



wwPDB EM Validation Summary Report ⓘ

Mar 15, 2026 – 09:59 AM UTC

PDB ID : 6MIZ / pdb_00006miz
EMDB ID : EMD-9133
Title : Human TRPM2 ion channel in an ADPR-bound state
Authors : Wang, L.; Fu, T.M.; Xia, S.; Wu, H.
Deposited on : 2018-09-20
Resolution : 6.10 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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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.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

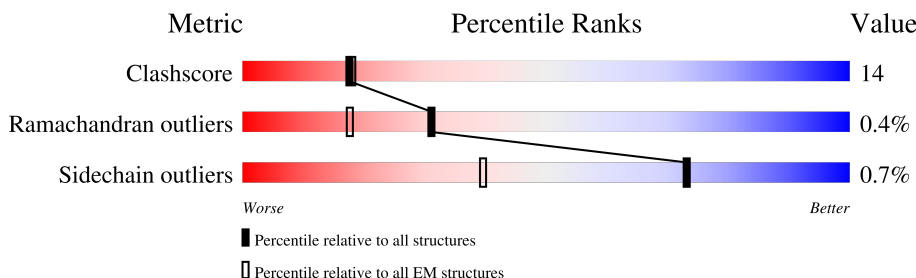
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.10 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	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

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	83% 58% 30% • 11%
1	B	1503	89% 57% 31% • 11%
1	C	1503	89% 57% 31% • 11%
1	D	1503	89% 58% 31% • 11%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 43120 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.

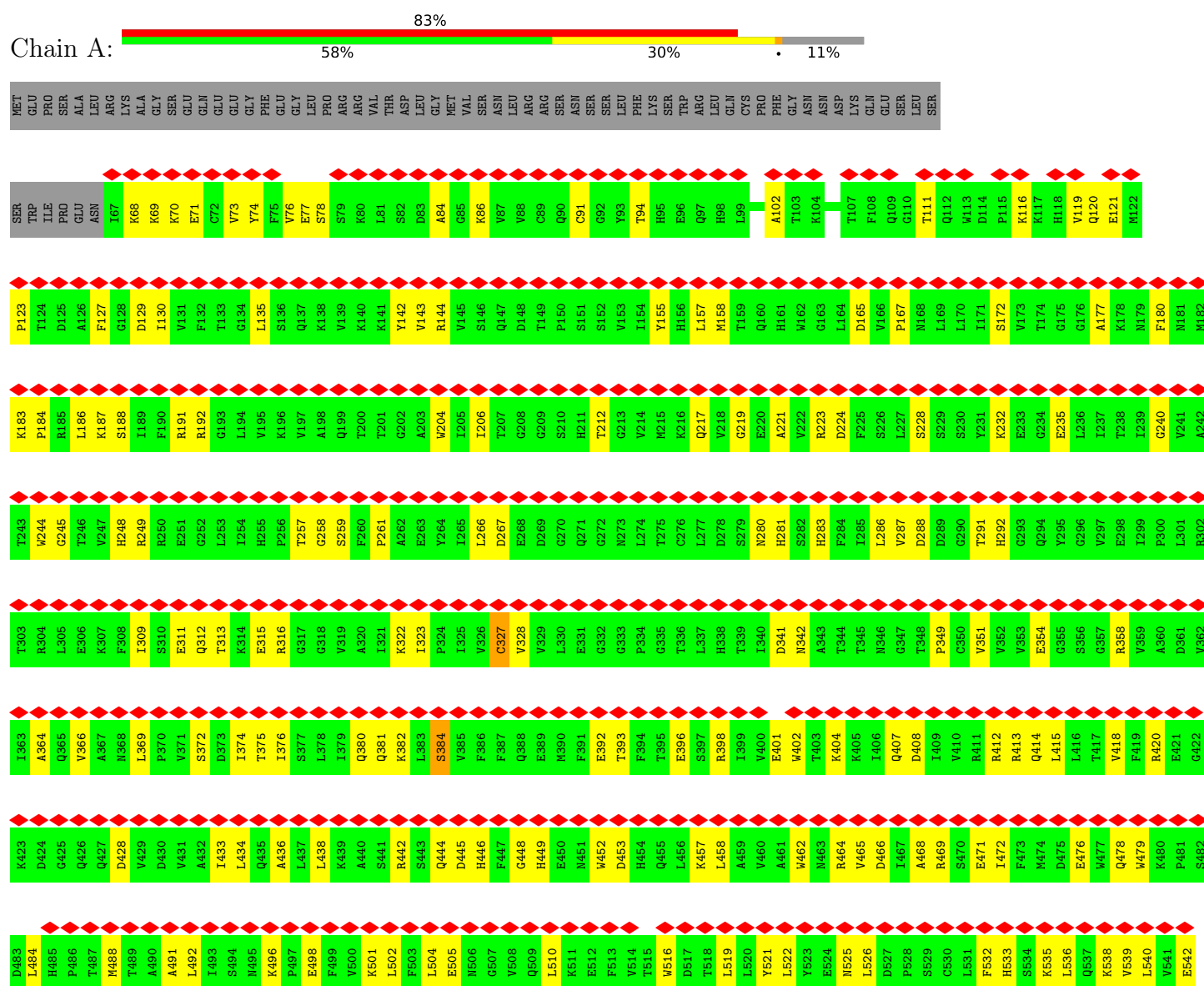
- Molecule 1 is a protein called Transient receptor potential cation channel subfamily M member 2.

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

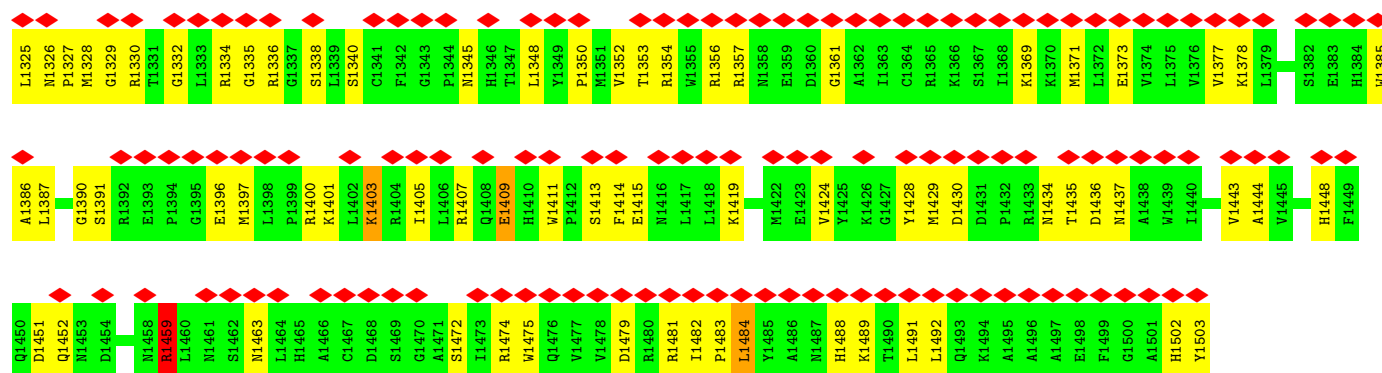
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

