



## Full wwPDB EM Validation Report ⓘ

Nov 14, 2022 – 02:54 AM EST

PDB ID : 7K10  
EMDB ID : EMD-22619  
Title : CryoEM structure of activated-form FATKIN domain of DNA-PK  
Authors : Chen, X.; Gellert, M.; Yang, W.  
Deposited on : 2020-09-06  
Resolution : 3.30 Å(reported)

This is a Full wwPDB EM Validation 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) : 2.31.2

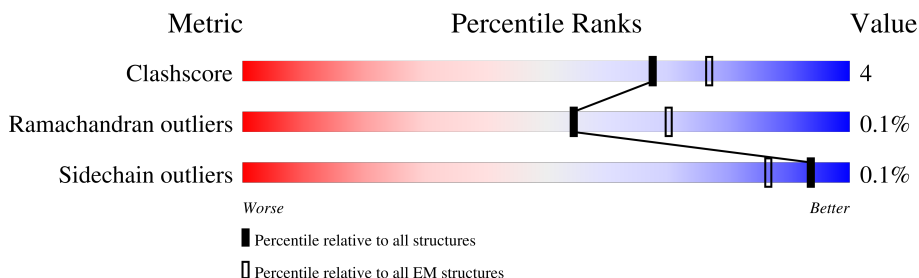
# 1 Overall quality at a glance

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)
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	4128	

## 2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 10037 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 DNA-dependent protein kinase catalytic subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1259	10037	6396	1714	1870	57	0	0





V3514	E3350	T3198	LEU	LEU	LEU	GLN	GLN	LEU	ILE	PHE	VAL	LEU	MET	LYS	ALA	ALA	VAL	LEU	VAL	SER
E3519	I3351	P3199	LEU	PRO	ALA	PHE	ASP	GLU	ARG	VAL	GLN	CYS	ASN	GLY	ASN	GLN	GLN	GLN	HIS	GLN
T3522	L3362	PRO	GLU	GLU	GLU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
V3530	SER	ASP	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
Y3531	GLY	ASN	PRO	PRO	ALA	THR	THR	GLN	HIS	SER	GLY	GLN	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
P3532	SER	MET	ALA	ALA	VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
Y3540	D3369	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
D3544	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
H3549	E3395	GLN	GLN	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
K3550	ALA	ASP	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
E3553	PRO	GLY	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
I3558	THR	SER	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
L3562	CYS	MET	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
D3563	GLY	VAL	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
Q3564	PRO	PRO	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
L3576	A3406	D3226	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
Q3577	D3411	I3227	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
L3584	R2940	D3228	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
F3585	P2917	I3227	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
K3586	R2940	S3228	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
N3590	E3395	I3243	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
D3591	ALA	L3259	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
V3592	ASN	L3259	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
R3593	VAL	K3267	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
A3594	ILE	T3268	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
E3595	ASP	R3269	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
L3596	SER	L3273	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
A3597	GLU	C3281	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
K3598	LEU	Q3440	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
T3599	ALA	S9294	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
P3600	VAL	L3451	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
V3601	ILE	N3457	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
K3602	ASP	S3458	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
K3603	SER	N3459	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
K3604	THR	E3309	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
N3605	GLY	S3313	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
I3606	VAL	L3329	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
K3608	THR	Y3334	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
N3609	ASP	T3484	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
Y3610	ILE	I3499	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
E3611	LYS	A3340	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
Y3614	THR	L3348	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
A3615	THR	A3349	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
A3616	GLU		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
L3617	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	254646	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 ( $e^-/\text{\AA}^2$ )	45	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	0.177	Depositor
Minimum map value	-0.103	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.018	Depositor
Map size (Å)	408.31998, 408.31998, 408.31998	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.16, 1.16, 1.16	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	0.32	0/10246	0.57	4/13844 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	3563	ASP	CB-CG-OD1	9.15	126.53	118.30
1	A	3695	LEU	CA-CB-CG	6.27	129.72	115.30
1	A	3129	LEU	CA-CB-CG	5.35	127.61	115.30
1	A	3668	LEU	CA-CB-CG	5.11	127.06	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	3698	GLU	Peptide

### 5.2 Too-close contacts

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	10037	0	9993	79	0
All	All	10037	0	9993	79	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.

