Full wwPDB EM Validation Report

May 4, 2025 – 10:54 PM EDT

PDB ID	:	6N88 / pdb_00006n88
EMDB ID	:	EMD-0366
Title	:	Cryo-EM structure of the Importin7:Importin beta:Histone H1.0 complex
Authors	:	Bilokapic, S.; Ivic, N.; Halic, M.
Deposited on	:	2018-11-28
Resolution	:	6.20 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

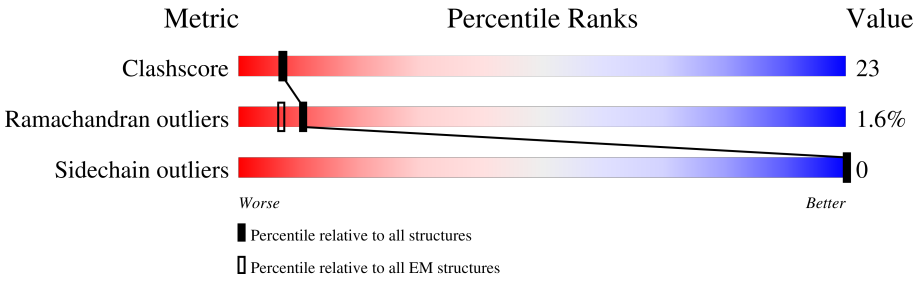
EMDB validation analysis	:	0.0.1.dev118
MolProbity	:	4-5-2 with Phenix2.0rc1
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

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 6.20 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1038	6%, 46%, 12%, 40%
2	B	876	77%, 21%
3	C	194	36%, 62%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6446 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 MGC52556 protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	A	619	2540	1302	619	619	0	0

- Molecule 2 is a protein called Importin subunit beta-1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	B	873	3607	1861	873	873	0	0

- Molecule 3 is a protein called Histone H1.0.

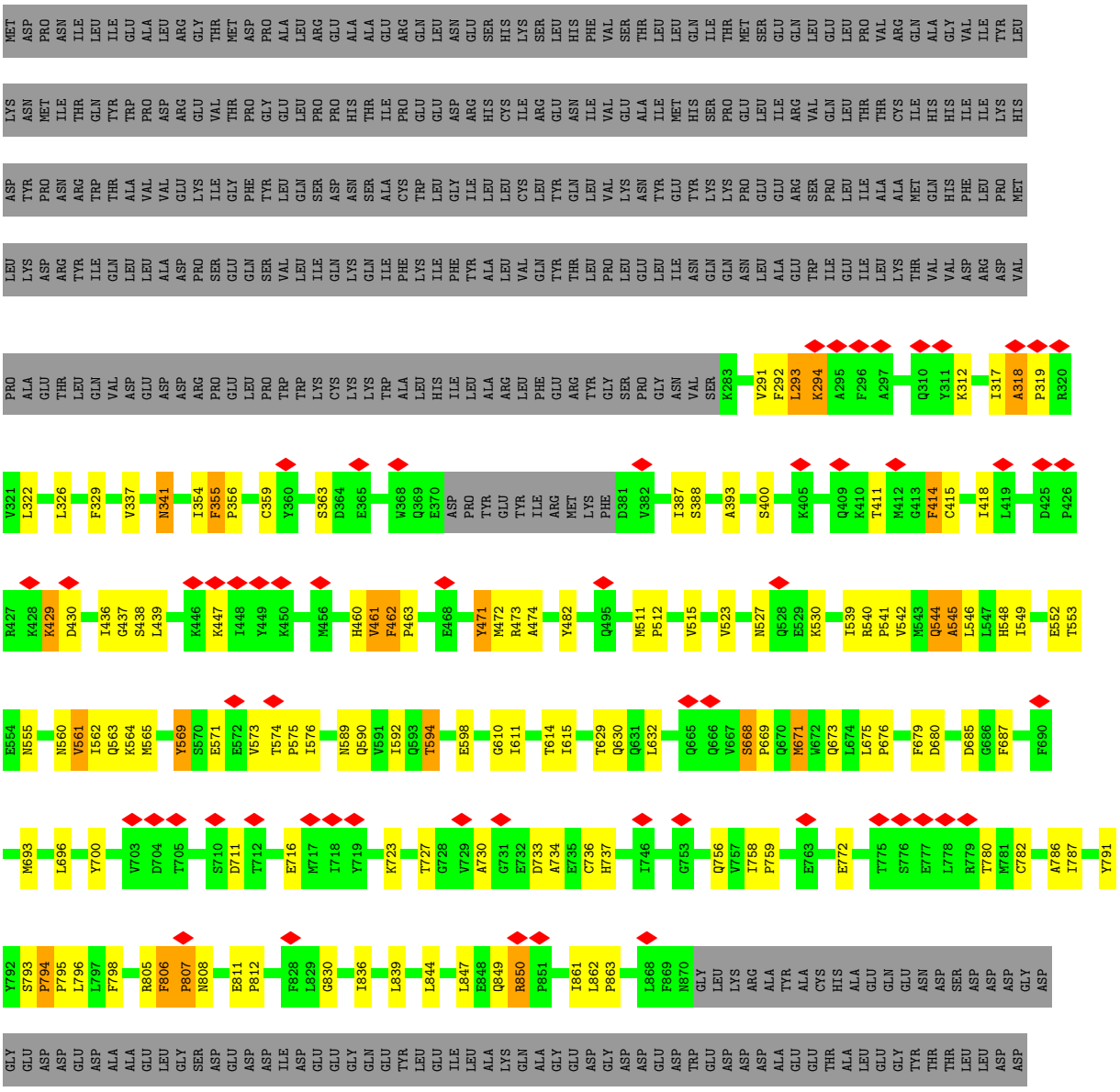
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	C	74	299	151	74	74	0	0

