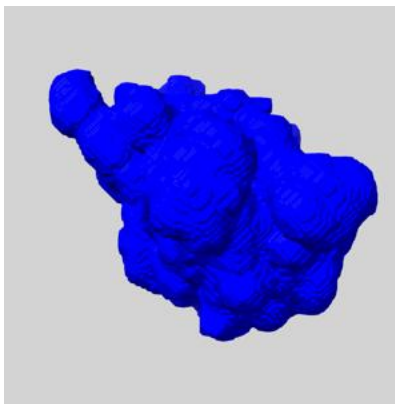
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

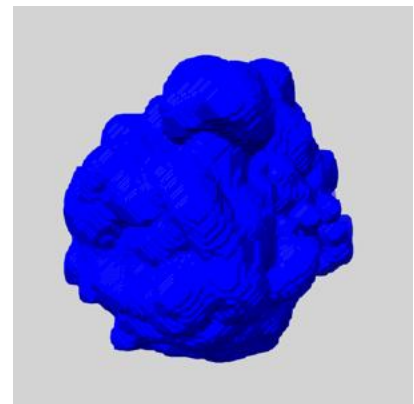
6.5.1 emd_13286_msk_1.map [i](#)



X



Y

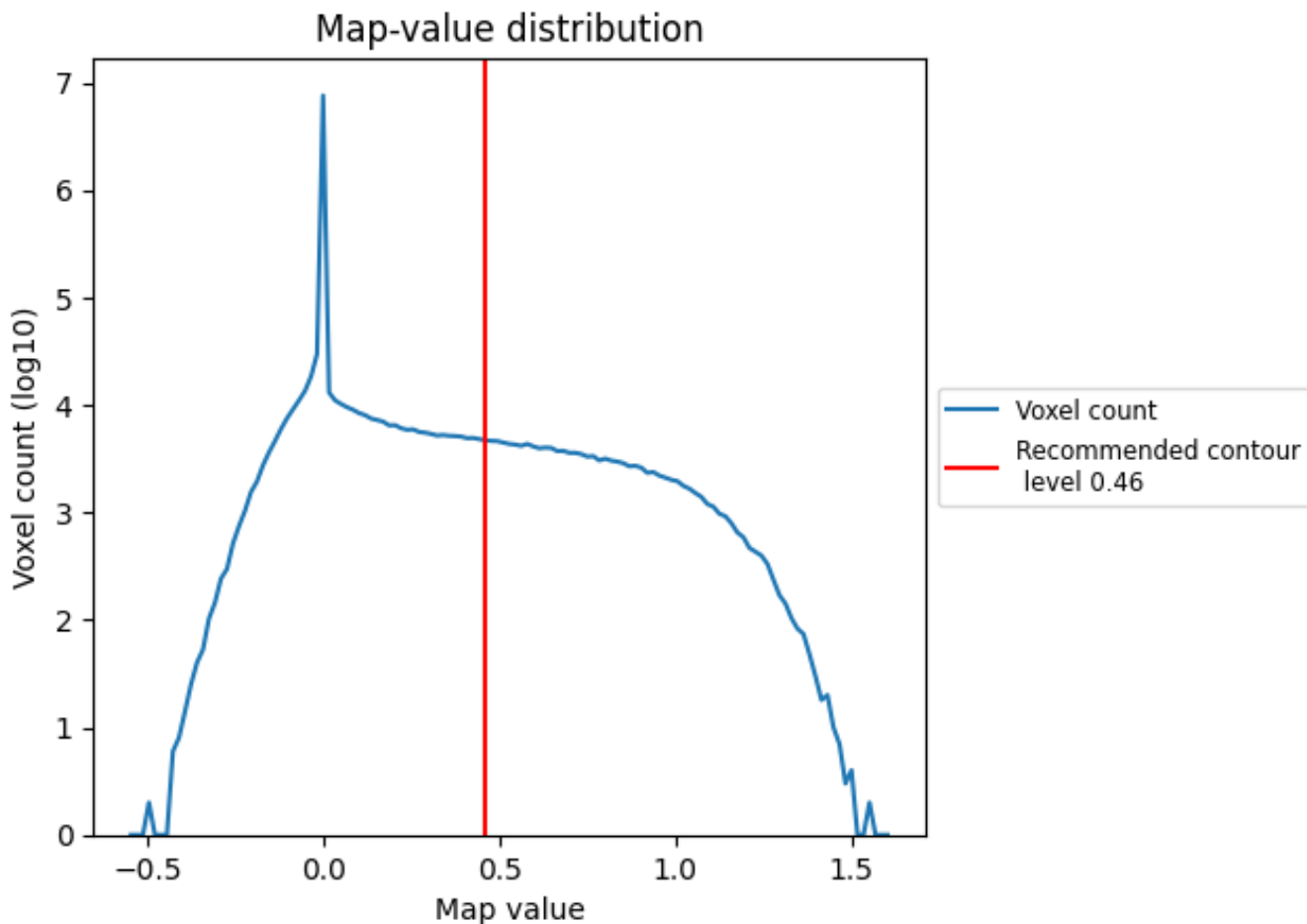


Z

7 Map analysis [i](#)

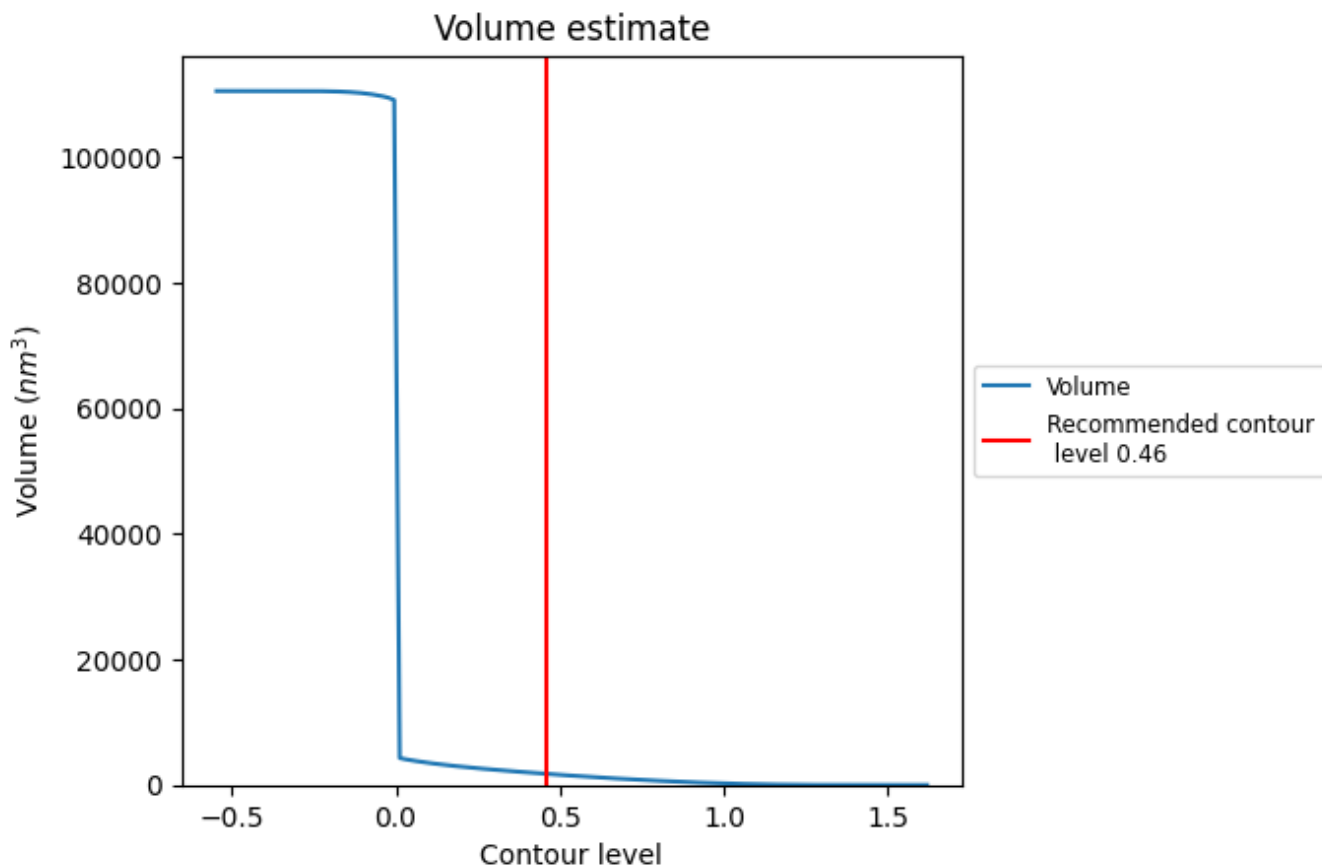
This section contains the results of statistical analysis of the map.

