



wwPDB EM Validation Summary Report ⓘ

Nov 6, 2022 – 01:19 PM EST

PDB ID : 6MJ2
EMDB ID : EMD-9134
Title : Human TRPM2 ion channel in a calcium- and ADPR-bound state
Authors : Wang, L.; Fu, T.M.; Xia, S.; Wu, H.
Deposited on : 2018-09-20
Resolution : 6.36 Å(reported)

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<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

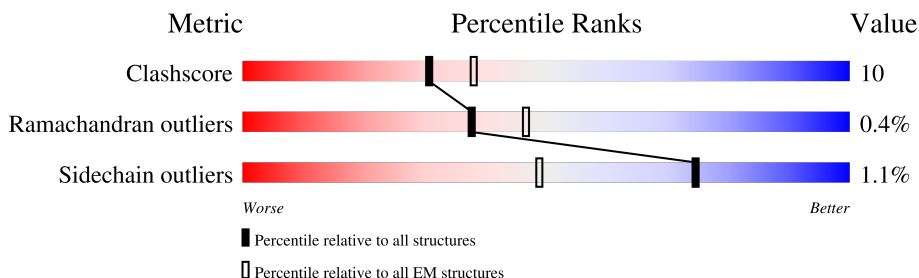
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.36 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	1503	84%
1	B	1503	89%
1	C	1503	89%
1	D	1503	88%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 43124 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.

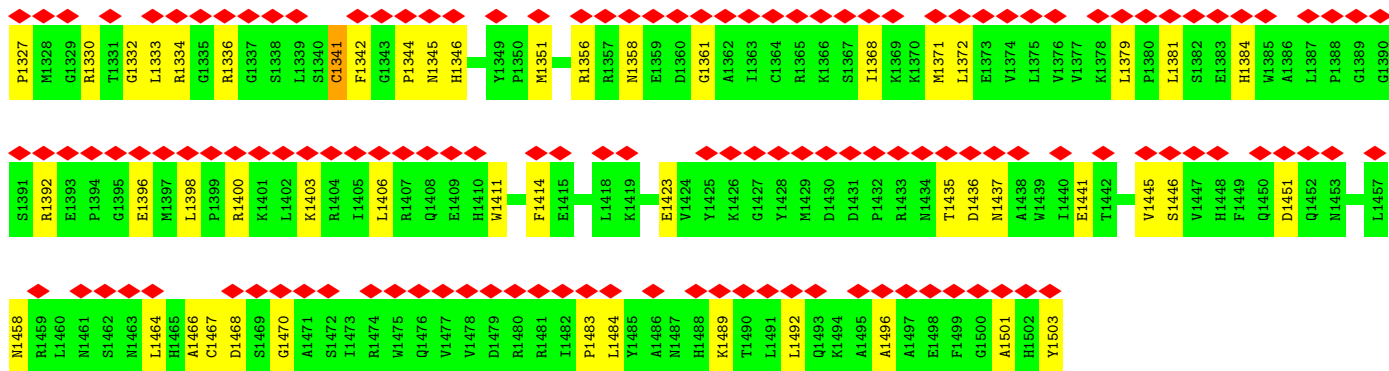
- Molecule 1 is a protein called Transient receptor potential cation channel subfamily M member 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1337	10780	6942	1865	1919	54	0	0
1	B	1337	10780	6942	1865	1919	54	0	0
1	C	1337	10780	6942	1865	1919	54	0	0
1	D	1337	10780	6942	1865	1919	54	0	0

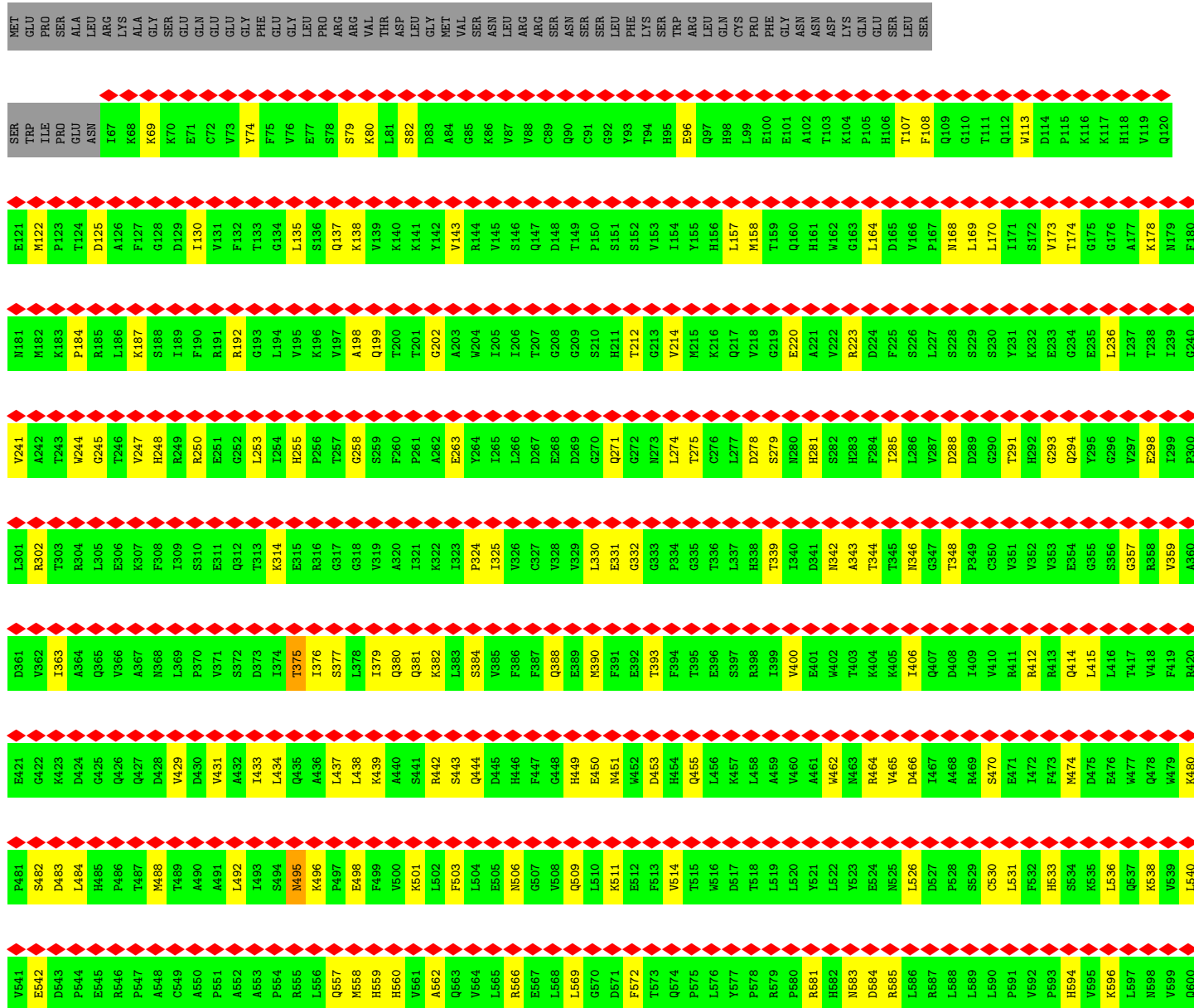
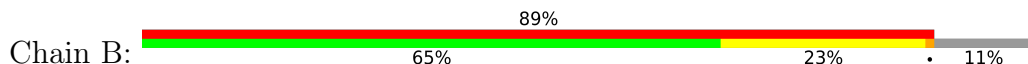
- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
			Total	Ca	
2	A	1	1	1	0
2	B	1	1	1	0
2	C	1	1	1	0
2	D	1	1	1	0

