



wwPDB EM Validation Summary Report ⓘ

Mar 17, 2026 – 02:57 PM UTC

PDB ID : 8XXT / pdb_00008xxt
EMDB ID : EMD-38760
Title : ASFV RNAP M1249L C-tail occupied complex2 (MCOC2)
Authors : Zhu, G.L.; Zhu, Y.; Zhu, Z.X.; Sun, F.; Zheng, H.X.
Deposited on : 2024-01-19
Resolution : 2.85 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:

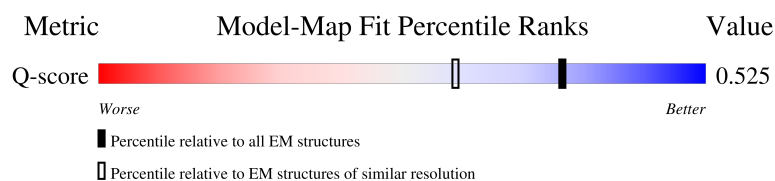
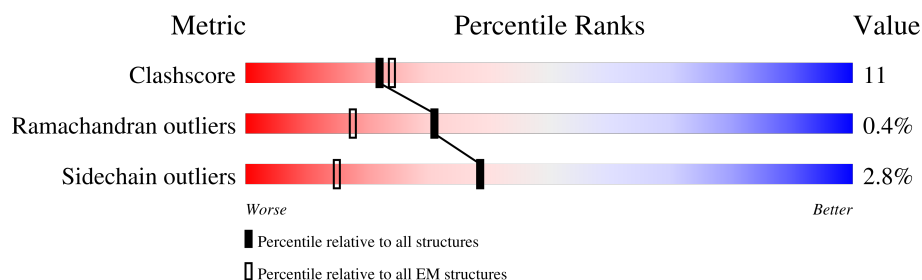
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

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 2.85 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.



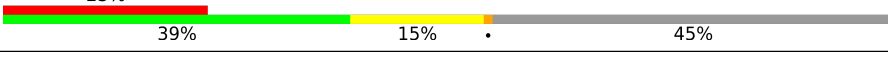
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11965 (2.35 - 3.35)

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	A	1441	
2	B	1235	
3	C	358	
4	D	205	

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Mol	Chain	Length	Quality of chain
5	E	139	
6	F	334	
7	G	105	
8	H	80	
9	I	1170	

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 35783 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 DNA-directed RNA polymerase subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1415	Total	C	N	O	S	0	0
			11244	7135	1955	2092	62		

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1226	Total	C	N	O	S	0	0
			9701	6124	1706	1819	52		

- Molecule 3 is a protein called DNA-directed RNA polymerase RPB3-11 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	358	Total	C	N	O	S	0	0
			2907	1885	481	529	12		

- Molecule 4 is a protein called DNA-directed RNA polymerase RPB5 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	205	Total	C	N	O	S	0	0
			1669	1088	278	295	8		

- Molecule 5 is a protein called C147L.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	129	Total	C	N	O	S	0	0
			1021	648	167	200	6		

- Molecule 6 is a protein called D339L.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	334	Total	C	N	O	S	0	0
			2687	1726	444	503	14		

- Molecule 7 is a protein called C122R.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	105	Total	C	N	O	S	0	0
			816	507	141	153	15		

- Molecule 8 is a protein called DNA-directed RNA polymerase RPB10 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	69	Total	C	N	O	S	0	0
			553	362	89	95	7		

- Molecule 9 is a protein called M1249L.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	638	Total	C	N	O	S	0	0
			5177	3329	858	968	22		

- Molecule 10 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
10	A	3	Total	Zn	0
			3	3	
10	B	1	Total	Zn	0
			1	1	
10	G	2	Total	Zn	0
			2	2	
10	H	1	Total	Zn	0
			1	1	

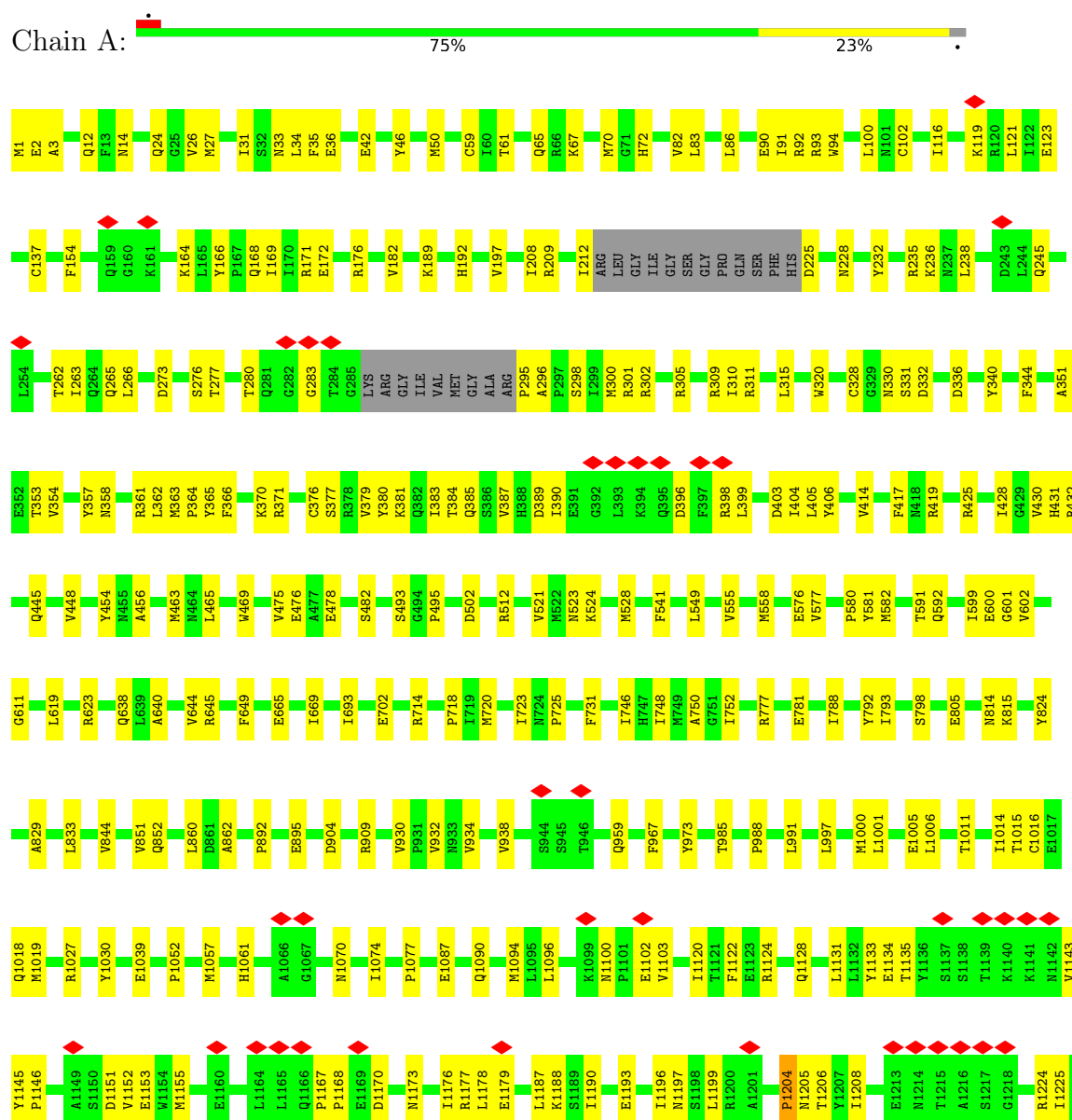
- Molecule 11 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

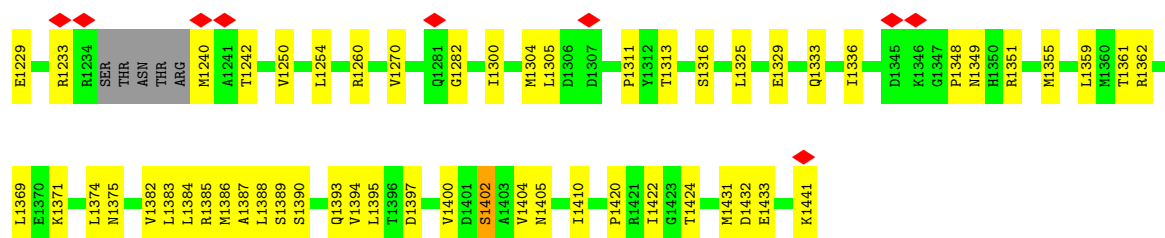
Mol	Chain	Residues	Atoms		AltConf
11	A	1	Total	Mg	0
			1	1	

