



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:58 AM UTC

PDB ID : 6RLB / pdb_00006rlb
EMDB ID : EMD-4918
Title : Structure of the dynein-2 complex; tail domain
Authors : Toropova, K.; Zalyte, R.; Mukhopadhyay, A.G.; Mladenov, M.; Carter, A.P.;
Roberts, A.J.
Deposited on : 2019-05-01
Resolution : 4.50 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:

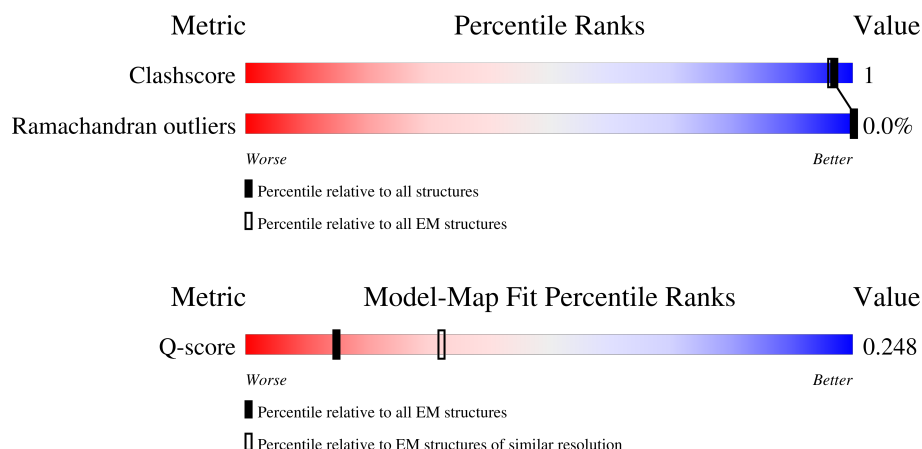
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.50 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	-
Q-score	-	25397	2937 (4.00 - 5.00)

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	4513	
1	B	4513	
2	C	1066	
3	D	564	
4	E	351	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	F	351	34% 87% 12%
5	G	96	97%
5	H	96	97%
6	I	89	96%
6	J	89	93%
6	K	89	96%
6	L	89	93%
6	M	89	96%
6	N	89	93%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 20407 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 O6-alkylguanine-DNA alkyltransferase mutant,DYNC2H1 variant protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	969	Total	C	N	O	0	0
			4805	2867	969	969		
1	B	889	Total	C	N	O	0	0
			4405	2627	889	889		

There are 62 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-205	GLY	-	expression tag	UNP E5BBQ0
A	-176	ARG	GLU	conflict	UNP E5BBQ0
A	-27	PRO	-	linker	UNP E5BBQ0
A	-26	GLY	-	linker	UNP E5BBQ0
A	-25	LEU	-	linker	UNP E5BBQ0
A	-24	GLY	-	linker	UNP E5BBQ0
A	-23	GLY	-	linker	UNP E5BBQ0
A	-22	SER	-	linker	UNP E5BBQ0
A	-21	LEU	-	linker	UNP E5BBQ0
A	-20	GLU	-	linker	UNP E5BBQ0
A	-19	VAL	-	linker	UNP E5BBQ0
A	-18	LEU	-	linker	UNP E5BBQ0
A	-17	PHE	-	linker	UNP E5BBQ0
A	-16	GLN	-	linker	UNP E5BBQ0
A	-15	GLY	-	linker	UNP E5BBQ0
A	-14	PRO	-	linker	UNP E5BBQ0
A	-13	ASP	-	linker	UNP E5BBQ0
A	-12	TYR	-	linker	UNP E5BBQ0
A	-11	ASP	-	linker	UNP E5BBQ0
A	-10	ILE	-	linker	UNP E5BBQ0
A	-9	PRO	-	linker	UNP E5BBQ0
A	-8	THR	-	linker	UNP E5BBQ0
A	-7	THR	-	linker	UNP E5BBQ0
A	-6	LEU	-	linker	UNP E5BBQ0
A	-5	GLU	-	linker	UNP E5BBQ0

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	VAL	-	linker	UNP E5BBQ0
A	-3	LEU	-	linker	UNP E5BBQ0
A	-2	PHE	-	linker	UNP E5BBQ0
A	-1	GLN	-	linker	UNP E5BBQ0
A	0	GLY	-	linker	UNP E5BBQ0
A	1	PRO	-	linker	UNP E5BBQ0
B	-205	GLY	-	expression tag	UNP E5BBQ0
B	-176	ARG	GLU	conflict	UNP E5BBQ0
B	-27	PRO	-	linker	UNP E5BBQ0
B	-26	GLY	-	linker	UNP E5BBQ0
B	-25	LEU	-	linker	UNP E5BBQ0
B	-24	GLY	-	linker	UNP E5BBQ0
B	-23	GLY	-	linker	UNP E5BBQ0
B	-22	SER	-	linker	UNP E5BBQ0
B	-21	LEU	-	linker	UNP E5BBQ0
B	-20	GLU	-	linker	UNP E5BBQ0
B	-19	VAL	-	linker	UNP E5BBQ0
B	-18	LEU	-	linker	UNP E5BBQ0
B	-17	PHE	-	linker	UNP E5BBQ0
B	-16	GLN	-	linker	UNP E5BBQ0
B	-15	GLY	-	linker	UNP E5BBQ0
B	-14	PRO	-	linker	UNP E5BBQ0
B	-13	ASP	-	linker	UNP E5BBQ0
B	-12	TYR	-	linker	UNP E5BBQ0
B	-11	ASP	-	linker	UNP E5BBQ0
B	-10	ILE	-	linker	UNP E5BBQ0
B	-9	PRO	-	linker	UNP E5BBQ0
B	-8	THR	-	linker	UNP E5BBQ0
B	-7	THR	-	linker	UNP E5BBQ0
B	-6	LEU	-	linker	UNP E5BBQ0
B	-5	GLU	-	linker	UNP E5BBQ0
B	-4	VAL	-	linker	UNP E5BBQ0
B	-3	LEU	-	linker	UNP E5BBQ0
B	-2	PHE	-	linker	UNP E5BBQ0
B	-1	GLN	-	linker	UNP E5BBQ0
B	0	GLY	-	linker	UNP E5BBQ0
B	1	PRO	-	linker	UNP E5BBQ0

- Molecule 2 is a protein called WD repeat-containing protein 60.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	C	494	Total	C	N	O	0	0
			2443	1455	494	494		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	225	LYS	ASN	conflict	UNP Q8WVS4
C	292	PHE	SER	conflict	UNP Q8WVS4

- Molecule 3 is a protein called WD repeat-containing protein 34.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	D	446	Total	C	N	O	0	0
			2200	1308	446	446		

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	537	TRP	-	expression tag	UNP Q96EX3
D	538	SER	-	expression tag	UNP Q96EX3
D	539	HIS	-	expression tag	UNP Q96EX3
D	540	PRO	-	expression tag	UNP Q96EX3
D	541	GLN	-	expression tag	UNP Q96EX3
D	542	PHE	-	expression tag	UNP Q96EX3
D	543	GLU	-	expression tag	UNP Q96EX3
D	544	LYS	-	expression tag	UNP Q96EX3
D	545	GLY	-	expression tag	UNP Q96EX3
D	546	SER	-	expression tag	UNP Q96EX3
D	547	ALA	-	expression tag	UNP Q96EX3
D	548	GLY	-	expression tag	UNP Q96EX3
D	549	SER	-	expression tag	UNP Q96EX3
D	550	ALA	-	expression tag	UNP Q96EX3
D	551	ALA	-	expression tag	UNP Q96EX3
D	552	GLY	-	expression tag	UNP Q96EX3
D	553	SER	-	expression tag	UNP Q96EX3
D	554	GLY	-	expression tag	UNP Q96EX3
D	555	ALA	-	expression tag	UNP Q96EX3
D	556	GLY	-	expression tag	UNP Q96EX3
D	557	TRP	-	expression tag	UNP Q96EX3
D	558	SER	-	expression tag	UNP Q96EX3
D	559	HIS	-	expression tag	UNP Q96EX3
D	560	PRO	-	expression tag	UNP Q96EX3
D	561	GLN	-	expression tag	UNP Q96EX3
D	562	PHE	-	expression tag	UNP Q96EX3
D	563	GLU	-	expression tag	UNP Q96EX3
D	564	LYS	-	expression tag	UNP Q96EX3

- Molecule 4 is a protein called Cytoplasmic dynein 2 light intermediate chain 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	E	312	Total	C	N	O	0	0
			1542	918	312	312		
4	F	310	Total	C	N	O	0	0
			1532	912	310	310		

- Molecule 5 is a protein called Dynein light chain roadblock-type 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	G	93	Total	C	N	O	0	0
			462	276	93	93		
5	H	93	Total	C	N	O	0	0
			462	276	93	93		

