wwPDB EM Validation Summary Report (i)

Sep 3, 2026 – 04:19 PM JST

PDB ID	:	9X0C / pdb_00009x0c
EMDB ID	:	EMD-66432
Title	:	Cryo-EM structure of AKT5 - D403A
Authors	:	Muraoka, Y.; Tanaka, Y.; Yokoyama, T.; Furuta, T.; Yamanashi, T.; Tsujii, M.; Tsubota, R.; Uozumi, N.
Deposited on	:	2025-09-30
Resolution	:	2.60 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

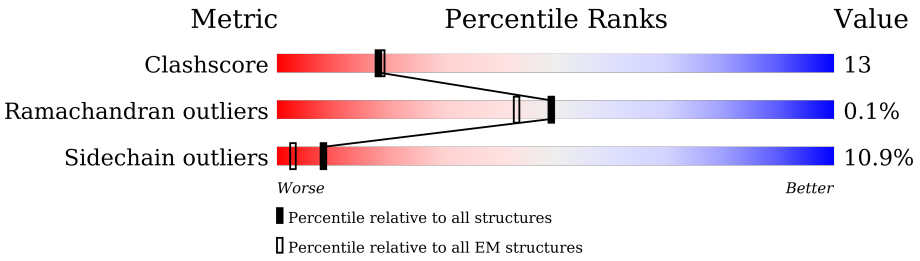
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

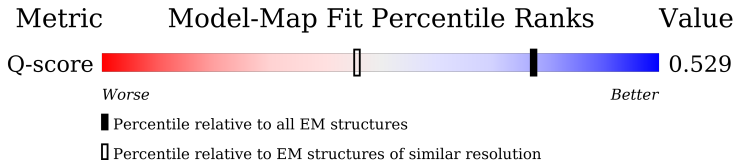
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.60 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	8728 (2.10 - 3.10)

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 <=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	894	9% 32% 15% • 50%
1	B	894	8% 33% 15% • 50%
1	C	894	8% 34% 14% • 50%
1	D	894	9% 34% 15% • 50%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 14592 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 Probable potassium channel AKT5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	B	449	3648	2384	613	635	16	0	0
1	C	449	3648	2384	613	635	16	0	0
1	A	449	3648	2384	613	635	16	0	0
1	D	449	3648	2384	613	635	16	0	0

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-7	MET	-	initiating methionine	UNP Q9SCX5
B	-6	ASP	-	expression tag	UNP Q9SCX5
B	-5	TYR	-	expression tag	UNP Q9SCX5
B	-4	LYS	-	expression tag	UNP Q9SCX5
B	-3	ASP	-	expression tag	UNP Q9SCX5
B	-2	ASP	-	expression tag	UNP Q9SCX5
B	-1	ASP	-	expression tag	UNP Q9SCX5
B	0	ASP	-	expression tag	UNP Q9SCX5
B	1	LYS	-	expression tag	UNP Q9SCX5
B	403	ALA	ASP	engineered mutation	UNP Q9SCX5
B	881	HIS	-	expression tag	UNP Q9SCX5
B	882	HIS	-	expression tag	UNP Q9SCX5
B	883	HIS	-	expression tag	UNP Q9SCX5
B	884	HIS	-	expression tag	UNP Q9SCX5
B	885	HIS	-	expression tag	UNP Q9SCX5
B	886	HIS	-	expression tag	UNP Q9SCX5
C	-7	MET	-	initiating methionine	UNP Q9SCX5
C	-6	ASP	-	expression tag	UNP Q9SCX5
C	-5	TYR	-	expression tag	UNP Q9SCX5
C	-4	LYS	-	expression tag	UNP Q9SCX5
C	-3	ASP	-	expression tag	UNP Q9SCX5
C	-2	ASP	-	expression tag	UNP Q9SCX5

Continued on next page...

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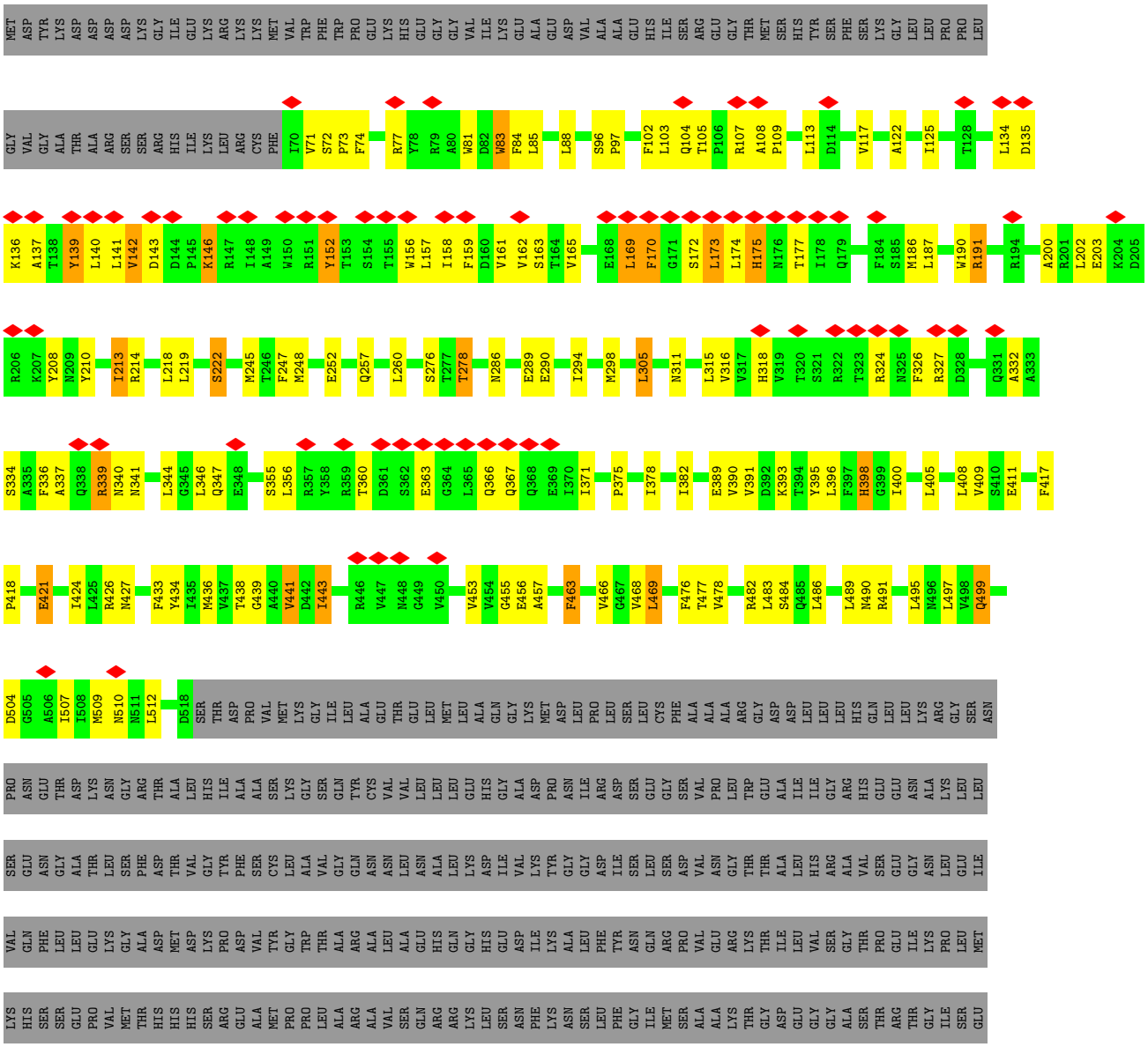
Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	ASP	-	expression tag	UNP Q9SCX5
C	0	ASP	-	expression tag	UNP Q9SCX5
C	1	LYS	-	expression tag	UNP Q9SCX5
C	403	ALA	ASP	engineered mutation	UNP Q9SCX5
C	881	HIS	-	expression tag	UNP Q9SCX5
C	882	HIS	-	expression tag	UNP Q9SCX5
C	883	HIS	-	expression tag	UNP Q9SCX5
C	884	HIS	-	expression tag	UNP Q9SCX5
C	885	HIS	-	expression tag	UNP Q9SCX5
C	886	HIS	-	expression tag	UNP Q9SCX5
A	-7	MET	-	initiating methionine	UNP Q9SCX5
A	-6	ASP	-	expression tag	UNP Q9SCX5
A	-5	TYR	-	expression tag	UNP Q9SCX5
A	-4	LYS	-	expression tag	UNP Q9SCX5
A	-3	ASP	-	expression tag	UNP Q9SCX5
A	-2	ASP	-	expression tag	UNP Q9SCX5
A	-1	ASP	-	expression tag	UNP Q9SCX5
A	0	ASP	-	expression tag	UNP Q9SCX5
A	1	LYS	-	expression tag	UNP Q9SCX5
A	403	ALA	ASP	engineered mutation	UNP Q9SCX5
A	881	HIS	-	expression tag	UNP Q9SCX5
A	882	HIS	-	expression tag	UNP Q9SCX5
A	883	HIS	-	expression tag	UNP Q9SCX5
A	884	HIS	-	expression tag	UNP Q9SCX5
A	885	HIS	-	expression tag	UNP Q9SCX5
A	886	HIS	-	expression tag	UNP Q9SCX5
D	-7	MET	-	initiating methionine	UNP Q9SCX5
D	-6	ASP	-	expression tag	UNP Q9SCX5
D	-5	TYR	-	expression tag	UNP Q9SCX5
D	-4	LYS	-	expression tag	UNP Q9SCX5
D	-3	ASP	-	expression tag	UNP Q9SCX5
D	-2	ASP	-	expression tag	UNP Q9SCX5
D	-1	ASP	-	expression tag	UNP Q9SCX5
D	0	ASP	-	expression tag	UNP Q9SCX5
D	1	LYS	-	expression tag	UNP Q9SCX5
D	403	ALA	ASP	engineered mutation	UNP Q9SCX5
D	881	HIS	-	expression tag	UNP Q9SCX5
D	882	HIS	-	expression tag	UNP Q9SCX5
D	883	HIS	-	expression tag	UNP Q9SCX5
D	884	HIS	-	expression tag	UNP Q9SCX5
D	885	HIS	-	expression tag	UNP Q9SCX5
D	886	HIS	-	expression tag	UNP Q9SCX5