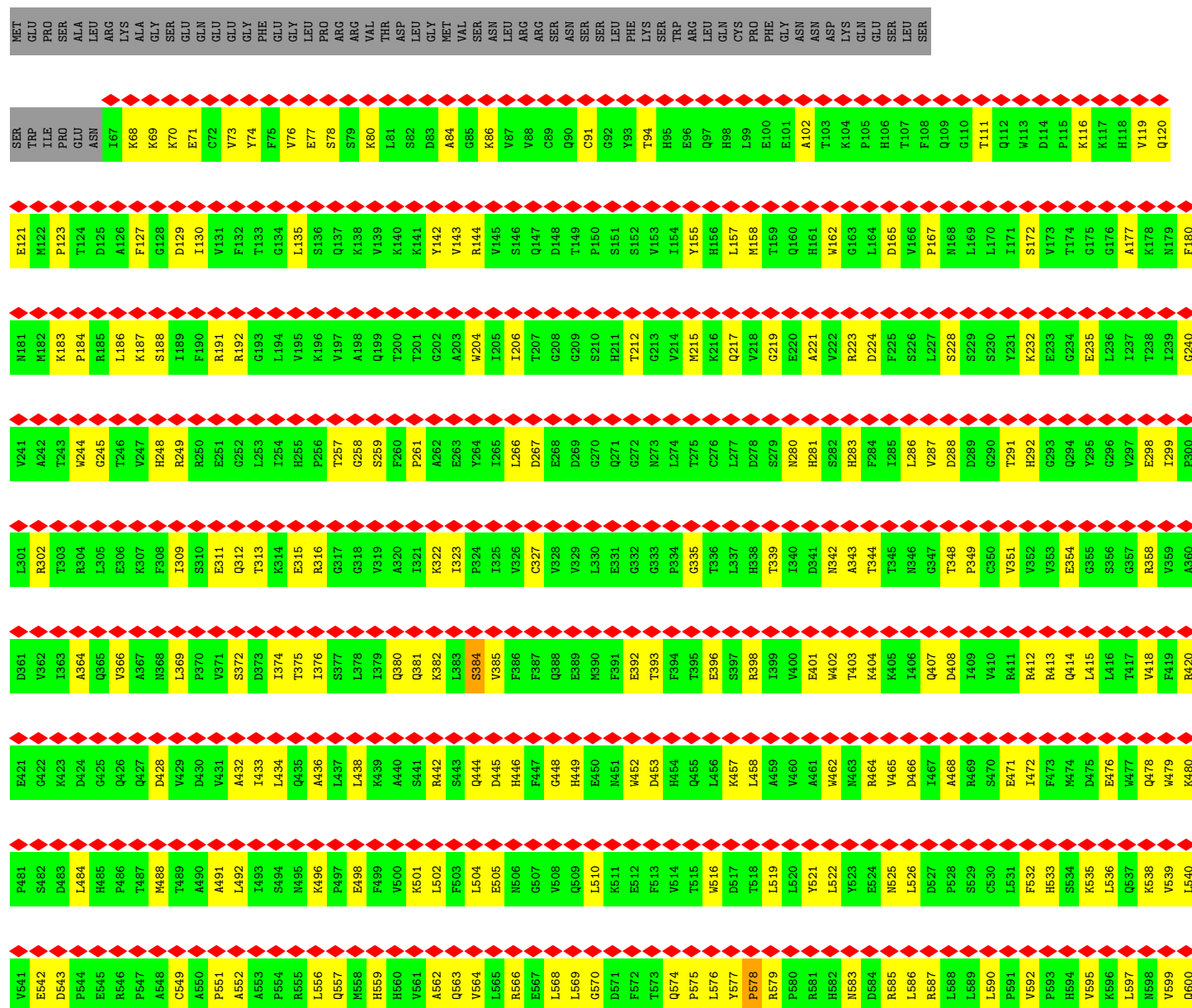
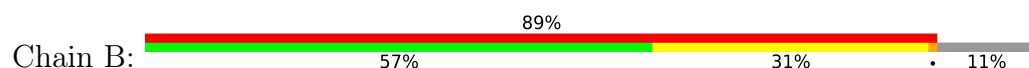
- Molecule 1: Transient receptor potential cation channel subfamily M member 2



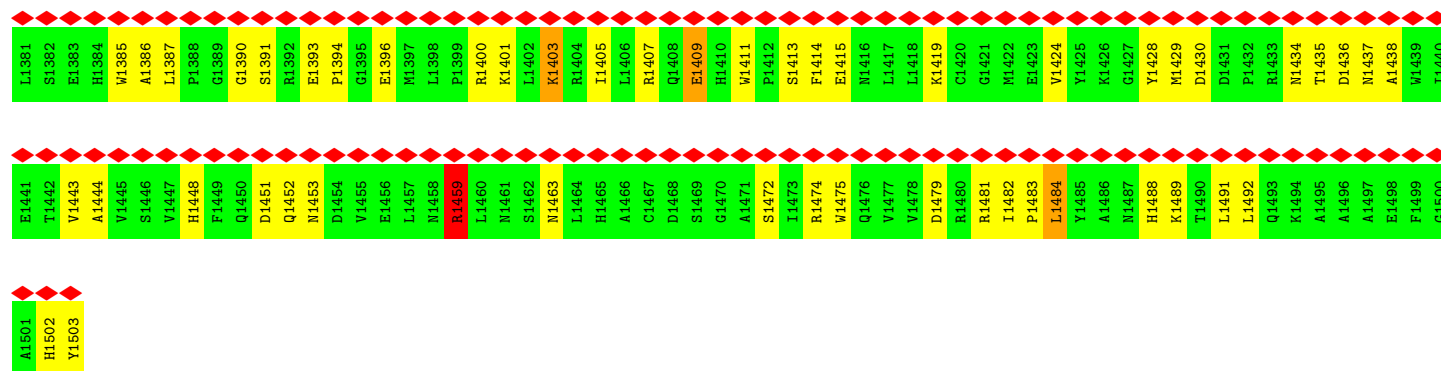
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SER	GLU	ALA	ASP	VAL	PRO	THR	LEU	SER	ALA	GLN	LYS	ALA	GLU	GLU	PRO	ASP	ALA	GLU	GLY	ARG	LYS	THR	GLU	GLU	PRO	G1235	D1236	S1237	H1238	V1239	V1240	M1241	A1242	R1243	H1244	L1245	L1246	Y1247	P1248	N1249	C1250	P1251	V1252	T1253	R1254	F1255	P1256	V1257	P1258	R1259	E1260	K1261	V1262	P1263	PHE	SER	W1264				
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L604	R605	S606	L607	R610	S611	S612	G613	H614	V615	T616	F617	T618	M619	D620	P621	I622	R623	D624	L625	L626	I627	W628	A629	I630	V631	Q632	N633	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	V660	E661	L662	S663	K664			
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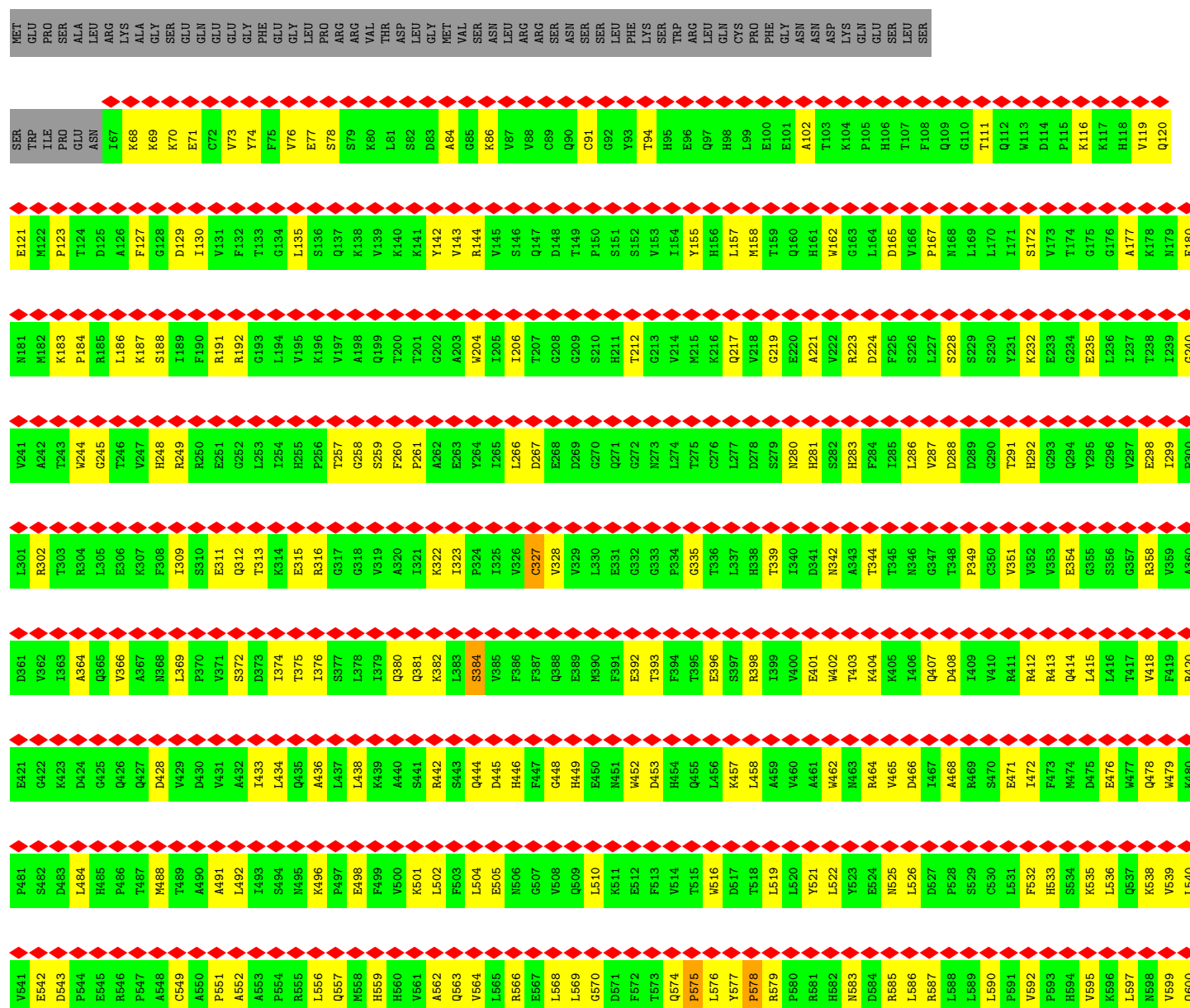
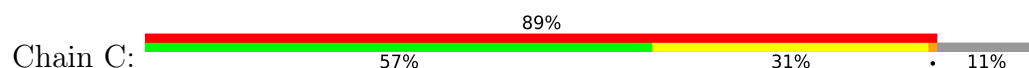
- Molecule 1: Transient receptor potential cation channel subfamily M member 2