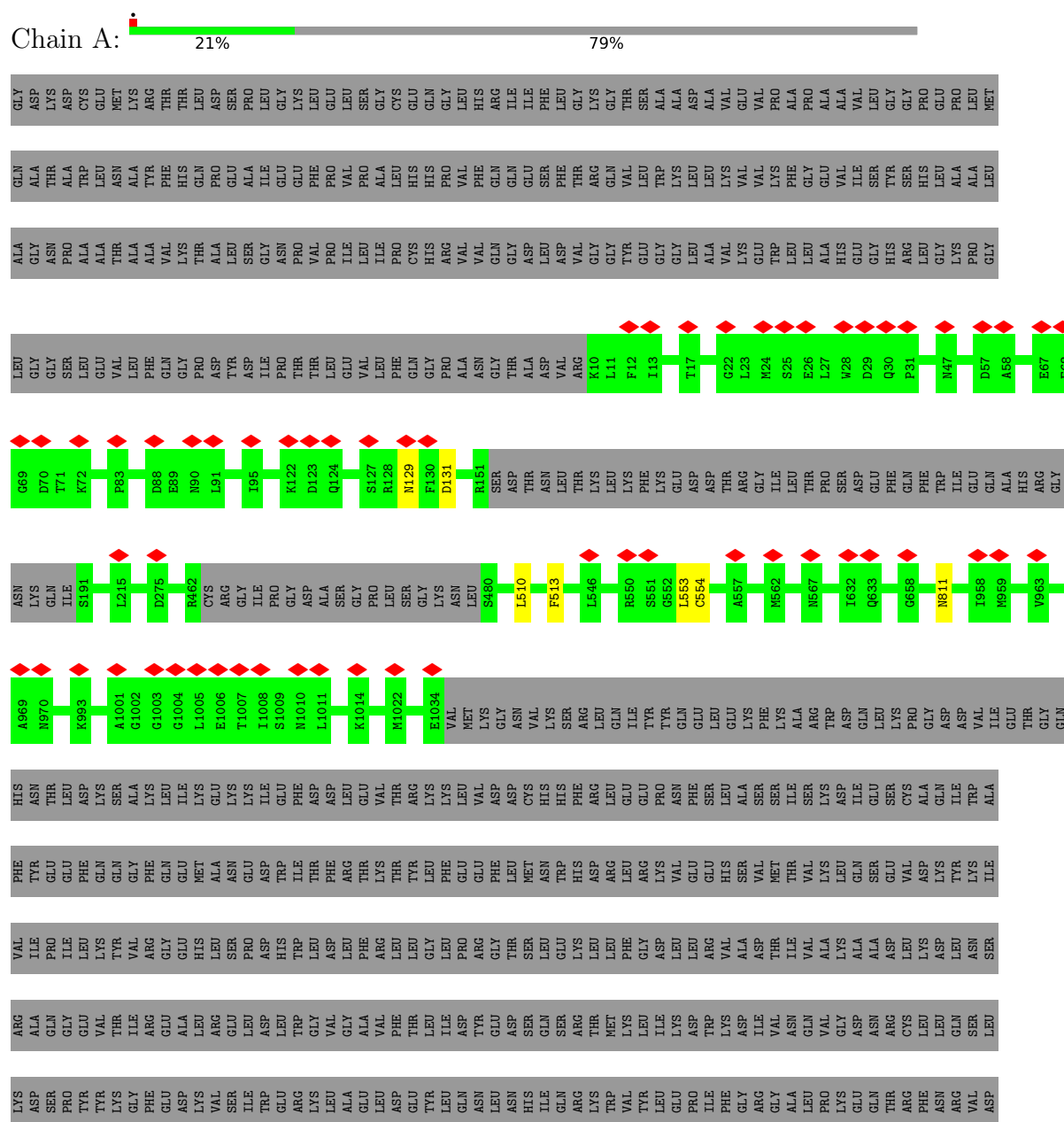
- Molecule 6 is a protein called Dynein light chain 1, cytoplasmic.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	I	86	Total	C	N	O	0	0
			426	254	86	86		
6	J	86	Total	C	N	O	0	0
			426	254	86	86		
6	K	86	Total	C	N	O	0	0
			426	254	86	86		
6	L	86	Total	C	N	O	0	0
			426	254	86	86		
6	M	86	Total	C	N	O	0	0
			426	254	86	86		
6	N	86	Total	C	N	O	0	0
			426	254	86	86		

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: O6-alkylguanine-DNA alkyltransferase mutant,DYNC2H1 variant protein

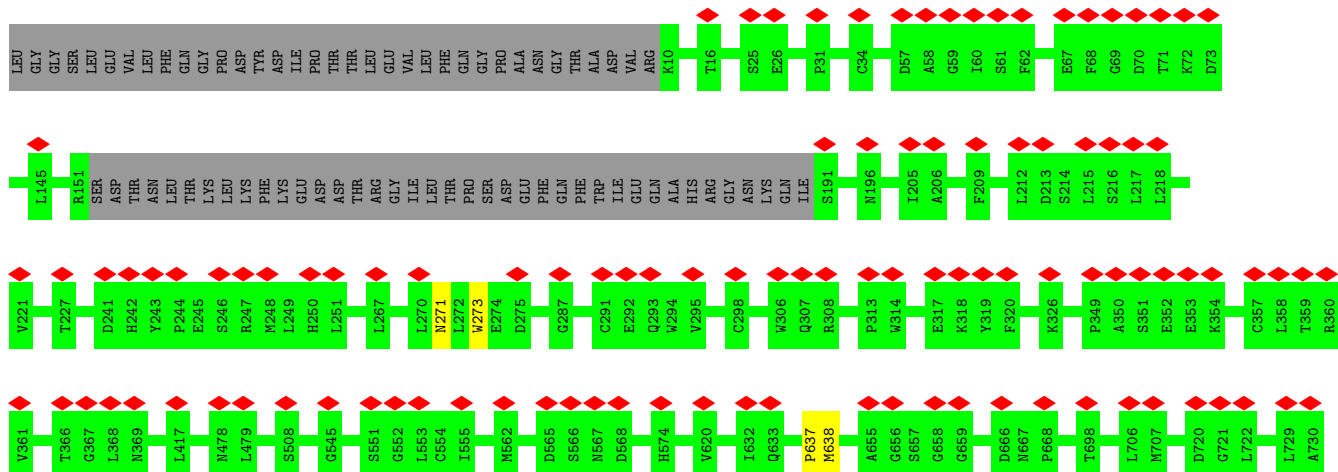






[illegible]

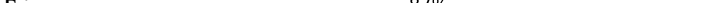
- Molecule 1: O6-alkylguanine-DNA alkyltransferase mutant,DYNC2H1 variant protein

[illegible]

