



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 01:51 AM UTC

PDB ID : 3JBH / pdb_00003jbh
EMDB ID : EMD-1950
Title : TWO HEAVY MEROMYOSIN INTERACTING-HEADS MOTIFS FLEXIBLE DOCKED INTO TARANTULA THICK FILAMENT 3D-MAP ALLOWS IN DEPTH STUDY OF INTRA- AND INTERMOLECULAR INTERACTIONS
Authors : Alamo, L.; Qi, D.; Wriggers, W.; Pinto, A.; Zhu, J.; Bilbao, A.; Gillilan, R.E.; Hu, S.; Padron, R.
Deposited on : 2015-09-01
Resolution : 20.00 Å(reported)
Based on initial model : 3DTP

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ 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:

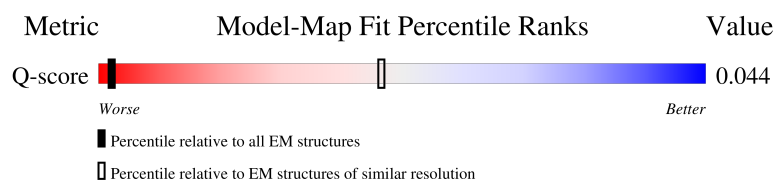
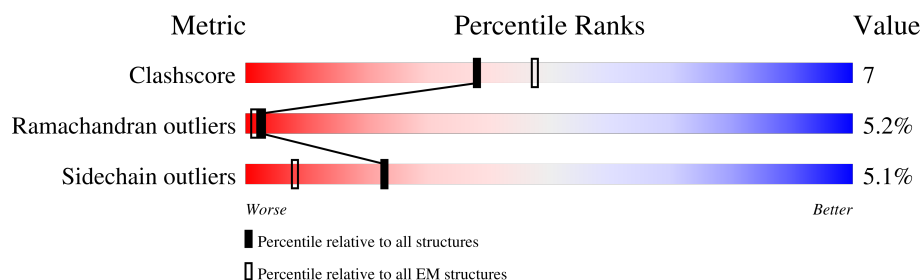
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 20.00 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.



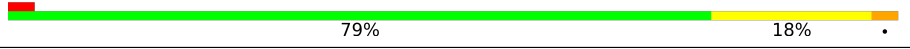
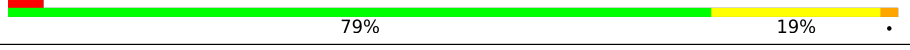
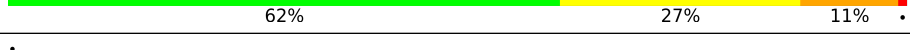
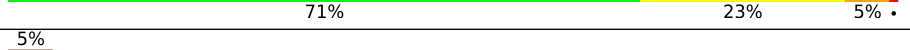
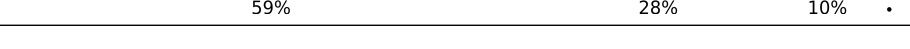
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	28 (19.50 - 20.50)

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	1953	
1	B	1953	
1	G	1953	

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Mol	Chain	Length	Quality of chain
1	H	1953	
2	C	156	
2	D	156	
2	I	156	
2	J	156	
3	E	196	
3	F	196	
3	K	196	
3	L	196	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 41968 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 MYOSIN 2 HEAVY CHAIN STRIATED MUSCLE.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	962	Total	C	N	O	S	0	0
			7721	4907	1334	1450	30		
1	B	964	Total	C	N	O	S	0	0
			7739	4918	1338	1453	30		
1	G	962	Total	C	N	O	S	0	0
			7721	4907	1334	1450	30		
1	H	964	Total	C	N	O	S	0	0
			7739	4918	1338	1453	30		

- Molecule 2 is a protein called MYOSIN 2 ESSENTIAL LIGHT CHAIN STRIATED MUSCLE.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	156	Total	C	N	O	S	0	0
			1233	779	199	247	8		
2	D	156	Total	C	N	O	S	0	0
			1233	779	199	247	8		
2	I	156	Total	C	N	O	S	0	0
			1233	779	199	247	8		
2	J	156	Total	C	N	O	S	0	0
			1233	779	199	247	8		

- Molecule 3 is a protein called MYOSIN 2 REGULATORY LIGHT CHAIN STRIATED MUSCLE.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	196	Total	C	N	O	S	0	0
			1529	952	257	314	6		
3	F	196	Total	C	N	O	S	0	0
			1529	952	257	314	6		
3	K	196	Total	C	N	O	S	0	0
			1529	952	257	314	6		
3	L	196	Total	C	N	O	S	0	0
			1529	952	257	314	6		

