



wwPDB EM Validation Summary Report ⓘ

Nov 6, 2022 – 05:33 AM EST

PDB ID : 6B3R
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.

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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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

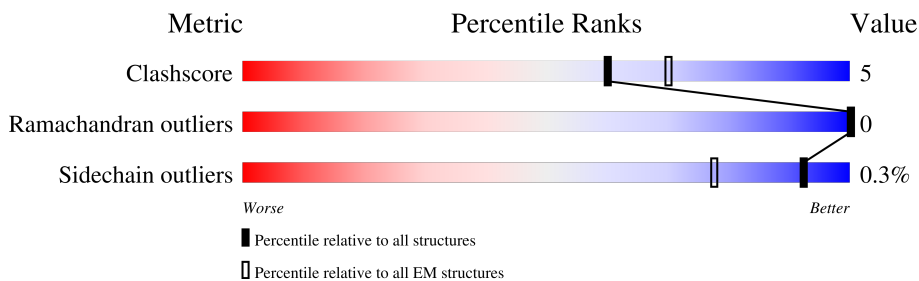
1 Overall quality at a glance

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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	
1	C	2547	
1	E	2547	
2	B	16	
2	D	16	
2	F	16	

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.

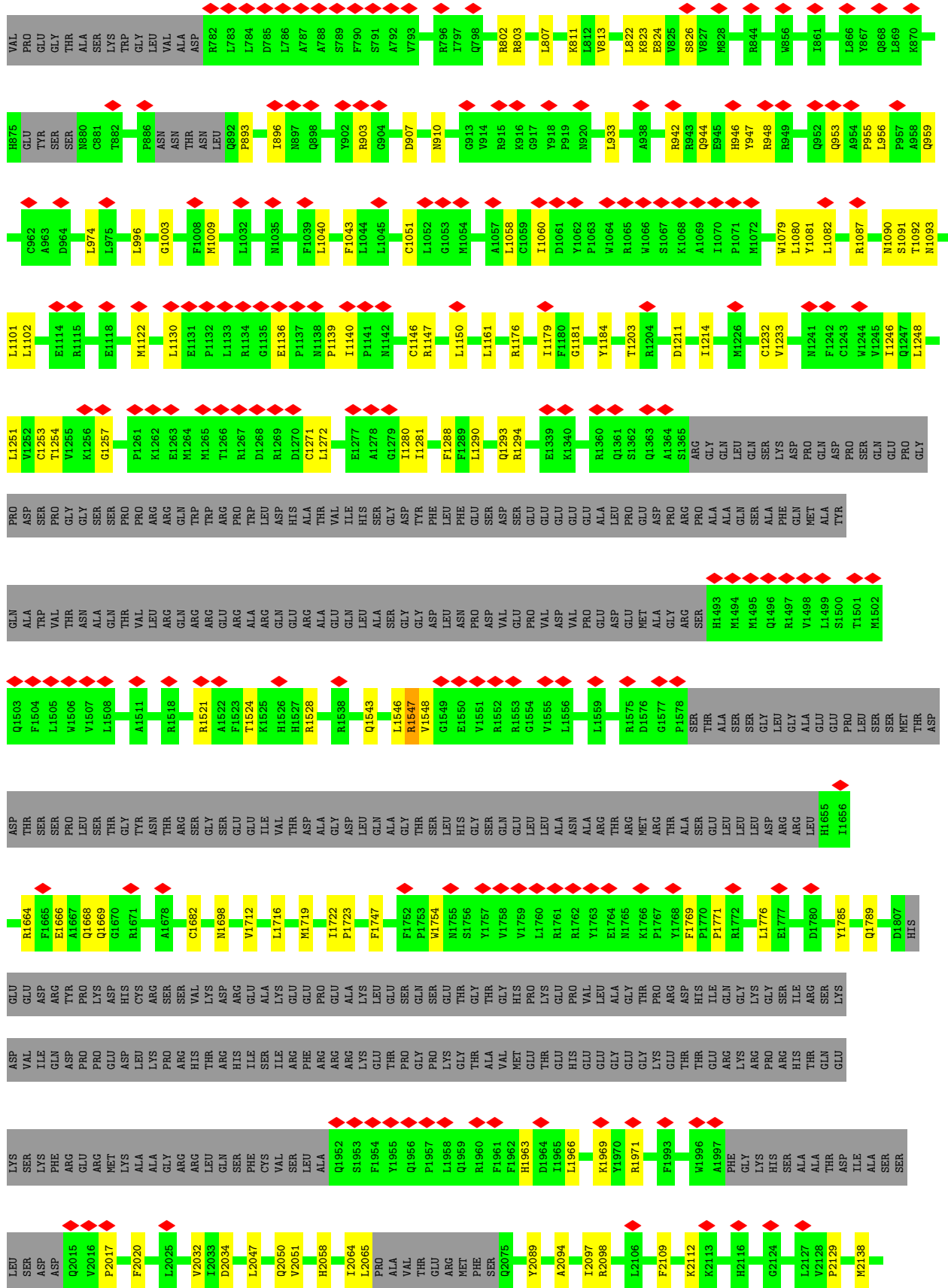
In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

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

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

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

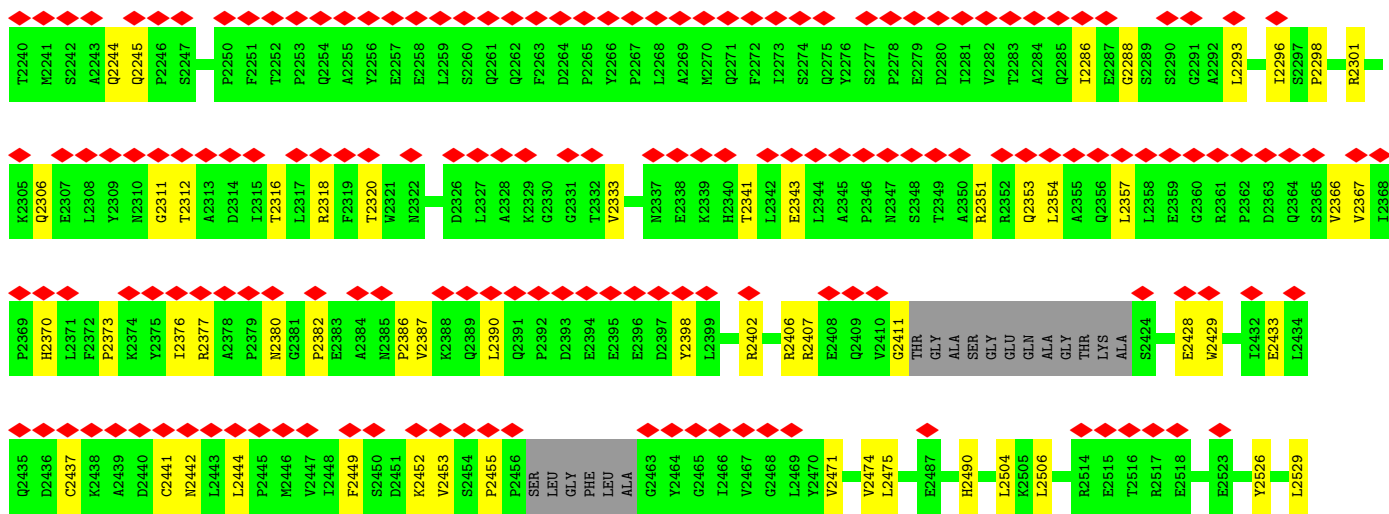
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	B	16	80	48	16	16	0	0
2	D	16	80	48	16	16	0	0
2	F	16	80	48	16	16	0	0