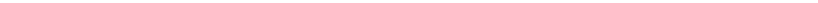
T731	T732	E733	A734	A739	Y761	G764	L768	N769	E770	N771	L772	P773	E774	I775	N776	I777	D778	L779	T780	Y781	K782	Q783	G784	R785	L786	Q787	F788	R789	P790	F791	F792	E793	E794	I809	P810	N811	A833	R849	L850	S851	A852	V853	L854	H855	Q856	H857	K858	E859	W860	I861	V862	I863																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
G864	Q865	V866	D867	M868	E869	A870	L871	V872	E873	K874	H875	T878	V879	H880	D881	W882	E883	K884	N885	F886	K887	A888	L889	K890	I891	K892	G893	K894	E895	V896	E897	R898	L899	P900	S901	A902	V903	K904	V905	D906	C907	L908	N909	I910	N911	C912	N913	P914	V915	K916	T917	V918	I919	D920	D921	L922	K925																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
D928	L929	L930	L931	V931	L932	S933	L934	K935	K936	S937	I938	L939	L940	L941	L942	L943	L944	L945	L946	L947	L948	L949	L950	L951	L952	L953	L954	L955	L956	L957	L958	L959	L960	L961	L962	L963	L964	L965	L966	L967	L968	L969	L970	L971	L972	L973	L974	L975	L976	L977	L978	L979	L980	L981	L982	L983	L984	L985	L986	L987	L988	L989	L990	L991	L992	L993	L994	L995	L996	L997	L998	L999	L1000	L1001	L1002	L1003	L1004	L1005	L1006	L1007	L1008	L1009	L1010	L1011	L1012	L1013	L1014	L1015	L1016	L1017	L1018	L1019	L1020	L1021	L1022	L1023	L1024	L1025	L1026	L1027	L1028	L1029	L1030	L1031	L1032	L1033	L1034	L1035	L1036	L1037	L1038	L1039	L1040	L1041	L1042	L1043	L1044	L1045	L1046	L1047	L1048	L1049	L1050	L1051	L1052	L1053	L1054	L1055	L1056	L1057	L1058	L1059	L1060	L1061	L1062	L1063	L1064	L1065	L1066	L1067	L1068	L1069	L1070	L1071	L1072	L1073	L1074	L1075	L1076	L1077	L1078	L1079	L1080	L1081	L1082	L1083	L1084	L1085	L1086	L1087	L1088	L1089	L1090	L1091	L1092	L1093	L1094	L1095	L1096	L1097	L1098	L1099	L1100	L1101	L1102	L1103	L1104	L1105	L1106	L1107	L1108	L1109	L1110	L1111	L1112	L1113	L1114	L1115	L1116	L1117	L1118	L1119	L1120	L1121	L1122	L1123	L1124	L1125	L1126	L1127	L1128	L1129	L1130	L1131	L1132	L1133	L1134	L1135	L1136	L1137	L1138	L1139	L1140	L1141	L1142	L1143	L1144	L1145	L1146	L1147	L1148	L1149	L1150	L1151	L1152	L1153	L1154	L1155	L1156	L1157	L1158	L1159	L1160	L1161	L1162	L1163	L1164	L1165	L1166	L1167	L1168	L1169	L1170	L1171	L1172	L1173	L1174	L1175	L1176	L1177	L1178	L1179	L1180	L1181	L1182	L1183	L1184	L1185	L1186	L1187	L1188	L1189	L1190	L1191	L1192	L1193	L1194	L1195	L1196	L1197	L1198	L1199	L1200	L1201	L1202	L1203	L1204	L1205	L1206	L1207	L1208	L1209	L1210	L1211	L1212	L1213	L1214	L1215	L1216	L1217	L1218	L1219	L1220	L1221	L1222	L1223	L1224	L1225	L1226	L1227	L1228	L1229	L1230	L1231	L1232	L1233	L1234	L1235	L1236	L1237	L1238	L1239	L1240	L1241	L1242	L1243	L1244	L1245	L1246	L1247	L1248	L1249	L1250	L1251	L1252	L1253	L1254	L1255	L1256	L1257	L1258	L1259	L1260	L1261	L1262	L1263	L1264	L1265	L1266	L1267	L1268	L1269	L1270	L1271	L1272	L1273	L1274	L1275	L1276	L1277	L1278	L1279	L1280	L1281	L1282	L1283	L1284	L1285	L1286	L1287	L1288	L1289	L1290	L1291	L1292	L1293	L1294	L1295	L1296	L1297	L1298	L1299	L1300	L1301	L1302	L1303	L1304	L1305	L1306	L1307	L1308	L1309	L1310	L1311	L1312	L1313	L1314	L1315	L1316	L1317	L1318	L1319	L1320	L1321	L1322	L1323	L1324	L1325	L1326	L1327	L1328	L1329	L1330	L1331	L1332	L1333	L1334	L1335	L1336	L1337	L1338	L1339	L1340	L1341	L1342	L1343	L1344	L1345	L1346	L1347	L1348	L1349	L1350	L1351	L1352	L1353	L1354	L1355	L1356	L1357	L1358	L1359	L1360	L1361	L1362	L1363	L1364	L1365	L1366	L1367	L1368	L1369	L1370	L1371	L1372	L1373	L1374	L1375	L1376	L1377	L1378	L1379	L1380	L1381	L1382	L1383	L1384	L1385	L1386	L1387	L1388	L1389	L1390	L1391	L1392	L1393	L1394	L1395	L1396	L1397	L1398	L1399	L1400	L1401	L1402	L1403	L1404	L1405	L1406	L1407	L1408	L1409	L1410	L1411	L1412	L1413	L1414	L1415	L1416	L1417	L1418	L1419	L1420	L1421	L1422	L1423	L1424	L1425	L1426	L1427	L1428	L1429	L1430	L1431	L1432	L1433	L1434	L1435	L1436	L1437	L1438	L1439	L1440	L1441	L1442	L1443	L1444	L1445	L1446	L1447	L1448	L1449	L1450	L1451	L1452	L1453	L1454	L1455	L1456	L1457	L1458	L1459	L1460	L1461	L1462	L1463	L1464	L1465	L1466	L1467	L1468	L1469	L1470	L1471	L1472	L1473	L1474	L1475	L1476	L1477	L1478	L1479	L1480	L1481	L1482	L1483	L1484	L1485	L1486	L1487	L1488	L1489	L1490	L1491	L1492	L1493	L1494	L1495	L1496	L1497	L1498	L1499	L1500	L1501	L1502	L1503	L1504	L1505	L1506	L1507	L1508	L1509	L1510	L1511	L1512	L1513	L1514	L1515	L1516	L1517	L1518	L1519	L1520	L1521	L1522	L1523	L1524	L1525	L1526	L1527	L1528	L1529	L1530	L1531	L1532	L1533	L1534	L1535	L1536	L1537	L1538	L1539	L1540	L1541	L1542	L1543	L1544	L1545	L1546	L1547	L1548	L1549	L1550	L1551	L1552	L1553	L1554	L1555	L1556	L1557	L1558	L1559	L1560	L1561	L1562	L1563	L1564	L1565	L1566	L1567	L1568	L1569	L1570	L1571	L1572	L1573	L1574	L1575	L1576	L1577	L1578	L1579	L1580	L1581	L1582	L1583	L1584	L1585	L1586	L1587	L1588	L1589	L1590	L1591	L1592	L1593	L1594	L1595	L1596	L1597	L1598	L1599	L1600	L1601	L1602	L1603	L1604	L1605	L1606	L1607	L1608	L1609	L1610	L1611	L1612	L1613	L1614	L1615	L1616	L1617	L1618	L1619	L1620	L1621	L1622	L1623	L1624	L1625	L1626	L1627	L1628	L1629	L1630	L1631	L1632	L1633	L1634	L1635	L1636	L1637	L1638	L1639	L1640	L1641	L1642	L1643	L1644	L1645	L1646	L1647	L1648	L1649	L1650	L1651	L1652	L1653	L1654	L1655	L1656	L1657	L1658	L1659	L1660	L1661	L1662	L1663	L1664	L1665	L1666	L1667	L1668	L1669	L1670	L1671	L1672	L1673	L1674	L1675	L1676	L1677	L1678	L1679	L1680	L1681	L1682	L1683	L1684	L1685	L1686	L1687	L1688	L1689	L1690	L1691	L1692	L1693	L1694	L1695	L1696	L1697	L1698	L1699	L1700	L1701	L1702	L1703	L1704	L1705	L1706	L1707	L1708	L1709	L1710	L1711	L1712	L1713	L1714	L1715	L1716	L1717	L1718	L1719	L1720	L1721	L1722	L1723	L1724	L1725	L1726	L1727	L1728	L1729	L1730	L1731	L1732	L1733	L1734	L1735	L1736	L1737	L1738	L1739	L1740	L1741	L1742	L1743	L1744	L1745	L1746	L1747	L1748	L1749	L1750	L1751	L1752	L1753	L1754	L1755	L1756	L1757	L1758	L1759	L1760	L1761	L1762	L1763	L1764	L1765	L1766	L1767	L1768	L1769	L1770	L1771	L1772	L1773	L1774	L1775	L1776	L1777	L1778	L1779	L1780	L1781	L1782	L1783	L1784	L1785	L1786	L1787	L1788	L1789	L1790	L1791	L1792	L1793	L1794	L1795	L1796	L1797	L1798	L1799	L1800	L1801	L1802	L1803	L1804	L1805	L1806	L1807	L1808	L1809	L1810	L1811	L1812	L1813	L1814	L1815	L1816	L1817	L1818	L1819	L1820	L1821	L1822	L1823	L1824	L1825	L1826	L1827	L1828	L1829	L1830	L1831	L1832	L1833	L1834	L1835	L1836	L1837	L1838	L1839	L1840	L1841	L1842	L1843	L1844	L1845	L1846	L1847	L1848	L1849	L1850	L1851	L1852	L1853	L1854	L1855	L1856	L1857	L1858	L1859	L1860	L1861	L1862	L1863	L1864	L1865	L1866	L1867	L1868	L1869	L1870	L1871	L1872	L1873	L1874	L1875	L1876	L1877	L1878	L1879	L1880	L1881	L1882	L1883	L1884	L1885	L1886	L1887	L1888	L1889	L1890	L1891	L1892	L1893	L1894	L1895	L1896	L1897	L1898	L1899	L1900	L1901	L1902	L1903	L1904	L1905	L1906	L1907	L1908	L1909	L1910	L1911	L1912	L1913	L1914	L1915	L1916	L1917	L1918	L1919	L1920	L1921	L1922	L1923	L1924	L1925	L1926	L1927	L1928	L1929	L1930	L1931	L1932	L1933	L1934	L1935	L1936	L1937	L1938	L1939	L1940	L1941	L1942	L1943	L1944	L1945	L1946	L1947	L1948	L1949	L1950	L1951	L1952	L1953	L1954	L1955	L1956	L1957	L1958	L1959	L1960	L1961	L1962	L1963	L1964	L1965	L1966	L1967	L1968	L1969	L1970	L1971	L1972	L1973	L1974	L1975	L1976	L1977	L1978	L1979	L1980	L1981	L1982	L1983	L1984	L1985	L1986	L1987	L1988	L1989	L1990	L1991	L1992	L1993	L1994	L1995	L1996	L1997	L1998	L1999	L2000	L2001	L2002	L2003	L2004	L2005	L2006	L2007	L2008	L2009	L2010	L2011	L2012	L2013	L2014	L2015	L2016	L2017	L2018	L2019	L2020	L2021	L2022	L2023	L2024	L2025	L2026	L2027	L2028	L2029	L2030	L2031	L2032	L2033	L2034	L2035	L2036	L2037	L2038	L2039	L2040	L2041	L2042	L2043	L2044	L2045	L2046	L2047	L2048	L2049	L2050	L2051	L2052	L2053	L2054	L2055	L2056	L2057	L2058	L2059	L2060	L2061	L2062	L2063	L2064	L2065	L2066	L2067	L2068	L2069	L2070	L2071	L2072	L2073	L2074	L2075	L2076	L2077	L2078	L2079	L2080	L2081	L2082	L2083	L2084	L2085	L2086	L2087	L2088	L2089	L2090	L2091	L2092	L2093	L2094	L2095	L2096	L2097	L2098	L2099	L2100	L2101	L2102	L2103	L2104	L2105	L2106	L2107	L2108	L2109	L2110	L2111	L2112	L2113	L2114	L2115	L2116	L2117	L2118	L2119	L2120	L2121	L2122	L2123	L2124	L2125	L2126	L2127	L2128	L2129	L2130	L2131	L2132	L2133	L2134	L2135	L2136	L2137	L2138	L2139	L2140	L2141	L2142	L2143	L2144	L2145	L2146	L2147	L2148	L2149	L2150	L2151	L2152	L2153	L2154	L2155	L2156	L2157	L2158	L2159	L2160	L2161	L2162	L2163	L2164	L2165	L2166	L2167	L2168	L2169	L2170	L2171	L2172	L2173	L2174	L2175	L2176	L2177	L2178	L2179	L2180	L2181	L2182	L2183	L2184	L2185	L2186	L2187	L2188	L2189	L2190	L2191	L2192	L2193	L2194	L21



