



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 04:51 AM UTC

PDB ID : 7K11 / pdb_00007k11
EMDB ID : EMD-22620
Title : CryoEM structure of inactivated-form FATKIN domain of DNA-PK
Authors : Chen, X.; Gellert, M.; Yang, W.
Deposited on : 2020-09-06
Resolution : 3.21 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

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

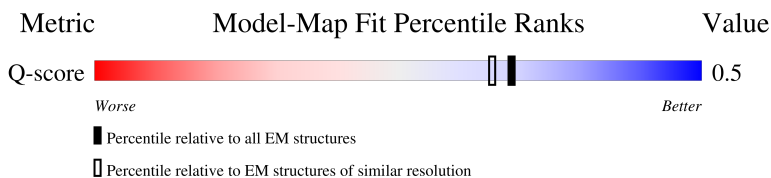
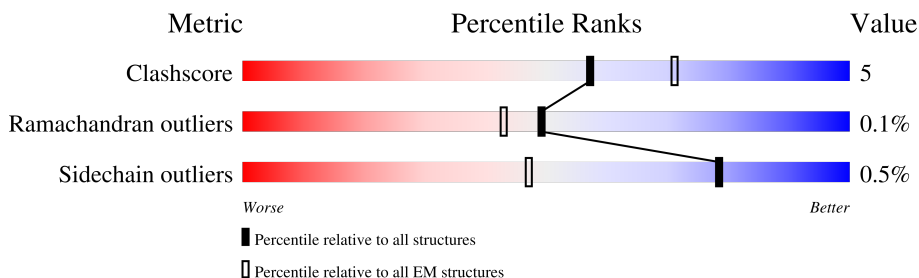
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.21 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	14613 (2.71 - 3.71)

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	4128	

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 10011 atoms, of which 0 are hydrogens and 0 are deuteriums.

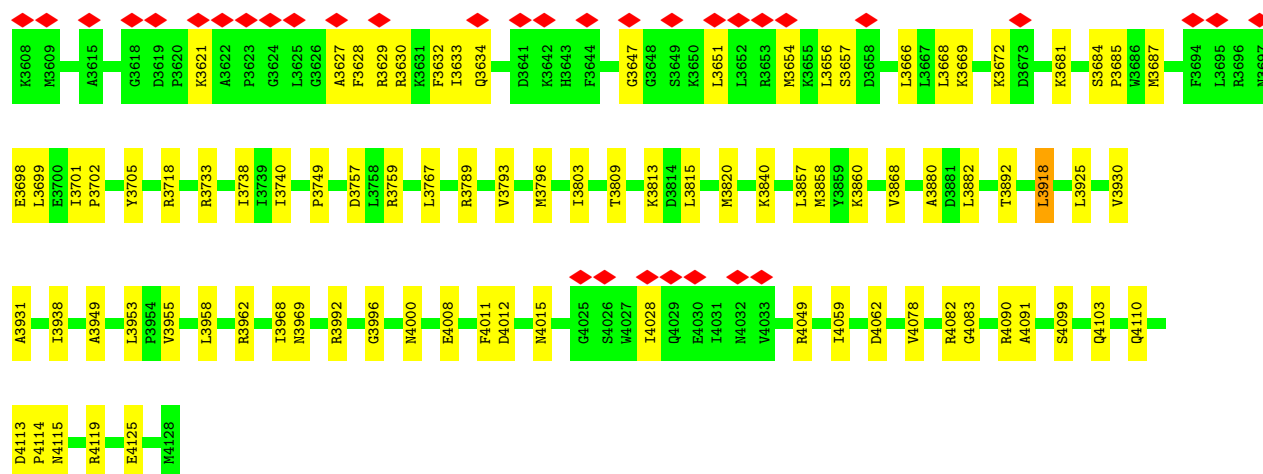
In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- 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	1254	10011	6378	1716	1860	57	0	0



VAL	ILE	ASP	SER	ALA	GLU	LEU	G3440	K3462	K3462	K3462	K3463	K3464	L3468	I3471	I3472	K3483	T3484	K3485	E3486	I3496	S3497	H3501	A3513	Q3527	V3530	K3543	H3549	K3552	I3558	K3561	L3562	D3563	I3568	N3573	L3583	L3586	A3597	P3600	V3601				
D3308	N3311	V3312	S3313	S3314	K3318	A3322	T3332	I3336	N3339	C3347	I3359	L3360	E3361	I3362	SER	GLY	SER	SER	SER	SER	GLN	ASP	V3373	Y3378	A3391	ALA	GLU	GLU	GLU	ALA	GLN	PRO	PRO	SER	CYS	GLY	A3406	M3414	K3426	E3429	ASN	ALA	SER
LEU	PRO	ALA	GLU	LEU	ALA	LYS	ARG	ARG	VAL	VAL	VAL	VAL	VAL	VAL	PRO	LEU	HIS	GLY	ASP	LEU	GLN	ASP	W3031	I3045	R3046	S3047	Q3059	S3060	L3061	L3062	D3065	I3065	M3069	H3070	L3078	S3083	Q3093	Q3123	L3126	E3137	LEU		
GLY	LYS	ARG	LYS	LEU	LEU	PRO	GLY	ASP	ASN	VAL	VAL	VAL	VAL	VAL	GLY	ALA	ALA	GLY	THR	LEU	LEU	ARG	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		
LEU	LYS	MET	LYS	GLN	ASP	ALA	GLN	VAL	LEU	TYR	SER	TYR	HIS	ASP	ASP	THR	LEU	THR	LEU	VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR		
LEU	CYS	GLU	ASN	LEU	VAL	ALA	GLN	LYS	HIS	GLN	ASN	THR	TYR	PHE	ILE	VAL	GLN	PRO	PHE	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL			
LEU	LYS	ASP	LEU	PRO	TYR	PRO	LYS	GLN	ALA	GLY	ASN	ILE	GLY	TYR	ASN	GLN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN			
VAL	LYS	HIS	TRP	HIS	ARG	SER	PRO	LEU	GLY	GLN	GLY	THR	CYS	THR	GLN	GLN	GLN	GLN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR		
ALA	LYS	HIS	TRP	HIS	ARG	SER	PRO	LEU	GLY	GLN	GLY	THR	CYS	THR	GLN	GLN	GLN	GLN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR		
SER	GLN	PHE	PHE	PHE	THR	GLY	VAL	GLN	VAL	TYR	SER	TYR	HIS	ASP	ASP	THR	LEU	THR	LEU	VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR		



