



## wwPDB EM Validation Summary Report ⓘ

Apr 13, 2026 – 10:46 AM EDT

PDB ID : 9ELD / pdb\_00009eld  
EMDB ID : EMD-48145  
Title : Full-length and internally HIS-tagged yeast E3 ubiquitin ligase Tom1p in an open-conformation  
Authors : Madrigal, J.M.  
Deposited on : 2024-12-04  
Resolution : 7.10 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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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.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

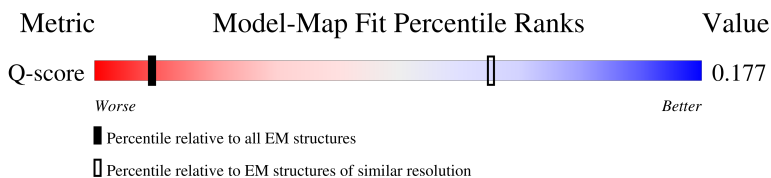
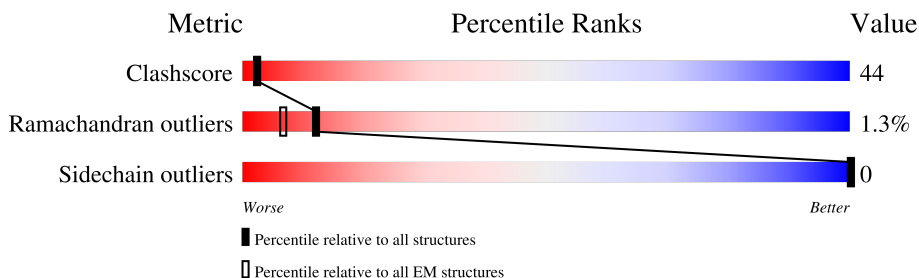
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 7.10 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	464 ( 6.60 - 7.60 )

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	3289	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 43025 atoms, of which 21527 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 E3 ubiquitin-protein ligase TOM1.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	A	2680	43025	13817	21527	3550	4035	96	0	0

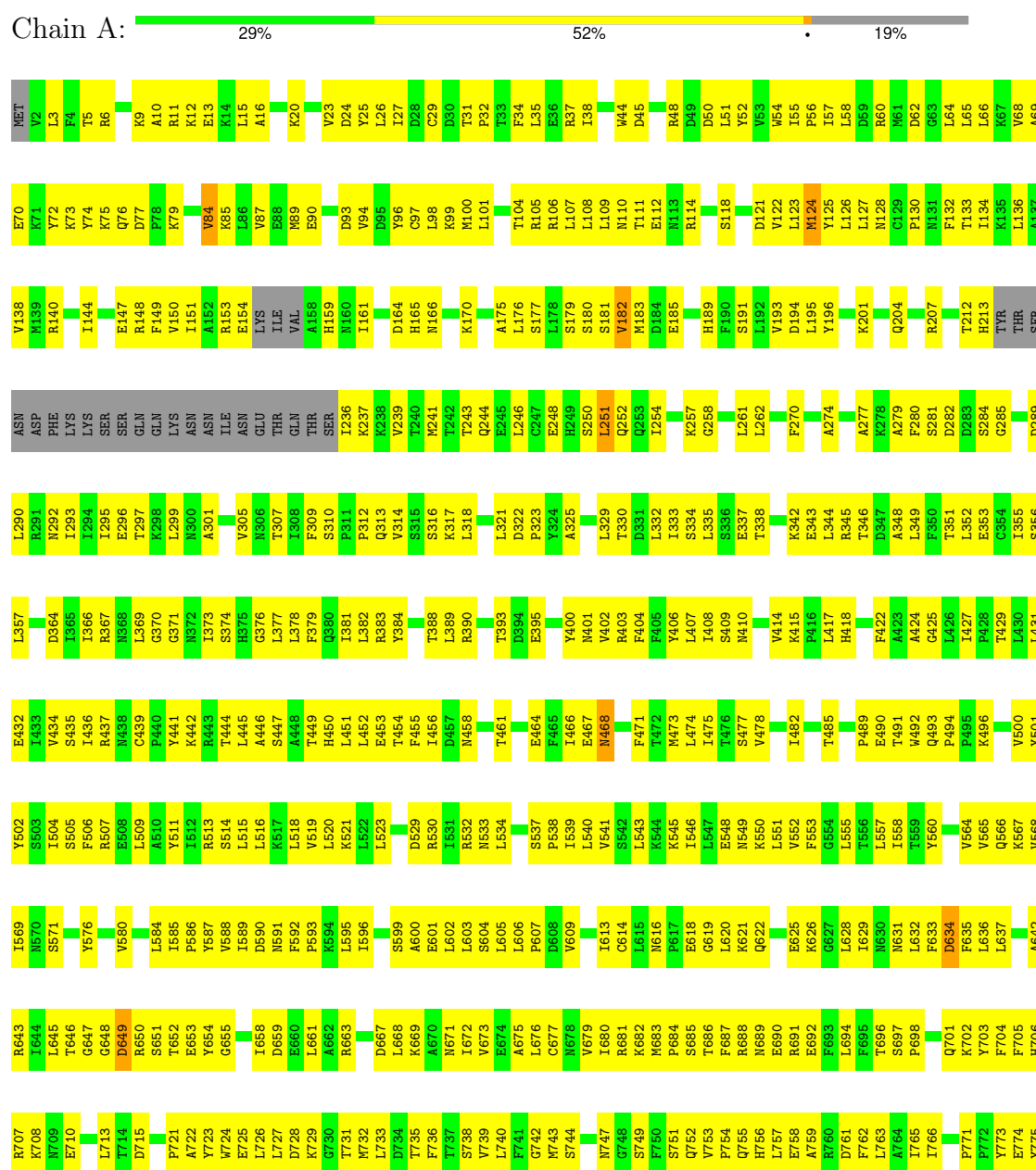
There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1073B	SER	-	insertion	UNP Q03280
A	1073C	GLY	-	insertion	UNP Q03280
A	1073D	GLY	-	insertion	UNP Q03280
A	1073E	GLY	-	insertion	UNP Q03280
A	1073F	GLY	-	insertion	UNP Q03280
A	1073G	GLY	-	insertion	UNP Q03280
A	1073H	GLY	-	insertion	UNP Q03280
A	1073I	SER	-	insertion	UNP Q03280
A	1073J	ARG	-	insertion	UNP Q03280
A	1073K	HIS	-	insertion	UNP Q03280
A	1073L	HIS	-	insertion	UNP Q03280
A	1073M	HIS	-	insertion	UNP Q03280
A	1073N	HIS	-	insertion	UNP Q03280
A	1073O	HIS	-	insertion	UNP Q03280
A	1073P	HIS	-	insertion	UNP Q03280
A	1073Q	HIS	-	insertion	UNP Q03280
A	1073R	HIS	-	insertion	UNP Q03280
A	1073S	HIS	-	insertion	UNP Q03280
A	1073T	HIS	-	insertion	UNP Q03280
A	1073U	HIS	-	insertion	UNP Q03280
A	1073V	HIS	-	insertion	UNP Q03280

