



wwPDB EM Validation Summary Report ⓘ

Mar 22, 2026 – 09:46 PM UTC

PDB ID : 7BL6 / pdb_00007bl6
EMDB ID : EMD-12219
Title : 50S-ObgE-GMPPNP particle
Authors : Hilal, T.; Nikolay, R.; Schmidt, S.; Spahn, C.M.T.
Deposited on : 2021-01-18
Resolution : 4.00 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:

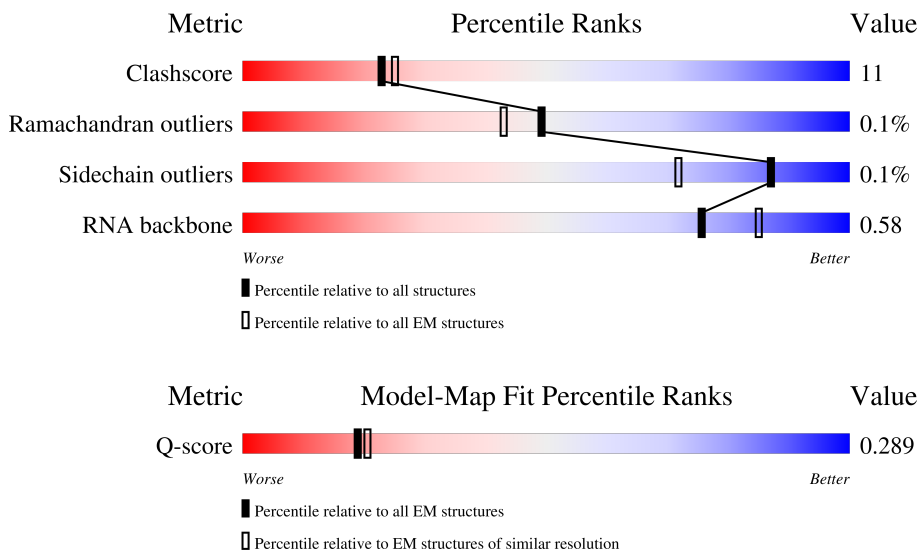
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 4.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7587 (3.50 - 4.50)

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	g	38	 68% 32%
2	C	273	 72% 27% .
3	D	209	 71% 29%





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Mol	Chain	Length	Quality of chain
4	E	201	76% 20%
5	F	179	66% 33%
6	G	177	5% 73% 26%
7	J	142	80% 20%
8	L	144	77% 23%
9	N	120	77% 23%
10	O	117	71% 28%
11	Q	118	81% 17%
12	R	103	74% 26%
13	S	110	72% 28%
14	T	100	64% 29% 7%
15	U	104	81% 17%
16	V	94	71% 29%
17	W	85	72% 18% 11%
18	X	78	69% 29%
19	Y	63	5% 60% 38%
20	Z	59	76% 22%
21	0	57	70% 28%
22	1	55	65% 25% 9%
23	2	46	70% 30%
24	K	123	70% 29%
25	P	115	81% 17%
26	M	136	75% 24%
27	H	149	40% 74% 26%
28	d	70	17% 47% 20% 33%

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Mol	Chain	Length	Quality of chain
29	A	2904	 47% 47% 6%
30	B	119	 48% 49% .
31	9	390	 7% 70% 17% 13%
32	3	65	 68% 29% . .

2 Entry composition [i](#)

There are 36 unique types of molecules in this entry. The entry contains 92769 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 L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	g	38	302	185	65	48	4	0	0

- Molecule 2 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	C	271	2082	1288	423	364	7	0	0

- Molecule 3 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	D	209	1565	979	288	294	4	0	0

- Molecule 4 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	E	193	1483	932	266	280	5	0	0

- Molecule 5 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	F	177	1410	899	249	256	6	0	0

- Molecule 6 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	G	176	1323	832	243	246	2	0	0

- Molecule 7 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	J	142	1129	714	212	199	4	0	0

- Molecule 8 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	L	144	1053	654	207	190	2	0	0

- Molecule 9 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	N	120	961	593	196	167	5	0	0

- Molecule 10 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	O	116	892	552	178	162	0	0

- Molecule 11 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
11	Q	117	947	604	192	151	0	0

- Molecule 12 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	R	103	816	516	153	145	2	0	0

- Molecule 13 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	S	110	857	532	166	156	3	0	0

- Molecule 14 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	T	93	738	466	139	131	2	0	0

- Molecule 15 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	U	102	779	492	146	141		0	0

- Molecule 16 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	V	94	753	479	137	134	3	0	0

- Molecule 17 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	W	76	577	357	117	102	1	0	0

- Molecule 18 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	X	77	625	388	129	106	2	0	0

- Molecule 19 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	Y	63	509	313	99	95	2	0	0

- Molecule 20 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	Z	58	449	281	87	79	2	0	0

- Molecule 21 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 22 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	1	50	Total	C	N	O	S	0	0
			409	263	75	71			

- Molecule 23 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 24 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	K	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 25 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	P	113	Total	C	N	O	S	0	0
			911	571	178	161	1		

- Molecule 26 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 27 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	H	149	Total	C	N	O	S	0	0
			1110	699	197	213	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d	47	Total	C	N	O	S	0	0
			364	227	64	67	6		

- Molecule 29 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	A	2897	Total	C	N	O	P	0	0
			62195	27745	11446	20107	2897		

- Molecule 30 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	B	119	Total	C	N	O	P	0	0
			2548	1135	466	829	118		

- Molecule 31 is a protein called GTPase ObgE/CgtA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	9	338	Total	C	N	O	S	0	0
			2582	1626	453	490	13		

- Molecule 32 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 33 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
33	g	1	Total	Zn	0
			1	1	
33	d	1	Total	Zn	0
			1	1	

- Molecule 34 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
34	A	1	Total	Mg	0
			1	1	
34	9	1	Total	Mg	0
			1	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.

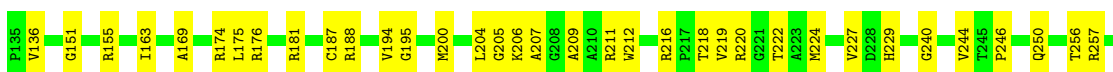
- Molecule 1: 50S ribosomal protein L36

Chain g:  68% 32%



- Molecule 2: 50S ribosomal protein L2

Chain C:  72% 27%




- Molecule 3: 50S ribosomal protein L3

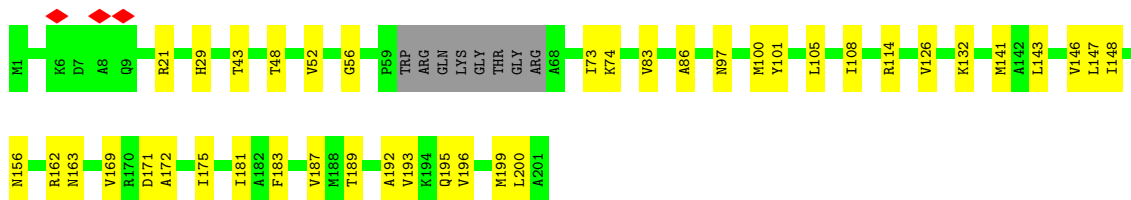
Chain D:  71% 29%



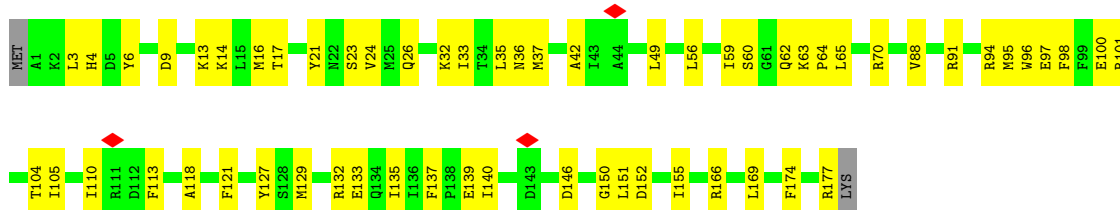
- Molecule 4: 50S ribosomal protein L4

Chain E:  76% 20%

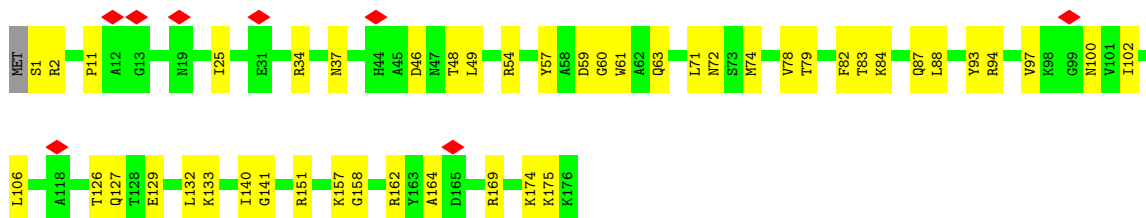
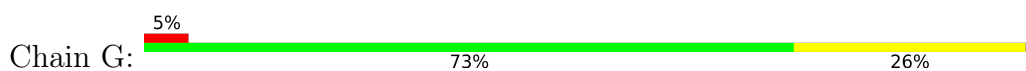




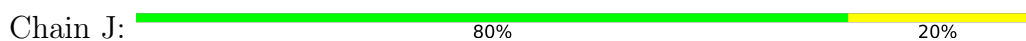
- Molecule 5: 50S ribosomal protein L5



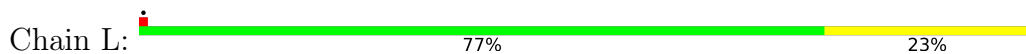
- Molecule 6: 50S ribosomal protein L6



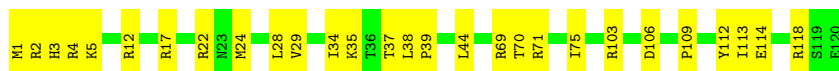
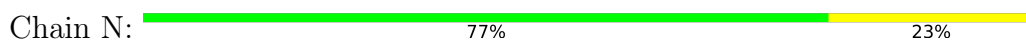
- Molecule 7: 50S ribosomal protein L13



- Molecule 8: 50S ribosomal protein L15

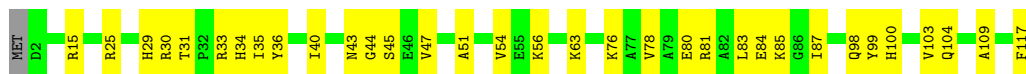


- Molecule 9: 50S ribosomal protein L17




- Molecule 10: 50S ribosomal protein L18

Chain O:  71% 28%



- Molecule 11: 50S ribosomal protein L20

Chain Q:  81% 17%



- Molecule 12: 50S ribosomal protein L21

Chain R:  74% 26%



- Molecule 13: 50S ribosomal protein L22

Chain S:  72% 28%




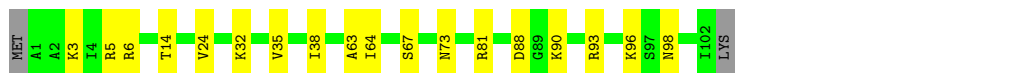
- Molecule 14: 50S ribosomal protein L23