E1265	T1266	F1084	L1024	D964	M844	F784	A724	K664	L604	P544
T1266	E1267	I1085	T1025	W965	R845	A785	K725	E665	R605	E545
F1268	E1268	L1086	V1026	L966	Q846	A786	D726	E666	S806	R546
L1269	F1268	L1087	L1027	F967	L847	R787	M727	E667	L607	P547
I1270	E1148	S1088	L1028	R968	F948	A788	K728	D668	Y608	A548
Y1271	E1149	H1089	L1029	G969	Y849	R789	F729	D669	K608	C549
D1272	D1150	L1090	C1030	A970	D850	A790	V730	D670	R610	A550
P1273	I1151	Q1091	L1031	W971	P851	F791	S731	S671	S811	P551
F1274	S1152	F1093	L1032	Y972	D852	F792	H732	S672	G613	A552
F1275	K1154	L1094	L1034	H973	E853	F793	G733	E673	G613	A553
Y1276	V1155	I1095	F1035	S974	C854	A794	G734	E674	H614	P554
T1277	R1096	R1095	T1036	Y975	G855	P795	I735	M675	V615	R555
A1278	V1097	V1097	L1037	L976	L856	V796	Q736	L676	T616	L556
E1279	V1098	T977	M1037	M857	L856	V797	A737	E677	F617	Q557
R1280	L1099	Y978	I1038	K958	K958	V798	F738	L678	T618	M558
K1281	K1100	F979	L1039	K859	K859	F799	F739	A679	M619	H559
D1282	T1101	G980	L1040	G860	G860	H800	T740	E680	D620	H560
A1283	P1102	Q981	L1041	A861	A861	L801	K741	E681	P621	V561
D1287	A1103	I982	M1042	L862	L862	N802	V742	E682	I622	A562
P1288	K1104	P983	L1043	Y863	Y863	I803	M743	E683	R623	Q563
M1289	R1105	G984	L1044	F864	F864	L804	W744	H884	D624	V564
G1290	H1106	Y985	I1045	S865	S865	S805	G745	E685	L625	L565
D1291	K1107	I986	A1046	D866	D866	Y806	Q746	A686	L626	R566
L1293	Q1108	D987	M1047	F867	F867	F907	L747	I687	I627	E567
E1294	L1109	G988	F1048	M868	M868	A808	S748	G688	W628	L568
P1295	K1110	R929	N1050	N869	N869	F909	V749	V689	A629	L569
L1296	M1111	W930	T1051	K970	K970	L810	D750	I630	I630	G570
S1297	L1113	PHE	F1052	L871	L871	C811	N751	F631	D571	D571
N1298	E1114	ASN	Q1053	D872	D872	C811	G752	Q632	F572	F572
A1242	K1115	GLU	Q1054	V873	V873	F813	L753	N633	T573	T573
R1243	M1116	HIS	Q1054	G874	G874	A814	W754	R634	Q574	Q574
L1244	E1117	CYS	Q1055	A875	A875	Y815	R755	R635	P575	P575
L1245	E1118	SER	Q1056	I876	I876	W816	V756	E636	L576	L576
L1246	A1119	ASN	Q1057	L877	L877	V817	F757	K697	Y577	Y577
Y1247	A1120	GLY	H1058	L878	L878	M818	L758	A638	P578	P578
P1248	A1121	THR	T1059	F879	F879	V819	C759	G639	R579	R579
N1249	L1121	PRO	D1060	N880	N880	D820	M760	I640	I640	I640
C1250	L1122	TYR	Q1061	G881	G881	F821	A761	R700	I641	P580
V1251	S1123	LYS	I1062	G882	G882	Q822	A762	A701	I641	P580
V1252	W1124	PRO	W1063	L883	L883	P823	F763	Q702	W642	H582
T1253	E1125	CYS	W1064	T884	T884	V824	W764	K703	A643	N583
R1254	I1126	PRO	F1065	C885	C885	P825	L765	L704	Q644	D584
F1255	Y1127	GLU	Q1066	R886	R886	S826	L766	L705	S645	R585
F1256	L1128	SER	Q1067	L887	L887	S826	L766	T706	Q646	L586
P1257	K1129	ASP	R1068	S887	S887	W827	L767	R707	D647	R587
P1258	E1130	ALA	H1068	I888	I888	C828	T768	V708	D648	L588
N1259	M1131	THR	D1069	F948	F948	C829	G769	I649	E649	L589
K1261	Y1132	GLN	L1070	G949	G949	E829	L770	A650	A650	L590
E1260	L1133	GLN	I1071	V950	V950	C830	I771	A651	A651	P591
L1262	Q1134	ARG	E1072	T991	T991	A831	I771	A711	A652	V592
P1263	M1135	PRO	E1073	L892	L892	I832	S772	W712	L653	P593
W1264	R1136	ALA	Y1074	G953	G953	I832	S772	G713	L653	P593
Q1320	Q1137	ALA	H1075	Q954	Q954	Y833	R774	K714	A654	H594
G1322	F1138	ALA	G1076	A954	A954	Y834	E775	K715	A654	H594
L1323	Q1139	ALA	R1077	P955	P955	W835	K776	T715	C655	V595
P1324	Q1140	ALA	P1078	L956	L956	L836	K776	T716	S656	K596
L1325	K1141	ALA	A1079	V957	V957	L836	K777	T717	K657	L597
M1326	Q1142	ALA	P1080	H958	H958	F837	L778	C717	I658	M598
	R1143	ALA	P1082	N959	N959	S838	L778	L718	L659	V599
		ALA		E960	E960	L839	Q779	Q719	K660	Q600
		ALA		R961	R961	V840	D780	L720	E661	G601
		ALA		R962	R962	C841	G782	L722	L662	V602
		ALA		V963	V963	E843	T783	E723	S663	S603

