



## wwPDB EM Validation Summary Report ⓘ

Oct 12, 2024 – 01:14 PM EDT

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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The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev113  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

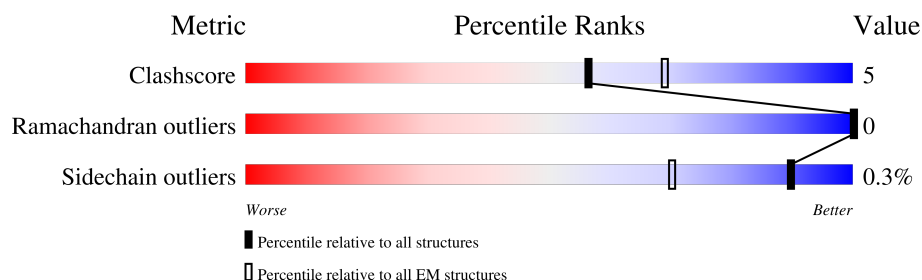
# 1 Overall quality at a glance

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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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  $\geq 3$ , 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
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	VAL	VAL
M1265	A1205	H1145	F1085	R1025	G965	P905	R845	D785	ARG	VAL	VAL
T1266	Q1206	C1146	F1086	R1026	T966	Y906	R846	L786	HIS	VAL	VAL
R1267	L1207	R1147	R1087	E1027	R967	D907	P847	A787	PRO	VAL	VAL
R1268	V1208	S1148	A1088	A1028	Q968	P908	H848	A788	TRP	VAL	VAL
R1269	L1209	Y1149	P1089	I1029	R969	A909	A849	S789	ALA	VAL	VAL
D1270	W1210	L1150	N1090	A1030	L970	N910	S850	F790	HIS	ALA	ALA
C1271	D1211	D1151	S1091	R1031	D971	W911	C851	S791	GLN	ALA	ALA
L1272	C1212	M1152	T1092	L1032	Q972	F912	L852	A792	ASP	LEU	LEU
L1273	L1213	L1153	N1093	W1033	D973	G913	S853	V793	VAL	LEU	LEU
P1274	I1214	K1154	L1094	P1034	L974	V914	T854	L794	SER	LEU	THR
V1275	L1215	V1155	I1095	N1035	L975	R915	W855	D675	GLU	THR	THR
E1276	Y1216	A1156	S1096	Y1036	S976	K916	W856	L676	ALA	THR	THR
E1277	M1217	V1157	D1097	C1037	C977	G917	W857	G677	PRO	THR	THR
A1278	V1218	F1158	F1098	L1038	L978	Y918	C858	L678	LEU	THR	THR
G1279	T1219	R1159	L1099	F1039	K979	P919	I859	E679	GLU	THR	THR
Y1280	V1220	Y1160	L1100	L1040	Y980	N920	I860	Q680	HIS	THR	THR
Y1281	I1221	L1161	L1101	T1041	F981	L921	I861	F681	GLN	THR	THR
W1282	I1222	F1162	L1102	L1042	I982	G922	W862	S682	GLU	THR	THR
D1283	S1223	W1163	C1103	F1043	N983	Y923	C863	V683	GLU	THR	THR
S1284	K1224	L1164	A1104	L1044	F984	I924	K864	Y624	VAL	THR	THR
M1285	M1225	V1165	S1105	L1045	F985	Q925	M865	Y625	VAL	THR	THR
C1286	M1226	L1166	Q1106	Y1046	F986	N926	L866	E626	PHE	THR	THR
F1287	L1227	V1167	Q1107	Q1047	Y987	H927	W867	L627	ARG	THR	THR
F1288	S1228	V1168	W1108	Y1048	K988	L928	Q868	W628	GLU	THR	THR
F1289	L1229	V1169	Q1109	L1049	F989	Q929	L869	R629	GLN	THR	THR
L1290	L1230	F1170	W1110	L1050	G990	I930	K870	K630	GLY	THR	THR
L1291	S1231	V1171	F1111	C1051	L991	L931	I871	L631	ASP	THR	THR
L1292	C1232	A1172	S1112	L1052	E992	L932	W872	L632	GLY	THR	THR
Q1293	V1233	A1173	A1113	G1053	I993	L933	M873	R633	PRO	THR	THR
R1294	F1234	A1174	E1114	M1054	C994	L934	R874	P634	HIS	THR	THR
R1295	V1235	T1175	R1115	P1055	F995	Y935	H875	F635	GLN	THR	THR
I1296	E1236	R1176	T1116	P1056	L996	F936	W876	W636	ALA	THR	THR
F1297	Q1237	E1177	E1117	A1057	M997	E937	TYR	W637	THR	THR	THR
L1298	M1238	S1178	E1118	L1058	A998	A938	SER	L638	VAL	THR	THR
S1299	Q1239	I1179	W1119	C1059	V999	V939	W878	V639	PRO	THR	THR
H1300	S1240	F1180	Q1120	I1060	N1000	V940	C881	W640	GLY	THR	THR
Y1301	M1241	G1181	R1121	D1061	V1001	Y941	T882	A641	ALA	THR	THR
F1302	F1242	L1182	M1122	Y1062	I1002	R942	E883	Y642	ALA	THR	THR
L1303	C1243	G1183	A1123	P1063	G1003	R943	P884	M644	LYS	THR	THR
H1304	V1244	Y1184	G1124	W1064	Q1004	Q944	F885	L645	TRP	THR	THR
V1305	V1245	L1185	I1125	R1065	R1005	E945	P886	V646	GLY	THR	THR
S1306	I1246	L1186	N1126	W1066	R1006	E946	ASN	L647	LEU	THR	THR
A1307	Q1247	A1187	T1127	S1067	N1007	Y947	THR	F707	VAL	THR	THR
D1308	L1248	C1188	D1128	K1068	F1008	R948	ASN	I648	ALA	THR	THR
L1309	F1249	F1189	M1129	A1069	M1009	R949	LEU	A649	VAL	THR	THR
K1310	S1250	Y1190	L1130	I1070	V1010	Q950	Q892	V650	ALA	THR	THR
A1311	L1251	L1191	E1131	P1071	I1011	H951	P893	T651	VAL	THR	THR
T1312	V1252	L1192	P1132	M1072	L1012	Q952	L894	T652	VAL	THR	THR
A1313	C1253	L1193	L1133	N1073	H1013	Q953	E895	F653	VAL	THR	THR
T1314	T1254	F1194	R1134	S1074	G1014	A954	I896	Q654	VAL	THR	THR
Q1315	V1255	G1195	G1135	A1075	C1015	P955	M897	L715	VAL	THR	THR
A1316	K1256	T1196	E1136	I1076	W1016	L956	Q898	Q656	VAL	THR	THR
G1257	G1257	T1197	P1137	I1077	L1017	P957	S899	D657	VAL	THR	THR
R1318	Y1258	L1198	N1138	K1078	V1018	F958	L900	F658	VAL	THR	THR
G1319	Y1259	L1199	P1139	W1079	A1019	Q959	A839	T660	VAL	THR	THR
F1320	D1260	Q1200	I1140	L1080	I1020	A960	L840				

