



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 10:48 AM UTC

PDB ID : 8VHZ / pdb_00008vhz
EMDB ID : EMD-43244
Title : Cryo EM structure of a soybean CesA1 homotrimer
Authors : Ho, R.; Palliniti, P.; Zimmer, J.
Deposited on : 2024-01-02
Resolution : 3.30 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

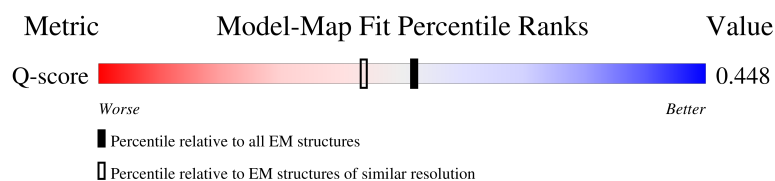
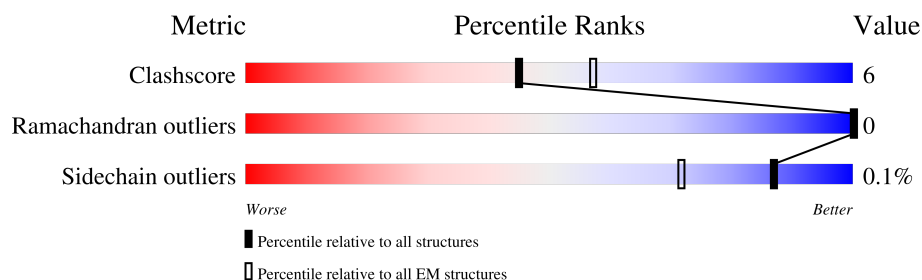
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	15087 (2.80 - 3.80)

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	1084	
1	B	1084	
1	C	1084	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 17208 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 Cellulose synthase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	714	Total	C	N	O	S	0	0
			5736	3760	952	995	29		
1	B	714	Total	C	N	O	S	0	0
			5736	3760	952	995	29		
1	C	714	Total	C	N	O	S	0	0
			5736	3760	952	995	29		

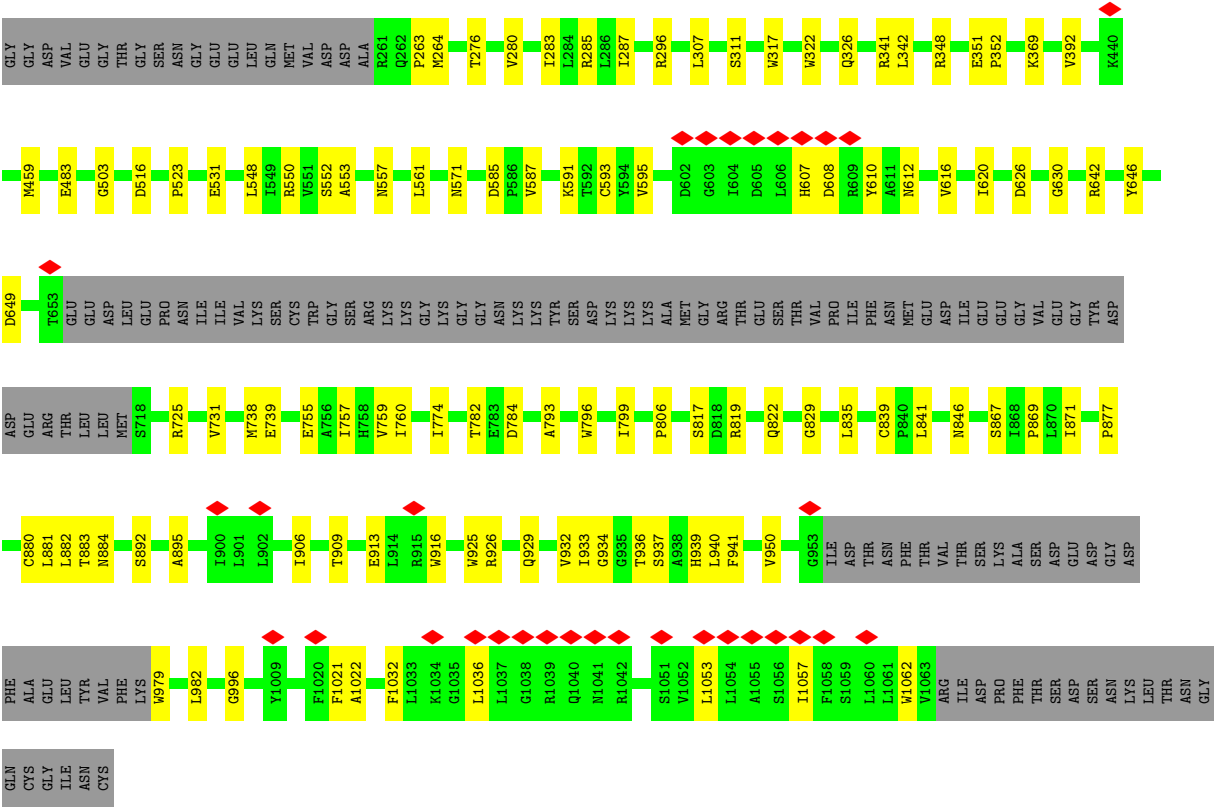
Chain B:



CYS	GLY	ILE	ASN	CYS	VAL	PHE	LYS	W979	L982	P986	L994	V995	G996	I997	V1001	F1016	F1020	F1021	A1022	F1032	L1033	K1034	G1035	L1036	L1037	G1038	L1039	Q1040	N1041	R1042	L1053	L1054	A1055	S1056	I1057	F1058	S1059	L1060	V1063	ARG	ILE	PRO	PHE	THR	SER	ASP	SER	ASN	LEU	THR	ASN	GLY																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
T883	M884	S892	M895	S896	T897	M901	S902	M903	S904	T905	M906	S907	M908	T909	S910	M911	S912	T913	M914	S915	T916	M917	S918	T919	M920	S921	T922	M923	S924	T925	M926	S927	T928	M929	S930	T931	M932	S933	T934	M935	S936	T937	M938	S939	T940	M941	S942	T943	M944	S945	T946	M947	S948	T949	M950	S951	T952	M953	S954	T955	M956	S957	T958	M959	S960	T961	M962	S963	T964	M965	S966	T967	M968	S969	T970	M971	S972	T973	M974	S975	T976	M977	S978	T979	M980	S981	T982	M983	S984	T985	M986	S987	T988	M989	S990	T991	M992	S993	T994	M995	S996	T997	M998	S999	T1000	M1001	S1002	T1003	M1004	S1005	T1006	M1007	S1008	T1009	M1010	S1011	T1012	M1013	S1014	T1015	M1016	S1017	T1018	M1019	S1020	T1021	M1022	S1023	T1024	M1025	S1026	T1027	M1028	S1029	T1030	M1031	S1032	T1033	M1034	S1035	T1036	M1037	S1038	T1039	M1040	S1041	T1042	M1043	S1044	T1045	M1046	S1047	T1048	M1049	S1050	T1051	M1052	S1053	T1054	M1055	S1056	T1057	M1058	S1059	T1060	M1061	S1062	T1063	M1064	S1065	T1066	M1067	S1068	T1069	M1070	S1071	T1072	M1073	S1074	T1075	M1076	S1077	T1078	M1079	S1080	T1081	M1082	S1083	T1084	M1085	S1086	T1087	M1088	S1089	T1090	M1091	S1092	T1093	M1094	S1095	T1096	M1097	S1098	T1099	M1100	S1101	T1102	M1103	S1104	T1105	M1106	S1107	T1108	M1109	S1110	T1111	M1112	S1113	T1114	M1115	S1116	T1117	M1118	S1119	T1120	M1121	S1122	T1123	M1124	S1125	T1126	M1127	S1128	T1129	M1130	S1131	T1132	M1133	S1134	T1135	M1136	S1137	T1138	M1139	S1140	T1141	M1142	S1143	T1144	M1145	S1146	T1147	M1148	S1149	T1150	M1151	S1152	T1153	M1154	S1155	T1156	M1157	S1158	T1159	M1160	S1161	T1162	M1163	S1164	T1165	M1166	S1167	T1168	M1169	S1170	T1171	M1172	S1173	T1174	M1175	S1176	T1177	M1178	S1179	T1180	M1181	S1182	T1183	M1184	S1185	T1186	M1187	S1188	T1189	M1190	S1191	T1192	M1193	S1194	T1195	M1196	S1197	T1198	M1199	S1200	T1201	M1202	S1203	T1204	M1205	S1206	T1207	M1208	S1209	T1210	M1211	S1212	T1213	M1214	S1215	T1216	M1217	S1218	T1219	M1220	S1221	T1222	M1223	S1224	T1225	M1226	S1227	T1228	M1229	S1230	T1231	M1232	S1233	T1234	M1235	S1236	T1237	M1238	S1239	T1240	M1241	S1242	T1243	M1244	S1245	T1246	M1247	S1248	T1249	M1250	S1251	T1252	M1253	S1254	T1255	M1256	S1257	T1258	M1259	S1260	T1261	M1262	S1263	T1264	M1265	S1266	T1267	M1268	S1269	T1270	M1271	S1272	T1273	M1274	S1275	T1276	M1277	S1278	T1279	M1280	S1281	T1282	M1283	S1284	T1285	M1286	S1287	T1288	M1289	S1290	T1291	M1292	S1293	T1294	M1295	S1296	T1297	M1298	S1299	T1300	M1301	S1302	T1303	M1304	S1305	T1306	M1307	S1308	T1309	M1310	S1311	T1312	M1313	S1314	T1315	M1316	S1317	T1318	M1319	S1320	T1321	M1322	S1323	T1324	M1325	S1326	T1327	M1328	S1329	T1330	M1331	S1332	T1333	M1334	S1335	T1336	M1337	S1338	T1339	M1340	S1341	T1342	M1343	S1344	T1345	M1346	S1347	T1348	M1349	S1350	T1351	M1352	S1353	T1354	M1355	S1356	T1357	M1358	S1359	T1360	M1361	S1362	T1363	M1364	S1365	T1366	M1367	S1368	T1369	M1370	S1371	T1372	M1373	S1374	T1375	M1376	S1377	T1378	M1379	S1380	T1381	M1382	S1383	T1384	M1385	S1386	T1387	M1388	S1389	T1389	M1390	S1391	T1392	M1393	S1394	T1395	M1396	S1397	T1398	M1399	S1400	T1401	M1402	S1403	T1404	M1405	S1406	T1407	M1408	S1409	T1410	M1411	S1412	T1413	M1414	S1415	T1416	M1417	S1418	T1419	M1420	S1421	T1422	M1423	S1424	T1425	M1426	S1427	T1428	M1429	S1430	T1431	M1432	S1433	T1434	M1435	S1436	T1437	M1438	S1439	T1440	M1441	S1442	T1443	M1444	S1445	T1446	M1447	S1448	T1449	M1450	S1451	T1452	M1453	S1454	T1455	M1456	S1457	T1458	M1459	S1459	T1460	M1460	S1461	T1461	M1461	S1462	T1462	M1462	S1463	T1463	M1463	S1464	T1464	M1464	S1465	T1465	M1465	S1466	T1466	M1466	S1467	T1467	M1467	S1468	T1468	M1468	S1469	T1469	M1469	S1470	T1470	M1470	S1471	T1471	M1471	S1472	T1472	M1472	S1473	T1473	M1473	S1474	T1474	M1474	S1475	T1475	M1475	S1476	T1476	M1476	S1477	T1477	M1477	S1478	T1478	M1478	S1479	T1479	M1479	S1480	T1480	M1480	S1481	T1481	M1481	S1482	T1482	M1482	S1483	T1483	M1483	S1484	T1484	M1484	S1485	T1485	M1485	S1486	T1486	M1486	S1487	T1487	M1487	S1488	T1488	M1488	S1489	T1489	M1489	S1490	T1490	M1490	S1491	T1491	M1491	S1492	T1492	M1492	S1493	T1493	M1493	S1494	T1494	M1494	S1495	T1495	M1495	S1496	T1496	M1496	S1497	T1497	M1497	S1498	T1498	M1498	S1499	T1499	M1499	S1500	T1500	M1500	S1501	T1501	M1501	S1502	T1502	M1502	S1503	T1503	M1503	S1504	T1504	M1504	S1505	T1505	M1505	S1506	T1506	M1506	S1507	T1507	M1507	S1508	T1508	M1508	S1509	T1509	M1509	S1510	T1510	M1510	S1511	T1511	M1511	S1512	T1512	M1512	S1513	T1513	M1513	S1514	T1514	M1514	S1515	T1515	M1515	S1516	T1516	M1516	S1517	T1517	M1517	S1518	T1518	M1518	S1519	T1519	M1519	S1520	T1520	M1520	S1521	T1521	M1521	S1522	T1522	M1522	S1523	T1523	M1523	S1524	T1524	M1524	S1525	T1525	M1525	S1526	T1526	M1526	S1527	T1527	M1527	S1528	T1528	M1528	S1529	T1529	M1529	S1530	T1530	M1530	S1531	T1531	M1531	S1532	T1532	M1532	S1533	T1533	M1533	S1534	T1534	M1534	S1535	T1535	M1535	S1536	T1536	M1536	S1537	T1537	M1537	S1538	T1538	M1538	S1539	T1539	M1539	S1540	T1540	M1540	S1541	T1541	M1541	S1542	T1542	M1542	S1543	T1543	M1543	S1544	T1544	M1544	S1545	T1545	M1545	S1546	T1546	M1546	S1547	T1547	M1547	S1548	T1548	M1548	S1549	T1549	M1549	S1550	T1550	M1550	S1551	T1551	M1551	S1552	T1552	M1552	S1553	T1553	M1553	S1554	T1554	M1554	S1555	T1555	M1555	S1556	T1556	M1556	S1557	T1557	M1557	S1558	T1558	M1558	S1559	T1559	M1559	S1560	T1560	M1560	S1561	T1561	M1561	S1562	T1562	M1562	S1563	T1563	M1563	S1564	T1564	M1564	S1565	T1565	M1565	S1566	T1566	M1566	S1567	T1567	M1567	S1568	T1568	M1568	S1569	T1569	M1569	S1570	T1570	M1570	S1571	T1571	M1571	S1572	T1572	M1572	S1573	T1573	M1573	S1574	T1574	M1574	S1575	T1575	M1575	S1576	T1576	M1576	S1577	T1577	M1577	S1578	T1578	M1578	S1579	T1579	M1579	S1580	T1580	M1580	S1581	T1581	M1581	S1582	T1582	M1582	S1583	T1583	M1583	S1584	T1584	M1584	S1585	T1585	M1585	S1586	T1586	M1586	S1587	T1587	M1587	S1588	T1588	M1588	S1589	T1589	M1589	S1590	T1590	M1590	S1591	T1591	M1591	S1592	T1592	M1592	S1593	T1593	M1593	S1594	T1594	M1594	S1595	T1595	M1595	S1596	T1596	M1596	S1597	T1597	M1597	S1598	T1598	M1598	S1599	T1599	M1599	S1600	T1600	M1600	S1601	T1601	M1601	S1602	T1602	M1602	S1603	T1603	M1603	S1604	T1604	M1604	S1605	T1605	M1605	S1606	T1606	M1606	S1607	T1607	M1607	S1608	T1608	M1608	S1609	T1609	M1609	S1610	T1610	M1610	S1611	T1611	M1611	S1612	T1612	M1612	S1613	T1613	M1613	S1614	T1614	M1614	S1615	T1615	M1615	S1616	T1616	M1616	S1617	T1617	M1617	S1618	T1618	M1618	S1619	T1619	M1619	S1620	T1620	M1620	S1621	T1621	M1621	S1622	T1622	M1622	S1623	T1623	M1623	S1624	T1624	M1624	S1625	T1625	M1625	S1626	T1626	M1626	S1627	T1627	M1627	S1628	T1628	M1628	S1629	T1629	M1629	S1630	T1630	M1630	S1631	T1631	M1631	S1632	T1632	M1632	S1633	T1633	M1633	S1634	T1634	M1634	S1635	T1635	M1635	S1636	T1636	M1636	S1637	T1637	M1637	S1638	T1638	M1638	S1639	T1639	M1639	S1640	T1640	M1640	S1641	T1641	M1641	S1642	T1642	M1642	S1643	T1643	M1643	S1644	T1644	M1644	S1645	T1645	M1645	S1646	T1646	M1646	S1647	T1647	M1647	S1648	T1648	M1648	S1649	T1649	M1649	S1650	T1650	M1650	S1651	T1651	M1651	S1652	T1652	M1652	S1653	T1653	M1653	S1654	T1654	M1654	S1655	T1655	M1655	S1656	T1656	M1656	S1657	T1657	M1657	S1658	T1658	M1658	S1659	T1659	M1659	S1660	T1660	M1660	S1661	T1661	M1661	S1662	T1662	M1662	S1663	T1663	M1663	S1664	T1664	M1664	S1665	T1665	M1665	S1666	T1666	M1666	S1667	T1667	M1667	S1668	T1668	M1668	S1669	T1669	M1669	S1670	T1670	M1670	S1671	T1671	M1671	S1672	T1672	M1672	S1673	T1673	M1673	S1674	T1674	M1674	S1675	T1675	M1675	S1676	T1676	M1676	S1677	T1677	M1677	S1678	T1678	M1678	S1679	T1679	M1679	S1680	T1680	M1680	S1681	T1681	M1681	S1682	T1682	M1682	S1683	T1683	M1683	S1684	T1684	M1684	S1685	T1685	M1685	S1686	T1686	M1686	S1687	T1687	M1687	S1688	T1688	M1688	S1689	T1689	M1689	S1690	T1690	M1690	S1691	T1691	M1691	S1692	T1692	M1692	S1693	T1693	M1693	S1694	T1694	M1694	S1695	T1695	M1695	S1696	T1696	M1696	S1697	T1697	M1697	S1698	T1698	M1698	S1699	T1699	M1699	S1700	T1700	M1700	S1701	T1701	M1701	S1702	T1702	M1702	S1703	T1703	M1703	S1704	T1704	M1704	S1705	T1705	M1705	S1706	T1706	M1706	S1707	T1707	M1707	S1708	T1708	M1708	S1709	T1709	M1709	S1710	T1710	M1710	S1711	T1711	M1711	S1712	T1712	M1712	S1713	T1713	M1713	S1714	T1714	M1714	S1715	T1715	M1715	S1716	T1716	M1716	S1717	T1717	M1717	S1718

