



wwPDB EM Validation Summary Report ⓘ

Dec 12, 2022 – 03:44 PM EST

PDB ID : 3J3V
EMDB ID : EMD-5642
Title : Atomic model of the immature 50S subunit from *Bacillus subtilis* (state I-a)
Authors : Li, N.; Guo, Q.; Zhang, Y.; Yuan, Y.; Ma, C.; Lei, J.; Gao, N.
Deposited on : 2013-04-28
Resolution : 13.30 Å (reported)
Based on initial models : 2J01, 2AW4

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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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:

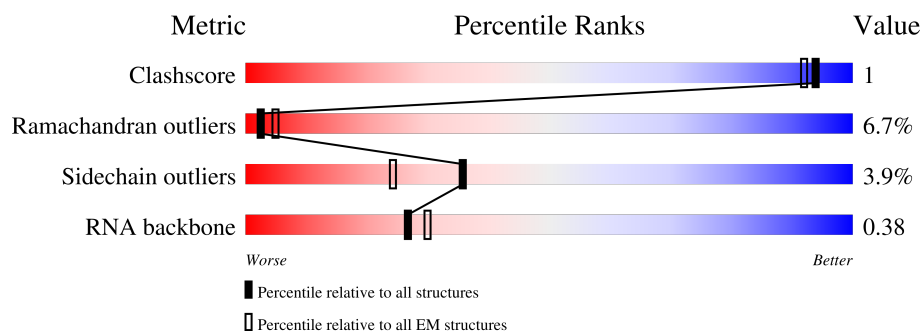
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 13.30 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.















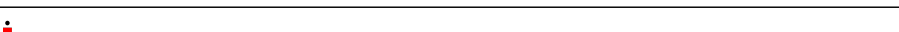



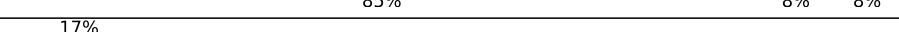
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	59	<div> <div>5%</div> <div>86%</div> <div>7%</div> <div>7%</div> </div>
2	2	44	<div> <div>93%</div> <div>7%</div> </div>
3	5	232	<div> <div>18%</div> <div>44%</div> <div>7%</div> <div>48%</div> </div>
4	6	141	<div> <div>77%</div> <div>94%</div> <div>6%</div> </div>
5	A	2927	<div> <div>53%</div> <div>36%</div> <div>9%</div> </div>
6	B	119	<div> <div>7%</div> <div>66%</div> <div>25%</div> <div>8%</div> </div>
7	C	277	<div> <div>90%</div> <div>9%</div> </div>

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Mol	Chain	Length	Quality of chain
8	D	209	 89% 9% ..
9	E	207	 86% 12% .
10	F	179	 11% 86% 13% .
11	G	179	 7% 87% . 9%
12	J	145	 86% 11% ..
13	K	122	 93% 7%
14	L	146	 85% 12% .
15	N	120	 94% 6%
16	O	120	 5% 83% 15% .
17	P	115	 73% 20% . .
18	Q	119	 94% . . .
19	R	102	 88% 11% .
20	S	113	 93% 5% ..
21	T	95	 86% 12% .
22	U	103	 84% 15% .
23	X	66	 85% 8% 8%
24	Y	59	 17% 92% . 5%

2 Entry composition

There are 24 unique types of molecules in this entry. The entry contains 86157 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 L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	55	Total	C	N	O	S	0	0
			433	267	87	72	7		

- Molecule 2 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	44	Total	C	N	O	S	0	0
			368	222	89	55	2		

- Molecule 3 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	5	120	Total	C	N	O	S	0	0
			910	576	156	176	2		

- Molecule 4 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	6	141	Total	C	N	O	S	0	0
			1044	657	184	196	7		

- Molecule 5 is a RNA chain called ribosome RNA 23S.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	2884	Total	C	N	O	P	0	0
			61914	27625	11428	19979	2882		

- Molecule 6 is a RNA chain called ribosome RNA 5S.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	119	Total	C	N	O	P	0	0
			2542	1135	462	827	118		

- Molecule 7 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	277	Total	C	N	O	S	0	0
			2129	1323	419	380	7		

- Molecule 8 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	206	Total	C	N	O	S	0	0
			1568	984	289	290	5		

- Molecule 9 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E	206	Total	C	N	O	S	0	0
			1567	983	290	292	2		

- Molecule 10 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	179	Total	C	N	O	S	0	0
			1413	898	246	261	8		

- Molecule 11 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	G	163	Total	C	N	O	S	0	0
			1246	776	226	242	2		

- Molecule 12 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J	143	Total	C	N	O	S	0	0
			1134	717	207	204	6		

- Molecule 13 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	K	122	Total	C	N	O	S	0	0
			921	571	173	173	4		

- Molecule 14 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L	146	Total	C	N	O	S	0	0
			1082	671	207	202	2		

- Molecule 15 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	120	Total	C	N	O	S	0	0
			962	588	187	182	5		

- Molecule 16 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	120	Total	C	N	O	S	0	0
			913	564	176	172	1		

- Molecule 17 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	P	112	Total	C	N	O		
			916	584	178	154	0	0

- Molecule 18 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 19 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	102	Total	C	N	O	S	0	0
			795	506	140	148	1		

- Molecule 20 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	112	Total	C	N	O	S	0	0
			868	541	168	155	4		

- Molecule 21 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	95	Total	C	N	O	S	0	0
			767	480	139	144	4		

- Molecule 22 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	103	Total	C	N	O	S	0	0
			780	488	145	143	4		

- Molecule 23 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	61	Total	C	N	O	S	0	0
			504	312	97	93	2		

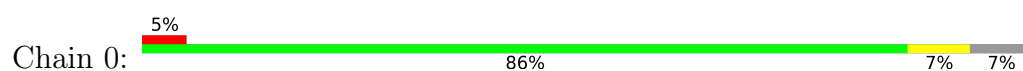
- Molecule 24 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	56	Total	C	N	O	S	0	0
			441	273	86	81	1		

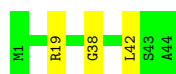
3 Residue-property plots [i](#)

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.

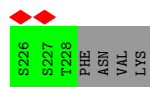
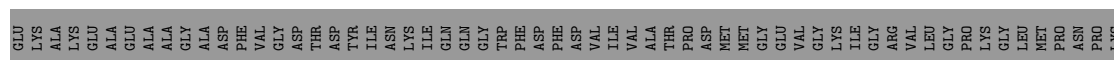
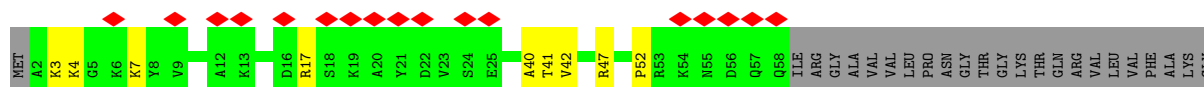
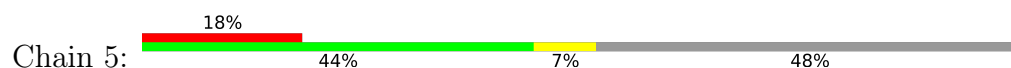
- Molecule 1: 50S ribosomal protein L32



