



## wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 08:43 PM UTC

PDB ID : 6VAA / pdb\_00006vaa  
EMDB ID : EMD-21134  
Title : Structure of the Fanconi Anemia ID complex bound to ICL DNA  
Authors : Pavletich, N.P.  
Deposited on : 2019-12-17  
Resolution : 3.40 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](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:

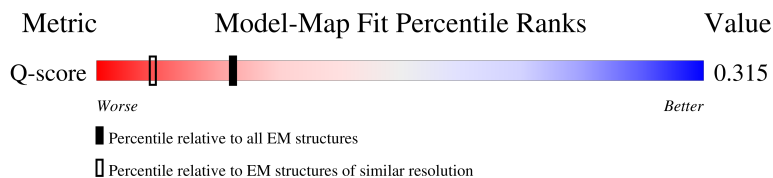
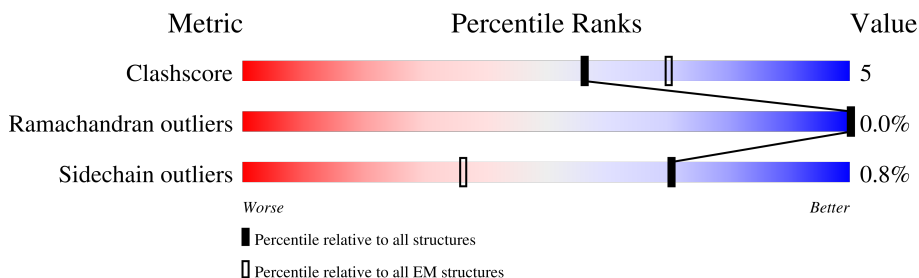
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:  
*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.40 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.



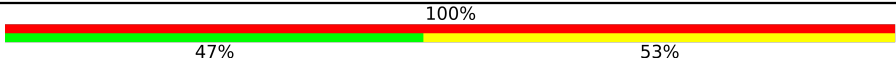

Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14717 ( 2.90 - 3.90 )

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	1328	
2	B	1451	
3	W	27	
4	X	18	

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Mol	Chain	Length	Quality of chain
5	Y	15	 <p>100% 47% 53%</p>
6	Z	16	 <p>100% 75% 25%</p>

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 40016 atoms, of which 19961 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
			Total	C	H	N	O	S		
1	A	1168	18879	5934	9619	1549	1723	54	0	0

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
			Total	C	H	N	O	S		
2	B	1153	18734	5969	9477	1527	1709	52	0	0

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

- Molecule 3 is a DNA chain called DNA (26-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
3	W	26	834	260	288	130	130	26	0	0

- Molecule 4 is a DNA chain called DNA (5'-D(P\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*TP

\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*T)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			P
4	X	18	577	180	217	36	126	18	0	0

- Molecule 5 is a DNA chain called DNA (5'-D(P\*AP\*AP\*AP\*AP\*AP\*AP\*AP\*AP\*AP\*AP\*AP\*AP\*AP\*AP\*AP\*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			P
5	Y	15	481	150	166	75	75	15	0	0

- Molecule 6 is a DNA chain called DNA (5'-D(\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*T)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			P
6	Z	16	511	160	194	32	110	15	0	0







T21	T22	T23	T24	T25	T26	T27	T28	T29	T30	T31	T32	T33	T34	T35	T36
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## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	231943	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	0.135	Depositor
Minimum map value	-0.092	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.012	Depositor
Map size ( $\text{\AA}$ )	279.04, 279.04, 279.04	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.09, 1.09, 1.09	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	1.04	31/9403 (0.3%)	1.20	11/12681 (0.1%)
2	B	0.84	3/9427 (0.0%)	1.12	1/12745 (0.0%)
3	W	0.32	0/622	0.61	0/954
4	X	0.32	0/395	0.82	0/608
5	Y	0.29	0/359	0.56	0/551
6	Z	0.31	0/348	0.83	0/536
All	All	0.91	34/20554 (0.2%)	1.13	12/28075 (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	4
2	B	0	2
All	All	0	6

The worst 5 of 34 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	315	SER	C-O	-8.31	1.13	1.24
2	B	387	ILE	C-O	-7.95	1.14	1.24
1	A	356	HIS	CE1-NE2	7.80	1.40	1.32
1	A	458	HIS	CG-ND1	-7.77	1.29	1.38
1	A	445	LEU	C-O	-7.54	1.15	1.24

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	362	THR	CA-CB-OG1	-7.55	98.28	109.60
1	A	310	ILE	N-CA-C	-5.97	106.67	111.81
1	A	636	GLU	CB-CA-C	5.94	116.76	110.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	387	PHE	CA-C-O	-5.52	112.47	119.31
1	A	578	VAL	N-CA-C	-5.52	107.07	111.81