Chain T:  64% 29% 7%



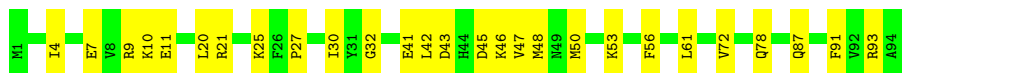
- Molecule 15: 50S ribosomal protein L24

Chain U:  81% 17%

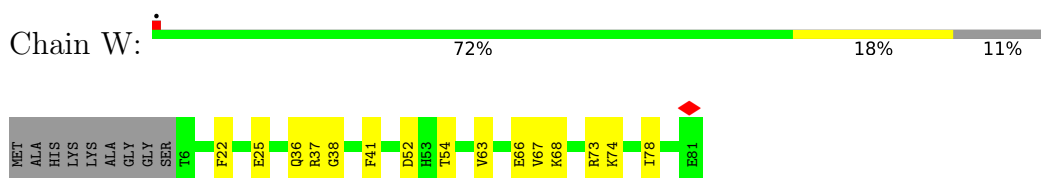


- Molecule 16: 50S ribosomal protein L25

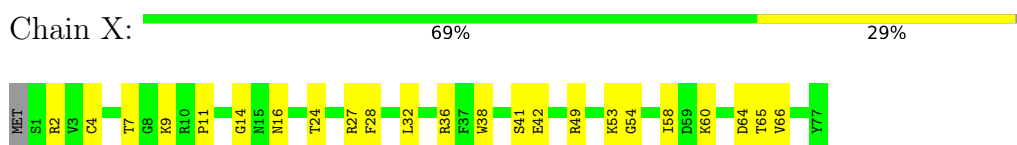
Chain V:  71% 29%



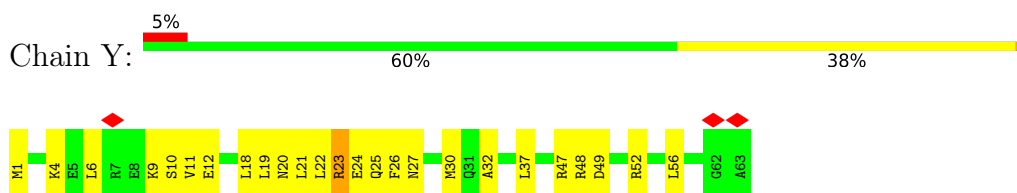
- Molecule 17: 50S ribosomal protein L27



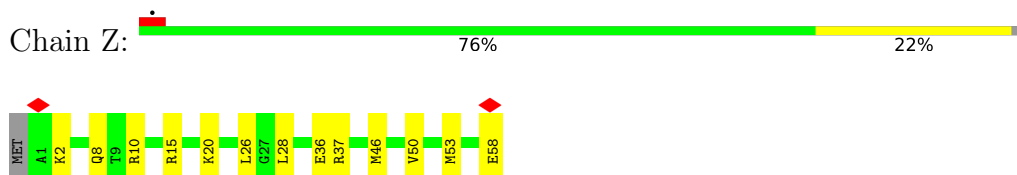
- Molecule 18: 50S ribosomal protein L28



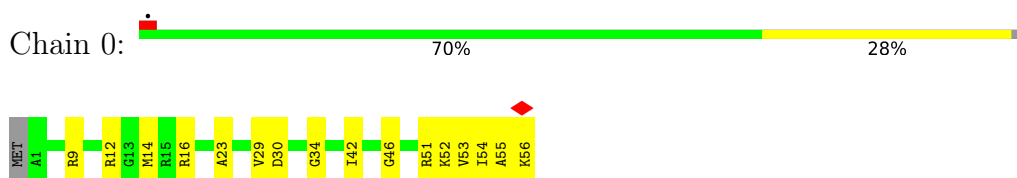
- Molecule 19: 50S ribosomal protein L29



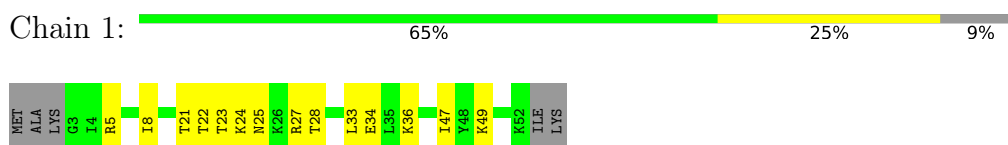
- Molecule 20: 50S ribosomal protein L30



- Molecule 21: 50S ribosomal protein L32



- Molecule 22: 50S ribosomal protein L33



- Molecule 23: 50S ribosomal protein L34

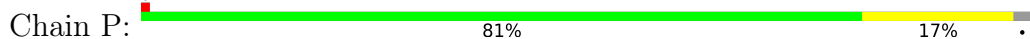




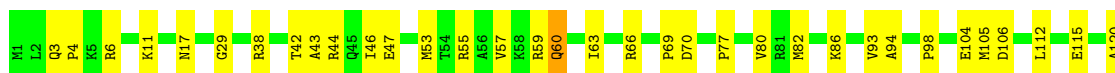
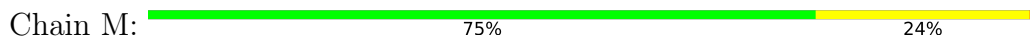
• Molecule 24: 50S ribosomal protein L14



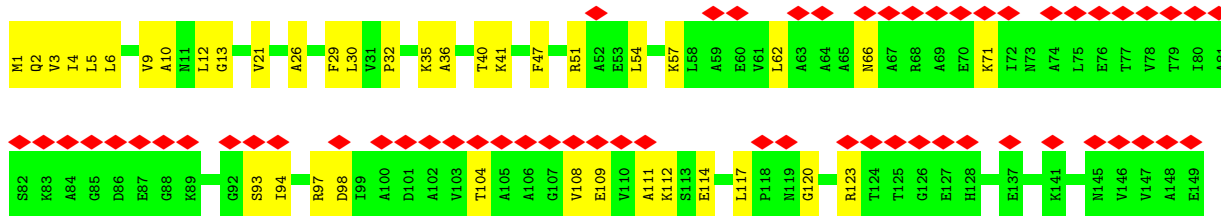
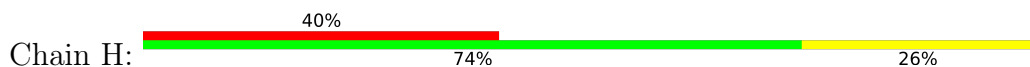
• Molecule 25: 50S ribosomal protein L19



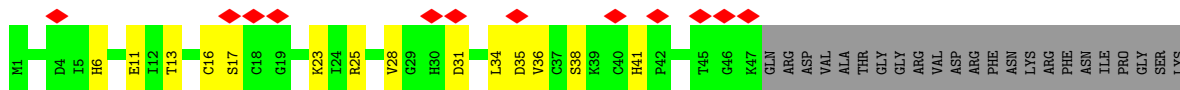
• Molecule 26: 50S ribosomal protein L16