All (79) 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:3577:GLN:HB3	1:A:3630:ARG:HD2	1.75	0.67
1:A:3718:ARG:H	1:A:3743:HIS:HD2	1.47	0.63
1:A:3631:LYS:HG2	1:A:3683:CYS:HA	1.83	0.61
1:A:2940:ARG:NH1	1:A:3977:THR:OG1	2.38	0.57
1:A:3294:SER:HB3	1:A:3348:LEU:HD22	1.86	0.56
1:A:4064:LEU:HD21	1:A:4077:TYR:HB3	1.86	0.56
1:A:3457:ASN:OD1	1:A:3708:ARG:NH1	2.39	0.55
1:A:3113:ASN:HD22	1:A:3128:LYS:HE3	1.71	0.55
1:A:3992:ARG:NH1	1:A:4103:GLN:OE1	2.40	0.55
1:A:4115:ASN:OD1	1:A:4119:ARG:NH1	2.40	0.55
1:A:3137:GLU:OE2	1:A:3167:ARG:NH2	2.41	0.54
1:A:3243:ILE:HD13	1:A:3259:LEU:HD22	1.90	0.54
1:A:3499:ILE:HD12	1:A:3532:PRO:HG3	1.89	0.54
1:A:3815:LEU:HD22	1:A:3930:VAL:HG11	1.90	0.54
1:A:3586:LYS:HE3	1:A:3667:LEU:HD13	1.89	0.53
1:A:3647:GLY:HA2	1:A:3651:LEU:HD13	1.90	0.53
1:A:3903:HIS:ND1	1:A:3935:GLY:O	2.39	0.53
1:A:3868:VAL:HG22	1:A:4114:PRO:HB2	1.91	0.52
1:A:3666:LEU:HA	1:A:3669:LYS:HG2	1.90	0.52
1:A:3631:LYS:HD3	1:A:3682:GLU:HG3	1.90	0.52
1:A:3913:ILE:HD11	1:A:3988:LEU:HD22	1.92	0.51
1:A:3721:GLY:HA3	1:A:3741:ARG:HH21	1.75	0.51
1:A:3170:ASP:N	1:A:3170:ASP:OD1	2.42	0.51
1:A:4083:GLY:HA3	1:A:4091:ALA:HB2	1.93	0.50
1:A:3607:GLU:OE2	1:A:3655:LYS:NZ	2.45	0.50
1:A:3831:ASP:HB3	1:A:3834:ALA:HB2	1.94	0.49
1:A:3522:THR:HG21	1:A:3558:ILE:HG23	1.94	0.49
1:A:3575:LEU:HD13	1:A:3802:LEU:HD11	1.94	0.49
1:A:3267:LYS:HG2	1:A:3273:LEU:HD21	1.95	0.49
1:A:3421:ASP:OD2	1:A:3425:ARG:NH2	2.46	0.48
1:A:3749:PRO:HB2	1:A:3805:TRP:HB3	1.96	0.48
1:A:3530:VAL:HG22	1:A:3562:LEU:HD22	1.97	0.47
1:A:3650:LYS:HG3	1:A:3651:LEU:HD12	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3421:ASP:OD1	1:A:3467:ARG:NE	2.47	0.46
1:A:3855:TYR:OH	1:A:4122:GLU:OE1	2.30	0.46
1:A:3306:LEU:HA	1:A:3309:GLU:HG2	1.98	0.46
1:A:3633:ILE:HD12	1:A:3636:PHE:HB3	1.97	0.46
1:A:3228:SER:O	1:A:3228:SER:OG	2.32	0.46
1:A:4026:SER:HB3	1:A:4066:LEU:HG	1.98	0.46
1:A:3753:LYS:HD3	1:A:3758:LEU:HD11	1.97	0.45
1:A:3020:ASP:HB2	1:A:3024:PRO:HB3	1.98	0.45
1:A:2978:LYS:O	1:A:2981:TRP:NE1	2.49	0.45
1:A:2866:ALA:HA	1:A:2869:LEU:HD12	1.99	0.45
1:A:3699:LEU:HG	1:A:3719:ILE:HD12	1.99	0.45
1:A:2841:ASN:O	1:A:2845:ASN:ND2	2.38	0.45
1:A:3334:TYR:HE1	1:A:3362:LEU:HD13	1.82	0.44
1:A:3692:VAL:HG23	1:A:3696:ARG:HH11	1.82	0.44
1:A:3815:LEU:O	1:A:3819:THR:OG1	2.32	0.44
1:A:3268:THR:OG1	1:A:3269:ARG:N	2.51	0.44
1:A:3281:CYS:HB3	1:A:3329:LEU:HD13	2.00	0.44
1:A:3505:LEU:HD23	1:A:3514:VAL:HG21	1.99	0.44
1:A:3884:LYS:HG3	1:A:3897:PHE:HZ	1.83	0.43
1:A:4071:ALA:HB3	1:A:4074:PHE:HB2	2.00	0.43
1:A:3716:HIS:O	1:A:3718:ARG:NH2	2.51	0.43
1:A:3459:ASN:HD22	1:A:3708:ARG:HE	1.66	0.43
1:A:3550:LYS:HA	1:A:3553:GLU:HG2	2.00	0.43
1:A:3651:LEU:HA	1:A:3654:MET:HB2	1.99	0.42
1:A:3763:ARG:HH21	1:A:4004:VAL:HG12	1.84	0.42
1:A:3195:GLU:O	1:A:3198:THR:OG1	2.37	0.42
1:A:3481:SER:O	1:A:3484:THR:OG1	2.37	0.42
1:A:3800:LEU:HD12	1:A:3800:LEU:HA	1.93	0.42
1:A:3929:MET:O	1:A:3938:ILE:N	2.48	0.42
1:A:3959:MET:SD	1:A:3959:MET:N	2.90	0.42
1:A:3781:CYS:HB3	1:A:3786:LEU:HD12	2.01	0.42
1:A:2940:ARG:NH1	1:A:3977:THR:HG1	2.18	0.41
1:A:4026:SER:O	1:A:4026:SER:OG	2.36	0.41
1:A:2851:PHE:HA	1:A:2852:PRO:HD3	1.95	0.41
1:A:3575:LEU:HD23	1:A:3575:LEU:HA	1.93	0.41
1:A:3955:VAL:HA	1:A:3956:PRO:HD3	1.90	0.41
1:A:2952:ILE:HG12	1:A:2975:ALA:HB2	2.02	0.41
1:A:3175:PRO:HD2	1:A:3178:ILE:HD12	2.03	0.41
1:A:3929:MET:HB2	1:A:3938:ILE:HB	2.03	0.41
1:A:2837:LEU:HD11	1:A:2871:LEU:HA	2.01	0.41
1:A:3630:ARG:HB2	1:A:3633:ILE:HG22	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2835:LYS:HE3	1:A:2835:LYS:HB2	1.91	0.41
1:A:3451:LEU:HD23	1:A:3451:LEU:HA	1.98	0.40
1:A:3596:LEU:HG	1:A:3657:SER:HB2	2.02	0.40
1:A:2870:SER:HB3	1:A:2899:ARG:HH12	1.87	0.40
1:A:3123:GLN:HA	1:A:3126:LEU:HB2	2.04	0.40

