



# wwPDB EM Validation Summary Report ⓘ

May 11, 2026 – 09:20 PM EDT

PDB ID : 11FH / pdb\_000011fh  
EMDB ID : EMD-75664  
Title : RNA Vault cap (MVP/PARP4/TEP1 sample)  
Authors : Osinski, A.; Tagliabracci, V.S.  
Deposited on : 2026-02-20  
Resolution : 1.92 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

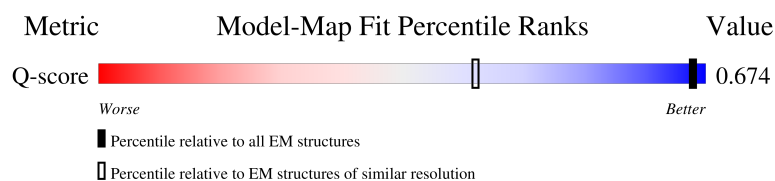
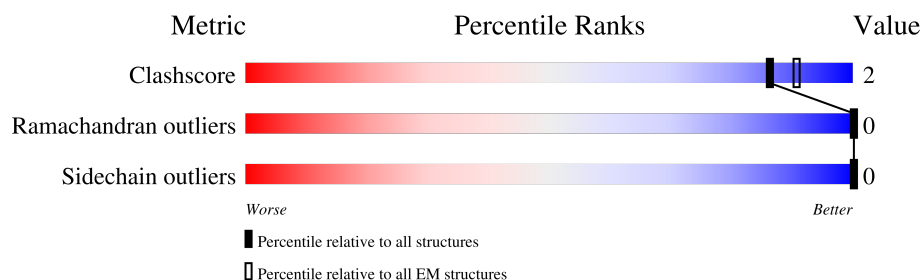
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 1.92 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	1227 ( 1.42 - 2.42 )

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	893	
1	B	893	
1	C	893	
1	D	893	

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Mol	Chain	Length	Quality of chain	
1	E	893		
1	F	893		
1	G	893		
1	H	893		
1	I	893		
1	J	893		
1	K	893		
1	L	893		
1	M	893		
1	N	893		
1	O	893		
1	P	893		
1	Q	893		
1	R	893		
1	S	893		
1	T	893		
1	U	893		
1	V	893		
1	W	893		
1	X	893		
1	Y	893		
1	Z	893		
1	a	893		
1	b	893		
1	c	893		

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Mol	Chain	Length	Quality of chain	
1	d	893	<div><div></div></div> 10%90%	
1	e	893	<div><div></div></div> 7%92%	
1	f	893	<div><div></div></div> 8%91%	
1	g	893	<div><div></div></div> 10%90%	
1	h	893	<div><div></div></div> 8%92%	
1	i	893	<div><div></div></div> 8%91%	
1	j	893	<div><div></div></div> 10%90%	
1	k	893	<div><div></div></div> 8%92%	
1	l	893	<div><div></div></div> 8%91%	
1	m	893	<div><div></div></div> 10%90%	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 50089 atoms, of which 25662 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 Major vault protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	74	Total	C	H	N	O	S	0	0
			1173	366	601	96	107	3		
1	B	78	Total	C	H	N	O	S	0	0
			1237	382	635	101	117	2		
1	C	93	Total	C	H	N	O	S	0	0
			1443	449	738	117	136	3		
1	D	74	Total	C	H	N	O	S	0	0
			1173	366	601	96	107	3		
1	E	78	Total	C	H	N	O	S	0	0
			1237	382	635	101	117	2		
1	F	93	Total	C	H	N	O	S	0	0
			1443	449	738	117	136	3		
1	G	74	Total	C	H	N	O	S	0	0
			1173	366	601	96	107	3		
1	H	78	Total	C	H	N	O	S	0	0
			1237	382	635	101	117	2		
1	I	93	Total	C	H	N	O	S	0	0
			1443	449	738	117	136	3		
1	J	74	Total	C	H	N	O	S	0	0
			1173	366	601	96	107	3		
1	K	78	Total	C	H	N	O	S	0	0
			1237	382	635	101	117	2		
1	L	93	Total	C	H	N	O	S	0	0
			1443	449	738	117	136	3		
1	M	74	Total	C	H	N	O	S	0	0
			1173	366	601	96	107	3		
1	N	78	Total	C	H	N	O	S	0	0
			1237	382	635	101	117	2		
1	O	93	Total	C	H	N	O	S	0	0
			1443	449	738	117	136	3		
1	P	74	Total	C	H	N	O	S	0	0
			1173	366	601	96	107	3		
1	Q	78	Total	C	H	N	O	S	0	0
			1237	382	635	101	117	2		

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	R	93	Total	C	H	N	O	S	0	0
			1443	449	738	117	136	3		
1	S	74	Total	C	H	N	O	S	0	0
			1173	366	601	96	107	3		
1	T	78	Total	C	H	N	O	S	0	0
			1237	382	635	101	117	2		
1	U	93	Total	C	H	N	O	S	0	0
			1443	449	738	117	136	3		
1	V	74	Total	C	H	N	O	S	0	0
			1173	366	601	96	107	3		
1	W	78	Total	C	H	N	O	S	0	0
			1237	382	635	101	117	2		
1	X	93	Total	C	H	N	O	S	0	0
			1443	449	738	117	136	3		
1	Y	74	Total	C	H	N	O	S	0	0
			1173	366	601	96	107	3		
1	Z	78	Total	C	H	N	O	S	0	0
			1237	382	635	101	117	2		
1	a	93	Total	C	H	N	O	S	0	0
			1443	449	738	117	136	3		
1	b	74	Total	C	H	N	O	S	0	0
			1173	366	601	96	107	3		
1	c	78	Total	C	H	N	O	S	0	0
			1237	382	635	101	117	2		
1	d	93	Total	C	H	N	O	S	0	0
			1443	449	738	117	136	3		
1	e	74	Total	C	H	N	O	S	0	0
			1173	366	601	96	107	3		
1	f	78	Total	C	H	N	O	S	0	0
			1237	382	635	101	117	2		
1	g	93	Total	C	H	N	O	S	0	0
			1443	449	738	117	136	3		
1	h	74	Total	C	H	N	O	S	0	0
			1173	366	601	96	107	3		
1	i	78	Total	C	H	N	O	S	0	0
			1237	382	635	101	117	2		
1	j	93	Total	C	H	N	O	S	0	0
			1443	449	738	117	136	3		
1	k	74	Total	C	H	N	O	S	0	0
			1173	366	601	96	107	3		
1	l	78	Total	C	H	N	O	S	0	0
			1237	382	635	101	117	2		

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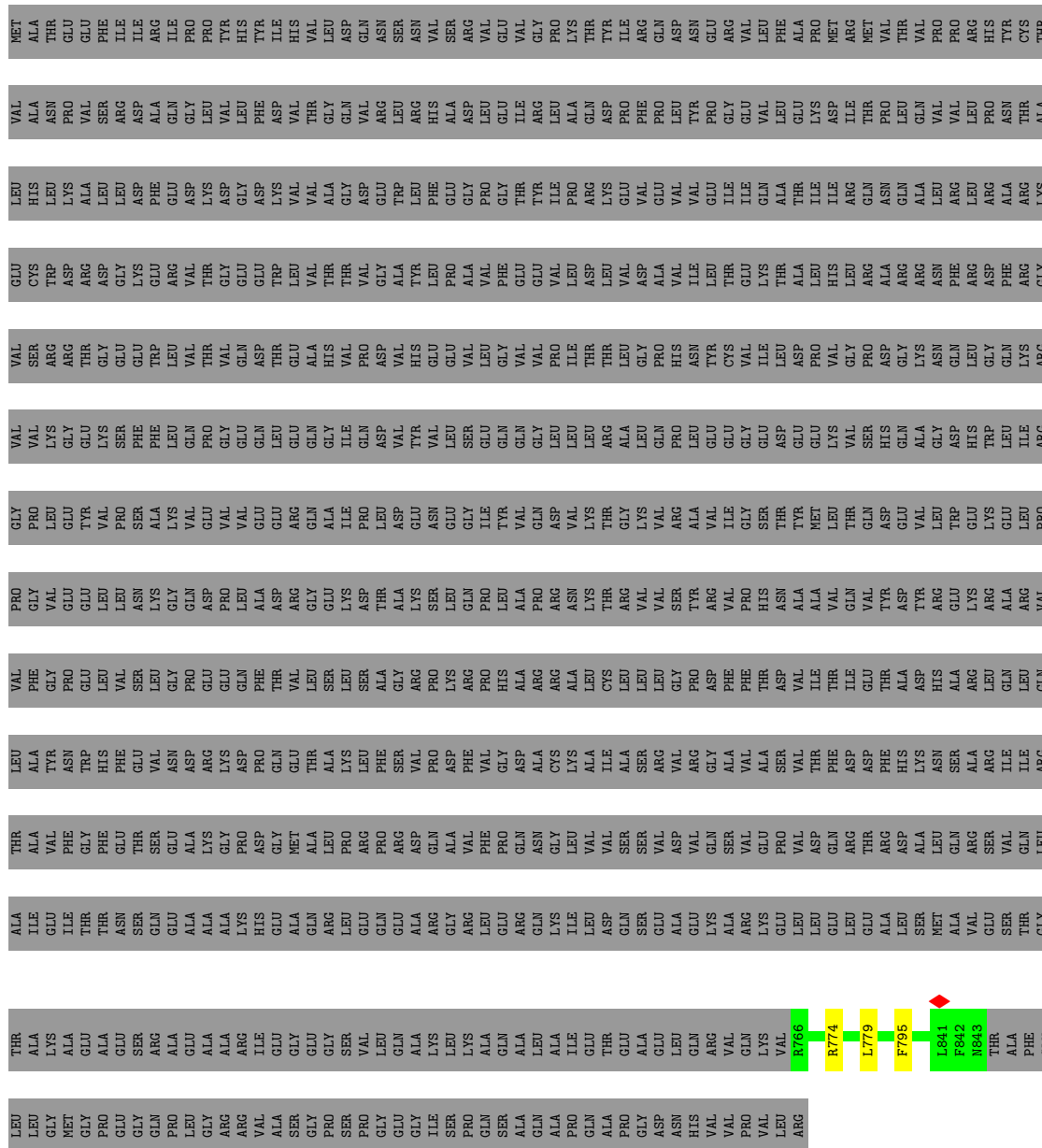
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Mol	Chain	Residues	Atoms						AltConf	Trace
1	m	93	Total	C	H	N	O	S	0	0
			1443	449	738	117	136	3		