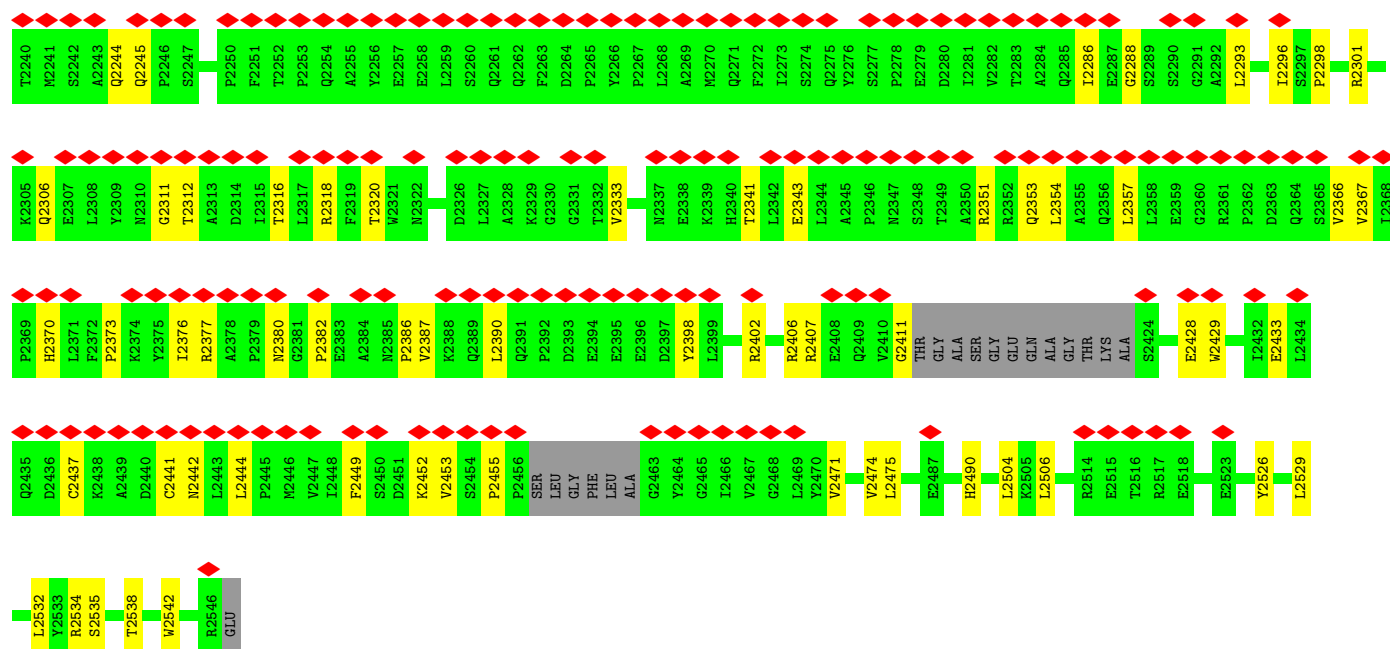






P1261	K1201	P1141	Y1081	L1021	V961	L901	P841	ASP	PRO	PRO	LYS
K1262	D1202	N1142	L1082	T1022	C962	Y902	Y842	R782	PRO	PRO	GLY
E1263	T1203	F1143	P1083	R1023	A963	R903	P843	L783	PRO	GLY	VAL
M1264	R1204	I1144	D1084	R1024	D964	G904	R844	L784	THR	ARG	V605
M1265	A1205	H1145	F1085	R1025	G965	P905	R845	D785	THR	ARG	Y606
T1266	Q1206	C1146	F1086	R1026	T966	Y906	R846	L786	HIS	HIS	K607
R1267	L1207	R1147	R1087	E1027	R967	D907	P847	A787	PRO	ARG	K608
R1268	V1208	S1148	A1088	A1028	Q968	P908	H848	A788	TRP	ALA	V609
R1269	L1209	Y1149	P1089	I1029	R969	A909	A849	S789	ALA	ALA	V610
D1270	W1210	L1150	N1090	A1030	L970	N910	S850	F790	ARG	ARG	M611
C1271	D1211	D1151	S1091	R1031	D971	W911	C851	S791	GLN	GLN	E671
L1272	C1212	M1152	T1092	L1032	Q972	F912	L852	A792	ASP	ASP	F612
L1273	L1213	L1153	N1093	W1033	D973	G913	S853	V793	VAL	VAL	L613
P1274	I1214	K1154	L1094	P1034	L974	V914	T854	L794	SER	SER	F614
V1275	L1215	V1155	T1095	N1035	L975	R915	W855	T795	GLU	GLU	L615
Y1216	V1216	A1156	S1096	Y1036	S976	K916	W856	R796	ALA	ALA	L616
E1277	M1217	V1157	D1097	C1037	C977	G917	T857	L797	PRO	PRO	C617
A1278	V1218	F1158	F1098	L1038	L978	Y918	C858	Q798	LEU	LEU	L618
G1279	T1219	R1159	L1099	F1039	K979	P919	T859	V799	GLU	GLU	T619
Y1280	V1220	Y1160	L1100	L1040	Y980	N920	T860	F800	HIS	HIS	L620
L1281	I1221	L1161	L1101	T1041	F981	L921	T861	W801	GLN	GLN	F621
W1282	I1222	F1162	L1102	L1042	I982	Q922	W862	R802	GLU	GLU	Q622
D1283	S1223	W1163	C1103	F1043	N983	Y923	C863	R803	GLU	GLU	Q623
S1284	K1224	L1164	A1104	L1044	F984	I924	K864	L804	VAL	VAL	Y624
M1225	M1225	V1165	S1105	L1045	F985	Q925	M865	L805	VAL	VAL	Y625
M1226	M1226	L1166	Q1106	Y1046	F986	N926	L866	E806	PHE	ARG	T626
L1227	L1227	V1167	Q1107	Q1047	Y987	H927	Y867	L807	GLU	GLU	L627
S1228	S1228	V1168	W1108	Y1048	K988	L928	Q868	H808	GLN	GLN	W628
L1229	L1229	V1169	Q1109	L1049	F989	Q929	L869	W809	GLY	GLY	R629
L1230	L1230	F1170	V1110	L1050	G990	I930	K870	F810	SER	SER	K630
S1231	S1231	V1171	F1111	C1051	L991	L931	T871	K811	ASP	ASP	L631
C1232	C1232	A1172	S1112	L1052	E992	L932	W872	L812	GLY	GLY	L632
V1233	V1233	G1173	A1113	G1053	I993	L933	M873	W813	PRO	PRO	R633
F1234	F1234	A1174	E1114	M1054	C994	L934	P874	A814	HIS	HIS	V634
V1235	V1235	T1175	R1115	P1055	F995	Y935	H875	L815	GLN	GLN	F635