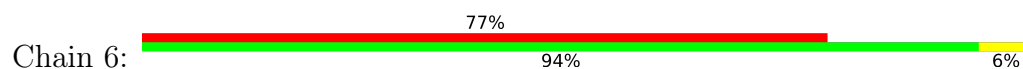
- Molecule 2: 50S ribosomal protein L34

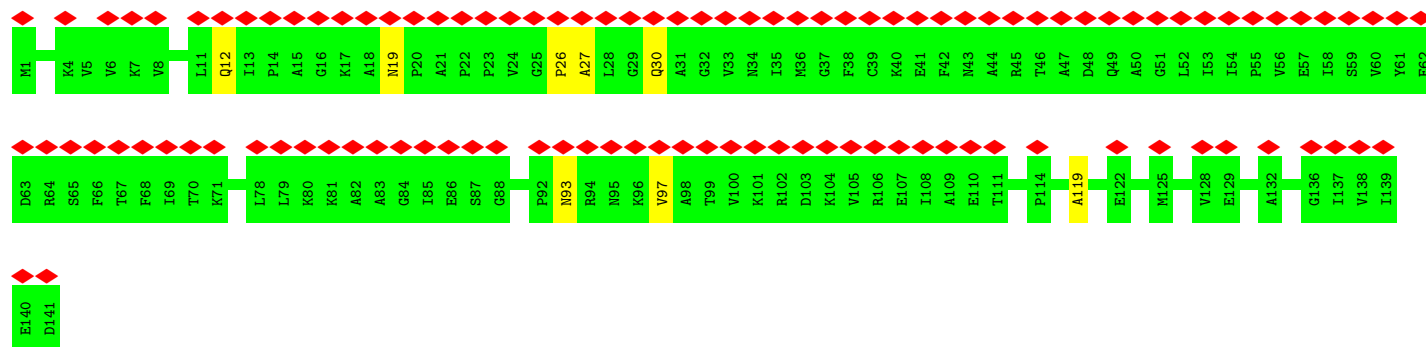


- Molecule 3: 50S ribosomal protein L1



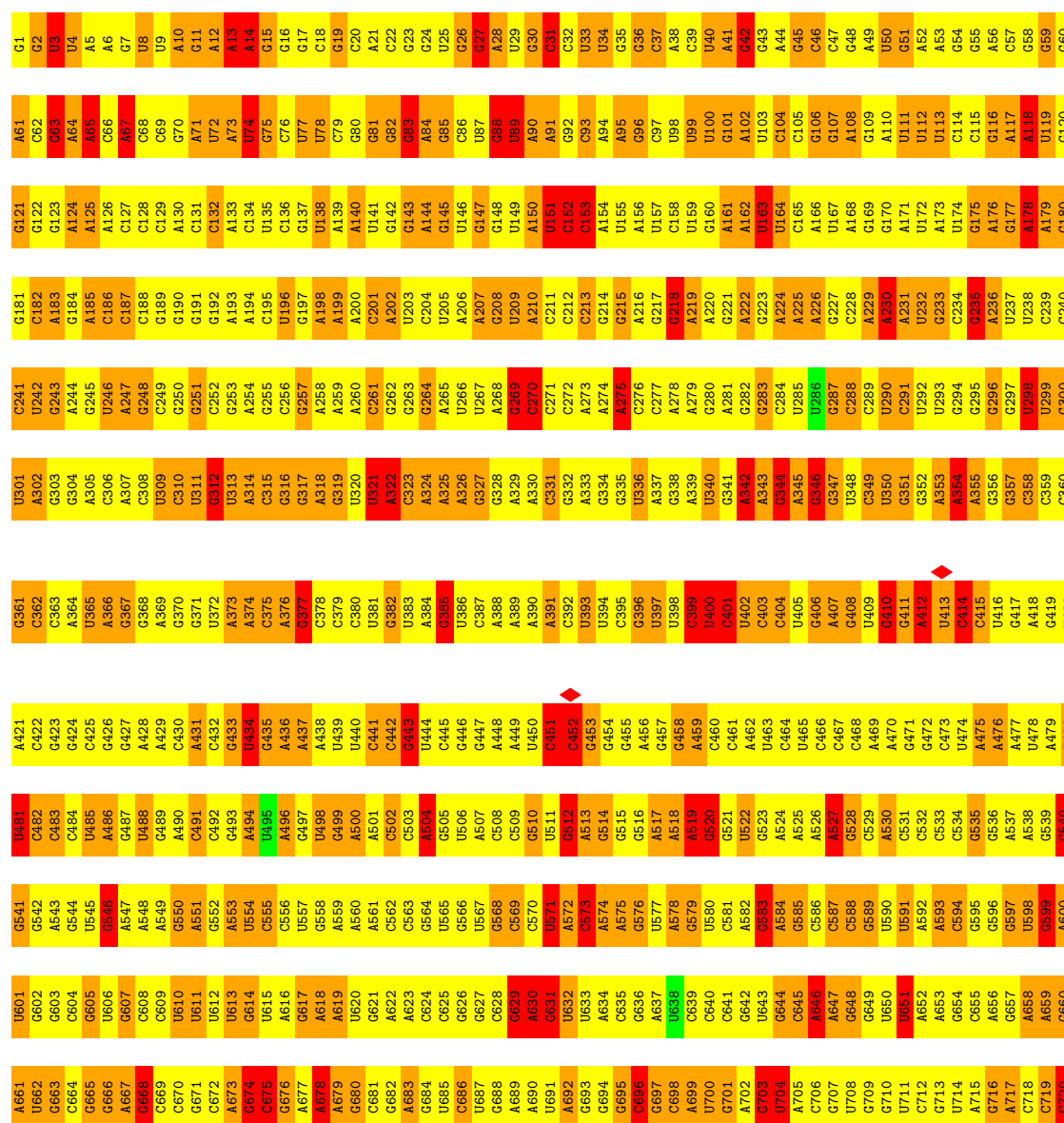
- Molecule 4: 50S ribosomal protein L11





• Molecule 5: ribosome RNA 23S

Chain A: 53% 36% 9%




U1501	U1441	A1381	U1321	C1261	A1201	A1141	U1081	A1021	C961	U901	A841	A781	G721
G1502	A1442	G1382	G1322	C1262	A1202	A1142	G1082	G1022	C962	G902	C842	A782	A722
G1503	C1443	U1383	A1323	G1263	G1203	U1143	G1083	G1023	G963	G903	C843	A783	A723
A1504	C1384	G1264	G1324	G1264	G1204	U1144	A1084	G1024	A964	G904	C844	A784	A724
U1505	A1445	A1265	A1325	A1265	U1205	G1145	U1085	A1025	A965	G905	G845	A785	C725
A1506	G1386	A1266	A1326	A1266	G1206	C1146	U1086	A1026	U966	G906	G846	A786	C726
U1507	C1387	G1267	U1327	G1267	G1207	U1147	U1087	A1027	C967	U907	A847	A787	A727
C1508	U1388	G1268	C1328	G1268	G1208	U1147	C1088	C1028	C968	A908	G848	A788	G728
C1509	C1389	A1269	C1329	A1269	G1209	U1148	C1089	A1029	C969	G909	A849	C789	G729
G1510	C1390	C1270	C1330	A1270	A1210	C1149	U1090	G1030	U970	A910	U850	A790	U730
C1511	U1391	C1271	C1331	U1271	C1211	U1151	U1091	C1031	A971	G911	A851	C791	G731
G1512	A1392	G1272	U1332	U1272	U1212	G1152	A1092	C1032	U972	C912	G852	U792	A732
U1513	C1393	G1273	C1333	G1273	G1213	G1153	G1093	C1033	G973	A913	C853	U793	U733
C1514	G1394	U1274	C1334	U1274	U1214	U1154	A1094	A1034	A974	C914	U854	U794	C734
C1515	C1395	G1275	A1335	G1275	U1215	U1155	C1095	G1035	C975	U915	G855	G795	U735
A1516	A1456	G1276	C1336	G1276	G1216	G1156	A1096	A1036	U976	G916	G856	A796	A736
A1517	U1457	A1277	C1337	A1277	U1217	A1157	A1097	C1037	U977	A917	U857	A797	C737
G1518	U1458	G1278	G1338	G1278	U1218	G1158	C1098	C1038	A978	U918	U858	A798	C738
U1519	U1459	C1279	A1339	C1279	C1219	U1159	C1099	G1039	U979	U919	C859	A799	C739
A1520	G1460	G1280	U1340	G1280	G1220	U1160	C1100	C1040	C980	G920	U860	G800	A740
G1521	A1461	C1281	A1341	C1281	A1221	A1161	C1101	C1041	C981	G921	C861	U801	U741
U1522	G1462	U1282	G1342	U1282	A1222	C1162	G1102	A1042	U982	A922	U862	G802	G742
U1523	C1463	U1283	C1343	U1283	C1223	U1163	G1103	G1043	U983	C923	C863	C803	U743
A1524	A1464	A1284	C1344	A1284	A1224	C1164	U1104	C1044	G984	U924	C864	C804	C744
G1525	A1465	G1285	U1345	G1285	G1225	U1165	G1105	U1045	G985	A925	G865	G805	C745
G1526	U1466	A1286	A1346	A1286	U1226	G1166	U1106	A1046	G986	G926	A866	G806	A746
C1527	G1467	G1287	A1347	G1287	G1227	C1167	U1107	A1047	A987	G927	A867	G807	G747
U1528	G1468	G1288	G1348	G1288	G1228	G1168	G1108	G1048	C988	G928	A868	A808	G748
G1529	G1469	A1409	U1349	U1289	U1229	C1169	G1109	G1049	U989	G929	U869	A809	G749
G1530	G1470	G1410	U1350	G1290	A1230	C1170	C1110	U1050	C990	C930	A870	G810	U750
G1531	G1471	U1411	U1351	A1291	G1231	G1171	U1111	C1051	A991	C931	G871	A811	G751
A1532	G1472	A1412	U1352	G1292	G1232	A1172	U1112	C1052	G992	C932	C872	G812	A752
C1533	A1473	C1293	C1353	A1293	A1233	A1173	A993	C1053	C993	C933	G873	A813	A753
A1534	C1474	A1414	C1354	A1294	G1234	A1174	G1114	A1054	C994	C934	U874	U814	G754
U1535	G1475	G1415	U1355	U1295	A1235	A1175	U995	A1055	U995	U934	U875	G815	U755
A1536	C1476	G1416	G1356	G1296	G1236	U1176	A1116	A1056	G996	A935	A876	U816	U756
G1537	A1477	A1417	A1357	C1297	C1237	G1177	C997	G1057	C997	C936	G877	G817	C757
G1538	G1478	U1418	G1358	C1298	G1238	U1178	G998	U1058	G998	C937	G878	G818	A758
C1539	G1479	G1419	G1359	G1299	U1239	A1179	A999	A1059	A999	G938	G879	G819	G759
A1540	A1480	G1420	A1360	G1300	U1240	C1180	G1000	U1060	G1000	G939	C880	U820	G760
A1541	G1481	A1421	A1361	U1301	C1241	G1181	U1001	A1061	U1001	G940	U881	A821	U761
A1542	G1482	C1422	G1362	A1302	U1242	G1182	G1002	A1062	G1002	U941	A882	G822	A762
U1543	U1483	A1423	C1363	U1303	A1243	G1183	A1003	G1063	A1003	U942	G883	G823	A763
C1544	U1484	A1424	G1364	G1304	A1244	G1184	U1004	U1064	C884	A943	C884	G824	C764
C1545	A1485	C1425	U1365	A1305	G1245	G1185	A1005	U1065	C885	C944	C885	G825	A765
G1546	G1486	A1426	G1366	G1306	G1246	C1186	A1006	A1066	U886	C945	U886	U826	C766
U1547	G1487	G1427	U1367	U1307	G1247	U1187	G1007	A1067	C887	G946	A888	G827	U767
U1548	G1488	G1428	U1368	A1308	C1248	A1188	U1008	A1068	A888	G947	A889	A829	G768
U1549	U1489	U1429	G1369	G1309	U1249	A1189	U1009	U1069	A889	A948	G890	A830	A769
C1550	A1490	U1430	C1370	C1310	G1250	U1189	C1010	G1070	G890	U949	G891	A831	A770
C1551	A1491	G1431	C1371	G1311	U1251	C1190	C1011	G1071	U892	U950	U892	G832	U771
C1552	G1492	A1432	C1372	A1312	G1252	C1191	G1012	A1072	A893	C951	A893	C833	G772
A1553	C1493	U1433	U1373	A1313	A1253	U1193	U1013	A1073	A894	C952	A894	C834	G773
U1554	G1494	A1434	C1374	A1314	A1254	A1194	A1014	A1074	G953	G953	G895	A835	A774
A1555	G1495	U1435	A1375	G1315	G1255	U1195	G1015	A1075	G954	C955	G896	A836	G775
G1556	C1496	G1436	G1376	A1316	C1256	C1196	U1016	G1076	C956	C956	G897	U837	G776
G1557	G1497	G1437	G1377	A1197	C1257	A1197	U1017	G1077	U898	A957	G898	C838	C777
U1498	U1498	G1438	G1378	C1198	A1258	C1198	G1018	U1078	C959	A957	U899	G839	C778
G1558	U1499	G1319	U1379	G1319	G1259	C1199	A1019	U1079	A958	A958	G840	A840	G780
C1559	U1500	G1440	U1380	G1320	A1260	G1200	U1140	G1080	U960	U960	U900	A840	G780