- Molecule 1: MYOSIN 2 HEAVY CHAIN STRIATED MUSCLE

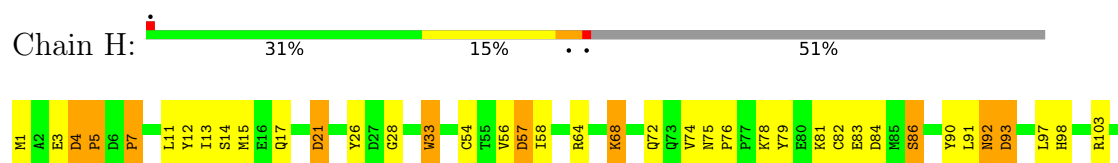


WORLDWIDE
PDB
PROTEIN DATA BANK

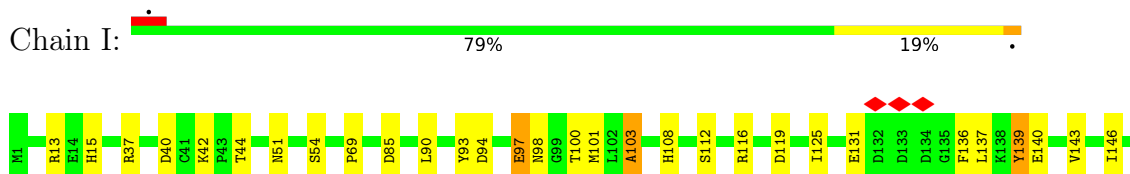
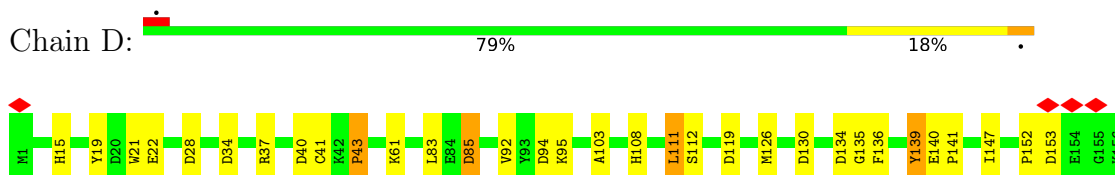
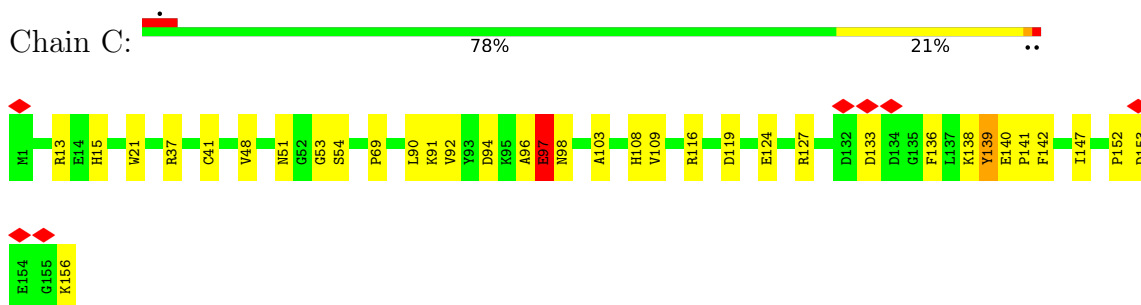
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ARG	GLN	ASP	SER	ASP	ARG	LYS	GLY	LEU	LEU	GLN	E868	T762	V584	L493	S279	
LEU	TRP	ALA	GLU	ALA	ALA	ARG	ALA	ASP	ASP	ILE	K869	V764	N587	E494	Y280	
GLN	LYS	GLY	LYS	LEU	THR	LEU	THR	GLU	SER	ASN	R870	I675	L592	E496	I281	
LYS	LYS	GLY	HIS	ASP	GLY	LYS	GLN	GLY	LEU	ASN	R871	I676	L593	E497	I282	
VAL	VAL	ASP	ASP	LEU	GLN	GLY	ALA	LEU	GLU	ASP	K872	L680	E594	E498	F283	
ASP	THR	THR	THR	VAL	VAL	VAL	VAL	VAL	ARG	ASP	D873	L771	N596	Y499	I291	
THR	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	ILE	E875	G772	K596	K402	E292	
ASN	THR	ASN	ASN	ASN	ASN	ASN	ASN	ASN	LEU	HIS	N878	E776	D597	M403	E292	
GLY	THR	LYS	LYS	LYS	LYS	LYS	LYS	LYS	ARG	GLN	N878	D779	N600	M405	D303	
GLN	GLY	GLY	GLY	GLY	ARG	ARG	ARG	LYS	GLY	ASP	N886	L782	D801	M413	H308	
ILE	ILE	THR	THR	THR	THR	THR	THR	THR	VAL	ASP	S894	L782	K608	A414	F309	
ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	VAL	LEU	E895	I785	L701	T415	Q312	
LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	VAL	ILE	R896	V786	L520	T416	Q312	
GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	LYS	ASN	S897	T787	L521	Q416	I315	
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	THR	LYS	V902	Q790	L613	V417	I315	
SER	SER	SER	SER	SER	SER	SER	SER	SER	LYS	LEU	E903	R794	L614	S418	D321	
LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	ASP	ASN	R905	E801	L615	Y419	D322	
VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	ASP	GLN	T907	E804	V617	S420	D330	
THR	THR	THR	THR	THR	THR	THR	THR	THR	LEU	MET	K908	L805	Q616	G422	T331	
LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LEU	GLN	S911	Q806	E620	G423	A332	
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	MET	L906	R718	E621	L424	H340	
ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	LEU	GLN	E911	P718	H622	A425	E341	
LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	ALA	GLY	Q924	K721	A627	D430	Y342	
LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	GLN	GLY	E925	Q722	E628	R431	Y343	
ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	GLY	GLY	R926	T722	S835	T344	D345	
THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL	THR	L927	Y724	E629	R439		
GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	VAL	GLY	S928	T725	F837	L440		
ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ASP	ALA	R929	L726	M441	M441		
LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	ASP	LEU	E930	L727	T541	M354		
LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LEU	ASN	A933	S730	Q546	L356		
GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	LEU	GLN	H934	A731	D547	E358		
LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	ASN	ALA	E934	V732	K548	M359		
ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	LYS	THR	R941	P733	N552	Q451		
THR	THR	THR	THR	THR	THR	THR	THR	THR	LYS	GLY	I948	K734	H553	Y452		
GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLY	ASP	L948	K734	K556	F453		
LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	I948	K734	K556	I464		
ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	GLY	ASN	L948	K734	K556	G455		
THR	THR	THR	THR	THR	THR	THR	THR	THR	GLY	THR	L948	K734	K556	V456		
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	VAL	VAL	L948	K734	K556	L457		
LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	ALA	ALA	L948	K734	K556	D458		
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	ALA	L948	K734	K556	F462		
ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ARG	ARG	L948	K734	K556	E463		
LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LYS	VAL	L948	K734	K556	T478		
THR	THR	THR	THR	THR	THR	THR	THR	THR	LYS	LYS	L948	K734	K556	M479		
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	L948	K734	K556	E480		
LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	GLY	GLY	L948	K734	K556	K481		
ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ALA	ALA	L948	K734	K556	F575		
THR	THR	THR	THR	THR	THR	THR	THR	THR	ALA	ALA	L948	K734	K556	H574		
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	SER	GLN	L948	K734	K556	F575		
LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	SER	GLN	L948	K734	K556	F575		
ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	LEU	THR	L948	K734	K556	H488		
ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	LEU	THR	L948	K734	K556	H488		
LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	L948	K734	K556	H488		
ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	LEU	LEU	L948	K734	K556	H488		
SER	SER	SER	SER	SER	SER	SER	SER	SER	ASP	ASP	L948	K734	K556	H488		