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	367072	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	0.181	Depositor
Minimum map value	-0.128	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 [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	0.24	0/10218	0.54	0/13801

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	10011	0	9993	95	0
All	All	10011	0	9993	95	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.

All (95) 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:4078:VAL:O	1:A:4082:ARG:HB2	1.85	0.75
1:A:3274:VAL:HG12	1:A:3311:ASN:HD22	1.63	0.62
1:A:4049:ARG:NH2	1:A:4062:ASP:OD2	2.36	0.58
1:A:3062:LEU:HD22	1:A:3093:GLN:HE21	1.67	0.58
1:A:3647:GLY:O	1:A:3651:LEU:HB3	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4083:GLY:HA3	1:A:4091:ALA:HB2	1.84	0.58
1:A:3738:ILE:O	1:A:3749:PRO:HA	2.04	0.56
1:A:3789:ARG:HG2	1:A:3938:ILE:HD12	1.87	0.56
1:A:4115:ASN:OD1	1:A:4119:ARG:NH1	2.37	0.56
1:A:3123:GLN:HA	1:A:3126:LEU:HB2	1.88	0.56
1:A:4082:ARG:NH1	1:A:4082:ARG:O	2.39	0.55
1:A:3378:TYR:OH	1:A:3426:LYS:NZ	2.39	0.55
1:A:3815:LEU:HD22	1:A:3930:VAL:HG21	1.89	0.55
1:A:3992:ARG:NH1	1:A:4103:GLN:OE1	2.40	0.55
1:A:3949:ALA:HA	1:A:3953:LEU:HD13	1.89	0.54
1:A:4011:PHE:HA	1:A:4015:ASN:HB2	1.90	0.54
1:A:3360:LEU:HG	1:A:3373:VAL:HG21	1.90	0.54
1:A:3629:ARG:HD2	1:A:3633:ILE:HD11	1.90	0.54
1:A:3583:LEU:HD13	1:A:3733:ARG:HE	1.73	0.53
1:A:2823:PHE:HD2	1:A:2824:LYS:HG2	1.72	0.53
1:A:3996:GLY:O	1:A:4000:ASN:ND2	2.41	0.53
1:A:3011:LEU:HD23	1:A:3047:SER:HB3	1.89	0.52
1:A:3028:ASN:HA	1:A:3031:TRP:HD1	1.74	0.52
1:A:4012:ASP:OD2	1:A:4012:ASP:N	2.42	0.52
1:A:3666:LEU:HA	1:A:3669:LYS:HG2	1.93	0.51
1:A:3701:ILE:HD12	1:A:3740:ILE:HD11	1.93	0.51
1:A:4099:SER:O	1:A:4103:GLN:HB2	2.10	0.51
1:A:3630:ARG:HG2	1:A:3632:PHE:H	1.76	0.50
1:A:4049:ARG:HH21	1:A:4059:ILE:HD13	1.76	0.50
1:A:4078:VAL:O	1:A:4082:ARG:CB	2.57	0.50
1:A:3681:LYS:HD2	1:A:3687:MET:HE3	1.93	0.49
1:A:3654:MET:HG3	1:A:3656:LEU:HD13	1.94	0.49
1:A:3558:ILE:HA	1:A:3561:LYS:HG2	1.95	0.49
1:A:3629:ARG:NH2	1:A:3630:ARG:O	2.44	0.49
1:A:3472:ILE:HD13	1:A:3483:MET:HE2	1.95	0.49
1:A:3468:LEU:HA	1:A:3471:ILE:HG22	1.95	0.48
1:A:3880:ALA:HB1	1:A:3969:ASN:HD22	1.77	0.48
1:A:3190:LEU:HD22	1:A:3231:ILE:HG23	1.94	0.48
1:A:3314:SER:OG	1:A:3318:LYS:NZ	2.45	0.48
1:A:3767:LEU:HD13	1:A:3918:LEU:HD22	1.96	0.48
1:A:3698:GLU:HG3	1:A:3718:ARG:HD2	1.96	0.47
1:A:3271:ASP:OD1	1:A:3271:ASP:N	2.48	0.47
1:A:3813:LYS:HB2	1:A:3925:LEU:HB3	1.96	0.47
1:A:3549:HIS:HA	1:A:3552:LYS:HE2	1.96	0.46
1:A:3462:ARG:NH1	1:A:3497:SER:OG	2.49	0.46
1:A:2879:GLY:O	1:A:2883:SER:HB3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3796:MET:HE3	1:A:3796:MET:HB2	1.78	0.46
1:A:3501:HIS:NE2	1:A:4008:GLU:OE2	2.49	0.46
1:A:2940:ARG:HG3	1:A:2957:LEU:HD22	1.97	0.46