E1236	E1236	R1176	T1116	P1056	L996	F936	GLU	Y816	THR	THR	W636
Q1237	Q1237	E1177	E1117	A1057	M997	E937	TYR	T817	GLN	GLN	W637
L1238	L1238	S1178	E1118	L1058	A998	A938	SER	W818	VAL	VAL	L638
Q1239	Q1239	I1179	W1119	C1059	V999	V939	N880	W819	PRO	PRO	W639
S1240	S1240	F1180	Q1120	I1060	N1000	V940	C891	W820	GLY	GLY	V640
M1241	M1241	G1181	R1121	D1061	V1001	Y941	T882	A821	ALA	ALA	A641
F1242	F1242	L1182	M1122	Y1062	I1002	R942	E883	L822	THR	THR	Y642
C1243	C1243	G1183	A1123	P1063	G1003	R943	P884	K823	SER	SER	M644
Y1244	Y1244	Y1184	G1124	W1064	Q1004	Q944	F885	E824	TRP	TRP	L645
V1245	V1245	L1185	I1125	R1065	R1005	E945	P886	W825	GLY	GLY	V646
I1246	I1246	L1186	N1126	W1066	R1006	E946	ASN	S826	VAL	VAL	L647
Q1247	Q1247	A1187	T1127	S1067	N1007	Y947	THR	V827	ALA	ALA	L648
L1248	L1248	C1188	D1128	K1068	F1008	R948	ASN	M828	THR	THR	A649
F1249	F1249	F1189	L1129	A1069	M1009	R949	LEU	N829	PRO	PRO	V650
K1250	S1250	Y1190	L1130	I1070	V1010	Q950	Q892	N830	GLY	GLY	Y651
L1251	L1251	L1191	E1131	P1071	I1011	H951	P893	L831	VAL	VAL	T652
V1252	V1252	L1192	P1132	M1072	L1012	Q952	L894	L832	GLY	GLY	F653
C1253	C1253	L1193	L1133	N1073	H1013	Q953	E895	W833	TRP	TRP	Q654
T1254	T1254	F1194	R1134	S1074	G1014	A954	I896	W834	LYS	LYS	L714
V1255	V1255	G1195	G1135	A1075	C1015	P955	N897	L835	GLY	GLY	T715
K1256	K1256	T1196	E1136	L1076	W1016	L956	Q898	W836	LEU	LEU	Q656
G1257	G1257	T1197	P1137	I1077	L1017	P957	S899	A837	VAL	VAL	D716
Y1258	Y1258	L1198	N1138	K1078	V1018	F958	L900	F838	ALA	ALA	F658
G1319	G1319	L1199	P1139	W1079	A1019	Q959	L900	A839	GLY	GLY	P659
F1320	D1260	Q1200	T1140	L1080	I1020	A960	L840	L840	HIS	HIS	T660





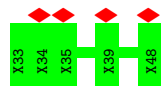
- Molecule 2: Piezo-type mechanosensitive ion channel component 1, unknown fragment



- 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%)	91	92
1	C	1198/2246 (53%)	1195 (100%)	3 (0%)	91	92
1	E	1198/2246 (53%)	1195 (100%)	3 (0%)	91	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	3594/6738 (53%)	3585 (100%)	9 (0%)	90 92

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 ⓘ

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.

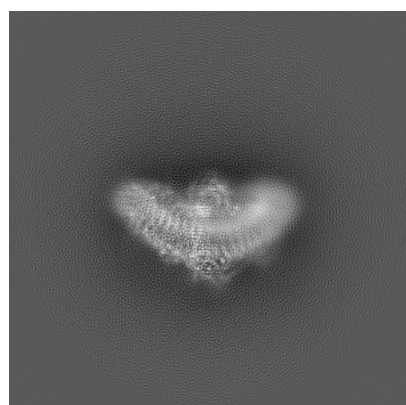
## 6 Map visualisation [i](#)

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.