3 Residue-property plots

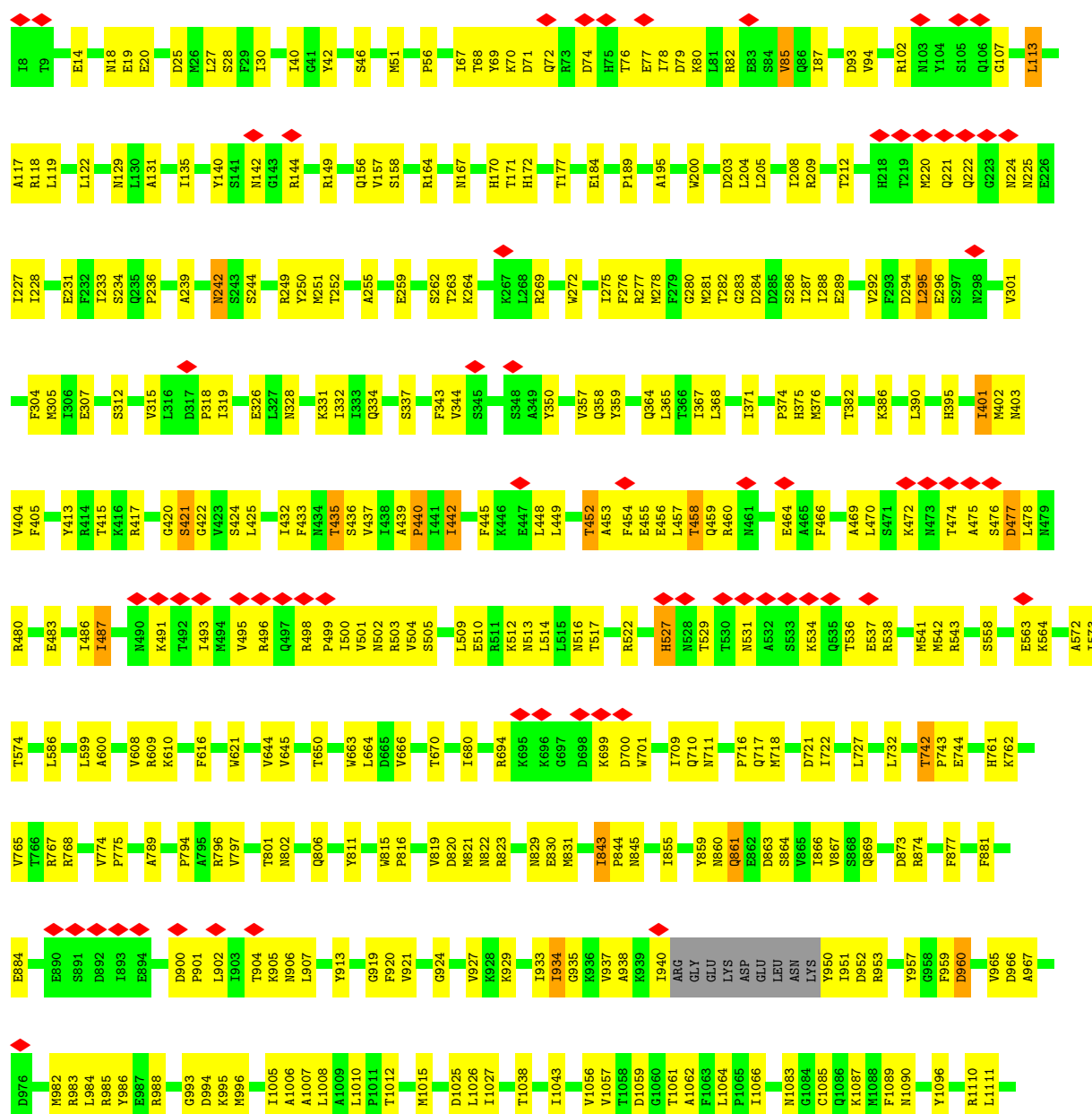
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

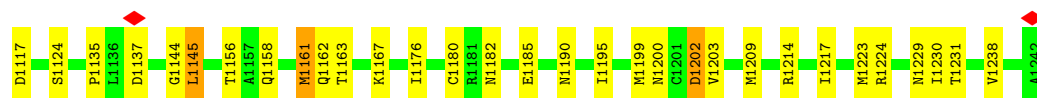
• Molecule 1: DNA-directed RNA polymerase subunit



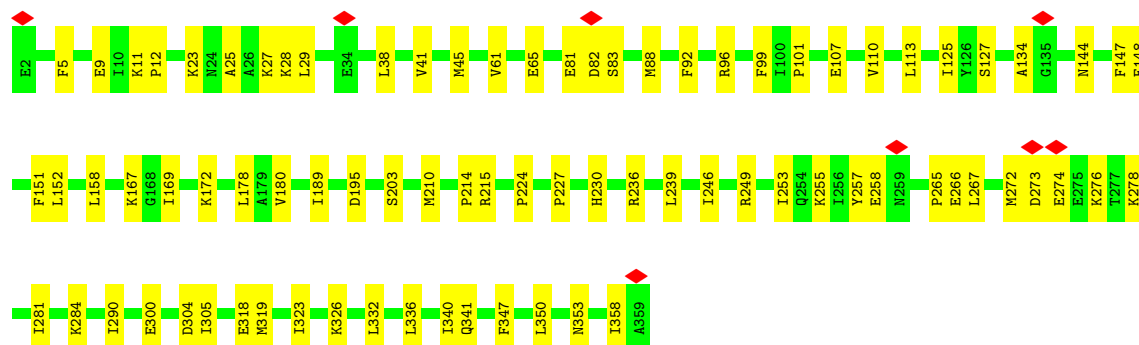
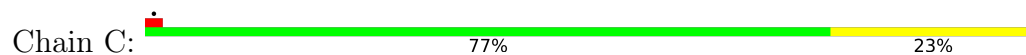


• Molecule 2: DNA-directed RNA polymerase subunit beta

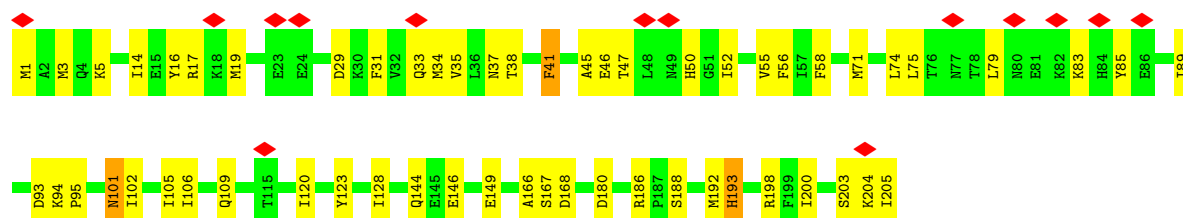
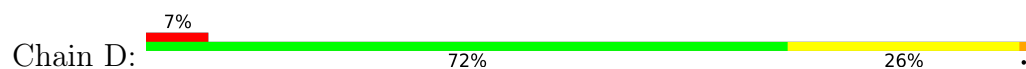




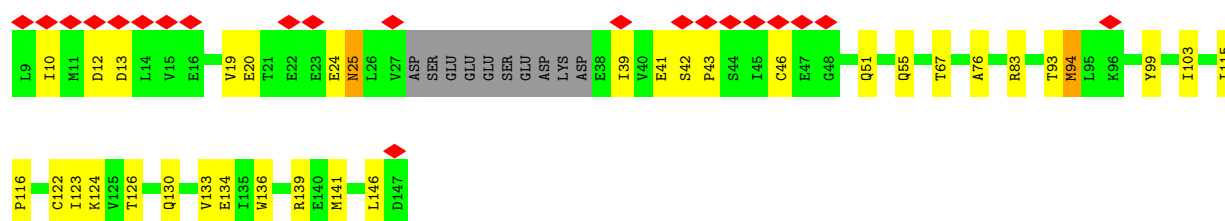
- Molecule 3: DNA-directed RNA polymerase RPB3-11 homolog



- Molecule 4: DNA-directed RNA polymerase RPB5 homolog

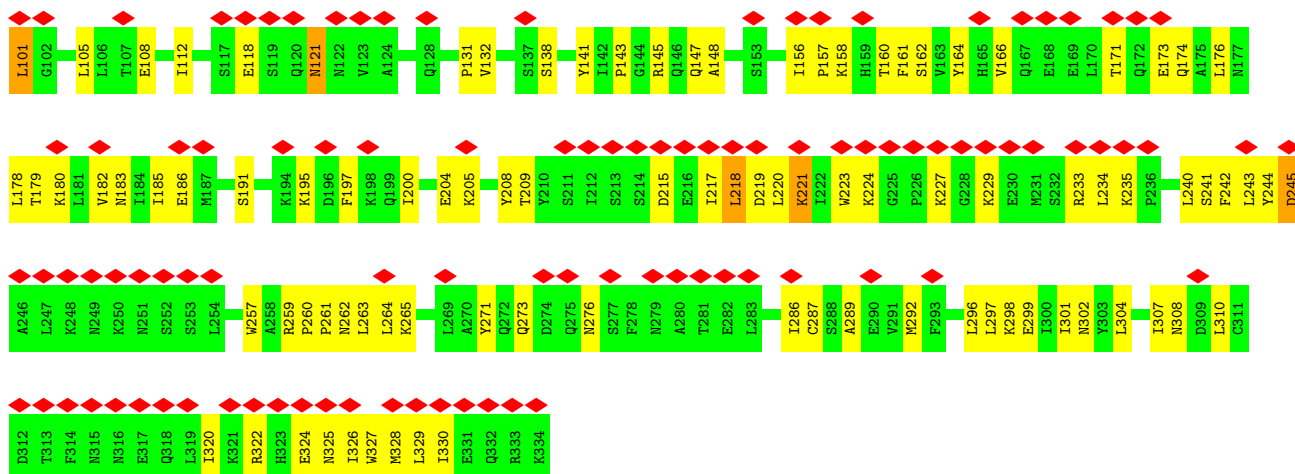


- Molecule 5: C147L

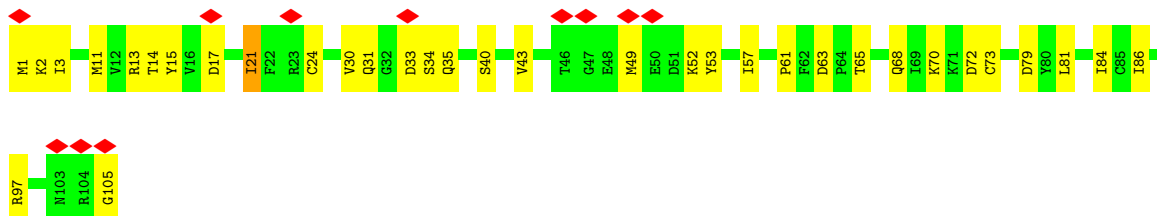


- Molecule 6: D339L

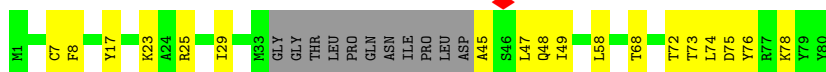




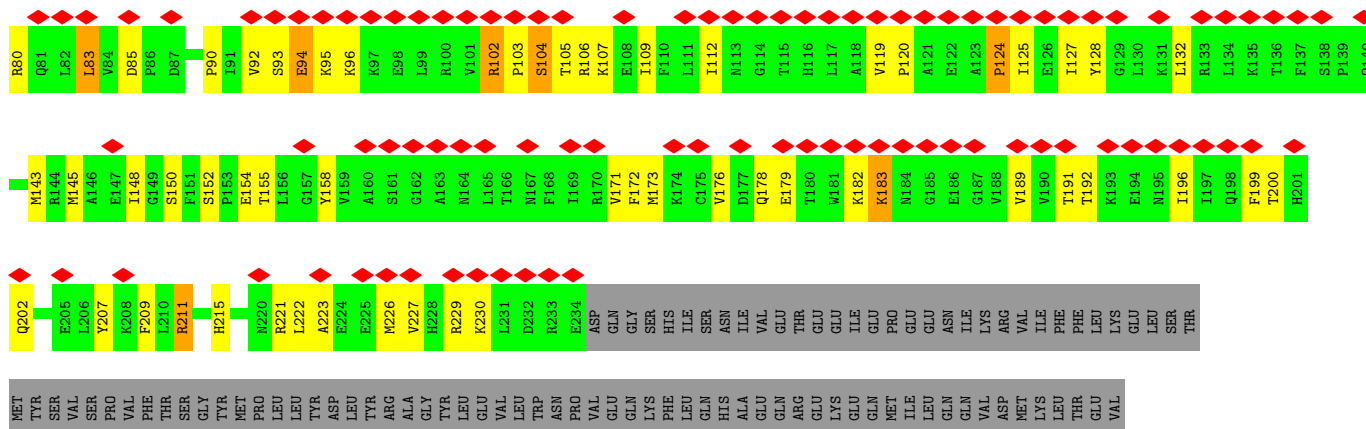
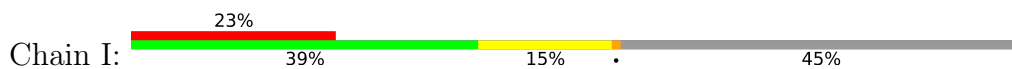
• Molecule 7: C122R