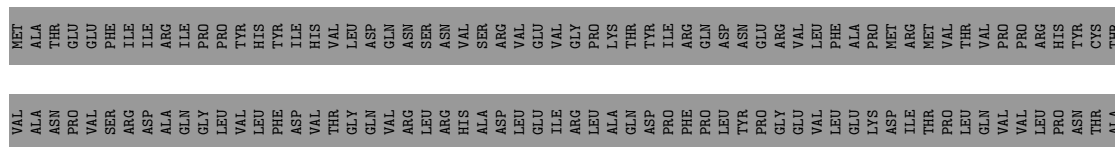
- Molecule 1: Major vault protein

Chain B:  8%  91%



- Molecule 1: Major vault protein

Chain C:  10% 90%

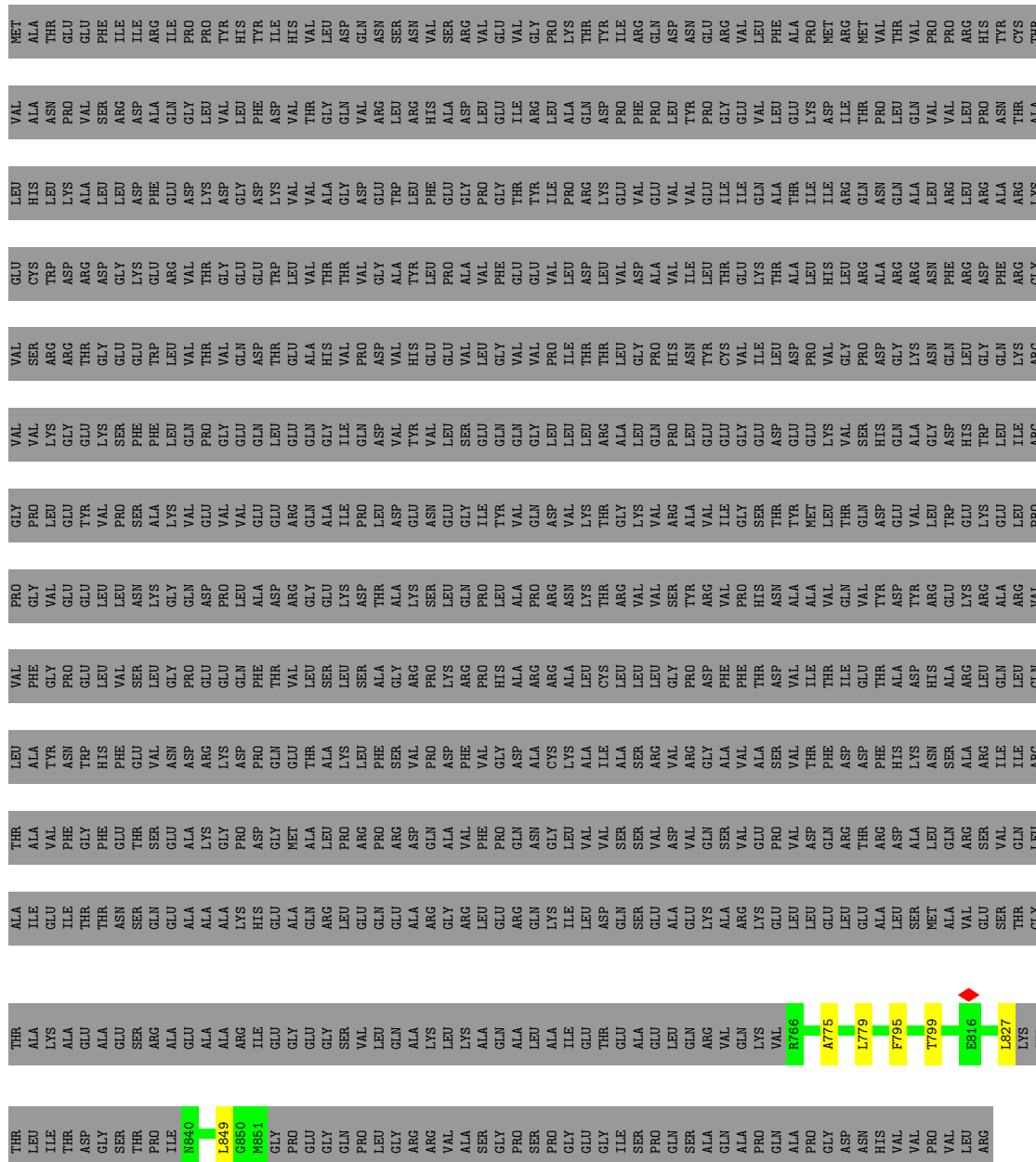


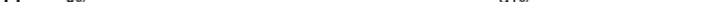


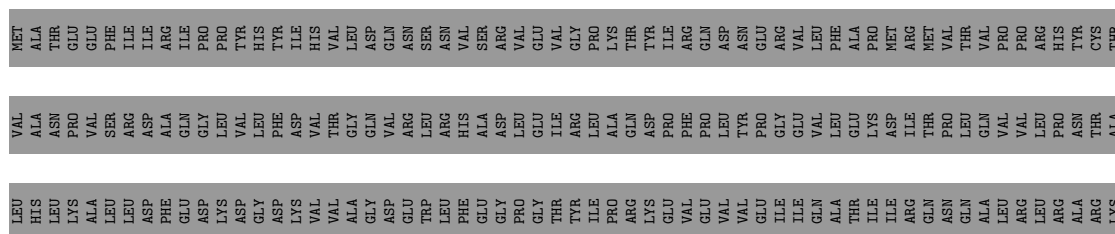




Chain G:  8% . 92%



Chain H:  8% 91%

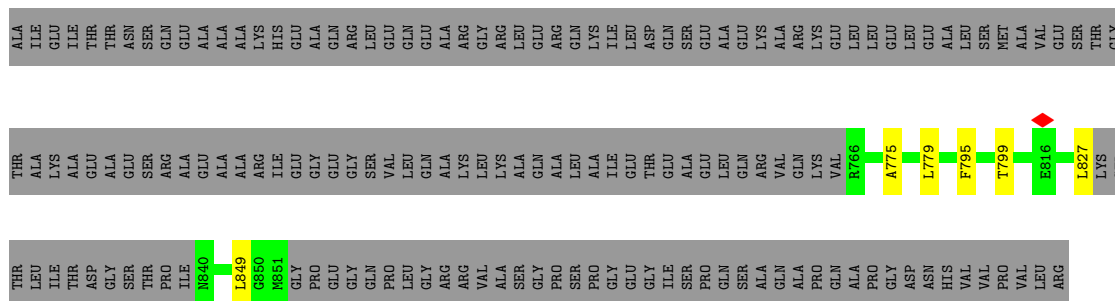


LEU	LEU	GLY	MET	GLY	PRO	GLU	GLY	GLN	PRO	LEU	GLY	ARG	ARG	VAL	ALA	GLY	PRO	PRO	PRO	GLY	GLY	ILE	SER	PRO	PRO	GLN	SER	ALA	GLN	ALA	PRO	GLN	ALA	PRO	GLY	ASP	ASN	HIS	VAL	VAL	VAL	PRO	VAL	LEU	ARG
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- Chain I:  10% 90%

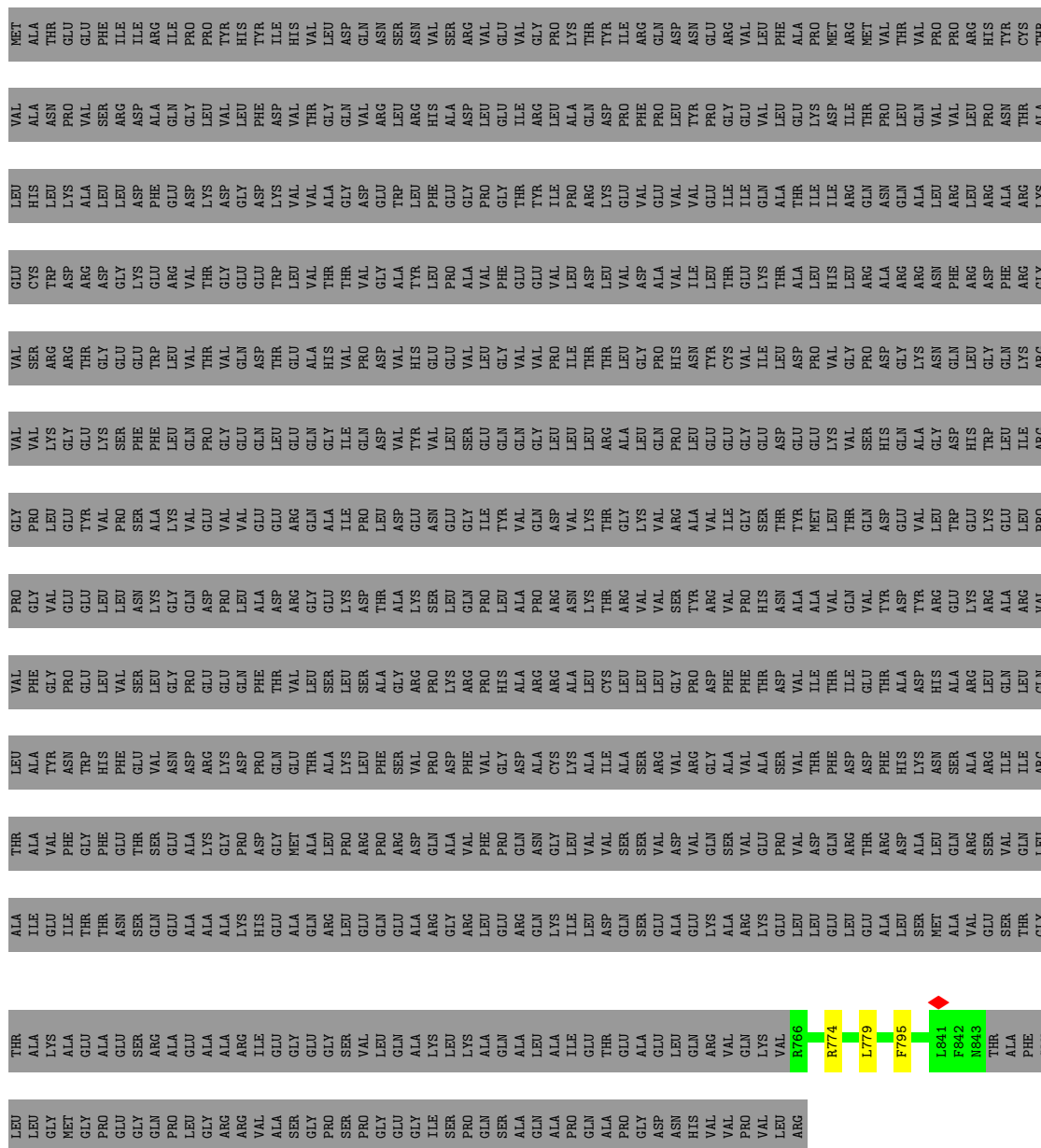






- Molecule 1: Major vault protein

Chain K:  8%  91%



- Molecule 1: Major vault protein

90%

- Molecule 1: Major vault protein

92%

[illegible]

[illegible]

- Molecule 1: Major vault protein

Chain N:  8% 91%

[illegible]











- Molecule 1: Major vault protein

- Molecule 1: Major vault protein











Chain Z:  8%  91%

- Molecule 1: Major vault protein

90%

- Molecule 1: Major vault protein

92%

[illegible]





ALA  
SER  
GLY  
GLY  
SER  
PRO  
GLY  
GLU  
GLY  
ILE  
SER  
PRO  
GLN  
SER  
SER  
ALA  
GLN  
ALA  
PRO  
GLN  
ALA  
PRO  
GLY  
ASP  
ASN  
HIS  
VAL  
VAL  
PRO  
VAL  
LEU  
ARG