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.

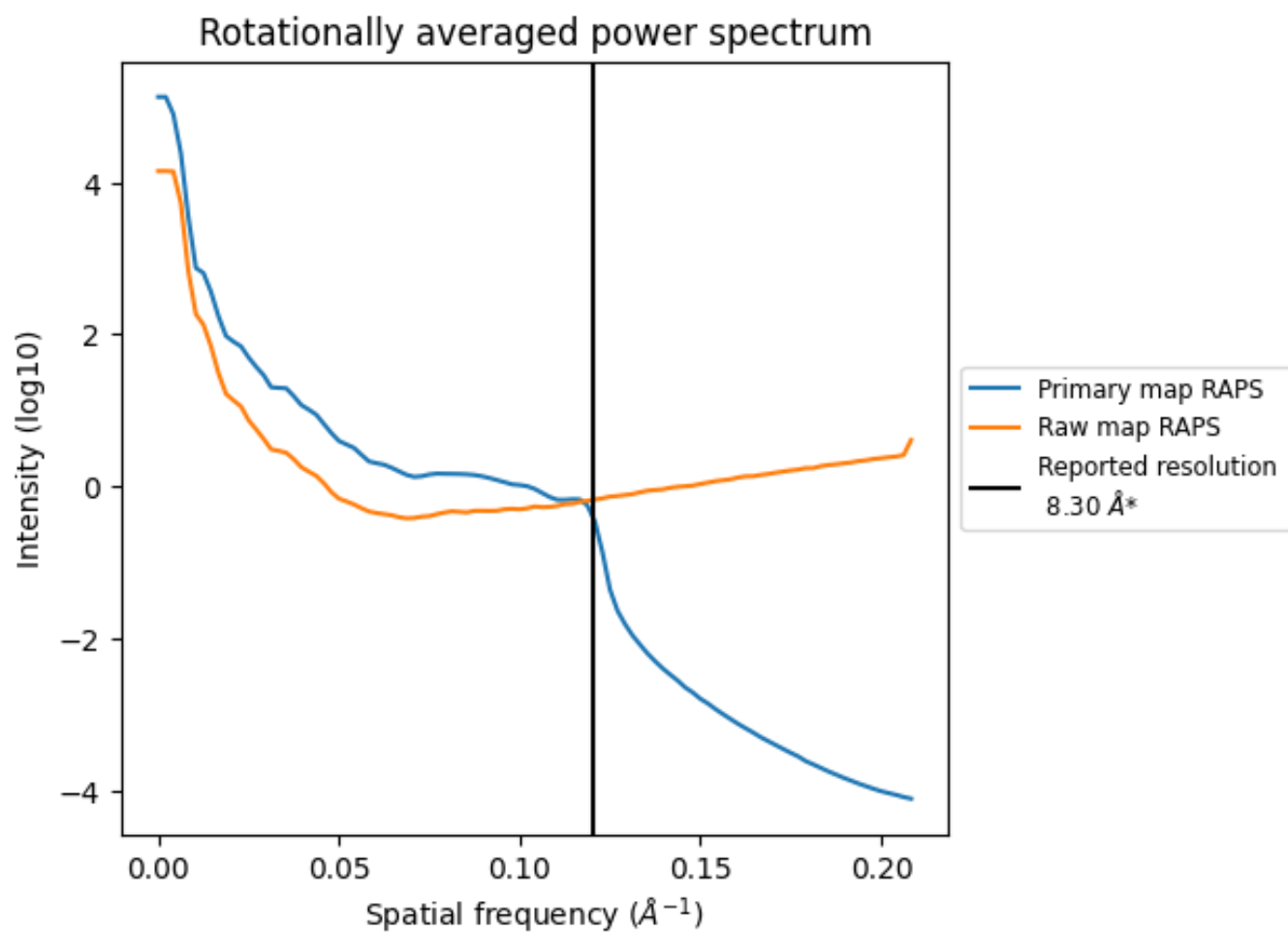
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1764 nm³; this corresponds to an approximate mass of 1593 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 i