• Molecule 27: 50S ribosomal protein L9



• Molecule 28: 50S ribosomal protein L31



• Molecule 29: 23S ribosomal RNA



U1132	U1133	C1134	C1135	G1136	G1137	G1138	C1139	U1140	U1141	U1142	A1147	C1153	G1154	A1155	G1156	G1157	C1161	G1162	C1163	C1164	A1165	G1166	C1167	G1168	G1169	C1170	G1171	G1172	C1173	G1174	C1175	G1176	G1177	G1178	C1179	G1180	C1181	G1182	C1183	A1184	G1185	C1186	G1187	A1188	C1189	G1190	C1191	G1192	C1193	G1194	C1195	G1196	C1197	G1198	C1199	G1200	C1201	G1202	C1203	G1204	C1205	G1206	C1207	G1208	C1209	G1210	C1211	G1212	C1213	G1214	C1215	G1216	C1217	G1218	C1219	G1220	C1221	G1222	C1223	G1224	C1225	G1226	C1227	G1228	C1229	G1230	C1231	G1232	C1233	G1234	C1235	G1236	C1237	G1238	C1239	G1240	C1241	G1242	C1243	G1244	C1245	G1246	C1247	G1248	C1249	G1250	C1251	G1252	C1253	G1254	C1255	G1256	C1257	G1258	C1259	G1260	C1261	G1262	C1263	G1264	C1265	G1266	C1267	G1268	C1269	G1270	C1271	G1272	C1273	G1274	C1275	G1276	C1277	G1278	C1279	G1280	C1281	G1282	C1283	G1284	C1285	G1286	C1287	G1288	C1289	G1290	C1291	G1292	C1293	G1294	C1295	G1296	C1297	G1298	C1299	G1300	C1301	G1302	C1303	G1304	C1305	G1306	C1307	G1308	C1309	G1310	C1311	G1312	C1313	G1314	C1315	G1316	C1317	G1318	C1319	G1320	C1321	G1322	C1323	G1324	C1325	G1326	C1327	G1328	C1329	G1330	C1331	G1332	C1333	G1334	C1335	G1336	C1337	G1338	C1339	G1340	C1341	G1342	C1343	G1344	C1345	G1346	C1347	G1348	C1349	G1350	C1351	G1352	C1353	G1354	C1355	G1356	C1357	G1358	C1359	G1360	C1361	G1362	C1363	G1364	C1365	G1366	C1367	G1368	C1369	G1370	C1371	G1372	C1373	G1374	C1375	G1376	C1377	G1378	C1379	G1380	C1381	G1382	C1383	G1384	C1385	G1386	C1387	G1388	C1389	G1390	C1391	G1392	C1393	G1394	C1395	G1396	C1397	G1398	C1399	G1400	C1401	G1402	C1403	G1404	C1405	G1406	C1407	G1408	C1409	G1410	C1411	G1412	C1413	G1414	C1415	G1416	C1417	G1418	C1419	G1420	C1421	G1422	C1423	G1424	C1425	G1426	C1427	G1428	C1429	G1430	C1431	G1432	C1433	G1434	C1435	G1436	C1437	G1438	C1439	G1440	C1441	G1442	C1443	G1444	C1445	G1446	C1447	G1448	C1449	G1450	C1451	G1452	C1453	G1454	C1455	G1456	C1457	G1458	C1459	G1460	C1461	G1462	C1463	G1464	C1465	G1466	C1467	G1468	C1469	G1470	C1471	G1472	C1473	G1474	C1475	G1476	C1477	G1478	C1479	G1480	C1481	G1482	C1483	G1484	C1485	G1486	C1487	G1488	C1489	G1490	C1491	G1492	C1493	G1494	C1495	G1496	C1497	G1498	C1499	G1500	C1501	G1502	C1503	G1504	C1505	G1506	C1507	G1508	C1509	G1510	C1511	G1512	C1513	G1514	C1515	G1516	C1517	G1518	C1519	G1520	C1521	G1522	C1523	G1524	C1525	G1526	C1527	G1528	C1529	G1530	C1531	G1532	C1533	G1534	C1535	G1536	C1537	G1538	C1539	G1540	C1541	G1542	C1543	G1544	C1545	G1546	C1547	G1548	C1549	G1550	C1551	G1552	C1553	G1554	C1555	G1556	C1557	G1558	C1559	G1560	C1561	G1562	C1563	G1564	C1565	G1566	C1567	G1568	C1569	G1570	C1571	G1572	C1573	G1574	C1575	G1576	C1577	G1578	C1579	G1580	C1581	G1582	C1583	G1584	C1585	G1586	C1587	G1588	C1589	G1590	C1591	G1592	C1593	G1594	C1595	G1596	C1597	G1598	C1599	G1600	C1601	G1602	C1603	G1604	C1605	G1606	C1607	G1608	C1609	G1610	C1611	G1612	C1613	G1614	C1615	G1616	C1617	G1618	C1619	G1620	C1621	G1622	C1623	G1624	C1625	G1626	C1627	G1628	C1629	G1630	C1631	G1632	C1633	G1634	C1635	G1636	C1637	G1638	C1639	G1640	C1641	G1642	C1643	G1644	C1645	G1646	C1647	G1648	C1649	G1650	C1651	G1652	C1653	G1654	C1655	G1656	C1657	G1658	C1659	G1660	C1661	G1662	C1663	G1664	C1665	G1666	C1667	G1668	C1669	G1670	C1671	G1672	C1673	G1674	C1675	G1676	C1677	G1678	C1679	G1680	C1681	G1682	C1683	G1684	C1685	G1686	C1687	G1688	C1689	G1690	C1691	G1692	C1693	G1694	C1695	G1696	C1697	G1698	C1699	G1700	C1701	G1702	C1703	G1704	C1705	G1706	C1707	G1708	C1709	G1710	C1711	G1712	C1713	G1714	C1715	G1716	C1717	G1718	C1719	G1720	C1721	G1722	C1723	G1724	C1725	G1726	C1727	G1728	C1729	G1730	C1731	G1732	C1733	G1734	C1735	G1736	C1737	G1738	C1739	G1740	C1741	G1742	C1743	G1744	C1745	G1746	C1747	G1748	C1749	G1750	C1751	G1752	C1753	G1754	C1755	G1756	C1757	G1758	C1759	G1760	C1761	G1762	C1763	G1764	C1765	G1766	C1767	G1768	C1769	G1770	C1771	G1772	C1773	G1774	C1775	G1776	C1777	G1778	C1779	G1780	C1781	G1782	C1783	G1784	C1785	G1786	C1787	G1788	C1789	G1790	C1791	G1792	C1793	G1794	C1795	G1796	C1797	G1798	C1799	G1800	C1801	G1802	C1803	G1804	C1805	G1806	C1807	G1808	C1809	G1810	C1811	G1812	C1813	G1814	C1815	G1816	C1817	G1818	C1819	G1820	C1821	G1822	C1823	G1824	C1825	G1826	C1827	G1828	C1829	G1830	C1831	G1832	C1833	G1834	C1835	G1836	C1837	G1838	C1839	G1840	C1841	G1842	C1843	G1844	C1845	G1846	C1847	G1848	C1849	G1850	C1851	G1852	C1853	G1854	C1855	G1856	C1857	G1858	C1859	G1860	C1861	G1862	C1863	G1864	C1865	G1866	C1867	G1868	C1869	G1870	C1871	G1872	C1873	G1874	C1875	G1876	C1877	G1878	C1879	G1880	C1881	G1882	C1883	G1884	C1885	G1886	C1887	G1888	C1889	G1890	C1891	G1892	C1893	G1894	C1895	G1896	C1897	G1898	C1899	G1900	C1901	G1902	C1903	G1904	C1905	G1906	C1907	G1908	C1909	G1910	C1911	G1912	C1913	G1914	C1915	G1916	C1917	G1918	C1919	G1920	C1921	G1922	C1923	G1924	C1925	G1926	C1927	G1928	C1929	G1930	C1931	G1932	C1933	G1934	C1935	G1936	C1937	G1938	C1939	G1940	C1941	G1942	C1943	G1944	C1945	G1946	C1947	G1948	C1949	G1950	C1951	G1952	C1953	G1954	C1955	G1956	C1957	G1958	C1959	G1960	C1961	G1962	C1963	G1964	C1965	G1966	C1967	G1968	C1969	G1970	C1971	G1972	C1973	G1974	C1975	G1976	C1977	G1978	C1979	G1980	C1981	G1982	C1983	G1984	C1985	G1986	C1987	G1988	C1989	G1990	C1991	G1992	C1993	G1994	C1995	G1996	C1997	G1998	C1999	G2000	C2001	G2002	C2003	G2004	C2005	G2006	C2007	G2008	C2009	G2010	C2011	G2012	C2013	G2014	C2015	G2016	C2017	G2018	C2019	G2020	C2021	G2022	C2023	G2024	C2025	G2026	C2027	G2028	C2029	G2030	C2031	G2032	C2033	G2034	C2035	G2036	C2037	G2038	C2039	G2040	C2041	G2042	C2043	G2044	C2045	G2046	C2047	G2048	C2049	G2050	C2051	G2052	C2053	G2054	C2055	G2056	C2057	G2058	C2059	G2060	C2061	G2062	C2063	G2064	C2065	G2066	C2067	G2068	C2069	G2070	C2071	G2072	C2073	G2074	C2075	G2076	C2077	G2078	C2079	G2080	C2081	G2082	C2083	G2084	C2085	G2086	C2087	G2088	C2089	G2090	C2091	G2092	C2093	G2094	C2095	G2096	C2097	G2098	C2099	G2100	C2101	G2102	C2103	G2104	C2105	G2106	C2107	G2108	C2109	G2110	C2111	G2112	C2113	G2114	C2115	G2116	C2117	G2118	C2119	G2120	C2121	G2122	C2123	G2124	C2125	G2126	C2127	G2128	C2129	G2130	C2131	G2132	C2133	G2134	C2135	G2136	C2137	G2138	C2139	G2140	C2141	G2142	C2143	G2144	C2145	G2146	C2147	G2148	C2149	G2150	C2151	G2152	C2153	G2154	C2155	G2156	C2157	G2158	C2159	G2160	C2161	G2162	C2163	G2164	C2165	G2166	C2167	G2168	C2169	G2170	C2171	G2172	C2173	G2174	C2175	G2176	C2177	G2178	C2179	G2180	C2181	G2182	C2183	G2184	C2185	G2186	C2187	G2188	C2189	G2190	C2191	G2192	C2193	G2194	C2195	G2196	C2197	G2198	C2199	G2200	C2201	G2202	C2203	G2204	C2205	G2206	C2207	G2208	C2209	G2210	C2211	G2212	C2213	G2214	C2215	G2216	C2217	G2218	C2219	G2220	C2221	G2222	C2223	G2224	C2225	G2226	C2227	G2228	C2229	G2230	C2231	G2232	C2233	G2234	C2235	G2236	C2237	G2238	C2239	G2240	C2241	G2242	C2243	G2244	C2245	G2246	C2247	G2248	C2249	G2250	C2251	G2252	C2253	G2254	C2255	G2256	C2257	G2258	C2259	G2260	C2261	G2262	C2263	G2264	C2265	G2266	C2267	G2268	C2269	G2270	C2271	G2272	C2273	G2274	C2275	G2276	C2277	G2278	C2279	G2280	C2281	G2282	C2283	G2284	C2285	G2286	C2287	G2288	C2289	G2290	C2291	G2292	C2293	G2294	C2295	G2296	C2297	G2298	C2299	G2300	C2301	G2302	C2303	G2304	C2305	G2306	C2307	G2308	C2309	G2310	C2311	G2312	C2313	G2314	C2315	G2316	C2317	G2318	C2319	G2320	C2321	G2322	C2323	G2324	C2325	G2326	C2327	G2328	C2329	G2330	C2331	G2332	C2333	G2334	C2335	G2336	C2337	G2338	C2339	G2340	C2341	G2342	C2343	G2344	C2345	G2346	C2347	G2348	C2349	G2350	C2351	G2352	C2353	G2354	C2355	G2356	C2357	G2358	C2359	G2360	C2361	G2362	C2363	G2364	C2365	G2366	C2367	G2368	C2369	G2370	C2371	G2372	C2373	G2374	C2375	G2376	C2377	G2378	C2379	G2380	C2381	G2382	C2383	G2384	C2385	G2386	C2387	G2388	C2389	G2390	C2391	G2392	C2393	G2394	C2395	G2396	C2397	G2398	C2399	G2400	C2401	G2402	C2403	G2404	C2405	G2406	C2407	G2408	C2409	G2410	C2411	G2412	C2413	G2414	C2415	G2416	C2417	G2418	C2419	G2420	C2421	G2422	C2423	G2424	C2425	G2426	C2427	G2428	C2429	G2430	C2431	G2432	C2433	G2434	C2435	G2436	C2437	G2438	C2439	G2440	C2441	G2442	C2443	G2444	C2445	G2446	C2447	G2448	C2449	G2450	C2451	G2452	C2453	G2454	C2455	G2456	C2457	G2458	C2459	G2460	C2461	G2462	C2463	G2464	C2465	G2466	C2467	G2468	C2469	G2470	C2471	G2472	C2473	G2474	C2475	G2476	C2477	G2478	C2479	G2480	C2481	G2482	C2483	G2484	C2485	G2486	C2487	G2488	C2489	G2490	C2491	G2492	C2493	G2494	C2495	G2496	C2497	G2498	C2499	G2500	C2501
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A2336	U2249	U2166	C2072	G1907	A1802	U1720	U1629	U1539	G1444	U1372	A1286	U1217
C2339	G2250	A2170	U2076	C1908	G1808	G1721	G1630	G1540	U1442	G1377	A1287	G1218
A2340	C2254	A2171	U2077	A1909	A1807	G1722	G1631	G1543	U1443	A1378	G1288	A1219
G2341	G2255	U2081	A2062	U1910	A1809	G1723	A1634	A1544	G1444	U1379	G1291	G1220
C2342	G2256	A2173	A2062	A1810	U1724	U1724	A1634	A1544	G1445	G1380	G1292	G1221
U2343	U2057	C2178	U2086	A1913	G1811	C1726	A1637	A1548	G1446	G1381	G1293	U1222
U2344	C2258	U2087	G2087	C1914	U1812	C1727	C1638	A1549	G1452	G1382	U1294	U1223
G2345	U2262	A2088	A2088	U1915	G1813	C1728	C1639	A1550	G1453	A1383	U1295	G1224
A2346	C2263	U2183	C2089	A1918	C1816	U1729	G1645	C1551	U1458	C1386	C1298	A1225
C2347	U2264	A2090	A2090	A1919	G1817	G1730	U1647	A1551	A1453	A1387	C1299	A1226
C2350	U2265	U2187	G2093	U1923	U1818	G1731	G1648	G1555	U1458	G1388	C1299	C1229
G2357	A2267	A2191	U2022	U1923	A1821	G1732	U1649	C1556	C1461	G1389	A1300	A1230
G2360	G2271	U2192	C2023	U1926	G1822	A1735	G1649	C1558	C1462	U1390	A1301	U1231
G2361	G2193	G2024	U2024	U1927	U1823	G1736	A1650	U1559	G1463	U1391	A1302	G1232
C2362	U2099	C2025	A2025	A1927	G1824	G1737	A1651	G1560	G1464	A1392	A1308	C1233
G2363	G2100	U2026	U2026	U1825	U1825	G1738	A1652	C1561	G1465	A1393	G1309	G1235
C2364	A2101	G2027	G2102	G1930	U1826	A1739	A1653	U1562	U1467	U1394	G1310	G1236
G2365	C2285	U2028	G2102	U1931	U1827	G1740	A1654	U1563	U1468	U1395	U1237	G1238
A2368	G2286	G2029	U2109	A1936	G1828	U1742	A1655	C1564	A1469	U1397	C1314	U1242
A2369	A2287	A2030	G2110	A1937	A1829	G1743	A1664	C1565	G1475	U1398	C1315	C1243
G2370	G2288	U2202	G2111	A1941	G1830	A1744	A1665	A1566	U1476	C1399	G1319	U1244
G2371	G2289	G2203	U2111	C1942	G1831	A1745	G1666	A1569	U1477	U1400	C1320	C1243
G2372	G2290	A2033	G2112	G1943	C1832	G1746	G1667	A1570	A1482	G1401	A1321	A1244
G2373	U2291	U2034	G2116	U1943	G1833	C1748	A1668	A1571	G1482	C1404	C1314	G1250
C2374	U2292	G2035	A2117	U1944	U1834	A1749	A1669	A1572	U1405	U1405	U1325	G1251
A2377	G2293	A2036	U2118	U1944	G1835	G1750	A1670	A1572	U1406	U1406	U1326	G1252
G2383	A2297	G2038	U2119	C1947	C1836	U1751	U1671	U1578	G1407	G1407	A1327	A1253
U2384	A2298	U2039	G2120	G1948	G1837	G1752	A1672	C1582	G1408	G1408	A1254	A1254
C2385	G2304	G2040	G2121	U1841	U1841	A1754	G1673	C1583	U1409	U1409	U1256	U1256
A2386	U2305	C2043	U2122	G1954	G1842	A1757	A1674	U1584	G1410	G1410	C1336	C1257
G2389	G2308	C2044	A2126	U1955	A1847	A1757	A1675	C1585	U1412	U1412	U1258	U1258
U2390	A2311	G2045	G2127	U1956	A1848	A1762	A1676	C1585	U1413	U1413	G1341	A1260
G2391	C2312	C2046	C2128	C1965	C1849	G1763	G1680	U1589	G1416	G1416	C1261	C1261
C2394	C2313	G2047	C2129	U1966	G1850	G1764	G1681	A1590	C1417	C1417	A1262	A1262
U2402	A2314	U2048	U2130	A1967	U1851	C1771	G1682	C1591	A1502	G1418	U1263	U1263
C2403	G2315	A2052	U2132	G1968	U1852	A1772	U1688	A1593	A1504	G1419	A1264	A1264
U2404	G2316	G2052	G2133	A1969	A1853	A1773	U1693	U1594	A1515	A1420	G1265	G1265
G2405	A2317	C2055	A2135	A1970	U1854	A1773	U1693	U1594	A1516	A1420	U1267	U1267
A2406	U2320	G2056	G2136	U1971	G1862	U1779	G1696	A1597	G1516	G1424	A1268	A1268
G2410	C2322	G2057	G2136	U1972	U1863	A1780	G1697	A1598	G1517	G1425	A1269	A1269
A2411	U2321	A2059	U2139	G1972	U1864	A1784	A1698	G1601	C1518	C1428	C1270	C1270
A2412	A2322	G2060	G2140	A1977	U1864	A1784	G1699	U1602	U1520	G1429	G1271	G1271
G2413	G2323	G2061	G2140	U1977	G1869	C1788	A1700	A1603	G1521	G1430	C1357	A1272
G2414	G2324	G2062	G2140	A1987	G1870	A1789	C1704	C1607	A1522	A1431	G1358	G1358
G2415	U2245	C2063	G2145	G1988	A1871	A1790	A1705	A1608	U1523	G1432	G1361	A1275
C2416	G2246	G2064	C2146	U1991	C1874	A1791	A1705	A1608	G1524	A1433	C1362	A1276
G2417	A2247	C2065	C2147	G1992	G1875	U1796	U1709	G1611	A1528	A1434	C1363	G1277
A2418	C2248	G2066	G2148	U1993	U1880	G1797	A1711	A1614	A1533	G1436	G1364	G1278
U2419	A2335	U2069	G2157	C1996	C1881	U1798	A1711	A1614	U1533	C1437	A1365	G1280
		A2071	C2165	C1997	A1890	G1799	G1715	C1615	U1534	U1438	U1281	U1281
				A1999	A1801	A1801		G1620	A1535	U1440	G1368	G1283

