



Full wwPDB EM Validation Report ⓘ

May 11, 2026 – 07:23 pm BST

PDB ID : 9TIP / pdb_00009tip
EMDB ID : EMD-55964
Title : Phage 812 baseplate in the pre-contraction state - upper arm (segment CDEF)
Authors : Binovsky, J.; Plevka, P.
Deposited on : 2025-12-05
Resolution : 5.20 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

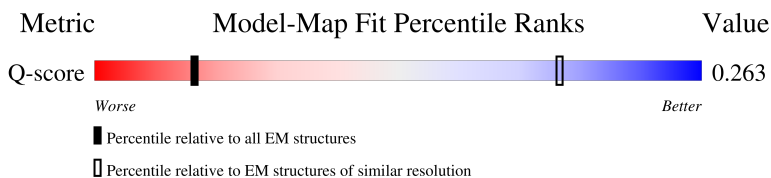
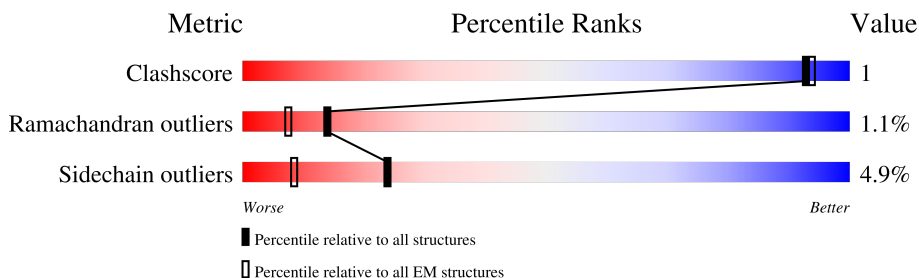
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.20 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	712 (4.70 - 5.70)

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	1019	<div> <div>17%</div> <div>25%</div> <div>73%</div> </div>
2	B	173	<div> <div>23%</div> <div>86%</div> <div>11%</div> <div>..</div> </div>
2	C	173	<div> <div>17%</div> <div>90%</div> <div>8%</div> <div>..</div> </div>
2	D	173	<div> <div>15%</div> <div>86%</div> <div>10%</div> <div>...</div> </div>

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Mol	Chain	Length	Quality of chain
2	E	173	
2	F	173	
2	G	173	
2	H	173	
2	I	173	
3	J	458	
3	K	458	
3	L	458	
4	M	640	
4	N	640	
4	O	640	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 15113 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 ORF63.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	278	Total	C	N	O	S	0	0
			2197	1394	353	448	2		

- Molecule 2 is a protein called ORF64.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	172	Total	C	N	O	S	0	0
			1349	858	221	269	1		
2	C	172	Total	C	N	O	S	0	0
			1349	858	221	269	1		
2	D	172	Total	C	N	O	S	0	0
			1349	858	221	269	1		
2	E	172	Total	C	N	O	S	0	0
			1349	858	221	269	1		
2	F	172	Total	C	N	O	S	0	0
			1349	858	221	269	1		
2	G	172	Total	C	N	O	S	0	0
			1349	858	221	269	1		
2	H	172	Total	C	N	O	S	0	0
			1349	858	221	269	1		
2	I	172	Total	C	N	O	S	0	0
			1349	858	221	269	1		

- Molecule 3 is a protein called ORF68.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	J	50	Total	C	N	O	S	0	0
			409	254	69	85	1		
3	K	50	Total	C	N	O	S	0	0
			409	254	69	85	1		
3	L	50	Total	C	N	O	S	0	0
			409	254	69	85	1		

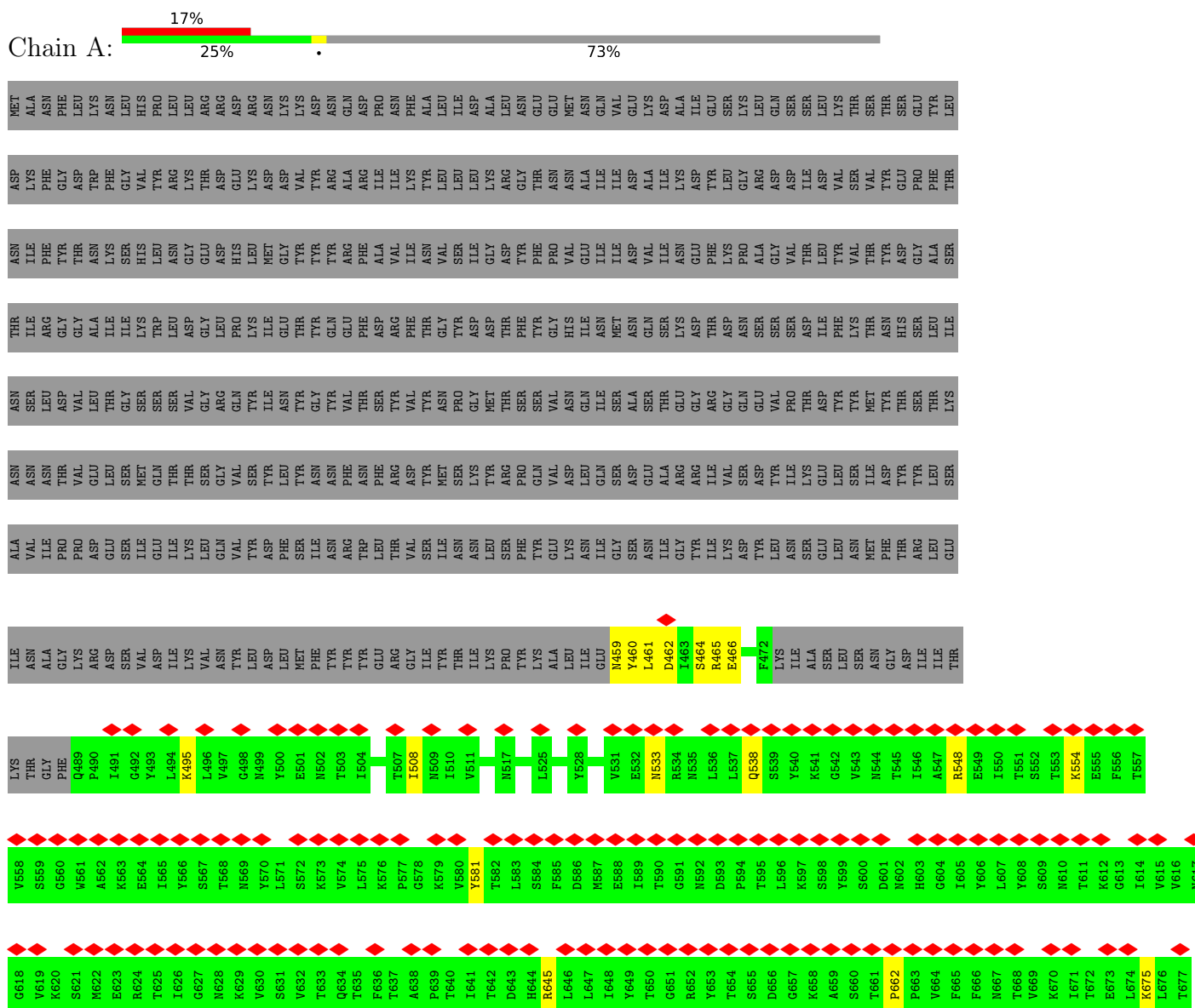
- Molecule 4 is a protein called CBM-cenC domain-containing protein.

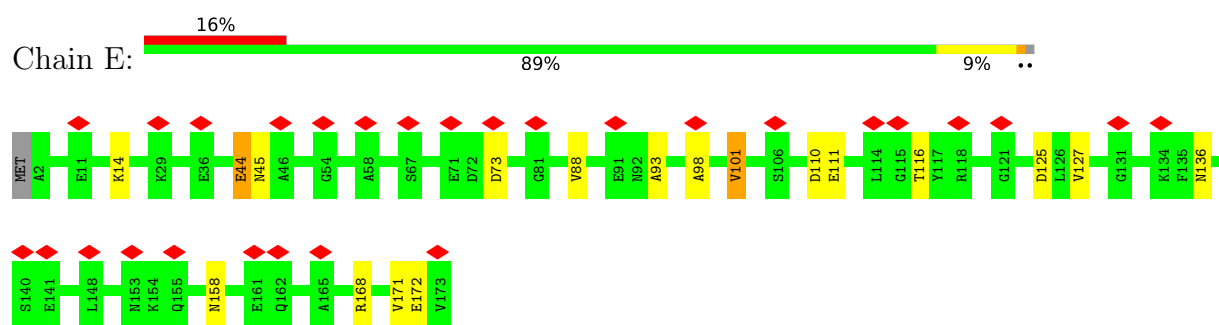
Mol	Chain	Residues	Atoms					AltConf	Trace
4	M	37	Total 299	C 192	N 46	O 59	S 2	0	0
4	N	37	Total 299	C 192	N 46	O 59	S 2	0	0
4	O	37	Total 299	C 192	N 46	O 59	S 2	0	0

3 Residue-property plots

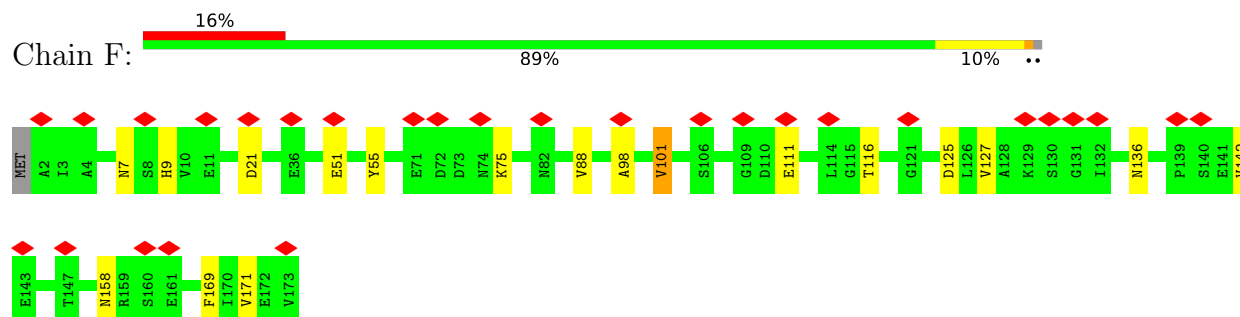
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: ORF63