P1261	K1201	P1141	Y1081	L1021	V961	L901	P841	ASP	PRO	GLY	Y661	GLY	LYS
K1262	D1202	N1142	L1082	T1022	C962	Y902	Y842	R782	PRO	PRO	W662	ARG	GLU
E1263	T1203	F1143	P1083	R1023	A963	R903	P843	L783	PRO	GLY	R663	LEU	LYS
M1264	R1204	I1144	D1084	R1024	D964	G904	R844	L784	THR	ARG	M664	LEU	LEU
M1265	A1205	H1145	F1085	R1025	G965	P905	P845	D785	HIS	HIS	L665	LYS	LYS
T1266	Q1206	C1146	F1086	R1026	T966	V906	R846	L786	PRO	PRO	T666	GLN	GLN
R1267	L1207	R1147	R1087	E1027	R967	D907	P847	A787	ARG	ARG	G667	LYS	LYS
D1268	V1208	S1148	A1088	A1028	Q968	P908	M848	A788	TRP	ALA	F668	VAL	VAL
R1269	L1209	Y1149	P1089	R1029	R969	A909	M849	S789	ALA	ALA	T669	PRO	PRO
D1270	W1210	L1150	M1090	A1030	L970	N910	S850	F790	HIS	ALA	F610	ALA	ALA
C1271	D1211	D1151	S1091	R1031	D971	W911	C851	S791	GLN	GLN	E671	ALA	ALA
L1272	C1212	M1152	T1092	L1032	Q972	F912	L852	A792	ASP	ASP	Q672	LEU	LEU
L1273	L1213	L1153	M1093	W1033	D973	G913	S853	V793	ALA	ALA	L613	GLU	GLU
P1274	I1214	K1154	L1094	P1034	L974	V914	T854	L794	VAL	VAL	G674	THR	THR
V1275	L1215	V1155	I1095	M1035	L975	R915	W855	T795	GLU	GLU	D675	VAL	VAL
E1276	Y1216	A1156	S1096	Y1036	S976	K916	W856	R796	ALA	ALA	L676	ALA	ALA
E1277	M1217	V1157	D1097	C1037	C977	G917	T857	I797	PRO	PRO	G677	ASP	ASP
A1278	V1218	F1158	F1098	L1038	L978	Y918	C858	Q798	LEU	LEU	L678	THR	THR
G1279	T1219	R1159	F1099	F1039	K979	P919	M859	V799	GLU	GLU	E679	PRO	PRO
I1280	Y1220	Y1160	L1100	L1040	Y980	N920	I860	F800	HIS	HIS	Q680	THR	THR
I1281	I1221	L1161	L1101	T1041	F981	R921	I861	W801	GLN	GLN	F621	GLN	GLN
W1282	I1222	F1162	L1102	L1042	I982	G922	W862	R802	GLU	GLU	Q622	THR	THR
D1283	S1223	W1163	C1103	F1043	N983	Y923	C863	R803	GLU	GLU	S623	GLN	GLN
S1284	K1224	L1164	A1104	L1044	F984	I924	K864	L804	VAL	VAL	Y624	LEU	LEU
I1285	M1225	V1165	S1105	L1045	F985	Q925	M865	L805	PHE	PHE	Y625	LEU	LEU
C1286	M1226	L1166	Q1106	Y1046	F986	N926	L866	E806	ARG	ARG	T626	SER	SER
F1287	L1227	V1167	Q1107	Q1047	Y987	H927	Y867	L807	ASP	ASP	L627	GLY	GLY
F1288	S1228	V1168	W1108	Y1048	K988	L928	Q868	H808	GLY	GLY	W628	GLY	GLY
F1289	L1229	V1169	Q1109	L1049	F989	Q929	Q869	W809	GLN	GLN	R629	GLU	GLU
L1290	L1230	F1170	W1110	L1050	G990	I930	K870	F810	SER	SER	K630	THR	THR
L1291	S1231	V1171	F1111	C1051	L991	L931	I871	K811	MET	MET	L631	LEU	LEU
L1292	C1232	A1172	S1112	L1052	E992	L932	W872	L812	ASP	ASP	P632	LEU	LEU
Q1293	V1233	A1173	A1113	G1053	I993	L933	M873	W813	PRO	PRO	P633	GLY	GLY
R1294	F1234	A1174	A1114	M1054	C994	G934	P874	A814	HIS	HIS	P634	PRO	PRO
R1295	V1235	T1175	R1115	P1055	F995	Y935	H875	L815	GLN	GLN	G694	GLN	GLN
I1296	E1236	R1176	T1116	P1056	L996	F936	W876	L816	ALA	ALA	F695	ALA	ALA
F1297	Q1237	I1177	E1117	A1057	M997	E937	TYR	T817	THR	THR	F696	THR	THR
M1298	M1238	S1178	A1118	L1058	A998	E938	SER	W818	VAL	VAL	L638	GLN	GLN
S1299	Q1239	I1179	W1119	C1059	V999	V939	SER	W819	PRO	PRO	W639	PRO	PRO
H1300	S1240	F1180	Q1120	I1060	M1000	V940	C881	W820	GLU	GLU	V640	GLY	GLY
Y1301	M1241	G1181	R1121	D1061	V1001	Y941	T882	A821	THR	THR	A641	ALA	ALA
F1302	F1242	L1182	M1122	Y1062	I1002	R942	E883	L822	ALA	ALA	I701	ALA	ALA
L1303	C1243	G1183	A1123	P1063	G1003	R943	P884	K823	SER	SER	L702	SER	SER
H1304	V1244	Y1184	G1124	W1064	Q1004	Q944	P885	E824	LYS	LYS	T642	TRP	TRP
V1305	V1245	L1185	I1125	R1065	R1005	E945	F886	W825	GLY	GLY	L645	GLY	GLY
S1306	I1246	L1186	M1126	W1066	M1006	R946	ASN	S826	VAL	VAL	Y706	VAL	VAL
A1307	Q1247	A1187	T1127	S1067	M1007	Y947	THR	W827	THR	THR	F707	THR	THR
L1308	L1248	C1188	D1128	K1068	F1008	R948	ASN	M828	ASN	ASN	A649	ALA	ALA
L1309	F1249	F1189	H1129	A1069	M1009	R949	LEU	M829	LEU	LEU	R709	LEU	LEU
K1310	S1250	Y1190	L1130	I1070	V1010	Q950	Q892	N829	LEU	LEU	W650	GLU	GLU
A1311	L1251	L1191	E1131	P1071	I1011	H951	P893	L831	LEU	LEU	F711	GLU	GLU
T1312	V1252	L1192	P1132	M1072	L1012	Q952	L894	L832	LEU	LEU	M712	HIS	HIS
A1313	C1253	L1193	L1133	M1073	H1013	Q953	E895	W833	VAL	VAL	Q713	VAL	VAL
L1314	T1254	F1194	R1134	S1074	G1014	A954	W834	L835	ALA	ALA	L714	ALA	ALA
Q1315	V1255	G1195	G1135	A1075	C1015	P955	M897	L836	THR	THR	T715	THR	THR
A1316	K1256	T1196	E1136	I1076	W1016	L956	Q898	W836	THR	THR	D716	THR	THR
S1317	G1257	T1197	P1137	I1077	L1017	P957	S899	A837	THR	THR	L717	THR	THR
L1318	Y1258	L1198	M1138	K1078	V1018	A958	L900	F838	ALA	ALA	F658	GLU	GLU
G1319	Y1259	L1199	P1139	W1079	A1019	Q959	A839	L840	ALA	ALA	VAL	VAL	VAL
F1320	D1260	Q1200	I1140	L1080	I1020	A960	L840	L840	ALA	ALA	VAL	VAL	VAL