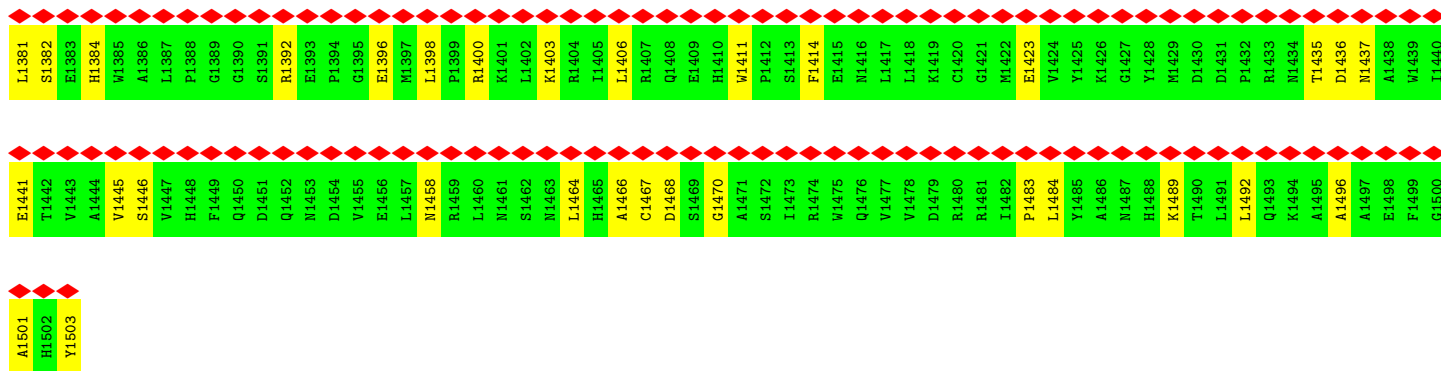


● Molecule 1: Transient receptor potential cation channel subfamily M member 2

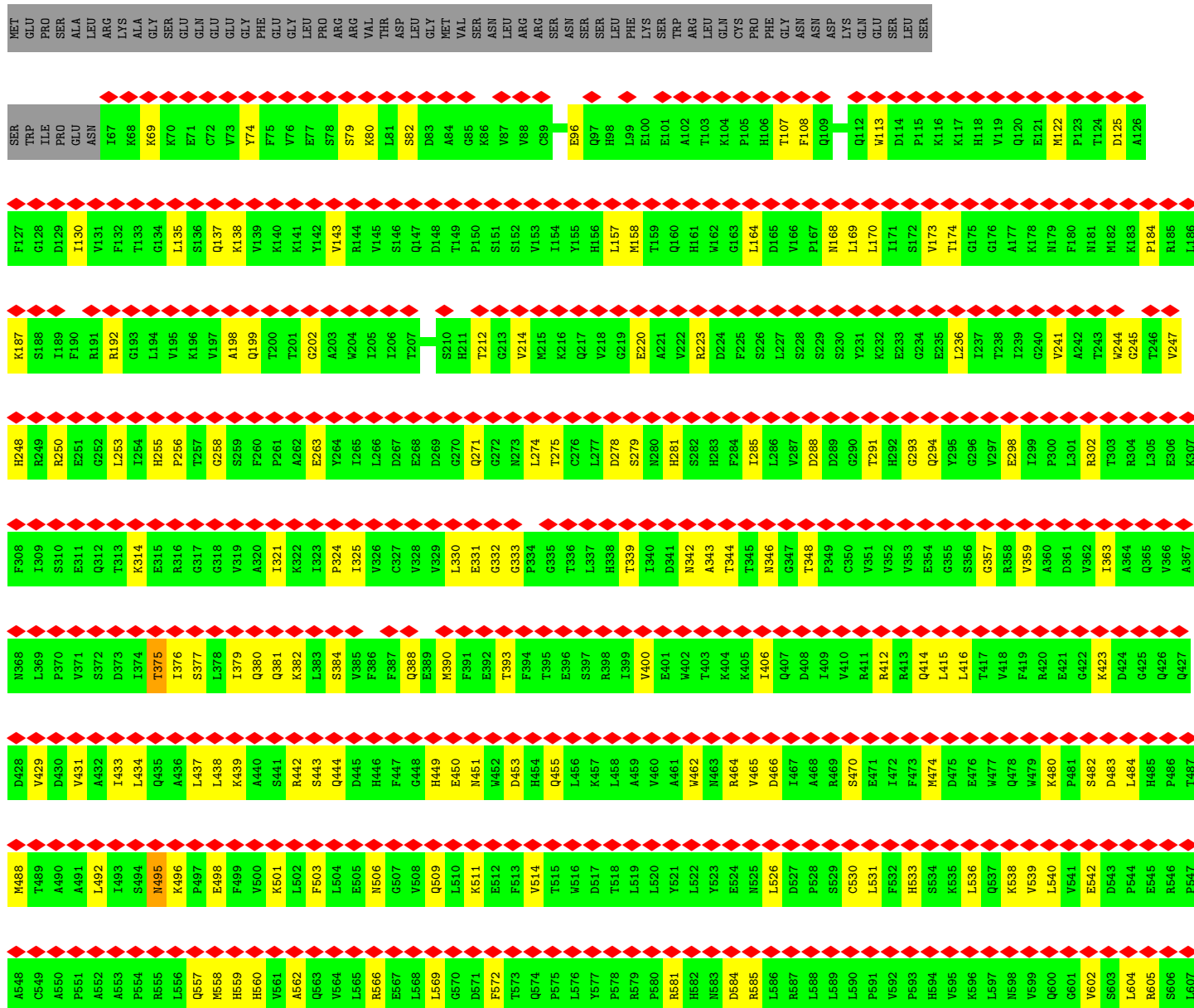
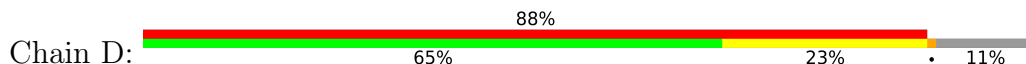


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SER	GLY	PHE	SER	GLU	ALA	ASP	PRO	THR	LEU	ALA	SER	GLN	LYS	ALA	GLU	PRO	ASP	ALA	GLU	PRO	GLY	ARG	LYS	THR	GLU	PRO	LYS	ARG	GLY	GLN	ARG	LEU	LEU	GLU	GLU	GLN	VAL	ALA	GLN	THR	ALA	GLN	LEU	HIS	TRP	ILE	VAL	ARG	THR	LEU	ARG	ALA	ALA	ALA	GLN	LEU	LEU	THR	LEU	ARG	ALA	ALA
G601	V602	S603	L604	R605	S606	L607	Y608	K609	R610	S611	S612	G613	H614	V615	T616	F617	T618	M619	D620	P621	I622	R623	D624	L625	L626	I627	W628	A629	I630	V631	G632	M633	R634	R635	E636	L637	A638	G639	I640	V641	W642	A643	Q644	S645	G646	D647	C648	I649	A650	A651	A652	L653	A654	C655	S656	K657	L658	L659	K660			
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V781	G782	T783	P784	R785	A786	R787	A788	R789	A790	F791	F792	T793	A794	F795	V796	V797	F798	A799	H800	L801	N802	I803	L804	S805	Y806	F807	A808	F809	L810	C811	L812	F813	A814	Y815	V816	L817	M818	V819	D820	F821	Q822	P823	V824	P825	S826	W827	C828	E829	G830	A831	I832	L833	L834	W835	L836	F837	L838	L839	V840			
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SER	GLY	PHE	SER	GLU	ALA	ASP	PRO	THR	LEU	ALA	SER	GLN	LYS	ALA	GLU	PRO	ASP	ALA	GLU	PRO	GLY	ARG	LYS	THR	GLU	PRO	LYS	ARG	GLY	GLN	ARG	LEU	LEU	GLU	GLU	GLN	VAL	ALA	GLN	THR	ALA	GLN	LEU	HIS	TRP	ILE	VAL	ARG	THR	LEU	ARG	ALA	ALA									
G1235	D1236	S1237	L1238	H1239	V1240	N1241	A1242	R1243	H1244	L1245	L1246	Y1247	N1249	C1250	P1251	V1252	T1253	R1254	F1255	P1256	V1257	P1258	M1259	E1260																																						