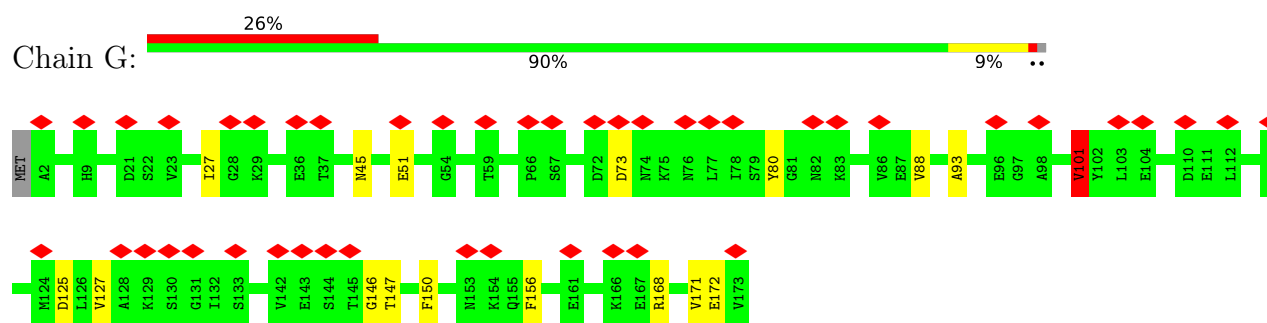




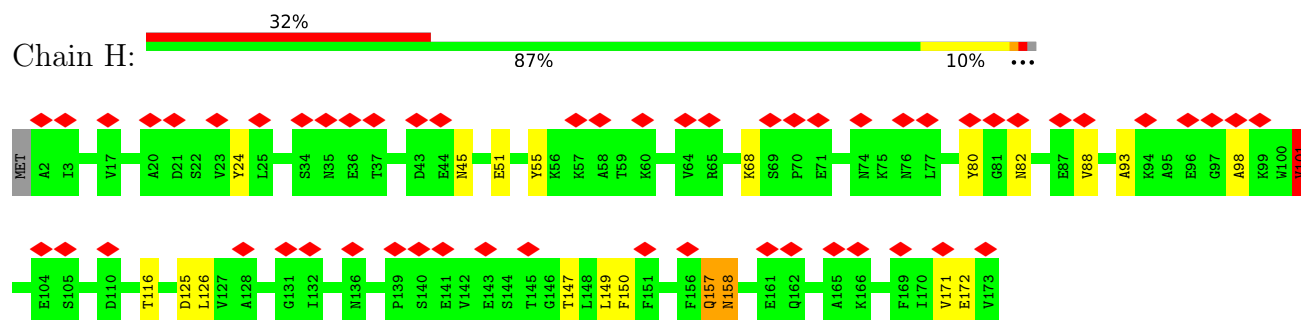
- Molecule 2: ORF64



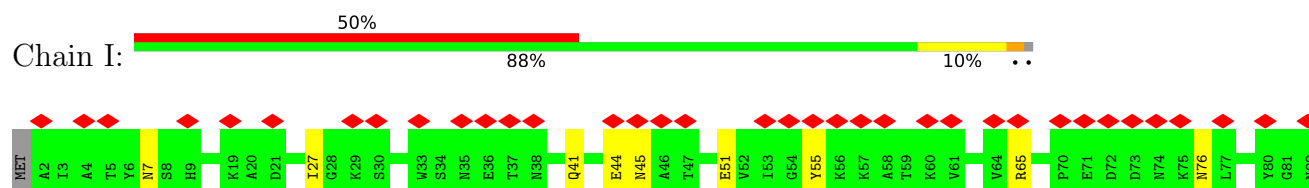
- Molecule 2: ORF64



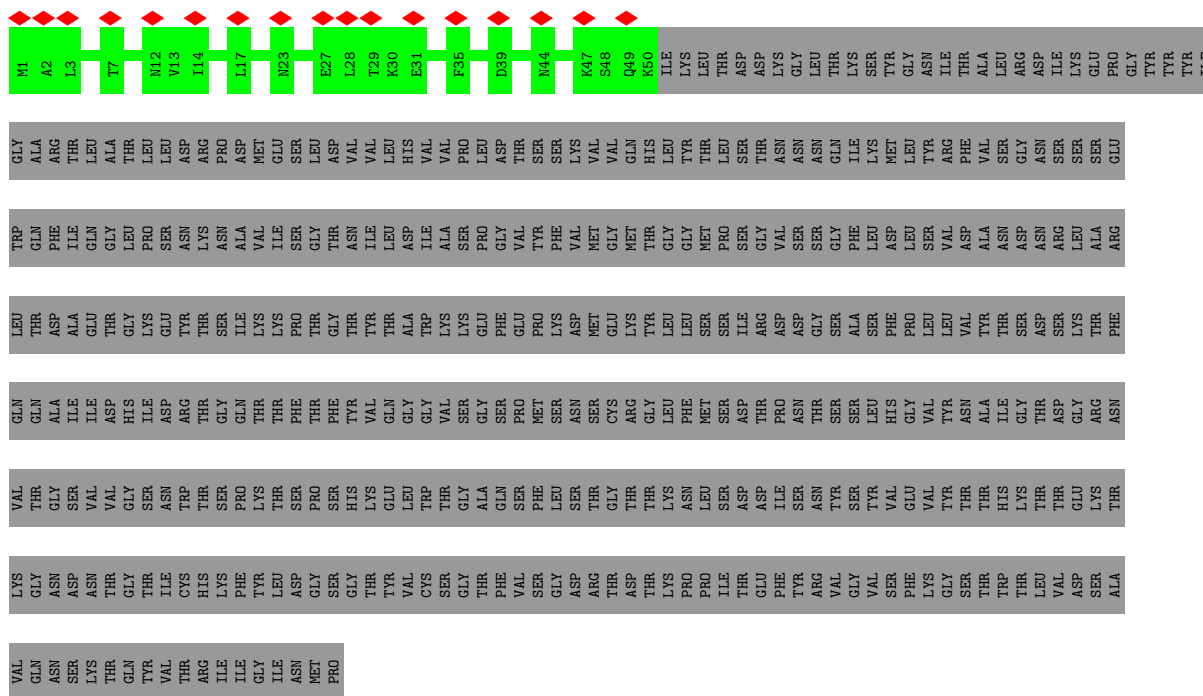
- Molecule 2: ORF64



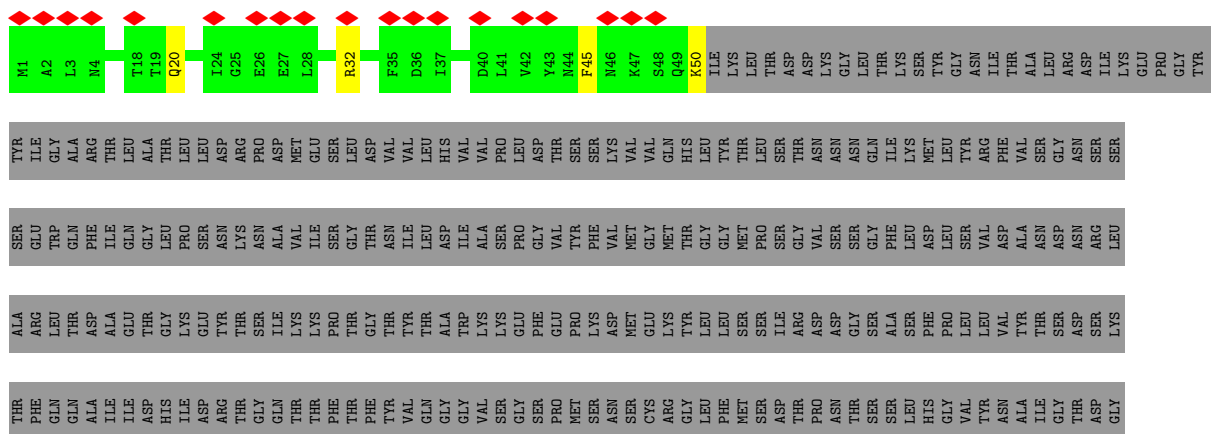
- Molecule 2: ORF64



- Molecule 3: ORF68



- Molecule 3: ORF68



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ALA
VAL
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GLN
TYR
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ARG
ILE
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GLY
ILE
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MET
PRO

- Molecule 3: ORF68



M1	A2	L3	M4	E10	I14	L17	T18	G25	E26	E27	L28	R32	N39	I34	F35	D36	I37	L41	M44	F45	M46	K47	S48	Q49	K50	I51	L52	L53	LEU	LEU	THR	ASP	ASP	L58	GLY	LEU	THR	L59	LYS	SER	TYR	GLY	ASN	ILE	THR	ALA	LEU	ARG	ASP	ILE	LYS	GLY	PRO	GLY
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TYR	TYR	ILE	GLY	ALA	ARG	THR	LEU	ALA	ALA	THR	LEU	LEU	ASP	ARG	PRO	ASP	MET	GLU	SER	LEU	ASP	VAL	VAL	HIS	VAL	VAL	LEU	PRO	LEU	ASP	THR	SER	SER	LYS	VAL	VAL	GLN	HIS	LEU	TYR	THR	LEU	SER	THR	ASN	ASN	ASN	GLN	GLN	ILE	LYS	MET	LEU	TYR	ARG	PHE	VAL	VAL	SER	GLY	ASN	SER
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SER	SER	GLU	TRP	GLN	PHE	ILE	GLN	GLY	LEU	PRO	SER	ASN	LYS	ASN	ALA	VAL	ILE	SER	GLY	THR	ASN	LEU	ASP	VAL	TYR	PHE	VAL	VAL	MET	GLY	MET	THR	GLY	GLY	PRO	SER	GLY	VAL	VAL	ASP	ALA	ALA	ASN	ASP	SER	SER	GLY	PHE	LEU	LEU	SER	VAL	ASP	ASN	ASN	ASP	ASP	PC
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LEU	ALA	ARG	LEU	THR	ASP	ALA	GLU	GLY	THR	LYS	GLU	TYR	THR	PRO	THR	GLY	GLY	TYR	THR	ALA	TRP	LYS	LYS	GLU	PHE	GLU	GLY	LYS	ASP	ASP	MET	GLY	LYS	LEU	LEU	SER	SER	ILE	ARG	ASP	ASP	GLY	SER	ALA	SER	PHE	PRO	LEU	LEU	VAL	TYR	THR	SER	ASP	SER
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Lys	Thr	Phe	Gln	Ala	Ile	Ile	Asp	His	Ile	Asp	Arg	Thr	Gly	Gln	Thr	Thr	Phe	Thr	Phe	Tyr	Val	Gln	Gly	Gly	Val	Ser	Gly	Ser	Ser	Pro	Met	Ser	Asn	Cys	Arg	Gly	Leu	Phe	Met	Ser	Asp	Thr	Pro	Asn	Thr	Ser	Ser	His	Gly	Val	Tyr	Asn	Ala	Ile	Gly	Gly	Thr	Ser
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GLY	ARG	ASN	VAL	THR	GLY	SER	VAL	VAL	GLY	SER	ASN	TRP	THR	SER	SER	LYS	THR	PRO	PRO	HIS	LYS	GLU	LEU	TRP	THR	ALA	GLN	SER	PHE	LEU	SER	THR	GLY	THR	THR	LYS	ASN	SER	SER	ASP	ILE	SER	ASN	Tyr	SER	Tyr	Val	GLU	Val	Tyr	Thr	Thr	His	Lys	Thr
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GLU	LYS	THR	THR	GLY	ASN	ASP	ASN	THR	GLY	ILE	CYS	HIS	LYS	PHE	TYR	LEU	ASP	GLY	SER	THR	THR	VAL	CYS	SER	GLY	THR	PHE	VAL	SER	GLY	ASP	ARG	THR	ASP	THR	LYS	PRO	PRO	ILE	THR	GLU	PHE	TYR	ARG	VAL	GLY	VAL	SER	PHE	LYS	PHE	GLY	SER	THR	THR	THR	LEU	VAL
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ILE
ASN
MET
PRO