P1261	K1201	P1141	Y1081	L1021	V961	L901	P841	ASP	PRO	GLY	Y661
K1262	D1202	N1141	L1082	T1022	C962	Y902	Y842	R782	PRO	ARG	W662
E1263	T1203	F1143	P1083	R1023	A963	R903	P843	L783	PRO	LEU	R663
M1264	R1204	I1144	D1084	R1024	D964	G904	R844	L784	THR	ARG	M664
M1265	A1205	H1145	F1085	R1025	G965	P905	P845	D785	ARG	HIS	L665
T1266	Q1206	C1146	F1086	R1026	T966	Y906	R846	L786	PRO	GLN	T666
R1267	L1207	R1147	R1087	E1027	R967	D907	P847	A787	ARG	ARG	G667
D1268	V1208	S1148	A1088	A1028	Q968	P908	M848	A788	TRP	ALA	F668
R1269	L1209	Y1149	P1089	R1029	R969	A909	A849	S789	ALA	HIS	T669
D1270	W1210	L1150	M1090	A1030	L970	N910	S850	F790	ARG	ALA	Y610
C1271	D1211	D1151	S1091	R1031	D971	W911	C851	S791	GLN	ALA	M611
L1272	C1212	M1152	T1092	L1032	Q972	F912	L852	A792	ASP	ALA	F612
L1273	L1213	L1153	M1093	W1033	D973	G913	S853	V793	VAL	VAL	L613
P1274	I1214	K1154	L1094	P1034	L974	V914	T854	L794	SER	GLU	F614
V1275	L1215	V1155	I1095	M1035	L975	R915	W855	T795	GLU	ALA	L615
E1276	Y1216	A1156	S1096	Y1036	S976	K916	W856	R796	ALA	ALA	L616
E1277	M1217	V1157	D1097	C1037	C977	G917	T857	I797	PRO	ASP	C617
A1278	V1218	F1158	F1098	L1038	L978	Y918	C858	Q798	LEU	LEU	L618
G1279	T1219	R1159	F1099	F1039	K979	P919	I859	V799	GLU	THR	T619
I1280	Y1220	Y1160	L1100	L1040	Y980	N920	I860	F800	HIS	THR	L620
I1281	I1221	L1161	L1101	T1041	F981	R921	I861	W801	GLN	GLN	F621
W1282	I1222	F1162	L1102	L1042	I982	G922	V862	R802	GLU	GLU	Q622
D1283	S1223	W1163	C1103	F1043	N983	Y923	C863	R803	GLU	THR	V623
S1284	K1224	L1164	A1104	L1044	F984	I924	K864	L804	GLU	THR	Y624
I1285	M1225	V1165	S1105	L1045	F985	Q925	M865	L805	VAL	LEU	Y625
C1286	M1226	L1166	Q1106	Y1046	F986	N926	L866	E806	PHE	ARG	E626
F1287	L1227	V1167	Q1107	Q1047	Y987	H927	Y867	L807	ASP	GLU	L627
F1288	S1228	V1168	W1108	Y1048	K988	L928	Q868	H808	GLY	GLY	W628
F1289	L1229	V1169	Q1109	L1049	F989	Q929	L869	W809	GLN	GLN	R629
L1290	L1230	F1170	W1110	L1050	G990	I930	K870	F810	SER	THR	K630
L1291	S1231	V1171	F1111	C1051	L991	L931	I871	K811	ASP	ASP	L631
L1292	C1232	A1172	S1112	L1052	E992	L932	V872	L812	GLY	GLY	L632
Q1293	V1233	L1173	A1113	G1053	I993	L933	M873	W813	PRO	HIS	R633
R1294	F1234	A1174	E1114	M1054	C994	R934	P874	A814	PRO	GLN	F634
R1295	V1235	T1175	R1115	P1055	F995	Y935	H875	L815	ALA	ALA	F635
I1296	E1236	R1176	T1116	P1056	L996	F936	W876	L816	THR	THR	W636
F1297	Q1237	I1177	E1117	A1057	M997	E937	TYR	T817	VAL	GLN	W637
M1298	M1238	S1178	A1118	L1058	A998	E937	SER	W818	PRO	VAL	L638
S1299	Q1239	I1179	W1119	C1059	V999	Y939	SER	W819	PRO	GLU	W639
H1300	S1240	F1180	Q1120	I1060	M1000	V940	C881	W820	GLY	GLY	V640
Y1301	M1241	G1181	R1121	D1061	V1001	Y941	T882	A821	THR	ALA	A641
F1302	F1242	L1182	M1122	Y1062	I1002	R942	E883	L822	ALA	ALA	I701
L1303	C1243	G1183	A1123	P1063	G1003	R943	P884	K823	SER	LYS	L702
H1304	V1244	Y1184	G1124	W1064	Q1004	Q944	F885	E824	TRP	TRP	T642
V1305	V1245	L1185	I1125	R1065	R1005	E945	F886	W825	GLY	GLY	L645
S1306	I1246	L1186	M1126	W1066	M1006	R946	ASN	S826	VAL	VAL	W646
A1307	Q1247	A1187	T1127	S1067	M1007	Y947	THR	W827	GLY	VAL	L647
L1308	L1248	C1188	D1128	K1068	F1008	R948	ASN	M828	PRO	ALA	I648
L1309	F1249	F1189	H1129	A1069	M1009	R949	LEU	M829	GLU	GLY	A649
K1310	S1250	Y1190	L1130	I1070	V1010	Q950	Q892	R829	THR	THR	W650
A1311	L1251	L1191	E1131	P1071	I1011	H951	P893	L831	LEU	LEU	R651
T1312	V1252	L1192	P1132	M1072	L1012	Q952	L894	L832	GLY	GLY	T652
A1313	C1253	L1193	L1133	M1073	H1013	Q953	E895	W833	VAL	VAL	F653
L1314	T1254	F1194	R1134	S1074	G1014	A954	W834	V834	TRP	TRP	Q654
Q1315	V1255	G1195	G1135	A1075	C1015	P955	M897	L835	GLY	GLY	F655
A1316	K1256	T1196	A1136	L1076	W1016	L956	Q898	W836	LEU	LEU	Q656
S1317	G1257	T1197	P1137	I1077	L1017	P957	S899	A837	VAL	VAL	D657
R1318	Y1258	L1198	N1138	K1078	V1018	A958	L900	F838	ALA	ALA	F658
G1319	Y1259	L1199	P1139	W1079	A1019	Q959	A839	L840	ALA	ALA	P659
F1320	D1260	Q1200	I1140	L1080	I1020	A960	L840	L840	ALA	ALA	T660

