



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 04:32 AM UTC

PDB ID : 6B3R / pdb_00006b3r
EMDB ID : EMD-7042
Title : Structure of the mechanosensitive channel Piezo1
Authors : Guo, Y.R.; MacKinnon, R.
Deposited on : 2017-09-22
Resolution : 3.80 Å (reported)
Based on initial model : 4RAX

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:

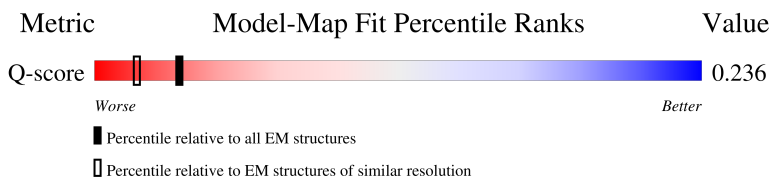
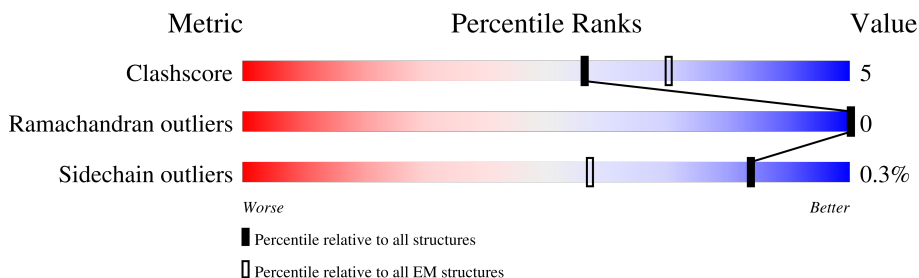
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.80 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	10198 (3.30 - 4.30)

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	2547	17% 51% 8% 41%
1	C	2547	50% 51% 8% 41%
1	E	2547	49% 51% 8% 41%
2	B	16	6% 100%

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Mol	Chain	Length	Quality of chain
2	D	16	6% 100%
2	F	16	25% 100%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 35718 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.

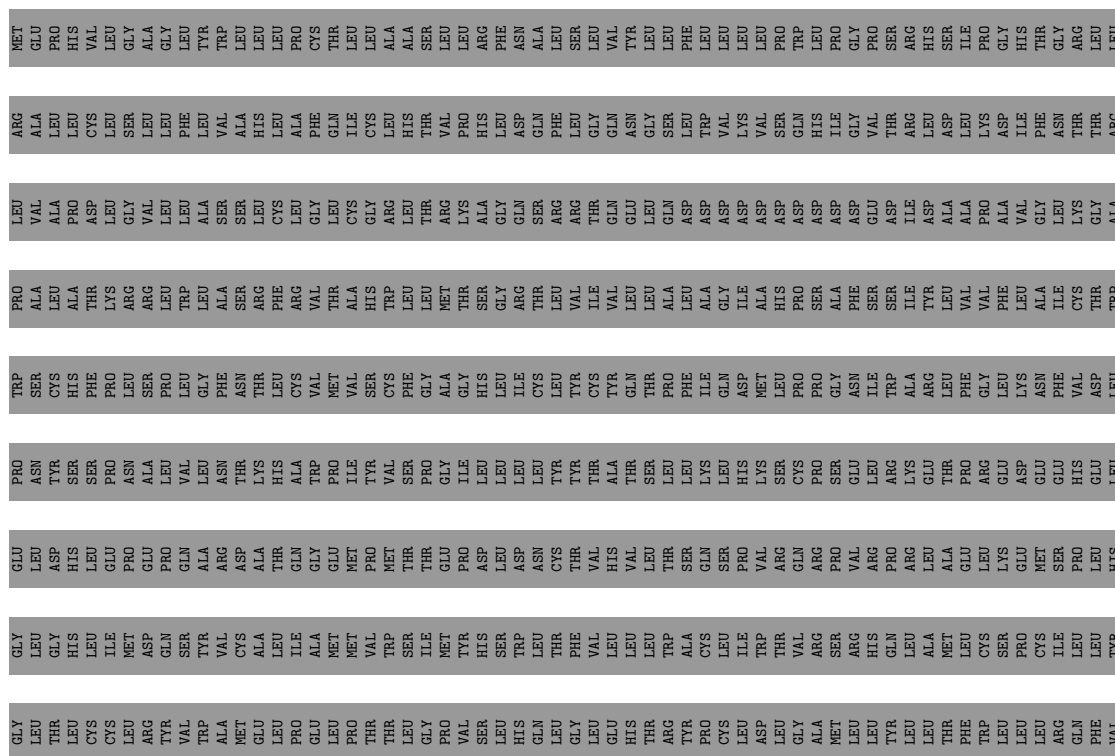
- Molecule 1 is a protein called Piezo-type mechanosensitive ion channel component 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1502	Total	C	N	O	S	0	0
			11826	7739	2004	2013	70		
1	C	1502	Total	C	N	O	S	0	0
			11826	7739	2004	2013	70		
1	E	1502	Total	C	N	O	S	0	0
			11826	7739	2004	2013	70		

- Molecule 2 is a protein called Piezo-type mechanosensitive ion channel component 1, unknown fragment.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	16	Total	C	N	O	0	0
			80	48	16	16		
2	D	16	Total	C	N	O	0	0
			80	48	16	16		
2	F	16	Total	C	N	O	0	0
			80	48	16	16		