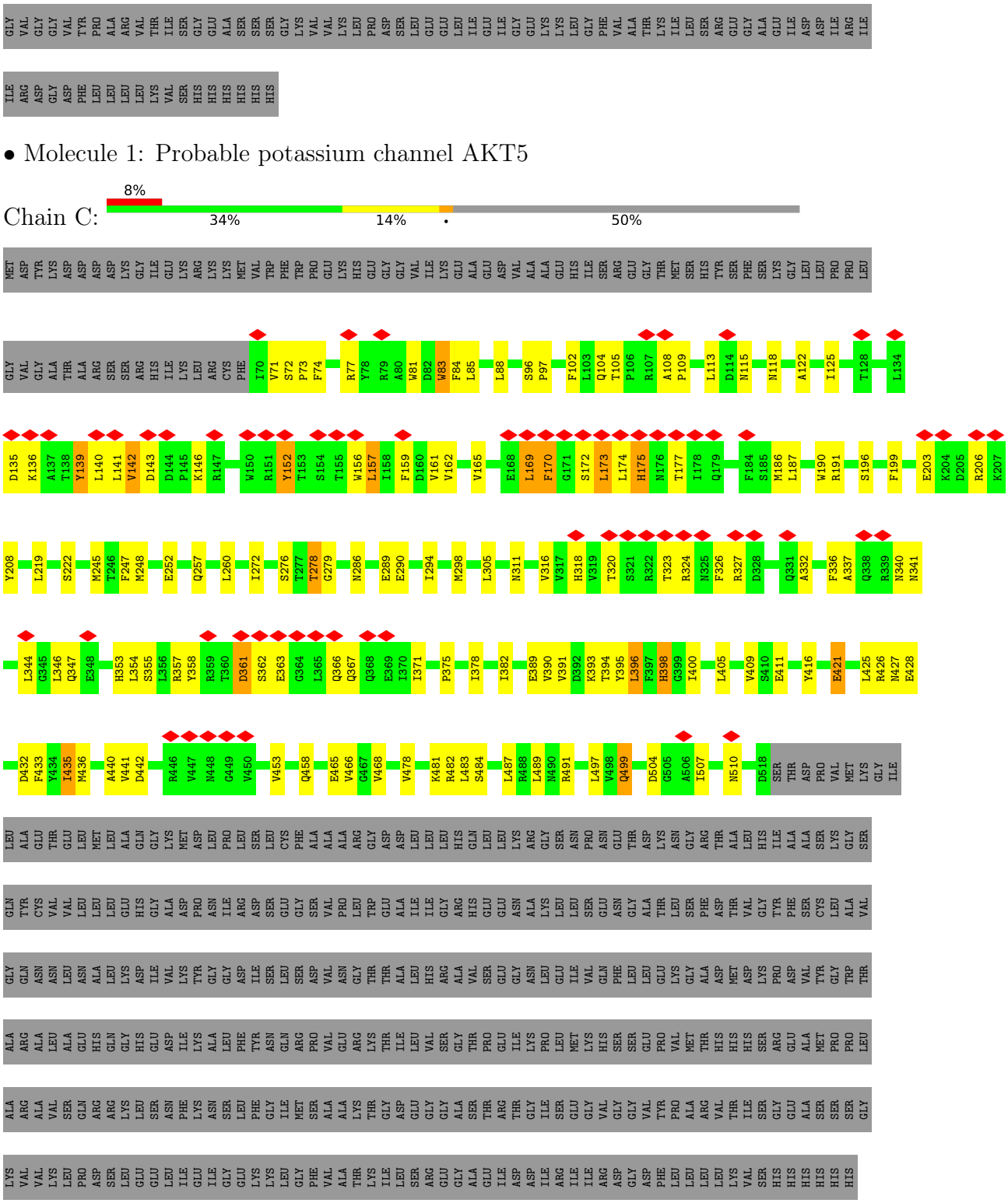
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

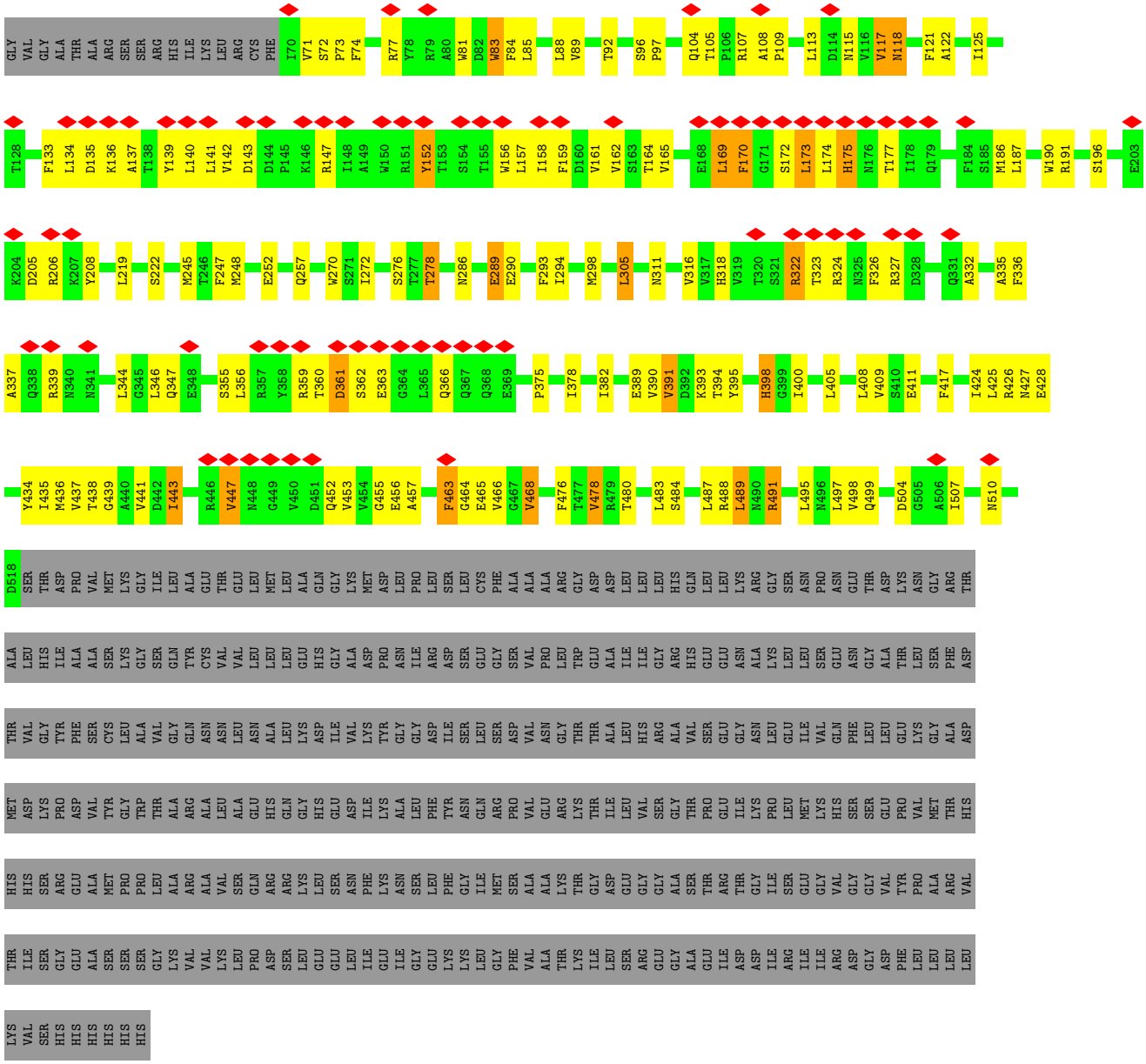
- Molecule 1: Probable potassium channel AKT5