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	1247/4128 (30%)	1114 (89%)	132 (11%)	1 (0%)	51	81

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3083	SER

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1094/3671 (30%)	1093 (100%)	1 (0%)	93	97

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3540	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2886	GLN
1	A	3104	GLN
1	A	3113	ASN
1	A	3139	GLN
1	A	3459	ASN
1	A	3590	ASN
1	A	3605	ASN
1	A	3743	HIS
1	A	3760	GLN
1	A	4088	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

### 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

### 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

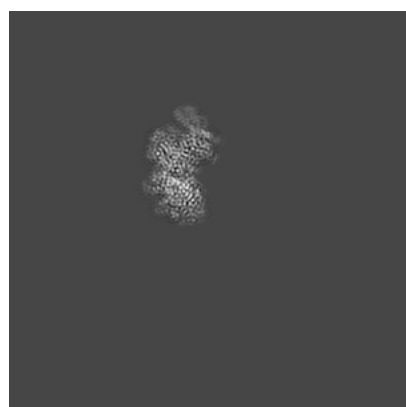
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22619. These allow visual inspection of the internal detail of the map and identification of artifacts.

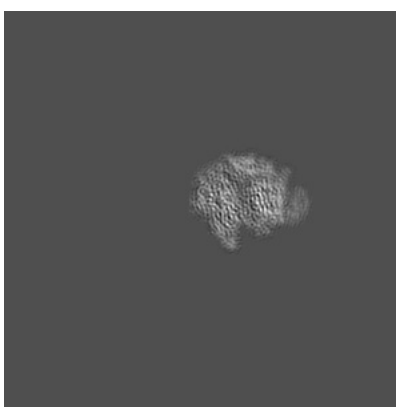
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