U2341	G2281	G2221	G2161	G2101	G2041	A1981	C1921	C1861	G1801	G1741	U1681	G1621	G1561
C2342	G2282	C2222	G2162	C2102	A2042	A1982	C1922	C1862	A1802	G1742	C1682	C1622	A1562
U2343	C2283	U2223	A2163	U2103	A2043	G1983	C1923	U1863	C1803	A1743	U1683	C1623	C1563
U2344	G2284	U2224	A2164	U2104	A2044	U1984	C1924	G1864	C1804	G1744	U1684	U1624	C1564
U2345	C2285	C2225	A2165	U2105	U2045	U1985	A1925	C1865	G1805	A1745	A1685	C1625	U1565
U2346	U2286	U2226	C2166	A2106	U2046	C1986	G1926	C1867	U1806	G1746	A1686	U1626	U1566
U2347	C2287	A2227	C2167	C2107	A2047	C1987	G1927	G1868	U1807	G1747	G1687	A1627	U1567
C2348	G2288	A2228	C2168	U2108	U2048	G1988	U1928	G1869	U1808	G1748	G1688	C1628	G1568
U2349	C2289	C2229	G2169	G2109	A2049	A1989	A1929	U1869	A1809	G1749	U1689	G1630	U1569
C2350	C2290	C2230	C2170	C2110	G2050	C1990	A1930	U1870	G1810	U1750	G1690	U1570	U1570
A2351	U2291	C2231	A2170	A2110	U2051	C1991	C1931	C1871	C1811	U1751	A1691	A1631	G1571
U2352	C2292	G2232	G2171	G2112	A2052	C1992	G1932	U1872	A1812	G1752	U1692	G1632	G1572
C2353	C2293	C2233	C2172	C2113	C2053	G1993	G1933	C1873	A1813	C1753	G1693	G1633	C1573
G2354	G2294	C2234	G2173	C2114	C2054	C1994	C1934	G1874	A1814	U1754	G1694	U1634	G1574
U2355	A2295	G2235	C2174	U2115	U2055	A1995	G1935	G1875	A1815	C1755	A1695	G1635	A1575
A2356	A2296	C2236	C2175	G2116	G2056	C1996	G1936	A1876	A1816	U1756	G1696	A1636	G1576
A2357	A2297	C2237	A2176	A2117	U2057	G1997	C1937	A1877	C1817	G1757	G1697	C1637	C1577
A2358	A2298	C2238	G2177	U2118	G2058	A1998	G1938	G1878	A1818	U1758	G1698	A1638	G1578
G2359	C2299	U2239	C2178	A2119	A2059	U1999	U1939	G	C1819	U1759	A1699	G1639	A1579
C2360	U2300	U2240	G2179	U2120	A2060	A2000	G1940	G	A1820	A1760	A1700	G1640	U1580
C2361	U2301	A2241	U2180	U2121	G2061	G2001	U1941	U	G1821	G1761	C1701	U1641	A1581
A2362	A2302	U2242	C2181	G2122	A2062	G2002	A1941	U	G1822	G1762	U1702	G1642	U1582
C2363	A2303	C2243	G2182	A2123	U2063	C2003	A1942	A	U1823	G1763	C1703	C1643	A1583
A2364	C2304	G2244	G2183	A2124	G2064	G2004	A1943	A	C1824	U1764	U1704	C1644	U1584
A2365	G2305	G2245	U2184	U2125	C2065	C2005	U1944	G	U1825	G1765	G1705	C1645	A1585
G2366	G2306	G2246	G2185	G2126	A2066	A2006	U1945	A	C1826	C1766	G1706	G1646	G1586
G2367	A2307	C2247	G2186	U2127	G2067	A2007	A1946	G	U1827	A1767	U1707	U1647	U1587
G2368	G2308	G2248	A2187	U2128	G2068	C2008	U1947	G	G1828	A1768	U1708	A1648	A1588
A2369	G2309	G2249	G2188	U2129	U2069	G2009	A1948	A	G1829	G1769	A1709	C1649	G1589
C2370	C2310	G2250	G2189	G2130	U2070	A2010	U1949	C	G1830	C1770	A1710	C1650	C1590
C2371	G2311	G2251	G2190	U2131	A2071	U2011	C1950	C	A1831	C1771	G1711	C1651	C1591
U2372	C2312	A2252	C2191	C2132	C2072	C2012	G1951	C	A1832	C1772	G1712	C1652	A1592
U2373	C2313	U2253	U2192	A2133	C2073	U2013	U1952	C	G1833	C1773	A1713	A1653	A1593
G2374	C2314	A2254	C2193	A2134	C2074	G2014	C1953	U	A1834	A1774	A1714	A1654	G1594
A2375	C2315	C2255	C2194	G2135	G2075	G2015	U1954	U	C1835	G1775	C1715	A1655	U1595
C2376	A2316	A2256	G2195	C2136	G2076	G2016	C1955	A	U1836	A1776	U1716	C1656	U1596
U2377	A2317	G2257	G2196	U2137	G2077	C2017	C1956	C	U1837	G1777	C1717	C1657	C1597
C2378	C2318	U2258	G2197	U2138	A2078	A2018	C1957	C	A1838	A1778	G1718	G1658	C1598
G2379	G2319	G2259	C2197	G2139	C2079	C2019	U1958	G	A1839	G1779	G1719	A1659	U1599
U2380	U2320	C2261	G2198	U2140	A2080	U2020	U1959	U	G1840	C1780	C1720	C1660	G1600
U2381	C2321	C2262	G2199	A2141	G2081	G2021	A1960	A	C1841	A1781	A1721	A1661	A1601
C2382	C2322	A2263	G2200	C2142	A2082	U2022	G1959	C	G1842	G1782	A1722	C1662	U1602
A2383	C2323	C2264	U2201	A2143	C2083	C2023	C1960	C	A1843	A1783	A1723	A1663	U1603
C2384	C2324	G2265	A2202	G2144	G2084	C2024	A1961	C	A1844	A1784	A1724	G1664	C1604
C2385	U2325	U2266	C2203	G2145	G2085	C2025	C1962	C	A1845	G1785	U1725	G1665	C1605
U2386	A2326	G2267	U2204	G2146	A2086	A2026	C1963	A	U1846	G1786	A1726	U1666	A1606
C2387	C2327	G2268	A2205	U2147	A2087	A2027	C1964	A	A1847	U1787	A1727	A1667	C1607
C2388	G2328	G2269	G2206	U2148	A2088	C2028	G1965	C	U1848	A1788	C1728	G1668	A1608
A2389	A2329	C2270	C2207	A2149	A2089	G2029	U1966	G	U1849	A1789	C1729	G1669	C1609
U2390	C2330	G2271	C2208	G2150	A2090	A2030	A1967	U	A1850	U1790	C1730	C1670	U1610
G2391	C2331	U2272	U2209	U2151	A2091	G2031	U1968	C	G1851	A1791	C1731	G1671	G1611
C2392	G2332	U2273	G2210	A2152	C2092	A2032	U1969	G	G1852	G1792	G1732	A1672	C1612
U2393	U2333	U2274	G2211	C2153	C2093	G2033	C1970	A	G1853	C1793	U1733	C1673	C1613
A2394	C2334	G2275	G2212	G2154	C2094	A2034	C1971	A	C1854	G1794	A1734	G1674	A1614
A2395	U2335	A2276	U2213	G2155	C2095	C2035	U1972	A	C1855	G1795	A1735	A1675	A1615
G2396	G2336	C2277	G2214	A2156	G2096	U2036	U1973	U	U1856	A1796	C1736	G1676	G1616
A2397	A2337	U2278	G2215	G2157	U2097	C2037	U1974	G	G1857	A1797	U1737	A1677	A1617
C2398	C2338	U2279	U2216	C2158	G2098	G2038	G1975	A	A1858	G1798	U1738	A1678	A1618
A2399	A2339	G2280	A2217	U2159	G2099	G2039	C1976	G	G1859	C1799	C1739	A1679	A1619
G2400	C2340		U2218	U2160	A2100	U2040	G1977	A	G1860	C1800	G1740	A1680	




