



## wwPDB EM Validation Summary Report ⓘ

Jan 5, 2023 – 02:41 PM JST

PDB ID : 8HGG  
EMDB ID : EMD-34738  
Title : Structure of 2:2 PAPP-A.ProMBP complex  
Authors : Zhong, Q.H.; Chu, H.L.; Wang, G.P.; Zhang, C.; Wei, Y.; Qiao, J.; Hang, J.  
Deposited on : 2022-11-14  
Resolution : 3.64 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.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.3

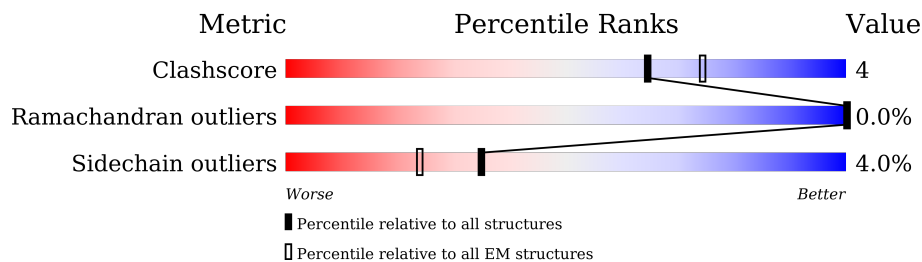
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.64 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	222	 13% 52% 8% 39%
1	B	222	 14% 51% 9% 39%
2	C	1627	 28% 78% 12% 9%
2	D	1627	 28% 78% 12% 9%

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 25404 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 Bone marrow proteoglycan.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	135	Total	C	N	O	S	0	0
			1101	691	218	181	11		
1	B	135	Total	C	N	O	S	0	0
			1101	691	218	181	11		

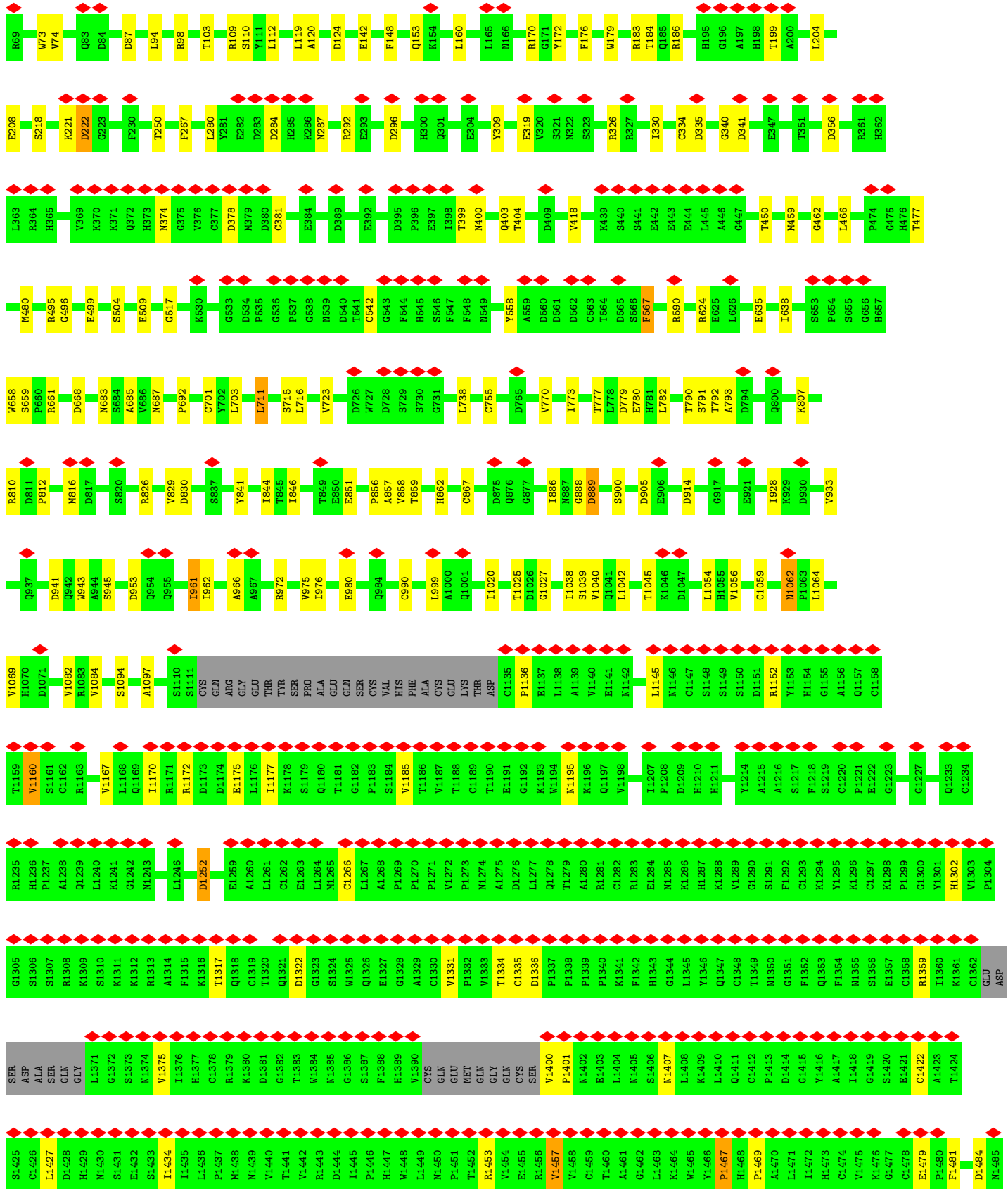
- Molecule 2 is a protein called Pappalysin-1.

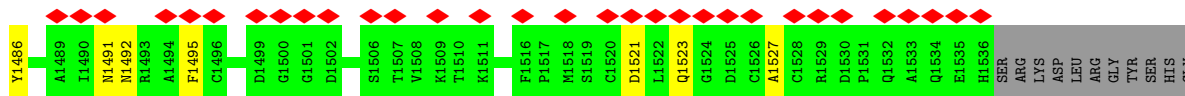
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	C	1484	Total	C	N	O	S	0	0
			11600	7267	2009	2225	99		
2	D	1484	Total	C	N	O	S	0	0
			11600	7267	2009	2225	99		