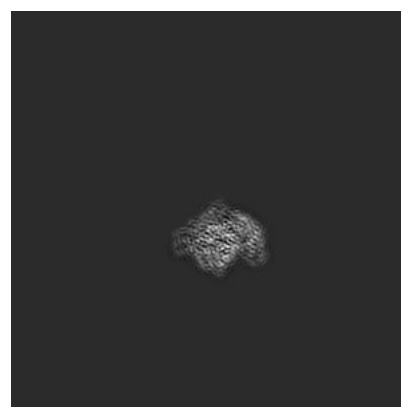
#### 6.1.1 Primary map



X



Y

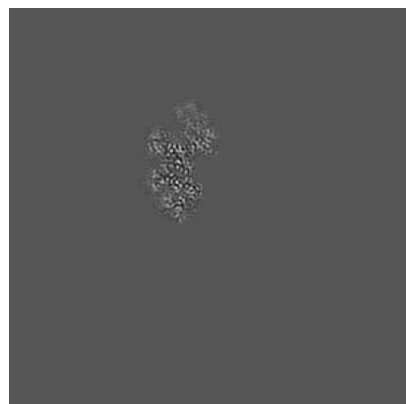


Z

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

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

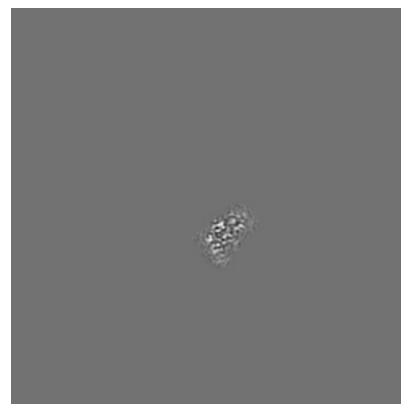
#### 6.2.1 Primary map



X Index: 176



Y Index: 176

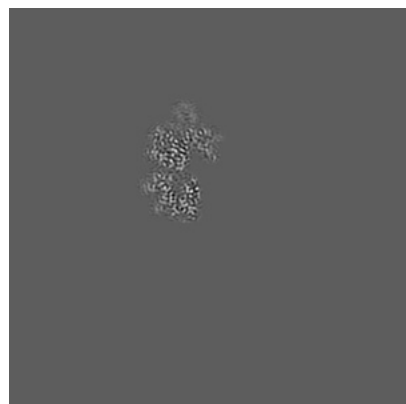


Z Index: 176

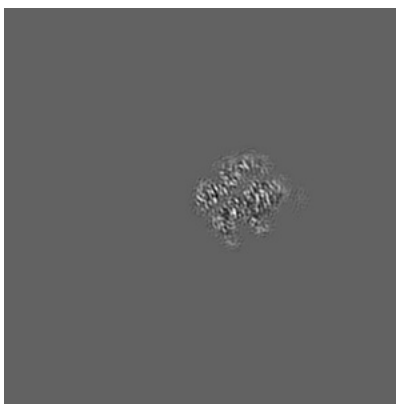
The images above show central slices of the map in three orthogonal directions.

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

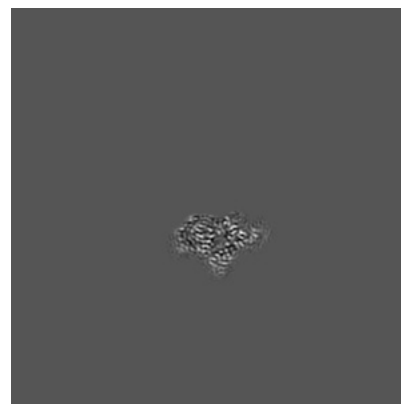
### 6.3.1 Primary map



X Index: 186



Y Index: 144



Z Index: 195

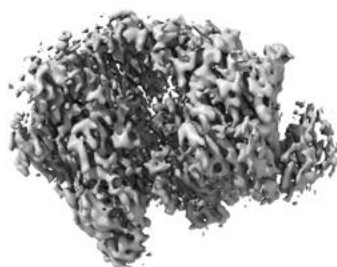
The images above show the largest variance slices of the map in three orthogonal directions.

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

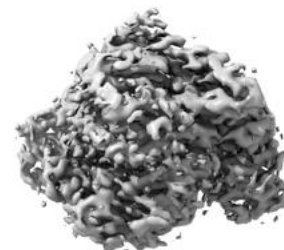
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.018. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.