1:A:3026:ASP:OD1	1:A:3026:ASP:N	2.49	0.46
1:A:3496:ILE:HG21	1:A:3705:TYR:HB3	1.97	0.46
1:A:3299:THR:HG23	1:A:3300:VAL:HG13	1.98	0.45
1:A:3684:SER:HB3	1:A:3687:MET:HE2	1.98	0.45
1:A:3065:ILE:HD12	1:A:3078:LEU:HD21	1.99	0.45
1:A:3527:GLN:NE2	1:A:3699:LEU:O	2.50	0.45
1:A:2824:LYS:O	1:A:2829:LYS:NZ	2.43	0.45
1:A:3175:PRO:HD2	1:A:3178:ILE:HD13	1.99	0.45
1:A:3958:LEU:O	1:A:4110:GLN:NE2	2.49	0.45
1:A:3069:MET:O	1:A:3070:HIS:ND1	2.50	0.44
1:A:3530:VAL:HG11	1:A:3568:ILE:HG21	1.99	0.44
1:A:3297:VAL:HG11	1:A:3359:ILE:HD11	1.99	0.44
1:A:3793:VAL:HG22	1:A:3803:ILE:HG23	1.98	0.44
1:A:3757:ASP:OD2	1:A:3759:ARG:NH2	2.49	0.44
1:A:3227:ILE:HD12	1:A:3227:ILE:HA	1.89	0.44
1:A:3414:MET:HE1	1:A:3464:LYS:HD2	2.00	0.44
1:A:3339:ASN:ND2	1:A:3378:TYR:OH	2.51	0.44
1:A:3543:LYS:HD3	1:A:3543:LYS:HA	1.73	0.44
1:A:3868:VAL:HG22	1:A:4114:PRO:HB2	2.00	0.43
1:A:3573:ASN:HB3	1:A:3627:ALA:HB2	2.01	0.43
1:A:2837:LEU:HD12	1:A:2871:LEU:HD12	2.00	0.43
1:A:3145:ILE:HD11	1:A:3196:LYS:HD2	2.00	0.43
1:A:3628:PHE:HB3	1:A:3685:PRO:HD2	2.01	0.43
1:A:3962:ARG:NH1	1:A:4125:GLU:O	2.41	0.43
1:A:3452:LYS:NZ	1:A:3486:GLU:OE2	2.52	0.42
1:A:3858:MET:HE3	1:A:3858:MET:HB3	1.92	0.42
1:A:3857:LEU:HD23	1:A:3860:LYS:HD3	2.01	0.42
1:A:3668:LEU:O	1:A:3672:LYS:NZ	2.53	0.42
1:A:3281:CYS:SG	1:A:3303:THR:OG1	2.75	0.42
1:A:3809:THR:HG22	1:A:3931:ALA:HA	2.02	0.42
1:A:3170:ASP:OD1	1:A:3170:ASP:N	2.43	0.42
1:A:2859:GLN:NE2	1:A:2880:CYS:SG	2.92	0.42
1:A:3968:ILE:HD13	1:A:3968:ILE:HA	1.94	0.42
1:A:2978:LYS:HD2	1:A:2981:TRP:CG	2.55	0.41
1:A:2978:LYS:HD2	1:A:2981:TRP:CD2	2.54	0.41
1:A:3597:ALA:HA	1:A:3657:SER:HB3	2.01	0.41
1:A:3484:THR:HG22	1:A:3513:ALA:HA	2.01	0.41
1:A:3621:LYS:HE2	1:A:3621:LYS:HB2	1.87	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3820:MET:HG2	1:A:3882:LEU:HD11	2.02	0.41
1:A:4090:ARG:NH1	1:A:4113:ASP:OD2	2.50	0.41
1:A:3840:LYS:HE2	1:A:3840:LYS:HB3	1.93	0.40
1:A:3045:ILE:HG13	1:A:3061:LEU:HD21	2.04	0.40
1:A:3629:ARG:HH12	1:A:3634:GLN:HB2	1.86	0.40
1:A:3137:GLU:OE1	1:A:3164:TRP:NE1	2.54	0.40
1:A:3332:THR:O	1:A:3336:ILE:HG13	2.22	0.40
1:A:3701:ILE:HA	1:A:3702:PRO:HD3	1.87	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	1242/4128 (30%)	1122 (90%)	119 (10%)	1 (0%)	48	78

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	1093/3671 (30%)	1088 (100%)	5 (0%)	81 84

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3178	ILE
1	A	3892	THR
1	A	3918	LEU
1	A	3955	VAL
1	A	4028	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2885	GLN
1	A	2977	ASN
1	A	3093	GLN
1	A	3122	HIS
1	A	3123	GLN
1	A	3139	GLN
1	A	3154	GLN
1	A	3251	ASN
1	A	3311	ASN
1	A	3327	ASN
1	A	3339	ASN
1	A	3384	HIS
1	A	3524	ASN
1	A	3590	ASN
1	A	3762	GLN
1	A	3951	GLN

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 [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.

