



Full wwPDB EM Validation Report ⓘ

Mar 28, 2026 – 01:19 PM UTC

PDB ID : 8T17 / pdb_00008t17
EMDB ID : EMD-40956
Title : Cryo-EM structure of tetradecameric hub domain of CaMKII beta
Authors : Chien, C.-T.; Chiu, W.; Khan, S.
Deposited on : 2023-06-02
Resolution : 2.60 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

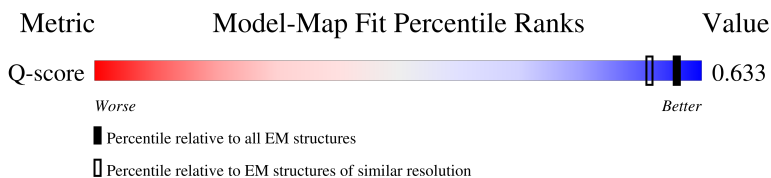
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 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.



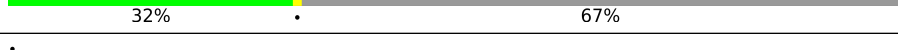
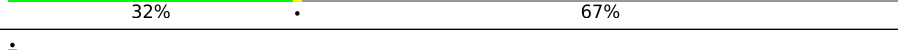
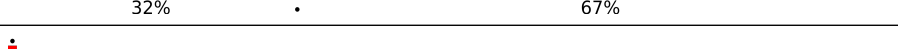
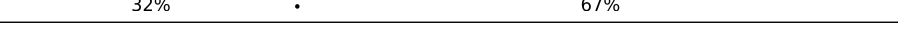
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	8728 (2.10 - 3.10)

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 $\leq 5\%$. 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	407	 32% 67%
1	B	407	 32% 67%
1	C	407	 32% 67%
1	D	407	 32% 67%

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Mol	Chain	Length	Quality of chain
1	E	407	
1	F	407	
1	G	407	
1	H	407	
1	I	407	
1	J	407	
1	K	407	
1	L	407	
1	M	407	
1	N	407	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 29554 atoms, of which 14462 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 Venus-tagged CaMKII Beta Association Domain.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	135	Total	C	H	N	O	S	0	0
			2111	679	1033	192	203	4		
1	B	135	Total	C	H	N	O	S	0	0
			2111	679	1033	192	203	4		
1	C	135	Total	C	H	N	O	S	0	0
			2111	679	1033	192	203	4		
1	D	135	Total	C	H	N	O	S	0	0
			2111	679	1033	192	203	4		
1	E	135	Total	C	H	N	O	S	0	0
			2111	679	1033	192	203	4		
1	F	135	Total	C	H	N	O	S	0	0
			2111	679	1033	192	203	4		
1	G	135	Total	C	H	N	O	S	0	0
			2111	679	1033	192	203	4		
1	H	135	Total	C	H	N	O	S	0	0
			2111	679	1033	192	203	4		
1	I	135	Total	C	H	N	O	S	0	0
			2111	679	1033	192	203	4		
1	J	135	Total	C	H	N	O	S	0	0
			2111	679	1033	192	203	4		
1	K	135	Total	C	H	N	O	S	0	0
			2111	679	1033	192	203	4		
1	L	135	Total	C	H	N	O	S	0	0
			2111	679	1033	192	203	4		
1	M	135	Total	C	H	N	O	S	0	0
			2111	679	1033	192	203	4		
1	N	135	Total	C	H	N	O	S	0	0
			2111	679	1033	192	203	4		