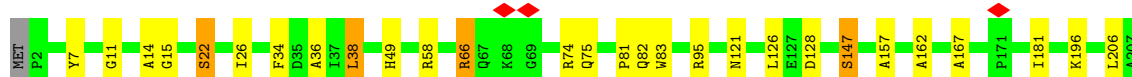
- Molecule 8: 50S ribosomal protein L3

Chain D:  89% 9% ..




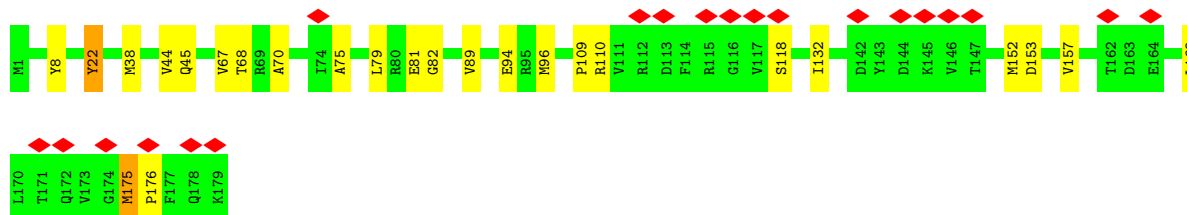
- Molecule 9: 50S ribosomal protein L4

Chain E:  86% 12% .




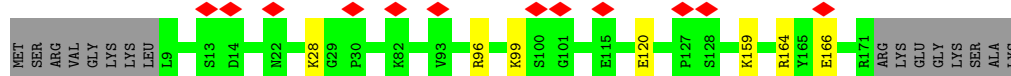
- Molecule 10: 50S ribosomal protein L5

Chain F:  11% 86% 13% .




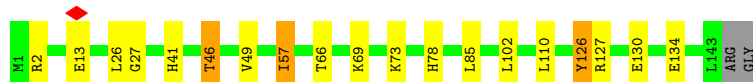
- Molecule 11: 50S ribosomal protein L6

Chain G:  7% 87% 9% .



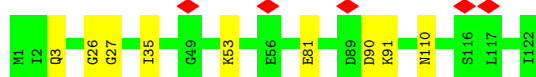
- Molecule 12: 50S ribosomal protein L13

Chain J:  86% 11% ..




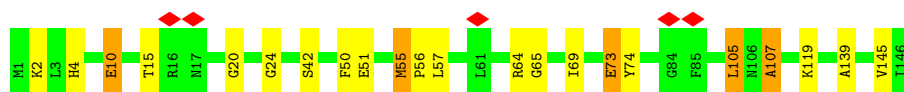
- Molecule 13: 50S ribosomal protein L14

Chain K:  93% 7%



- Molecule 14: 50S ribosomal protein L15

Chain L:  85% 12%




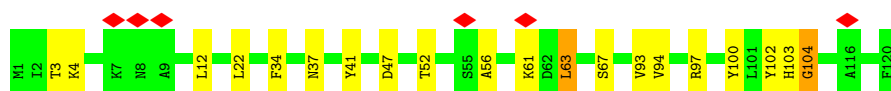
- Molecule 15: 50S ribosomal protein L17

Chain N:  94% 6%



- Molecule 16: 50S ribosomal protein L18

Chain O:  83% 15%



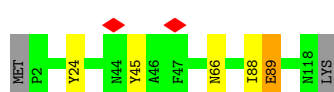
- Molecule 17: 50S ribosomal protein L19

Chain P:  73% 20%




- Molecule 18: 50S ribosomal protein L20

Chain Q:  94%



- Molecule 19: 50S ribosomal protein L21

Chain R:  88% 11%




- Molecule 20: 50S ribosomal protein L22

Chain S:  93% 5%




- Molecule 21: 50S ribosomal protein L23

Chain T:  86% 12%




- Molecule 22: 50S ribosomal protein L24

Chain U:  84% 15%



- Molecule 23: 50S ribosomal protein L29

Chain X:  85% 8% 8%



- Molecule 24: 50S ribosomal protein L30

Chain Y:  17% 92% 5%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	21020	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	59000	Depositor
Image detector	FEI EAGLE (4k x 4k)	Depositor
Maximum map value	10.841	Depositor
Minimum map value	-4.301	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2.7	Depositor
Map size (\AA)	384.0, 384.0, 384.0	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.5, 1.5, 1.5	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	1.04	0/440	1.06	1/584 (0.2%)
2	2	1.26	0/371	1.06	0/483
3	5	0.87	0/921	1.10	1/1239 (0.1%)
4	6	0.91	0/1058	1.02	0/1427
5	A	1.69	134/69349 (0.2%)	2.70	8798/108189 (8.1%)
6	B	1.64	4/2843 (0.1%)	2.64	336/4432 (7.6%)
7	C	1.01	0/2166	1.09	2/2902 (0.1%)
8	D	0.96	0/1590	1.07	0/2130
9	E	0.97	0/1586	1.08	2/2139 (0.1%)
10	F	0.96	0/1432	1.09	2/1920 (0.1%)
11	G	0.98	0/1264	1.05	0/1709
12	J	0.94	0/1157	1.04	0/1557
13	K	1.03	0/928	1.05	0/1245
14	L	0.98	0/1094	1.09	2/1457 (0.1%)
15	N	1.08	0/969	1.06	0/1294
16	O	1.01	0/922	1.05	1/1236 (0.1%)
17	P	1.10	0/929	1.21	5/1243 (0.4%)
18	Q	1.06	0/952	1.08	4/1266 (0.3%)
19	R	0.91	0/806	1.09	0/1080
20	S	1.01	0/877	1.13	1/1179 (0.1%)
21	T	1.00	0/774	1.11	1/1030 (0.1%)
22	U	0.87	0/790	1.15	0/1054
23	X	1.05	0/505	1.02	0/671
24	Y	0.97	0/443	1.01	0/594
All	All	1.55	138/94166 (0.1%)	2.45	9156/142060 (6.4%)

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
5	A	0	447

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Mol	Chain	#Chirality outliers	#Planarity outliers
6	B	0	15
8	D	0	2
9	E	0	1
14	L	0	2
15	N	0	1
17	P	0	3
21	T	0	3
All	All	0	474

The worst 5 of 138 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1253	A	N7-C5	-7.44	1.34	1.39
5	A	353	A	N7-C5	-7.42	1.34	1.39
5	A	629	G	C2'-C1'	-7.08	1.45	1.53
5	A	1449	C	P-O5'	-7.08	1.52	1.59
5	A	2297	A	N7-C5	-6.86	1.35	1.39

The worst 5 of 9156 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	10	G	P-O3'-C3'	26.30	151.26	119.70
5	A	1339	A	P-O3'-C3'	26.04	150.94	119.70
5	A	178	A	P-O3'-C3'	22.26	146.41	119.70
5	A	2062	A	P-O3'-C3'	21.01	144.91	119.70
5	A	74	U	P-O3'-C3'	20.60	144.42	119.70

There are no chirality outliers.