- Molecule 1: Major vault protein

Chain e:  7% • 92%

VAL	ALA	ASN	PRO	VAL	SER	ARG	ASP	ALA	GLN	GLY	LEU	VAL	LEU	PHE	ASP	GLN	GLY	THR	GLY	GLN	VAL	ARG	LEU	ARG	HIS	ALA	ASP	GLU	ILE	ARG	LEU	GLN	ASP	PRO	PHE	PRO	LEU	TYR	PRO	GLY	GLU	VAL	LEU	LYS	ASP	THR	PRO	ASN	THR	ALA
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GLU CYS TRP TRP ASP ARG ASP GLY LYS GLU GLU ARG VAL VAL THR GLY GLU GLU TRP TRP VAL VAL LEU LEU THR THR VAL VAL TYR LEU PRO ALA ALA PHE PHE GLU GLU VAL VAL LEU LEU ASP ASP LEU LEU VAL VAL ASP ALA VAL VAL ILE LEU LEU THR THR GLU GLU LYS THR ALA ALA HIS LEU LEU ARG ALA ARG ARG ARG ASN PHE ARG ASP PHE ASP ARG GLY

VAL	VAL	LYS	GLY	GLY	LYS	SER	PHE	PHE	LEU	GLN	PRO	GLY	GLY	GLN	GLN	LEU	GLY	GLY	ILE	ASP	ASP	TYR	VAL	VAL	LEU	SER	SER	GLY	GLN	GLN	GLY	LEU	LEU	LEU	LEU	ARG	ALA	ALA	LEU	GLN	GLN	PRO	PRO	GLY	GLY	GLY	LYS	VAL	VAL	SER	HIS	HIS	TRP	TRP	LEU	LEU	ILE	ILE	BC
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PRO	GLY	VAL	GLU	LEU	ASN	LYS	GLN	ASP	PRO	LEU	ALA	ASP	ARG	GLY	GLU	LYS	ASP	THR	LYS	SER	LYS	THR	ARG	VAL	VAL	PRO	HIS	ASN	ALA	ALA	VAL	GLN	VAL	TYR	ASP	TYR	ARG	GLU	LYS	ARG	ALA	VAL	ASN
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LEU	TYR	ASN	TRP	HIS	PHE	GLU	VAL	ASN	ASP	ARG	LYS	ASP	PRO	GLN	GLU	THR	ALA	LYS	LEU	PHE	SER	VAL	ASP	PRO	PHE	GLY	ASP	ALA	CYS	LYS	ALA	ILE	ALA	SER	ARG	VAL	ARG	GLY	ALA	VAL	ALA	SER	THR	PHE	ASP	ASP	PHE	HIS	LYS	ASN	SER	ALA	ARG	ILE	ILE	PCG
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ALA ILE LEU LEU THR THR ASN SER SER GLN GLU ALA ALA ALA LYS HIS HIS GLU GLU GLN GLN GLU GLU ALA ARG ARG LEU LEU GLU GLN GLN GLU GLU GLU GLU ARG ARG ARG ARG GLN LYS LYS LEU LEU ASP ASP GLN SER SER GLU GLU ALA ALA ALA GLU GLU LYS LYS LEU LEU GLU GLU ALA ALA ALA MET MET ALA ALA VAL VAL GLU GLU SER SER THR THR TYR TYR

THR	ALA	LYS	ALA	GLU	ALA	GLU	SER	ARG	ALA	GLU	ALA	ALA	ARG	ILE	GLU	GLY	GLU	GLY	SER	VAL	LEU	GLN	ALA	LYS	LEU	LYS	ALA	GLN	ALA	LEU	ALA	ALA	ILE	GLU	THR	GLU	ALA	GLU	LEU	GLN	ARG	VAL	GLN	LYS	VAL

L827	L837	L841	L849	L850	M851	L859	L860	L861	L862	L863	L864	L865	L866	L867	L868	L869	L870	L871	L872	L873	L874	L875	L876	L877	L878	L879	L880	L881	L882	L883	L884	L885	L886	L887	L888	L889	L890	L891	L892	L893	L894	L895	L896	L897	L898	L899	L900	L901	L902	L903	L904	L905	L906	L907	L908	L909	L910	L911	L912	L913	L914	L915	L916	L917	L918	L919	L920	L921	L922	L923	L924	L925	L926	L927	L928	L929	L930	L931	L932	L933	L934	L935	L936	L937	L938	L939	L940	L941	L942	L943	L944	L945	L946	L947	L948	L949	L950	L951	L952	L953	L954	L955	L956	L957	L958	L959	L960	L961	L962	L963	L964	L965	L966	L967	L968	L969	L970	L971	L972	L973	L974	L975	L976	L977	L978	L979	L980	L981	L982	L983	L984	L985	L986	L987	L988	L989	L990	L991	L992	L993	L994	L995	L996	L997	L998	L999	L1000	L1001	L1002	L1003	L1004	L1005	L1006	L1007	L1008	L1009	L1010	L1011	L1012	L1013	L1014	L1015	L1016	L1017	L1018	L1019	L1020	L1021	L1022	L1023	L1024	L1025	L1026	L1027	L1028	L1029	L1030	L1031	L1032	L1033	L1034	L1035	L1036	L1037	L1038	L1039	L1040	L1041	L1042	L1043	L1044	L1045	L1046	L1047	L1048	L1049	L1050	L1051	L1052	L1053	L1054	L1055	L1056	L1057	L1058	L1059	L1060	L1061	L1062	L1063	L1064	L1065	L1066	L1067	L1068	L1069	L1070	L1071	L1072	L1073	L1074	L1075	L1076	L1077	L1078	L1079	L1080	L1081	L1082	L1083	L1084	L1085	L1086	L1087	L1088	L1089	L1090	L1091	L1092	L1093	L1094	L1095	L1096	L1097	L1098	L1099	L1100	L1101	L1102	L1103	L1104	L1105	L1106	L1107	L1108	L1109	L1110	L1111	L1112	L1113	L1114	L1115	L1116	L1117	L1118	L1119	L1120	L1121	L1122	L1123	L1124	L1125	L1126	L1127	L1128	L1129	L1130	L1131	L1132	L1133	L1134	L1135	L1136	L1137	L1138	L1139	L1140	L1141	L1142	L1143	L1144	L1145	L1146	L1147	L1148	L1149	L1150	L1151	L1152	L1153	L1154	L1155	L1156	L1157	L1158	L1159	L1160	L1161	L1162	L1163	L1164	L1165	L1166	L1167	L1168	L1169	L1170	L1171	L1172	L1173	L1174	L1175	L1176	L1177	L1178	L1179	L1180	L1181	L1182	L1183	L1184	L1185	L1186	L1187	L1188	L1189	L1190	L1191	L1192	L1193	L1194	L1195	L1196	L1197	L1198	L1199	L1200	L1201	L1202	L1203	L1204	L1205	L1206	L1207	L1208	L1209	L1210	L1211	L1212	L1213	L1214	L1215	L1216	L1217	L1218	L1219	L1220	L1221	L1222	L1223	L1224	L1225	L1226	L1227	L1228	L1229	L1230	L1231	L1232	L1233	L1234	L1235	L1236	L1237	L1238	L1239	L1240	L1241	L1242	L1243	L1244	L1245	L1246	L1247	L1248	L1249	L1250	L1251	L1252	L1253	L1254	L1255	L1256	L1257	L1258	L1259	L1260	L1261	L1262	L1263	L1264	L1265	L1266	L1267	L1268	L1269	L1270	L1271	L1272	L1273	L1274	L1275	L1276	L1277	L1278	L1279	L1280	L1281	L1282	L1283	L1284	L1285	L1286	L1287	L1288	L1289	L1290	L1291	L1292	L1293	L1294	L1295	L1296	L1297	L1298	L1299	L1300	L1301	L1302	L1303	L1304	L1305	L1306	L1307	L1308	L1309	L1310	L1311	L1312	L1313	L1314	L1315	L1316	L1317	L1318	L1319	L1320	L1321	L1322	L13
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LEU  
ARG



ALA SER GLY PRO SER PRO GLY GLY ILE SER PRO GLN SER ALA GLN ALA PRO GLN ALA PRO GLY ASP ASN HIS VAL VAL PRO VAL LEU ARG

- Chain h:  8% . 92%

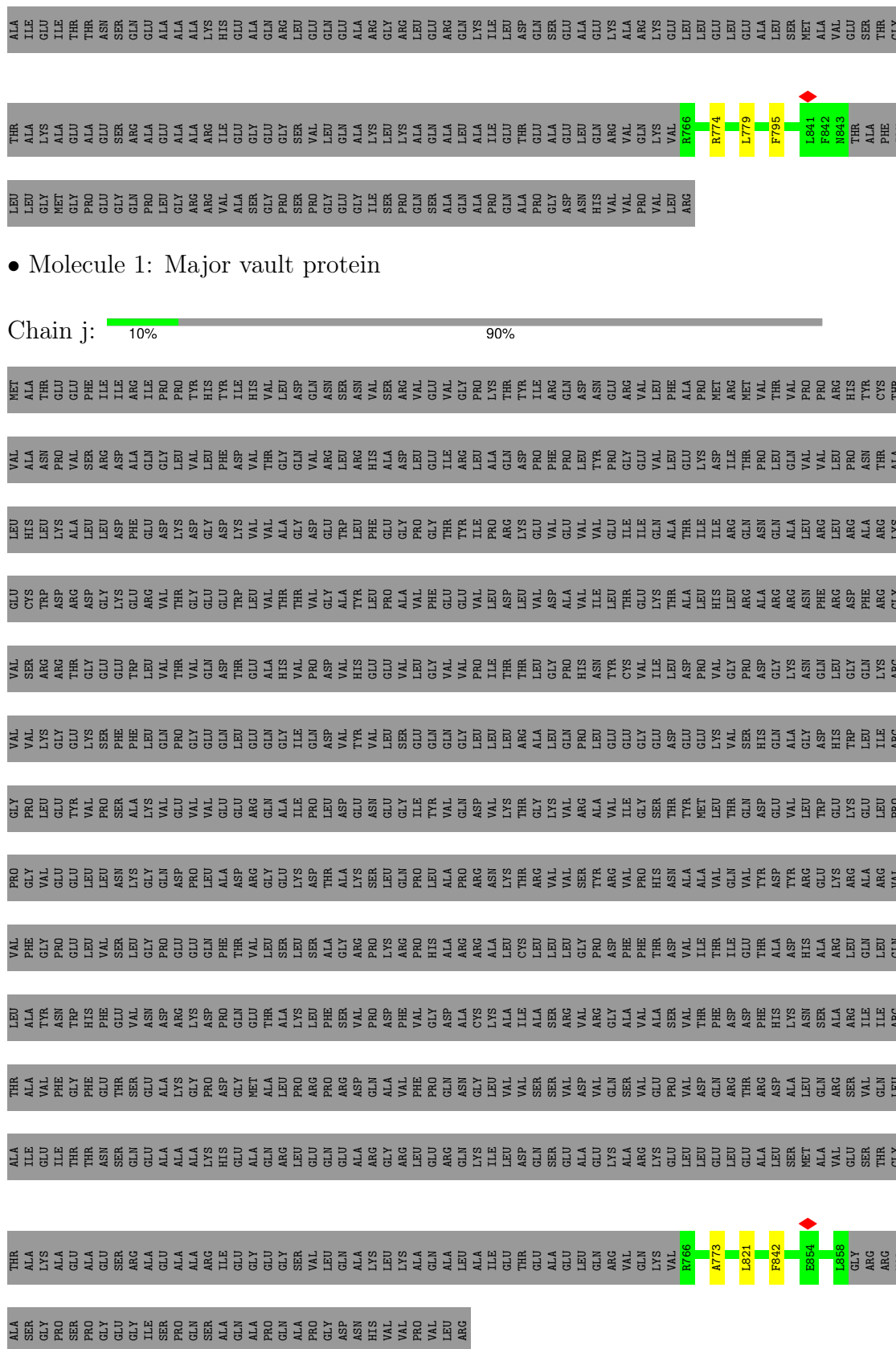
GLY	PRO	LEU	GLU	TYR	VAL	PRO	SER	ALA	LYS	VAL	GLU	VAL	VAL	GLU	GLU	GLU	ARG	GLN	ALA	ILE	GLY	GLY	ILE	TYR	VAL	GLN	ASP	VAL	VAL	LYS	THR	GLY	LYS	VAL	ARG	ALA	VAL	ILE	GLY	SER	THR	TYR	MET	LEU	THR	GLN	ASP	GLU	VAL	LEU	TRP	GLU	LYS	GLU	LEU	PRO
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THR	THR	THR	ASP	GLY	SER	THR	THR	PRO	ILE	<b>M840</b>	<b>L841</b>	<b>M851</b>	<b>G850</b>	<b>M851</b>	GLY	PRO	GLY	GLN	PRO	LEU	GLY	ARG	ALA	SER	ALA	GLY	PRO	SER	PRO	GLY	GLY	GLY	ILE	SER	PRO	GLN	GLN	PRO	ALA	PRO	GLY	ASP	ASN	HIS	VAL	VAL	VAL	PRO	VAL	LEU	ARG
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- Molecule 1: Major vault protein