There are 658 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	136	MET	-	initiating methionine	UNP P42212
A	137	GLY	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
A	138	SER	-	expression tag	UNP P42212
A	139	SER	-	expression tag	UNP P42212
A	140	HIS	-	expression tag	UNP P42212
A	141	HIS	-	expression tag	UNP P42212
A	142	HIS	-	expression tag	UNP P42212
A	143	HIS	-	expression tag	UNP P42212
A	144	HIS	-	expression tag	UNP P42212
A	145	HIS	-	expression tag	UNP P42212
A	146	SER	-	expression tag	UNP P42212
A	147	SER	-	expression tag	UNP P42212
A	148	GLY	-	expression tag	UNP P42212
A	149	LEU	-	expression tag	UNP P42212
A	150	VAL	-	expression tag	UNP P42212
A	151	PRO	-	expression tag	UNP P42212
A	152	ARG	-	expression tag	UNP P42212
A	153	GLY	-	expression tag	UNP P42212
A	154	SER	-	expression tag	UNP P42212
A	155	HIS	-	expression tag	UNP P42212
A	156	VAL	-	expression tag	UNP P42212
A	201	LEU	PHE	conflict	UNP P42212
A	219	LEU	PHE	conflict	UNP P42212
A	220	GLY	SER	conflict	UNP P42212
A	223	LEU	VAL	conflict	UNP P42212
A	227	ALA	SER	conflict	UNP P42212
A	308	THR	MET	conflict	UNP P42212
A	318	ALA	VAL	conflict	UNP P42212
A	330	GLY	SER	conflict	UNP P42212
A	358	TYR	THR	conflict	UNP P42212
A	361	LYS	ALA	conflict	UNP P42212
A	386	LEU	HIS	conflict	UNP P42212
A	394	SER	-	linker	UNP P42212
A	395	GLY	-	linker	UNP P42212
A	396	LEU	-	linker	UNP P42212
A	397	ARG	-	linker	UNP P42212
A	398	SER	-	linker	UNP P42212
A	399	ARG	-	linker	UNP P42212
A	400	ALA	-	linker	UNP P42212
A	401	GLN	-	linker	UNP P42212
A	402	ALA	-	linker	UNP P42212
A	403	SER	-	linker	UNP P42212
A	404	ASN	-	linker	UNP P42212
A	405	SER	-	linker	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
A	406	ALA	-	linker	UNP P42212
A	407	VAL	-	linker	UNP P42212
A	408	ASP	-	linker	UNP P42212
B	136	MET	-	initiating methionine	UNP P42212
B	137	GLY	-	expression tag	UNP P42212
B	138	SER	-	expression tag	UNP P42212
B	139	SER	-	expression tag	UNP P42212
B	140	HIS	-	expression tag	UNP P42212
B	141	HIS	-	expression tag	UNP P42212
B	142	HIS	-	expression tag	UNP P42212
B	143	HIS	-	expression tag	UNP P42212
B	144	HIS	-	expression tag	UNP P42212
B	145	HIS	-	expression tag	UNP P42212
B	146	SER	-	expression tag	UNP P42212
B	147	SER	-	expression tag	UNP P42212
B	148	GLY	-	expression tag	UNP P42212
B	149	LEU	-	expression tag	UNP P42212
B	150	VAL	-	expression tag	UNP P42212
B	151	PRO	-	expression tag	UNP P42212
B	152	ARG	-	expression tag	UNP P42212
B	153	GLY	-	expression tag	UNP P42212
B	154	SER	-	expression tag	UNP P42212
B	155	HIS	-	expression tag	UNP P42212
B	156	VAL	-	expression tag	UNP P42212
B	201	LEU	PHE	conflict	UNP P42212
B	219	LEU	PHE	conflict	UNP P42212
B	220	GLY	SER	conflict	UNP P42212
B	223	LEU	VAL	conflict	UNP P42212
B	227	ALA	SER	conflict	UNP P42212
B	308	THR	MET	conflict	UNP P42212
B	318	ALA	VAL	conflict	UNP P42212
B	330	GLY	SER	conflict	UNP P42212
B	358	TYR	THR	conflict	UNP P42212
B	361	LYS	ALA	conflict	UNP P42212
B	386	LEU	HIS	conflict	UNP P42212
B	394	SER	-	linker	UNP P42212
B	395	GLY	-	linker	UNP P42212
B	396	LEU	-	linker	UNP P42212
B	397	ARG	-	linker	UNP P42212
B	398	SER	-	linker	UNP P42212
B	399	ARG	-	linker	UNP P42212
B	400	ALA	-	linker	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
B	401	GLN	-	linker	UNP P42212
B	402	ALA	-	linker	UNP P42212
B	403	SER	-	linker	UNP P42212
B	404	ASN	-	linker	UNP P42212
B	405	SER	-	linker	UNP P42212
B	406	ALA	-	linker	UNP P42212
B	407	VAL	-	linker	UNP P42212
B	408	ASP	-	linker	UNP P42212
C	136	MET	-	initiating methionine	UNP P42212
C	137	GLY	-	expression tag	UNP P42212
C	138	SER	-	expression tag	UNP P42212
C	139	SER	-	expression tag	UNP P42212
C	140	HIS	-	expression tag	UNP P42212
C	141	HIS	-	expression tag	UNP P42212
C	142	HIS	-	expression tag	UNP P42212
C	143	HIS	-	expression tag	UNP P42212
C	144	HIS	-	expression tag	UNP P42212
C	145	HIS	-	expression tag	UNP P42212
C	146	SER	-	expression tag	UNP P42212
C	147	SER	-	expression tag	UNP P42212
C	148	GLY	-	expression tag	UNP P42212
C	149	LEU	-	expression tag	UNP P42212
C	150	VAL	-	expression tag	UNP P42212
C	151	PRO	-	expression tag	UNP P42212
C	152	ARG	-	expression tag	UNP P42212
C	153	GLY	-	expression tag	UNP P42212
C	154	SER	-	expression tag	UNP P42212
C	155	HIS	-	expression tag	UNP P42212
C	156	VAL	-	expression tag	UNP P42212
C	201	LEU	PHE	conflict	UNP P42212
C	219	LEU	PHE	conflict	UNP P42212
C	220	GLY	SER	conflict	UNP P42212
C	223	LEU	VAL	conflict	UNP P42212
C	227	ALA	SER	conflict	UNP P42212
C	308	THR	MET	conflict	UNP P42212
C	318	ALA	VAL	conflict	UNP P42212
C	330	GLY	SER	conflict	UNP P42212
C	358	TYR	THR	conflict	UNP P42212
C	361	LYS	ALA	conflict	UNP P42212
C	386	LEU	HIS	conflict	UNP P42212
C	394	SER	-	linker	UNP P42212
C	395	GLY	-	linker	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
C	396	LEU	-	linker	UNP P42212
C	397	ARG	-	linker	UNP P42212
C	398	SER	-	linker	UNP P42212
C	399	ARG	-	linker	UNP P42212
C	400	ALA	-	linker	UNP P42212
C	401	GLN	-	linker	UNP P42212
C	402	ALA	-	linker	UNP P42212
C	403	SER	-	linker	UNP P42212
C	404	ASN	-	linker	UNP P42212
C	405	SER	-	linker	UNP P42212
C	406	ALA	-	linker	UNP P42212
C	407	VAL	-	linker	UNP P42212
C	408	ASP	-	linker	UNP P42212
D	136	MET	-	initiating methionine	UNP P42212
D	137	GLY	-	expression tag	UNP P42212
D	138	SER	-	expression tag	UNP P42212
D	139	SER	-	expression tag	UNP P42212
D	140	HIS	-	expression tag	UNP P42212
D	141	HIS	-	expression tag	UNP P42212
D	142	HIS	-	expression tag	UNP P42212
D	143	HIS	-	expression tag	UNP P42212
D	144	HIS	-	expression tag	UNP P42212
D	145	HIS	-	expression tag	UNP P42212
D	146	SER	-	expression tag	UNP P42212
D	147	SER	-	expression tag	UNP P42212
D	148	GLY	-	expression tag	UNP P42212
D	149	LEU	-	expression tag	UNP P42212
D	150	VAL	-	expression tag	UNP P42212
D	151	PRO	-	expression tag	UNP P42212
D	152	ARG	-	expression tag	UNP P42212
D	153	GLY	-	expression tag	UNP P42212
D	154	SER	-	expression tag	UNP P42212
D	155	HIS	-	expression tag	UNP P42212
D	156	VAL	-	expression tag	UNP P42212
D	201	LEU	PHE	conflict	UNP P42212
D	219	LEU	PHE	conflict	UNP P42212
D	220	GLY	SER	conflict	UNP P42212
D	223	LEU	VAL	conflict	UNP P42212
D	227	ALA	SER	conflict	UNP P42212
D	308	THR	MET	conflict	UNP P42212
D	318	ALA	VAL	conflict	UNP P42212
D	330	GLY	SER	conflict	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
D	358	TYR	THR	conflict	UNP P42212
D	361	LYS	ALA	conflict	UNP P42212
D	386	LEU	HIS	conflict	UNP P42212
D	394	SER	-	linker	UNP P42212
D	395	GLY	-	linker	UNP P42212
D	396	LEU	-	linker	UNP P42212
D	397	ARG	-	linker	UNP P42212
D	398	SER	-	linker	UNP P42212
D	399	ARG	-	linker	UNP P42212
D	400	ALA	-	linker	UNP P42212
D	401	GLN	-	linker	UNP P42212
D	402	ALA	-	linker	UNP P42212
D	403	SER	-	linker	UNP P42212
D	404	ASN	-	linker	UNP P42212
D	405	SER	-	linker	UNP P42212
D	406	ALA	-	linker	UNP P42212
D	407	VAL	-	linker	UNP P42212
D	408	ASP	-	linker	UNP P42212
E	136	MET	-	initiating methionine	UNP P42212
E	137	GLY	-	expression tag	UNP P42212
E	138	SER	-	expression tag	UNP P42212
E	139	SER	-	expression tag	UNP P42212
E	140	HIS	-	expression tag	UNP P42212
E	141	HIS	-	expression tag	UNP P42212
E	142	HIS	-	expression tag	UNP P42212
E	143	HIS	-	expression tag	UNP P42212
E	144	HIS	-	expression tag	UNP P42212
E	145	HIS	-	expression tag	UNP P42212
E	146	SER	-	expression tag	UNP P42212
E	147	SER	-	expression tag	UNP P42212
E	148	GLY	-	expression tag	UNP P42212
E	149	LEU	-	expression tag	UNP P42212
E	150	VAL	-	expression tag	UNP P42212
E	151	PRO	-	expression tag	UNP P42212
E	152	ARG	-	expression tag	UNP P42212
E	153	GLY	-	expression tag	UNP P42212
E	154	SER	-	expression tag	UNP P42212
E	155	HIS	-	expression tag	UNP P42212
E	156	VAL	-	expression tag	UNP P42212
E	201	LEU	PHE	conflict	UNP P42212
E	219	LEU	PHE	conflict	UNP P42212
E	220	GLY	SER	conflict	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
E	223	LEU	VAL	conflict	UNP P42212
E	227	ALA	SER	conflict	UNP P42212
E	308	THR	MET	conflict	UNP P42212
E	318	ALA	VAL	conflict	UNP P42212
E	330	GLY	SER	conflict	UNP P42212
E	358	TYR	THR	conflict	UNP P42212
E	361	LYS	ALA	conflict	UNP P42212
E	386	LEU	HIS	conflict	UNP P42212
E	394	SER	-	linker	UNP P42212
E	395	GLY	-	linker	UNP P42212
E	396	LEU	-	linker	UNP P42212
E	397	ARG	-	linker	UNP P42212
E	398	SER	-	linker	UNP P42212
E	399	ARG	-	linker	UNP P42212
E	400	ALA	-	linker	UNP P42212
E	401	GLN	-	linker	UNP P42212
E	402	ALA	-	linker	UNP P42212
E	403	SER	-	linker	UNP P42212
E	404	ASN	-	linker	UNP P42212
E	405	SER	-	linker	UNP P42212
E	406	ALA	-	linker	UNP P42212
E	407	VAL	-	linker	UNP P42212
E	408	ASP	-	linker	UNP P42212
F	136	MET	-	initiating methionine	UNP P42212
F	137	GLY	-	expression tag	UNP P42212
F	138	SER	-	expression tag	UNP P42212
F	139	SER	-	expression tag	UNP P42212
F	140	HIS	-	expression tag	UNP P42212
F	141	HIS	-	expression tag	UNP P42212
F	142	HIS	-	expression tag	UNP P42212
F	143	HIS	-	expression tag	UNP P42212
F	144	HIS	-	expression tag	UNP P42212
F	145	HIS	-	expression tag	UNP P42212
F	146	SER	-	expression tag	UNP P42212
F	147	SER	-	expression tag	UNP P42212
F	148	GLY	-	expression tag	UNP P42212
F	149	LEU	-	expression tag	UNP P42212
F	150	VAL	-	expression tag	UNP P42212
F	151	PRO	-	expression tag	UNP P42212
F	152	ARG	-	expression tag	UNP P42212
F	153	GLY	-	expression tag	UNP P42212
F	154	SER	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
F	155	HIS	-	expression tag	UNP P42212
F	156	VAL	-	expression tag	UNP P42212
F	201	LEU	PHE	conflict	UNP P42212
F	219	LEU	PHE	conflict	UNP P42212
F	220	GLY	SER	conflict	UNP P42212
F	223	LEU	VAL	conflict	UNP P42212
F	227	ALA	SER	conflict	UNP P42212
F	308	THR	MET	conflict	UNP P42212
F	318	ALA	VAL	conflict	UNP P42212
F	330	GLY	SER	conflict	UNP P42212
F	358	TYR	THR	conflict	UNP P42212
F	361	LYS	ALA	conflict	UNP P42212
F	386	LEU	HIS	conflict	UNP P42212
F	394	SER	-	linker	UNP P42212
F	395	GLY	-	linker	UNP P42212
F	396	LEU	-	linker	UNP P42212
F	397	ARG	-	linker	UNP P42212
F	398	SER	-	linker	UNP P42212
F	399	ARG	-	linker	UNP P42212
F	400	ALA	-	linker	UNP P42212
F	401	GLN	-	linker	UNP P42212
F	402	ALA	-	linker	UNP P42212
F	403	SER	-	linker	UNP P42212
F	404	ASN	-	linker	UNP P42212
F	405	SER	-	linker	UNP P42212
F	406	ALA	-	linker	UNP P42212
F	407	VAL	-	linker	UNP P42212
F	408	ASP	-	linker	UNP P42212
G	136	MET	-	initiating methionine	UNP P42212
G	137	GLY	-	expression tag	UNP P42212
G	138	SER	-	expression tag	UNP P42212
G	139	SER	-	expression tag	UNP P42212
G	140	HIS	-	expression tag	UNP P42212
G	141	HIS	-	expression tag	UNP P42212
G	142	HIS	-	expression tag	UNP P42212
G	143	HIS	-	expression tag	UNP P42212
G	144	HIS	-	expression tag	UNP P42212
G	145	HIS	-	expression tag	UNP P42212
G	146	SER	-	expression tag	UNP P42212
G	147	SER	-	expression tag	UNP P42212
G	148	GLY	-	expression tag	UNP P42212
G	149	LEU	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
G	150	VAL	-	expression tag	UNP P42212
G	151	PRO	-	expression tag	UNP P42212
G	152	ARG	-	expression tag	UNP P42212
G	153	GLY	-	expression tag	UNP P42212
G	154	SER	-	expression tag	UNP P42212
G	155	HIS	-	expression tag	UNP P42212
G	156	VAL	-	expression tag	UNP P42212
G	201	LEU	PHE	conflict	UNP P42212
G	219	LEU	PHE	conflict	UNP P42212
G	220	GLY	SER	conflict	UNP P42212
G	223	LEU	VAL	conflict	UNP P42212
G	227	ALA	SER	conflict	UNP P42212
G	308	THR	MET	conflict	UNP P42212
G	318	ALA	VAL	conflict	UNP P42212
G	330	GLY	SER	conflict	UNP P42212
G	358	TYR	THR	conflict	UNP P42212
G	361	LYS	ALA	conflict	UNP P42212
G	386	LEU	HIS	conflict	UNP P42212
G	394	SER	-	linker	UNP P42212
G	395	GLY	-	linker	UNP P42212
G	396	LEU	-	linker	UNP P42212
G	397	ARG	-	linker	UNP P42212
G	398	SER	-	linker	UNP P42212
G	399	ARG	-	linker	UNP P42212
G	400	ALA	-	linker	UNP P42212
G	401	GLN	-	linker	UNP P42212
G	402	ALA	-	linker	UNP P42212
G	403	SER	-	linker	UNP P42212
G	404	ASN	-	linker	UNP P42212
G	405	SER	-	linker	UNP P42212
G	406	ALA	-	linker	UNP P42212
G	407	VAL	-	linker	UNP P42212
G	408	ASP	-	linker	UNP P42212
H	136	MET	-	initiating methionine	UNP P42212
H	137	GLY	-	expression tag	UNP P42212
H	138	SER	-	expression tag	UNP P42212
H	139	SER	-	expression tag	UNP P42212
H	140	HIS	-	expression tag	UNP P42212
H	141	HIS	-	expression tag	UNP P42212
H	142	HIS	-	expression tag	UNP P42212
H	143	HIS	-	expression tag	UNP P42212
H	144	HIS	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
H	145	HIS	-	expression tag	UNP P42212
H	146	SER	-	expression tag	UNP P42212
H	147	SER	-	expression tag	UNP P42212
H	148	GLY	-	expression tag	UNP P42212
H	149	LEU	-	expression tag	UNP P42212
H	150	VAL	-	expression tag	UNP P42212
H	151	PRO	-	expression tag	UNP P42212
H	152	ARG	-	expression tag	UNP P42212
H	153	GLY	-	expression tag	UNP P42212
H	154	SER	-	expression tag	UNP P42212
H	155	HIS	-	expression tag	UNP P42212
H	156	VAL	-	expression tag	UNP P42212
H	201	LEU	PHE	conflict	UNP P42212
H	219	LEU	PHE	conflict	UNP P42212
H	220	GLY	SER	conflict	UNP P42212
H	223	LEU	VAL	conflict	UNP P42212
H	227	ALA	SER	conflict	UNP P42212
H	308	THR	MET	conflict	UNP P42212
H	318	ALA	VAL	conflict	UNP P42212
H	330	GLY	SER	conflict	UNP P42212
H	358	TYR	THR	conflict	UNP P42212
H	361	LYS	ALA	conflict	UNP P42212
H	386	LEU	HIS	conflict	UNP P42212
H	394	SER	-	linker	UNP P42212
H	395	GLY	-	linker	UNP P42212
H	396	LEU	-	linker	UNP P42212
H	397	ARG	-	linker	UNP P42212
H	398	SER	-	linker	UNP P42212
H	399	ARG	-	linker	UNP P42212
H	400	ALA	-	linker	UNP P42212
H	401	GLN	-	linker	UNP P42212
H	402	ALA	-	linker	UNP P42212
H	403	SER	-	linker	UNP P42212
H	404	ASN	-	linker	UNP P42212
H	405	SER	-	linker	UNP P42212
H	406	ALA	-	linker	UNP P42212
H	407	VAL	-	linker	UNP P42212
H	408	ASP	-	linker	UNP P42212
I	136	MET	-	initiating methionine	UNP P42212
I	137	GLY	-	expression tag	UNP P42212
I	138	SER	-	expression tag	UNP P42212
I	139	SER	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
I	140	HIS	-	expression tag	UNP P42212
I	141	HIS	-	expression tag	UNP P42212
I	142	HIS	-	expression tag	UNP P42212
I	143	HIS	-	expression tag	UNP P42212
I	144	HIS	-	expression tag	UNP P42212
I	145	HIS	-	expression tag	UNP P42212
I	146	SER	-	expression tag	UNP P42212
I	147	SER	-	expression tag	UNP P42212
I	148	GLY	-	expression tag	UNP P42212
I	149	LEU	-	expression tag	UNP P42212
I	150	VAL	-	expression tag	UNP P42212
I	151	PRO	-	expression tag	UNP P42212
I	152	ARG	-	expression tag	UNP P42212
I	153	GLY	-	expression tag	UNP P42212
I	154	SER	-	expression tag	UNP P42212
I	155	HIS	-	expression tag	UNP P42212
I	156	VAL	-	expression tag	UNP P42212
I	201	LEU	PHE	conflict	UNP P42212
I	219	LEU	PHE	conflict	UNP P42212
I	220	GLY	SER	conflict	UNP P42212
I	223	LEU	VAL	conflict	UNP P42212
I	227	ALA	SER	conflict	UNP P42212
I	308	THR	MET	conflict	UNP P42212
I	318	ALA	VAL	conflict	UNP P42212
I	330	GLY	SER	conflict	UNP P42212
I	358	TYR	THR	conflict	UNP P42212
I	361	LYS	ALA	conflict	UNP P42212
I	386	LEU	HIS	conflict	UNP P42212
I	394	SER	-	linker	UNP P42212
I	395	GLY	-	linker	UNP P42212
I	396	LEU	-	linker	UNP P42212
I	397	ARG	-	linker	UNP P42212
I	398	SER	-	linker	UNP P42212
I	399	ARG	-	linker	UNP P42212
I	400	ALA	-	linker	UNP P42212
I	401	GLN	-	linker	UNP P42212
I	402	ALA	-	linker	UNP P42212
I	403	SER	-	linker	UNP P42212
I	404	ASN	-	linker	UNP P42212
I	405	SER	-	linker	UNP P42212
I	406	ALA	-	linker	UNP P42212
I	407	VAL	-	linker	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
I	408	ASP	-	linker	UNP P42212
J	136	MET	-	initiating methionine	UNP P42212
J	137	GLY	-	expression tag	UNP P42212
J	138	SER	-	expression tag	UNP P42212
J	139	SER	-	expression tag	UNP P42212
J	140	HIS	-	expression tag	UNP P42212
J	141	HIS	-	expression tag	UNP P42212
J	142	HIS	-	expression tag	UNP P42212
J	143	HIS	-	expression tag	UNP P42212
J	144	HIS	-	expression tag	UNP P42212
J	145	HIS	-	expression tag	UNP P42212
J	146	SER	-	expression tag	UNP P42212
J	147	SER	-	expression tag	UNP P42212
J	148	GLY	-	expression tag	UNP P42212
J	149	LEU	-	expression tag	UNP P42212
J	150	VAL	-	expression tag	UNP P42212
J	151	PRO	-	expression tag	UNP P42212
J	152	ARG	-	expression tag	UNP P42212
J	153	GLY	-	expression tag	UNP P42212
J	154	SER	-	expression tag	UNP P42212
J	155	HIS	-	expression tag	UNP P42212
J	156	VAL	-	expression tag	UNP P42212
J	201	LEU	PHE	conflict	UNP P42212
J	219	LEU	PHE	conflict	UNP P42212
J	220	GLY	SER	conflict	UNP P42212
J	223	LEU	VAL	conflict	UNP P42212
J	227	ALA	SER	conflict	UNP P42212
J	308	THR	MET	conflict	UNP P42212
J	318	ALA	VAL	conflict	UNP P42212
J	330	GLY	SER	conflict	UNP P42212
J	358	TYR	THR	conflict	UNP P42212
J	361	LYS	ALA	conflict	UNP P42212
J	386	LEU	HIS	conflict	UNP P42212
J	394	SER	-	linker	UNP P42212
J	395	GLY	-	linker	UNP P42212
J	396	LEU	-	linker	UNP P42212
J	397	ARG	-	linker	UNP P42212
J	398	SER	-	linker	UNP P42212
J	399	ARG	-	linker	UNP P42212
J	400	ALA	-	linker	UNP P42212
J	401	GLN	-	linker	UNP P42212
J	402	ALA	-	linker	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
J	403	SER	-	linker	UNP P42212
J	404	ASN	-	linker	UNP P42212
J	405	SER	-	linker	UNP P42212
J	406	ALA	-	linker	UNP P42212
J	407	VAL	-	linker	UNP P42212
J	408	ASP	-	linker	UNP P42212
K	136	MET	-	initiating methionine	UNP P42212
K	137	GLY	-	expression tag	UNP P42212
K	138	SER	-	expression tag	UNP P42212
K	139	SER	-	expression tag	UNP P42212
K	140	HIS	-	expression tag	UNP P42212
K	141	HIS	-	expression tag	UNP P42212
K	142	HIS	-	expression tag	UNP P42212
K	143	HIS	-	expression tag	UNP P42212
K	144	HIS	-	expression tag	UNP P42212
K	145	HIS	-	expression tag	UNP P42212
K	146	SER	-	expression tag	UNP P42212
K	147	SER	-	expression tag	UNP P42212
K	148	GLY	-	expression tag	UNP P42212
K	149	LEU	-	expression tag	UNP P42212
K	150	VAL	-	expression tag	UNP P42212
K	151	PRO	-	expression tag	UNP P42212
K	152	ARG	-	expression tag	UNP P42212
K	153	GLY	-	expression tag	UNP P42212
K	154	SER	-	expression tag	UNP P42212
K	155	HIS	-	expression tag	UNP P42212
K	156	VAL	-	expression tag	UNP P42212
K	201	LEU	PHE	conflict	UNP P42212
K	219	LEU	PHE	conflict	UNP P42212
K	220	GLY	SER	conflict	UNP P42212
K	223	LEU	VAL	conflict	UNP P42212
K	227	ALA	SER	conflict	UNP P42212
K	308	THR	MET	conflict	UNP P42212
K	318	ALA	VAL	conflict	UNP P42212
K	330	GLY	SER	conflict	UNP P42212
K	358	TYR	THR	conflict	UNP P42212
K	361	LYS	ALA	conflict	UNP P42212
K	386	LEU	HIS	conflict	UNP P42212
K	394	SER	-	linker	UNP P42212
K	395	GLY	-	linker	UNP P42212
K	396	LEU	-	linker	UNP P42212
K	397	ARG	-	linker	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
K	398	SER	-	linker	UNP P42212
K	399	ARG	-	linker	UNP P42212
K	400	ALA	-	linker	UNP P42212
K	401	GLN	-	linker	UNP P42212
K	402	ALA	-	linker	UNP P42212
K	403	SER	-	linker	UNP P42212
K	404	ASN	-	linker	UNP P42212
K	405	SER	-	linker	UNP P42212
K	406	ALA	-	linker	UNP P42212
K	407	VAL	-	linker	UNP P42212
K	408	ASP	-	linker	UNP P42212
L	136	MET	-	initiating methionine	UNP P42212
L	137	GLY	-	expression tag	UNP P42212
L	138	SER	-	expression tag	UNP P42212
L	139	SER	-	expression tag	UNP P42212
L	140	HIS	-	expression tag	UNP P42212
L	141	HIS	-	expression tag	UNP P42212
L	142	HIS	-	expression tag	UNP P42212
L	143	HIS	-	expression tag	UNP P42212
L	144	HIS	-	expression tag	UNP P42212
L	145	HIS	-	expression tag	UNP P42212
L	146	SER	-	expression tag	UNP P42212
L	147	SER	-	expression tag	UNP P42212
L	148	GLY	-	expression tag	UNP P42212
L	149	LEU	-	expression tag	UNP P42212
L	150	VAL	-	expression tag	UNP P42212
L	151	PRO	-	expression tag	UNP P42212
L	152	ARG	-	expression tag	UNP P42212
L	153	GLY	-	expression tag	UNP P42212
L	154	SER	-	expression tag	UNP P42212
L	155	HIS	-	expression tag	UNP P42212
L	156	VAL	-	expression tag	UNP P42212
L	201	LEU	PHE	conflict	UNP P42212
L	219	LEU	PHE	conflict	UNP P42212
L	220	GLY	SER	conflict	UNP P42212
L	223	LEU	VAL	conflict	UNP P42212
L	227	ALA	SER	conflict	UNP P42212
L	308	THR	MET	conflict	UNP P42212
L	318	ALA	VAL	conflict	UNP P42212
L	330	GLY	SER	conflict	UNP P42212
L	358	TYR	THR	conflict	UNP P42212
L	361	LYS	ALA	conflict	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
L	386	LEU	HIS	conflict	UNP P42212
L	394	SER	-	linker	UNP P42212
L	395	GLY	-	linker	UNP P42212
L	396	LEU	-	linker	UNP P42212
L	397	ARG	-	linker	UNP P42212
L	398	SER	-	linker	UNP P42212
L	399	ARG	-	linker	UNP P42212
L	400	ALA	-	linker	UNP P42212
L	401	GLN	-	linker	UNP P42212
L	402	ALA	-	linker	UNP P42212
L	403	SER	-	linker	UNP P42212
L	404	ASN	-	linker	UNP P42212
L	405	SER	-	linker	UNP P42212
L	406	ALA	-	linker	UNP P42212
L	407	VAL	-	linker	UNP P42212
L	408	ASP	-	linker	UNP P42212
M	136	MET	-	initiating methionine	UNP P42212
M	137	GLY	-	expression tag	UNP P42212
M	138	SER	-	expression tag	UNP P42212
M	139	SER	-	expression tag	UNP P42212
M	140	HIS	-	expression tag	UNP P42212
M	141	HIS	-	expression tag	UNP P42212
M	142	HIS	-	expression tag	UNP P42212
M	143	HIS	-	expression tag	UNP P42212
M	144	HIS	-	expression tag	UNP P42212
M	145	HIS	-	expression tag	UNP P42212
M	146	SER	-	expression tag	UNP P42212
M	147	SER	-	expression tag	UNP P42212
M	148	GLY	-	expression tag	UNP P42212
M	149	LEU	-	expression tag	UNP P42212
M	150	VAL	-	expression tag	UNP P42212
M	151	PRO	-	expression tag	UNP P42212
M	152	ARG	-	expression tag	UNP P42212
M	153	GLY	-	expression tag	UNP P42212
M	154	SER	-	expression tag	UNP P42212
M	155	HIS	-	expression tag	UNP P42212
M	156	VAL	-	expression tag	UNP P42212
M	201	LEU	PHE	conflict	UNP P42212
M	219	LEU	PHE	conflict	UNP P42212
M	220	GLY	SER	conflict	UNP P42212
M	223	LEU	VAL	conflict	UNP P42212
M	227	ALA	SER	conflict	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
M	308	THR	MET	conflict	UNP P42212
M	318	ALA	VAL	conflict	UNP P42212
M	330	GLY	SER	conflict	UNP P42212
M	358	TYR	THR	conflict	UNP P42212
M	361	LYS	ALA	conflict	UNP P42212
M	386	LEU	HIS	conflict	UNP P42212
M	394	SER	-	linker	UNP P42212
M	395	GLY	-	linker	UNP P42212
M	396	LEU	-	linker	UNP P42212
M	397	ARG	-	linker	UNP P42212
M	398	SER	-	linker	UNP P42212
M	399	ARG	-	linker	UNP P42212
M	400	ALA	-	linker	UNP P42212
M	401	GLN	-	linker	UNP P42212
M	402	ALA	-	linker	UNP P42212
M	403	SER	-	linker	UNP P42212
M	404	ASN	-	linker	UNP P42212
M	405	SER	-	linker	UNP P42212
M	406	ALA	-	linker	UNP P42212
M	407	VAL	-	linker	UNP P42212
M	408	ASP	-	linker	UNP P42212
N	136	MET	-	initiating methionine	UNP P42212
N	137	GLY	-	expression tag	UNP P42212
N	138	SER	-	expression tag	UNP P42212
N	139	SER	-	expression tag	UNP P42212
N	140	HIS	-	expression tag	UNP P42212
N	141	HIS	-	expression tag	UNP P42212
N	142	HIS	-	expression tag	UNP P42212
N	143	HIS	-	expression tag	UNP P42212
N	144	HIS	-	expression tag	UNP P42212
N	145	HIS	-	expression tag	UNP P42212
N	146	SER	-	expression tag	UNP P42212
N	147	SER	-	expression tag	UNP P42212
N	148	GLY	-	expression tag	UNP P42212
N	149	LEU	-	expression tag	UNP P42212
N	150	VAL	-	expression tag	UNP P42212
N	151	PRO	-	expression tag	UNP P42212
N	152	ARG	-	expression tag	UNP P42212
N	153	GLY	-	expression tag	UNP P42212
N	154	SER	-	expression tag	UNP P42212
N	155	HIS	-	expression tag	UNP P42212
N	156	VAL	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
N	201	LEU	PHE	conflict	UNP P42212
N	219	LEU	PHE	conflict	UNP P42212
N	220	GLY	SER	conflict	UNP P42212
N	223	LEU	VAL	conflict	UNP P42212
N	227	ALA	SER	conflict	UNP P42212
N	308	THR	MET	conflict	UNP P42212
N	318	ALA	VAL	conflict	UNP P42212
N	330	GLY	SER	conflict	UNP P42212
N	358	TYR	THR	conflict	UNP P42212
N	361	LYS	ALA	conflict	UNP P42212
N	386	LEU	HIS	conflict	UNP P42212
N	394	SER	-	linker	UNP P42212
N	395	GLY	-	linker	UNP P42212
N	396	LEU	-	linker	UNP P42212
N	397	ARG	-	linker	UNP P42212
N	398	SER	-	linker	UNP P42212
N	399	ARG	-	linker	UNP P42212
N	400	ALA	-	linker	UNP P42212
N	401	GLN	-	linker	UNP P42212
N	402	ALA	-	linker	UNP P42212
N	403	SER	-	linker	UNP P42212
N	404	ASN	-	linker	UNP P42212
N	405	SER	-	linker	UNP P42212
N	406	ALA	-	linker	UNP P42212
N	407	VAL	-	linker	UNP P42212
N	408	ASP	-	linker	UNP P42212