### 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: E3 ubiquitin-protein ligase TOM1



I1725	N1641	F1571	E1511	K1436	M1367	K1301	L1230	T1160	G1090	T1044	S978	T910	C844	F776
L1728	A1644	H1572	T1512	L1437	Q1368	L1302	I1236	Q1161	I1091	I1045	R379	E911	R845	T777
A1729	Q1645	E1573	T1513	F1438	R1369	L1303	I1237	R1163	T1092	P1046	N980	M913	L846	S778
L1730	L1646	F1574	E1514	D1439	F1370	M1304	I1238	R1164	T1093	A1047	M981	M913	A847	A847
S1731	D1647	D1576	N1516	I1440	I1371	F1305	A1239	M1165	S1095	Y1048	L982	P914	L848	A780
	P1648	Q1577	D1517	L1442	Y1373	A1307	S1240	P1166	C1096	F1050	L983	P916	L849	I781
			A1518	R1443	Y1374	K1308	F1241	Y1167	L1097	Y1051	E984	I917	L850	S782
			E1519	L1444	E1375	T1309	E1242	Y1168	L1098	Q1052	H985	V918	L851	H783
			L1510	Y1444	E1376	L1309	F1242	V1169	T1098	K1053	K986	V918	L852	V784
			E1520	S1445	K1377	L1310			A1100	G1054	L987	V920	L853	T785
			R1521	D1446	E1378	L1311			M1099	G1055	L988	G921	T854	
			A1522	I1447	K1378	Y1313	K1249	Q1172	L1101	G1056	T989	G922	L855	Q789
			E1523	S1448	L1379	F1313	L1250	L1173	T1102	Y1056	T990	G923	L856	Y790
			I1524	N1449	P1380	F1314	I1251	L1174	F1103	L1057	E991	D923	L857	L791
			N1525	Y1450	E1381			S1175	M1105	Y1058	Y992	G924	L858	D792
			R1526	F1451	H1382			M1176	L1106	D1065	E1000	P926	L859	D793
			S1527		K1383	Y1317	S1256	K1178	K1106	H1061	F995	L927	L860	K794
			F1528	L1454	N1384	D1318			M1114	L1062	E996	Q928	L863	Y795
			T1529	A1455	F1385	E1319	Y1269	M1179	S1107	I1063	N997	I929	L864	E796
			A1530	T1456	T1386	P1320	P1260	I1180	T1110	R1064	V998	Y930	L865	D797
			R1531	S1457	W1387		Q1261	F1181		D1066	Y999	I931	K866	A799
			P1532	R1458	F1388	R1327	M1262	T1182		L1067	L1068	I931	L867	F800
			L1533	I1459	S1389	I1328	M1263	M1183		T1068	N1001	Q939	L868	M801
			G1534	L1460	K1390	L1329	Q1264			R1069	Y1002		L869	
			GLY	I1461	A1391	D1330	A1265	Y1187			I1003		Q870	V803
			GLY	F1462	L1392	R1331	Q1266	T1188			I1004		L871	M804
			ASP	Y1463	F1393	I1332	Y1267			K1072	E1004		L872	K805
			ASP	S1464	Y1394	L1333	E1268			I1073	M1005		L873	V806
			A1539	R1465	Y1395	E1334	K1269	Y1192		LYS	L1006		L874	L807
			V1540	D1466	K1396	E1335	G1270	E1193		GLY	K1007		L875	N808
			R1541	E1467	T1397	D1336	C1271	L1194		GLY	E1012		L876	D809
			E1542	L1468	F1398	L1337	S1272	H1195		GLY			L877	Q810
			L1543		L1399	D1338	S1273	W1196		GLY	L1015		L878	L811
			T1544	M1471	A1400	P1339	E1274	D1197		GLY	P1016		L879	E812
			T1545		K1401	F1340	E1275	L1198		GLY	Y1017		L880	F880
			I1546	A1474	S1402	A1341	L1276			GLY	I1018		L881	L814
			L1547	R1475	E1403	T1342	D1277	K1205		GLY	G953		L882	N815
			E1548	S1476	L1404	L1343	E1278	I1206		GLY	M954		L883	D816
			E1549	G1477	P1405	S1344	L1279	S1207		GLY	V1020		L884	F817
			K1550	L1478	L1406	S1345	D1280	L1208		GLY	L1019		L885	L818
			A1551	L1479	L1407	L1346	D1281	F1209		GLY	L1021		L886	N819
			H1552	S1480	E1408	I1347	T1282	E1210		HIS	N1025		L887	S820
			V1553	R1481	E1409	H1348	F1283	G1211		HIS	T1026		F890	F826
			V1554		L1410	L1349	E1284	Y1212		HIS	F1027		Q891	F827
			M1555	Q1490		F1350	M1285	G1213		HIS	V1028		E896	R830
			R1556	K1491	V1414	G1351	D1286	G1213		HIS	F1029		E897	D831
			S1557	L1492	L1415	I1352	G1287	I1214		HIS	T1030		Y898	E832
			P1558		L1416	F1353	L1288	P1215		HIS	I1031		Y899	E833
			S1559	L1498		L1354	P1289	G1216		HIS	P1032		M898	N834
			Q1560		S1422		S1290	V1218		HIS	K1033		Y899	S835
			F1561	S1501		K1357	R1291	A1219		HIS	A1034		Y899	R901
			I1562	F1502	V1426	Y1358	I1292	A1220		ASP	S1035		Y899	Q902
			L1563	L1503	F1427	I1359	F1293	N1221		L1076	P1036		Y899	H903
			V1564	L1504	R1428	Y1360	T1294	Y1222			N1037		Y899	R837
			L1565	L1505	I1429	Q1361	L1296	D1152			S1038		Y899	F972
			L1566	T1506	I1429	G1362	L1296	D1155			T1039		Y899	M904
			C1566	P1430	P1430	A1363	P1297	S1156			E1040		Y899	P905
			E1567	D1431	D1431	A1363	P1297	T1226			E1040		Y899	C839
			T1568	C1508	P1432	H1364	Y1298	D1227			I1041		Y899	H840
			A1569	C1509	P1432	S1364	Y1298	D1228			I1042		Y899	
			E1569	E1510	Q1435	L1366	P1300	D1229			Q1043		Y899	L843



P3230	N3156	E3085	I3008	F2929	N2864
S3231	K3157	K3088	I3009	F2930	Q2865
H3232	N3158	D3089	G3010	K2931	N2866
T3233	N3159	I3090	K3011	E2935	I2867
C3234	T3160	I3091	A3012	I2936	R2868
C3235	T3161	I3092	I3013	K2937	S2869
F3236	V3162	T3093	R3014	N2938	N2870
N3237	V3163		D3015	S2939	
Q3238	N3164	N3096	Q3016	K2940	N2874
L3239	T3165	K3097	F3017	L2941	S2875
N3240	T3166		F3018	E2942	G2876
L3241	A3167	Y3100	L3019	I2943	P2877
F3242	T3168	V3101	C3021	R2944	F2878
Y3244		K3102	H3022		A2879
	E3171	K3103	F3023	V2951	L2880
	S3173	V3104	S3024		L2881
		V3105	R3025	G2955	V2882
L3255	V3176	E3106	E3026	V2956	K2883
L3256	R3177	Y3107	V3027		N2884
A3257	A3178	K3108		E2959	P2885
I3258	V3179	L3109	N3030	W2960	K2886
		Q3110		V2963	L2887
G3261	D3183	T3111	V3036	L2964	L2888
H3262	A3184	S3112	S3037		F2889
E3263	E3185	V3113	L3038		D2890
G3264	E3186		K3039	M2968	I2891
F3265	R3187	Q3116	D3040	F2969	N2892
	A3188	M3117	N3041	N2970	K2893
	K3189	D3118	E3042		R2894
		N3119	S3043	Y2973	Y2895
Q3192		F3120	L3044	A2974	F2896
F3193		L3121		F2976	F2897
V3194		V3122	Y3048		N2898
T3195		G3123		V2979	K2900
G3196					L2901
T3197		L3127	L3052	P2980	K2902
S3198		I3128		S2981	S2903
K3199			I3055	D2982	ASP
V3200		D3131	L3056	K2983	ASN
		L3132	E3057	T2984	GLN
		I3133	N3058	T2985	E2907
N3203	G3204	T3134	D3059	F2986	
F3205	K3206	I3135	I3060	H2987	L2911
K3206	E3207	F3136		P2988	F2912
		D3137	T3067	N2989	L2913
		E3138	F3068	R2990	T2914
S3209	S3209	Q3139	S3069	T2991	T2915
G3210	G3210	E3140	V3070	S2992	R2916
V3211	V3211	L3141	E3071	G2993	R2917
N3212	N3212	E3142	T3072	I2994	E2918
G3213	G3213	L3143	D3073	N2995	Q2919
V3214	V3214	L3144	D3074		V2920
C3215	C3215	I3145		L2999	F2921
K3216	K3216	S3146	E3077		L2922
F3217	F3217		H3078	F3002	D2923
S3218	S3218	D3152	K3079		S2924
I3219	I3219	V3153	V3080		
H3220	H3220	D3154		I3005	A2927
		D3155	I3084	G3006	L2928
				M3007	