H2116	V2054	I1992	SER	VAL	GLU	G1750	L1690	G1570	GLN	GLN	Q1510	GLN	SER	PRO	A1321
L2117	V2055	F1993	LYS	ILE	ASP	F1751	C1691	P1571	THR	VAL	A1511	THR	PRO	PRO	L1322
N2118	V2056	G1994	ARG	GLN	TYR	F1752	Y1692	V1572	GLN	LEU	T1512	VAL	PRO	ARG	V1323
L2119	A2056	G1994	ARG	ASP	GLU	F1753	F1693	E1573	LEU	ARG	V1513	ARG	ARG	ARG	N1324
F2120	I2057	F1995	PRO	PRO	PRO	P1753	F1694	R1574	LEU	GLN	D1514	GLN	TRP	TRP	A1325
L2121	H2058	M1996	GLU	GLU	ASP	W1754	I1695	T1575	ALA	ARG	G1515	ARG	ALA	ALA	I1326
F2130	I2059	PHE	HIS	ASP	HIS	M1755	I1696	D1576	ASN	ALA	G1516	ARG	ALA	ALA	N1327
L2131	W2060	GLY	LYS	LYS	CYS	S1756	I1697	G1577	ALA	ARG	L1517	GLU	ALA	ALA	L1328
L2132	M2061	LYS	PRO	PRO	PRO	V1757	L1697	P1578	ARG	ALA	L1518	ARG	ALA	ALA	K1329
F2062	F2062	HIS	ARG	ARG	ARG	V1758	M1698	SER	THR	ARG	R1518	ARG	ALA	ALA	K1330
F2063	F2063	ARG	VAL	VAL	VAL	V1759	L1699	P1578	MET	ARG	W1519	GLN	ASP	ASP	S1331
E2133	I2064	ALA	THR	THR	LYS	L1760	M1700	THR	ARG	ALA	L1520	GLU	HIS	HIS	I1331
W2138	L2065	THR	GLN	ARG	ASP	R1761	V1701	ALA	THR	ALA	R1521	ARG	ALA	ALA	N1332
T2143	PRO	ASP	SER	HIS	ARG	R1762	I1702	SER	THR	ALA	A1522	ARG	THR	THR	N1332
D2144	ALA	ILE	GLU	ILE	GLU	V1763	A1703	GLY	ALA	ALA	F1523	GLN	VAL	VAL	F1333
T2145	THR	VAL	ALA	SER	ALA	E1764	A1704	LEU	GLU	GLN	A1524	GLN	ILE	ILE	H1334
T2146	GLU	SER	VAL	ARG	LYS	N1765	S1704	ALA	LEU	LEU	T1524	ALA	HIS	HIS	R1335
N2151	LEU	SER	ARG	PHE	GLU	N1766	A1705	GLY	ALA	ALA	K1525	SER	GLY	GLY	Q1336
W2152	ALA	Q1952	ALA	ARG	PRO	P1767	A1706	GLU	LEU	GLU	H1526	GLY	ASP	ASP	I1337
E2172	SER	S1953	ALA	ARG	ALA	Y1768	S1707	PRO	PRO	ASP	H1527	GLY	TYR	TYR	E1338
Q2075	Q2075	F1954	LYS	ARG	LYS	F1769	L1708	LEU	LEU	LEU	R1528	LEU	PHE	PHE	E1339
N2076	N2076	Y1955	LEU	GLU	LEU	P1770	V1709	SER	SER	ASN	T1529	ASN	PHE	PHE	K1340
A2077	A2077	Y1956	GLU	THR	GLU	P1771	L1710	THR	THR	GLU	M1530	PRO	GLU	GLU	S1341
V2078	V2078	Q1956	GLN	PRO	GLY	R1772	P1711	MET	THR	ASP	S1531	ASP	SER	SER	L1342
A2079	A2079	P1957	PRO	PRO	PRO	I1773	V1712	ASP	ASP	VAL	D1532	VAL	ASP	ASP	L1343
Q2080	Q2080	L1958	LYS	LYS	LYS	I1774	L1713	THR	THR	GLU	V1533	PRO	SER	SER	A1343
L2081	L2081	Q1959	GLY	GLY	THR	G1775	V1714	SER	SER	VAL	L1534	VAL	GLU	GLU	Q1344
W2082	W2082	R1960	THR	VAL	ALA	L1776	F1715	SER	SER	VAL	C1535	ASP	GLU	GLU	L1345
F2084	F2084	F1961	VAL	VAL	THR	E1777	L1716	PRO	PRO	VAL	A1536	ASP	GLU	GLU	L1346
V2085	V2085	F1962	HIS	MET	HIS	E1778	W1717	LEU	LEU	LEU	E1537	ASP	ALA	ALA	R1347
K2086	K2086	D1963	GLU	THR	GLU	I1779	A1718	THR	THR	GLU	R1538	ASP	LEU	LEU	E1357
C2087	C2087	I1964	THR	GLU	LYS	T1779	M1719	GLY	GLY	GLU	Y1539	GLU	PRO	PRO	E1357
I2088	I2088	I1965	GLU	HIS	PRO	D1780	L1720	THR	THR	MET	R1540	GLU	GLU	GLU	R1360
Y2089	Y2089	L1966	GLU	GLU	VAL	S1781	I1721	ASN	ASN	ALA	L1540	ALA	ASP	ASP	Q1361
F2090	F2090	L1967	GLY	GLY	ALA	I1782	T1722	THR	THR	GLY	L1541	ALA	PRO	PRO	S1362
A2091	A2091	T1968	GLY	GLY	ALA	N1783	P1723	ARG	ARG	ARG	T1542	ARG	ARG	ARG	Q1363
S2093	S2093	K1969	THR	THR	THR	K1784	R1724	GLY	GLY	ALA	Q1543	ALA	ALA	ALA	S1364
A2094	A2094	Y1970	LYS	LYS	PRO	Y1785	R1725	SER	SER	GLN	E1544	GLN	ALA	ALA	S1365
Y2095	Y2095	R1971	ARG	ARG	ARG	D1786	P1726	GLU	GLU	GLU	L1545	SER	GLN	GLN	ARG
Q2096	Q2096	A1972	ASP	ASP	ASP	L1787	S1726	LEU	LEU	LEU	L1546	ALA	ALA	ALA	GLY
I2097	I2097	I1973	ILE	ILE	ILE	V1788	K1727	VAL	VAL	VAL	R1547	PHE	PHE	PHE	LEU
R2098	R2098	T1974	ARG	ARG	ARG	Q1789	R1728	THR	THR	THR	V1548	GLN	GLN	GLN	LEU
G2100	G2100	D1975	GLY	GLY	GLY	L1790	F1729	ASP	ASP	ASP	G1549	ALA	ALA	ALA	LYS
Y2101	Y2101	V1976	PRO	PRO	PRO	M1791	W1730	ALA	ALA	ALA	E1550	TYR	TYR	TYR	ASP
R2104	R2104	I1979	GLY	GLY	GLY	A1792	M1731	GLY	GLY	GLY	V1551	GLN	GLN	GLN	PRO
I2105	I2105	M1980	ILE	ILE	ILE	L1793	I1732	ASP	ASP	ASP	R1552	ALA	ALA	ALA	PRO
L2106	L2106	A1983	ARG	ARG	ARG	F1794	A1733	GLN	GLN	GLN	G1553	VAL	VAL	VAL	TRP
G2107	G2107	D1984	SER	SER	SER	P1795	I1734	GLY	GLY	GLY	G1554	THR	THR	THR	ASP
F2109	F2109	I1988	LYS	LYS	LYS	H1796	V1735	THR	THR	THR	V1555	F1504	F1504	F1504	PRO
K2112	K2112	V2051	ASP	ASP	ASP	R1797	F1736	SER	SER	SER	L1556	W1506	W1506	W1506	GLN
K2113	K2113	V2052	HIS	HIS	HIS	R1797	T1737	LEU	LEU	LEU	D1557	W1507	W1507	W1507	GLY
Y2114	Y2114	L2053	LYS	LYS	LYS	Q1798	E1738	HIS	HIS	HIS	Q1558	L1508	L1508	L1508	PRO
N2115	N2115	L2053	LYS	LYS	LYS	Q1799	I1739	ALA	ALA	ALA	Q1559	G1509	G1509	G1509	ASP
						L1800	A1684	ALA	ALA	ALA	Y1560	ASP	ASP	ASP	PRO
						L1801	A1685	ALA	ALA	ALA	V1561	GLY	GLY	GLY	SER
						L1802	H1686	ALA	ALA	ALA	G1562	GLY	GLY	GLY	PRO
						L1803	S1687	ALA	ALA	ALA	E1563	GLY	GLY	GLY	GLY
						G1804	E1688	ALA	ALA	ALA	D1564	GLY	GLY	GLY	SER
						L1805	E1688	ALA	ALA	ALA	E1565	GLY	GLY	GLY	GLY
						W1806	E1688	ALA	ALA	ALA	T1567	GLY	GLY	GLY	SER
						L1807	F1747	ALA	ALA	ALA	L1568	GLY	GLY	GLY	SER
						HIS	F1748	ALA	ALA	ALA	S1569	GLY	GLY	GLY	SER
						GLU	F1749	ALA	ALA	ALA					