67%

ILE	LYS	ALA	ASN	PHE	LYS	ILE	ARG	HIS	ASN	ILE	GLU	ASP	GLY	VAL	GLN	LEU	ALA	ASP	HIS	ASP	TYR	GLN	GLN	ASN	THR	THR	ILE	GLY	ASP	GLY	PRO	VAL	LEU	LEU	LEU	PRO	ASP	ASN	HIS	TYR	LEU	LEU	SER	SER	GLN	TYR	GLN	SER	LYS	LEU	LYS	VAL	ARG	ASP	HIS	HIS	MET	VAL
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67%

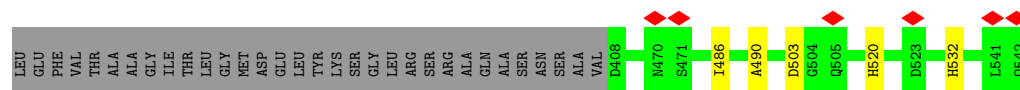
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67%

ILE	LYS	ALA	ASN	PHE	LYS	ILE	ARG	HIS	ASN	ILE	GLU	ASP	GLY	GLY	VAL	GLN	LEU	ALA	ASP	HIS	TYR	GLN	GLN	ASN	THR	PRO	ILE	ILE	GLY	ASP	GLY	PRO	VAL	LEU	LEU	LEU	LEU	ASP	ASN	HIS	TYR	LEU	SER	LYS	LYS	GLU	ASN	PRO	PRO	GLU	LYS	ARG	ASP	HIS	MET	VAL
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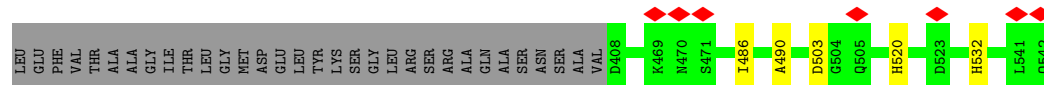
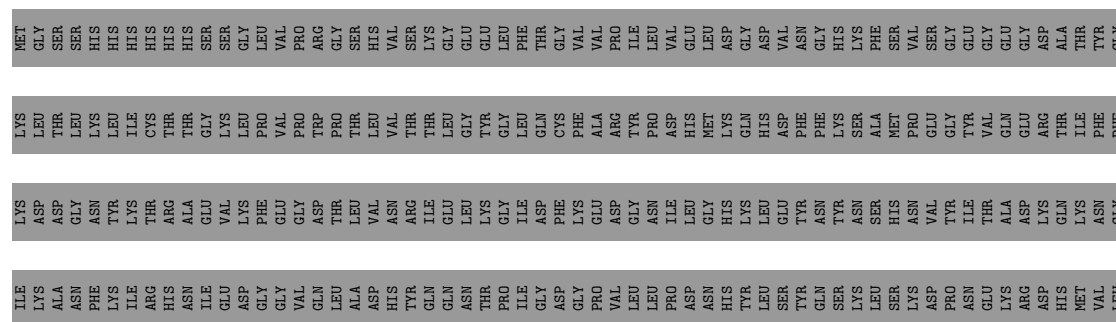
Chain F:

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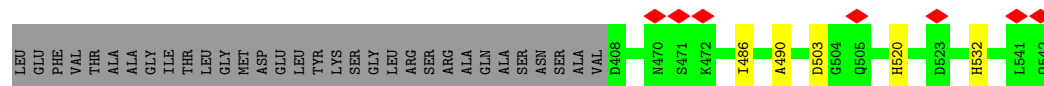
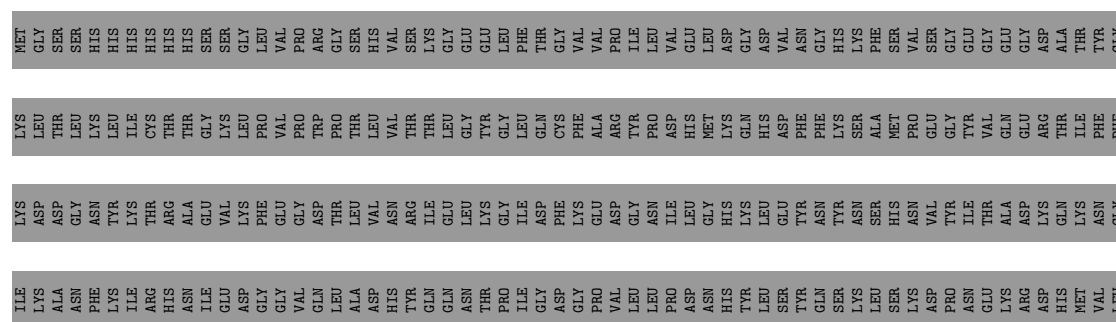
• Molecule 1: Venus-tagged CaMKII Beta Association Domain

Chain I: 32% 67%



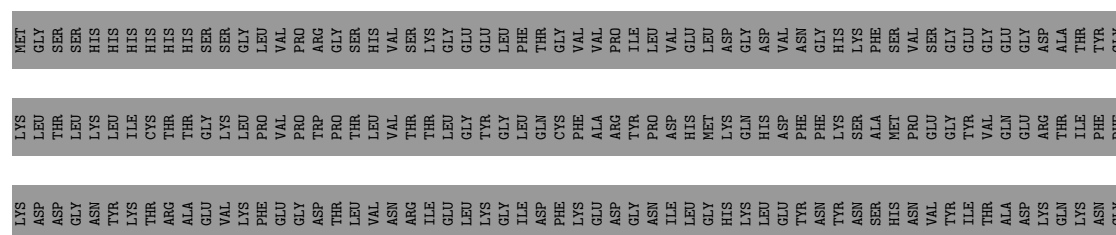
• Molecule 1: Venus-tagged CaMKII Beta Association Domain

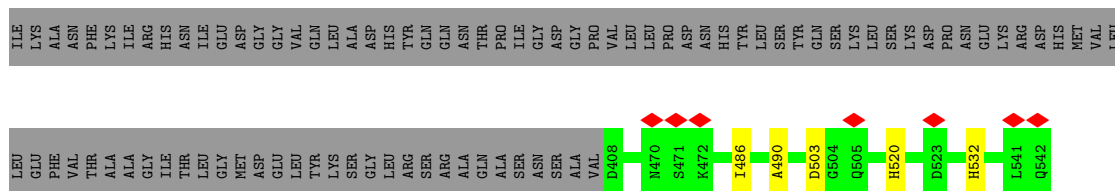
Chain J: 32% 67%



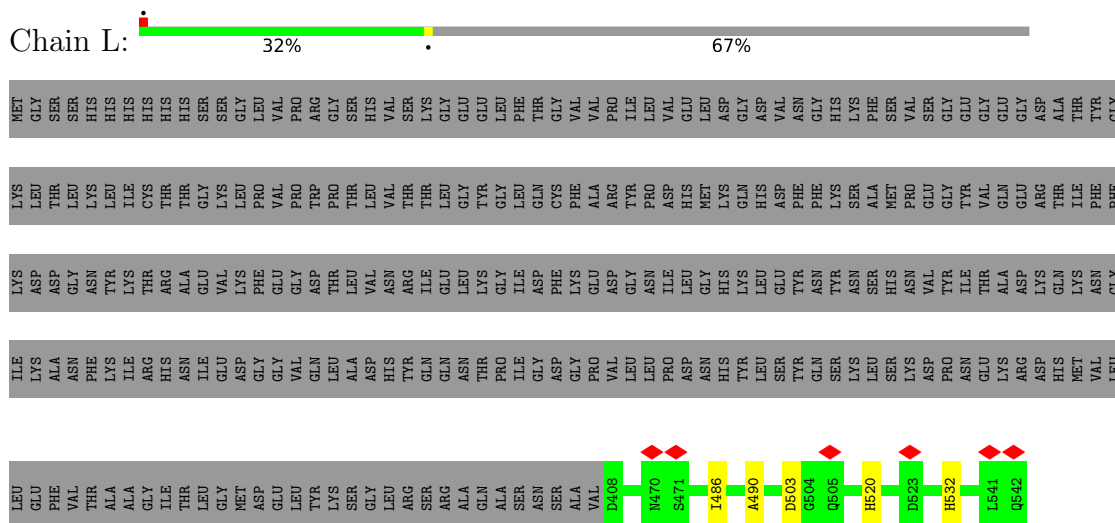
• Molecule 1: Venus-tagged CaMKII Beta Association Domain

Chain K: 32% 67%

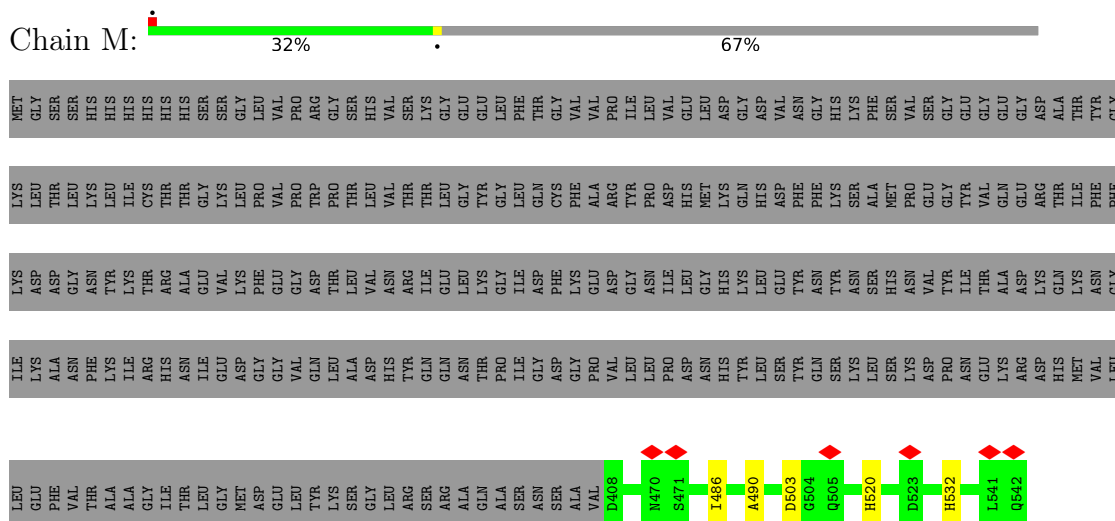




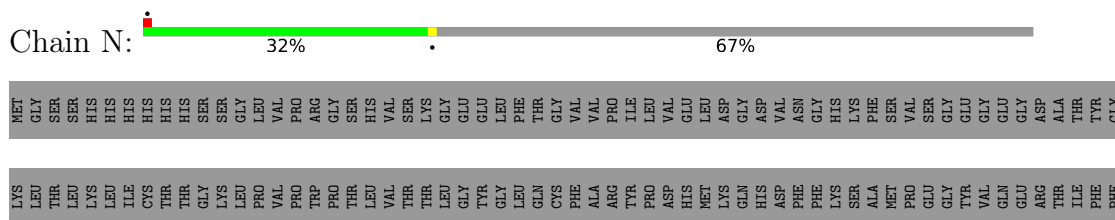
- Molecule 1: Venus-tagged CaMKII Beta Association Domain



- Molecule 1: Venus-tagged CaMKII Beta Association Domain



- Molecule 1: Venus-tagged CaMKII Beta Association Domain



LYS	ASP	GLY	ASN	ASN	TYR	LYS	THR	ARG	ALA	VAL	LYS	PHE	GLY	GLY	ASP	THR	LEU	VAL	ASP	ASN	ILE	GLN	ASN	LEU	LYS	GLY	ASP	PHE	LYS	GLU	ASP	GLY	ASN	TYR	ASN	TYR	ASN	LYS	HIS	GLY	HIS	LYS	LEU	GLU	TYR	ASN	TYR	ASN	LYS	ASN	VAL	TYR	THR	ALA	LYS	GLN	ASP	LYS	GLN	LYS	ASN	VAL	GLY
ILE	LYS	ALA	ASN	PHE	THR	LYS	ILE	ARG	HIS	ASN	ALA	ILE	GLU	GLY	VAL	GLN	LEU	ALA	ASP	HIS	TYR	GLN	ASN	THR	PRO	ILE	GLY	ASP	GLY	PRO	VAL	VAL	LEU	ASN	PRO	ASN	ASN	TYR	LEU	SER	TYR	GLN	SER	LYS	LEU	SER	HIS	LYS	ASP	PRO	ASN	GLU	LYS	ARG	ASP	LYS	HIS	MET	VAL	LEU			
LEU	GLU	PHE	VAL	THR	ALA	ALA	GLY	ILE	THR	LEU	GLY	MET	ASP	GLU	LEU	TYR	LYS	SER	GLY	LEU	ARG	SER	ARG	ALA	GLN	ALA	SER	ASN	SER	ALA	VAL	D408	N470	S471	I486	A490	D503	G504	Q505	H520	D523	H532	L541	Q542																			

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	126970	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.960	Depositor
Minimum map value	-1.785	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.048	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	331.85278, 331.85278, 331.85278	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.86419994, 0.86419994, 0.86419994	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	0.84	0/1106	1.39	2/1501 (0.1%)
1	B	0.84	0/1106	1.40	2/1501 (0.1%)
1	C	0.84	0/1106	1.39	2/1501 (0.1%)
1	D	0.84	0/1106	1.39	2/1501 (0.1%)
1	E	0.84	0/1106	1.39	2/1501 (0.1%)
1	F	0.84	0/1106	1.40	2/1501 (0.1%)
1	G	0.84	0/1106	1.39	2/1501 (0.1%)
1	H	0.84	0/1106	1.39	2/1501 (0.1%)
1	I	0.84	0/1106	1.40	2/1501 (0.1%)
1	J	0.85	0/1106	1.40	2/1501 (0.1%)
1	K	0.84	0/1106	1.39	2/1501 (0.1%)
1	L	0.84	0/1106	1.40	2/1501 (0.1%)
1	M	0.85	0/1106	1.39	2/1501 (0.1%)
1	N	0.84	0/1106	1.39	2/1501 (0.1%)
All	All	0.84	0/15484	1.39	28/21014 (0.1%)

There are no bond length outliers.