• Molecule 8: DNA-directed RNA polymerase RPB10 homolog



• Molecule 9: M1249L



V1161	V1162	V1165	R1166	E1172	I1177	K1181	L1182	P1186	M1192	I1193	F1194	G1195	E1196	D1197	F1198	V1199	C1200	S1206	M1207	D1208	D1209	I1210	P1216	G1217	L1218	F1219	G1220	E1221	D1222	I1223	I1224	D1225	R1226	L1227	D1228	S1232	I1233	E1234	D1235	V1236	S1239	L1240	D1241	V1242	P1248	Q1249																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
L1027	D1028	I1029	V1033	I1034	I1037	E1050	S1060	D1070	R1074	I1075	F1076	M1079	N1090	K1091	I1094	H1095	V1096	E1097	R1098	I1099	V1100	K1101	H1102	L1103	S1104	E1105	E1106	E1107	K1108	E1109	E1112	K1113	Y1122	I1142	F1149	L1150	T1151	L1152	Y1153	E1154	I1155	P1158	S1159	W1160																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
L969	I960	Y961	D962	H963	L964	S965	Q966	P967	E968	L969	V970	H971	D972	Y973	Y974	N975	Y976	Y977	K978	D979	Q980	Y981	D982	K983	E984	K985	M986	S987	I988	A989	I990	E991	E992	E993	C994	L995	H996	D997	L998	P999	G1000	S1001	D1002	E1003	I1004	L1005	F1006	G1007	H1008	I1009	K1010	L1011	S1012	E1013	E1014	E1015	E1016	E1017	E1018	E1019	E1020	E1021	E1022	E1023	E1024	E1025	E1026	E1027	E1028	E1029	E1030	E1031	E1032	E1033	E1034	E1035	E1036	E1037	E1038	E1039	E1040	E1041	E1042	E1043	E1044	E1045	E1046	E1047	E1048	E1049	E1050	E1051	E1052	E1053	E1054	E1055	E1056	E1057	E1058	E1059	E1060	E1061	E1062	E1063	E1064	E1065	E1066	E1067	E1068	E1069	E1070	E1071	E1072	E1073	E1074	E1075	E1076	E1077	E1078	E1079	E1080	E1081	E1082	E1083	E1084	E1085	E1086	E1087	E1088	E1089	E1090	E1091	E1092	E1093	E1094	E1095	E1096	E1097	E1098	E1099	E1100	E1101	E1102	E1103	E1104	E1105	E1106	E1107	E1108	E1109	E1110	E1111	E1112	E1113	E1114	E1115	E1116	E1117	E1118	E1119	E1120	E1121	E1122	E1123	E1124	E1125	E1126	E1127	E1128	E1129	E1130	E1131	E1132	E1133	E1134	E1135	E1136	E1137	E1138	E1139	E1140	E1141	E1142	E1143	E1144	E1145	E1146	E1147	E1148	E1149	E1150	E1151	E1152	E1153	E1154	E1155	E1156	E1157	E1158	E1159	E1160	E1161	E1162	E1163	E1164	E1165	E1166	E1167	E1168	E1169	E1170	E1171	E1172	E1173	E1174	E1175	E1176	E1177	E1178	E1179	E1180	E1181	E1182	E1183	E1184	E1185	E1186	E1187	E1188	E1189	E1190	E1191	E1192	E1193	E1194	E1195	E1196	E1197	E1198	E1199	E1200	E1201	E1202	E1203	E1204	E1205	E1206	E1207	E1208	E1209	E1210	E1211	E1212	E1213	E1214	E1215	E1216	E1217	E1218	E1219	E1220	E1221	E1222	E1223	E1224	E1225	E1226	E1227	E1228	E1229	E1230	E1231	E1232	E1233	E1234	E1235	E1236	E1237	E1238	E1239	E1240	E1241	E1242	E1243	E1244	E1245	E1246	E1247	E1248	E1249	E1250	E1251	E1252	E1253	E1254	E1255	E1256	E1257	E1258	E1259	E1260	E1261	E1262	E1263	E1264	E1265	E1266	E1267	E1268	E1269	E1270	E1271	E1272	E1273	E1274	E1275	E1276	E1277	E1278	E1279	E1280	E1281	E1282	E1283	E1284	E1285	E1286	E1287	E1288	E1289	E1290	E1291	E1292	E1293	E1294	E1295	E1296	E1297	E1298	E1299	E1300	E1301	E1302	E1303	E1304	E1305	E1306	E1307	E1308	E1309	E1310	E1311	E1312	E1313	E1314	E1315	E1316	E1317	E1318	E1319	E1320	E1321	E1322	E1323	E1324	E1325	E1326	E1327	E1328	E1329	E1330	E1331	E1332	E1333	E1334	E1335	E1336	E1337	E1338	E1339	E1340	E1341	E1342	E1343	E1344	E1345	E1346	E1347	E1348	E1349	E1350	E1351	E1352	E1353	E1354	E1355	E1356	E1357	E1358	E1359	E1360	E1361	E1362	E1363	E1364	E1365	E1366	E1367	E1368	E1369	E1370	E1371	E1372	E1373	E1374	E1375	E1376	E1377	E1378	E1379	E1380	E1381	E1382	E1383	E1384	E1385	E1386	E1387	E1388	E1389	E1390	E1391	E1392	E1393	E1394	E1395	E1396	E1397	E1398	E1399	E1400	E1401	E1402	E1403	E1404	E1405	E1406	E1407	E1408	E1409	E1410	E1411	E1412	E1413	E1414	E1415	E1416	E1417	E1418	E1419	E1420	E1421	E1422	E1423	E1424	E1425	E1426	E1427	E1428	E1429	E1430	E1431	E1432	E1433	E1434	E1435	E1436	E1437	E1438	E1439	E1440	E1441	E1442	E1443	E1444	E1445	E1446	E1447	E1448	E1449	E1450	E1451	E1452	E1453	E1454	E1455	E1456	E1457	E1458	E1459	E1460	E1461	E1462	E1463	E1464	E1465	E1466	E1467	E1468	E1469	E1470	E1471	E1472	E1473	E1474	E1475	E1476	E1477	E1478	E1479	E1480	E1481	E1482	E1483	E1484	E1485	E1486	E1487	E1488	E1489	E1490	E1491	E1492	E1493	E1494	E1495	E1496	E1497	E1498	E1499	E1500	E1501	E1502	E1503	E1504	E1505	E1506	E1507	E1508	E1509	E1510	E1511	E1512	E1513	E1514	E1515	E1516	E1517	E1518	E1519	E1520	E1521	E1522	E1523	E1524	E1525	E1526	E1527	E1528	E1529	E1530	E1531	E1532	E1533	E1534	E1535	E1536	E1537	E1538	E1539	E1540	E1541	E1542	E1543	E1544	E1545	E1546	E1547	E1548	E1549	E1550	E1551	E1552	E1553	E1554	E1555	E1556	E1557	E1558	E1559	E1560	E1561	E1562	E1563	E1564	E1565	E1566	E1567	E1568	E1569	E1570	E1571	E1572	E1573	E1574	E1575	E1576	E1577	E1578	E1579	E1580	E1581	E1582	E1583	E1584	E1585	E1586	E1587	E1588	E1589	E1590	E1591	E1592	E1593	E1594	E1595	E1596	E1597	E1598	E1599	E1600	E1601	E1602	E1603	E1604	E1605	E1606	E1607	E1608	E1609	E1610	E1611	E1612	E1613	E1614	E1615	E1616	E1617	E1618	E1619	E1620	E1621	E1622	E1623	E1624	E1625	E1626	E1627	E1628	E1629	E1630	E1631	E1632	E1633	E1634	E1635	E1636	E1637	E1638	E1639	E1640	E1641	E1642	E1643	E1644	E1645	E1646	E1647	E1648	E1649	E1650	E1651	E1652	E1653	E1654	E1655	E1656	E1657	E1658	E1659	E1660	E1661	E1662	E1663	E1664	E1665	E1666	E1667	E1668	E1669	E1670	E1671	E1672	E1673	E1674	E1675	E1676	E1677	E1678	E1679	E1680	E1681	E1682	E1683	E1684	E1685	E1686	E1687	E1688	E1689	E1690	E1691	E1692	E1693	E1694	E1695	E1696	E1697	E1698	E1699	E1700	E1701	E1702	E1703	E1704	E1705	E1706	E1707	E1708	E1709	E1710	E1711	E1712	E1713	E1714	E1715	E1716	E1717	E1718	E1719	E1720	E1721	E1722	E1723	E1724	E1725	E1726	E1727	E1728	E1729	E1730	E1731	E1732	E1733	E1734	E1735	E1736	E1737	E1738	E1739	E1740	E1741	E1742	E1743	E1744	E1745	E1746	E1747	E1748	E1749	E1750	E1751	E1752	E1753	E1754	E1755	E1756	E1757	E1758	E1759	E1760	E1761	E1762	E1763	E1764	E1765	E1766	E1767	E1768	E1769	E1770	E1771	E1772	E1773	E1774	E1775	E1776	E1777	E1778	E1779	E1780	E1781	E1782	E1783	E1784	E1785	E1786	E1787	E1788	E1789	E1790	E1791	E1792	E1793	E1794	E1795	E1796	E1797	E1798	E1799	E1800	E1801	E1802	E1803	E1804	E1805	E1806	E1807	E1808	E1809	E1810	E1811	E1812	E1813	E1814	E1815	E1816	E1817	E1818	E1819	E1820	E1821	E1822	E1823	E1824	E1825	E1826	E1827	E1828	E1829	E1830	E1831	E1832	E1833	E1834	E1835	E1836	E1837	E1838	E1839	E1840	E1841	E1842	E1843	E1844	E1845	E1846	E1847	E1848	E1849	E1850	E1851	E1852	E1853	E1854	E1855	E1856	E1857	E1858	E1859	E1860	E1861	E1862	E1863	E1864	E1865	E1866	E1867	E1868	E1869	E1870	E1871	E1872	E1873	E1874	E1875	E1876	E1877	E1878	E1879	E1880	E1881	E1882	E1883	E1884	E1885	E1886	E1887	E1888	E1889	E1890	E1891	E1892	E1893	E1894	E1895	E1896	E1897	E1898	E1899	E1900	E1901	E1902	E1903	E1904	E1905	E1906	E1907	E1908	E1909	E1910	E1911	E1912	E1913	E1914	E1915	E1916	E1917	E1918	E1919	E1920	E1921	E1922	E1923	E1924	E1925	E1926	E1927	E1928	E1929	E1930	E1931	E1932	E1933	E1934	E1935	E1936	E1937	E1938	E1939	E1940	E1941	E1942	E1943	E1944	E1945	E1946	E1947	E1948	E1949	E1950	E1951	E1952	E1953	E1954	E1955	E1956	E1957	E1958	E1959
L969	I960	Y961	D962	H963	L964	S965	Q966	P967	E968	L969	V970	H971	D972	Y973	Y974	N975	Y976	Y977	K978	D979	Q980	Y981	D982	K983	E984	K985	M986	S987	I988	A989	I990	E991	E992	E993	C994	L995	H996	D997	L998	P999	G1000	S1001	D1002	E1003	I1004	L1005	F1006	G1007	H1008	I1009	K1010	L1011	S1012	E1013	E1014	E1015	E1016	E1017	E1018	E1019	E1020	E1021	E1022	E1023	E1024	E1025	E1026	E1027	E1028	E1029	E1030	E1031	E1032	E1033	E1034	E1035	E1036	E1037	E1038	E1039	E1040	E1041	E1042	E1043	E1044	E1045	E1046	E1047	E1048	E1049	E1050	E1051	E1052	E1053	E1054	E1055	E1056	E1057	E1058	E1059	E1060	E1061	E1062	E1063	E1064	E1065	E1066	E1067	E1068	E1069	E1070	E1071	E1072	E1073	E1074	E1075	E1076	E1077	E1078	E1079	E1080	E1081	E1082	E1083	E1084	E1085	E1086	E1087	E1088	E1089	E1090	E1091	E1092	E1093	E1094	E1095	E1096	E1097	E1098	E1099	E1100	E1101	E1102	E1103	E1104	E1105	E1106	E1107	E1108	E1109	E1110	E1111	E1112	E1113	E1114	E1115	E1116	E1117	E1118	E1119	E1120	E1121	E1122	E1123	E1124	E1125	E1126	E1127	E1128	E1129	E1130	E1131	E1132	E1133	E1134	E1135	E1136	E1137	E1138	E1139	E1140	E1141	E1142	E1143	E1144	E1145	E1146	E1147	E1148	E1149	E1150	E1151	E1152	E1153	E1154	E1155	E1156	E1157	E1158	E1159	E1160	E1161	E1162	E1163	E1164	E1165	E1166	E1167	E1168	E1169	E1170	E1171	E1172	E1173	E1174	E1175	E1176	E1177	E1178	E1179	E1180	E1181	E1182	E1183	E1184	E1185	E1186	E1187	E1188	E1189	E1190	E1191	E1192	E1193	E1194	E1195	E1196	E1197	E1198	E1199	E1200	E1201	E1202	E1203	E1204	E1205	E1206	E1207	E1208	E1209	E1210	E1211	E1212	E1213	E1214	E1215	E1216	E1217	E1218	E1219	E1220	E1221	E1222	E1223	E1224	E1225	E1226	E1227	E1228	E1229	E1230	E1231	E1232	E1233	E1234	E1235	E1236																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	83920	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.226	Depositor
Minimum map value	-1.107	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.072	Depositor
Recommended contour level	0.4	Depositor
Map size ($\text{\AA}$)	419.84, 419.84, 419.84	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.82, 0.82, 0.82	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	A	0.19	0/11462	0.32	1/15525 (0.0%)
2	B	0.20	0/9896	0.36	1/13394 (0.0%)
3	C	0.20	0/2969	0.33	0/4012
4	D	0.17	0/1708	0.37	0/2311
5	E	0.20	0/1033	0.36	0/1398
6	F	0.17	0/2740	0.42	0/3709
7	G	0.19	0/828	0.42	0/1109
8	H	0.24	0/563	0.41	0/758
9	I	0.17	0/5298	0.39	1/7172 (0.0%)
All	All	0.19	0/36497	0.36	3/49388 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	I	124	PRO	CA-N-CD	-9.28	99.01	112.00
1	A	1204	PRO	CA-N-CD	-8.63	99.92	112.00
2	B	440	PRO	CA-N-CD	-5.94	103.68	112.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	A	11244	0	11362	231	0
2	B	9701	0	9657	304	0
3	C	2907	0	2982	56	0
4	D	1669	0	1713	44	0
5	E	1021	0	1054	25	0
6	F	2687	0	2721	88	0
7	G	816	0	814	23	0
8	H	553	0	580	28	0
9	I	5177	0	5136	140	0
10	A	3	0	0	0	0
10	B	1	0	0	0	0
10	G	2	0	0	0	0
10	H	1	0	0	0	0
11	A	1	0	0	0	0
All	All	35783	0	36019	824	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 824 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)
8:H:48:GLN:HB2	9:I:821:PHE:H	1.24	1.03
3:C:29:LEU:HD22	8:H:23:LYS:HD3	1.54	0.88
4:D:192:MET:O	4:D:193:HIS:ND1	2.08	0.86
2:B:491:LYS:HE2	2:B:527:HIS:HB3	1.60	0.84
2:B:1161:MET:O	2:B:1163:THR:N	2.13	0.81

