



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 02:56 AM UTC

PDB ID : 6VAD / pdb_00006vad
EMDB ID : EMD-21137
Title : Fanconi Anemia ID complex
Authors : Pavletich, N.P.
Deposited on : 2019-12-17
Resolution : 3.30 Å (reported)
Based on initial model : 3S4W

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

We welcome your comments at 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>.

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

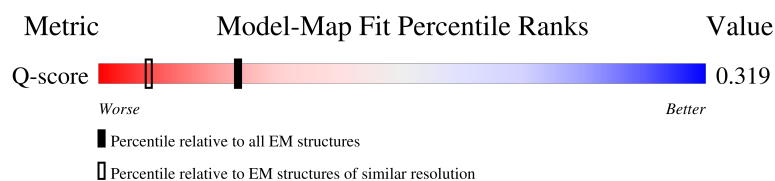
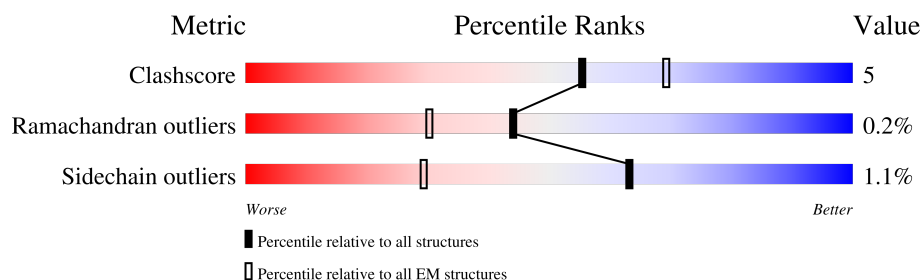
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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	15087 (2.80 - 3.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1328	
2	B	1451	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 37613 atoms, of which 19096 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 Fanconi anemia, complementation group I.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	1168	Total	C	H	N	O	S	0	0
			18879	5934	9619	1549	1723	54		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	136	VAL	ALA	conflict	UNP B7ZMF2
A	476	ASN	SER	conflict	UNP B7ZMF2
A	638	GLU	LYS	conflict	UNP B7ZMF2
A	657	GLN	LYS	conflict	UNP B7ZMF2
A	877	LEU	ILE	conflict	UNP B7ZMF2
A	1235	VAL	ALA	conflict	UNP B7ZMF2
A	1274	SER	ASN	conflict	UNP B7ZMF2

- Molecule 2 is a protein called Fanconi anemia group D2 protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	1153	Total	C	H	N	O	S	0	0
			18734	5969	9477	1527	1709	52		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	654	GLN	HIS	conflict	UNP Q9BXW9
B	693	ASN	ASP	conflict	UNP Q9BXW9

Chain B:



GLU	L1367	K1307	K1247	C1187	F1121
ASP	V1368	Q1308	K1248	I1188	H122
GLY	C1369	C1309	I1249	L1189	Q1123
GLU	R1370	M1310	E1250	L1190	S1124
ASP	V1371	P1311	P1251	E1191	
GLU	K1372	L1312	G1252	H1192	Q1129
VAL	A1373	L1313	T1253	T1193	C1130
SER	M1374	D1314	A1254	E1194	
ALA	L1375	F1315	A1255	S1195	Y1133
GLY	T1376	S1316	D1256	L1196	L1134
GLU	LEU	F1317	S1257	L1197	I1135
GLN	ASN	R1318	Q1258	K1198	R1136
ASN	ASN	K1319	Q1259	A1199	L1137
CYS	ARG	H1320	I1260	T1200	L1138
ASP	GLU	R1321	H1261	E1201	M1139
GLU	ALA	E1322	E1262	E1202	V1140
SER	PHE	D1323	E1263	I1203	I1141
TYR	TRP	V1324	K1264	A1204	L1342
ASP	LEU	L1325	L1265	G1205	E1143
GLY	GLY	S1326	L1266	V1206	K1344
SER	ASN	L1327	L1267	G1207	S1145
ASP	LEU	L1328	M1268	V1208	THR
	ASN	E1329	M1269	P1209	ALA
	ARG	T1330	M1270	E1210	ALA
LEU	LEU	F1331	A1271	L1211	Q1150
GLN	GLN	Q1332	V1272	I1212	M1151
GLY	GLU	L1333	R1273	N1213	K1152
GLU	GLU	D1334	D1274	S1214	E1153
ILE	ILE	T1335	F1275	P1215	K1154
LYS	LYS	R1336	S1276	LYS	I1155
SER	SER	L1337	I1277	ASP	
GLN	GLN	L1338	L1278	ALA	A1159
ASN	ASN	H1339	I1279	SER	R1160
GLU	GLU	H1340	N1280	S1220	Q1161
SER	SER	L1341	L1281	S1221	F1162
ALA	ALA	C1342	I1282	T1222	L1163
ASP	ASP	G1343	K1283	F1223	C1164
GLU	GLU	H1344	V1284	P1224	R1165
SER	SER	S1345	F1285	T1225	V1166
GLU	GLU	S1346	D1286	L1226	M1167
ASP	ASP	K1347	S1287	T1227	P1168
MET	MET	H1348	H1288	R1228	S1169
SER	SER	Q1349	P1289	H1229	GL170
SER	SER	D1350	P1290	T1230	D1171
GLN	GLN	T1351	L1291	F1231	K1172
LYS	LYS	R1352	H1292	V1232	E1173
SER	SER	L1353	V1293	F1234	K1174
LYS	LYS	T1354	C1294	F1235	S1175
ALA	ALA	Q1355	L1295	M1176	M1177
THR	THR	H1356	K1296	I1177	I1178
		V1357	Y1297	V1237	S1179
		P1358	Q1298	M1238	M1239
		L1359	R1299	M1239	D1180
		L1360	L1300	A1240	Q1181
		K1361	F1301	E1241	L1182
		V1362	V1302	L1242	H1183
		T1363	E1303	E1243	A1184
		L1364	A1304	K1244	L1185
		E1365	F1305	T1245	L1186
		L1366	L1306	V1246	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	251271	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 ($e^-/\text{\AA}^2$)	51	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	0.188	Depositor
Minimum map value	-0.114	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.012	Depositor
Map size (Å)	279.04, 279.04, 279.04	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.09, 1.09, 1.09	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	1.02	22/9403 (0.2%)	1.25	22/12681 (0.2%)
2	B	0.86	10/9427 (0.1%)	1.21	7/12745 (0.1%)
All	All	0.94	32/18830 (0.2%)	1.23	29/25426 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	4
2	B	0	4
All	All	0	8