- Molecule 32: 50S ribosomal protein L35

Chain 3:  68% 29% ..



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	45746	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	120000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	2.195	Depositor
Minimum map value	-0.000	Depositor
Average map value	0.034	Depositor
Map value standard deviation	0.170	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	417.6, 417.6, 417.6	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.74, 1.74, 1.74	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GNP, ZN, MG

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	g	0.12	0/303	0.33	0/397
2	C	0.10	0/2121	0.31	0/2852
3	D	0.09	0/1586	0.28	0/2134
4	E	0.10	0/1499	0.28	0/2016
5	F	0.12	0/1434	0.36	0/1926
6	G	0.10	0/1343	0.29	0/1816
7	J	0.10	0/1152	0.29	0/1551
8	L	0.10	0/1062	0.34	0/1413
9	N	0.12	0/974	0.34	0/1301
10	O	0.13	0/902	0.40	0/1209
11	Q	0.14	0/960	0.42	1/1278 (0.1%)
12	R	0.10	0/829	0.32	0/1107
13	S	0.10	0/864	0.29	0/1156
14	T	0.11	0/744	0.35	0/994
15	U	0.10	0/787	0.30	0/1051
16	V	0.12	0/766	0.39	0/1025
17	W	0.09	0/584	0.28	0/772
18	X	0.09	0/635	0.28	0/848
19	Y	0.18	0/510	0.58	1/677 (0.1%)
20	Z	0.10	0/453	0.32	0/605
21	0	0.11	0/450	0.40	0/599
22	1	0.09	0/416	0.26	0/554
23	2	0.10	0/380	0.34	0/498
24	K	0.10	0/947	0.31	0/1268
25	P	0.10	0/923	0.29	0/1234
26	M	0.10	0/1093	0.33	0/1460
27	H	0.12	0/1121	0.39	0/1515
28	d	0.11	0/371	0.33	0/496
29	A	0.07	0/69659	0.18	0/108672
30	B	0.06	0/2847	0.15	0/4440
31	9	0.11	0/2626	0.32	0/3542
32	3	0.10	0/513	0.38	0/676

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.08	0/100854	0.23	2/151082 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
11	Q	110	GLU	N-CA-CB	5.09	118.17	110.28
19	Y	23	ARG	CB-CG-CD	5.01	122.83	111.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	g	302	0	340	10	0
2	C	2082	0	2157	61	0
3	D	1565	0	1616	45	0
4	E	1483	0	1548	26	0
5	F	1410	0	1447	47	0
6	G	1323	0	1374	31	0
7	J	1129	0	1162	21	0
8	L	1053	0	1129	26	0
9	N	961	0	1000	22	0
10	O	892	0	923	23	0
11	Q	947	0	1022	17	0
12	R	816	0	839	19	0
13	S	857	0	922	21	0
14	T	738	0	807	23	0
15	U	779	0	834	15	0
16	V	753	0	780	21	0
17	W	577	0	594	12	0
18	X	625	0	655	16	0
19	Y	509	0	543	21	0
20	Z	449	0	491	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	0	444	0	461	12	0
22	1	409	0	440	12	0
23	2	377	0	418	11	0
24	K	938	0	1012	26	0
25	P	911	0	957	13	0
26	M	1074	0	1157	23	0
27	H	1110	0	1148	28	0
28	d	364	0	364	12	0
29	A	62195	0	31280	1125	0
30	B	2548	0	1292	55	0
31	9	2582	0	2606	45	0
32	3	504	0	574	16	0
33	d	1	0	0	0	0
33	g	1	0	0	0	0
34	9	1	0	0	0	0
34	A	1	0	0	0	0
35	9	32	0	13	2	0
36	A	20	0	0	0	0
36	B	1	0	0	0	0
36	C	1	0	0	0	0
36	F	1	0	0	0	0
36	N	3	0	0	0	0
36	S	1	0	0	0	0
All	All	92769	0	61905	1672	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 1672 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)
29:A:1433:A:N6	29:A:1560:G:H1	1.63	0.96
29:A:408:G:H1	29:A:419:U:H3	1.08	0.95
29:A:2102:G:H1	29:A:2187:U:H3	1.17	0.92
29:A:2475:C:H42	29:A:2529:G:H22	1.13	0.91
29:A:377:G:H1	29:A:397:U:H3	0.93	0.90