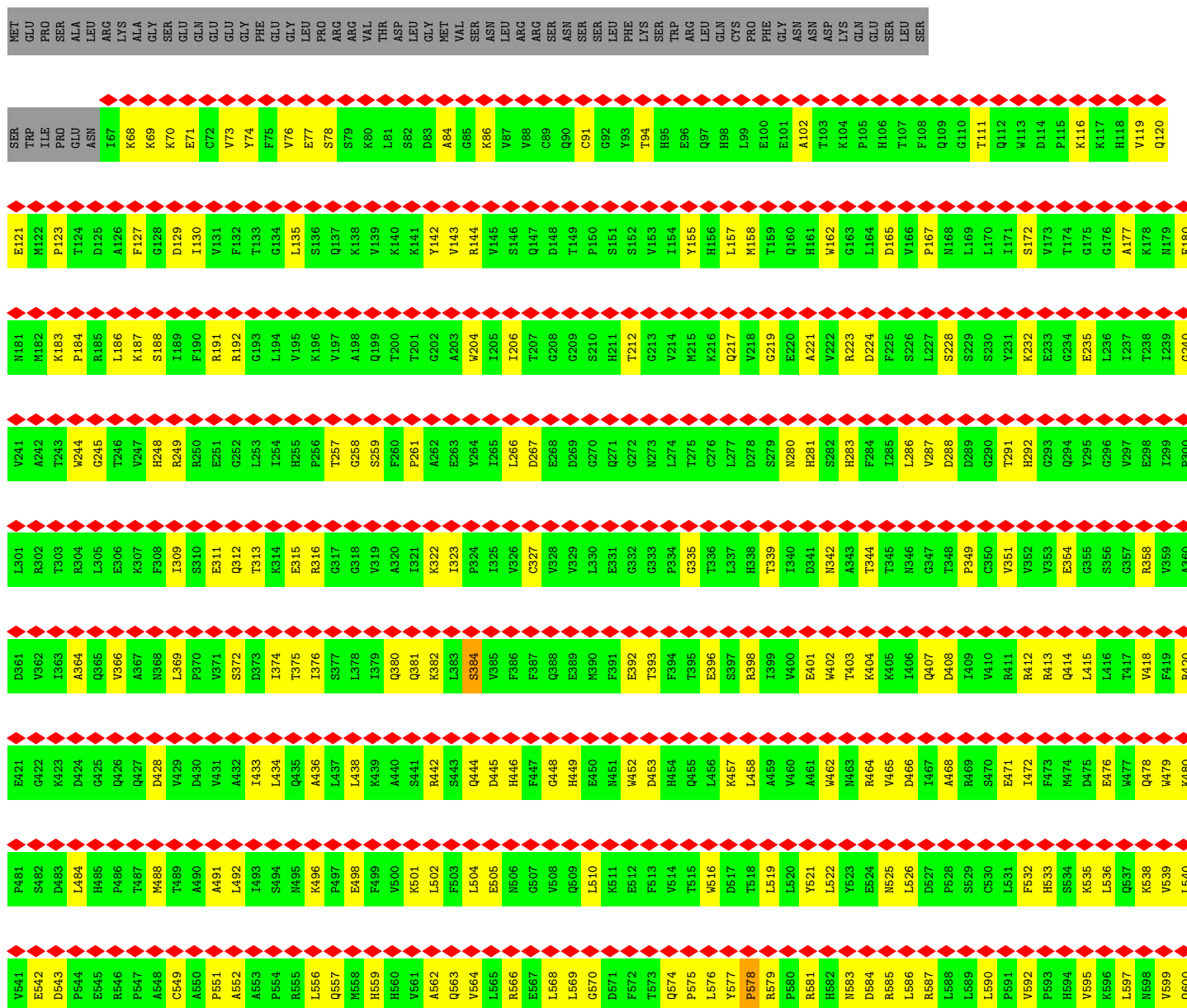
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- Molecule 1: Transient receptor potential cation channel subfamily M member 2