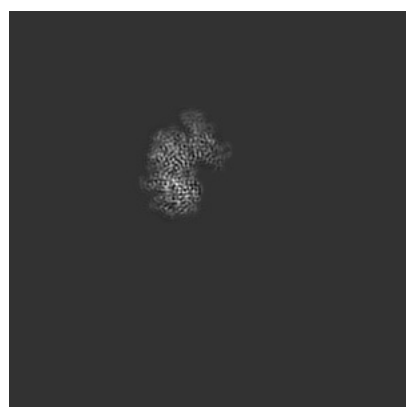
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22620. These allow visual inspection of the internal detail of the map and identification of artifacts.

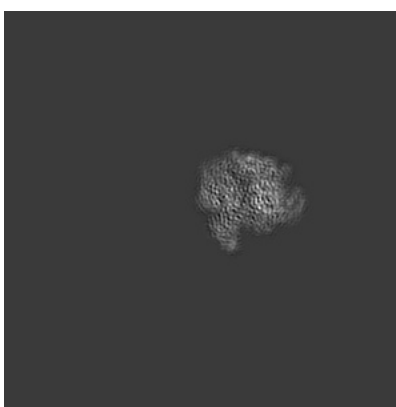
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

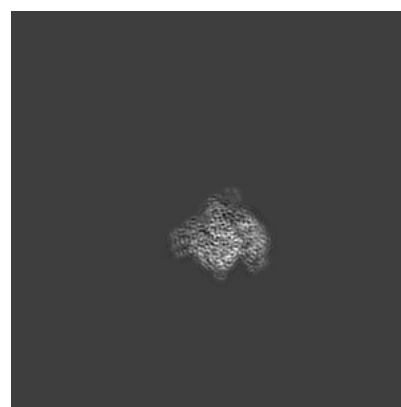
6.1.1 Primary map



X



Y

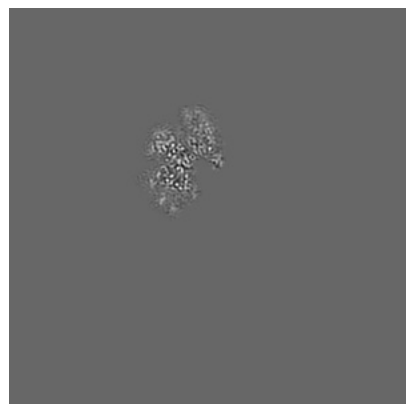


Z

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

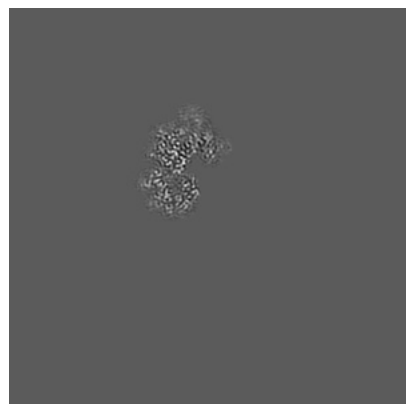


Z Index: 176

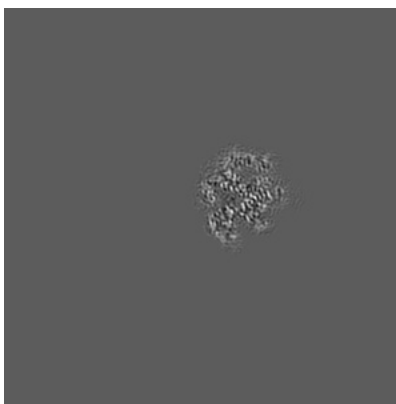
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

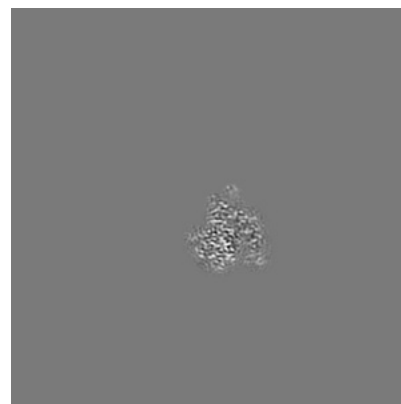
6.3.1 Primary map



X Index: 188



Y Index: 148

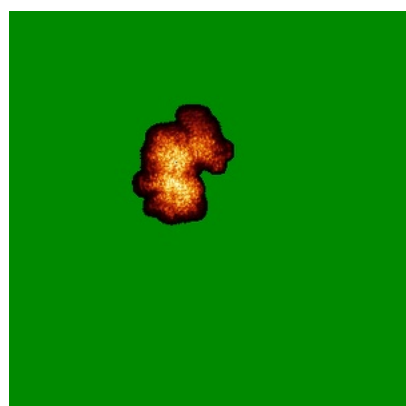


Z Index: 225

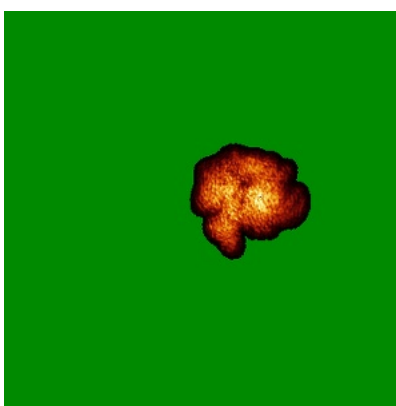
The images above show the largest variance slices of the map in three orthogonal directions.