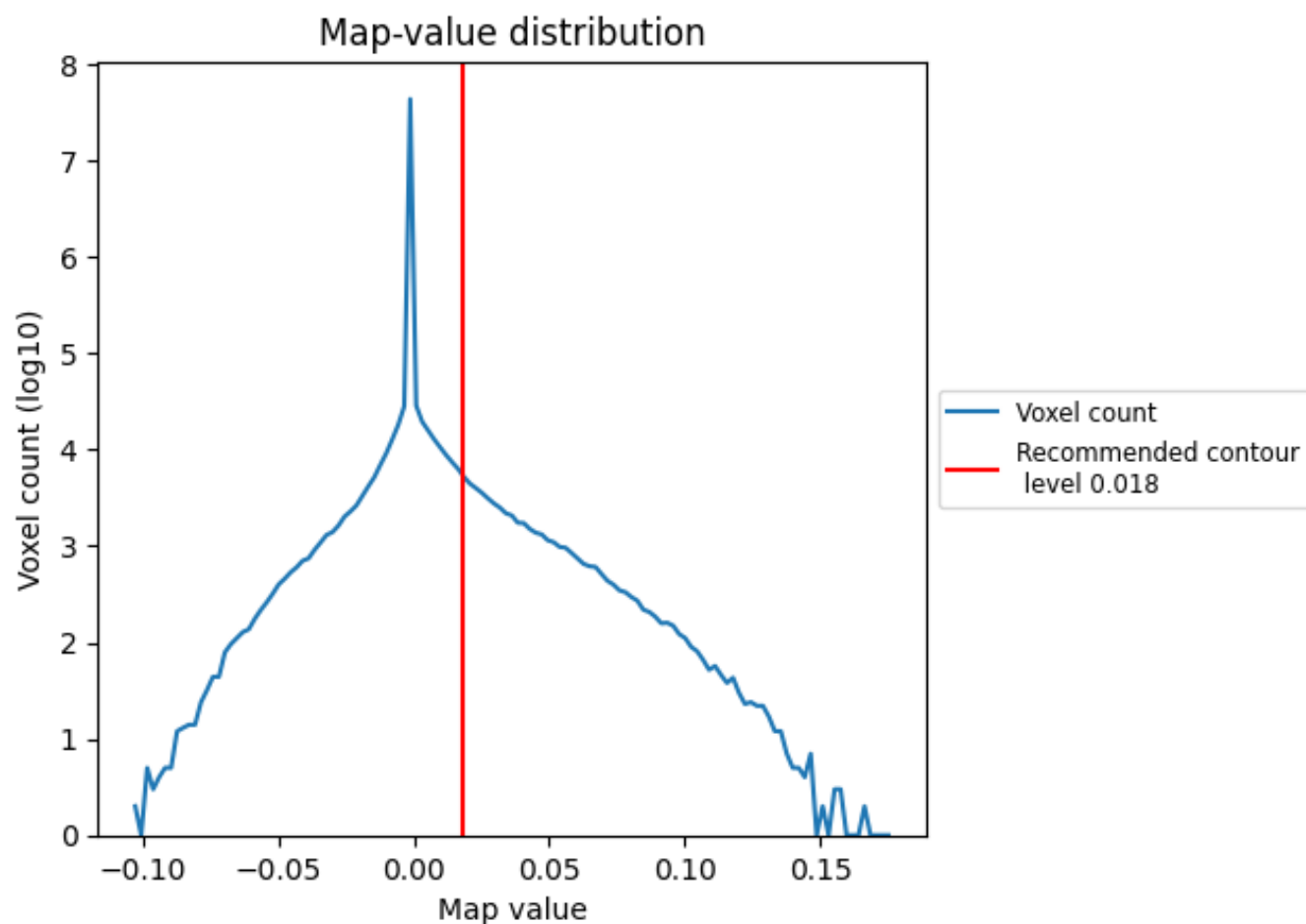
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