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	532	HIS	CA-CB-CG	5.82	119.62	113.80
1	C	532	HIS	CA-CB-CG	5.82	119.61	113.80
1	B	532	HIS	CA-CB-CG	5.80	119.60	113.80
1	I	532	HIS	CA-CB-CG	5.80	119.60	113.80
1	G	532	HIS	CA-CB-CG	5.79	119.59	113.80
1	A	532	HIS	CA-CB-CG	5.79	119.59	113.80
1	H	532	HIS	CA-CB-CG	5.79	119.59	113.80
1	M	532	HIS	CA-CB-CG	5.78	119.58	113.80
1	J	532	HIS	CA-CB-CG	5.77	119.57	113.80
1	E	532	HIS	CA-CB-CG	5.77	119.57	113.80
1	L	532	HIS	CA-CB-CG	5.77	119.57	113.80
1	N	532	HIS	CA-CB-CG	5.76	119.56	113.80
1	K	532	HIS	CA-CB-CG	5.76	119.56	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	532	HIS	CA-CB-CG	5.76	119.56	113.80
1	G	503	ASP	CA-CB-CG	5.10	117.70	112.60
1	B	503	ASP	CA-CB-CG	5.09	117.69	112.60
1	I	503	ASP	CA-CB-CG	5.09	117.69	112.60
1	K	503	ASP	CA-CB-CG	5.09	117.69	112.60
1	A	503	ASP	CA-CB-CG	5.09	117.69	112.60
1	H	503	ASP	CA-CB-CG	5.09	117.69	112.60
1	L	503	ASP	CA-CB-CG	5.09	117.69	112.60
1	F	503	ASP	CA-CB-CG	5.08	117.68	112.60
1	N	503	ASP	CA-CB-CG	5.08	117.68	112.60
1	D	503	ASP	CA-CB-CG	5.08	117.68	112.60
1	E	503	ASP	CA-CB-CG	5.07	117.67	112.60
1	J	503	ASP	CA-CB-CG	5.07	117.67	112.60
1	C	503	ASP	CA-CB-CG	5.06	117.66	112.60
1	M	503	ASP	CA-CB-CG	5.06	117.66	112.60

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	1078	1033	1034	9	0
1	B	1078	1033	1034	8	0
1	C	1078	1033	1034	8	0
1	D	1078	1033	1034	9	0
1	E	1078	1033	1034	10	0
1	F	1078	1033	1034	9	0
1	G	1078	1033	1034	9	0
1	H	1078	1033	1034	9	0
1	I	1078	1033	1034	9	0
1	J	1078	1033	1034	10	0
1	K	1078	1033	1034	9	0
1	L	1078	1033	1034	8	0
1	M	1078	1033	1034	8	0
1	N	1078	1033	1034	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	15092	14462	14476	62	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 2.

All (62) 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:520:HIS:CD2	1:L:486:ILE:HG23	2.03	0.93
1:A:486:ILE:HG23	1:N:520:HIS:CD2	2.04	0.93
1:F:486:ILE:HG23	1:I:520:HIS:CD2	2.04	0.93
1:E:520:HIS:CD2	1:J:486:ILE:HG23	2.04	0.93
1:G:486:ILE:HG23	1:H:520:HIS:CD2	2.04	0.93
1:D:486:ILE:HG23	1:K:520:HIS:CD2	2.04	0.92
1:D:520:HIS:CD2	1:K:486:ILE:HG23	2.04	0.92
1:A:520:HIS:CD2	1:N:486:ILE:HG23	2.04	0.92
1:B:520:HIS:CD2	1:M:486:ILE:HG23	2.04	0.92
1:B:486:ILE:HG23	1:M:520:HIS:CD2	2.04	0.92
1:F:520:HIS:CD2	1:I:486:ILE:HG23	2.04	0.91
1:G:520:HIS:CD2	1:H:486:ILE:HG23	2.05	0.91
1:C:486:ILE:HG23	1:L:520:HIS:CD2	2.05	0.91
1:E:486:ILE:HG23	1:J:520:HIS:CD2	2.05	0.91
1:E:520:HIS:CD2	1:J:486:ILE:CG2	2.74	0.71
1:A:486:ILE:CG2	1:N:520:HIS:CD2	2.74	0.71
1:G:486:ILE:CG2	1:H:520:HIS:CD2	2.74	0.70
1:B:520:HIS:CD2	1:M:486:ILE:CG2	2.74	0.70
1:B:486:ILE:CG2	1:M:520:HIS:CD2	2.75	0.70
1:C:520:HIS:CD2	1:L:486:ILE:CG2	2.74	0.70
1:E:486:ILE:CG2	1:J:520:HIS:CD2	2.74	0.70
1:F:486:ILE:CG2	1:I:520:HIS:CD2	2.74	0.69
1:D:486:ILE:CG2	1:K:520:HIS:CD2	2.74	0.69
1:F:520:HIS:CD2	1:I:486:ILE:CG2	2.75	0.69
1:C:486:ILE:CG2	1:L:520:HIS:CD2	2.75	0.69
1:G:520:HIS:CD2	1:H:486:ILE:CG2	2.75	0.69
1:D:520:HIS:CD2	1:K:486:ILE:CG2	2.74	0.68
1:A:520:HIS:CD2	1:N:486:ILE:CG2	2.75	0.68
1:G:486:ILE:HG22	1:H:490:ALA:HB2	1.87	0.56
1:G:490:ALA:HB2	1:H:486:ILE:HG22	1.87	0.56
1:A:490:ALA:HB2	1:N:486:ILE:HG22	1.87	0.56
1:F:490:ALA:HB2	1:I:486:ILE:HG22	1.88	0.55
1:F:486:ILE:HG22	1:I:490:ALA:HB2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:486:ILE:HG22	1:N:490:ALA:HB2	1.87	0.55
1:D:486:ILE:HG22	1:K:490:ALA:HB2	1.88	0.55
1:D:490:ALA:HB2	1:K:486:ILE:HG22	1.88	0.55
1:A:486:ILE:CG2	1:N:490:ALA:HB2	2.37	0.54
1:C:486:ILE:HG22	1:L:490:ALA:HB2	1.88	0.54
1:E:486:ILE:HG22	1:J:490:ALA:HB2	1.90	0.54
1:C:490:ALA:HB2	1:L:486:ILE:CG2	2.38	0.54
1:E:490:ALA:HB2	1:J:486:ILE:HG22	1.90	0.54
1:B:490:ALA:HB2	1:M:486:ILE:HG22	1.88	0.54
1:B:486:ILE:CG2	1:M:490:ALA:HB2	2.38	0.54
1:B:486:ILE:HG22	1:M:490:ALA:HB2	1.88	0.53
1:C:490:ALA:HB2	1:L:486:ILE:HG22	1.88	0.53
1:G:490:ALA:HB2	1:H:486:ILE:CG2	2.38	0.53
1:G:486:ILE:CG2	1:H:490:ALA:HB2	2.37	0.53
1:B:490:ALA:HB2	1:M:486:ILE:CG2	2.38	0.53
1:A:490:ALA:HB2	1:N:486:ILE:CG2	2.38	0.53
1:D:486:ILE:CG2	1:K:490:ALA:HB2	2.38	0.53
1:D:490:ALA:HB2	1:K:486:ILE:CG2	2.38	0.53
1:F:486:ILE:CG2	1:I:490:ALA:HB2	2.38	0.53
1:F:490:ALA:HB2	1:I:486:ILE:CG2	2.38	0.52
1:C:486:ILE:CG2	1:L:490:ALA:HB2	2.39	0.52
1:E:486:ILE:CG2	1:J:490:ALA:HB2	2.40	0.51
1:E:490:ALA:HB2	1:J:486:ILE:CG2	2.40	0.51
1:E:486:ILE:HG23	1:J:520:HIS:CG	2.53	0.43
1:E:520:HIS:CG	1:J:486:ILE:HG23	2.52	0.43
1:D:486:ILE:HG23	1:K:520:HIS:CG	2.53	0.41
1:A:486:ILE:HG23	1:N:520:HIS:CG	2.53	0.41
1:G:486:ILE:HG23	1:H:520:HIS:CG	2.53	0.40
1:F:520:HIS:CG	1:I:486:ILE:HG23	2.53	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	133/407 (33%)	129 (97%)	4 (3%)	0	100	100
1	B	133/407 (33%)	129 (97%)	4 (3%)	0	100	100
1	C	133/407 (33%)	129 (97%)	4 (3%)	0	100	100
1	D	133/407 (33%)	129 (97%)	4 (3%)	0	100	100
1	E	133/407 (33%)	129 (97%)	4 (3%)	0	100	100
1	F	133/407 (33%)	129 (97%)	4 (3%)	0	100	100
1	G	133/407 (33%)	129 (97%)	4 (3%)	0	100	100
1	H	133/407 (33%)	129 (97%)	4 (3%)	0	100	100
1	I	133/407 (33%)	129 (97%)	4 (3%)	0	100	100
1	J	133/407 (33%)	129 (97%)	4 (3%)	0	100	100
1	K	133/407 (33%)	129 (97%)	4 (3%)	0	100	100
1	L	133/407 (33%)	129 (97%)	4 (3%)	0	100	100
1	M	133/407 (33%)	129 (97%)	4 (3%)	0	100	100
1	N	133/407 (33%)	129 (97%)	4 (3%)	0	100	100
All	All	1862/5698 (33%)	1806 (97%)	56 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	115/347 (33%)	115 (100%)	0	100	100
1	B	115/347 (33%)	115 (100%)	0	100	100
1	C	115/347 (33%)	115 (100%)	0	100	100
1	D	115/347 (33%)	115 (100%)	0	100	100
1	E	115/347 (33%)	115 (100%)	0	100	100
1	F	115/347 (33%)	115 (100%)	0	100	100
1	G	115/347 (33%)	115 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	115/347 (33%)	115 (100%)	0	100	100
1	I	115/347 (33%)	115 (100%)	0	100	100
1	J	115/347 (33%)	115 (100%)	0	100	100
1	K	115/347 (33%)	115 (100%)	0	100	100
1	L	115/347 (33%)	115 (100%)	0	100	100
1	M	115/347 (33%)	115 (100%)	0	100	100
1	N	115/347 (33%)	115 (100%)	0	100	100
All	All	1610/4858 (33%)	1610 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (43) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	465	ASN
1	A	520	HIS
1	B	465	ASN
1	B	475	HIS
1	B	500	GLN
1	B	520	HIS
1	C	412	GLN
1	C	465	ASN
1	C	500	GLN
1	C	520	HIS
1	D	465	ASN
1	D	520	HIS
1	E	465	ASN
1	E	520	HIS
1	F	412	GLN
1	F	465	ASN
1	F	520	HIS
1	G	412	GLN
1	G	465	ASN
1	G	520	HIS
1	H	465	ASN
1	H	475	HIS
1	H	500	GLN
1	H	520	HIS
1	I	412	GLN

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Mol	Chain	Res	Type
1	I	465	ASN
1	I	520	HIS
1	J	412	GLN
1	J	465	ASN
1	J	475	HIS
1	J	500	GLN
1	J	520	HIS
1	K	465	ASN
1	K	520	HIS
1	L	412	GLN
1	L	465	ASN
1	L	475	HIS
1	L	500	GLN
1	L	520	HIS
1	M	465	ASN
1	M	520	HIS
1	N	465	ASN
1	N	520	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 ⓘ

There are no chain breaks in this entry.

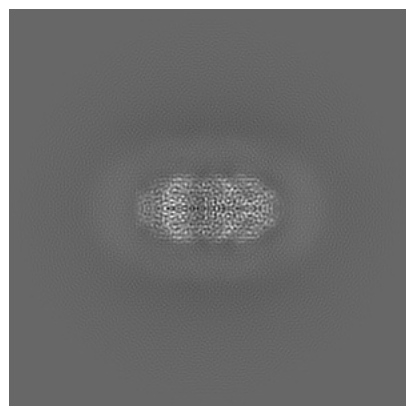
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-40956. These allow visual inspection of the internal detail of the map and identification of artifacts.

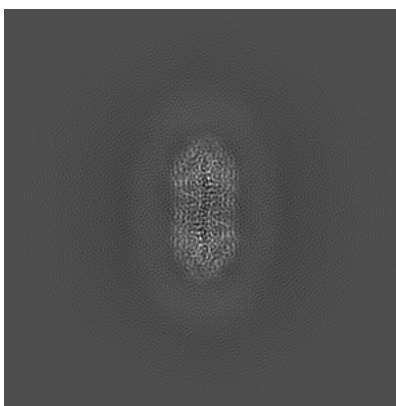
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

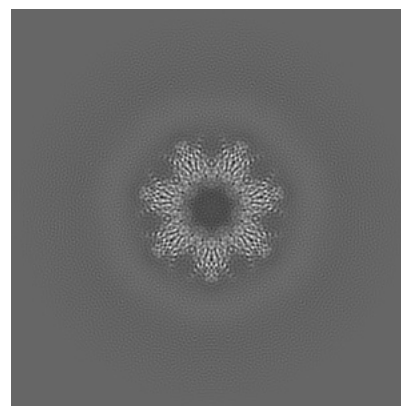
6.1.1 Primary map



X

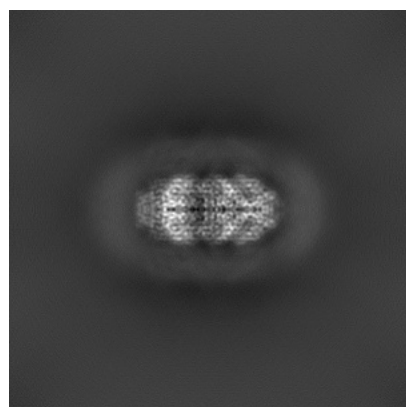


Y

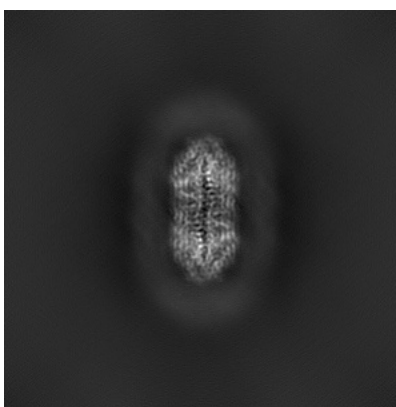


Z

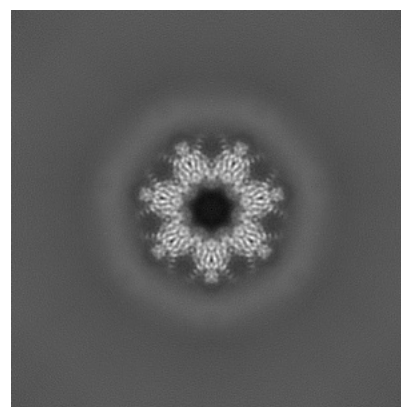
6.1.2 Raw map



X



Y

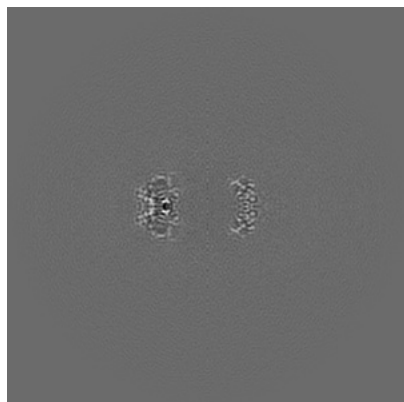


Z

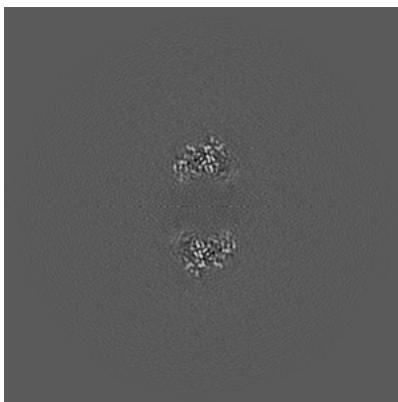
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