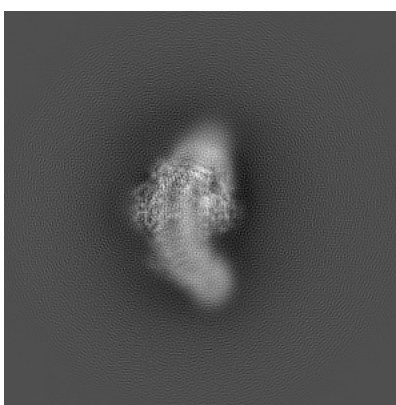
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

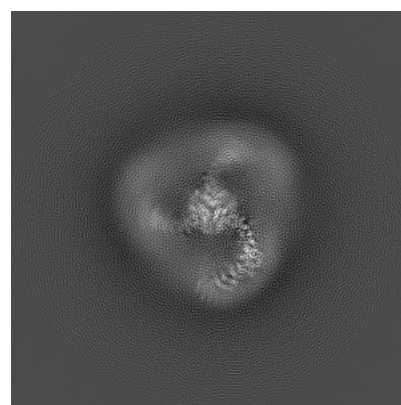
#### 6.1.1 Primary map



X



Y



Z

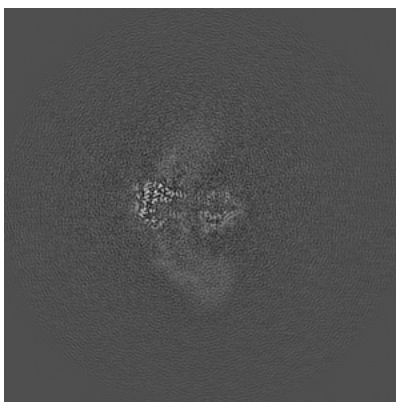
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

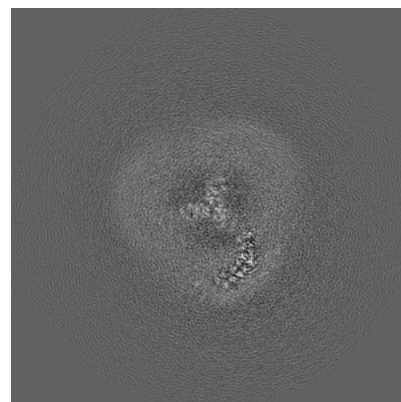
#### 6.2.1 Primary map



X Index: 200



Y Index: 200

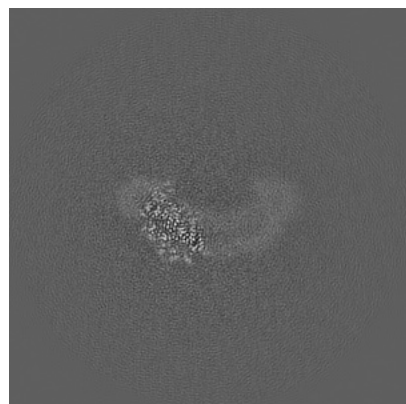


Z Index: 200

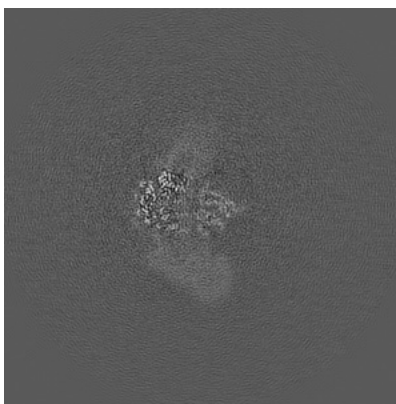
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

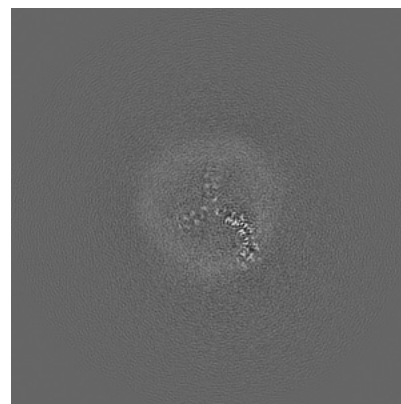
### 6.3.1 Primary map



X Index: 233



Y Index: 193

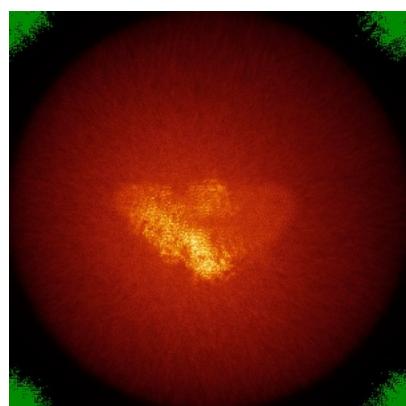


Z Index: 170

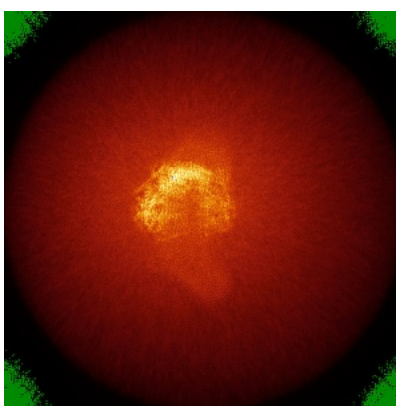
The images above show the largest variance slices of the map in three orthogonal directions.