A1321	G1322	L1323	P1324	L1325	N1326	P1327	M1328	G1329	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	A1362	I1363	C1364	R1365	K1366	S1367	R1368	K1369	K1370	M1371	L1372	E1373	V1374	L1375	V1376	V1377	K1378	L1379	P1380																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
K1261	V1262	P1263	W1264	E1265	T1266	E1267	F1268	L1269	I1270	Y1271	D1272	P1273	P1274	F1275	Y1276	T1277	G1278	E1279	R1280	K1281	D1282	A1283	A1284	A1285	M1286	D1287	P1288	M1289	G1290	D1291	T1292	L1293	E1294	P1295	L1296	S1297	T1298	I1299	Q1300	Y1301	N1302	V1303	V1304	D1305	K1306	L1307	R1308	D1309	R1310	R1311	S1312	F1313	H1314	G1315	P1316	T1317	T1318	V1319	Q1320																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
SER	GLY	PHE	SER	SER	GLU	ALA	ASP	VAL	THR	LEU	ALA	SER	GLN	LYS	ALA	GLU	PRO	ASP	ALA	GLU	PRO	LYS	ARG	GLY	GLY	MET	H1239	V1240	N1241	A1242	R1243	H1244	L1245	L1246	Y1247	P1248	N1249	C1250	T1251	V1252	T1253	R1254	F1255	P1256	V1257	N1258	P1259	E1260																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
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	SER	GLU	GLN	ARG	LEU	SER	LEU	GLY	GLU	GLN	VAL	ALA	GLN	THR	ALA	HIS	TRP	ILE	VAL	ARG	THR	LEU	ARG	ALA																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
P1081	P1082	P1083	F1084	I1085	L1086	L1087	S1088	H1089	L1090	Q1091	L1092	F1093	I1094	K1095	R1096	V1097	I1098	L1099	K1100	T1101	P1102	A1103	K1104	R1105	H1106	K1107	Q1108	L1109	K1110	M1111	K1112	L1113	E1114	K1115	N1116	E1117	E1118	A1119	A1120	L1121	L1122	S1123	W1124	I1125	I1126	Y1127	L1128	K1129	E1130	M1131	Y1132	L1133	Q1134	M1135	R1136	Q1137	F1138	Q1139	Q1140																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
G1235	D1236	S1237	Y1238	H1239	V1240	N1241	A1242	R1243	H1244	L1245	L1246	Y1247	P1248	N1249	C1250	T1251	V1252	T1253	R1254	F1255	P1256	V1257	N1258	P1259	E1260																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		</

A1501	H1502	Y1503	E1441	L1381
			T1442	S1382
			V1443	E1383
A1444	V1445	H1446	A1444	H1384
			V1446	W1385
			V1447	A1386
H1448	V1449	F1450	V1448	L1387
			V1449	P1388
			V1450	G1389
D1451	Q1452	R1453	D1451	G1390
			Q1452	S1391
			R1453	R1392
V1454	V1455	V1456	V1454	E1393
			V1455	P1394
			V1456	G1395
L1457	V1458	R1459	L1457	E1396
			V1458	M1397
			R1459	L1398
L1460	V1461	S1462	L1460	P1399
			V1461	R1400
			S1462	K1401
V1463	V1464	V1465	V1463	L1402
			V1464	K1403
			V1465	R1404
A1466	V1467	D1468	A1466	L1405
			V1467	L1406
			D1468	R1407
S1469	G1470	A1471	S1469	Q1408
			G1470	E1409
			A1471	H1410
T1472	T1473	R1474	T1472	W1411
			T1473	P1412
			R1474	S1413
V1475	Q1476	V1477	V1475	F1414
			Q1476	E1415
			V1477	N1416
V1478	R1480	R1481	V1478	L1417
			R1480	L1418
			R1481	L1419
D1479	G1420	G1421	D1479	G1420
			G1420	G1421
			G1421	M1422
P1483	V1424	V1425	P1483	E1423
			V1424	V1425
			V1425	K1426
V1485	V1486	V1487	V1485	G1427
			V1486	Y1428
			V1487	M1429
H1488	K1489	T1490	H1488	Y1428
			K1489	M1429
			T1490	D1430
L1491	Q1492	K1493	L1491	D1431
			Q1492	P1432
			K1493	R1433
K1494	A1495	A1496	K1494	N1434
			A1495	T1435
			A1496	D1436
A1497	V1498	F1499	A1497	M1437
			V1498	A1438
			F1499	W1439
G1500	G1501	G1502	G1500	L1440
			G1501	
			G1502	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	49383	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	31.379	Depositor
Minimum map value	-14.438	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3.6	Depositor
Map size ($\text{\AA}$)	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 ($\text{\AA}$)	1.07, 1.07, 1.07	Depositor

5 Model quality

5.1 Standard geometry

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	0.25	0/11050	0.69	11/14990 (0.1%)
1	B	0.26	0/11050	0.69	11/14990 (0.1%)
1	C	0.25	0/11050	0.69	11/14990 (0.1%)
1	D	0.25	0/11050	0.69	11/14990 (0.1%)
All	All	0.26	0/44200	0.69	44/59960 (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	10
1	B	0	10
1	C	0	10
1	D	0	10
All	All	0	40

There are no bond length outliers.

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	749	VAL	N-CA-C	-6.72	107.33	113.71
1	C	749	VAL	N-CA-C	-6.70	107.35	113.71
1	D	749	VAL	N-CA-C	-6.70	107.35	113.71
1	B	749	VAL	N-CA-C	-6.70	107.35	113.71
1	A	929	ARG	CD-NE-CZ	6.03	132.84	124.40

There are no chirality outliers.

5 of 40 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	375	THR	Peptide
1	A	452	TRP	Peptide
1	A	479	TRP	Peptide
1	A	616	THR	Peptide
1	A	618	THR	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	10780	0	10822	291	0
1	B	10780	0	10822	305	0
1	C	10780	0	10822	300	0
1	D	10780	0	10822	296	0
All	All	43120	0	43288	1169	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 14.

The worst 5 of 1169 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:559:HIS:H	1:A:585:ARG:HB2	1.54	0.73
1:B:559:HIS:H	1:B:585:ARG:HB2	1.54	0.73
1:D:559:HIS:H	1:D:585:ARG:HB2	1.54	0.73
1:C:559:HIS:H	1:C:585:ARG:HB2	1.54	0.72
1:B:471:GLU:HG3	1:B:472:ILE:HG12	1.72	0.70

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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%)	1115 (84%)	211 (16%)	5 (0%)	30	67
1	B	1331/1503 (89%)	1115 (84%)	211 (16%)	5 (0%)	30	67
1	C	1331/1503 (89%)	1114 (84%)	212 (16%)	5 (0%)	30	67
1	D	1331/1503 (89%)	1115 (84%)	211 (16%)	5 (0%)	30	67
All	All	5324/6012 (89%)	4459 (84%)	845 (16%)	20 (0%)	31	67

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	576	LEU
1	B	576	LEU
1	C	576	LEU
1	D	576	LEU
1	A	575	PRO

5.3.2 Protein sidechains

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%)	1168 (99%)	8 (1%)	76	81
1	B	1176/1318 (89%)	1168 (99%)	8 (1%)	76	81
1	C	1176/1318 (89%)	1168 (99%)	8 (1%)	76	81
1	D	1176/1318 (89%)	1168 (99%)	8 (1%)	76	81
All	All	4704/5272 (89%)	4672 (99%)	32 (1%)	73	81

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	1024	LEU
1	D	1043	LEU
1	B	1024	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	716	THR
1	D	1352	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 147 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	211	HIS
1	D	1410	HIS
1	D	495	ASN
1	D	633	ASN
1	B	506	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9133. These allow visual inspection of the internal detail of the map and identification of artifacts.