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	224	GLY	Peptide
1	A	436	ILE	Peptide
1	A	641	LEU	Peptide
1	A	717	GLU	Peptide
2	B	485	ASN	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	84	0
2	B	9257	9477	9421	94	0
3	W	546	288	288	10	0
4	X	360	217	217	4	0
5	Y	315	166	166	6	0
6	Z	317	194	194	2	0
All	All	20055	19961	19873	195	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 195 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	2.03	0.76
2:B:623:GLN:O	2:B:624:SER:N	2.30	0.65
1:A:534:LYS:HE2	1:A:600:ASP:OD1	1.98	0.64
2:B:1111:LEU:HD21	2:B:1144:LYS:HB2	1.80	0.63
1:A:504:GLN:HE21	1:A:508:LYS:HE3	1.65	0.61

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%)	1078 (94%)	70 (6%)	1 (0%)	48	78
2	B	1123/1451 (77%)	1057 (94%)	66 (6%)	0	100	100
All	All	2272/2779 (82%)	2135 (94%)	136 (6%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	452	ALA

### 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	1067/1205 (88%)	1059 (99%)	8 (1%)	76	78
2	B	1065/1324 (80%)	1057 (99%)	8 (1%)	73	77
All	All	2132/2529 (84%)	2116 (99%)	16 (1%)	70	77

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	1208	VAL
2	B	1021	THR

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Mol	Chain	Res	Type
2	B	198	GLN
2	B	816	LEU
1	A	1074	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 61 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1150	GLN
2	B	1083	ASN
2	B	112	ASN
2	B	1070	HIS
2	B	1349	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
3	W	1
1	A	1

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	W	28:DA	O3'	30:DA	P	7.74
1	B	773:SER	C	774:MET	N	3.70
1	A	260:PRO	C	261:SER	N	3.52
1	B	187:VAL	C	188:ASP	N	3.52
1	B	623:GLN	C	624:SER	N	3.11

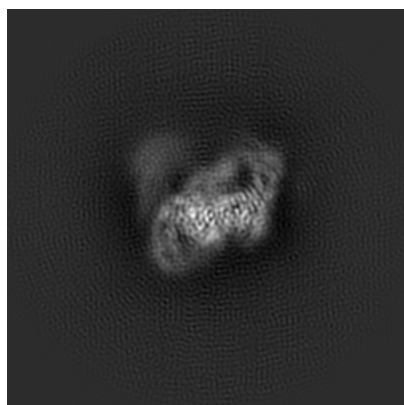
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21134. These allow visual inspection of the internal detail of the map and identification of artifacts.

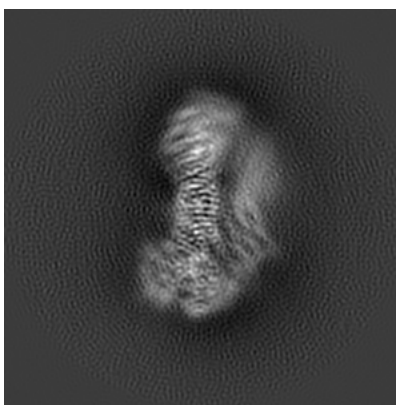
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

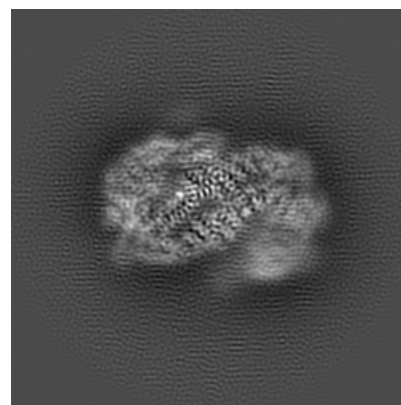
#### 6.1.1 Primary map



X



Y

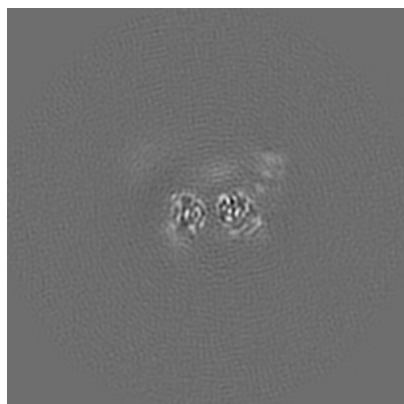


Z

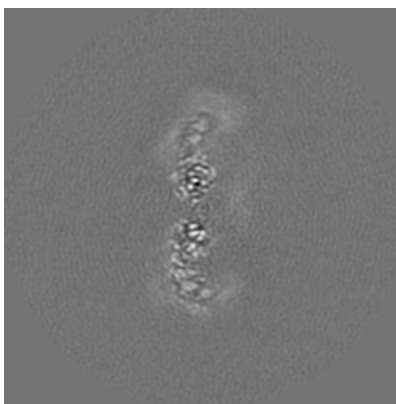
The images above show the map projected in three orthogonal directions.