G601	G602	S603	L604	R605	G606	L607	Y608	K609	R610	S611	S612	G613	H614	V615	T616	F617	T618	M619	D620	P621	E622	R623	D624	L625	L626	L627	W628	A629	I630	V631	G632	M633	R634	R635	E636	L637	A638	G639	I640	I641	W642	A643	Q644	S645	Q646	D647	C648	I649	A650	A651	A652	L653	A654	C655	S656	K657	I658	L659	K660	
E661	L662	S663	K664	E665	E666	D668	T669	D670	S671	S672	E673	E674	M675	L676	A677	A678	A679	E680	E681	E682	E683	H684	R685	A686	I687	G688	F689	T691	E692	C693	G694	R695	K696	D697	E698	E699	R700	A701	A702	K703	L704	L705	Q706	R707	V708	S709	A710	A711	A712	G713	A714	T715	T716	K717	L718	Q719	L720			
A721	L722	E723	A724	K725	M727	K728	F729	V730	S731	H732	G733	I735	Q736	A737	L738	L739	T740	K741	E742	E743	H744	R685	Q745	L747	S748	V749	D750	N751	G752	L753	A754	R755	V756	L757	L758	C759	M760	L761	A762	F763	P764	L765	L766	L767	T768	G769	L770	I771	S772	F773	E775	K776	L777	L778	Q779	D780				
V781	G782	T783	P784	A785	R787	A788	R789	A790	F791	F792	T793	A794	P795	V796	V797	V798	F799	H800	L801	N802	I803	L804	S805	Y806	F807	A808	F809	L810	C811	L812	F813	A814	Y815	V816	L817	M818	V819	D820	F821	Q822	P823	V824	P825	S826	W827	C828	E829	G830	A831	I832	L833	L834	W835	L836	F837	L838	L839	V840		
C841	E842	E843	M844	R845	Q846	L847	F848	Y849	D850	P851	D852	E853	C854	G855	L856	M857	K858	K859	A860	A861	L862	Y863	F864	S865	D866	F867	W868	N869	K870	L871	D872	V873	G874	A875	I876	L877	L878	F879	V880	A881	G882	L883	T884	C885	R886	L887	I888	P889	G890	V891	T891	L892	E893	P894	E895	R896	V897	I898	L899	S900
L901	D902	F903	I904	L905	F906	C907	L908	R909	L910	M911	H912	I913	F914	T915	I916	S917	K918	T919	L920	G921	P922	K923	I924	I925	I926	V927	K928	R929	N930	M931	K932	D933	V934	F935	F936	F937	L938	F939	L940	T941	A942	L943	V944	V945	V946	S947	F948	G949	V950	A951	K952	Q953	A954	I955	L956	I957	H958	N959	E960	
R961	R962	V963	D964	W965	L966	R968	G969	A970	V971	Y972	H973	A974	Y975	L976	T977	I978	F979	G980	Q981	I982	P983	G984	Y985	I986	D987	G988	VAL	ASN	PHE	ASN	PRO	GLU	HIS	CYS	SER	PRO	ASN	GLY	THR	ASP	PRO	TYR	LYS	PRO	LYS	CYS	PRO	GLU	SER	ASP	ALA	THR	GLN	ARG	PRO	ALA	F1020			
P1021	E1022	W1023	L1024	T1025	L1027	L1028	L1029	C1030	L1031	Y1032	L1033	L1034	F1035	T1036	M1037	L1038	L1039	L1040	L1041	L1042	L1043	L1044	L1045	A1046	M1047	F1048	R1049	Y1050	T1051	F1052	Q1053	Q1054	V1055	Q1056	E1057	H1058	T1059	D1060	Q1061	I1062	W1063	K1064	F1065	Q1066	R1067	H1068	D1069	L1070	I1071	A1072	E1073	Y1074	H1075	G1076	R1077	P1078	A1079	A1080		
P1081	P1082	P1083	F1084	I1085	L1086	L1087	S1088	H1089	L1090	Q1091	L1092	F1093	I1094	K1095	R1096	V1097	V1098	L1099	K1100	T1101	P1102	A1103	K1104	R1105	H1106	K1107	Q1108	L1109	K1110	M1111	K1112	L1113	E1114	K1115	M1116	E1117	E1118	A1119	L1120	L1121	L1122	S1123	W1124	E1125	I1126	Y1127	L1128	K1129	E1130	M1131	L1132	L1133	Q1134	M1135	R1136	Q1137	F1138	Q1139	Q1140	
K1141	Q1142	R1143	P1144	E1145	Q1146	K1147	I1148	E1149	D1150	I1151	S1152	M1153	K1154	V1155	D1156	A1157	M1158	V1159	D1160	L1161	L1162	D1163	L1164	D1165	PRO	LEU	LYS	ARG	SER	GLY	GLN	ARG	LEU	ALA	SER	LEU	GLY	GLU	GLN	ALA	LEU	HIS	TRP	ILE	VAL	ARG	THR	LEU	ARG	ARG	ALA									
SER	GLY	PHE	SER	GLU	ALA	ASP	PRO	THR	LEU	ALA	SER	GLN	LYS	ALA	GLU	PRO	ASP	ALA	GLU	PRO	GLY	GLY	ARG	LYS	LYS	THR	GLU	PRO	G1235	D1236	S1237	L1238	H1239	V1240	N1241	A1242	R1243	H1244	L1245	L1246	Y1247	P1248	N1249	C1250	P1251	V1252	T1253	R1254	F1255	P1256	V1257	P1258	M1259	E1260						
K1261	V1262	P1263	W1264	E1265	T1266	L1267	F1268	I1269	L1270	Y1271	D1272	P1273	P1274	F1275	Y1276	T1277	A1278	E1279	R1280	K1281	D1282	A1283	A1284	A1285	M1286	D1287	P1288	M1289	G1290	D1291	T1292	L1293	E1294	P1295	L1296	S1297	T1298	I1299	Q1300	M1301	V1302	V1303	V1304	D1305	G1306	L1307	R1308	D1309	R1310	R1311	S1312	F1313	H1314	G1315	P1316	V1317	L1318	T1319	V1319	Q1320
A1321	G1322	L1323	P1324	L1325	N1326	P1327	W1328	L1329	R1330	T1331	G1332	L1333	R1334	G1335	R1336	G1337	S1338	L1339	S1340	C1341	F1342	G1343	P1344	N1345	H1346	T1347	L1348	Y1349	P1350	M1351	V1352	T1353	R1354	W1355	R1356	R1357	N1358	E1359	D1360	G1361	I1363	C1364	R1365	K1366	S1367	I1368	K1369	L1370	M1371	L1372	E1373	V1374	L1375	V1376	V1377	K1378	L1379	P1380		



● Molecule 1: Transient receptor potential cation channel subfamily M member 2



P1388	G1389	G1390	S1391	R1392	E1393	P1394	G1395	E1396	M1397	L1398	P1399	R1400	K1401	L1402	K1403	R1404	I1405	L1406	R1407	Q1408	E1409	H1410	W1411	P1412	S1413	F1414	E1415	M1416	L1417	L1418	K1419	C1420	G1421	M1422	E1423	V1424	Y1425	K1426	G1427	Y1428	M1429	D1430	D1431	P1432	R1433	M1434	T1435	D1436	N1437	A1438	W1439	I1440	E1441	T1442	V1443	A1444	Y1445	S1446	V1447
H1448	F1449	Q1450	D1451	Q1452	N1453	D1454	V1455	E1456	L1457	N1458	R1459	L1460	N1461	S1462	N1463	L1464	H1465	A1466	C1467	D1468	S1469	G1470	A1471	S1472	I1473	R1474	W1475	Q1476	V1477	V1478	D1479	R1480	R1481	I1482	P1483	L1484	Y1485	A1486	N1487	H1488	K1489	T1490	L1491	L1492	Q1493	K1494	A1495	A1496	A1497	E1498	F1499	G1500	A1501	H1502	Y1503				

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	14199	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	70.072	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	21.981	Depositor
Minimum map value	-13.418	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2.77	Depositor
Map size (\AA)	321.00003, 321.00003, 321.00003	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.07, 1.07, 1.07	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA

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	0.30	0/11050	0.67	19/14990 (0.1%)
1	B	0.30	0/11050	0.67	19/14990 (0.1%)
1	C	0.30	0/11050	0.67	19/14990 (0.1%)
1	D	0.30	0/11050	0.67	19/14990 (0.1%)
All	All	0.30	0/44200	0.67	76/59960 (0.1%)

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
1	A	0	13
1	B	0	13
1	C	0	13
1	D	0	13
All	All	0	52

There are no bond length outliers.