Chain C:

[illegible]



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	186101	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	4.730	Depositor
Minimum map value	-3.035	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.061	Depositor
Recommended contour level	0.35	Depositor
Map size ($\text{\AA}$)	432.00003, 432.00003, 432.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.08, 1.08, 1.08	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	0.10	0/5908	0.28	0/8043
1	B	0.10	0/5908	0.28	0/8043
1	C	0.10	0/5908	0.28	0/8043
All	All	0.10	0/17724	0.28	0/24129

There are no bond length outliers.

There are no bond angle outliers.

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	A	5736	0	5755	71	0
1	B	5736	0	5755	72	0
1	C	5736	0	5755	73	0
All	All	17208	0	17265	216	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 6.

The worst 5 of 216 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)
1:B:871:ILE:HG21	1:B:940:LEU:HD21	1.74	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:871:ILE:HG21	1:A:940:LEU:HD21	1.74	0.69
1:C:871:ILE:HG21	1:C:940:LEU:HD21	1.74	0.69
1:C:877:PRO:HG3	1:C:1021:PHE:HE2	1.60	0.67
1:B:877:PRO:HG3	1:B:1021:PHE:HE2	1.61	0.66

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	708/1084 (65%)	687 (97%)	21 (3%)	0	100	100
1	B	708/1084 (65%)	688 (97%)	20 (3%)	0	100	100
1	C	708/1084 (65%)	686 (97%)	22 (3%)	0	100	100
All	All	2124/3252 (65%)	2061 (97%)	63 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	A	623/943 (66%)	621 (100%)	2 (0%)	86	86
1	B	623/943 (66%)	623 (100%)	0	100	100
1	C	623/943 (66%)	623 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1869/2829 (66%)	1867 (100%)	2 (0%)	87 90

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

Mol	Chain	Res	Type
1	A	267	VAL
1	A	802	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	497	ASN
1	C	568	HIS
1	B	377	ASN
1	B	497	ASN
1	B	568	HIS

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 ⓘ

There are no chain breaks in this entry.

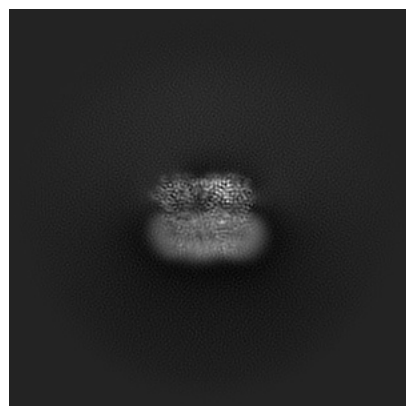
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43244. These allow visual inspection of the internal detail of the map and identification of artifacts.