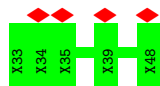
- Molecule 2: Piezo-type mechanosensitive ion channel component 1, unknown fragment



- 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	0.35	0/12117	0.59	0/16473
1	C	0.35	0/12117	0.59	0/16473
1	E	0.34	0/12117	0.59	0/16473
All	All	0.35	0/36351	0.59	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	118	0
1	C	11826	0	11563	119	0
1	E	11826	0	11563	122	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	333	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 333 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%)	92	96
1	C	1198/2246 (53%)	1195 (100%)	3 (0%)	92	96
1	E	1198/2246 (53%)	1195 (100%)	3 (0%)	92	96

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	3594/6738 (53%)	3585 (100%)	9 (0%)	92 96

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

Mol	Chain	Res	Type
1	E	1547	ARG
1	E	1971	ARG
1	C	903	ARG
1	C	1547	ARG
1	C	1971	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	1047	GLN
1	C	2050	GLN
1	E	2050	GLN
1	E	944	GLN
1	A	1669	GLN

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 monosaccharides 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.

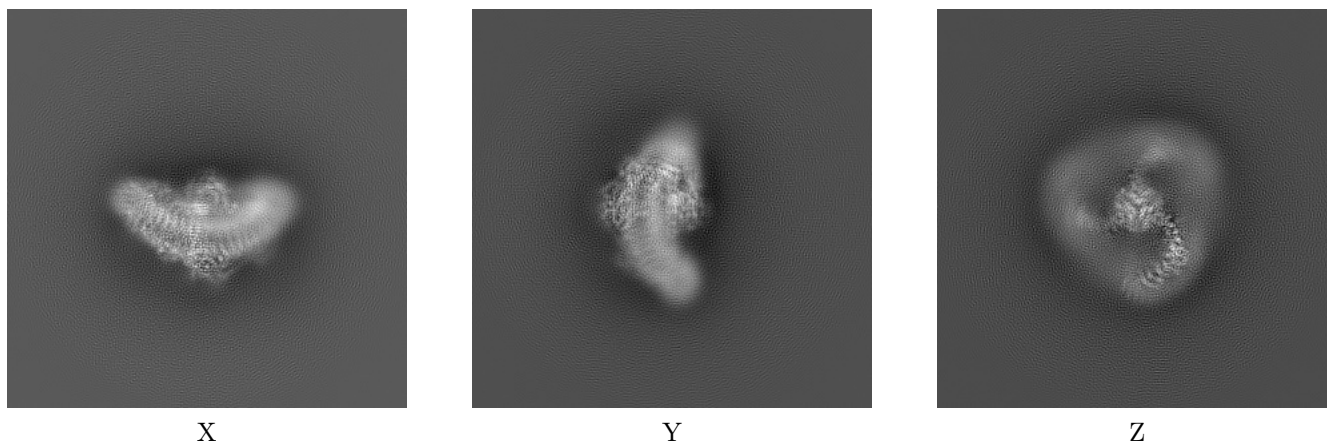
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-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](#)

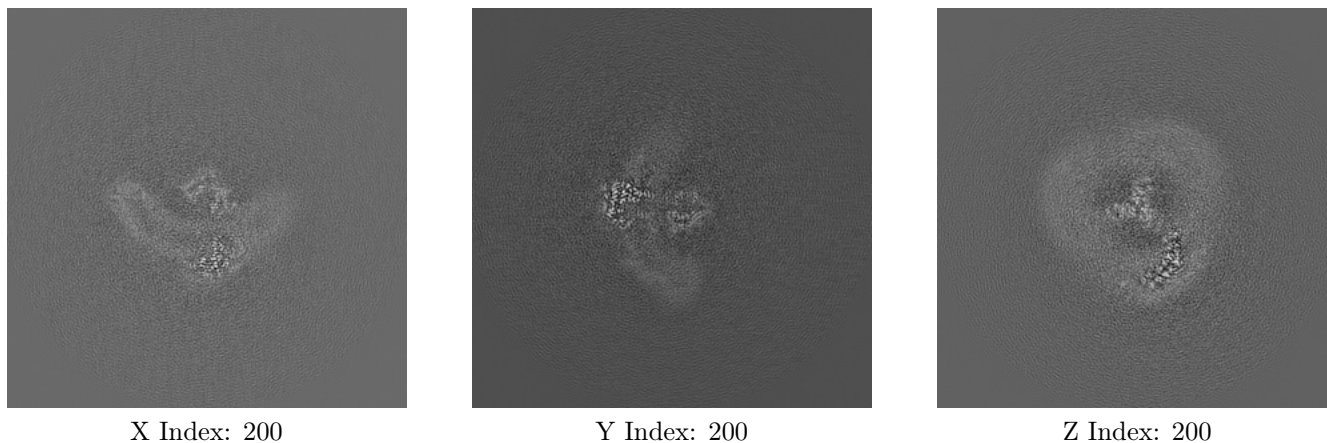
6.1.1 Primary map



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

6.2 Central slices [i](#)

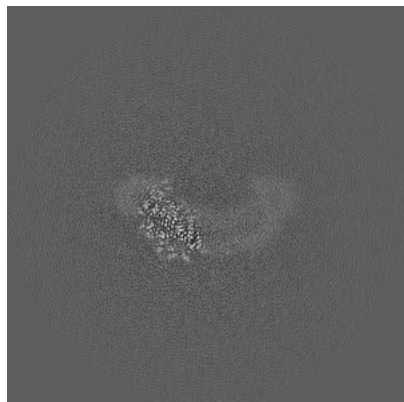
6.2.1 Primary map



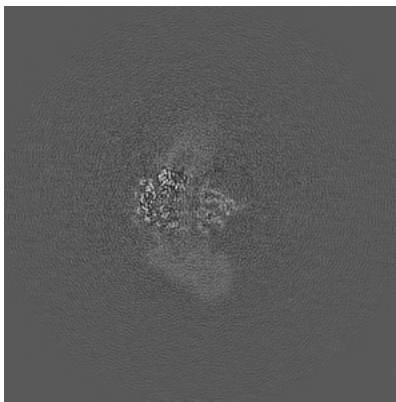
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

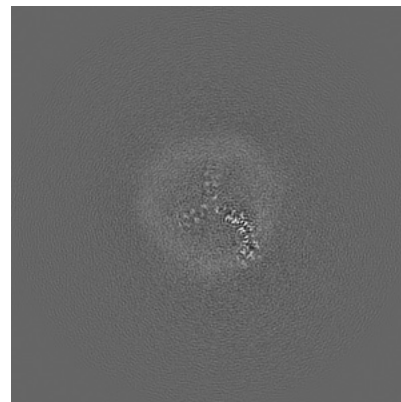
6.3.1 Primary map



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 surface views [i](#)

6.4.1 Primary map



X



Y



Z

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.