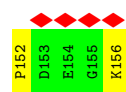
- Molecule 1: MYOSIN 2 HEAVY CHAIN STRIATED MUSCLE



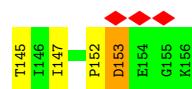




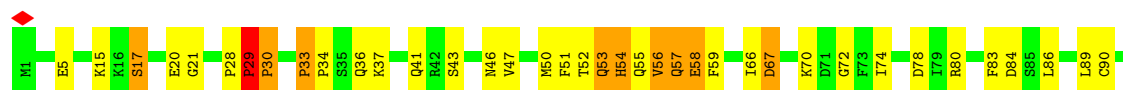




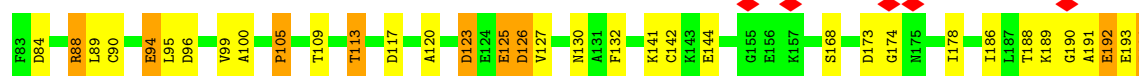
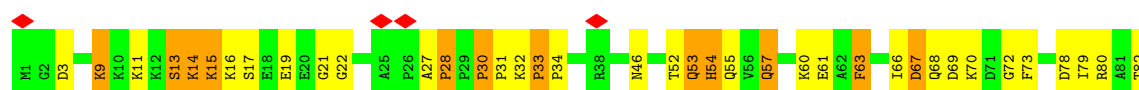
- Molecule 2: MYOSIN 2 ESSENTIAL LIGHT CHAIN STRIATED MUSCLE



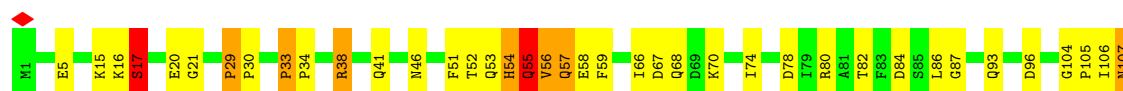
- Molecule 3: MYOSIN 2 REGULATORY LIGHT CHAIN STRIATED MUSCLE



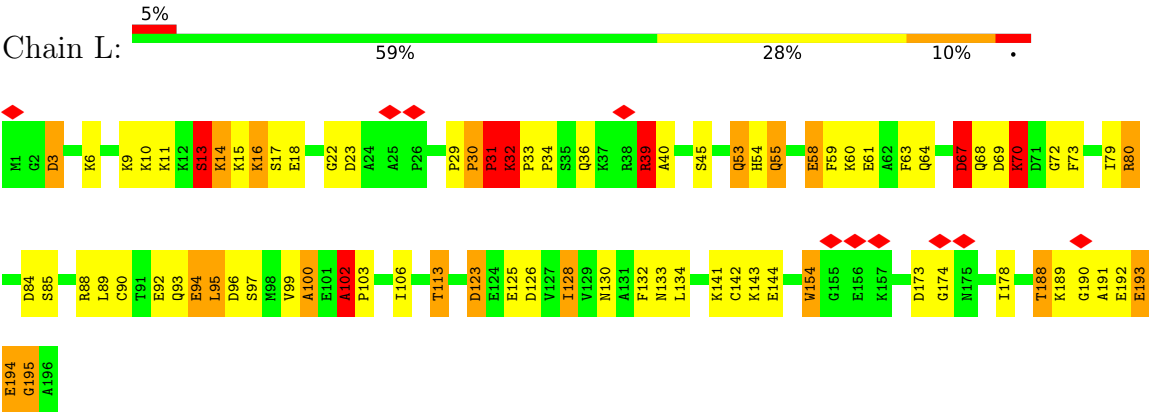
- Molecule 3: MYOSIN 2 REGULATORY LIGHT CHAIN STRIATED MUSCLE



- Molecule 3: MYOSIN 2 REGULATORY LIGHT CHAIN STRIATED MUSCLE



- Molecule 3: MYOSIN 2 REGULATORY LIGHT CHAIN STRIATED MUSCLE



4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=30°, rise=100 Å, axial sym=C4	Depositor
Number of segments used	Not provided	
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI/PHILIPS CM120T	Depositor
Voltage (kV)	120	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	1950	Depositor
Maximum defocus (nm)	1950	Depositor
Magnification	35000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	247.077	Depositor
Minimum map value	-0.037	Depositor
Average map value	10.023	Depositor
Map value standard deviation	28.567	Depositor
Recommended contour level	25	Depositor
Map size (Å)	620, 620, 620.5	wwPDB
Map dimensions	250, 250, 250	wwPDB
Map angles (°)	90, 90, 90	wwPDB
Pixel spacing (Å)	2.48, 2.48, 2.482	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	0.75	24/7867 (0.3%)	1.70	157/10591 (1.5%)
1	B	0.74	22/7885 (0.3%)	1.67	144/10614 (1.4%)
1	G	0.72	20/7867 (0.3%)	1.63	126/10591 (1.2%)
1	H	0.73	18/7885 (0.2%)	1.67	140/10614 (1.3%)
2	C	0.68	2/1251 (0.2%)	1.49	13/1674 (0.8%)
2	D	0.69	2/1251 (0.2%)	1.50	13/1674 (0.8%)
2	I	0.66	2/1251 (0.2%)	1.50	12/1674 (0.7%)
2	J	0.68	2/1251 (0.2%)	1.48	9/1674 (0.5%)
3	E	0.63	1/1554 (0.1%)	1.58	25/2081 (1.2%)
3	F	0.66	1/1554 (0.1%)	1.68	30/2081 (1.4%)
3	K	0.64	1/1554 (0.1%)	1.63	30/2081 (1.4%)
3	L	0.75	3/1554 (0.2%)	1.78	37/2081 (1.8%)
All	All	0.72	98/42724 (0.2%)	1.65	736/57430 (1.3%)