Chain i:  8% 91%

[illegible]



- Molecule 1: Major vault protein

[illegible][illegible]

LEU LEU GLY MET GLY PRO GLU GLY GLN LEU GLY ARG ARG VAL ALA SER SER PRO PRO GLY GLY ILE SER PRO GLN SER ALA ALA GLN ALA GLN PRO GLN ALA PRO PRO GLY ASP ASN HIS VAL VAL PRO PRO VAL VAL LEU ARG

- Chain m:  10% 90%





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C13	Depositor
Number of particles used	115486	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.518	Depositor
Minimum map value	-0.227	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	427.8, 427.8, 427.8	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.713, 0.713, 0.713	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	0.11	0/576	0.22	0/772
1	B	0.12	0/607	0.23	0/818
1	C	0.12	0/713	0.25	0/962
1	D	0.11	0/576	0.22	0/772
1	E	0.12	0/607	0.23	0/818
1	F	0.12	0/713	0.25	0/962
1	G	0.11	0/576	0.22	0/772
1	H	0.12	0/607	0.23	0/818
1	I	0.12	0/713	0.25	0/962
1	J	0.11	0/576	0.22	0/772
1	K	0.12	0/607	0.23	0/818
1	L	0.12	0/713	0.25	0/962
1	M	0.11	0/576	0.22	0/772
1	N	0.12	0/607	0.23	0/818
1	O	0.12	0/713	0.25	0/962
1	P	0.10	0/576	0.22	0/772
1	Q	0.12	0/607	0.23	0/818
1	R	0.12	0/713	0.25	0/962
1	S	0.11	0/576	0.22	0/772
1	T	0.12	0/607	0.23	0/818
1	U	0.12	0/713	0.25	0/962
1	V	0.11	0/576	0.22	0/772
1	W	0.12	0/607	0.23	0/818
1	X	0.12	0/713	0.25	0/962
1	Y	0.11	0/576	0.22	0/772
1	Z	0.12	0/607	0.23	0/818
1	a	0.12	0/713	0.25	0/962
1	b	0.11	0/576	0.22	0/772
1	c	0.12	0/607	0.23	0/818
1	d	0.12	0/713	0.25	0/962
1	e	0.11	0/576	0.22	0/772
1	f	0.12	0/607	0.23	0/818
1	g	0.12	0/713	0.25	0/962
1	h	0.11	0/576	0.22	0/772

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	i	0.12	0/607	0.23	0/818
1	j	0.12	0/713	0.25	0/962
1	k	0.11	0/576	0.22	0/772
1	l	0.12	0/607	0.23	0/818
1	m	0.12	0/713	0.25	0/962
All	All	0.12	0/24648	0.24	0/33176

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	572	601	601	6	0
1	B	602	635	635	3	0
1	C	705	738	738	5	0
1	D	572	601	601	5	0
1	E	602	635	635	3	0
1	F	705	738	738	5	0
1	G	572	601	601	5	0
1	H	602	635	635	3	0
1	I	705	738	738	5	0
1	J	572	601	601	5	0
1	K	602	635	635	3	0
1	L	705	738	738	5	0
1	M	572	601	601	5	0
1	N	602	635	635	3	0
1	O	705	738	738	5	0
1	P	572	601	601	5	0
1	Q	602	635	635	3	0
1	R	705	738	738	5	0
1	S	572	601	601	6	0
1	T	602	635	635	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	U	705	738	738	5	0
1	V	572	601	601	6	0
1	W	602	635	635	3	0
1	X	705	738	738	5	0
1	Y	572	601	601	6	0
1	Z	602	635	635	3	0
1	a	705	738	738	5	0
1	b	572	601	601	7	0
1	c	602	635	635	3	0
1	d	705	738	738	5	0
1	e	572	601	601	7	0
1	f	602	635	635	3	0
1	g	705	738	738	5	0
1	h	572	601	601	6	0
1	i	602	635	635	3	0
1	j	705	738	738	4	0
1	k	572	601	601	5	0
1	l	602	635	635	3	0
1	m	705	738	738	4	0
All	All	24427	25662	25662	106	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 2.

The worst 5 of 106 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:D:827:LEU:HD11	1:E:795:PHE:CE1	2.42	0.55
1:J:827:LEU:HD11	1:K:795:PHE:CE1	2.42	0.55
1:k:827:LEU:HD11	1:l:795:PHE:CE1	2.42	0.55
1:A:827:LEU:HD11	1:B:795:PHE:CE1	2.42	0.55
1:G:827:LEU:HD11	1:H:795:PHE:CE1	2.42	0.54

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	70/893 (8%)	70 (100%)	0	0	100	100
1	B	76/893 (8%)	76 (100%)	0	0	100	100
1	C	91/893 (10%)	90 (99%)	1 (1%)	0	100	100
1	D	70/893 (8%)	70 (100%)	0	0	100	100
1	E	76/893 (8%)	76 (100%)	0	0	100	100
1	F	91/893 (10%)	90 (99%)	1 (1%)	0	100	100
1	G	70/893 (8%)	70 (100%)	0	0	100	100
1	H	76/893 (8%)	76 (100%)	0	0	100	100
1	I	91/893 (10%)	90 (99%)	1 (1%)	0	100	100
1	J	70/893 (8%)	70 (100%)	0	0	100	100
1	K	76/893 (8%)	76 (100%)	0	0	100	100
1	L	91/893 (10%)	90 (99%)	1 (1%)	0	100	100
1	M	70/893 (8%)	70 (100%)	0	0	100	100
1	N	76/893 (8%)	76 (100%)	0	0	100	100
1	O	91/893 (10%)	90 (99%)	1 (1%)	0	100	100
1	P	70/893 (8%)	70 (100%)	0	0	100	100
1	Q	76/893 (8%)	76 (100%)	0	0	100	100
1	R	91/893 (10%)	90 (99%)	1 (1%)	0	100	100
1	S	70/893 (8%)	70 (100%)	0	0	100	100
1	T	76/893 (8%)	76 (100%)	0	0	100	100
1	U	91/893 (10%)	90 (99%)	1 (1%)	0	100	100
1	V	70/893 (8%)	70 (100%)	0	0	100	100
1	W	76/893 (8%)	76 (100%)	0	0	100	100
1	X	91/893 (10%)	90 (99%)	1 (1%)	0	100	100
1	Y	70/893 (8%)	70 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Z	76/893 (8%)	76 (100%)	0	0	100	100
1	a	91/893 (10%)	90 (99%)	1 (1%)	0	100	100
1	b	70/893 (8%)	70 (100%)	0	0	100	100
1	c	76/893 (8%)	76 (100%)	0	0	100	100
1	d	91/893 (10%)	90 (99%)	1 (1%)	0	100	100
1	e	70/893 (8%)	70 (100%)	0	0	100	100
1	f	76/893 (8%)	76 (100%)	0	0	100	100
1	g	91/893 (10%)	90 (99%)	1 (1%)	0	100	100
1	h	70/893 (8%)	70 (100%)	0	0	100	100
1	i	76/893 (8%)	76 (100%)	0	0	100	100
1	j	91/893 (10%)	90 (99%)	1 (1%)	0	100	100
1	k	70/893 (8%)	70 (100%)	0	0	100	100
1	l	76/893 (8%)	76 (100%)	0	0	100	100
1	m	91/893 (10%)	90 (99%)	1 (1%)	0	100	100
All	All	3081/34827 (9%)	3068 (100%)	13 (0%)	0	100	100

There are no Ramachandran outliers to report.

### 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	61/755 (8%)	61 (100%)	0	100	100
1	B	67/755 (9%)	67 (100%)	0	100	100
1	C	77/755 (10%)	77 (100%)	0	100	100
1	D	61/755 (8%)	61 (100%)	0	100	100
1	E	67/755 (9%)	67 (100%)	0	100	100
1	F	77/755 (10%)	77 (100%)	0	100	100
1	G	61/755 (8%)	61 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	67/755 (9%)	67 (100%)	0	100	100
1	I	77/755 (10%)	77 (100%)	0	100	100
1	J	61/755 (8%)	61 (100%)	0	100	100
1	K	67/755 (9%)	67 (100%)	0	100	100
1	L	77/755 (10%)	77 (100%)	0	100	100
1	M	61/755 (8%)	61 (100%)	0	100	100
1	N	67/755 (9%)	67 (100%)	0	100	100
1	O	77/755 (10%)	77 (100%)	0	100	100
1	P	61/755 (8%)	61 (100%)	0	100	100
1	Q	67/755 (9%)	67 (100%)	0	100	100
1	R	77/755 (10%)	77 (100%)	0	100	100
1	S	61/755 (8%)	61 (100%)	0	100	100
1	T	67/755 (9%)	67 (100%)	0	100	100
1	U	77/755 (10%)	77 (100%)	0	100	100
1	V	61/755 (8%)	61 (100%)	0	100	100
1	W	67/755 (9%)	67 (100%)	0	100	100
1	X	77/755 (10%)	77 (100%)	0	100	100
1	Y	61/755 (8%)	61 (100%)	0	100	100
1	Z	67/755 (9%)	67 (100%)	0	100	100
1	a	77/755 (10%)	77 (100%)	0	100	100
1	b	61/755 (8%)	61 (100%)	0	100	100
1	c	67/755 (9%)	67 (100%)	0	100	100
1	d	77/755 (10%)	77 (100%)	0	100	100
1	e	61/755 (8%)	61 (100%)	0	100	100
1	f	67/755 (9%)	67 (100%)	0	100	100
1	g	77/755 (10%)	77 (100%)	0	100	100
1	h	61/755 (8%)	61 (100%)	0	100	100
1	i	67/755 (9%)	67 (100%)	0	100	100
1	j	77/755 (10%)	77 (100%)	0	100	100
1	k	61/755 (8%)	61 (100%)	0	100	100
1	l	67/755 (9%)	67 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	m	77/755 (10%)	77 (100%)	0	100	100
All	All	2665/29445 (9%)	2665 (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 56 such sidechains are listed below:

Mol	Chain	Res	Type
1	S	786	GLN
1	l	797	GLN
1	W	797	GLN
1	l	786	GLN
1	h	786	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.