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	
1	g	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
2	C	269/273 (98%)	258 (96%)	11 (4%)	0	100	100
3	D	207/209 (99%)	195 (94%)	12 (6%)	0	100	100
4	E	189/201 (94%)	180 (95%)	9 (5%)	0	100	100
5	F	175/179 (98%)	163 (93%)	12 (7%)	0	100	100
6	G	174/177 (98%)	165 (95%)	9 (5%)	0	100	100
7	J	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
8	L	142/144 (99%)	129 (91%)	13 (9%)	0	100	100
9	N	118/120 (98%)	112 (95%)	6 (5%)	0	100	100
10	O	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
11	Q	115/118 (98%)	111 (96%)	4 (4%)	0	100	100
12	R	101/103 (98%)	100 (99%)	1 (1%)	0	100	100
13	S	108/110 (98%)	105 (97%)	3 (3%)	0	100	100
14	T	91/100 (91%)	85 (93%)	6 (7%)	0	100	100
15	U	100/104 (96%)	91 (91%)	9 (9%)	0	100	100
16	V	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
17	W	74/85 (87%)	71 (96%)	3 (4%)	0	100	100
18	X	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
19	Y	61/63 (97%)	54 (88%)	7 (12%)	0	100	100
20	Z	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
21	0	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
22	1	48/55 (87%)	48 (100%)	0	0	100	100
23	2	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
24	K	120/123 (98%)	114 (95%)	6 (5%)	0	100	100
25	P	111/115 (96%)	108 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	M	134/136 (98%)	131 (98%)	3 (2%)	0	100	100
27	H	147/149 (99%)	131 (89%)	16 (11%)	0	100	100
28	d	45/70 (64%)	44 (98%)	1 (2%)	0	100	100
31	9	336/390 (86%)	321 (96%)	15 (4%)	0	100	100
32	3	62/65 (95%)	59 (95%)	1 (2%)	2 (3%)	3	25
All	All	3538/3720 (95%)	3370 (95%)	166 (5%)	2 (0%)	49	81

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
32	3	31	ILE
32	3	32	LEU

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	g	34/34 (100%)	34 (100%)	0	100	100
2	C	216/218 (99%)	216 (100%)	0	100	100
3	D	164/164 (100%)	164 (100%)	0	100	100
4	E	159/165 (96%)	159 (100%)	0	100	100
5	F	148/150 (99%)	148 (100%)	0	100	100
6	G	137/138 (99%)	137 (100%)	0	100	100
7	J	116/116 (100%)	115 (99%)	1 (1%)	70	76
8	L	103/103 (100%)	103 (100%)	0	100	100
9	N	100/100 (100%)	100 (100%)	0	100	100
10	O	86/87 (99%)	86 (100%)	0	100	100
11	Q	89/90 (99%)	89 (100%)	0	100	100
12	R	84/84 (100%)	84 (100%)	0	100	100
13	S	93/93 (100%)	93 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	T	80/84 (95%)	80 (100%)	0	100	100
15	U	83/85 (98%)	83 (100%)	0	100	100
16	V	78/78 (100%)	78 (100%)	0	100	100
17	W	57/63 (90%)	57 (100%)	0	100	100
18	X	67/68 (98%)	67 (100%)	0	100	100
19	Y	55/55 (100%)	55 (100%)	0	100	100
20	Z	48/49 (98%)	48 (100%)	0	100	100
21	0	47/48 (98%)	47 (100%)	0	100	100
22	1	45/49 (92%)	45 (100%)	0	100	100
23	2	38/38 (100%)	38 (100%)	0	100	100
24	K	103/104 (99%)	103 (100%)	0	100	100
25	P	98/100 (98%)	98 (100%)	0	100	100
26	M	109/109 (100%)	108 (99%)	1 (1%)	70	76
27	H	114/114 (100%)	114 (100%)	0	100	100
28	d	43/62 (69%)	43 (100%)	0	100	100
31	9	273/321 (85%)	273 (100%)	0	100	100
32	3	51/52 (98%)	51 (100%)	0	100	100
All	All	2918/3021 (97%)	2916 (100%)	2 (0%)	87	89

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	J	128	ASN
26	M	60	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
24	K	5	GLN
28	d	41	HIS
27	H	73	ASN
6	G	47	ASN
21	0	3	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
29	A	2895/2904 (99%)	390 (13%)	9 (0%)
30	B	118/119 (99%)	9 (7%)	0
All	All	3013/3023 (99%)	399 (13%)	9 (0%)

5 of 399 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
29	A	10	A
29	A	12	U
29	A	14	A
29	A	27	G
29	A	46	G

5 of 9 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
29	A	2505	G
29	A	2756	U
29	A	1328	A
29	A	1378	A
29	A	2127	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](#)

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
35	GNP	9	402	34	34,34,34	1.32	5 (14%)	47,54,54	0.65	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
35	GNP	9	402	34	-	2/18/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	9	402	GNP	PB-O3A	4.59	1.64	1.59
35	9	402	GNP	PB-O1B	3.25	1.51	1.46
35	9	402	GNP	PG-N3B	3.04	1.71	1.63
35	9	402	GNP	PG-O1G	2.84	1.50	1.46
35	9	402	GNP	PB-O2B	-2.27	1.50	1.56

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
35	9	402	GNP	C4'-C5'-O5'-PA
35	9	402	GNP	O4'-C4'-C5'-O5'

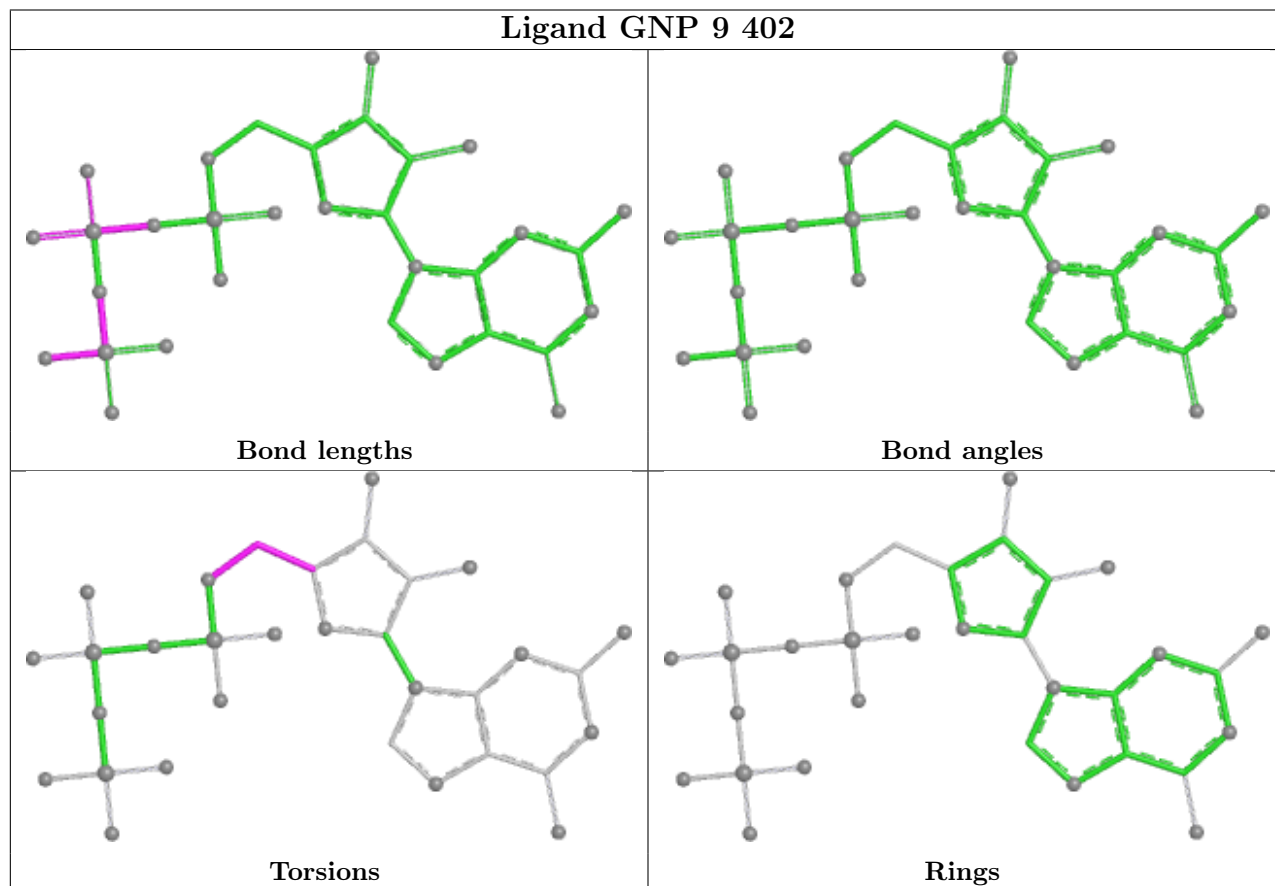
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
35	9	402	GNP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

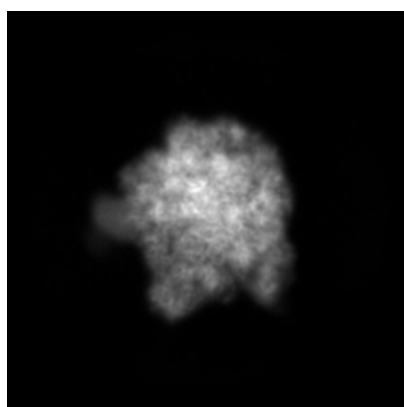
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12219. These allow visual inspection of the internal detail of the map and identification of artifacts.

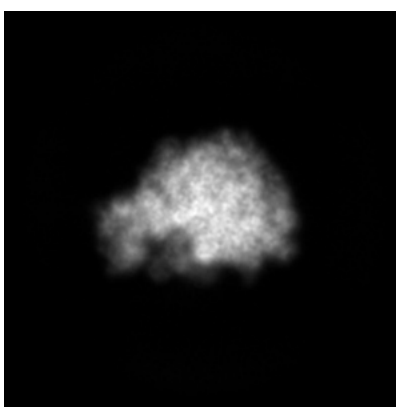
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

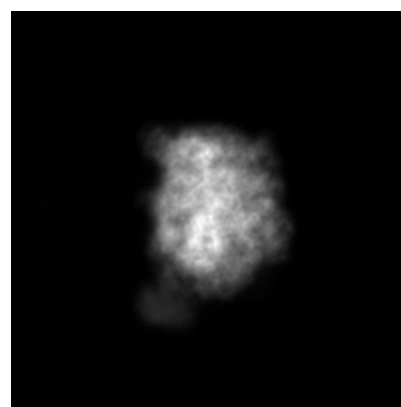
6.1.1 Primary map



X



Y

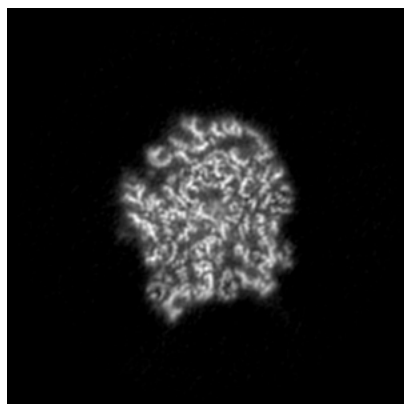


Z

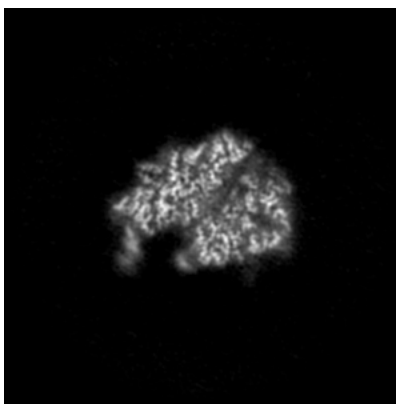
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