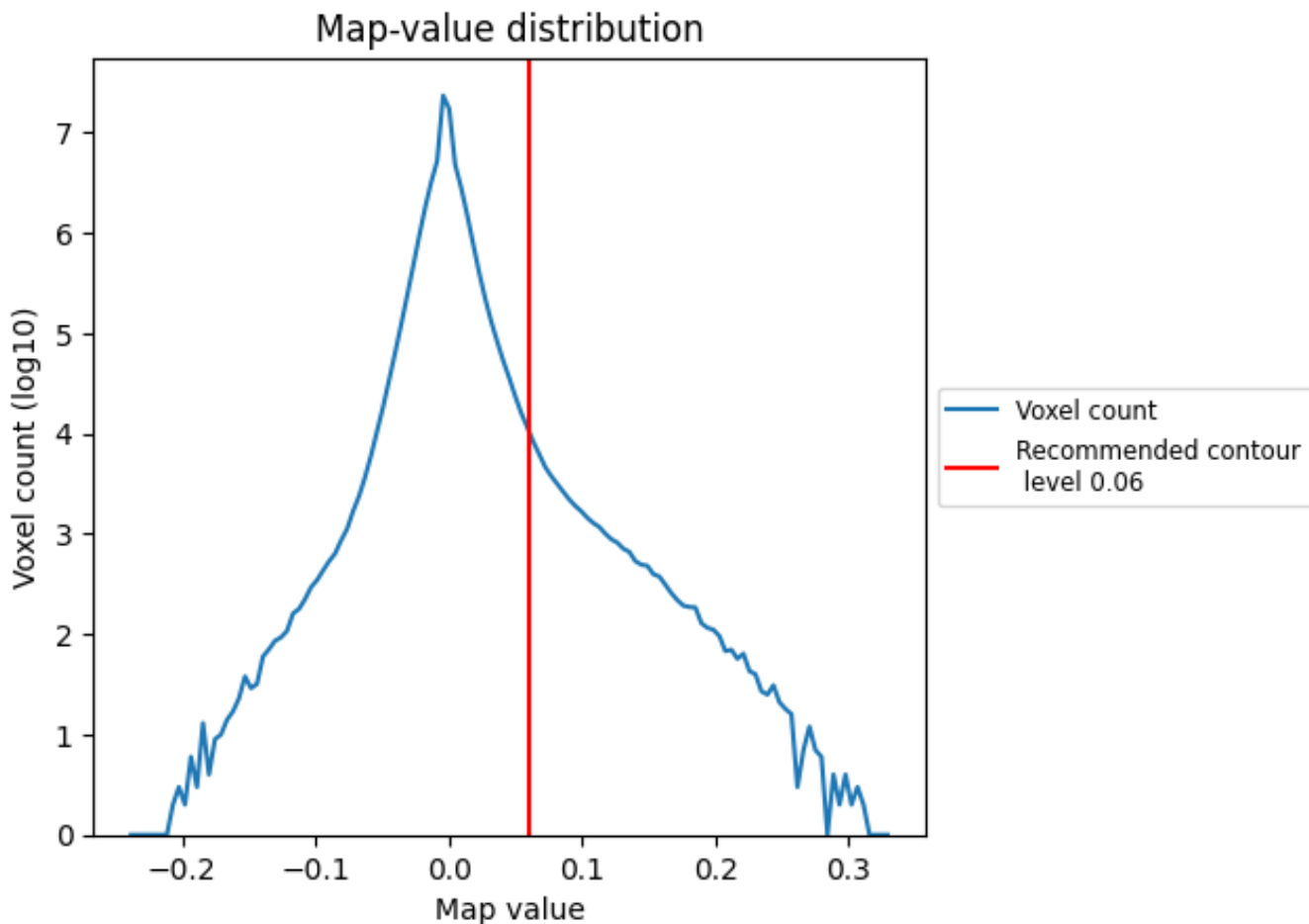
6.5 Mask visualisation

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

7 Map analysis [i](#)

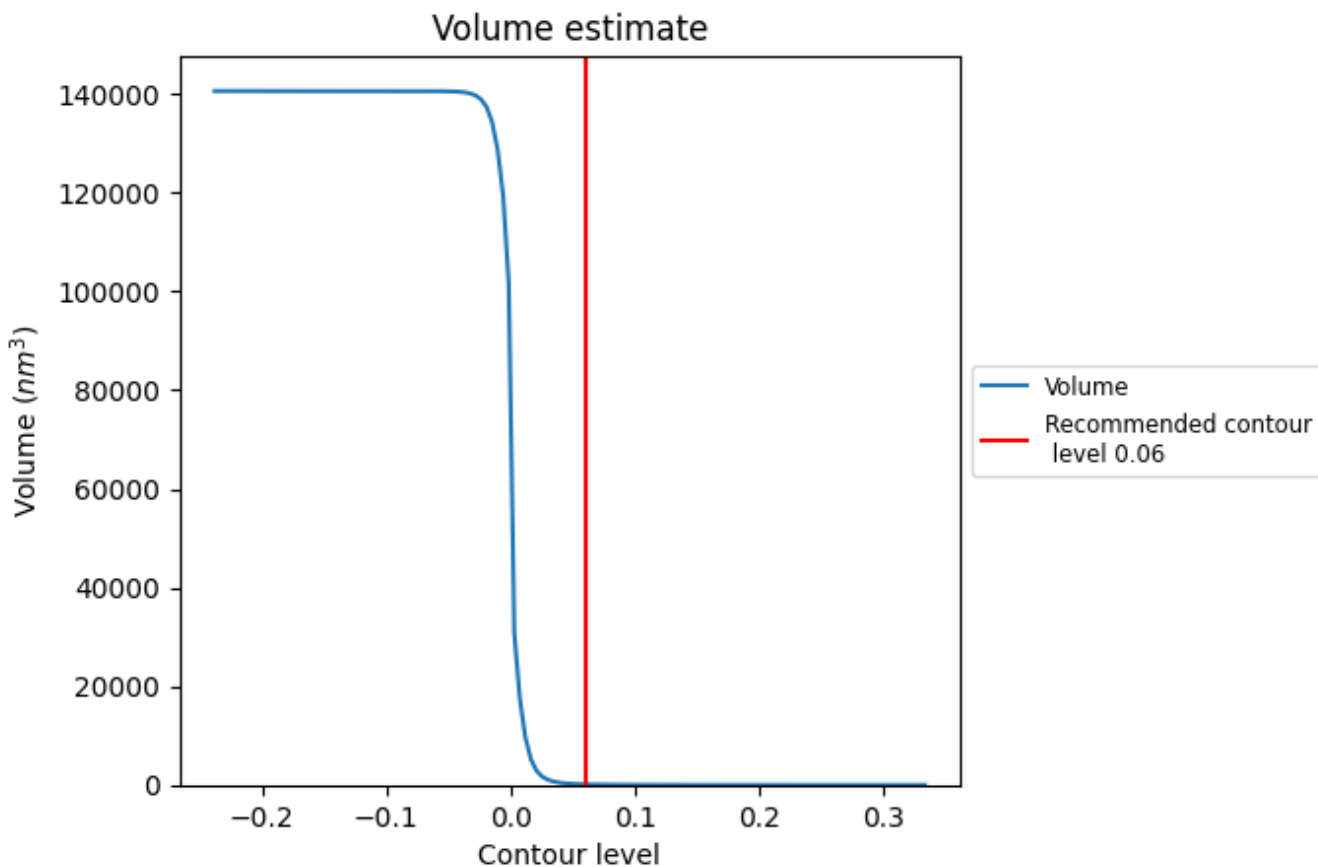
This section contains the results of statistical analysis of the map.