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	A	1407/1441 (98%)	1351 (96%)	51 (4%)	5 (0%)	30	48
2	B	1222/1235 (99%)	1130 (92%)	86 (7%)	6 (0%)	24	42
3	C	356/358 (99%)	338 (95%)	18 (5%)	0	100	100
4	D	203/205 (99%)	196 (97%)	7 (3%)	0	100	100
5	E	125/139 (90%)	108 (86%)	17 (14%)	0	100	100
6	F	332/334 (99%)	298 (90%)	30 (9%)	4 (1%)	10	22
7	G	103/105 (98%)	95 (92%)	7 (7%)	1 (1%)	12	25
8	H	65/80 (81%)	59 (91%)	6 (9%)	0	100	100
9	I	630/1170 (54%)	588 (93%)	40 (6%)	2 (0%)	36	54
All	All	4443/5067 (88%)	4163 (94%)	262 (6%)	18 (0%)	31	48

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	582	MET
2	B	421	SER
2	B	1162	GLN
2	B	1202	ASP
9	I	94	GLU

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	A	1250/1270 (98%)	1229 (98%)	21 (2%)	53	75
2	B	1066/1074 (99%)	1034 (97%)	32 (3%)	36	61
3	C	327/327 (100%)	325 (99%)	2 (1%)	78	89
4	D	185/185 (100%)	178 (96%)	7 (4%)	29	54
5	E	119/129 (92%)	114 (96%)	5 (4%)	26	51
6	F	308/308 (100%)	292 (95%)	16 (5%)	21	43
7	G	96/96 (100%)	93 (97%)	3 (3%)	35	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
8	H	61/70 (87%)	60 (98%)	1 (2%)	55 76
9	I	572/1057 (54%)	549 (96%)	23 (4%)	28 53
All	All	3984/4516 (88%)	3874 (97%)	110 (3%)	38 62

5 of 110 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	101	ASN
6	F	93	ILE
9	I	1218	LEU
9	I	775	THR
4	D	167	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 59 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	598	GLN
9	I	1123	HIS
2	B	1227	ASN
9	I	1085	HIS
9	I	812	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

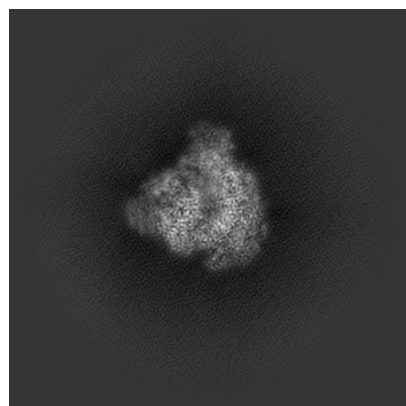
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38760. These allow visual inspection of the internal detail of the map and identification of artifacts.

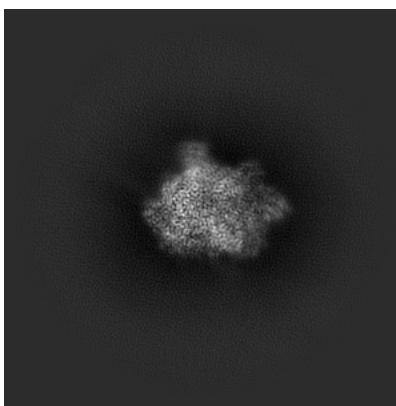
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