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	16098	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	47	Depositor
Minimum defocus (nm)	-800	Depositor
Maximum defocus (nm)	-2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.656	Depositor
Minimum map value	-0.166	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.1	Depositor
Map size ( $\text{\AA}$ )	387.2, 387.2, 387.2	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.5125, 1.5125, 1.5125	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	0.21	0/21920	0.43	6/29669 (0.0%)

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	1

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	468	ASN	CA-C-N	9.15	141.11	124.82
1	A	468	ASN	C-N-CA	9.15	141.11	124.82
1	A	1321	THR	OG1-CB-CG2	5.63	120.56	109.30
1	A	3128	ILE	CG1-CB-CG2	5.35	126.75	110.70
1	A	2943	ILE	CG1-CB-CG2	5.29	126.58	110.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	124	MET	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	21498	21527	21652	1912	0
All	All	21498	21527	21652	1912	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 44.

The worst 5 of 1912 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:1589:LEU:HD12	1:A:1592:LYS:HD2	1.41	0.98
1:A:74:TYR:OH	1:A:87:VAL:O	1.82	0.98
1:A:970:ARG:NE	1:A:1030:THR:O	1.98	0.96
1:A:2710:LEU:HD22	1:A:2785:VAL:HG11	1.44	0.95
1:A:1403:GLU:OE2	1:A:2239:TYR:OH	1.85	0.94

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	2660/3289 (81%)	2092 (79%)	533 (20%)	35 (1%)	9	42

5 of 35 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	84	VAL
1	A	182	VAL
1	A	634	ASP
1	A	799	ALA
1	A	1035	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	2416/3002 (80%)	2416 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2475	GLN
1	A	2680	ASN
1	A	3212	ASN
1	A	2555	GLN
1	A	2795	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 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.

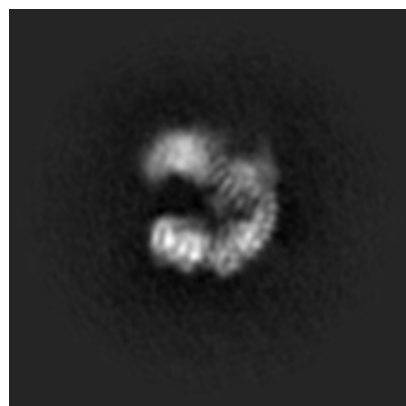
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-48145. These allow visual inspection of the internal detail of the map and identification of artifacts.

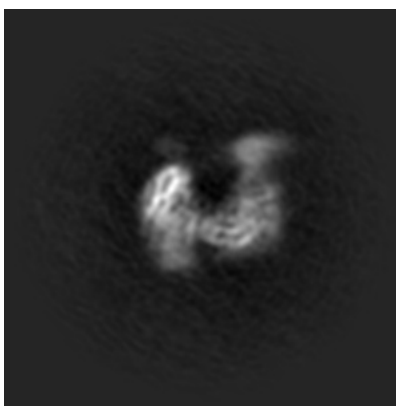
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

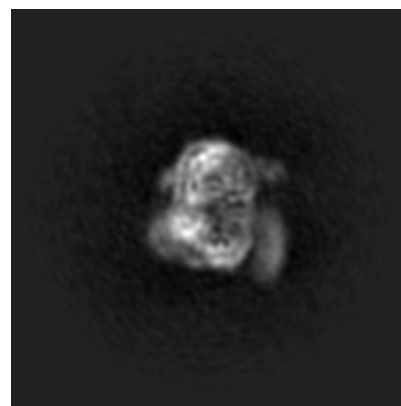
#### 6.1.1 Primary map



X

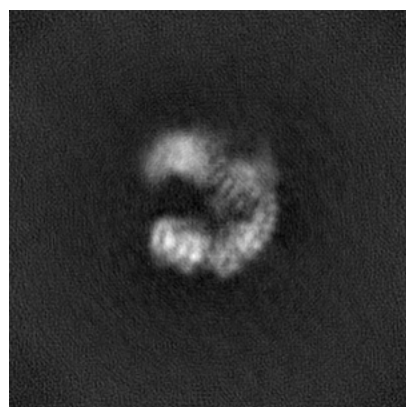


Y

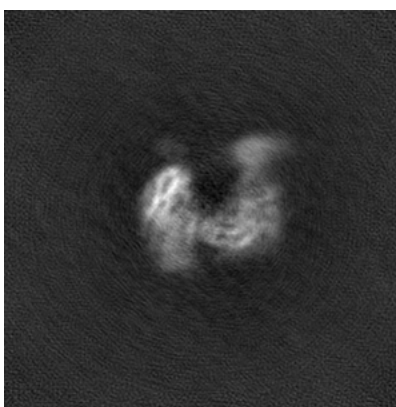


Z

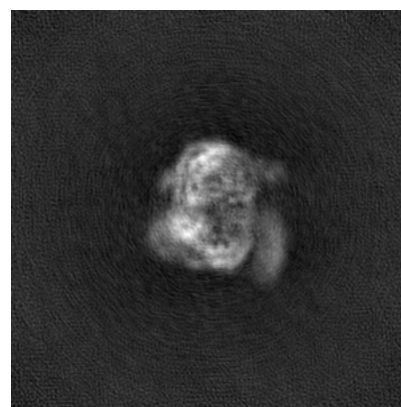
#### 6.1.2 Raw map



X



Y

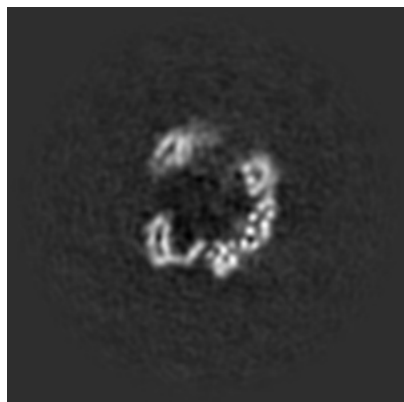


Z

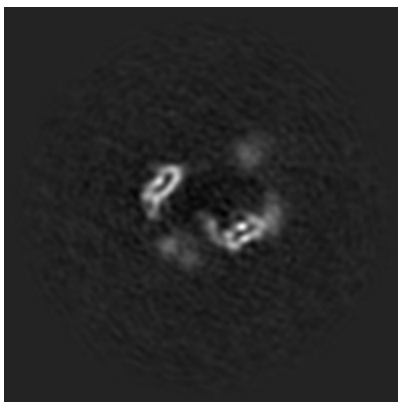
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