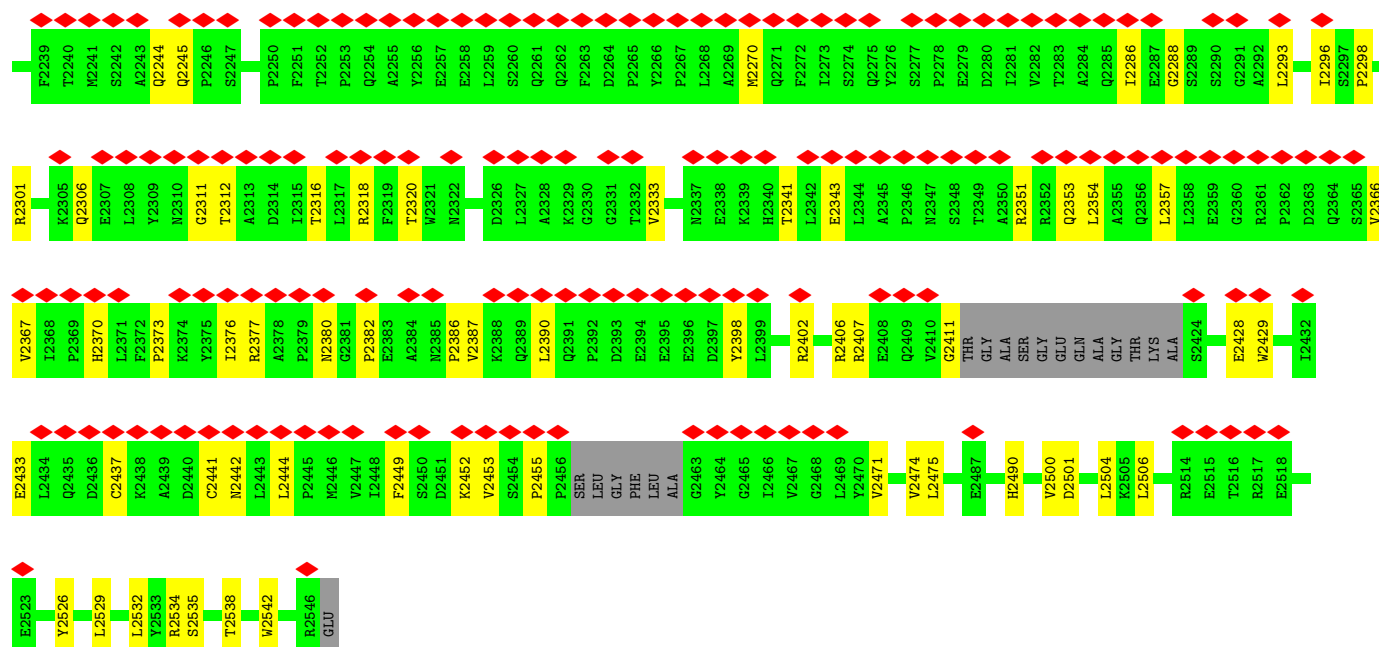
P1261	K1201	P1141	Y1081	L1021	V961	L901	P841	ASP	PRO	PRO	LYS
K1262	D1202	N1142	L1082	T1022	C962	Y902	Y842	R782	PRO	GLY	GLY
E1263	T1203	F1143	P1083	R1023	A963	R903	P843	L783	PRO	ARG	ARG
M1264	R1204	I1144	D1084	R1024	D964	G904	R844	L784	THR	THR	LYS
M1265	A1205	H1145	F1085	R1025	G965	P905	R845	D785	ARG	ARG	LYS
T1266	Q1206	C1146	F1086	R1026	T966	Y906	R846	L786	HIS	HIS	GLN
R1267	L1207	R1147	R1087	E1027	R967	D907	P847	A787	PRO	ARG	GLN
R1268	V1208	S1148	A1088	A1028	Q968	P908	H848	A788	TRP	TRP	VAL
R1269	L1209	Y1149	P1089	I1029	R969	A909	A849	S789	ALA	ALA	VAL
D1270	W1210	L1150	N1090	A1030	L970	N910	S850	F790	HIS	ARG	ALA
C1271	D1211	D1151	S1091	R1031	D971	W911	C851	S791	GLN	GLN	ALA
L1272	C1212	M1152	T1092	L1032	Q972	F912	L852	A792	ASP	ASP	LEU
L1273	L1213	L1153	N1093	W1033	D973	G913	S853	V793	VAL	VAL	GLU
P1274	I1214	K1154	L1094	P1034	L974	V914	T854	L794	SER	SER	THR
V1275	L1215	V1155	I1095	N1035	L975	R915	W855	T795	GLU	GLU	VAL
E1276	Y1216	A1156	S1096	Y1036	S976	K916	W856	R796	ALA	ALA	VAL
E1277	M1217	V1157	D1097	C1037	C977	G917	T857	L797	PRO	PRO	ASP
A1278	V1218	F1158	F1098	L1038	L978	Y918	C858	Q798	LEU	LEU	THR
G1279	T1219	R1159	L1099	F1039	K979	P919	T859	V799	GLU	GLU	GLU
Y1280	V1220	Y1160	L1100	L1040	Y980	N920	I860	F800	HIS	HIS	THR
L1281	I1221	L1161	L1101	T1041	F981	G921	R861	Q801	GLN	GLN	GLN
W1282	I1222	F1162	L1102	L1042	S982	L922	W862	R802	GLU	GLU	THR
D1283	S1223	W1163	C1103	F1043	N983	Y923	C863	R803	GLU	GLU	THR
S1284	K1224	L1164	A1104	L1044	F984	I924	K864	L804	VAL	VAL	LEU
M1285	M1225	V1165	S1105	L1045	F985	Q925	M865	L805	VAL	VAL	LEU
C1286	M1226	L1166	Q1106	Y1046	F986	N926	L866	E806	PHE	ARG	ARG
F1287	L1227	V1167	Q1107	Q1047	Y987	H927	W867	L807	GLU	GLU	GLY
F1288	S1228	V1168	W1108	Y1048	K988	L928	Q868	R808	ASP	ASP	GLU
F1289	L1229	V1169	Q1109	L1049	R989	Q929	L869	W809	GLN	GLN	LEU
L1290	L1230	F1170	W1110	L1050	G990	I930	K870	F810	SER	SER	SER
L1291	S1231	V1171	F1111	C1051	L991	L931	T871	K811	MET	ASP	GLY
L1292	C1232	A1172	S1112	L1052	E992	L932	W872	L812	GLY	GLY	LEU
Q1293	V1233	G1173	A1113	G1053	I993	L933	M873	W813	PRO	PRO	LEU
R1294	F1234	A1174	E1114	M1054	C994	L934	R874	L814	HIS	HIS	LEU
R1295	V1235	T1175	R1115	P1055	F995	Y935	W875	L815	GLN	GLN	LEU
I1296	E1236	R1176	T1116	P1056	L996	F936	GLU	Y816	THR	THR	LEU
F1297	Q1237	E1177	E1117	A1057	M997	E937	TYR	T817	VAL	VAL	LEU
L1298	M1238	S1178	E1118	L1058	A998	A938	SER	W818	PRO	PRO	LEU
S1299	Q1239	I1179	W1119	C1059	V999	V939	GLU	W819	GLU	GLU	LEU
H1300	S1240	F1180	Q1120	I1060	N1000	V940	C891	W820	GLY	GLY	LEU
Y1301	M1241	G1181	R1121	D1061	V1001	Y941	T882	A821	ALA	ALA	LEU
F1302	F1242	L1182	M1122	Y1062	I1002	R942	E883	L822	SER	SER	LEU
L1303	C1243	G1183	A1123	P1063	G1003	R943	P884	R823	LYS	LYS	LEU
H1304	V1244	Y1184	G1124	W1064	Q1004	Q944	F885	E824	TRP	TRP	LEU
V1305	V1245	L1185	I1125	R1065	R1005	E945	P886	W825	GLY	GLY	LEU
S1306	I1246	L1186	N1126	W1066	R1006	R946	ASN	S826	VAL	VAL	LEU
A1307	Q1247	A1187	T1127	S1067	N1007	Y947	THR	W827	ALA	ALA	LEU
D1308	L1248	C1188	D1128	K1068	F1008	R948	ASN	M828	GLY	GLY	LEU
L1309	F1249	F1189	L1129	A1069	M1009	R949	LEU	N829	PRO	PRO	LEU
K1310	S1250	Y1190	L1130	I1070	V1010	Q950	Q892	N830	GLY	GLY	LEU
A1311	L1251	L1191	E1131	P1071	I1011	H951	P893	L831	THR	THR	LEU
T1312	V1252	L1192	P1132	M1072	L1012	Q952	L894	L832	VAL	VAL	LEU
A1313	C1253	L1193	L1133	N1073	H1013	Q953	E895	W833	ALA	ALA	LEU
T1314	T1254	F1194	R1134	S1074	G1014	A954	I896	W834	LYS	LYS	LEU
Q1315	V1255	G1195	G1135	A1075	C1015	P955	N897	L835	TRP	TRP	LEU
A1316	K1256	T1196	E1136	I1076	W1016	L956	Q898	W836	GLY	GLY	LEU
G1257	G1257	T1197	P1137	I1077	L1017	P957	S899	A837	VAL	VAL	LEU
R1318	Y1258	L1198	N1138	K1078	V1018	F958	L900	F838	ALA	ALA	LEU
G1319	Y1259	L1199	P1139	W1079	A1019	Q959	S900	A839	GLY	GLY	LEU
F1320	D1260	Q1200	L1140	L1080	I1020	A960	L840	L840	HIS	HIS	VAL



[illegible]