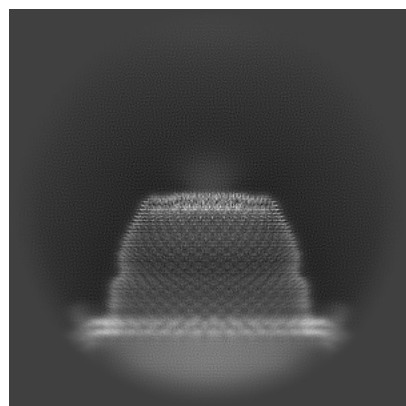
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75664. These allow visual inspection of the internal detail of the map and identification of artifacts.

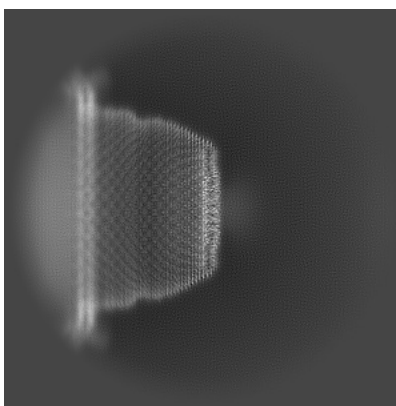
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

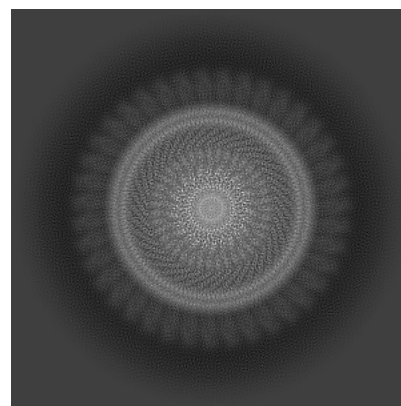
#### 6.1.1 Primary map



X

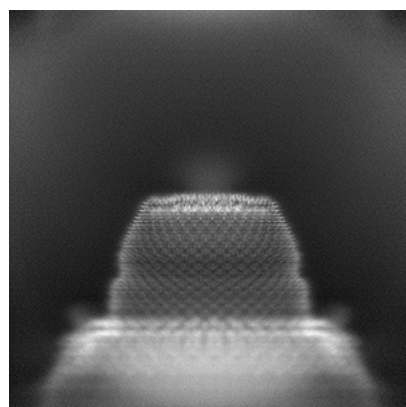


Y

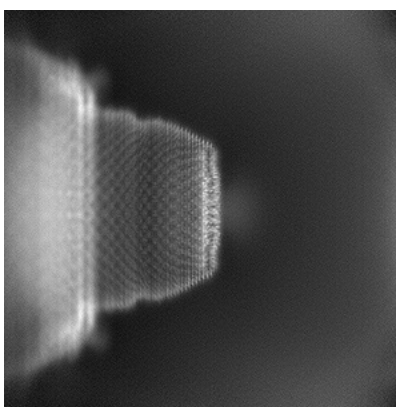


Z

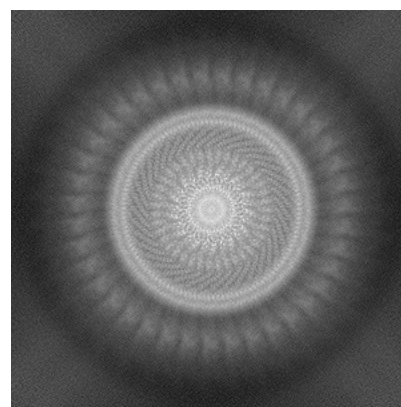
#### 6.1.2 Raw map



X



Y

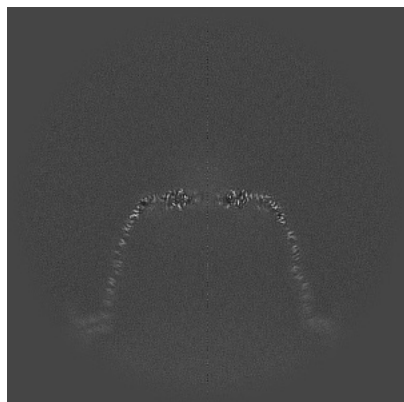


Z

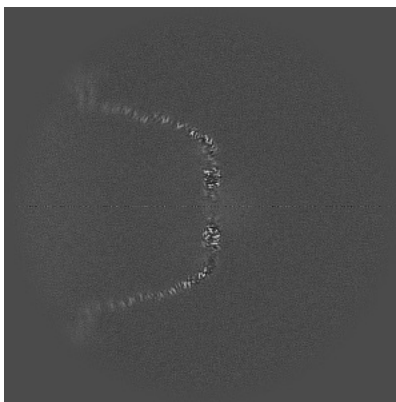
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

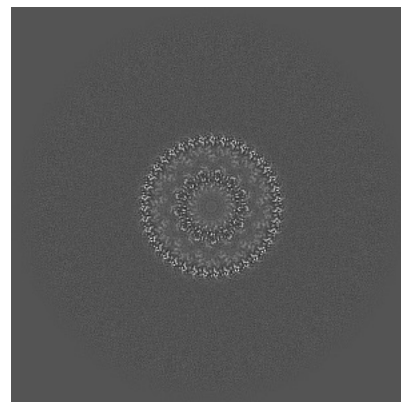
### 6.2.1 Primary map



X Index: 300

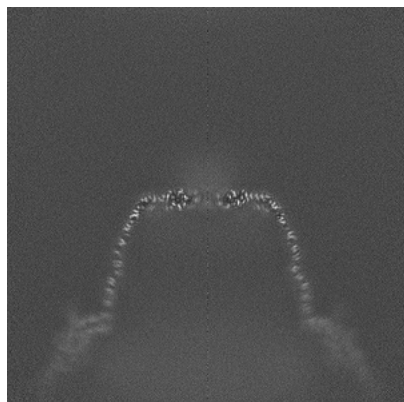


Y Index: 300

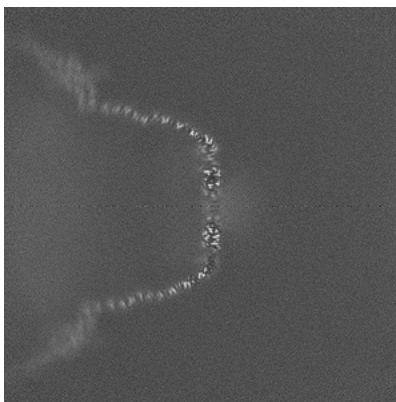


Z Index: 300

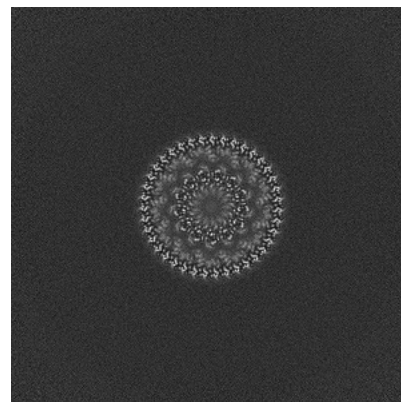
### 6.2.2 Raw map



X Index: 300



Y Index: 300



Z Index: 300

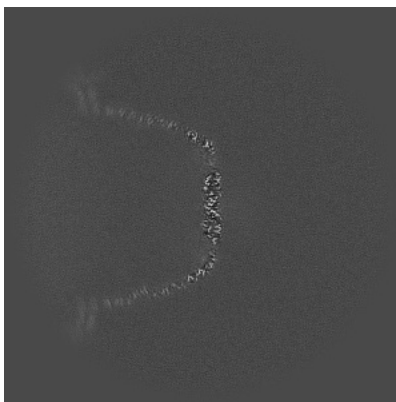
The images above show central slices of the map in three orthogonal directions.

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

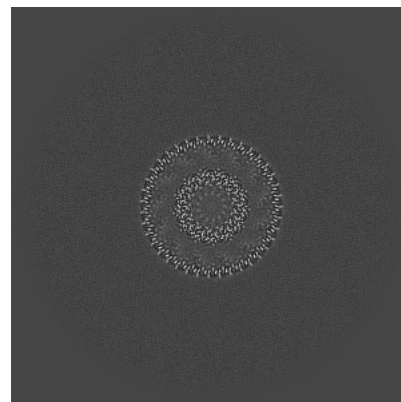
### 6.3.1 Primary map



X Index: 268



Y Index: 332

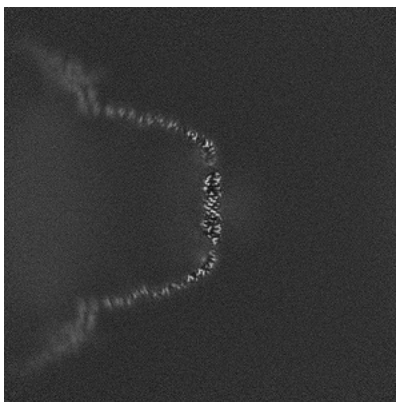


Z Index: 303

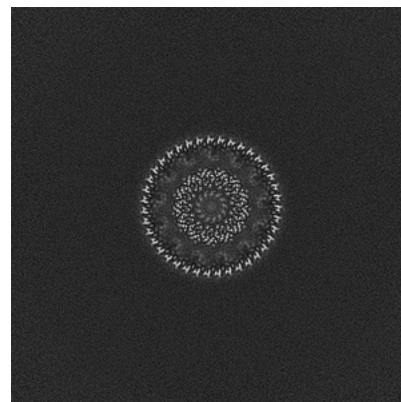
### 6.3.2 Raw map



X Index: 268



Y Index: 332

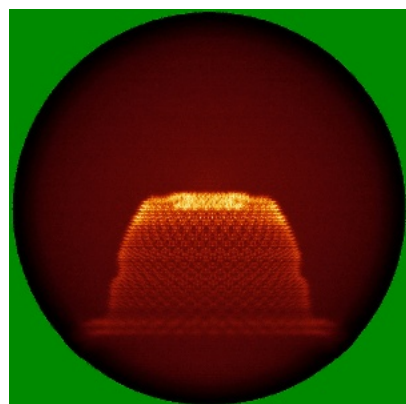


Z Index: 304

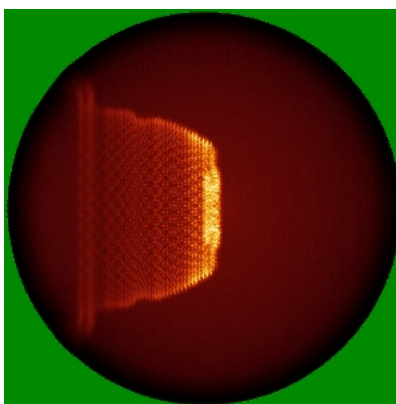
The images above show the largest variance slices of the map in three orthogonal directions.