The worst 5 of 76 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	933	ASP	CB-CG-OD2	-8.80	110.38	118.30
1	D	933	ASP	CB-CG-OD2	-8.77	110.41	118.30
1	C	933	ASP	CB-CG-OD2	-8.77	110.41	118.30
1	A	933	ASP	CB-CG-OD2	-8.74	110.44	118.30
1	C	933	ASP	CB-CG-OD1	8.54	125.99	118.30

There are no chirality outliers.

5 of 52 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	375	THR	Peptide
1	A	388	GLN	Peptide
1	A	495	ASN	Peptide
1	A	615	VAL	Peptide
1	A	82	SER	Peptide

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	10780	0	10822	212	0
1	B	10780	0	10822	209	0
1	C	10780	0	10822	215	0
1	D	10780	0	10822	215	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
All	All	43124	0	43288	843	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 10.

The worst 5 of 843 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:A:569:LEU:HD13	1:A:572:PHE:HB2	1.76	0.68
1:D:569:LEU:HD13	1:D:572:PHE:HB2	1.77	0.67
1:B:569:LEU:HD13	1:B:572:PHE:HB2	1.76	0.67
1:C:569:LEU:HD13	1:C:572:PHE:HB2	1.76	0.66
1:B:962:ARG:H	1:B:965:TRP:HB2	1.60	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	1331/1503 (89%)	1131 (85%)	195 (15%)	5 (0%)	34	72
1	B	1331/1503 (89%)	1133 (85%)	193 (14%)	5 (0%)	34	72
1	C	1331/1503 (89%)	1131 (85%)	195 (15%)	5 (0%)	34	72
1	D	1331/1503 (89%)	1131 (85%)	195 (15%)	5 (0%)	34	72
All	All	5324/6012 (89%)	4526 (85%)	778 (15%)	20 (0%)	38	72

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	376	ILE
1	B	376	ILE
1	C	376	ILE
1	D	376	ILE
1	A	384	SER

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	1176/1318 (89%)	1163 (99%)	13 (1%)	73	84
1	B	1176/1318 (89%)	1163 (99%)	13 (1%)	73	84
1	C	1176/1318 (89%)	1163 (99%)	13 (1%)	73	84
1	D	1176/1318 (89%)	1163 (99%)	13 (1%)	73	84
All	All	4704/5272 (89%)	4652 (99%)	52 (1%)	74	84

5 of 52 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	566	ARG
1	C	930	MET
1	D	941	LEU
1	C	610	ARG
1	C	839	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 70 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	446	HIS
1	D	506	ASN
1	D	684	HIS
1	B	506	ASN
1	B	454	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

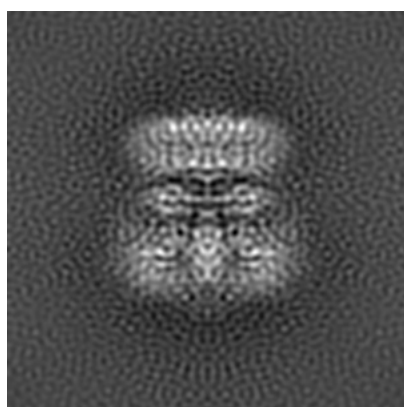
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9134. These allow visual inspection of the internal detail of the map and identification of artifacts.

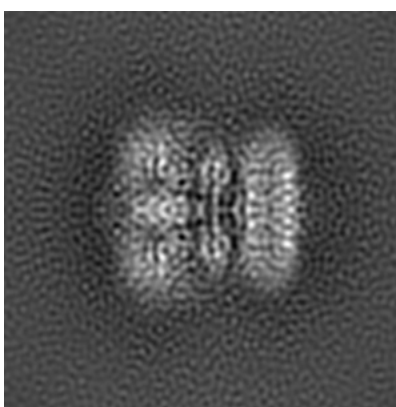
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

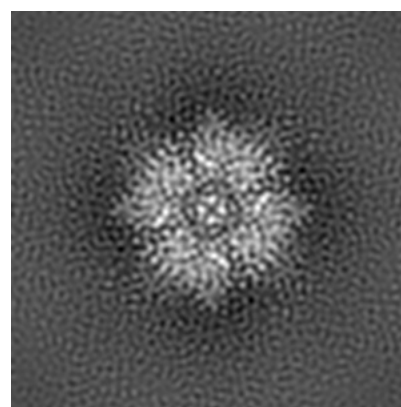
6.1.1 Primary map



X



Y

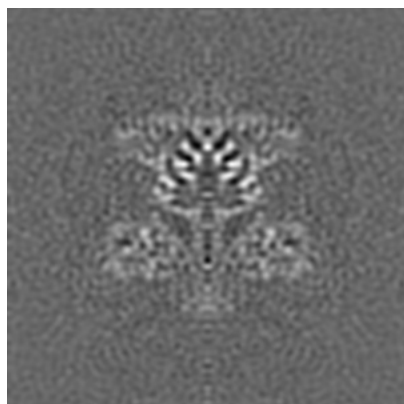


Z

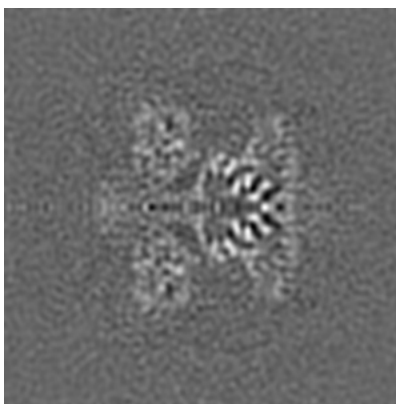
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

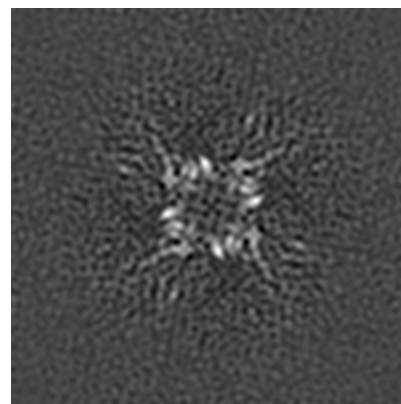
6.2.1 Primary map



X Index: 150



Y Index: 150

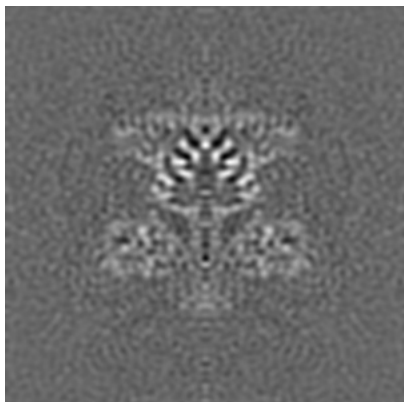


Z Index: 150

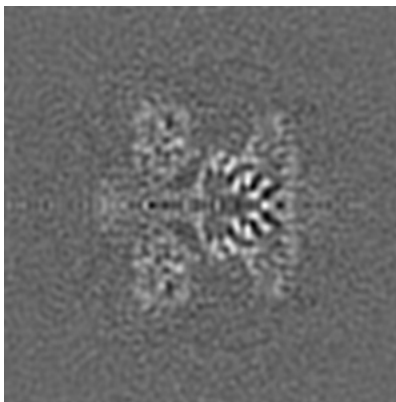
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