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	32
1	B	0	20
1	G	0	25
1	H	0	19
2	D	0	1
2	I	0	1
2	J	0	4
3	E	0	1
3	F	0	3
3	K	0	2
3	L	0	8
All	All	0	116

The worst 5 of 98 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	364	ARG	CA-C	9.44	1.64	1.52
1	G	148	HIS	CD2-NE2	-7.44	1.29	1.37
1	A	363	GLN	CA-C	7.29	1.62	1.52
2	D	108	HIS	CD2-NE2	-7.27	1.29	1.37
1	H	489	HIS	CD2-NE2	-7.18	1.29	1.37

The worst 5 of 736 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	565	PRO	N-CA-C	19.02	133.91	110.70
1	B	565	PRO	N-CA-C	18.55	133.34	110.70
1	A	364	ARG	CA-C-N	13.91	137.23	119.84
1	A	364	ARG	C-N-CA	13.91	137.23	119.84
1	A	365	PRO	CA-N-CD	-13.75	92.75	112.00

There are no chirality outliers.

5 of 116 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	110	TYR	Sidechain
1	A	142	ARG	Sidechain
1	A	157	TYR	Sidechain
1	A	41	TYR	Sidechain
1	A	64	ARG	Sidechain

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	7721	0	7778	127	0
1	B	7739	0	7799	169	0
1	G	7721	0	7778	111	0
1	H	7739	0	7799	134	0
2	C	1233	0	1227	10	0
2	D	1233	0	1227	11	0
2	I	1233	0	1227	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	J	1233	0	1227	14	0
3	E	1529	0	1491	27	0
3	F	1529	0	1491	28	0
3	K	1529	0	1491	23	0
3	L	1529	0	1491	51	0
All	All	41968	0	42026	623	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 7.

The worst 5 of 623 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:B:641:LYS:HE3	1:B:642:LYS:NZ	1.21	1.52
1:B:641:LYS:CE	1:B:642:LYS:NZ	2.16	1.08
1:A:364:ARG:HA	3:L:31:PRO:HG2	1.42	1.00
1:B:641:LYS:CE	1:B:642:LYS:HZ1	1.70	0.99
1:A:364:ARG:HA	3:L:31:PRO:CG	1.95	0.94

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	960/1953 (49%)	772 (80%)	149 (16%)	39 (4%)	2	18
1	B	962/1953 (49%)	779 (81%)	128 (13%)	55 (6%)	1	14
1	G	960/1953 (49%)	783 (82%)	136 (14%)	41 (4%)	2	17
1	H	962/1953 (49%)	779 (81%)	125 (13%)	58 (6%)	1	13
2	C	154/156 (99%)	137 (89%)	13 (8%)	4 (3%)	4	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	154/156 (99%)	139 (90%)	11 (7%)	4 (3%)	4	25
2	I	154/156 (99%)	135 (88%)	16 (10%)	3 (2%)	6	32
2	J	154/156 (99%)	131 (85%)	19 (12%)	4 (3%)	4	25
3	E	194/196 (99%)	139 (72%)	40 (21%)	15 (8%)	1	10
3	F	194/196 (99%)	136 (70%)	41 (21%)	17 (9%)	0	8
3	K	194/196 (99%)	144 (74%)	37 (19%)	13 (7%)	1	12
3	L	194/196 (99%)	129 (66%)	46 (24%)	19 (10%)	0	7
All	All	5236/9220 (57%)	4203 (80%)	761 (14%)	272 (5%)	3	15

5 of 272 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	6	ASP
1	A	22	GLN
1	A	138	LYS
1	A	269	ARG
1	A	310	VAL

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	833/1689 (49%)	792 (95%)	41 (5%)	22	43
1	B	835/1689 (49%)	778 (93%)	57 (7%)	14	36
1	G	833/1689 (49%)	795 (95%)	38 (5%)	24	45
1	H	835/1689 (49%)	788 (94%)	47 (6%)	19	40
2	C	132/132 (100%)	128 (97%)	4 (3%)	36	57
2	D	132/132 (100%)	128 (97%)	4 (3%)	36	57
2	I	132/132 (100%)	128 (97%)	4 (3%)	36	57
2	J	132/132 (100%)	127 (96%)	5 (4%)	29	50
3	E	164/164 (100%)	160 (98%)	4 (2%)	43	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	F	164/164 (100%)	151 (92%)	13 (8%)	11	32
3	K	164/164 (100%)	161 (98%)	3 (2%)	51	68
3	L	164/164 (100%)	155 (94%)	9 (6%)	19	41
All	All	4520/7940 (57%)	4291 (95%)	229 (5%)	23	42

5 of 229 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	F	55	GLN
3	L	45	SER
1	G	568	PRO
3	K	108	PHE
1	H	846	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 69 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	546	GLN
1	H	595	ASN
3	K	133	ASN
1	B	827	ASN
1	B	693	HIS

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 [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

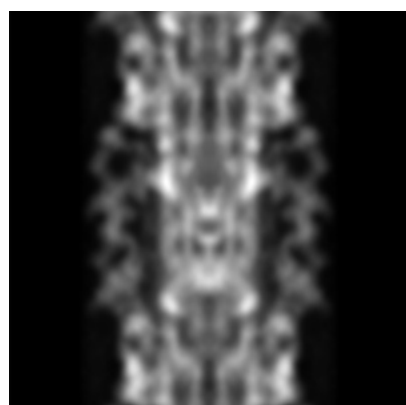
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1950. These allow visual inspection of the internal detail of the map and identification of artifacts.