Chain B:



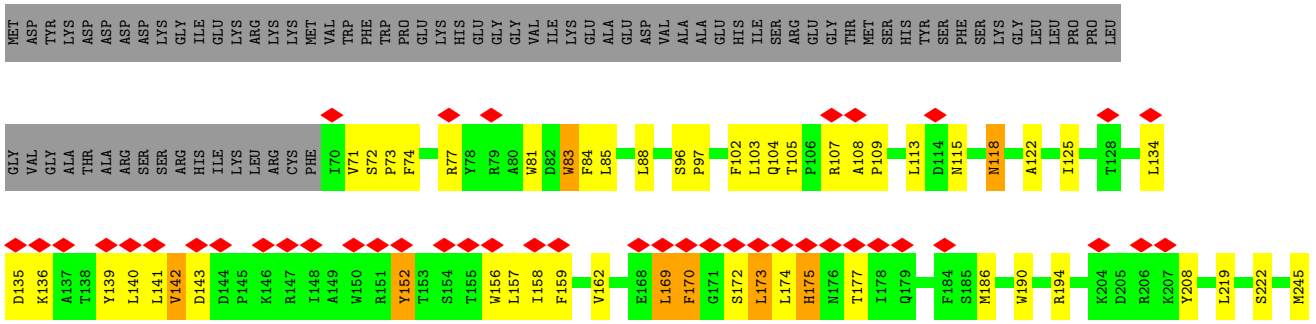


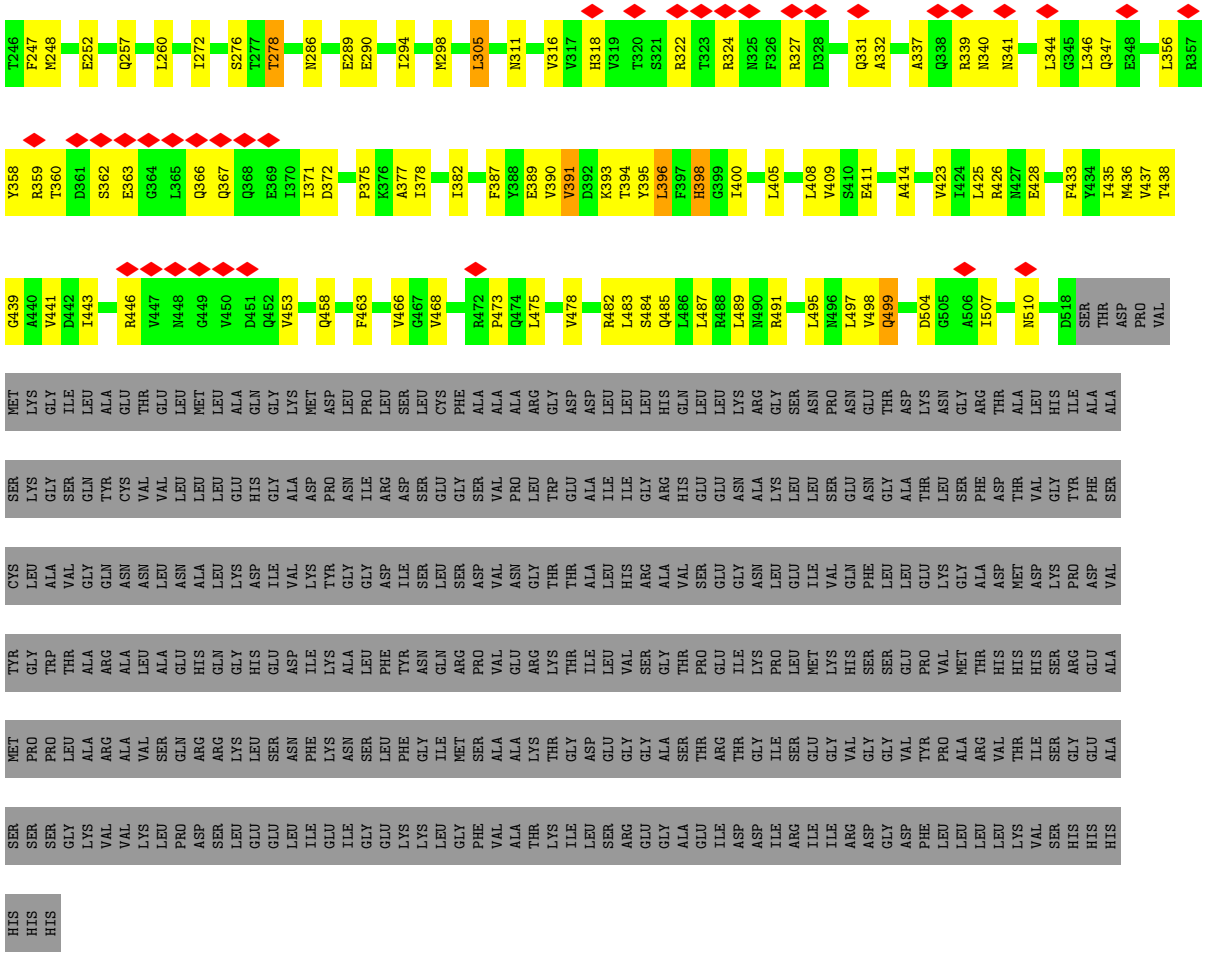
• Molecule 1: Probable potassium channel AKT5



- Molecule 1: Probable potassium channel AKT5

Chain D:




T246 F247 M248 E252 Q257 L260 I272 S276 T277 T278 N286 E289 E290 I294 M298 L305 N311 V316 V317 H318 V319 T320 S321 R322 T323 R324 N325 F326 R327 D328 Q331 A332 A337 Q338 R339 N340 N341 L344 G345 L346 Q347 E348 L356 R357
Y358 R359 T360 D361 S362 E363 G364 L365 Q366 Q367 Q368 E369 I370 I371 D372 P375 K376 A377 I378 I382 F387 Y388 E389 V390 V391 D392 K393 T394 Y395 L396 F397 H398 G399 I400 L405 L408 V409 S410 E411 A414 V423 I424 L425 R426 N427 E428 F433 Y434 I435 M436 V437 T438
G439 A440 V441 D442 I443 R446 V447 N448 G449 V450 D451 Q452 V453 Q458 F463 V466 G467 V468 R472 P473 Q474 L475 V478 R482 L483 S484 Q485 L486 L487 R488 L489 N490 R491 L495 N496 L497 V498 Q499 D504 G505 A506 I507 N510 D518 SER THR ASP PRO VAL
MET LYS GLY ILE LEU ALA GLU THR GLU LEU MET LEU ALA GLN GLY LYS MET ASP LEU PRO LEU SER LEU CYS PHE ALA ALA ARG GLY ASP ASP LEU LEU LEU HIS GLN LEU LEU LYS ARG GLY SER ASN PRO ASN GLU THR ASP LYS ASN GLY ARG THR ALA LEU HIS ILE ALA ALA
SER LYS GLY SER GLN TYR CYS VAL VAL LEU LEU LEU LEU GLU HIS GLY ALA ASP PRO ASN ILE ARG ASP SER GLU GLY SER VAL PRO LEU TRP GLU ALA ILE ILE GLY ARG HIS GLU GLU ASN ALA LYS LEU LEU SER GLU GLY ALA THR LEU SER PHE ASP THR VAL GLY TYR PHE SER
CYS LEU ALA VAL GLY GLN ASN ASN LEU ASN ALA LEU LYS ASP ILE VAL LYS TYR GLY GLY ASP ILE SER LEU SER ASP VAL ASN GLY THR THR ALA LEU HIS ARG ALA VAL SER GLU GLY ASN LEU GLU ILE VAL GLN PHE LEU LEU GLU LYS GLY ALA ASP MET ASP LYS PRO VAL
TYR GLY TRP THR ALA ARG ALA LEU ALA GLU HIS GLN GLY HIS GLU ASP ILE LYS ALA LEU PHE TYR ASN GLN ARG PRO VAL GLU ARG LYS THR ILE LEU VAL SER GLY THR PRO GLU ILE LYS PRO LEU MET LYS HIS SER SER GLU PRO VAL MET THR HIS HIS HIS SER ARG GLU ALA
MET PRO PRO LEU ALA ARG ALA VAL SER GLN ARG ARG LYS LEU SER ASN PHE LYS ASN SER LEU PHE GLY ILE MET SER ALA ALA LYS THR GLY ASP GLU GLY GLY ALA SER THR ARG THR GLY ILE SER GLU GLY VAL GLY GLY VAL TYR PRO ALA ARG VAL THR ILE SER GLY GLU ALA
SER SER SER GLY LYS VAL VAL LYS LEU PRO ASP SER LEU GLU GLU LEU ILE GLU ILE GLY GLU LYS LYS LEU GLY PHE VAL ALA THR LYS ILE LEU SER ARG GLU GLY ALA GLU ILE ASP ASP ILE ARG ILE ILE ARG ASP GLY ASP PHE LEU LEU LEU LYS VAL SER HIS HIS HIS
HIS HIS HIS

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	186912	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.762	Depositor
Minimum map value	-1.507	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.184	Depositor
Map size (Å)	369.6, 369.6, 369.6	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.825, 0.825, 0.825	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	0.96	0/3745	1.20	0/5094
1	B	0.96	0/3745	1.21	0/5094
1	C	0.96	0/3745	1.21	0/5094
1	D	0.96	0/3745	1.21	0/5094
All	All	0.96	0/14980	1.21	0/20376

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	3648	0	3646	118	0
1	B	3648	0	3646	114	0
1	C	3648	0	3646	99	0
1	D	3648	0	3646	105	0
All	All	14592	0	14584	385	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 13.