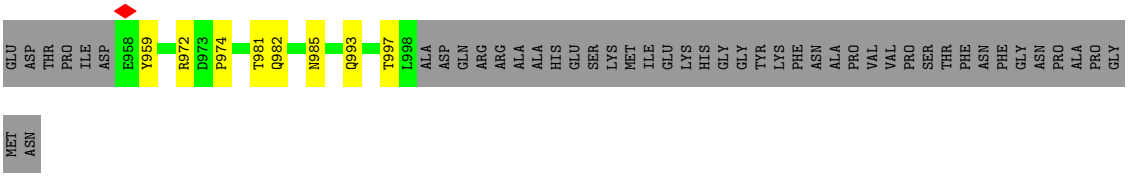
3 Residue-property plots (i)

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

- Molecule 1: MGC52556 protein

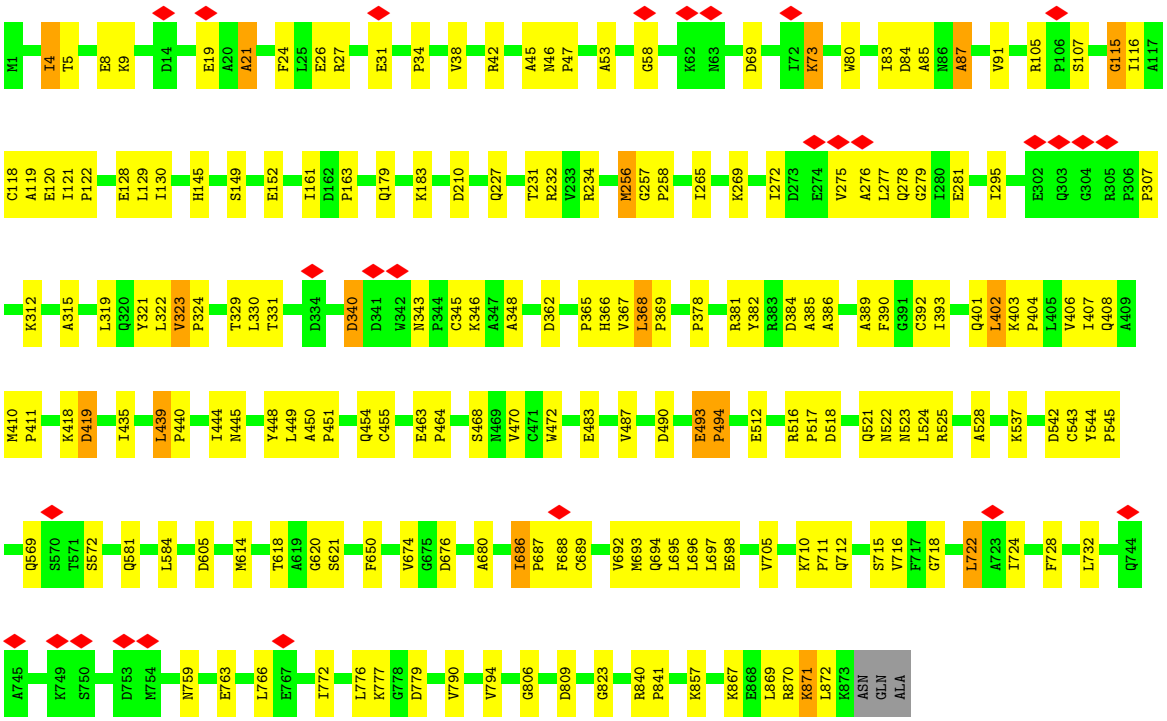
Chain A:





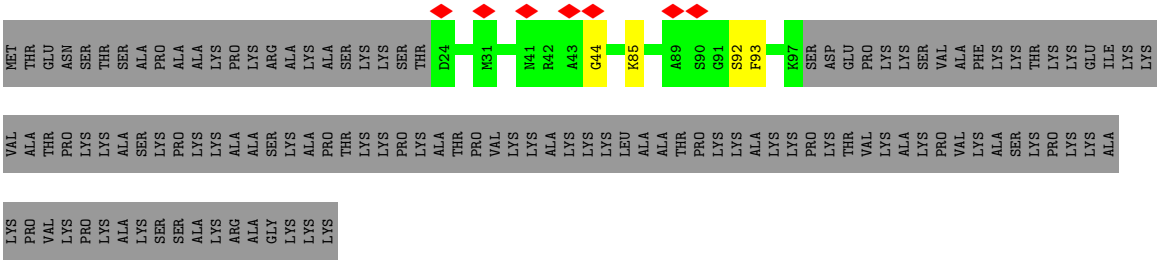
• Molecule 2: Importin subunit beta-1

Chain B:



• Molecule 3: Histone H1.0

Chain C:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	18900	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 ($e^-/Å^2$)	80	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 BASE (4k x 4k)	Depositor
Maximum map value	0.147	Depositor
Minimum map value	-0.049	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.0356	Depositor
Map size (Å)	240.23999, 240.23999, 240.23999	wwPDB
Map dimensions	168, 168, 168	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.43, 1.43, 1.43	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	0.47	0/2558	1.65	63/3235 (1.9%)
2	B	0.47	0/3643	1.55	68/4629 (1.5%)
3	C	0.44	0/299	0.99	0/374
All	All	0.47	0/6500	1.57	131/8238 (1.6%)

There are no bond length outliers.