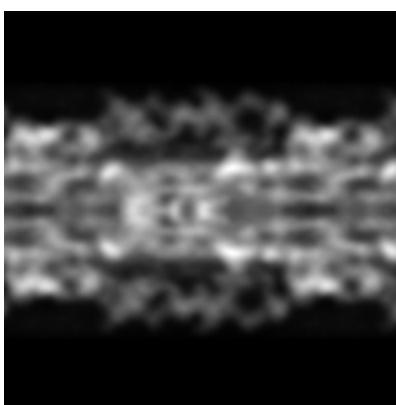
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y

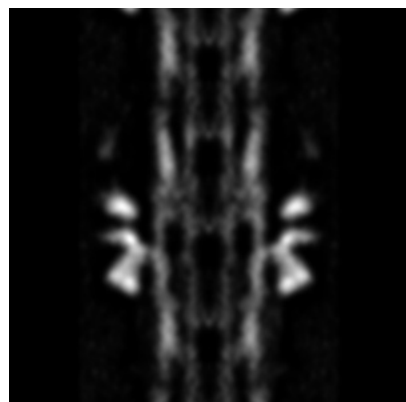


Z

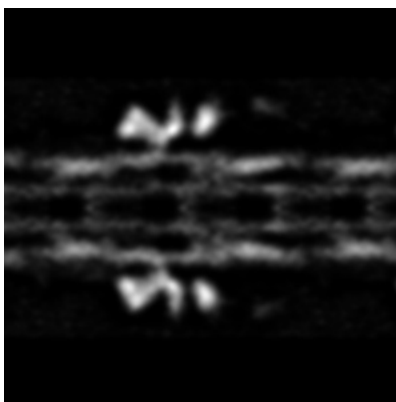
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

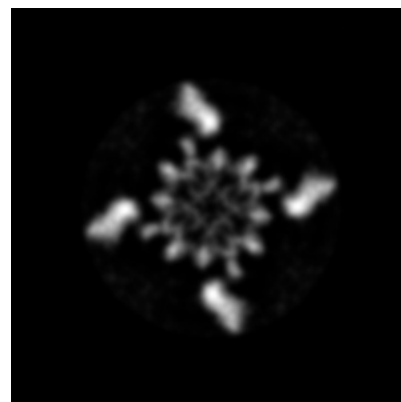
6.2.1 Primary map



X Index: 125



Y Index: 125

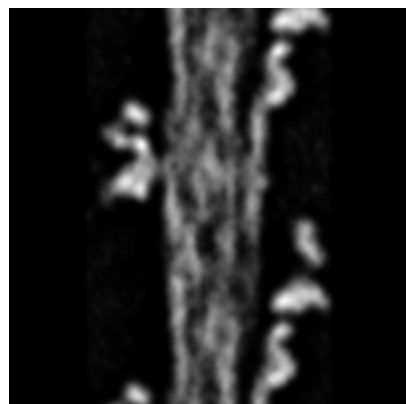


Z Index: 125

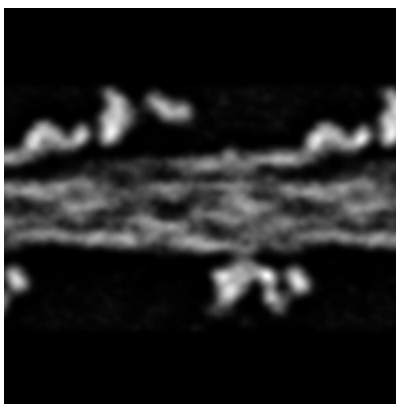
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 150



Y Index: 99

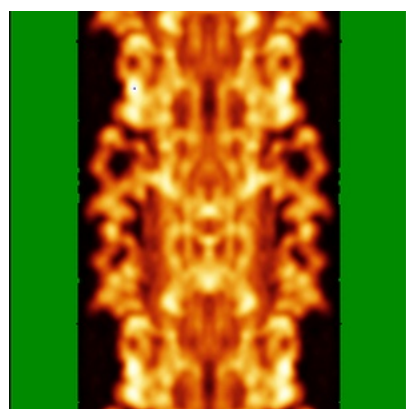


Z Index: 200

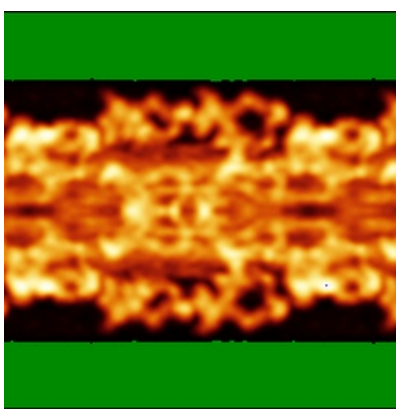
The images above show the largest variance slices of the map in three orthogonal directions.

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

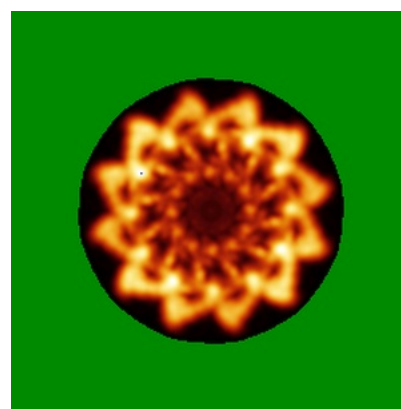
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views

This section was not generated.