- Molecule 4: CBM-cenC domain-containing protein



M1	A2	F4	N3	E10	T11	Q12	K13	L14	K15	G25	L28	F31	L34	S35	D36	V37	LYS	GLN	ILE	ILE	SER	GLN	GLN	PRO	ASP	PHE	ASN	ASN	ASN	LEU	ALA	ILE	ILE	ILE	ASP	PRO	SER	GLY	ASN	TYR	TYR	VAL	THR	ASN	SER	LYS	GLY	ALA	ALA	PRO	SER	GLY	GLU	ALA	ALA	THR	ALA	ALA	GLY
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VAL	ARG	LEU	ASP	LYS	ARG	ASN	VAL	ASN	TYR	TYR	LYS	ILE	TYR	TYR	SER	PRO	SER	ASN	LYS	MET	TYR	ILE	LYS	THR	TYR	ALA	ASN	GLY	THR	VAL	ASP	TRP	ILE	ILE	SER	PHE	LYS	LEU	TYR	ASN	GLU	GLY	ASN	THR	LEU	ASN	VAL	LYS	GLU	LEU	THR	THI
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SER	THR	THR	GLN	TYR	ALA	THR	LEU	VAL	ASN	PRO	PRO	LYS	GLU	ASN	LEU	ASN	THR	GLY	TRP	VAL	ASN	TYR	LYS	GLU	LYS	SER	ASN	GLY	VAL	SER	SER	LEU	VAL	GLU	PHE	ASN	VAL	PRO	VAL	ASN	SER	SER	THR	THR	SER	PHE	LYS	LYS	MET	ILE	ARG	LYS	LEU	PRO	PRO	ASN	LEU
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LEU LYS ASP SER LEU PHE VAL THR PRO GLU THR SER TYR SER ASN ILE LYS THR ASP ASN TRP THR PRO PHE TRP TYR SER SER ASN SER GLY ARG SER GLY VAL ARG PHE ARG GLY GLU ASN THR VAL GLN ILE ASP ASP GLY THR THR VAL VAL VAL VAL

ASN	ARG	PHE	LYS	GLY	LYS	GLU	LEU	VAL	GLY	ASP	THR	VAL	THR	VAL	VAL	TYR	ILE	ASN	ASP	PRO	ALA	LEU	LYS	ASP	ASN	GLU	THR	ASP	THR	VAL	ASP	THR	LYS	ASN	PRO	TYR	THR	GLY	GLY	ARG	GLU	GLU	ILE	THR
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Chain 0:  5% 94%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	14954	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.8	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.138	Depositor
Minimum map value	-0.079	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.04	Depositor
Map size (\AA)	300.096, 300.096, 300.096	wwPDB
Map dimensions	180, 180, 180	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.6672001, 1.6672001, 1.6672001	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	0.75	1/2238 (0.0%)	1.25	5/3046 (0.2%)
2	B	0.71	0/1377	1.41	8/1872 (0.4%)
2	C	0.70	0/1377	1.38	6/1872 (0.3%)
2	D	0.69	0/1377	1.38	7/1872 (0.4%)
2	E	0.68	0/1377	1.33	3/1872 (0.2%)
2	F	0.76	1/1377 (0.1%)	1.34	4/1872 (0.2%)
2	G	0.72	0/1377	1.37	4/1872 (0.2%)
2	H	0.74	0/1377	1.37	4/1872 (0.2%)
2	I	0.73	0/1377	1.33	4/1872 (0.2%)
3	J	0.68	0/412	1.24	0/557
3	K	0.69	0/412	1.28	1/557 (0.2%)
3	L	0.72	0/412	1.26	0/557
4	M	0.76	0/304	1.28	0/411
4	N	0.76	0/304	1.30	0/411
4	O	0.74	0/304	1.27	1/411 (0.2%)
All	All	0.72	2/15402 (0.0%)	1.33	47/20926 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
2	F	0	1
2	G	0	1
2	H	0	2
2	I	0	2
4	O	0	2
All	All	0	11

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	101	VAL	CB-CG2	-11.30	1.15	1.52
1	A	662	PRO	CA-C	5.48	1.54	1.51

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	101	VAL	CA-CB-CG1	11.26	129.54	110.40
2	D	158	ASN	CA-CB-CG	8.93	121.53	112.60
2	B	163	THR	CA-CB-CG2	8.77	125.40	110.50
2	E	101	VAL	N-CA-C	7.49	118.67	107.51
2	I	136	ASN	CA-CB-CG	7.18	119.78	112.60
2	C	158	ASN	CA-CB-CG	7.12	119.72	112.60
2	H	101	VAL	CA-CB-CG1	6.71	121.81	110.40
2	B	101	VAL	CA-CB-CG1	6.66	121.71	110.40
2	H	82	ASN	CA-CB-CG	6.57	119.17	112.60
2	F	101	VAL	CA-CB-CG1	6.52	121.49	110.40
2	G	101	VAL	CA-CB-CG1	6.38	121.25	110.40
2	B	9	HIS	CB-CG-CD2	-6.35	122.94	131.20
2	D	158	ASN	OD1-CG-ND2	-6.21	116.39	122.60
2	D	136	ASN	CA-CB-CG	6.17	118.77	112.60
2	D	157	GLN	OE1-CD-NE2	-6.07	116.53	122.60
1	A	464	SER	N-CA-C	5.99	121.25	113.88
2	B	106	SER	CA-C-N	5.95	127.24	121.65
2	B	106	SER	C-N-CA	5.95	127.24	121.65
2	E	110	ASP	N-CA-C	5.84	117.45	111.14
2	F	169	PHE	CA-CB-CG	5.82	119.62	113.80
2	D	101	VAL	CA-CB-CG1	5.78	120.23	110.40
2	B	136	ASN	CA-CB-CG	5.77	118.37	112.60
2	F	9	HIS	CB-CG-CD2	-5.77	123.70	131.20
2	C	156	PHE	CA-CB-CG	5.75	119.55	113.80
1	A	459	ASN	CA-C-N	5.71	131.23	121.87
1	A	459	ASN	C-N-CA	5.71	131.23	121.87
2	G	172	GLU	N-CA-CB	-5.69	101.46	110.28
2	C	157	GLN	CB-CG-CD	-5.69	102.92	112.60
2	G	146	GLY	N-CA-C	5.64	119.98	112.65
2	C	103	LEU	N-CA-CB	-5.62	102.16	110.37
2	D	158	ASN	CB-CG-ND2	5.49	124.63	116.40
2	I	111	GLU	CB-CG-CD	5.41	121.79	112.60
2	B	103	LEU	N-CA-CB	-5.40	102.48	110.37
2	D	162	GLN	OE1-CD-NE2	-5.32	117.28	122.60
2	B	110	ASP	N-CA-C	5.32	117.89	111.40
4	O	18	TYR	CA-CB-CG	5.29	123.42	113.90
2	I	169	PHE	CA-CB-CG	-5.28	108.52	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	169	PHE	CA-CB-CG	5.27	119.07	113.80
2	G	93	ALA	N-CA-C	5.26	117.42	111.11
1	A	645	ARG	NE-CZ-NH2	5.18	123.86	119.20
3	K	32	ARG	NE-CZ-NH2	5.13	123.82	119.20
2	I	65	ARG	NE-CZ-NH2	5.10	123.79	119.20
1	A	538	GLN	OE1-CD-NE2	-5.10	117.50	122.60
2	H	172	GLU	N-CA-CB	-5.08	102.11	110.40
2	F	21	ASP	CA-CB-CG	-5.08	107.52	112.60
2	H	157	GLN	OE1-CD-NE2	-5.07	117.53	122.60
2	C	158	ASN	N-CA-CB	5.01	117.10	110.29

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	460	TYR	Sidechain
1	A	548	ARG	Sidechain
1	A	581	TYR	Sidechain
2	F	55	TYR	Sidechain
2	G	80	TYR	Sidechain
2	H	55	TYR	Sidechain
2	H	80	TYR	Sidechain
2	I	169	PHE	Sidechain
2	I	55	TYR	Sidechain
4	O	18	TYR	Sidechain
4	O	5	TYR	Sidechain

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2197	0	2179	6	0
2	B	1349	0	1339	6	0
2	C	1349	0	1339	9	0
2	D	1349	0	1339	12	0
2	E	1349	0	1339	4	0
2	F	1349	0	1339	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	G	1349	0	1339	5	0
2	H	1349	0	1339	6	0
2	I	1349	0	1339	2	0
3	J	409	0	404	0	0
3	K	409	0	404	1	0
3	L	409	0	404	0	0
4	M	299	0	301	0	0
4	N	299	0	301	0	0
4	O	299	0	301	0	0
All	All	15113	0	15006	43	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 1.