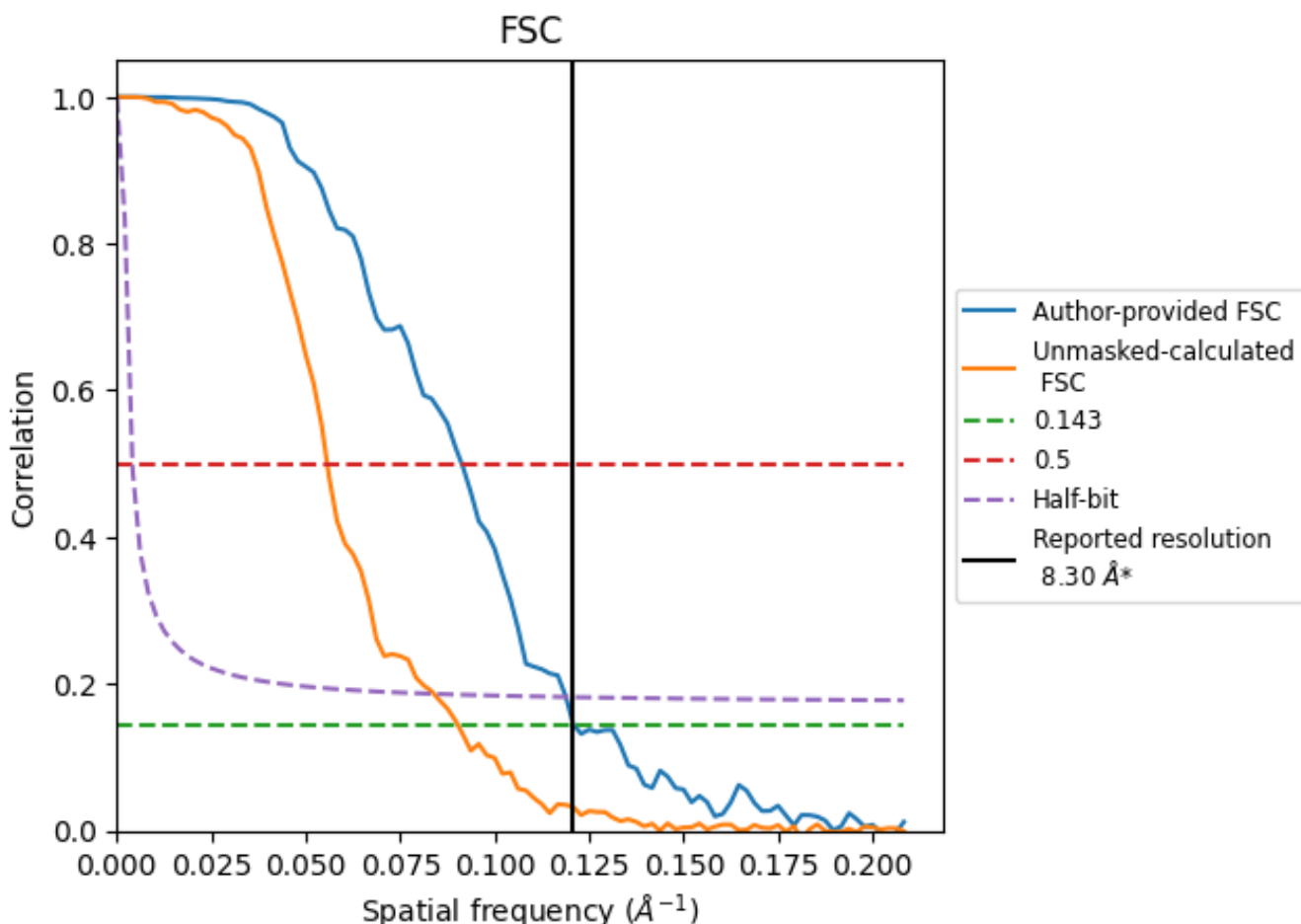


*Reported resolution corresponds to spatial frequency of 0.120 Å⁻¹

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 0.120 Å⁻¹

8.2 Resolution estimates [i](#)

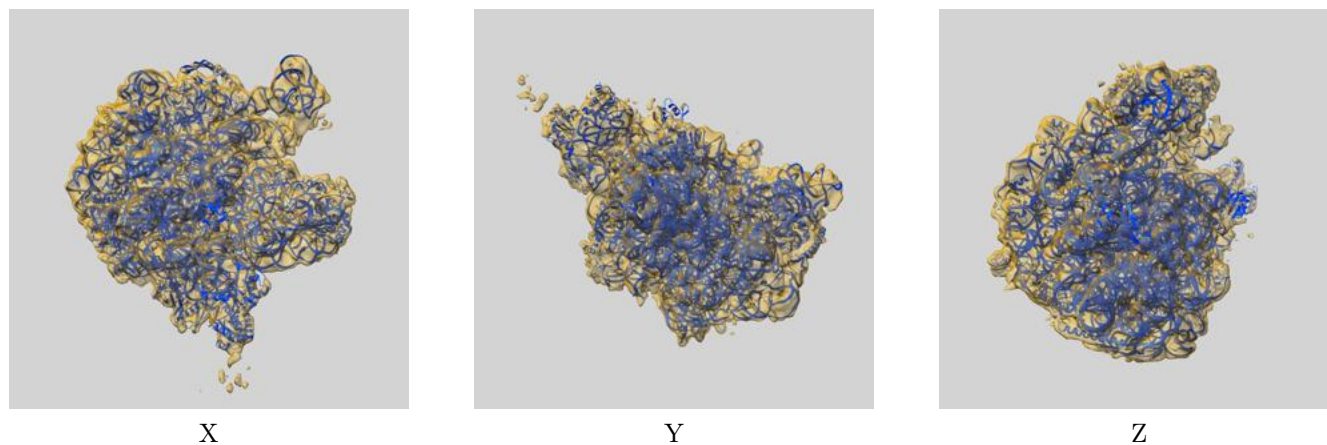
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	8.30	-	-
Author-provided FSC curve	8.26	10.96	8.42
Unmasked-calculated*	11.07	17.95	11.90