The worst 5 of 385 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:C:442:ASP:OD2	1:C:481:LYS:HD2	1.53	1.09
1:A:356:LEU:HD11	1:A:483:LEU:CD1	1.90	1.01
1:A:443:ILE:HG12	1:A:463:PHE:HZ	1.28	0.97
1:D:294:ILE:HG22	1:D:298:MET:HE2	1.51	0.92
1:B:294:ILE:HG22	1:B:298:MET:HE2	1.52	0.91

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	447/894 (50%)	416 (93%)	31 (7%)	0	100	100
1	B	447/894 (50%)	417 (93%)	30 (7%)	0	100	100
1	C	447/894 (50%)	418 (94%)	28 (6%)	1 (0%)	43	66
1	D	447/894 (50%)	415 (93%)	32 (7%)	0	100	100
All	All	1788/3576 (50%)	1666 (93%)	121 (7%)	1 (0%)	49	70

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	279	GLY

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	393/761 (52%)	347 (88%)	46 (12%)	5	11
1	B	393/761 (52%)	347 (88%)	46 (12%)	5	11
1	C	393/761 (52%)	351 (89%)	42 (11%)	6	14
1	D	393/761 (52%)	355 (90%)	38 (10%)	8	17
All	All	1572/3044 (52%)	1400 (89%)	172 (11%)	8	13

5 of 172 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	305	LEU
1	D	143	ASP
1	A	391	VAL
1	A	489	LEU
1	D	175	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	175	HIS
1	D	496	ASN
1	A	452	GLN
1	D	485	GLN
1	D	515	HIS

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)

There are no chain breaks in this entry.

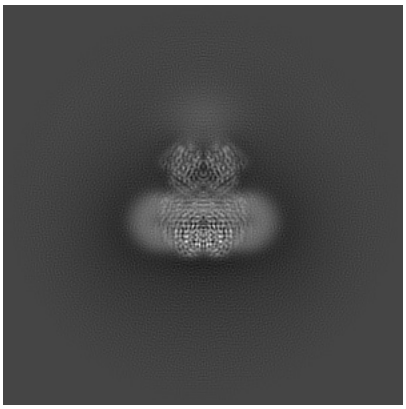
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-66432. These allow visual inspection of the internal detail of the map and identification of artifacts.

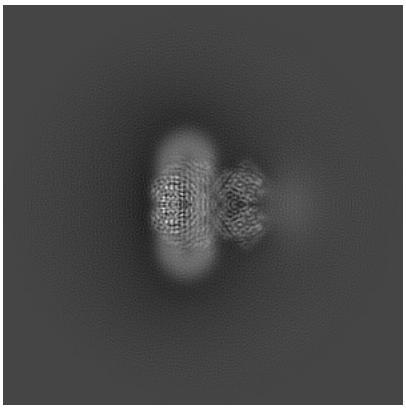
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

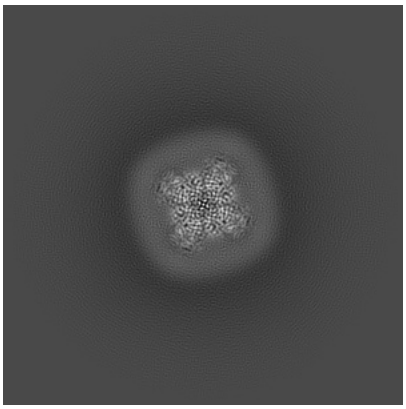
6.1.1 Primary map



X

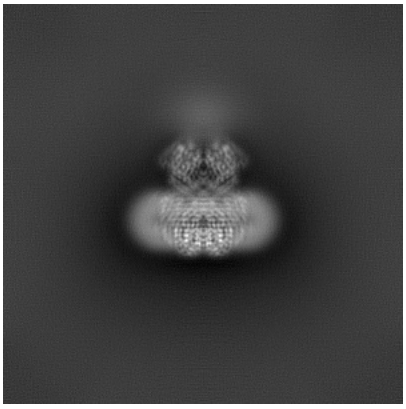


Y

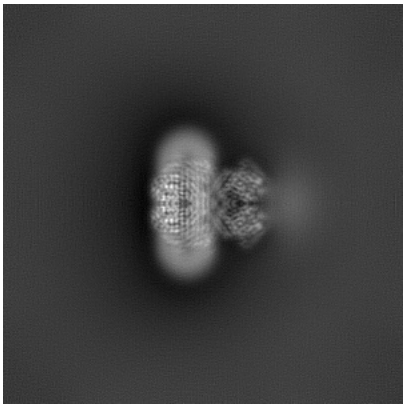


Z

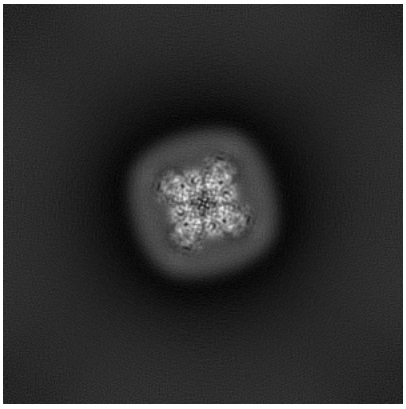
6.1.2 Raw map



X



Y

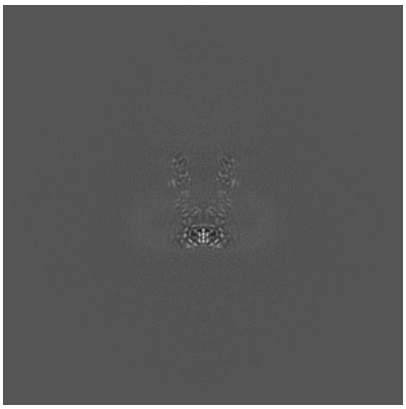


Z

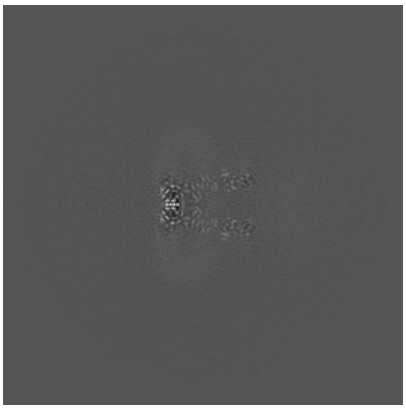
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

6.2.1 Primary map



X Index: 224



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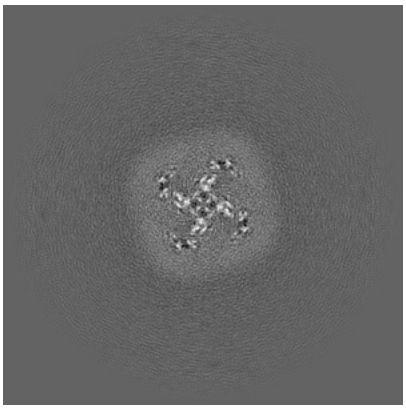
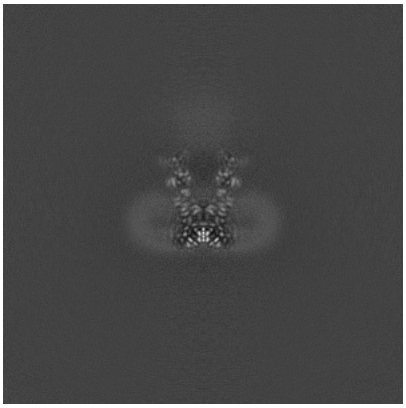
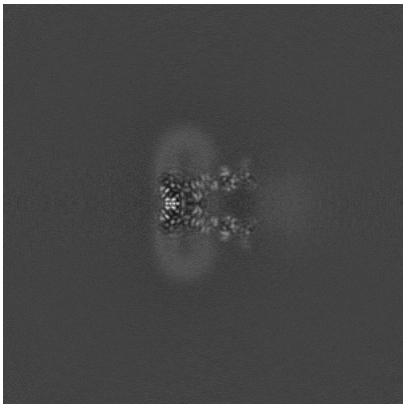