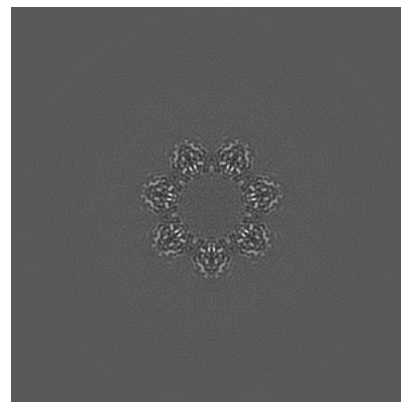
6.2.1 Primary map



X Index: 192

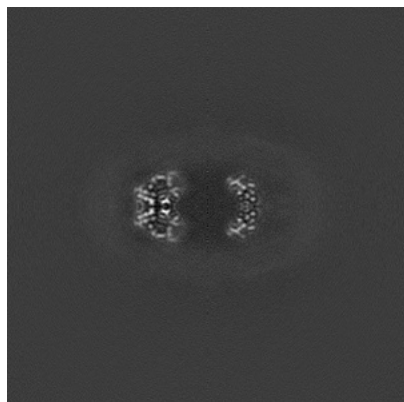


Y Index: 192

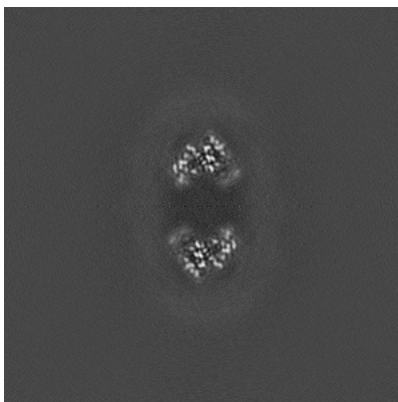


Z Index: 192

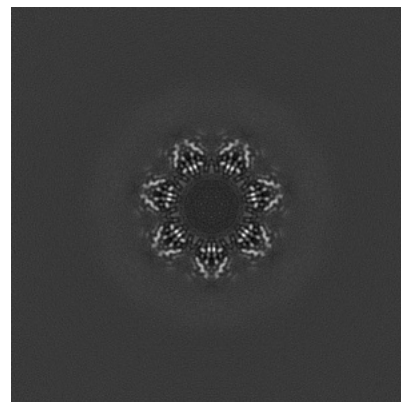
6.2.2 Raw map



X Index: 192



Y Index: 192

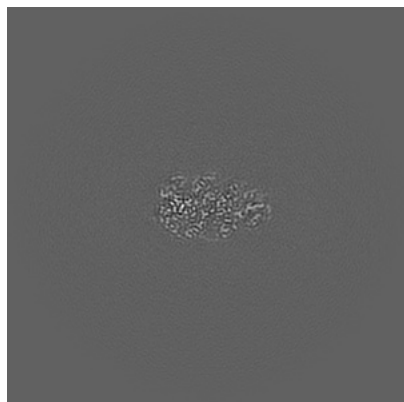


Z Index: 192

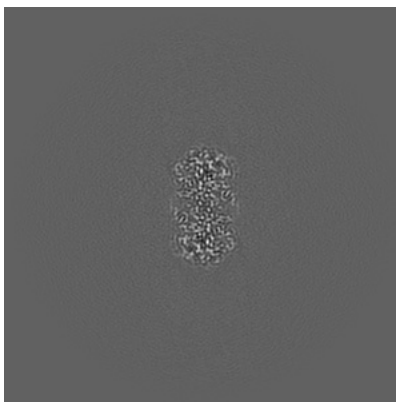
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

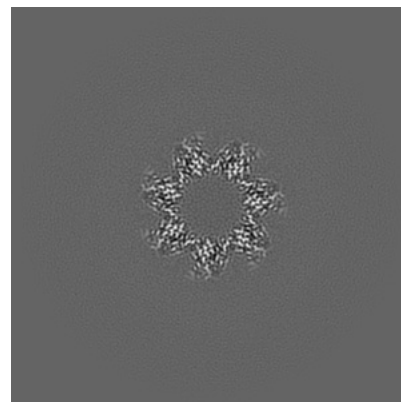
6.3.1 Primary map



X Index: 158

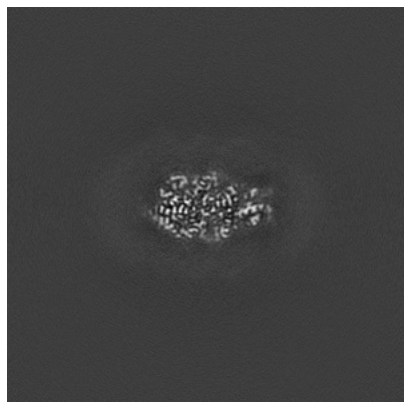


Y Index: 158

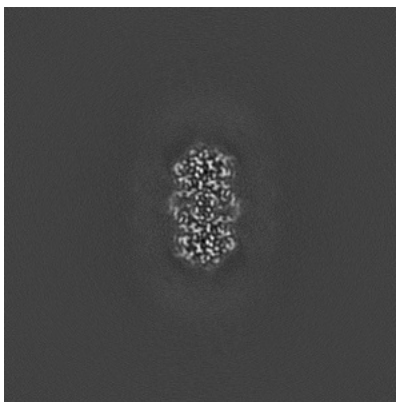


Z Index: 196

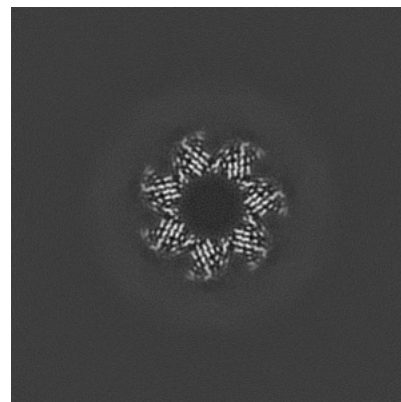
6.3.2 Raw map



X Index: 157



Y Index: 158

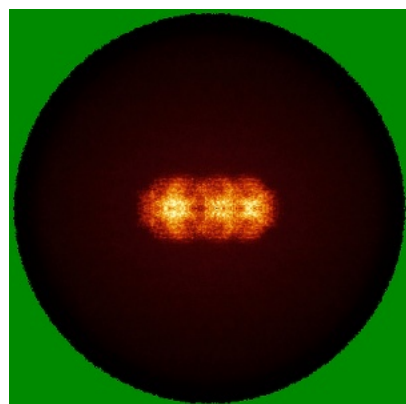


Z Index: 196

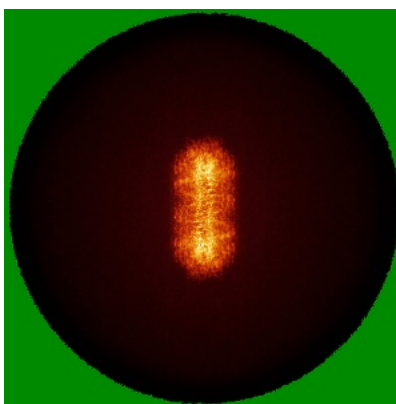
The images above show the largest variance slices of the map in three orthogonal directions.

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

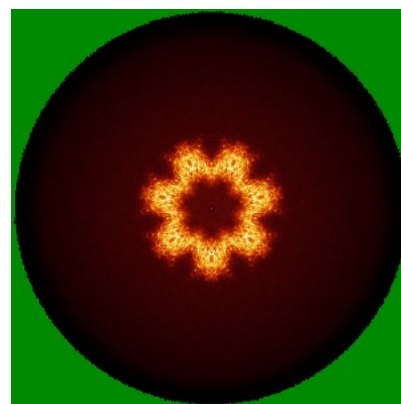
6.4.1 Primary map



X

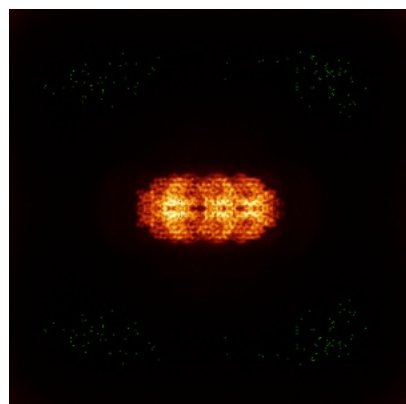


Y

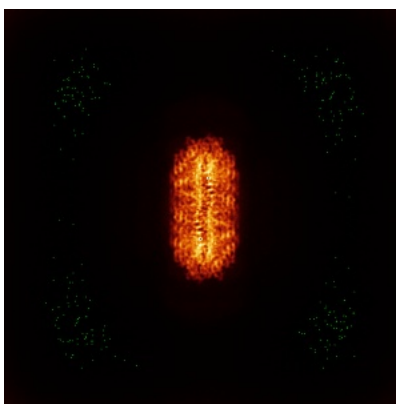


Z

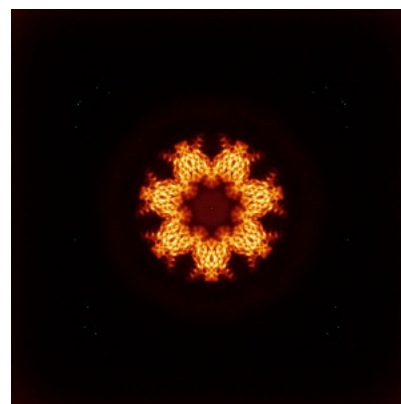
6.4.2 Raw map



X



Y

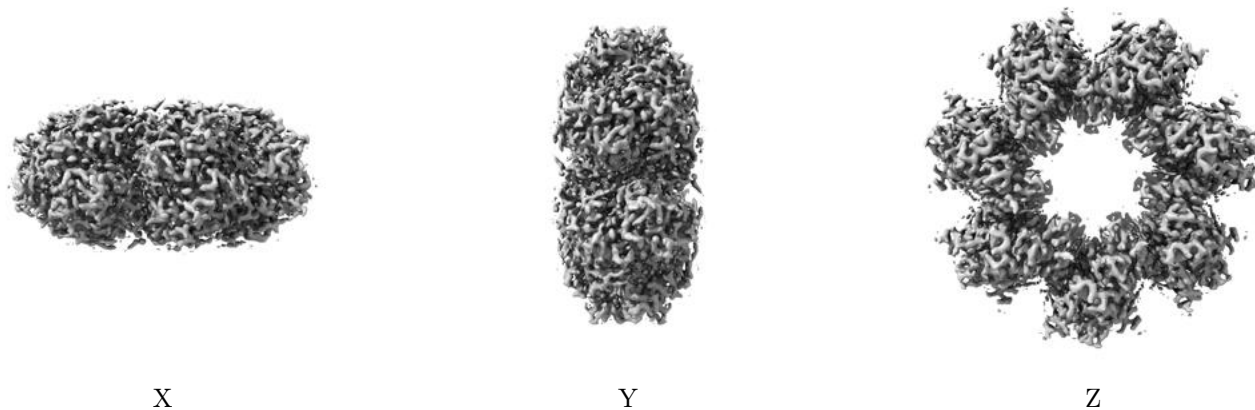


Z

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.