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

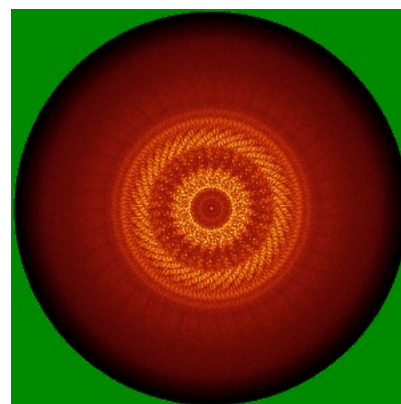
### 6.4.1 Primary map



X

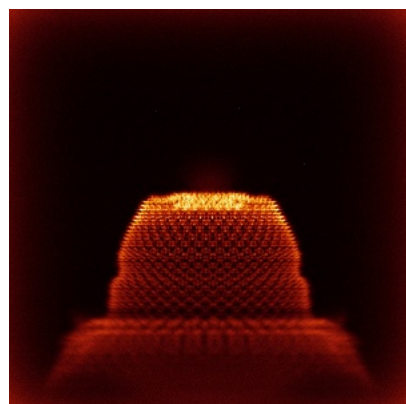


Y

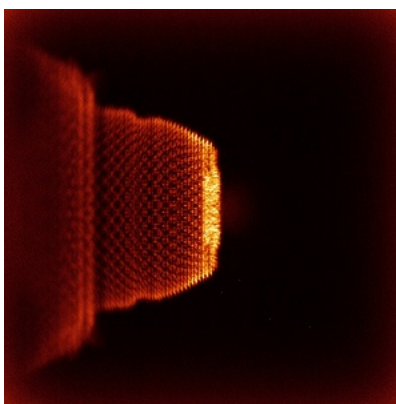


Z

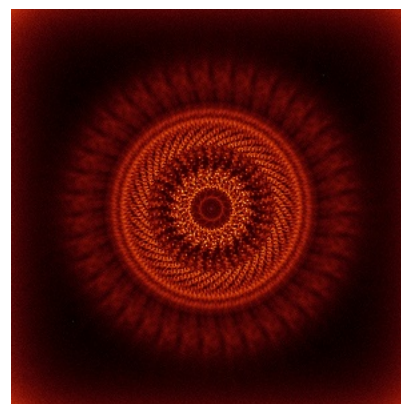
### 6.4.2 Raw map



X



Y

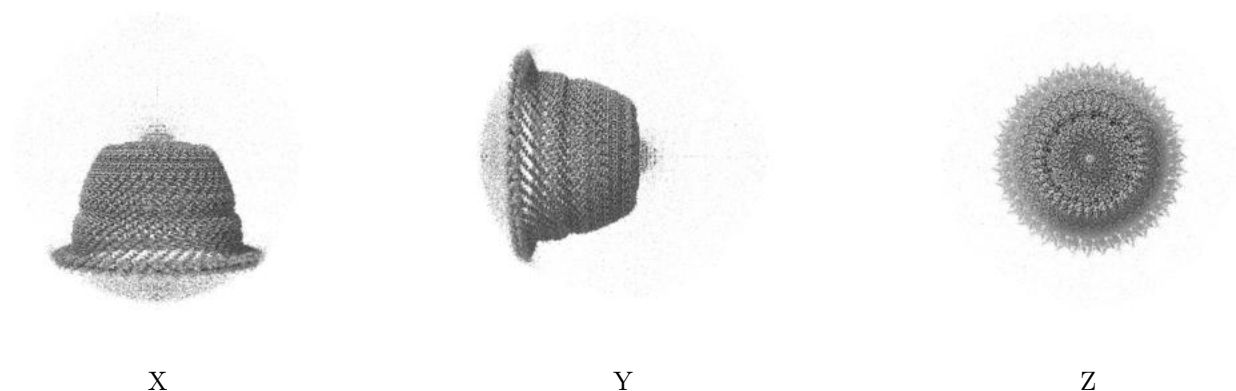


Z

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.

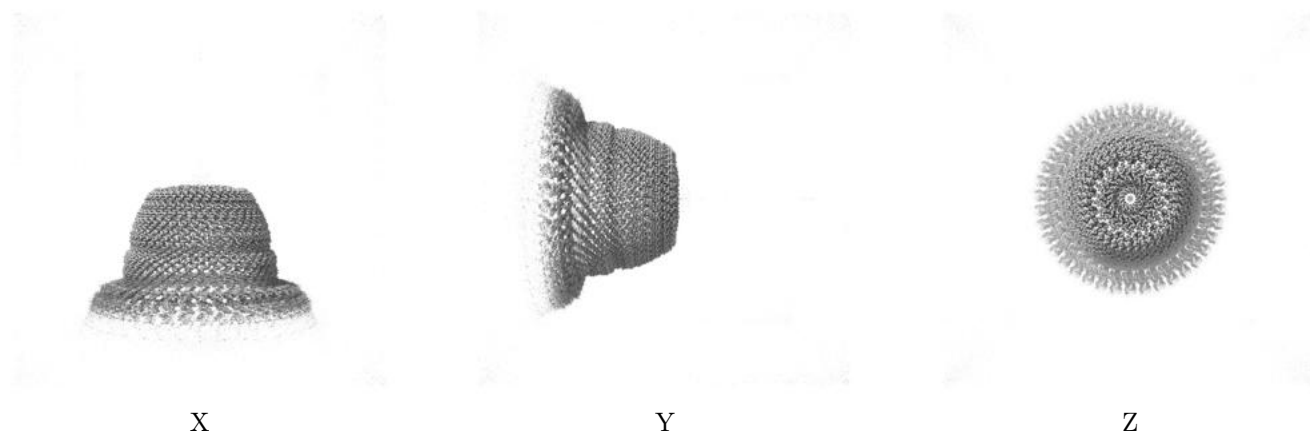
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. 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

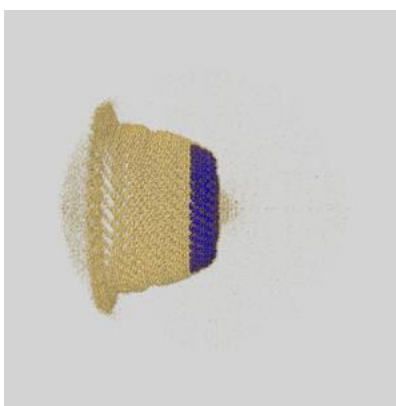
A mask typically either:

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

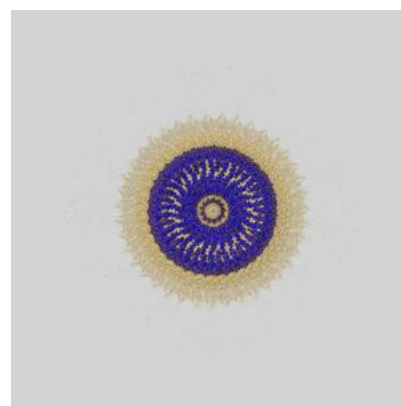
### 6.6.1 emd\_75664\_msk\_1.map [i](#)