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

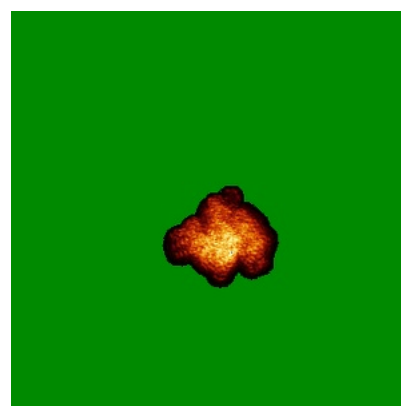
6.4.1 Primary map



X



Y

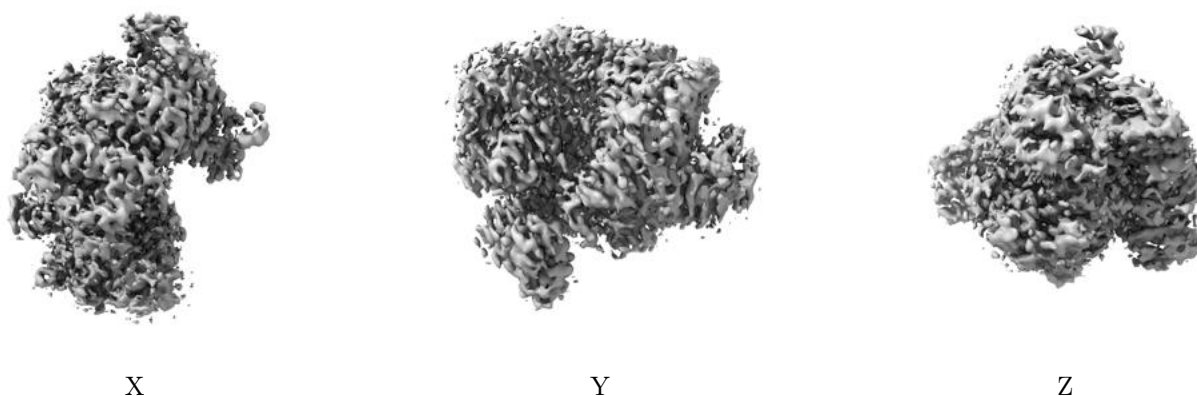


Z

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 0.018. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

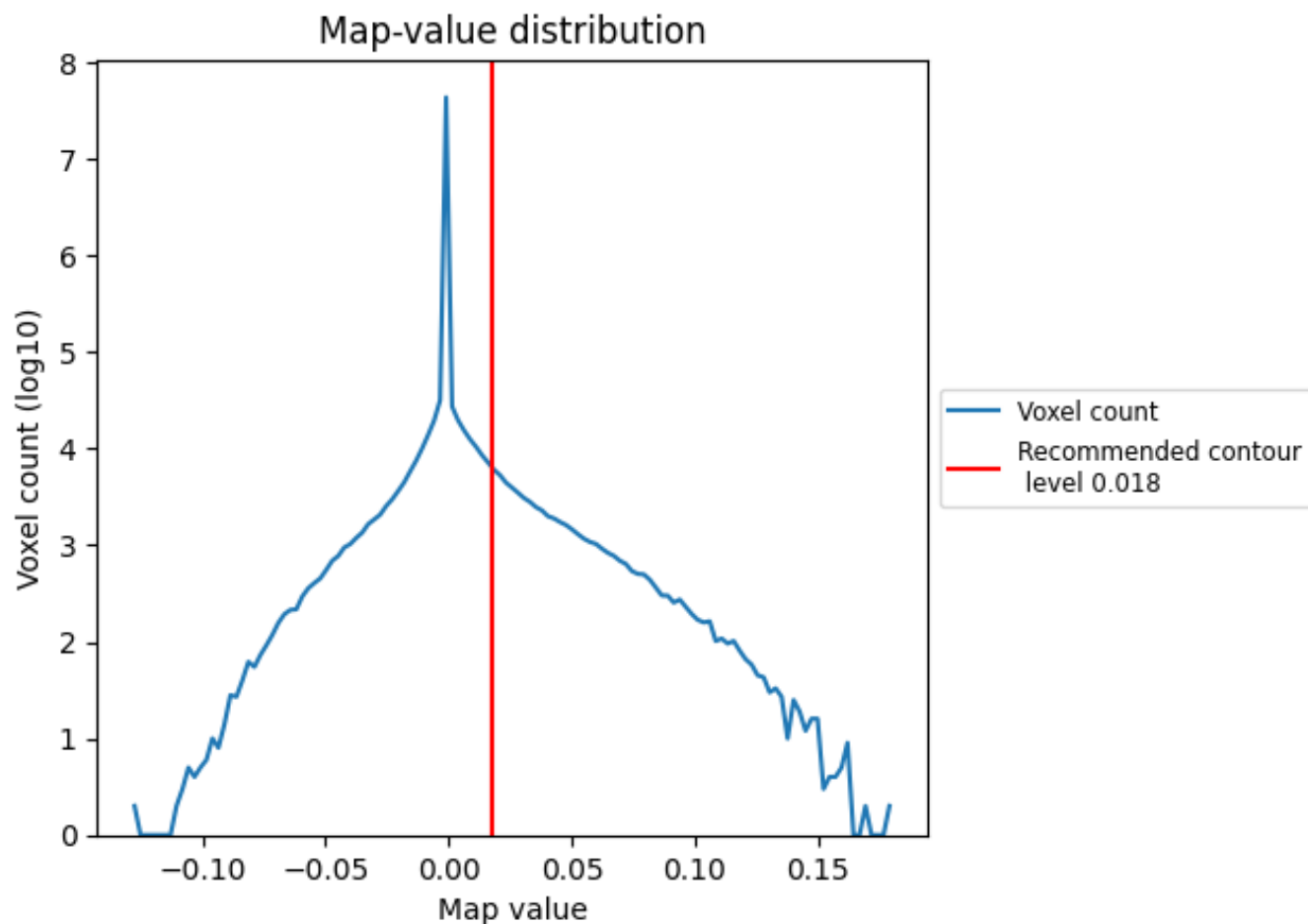
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