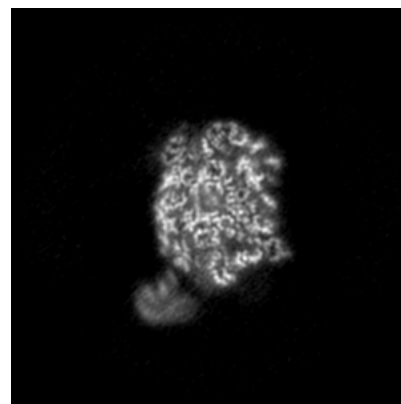
6.2.1 Primary map



X Index: 120



Y Index: 120

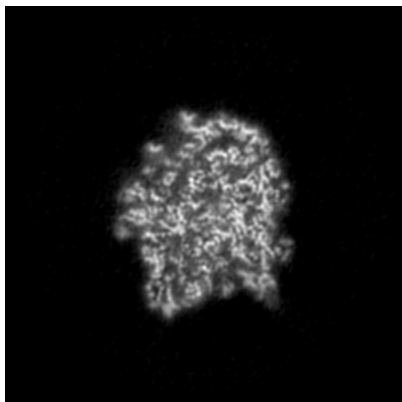


Z Index: 120

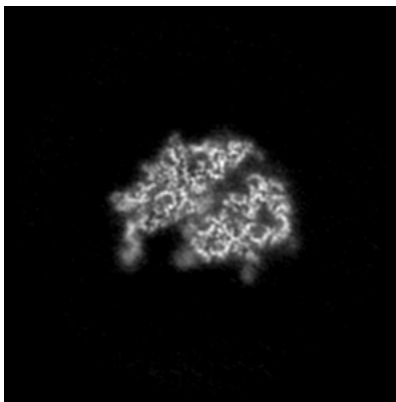
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

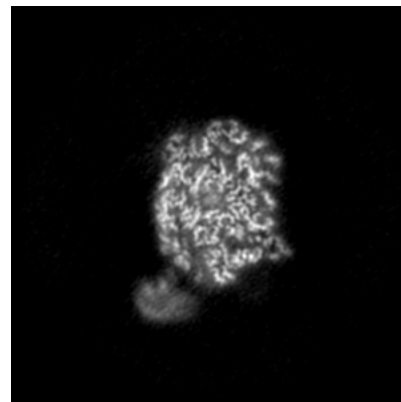
6.3.1 Primary map



X Index: 117



Y Index: 123

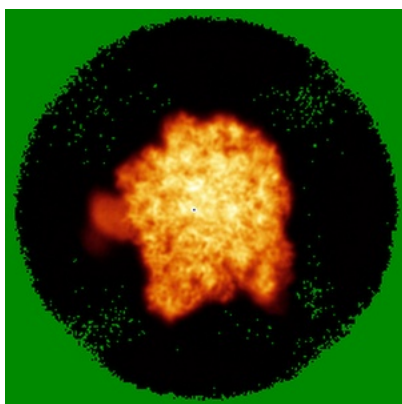


Z Index: 119

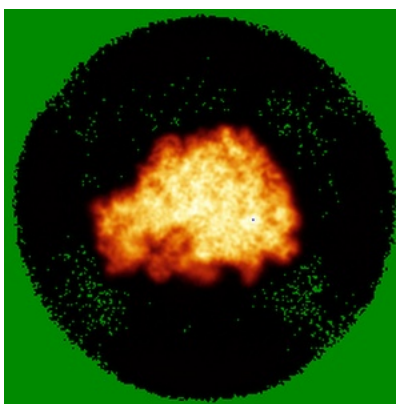
The images above show the largest variance slices of the map in three orthogonal directions.

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

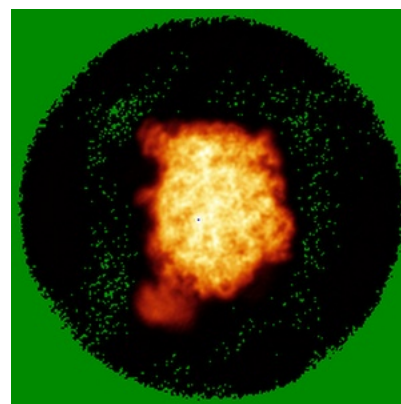
6.4.1 Primary map



X



Y

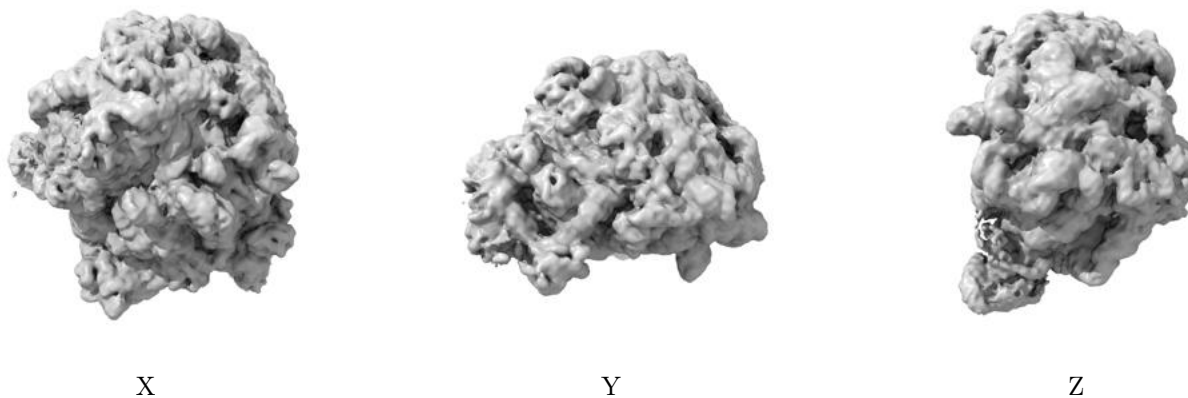


Z

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 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

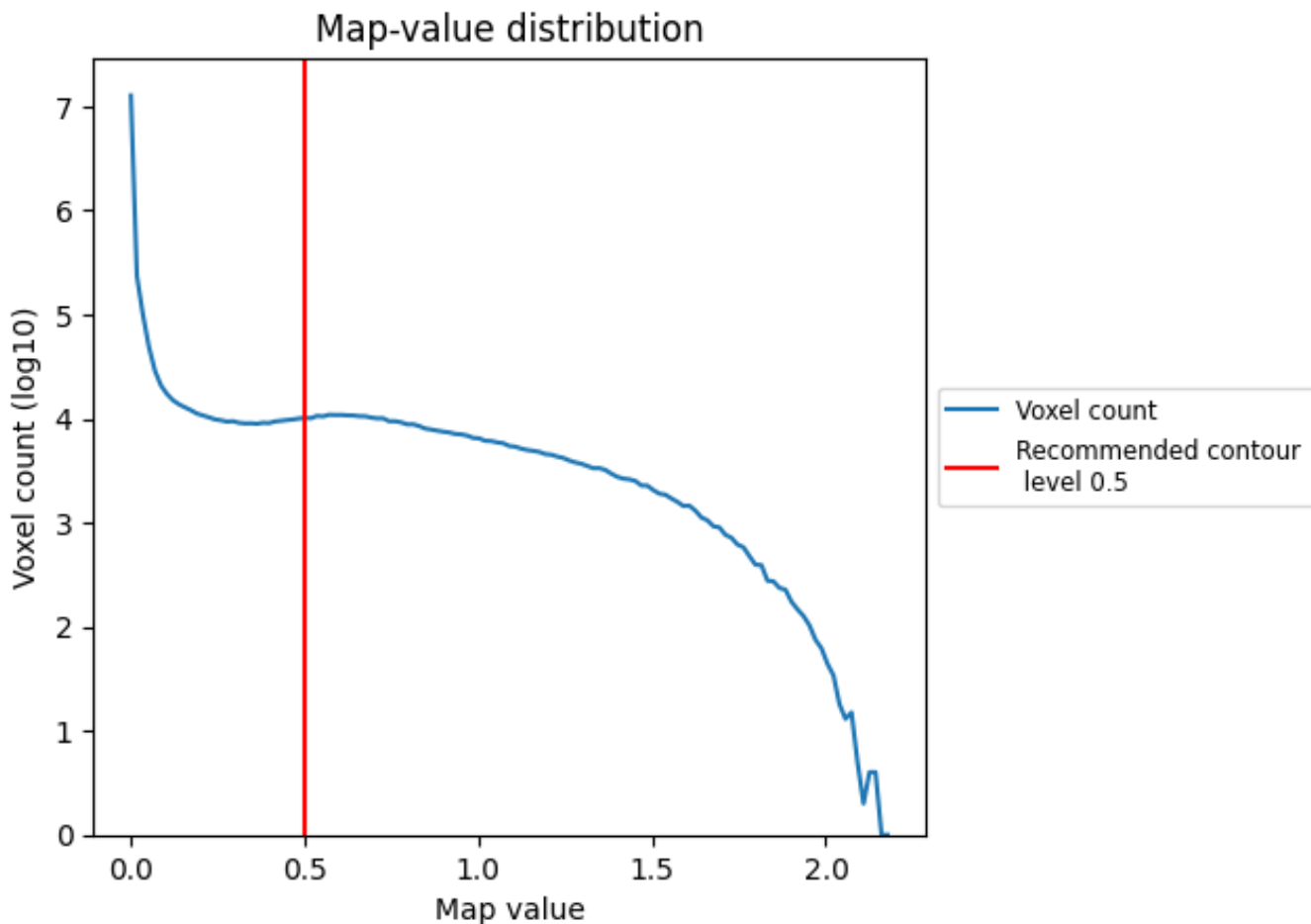
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