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

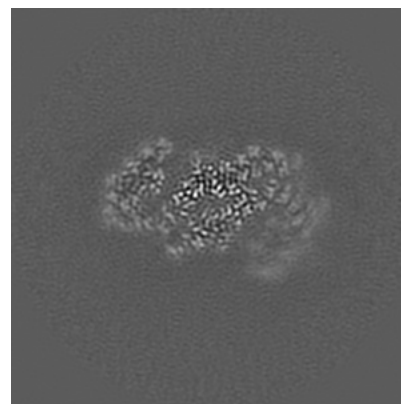
#### 6.2.1 Primary map



X Index: 128



Y Index: 128



Z Index: 128

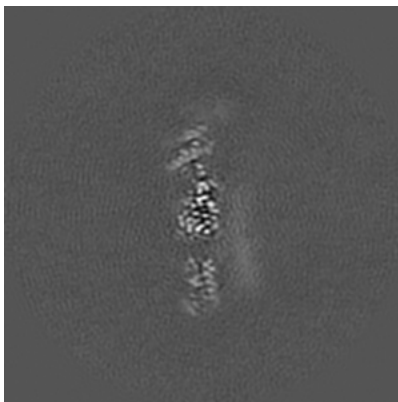
The images above show central slices of the map in three orthogonal directions.

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

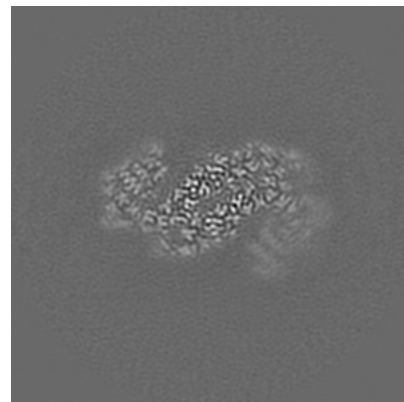
### 6.3.1 Primary map



X Index: 117



Y Index: 141

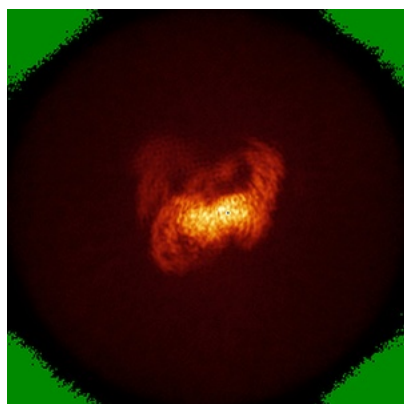


Z Index: 123

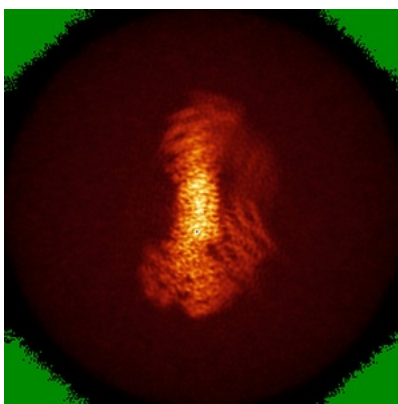
The images above show the largest variance slices of the map in three orthogonal directions.