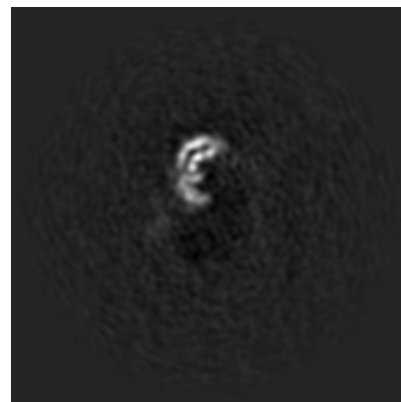
### 6.2.1 Primary map



X Index: 128

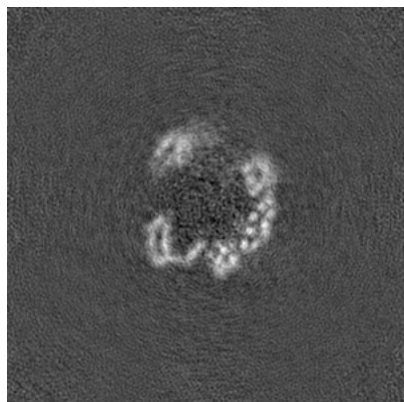


Y Index: 128

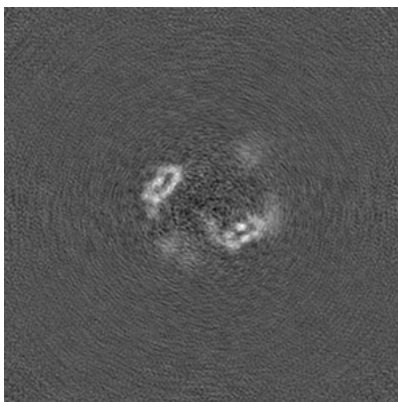


Z Index: 128

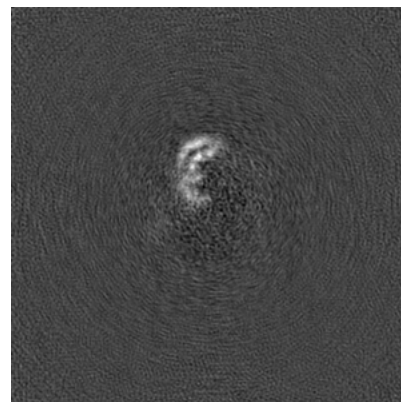
### 6.2.2 Raw map



X Index: 128



Y Index: 128

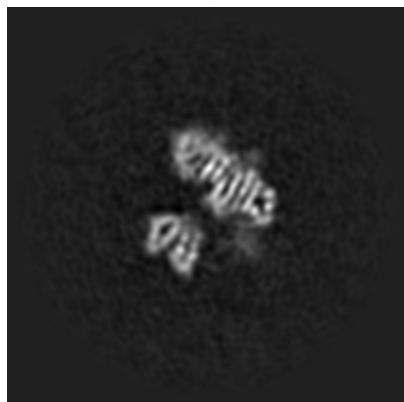


Z Index: 128

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

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

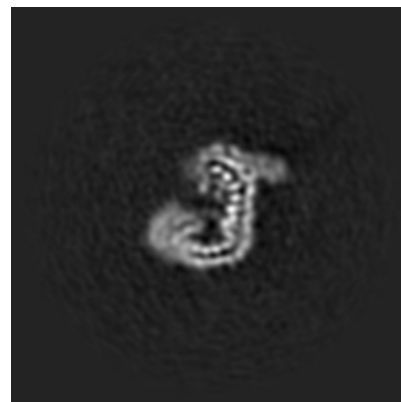
### 6.3.1 Primary map



X Index: 115

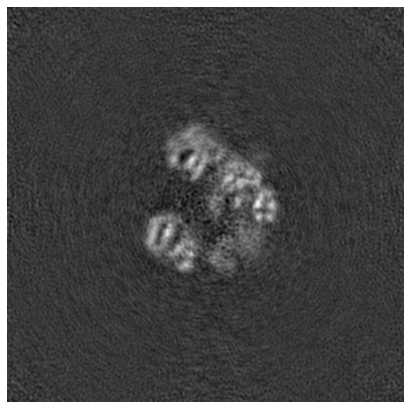


Y Index: 112

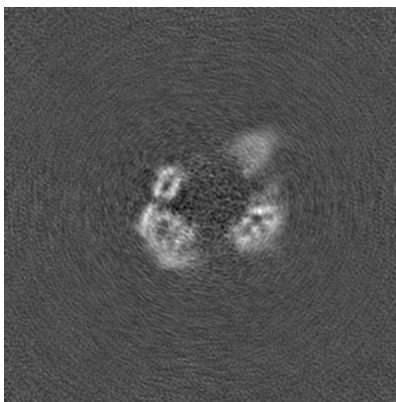


Z Index: 107

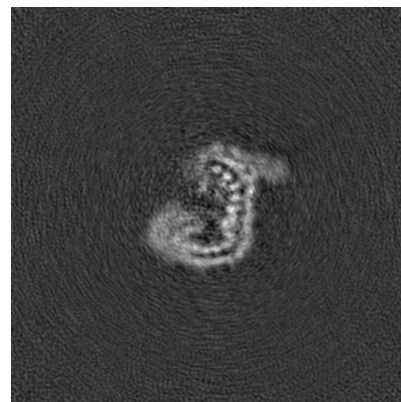
### 6.3.2 Raw map



X Index: 120



Y Index: 115



Z Index: 107

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