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	315	SER	C-N	-9.46	1.24	1.34
1	A	329	LEU	C-O	8.19	1.33	1.24
1	A	310	ILE	C-O	-8.18	1.15	1.23
2	B	480	HIS	CE1-NE2	7.70	1.40	1.32
2	B	387	ILE	C-O	-7.52	1.15	1.24

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	276	VAL	N-CA-C	-9.24	101.86	110.82
1	A	391	ASP	CA-CB-CG	8.01	120.61	112.60
1	A	219	VAL	N-CA-C	-6.50	104.16	110.72
1	A	390	MET	CA-C-O	-6.07	113.99	120.42
1	A	443	GLN	CB-CG-CD	-6.03	102.36	112.60

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	224	GLY	Peptide
1	A	641	LEU	Peptide
1	A	717	GLU	Peptide
1	A	801	SER	Peptide
2	B	222	SER	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	9260	9619	9587	67	0
2	B	9257	9477	9421	121	0
All	All	18517	19096	19008	187	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 187 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:425:ILE:O	1:A:429:THR:OG1	1.97	0.79
2:B:1122:HIS:O	2:B:1165:ARG:NH1	2.16	0.78
2:B:1279:ILE:HG23	2:B:1341:LEU:HD11	1.64	0.78
1:A:1170:TYR:OH	1:A:1209:CYS:SG	2.40	0.77
1:A:622:SER:O	1:A:626:THR:OG1	2.04	0.74

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	1149/1328 (86%)	1075 (94%)	72 (6%)	2 (0%)	43	71
2	B	1123/1451 (77%)	1050 (94%)	70 (6%)	3 (0%)	36	65
All	All	2272/2779 (82%)	2125 (94%)	142 (6%)	5 (0%)	44	71

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	376	ASP
1	A	120	SER
2	B	391	THR
2	B	767	PRO
2	B	220	GLY

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	1067/1205 (88%)	1053 (99%)	14 (1%)	61	74
2	B	1065/1324 (80%)	1055 (99%)	10 (1%)	70	78
All	All	2132/2529 (84%)	2108 (99%)	24 (1%)	63	76

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	243	VAL
2	B	392	ASN
2	B	391	THR
2	B	433	SER
1	A	590	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	615	GLN
2	B	1005	GLN
2	B	1349	GLN
2	B	1041	ASN
1	A	865	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	B	4
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	773:SER	C	774:MET	N	3.97
1	B	187:VAL	C	188:ASP	N	3.61

Continued on next page...