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

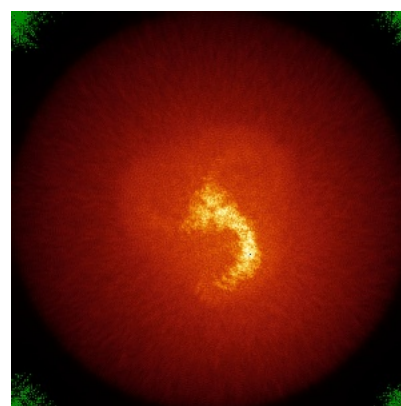
### 6.4.1 Primary map



X



Y

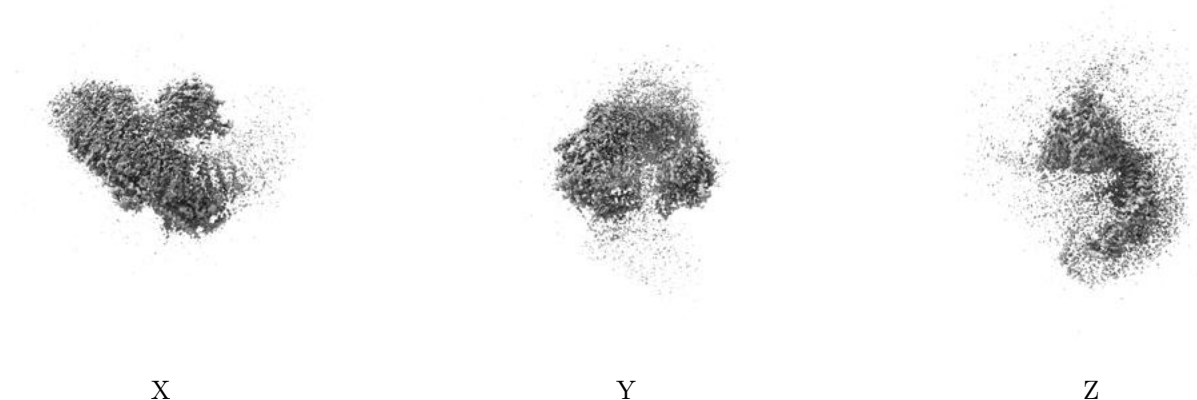


Z

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.

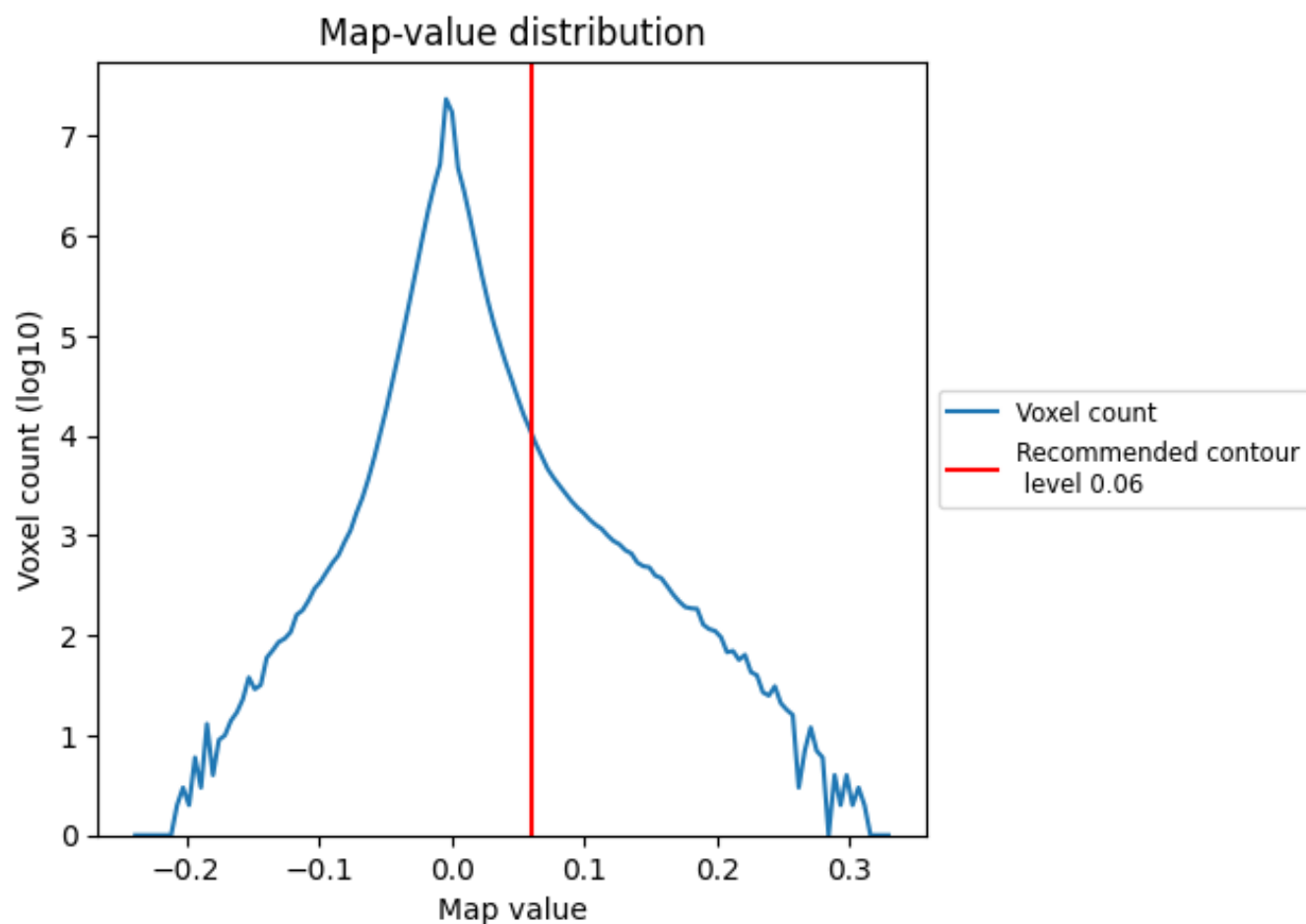
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