5 of 474 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	A	14	A	Sidechain
5	A	15	G	Sidechain
5	A	27	G	Sidechain
5	A	28	A	Sidechain
5	A	3	U	Sidechain

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	433	0	454	0	0
2	2	368	0	410	0	0
3	5	910	0	944	2	0
4	6	1044	0	1098	1	0
5	A	61914	0	31166	148	0
6	B	2542	0	1288	6	0
7	C	2129	0	2225	0	0
8	D	1568	0	1635	2	0
9	E	1567	0	1652	3	0
10	F	1413	0	1479	2	0
11	G	1246	0	1273	0	0
12	J	1134	0	1178	3	0
13	K	921	0	977	0	0
14	L	1082	0	1132	3	0
15	N	962	0	995	0	0
16	O	913	0	947	4	0
17	P	916	0	987	2	0
18	Q	940	0	1005	1	0
19	R	795	0	838	0	0
20	S	868	0	930	0	0
21	T	767	0	813	0	0
22	U	780	0	838	1	0
23	X	504	0	541	0	0
24	Y	441	0	478	0	0
All	All	86157	0	55283	174	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 1.

The worst 5 of 174 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:1799:G:H1	5:A:2011:U:H3	1.32	0.76
5:A:2557:U:H3	5:A:2564:A:H61	1.39	0.68
5:A:1672:A:H61	5:A:1684:U:H3	1.43	0.65
5:A:1339:A:C2	5:A:1679:A:C2	2.87	0.62
5:A:1976:C:H2'	5:A:1977:G:H5''	1.80	0.62

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	53/59 (90%)	40 (76%)	10 (19%)	3 (6%)	1	18
2	2	42/44 (96%)	38 (90%)	2 (5%)	2 (5%)	2	21
3	5	116/232 (50%)	96 (83%)	11 (10%)	9 (8%)	1	13
4	6	139/141 (99%)	117 (84%)	15 (11%)	7 (5%)	2	20
7	C	275/277 (99%)	224 (82%)	33 (12%)	18 (6%)	1	16
8	D	204/209 (98%)	158 (78%)	38 (19%)	8 (4%)	3	23
9	E	204/207 (99%)	166 (81%)	19 (9%)	19 (9%)	0	11
10	F	177/179 (99%)	136 (77%)	27 (15%)	14 (8%)	1	13
11	G	161/179 (90%)	150 (93%)	9 (6%)	2 (1%)	13	50
12	J	141/145 (97%)	117 (83%)	14 (10%)	10 (7%)	1	14
13	K	120/122 (98%)	103 (86%)	11 (9%)	6 (5%)	2	20
14	L	144/146 (99%)	105 (73%)	24 (17%)	15 (10%)	0	8
15	N	118/120 (98%)	96 (81%)	19 (16%)	3 (2%)	5	32
16	O	118/120 (98%)	87 (74%)	18 (15%)	13 (11%)	0	7
17	P	110/115 (96%)	71 (64%)	23 (21%)	16 (14%)	0	4
18	Q	115/119 (97%)	104 (90%)	10 (9%)	1 (1%)	17	57
19	R	100/102 (98%)	79 (79%)	13 (13%)	8 (8%)	1	12
20	S	110/113 (97%)	97 (88%)	8 (7%)	5 (4%)	2	22
21	T	93/95 (98%)	70 (75%)	14 (15%)	9 (10%)	0	10
22	U	101/103 (98%)	71 (70%)	18 (18%)	12 (12%)	0	6
23	X	59/66 (89%)	53 (90%)	4 (7%)	2 (3%)	3	26
24	Y	54/59 (92%)	47 (87%)	5 (9%)	2 (4%)	3	24
All	All	2754/2952 (93%)	2225 (81%)	345 (12%)	184 (7%)	2	15

5 of 184 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	5	41	THR
3	5	209	VAL
3	5	212	VAL
4	6	93	ASN
7	C	34	LEU

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	
1	0	49/53 (92%)	49 (100%)	0	100	100
2	2	39/39 (100%)	38 (97%)	1 (3%)	46	66
3	5	98/185 (53%)	93 (95%)	5 (5%)	24	48
4	6	110/110 (100%)	110 (100%)	0	100	100
7	C	225/225 (100%)	213 (95%)	12 (5%)	22	47
8	D	167/170 (98%)	157 (94%)	10 (6%)	19	44
9	E	169/170 (99%)	163 (96%)	6 (4%)	35	59
10	F	154/154 (100%)	147 (96%)	7 (4%)	27	52
11	G	138/151 (91%)	133 (96%)	5 (4%)	35	59
12	J	122/123 (99%)	113 (93%)	9 (7%)	13	38
13	K	101/101 (100%)	98 (97%)	3 (3%)	41	63
14	L	110/110 (100%)	107 (97%)	3 (3%)	44	65
15	N	100/100 (100%)	97 (97%)	3 (3%)	41	63
16	O	93/93 (100%)	90 (97%)	3 (3%)	39	61
17	P	97/100 (97%)	90 (93%)	7 (7%)	14	39
18	Q	96/98 (98%)	95 (99%)	1 (1%)	76	86
19	R	84/84 (100%)	79 (94%)	5 (6%)	19	44
20	S	93/93 (100%)	91 (98%)	2 (2%)	52	71
21	T	85/85 (100%)	83 (98%)	2 (2%)	49	69
22	U	87/87 (100%)	84 (97%)	3 (3%)	37	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	X	54/57 (95%)	51 (94%)	3 (6%)	21	46
24	Y	51/53 (96%)	51 (100%)	0	100	100
All	All	2322/2441 (95%)	2232 (96%)	90 (4%)	36	56

5 of 90 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	K	90	ASP
17	P	74	PHE
14	L	51	GLU
16	O	94	VAL
19	R	10	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
16	O	103	HIS
20	S	2	GLN
10	F	37	ASN
10	F	172	GLN
11	G	23	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	A	2882/2927 (98%)	895 (31%)	205 (7%)
6	B	118/119 (99%)	24 (20%)	3 (2%)
All	All	3000/3046 (98%)	919 (30%)	208 (6%)

5 of 919 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	A	2	G
5	A	3	U
5	A	4	U
5	A	8	U
5	A	10	A

5 of 208 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	A	1606	A
5	A	1999	A
5	A	2870	G
5	A	1629	C
5	A	1787	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 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.

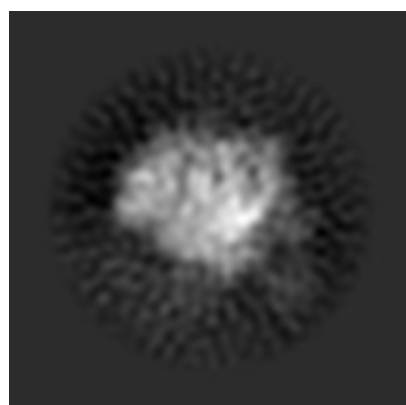
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5642. These allow visual inspection of the internal detail of the map and identification of artifacts.