P1261	K1201	P1141	Y1081	L1021	V961	L901	P841	ASP	PRO	LYS
K1262	D1202	N1142	L1082	T1022	C962	Y902	Y842	R782	PRO	GLY
E1263	T1203	F1143	P1083	R1023	A963	R903	P843	L783	PRO	LYS
M1264	R1204	I1144	D1084	R1024	D964	G904	R844	L784	THR	LEU
M1265	A1205	H1145	F1085	R1025	G965	P905	R845	D785	ARG	LYS
T1266	Q1206	C1146	F1086	R1026	T966	Y906	R846	L786	HIS	GLN
R1267	L1207	R1147	R1087	E1027	R967	D907	P847	A787	PRO	LYS
R1268	V1208	S1148	A1088	A1028	Q968	P908	H848	A788	TRP	VAL
R1269	L1209	Y1149	P1089	I1029	R969	A909	A849	S789	ALA	PRO
D1270	W1210	L1150	N1090	A1030	L970	N910	S850	F790	HIS	ALA
C1271	D1211	D1151	S1091	R1031	D971	W911	C851	S791	GLN	ALA
L1272	C1212	M1152	T1092	L1032	Q972	F912	L852	A792	ASP	LEU
L1273	L1213	L1153	N1093	W1033	D973	G913	S853	V793	VAL	GLY
P1274	I1214	K1154	L1094	P1034	L974	V914	T854	L794	SER	THR
V1275	L1215	V1155	T1095	N1035	L975	R915	W855	T795	GLU	VAL
E1276	Y1216	A1156	S1096	Y1036	S976	K916	W856	R796	ALA	ALA
E1277	M1217	V1157	D1097	C1037	C977	G917	T857	L797	PRO	ASP
A1278	V1218	F1158	F1098	L1038	L978	Y918	C858	Q798	LEU	THR
G1279	T1219	R1159	L1099	F1039	K979	P919	T859	V799	GLU	GLU
Y1280	V1220	Y1160	L1100	L1040	Y980	N920	I860	F800	HIS	THR
I1281	I1221	L1161	L1101	T1041	F981	L921	I861	W801	GLN	GLN
W1282	I1222	F1162	L1102	L1042	I982	G922	W862	R802	GLU	THR
D1283	S1223	W1163	C1103	F1043	N983	Y923	C863	R803	GLU	THR
S1284	K1224	L1164	A1104	L1044	F984	I924	K864	L804	VAL	LEU
M1285	M1225	V1165	S1105	L1045	F985	Q925	M865	L805	VAL	LEU
C1286	M1226	L1166	Q1106	Y1046	F986	N926	L866	E806	PHE	ARG
F1287	L1227	V1167	Q1107	Q1047	Y987	H927	Y867	L807	GLU	GLY
F1288	S1228	V1168	W1108	Y1048	K988	L928	Q868	R829	GLY	GLY
F1289	L1229	V1169	Q1109	L1049	R989	Q929	L869	W809	GLN	LEU
L1290	L1230	F1170	V1110	L1050	G990	I930	K870	F810	SER	ARG
L1291	S1231	V1171	F1111	C1051	L991	L931	I871	K811	ASP	LEU
L1292	C1232	A1172	S1112	L1052	E992	L932	W872	L812	GLY	GLY
Q1293	V1233	A1173	A1113	G1053	I993	L933	M873	W813	PRO	V577
R1294	F1234	A1174	E1114	M1054	C994	L934	P874	L814	HIS	V578
R1295	V1235	T1175	R1115	P1055	F995	Y935	H875	L815	GLN	T579
I1296	E1236	R1176	T1116	P1056	L996	F936	GLU	Y816	ALA	G580
F1297	Q1237	I1177	E1117	A1057	M997	E937	TYR	T817	THR	I581
L1298	M1238	S1178	E1118	L1058	A998	A938	SER	W818	VAL	Y582
S1299	Q1239	I1179	W1119	C1059	V999	V939	GLU	W819	PRO	Y583
H1300	S1240	F1180	Q1120	I1060	N1000	V940	C891	W820	GLY	K584
Y1301	M1241	G1181	R1121	D1061	V1001	Y941	T882	A821	THR	Y585
F1302	F1242	L1182	M1122	Y1062	I1002	R942	E883	L822	ALA	Y586
L1303	C1243	G1183	A1123	P1063	G1003	R943	P884	K823	SER	I587
H1304	V1244	Y1184	G1124	W1064	Q1004	Q944	F885	E824	LYS	V588
V1305	Y1245	L1185	I1125	R1065	R1005	E945	P886	W825	TRP	C590
S1306	I1246	L1186	M1126	W1066	R1006	H946	ASN	S826	GLY	G592
A1307	Q1247	A1187	T1127	S1067	N1007	Y947	THR	W827	VAL	M593
D1308	L1248	C1188	D1128	K1068	F1008	R948	ASN	M828	GLY	F594
L1309	F1249	F1189	L1129	A1069	M1009	R949	LEU	N829	PRO	I595
K1310	S1250	Y1190	L1130	I1070	V1010	Q950	Q892	N829	GLY	V596
A1311	L1251	L1191	E1131	P1071	I1011	H951	P893	L831	THR	V597
T1312	V1252	L1192	P1132	M1072	L1012	Q952	L894	L832	ALA	S598
A1313	C1253	L1193	L1133	N1073	H1013	Q953	E895	W833	LYS	F599
T1314	T1254	F1194	R1134	S1074	G1014	A954	I896	W834	TRP	Q654
Q1315	V1255	G1195	G1135	A1075	C1015	P955	N897	L835	GLY	F655
A1316	K1256	T1196	E1136	L1076	W1016	L956	Q898	W836	LEU	Q656
G1257	G1257	T1197	P1137	I1077	L1017	P957	S899	A837	VAL	D657
R1318	Y1258	L1198	N1138	K1078	V1018	F958	L900	F838	ALA	F658
G1319	Y1259	L1199	P1139	W1079	A1019	Q959	L900	A839	GLY	P659
F1320	D1260	Q1200	I1140	L1080	I1020	A960	L840	L840	HIS	T660
									VAL	