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

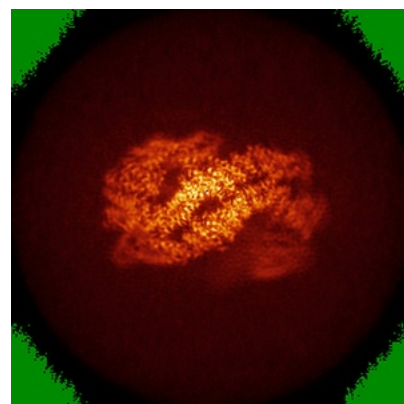
### 6.4.1 Primary map



X



Y

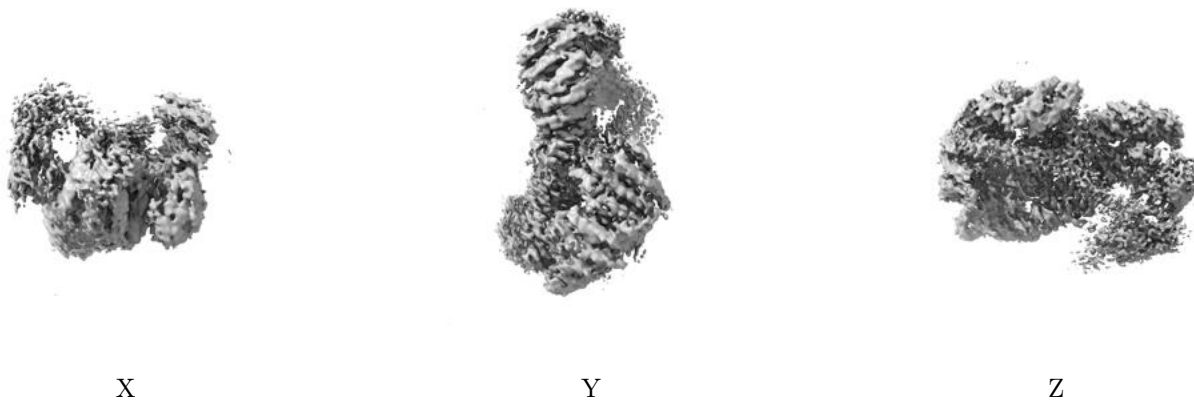


Z

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



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.

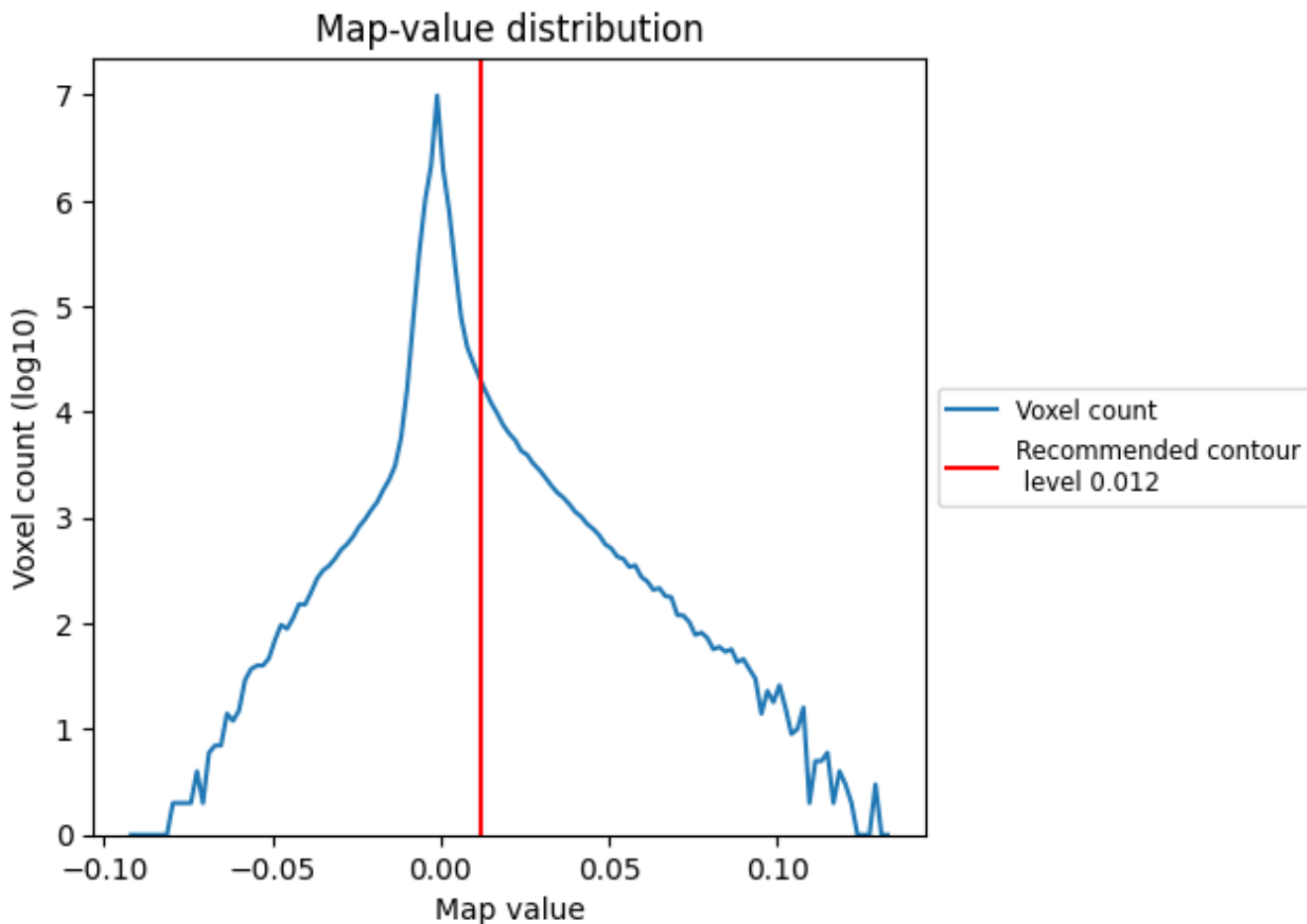
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