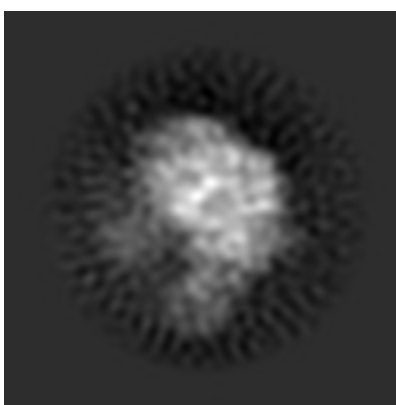
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

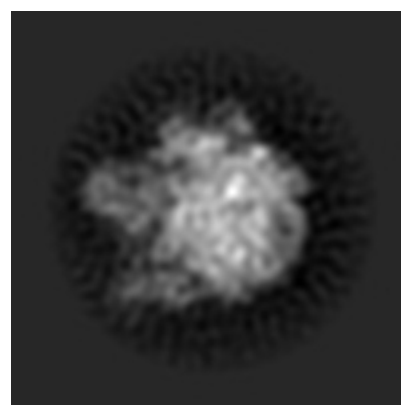
6.1.1 Primary map



X



Y

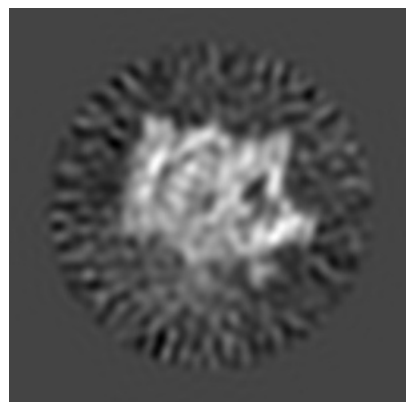


Z

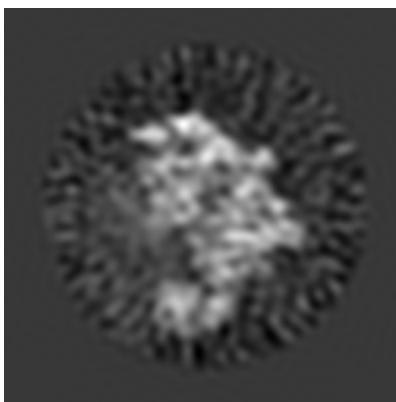
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

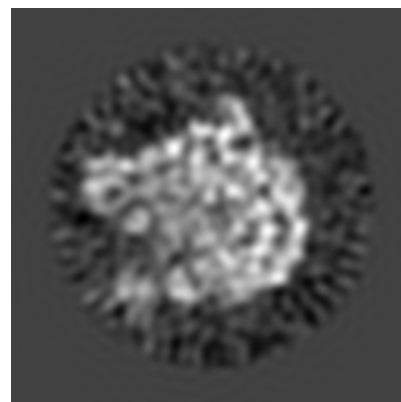
6.2.1 Primary map



X Index: 128



Y Index: 128

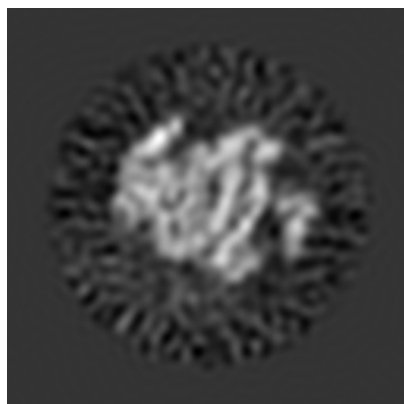


Z Index: 128

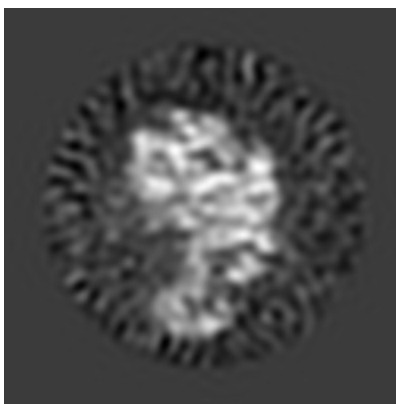
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

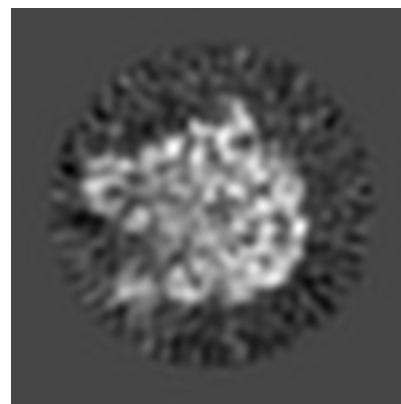
6.3.1 Primary map



X Index: 143



Y Index: 139

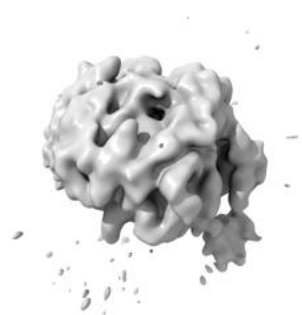


Z Index: 130

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

6.4 Orthogonal surface views [i](#)

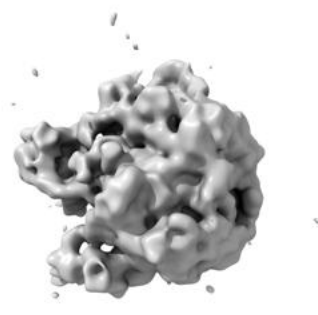
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.7. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