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	623:GLN	C	624:SER	N	3.18
1	B	643:LYS	C	644:LEU	N	3.18
1	A	260:PRO	C	261:SER	N	3.11

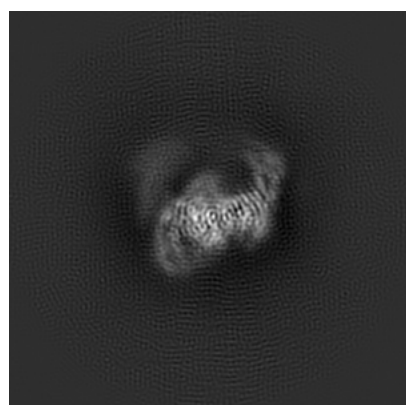
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21137. These allow visual inspection of the internal detail of the map and identification of artifacts.

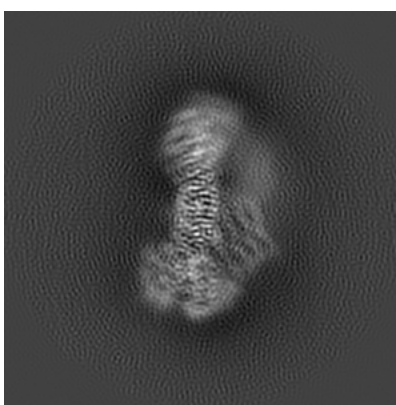
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

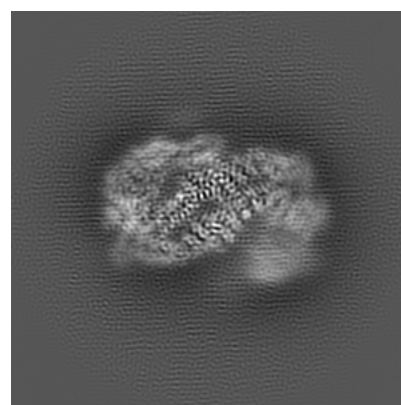
6.1.1 Primary map



X



Y

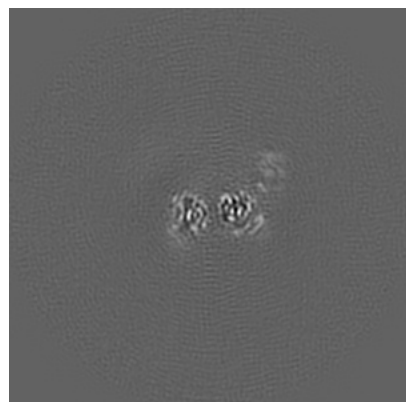


Z

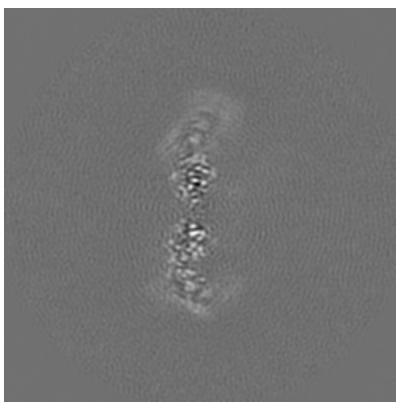
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

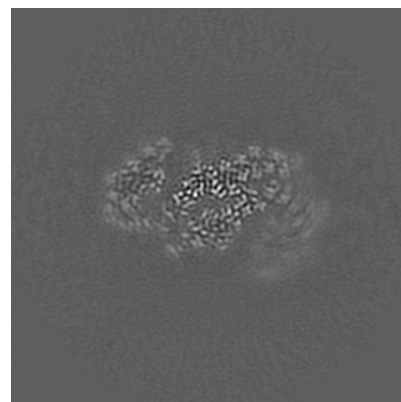
6.2.1 Primary map



X Index: 128



Y Index: 128

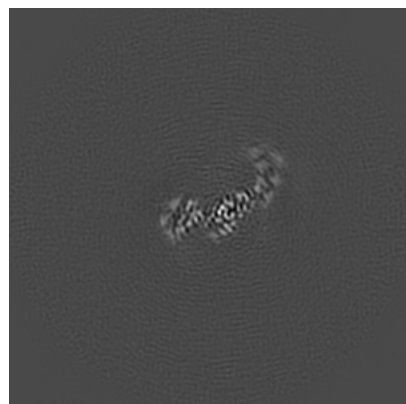


Z Index: 128

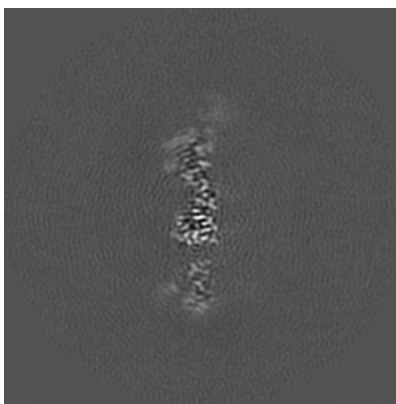
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