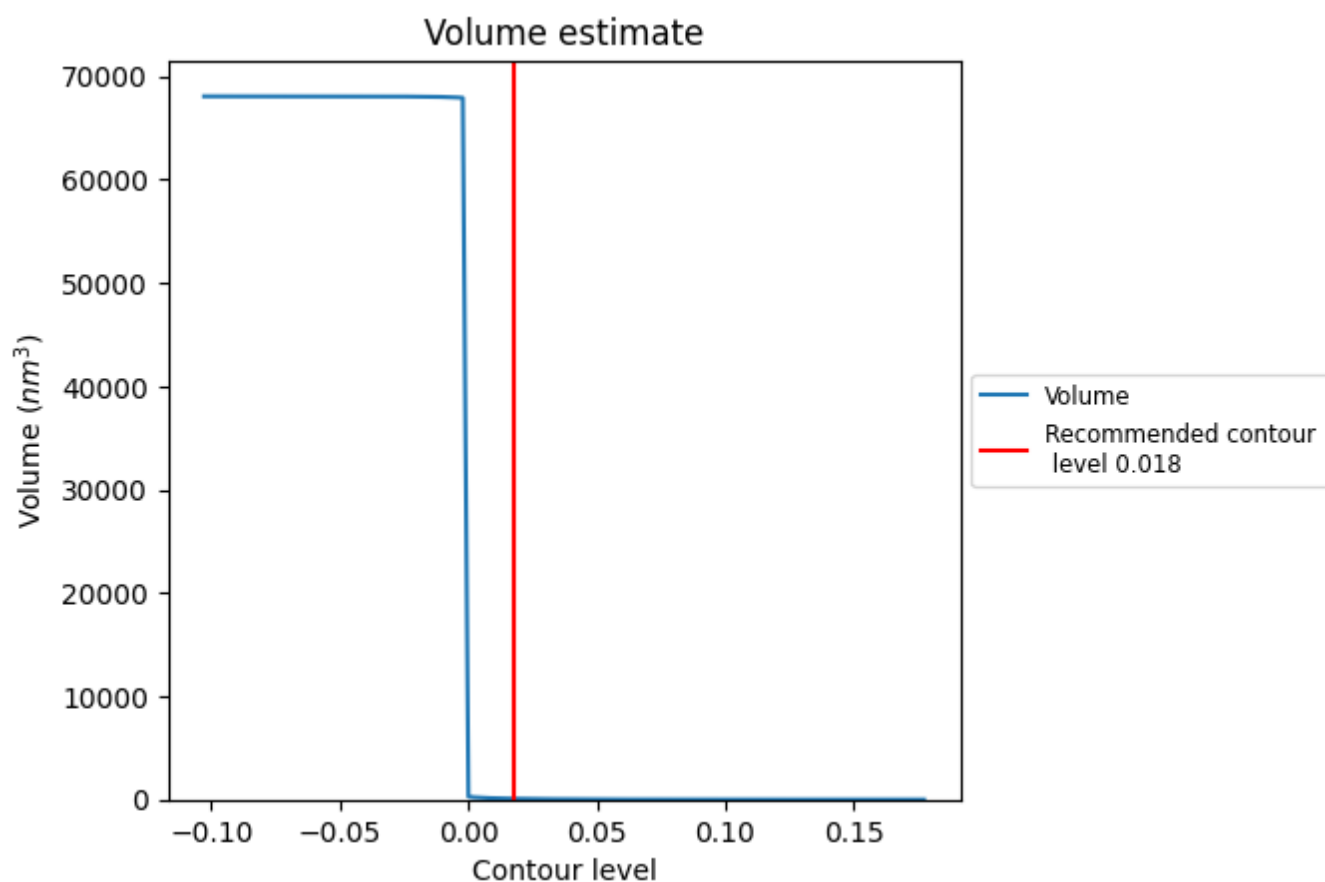
This section contains the results of statistical analysis of the map.

### 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.

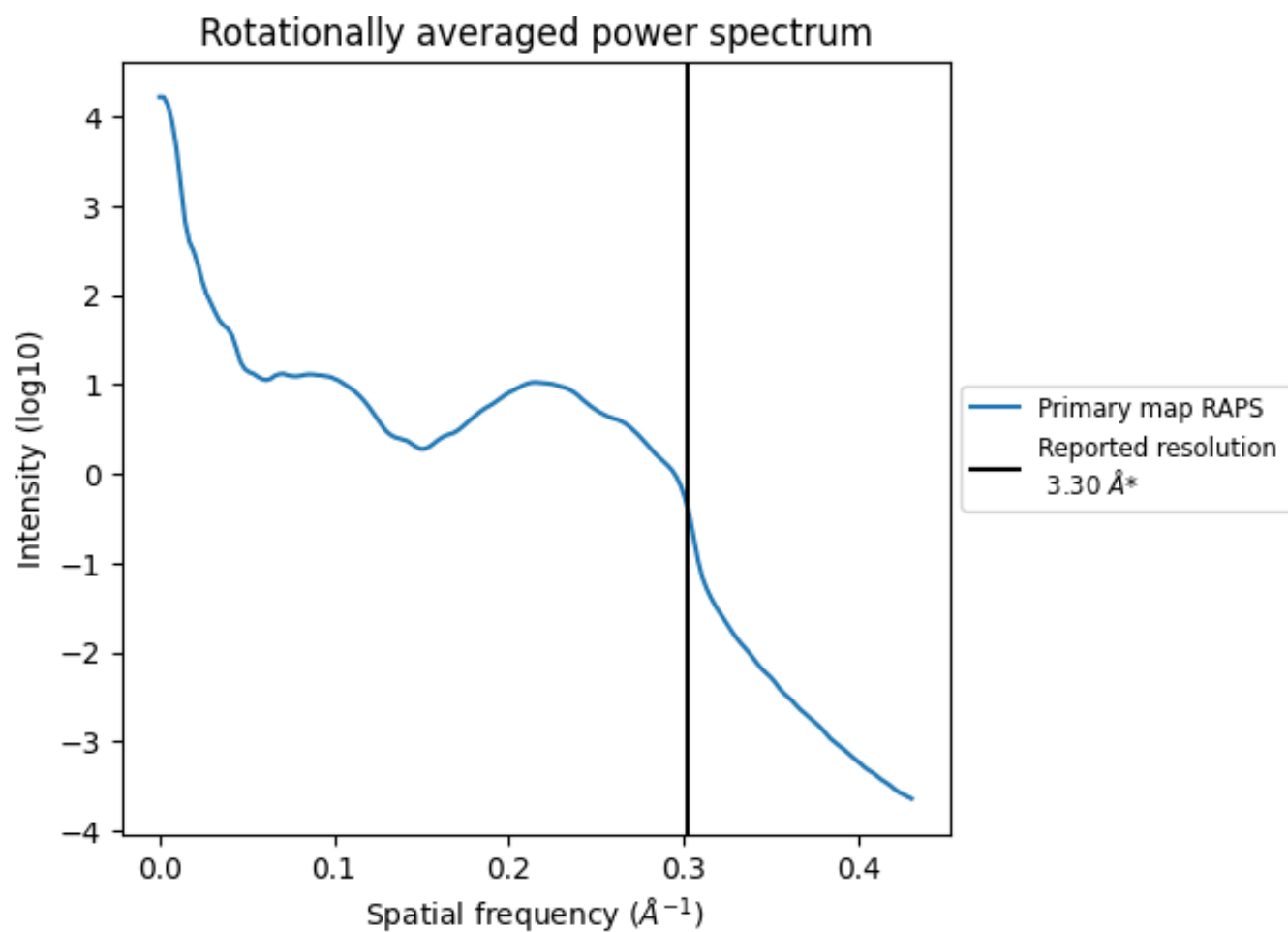
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 80  $\text{nm}^3$ ; this corresponds to an approximate mass of 72 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 0.303 Å<sup>-1</sup>