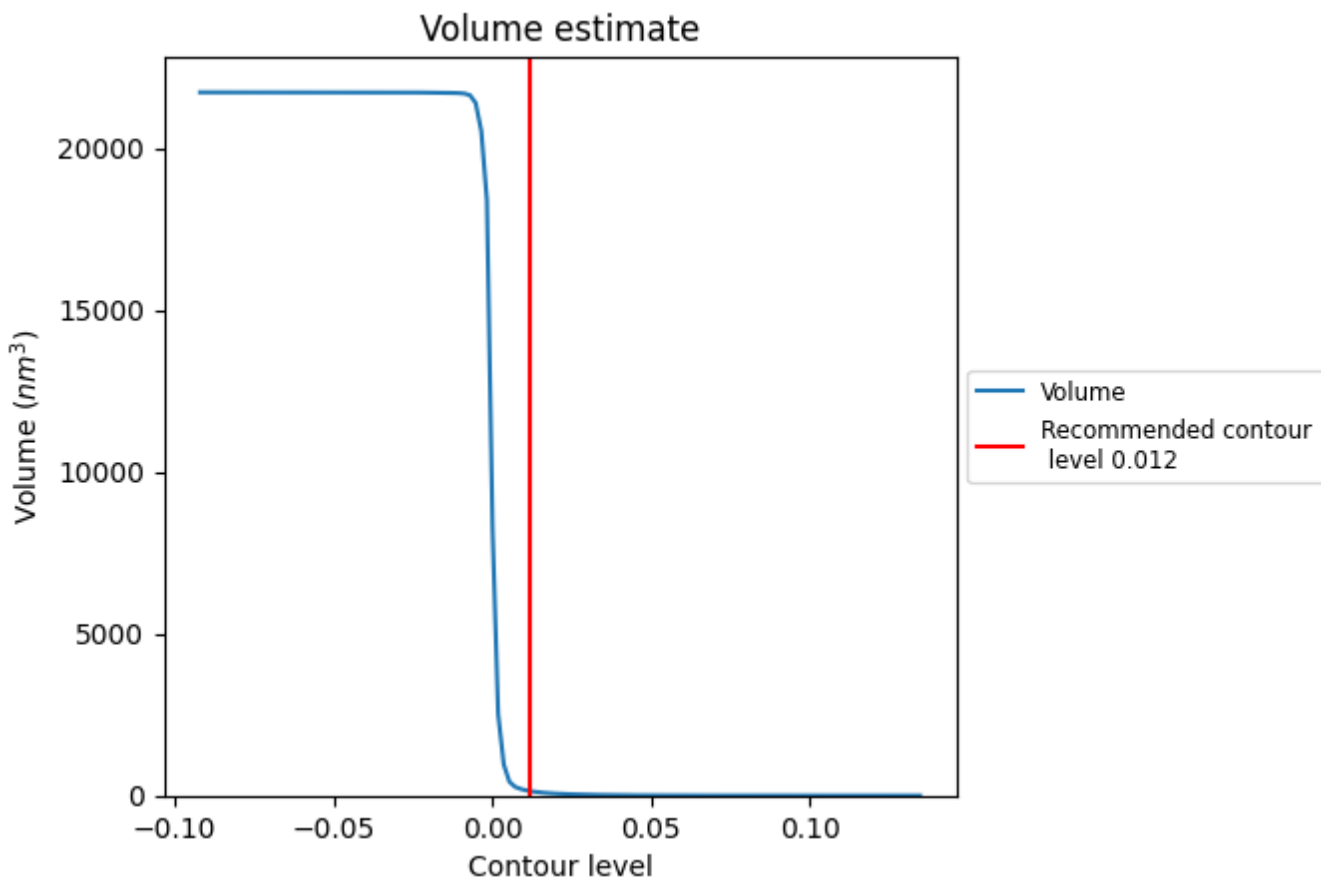
This section contains the results of statistical analysis of the map.