H2116	V2054	I1992	SER	VAL	GLU	G1750	L1690	GLY	G1570	H1510	GLN	SER	A1321
L2117	V2055	F1993	LYS	ILE	ASP	F1751	C1691	SER	P1571	A1511	THR	PRO	L1322
N2118	A2056	G1994	ARG	GLN	ARG	F1752	Y1692	GLN	V1572	T1512	VAL	PRO	Y1323
L2119	I2057	F1995	GLU	PRO	TYR	P1753	I1693	GLU	E1573	V1513	LEU	ARG	N1324
F2120	H2058	W1996	ARG	PRO	LYS	W1754	I1694	LEU	T1574	D1514	GLN	GLN	A1325
L2127	I2059	A1997	MET	GLU	ASP	N1755	I1695	ALA	E1575	G1515	ARG	TRP	A1326
F2130	W2060	PHE	LYS	ASP	HIS	S1756	I1696	ASN	D1576	L1516	ARG	TRP	A1327
L2131	M2061	GLY	ALA	LEU	CYS	Y1757	L1697	ALA	G1577	T1517	GLU	PRO	L1328
W2132	F2062	GLY	LYS	PRO	ARG	W1758	N1698	ARG	P1578	L1518	ALA	TRP	K1329
F2133	F2063	ARG	ARG	ARG	SER	V1759	H1699	THR	SER	W1519	ARG	ASP	K1330
L2064	L2064	ALA	LEU	HIS	VAL	L1760	M1700	MET	THR	L1520	GLN	ASP	I1331
L2065	PRO	ALA	GLN	ARG	LYS	R1761	V1701	ARG	ALA	R1521	GLU	HIS	I1331
W2138	ASP	THR	SER	ASP	ASP	R1762	T1702	THR	SER	A1522	ARG	ALA	N1332
T2143	ALA	ILE	SER	GLU	GLU	Y1763	A1703	ALA	SER	F1523	ALA	THR	F1333
D2144	VAL	CYS	SER	ALA	GLU	E1764	S1704	GLU	GLY	T1524	GLN	VAL	H1334
T2145	THR	ILE	VAL	LYS	LYS	N1765	A1705	LEU	GLY	K1525	LEU	ILE	R1335
T2146	GLU	ARG	ARG	GLU	GLU	K1766	A1706	LEU	ALA	H1526	ALA	SER	Q1336
N2151	ARG	PHE	SER	PHE	GLU	P1767	S1707	ASP	GLU	H1527	SER	GLY	I1337
W2152	ALA	ALA	ALA	ARG	PRO	Y1768	L1708	ARG	PRO	R1528	GLY	TYR	E1338
K2166	SER	LYS	LYS	ARG	ALA	F1769	V1709	LEU	LEU	T1529	ASP	PHE	E1339
E2172	Q2075	Q2015	F1954	GLU	LEU	P1770	I1710	H1655	SER	M1529	ASN	PHE	K1340
Y2175	N2076	V2016	Y1955	THR	GLU	R1771	P1711	I1656	THR	M1530	PRO	GLU	S1341
F2176	A2077	F2017	Q1956	PRO	SER	R1772	V1712	P1657	GLY	S1531	ASP	SER	L1342
Q2177	W2078	Q2018	P1957	GLY	GLN	I1773	L1713	E1658	ASP	D1532	VAL	ASP	A1343
F2178	A2079	A2019	L1958	LYS	GLU	L1774	V1714	E1659	THR	V1533	PRO	GLU	Q1344
L2081	Q2080	F2020	Q1959	THR	GLY	G1775	F1715	E1660	SER	L1534	VAL	GLU	L1345
W2082	L2081	F2021	R1960	ALA	THR	L1776	L1716	E1661	PRO	C1535	ASP	GLU	K1346
Y2083	Y2083	F2022	F1961	VAL	GLY	E1777	W1717	E1662	SER	A1536	VAL	GLU	R1347
F2084	V2085	N2023	F1962	GLU	HIS	K1778	A1718	E1663	THR	E1537	ASP	ALA	E1357
V2085	K2086	L2024	H1963	THR	LYS	T1779	M1719	R1664	TYR	Y1539	GLU	PRO	L1357
K2086	C2087	V2026	D1964	GLU	GLU	D1780	L1720	F1665	ASN	L1540	MET	GLU	Q1360
C2087	L2088	Q2027	L1965	VAL	VAL	S1781	T1721	E1666	THR	L1541	ALA	ASP	R1361
Y2088	F2089	F2028	L1966	GLU	LEU	Y1782	I1722	A1667	GLY	T1542	GLY	PRO	S1362
F2090	A2091	T2030	H1967	GLY	ALA	I1783	P1723	Q1668	SER	Q1543	SER	PRO	Q1363
L2092	S2093	Y2032	K1969	GLY	THR	K1784	R1724	Q1669	GLY	E1544	ALA	ALA	A1364
A2094	D2034	D2033	Y1970	THR	PRO	Y1785	P1725	G1670	SER	L1545	GLN	ALA	S1365
Y2095	R2035	L2033	R1971	ARG	ARG	D1786	S1726	R1671	GLU	L1546	GLY	GLN	ARG
Q2096	A2036	D2034	A1972	THR	ASP	L1787	K1727	T1672	LEU	R1547	ALA	PHE	GLY
L2097	R2037	R2037	A1973	GLU	ILE	W1788	R1728	L1673	VAL	V1498	GLN	GLN	LEU
R2098	Q2036	L2037	T1974	ARG	GLN	Q1789	F1729	R1674	THR	G1549	MET	SER	GLN
C2099	R2040	R2040	D1975	LYS	LYS	L1790	M1730	L1675	ASP	E1550	ALA	ALA	LYS
G2100	K2041	K2041	Y1976	ARG	GLY	M1791	M1731	L1676	GLY	S1500	TYR	ASP	ASP
Y2101	T2042	T2042	L1979	PRO	GLY	A1792	T1732	R1677	ASP	T1501	GLN	PRO	PRO
R2104	L2044	L2044	M1980	HIS	ILE	L1793	I1733	E1678	LEU	R1552	ALA	TRP	ASP
I2105	L2047	L2047	A1983	THR	ARG	F1794	A1733	G1679	GLN	R1553	VAL	THR	ASP
L2106	A2048	A2048	D1984	GLN	SER	F1795	I1735	V1680	GLY	F1554	THR	ASN	SER
G2107	F2049	F2049	I1985	LYS	ASP	H1796	F1736	Q1681	SER	V1555	GLN	GLN	GLN
Q2108	Q2050	Q2050	I1986	LYS	LYS	R1797	T1737	C1682	THR	L1556	L1505	GLU	L1505
F2109	V2051	V2051	I1987	LYS	LYS	R1797	T1737	Q1682	LEU	D1557	W1506	PRO	PRO
K2112	V2052	V2052	I1988	LYS	LYS	F1797	E1738	V1683	HIS	Q1558	V1507	GLY	GLY
K2113	L2053	L2053	I1989	LYS	LYS	S1798	I1739	A1684		L1559	L1508	ASP	ASP
Y2114	L2053	L2053	I1990	LYS	LYS	Q1799	M1740	A1685		Y1560	V1561	SER	SER
N2115	L2053	L2053	I1991	LYS	LYS	L1800	M1741	H1686		V1562	G1569	GLY	GLY
						L1801	V1742	S1687		E1563		ALA	ALA
						Y1803	T1743	E1688		D1564			
						G1804	K1744	L1689		E1565			
						L1805	Y1745			T1567			
						W1806	L1746			L1568			
						D1807	F1747						
						HIS	Q1748						
						GLU	F1749						



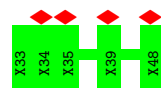
- Molecule 2: Piezo-type mechanosensitive ion channel component 1, unknown fragment



- Molecule 2: Piezo-type mechanosensitive ion channel component 1, unknown fragment



- Molecule 2: Piezo-type mechanosensitive ion channel component 1, unknown fragment



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	277548	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 ($e^-/\text{\AA}^2$)	47	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.334	Depositor
Minimum map value	-0.238	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	520.0, 520.0, 520.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3, 1.3, 1.3	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	0.27	0/12117	0.56	0/16473
1	C	0.27	0/12117	0.56	0/16473
1	E	0.27	0/12117	0.56	0/16473
All	All	0.27	0/36351	0.56	0/49419

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	11826	0	11563	125	0
1	C	11826	0	11563	124	0
1	E	11826	0	11563	126	0
2	B	80	0	19	0	0
2	D	80	0	19	0	0
2	F	80	0	19	0	0
All	All	35718	0	34746	346	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 5.