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.

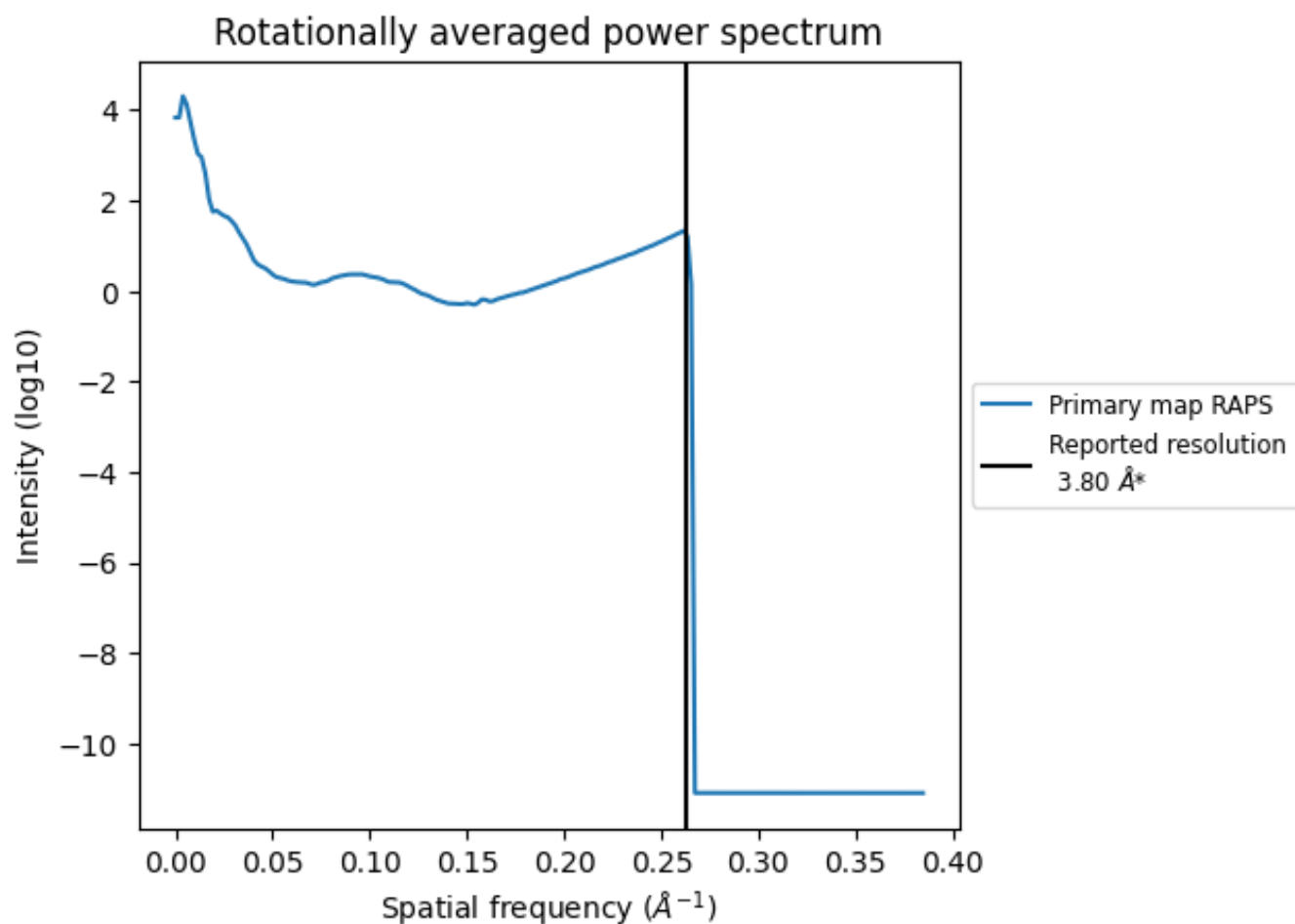
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 123 nm³; 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 [\(i\)](#)



*Reported resolution corresponds to spatial frequency of 0.263\AA^{-1}

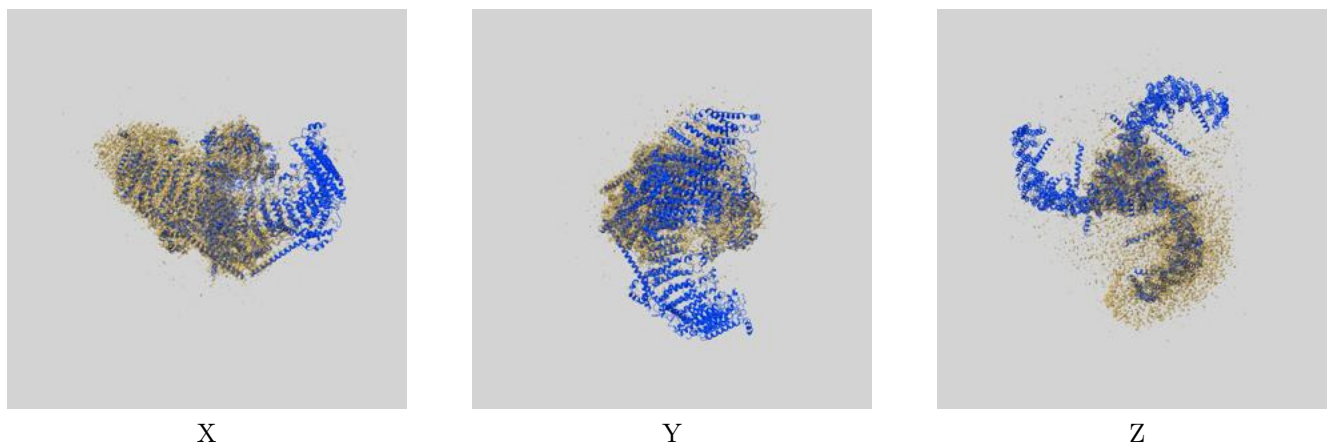
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