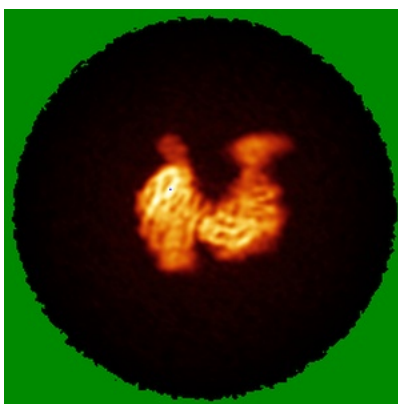


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

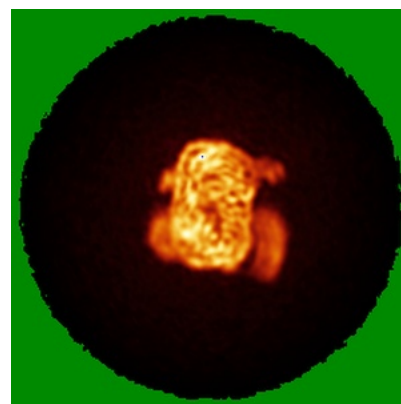
### 6.4.1 Primary map



X

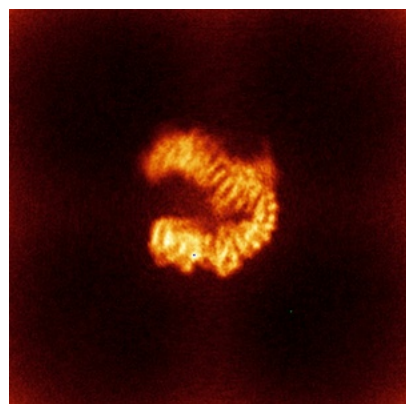


Y

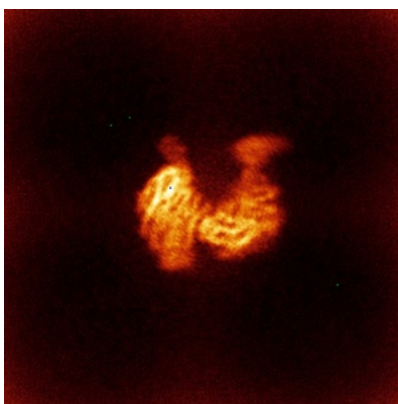


Z

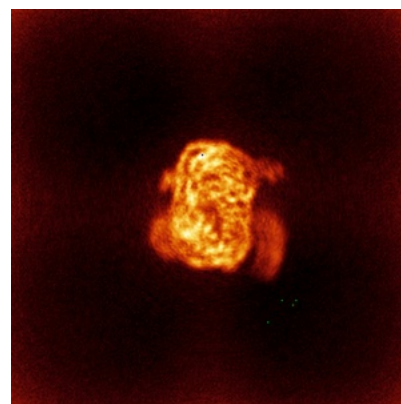
### 6.4.2 Raw map



X



Y



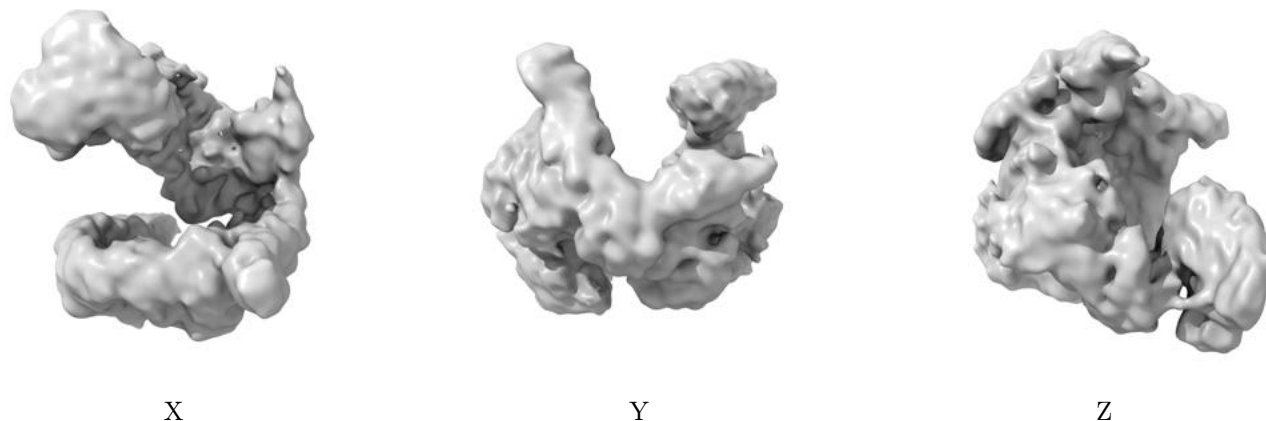
Z

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.



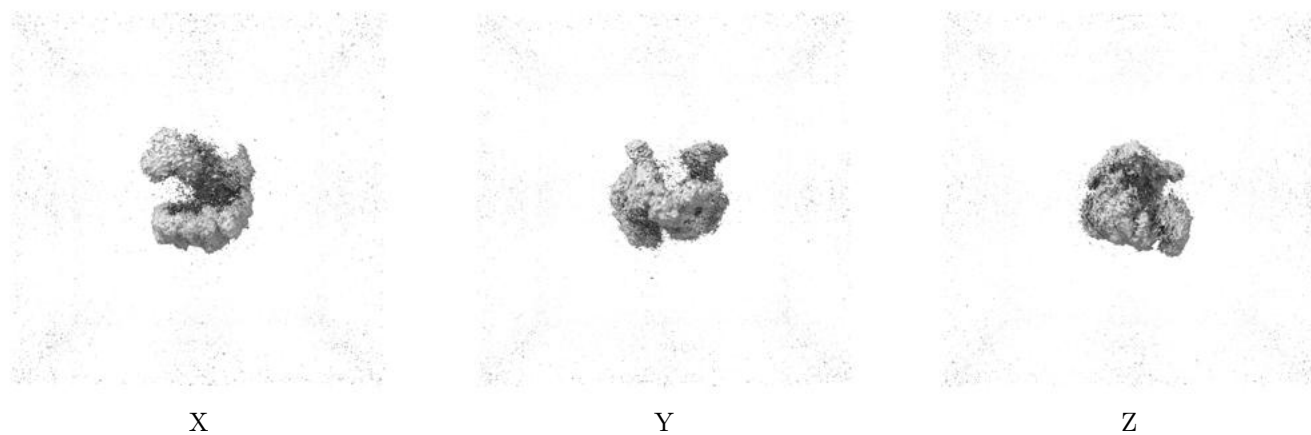
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

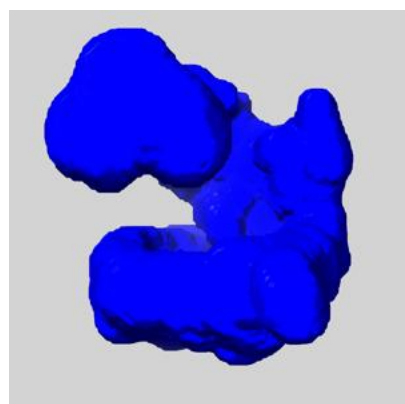
## 6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

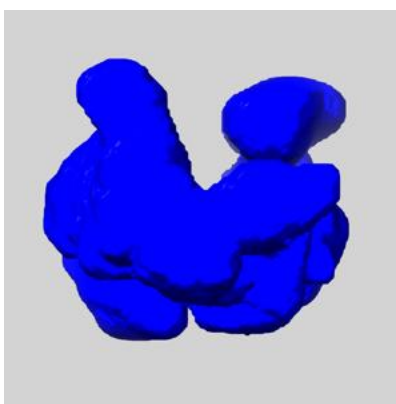
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

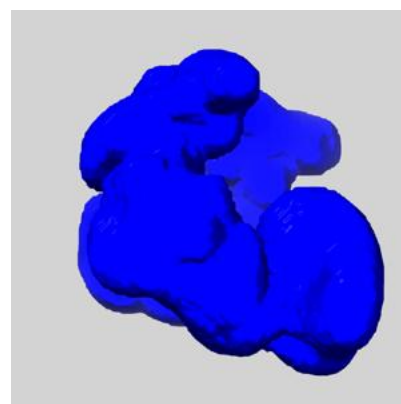
### 6.6.1 emd\_48145\_msk\_1.map [i](#)