### 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.

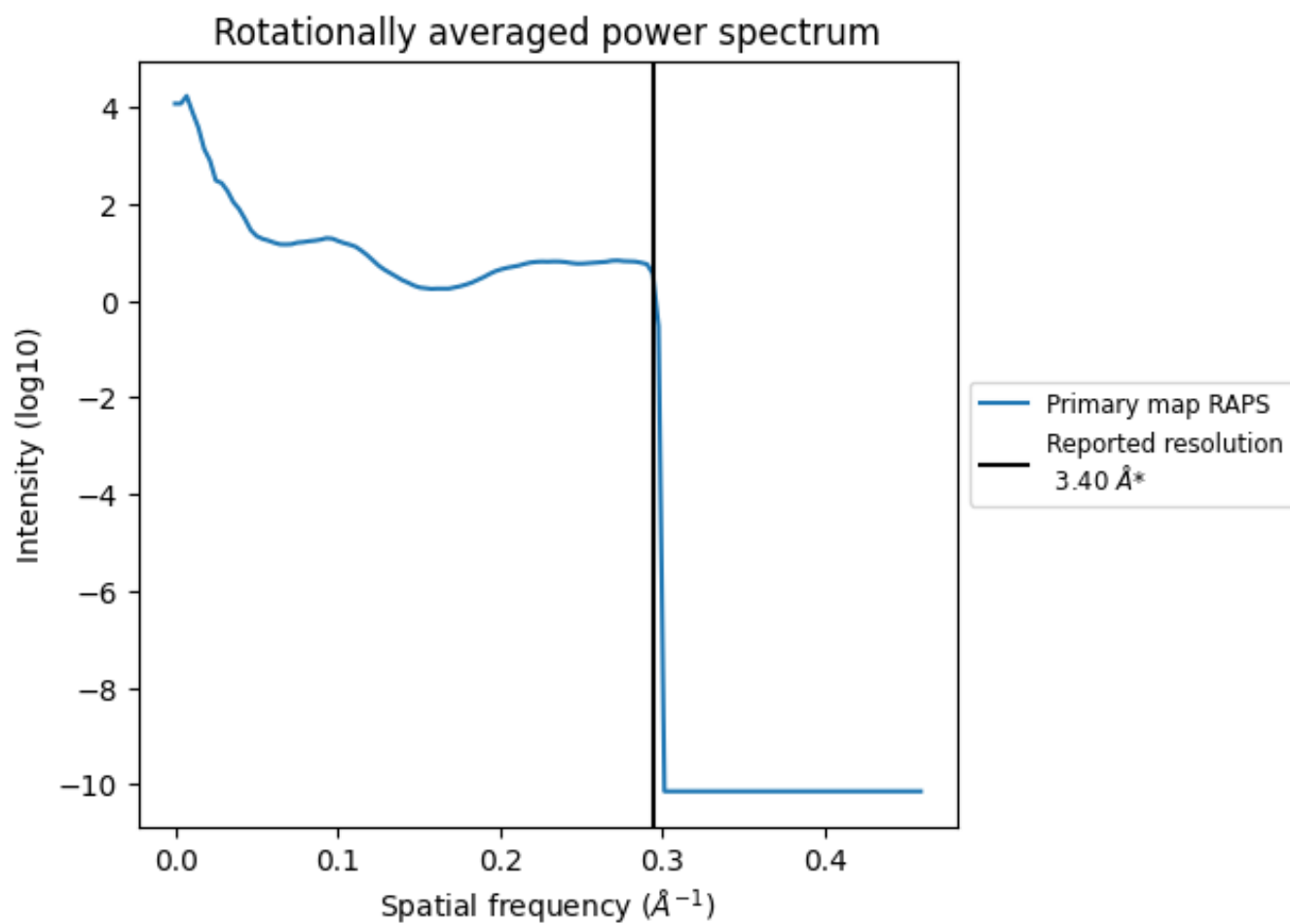
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 136 nm<sup>3</sup>; this corresponds to an approximate mass of 123 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 0.294 Å<sup>-1</sup>