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

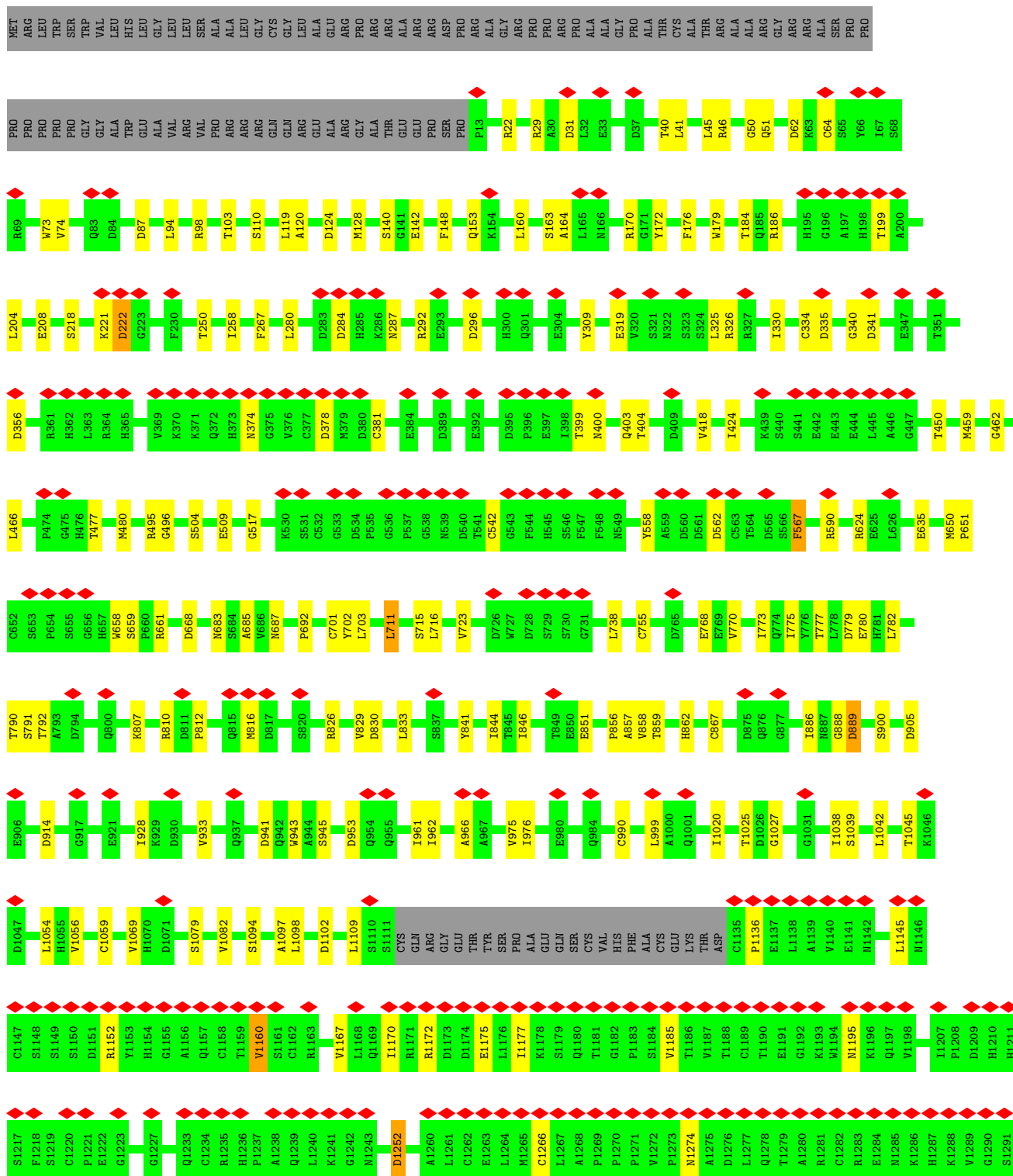
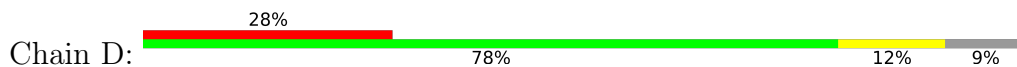
Mol	Chain	Residues	Atoms		AltConf
3	C	1	Total	Zn	0
			1	1	
3	D	1	Total	Zn	0
			1	1	







• Molecule 2: Pappalysin-1



GLY	K1296	S1356	Y1416	K1476	GLY
TYR	C1297	E1357	A1417	G1477	TYR
SER	K1298	C1358	I1418	C1478	SER
HIS	P1299	R1359	G1419	E1479	HIS
GLY	G1300	I1360	P1480	P1480	GLY
	Y1301	K1361	E1421	F1481	
	H1302	C1362	C1422	D1484	
	V1303	GLU	A1423	M1485	
	P1304	ASP	T1424	Y1486	
	G1305	SER	S1425	A1489	
	S1306	ASP	C1426	I1490	
	S1307	ALA	L1427	M1491	
	K1308	SER	D1428	M1492	
	R1309	GLY	H1429	R1493	
	S1310	L1371	M1430	A1494	
	K1311	G1372	S1431	F1495	
	K1312	S1373	E1432	C1496	
	R1313	N1374	S1433	D1499	
	A1314	V1375	I1434	G1500	
	F1315	I1376	I1435	G1501	
	F1316	H1377	L1436	D1502	
	K1317	C1378	P1437	C1503	
	Q1318	R1379	M1438	S1506	
	C1319	K1380	M1439	T1507	
	T1320	D1381	V1440	V1508	
	Q1321	G1382	T1441	K1509	
	D1322	T1383	V1442	T1510	
	G1323	W1384	R1443	K1511	
	S1324	N1385	D1444	F1516	
	W1325	G1386	I1445	P1517	
	Q1326	S1387	P1446	M1518	
	E1327	F1388	H1447	S1519	
	G1328	H1389	W1448	C1520	
	A1329	V1390	L1449	D1521	
	C1330	CYS	M1450	L1522	
	V1331	GLN	P1451	Q1523	
	P1332	GLU	T1452	G1524	
	V1333	GLY	R1453	D1525	
	T1334	GLN	W1454	C1526	
	C1335	CYS	E1455	A1527	
	D1336	SER	R1456	C1528	
	P1337	V1400	V1457	R1529	
	P1338	P1401	W1458	D1530	
	P1339	N1402	C1459	P1531	
	P1340	E1403	T1460	Q1532	
	K1341	L1404	A1461	A1533	
	F1342	N1405	G1462	Q1534	
	H1343	S1406	L1463	E1535	
	G1344	N1407	K1464	H1536	
	L1345	L1408	W1465	SER	
	Y1346	K1409	Y1466	ARG	
	Q1347	L1410	ARG	LYS	
	C1348	L1411	P1467	ASP	
	T1349	C1412	H1468	LEU	
	N1350	P1413	P1469	ARG	
	G1351	D1414	A1470		
	F1352	I1415	L1471		
	F1354	I1472	I1473		
	N1355	H1474	C1474		
		V1475			

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	261371	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 ( $e^-/\text{\AA}^2$ )	60.1	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1200	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.207	Depositor
Minimum map value	-0.128	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0262	Depositor
Map size (Å)	269.312, 269.312, 269.312	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.052, 1.052, 1.052	Depositor



## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section:  
ZN

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	0.26	0/1134	0.59	0/1535
1	B	0.26	0/1134	0.59	0/1535
2	C	0.27	0/11914	0.50	0/16222
2	D	0.27	0/11914	0.50	0/16222
All	All	0.27	0/26096	0.51	0/35514

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	1101	0	1051	14	0
1	B	1101	0	1051	14	0
2	C	11600	0	10964	101	0
2	D	11600	0	10964	94	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
All	All	25404	0	24030	206	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 4.