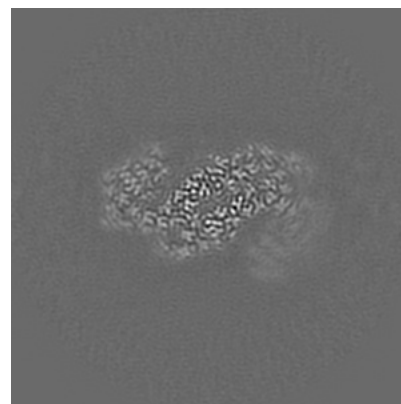
6.3.1 Primary map



X Index: 117



Y Index: 137

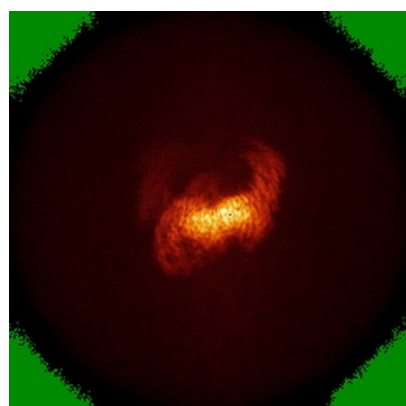


Z Index: 123

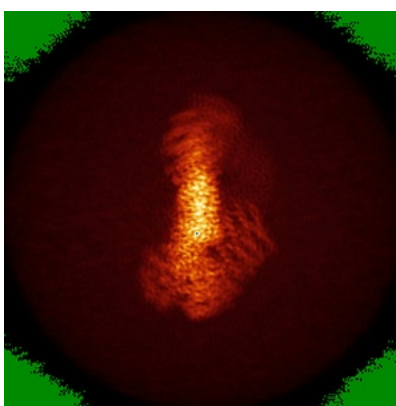
The images above show the largest variance slices of the map in three orthogonal directions.

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

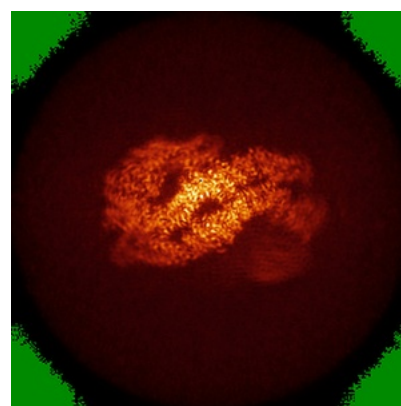
6.4.1 Primary map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.012. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

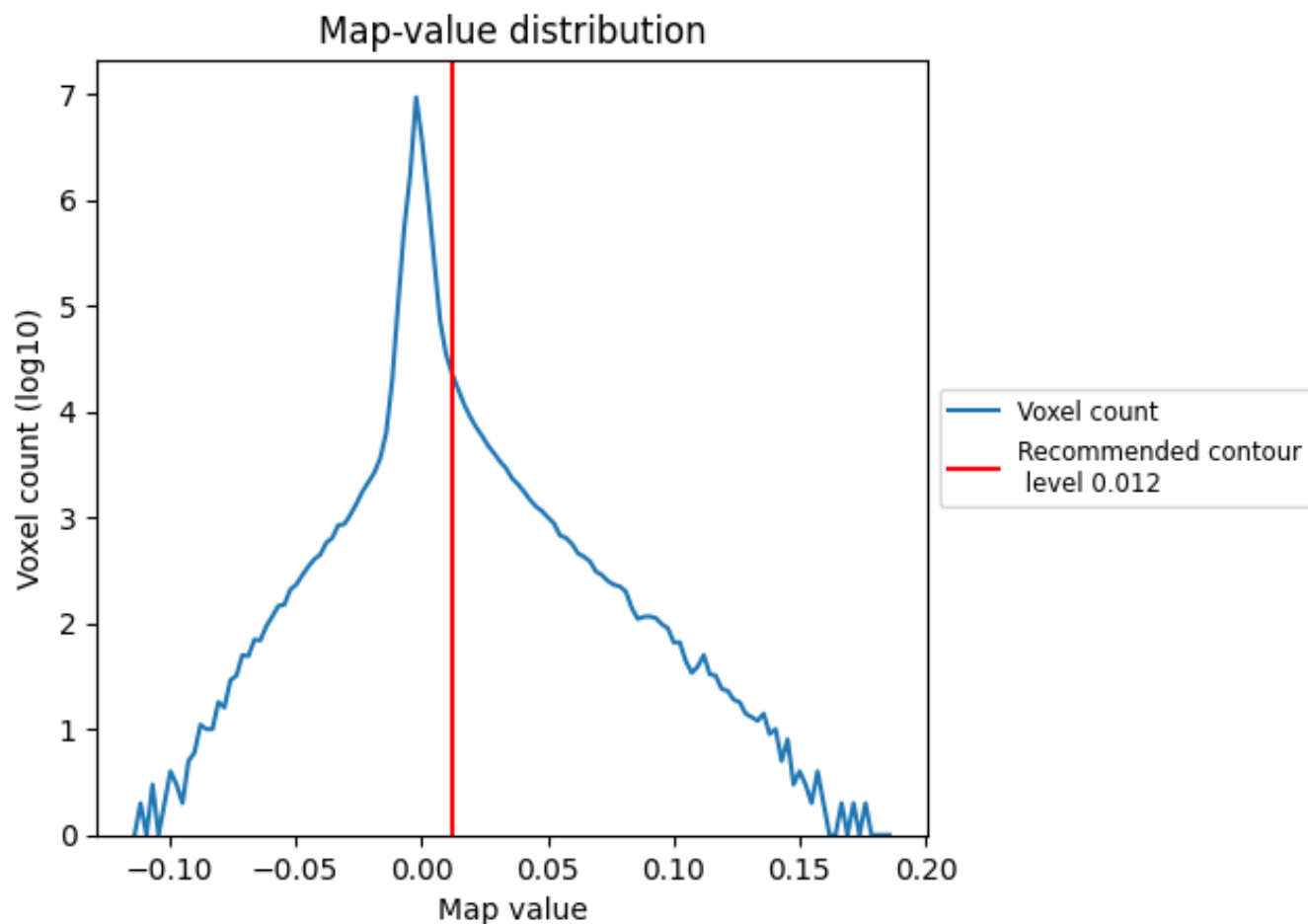
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