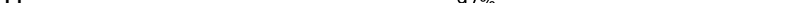
- Molecule 2: WD repeat-containing protein 60

- Chain F:  34% 87% 12%

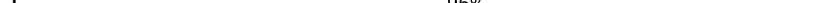
[illegible]

- Chain G:  97%

MET
ALA
E604
T696
GLU

- Chain H:  97%

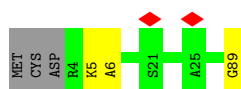
MET
ALA
E511
T603
GLU

- Chain I:  96%

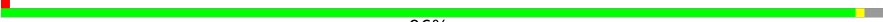


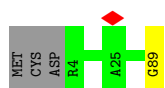
- Molecule 6: Dynein light chain 1, cytoplasmic

Chain J:  93% . .



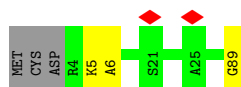
- Molecule 6: Dynein light chain 1, cytoplasmic

Chain K:  96% . .

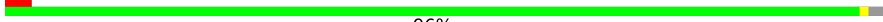


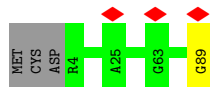
- Molecule 6: Dynein light chain 1, cytoplasmic

Chain L:  93% . .

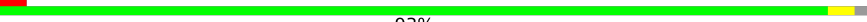


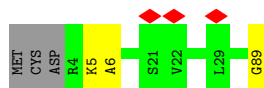
- Molecule 6: Dynein light chain 1, cytoplasmic

Chain M:  96% . .



- Molecule 6: Dynein light chain 1, cytoplasmic

Chain N:  93% . .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	68623	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 ($e^-/\text{\AA}^2$)	49.6	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.142	Depositor
Minimum map value	-0.064	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0318	Depositor
Map size (Å)	389.19998, 389.19998, 389.19998	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.39, 1.39, 1.39	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.29	0/4802	0.58	1/6694 (0.0%)
1	B	0.27	0/4403	0.56	0/6137
2	C	0.32	0/2437	0.63	2/3386 (0.1%)
3	D	0.32	0/2197	0.65	0/3053
4	E	0.30	0/1538	0.66	1/2136 (0.0%)
4	F	0.30	0/1528	0.66	1/2122 (0.0%)
5	G	0.35	0/461	0.55	0/642
5	H	0.36	0/461	0.55	0/642
6	I	1.24	1/425 (0.2%)	1.01	0/591
6	J	1.35	3/425 (0.7%)	1.03	1/591 (0.2%)
6	K	1.24	1/425 (0.2%)	1.00	0/591
6	L	1.35	3/425 (0.7%)	1.03	1/591 (0.2%)
6	M	1.23	1/425 (0.2%)	1.00	0/591
6	N	1.35	3/425 (0.7%)	1.02	1/591 (0.2%)
All	All	0.54	12/20377 (0.1%)	0.67	8/28358 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	E	0	1
4	F	0	1
All	All	0	2

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	L	6	ALA	N-CA	7.82	1.55	1.46
6	L	89	GLY	C-O	7.62	1.38	1.23
6	N	89	GLY	C-O	7.56	1.38	1.23
6	N	6	ALA	N-CA	7.53	1.55	1.46

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	J	89	GLY	C-O	7.52	1.38	1.23

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	J	89	GLY	CA-C-O	6.47	134.38	120.80
6	L	89	GLY	CA-C-O	6.43	134.30	120.80
6	N	89	GLY	CA-C-O	6.37	134.17	120.80
4	F	298	PRO	N-CA-C	5.96	117.97	110.70
4	E	298	PRO	N-CA-C	5.95	117.95	110.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	E	297	PHE	Mainchain
4	F	297	PHE	Mainchain

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	4805	0	2100	3	0
1	B	4405	0	1927	4	0
2	C	2443	0	1071	4	0
3	D	2200	0	1004	5	0
4	E	1542	0	672	4	0
4	F	1532	0	668	1	0
5	G	462	0	192	0	0
5	H	462	0	192	0	0
6	I	426	0	195	0	0
6	J	426	0	195	0	0
6	K	426	0	195	0	0
6	L	426	0	195	0	0
6	M	426	0	195	0	0
6	N	426	0	195	0	0
All	All	20407	0	8996	21	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 21 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)
2:C:555:TRP:O	2:C:565:VAL:CB	2.08	1.02
2:C:555:TRP:C	2:C:565:VAL:CB	2.60	0.74
3:D:494:GLN:O	3:D:496:GLN:N	2.37	0.57
4:E:29:ILE:O	4:E:30:ALA:C	2.52	0.52
1:B:764:GLY:O	1:B:768:LEU:N	2.44	0.51

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	963/4513 (21%)	937 (97%)	26 (3%)	0	100	100
1	B	885/4513 (20%)	859 (97%)	26 (3%)	0	100	100
2	C	482/1066 (45%)	463 (96%)	19 (4%)	0	100	100
3	D	440/564 (78%)	402 (91%)	37 (8%)	1 (0%)	43	77
4	E	304/351 (87%)	282 (93%)	21 (7%)	1 (0%)	36	71
4	F	302/351 (86%)	287 (95%)	15 (5%)	0	100	100
5	G	91/96 (95%)	87 (96%)	4 (4%)	0	100	100
5	H	91/96 (95%)	89 (98%)	2 (2%)	0	100	100
6	I	84/89 (94%)	82 (98%)	2 (2%)	0	100	100
6	J	84/89 (94%)	81 (96%)	3 (4%)	0	100	100
6	K	84/89 (94%)	82 (98%)	2 (2%)	0	100	100
6	L	84/89 (94%)	82 (98%)	2 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	M	84/89 (94%)	81 (96%)	3 (4%)	0	100	100
6	N	84/89 (94%)	82 (98%)	2 (2%)	0	100	100
All	All	4062/12084 (34%)	3896 (96%)	164 (4%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	D	495	THR
4	E	93	LEU

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

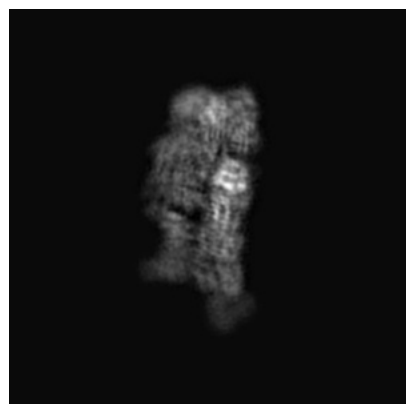
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4918. These allow visual inspection of the internal detail of the map and identification of artifacts.

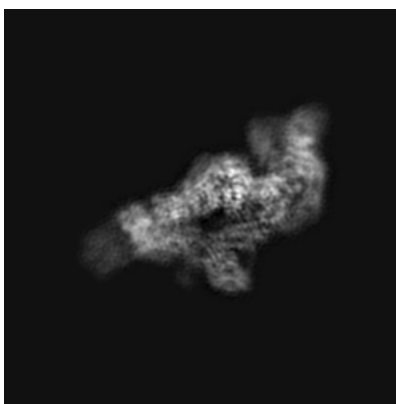
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