The worst 5 of 206 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)
2:D:777:THR:HG22	2:D:779:ASP:H	1.56	0.70
2:C:777:THR:HG22	2:C:779:ASP:H	1.56	0.69
1:A:214:ARG:HH21	2:C:1481:PHE:HB3	1.59	0.68
2:C:1020:ILE:HB	2:C:1097:ALA:HB3	1.79	0.63
1:B:214:ARG:HH21	2:D:1481:PHE:HB3	1.63	0.63

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	133/222 (60%)	128 (96%)	5 (4%)	0	100	100
1	B	133/222 (60%)	128 (96%)	5 (4%)	0	100	100
2	C	1476/1627 (91%)	1426 (97%)	49 (3%)	1 (0%)	51	83
2	D	1476/1627 (91%)	1425 (96%)	51 (4%)	0	100	100
All	All	3218/3698 (87%)	3107 (97%)	110 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	1467	PRO

### 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	115/191 (60%)	111 (96%)	4 (4%)	36	67
1	B	115/191 (60%)	111 (96%)	4 (4%)	36	67
2	C	1304/1414 (92%)	1253 (96%)	51 (4%)	32	64
2	D	1304/1414 (92%)	1250 (96%)	54 (4%)	30	63
All	All	2838/3210 (88%)	2725 (96%)	113 (4%)	35	64

5 of 113 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	1457	VAL
2	D	1336	ASP
2	D	319	GLU
2	D	1335	CYS
2	D	1160	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
2	C	168	ASN
2	C	492	HIS
2	D	492	HIS
2	D	587	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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.

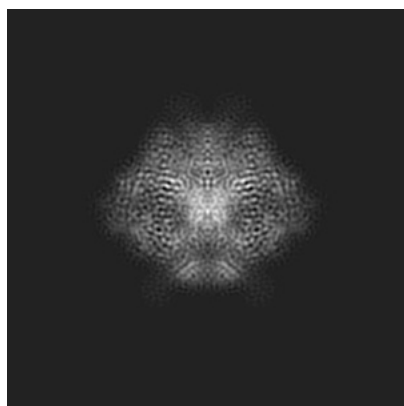
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34738. These allow visual inspection of the internal detail of the map and identification of artifacts.

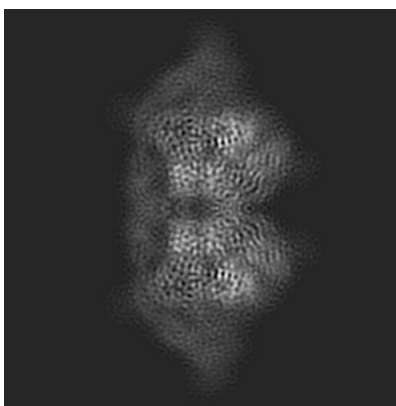
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

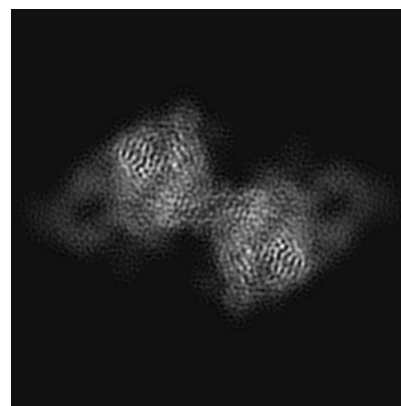
#### 6.1.1 Primary map



X

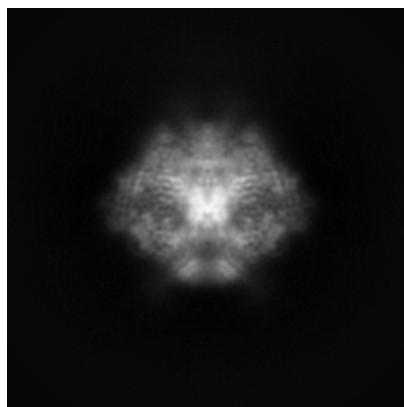


Y

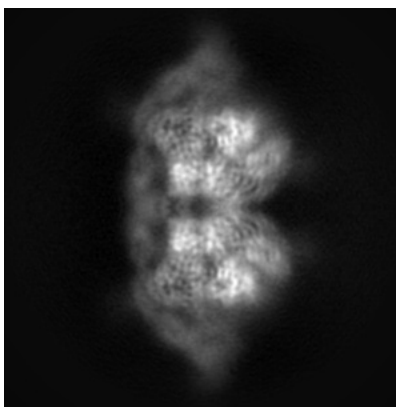


Z

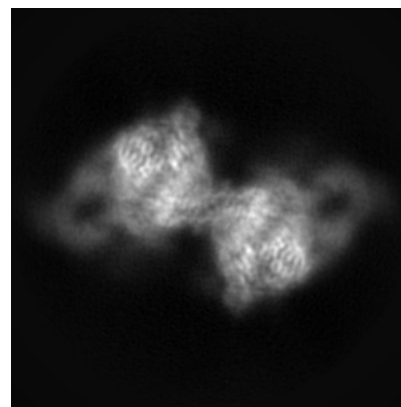
#### 6.1.2 Raw map



X



Y



Z

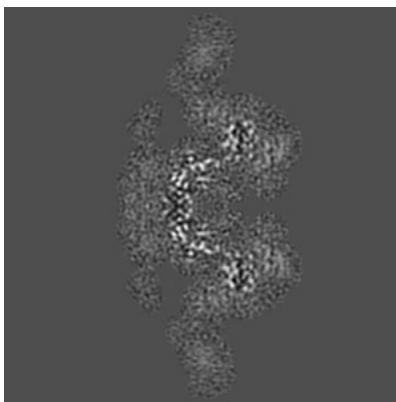
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