X



Y

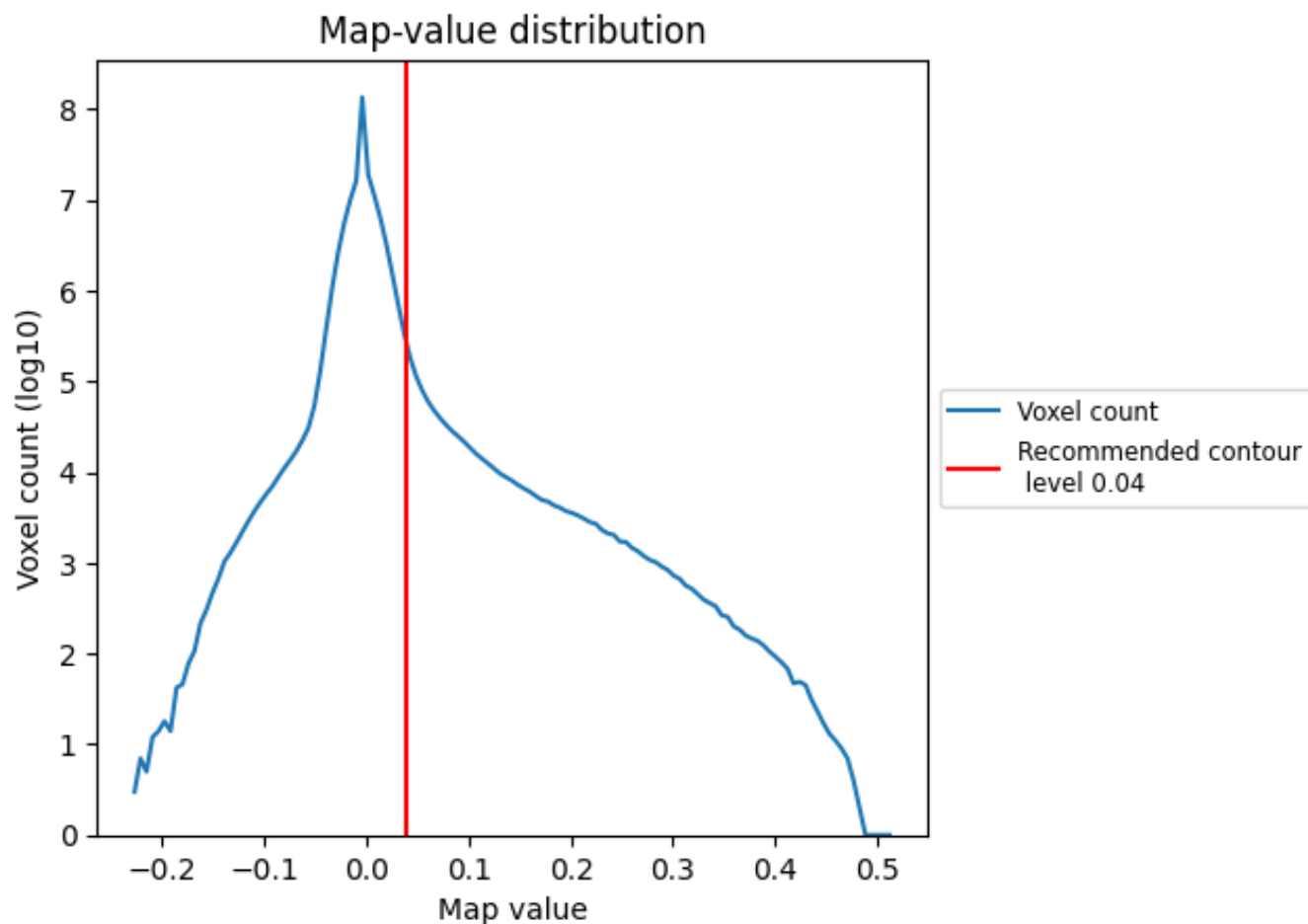


Z

## 7 Map analysis [i](#)

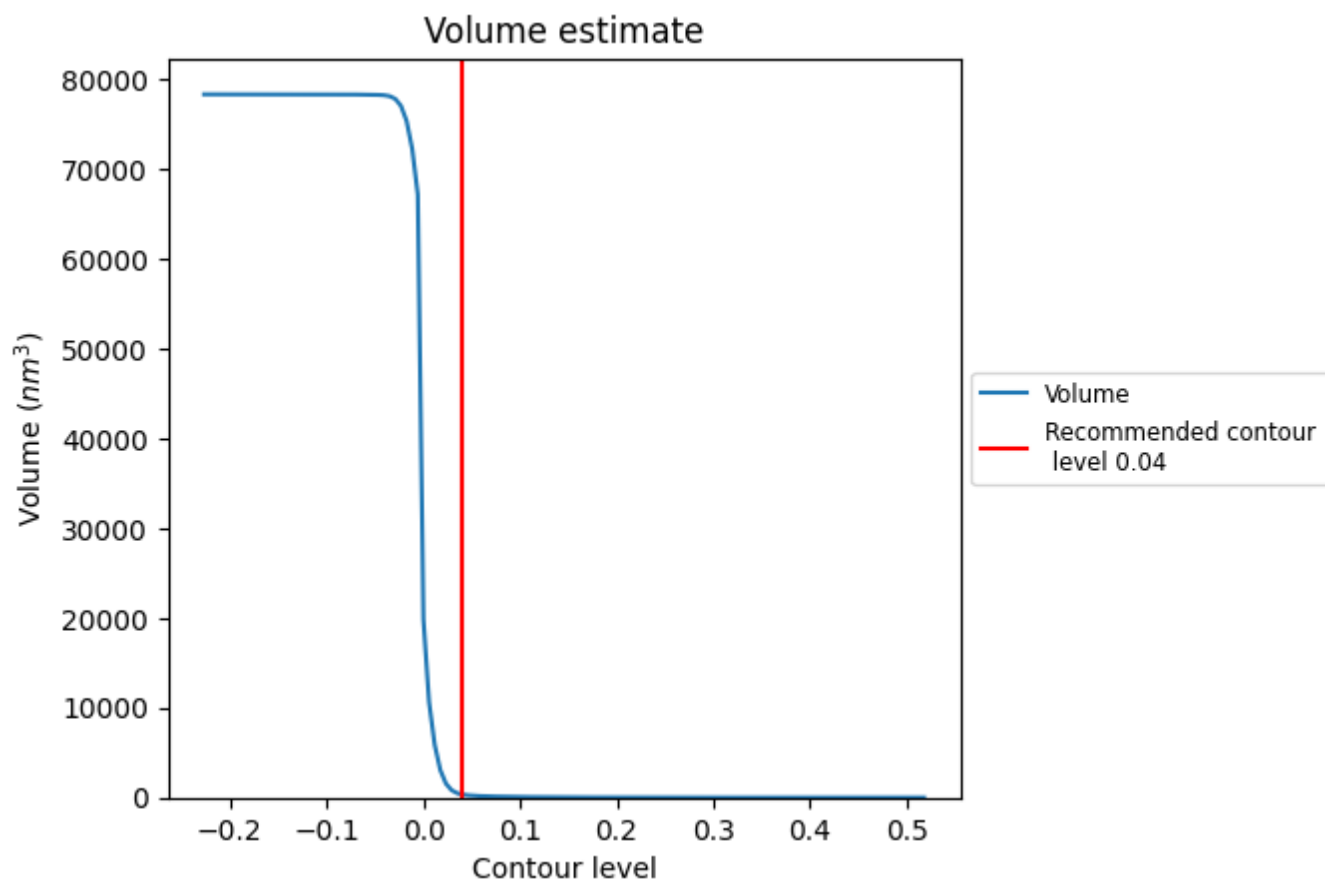
This section contains the results of statistical analysis of the map.

### 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.

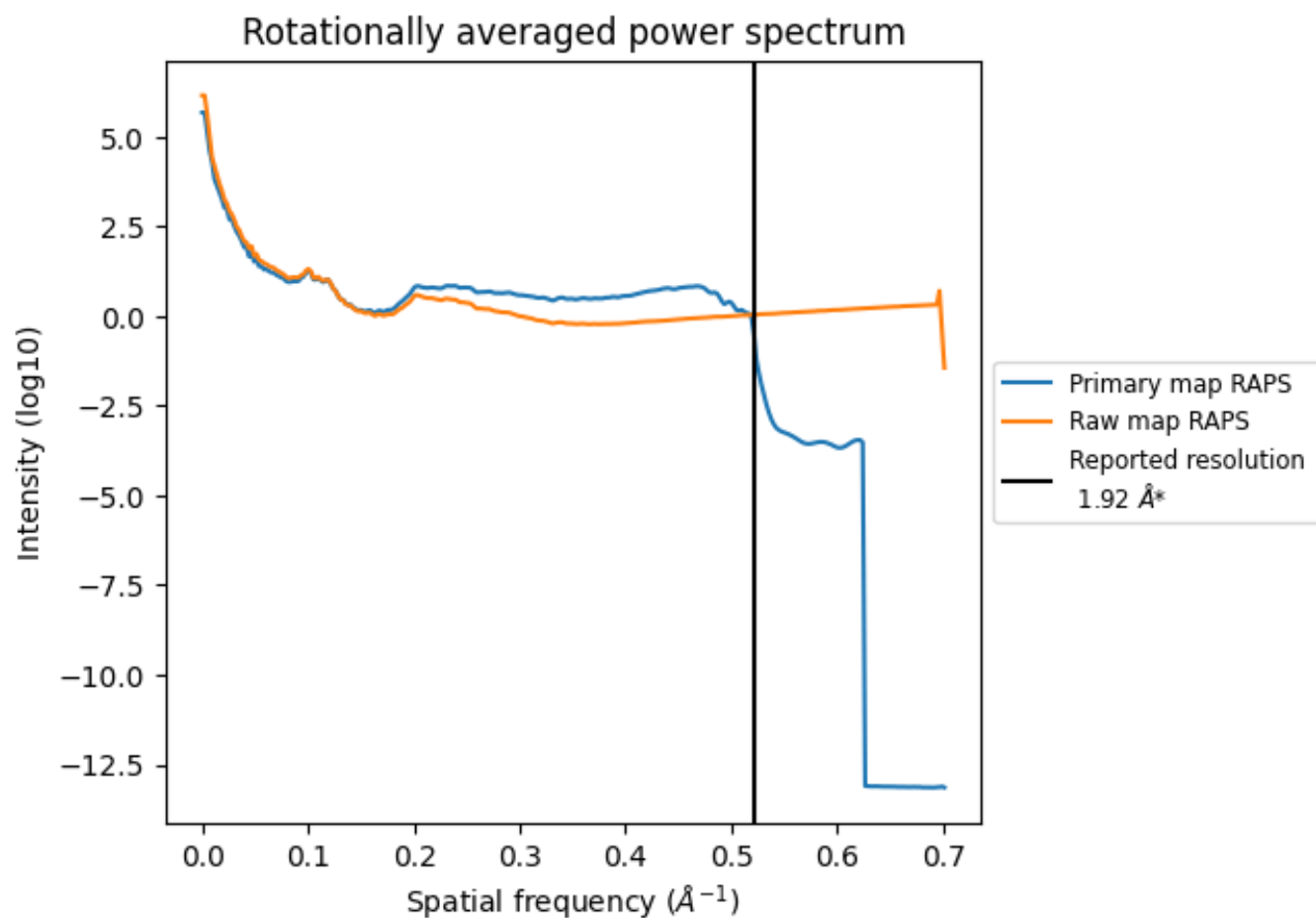
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 354  $\text{nm}^3$ ; this corresponds to an approximate mass of 320 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 ⓘ

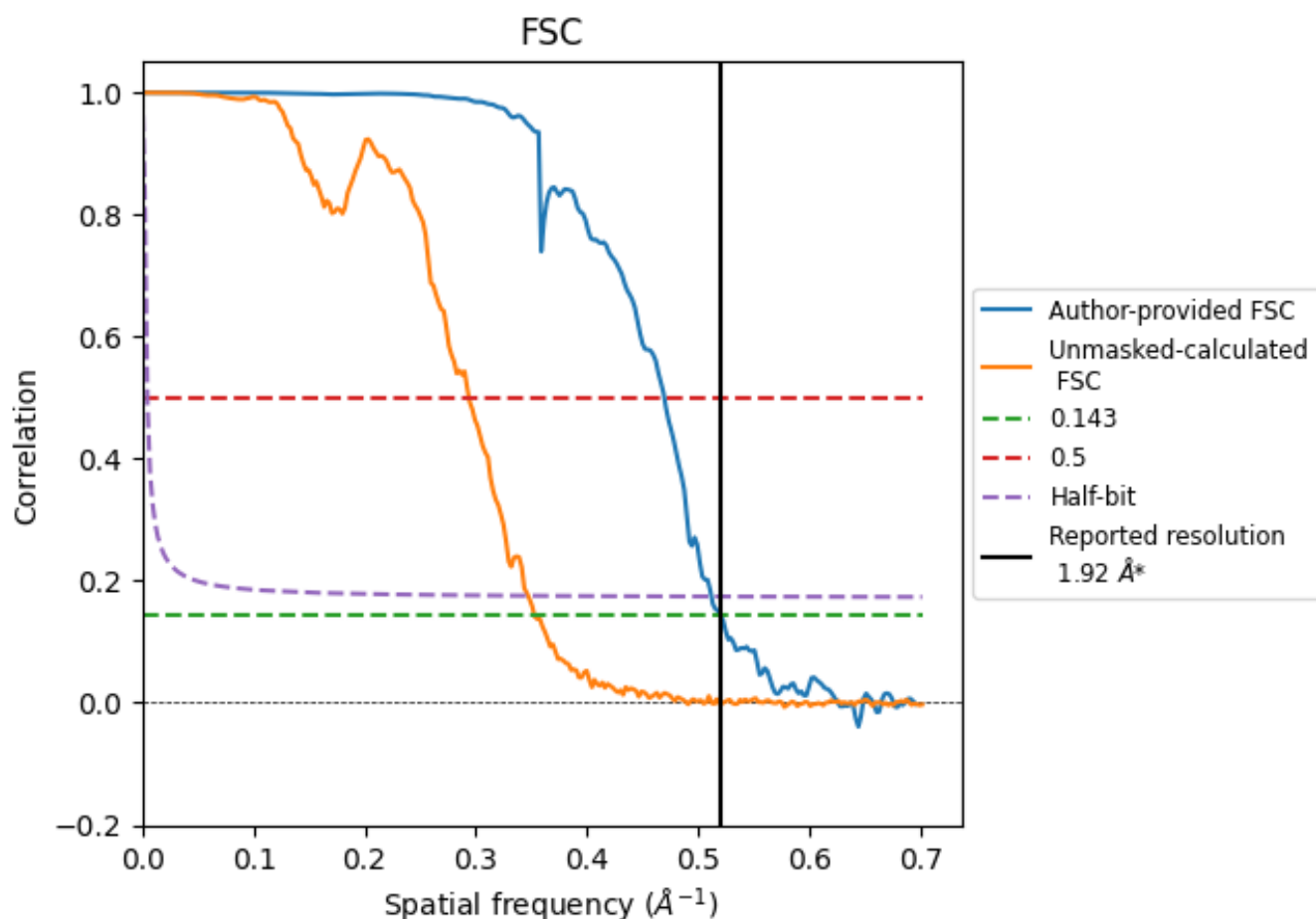


\*Reported resolution corresponds to spatial frequency of 0.521  $\text{\AA}^{-1}$