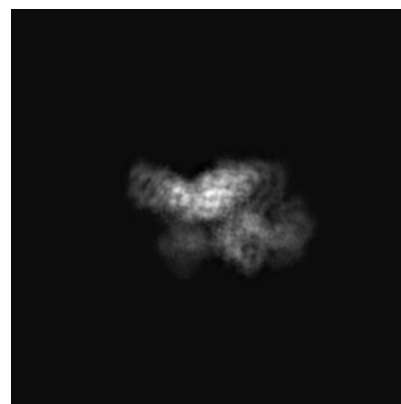
6.1.1 Primary map



X

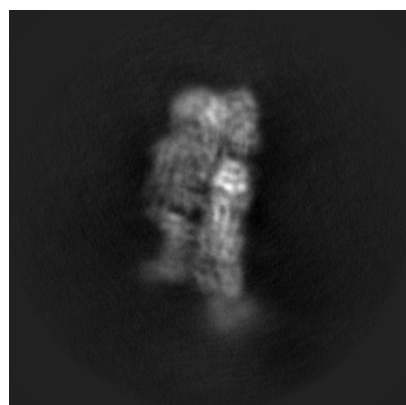


Y

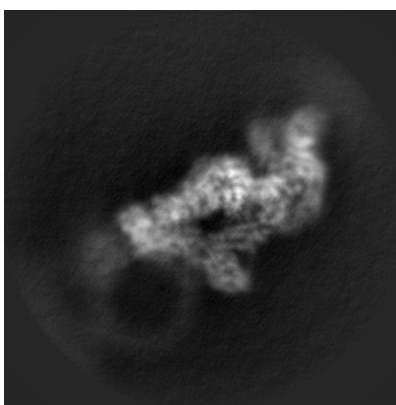


Z

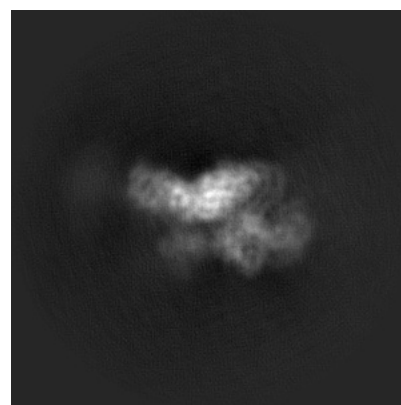
6.1.2 Raw map



X



Y

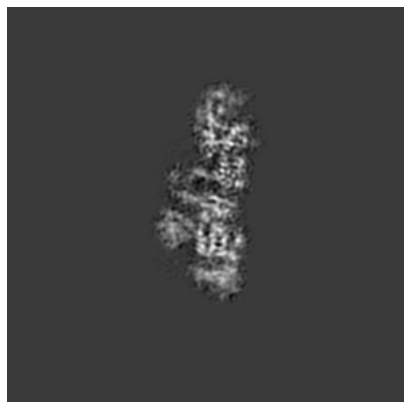


Z

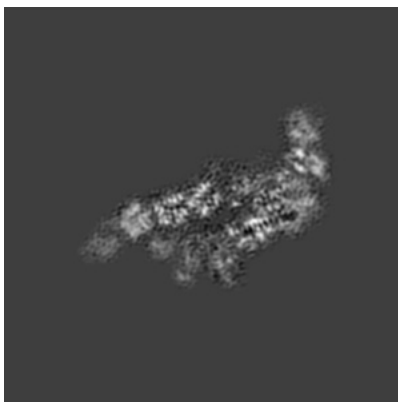
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

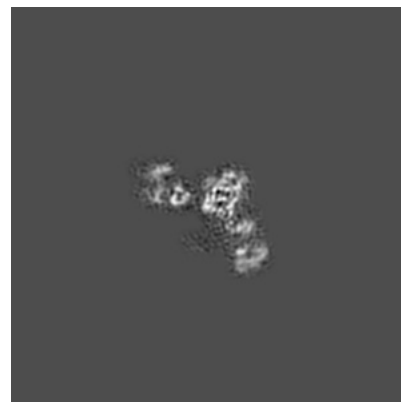
6.2.1 Primary map



X Index: 140

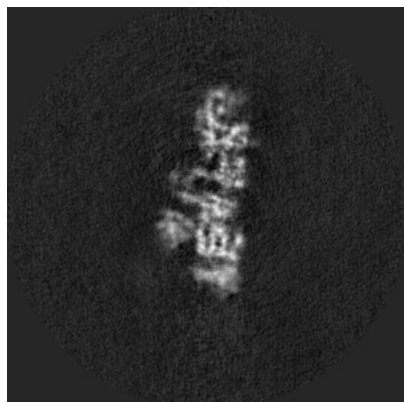


Y Index: 140

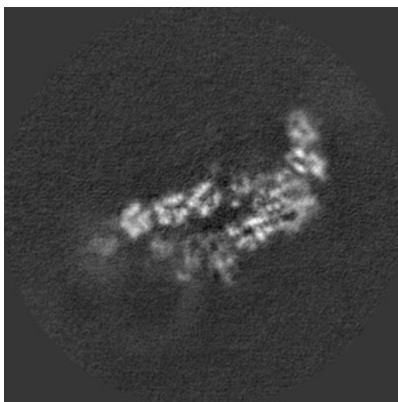


Z Index: 140

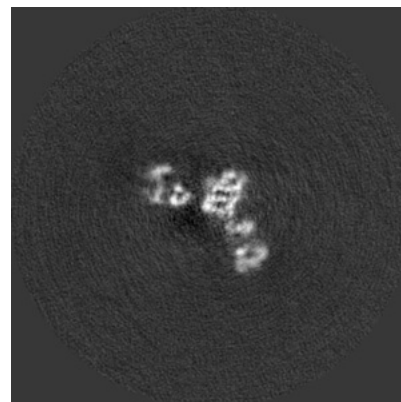
6.2.2 Raw map



X Index: 140



Y Index: 140



Z Index: 140

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

6.3 Largest variance slices [i](#)

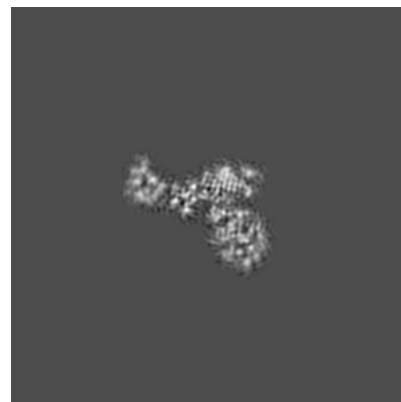
6.3.1 Primary map



X Index: 152

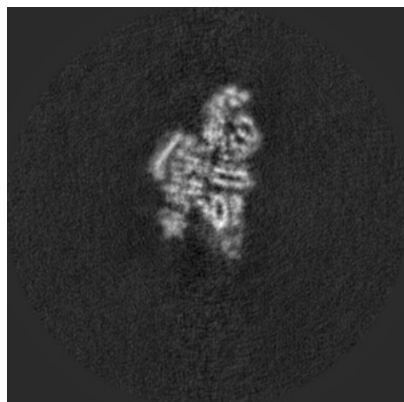


Y Index: 150

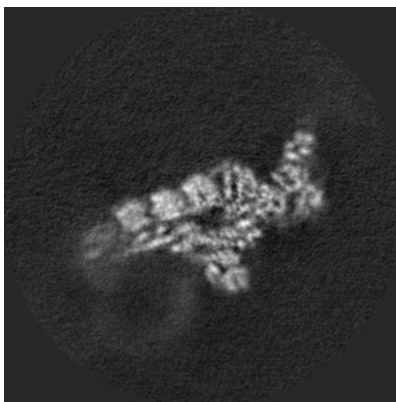


Z Index: 163

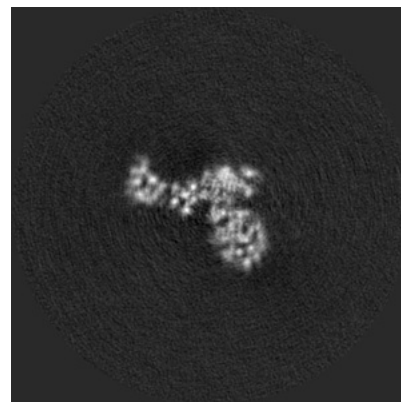
6.3.2 Raw map



X Index: 151



Y Index: 151

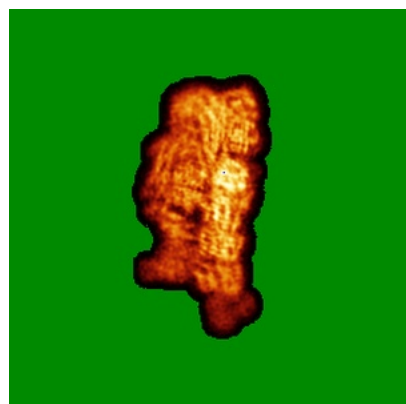


Z Index: 163

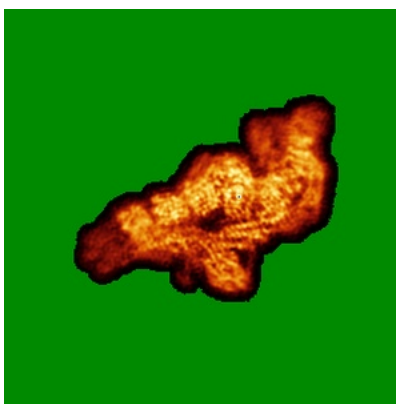
The images above show the largest variance slices of the map in three orthogonal directions.