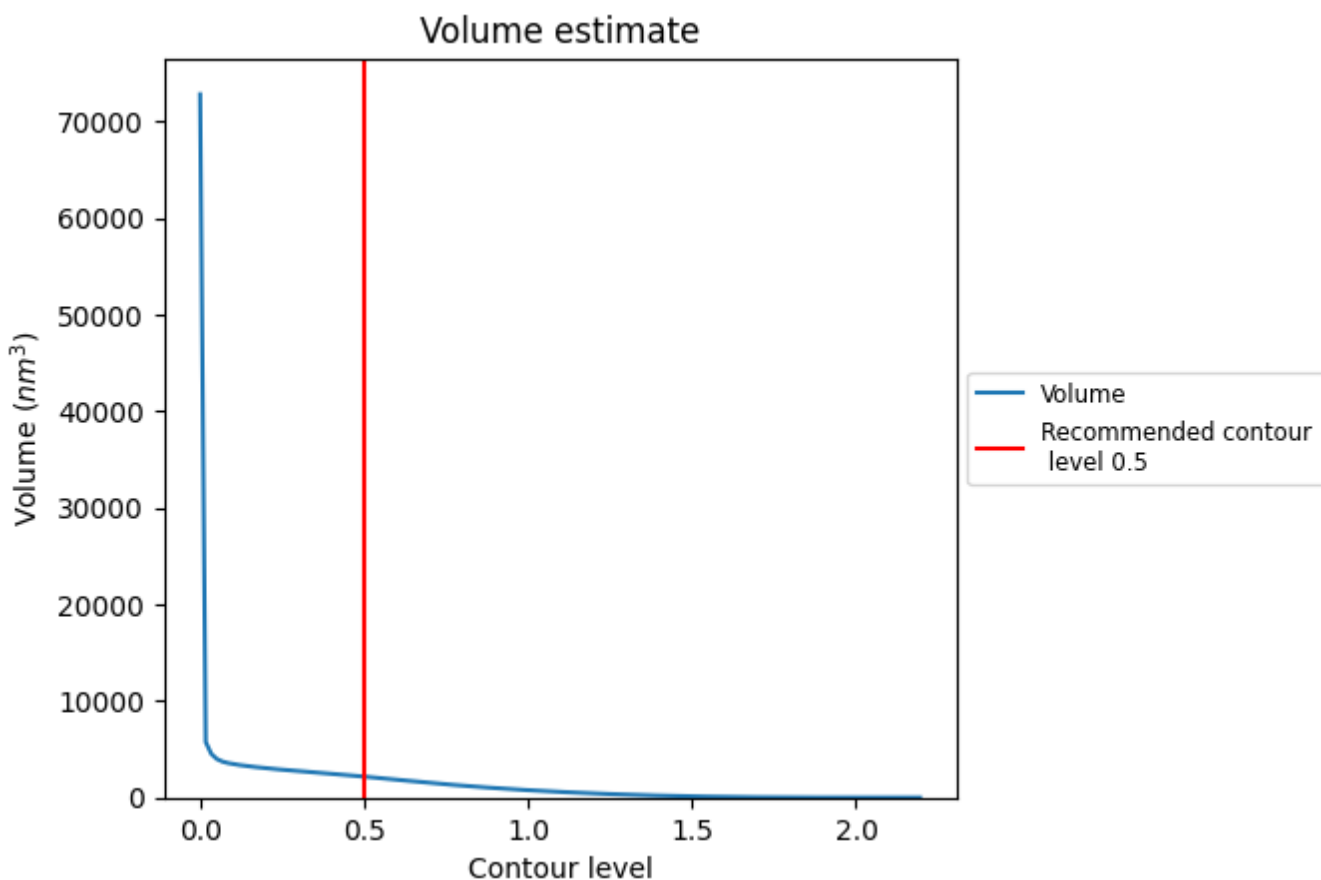
This section contains the results of statistical analysis of the map.

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.

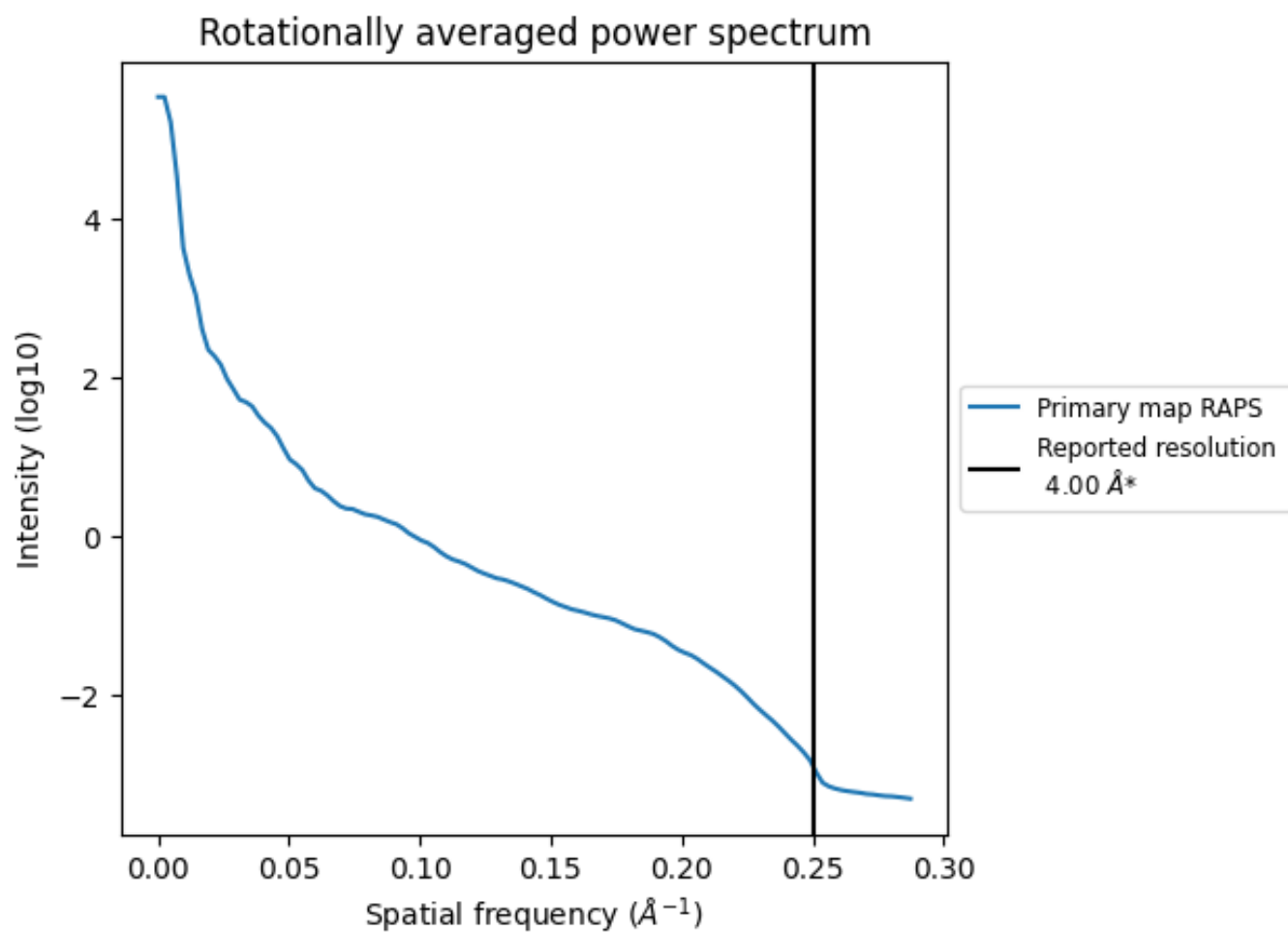
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2171 nm³; this corresponds to an approximate mass of 1962 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](#)