The worst 5 of 346 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:C:2050:GLN:HE22	1:C:2094:ALA:HB2	1.57	0.69
1:E:2050:GLN:HE22	1:E:2094:ALA:HB2	1.57	0.69
1:A:2050:GLN:HE22	1:A:2094:ALA:HB2	1.57	0.69
1:A:1161:LEU:O	1:A:1293:GLN:NE2	2.29	0.66
1:E:1161:LEU:O	1:E:1293:GLN:NE2	2.29	0.65

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	1478/2547 (58%)	1358 (92%)	120 (8%)	0	100	100
1	C	1478/2547 (58%)	1359 (92%)	119 (8%)	0	100	100
1	E	1478/2547 (58%)	1360 (92%)	118 (8%)	0	100	100
All	All	4434/7641 (58%)	4077 (92%)	357 (8%)	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	1198/2246 (53%)	1195 (100%)	3 (0%)	86	84
1	C	1198/2246 (53%)	1195 (100%)	3 (0%)	86	84
1	E	1198/2246 (53%)	1195 (100%)	3 (0%)	86	84

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	3594/6738 (53%)	3585 (100%)	9 (0%)	84 84

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	1976	VAL
1	E	2500	VAL
1	C	1694	ILE
1	C	1976	VAL
1	C	2500	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	2324	GLN
1	E	944	GLN
1	E	798	GLN
1	E	1668	GLN
1	A	2322	ASN

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 ⓘ

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.

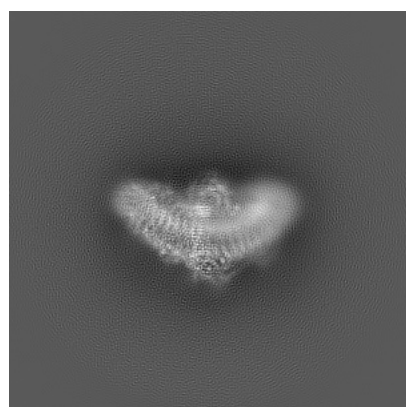
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7042. These allow visual inspection of the internal detail of the map and identification of artifacts.

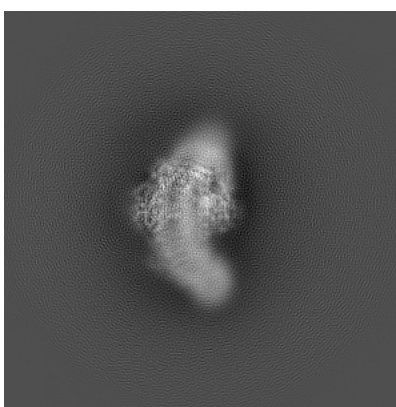
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

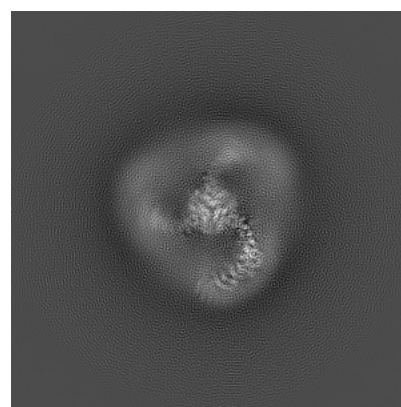
6.1.1 Primary map



X



Y



Z

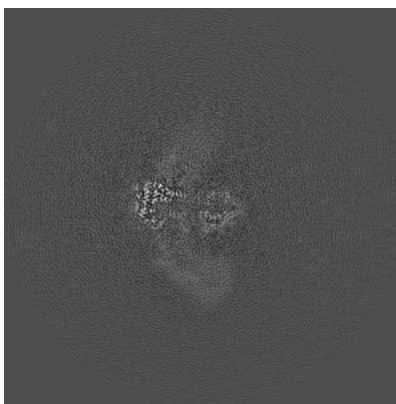
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

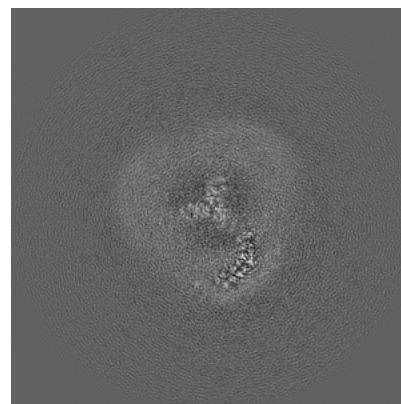
6.2.1 Primary map



X Index: 200



Y Index: 200

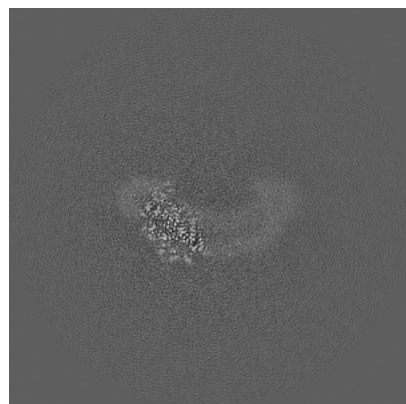


Z Index: 200

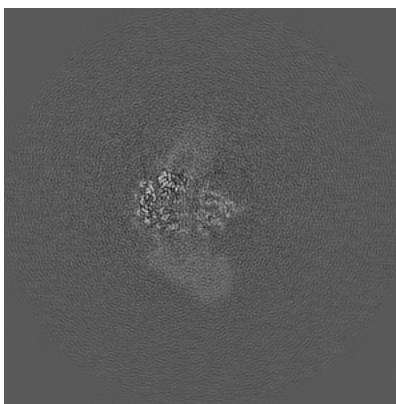
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

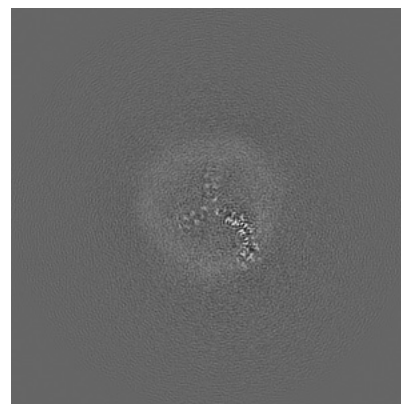
6.3.1 Primary map



X Index: 233



Y Index: 193

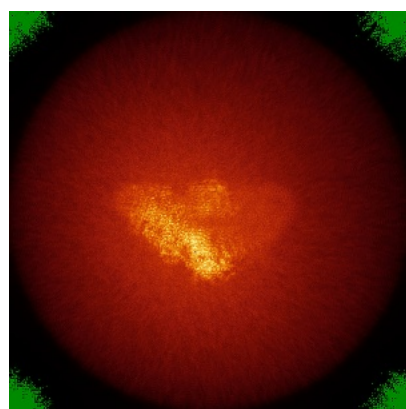


Z Index: 170

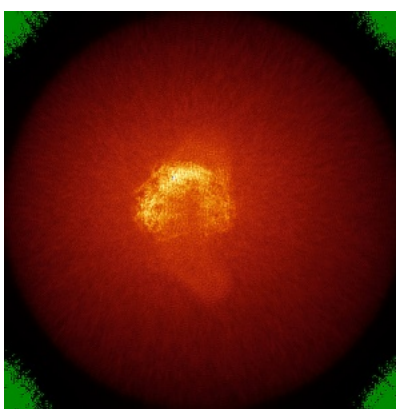
The images above show the largest variance slices of the map in three orthogonal directions.