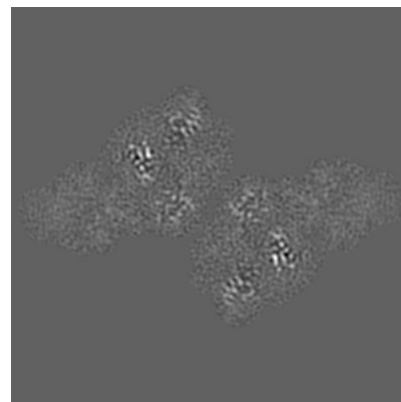
### 6.2.1 Primary map



X Index: 128

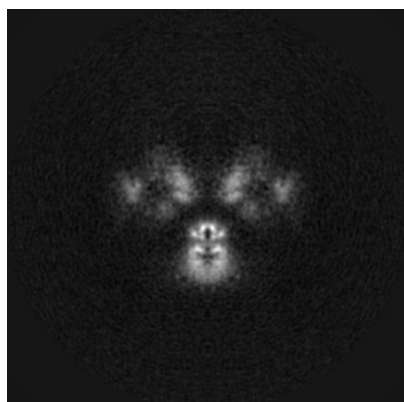


Y Index: 128

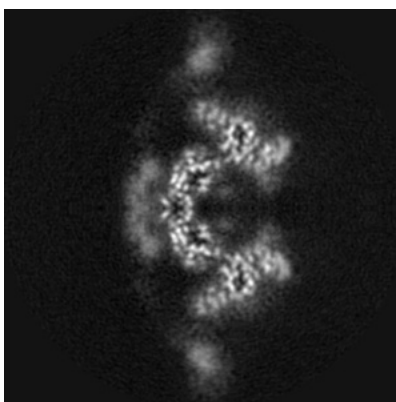


Z Index: 128

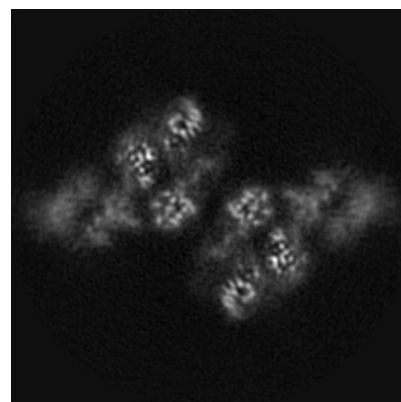
### 6.2.2 Raw map



X Index: 128



Y Index: 128



Z Index: 128

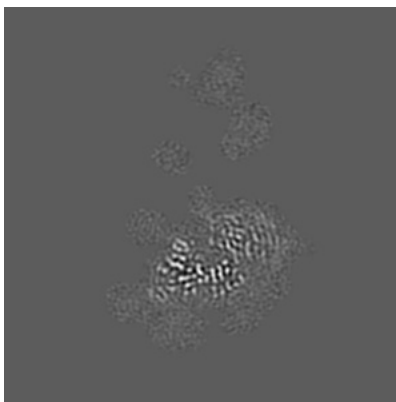
The images above show central slices of the map in three orthogonal directions.