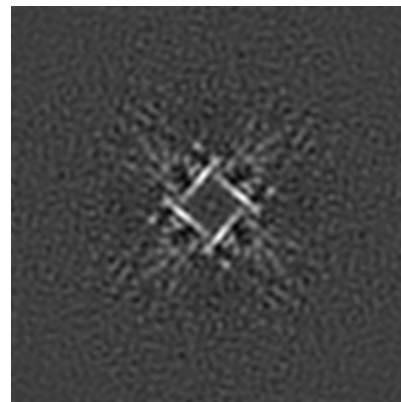
6.3.1 Primary map



X Index: 150



Y Index: 150



Z Index: 158

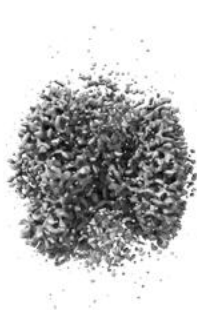
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

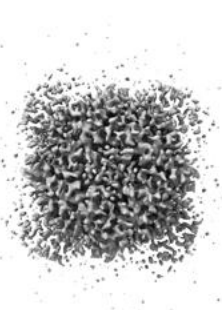
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.77. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

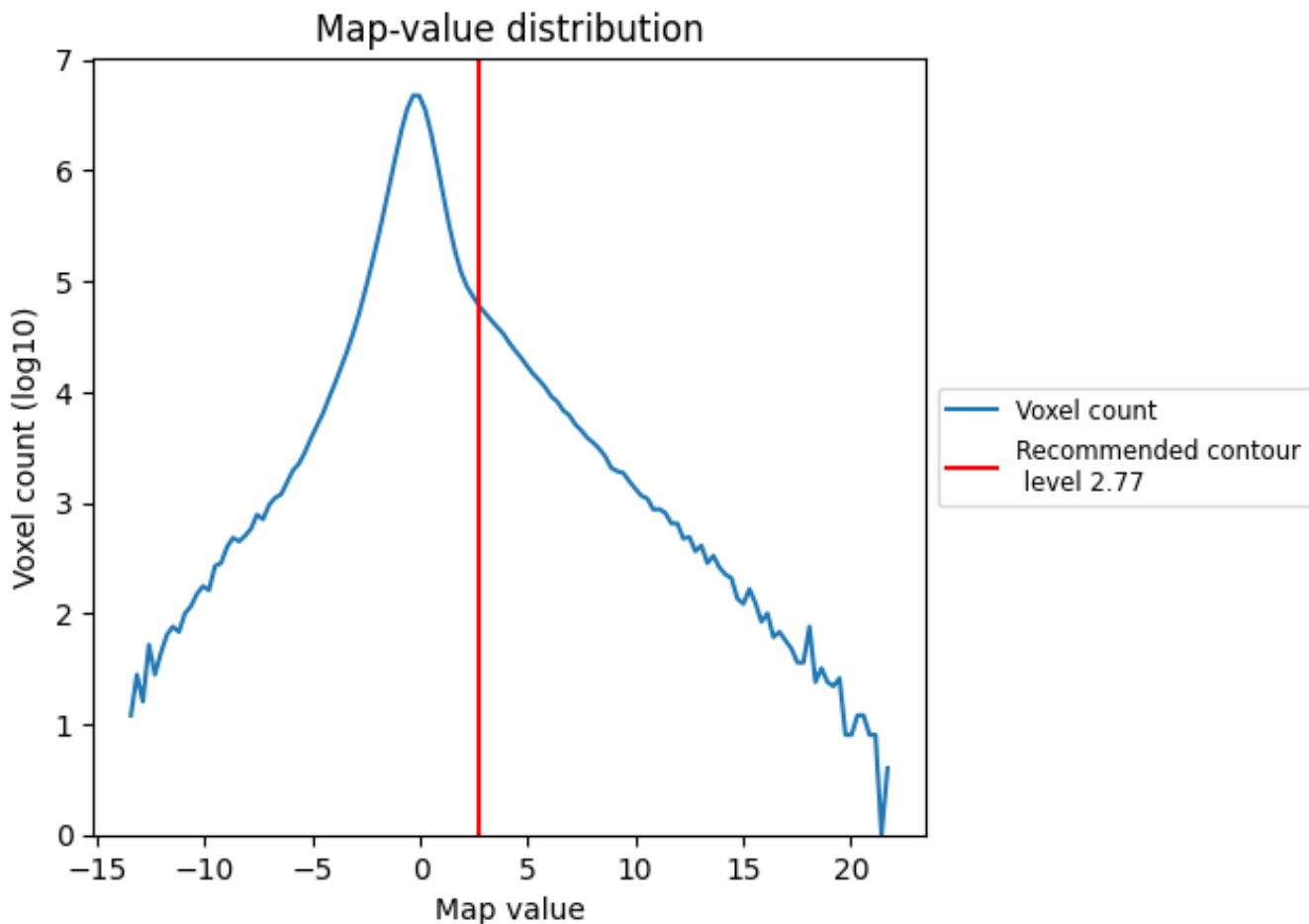
6.5 Mask visualisation

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

7 Map analysis [i](#)

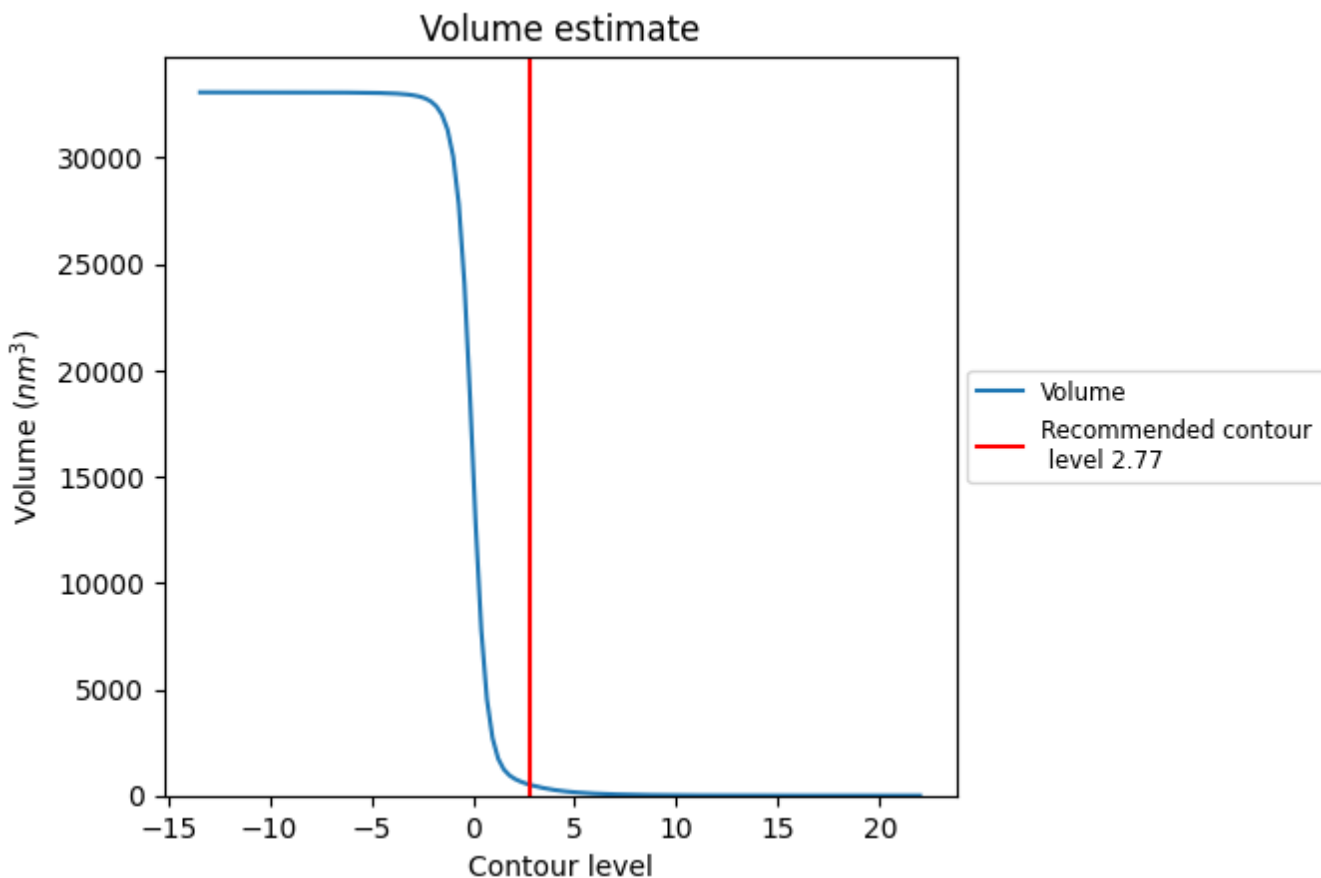
This section contains the results of statistical analysis of the map.