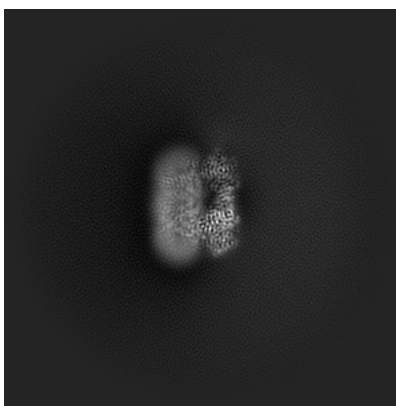
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

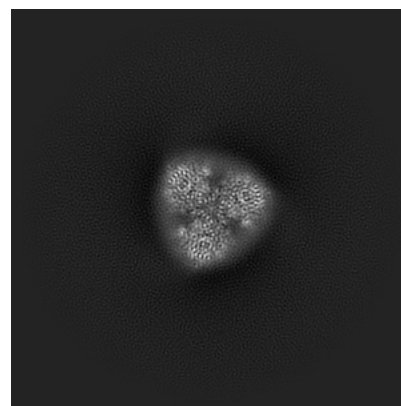
6.1.1 Primary map



X

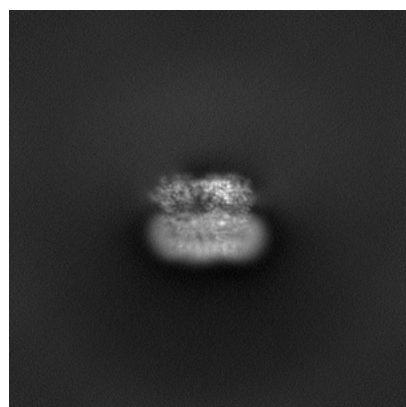


Y

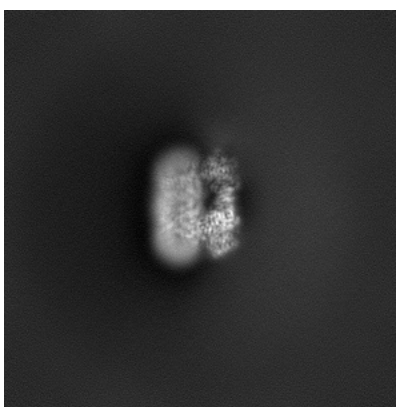


Z

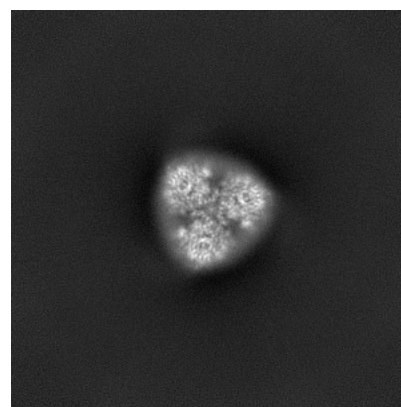
6.1.2 Raw map



X



Y



Z

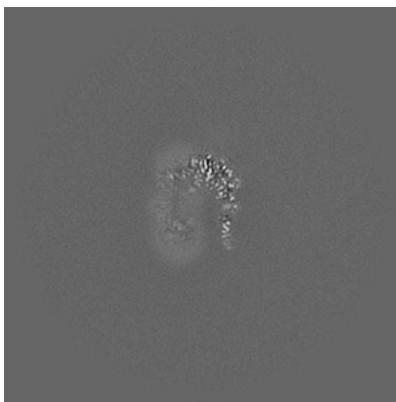
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

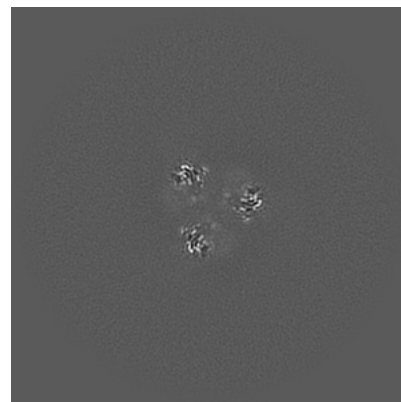
6.2.1 Primary map



X Index: 200

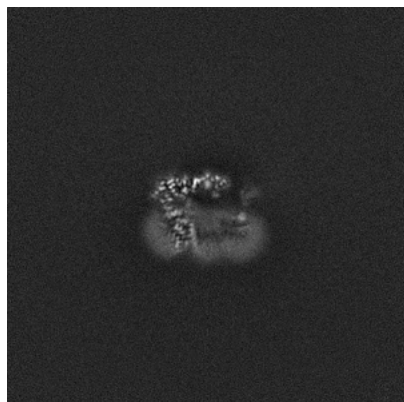


Y Index: 200

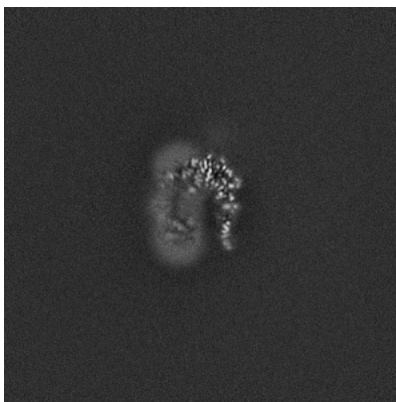


Z Index: 200

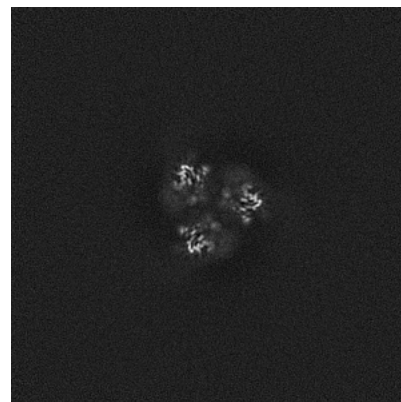
6.2.2 Raw map



X Index: 200



Y Index: 200

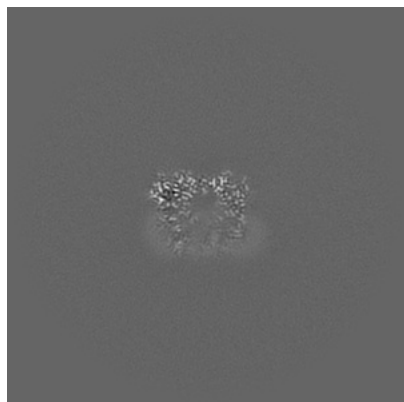


Z Index: 200

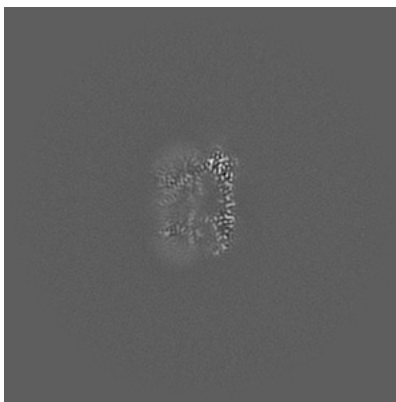
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