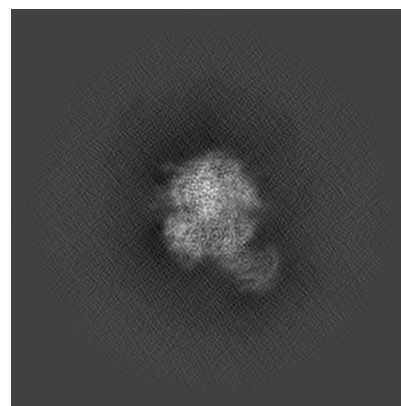
6.1.1 Primary map



X

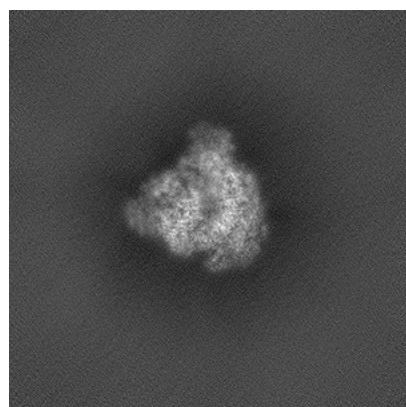


Y

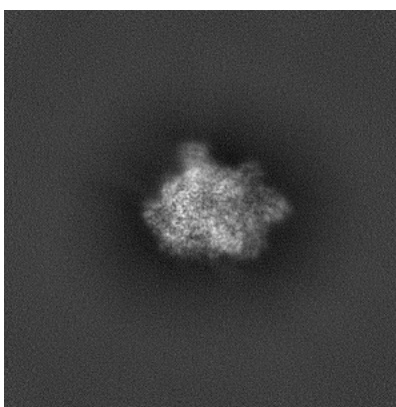


Z

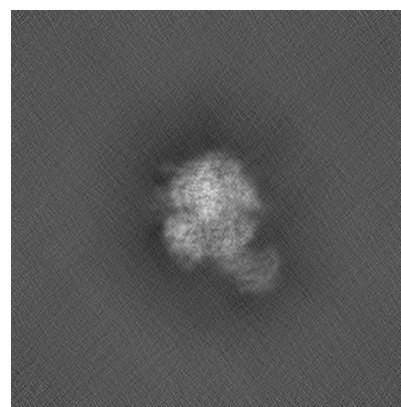
6.1.2 Raw map



X



Y

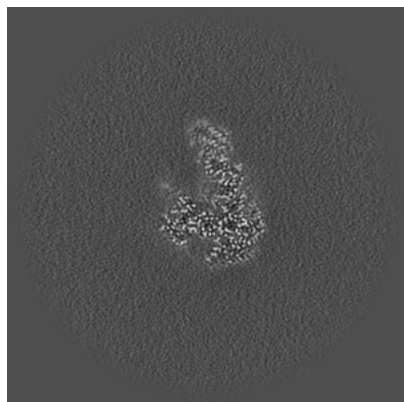


Z

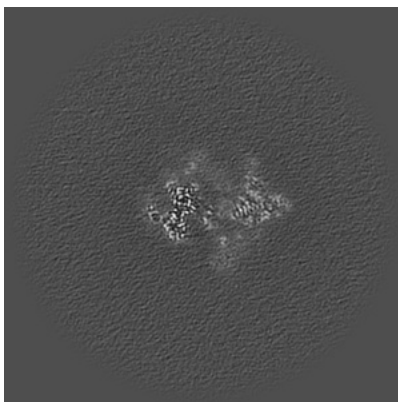
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

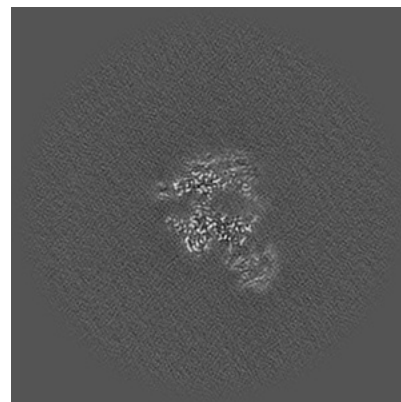
6.2.1 Primary map



X Index: 256

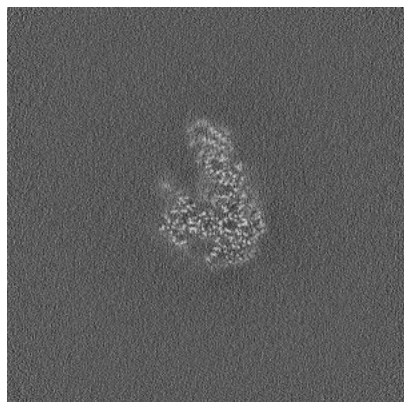


Y Index: 256

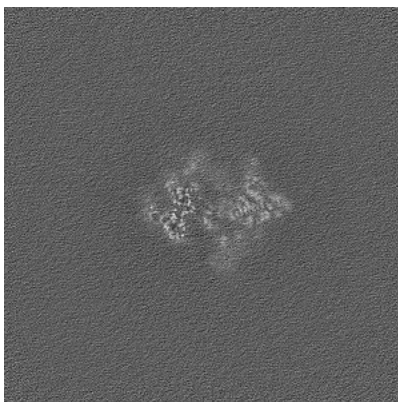


Z Index: 256

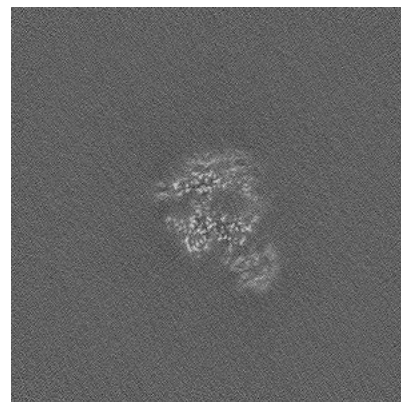
6.2.2 Raw map



X Index: 256



Y Index: 256

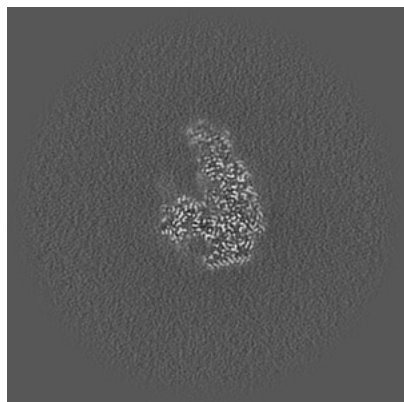


Z Index: 256

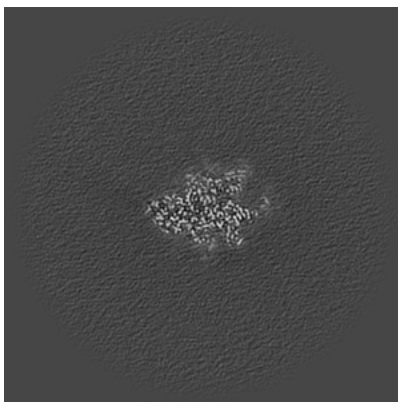
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

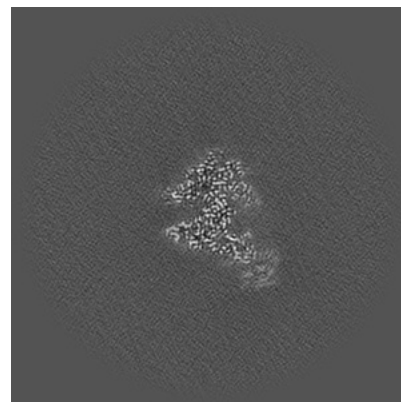
6.3.1 Primary map



X Index: 252

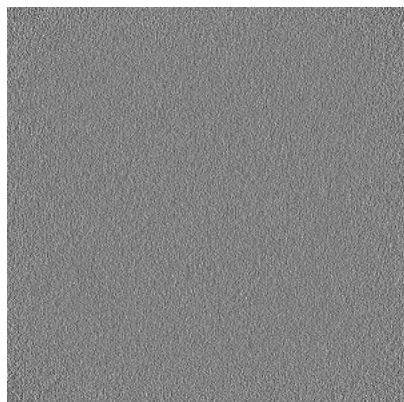


Y Index: 287

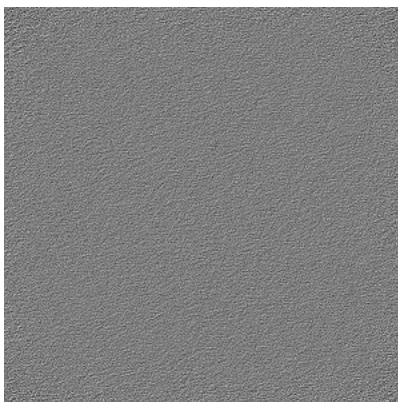


Z Index: 236

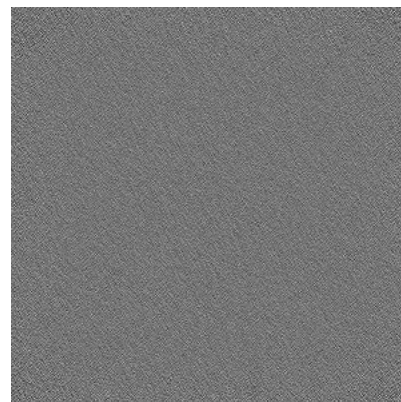
6.3.2 Raw map



X Index: 0



Y Index: 0

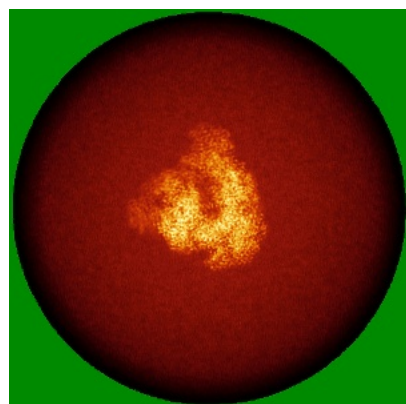


Z Index: 0

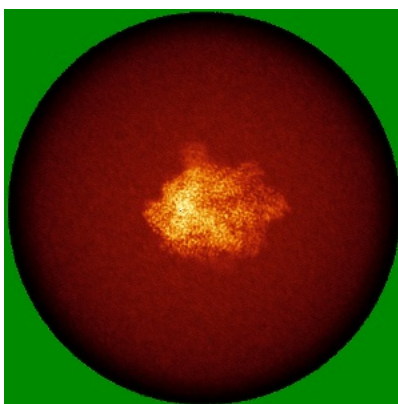
The images above show the largest variance slices of the map in three orthogonal directions.