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

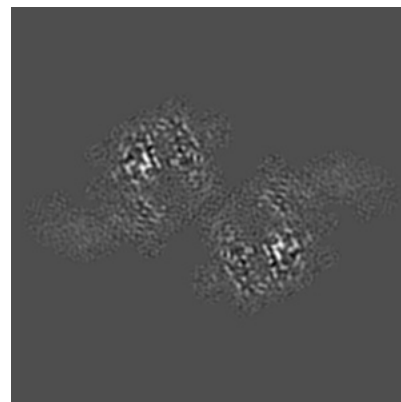
### 6.3.1 Primary map



X Index: 85

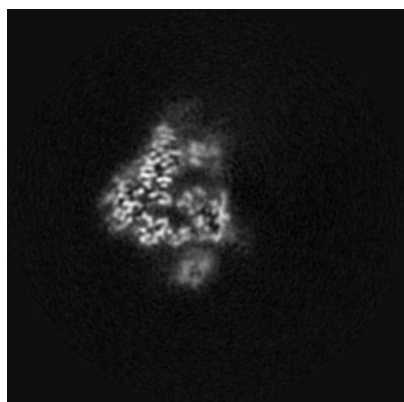


Y Index: 157

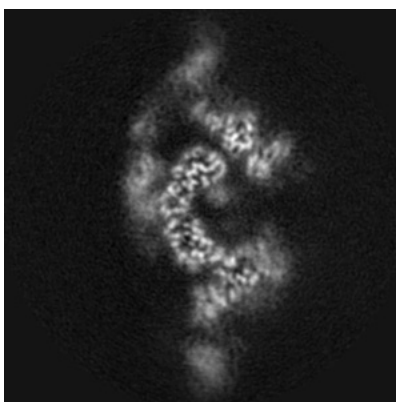


Z Index: 142

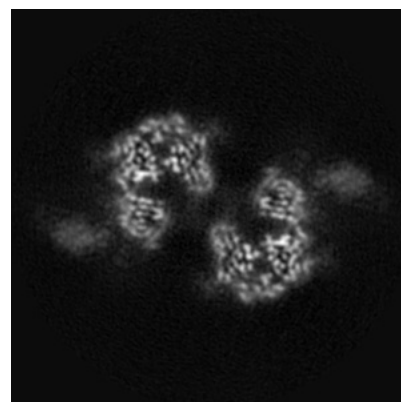
### 6.3.2 Raw map



X Index: 151



Y Index: 123

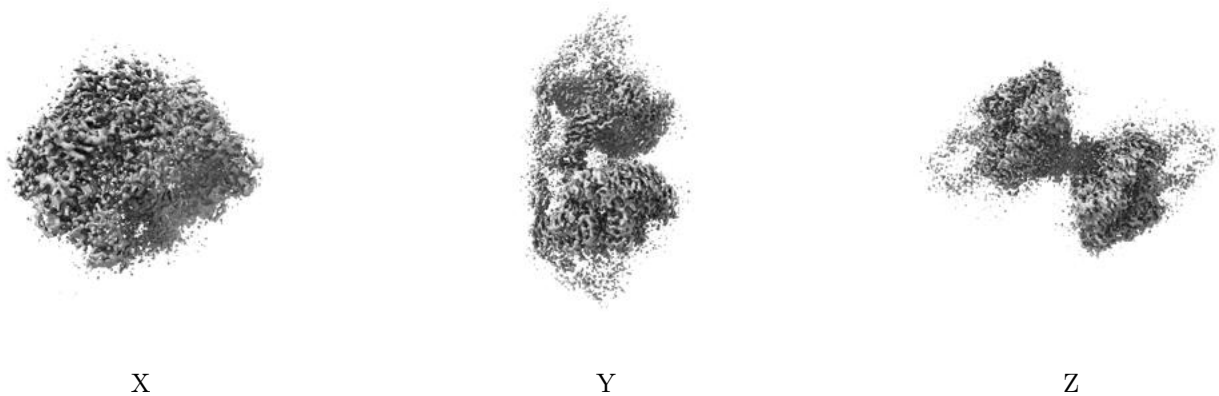


Z Index: 146

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

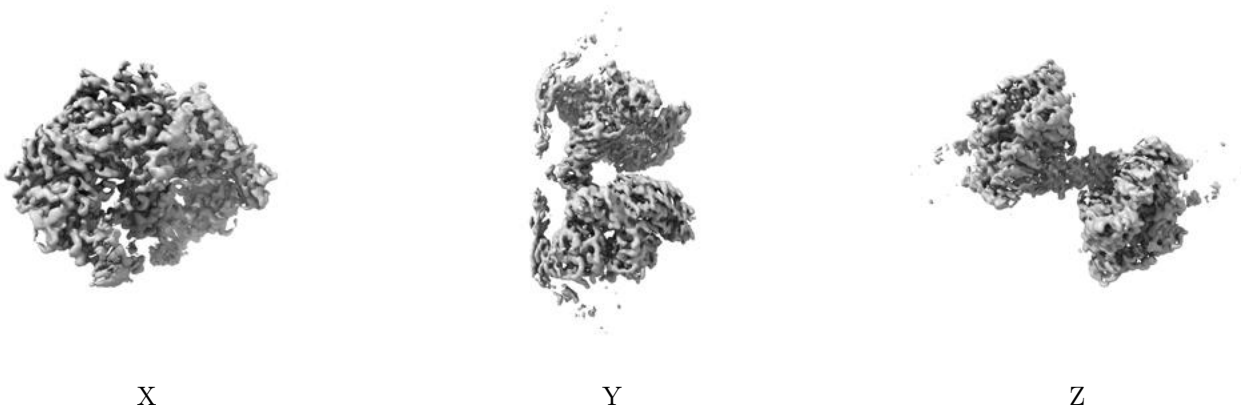
## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0262. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.4.2 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.

## 6.5 Mask visualisation [i](#)

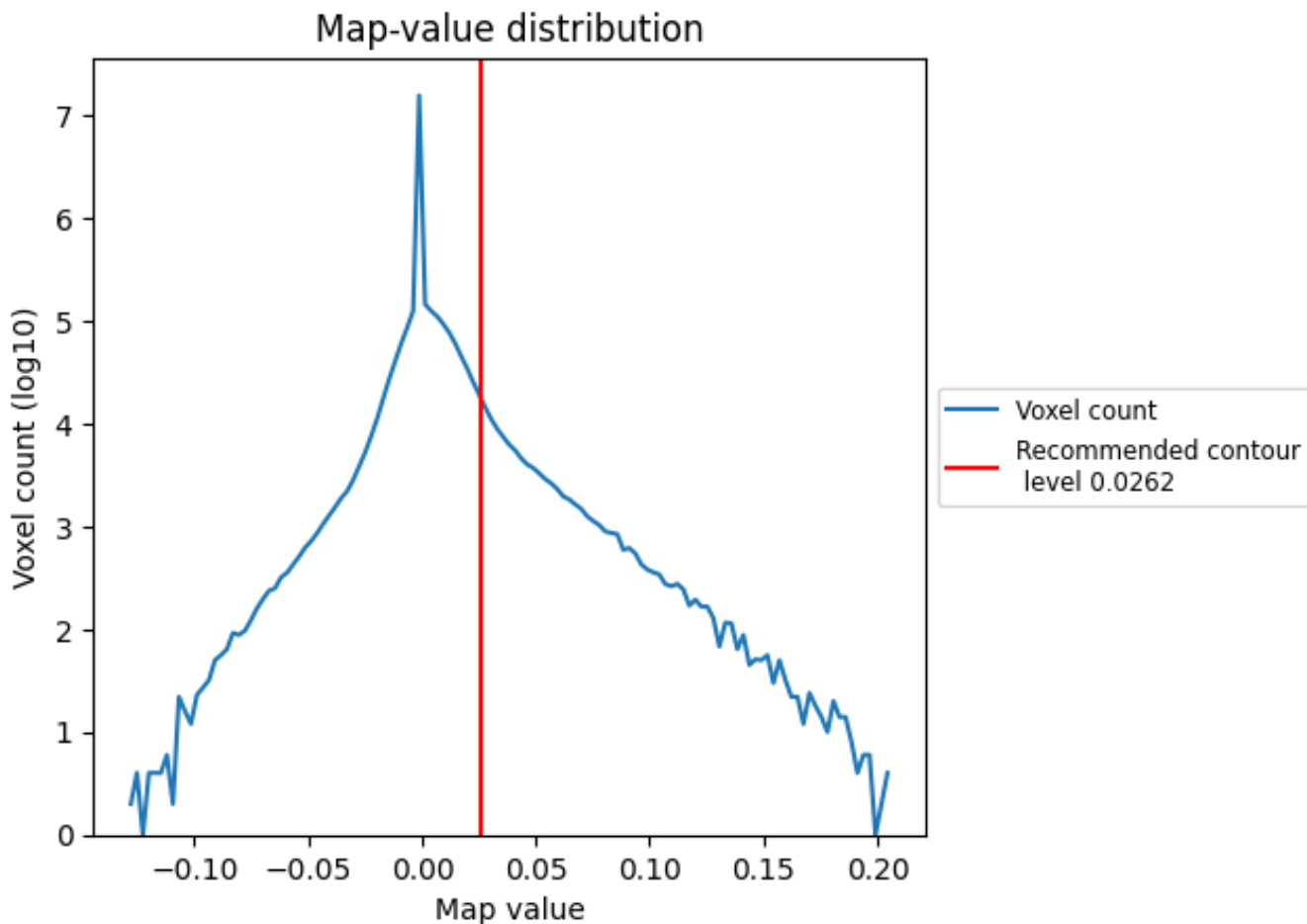
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