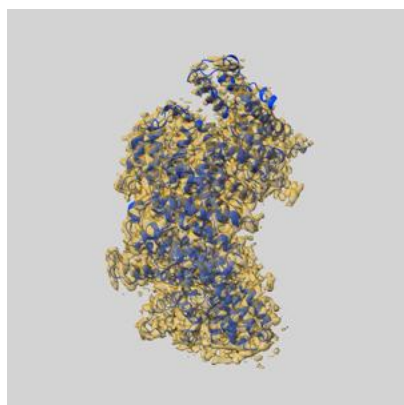
## 8 Fourier-Shell correlation ⓘ

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

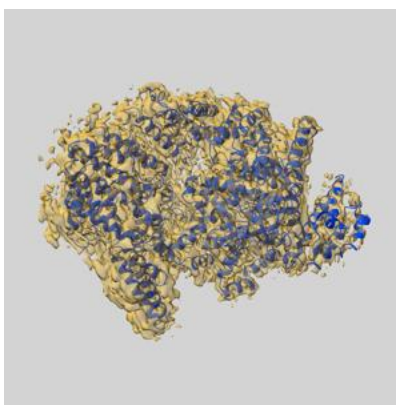
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-22619 and PDB model 7K10. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

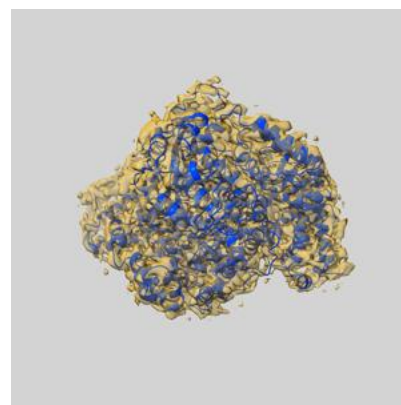
### 9.1 Map-model overlay [i](#)



X



Y



Z

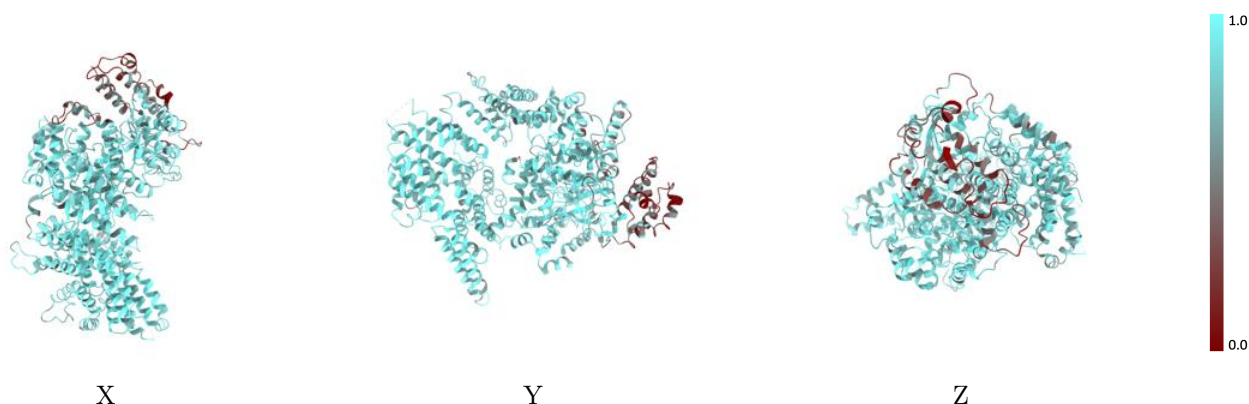
The images above show the 3D surface view of the map at the recommended contour level 0.018 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