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

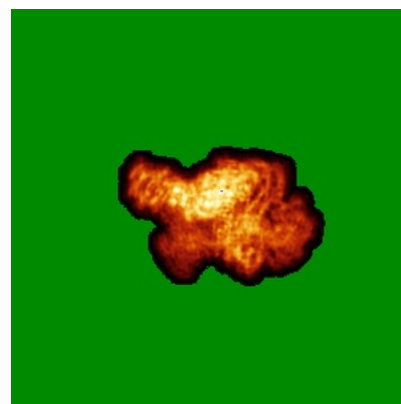
6.4.1 Primary map



X

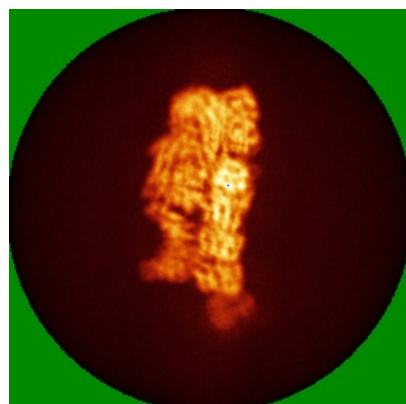


Y

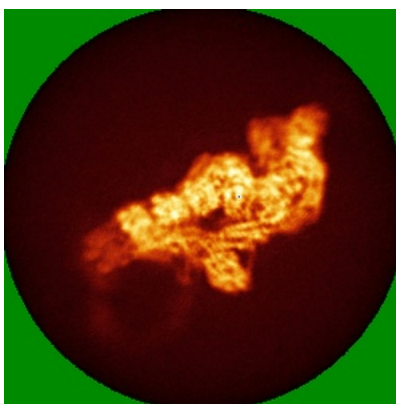


Z

6.4.2 Raw map



X



Y



Z

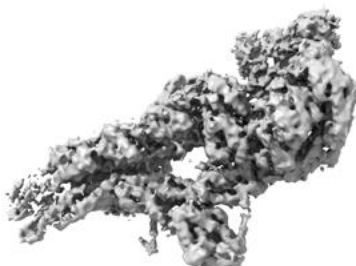
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

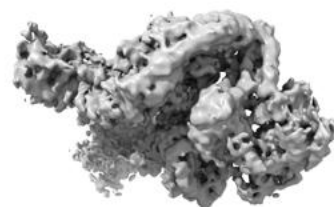
6.5.1 Primary map



X



Y



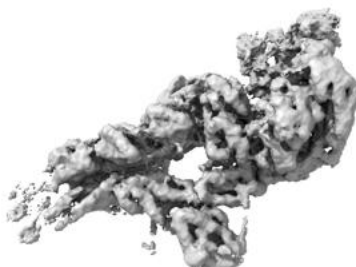
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0318. 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



X



Y



Z

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.

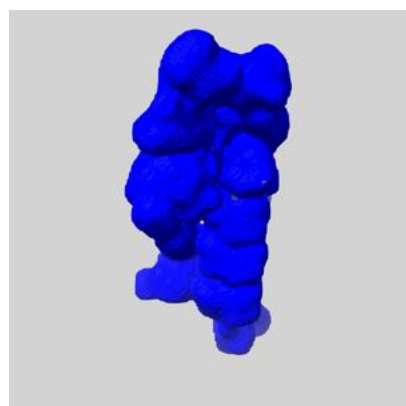
6.6 Mask visualisation [i](#)

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

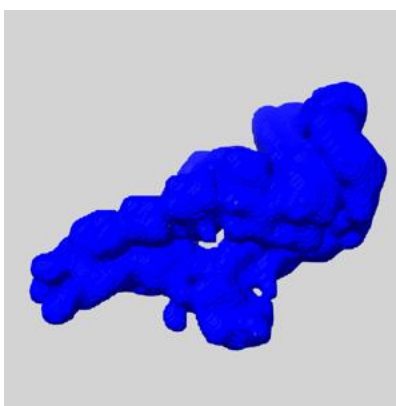
A mask typically either:

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

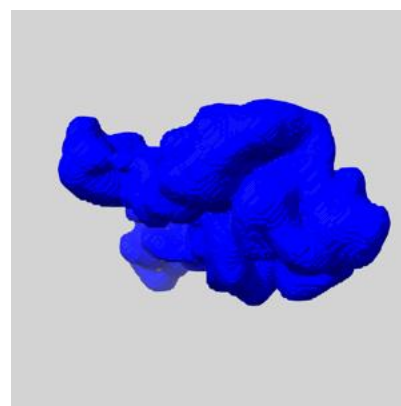
6.6.1 emd_4918_msk_1.map [i](#)