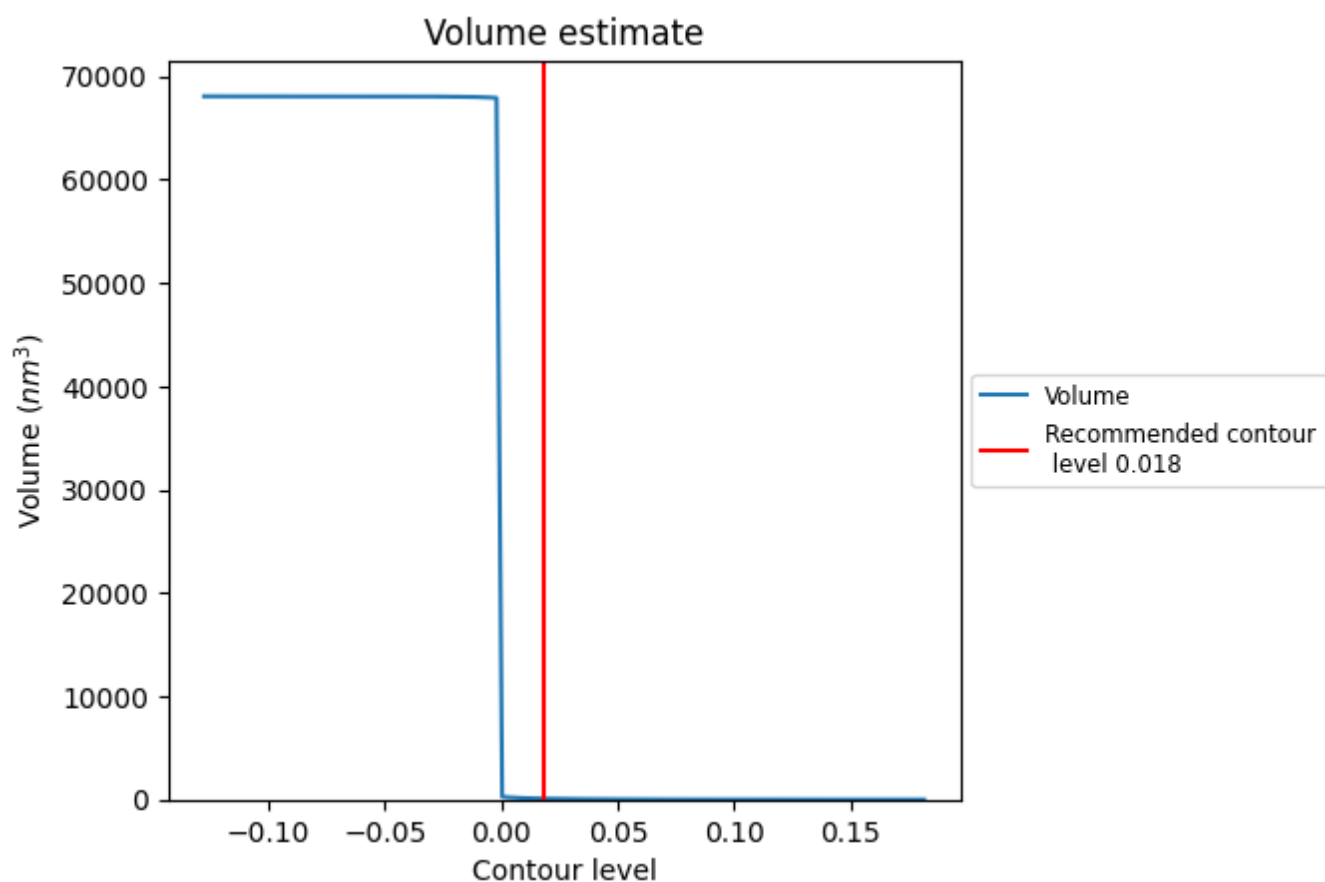
This section contains the results of statistical analysis of the map.

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.