All (43) 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)
2:F:101:VAL:HB	2:F:171:VAL:HG22	1.58	0.84
2:E:101:VAL:HB	2:E:171:VAL:HG22	1.65	0.78
2:F:101:VAL:HB	2:F:171:VAL:CG2	2.22	0.69
2:E:101:VAL:HB	2:E:171:VAL:CG2	2.24	0.67
2:B:147:THR:HG23	2:C:7:ASN:HB3	1.78	0.65
2:C:158:ASN:HD22	2:D:157:GLN:CA	2.17	0.58
2:H:101:VAL:HB	2:H:171:VAL:HG22	1.90	0.54
2:H:101:VAL:HB	2:H:171:VAL:CG2	2.40	0.52
2:D:103:LEU:HD11	2:D:122:PHE:CD2	2.46	0.50
1:A:554:LYS:HE2	1:A:685:TYR:CE2	2.48	0.49
2:D:101:VAL:HB	2:D:171:VAL:CG2	2.44	0.47
1:A:495:LYS:HB2	1:A:734:TRP:CH2	2.49	0.47
2:G:101:VAL:HB	2:G:171:VAL:CG2	2.45	0.47
1:A:675:LYS:HE3	1:A:686:SER:H	1.80	0.47
2:D:101:VAL:HB	2:D:171:VAL:HG22	1.97	0.47
2:C:158:ASN:HB2	2:D:157:GLN:HA	1.97	0.47
2:I:107:ILE:HD12	2:I:107:ILE:H	1.79	0.47
1:A:733:SER:HB3	2:C:35:ASN:CG	2.39	0.46
2:D:3:ILE:HD12	2:D:3:ILE:O	2.15	0.46
2:B:6:TYR:CE2	2:B:99:LYS:HE2	2.50	0.46
2:C:116:THR:HG22	2:C:158:ASN:HA	1.98	0.45
1:A:461:LEU:HD12	1:A:462:ASP:H	1.82	0.45
2:D:3:ILE:HG12	2:E:44:GLU:CB	2.47	0.45
2:G:150:PHE:CZ	2:G:171:VAL:HG11	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:116:THR:HG22	2:H:158:ASN:HA	1.99	0.45
2:D:33:TRP:CD1	2:D:118:ARG:HD3	2.52	0.44
2:H:147:THR:HG23	2:I:7:ASN:HB3	1.99	0.44
2:H:149:LEU:HD23	2:H:150:PHE:CE2	2.53	0.43
3:K:45:PHE:CE2	3:K:50:LYS:HE2	2.54	0.43
2:H:24:TYR:CE1	2:H:126:LEU:HD11	2.53	0.43
2:C:157:GLN:HA	2:D:158:ASN:HB2	2.00	0.42
2:B:3:ILE:HD13	2:B:3:ILE:H	1.84	0.42
2:F:7:ASN:HB3	2:G:147:THR:HG23	2.00	0.42
2:G:101:VAL:HB	2:G:171:VAL:HG22	2.00	0.42
2:C:158:ASN:CG	2:D:156:PHE:CD1	2.98	0.42
2:B:25:LEU:HD12	2:B:121:GLY:O	2.19	0.41
1:A:466:GLU:CG	2:B:168:ARG:HD2	2.51	0.41
2:E:116:THR:HG22	2:E:158:ASN:HA	2.03	0.41
2:C:158:ASN:HD22	2:D:157:GLN:N	2.19	0.41
2:G:150:PHE:CE2	2:G:171:VAL:HG11	2.56	0.41
2:F:116:THR:HG22	2:F:158:ASN:HA	2.03	0.41
2:B:107:ILE:H	2:B:107:ILE:HD12	1.85	0.41
2:C:158:ASN:HD22	2:D:157:GLN:HA	1.84	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	274/1019 (27%)	263 (96%)	9 (3%)	2 (1%)	18	55
2	B	170/173 (98%)	154 (91%)	14 (8%)	2 (1%)	10	42
2	C	170/173 (98%)	157 (92%)	11 (6%)	2 (1%)	10	42
2	D	170/173 (98%)	153 (90%)	12 (7%)	5 (3%)	3	23
2	E	170/173 (98%)	157 (92%)	10 (6%)	3 (2%)	6	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	F	170/173 (98%)	157 (92%)	12 (7%)	1 (1%)	21	58
2	G	170/173 (98%)	161 (95%)	8 (5%)	1 (1%)	21	58
2	H	170/173 (98%)	154 (91%)	13 (8%)	3 (2%)	6	32
2	I	170/173 (98%)	153 (90%)	16 (9%)	1 (1%)	21	58
3	J	48/458 (10%)	46 (96%)	2 (4%)	0	100	100
3	K	48/458 (10%)	46 (96%)	2 (4%)	0	100	100
3	L	48/458 (10%)	45 (94%)	3 (6%)	0	100	100
4	M	35/640 (6%)	35 (100%)	0	0	100	100
4	N	35/640 (6%)	35 (100%)	0	0	100	100
4	O	35/640 (6%)	35 (100%)	0	0	100	100
All	All	1883/5697 (33%)	1751 (93%)	112 (6%)	20 (1%)	14	45

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	465	ARG
2	B	93	ALA
2	C	93	ALA
2	C	111	GLU
2	D	93	ALA
2	D	114	LEU
2	E	93	ALA
2	H	93	ALA
2	I	93	ALA
1	A	694	ASN
2	D	98	ALA
2	H	98	ALA
2	D	156	PHE
2	E	98	ALA
2	F	98	ALA
2	G	73	ASP
2	B	163	THR
2	E	73	ASP
2	H	158	ASN
2	D	73	ASP

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	254/928 (27%)	251 (99%)	3 (1%)	63	74
2	B	152/153 (99%)	142 (93%)	10 (7%)	15	37
2	C	152/153 (99%)	146 (96%)	6 (4%)	28	49
2	D	152/153 (99%)	139 (91%)	13 (9%)	10	29
2	E	152/153 (99%)	142 (93%)	10 (7%)	15	37
2	F	152/153 (99%)	144 (95%)	8 (5%)	20	41
2	G	152/153 (99%)	143 (94%)	9 (6%)	18	39
2	H	152/153 (99%)	145 (95%)	7 (5%)	24	45
2	I	152/153 (99%)	138 (91%)	14 (9%)	8	27
3	J	48/405 (12%)	48 (100%)	0	100	100
3	K	48/405 (12%)	47 (98%)	1 (2%)	47	64
3	L	48/405 (12%)	47 (98%)	1 (2%)	47	64
4	M	35/577 (6%)	33 (94%)	2 (6%)	18	40
4	N	35/577 (6%)	35 (100%)	0	100	100
4	O	35/577 (6%)	35 (100%)	0	100	100
All	All	1719/5098 (34%)	1635 (95%)	84 (5%)	24	43

All (84) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	508	ILE
1	A	533	ASN
1	A	718	THR
2	B	3	ILE
2	B	45	ASN
2	B	51	GLU
2	B	68	LYS
2	B	88	VAL
2	B	101	VAL
2	B	136	ASN

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Mol	Chain	Res	Type
2	B	143	GLU
2	B	157	GLN
2	B	162	GLN
2	C	71	GLU
2	C	88	VAL
2	C	101	VAL
2	C	125	ASP
2	C	127	VAL
2	C	143	GLU
2	D	68	LYS
2	D	75	LYS
2	D	88	VAL
2	D	99	LYS
2	D	101	VAL
2	D	111	GLU
2	D	125	ASP
2	D	136	ASN
2	D	143	GLU
2	D	154	LYS
2	D	156	PHE
2	D	157	GLN
2	D	162	GLN
2	E	14	LYS
2	E	44	GLU
2	E	45	ASN
2	E	88	VAL
2	E	111	GLU
2	E	125	ASP
2	E	127	VAL
2	E	136	ASN
2	E	168	ARG
2	E	172	GLU
2	F	51	GLU
2	F	75	LYS
2	F	88	VAL
2	F	111	GLU
2	F	125	ASP
2	F	127	VAL
2	F	136	ASN
2	F	142	VAL
2	G	27	ILE
2	G	45	ASN

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Mol	Chain	Res	Type
2	G	51	GLU
2	G	88	VAL
2	G	101	VAL
2	G	125	ASP
2	G	127	VAL
2	G	156	PHE
2	G	168	ARG
2	H	45	ASN
2	H	51	GLU
2	H	68	LYS
2	H	88	VAL
2	H	101	VAL
2	H	125	ASP
2	H	157	GLN
2	I	27	ILE
2	I	41	GLN
2	I	44	GLU
2	I	45	ASN
2	I	51	GLU
2	I	76	ASN
2	I	88	VAL
2	I	101	VAL
2	I	111	GLU
2	I	125	ASP
2	I	127	VAL
2	I	136	ASN
2	I	161	GLU
2	I	172	GLU
3	K	20	GLN
3	L	49	GLN
4	M	4	ASN
4	M	15	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	523	ASN
1	A	667	ASN
2	B	38	ASN
2	B	157	GLN
2	C	7	ASN
2	C	9	HIS

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Mol	Chain	Res	Type
2	C	45	ASN
2	C	153	ASN
2	C	158	ASN
2	D	119	GLN
2	D	157	GLN
2	E	7	ASN
2	E	74	ASN
2	E	119	GLN
2	E	153	ASN
2	E	158	ASN
2	F	119	GLN
2	F	153	ASN
2	G	158	ASN
2	H	7	ASN
2	H	119	GLN
2	I	119	GLN
2	I	153	ASN
4	M	26	ASN
4	N	26	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

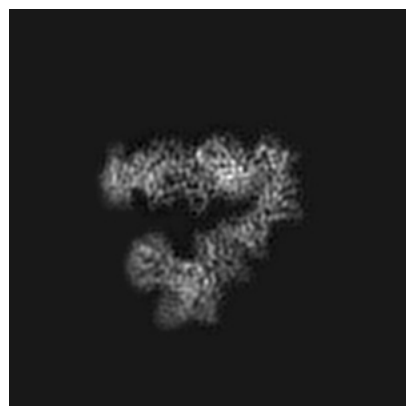
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55964. These allow visual inspection of the internal detail of the map and identification of artifacts.