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.

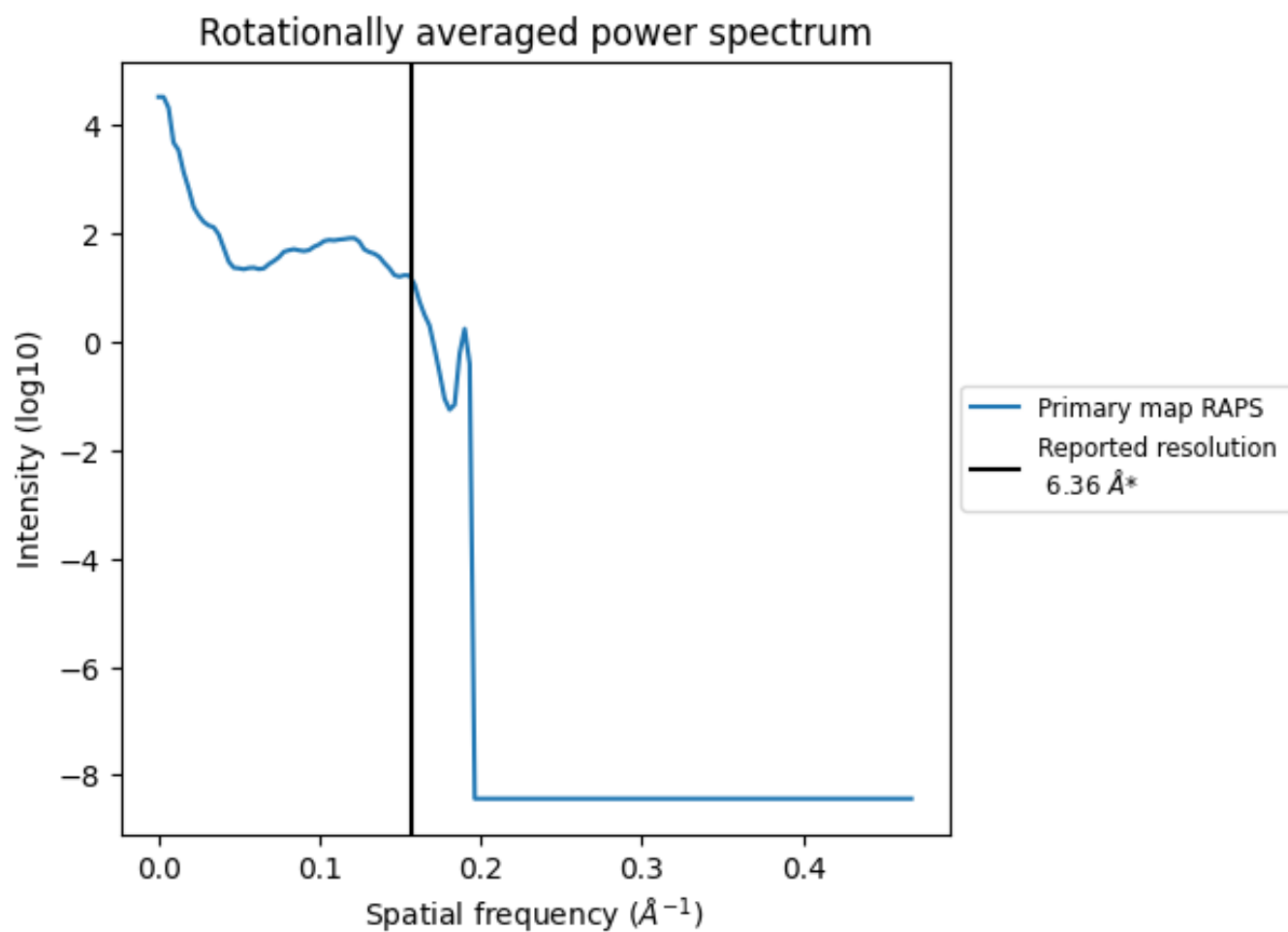
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 518 nm^3 ; this corresponds to an approximate mass of 468 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 0.157 Å⁻¹

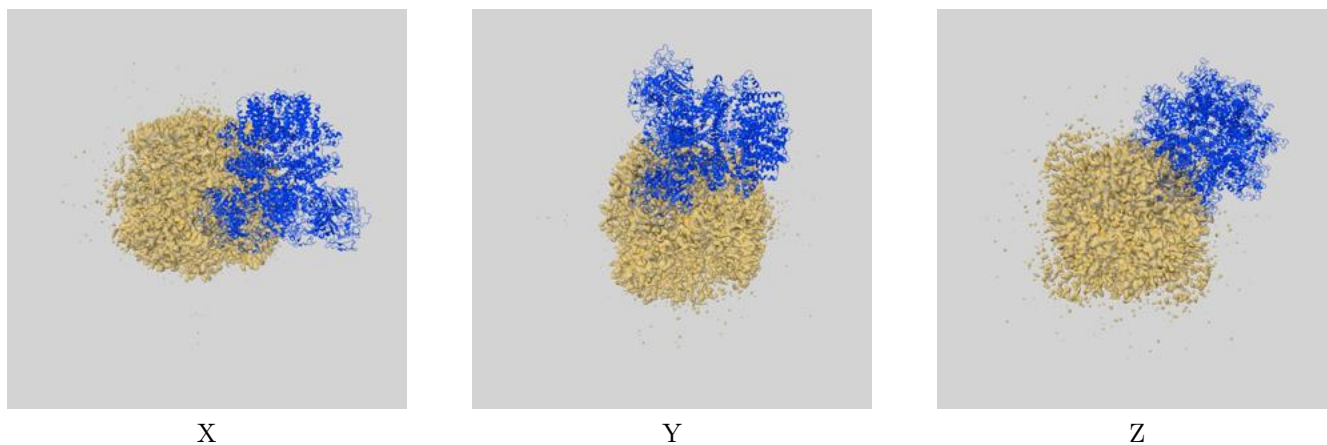
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