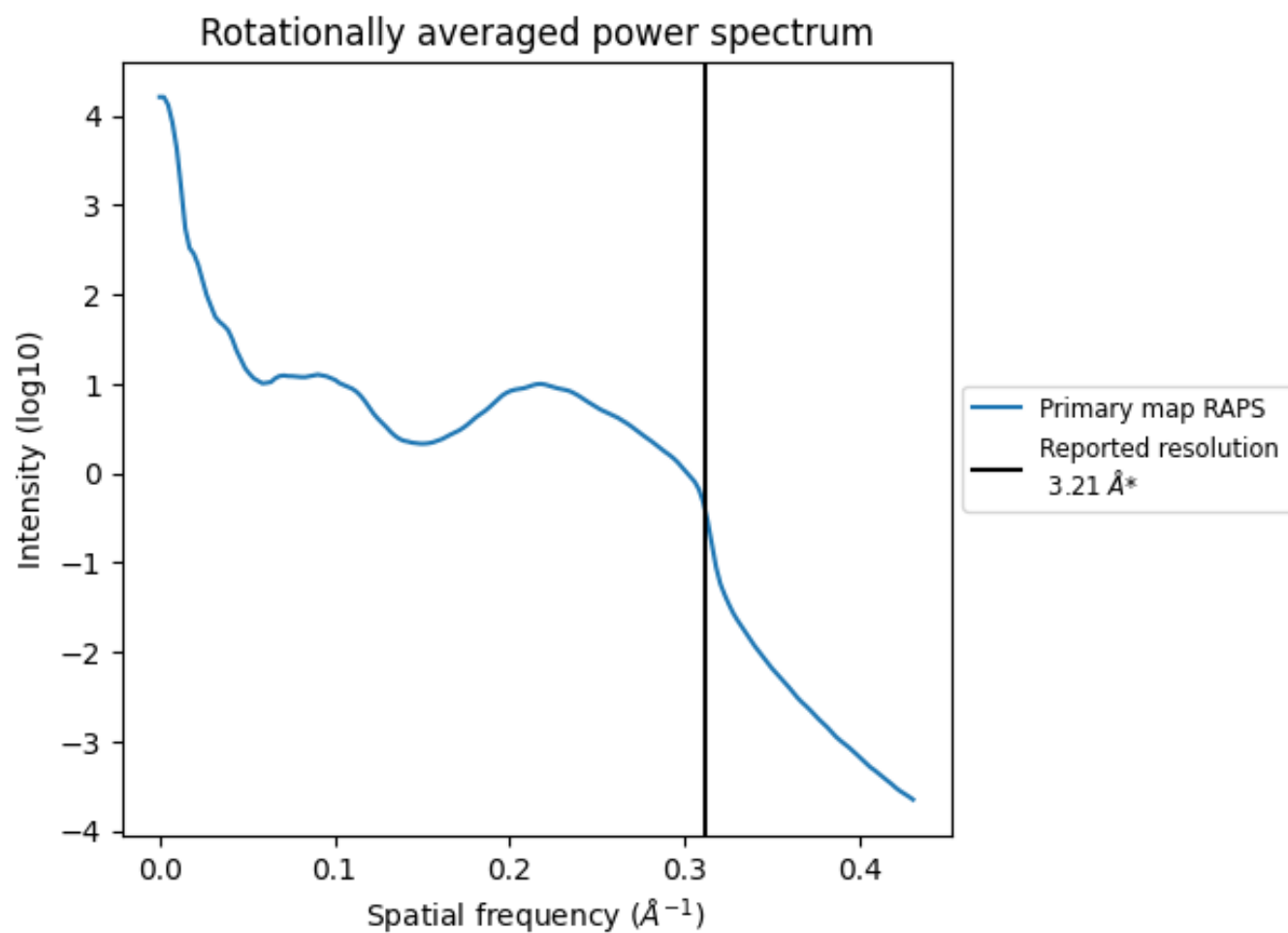
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 90 nm³; this corresponds to an approximate mass of 81 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 0.312 Å⁻¹

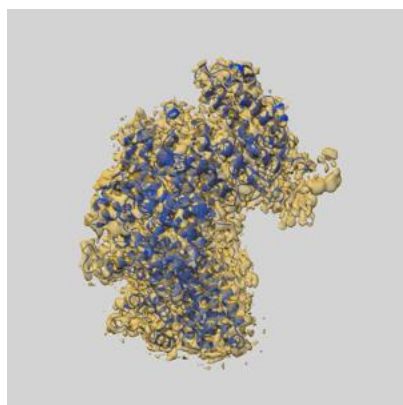
8 Fourier-Shell correlation ⓘ

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

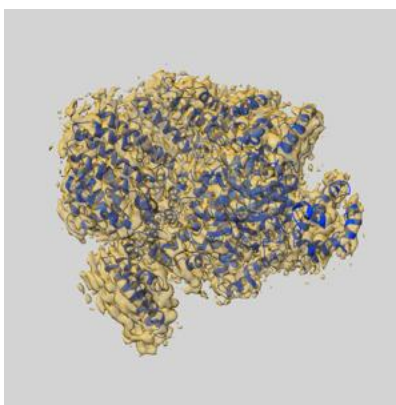
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-22620 and PDB model 7K11. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

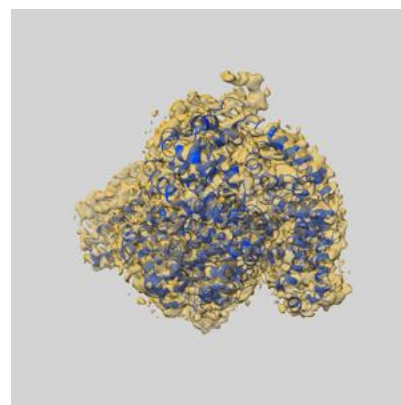
9.1 Map-model overlay [i](#)