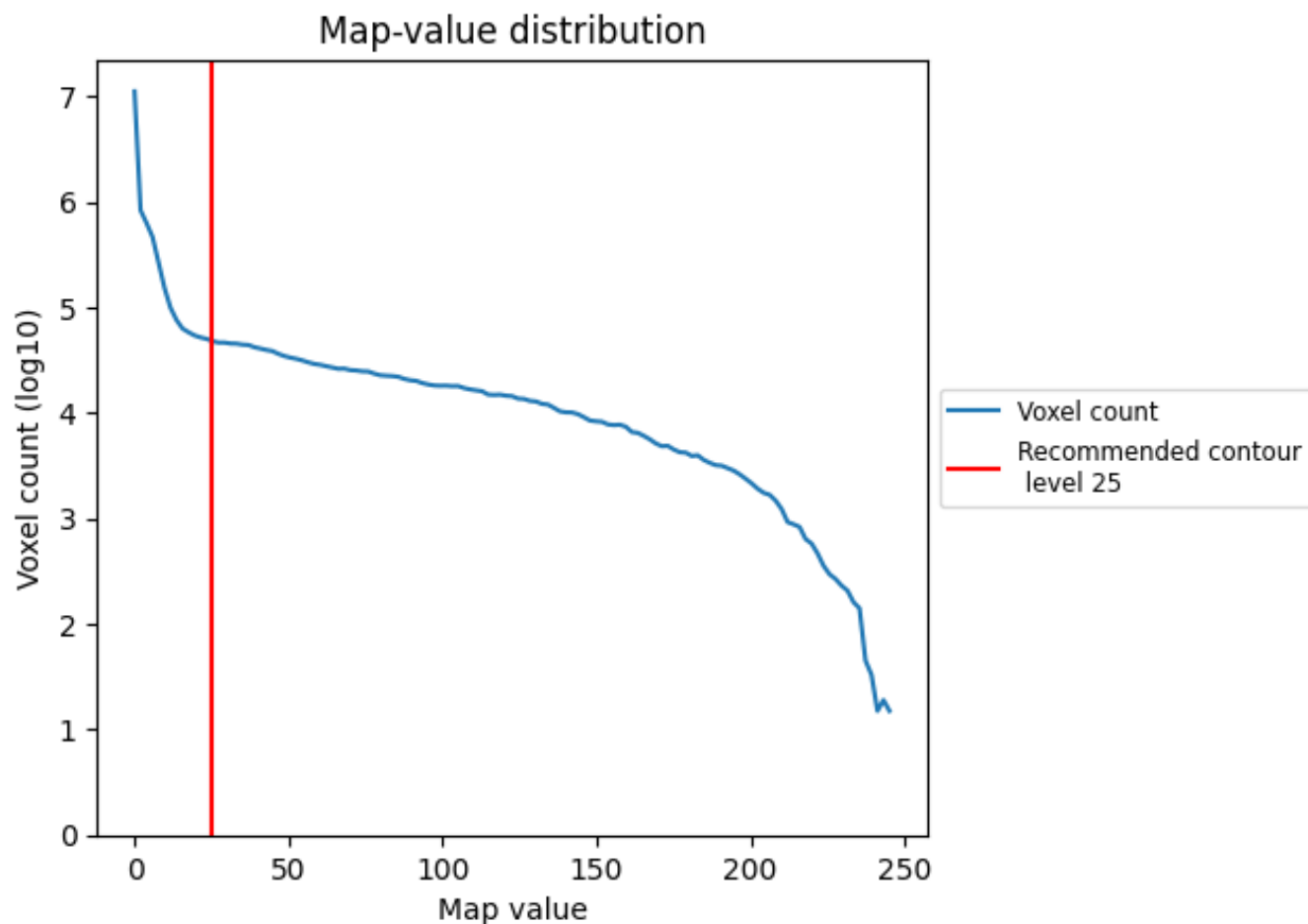
6.6 Mask visualisation

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

7 Map analysis [i](#)

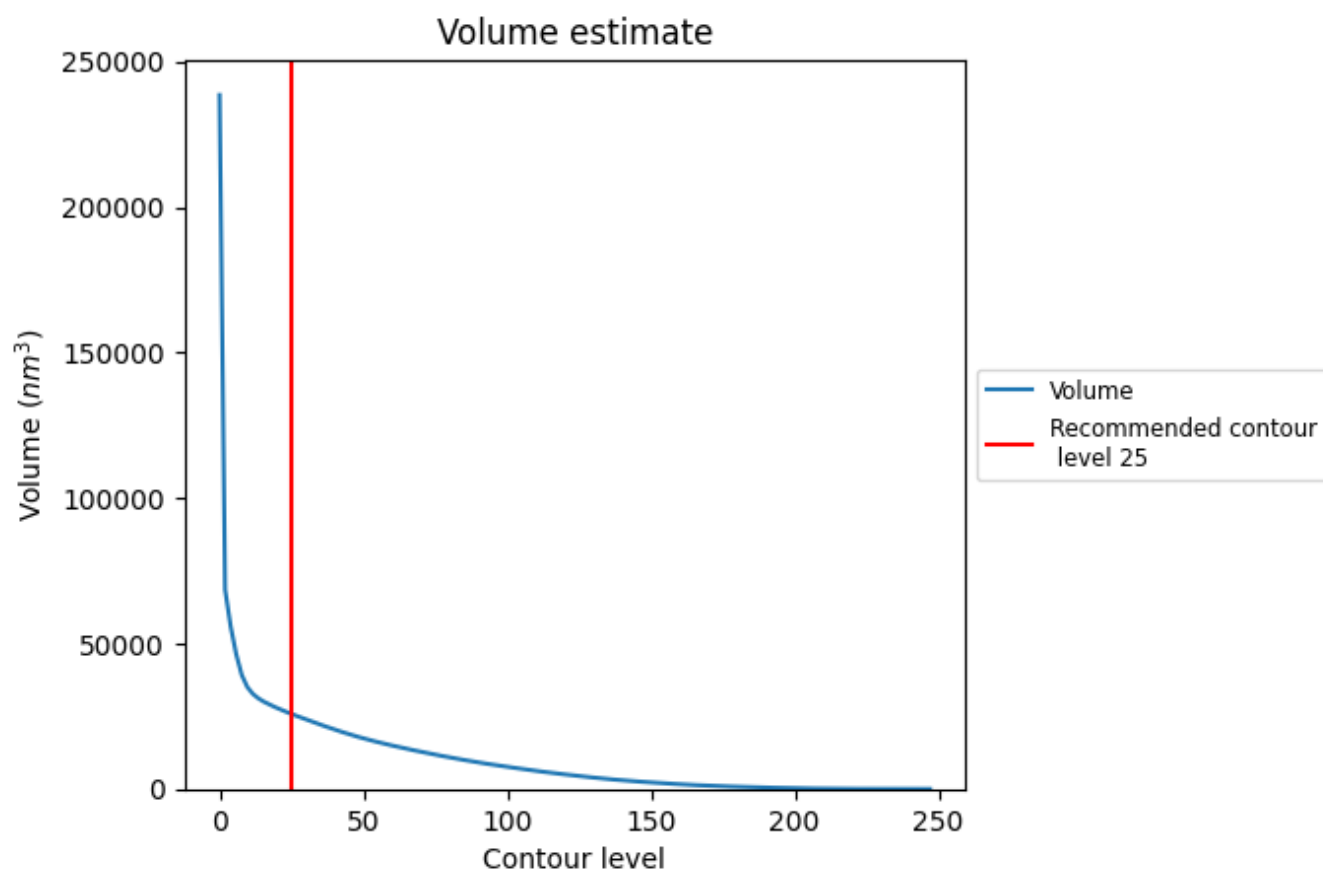
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