X



Y

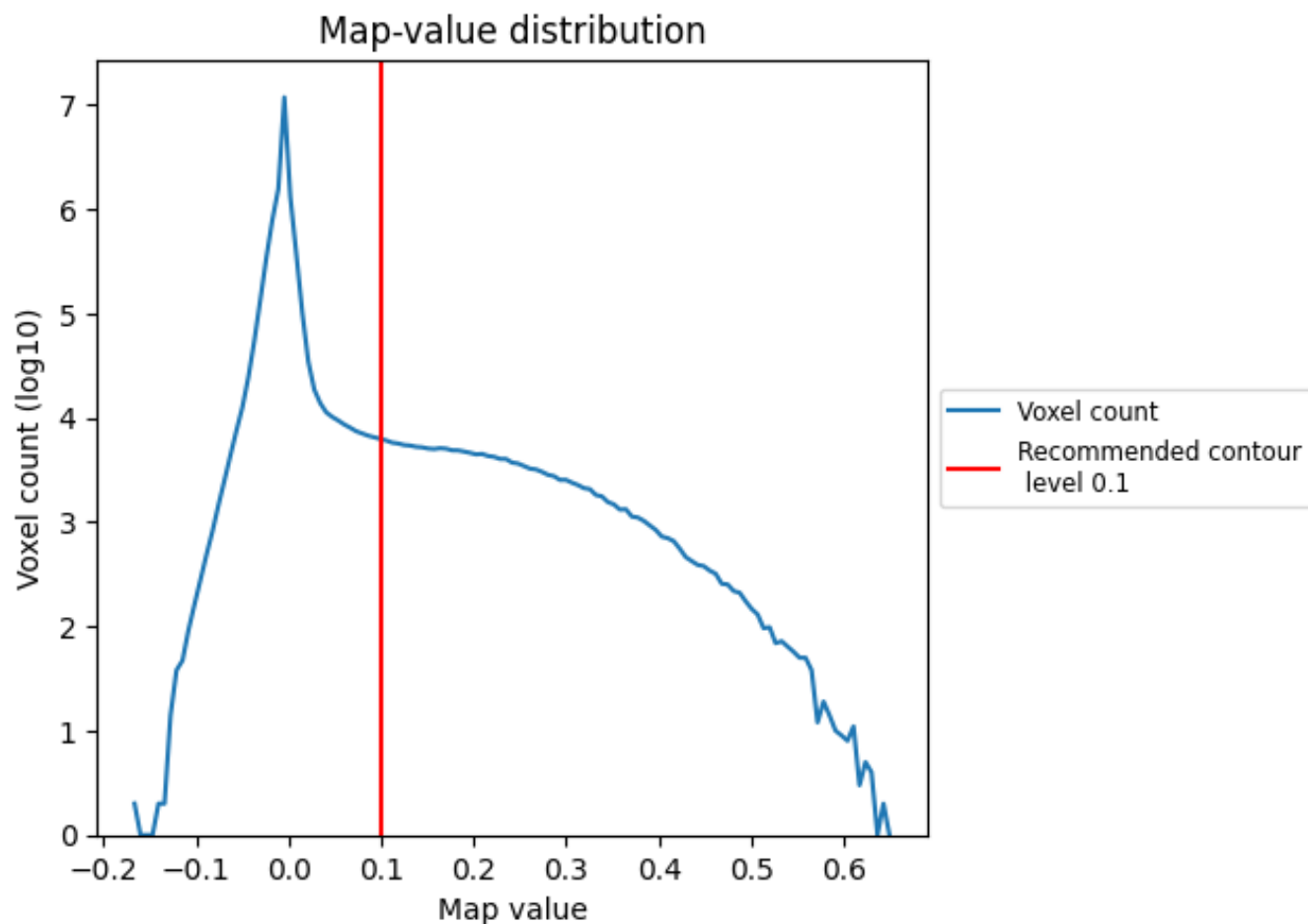


Z

## 7 Map analysis [i](#)

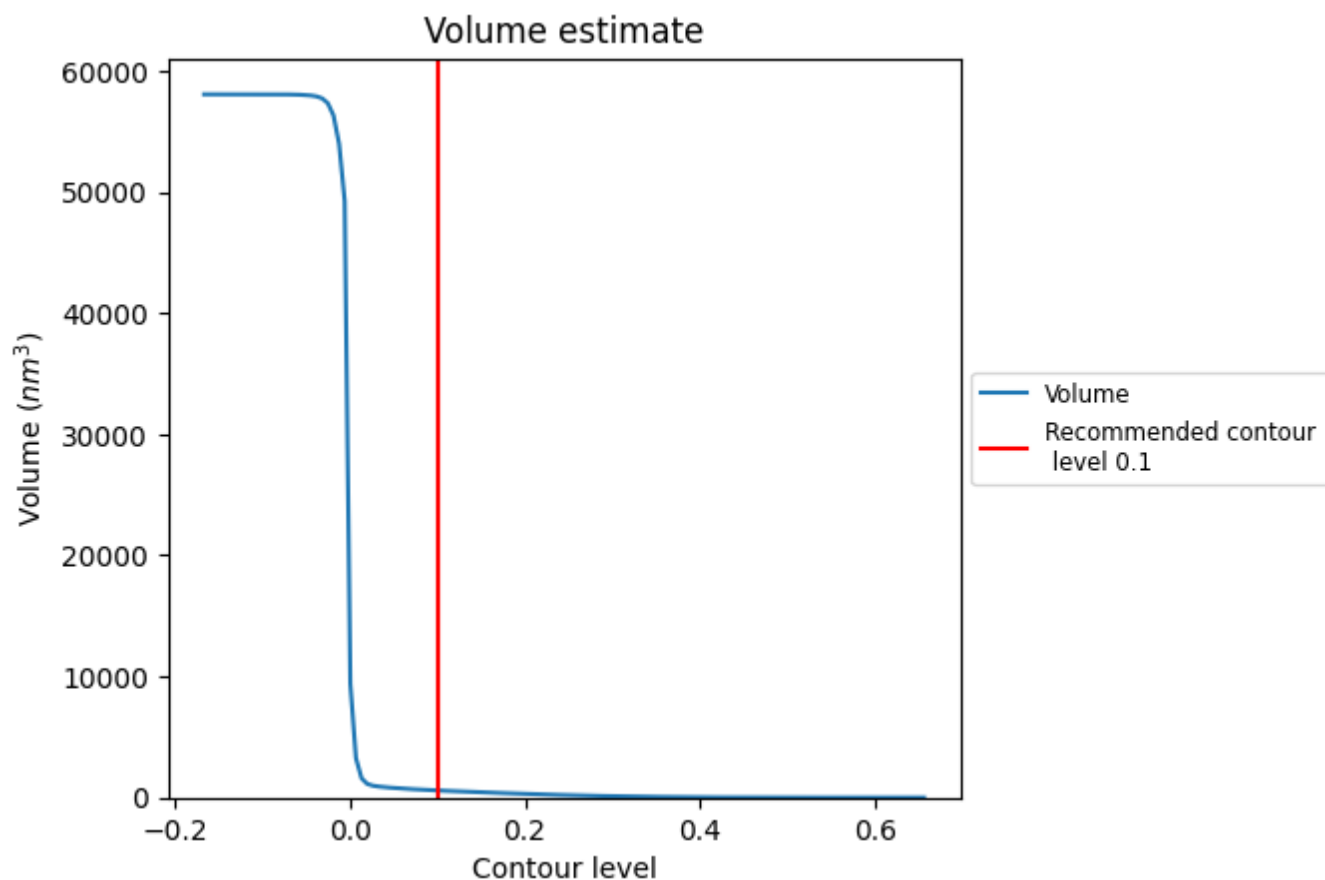
This section contains the results of statistical analysis of the map.