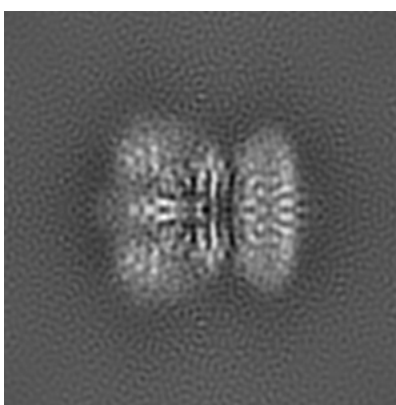
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

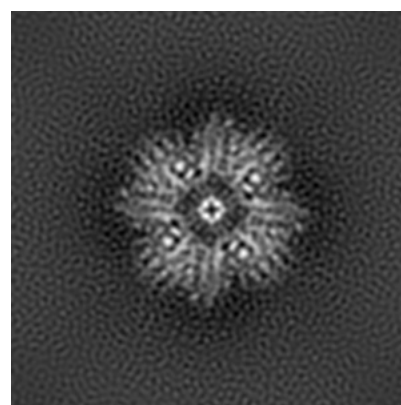
6.1.1 Primary map



X



Y

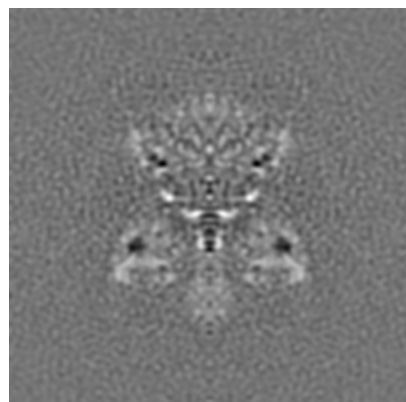


Z

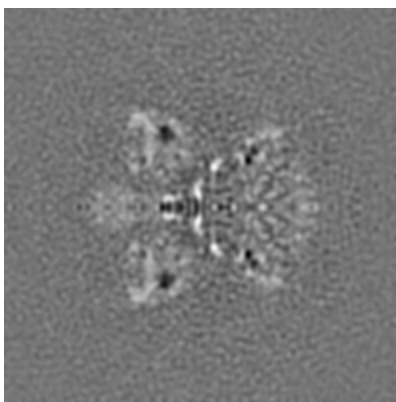
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

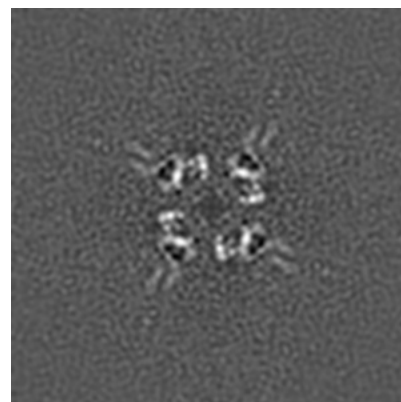
6.2.1 Primary map



X Index: 150



Y Index: 150

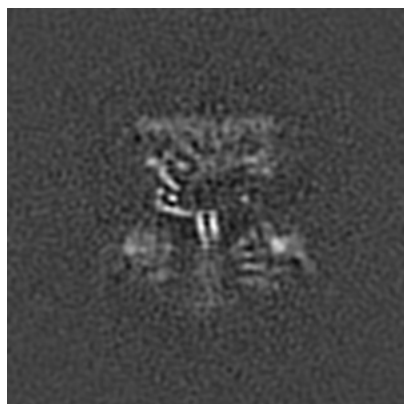


Z Index: 150

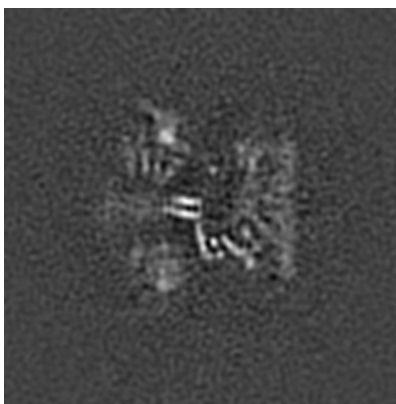
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

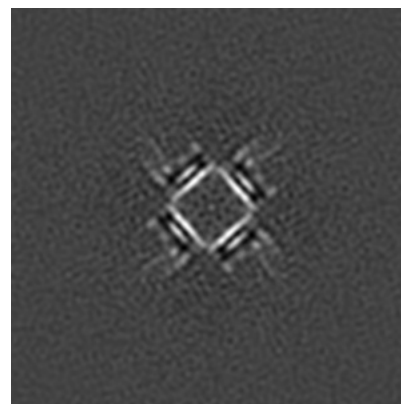
6.3.1 Primary map



X Index: 155



Y Index: 145

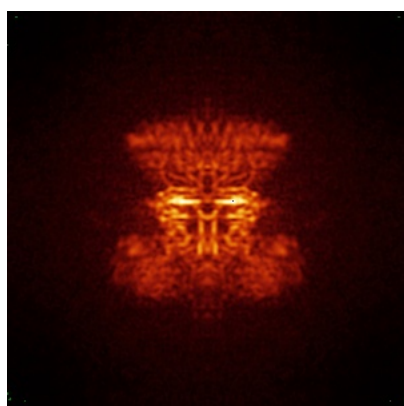


Z Index: 157

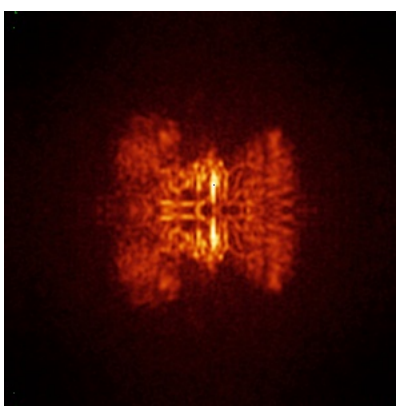
The images above show the largest variance slices of the map in three orthogonal directions.

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

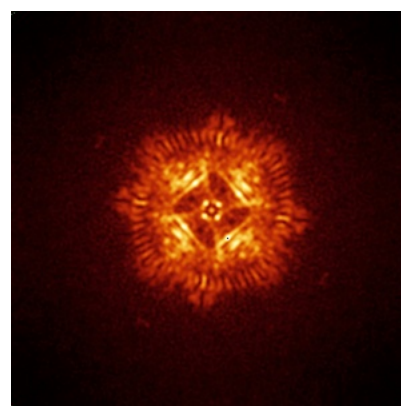
6.4.1 Primary map



X



Y

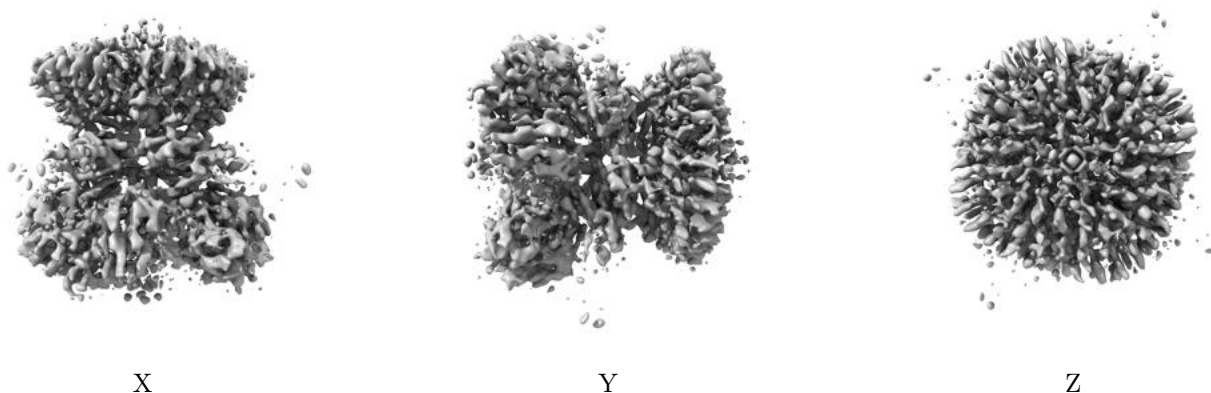


Z

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 3.6. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