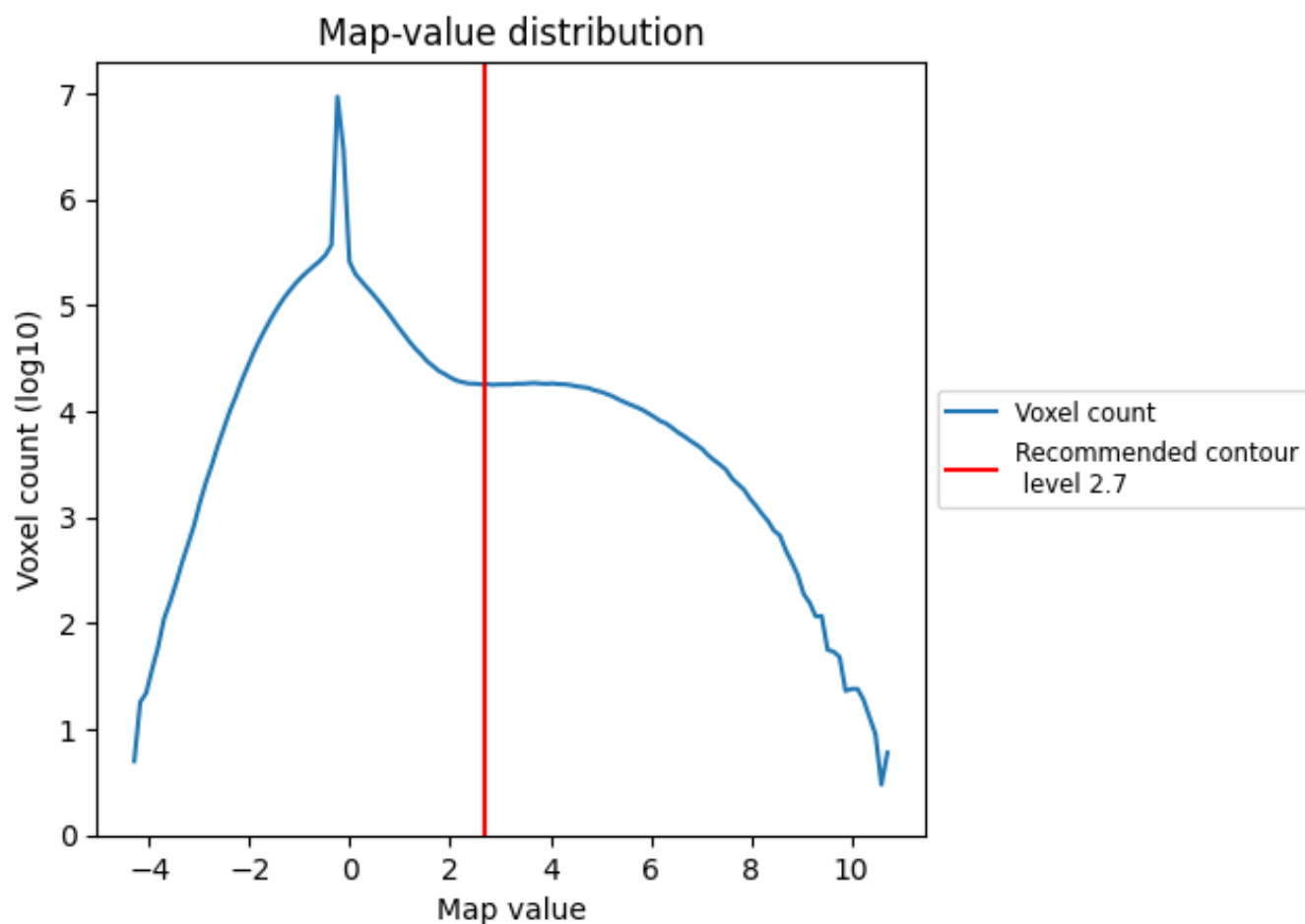
6.5 Mask visualisation

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

7 Map analysis [i](#)

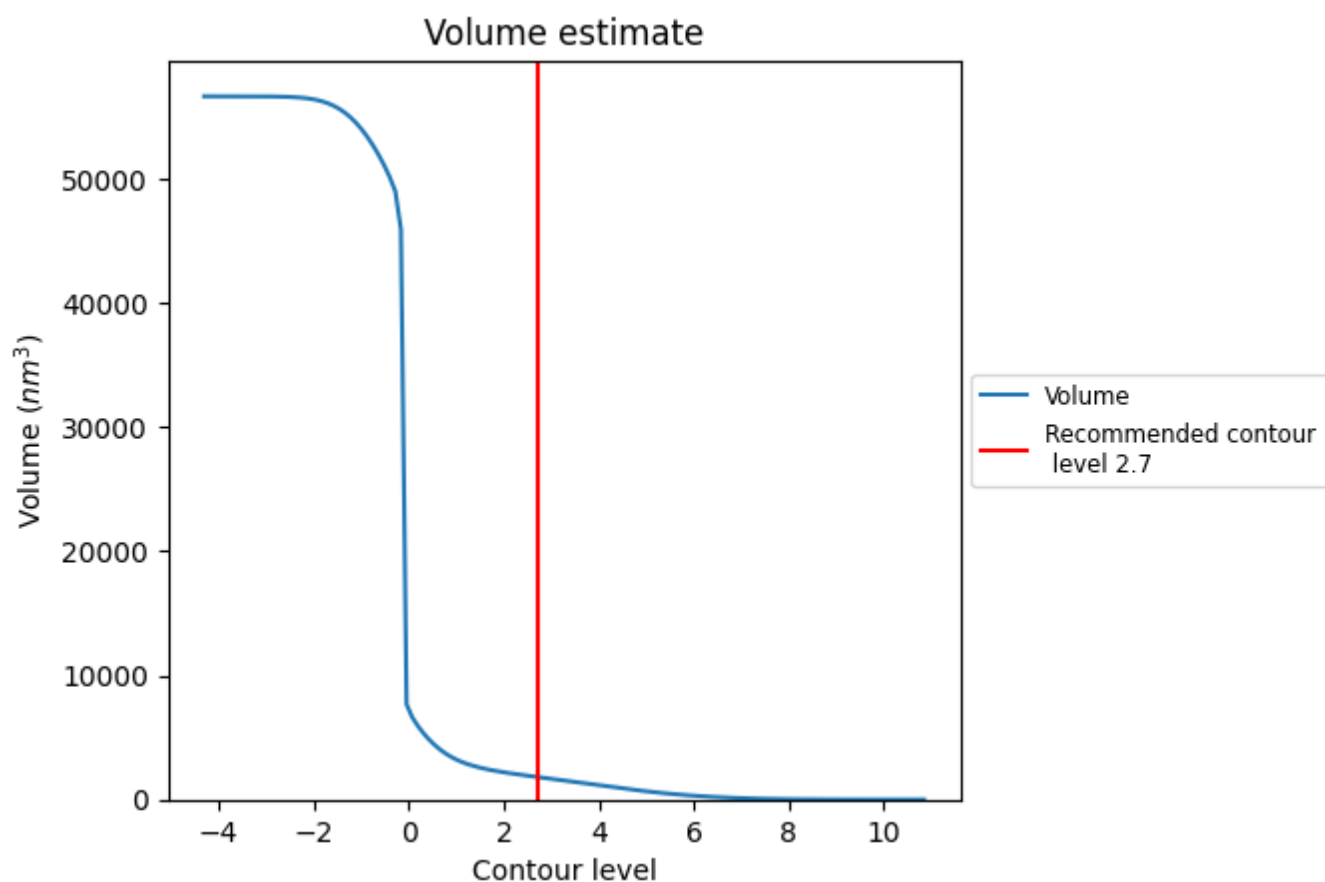
This section contains the results of statistical analysis of the map.

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.

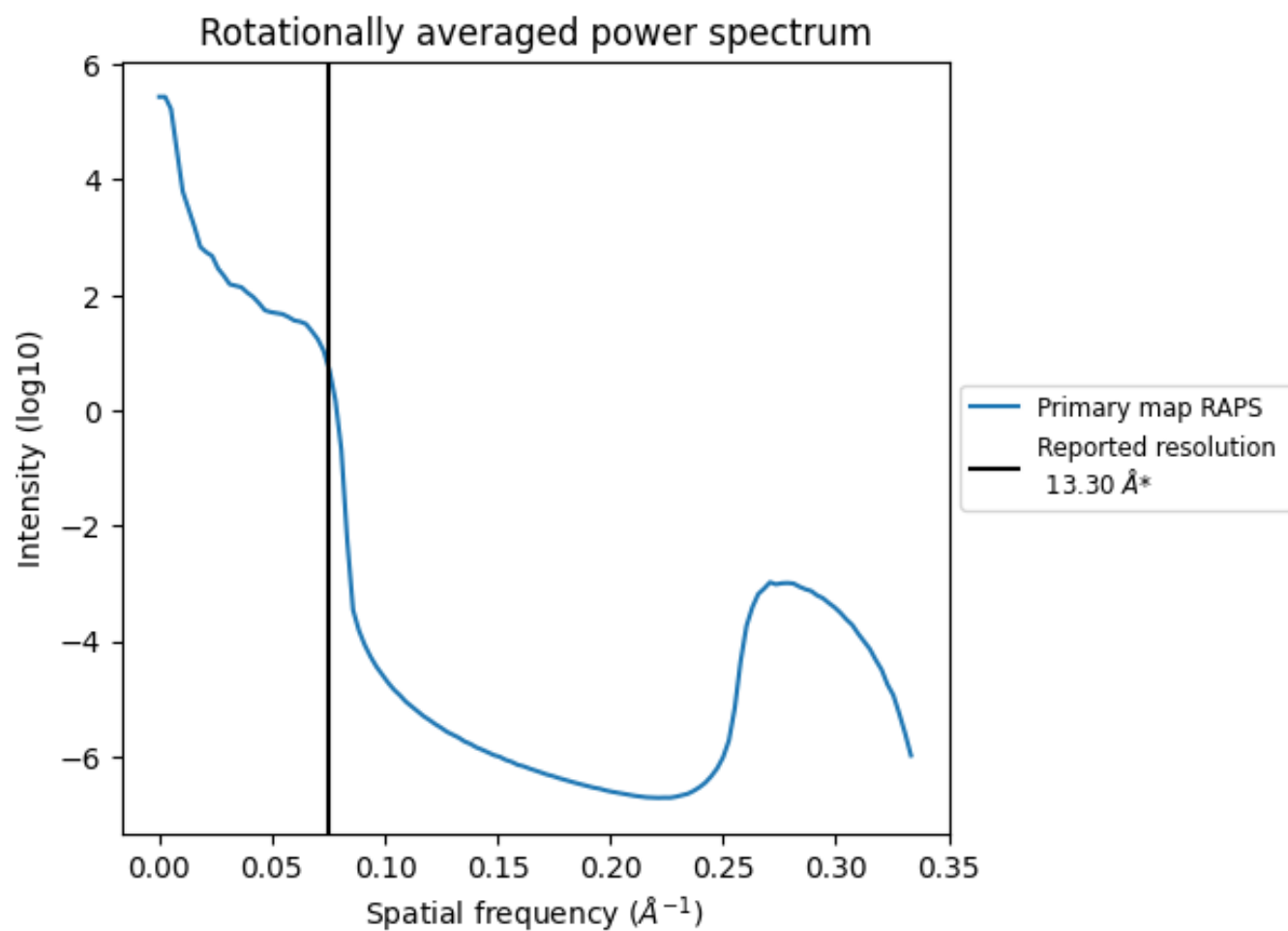
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1820 nm³; this corresponds to an approximate mass of 1644 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 0.075 Å⁻¹

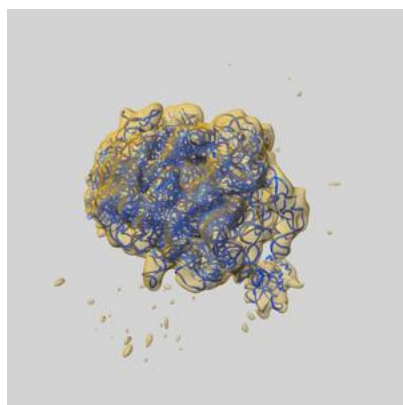
8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

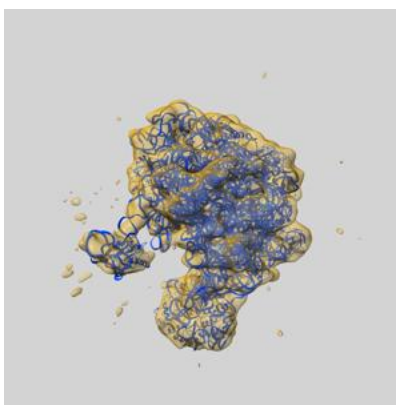
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5642 and PDB model 3J3V. Per-residue inclusion information can be found in section [3](#) on page [8](#).