Z Index: 224

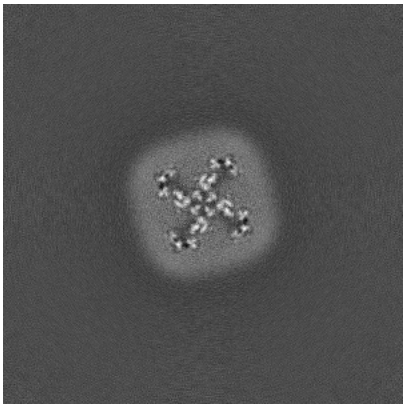
6.2.2 Raw map



X Index: 224



Y Index: 224

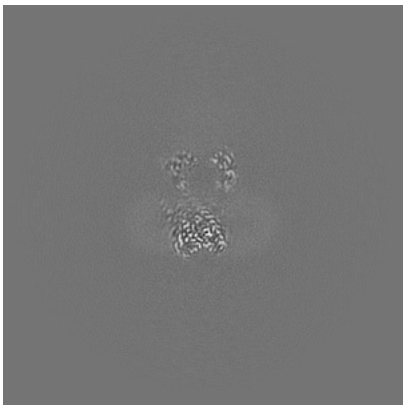


Z Index: 224

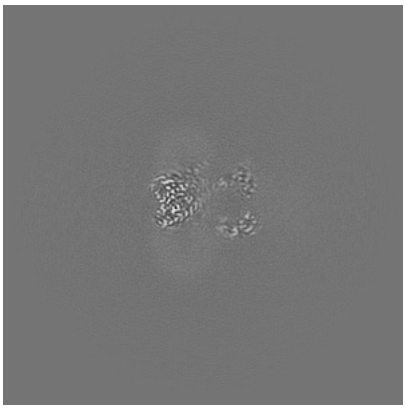
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

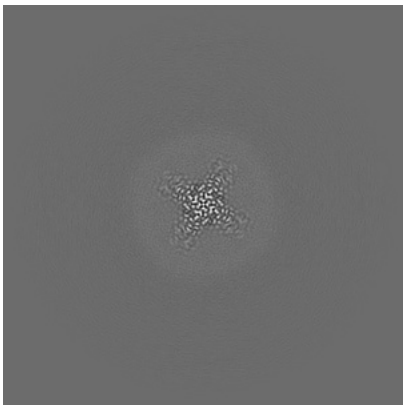
6.3.1 Primary map



X Index: 216

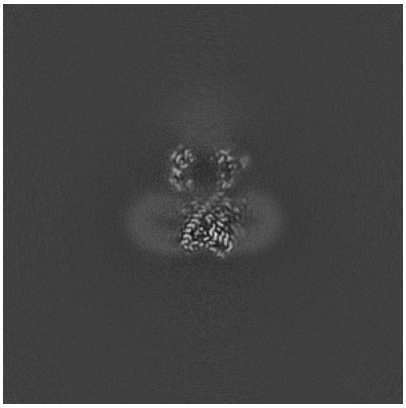


Y Index: 216

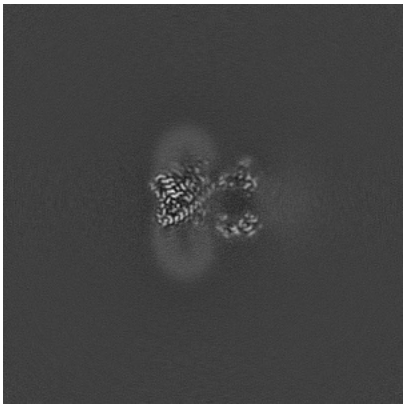


Z Index: 190

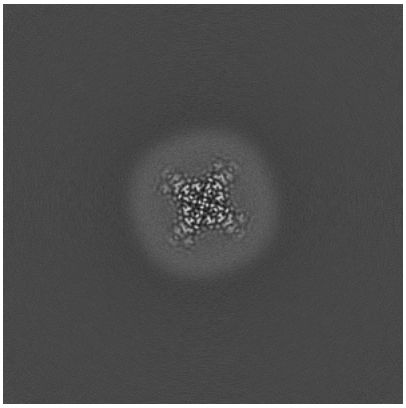
6.3.2 Raw map



X Index: 231



Y Index: 217

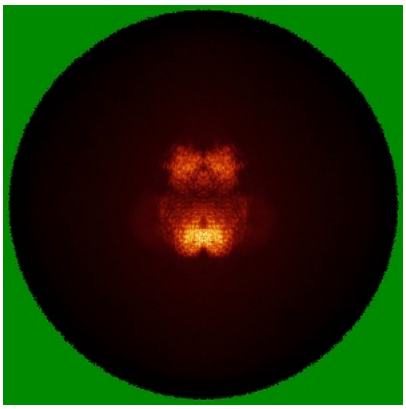


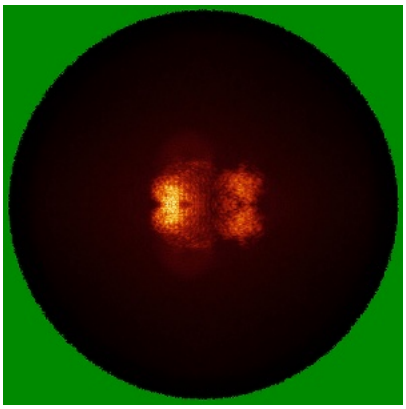
Z Index: 188

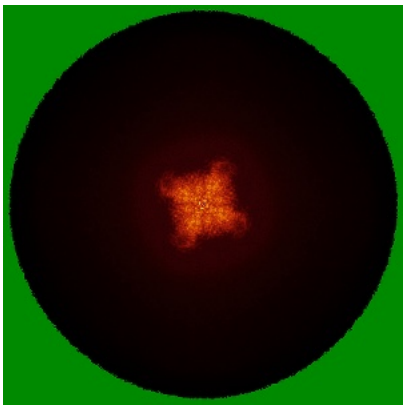
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

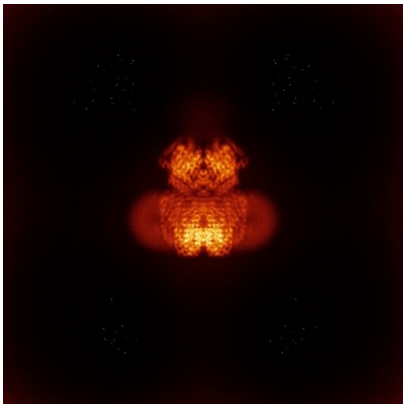
6.4.1 Primary map

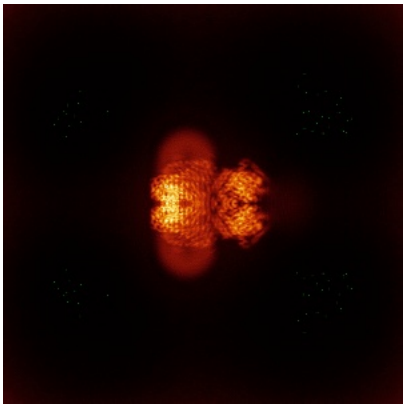

X

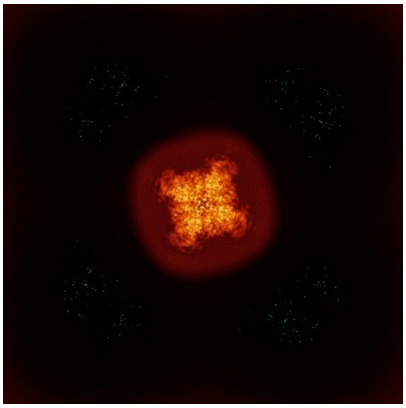

Y


Z

6.4.2 Raw map


X

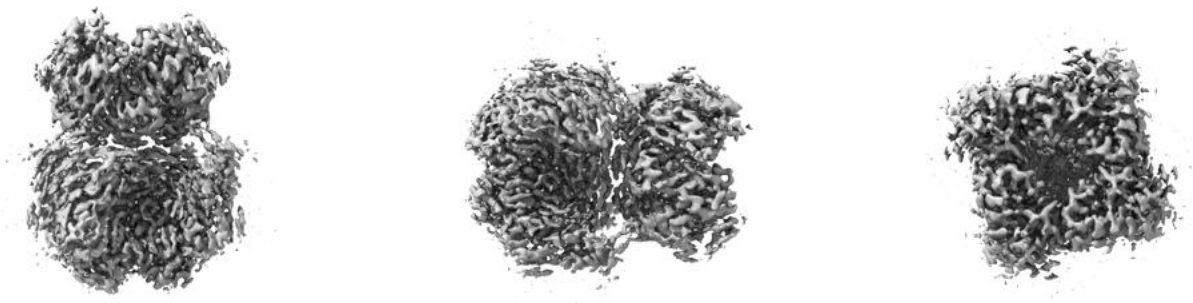

Y


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)