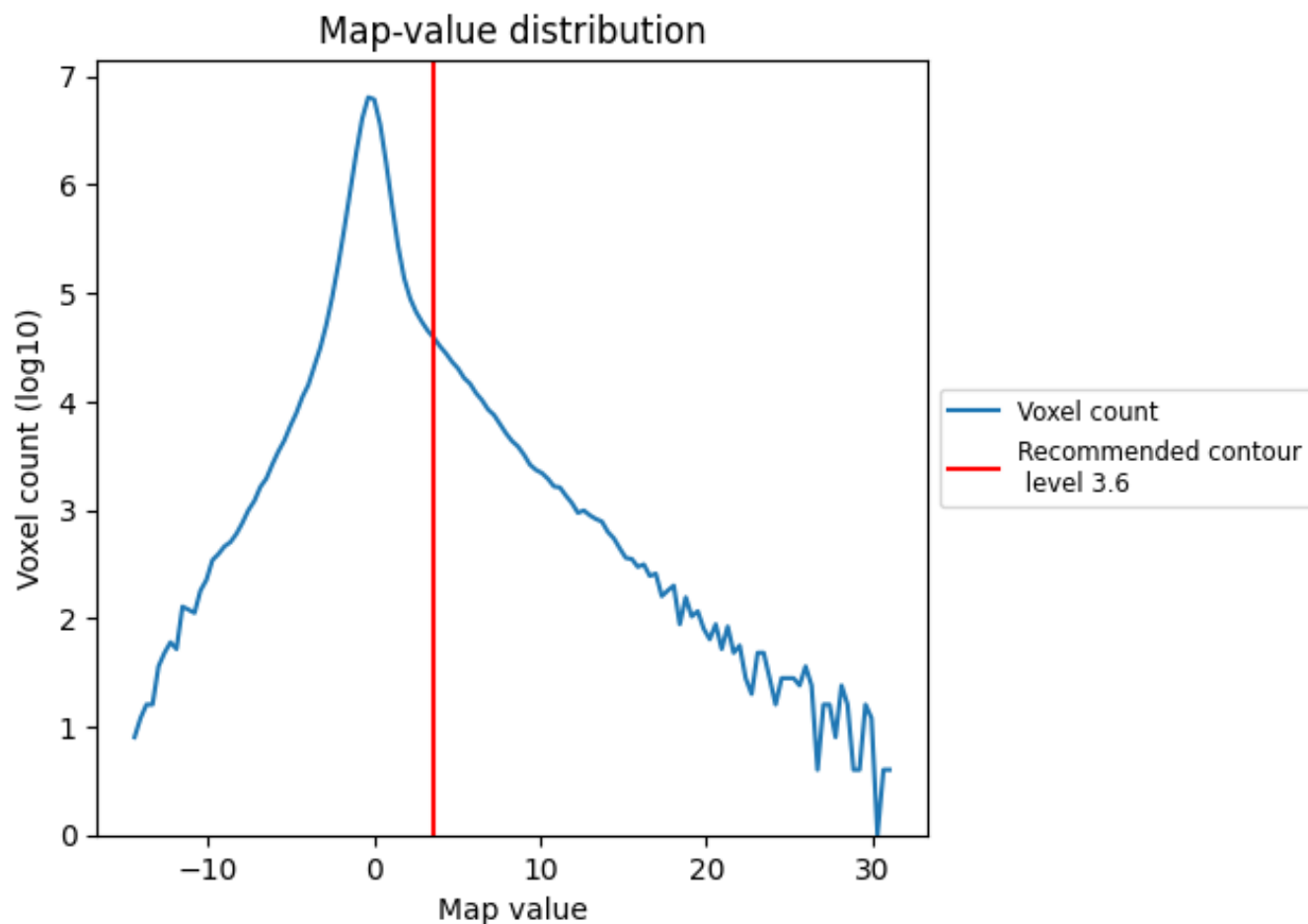
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

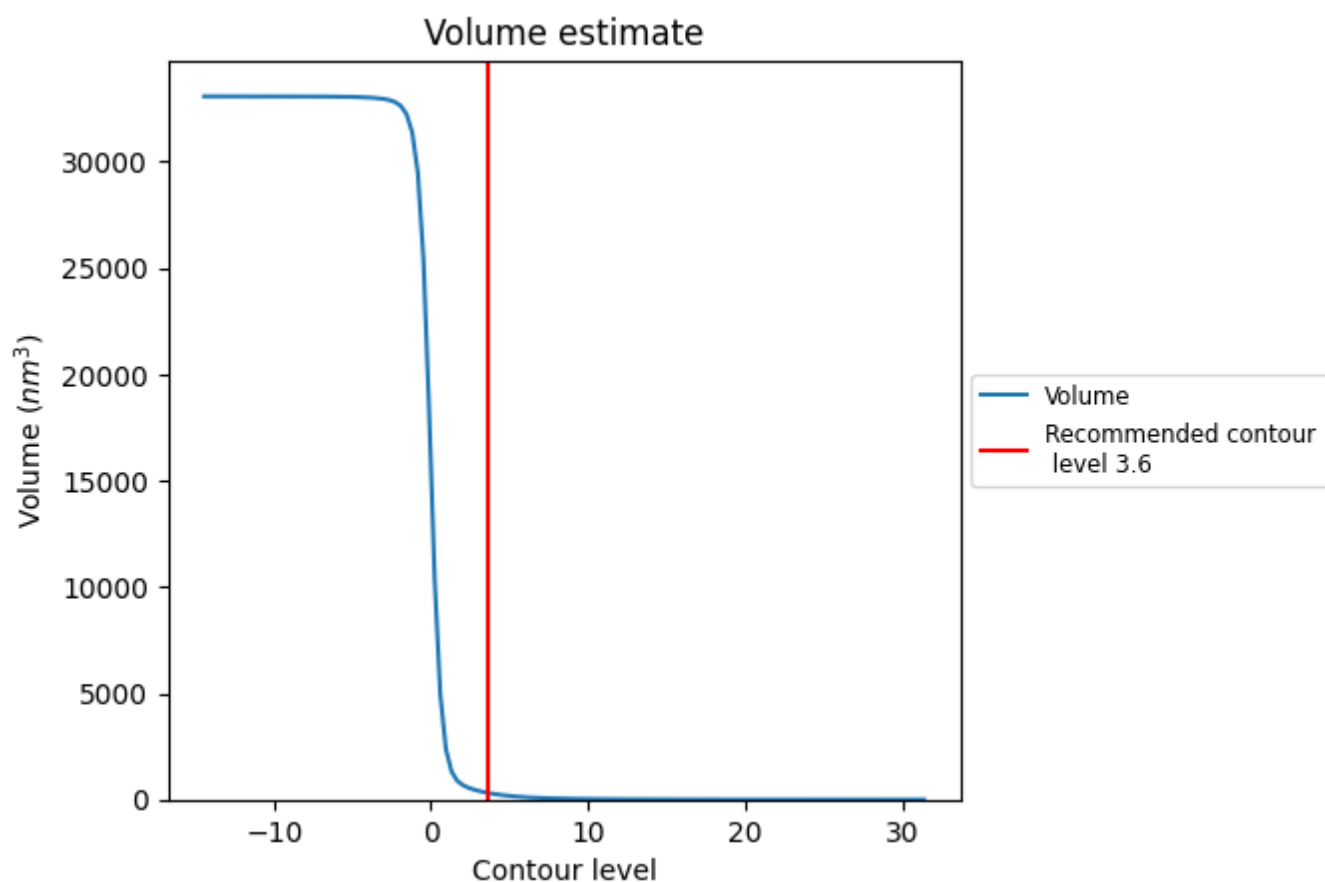
This section contains the results of statistical analysis of the map.