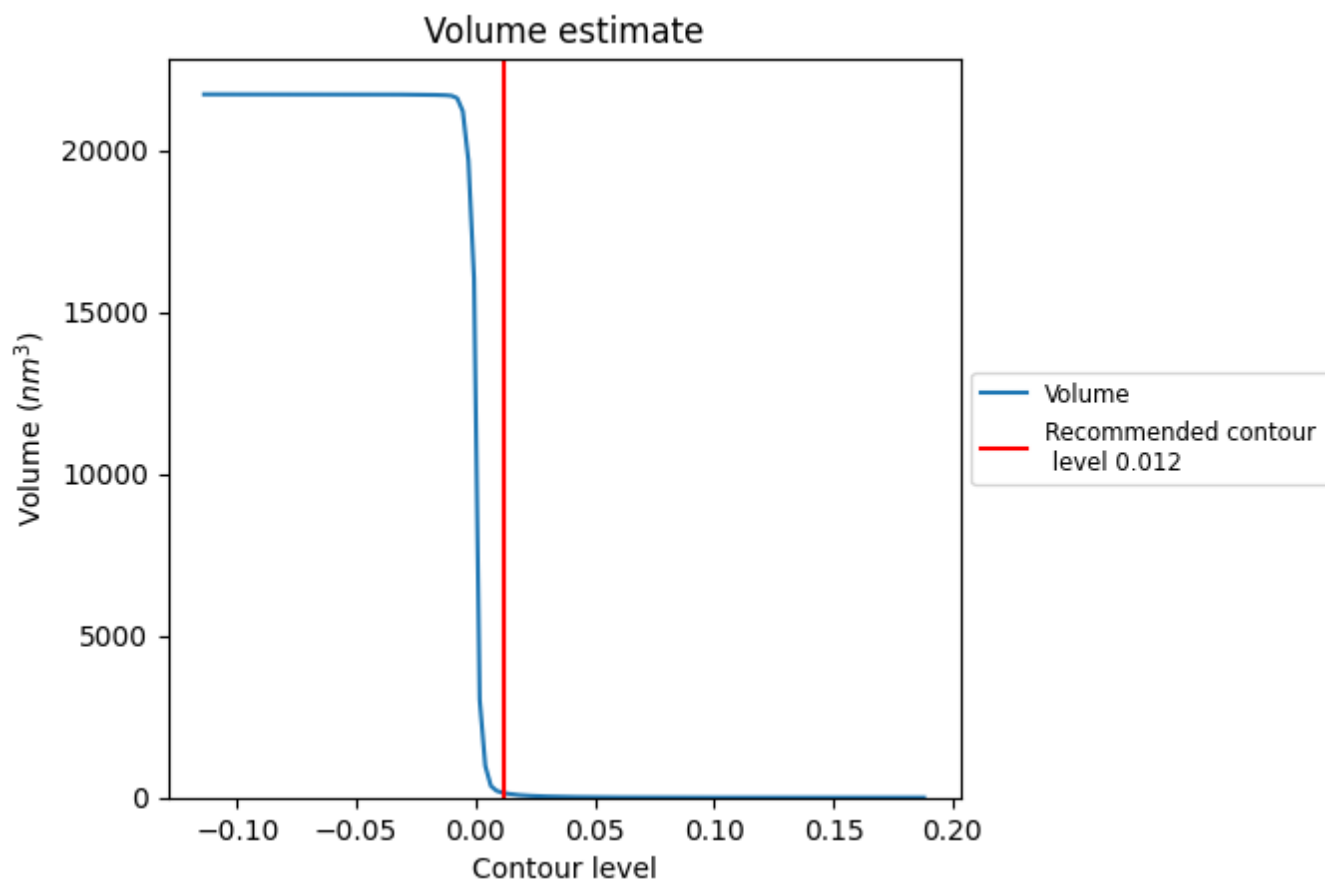
This section contains the results of statistical analysis of the map.