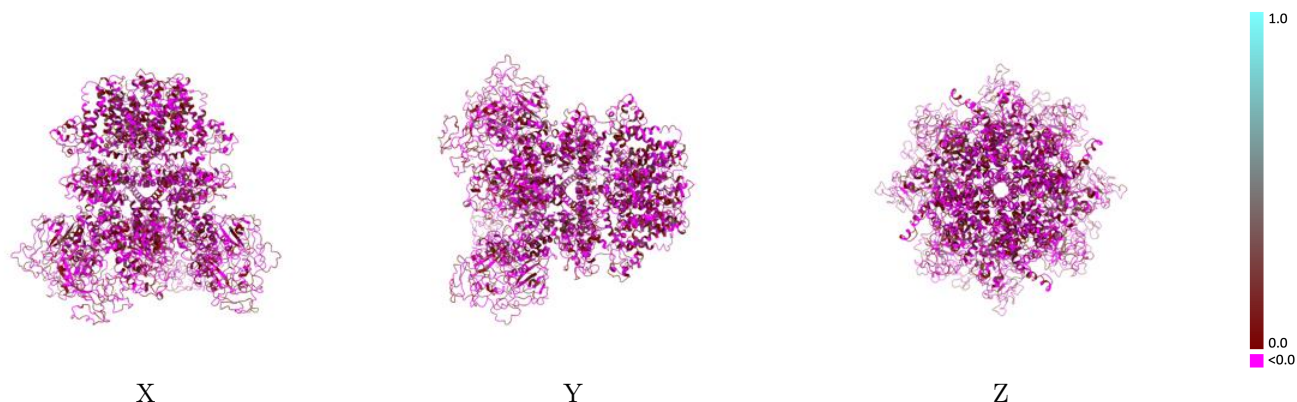
This section contains information regarding the fit between EMDB map EMD-9134 and PDB model 6MJ2. Per-residue inclusion information can be found in section [3](#) on page [4](#).

9.1 Map-model overlay [i](#)



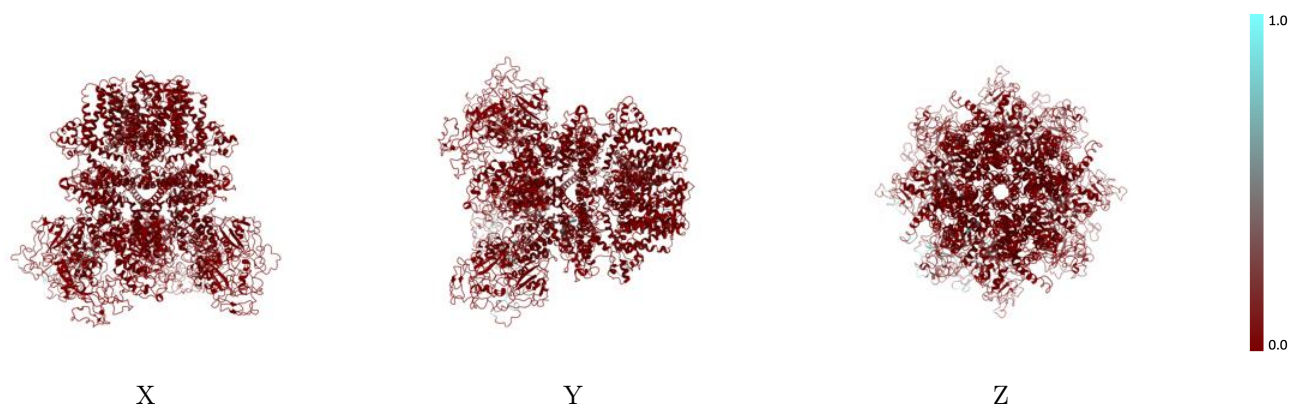
The images above show the 3D surface view of the map at the recommended contour level 2.77 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



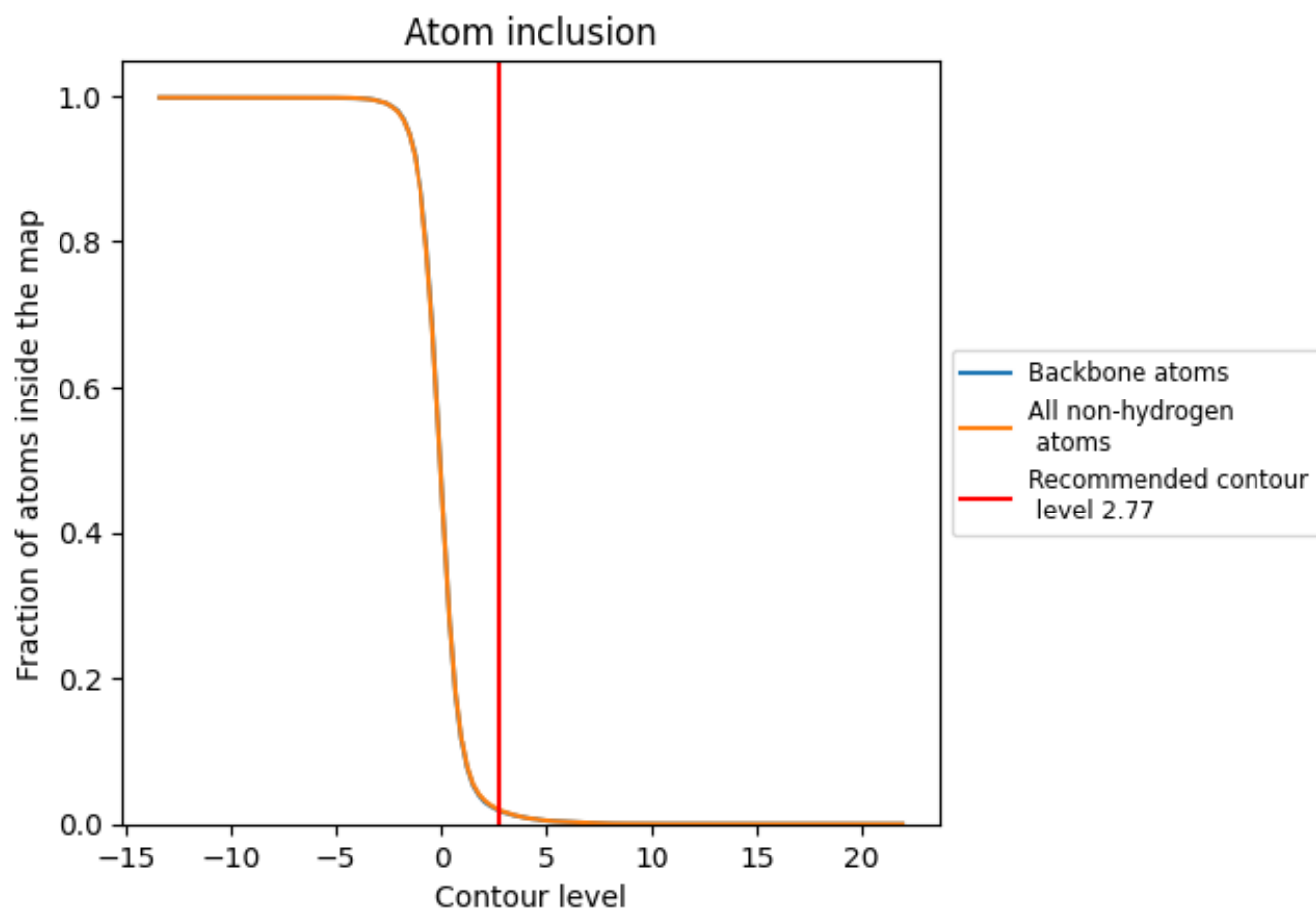
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.77).











9.4 Atom inclusion [i](#)



At the recommended contour level, 2% of all backbone atoms, 2% 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 (2.77) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.0188	 -0.0000
A	 0.0603	 -0.0020
B	 0.0003	 -0.0020
C	 0.0000	 0.0030
D	 0.0145	 -0.0000