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

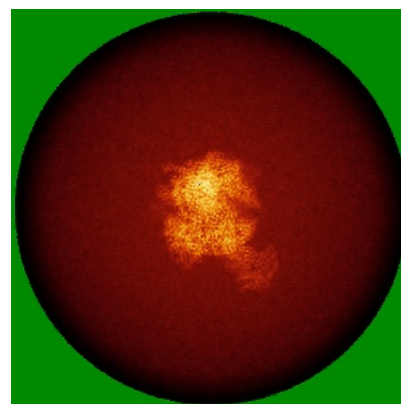
6.4.1 Primary map



X

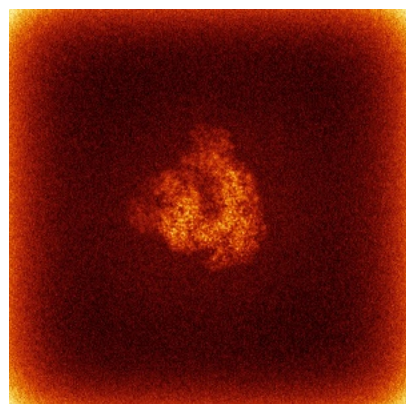


Y

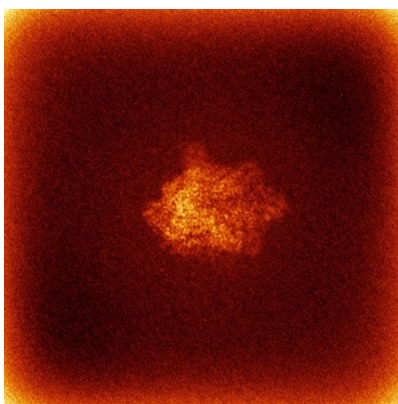


Z

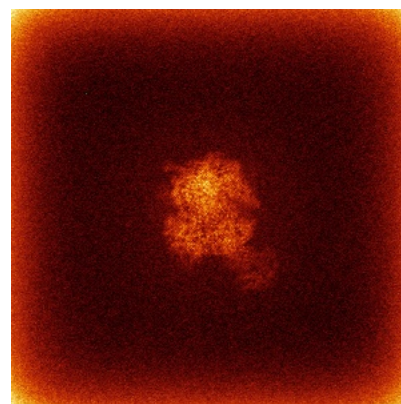
6.4.2 Raw map



X



Y

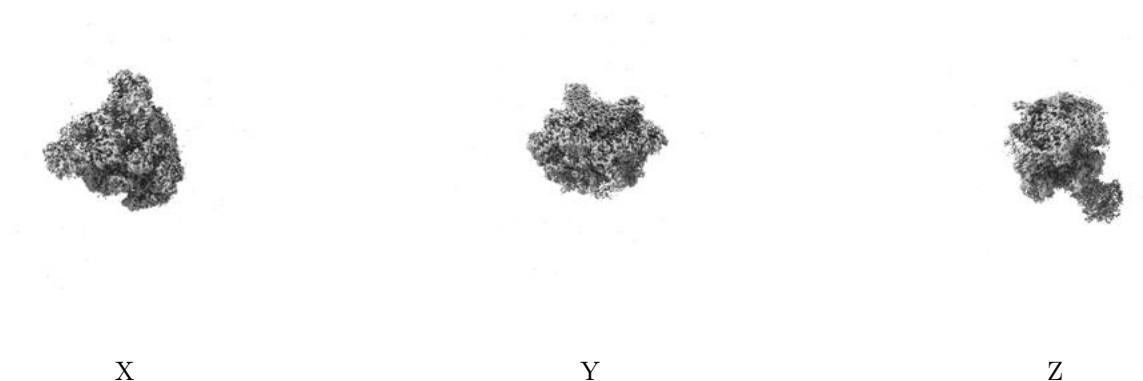


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

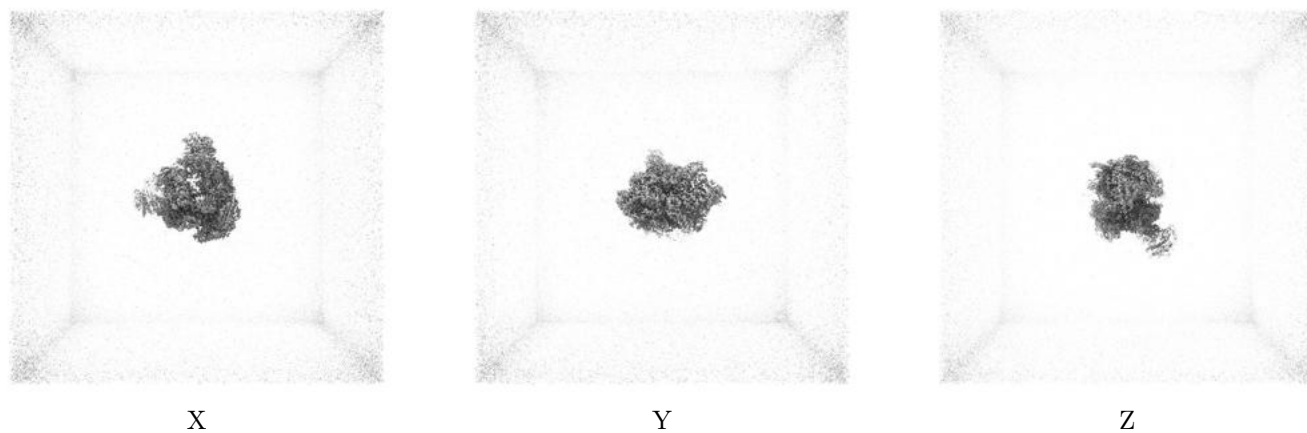
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

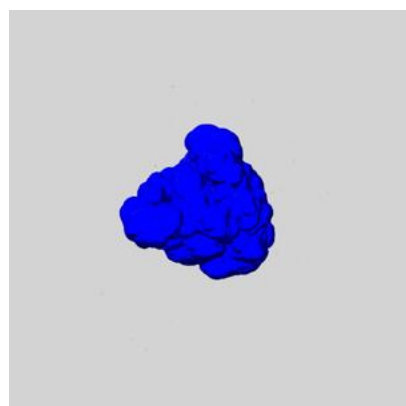
6.6 Mask visualisation [i](#)

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

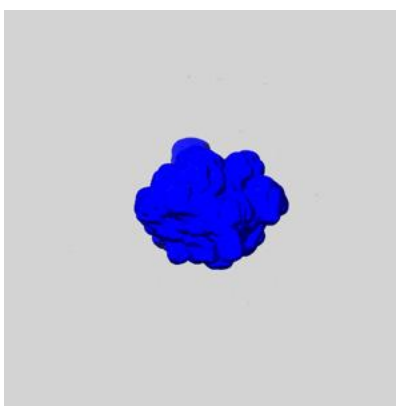
A mask typically either:

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

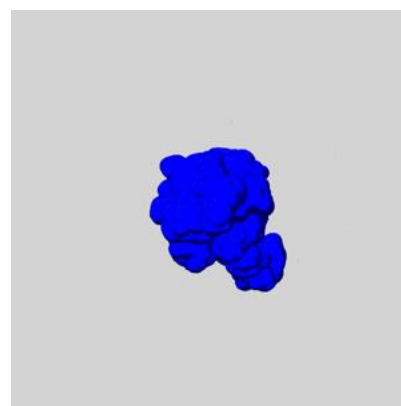
6.6.1 emd_38760_msk_1.map [i](#)