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.

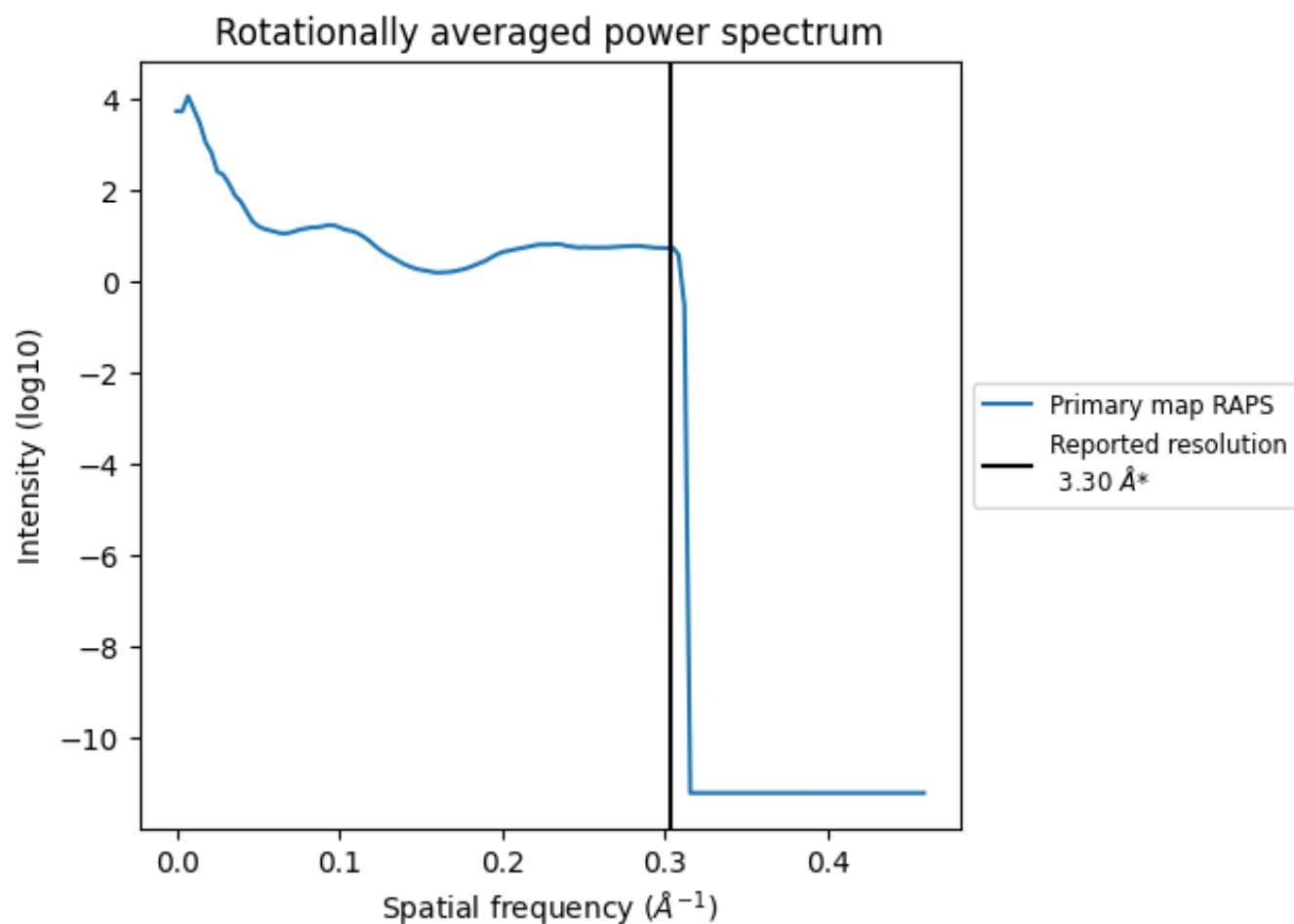
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 140 nm³; this corresponds to an approximate mass of 127 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