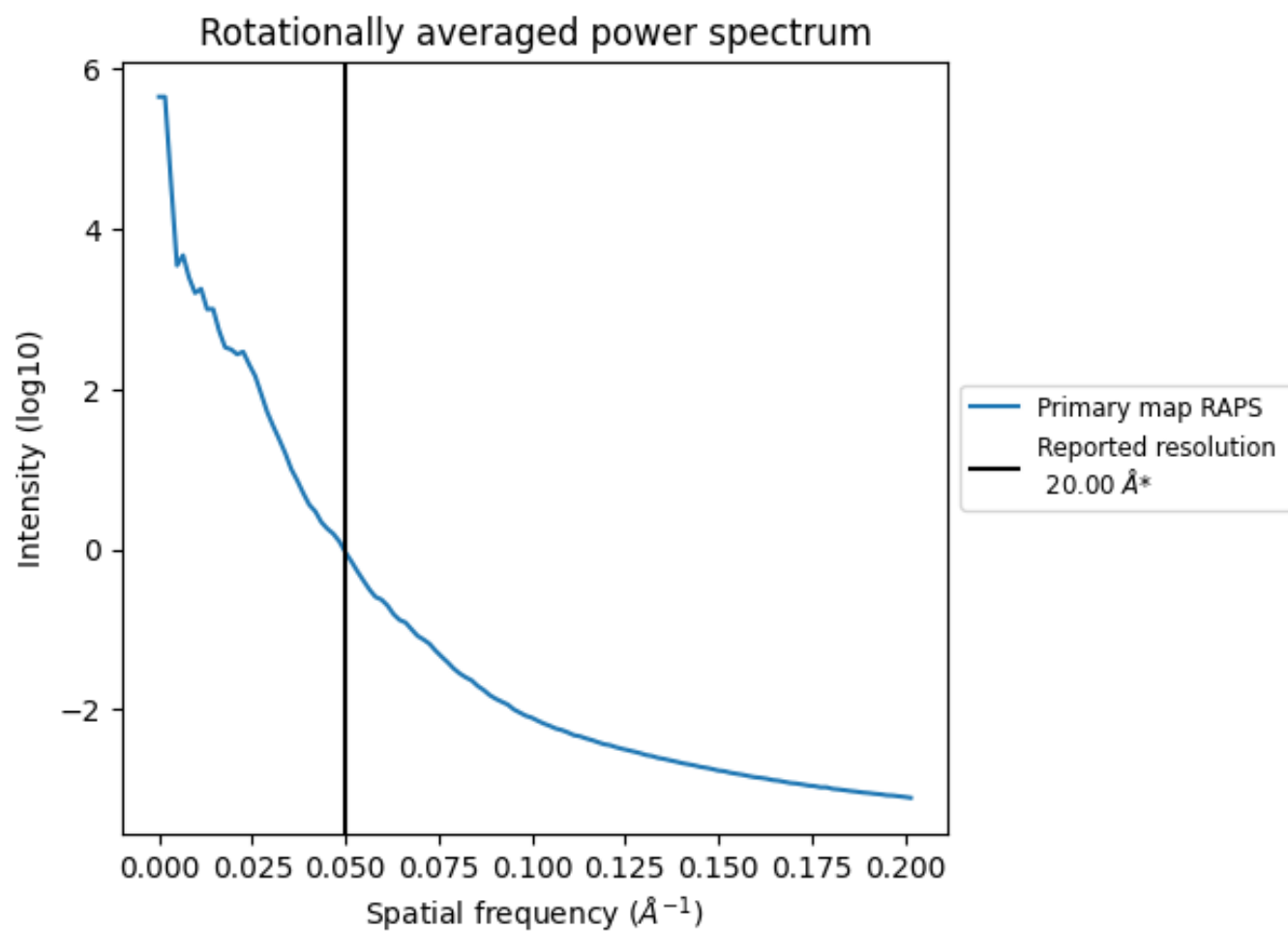
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 25767 nm^3 ; this corresponds to an approximate mass of 23276 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 0.050 Å⁻¹

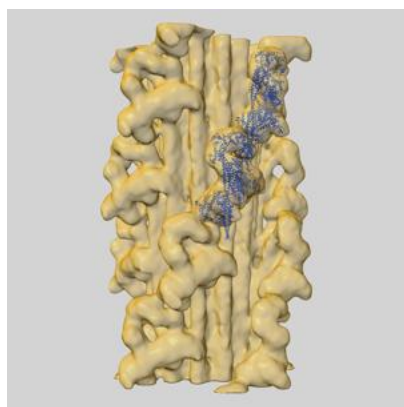
8 Fourier-Shell correlation

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

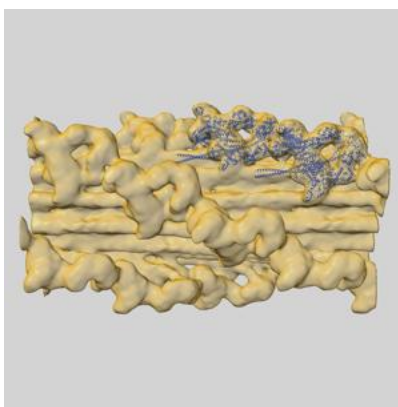
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1950 and PDB model 3JBH. Per-residue inclusion information can be found in section [3](#) on page [5](#).