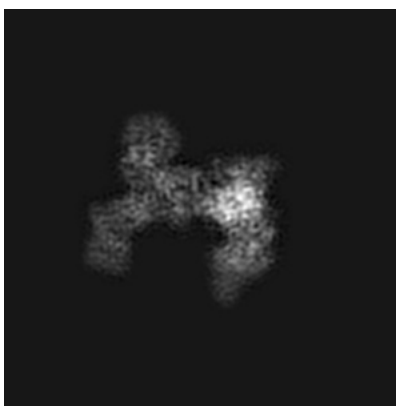
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

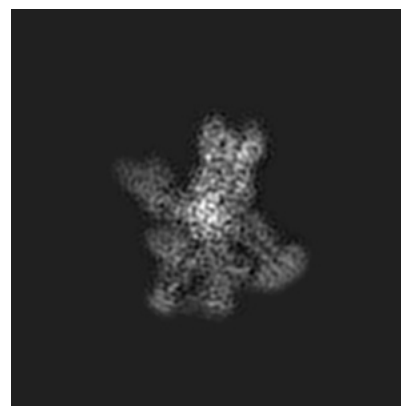
6.1.1 Primary map



X

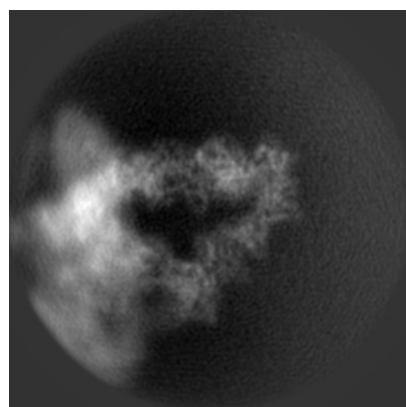


Y

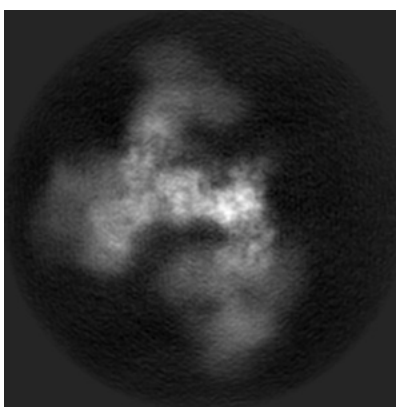


Z

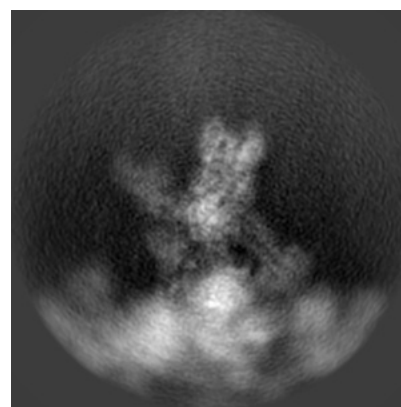
6.1.2 Raw map



X



Y



Z

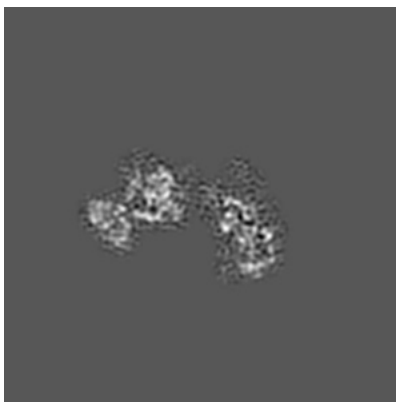
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

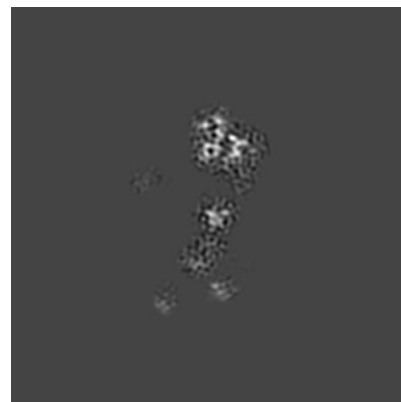
6.2.1 Primary map



X Index: 90

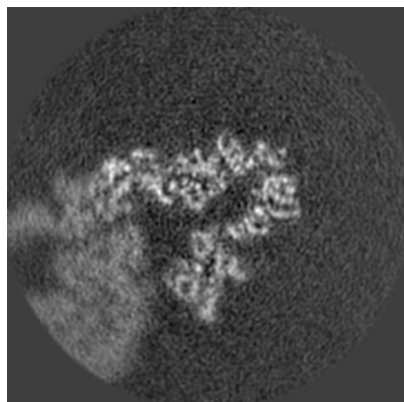


Y Index: 90

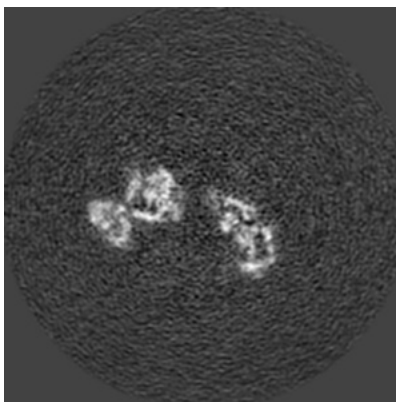


Z Index: 90

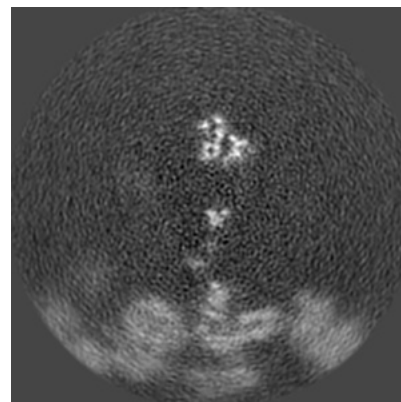
6.2.2 Raw map



X Index: 90



Y Index: 90

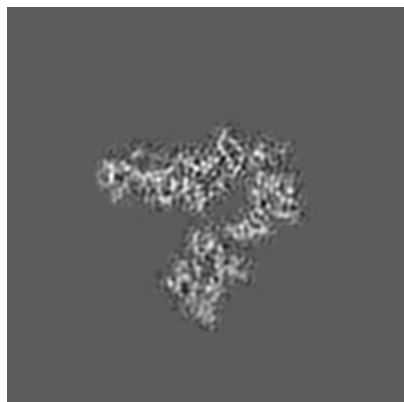


Z Index: 90

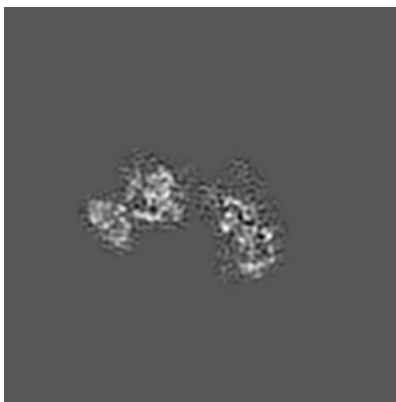
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

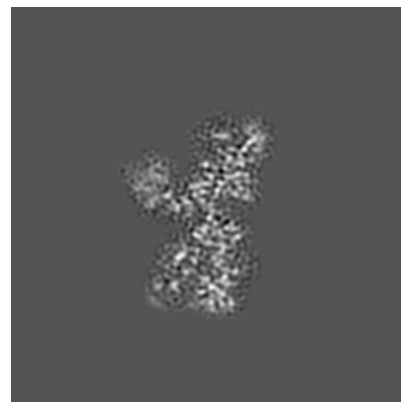
6.3.1 Primary map



X Index: 89

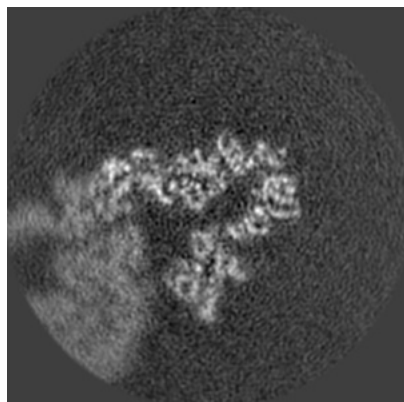


Y Index: 90

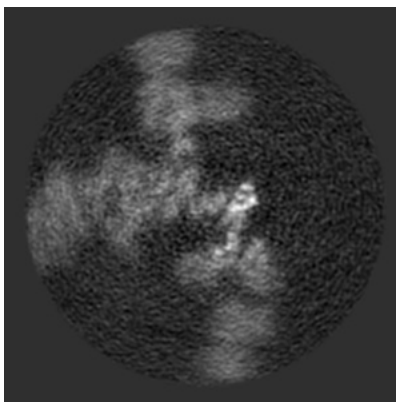


Z Index: 107

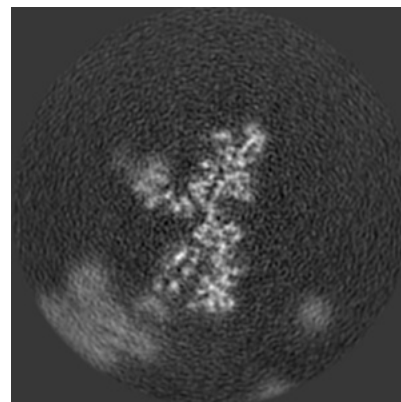
6.3.2 Raw map



X Index: 90



Y Index: 47



Z Index: 107

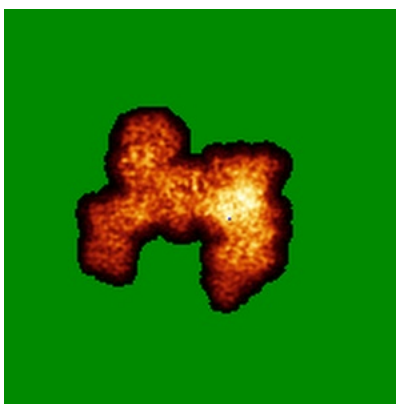
The images above show the largest variance slices of the map in three orthogonal directions.