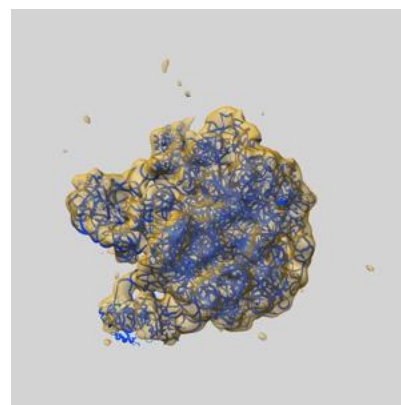
9.1 Map-model overlay [i](#)



X



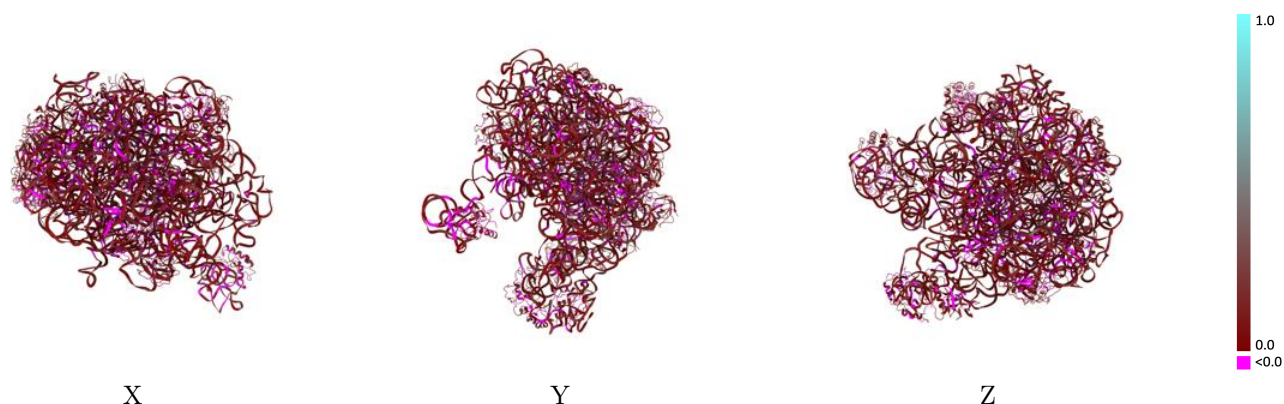
Y



Z

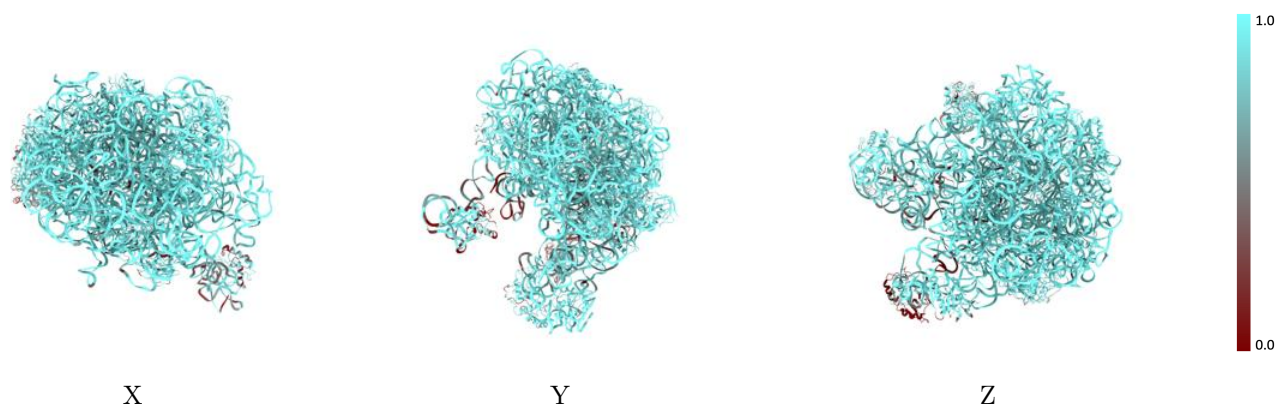
The images above show the 3D surface view of the map at the recommended contour level 2.7 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



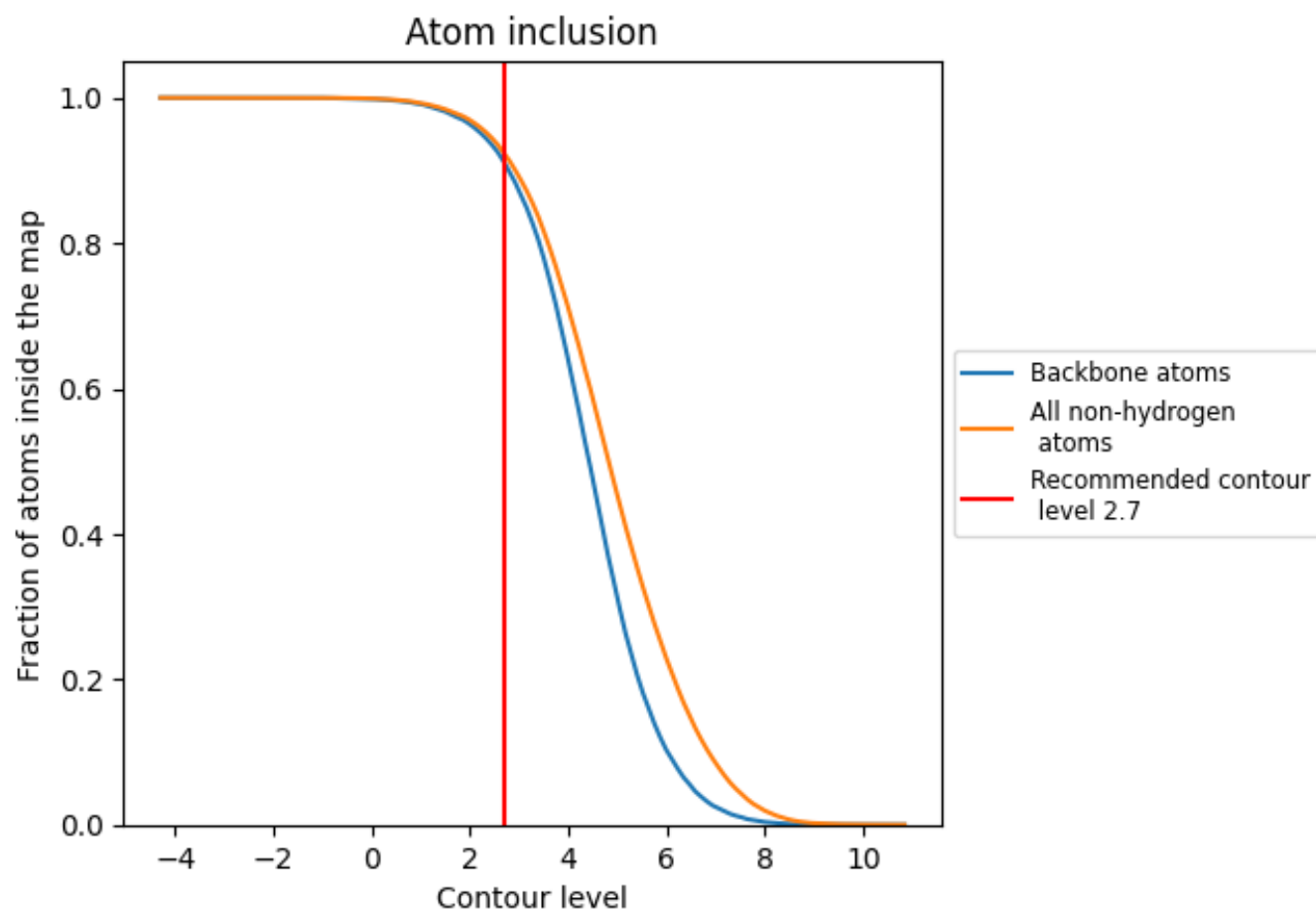
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.7).



















































9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 92% 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 (2.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9229	 0.0810
0	 0.9476	 0.0410
2	 1.0000	 0.0160
5	 0.6233	 0.0580
6	 0.2031	 0.0410
A	 0.9362	 0.0910
B	 0.8525	 0.0870
C	 0.9604	 0.0350
D	 0.9663	 0.0560
E	 0.9694	 0.0560
F	 0.8475	 0.0720
G	 0.8844	 0.0820
J	 0.9576	 0.0420
K	 0.9365	 0.0590
L	 0.9125	 0.0420
N	 1.0000	 0.0510
O	 0.9279	 0.0730
P	 0.9125	 0.0450
Q	 0.9670	 0.0250
R	 0.9796	 0.0700
S	 0.9680	 0.0470
T	 0.9906	 0.0490
U	 0.9547	 0.0470
X	 0.9918	 0.0830
Y	 0.7494	 0.0410