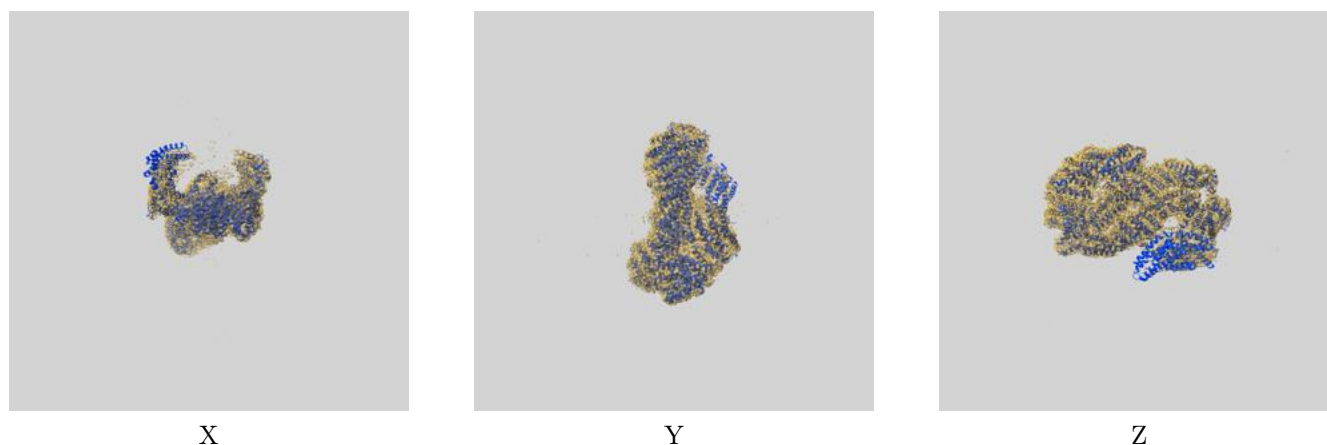
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

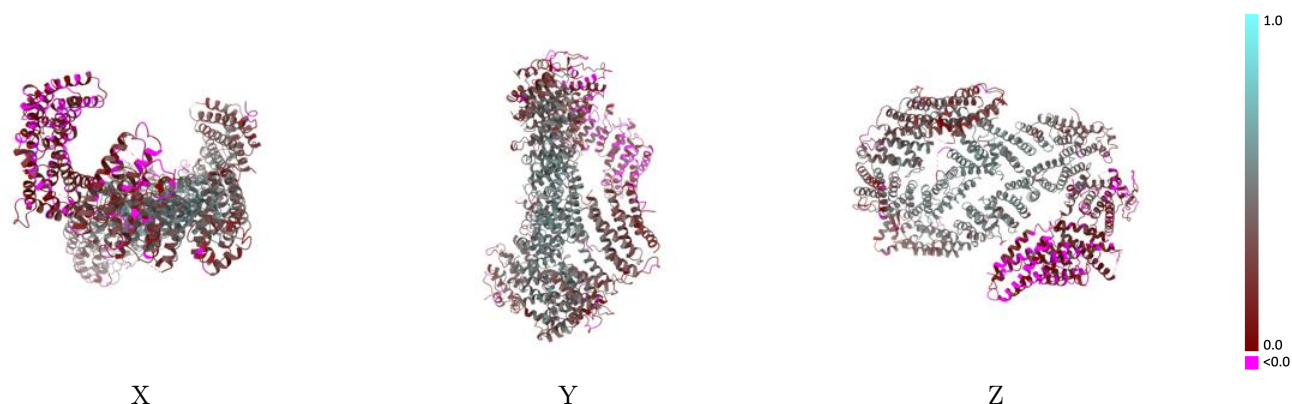
This section contains information regarding the fit between EMDB map EMD-21137 and PDB model 6VAD. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



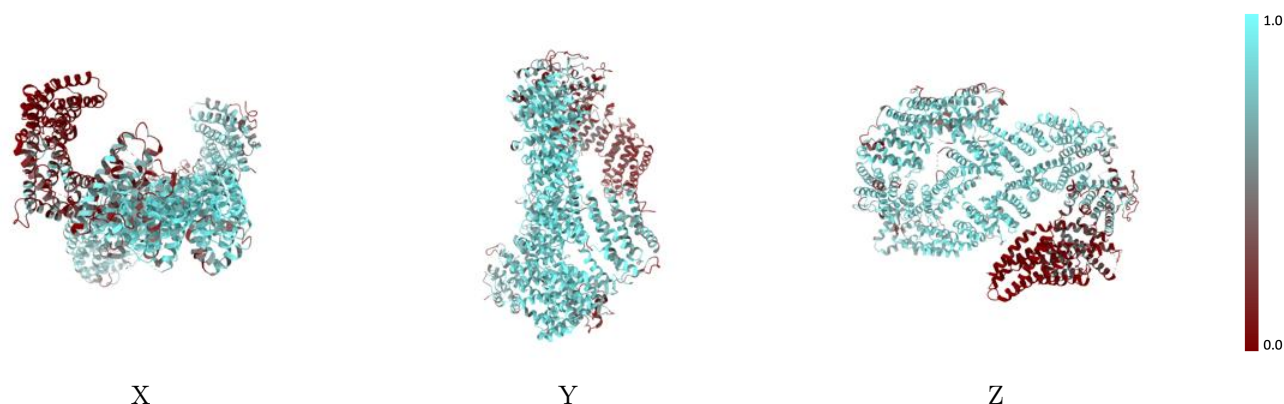
The images above show the 3D surface view of the map at the recommended contour level 0.012 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