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

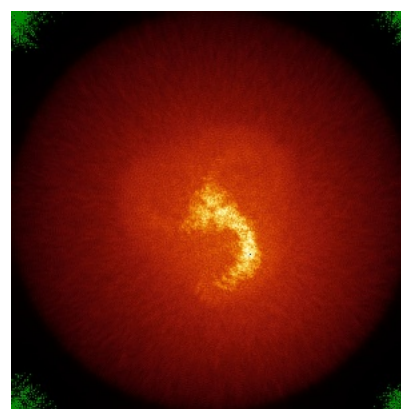
6.4.1 Primary map



X



Y

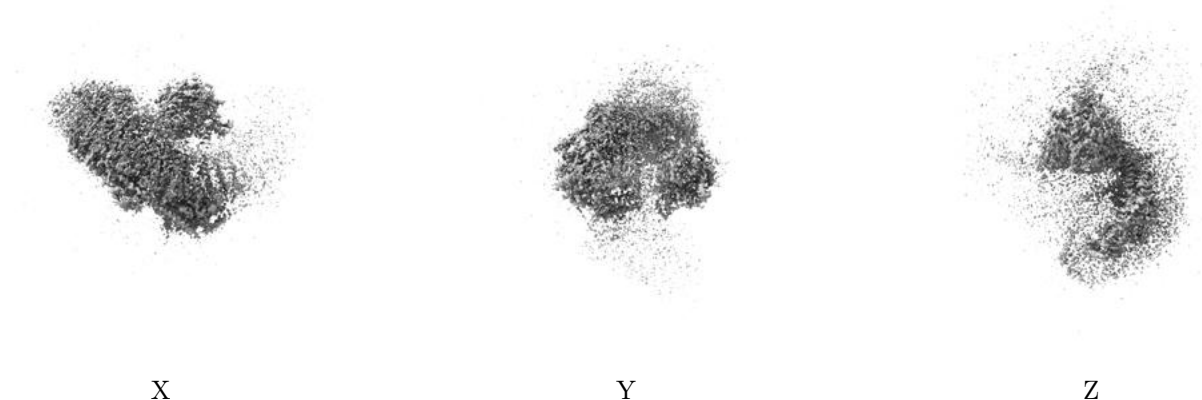


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

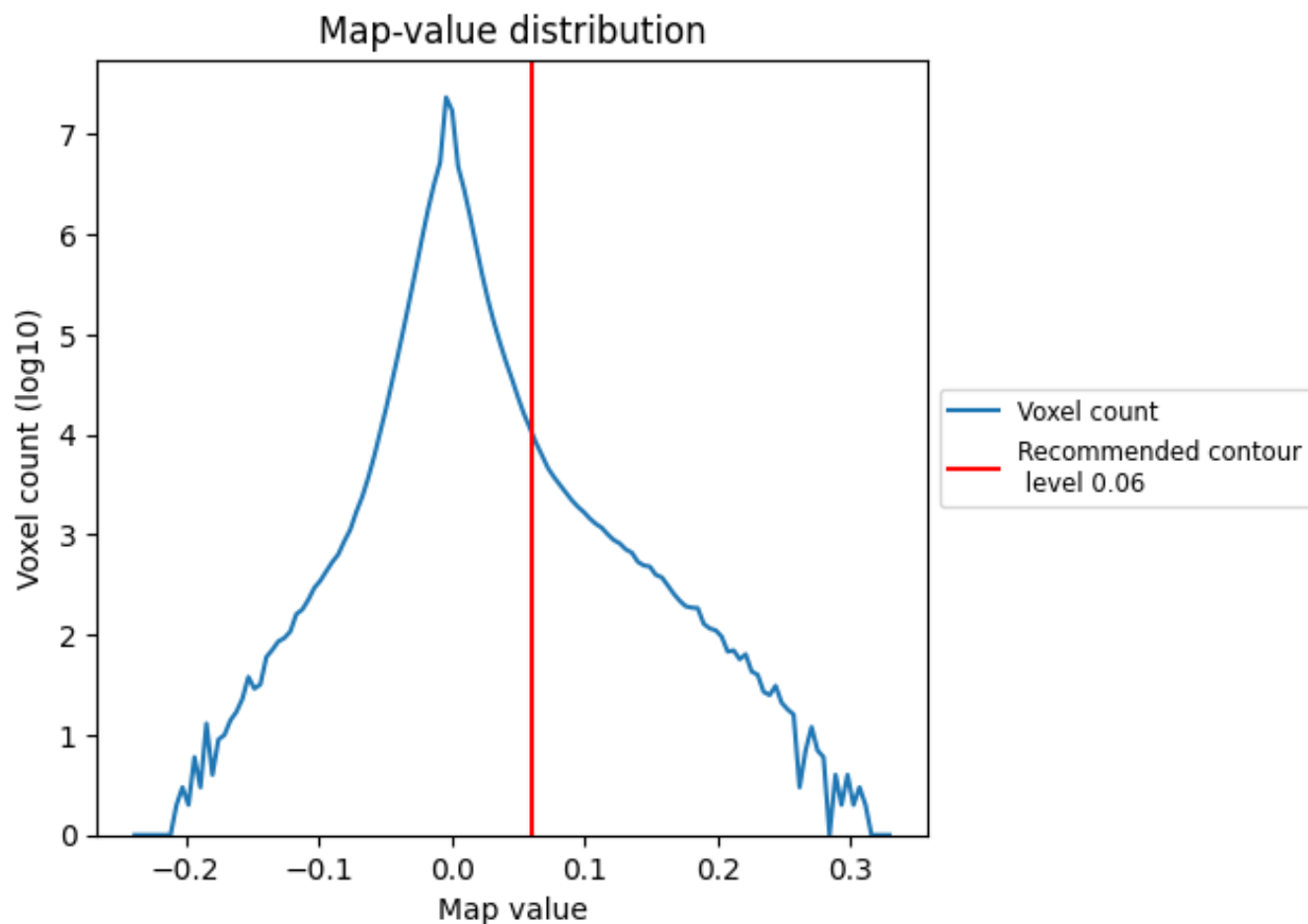
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

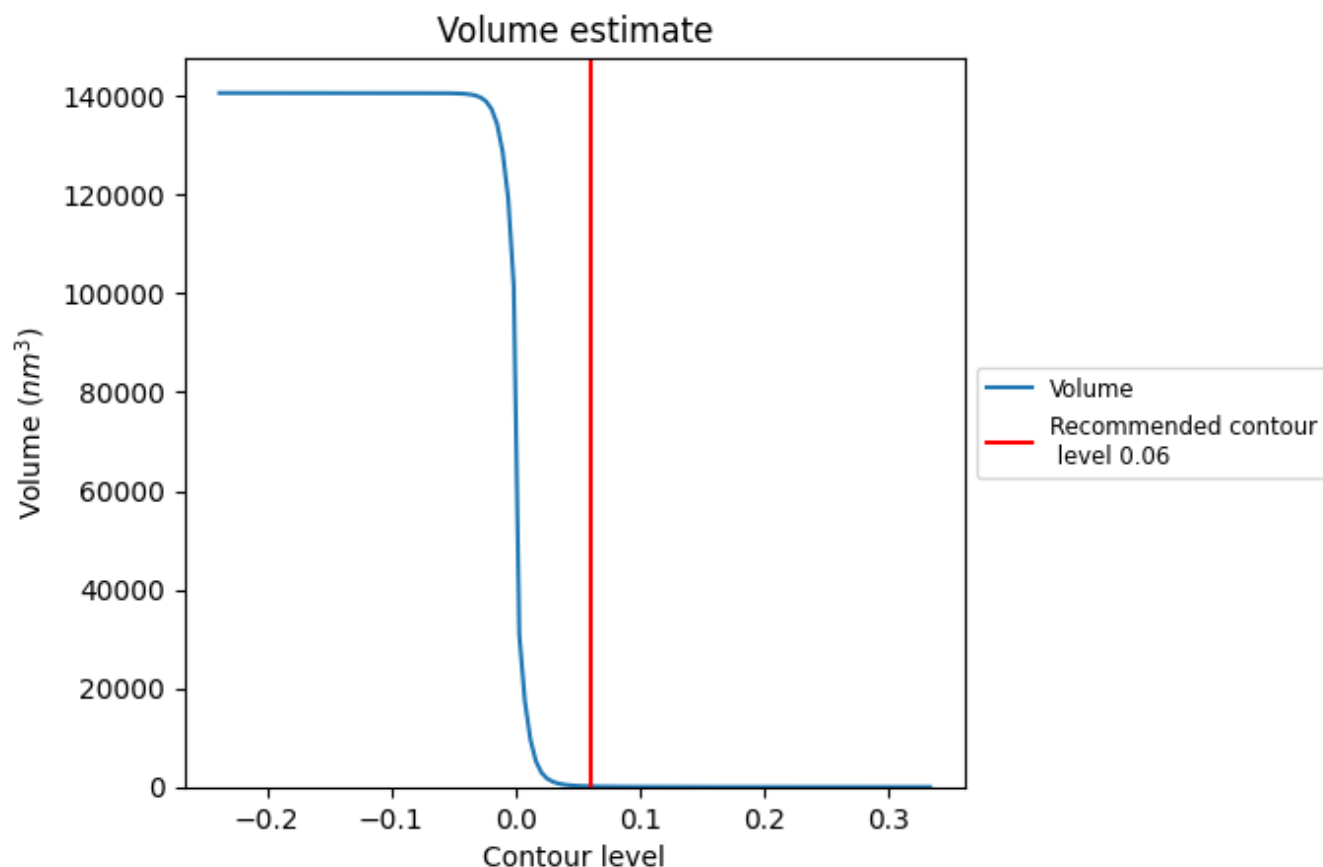
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