### 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.

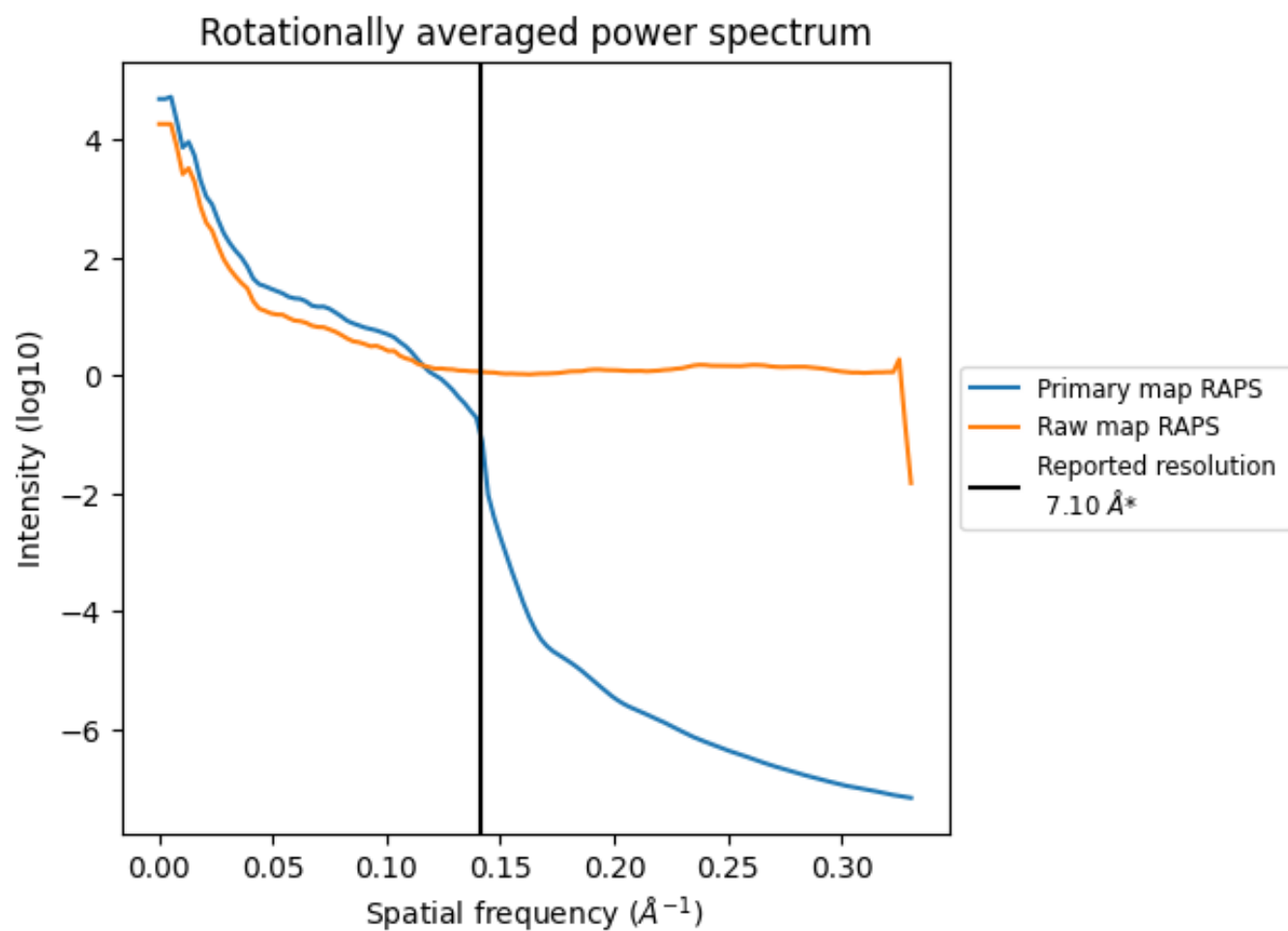
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 588  $\text{nm}^3$ ; this corresponds to an approximate mass of 531 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 ⓘ

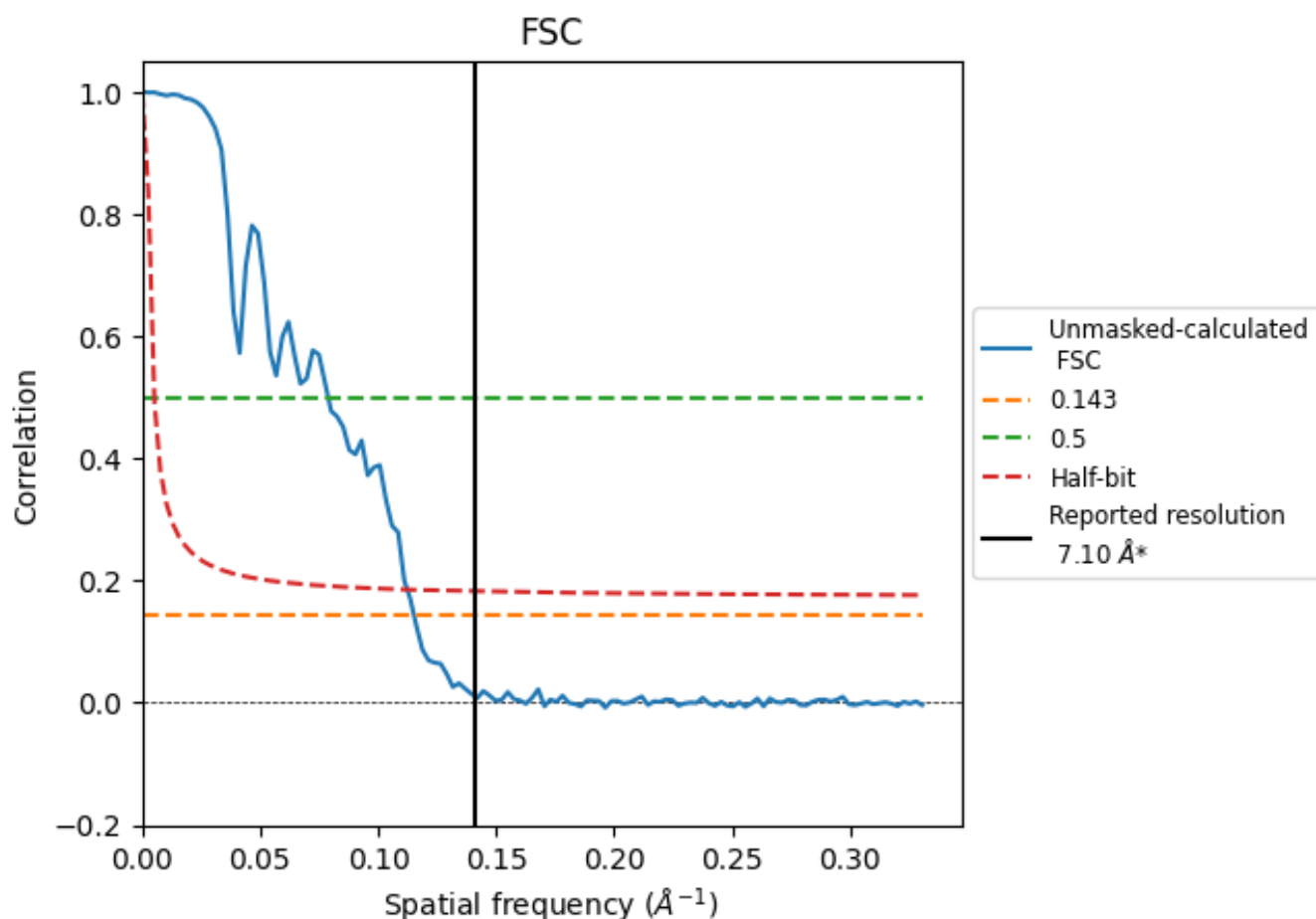


\*Reported resolution corresponds to spatial frequency of 0.141 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.141 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

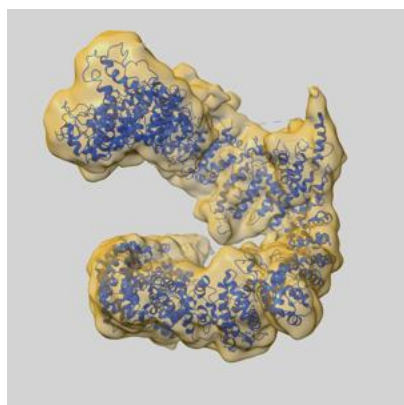
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	8.68	12.69	8.90

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.68 differs from the reported value 7.1 by more than 10 %

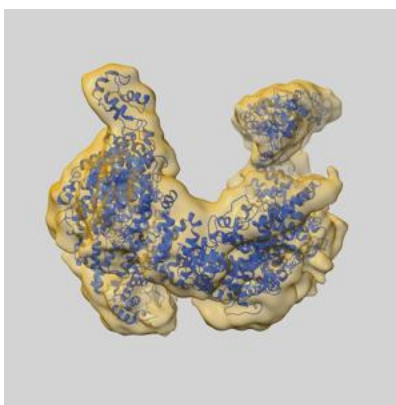
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-48145 and PDB model 9ELD. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

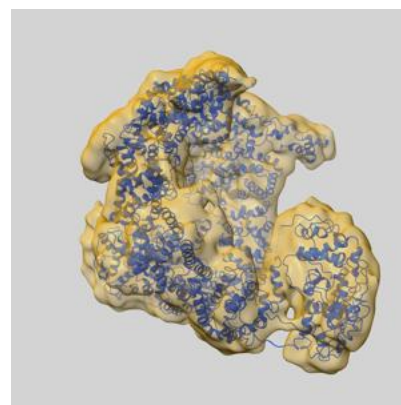
### 9.1 Map-model overlay [i](#)