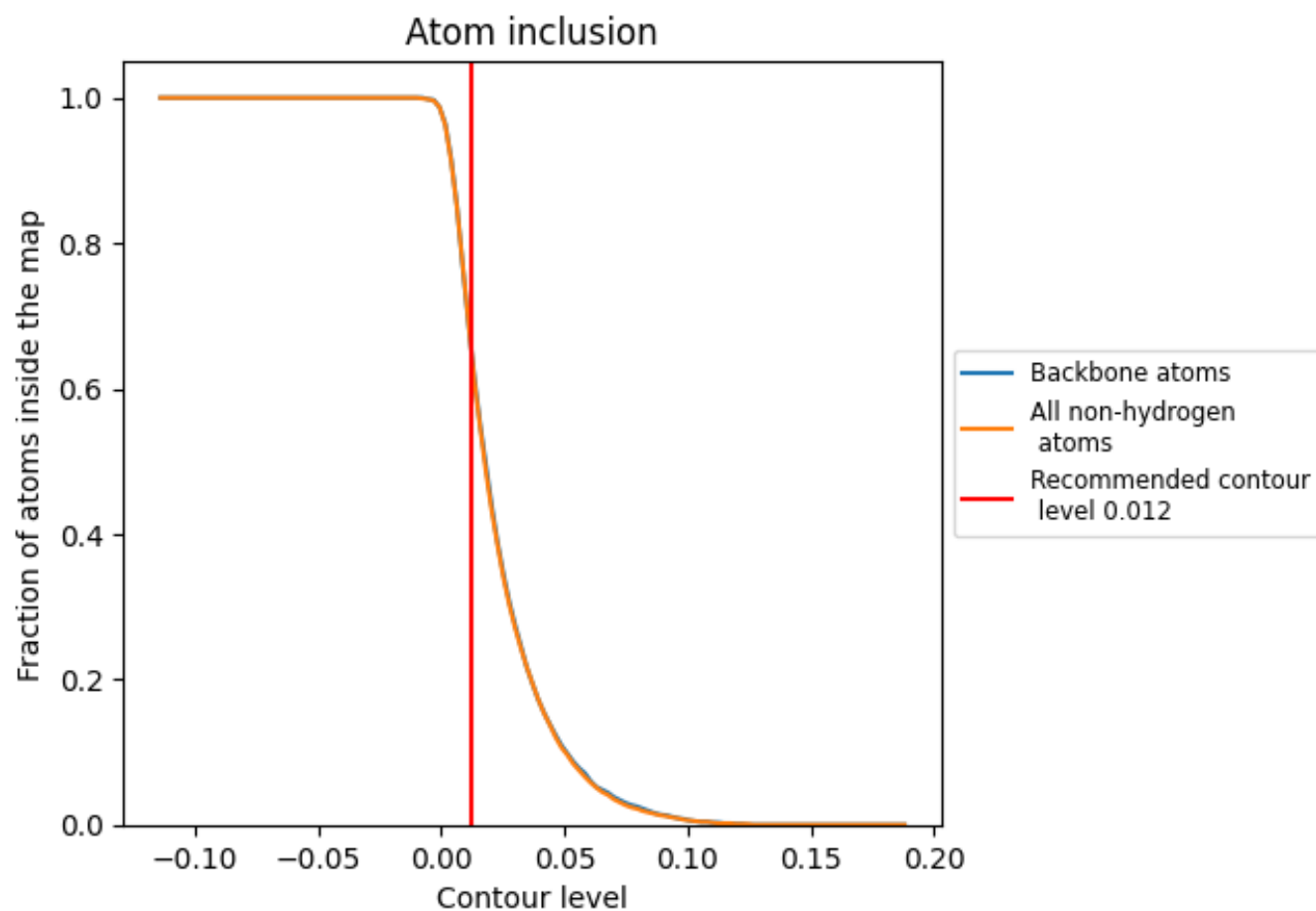
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.012).

9.4 Atom inclusion [i](#)



At the recommended contour level, 66% of all backbone atoms, 66% 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 (0.012) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6580	0.3190
A	0.7960	0.4010
B	0.5280	0.2360