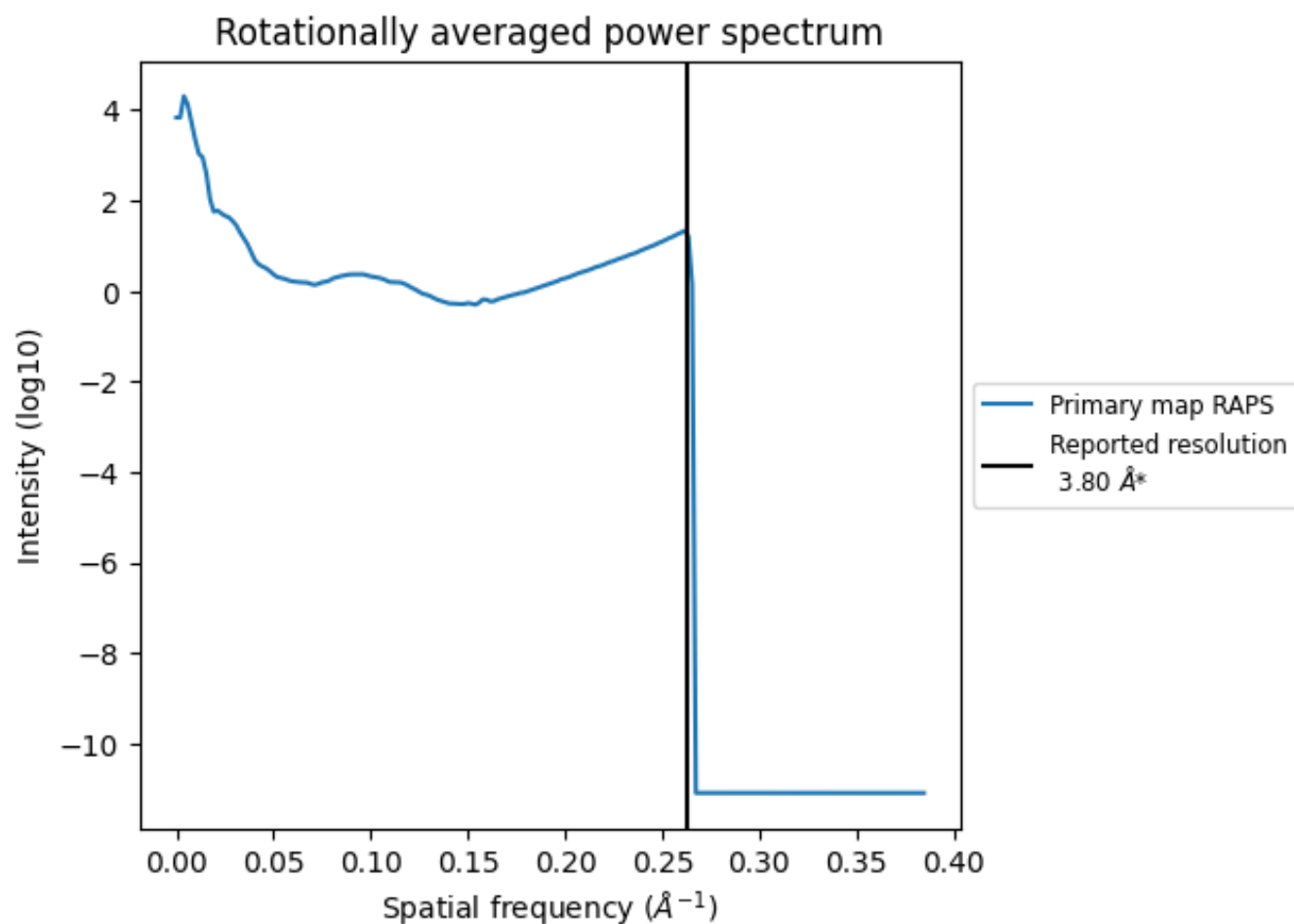
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 123 nm^3 ; this corresponds to an approximate mass of 111 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 0.263 Å⁻¹

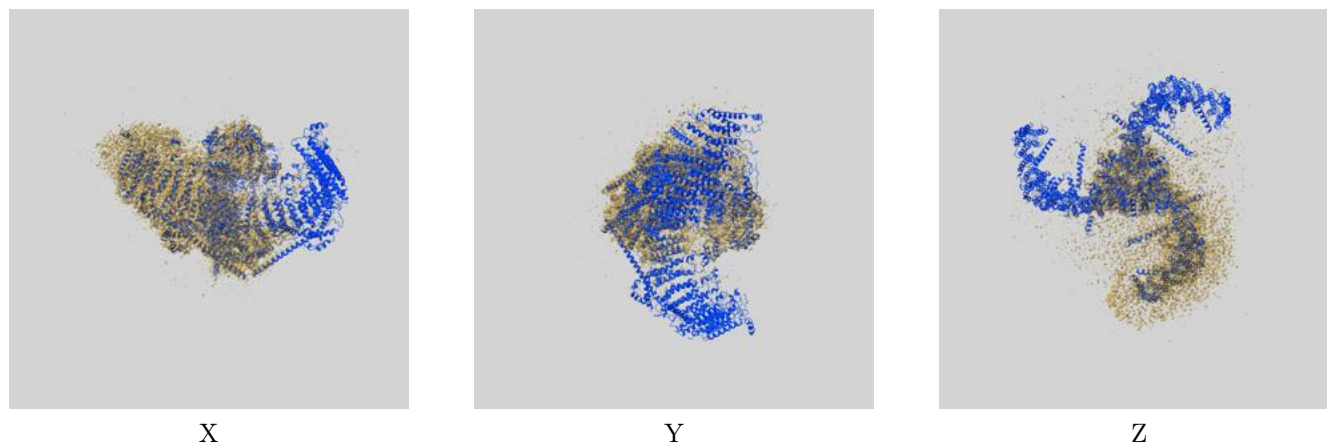
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