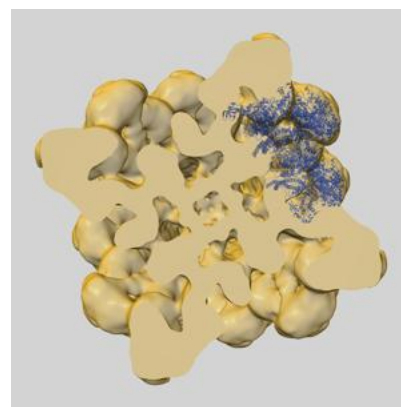
9.1 Map-model overlay [i](#)



X



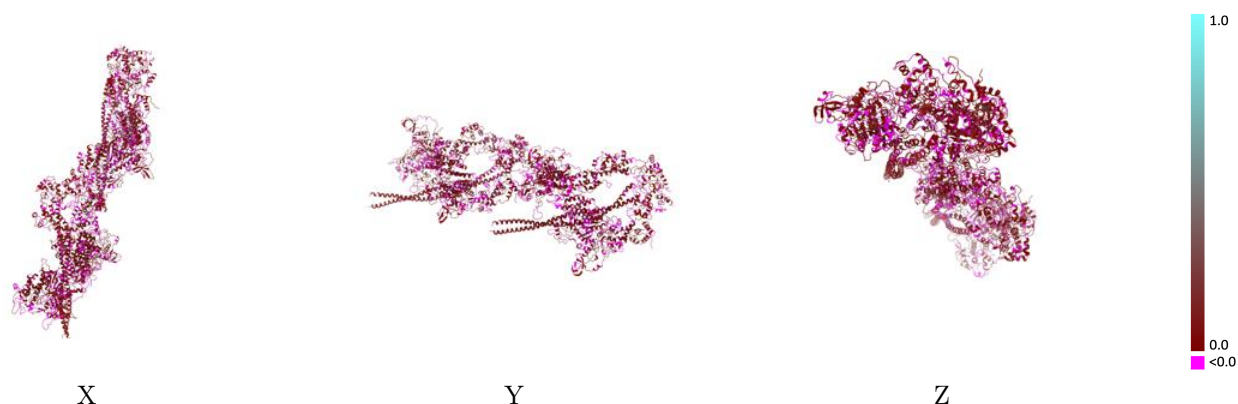
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 25.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

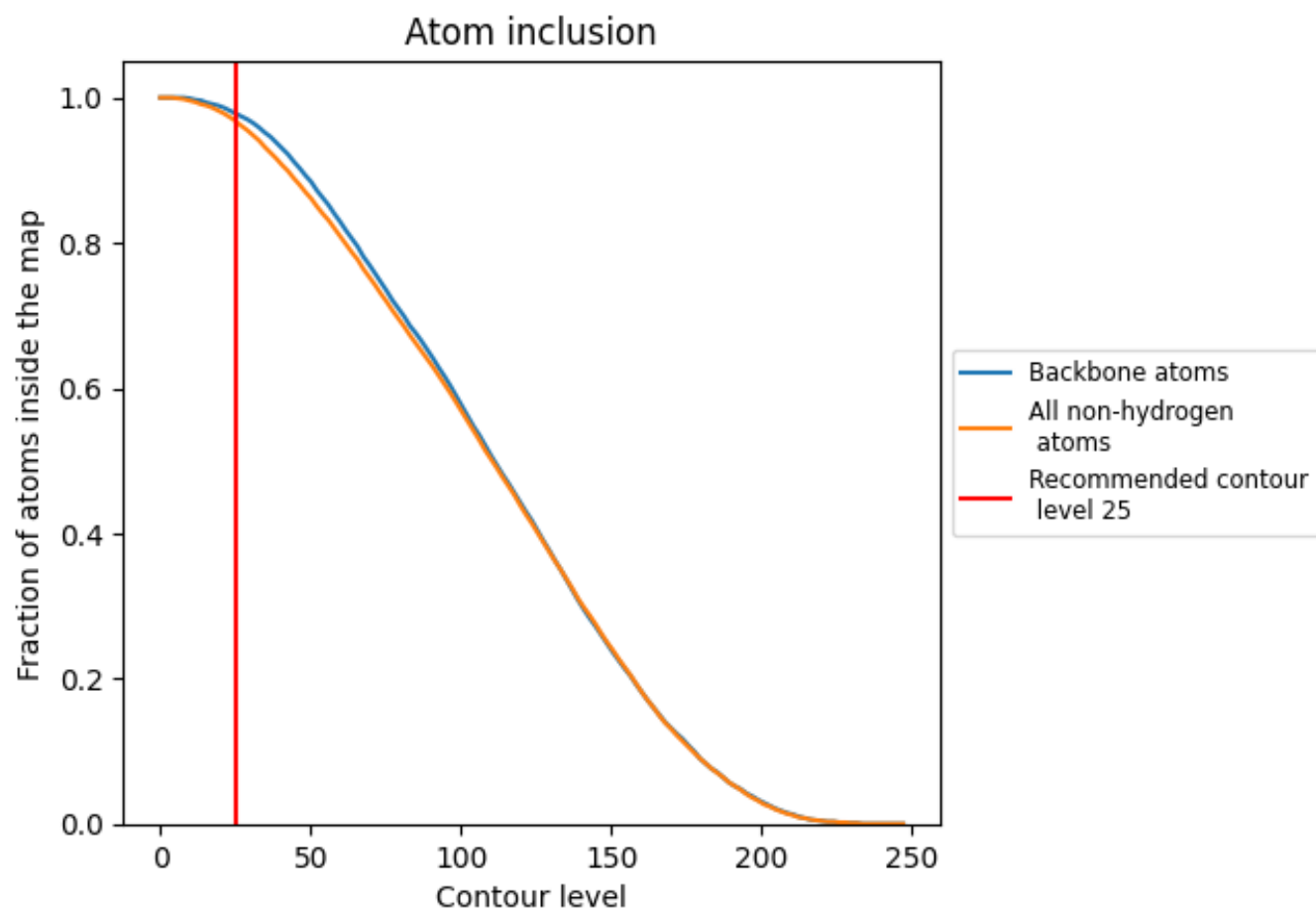


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 97% 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 (25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9680	0.0440
A	0.9730	0.0440
B	0.9670	0.0430
C	0.9540	0.0530
D	0.9590	0.0410
E	0.9720	0.0430
F	0.9460	0.0440
G	0.9770	0.0460
H	0.9680	0.0430
I	0.9550	0.0520
J	0.9610	0.0380
K	0.9680	0.0440
L	0.9440	0.0440

1.0

0.0

<0.0