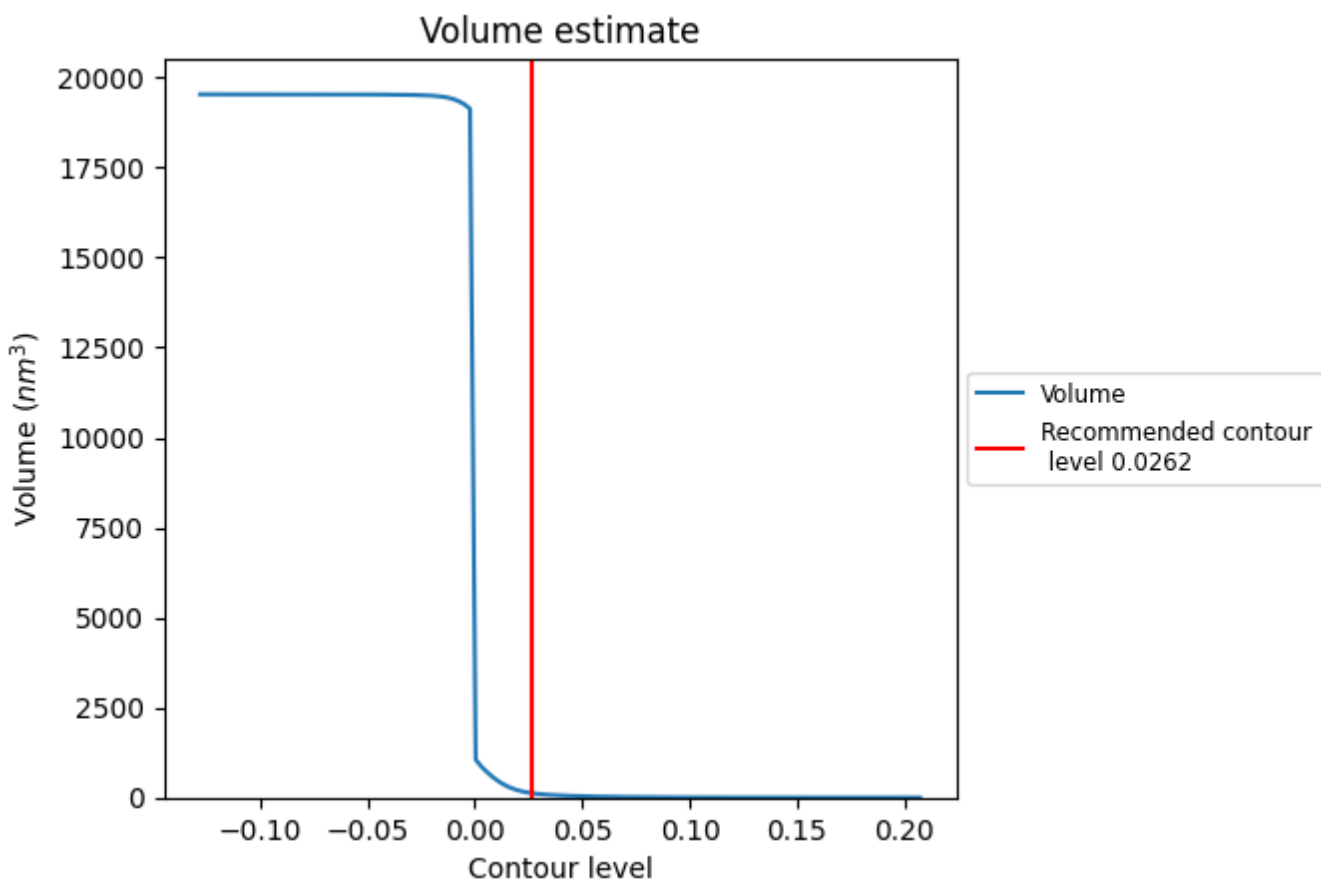
This section contains the results of statistical analysis of the map.

### 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.

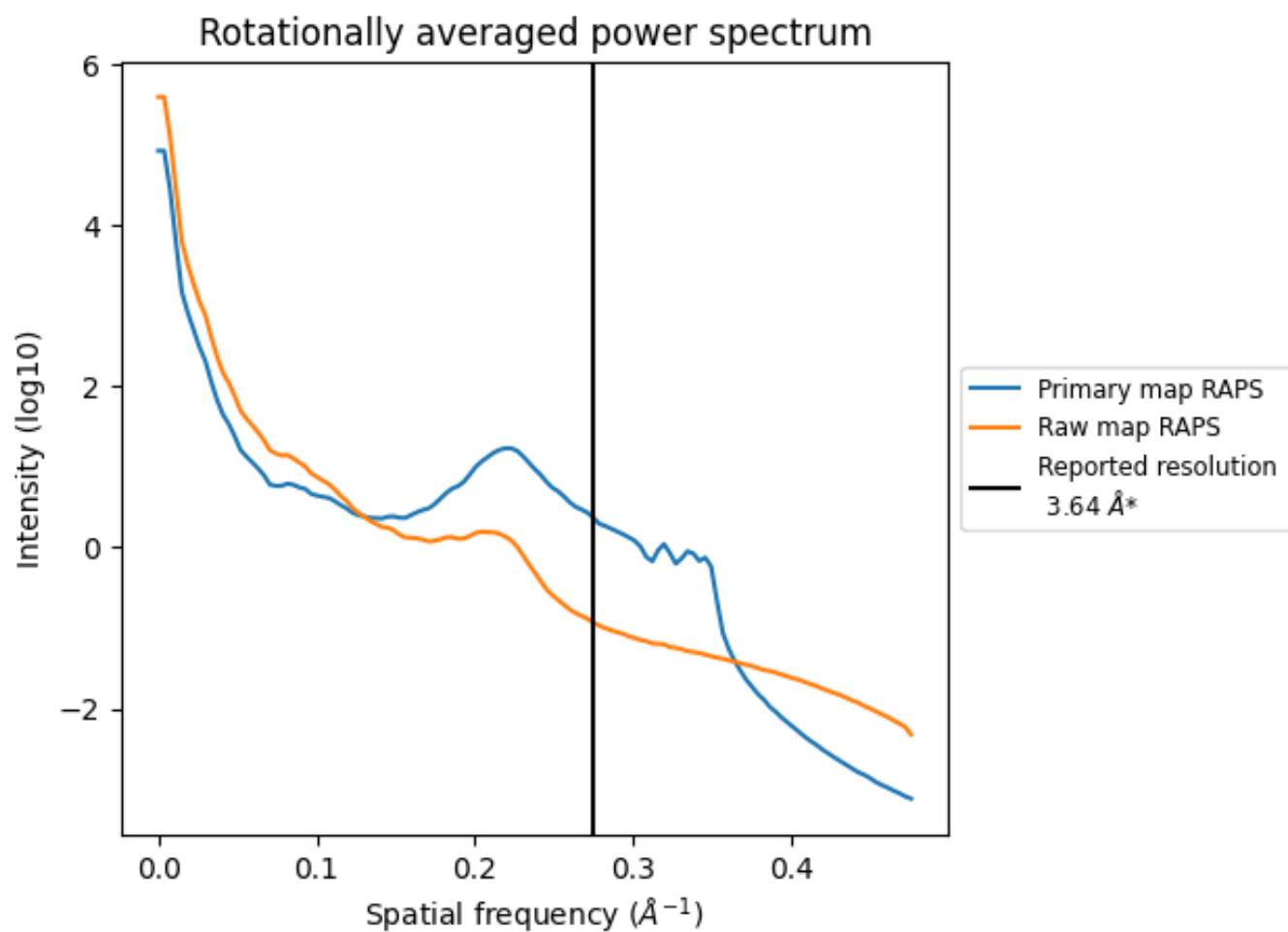
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 125 nm<sup>3</sup>; this corresponds to an approximate mass of 112 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