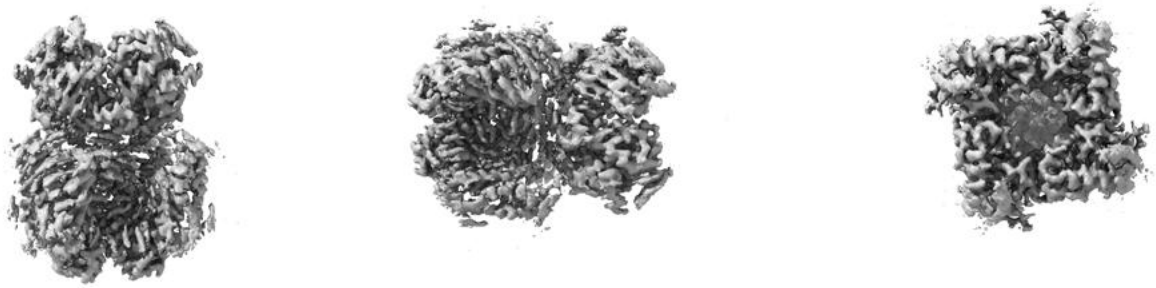
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.184. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

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.

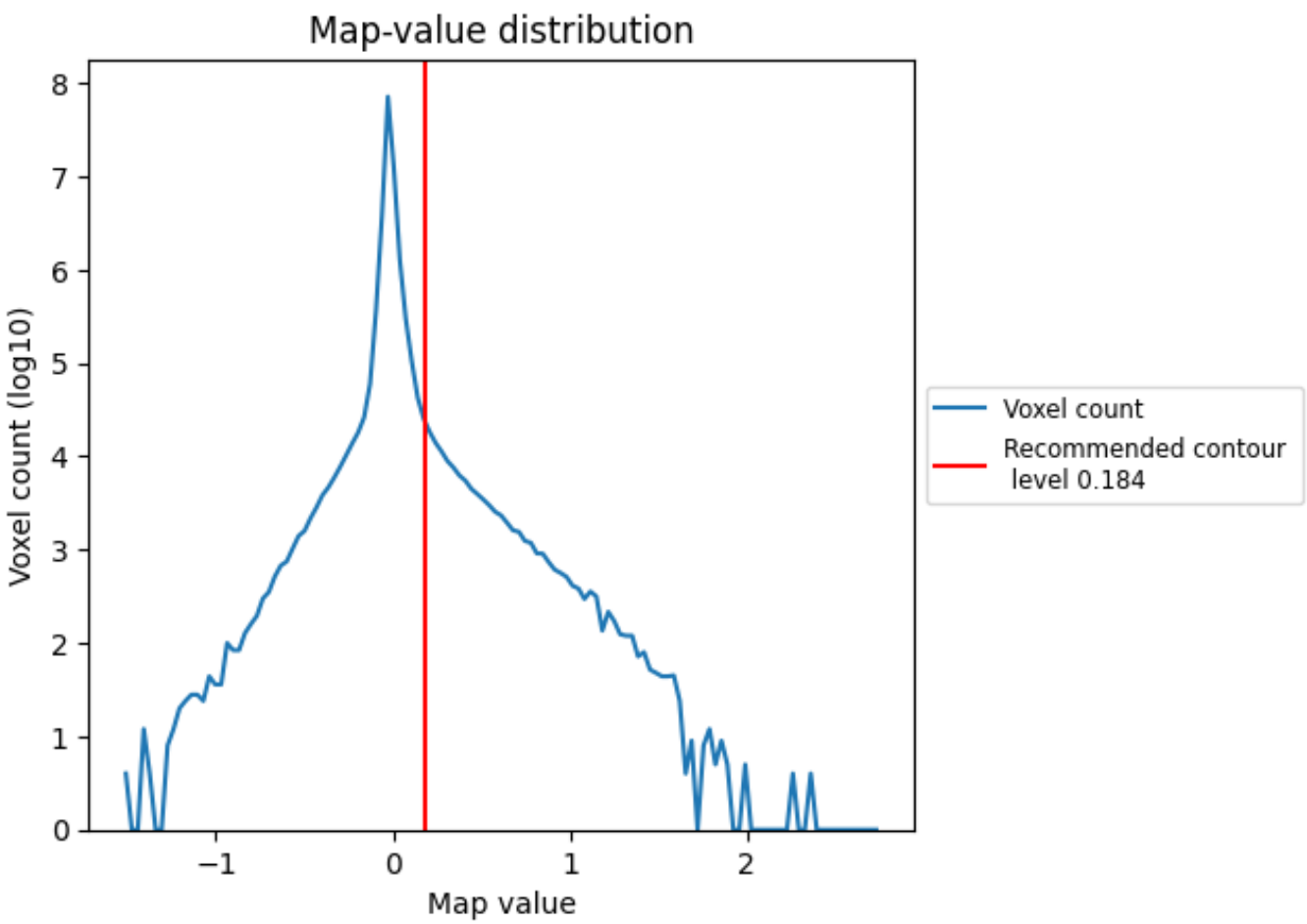
6.6 Mask visualisation (i)

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

7 Map analysis (i)

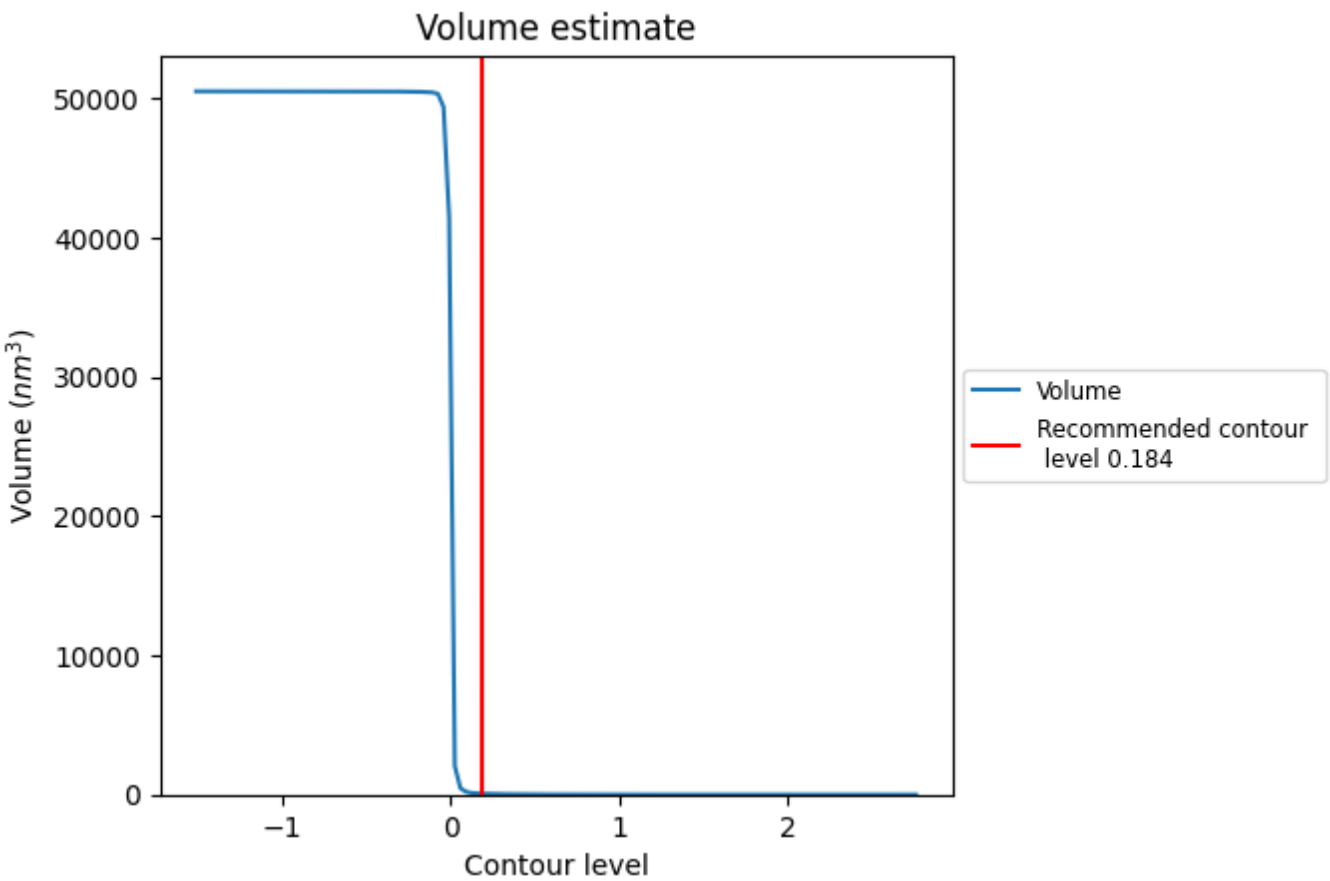
This section contains the results of statistical analysis of the map.