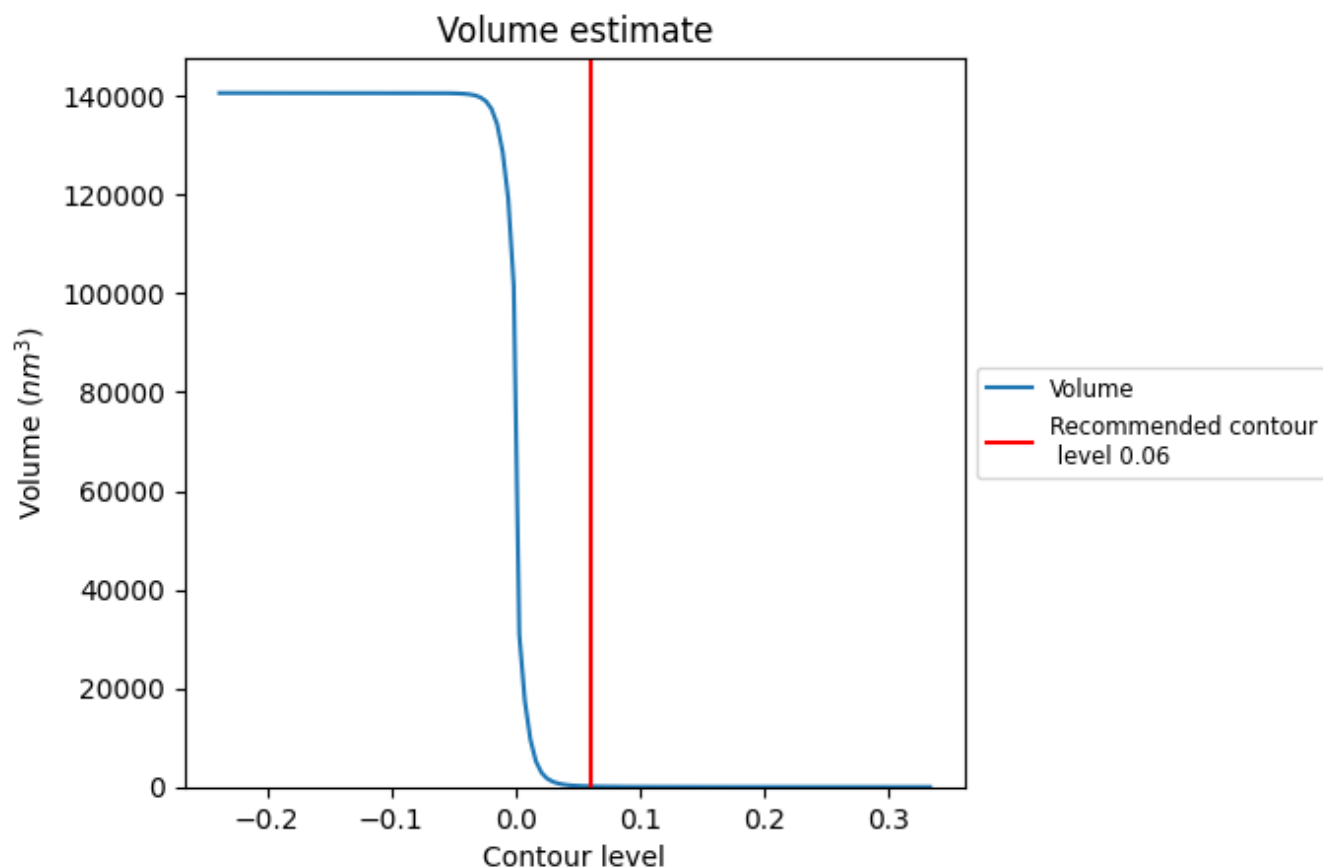
This section contains the results of statistical analysis of the map.

### 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.

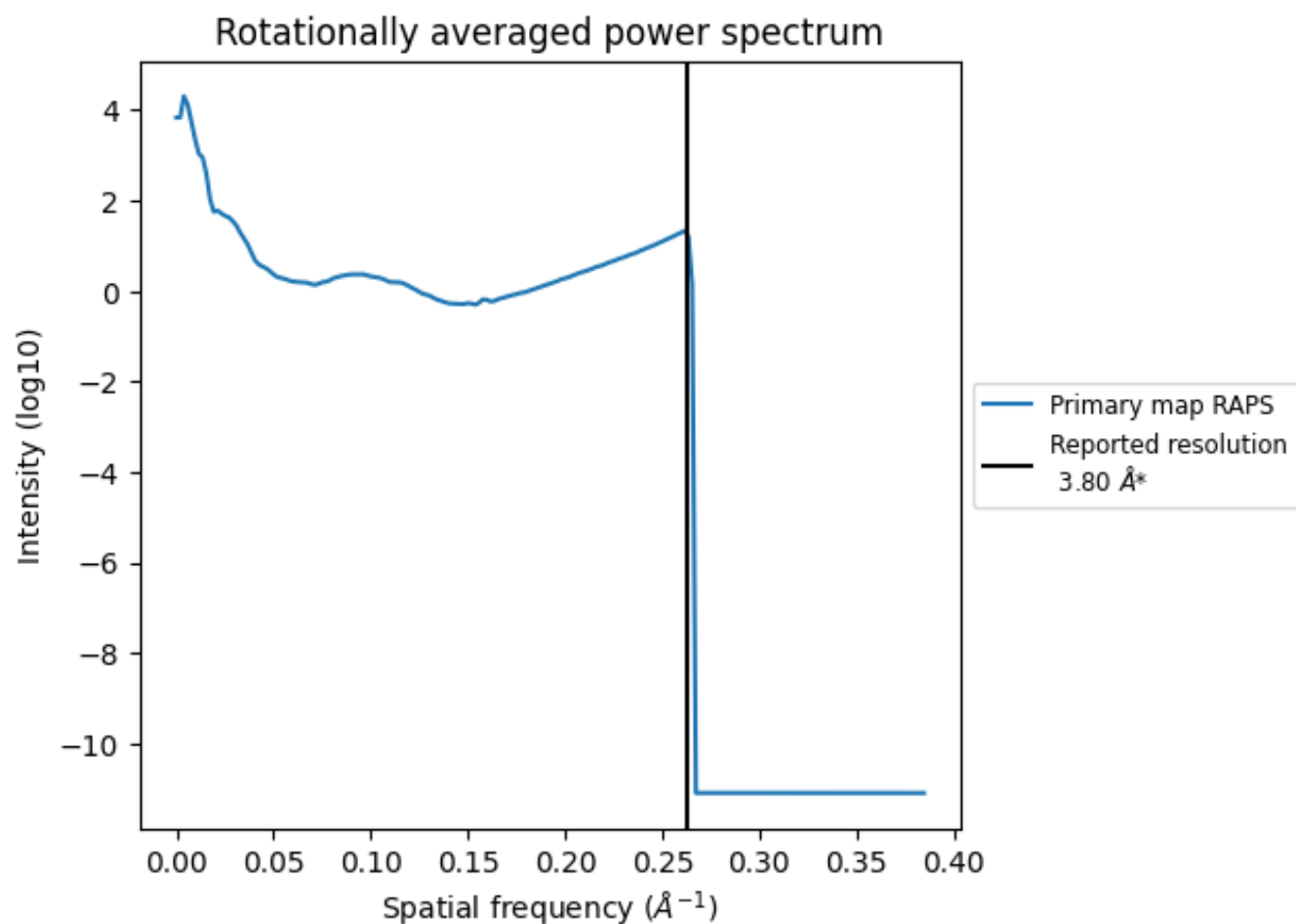
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 123 nm<sup>3</sup>; 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<sup>-1</sup>