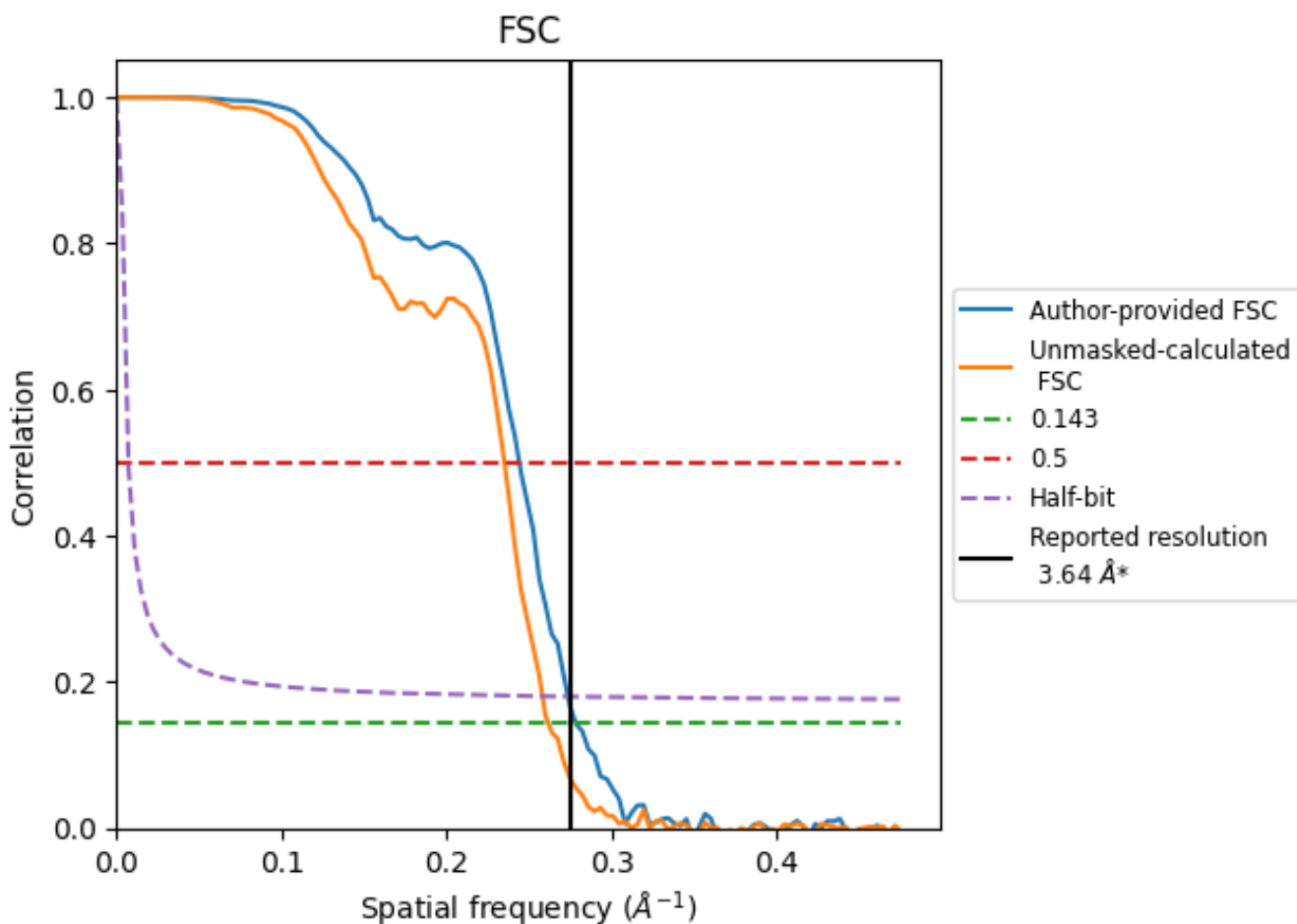


\*Reported resolution corresponds to spatial frequency of  $0.275 \text{ \AA}^{-1}$

## 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 0.275 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

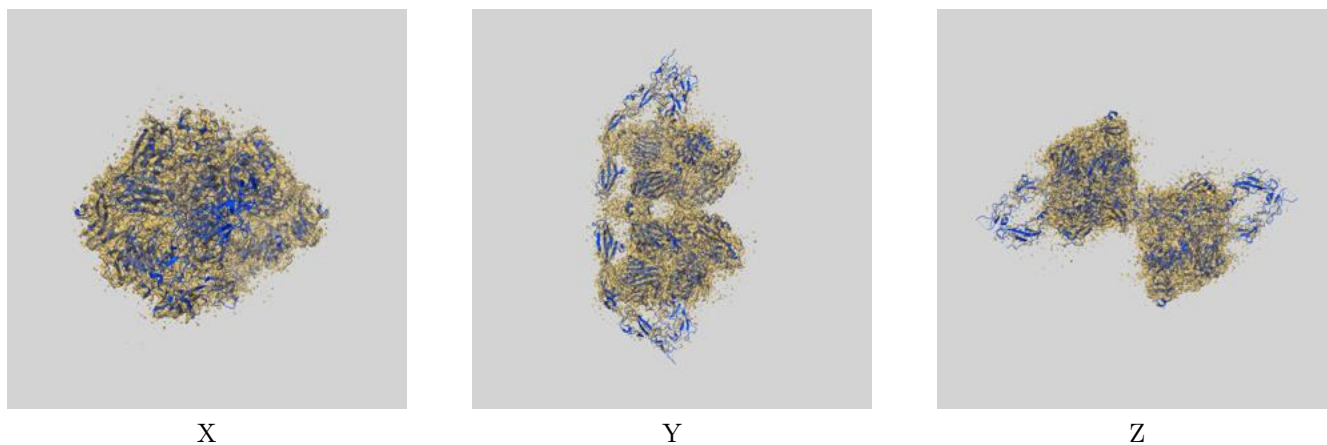
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.64	-	-
Author-provided FSC curve	3.59	4.10	3.66
Unmasked-calculated*	3.82	4.25	3.87

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

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

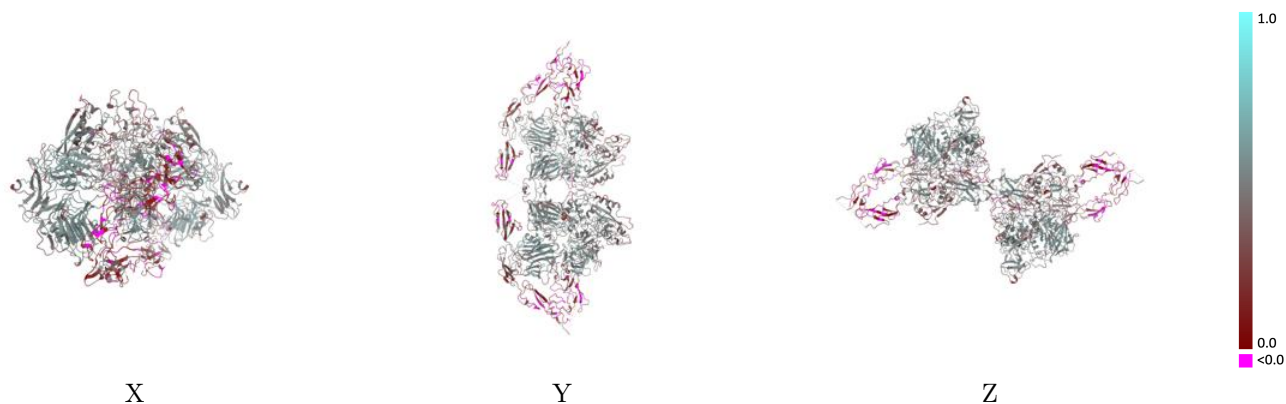
This section contains information regarding the fit between EMDB map EMD-34738 and PDB model 8HGG. Per-residue inclusion information can be found in section [3](#) on page [4](#).