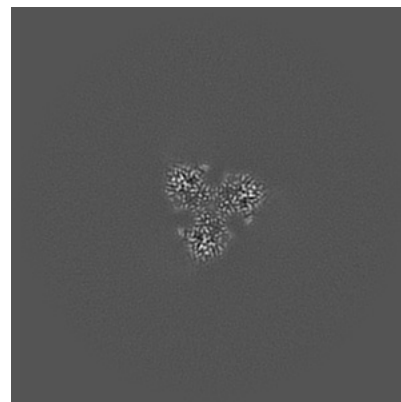
6.3.1 Primary map



X Index: 189

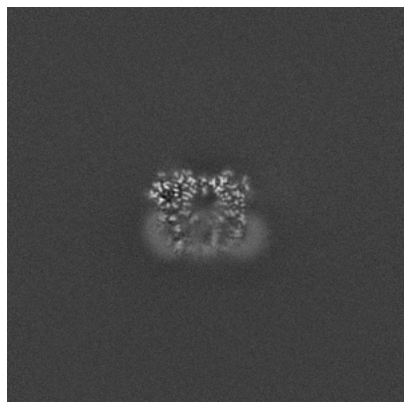


Y Index: 214

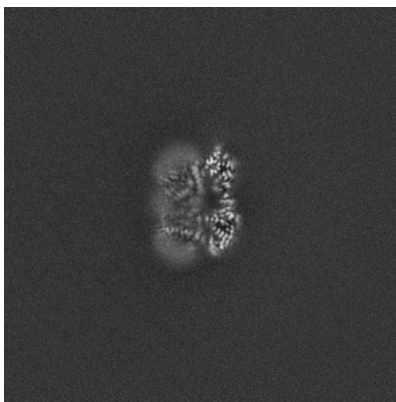


Z Index: 219

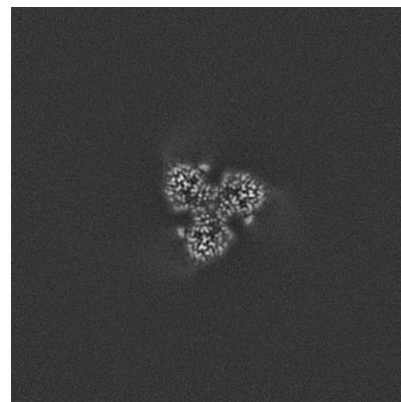
6.3.2 Raw map



X Index: 189



Y Index: 218

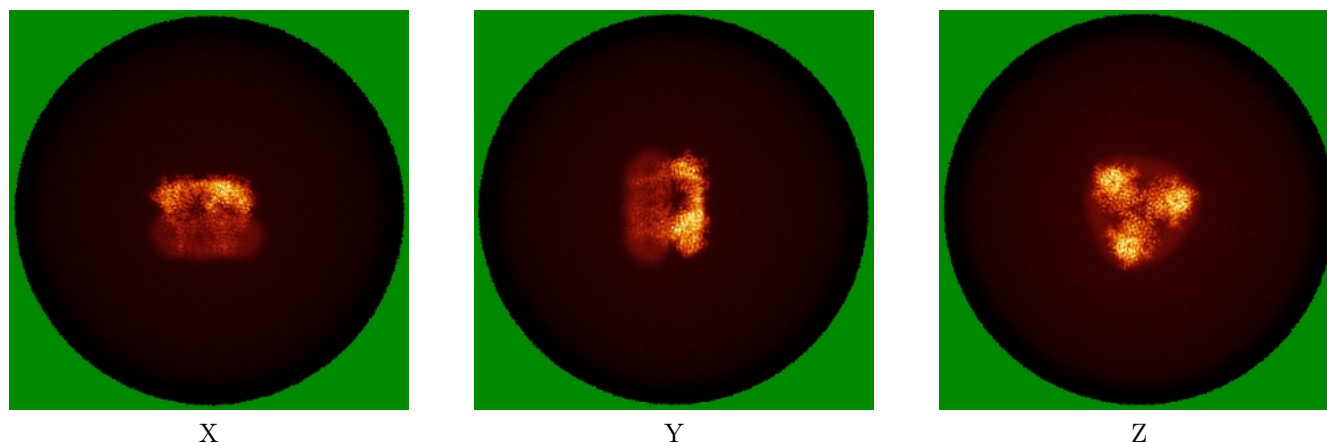


Z Index: 219

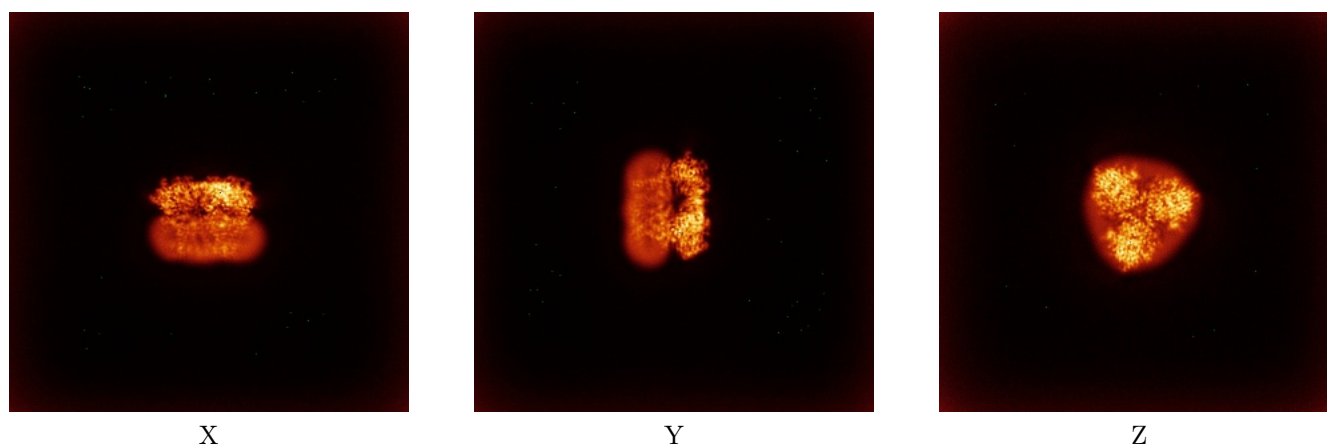
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