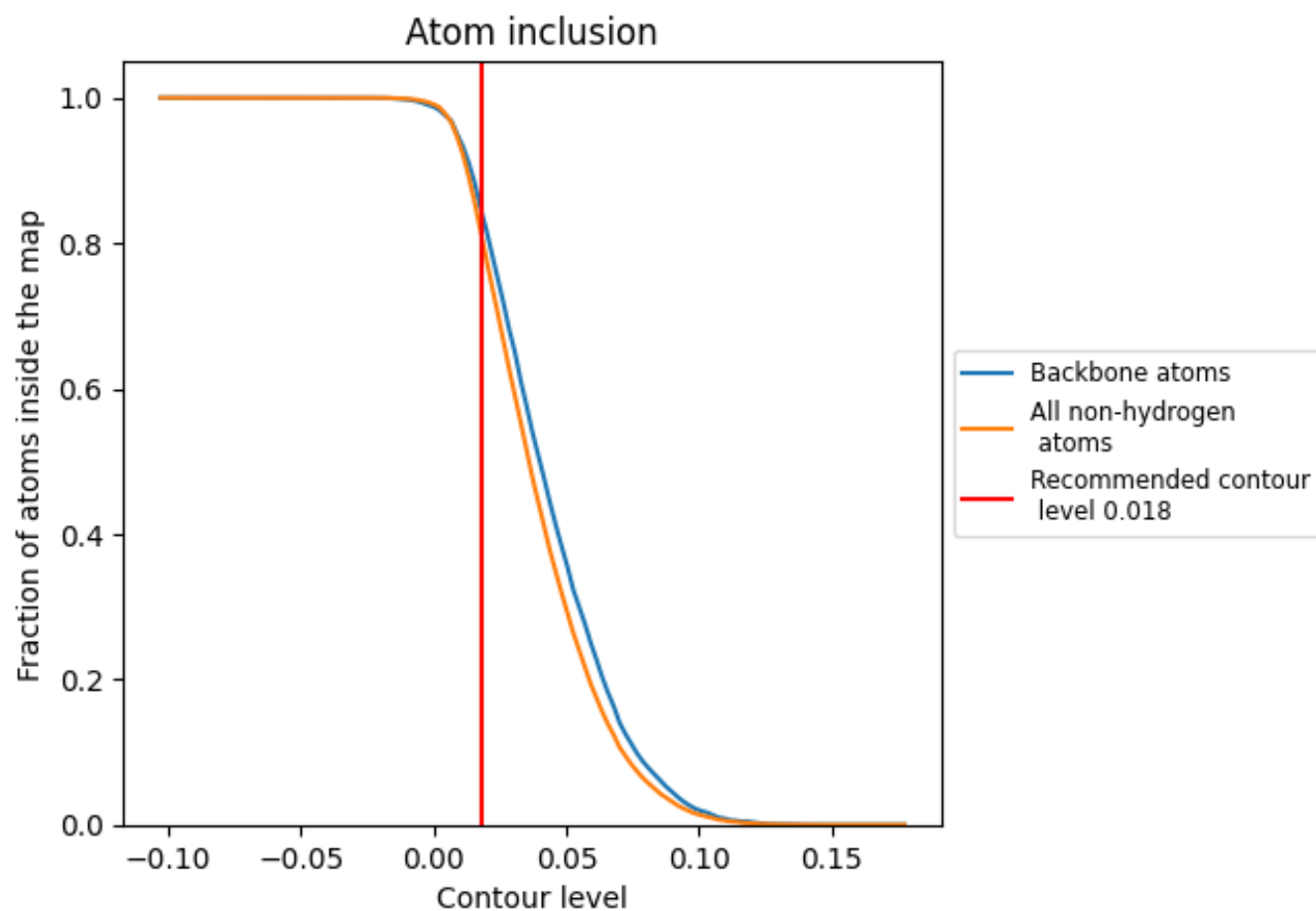
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.018).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 81% 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 (0.018) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.8116	<div><div></div></div> 0.4940
A	<div><div></div></div> 0.8116	<div><div></div></div> 0.4940