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 11.07 differs from the reported value 8.3 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13286 and PDB model 7PAU. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)



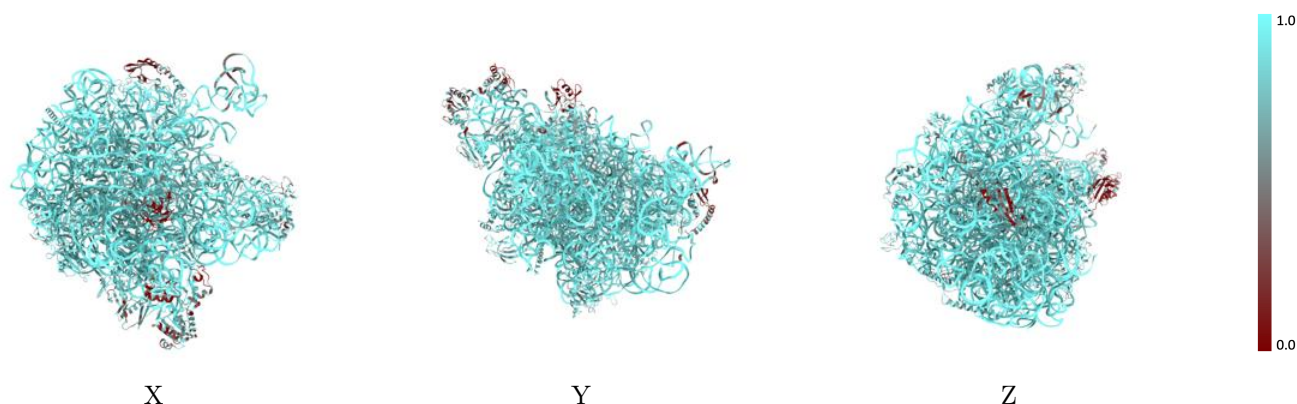
The images above show the 3D surface view of the map at the recommended contour level 0.46 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