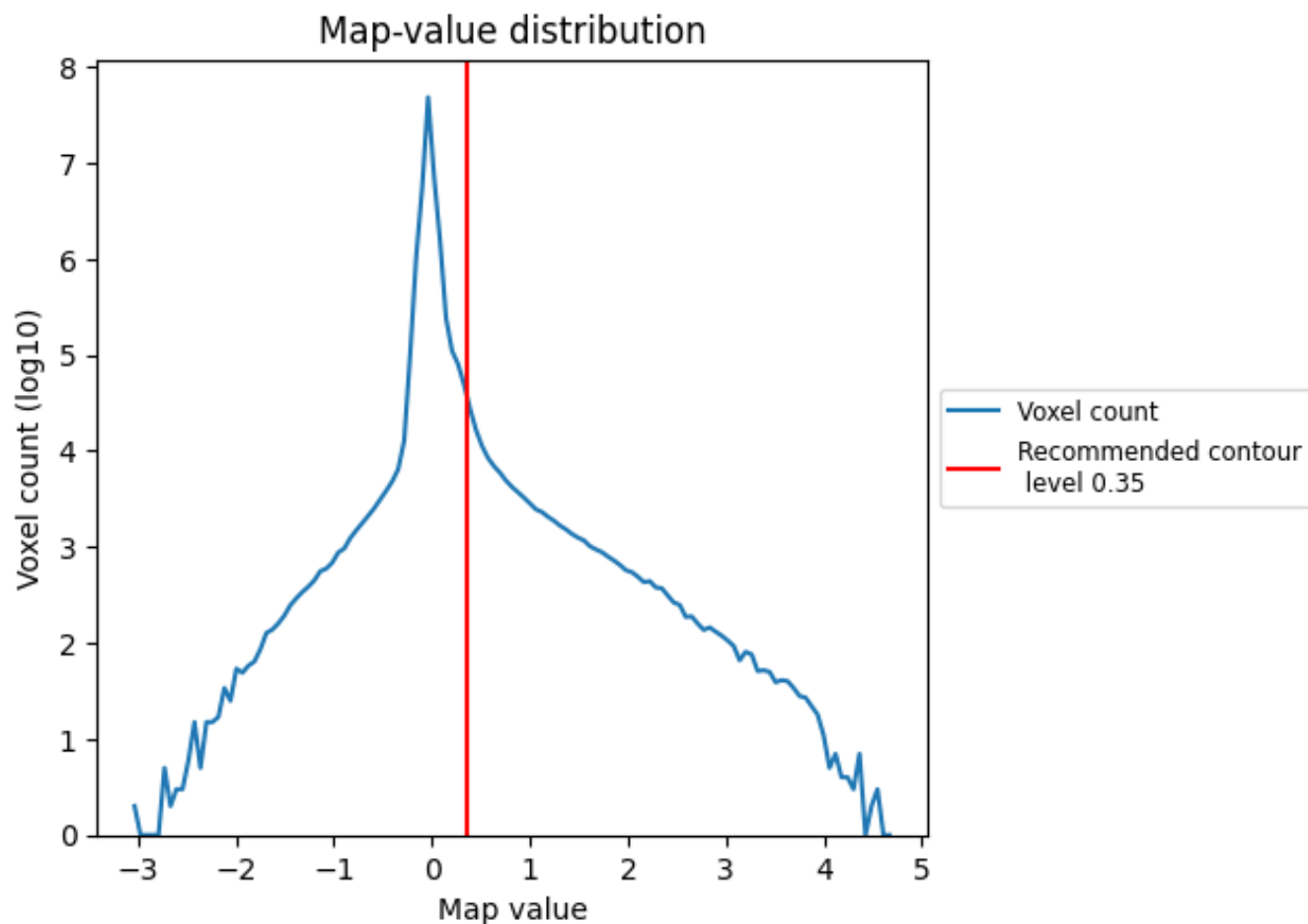
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

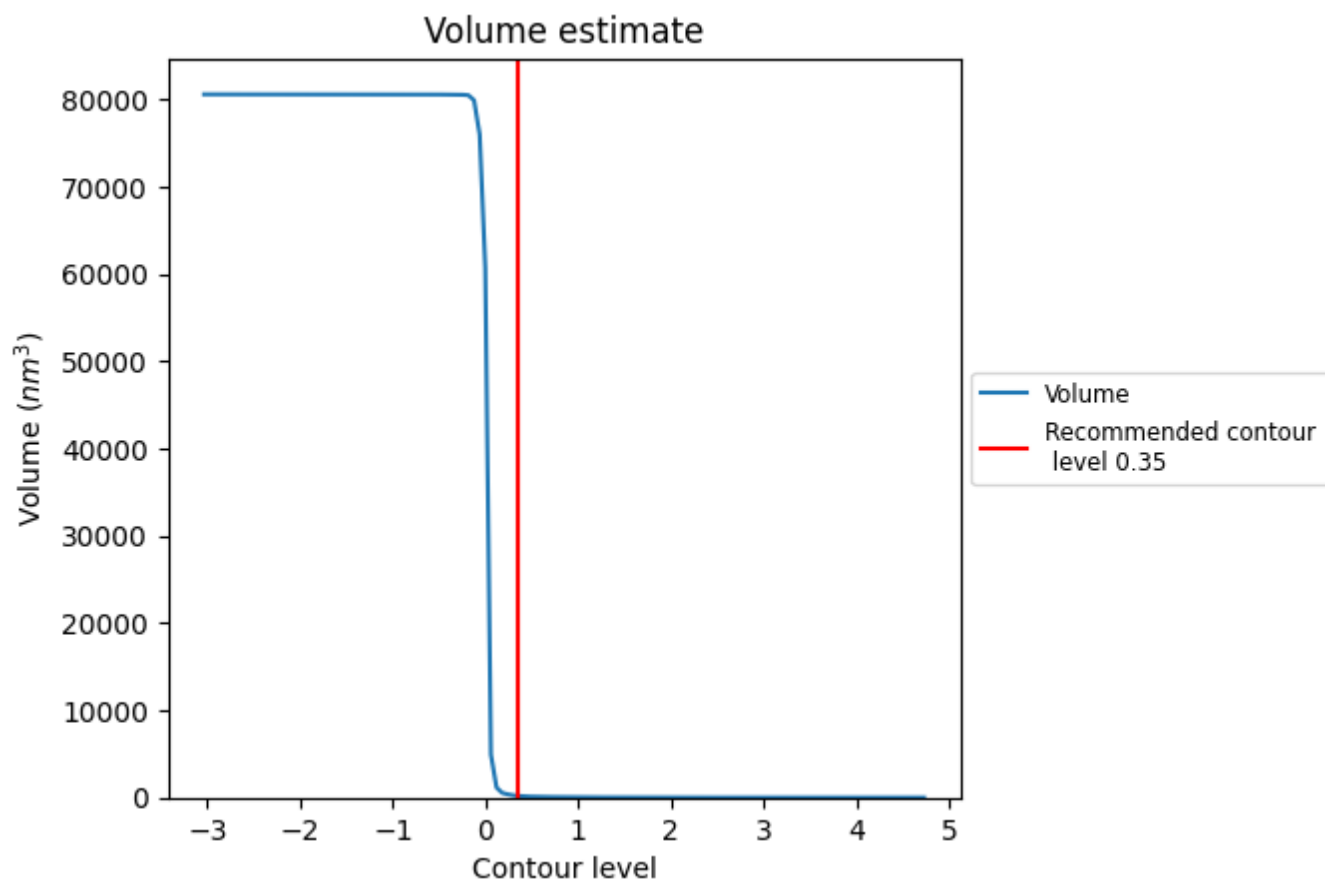
This section contains the results of statistical analysis of the map.

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.