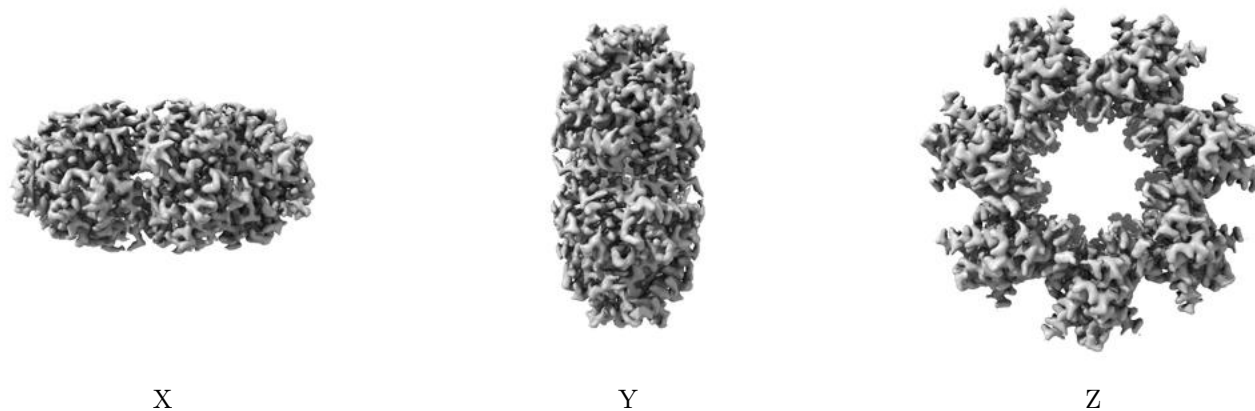
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.3. 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



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.

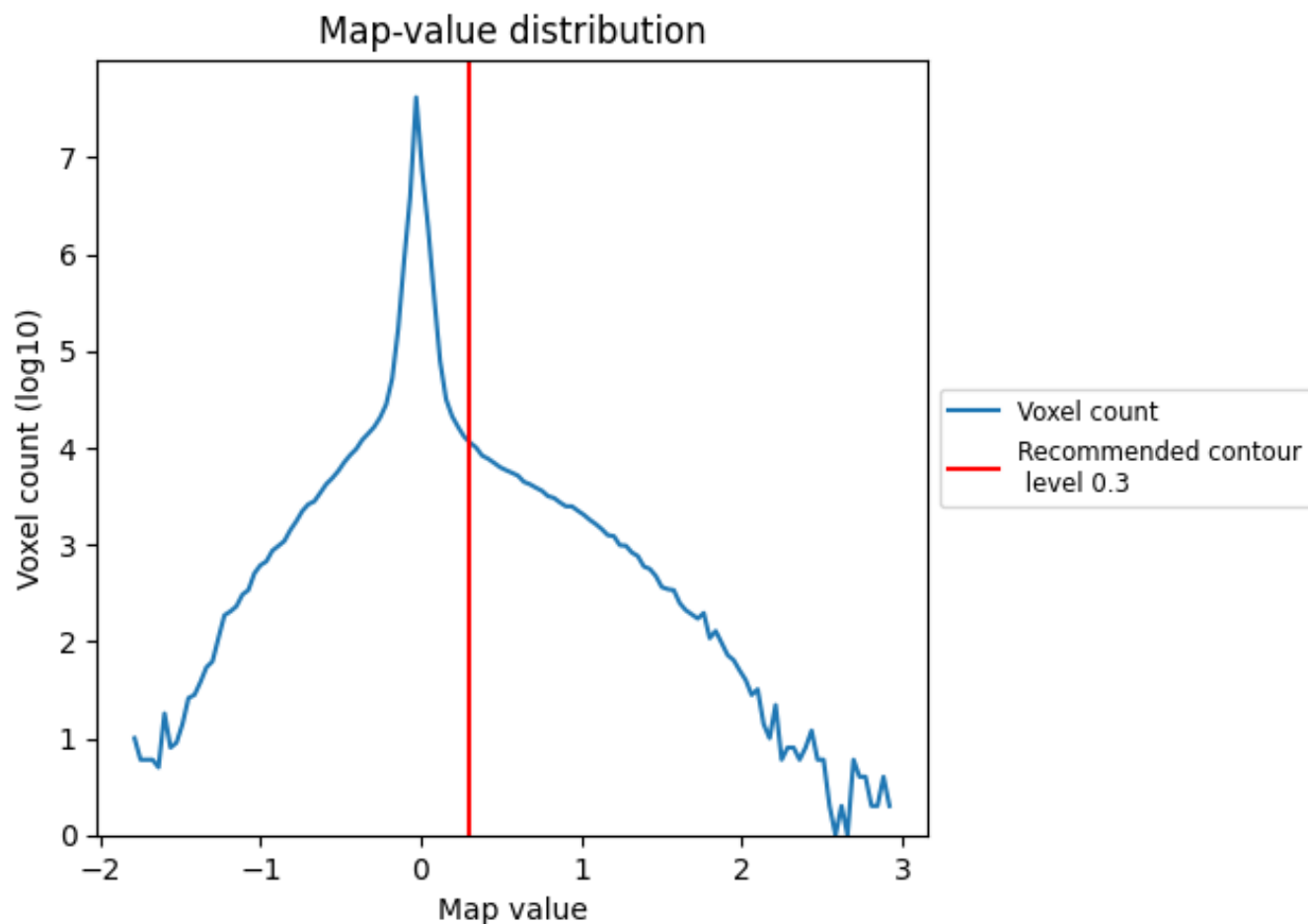
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

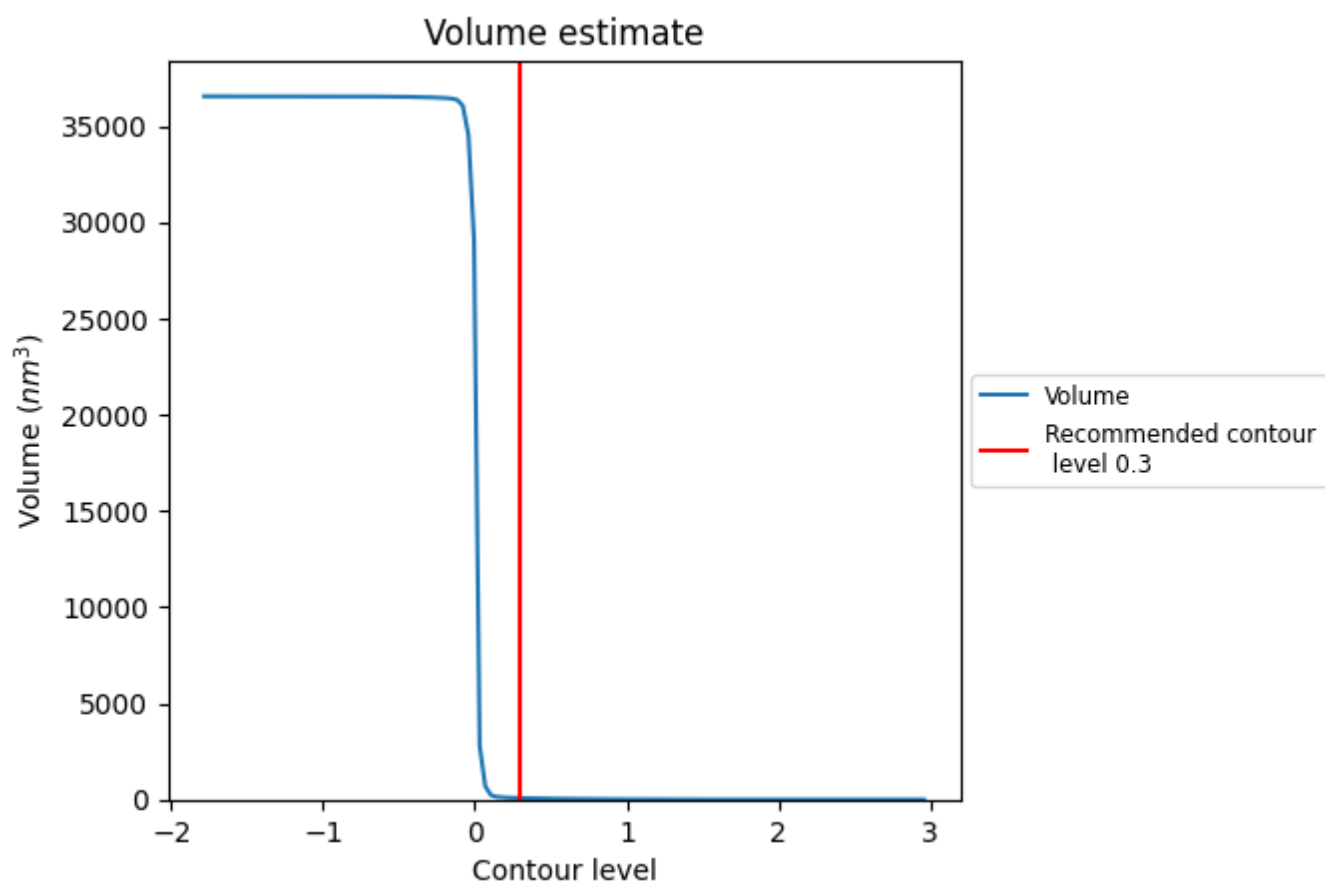
This section contains the results of statistical analysis of the map.

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.

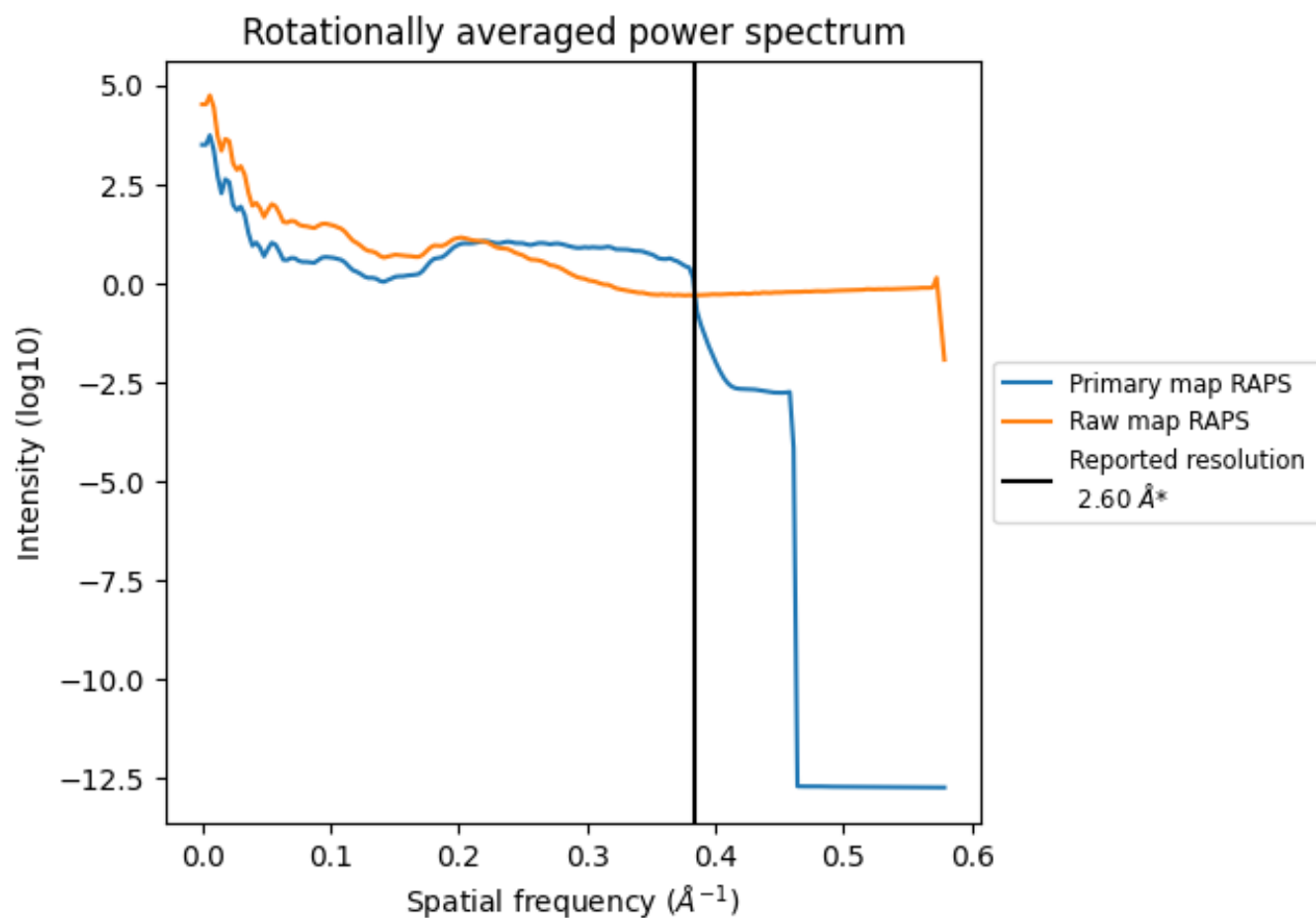
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 77 nm³; this corresponds to an approximate mass of 69 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 ⓘ