## 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  $0.521 \text{ \AA}^{-1}$

## 8.2 Resolution estimates [i](#)

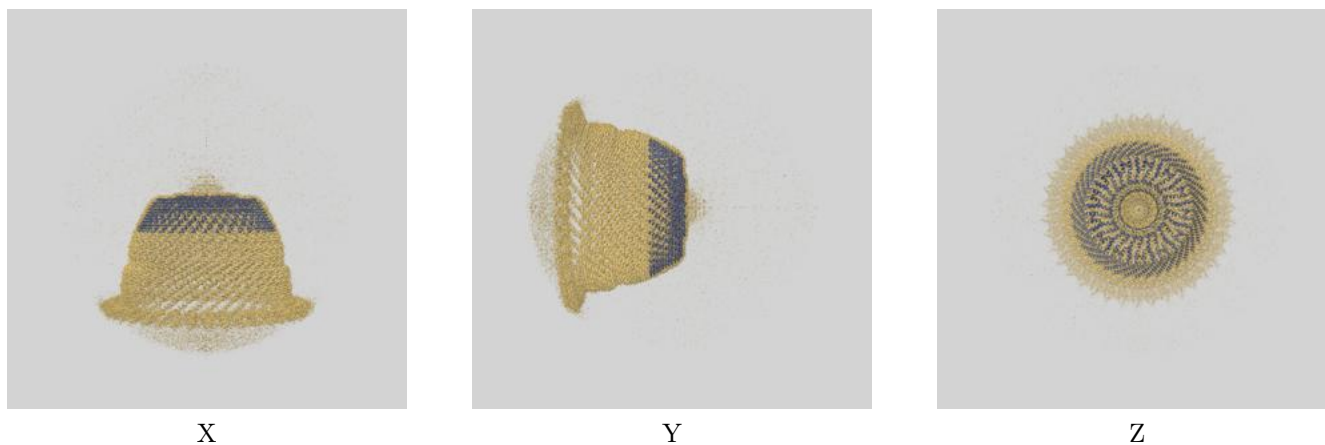
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	1.92	-	-
Author-provided FSC curve	1.92	2.13	1.95
Unmasked-calculated*	2.84	3.40	2.88

\*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 2.84 differs from the reported value 1.92 by more than 10 %

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

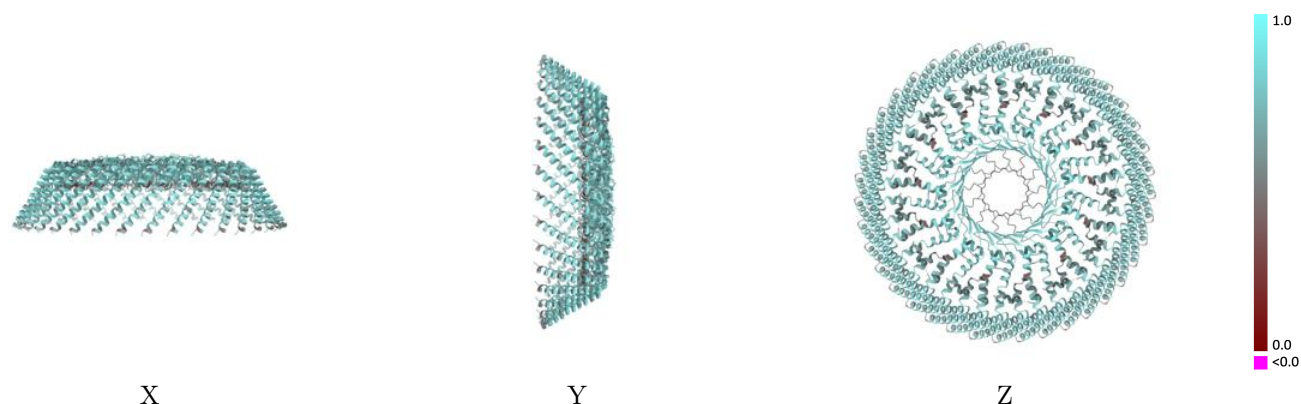
This section contains information regarding the fit between EMDB map EMD-75664 and PDB model 11FH. Per-residue inclusion information can be found in section [3](#) on page [8](#).

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



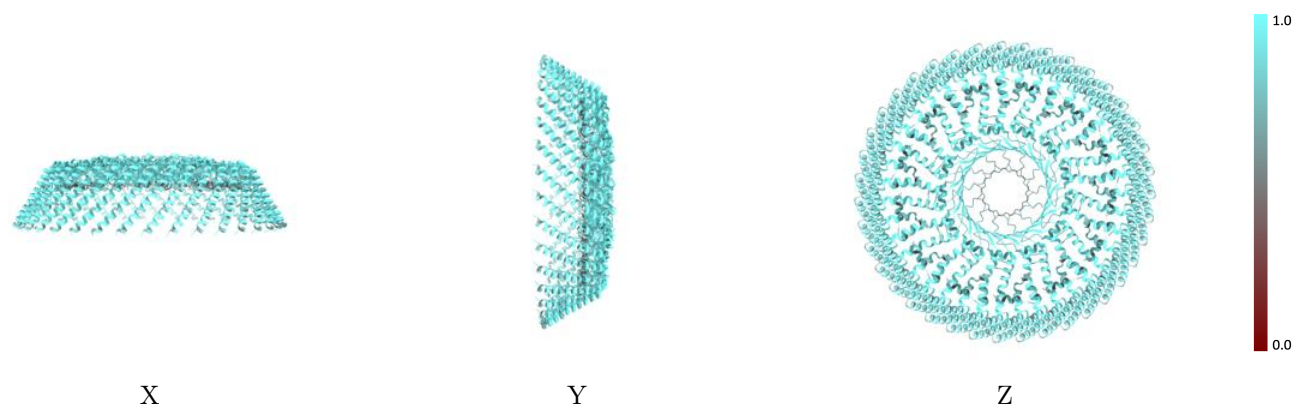
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



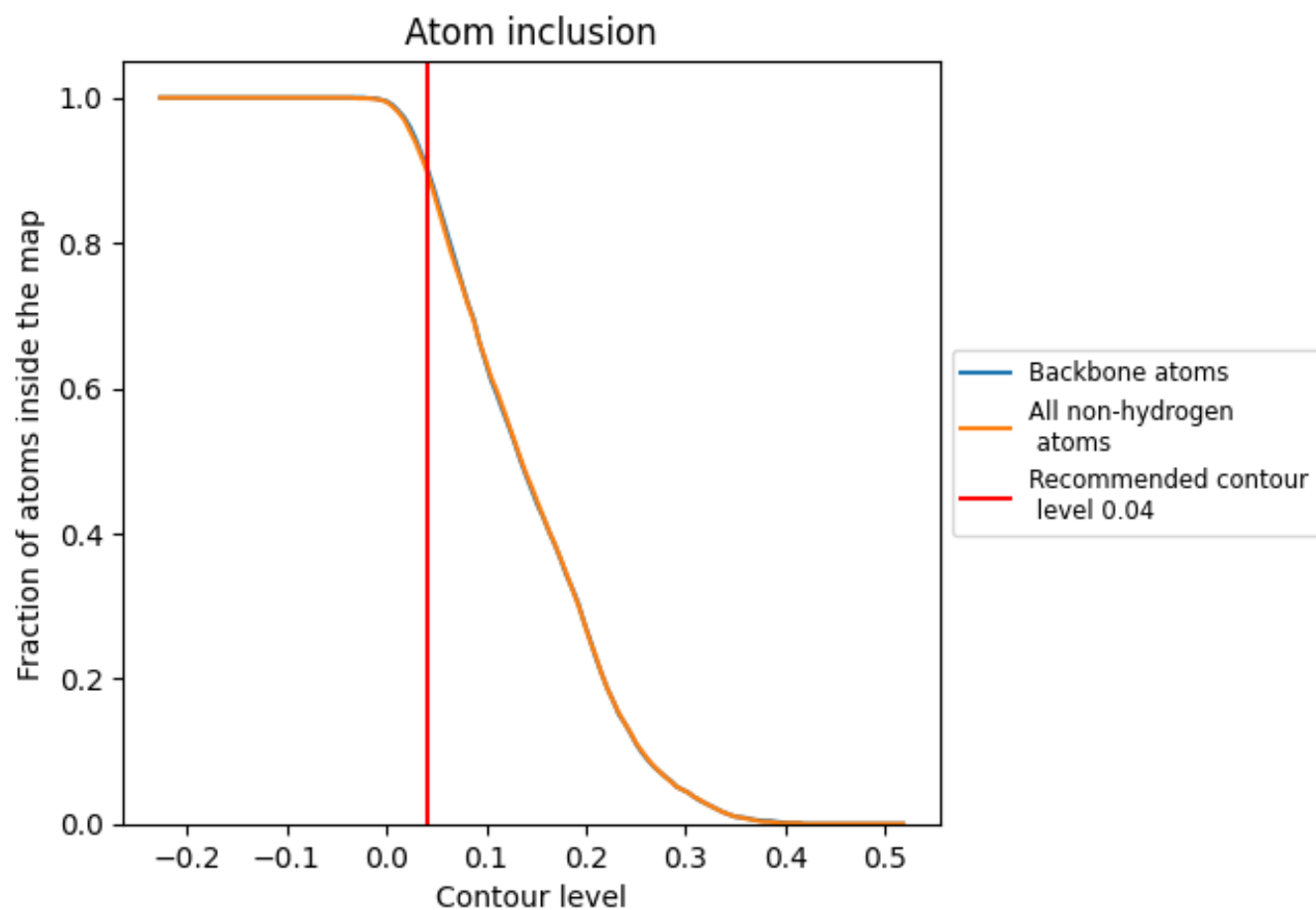
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).







































































## 9.4 Atom inclusion ⓘ



At the recommended contour level, 90% of all backbone atoms, 90% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9010	 0.6740
A	 0.8660	 0.6240
B	 0.9160	 0.6790
C	 0.9270	 0.7030
D	 0.8660	 0.6250
E	 0.9130	 0.6800
F	 0.9280	 0.7060
G	 0.8660	 0.6270
H	 0.9090	 0.6820
I	 0.9270	 0.7050
J	 0.8660	 0.6250
K	 0.9160	 0.6810
L	 0.9230	 0.7060
M	 0.8670	 0.6220
N	 0.9160	 0.6840
O	 0.9250	 0.7070
P	 0.8670	 0.6250
Q	 0.9110	 0.6830
R	 0.9250	 0.7070
S	 0.8670	 0.6270
T	 0.9090	 0.6840
U	 0.9280	 0.7060
V	 0.8670	 0.6280
W	 0.9140	 0.6840
X	 0.9250	 0.7070
Y	 0.8660	 0.6290
Z	 0.9110	 0.6840
a	 0.9280	 0.7060
b	 0.8620	 0.6280
c	 0.9130	 0.6830
d	 0.9240	 0.7040
e	 0.8690	 0.6260
f	 0.9090	 0.6800
g	 0.9250	 0.7050
h	 0.8660	 0.6270



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Chain	Atom inclusion	Q-score
i	 0.9160	 0.6800
j	 0.9240	 0.7040
k	 0.8620	 0.6240
l	 0.9180	 0.6800
m	 0.9210	 0.7030