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.

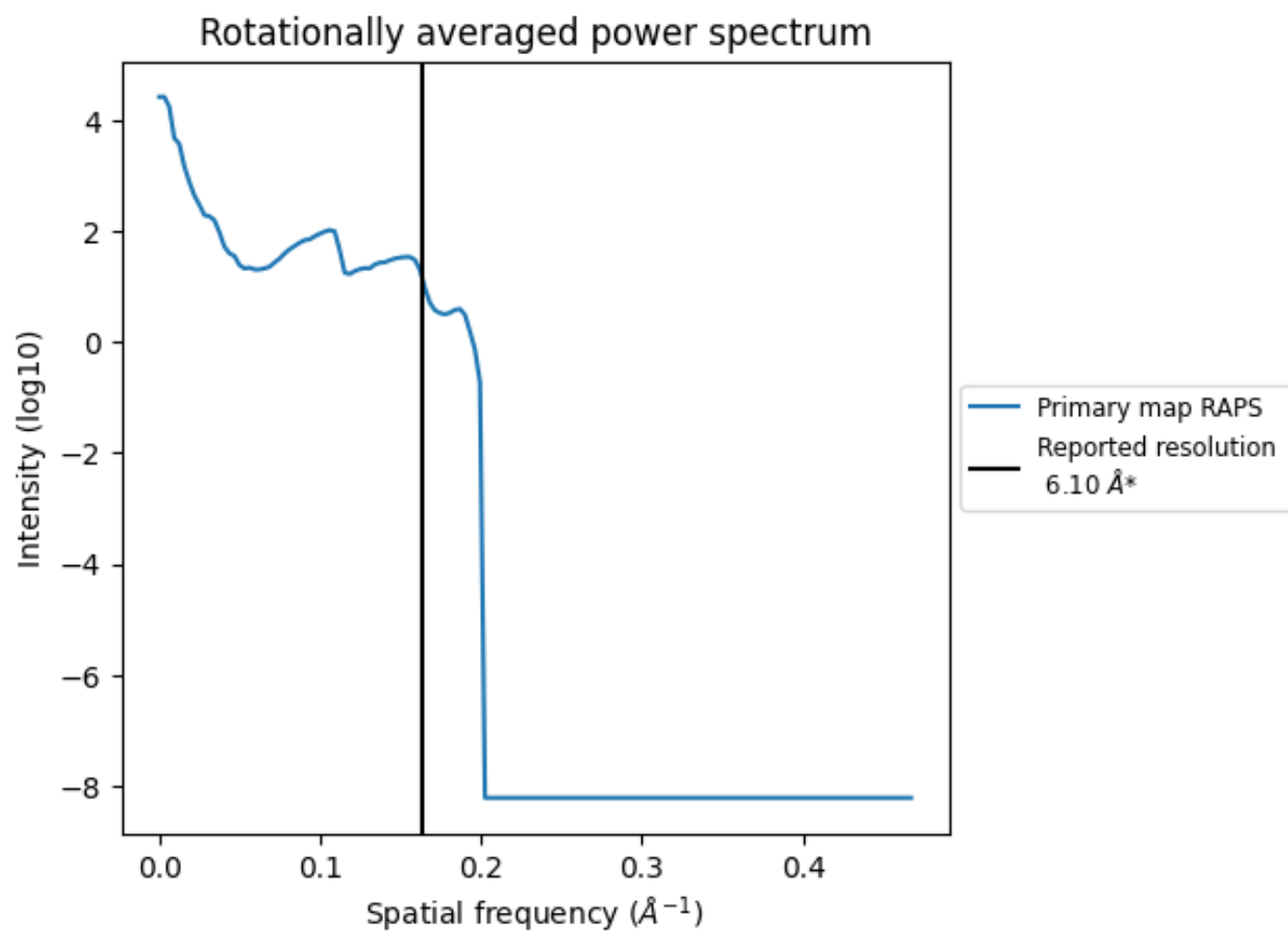
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 317 nm^3 ; this corresponds to an approximate mass of 286 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 0.164 Å⁻¹

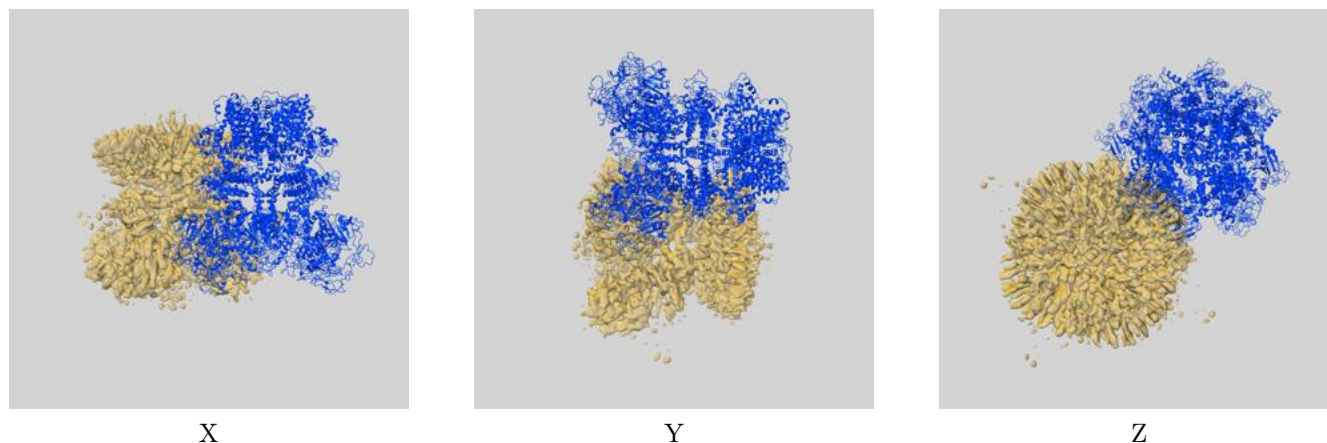
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