X



Y

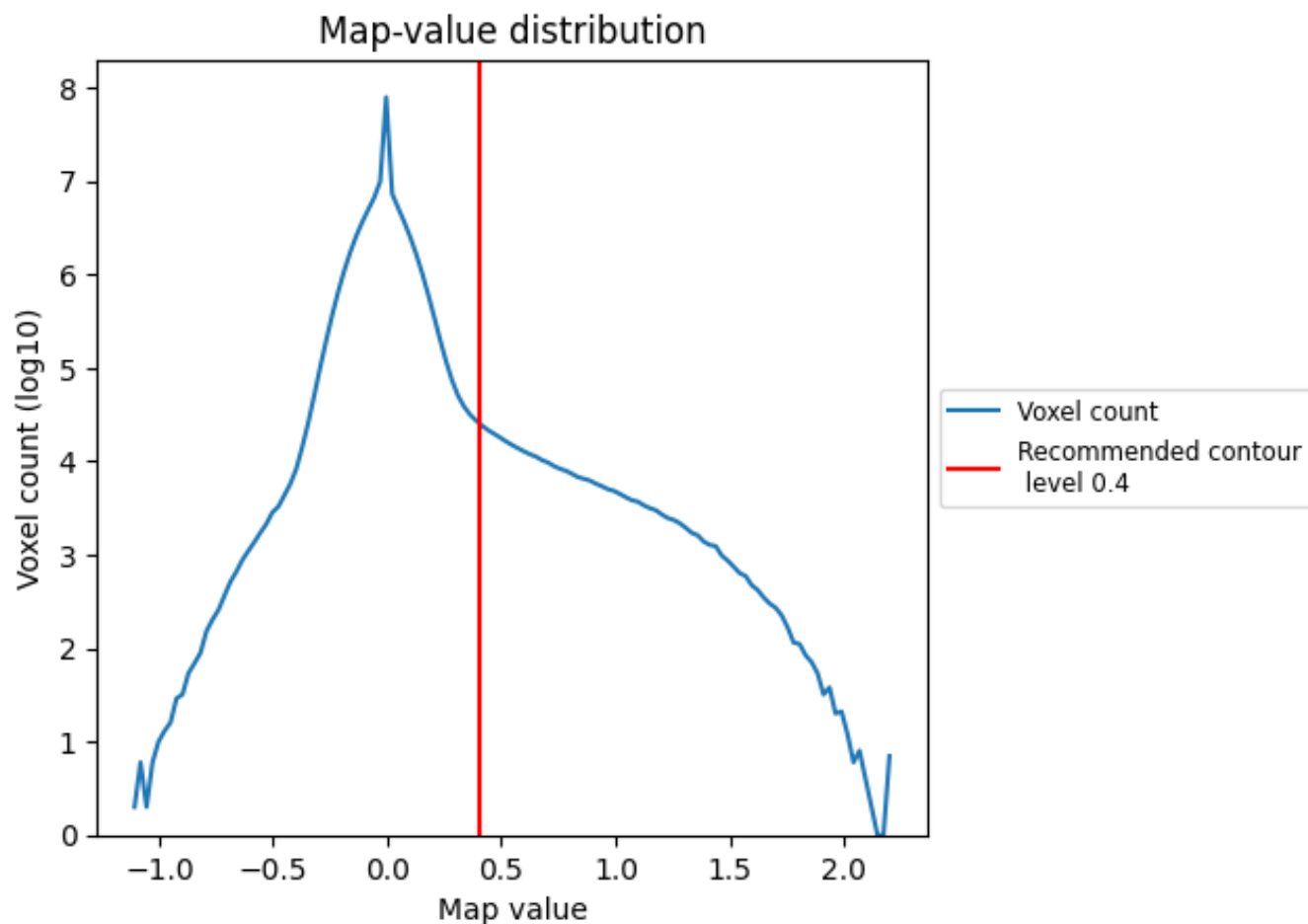


Z

7 Map analysis [i](#)

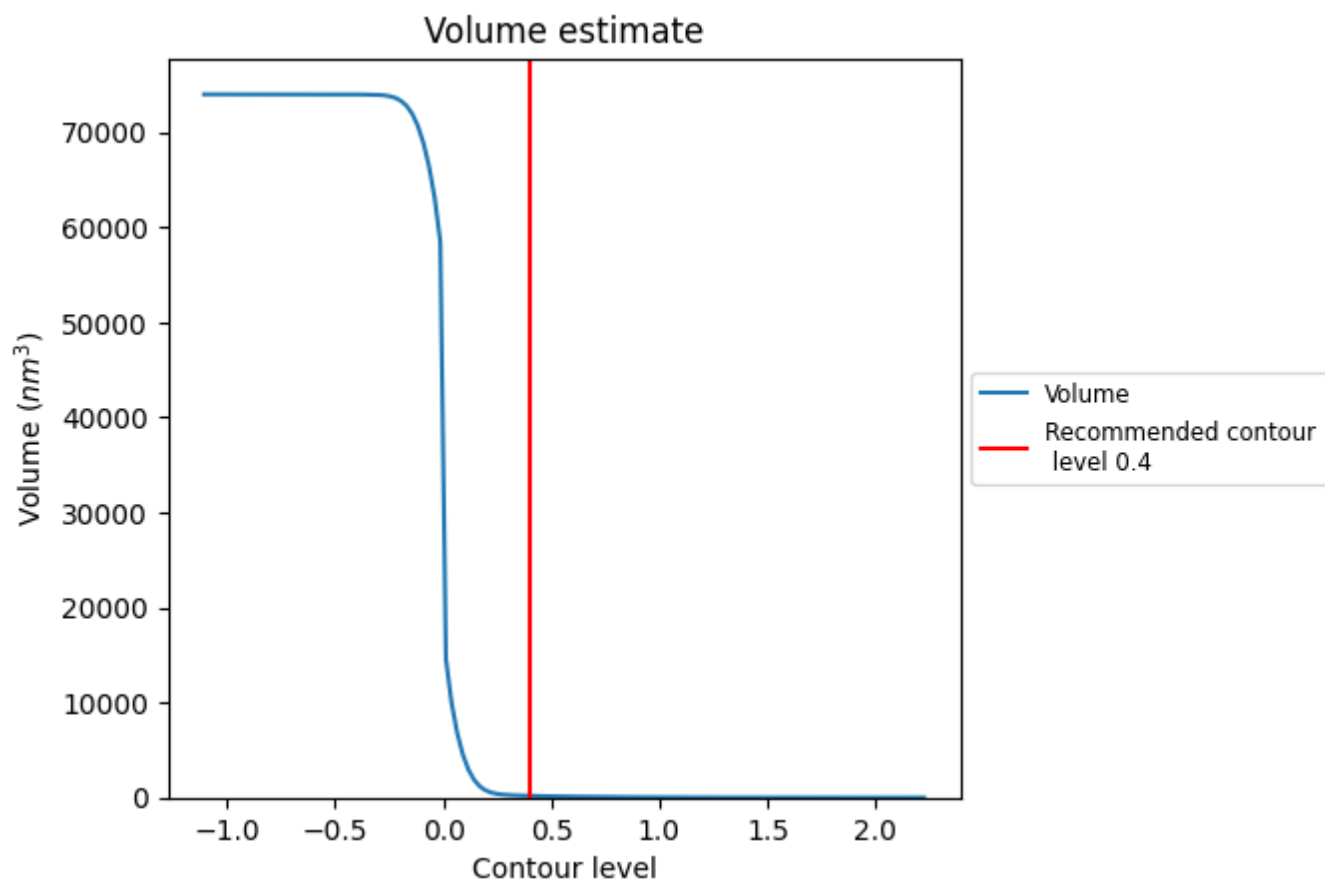
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

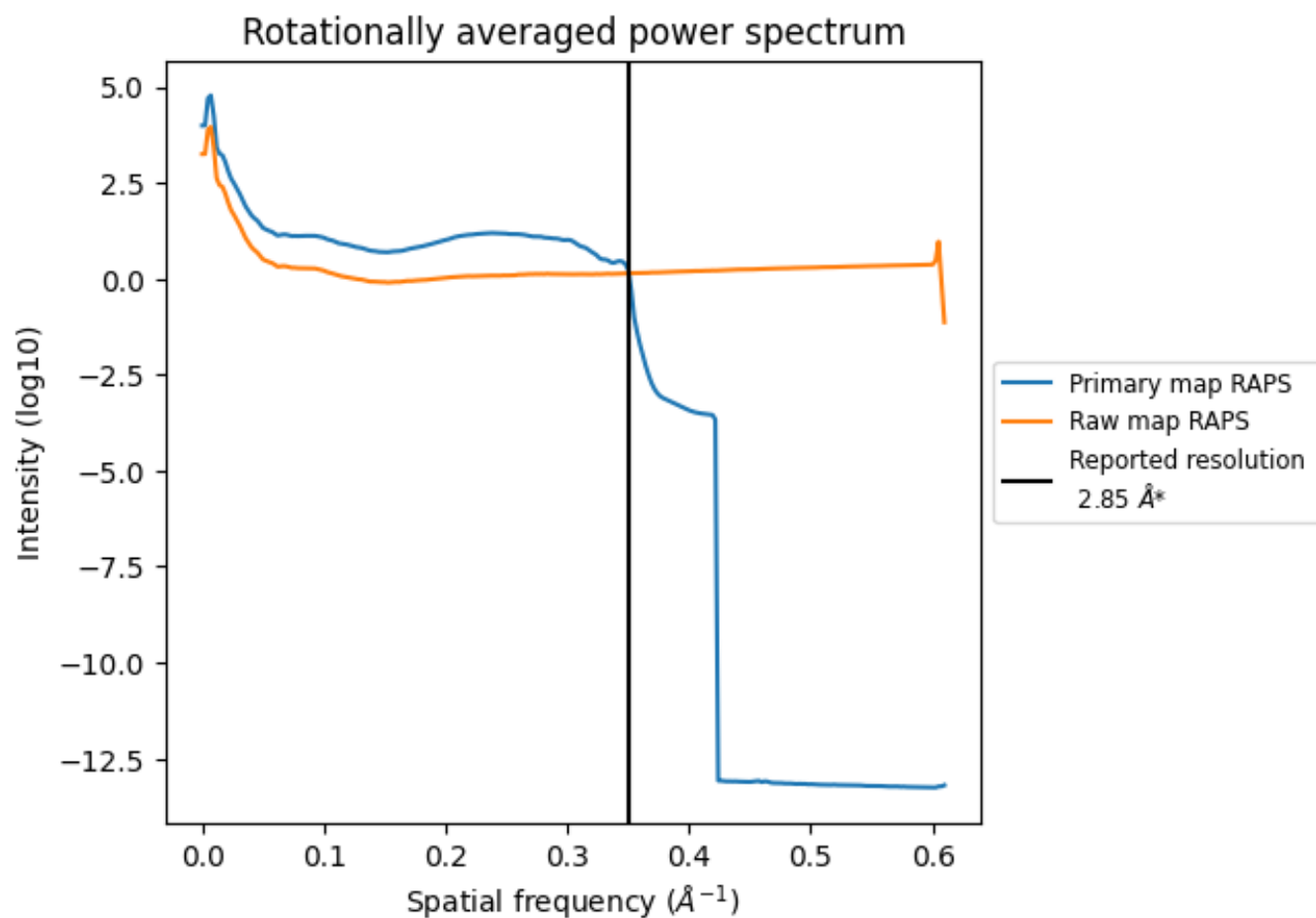
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 179 nm³; this corresponds to an approximate mass of 162 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 ⓘ

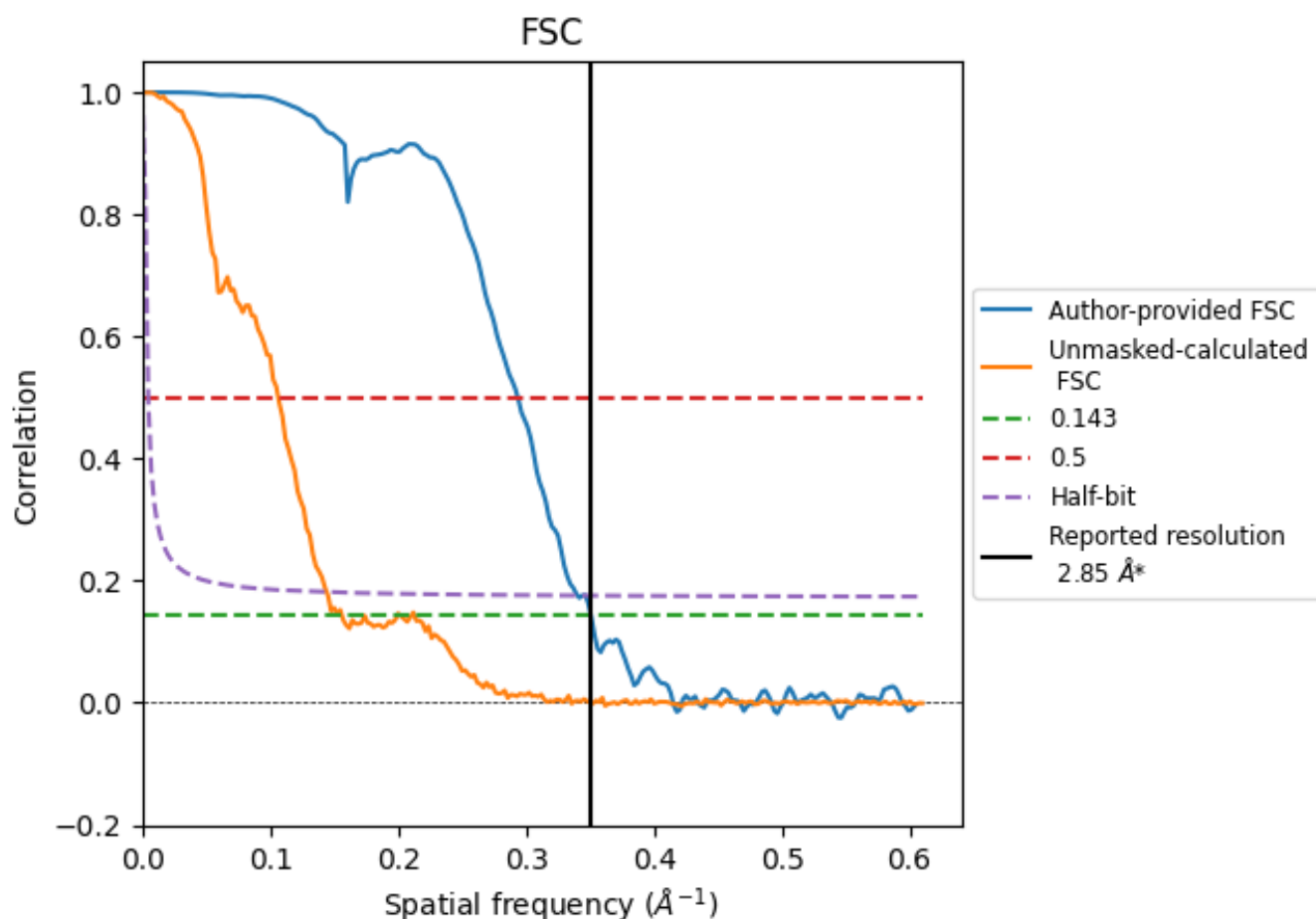


*Reported resolution corresponds to spatial frequency of 0.351 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.351 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