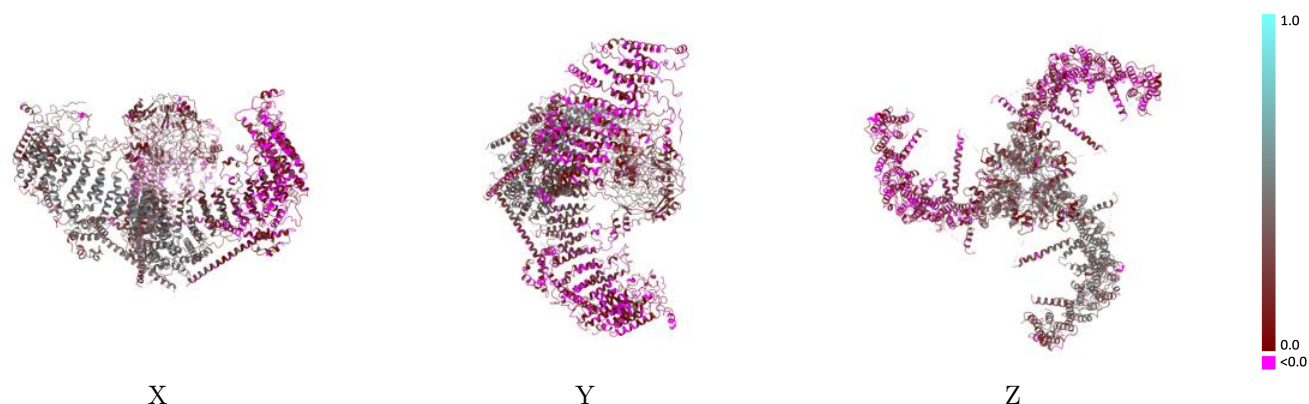
This section contains information regarding the fit between EMDB map EMD-7042 and PDB model 6B3R. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



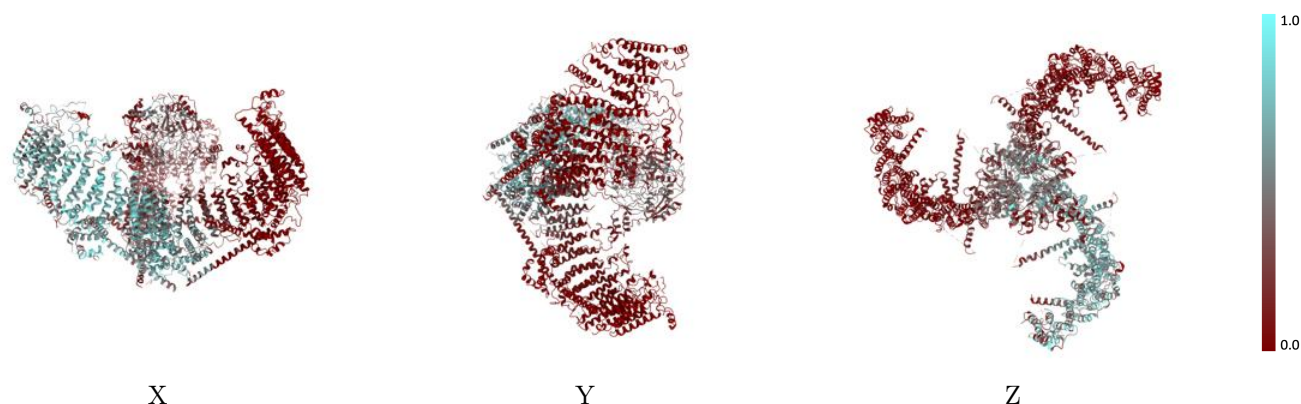
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



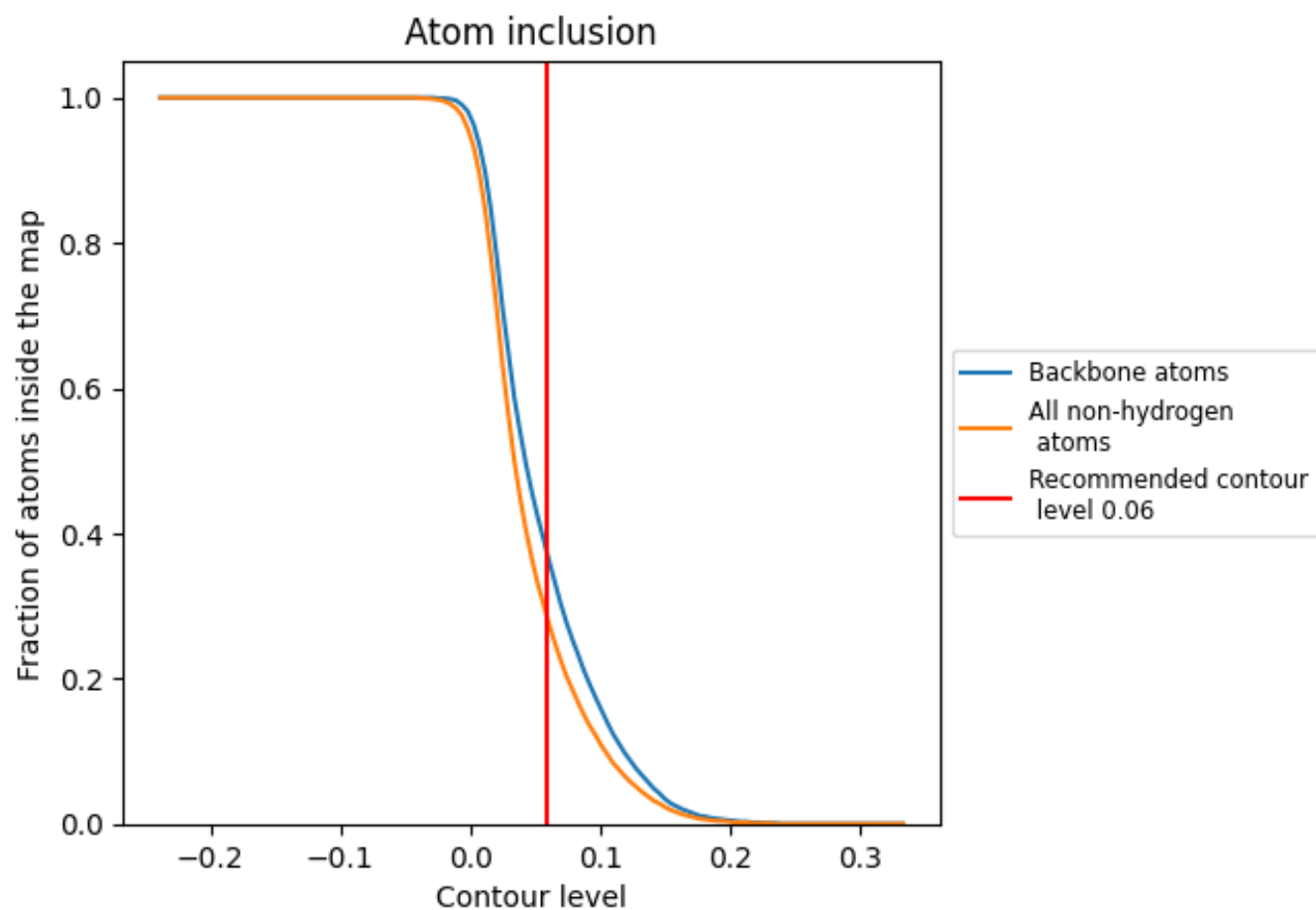
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.06).

9.4 Atom inclusion [i](#)



At the recommended contour level, 37% of all backbone atoms, 28% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.2810	0.2360
A	0.5390	0.3720
B	0.7250	0.4520
C	0.1470	0.1650
D	0.6880	0.4410
E	0.1470	0.1660
F	0.6250	0.4110

1.0

0.0

<0.0