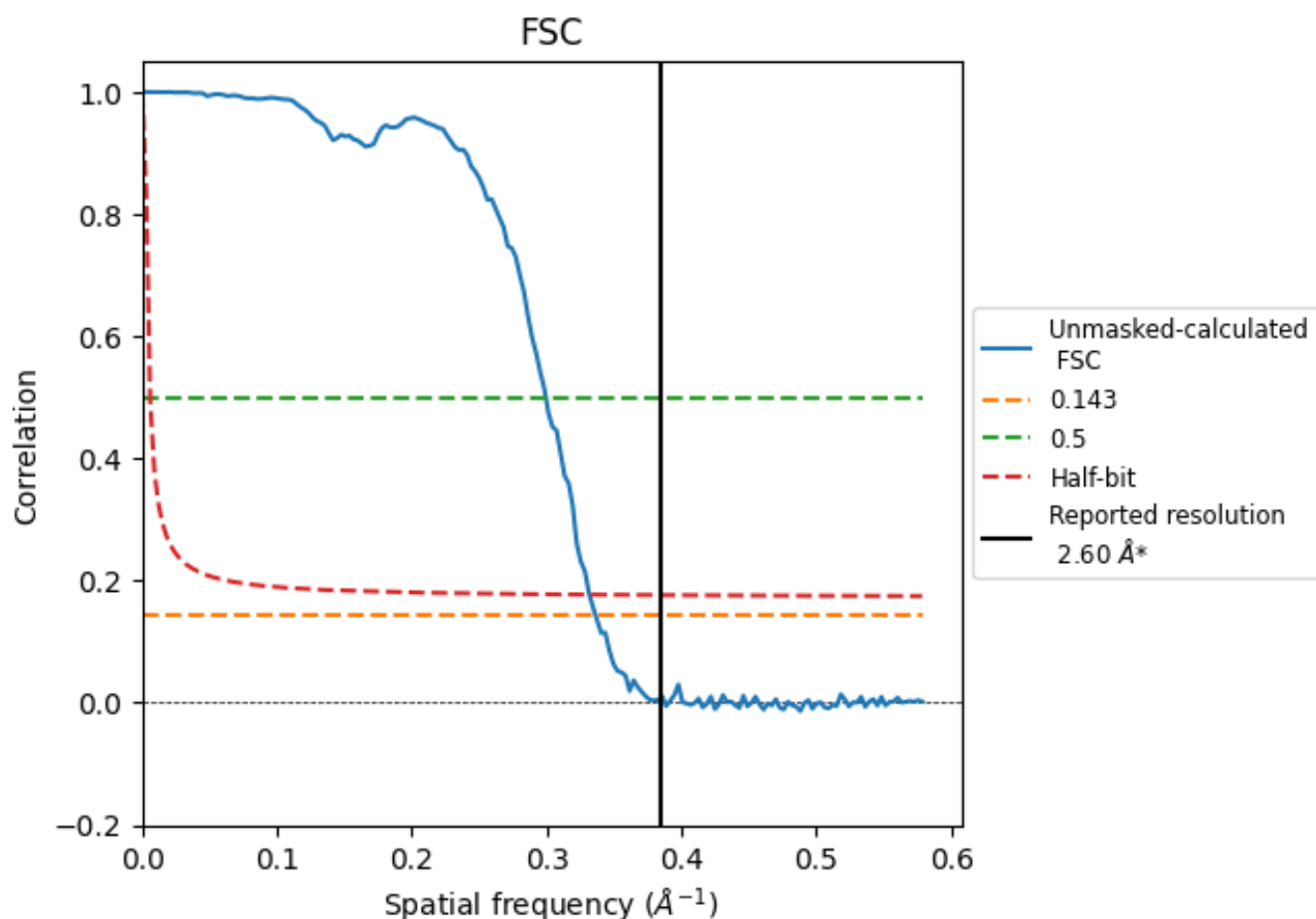


*Reported resolution corresponds to spatial frequency of 0.385 Å⁻¹

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](#)

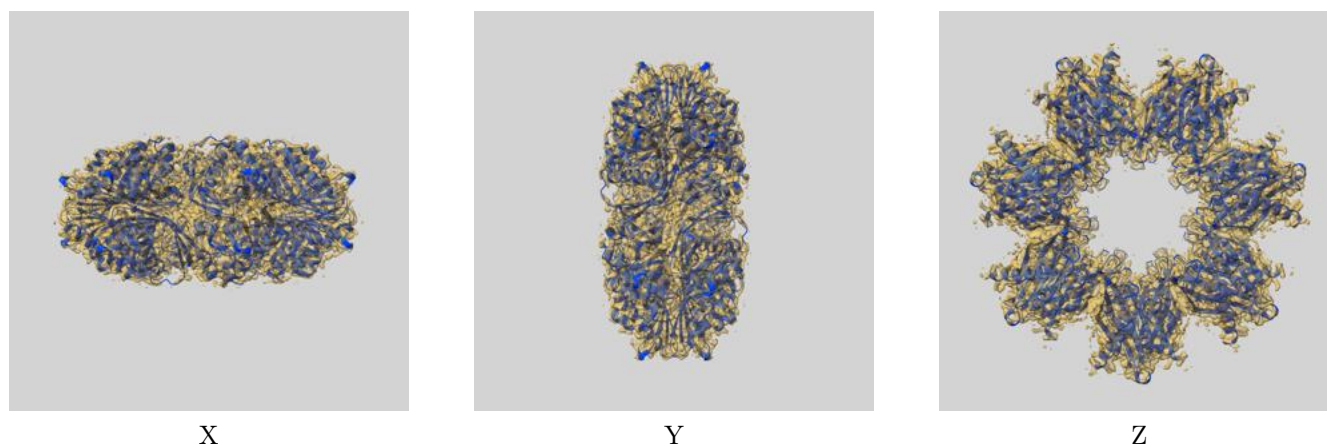
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.97	3.34	3.01

*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 2.97 differs from the reported value 2.6 by more than 10 %

9 Map-model fit [i](#)

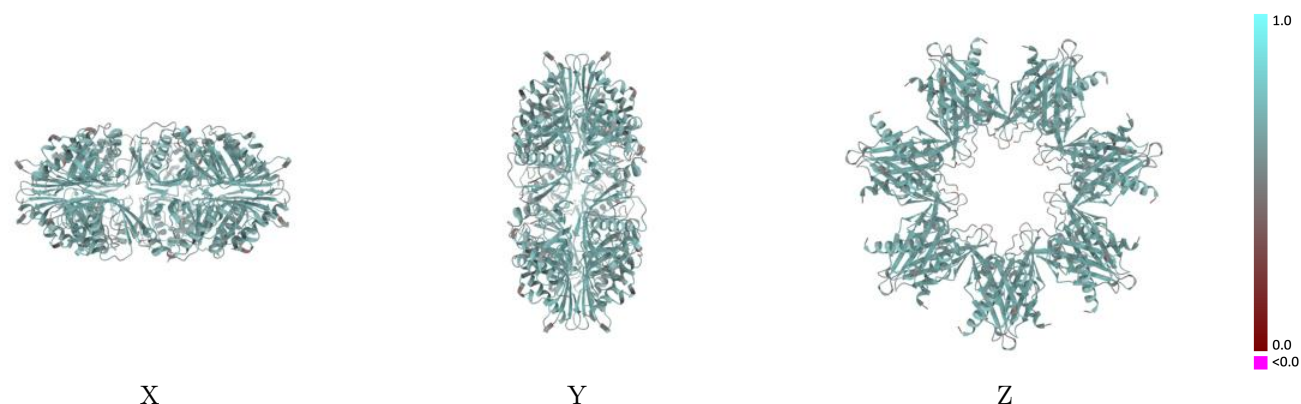
This section contains information regarding the fit between EMDB map EMD-40956 and PDB model 8T17. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



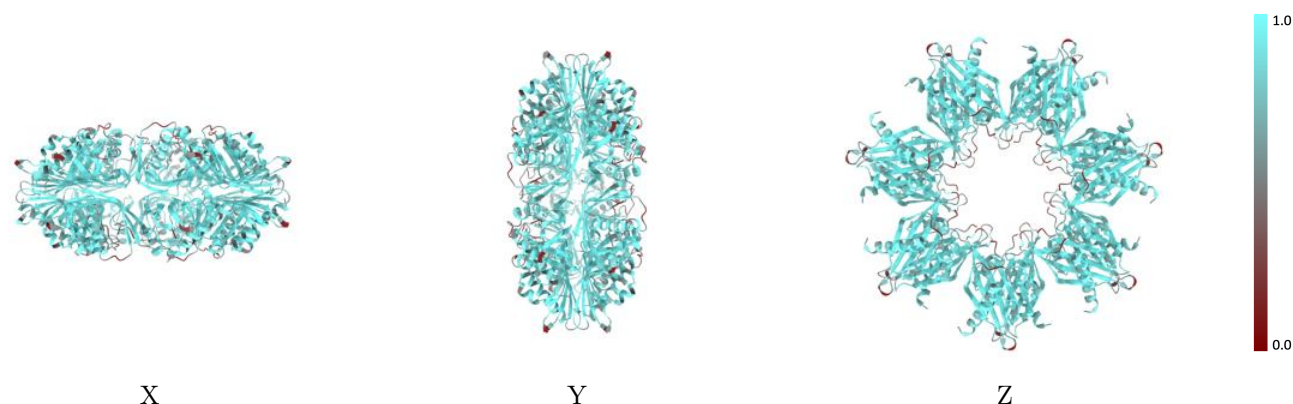
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



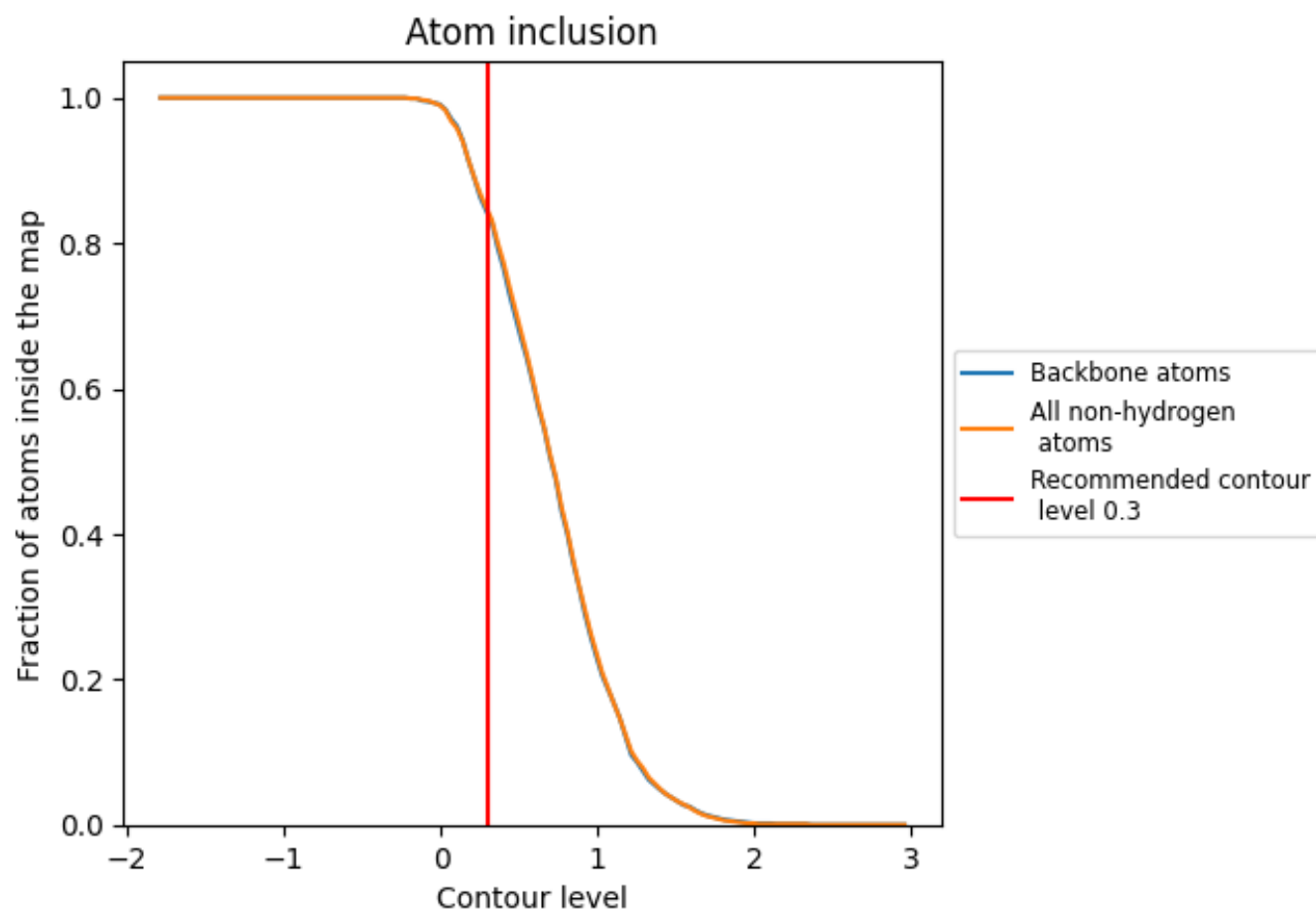
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 85% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8460	0.6330
A	0.8530	0.6350
B	0.8540	0.6330
C	0.8480	0.6330
D	0.8530	0.6320
E	0.8490	0.6330
F	0.8530	0.6330
G	0.8510	0.6330
H	0.8530	0.6330
I	0.8540	0.6310
J	0.8480	0.6310
K	0.8540	0.6340
L	0.8490	0.6330
M	0.8520	0.6330
N	0.8510	0.6320

1.0

0.0

<0.0