X



Y

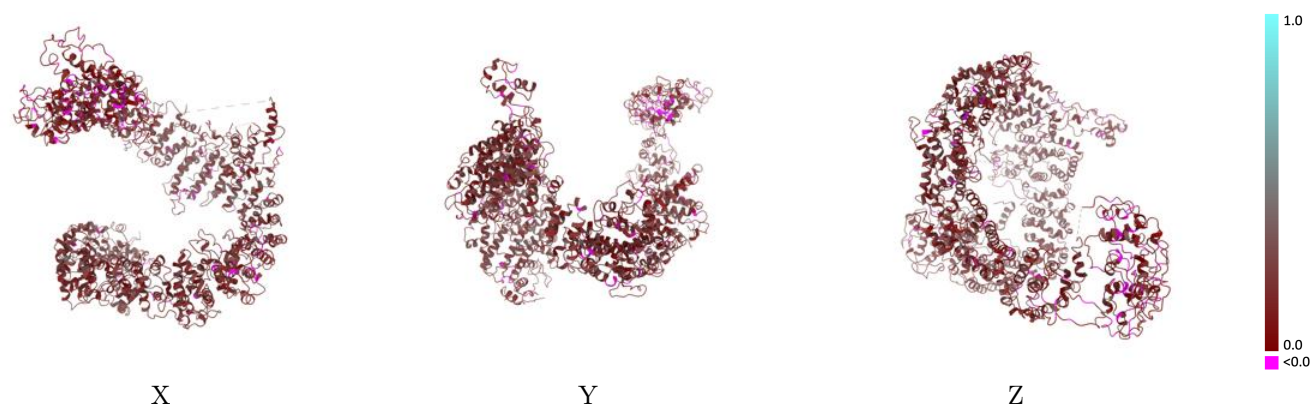


Z

The images above show the 3D surface view of the map at the recommended contour level 0.1 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.

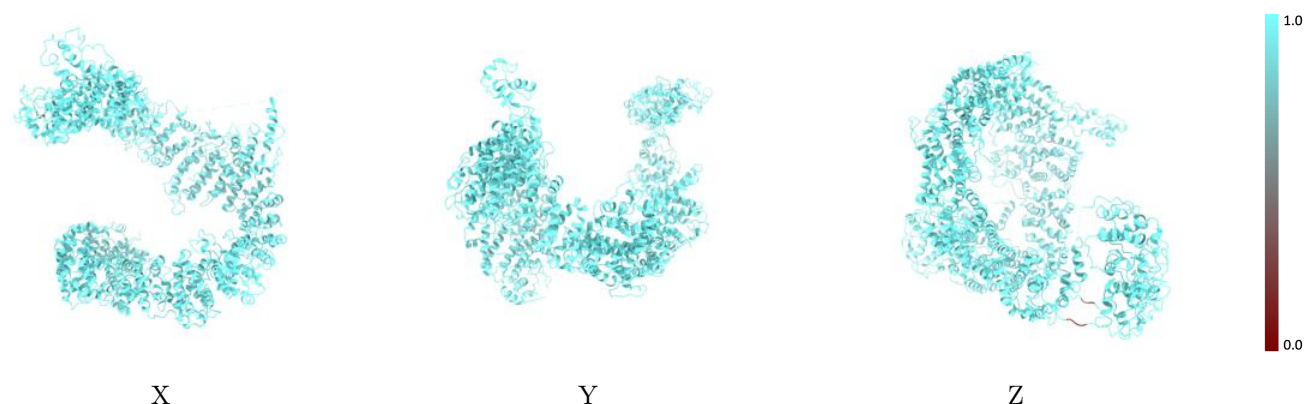


## 9.2 Q-score mapped to coordinate model [i](#)



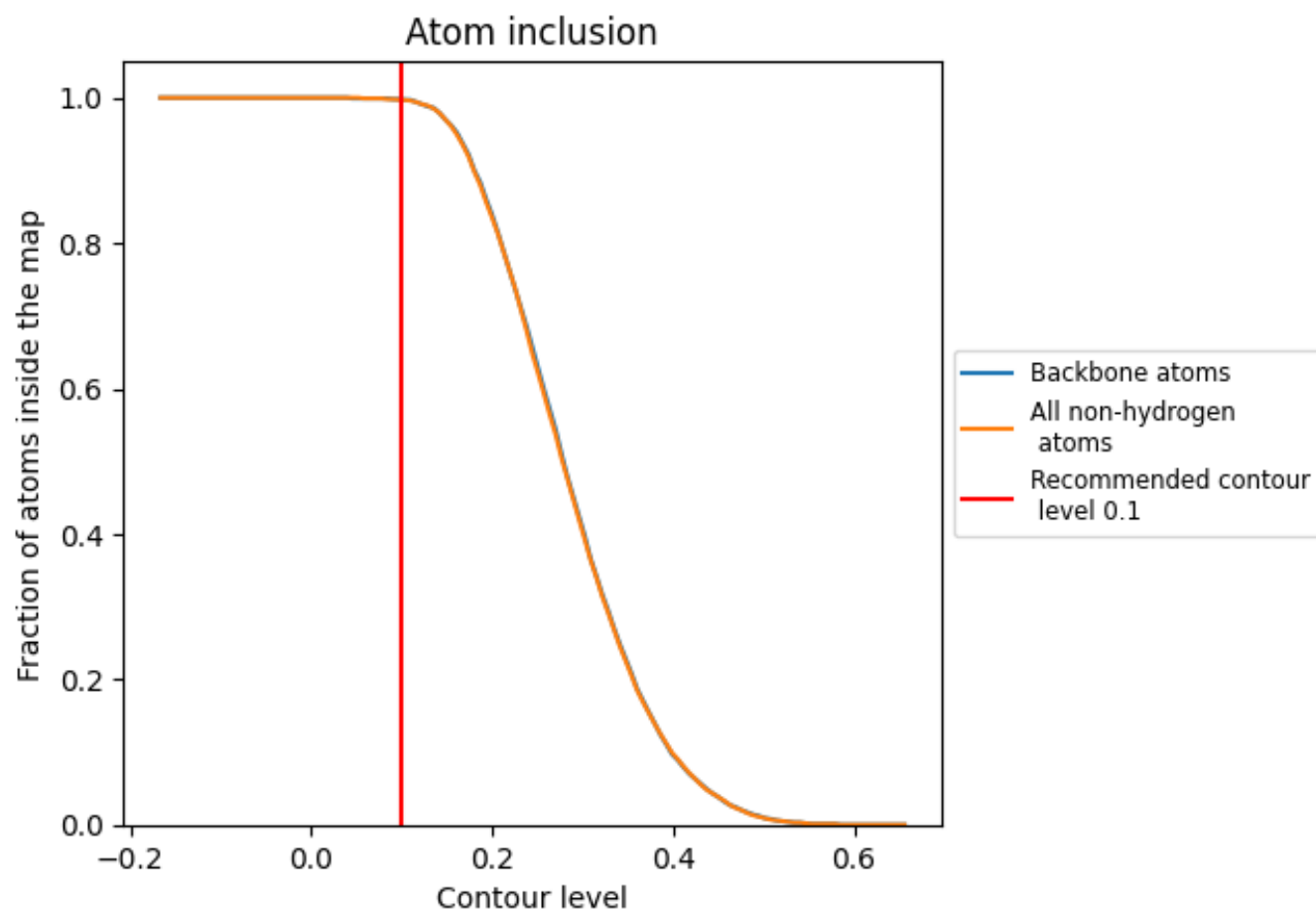
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 100% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.9970	<div><div></div></div> 0.1770
A	<div><div></div></div> 0.9980	<div><div></div></div> 0.1770