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



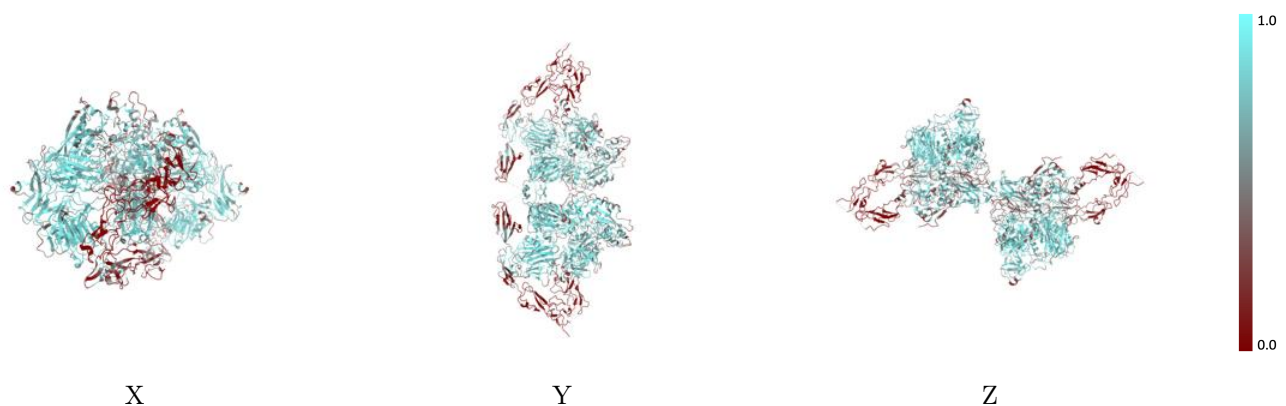
The images above show the 3D surface view of the map at the recommended contour level 0.0262 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



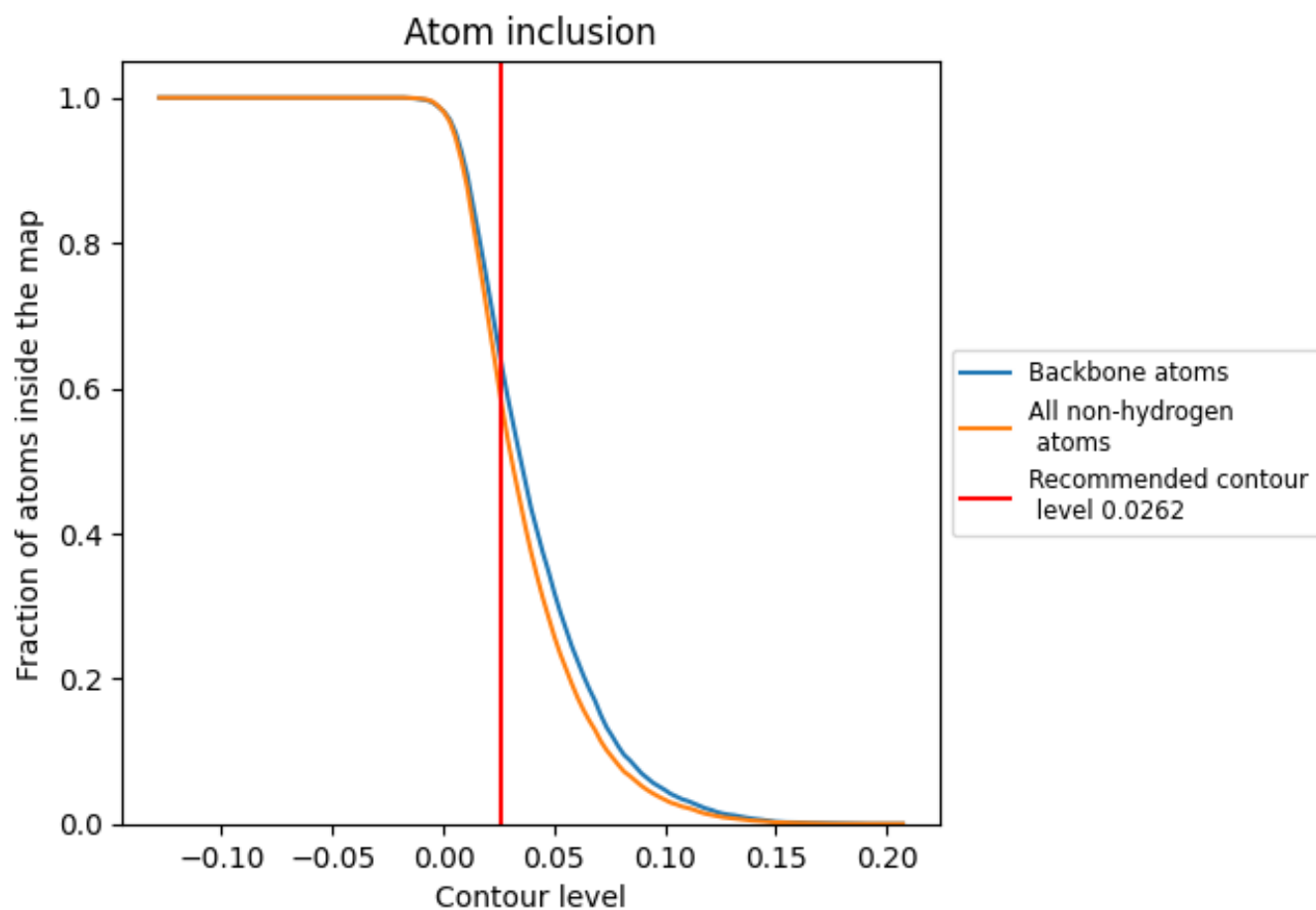
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0262).

## 9.4 Atom inclusion [i](#)











At the recommended contour level, 63% of all backbone atoms, 58% 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 (0.0262) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5802	 0.4080
A	 0.6199	 0.4430
B	 0.6227	 0.4420
C	 0.5767	 0.4060
D	 0.5761	 0.4030