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

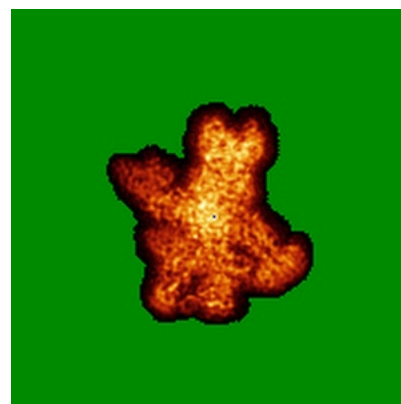
6.4.1 Primary map



X

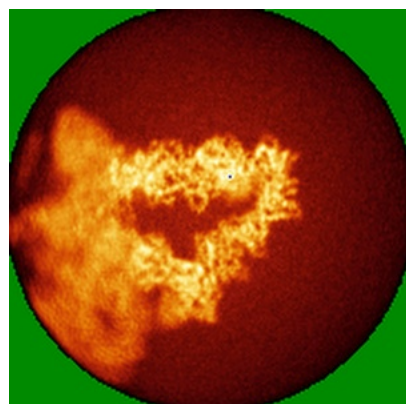


Y

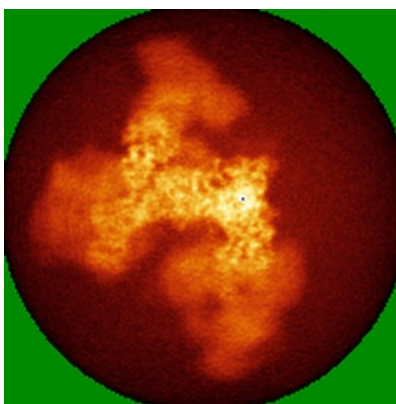


Z

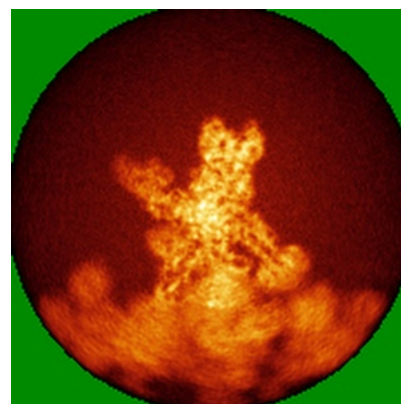
6.4.2 Raw map



X



Y

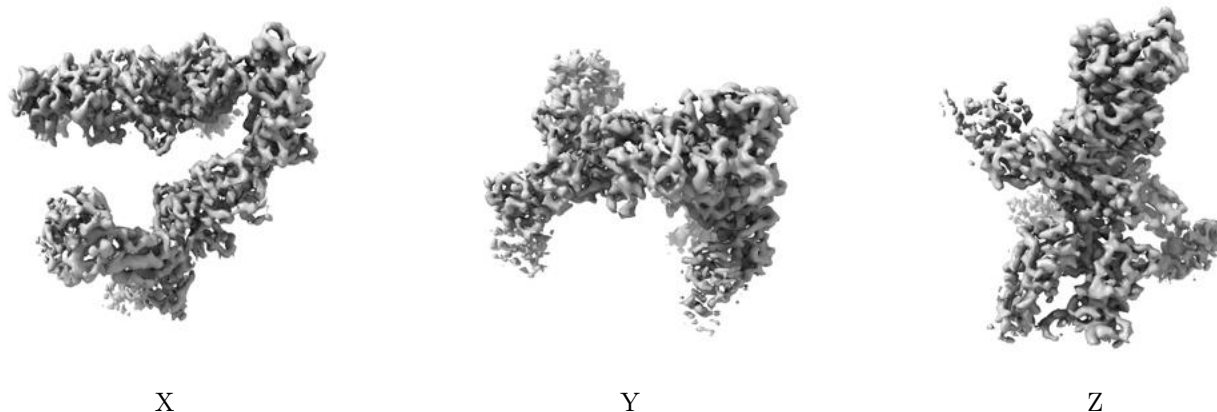


Z

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.

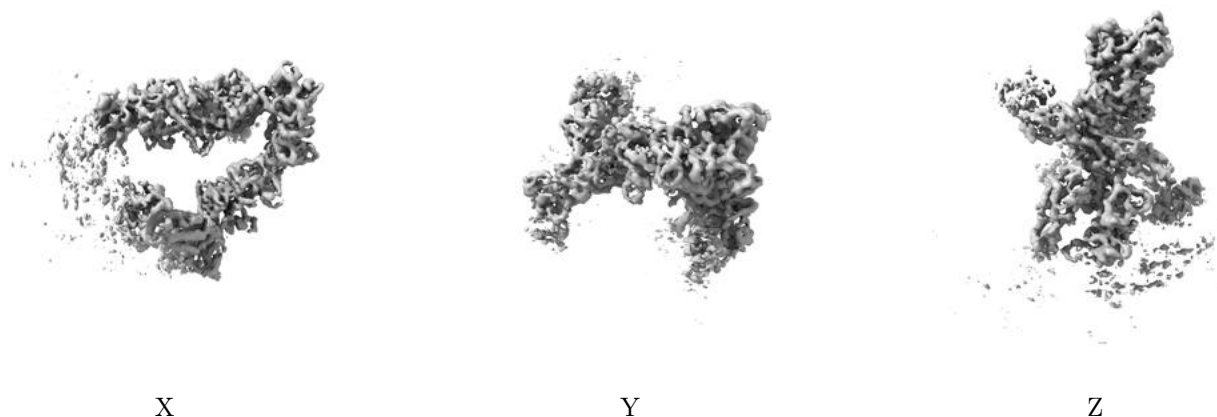
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. 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.

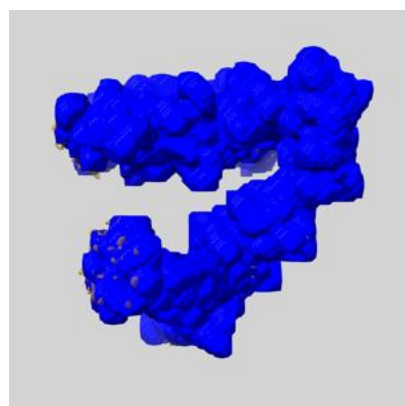
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

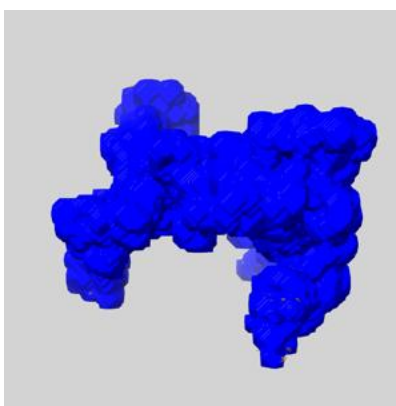
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

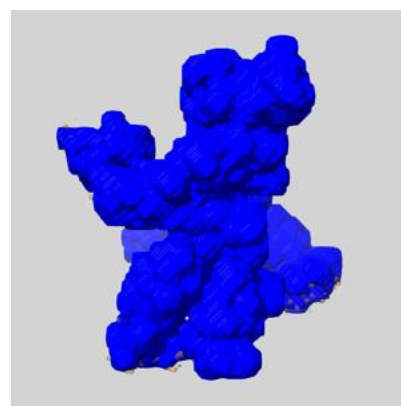
6.6.1 emd_55964_msk_1.map [i](#)