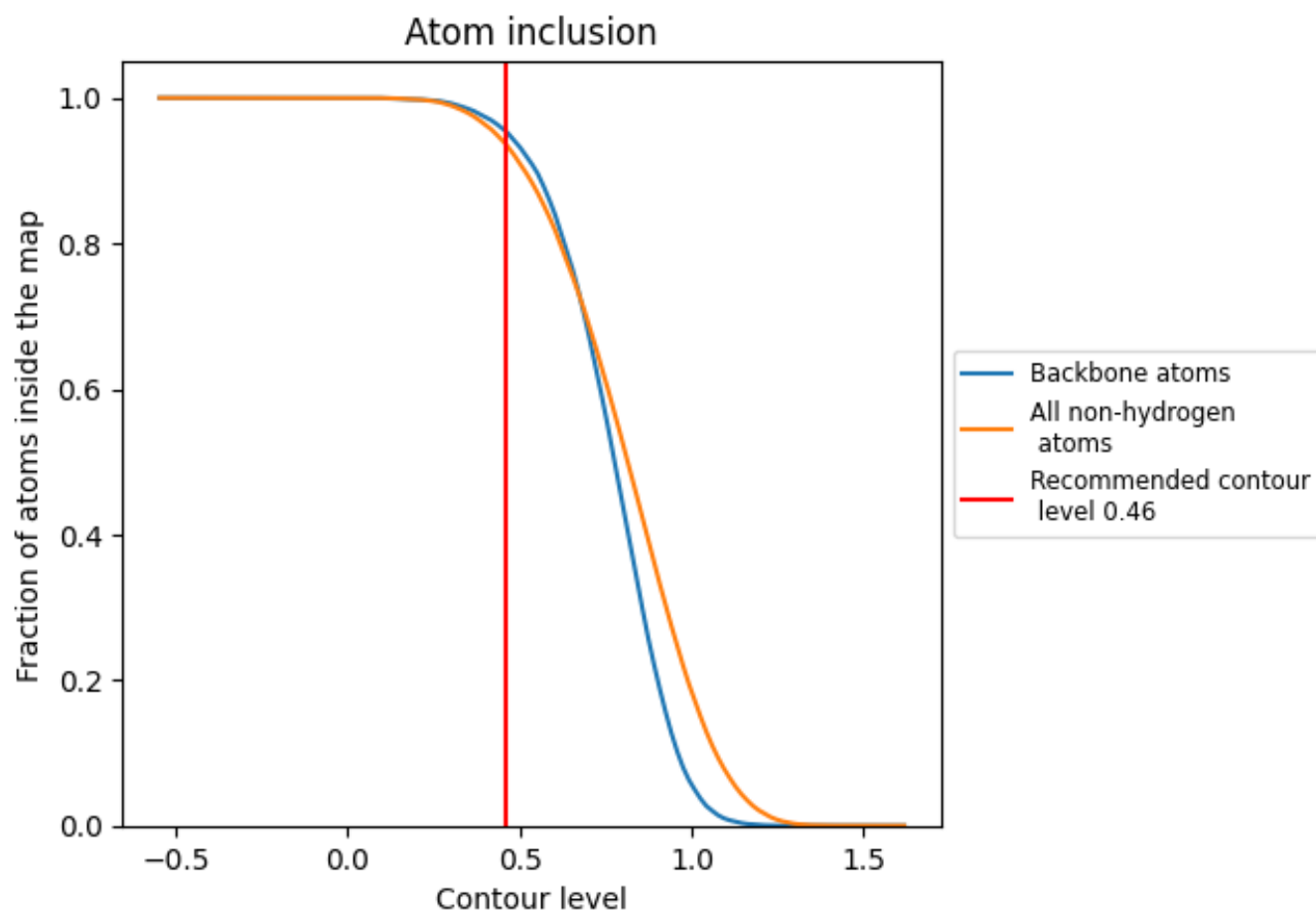
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.46).



































































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.46) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9365	 0.1700
0	 0.9836	 0.1250
1	 0.9721	 0.1360
2	 0.9324	 0.0950
3	 0.9858	 0.1820
4	 0.9808	 0.1820
7	 0.5421	 0.1310
a	 0.9373	 0.1320
b	 0.8980	 0.1330
c	 0.8784	 0.1540
d	 0.7636	 0.1510
e	 0.7427	 0.1610
f	 0.4952	 0.1440
g	 0.5821	 0.1350
h	 0.4556	 0.1170
i	 0.9369	 0.1510
j	 0.8902	 0.1390
k	 0.9011	 0.1450
l	 0.9213	 0.1460
m	 0.9252	 0.1480
n	 0.8431	 0.1510
o	 0.8551	 0.1580
p	 0.9191	 0.1360
q	 0.8523	 0.1370
r	 0.9542	 0.1610
s	 0.9365	 0.1520
t	 0.7654	 0.1330
u	 0.9422	 0.1330
v	 0.9616	 0.1290
w	 0.8477	 0.1880
x	 0.6297	 0.1540
y	 0.9493	 0.1370
z	 0.9496	 0.1610