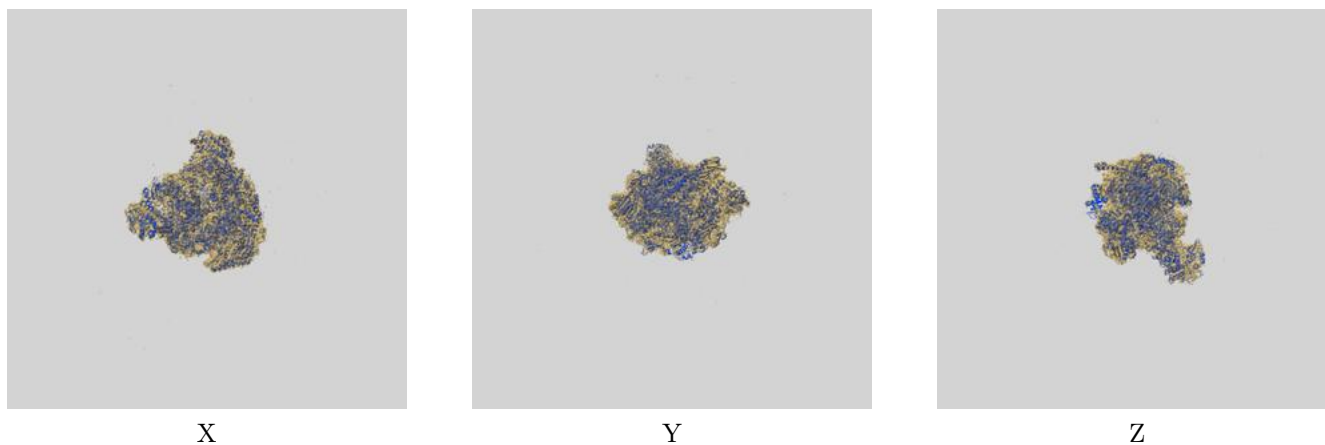
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.85	-	-
Author-provided FSC curve	2.85	3.41	2.94
Unmasked-calculated*	6.41	9.40	6.93

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.41 differs from the reported value 2.85 by more than 10 %

9 Map-model fit [i](#)

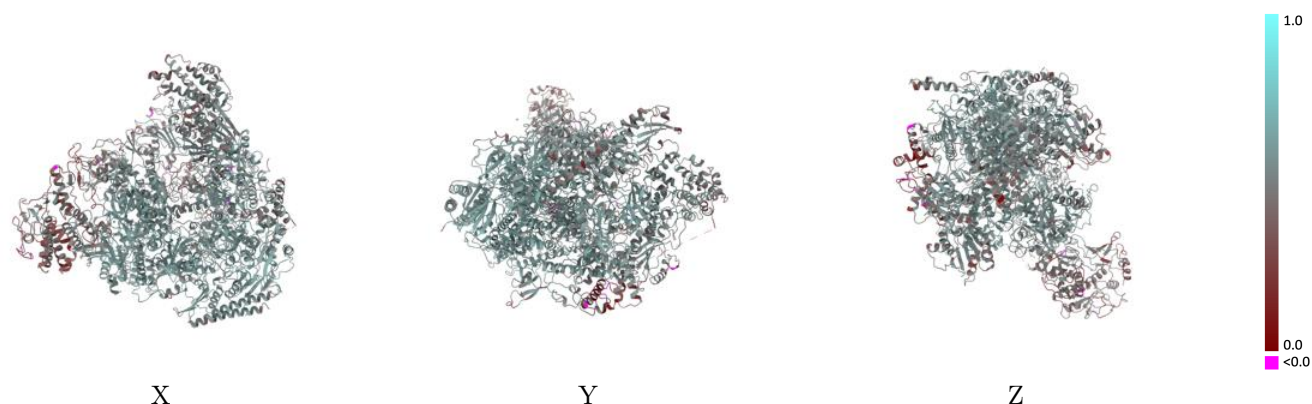
This section contains information regarding the fit between EMDB map EMD-38760 and PDB model 8XXT. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



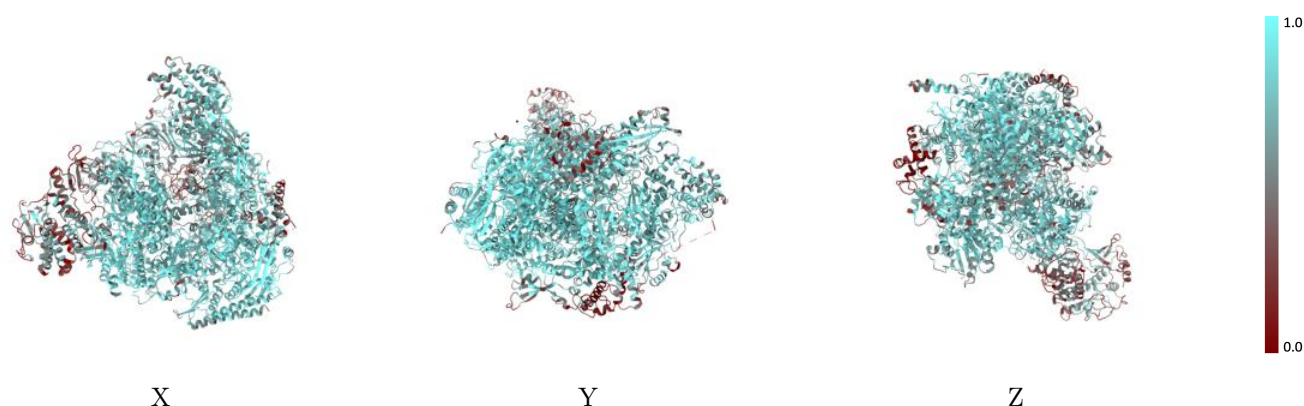
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



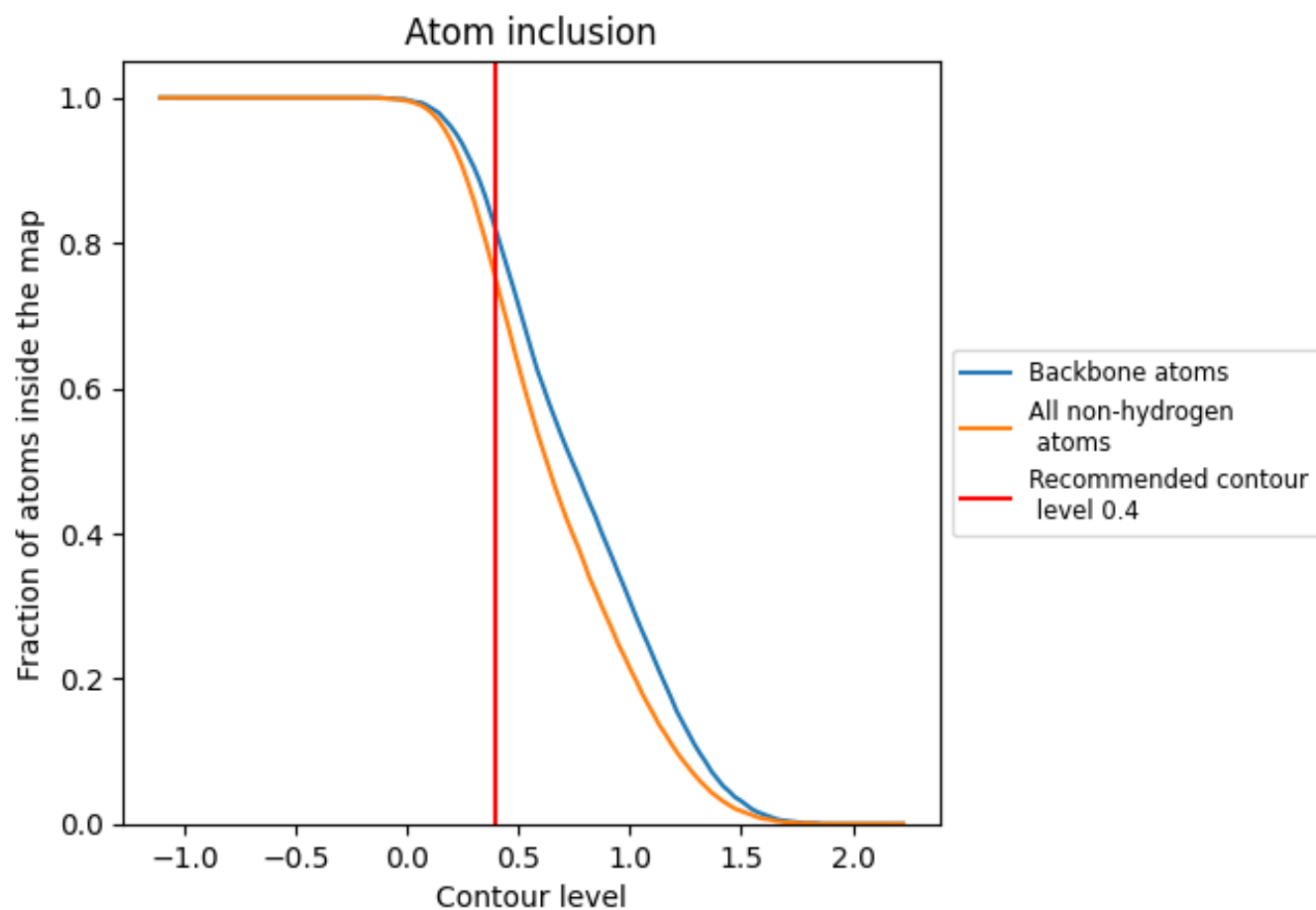
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 75% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7480	0.5250
A	0.8320	0.5600
B	0.8140	0.5490
C	0.8440	0.5700
D	0.7550	0.5130
E	0.7370	0.5400
F	0.5570	0.4370
G	0.7750	0.5230
H	0.8730	0.5620
I	0.4670	0.4200

1.0

0.0

<0.0