X



Y

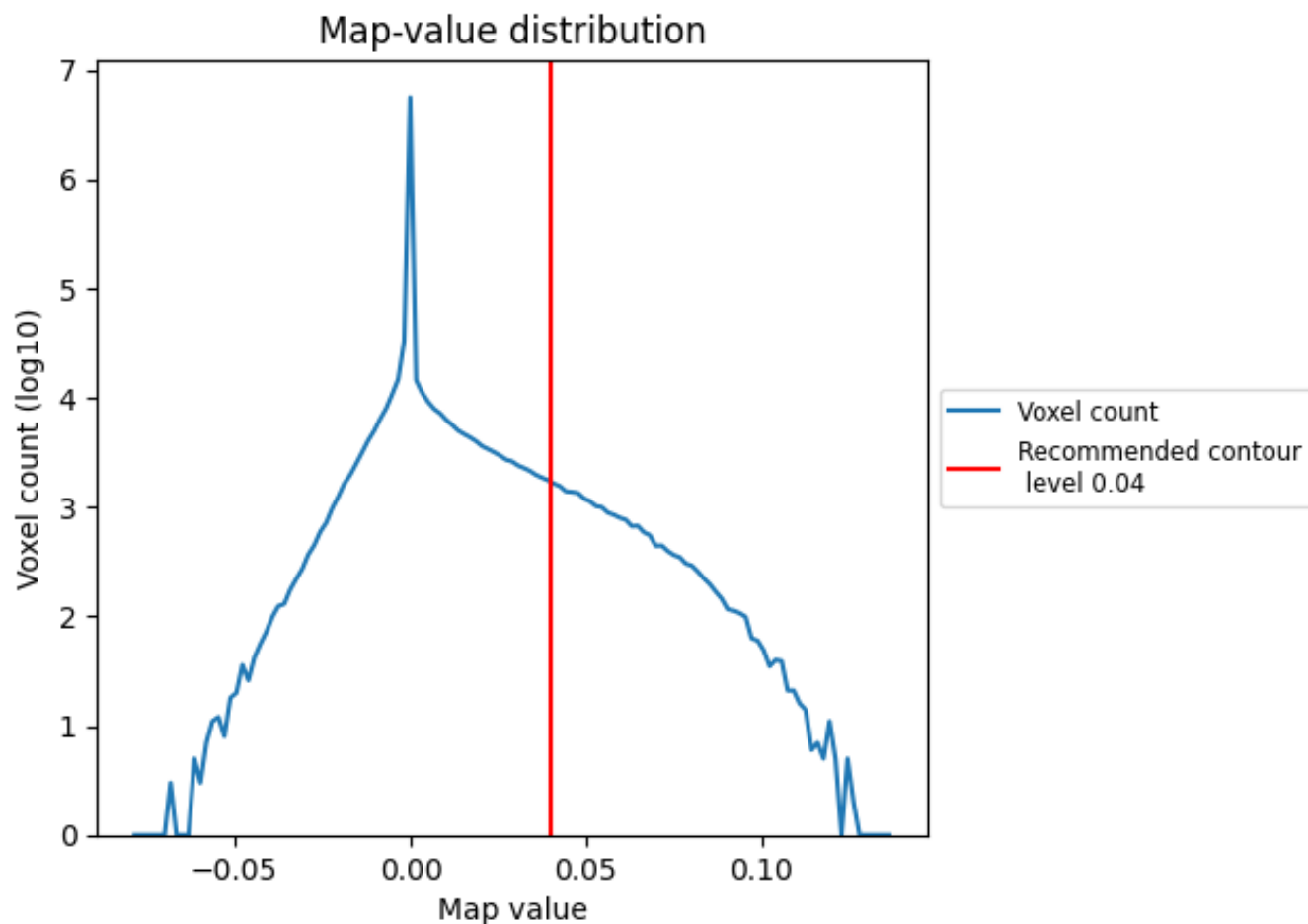


Z

7 Map analysis [i](#)

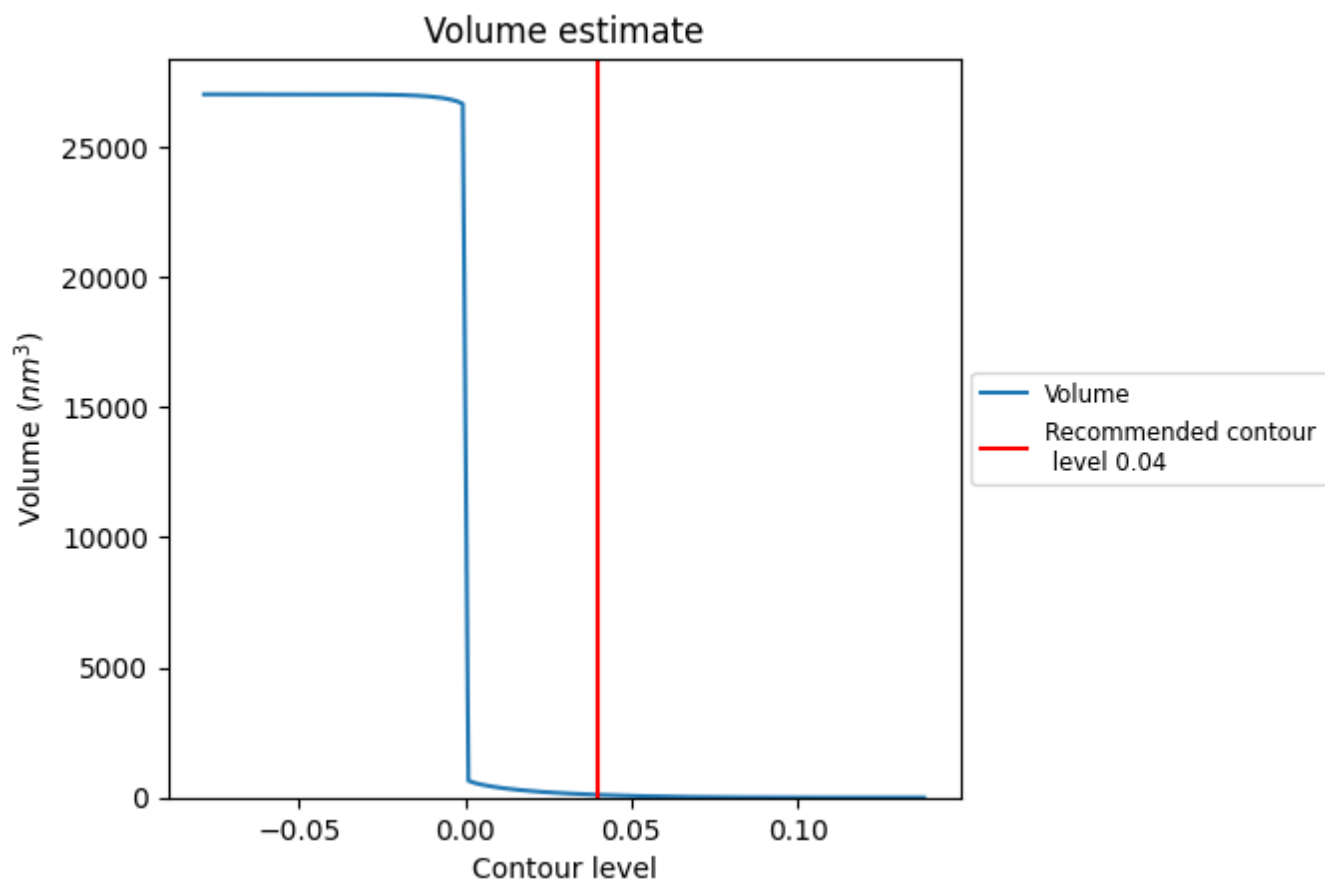
This section contains the results of statistical analysis of the map.

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.

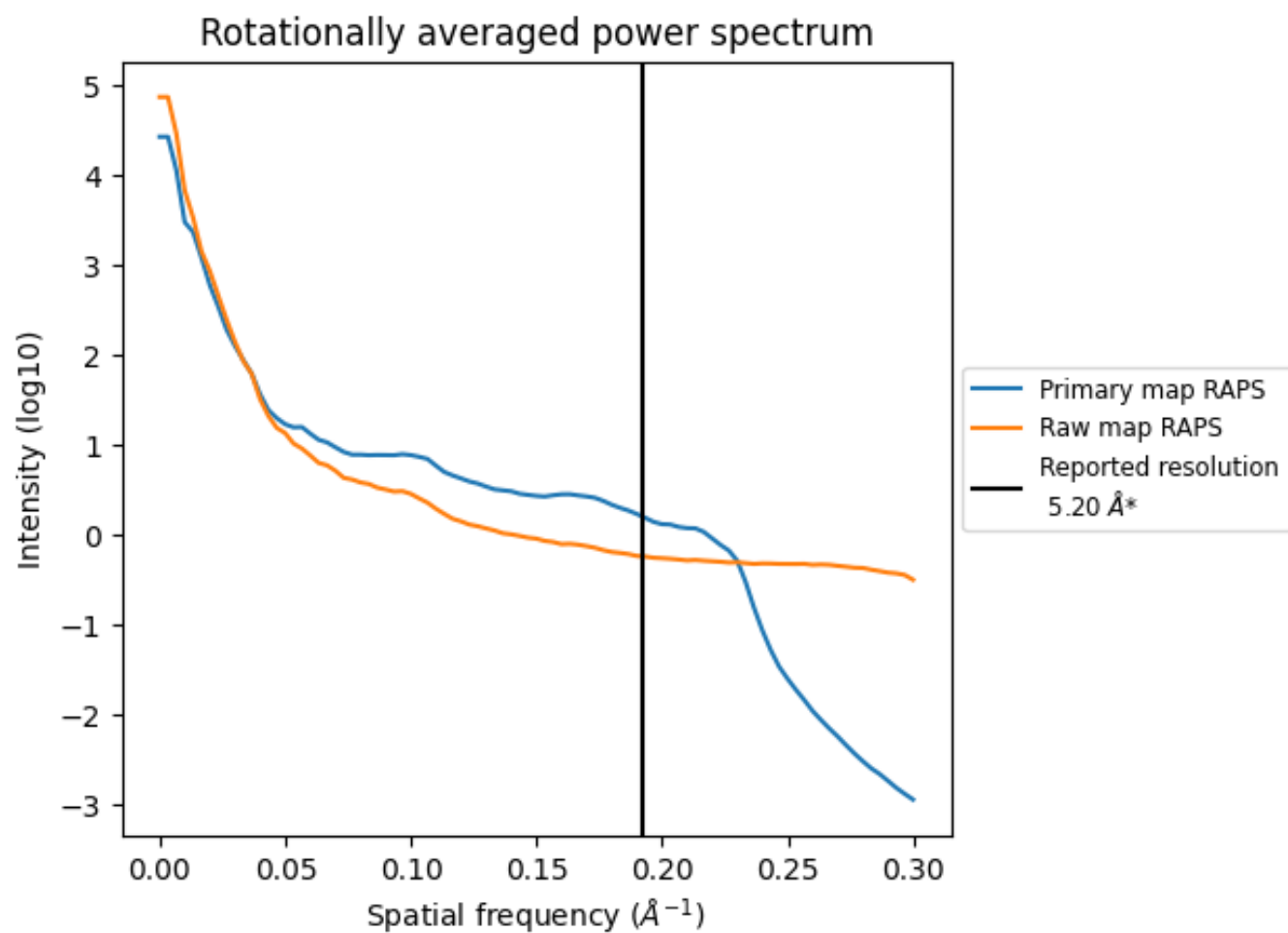
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 106 nm³; this corresponds to an approximate mass of 95 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 ⓘ

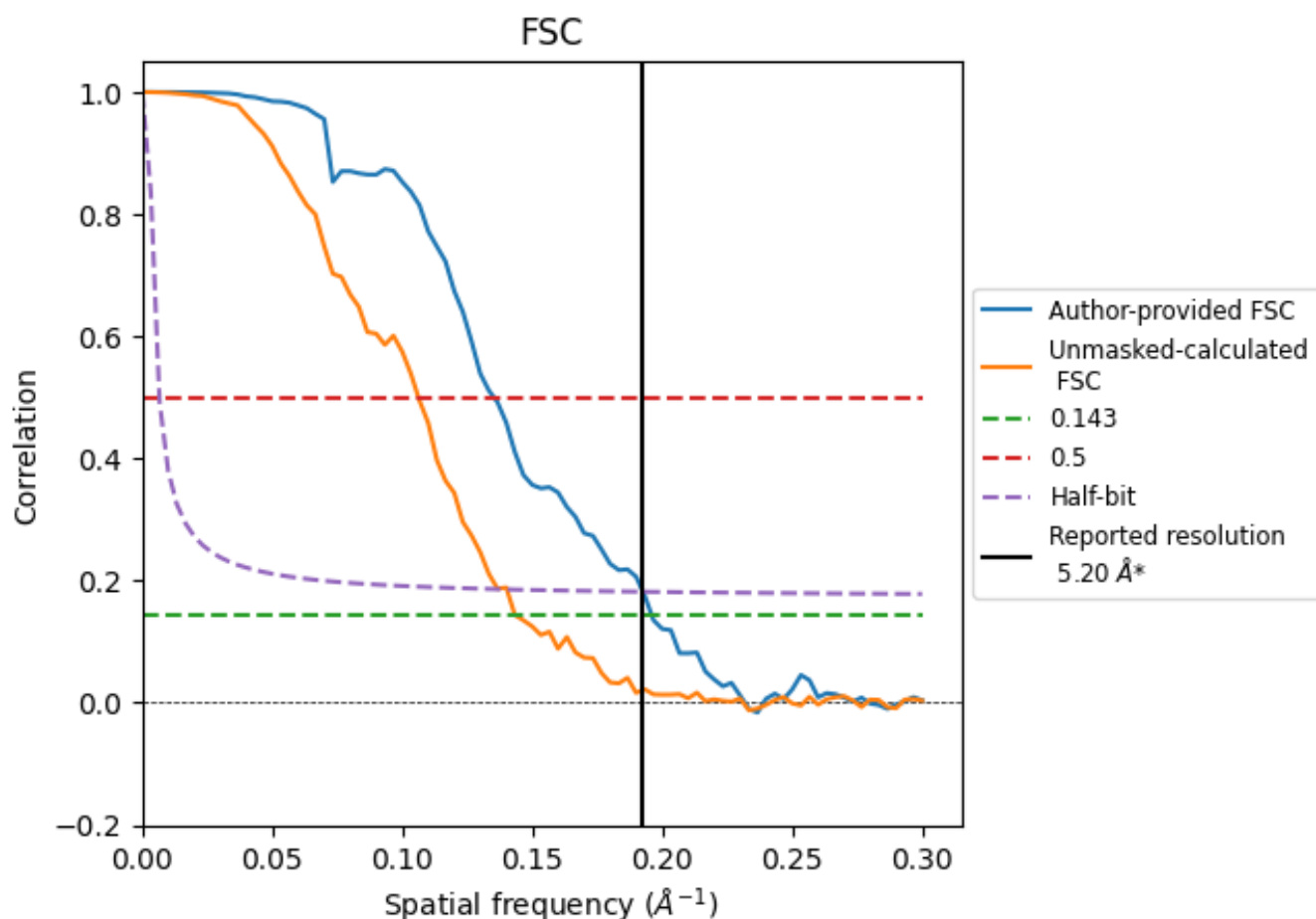


*Reported resolution corresponds to spatial frequency of 0.192 Å⁻¹

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 0.192 \AA^{-1}

8.2 Resolution estimates [i](#)

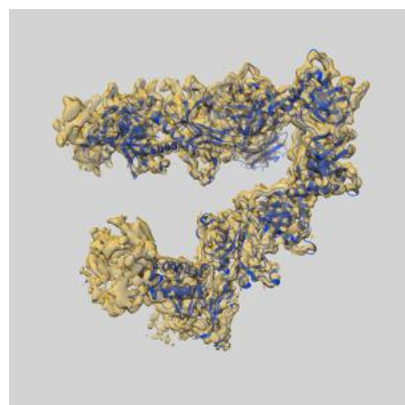
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.20	-	-
Author-provided FSC curve	5.10	7.39	5.19
Unmasked-calculated*	6.97	9.41	7.13