X



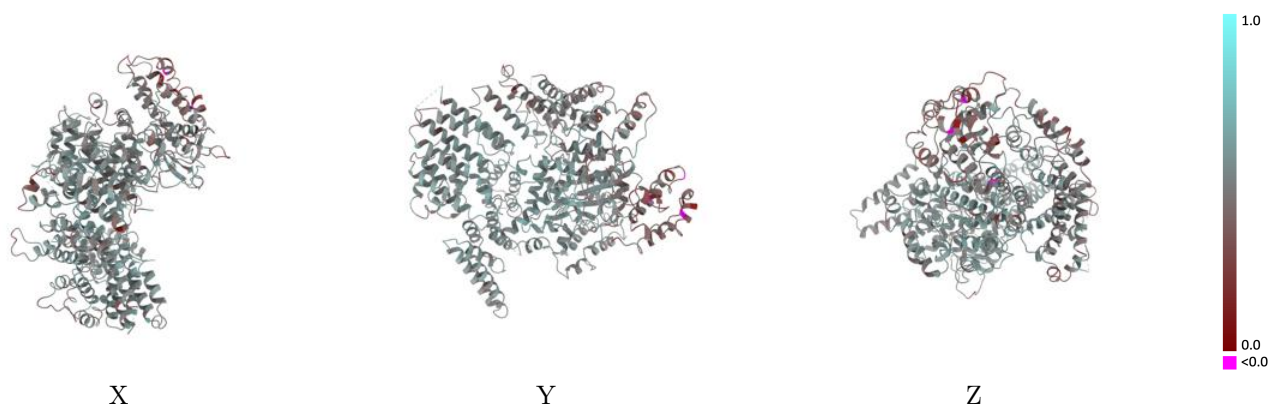
Y



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](#)

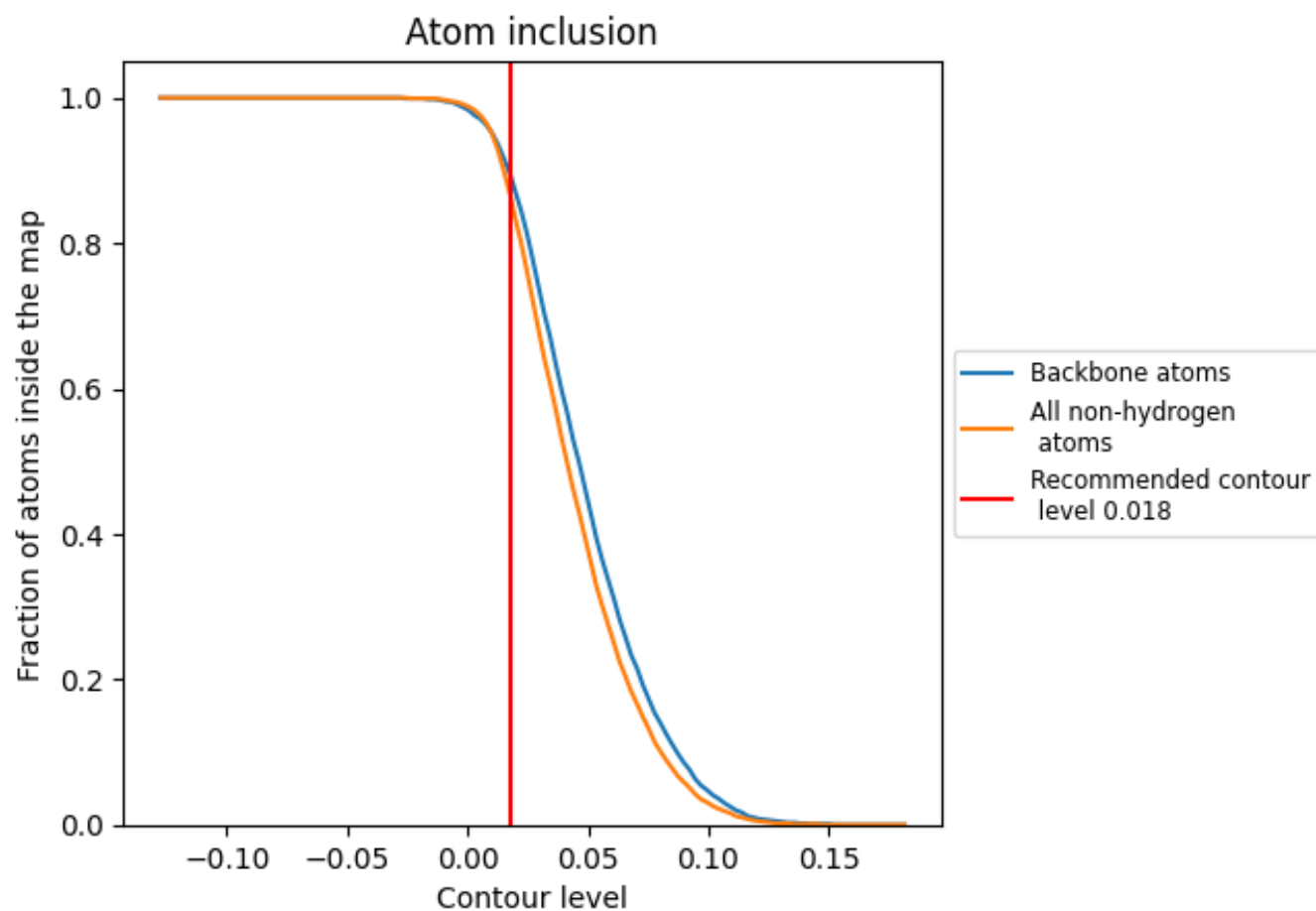


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 86% 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	0.8630	0.5000
A	0.8630	0.5000