## 8 Fourier-Shell correlation

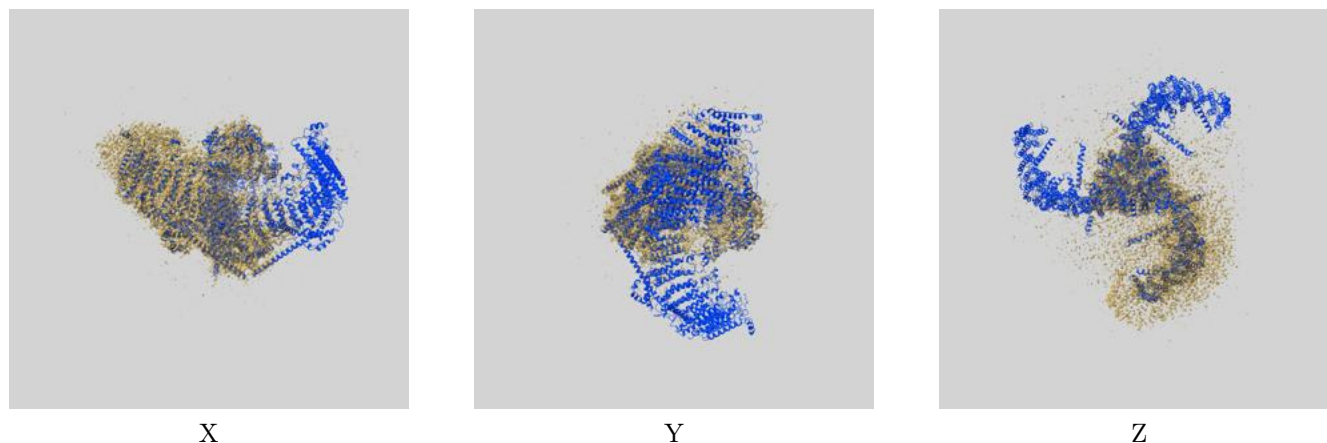
This section was not generated. No FSC curve or half-maps provided.



## 9 Map-model fit [i](#)

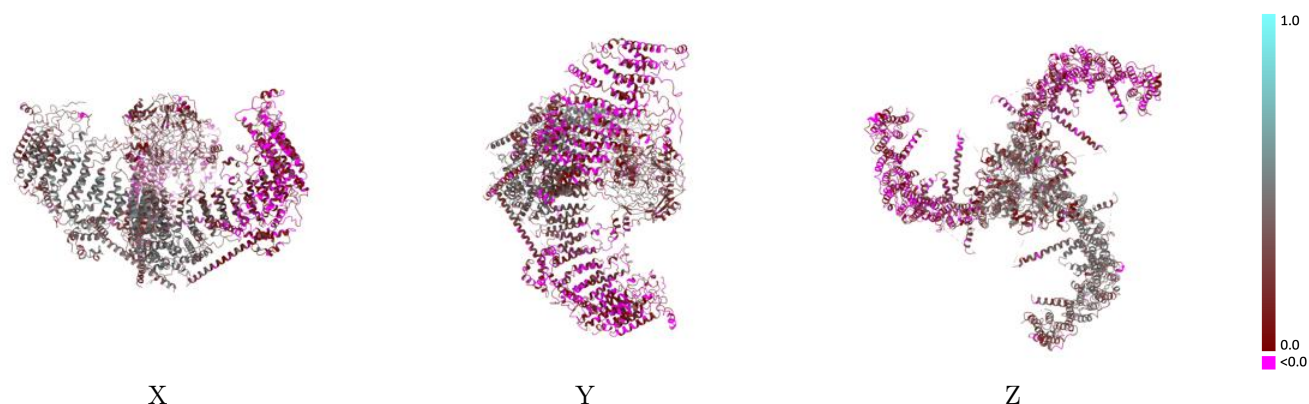
This section contains information regarding the fit between EMDB map EMD-7042 and PDB model 6B3R. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