*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 6.97 differs from the reported value 5.2 by more than 10 %

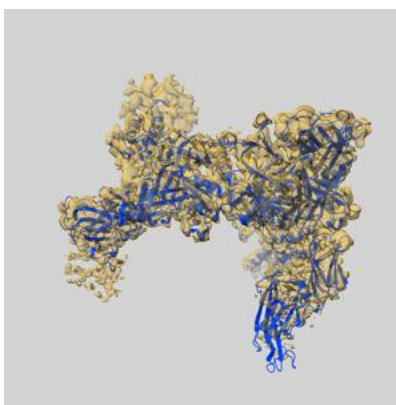
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-55964 and PDB model 9TIP. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

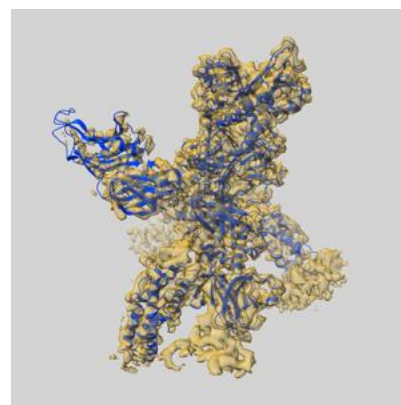
9.1 Map-model overlay [i](#)



X



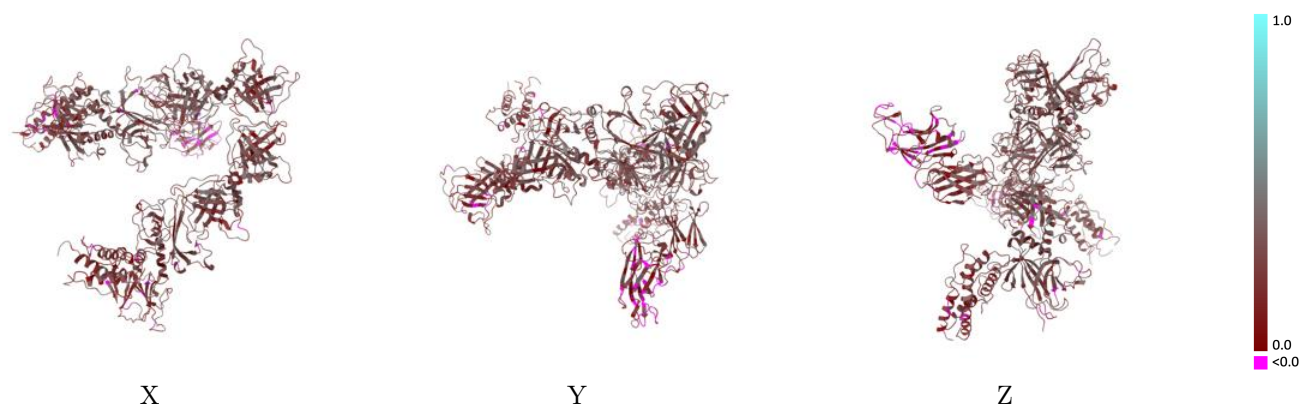
Y



Z

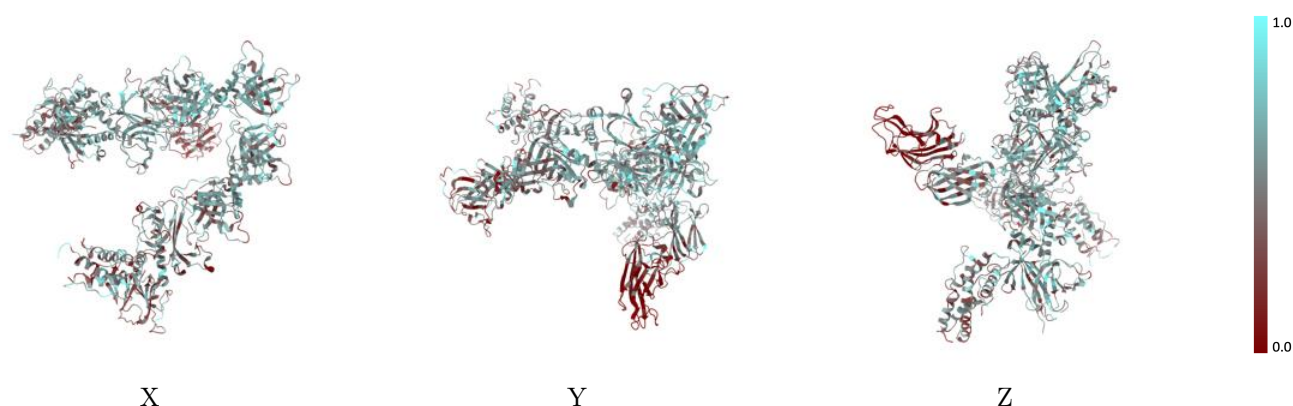
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



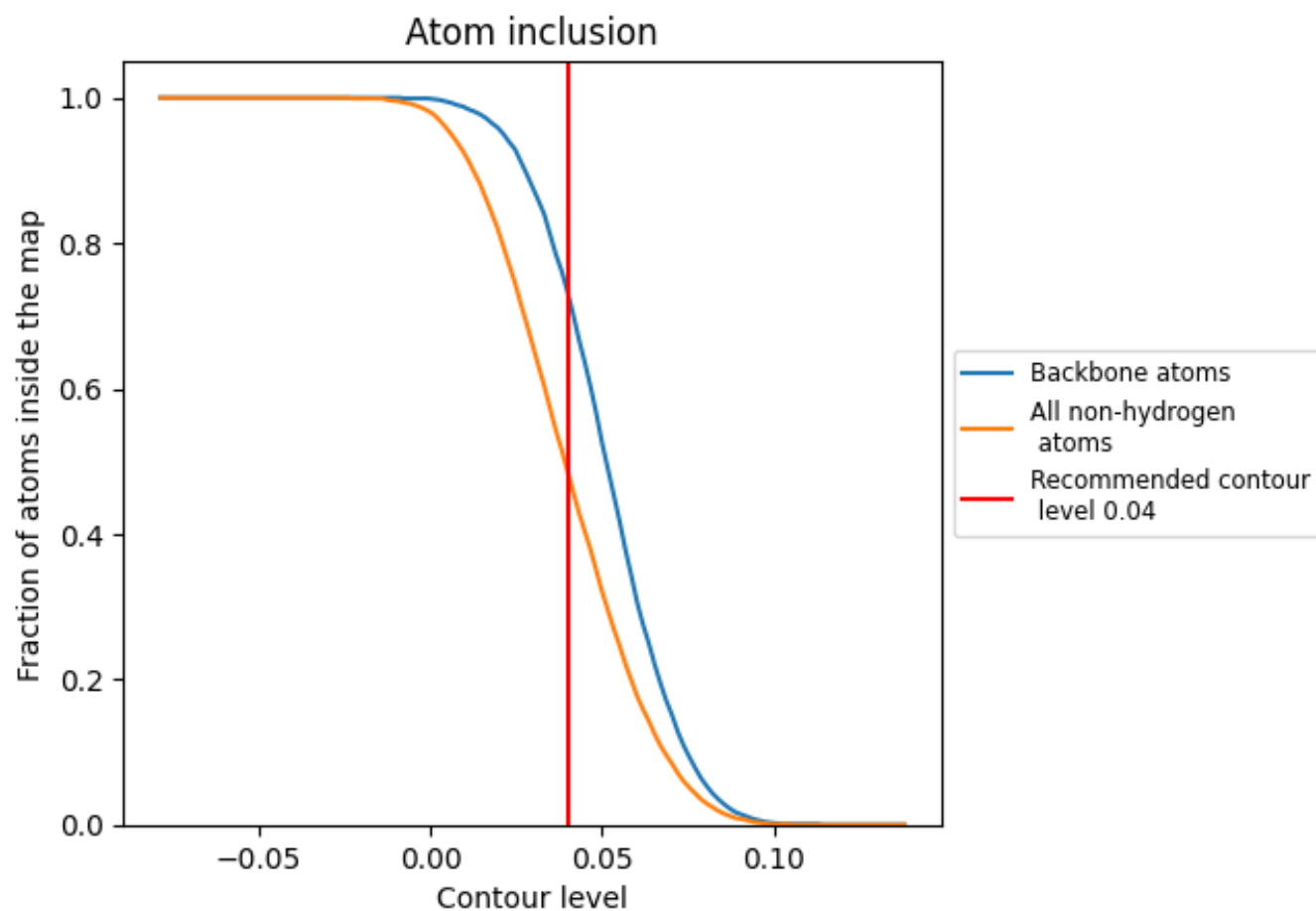
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 73% of all backbone atoms, 49% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.4860	<div></div> 0.2630
A	<div></div> 0.3020	<div></div> 0.1850
B	<div></div> 0.5350	<div></div> 0.2780
C	<div></div> 0.5680	<div></div> 0.3250
D	<div></div> 0.5890	<div></div> 0.3300
E	<div></div> 0.5880	<div></div> 0.2980
F	<div></div> 0.5540	<div></div> 0.2880
G	<div></div> 0.5160	<div></div> 0.2830
H	<div></div> 0.4750	<div></div> 0.2770
I	<div></div> 0.3970	<div></div> 0.2090
J	<div></div> 0.4700	<div></div> 0.2400
K	<div></div> 0.4480	<div></div> 0.2160
L	<div></div> 0.4310	<div></div> 0.2300
M	<div></div> 0.4680	<div></div> 0.2070
N	<div></div> 0.4850	<div></div> 0.2300
O	<div></div> 0.4980	<div></div> 0.2330

1.0

0.0

<0.0