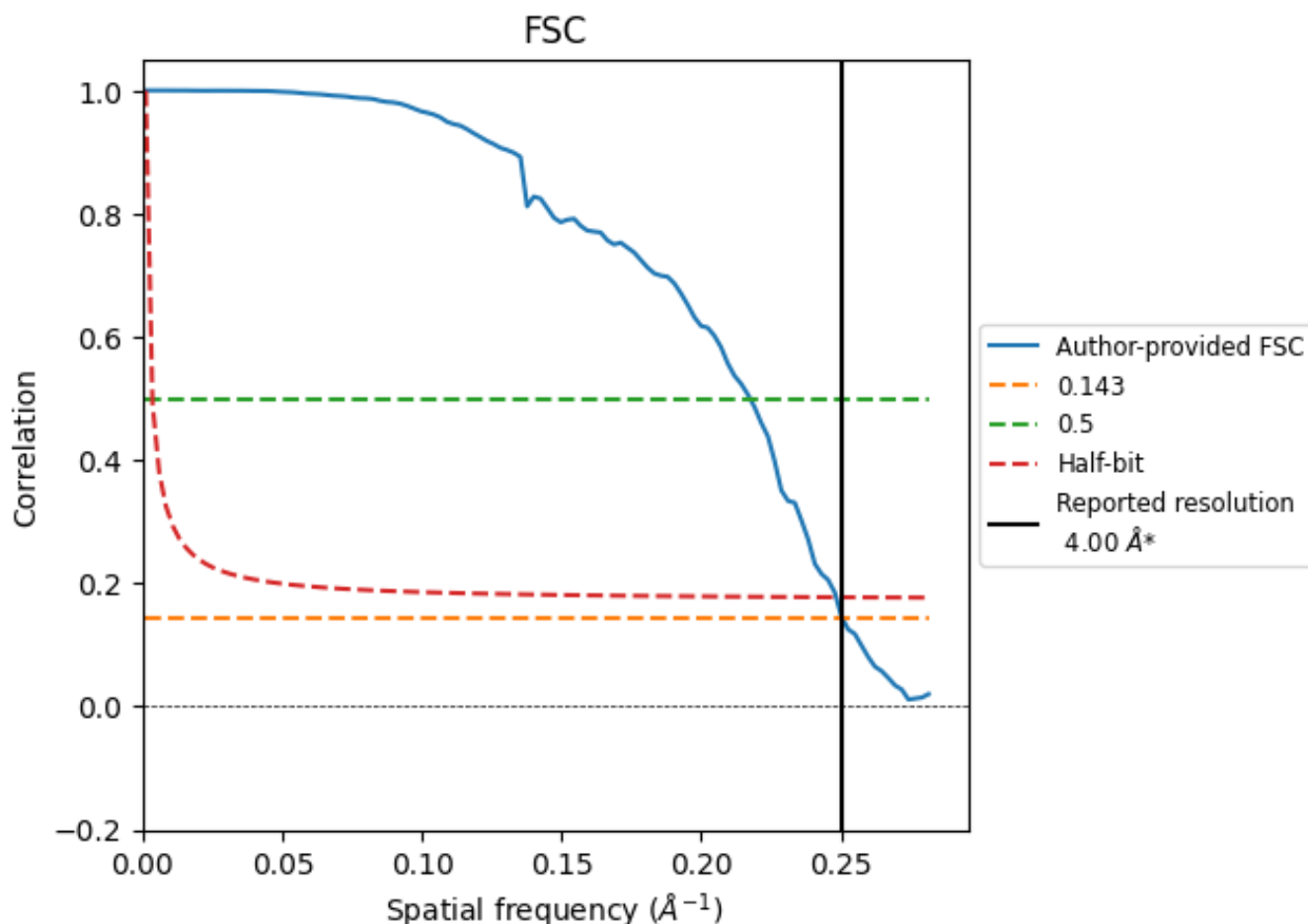


*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

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 0.250 Å⁻¹

8.2 Resolution estimates [i](#)

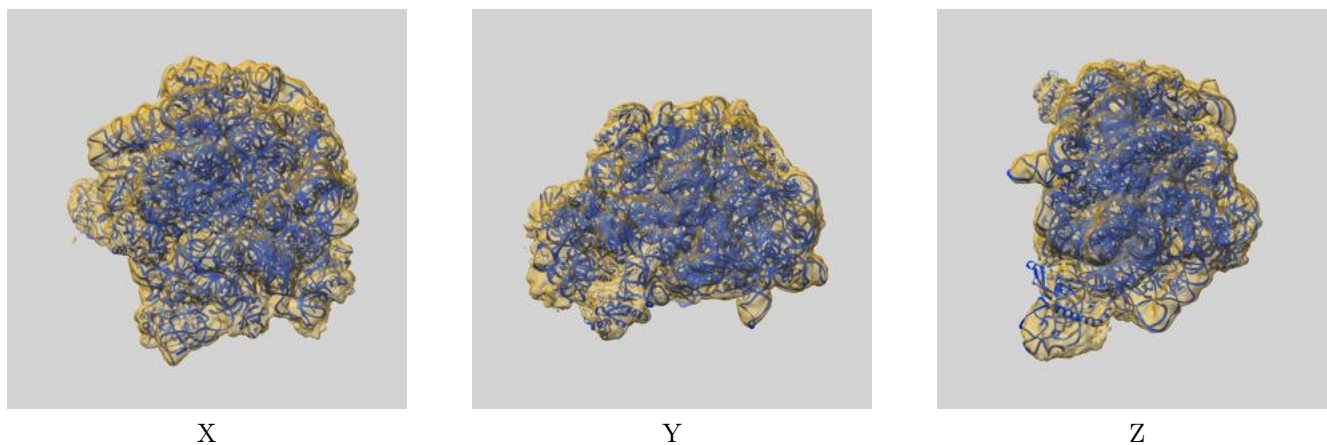
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	3.99	4.60	4.03
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

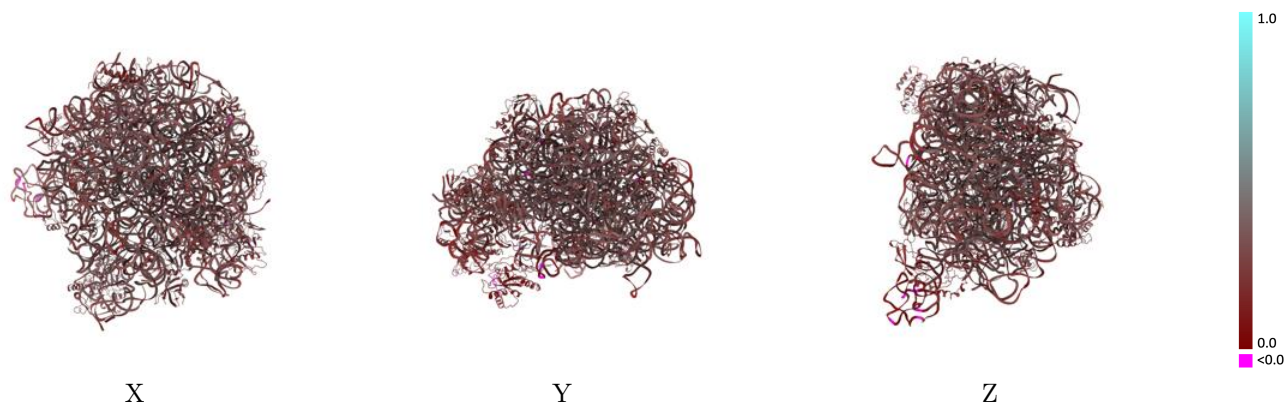
This section contains information regarding the fit between EMDB map EMD-12219 and PDB model 7BL6. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



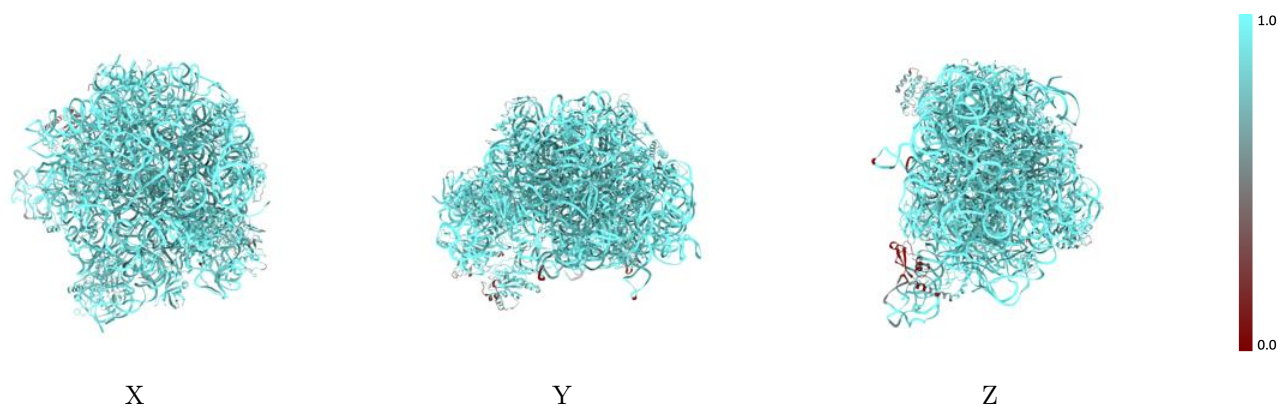
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



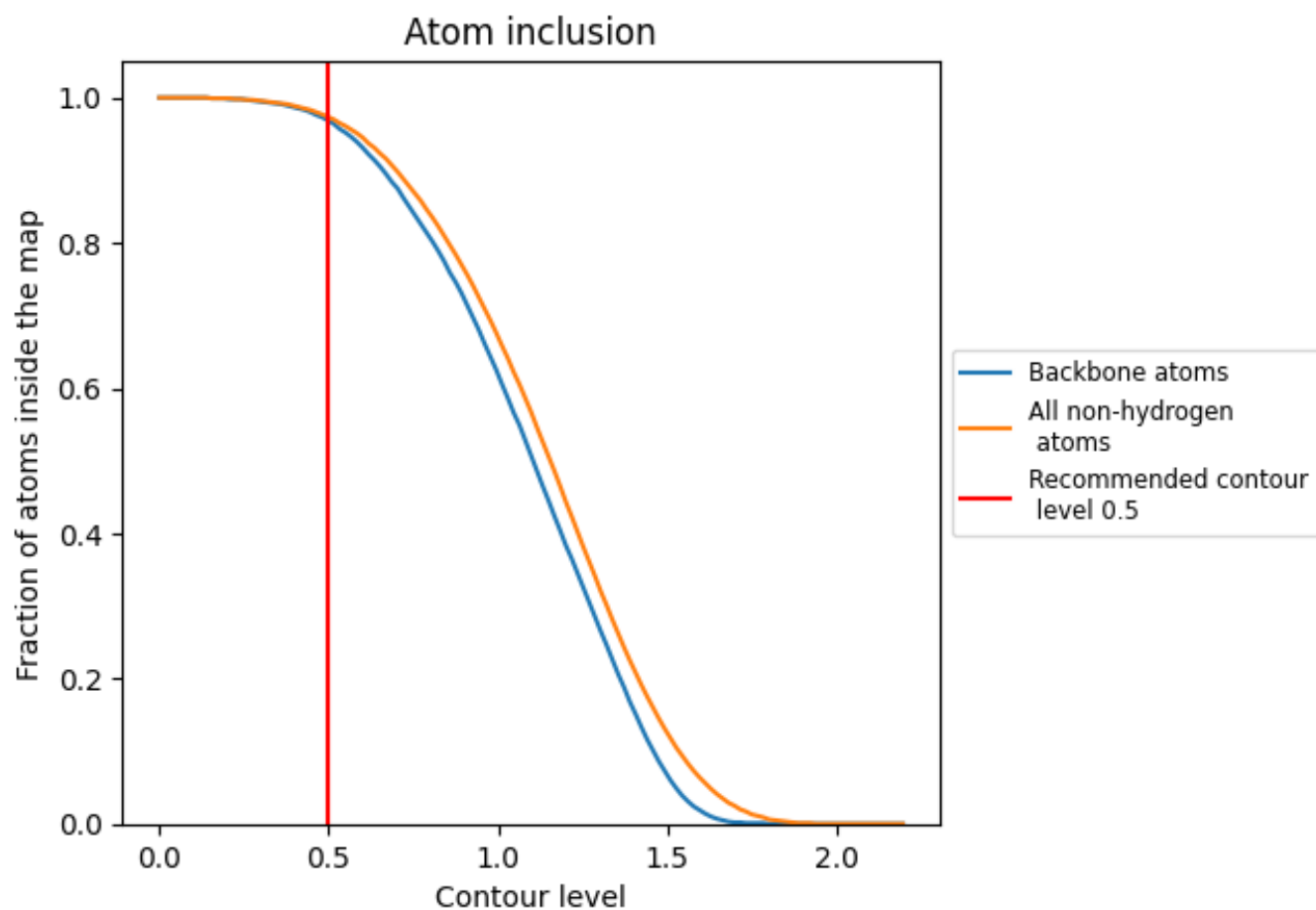
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).



































































9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 97% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9730	 0.2890
0	 0.9810	 0.2670
1	 0.9950	 0.2680
2	 0.9970	 0.2870
3	 1.0000	 0.2860
9	 0.8530	 0.1990
A	 0.9900	 0.3010
B	 0.9970	 0.2850
C	 0.9910	 0.3020
D	 0.9700	 0.3000
E	 0.9160	 0.2710
F	 0.8990	 0.2090
G	 0.9000	 0.2490
H	 0.5700	 0.2020
J	 0.9850	 0.2910
K	 0.9770	 0.2810
L	 0.9560	 0.2820
M	 0.9810	 0.2930
N	 0.9920	 0.2700
O	 0.9710	 0.2530
P	 0.9600	 0.2810
Q	 0.9850	 0.2690
R	 0.9270	 0.2820
S	 0.9820	 0.2780
T	 0.9830	 0.2920
U	 0.9620	 0.2600
V	 0.9510	 0.2710
W	 0.9930	 0.2860
X	 0.9900	 0.2870
Y	 0.9500	 0.2140
Z	 0.9410	 0.2580
d	 0.6740	 0.1790
g	 0.9930	 0.2860