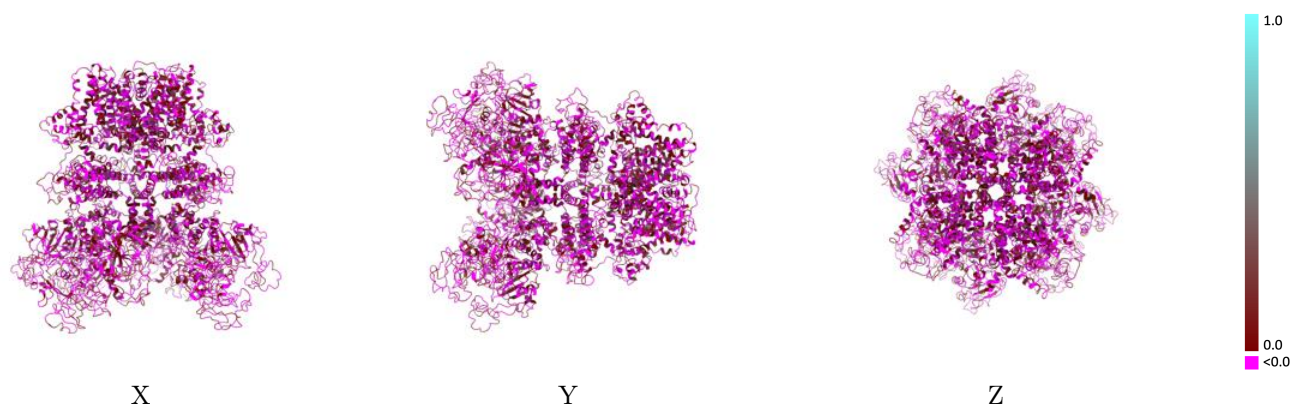
This section contains information regarding the fit between EMDB map EMD-9133 and PDB model 6MIZ. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



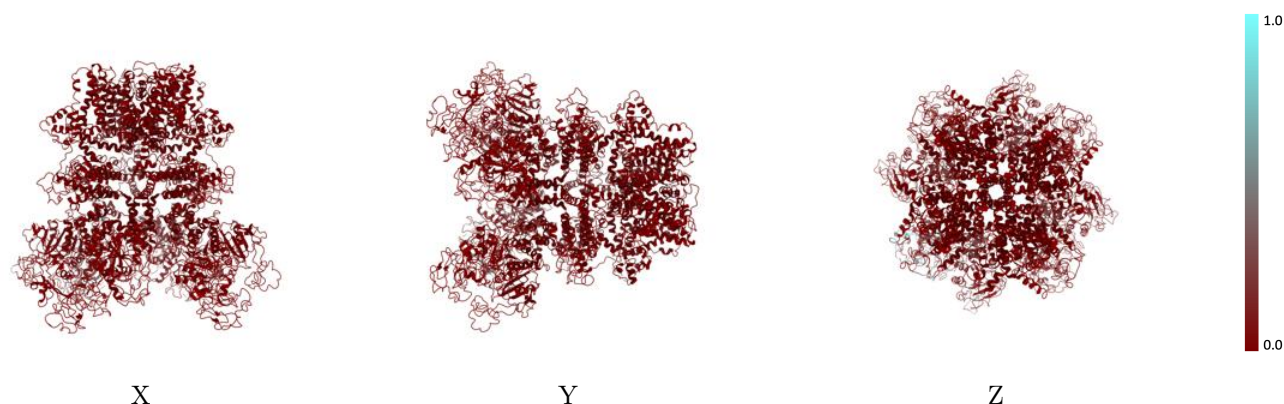
The images above show the 3D surface view of the map at the recommended contour level 3.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



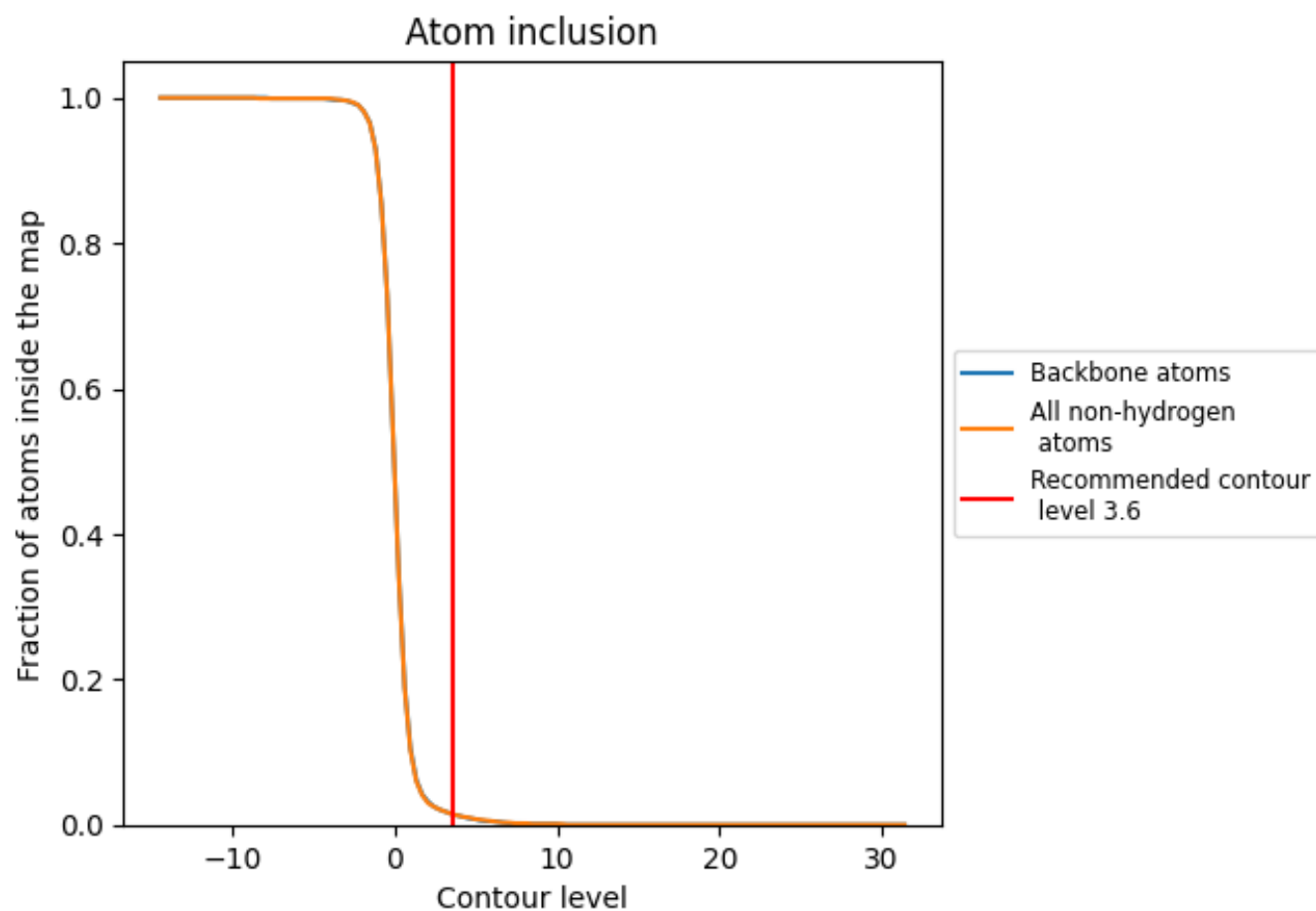
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.6).

9.4 Atom inclusion [i](#)



At the recommended contour level, 1% of all backbone atoms, 1% 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 (3.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.0140	-0.0020
A	0.0570	-0.0020
B	0.0000	0.0020
C	0.0000	-0.0030
D	0.0000	-0.0030