### 9.1 Map-model overlay [i](#)



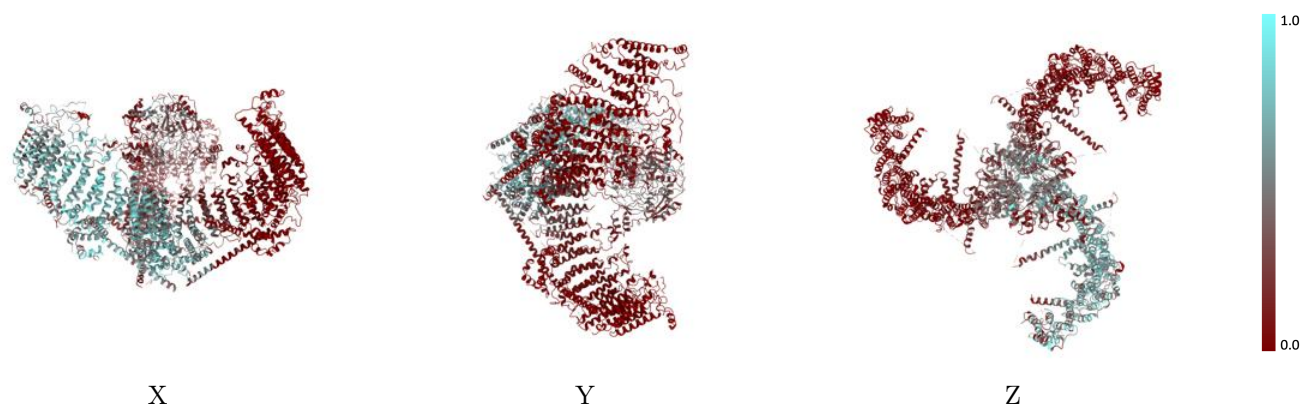
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



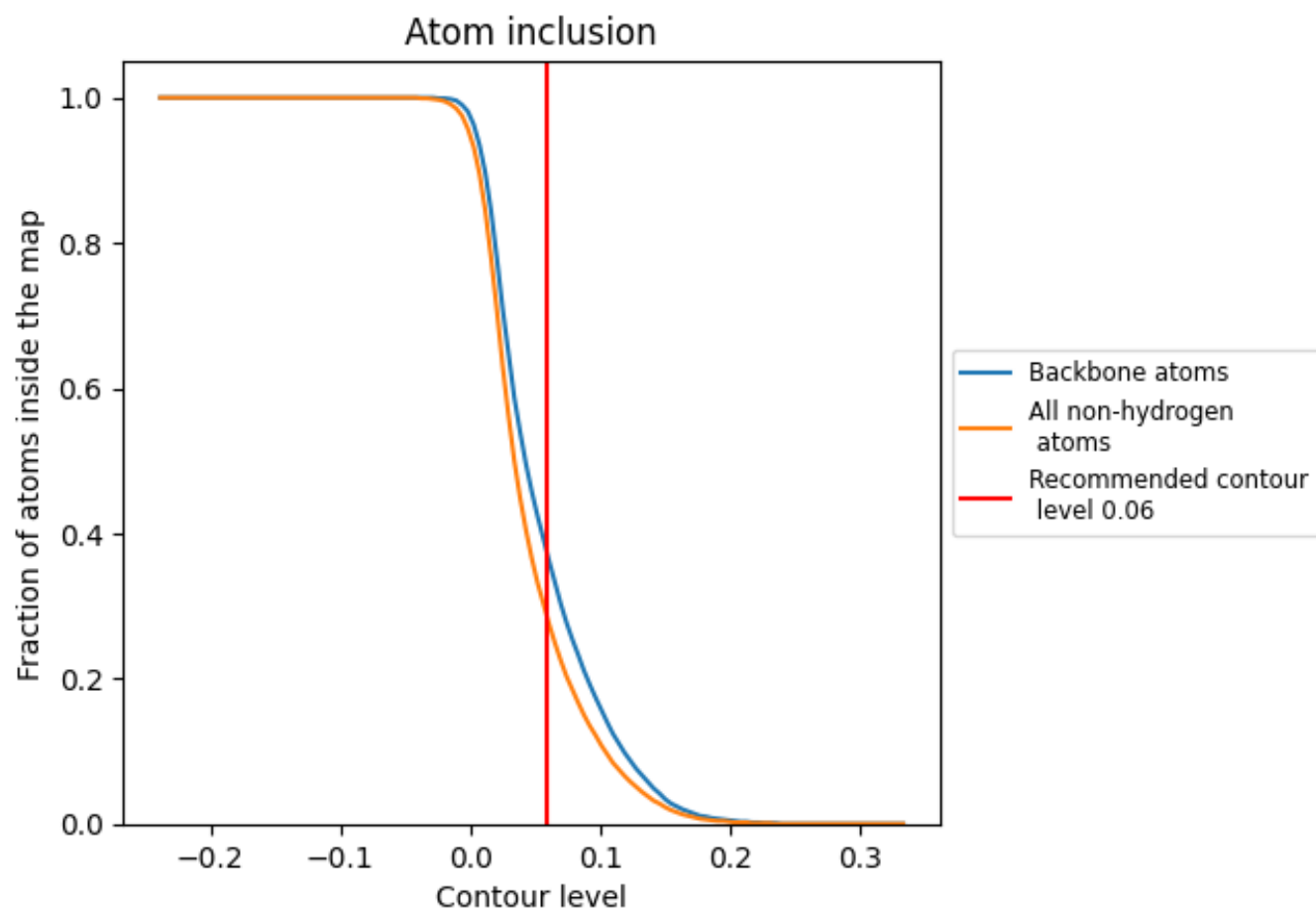
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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	<div></div> 0.2810	<div></div> 0.2360
A	<div></div> 0.5390	<div></div> 0.3720
B	<div></div> 0.7250	<div></div> 0.4520
C	<div></div> 0.1470	<div></div> 0.1650
D	<div></div> 0.6880	<div></div> 0.4410
E	<div></div> 0.1470	<div></div> 0.1660
F	<div></div> 0.6250	<div></div> 0.4110

1.0

0.0

<0.0