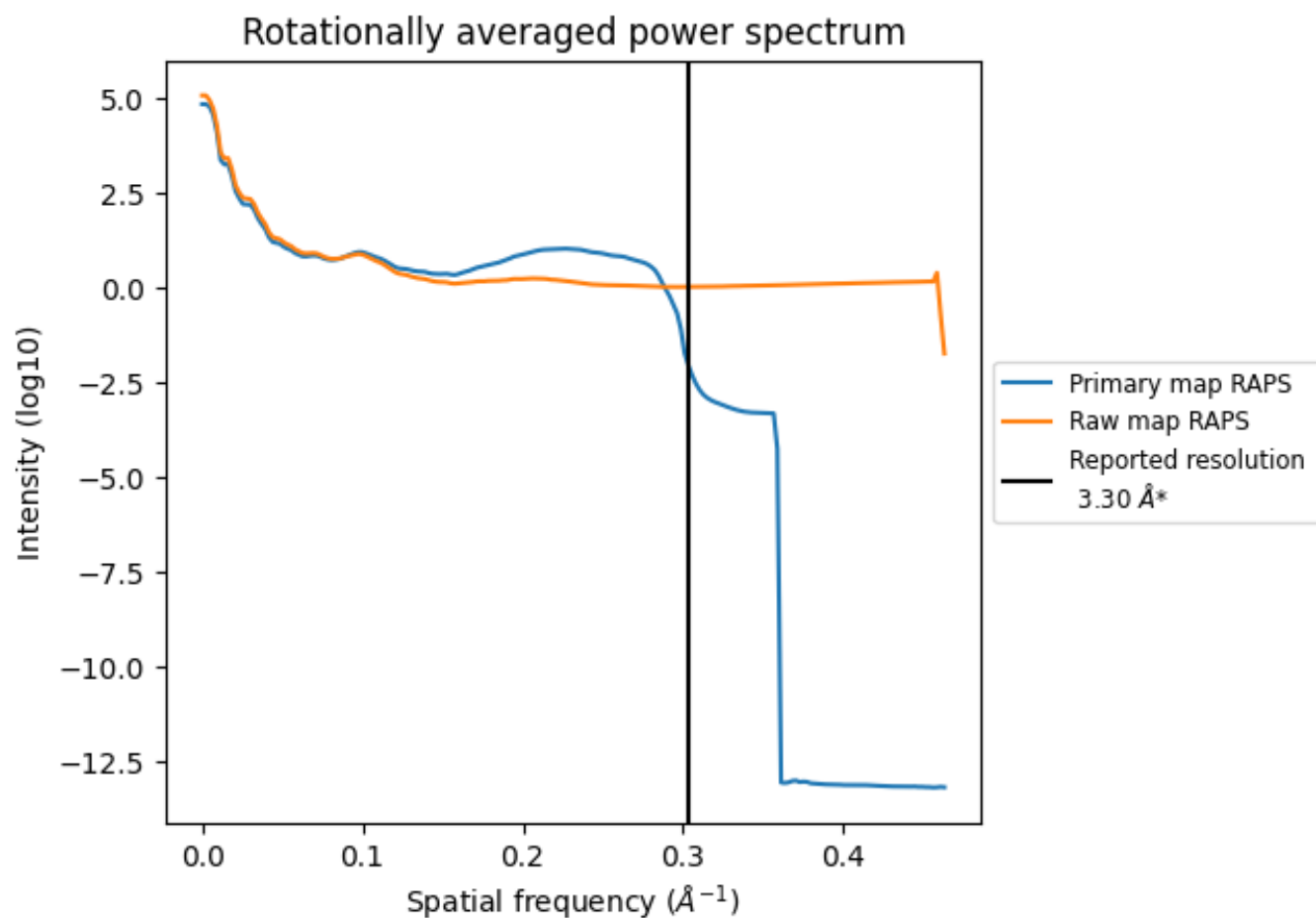
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 192 nm³; this corresponds to an approximate mass of 173 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 ⓘ