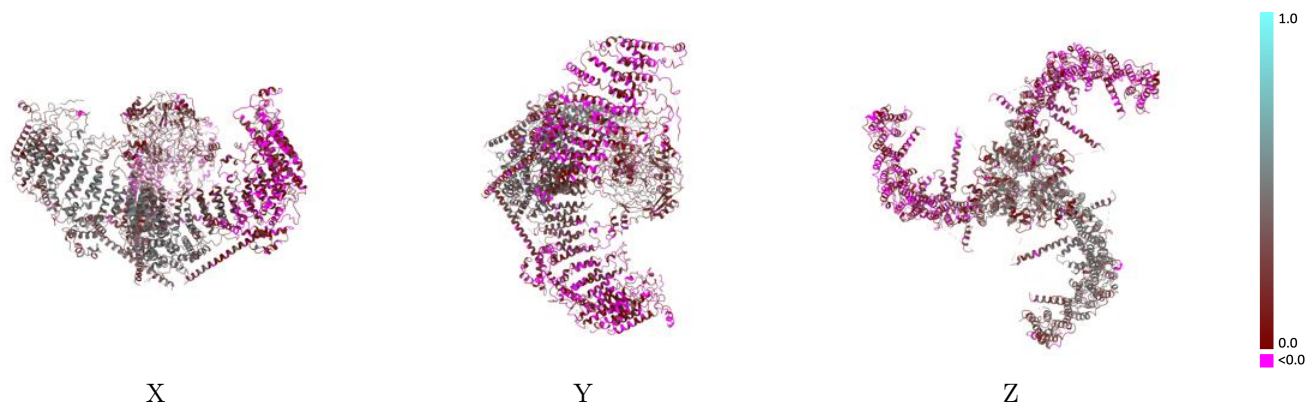
This section contains information regarding the fit between EMDB map EMD-7042 and PDB model 6B3R. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)



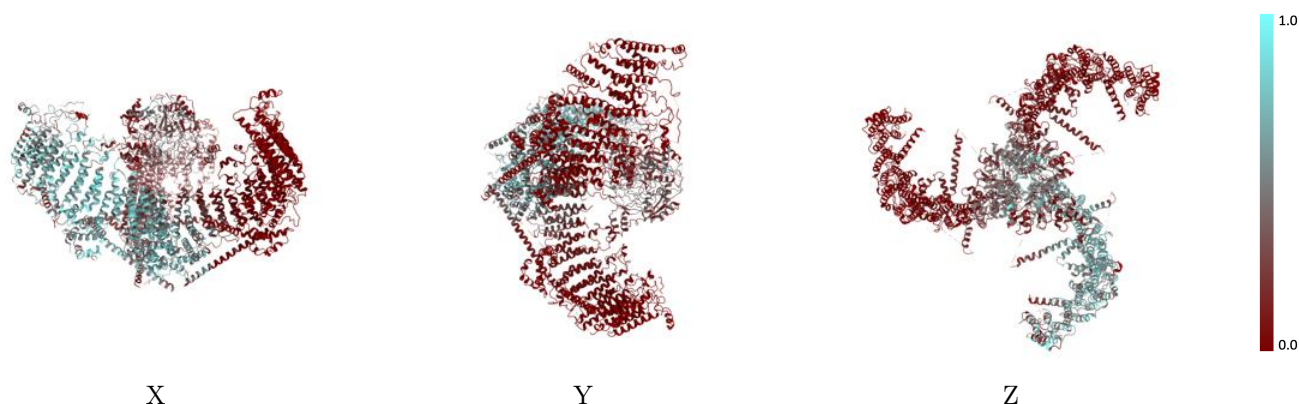
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



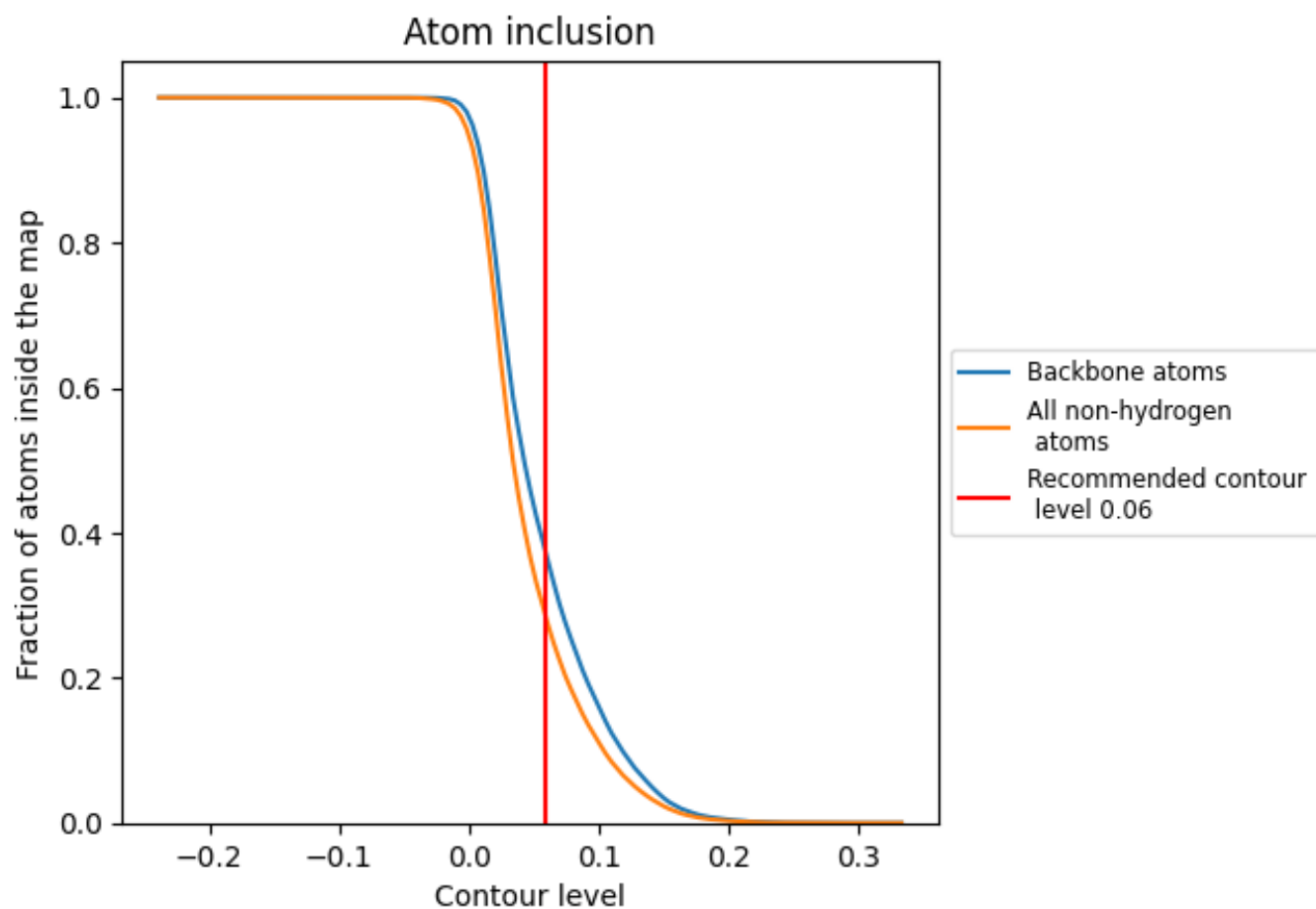
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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	 0.2806	 0.2360
A	 0.5392	 0.3720
B	 0.7250	 0.4520
C	 0.1472	 0.1650
D	 0.6875	 0.4410
E	 0.1473	 0.1660
F	 0.6250	 0.4110