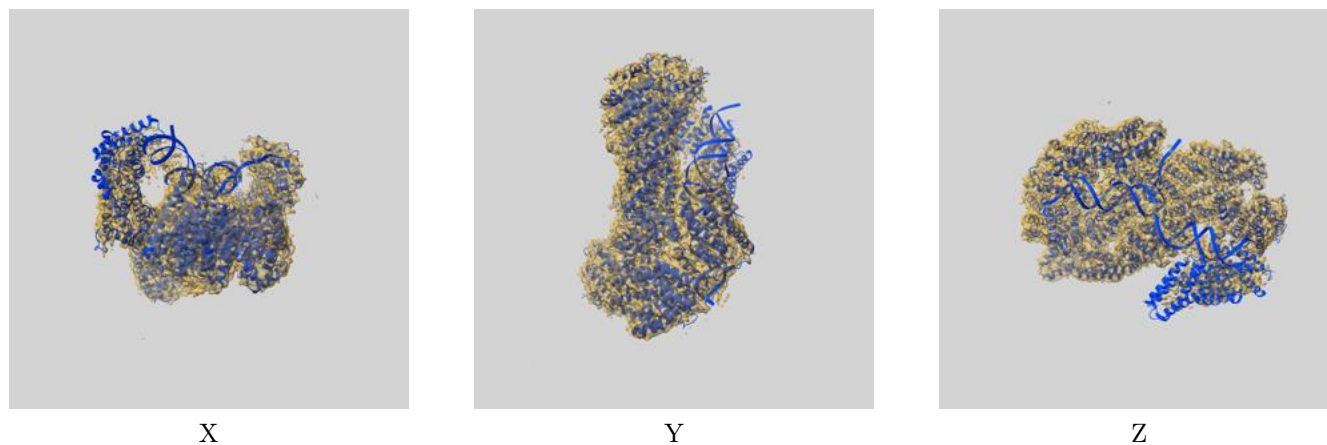
## 8 Fourier-Shell correlation

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

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

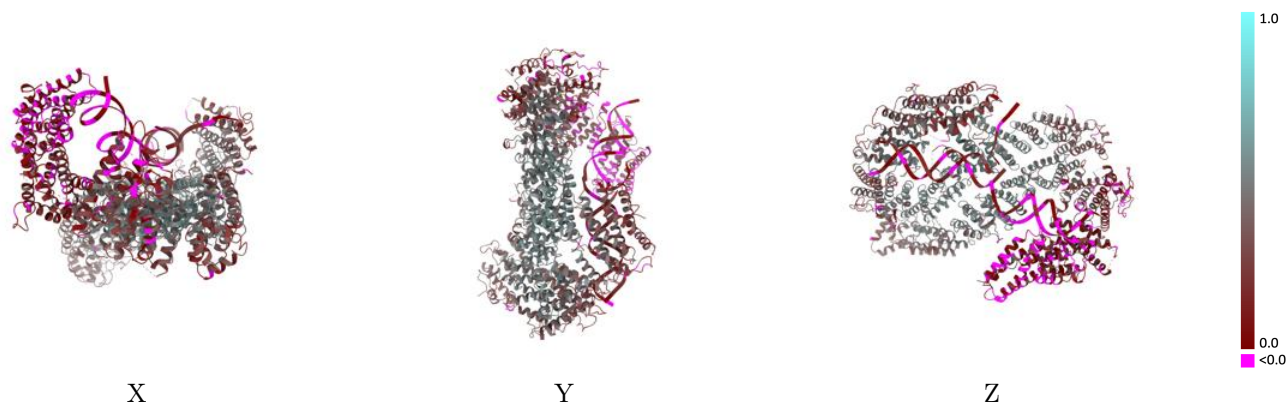
This section contains information regarding the fit between EMDB map EMD-21134 and PDB model 6VAA. Per-residue inclusion information can be found in section 3 on page 6.

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



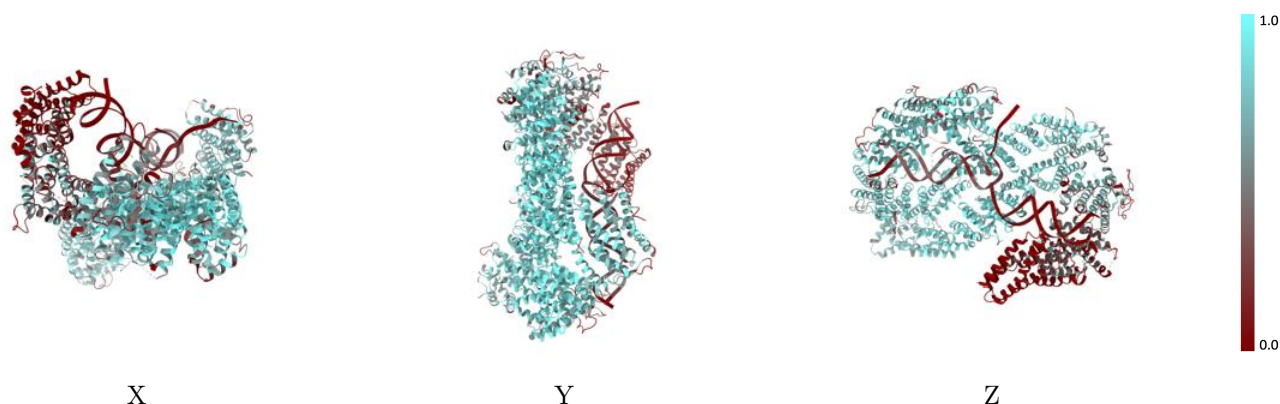
The images above show the 3D surface view of the map at the recommended contour level 0.012 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