X



Y

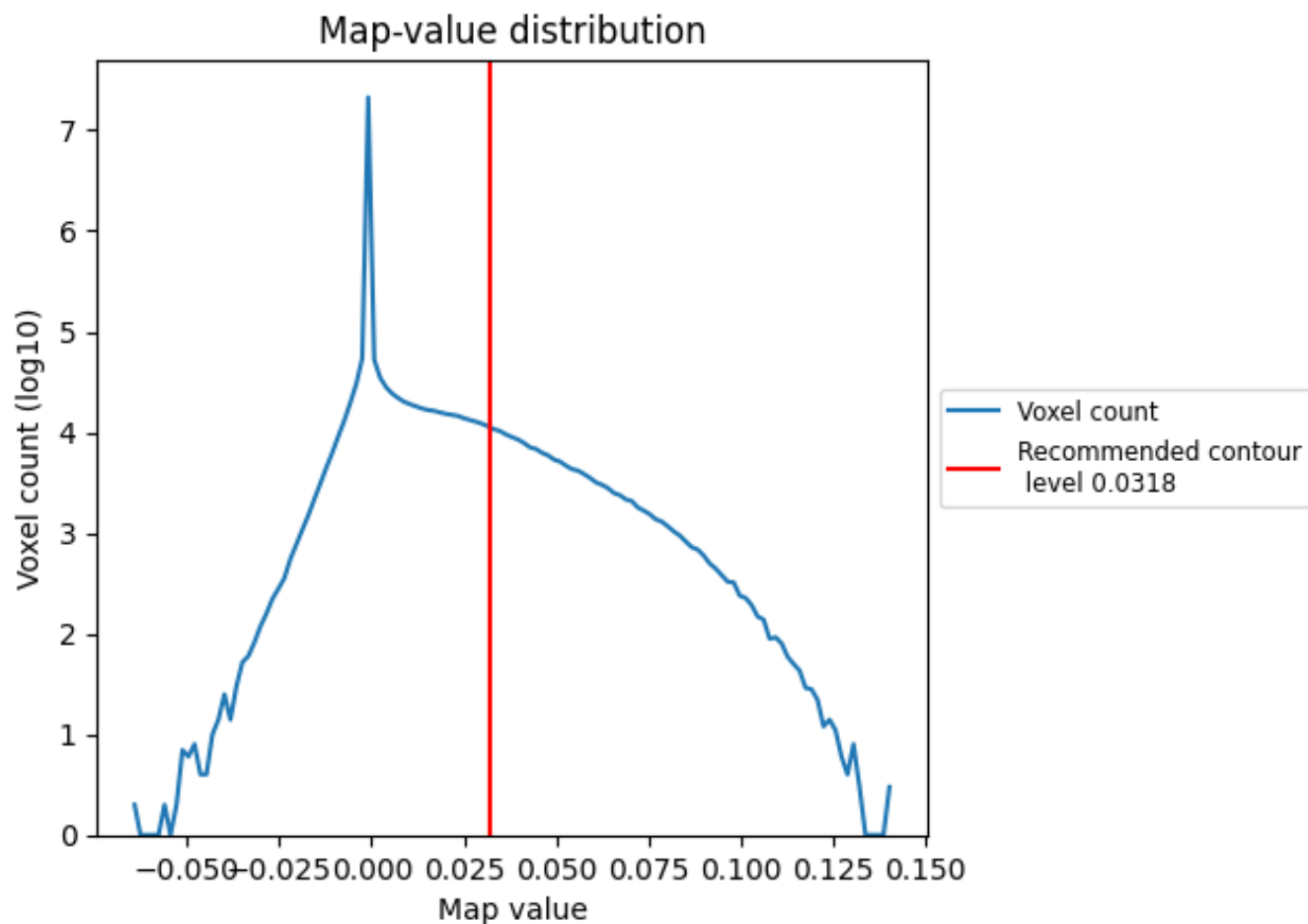


Z

7 Map analysis [i](#)

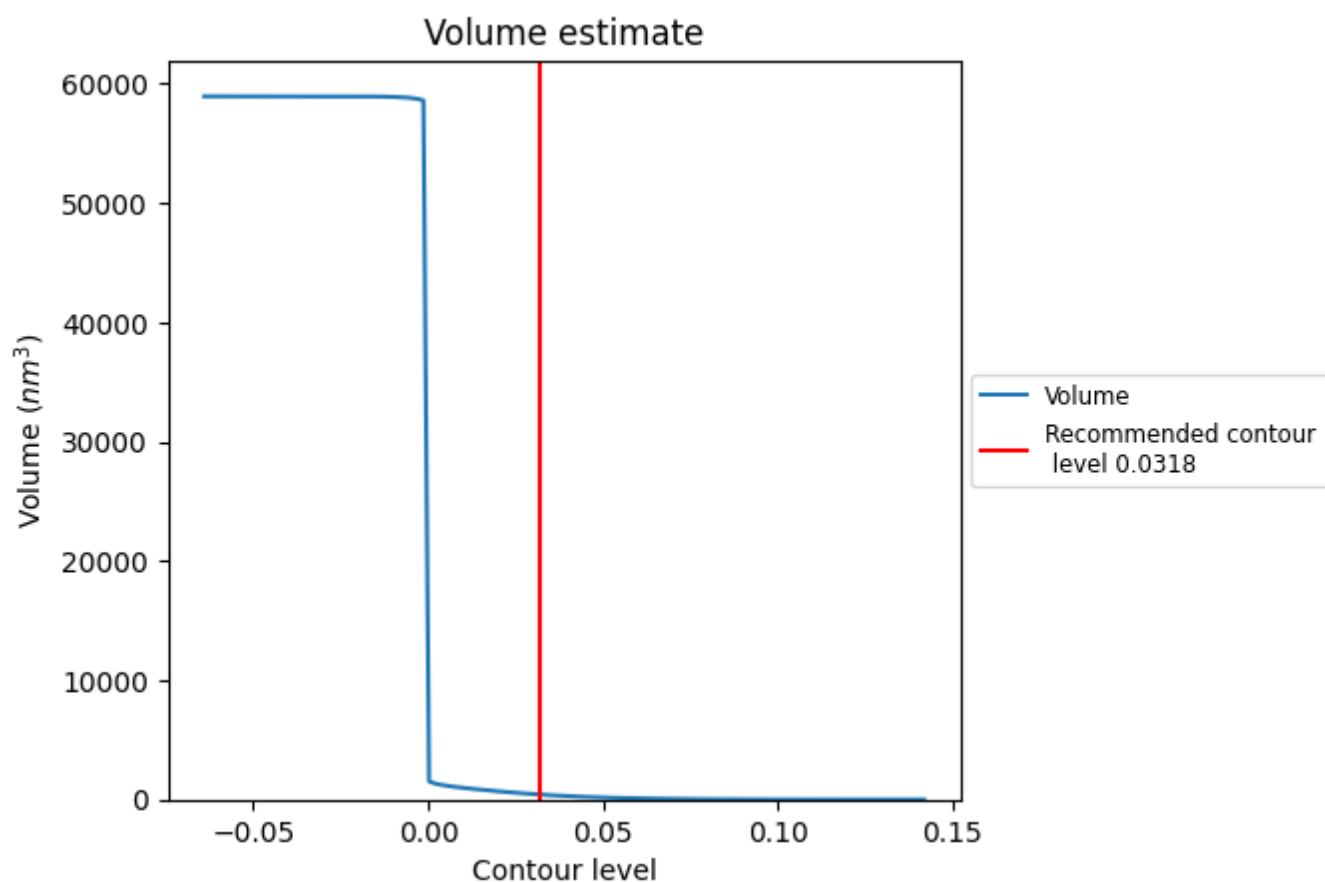
This section contains the results of statistical analysis of the map.

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.

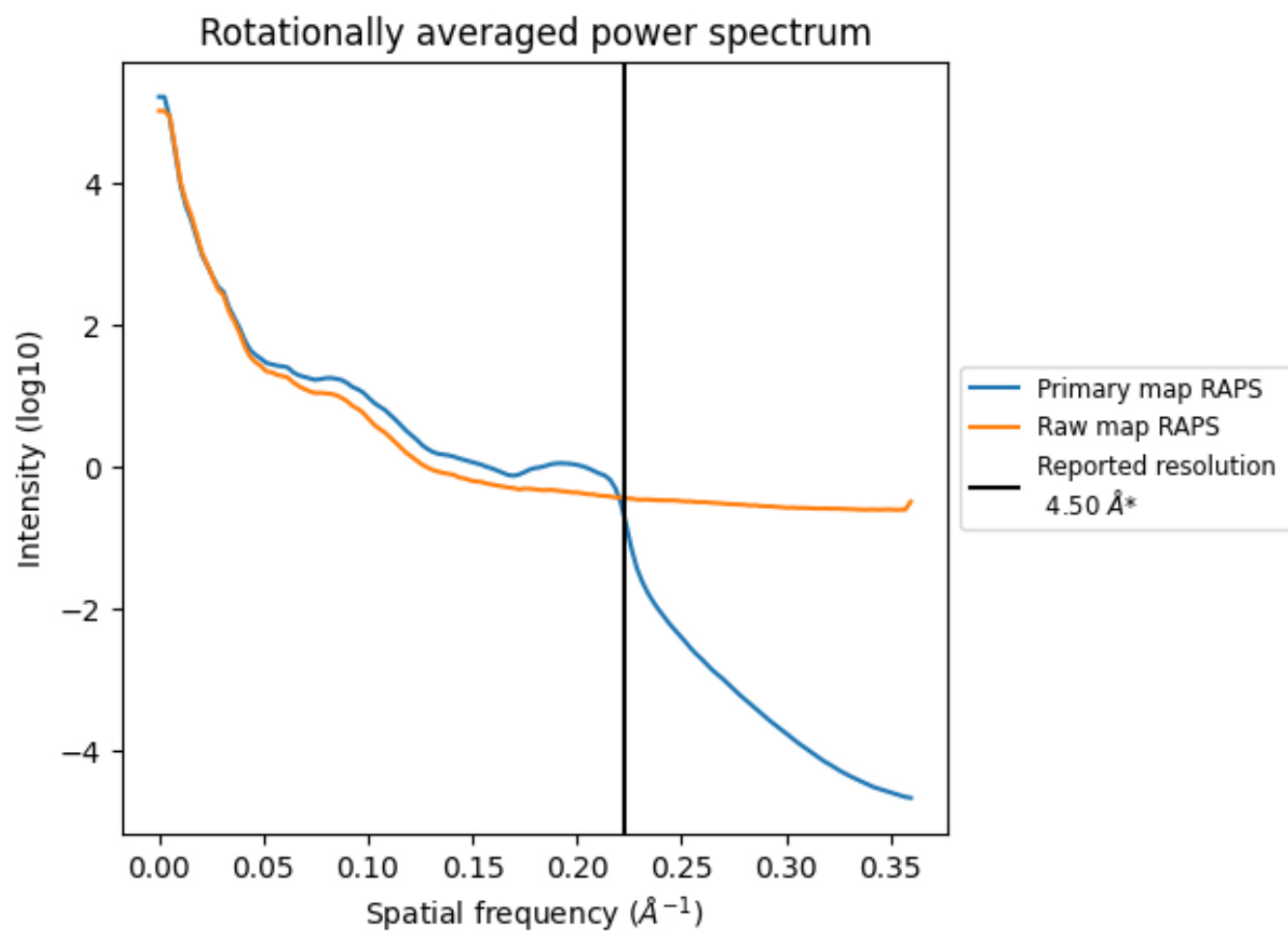
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 424 nm³; this corresponds to an approximate mass of 383 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 ⓘ

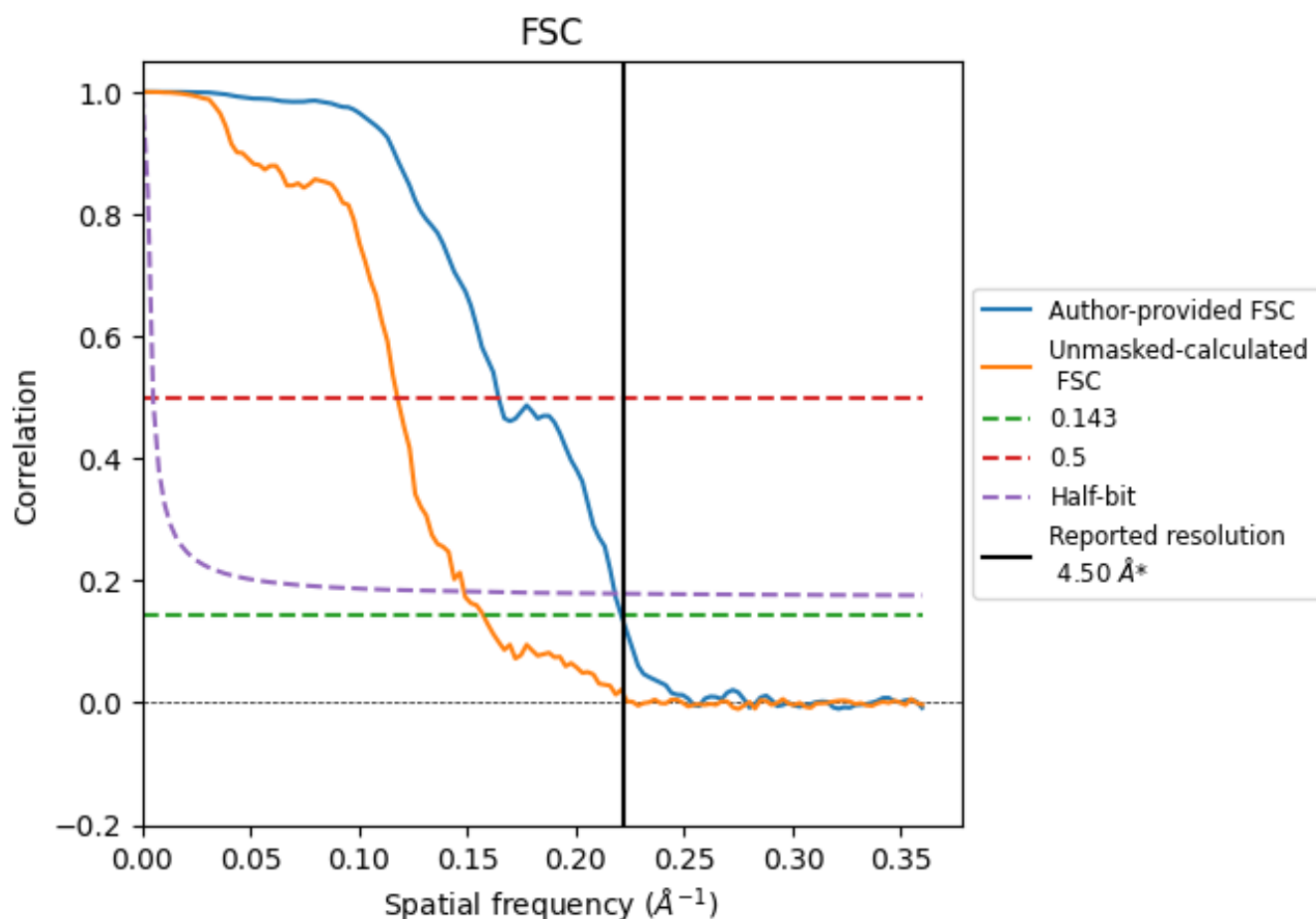


*Reported resolution corresponds to spatial frequency of 0.222 Å⁻¹

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 $0.222 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