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.

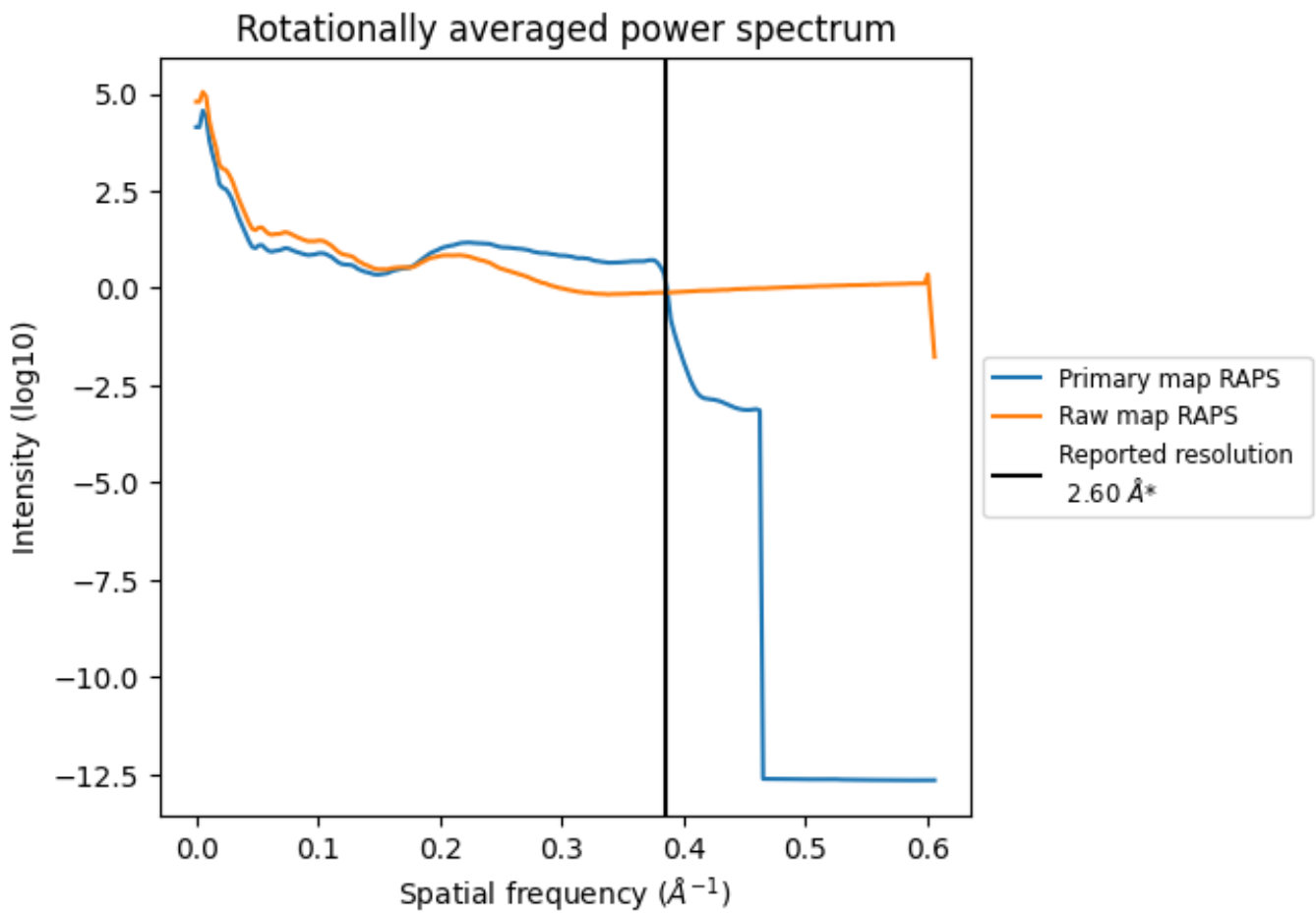
7.2 Volume estimate (i)



The volume at the recommended contour level is 70 nm^3; this corresponds to an approximate mass of 63 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)

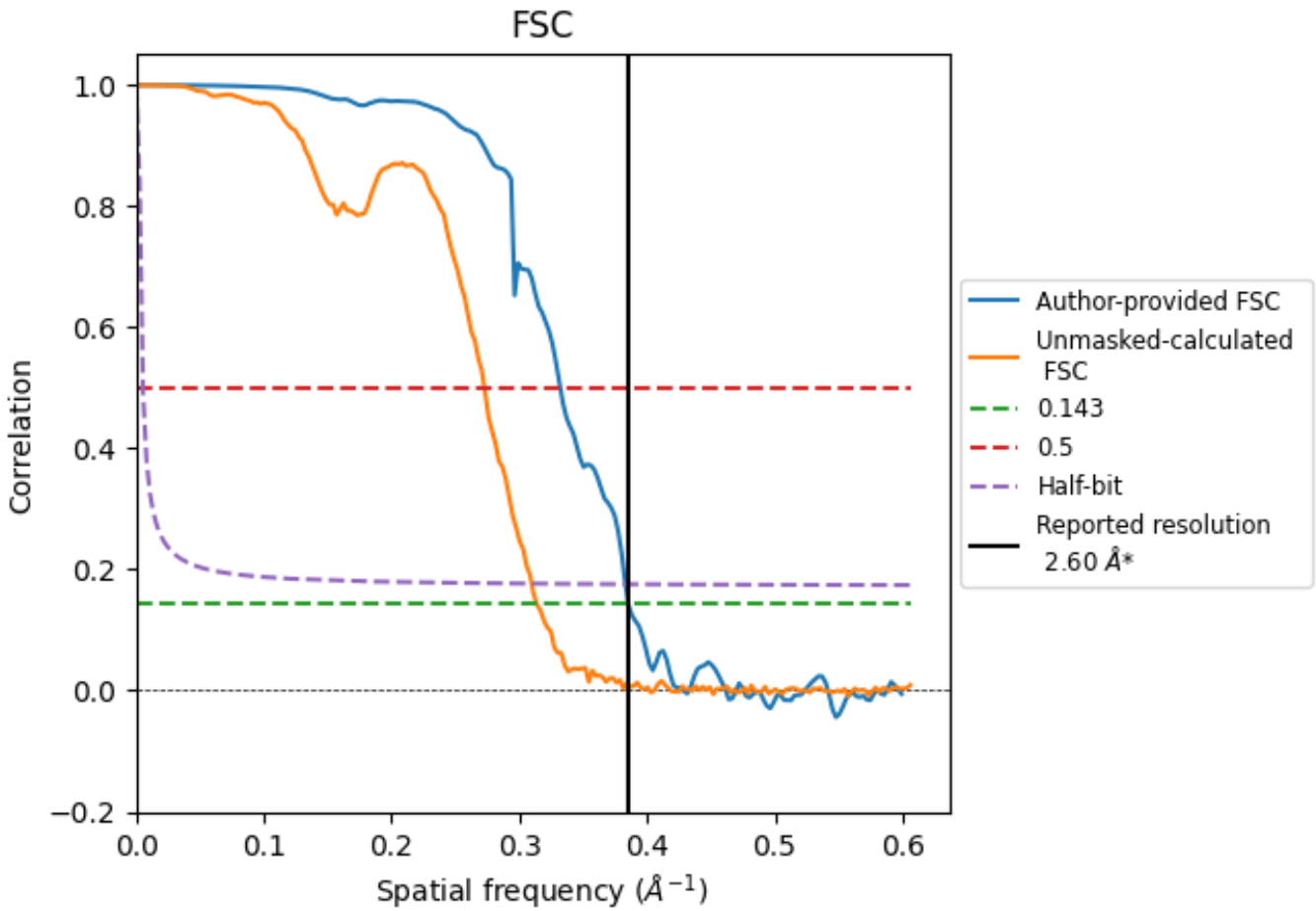


*Reported resolution corresponds to spatial frequency of 0.385 Å^{-1}

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 0.385 Å^{-1}

8.2 Resolution estimates (i)

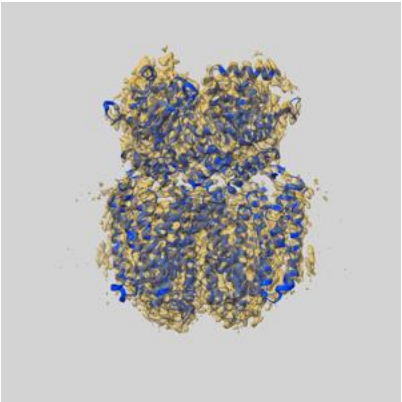
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.60	3.01	2.61
Unmasked-calculated*	3.19	3.67	3.23

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.19 differs from the reported value 2.6 by more than 10 %

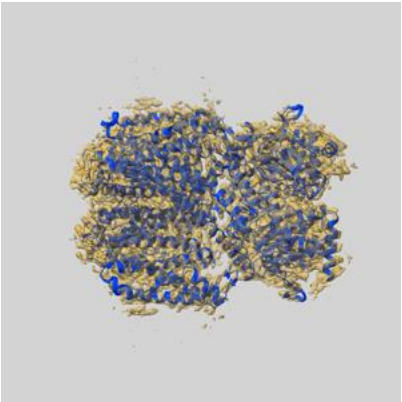
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-66432 and PDB model 9X0C. Per-residue inclusion information can be found in section 3 on page 5.