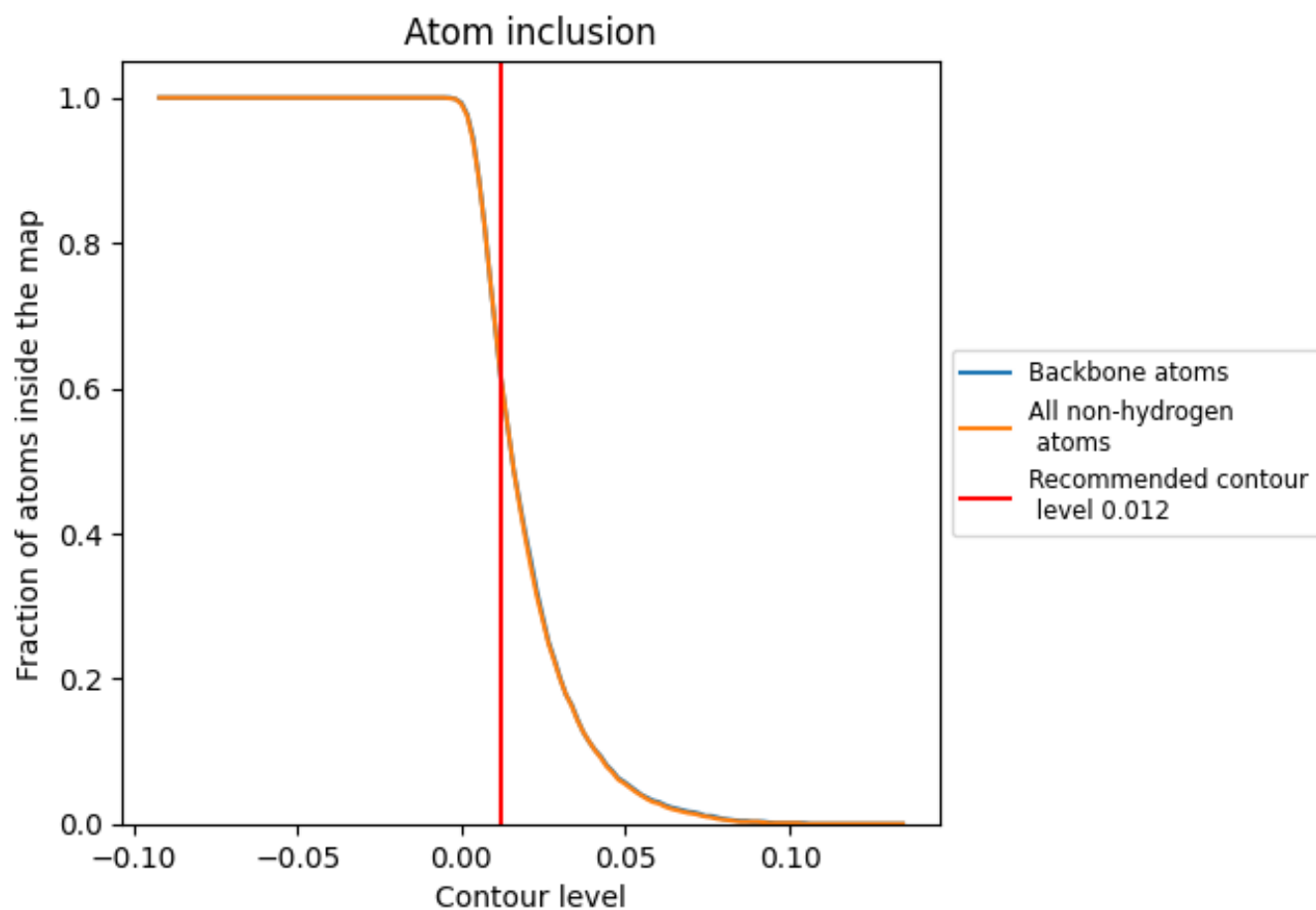
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 62% of all backbone atoms, 62% 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	 0.6170	 0.3150
A	 0.7760	 0.4090
B	 0.5490	 0.2630
W	 0.2490	 0.0900
X	 0.2670	 0.0940
Y	 0.0760	 0.0080
Z	 0.0320	 -0.0030