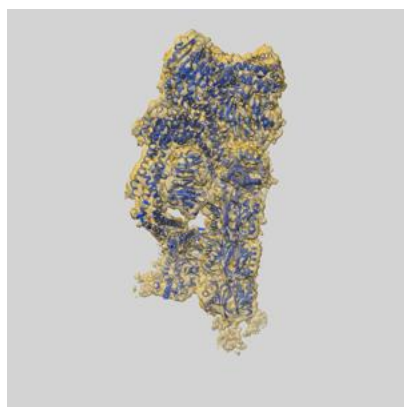
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.50	-	-
Author-provided FSC curve	4.53	6.09	4.59
Unmasked-calculated*	6.36	8.50	6.73

*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 6.36 differs from the reported value 4.5 by more than 10 %

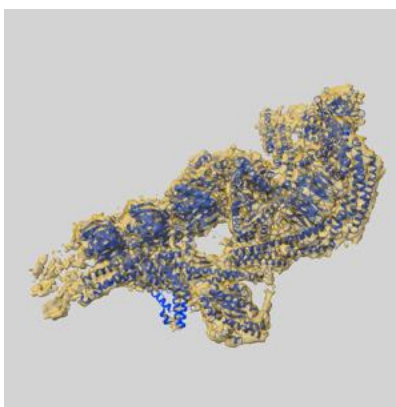
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4918 and PDB model 6RLB. Per-residue inclusion information can be found in section [3](#) on page [8](#).

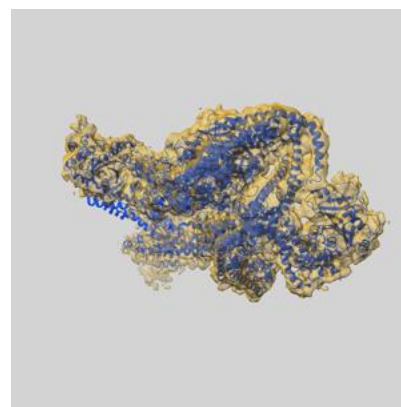
9.1 Map-model overlay [i](#)



X



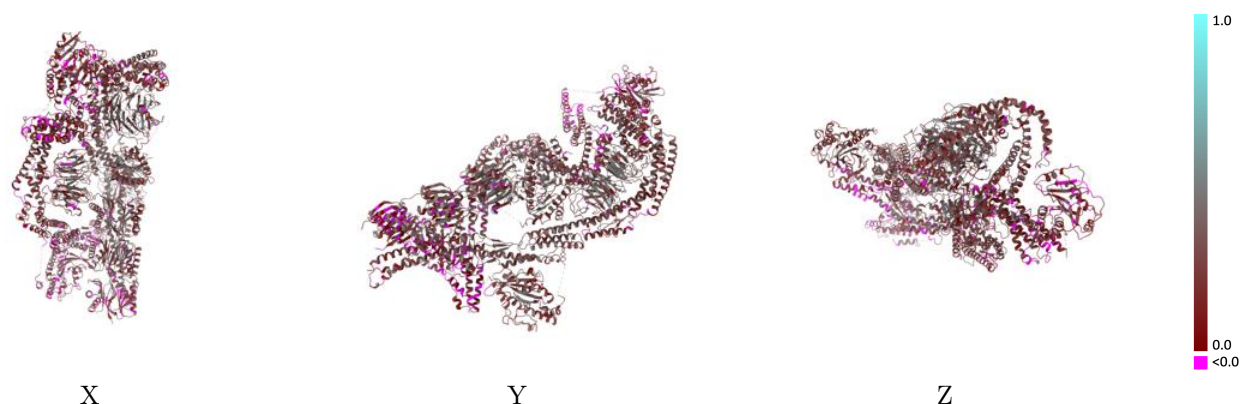
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0318 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](#)

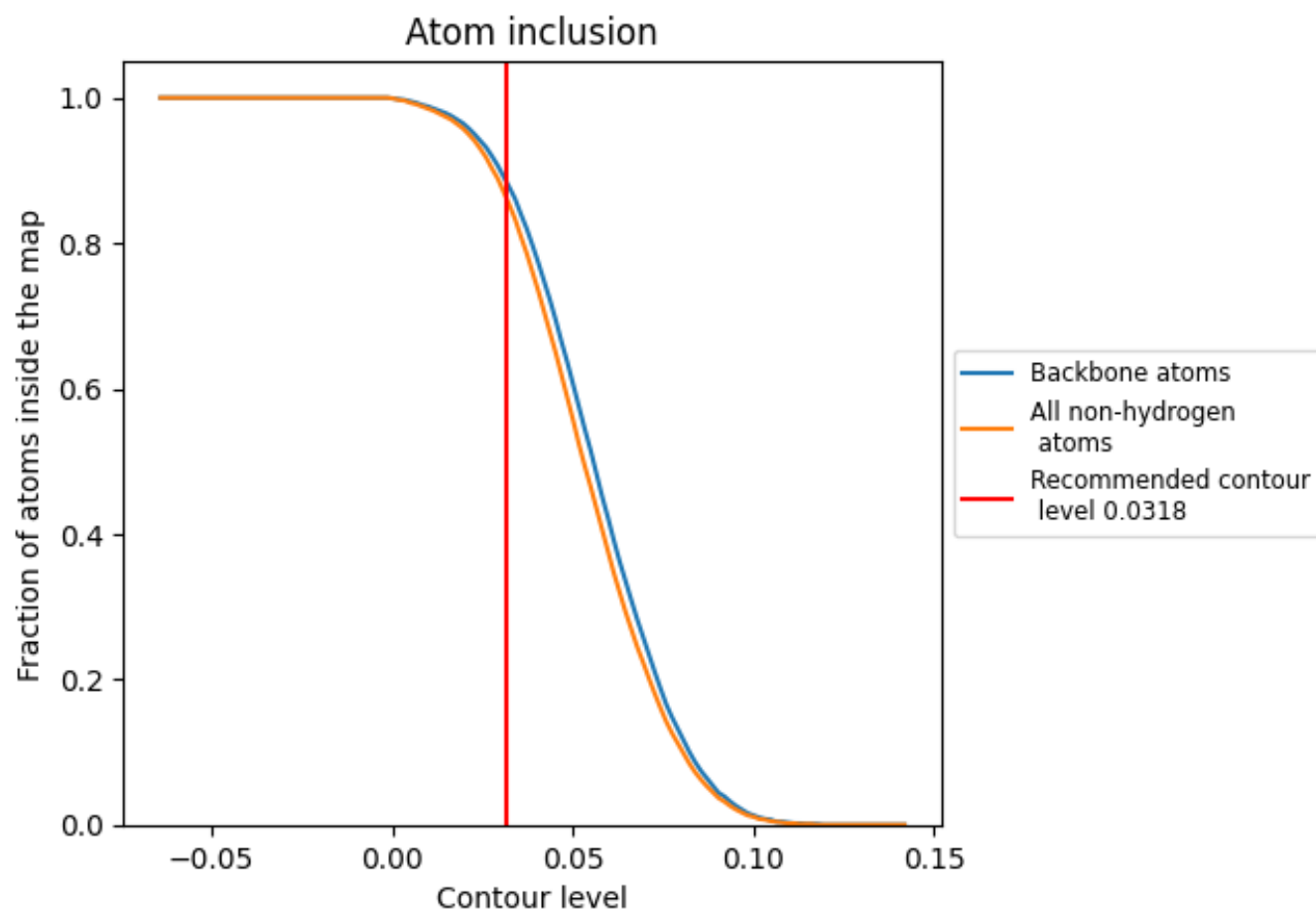


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 86% 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 (0.0318) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8600	0.2480
A	0.9190	0.2530
B	0.7190	0.1860
C	0.9320	0.3240
D	0.9180	0.2920
E	0.9260	0.2640
F	0.5890	0.1300
G	0.9500	0.3450
H	0.9700	0.3300
I	0.9790	0.3020
J	0.9650	0.3150
K	0.9720	0.2940
L	0.9720	0.2940
M	0.9390	0.1800
N	0.9480	0.2170

1.0

0.0

<0.0