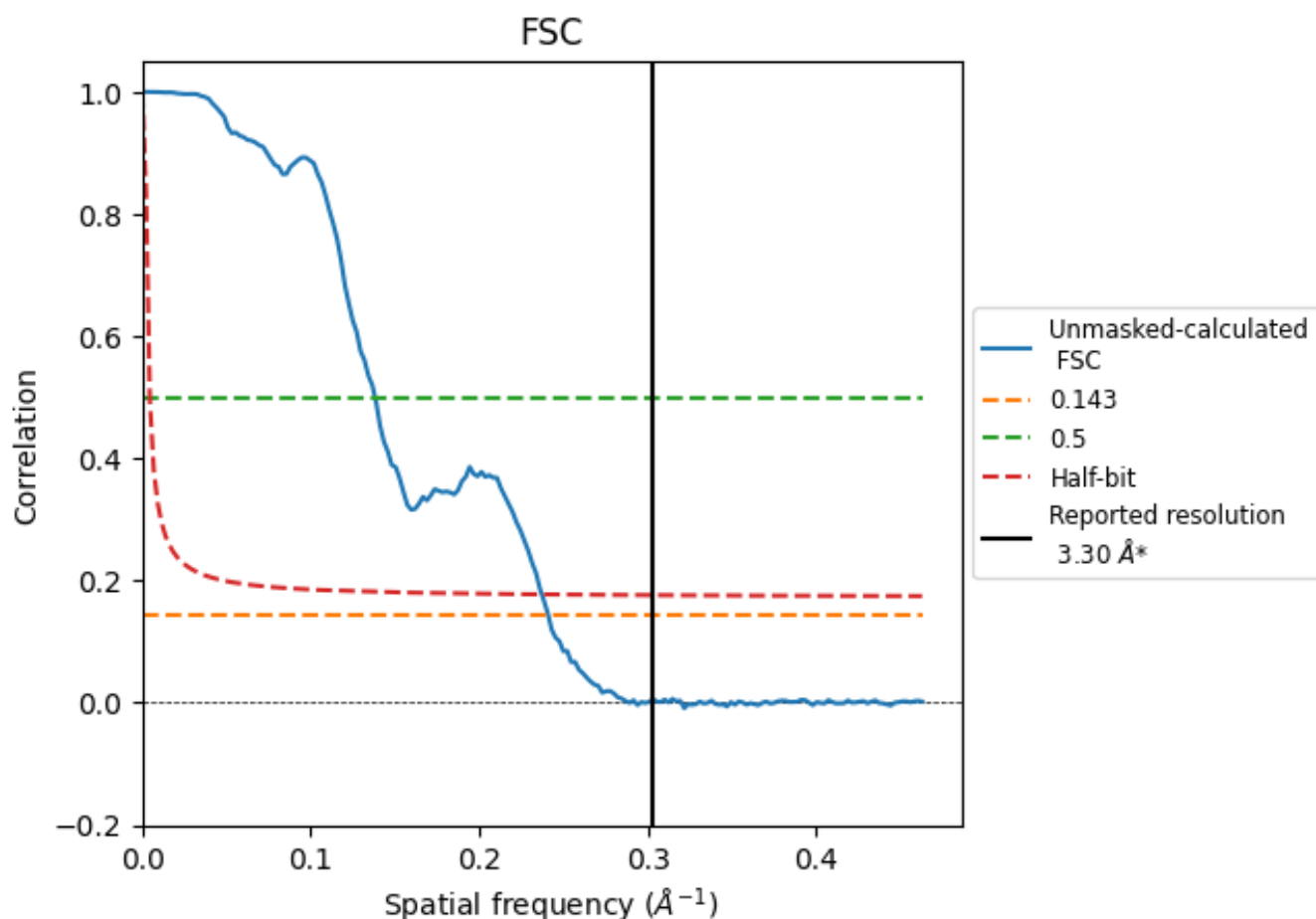


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

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 0.303 Å⁻¹

8.2 Resolution estimates [i](#)

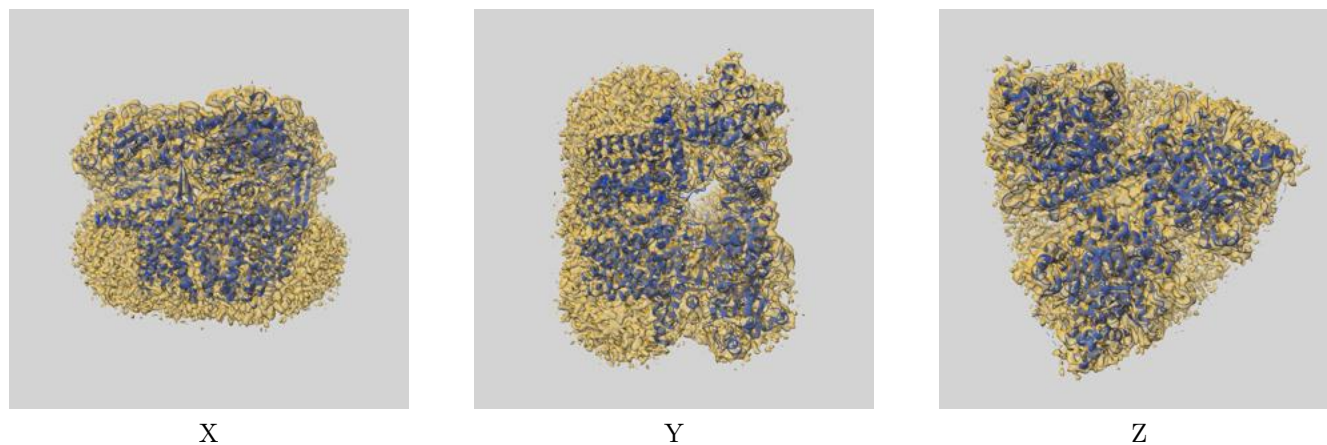
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.15	7.24	4.21

*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 4.15 differs from the reported value 3.3 by more than 10 %

9 Map-model fit [i](#)

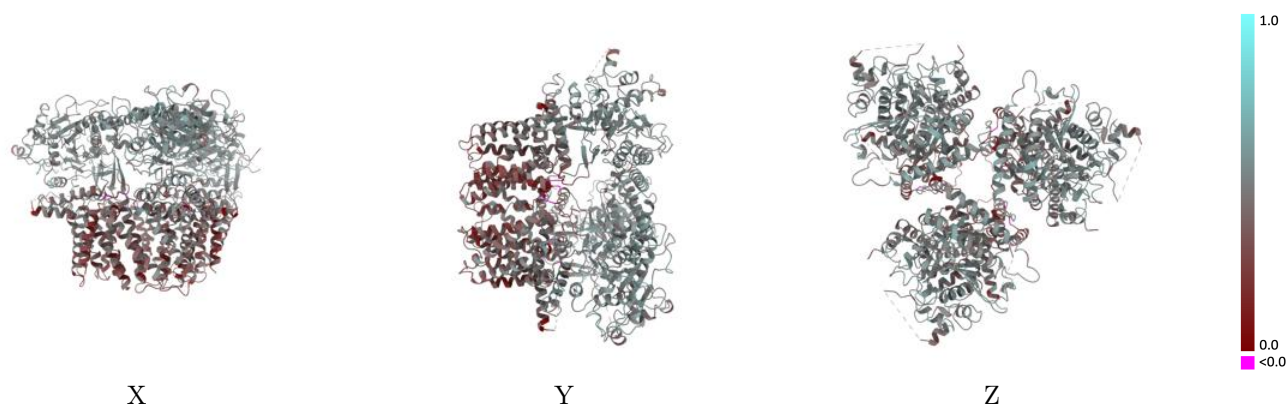
This section contains information regarding the fit between EMDB map EMD-43244 and PDB model 8VHZ. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.35 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](#)

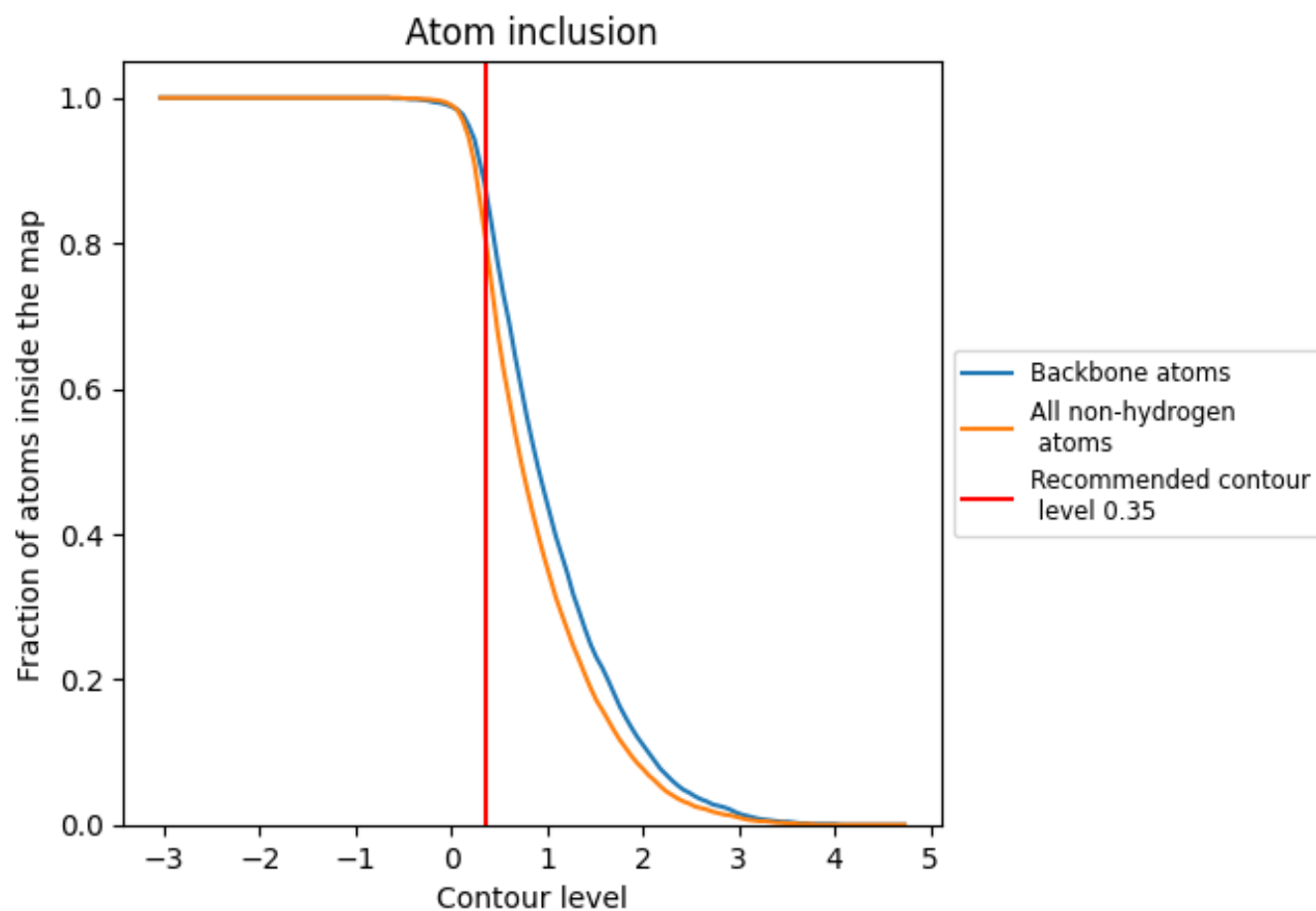


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 81% 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 (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8130	0.4480
A	0.8160	0.4520
B	0.8140	0.4510
C	0.8070	0.4420