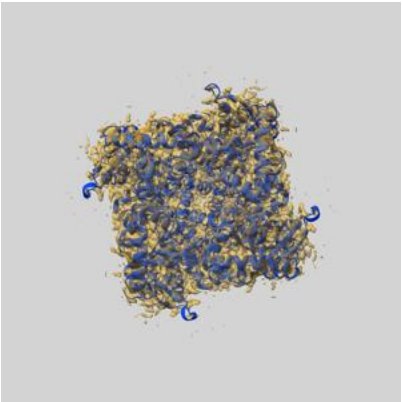
9.1 Map-model overlay (i)



X



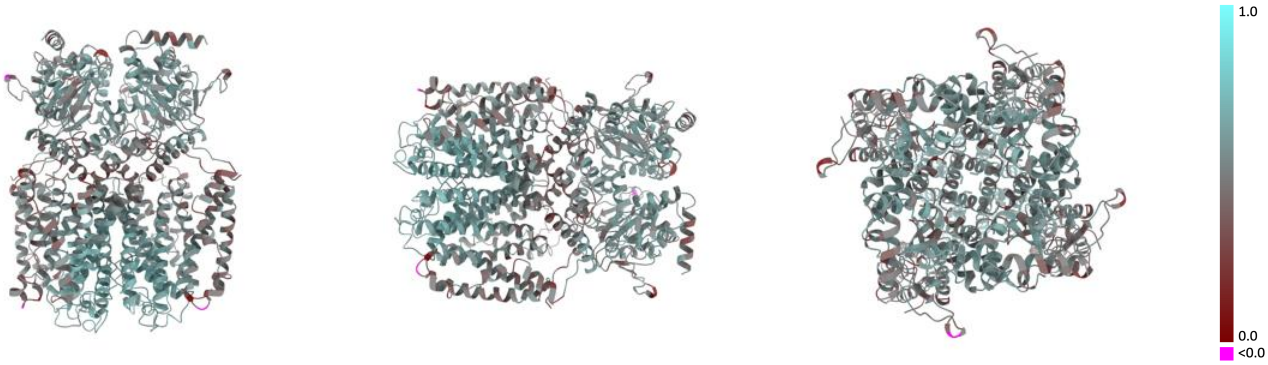
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.184 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.

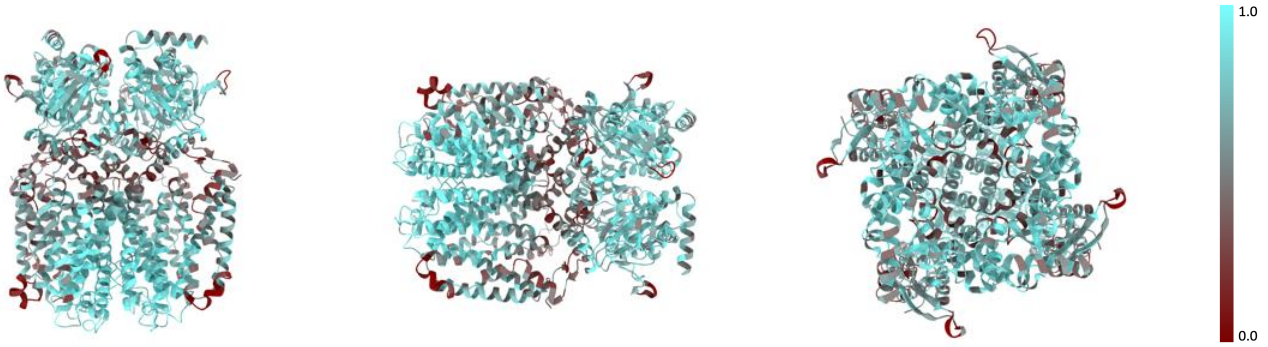
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

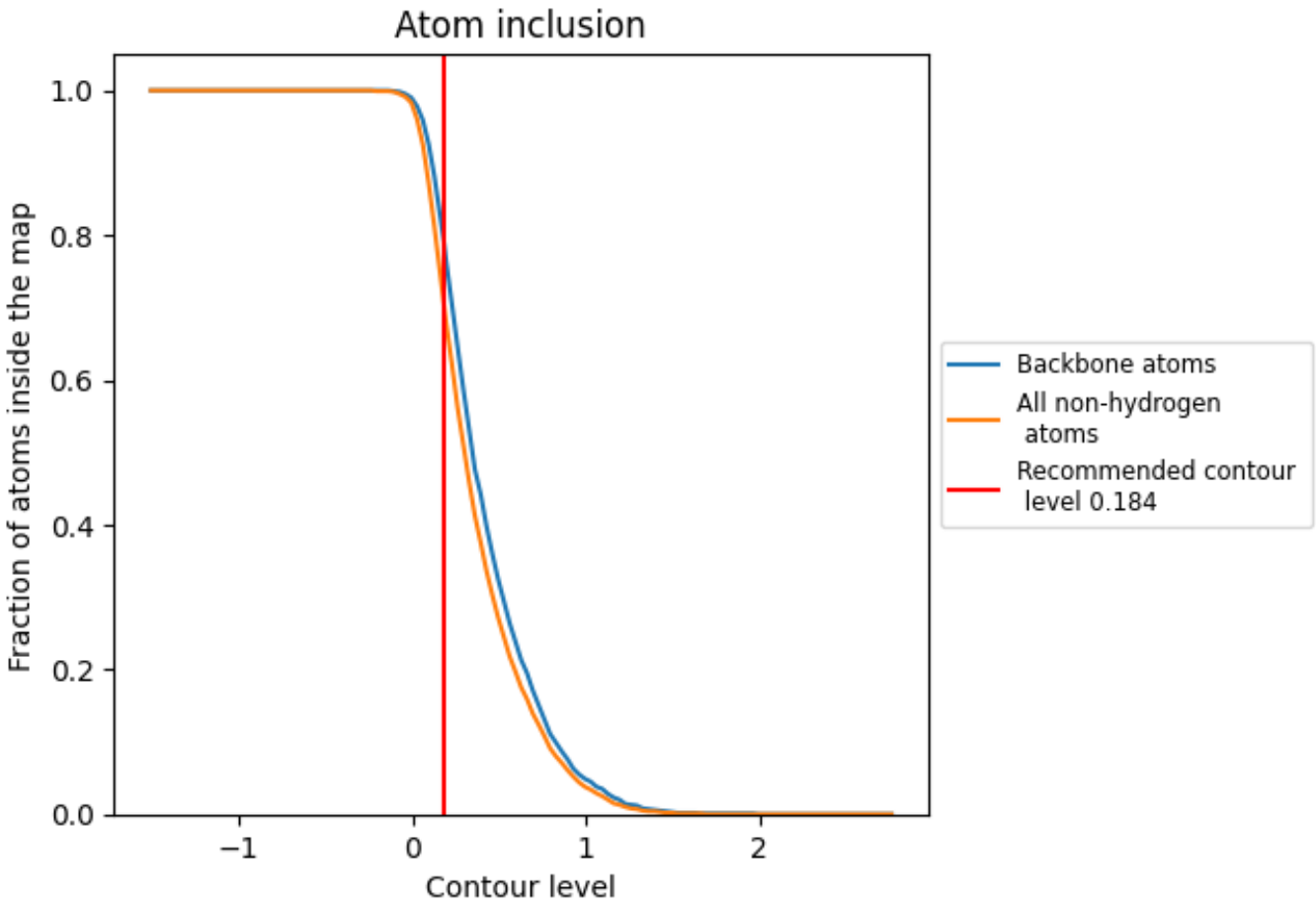
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.184).

9.4 Atom inclusion (i)



At the recommended contour level, 79% of all backbone atoms, 70% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.184) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7010	0.5290
A	0.7010	0.5300
B	0.6970	0.5260
C	0.7040	0.5300
D	0.7030	0.5300