All (131) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	323	VAL	CA-C-N	14.81	134.99	118.85
2	B	323	VAL	C-N-CA	14.81	134.99	118.85
1	A	354	ILE	N-CA-C	12.78	123.66	110.62
2	B	368	LEU	CA-C-N	12.12	132.50	119.05
2	B	368	LEU	C-N-CA	12.12	132.50	119.05
2	B	73	LYS	N-CA-C	11.74	124.07	111.28
1	A	387	ILE	N-CA-C	11.71	122.56	110.62
2	B	572	SER	N-CA-C	-11.39	98.95	111.36
2	B	129	LEU	N-CA-C	10.63	122.87	111.28
1	A	861	ILE	N-CA-C	10.25	121.08	110.62
1	A	461	VAL	N-CA-C	10.12	120.94	110.62
2	B	45	ALA	N-CA-C	10.11	122.30	111.28
1	A	471	TYR	N-CA-C	9.93	122.10	111.28
1	A	850	ARG	CA-C-N	9.70	129.81	119.05
1	A	850	ARG	C-N-CA	9.70	129.81	119.05
2	B	367	VAL	N-CA-C	9.68	120.50	110.62
1	A	437	GLY	N-CA-C	9.60	123.63	112.50
1	A	972	ARG	N-CA-C	9.36	121.48	111.28
1	A	429	LYS	N-CA-C	-9.31	101.00	111.71
2	B	152	GLU	N-CA-C	-9.16	101.30	111.28
1	A	836	ILE	N-CA-C	8.72	119.51	110.62
1	A	411	THR	N-CA-C	8.69	120.83	111.36
1	A	806	PHE	CA-C-N	-8.61	109.08	119.84
1	A	806	PHE	C-N-CA	-8.61	109.08	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	294	LYS	N-CA-C	8.60	120.66	111.28
2	B	794	VAL	N-CA-C	8.56	118.57	110.53
2	B	115	GLY	N-CA-C	-8.47	102.57	112.73
2	B	688	PHE	N-CA-C	8.45	120.49	111.28
1	A	355	PHE	CA-C-N	8.33	127.93	118.85
1	A	355	PHE	C-N-CA	8.33	127.93	118.85
2	B	620	GLY	N-CA-C	8.06	123.08	112.77
1	A	329	PHE	N-CA-C	7.93	119.92	111.28
2	B	128	GLU	N-CA-C	7.80	119.79	111.28
1	A	447	LYS	N-CA-C	7.77	122.48	112.92
1	A	462	PHE	CA-C-N	7.71	127.61	119.05
1	A	462	PHE	C-N-CA	7.71	127.61	119.05
2	B	449	LEU	N-CA-C	7.71	119.69	111.28
1	A	772	GLU	N-CA-C	7.70	119.45	111.14
1	A	555	ASN	N-CA-C	7.62	120.98	110.24
1	A	576	ILE	N-CA-C	-7.60	102.87	110.62
2	B	279	GLY	N-CA-C	-7.46	103.78	112.73
1	A	806	PHE	N-CA-C	7.40	119.53	109.24
2	B	470	VAL	N-CA-C	-7.38	103.09	110.62
1	A	687	PHE	N-CA-C	7.37	119.31	111.28
2	B	621	SER	N-CA-C	7.35	118.94	111.07
2	B	402	LEU	N-CA-C	7.32	119.25	111.28
2	B	537	LYS	N-CA-C	-7.32	103.31	111.28
2	B	107	SER	N-CA-C	7.31	120.83	109.07
2	B	680	ALA	N-CA-C	7.25	119.18	111.28
1	A	539	ILE	N-CA-C	7.20	117.97	110.62
2	B	210	ASP	N-CA-C	7.04	120.96	109.76
1	A	561	VAL	N-CA-C	-7.03	103.45	110.62
1	A	844	LEU	N-CA-C	6.95	118.85	111.28
2	B	722	LEU	N-CA-C	6.94	120.85	112.38
2	B	790	VAL	N-CA-C	6.76	117.51	110.62
1	A	414	PHE	N-CA-C	6.72	118.61	111.28
1	A	388	SER	CA-C-N	6.71	126.50	119.05
1	A	388	SER	C-N-CA	6.71	126.50	119.05
2	B	705	VAL	N-CA-C	6.63	117.38	110.62
2	B	419	ASP	CA-C-N	6.59	126.36	119.05
2	B	419	ASP	C-N-CA	6.59	126.36	119.05
2	B	525	ARG	N-CA-C	-6.54	104.24	111.36
1	A	393	ALA	N-CA-C	-6.47	104.23	111.28
1	A	796	LEU	N-CA-C	-6.46	104.23	111.28
1	A	569	TYR	N-CA-C	6.45	118.31	111.28
1	A	544	GLN	N-CA-C	-6.43	104.28	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	689	CYS	N-CA-C	6.37	118.23	111.28
2	B	323	VAL	O-C-N	6.26	124.52	120.07
2	B	809	ASP	N-CA-C	-6.22	104.26	113.40
2	B	278	GLN	N-CA-C	6.18	118.02	111.28
2	B	227	GLN	N-CA-C	6.13	117.96	111.28
2	B	439	LEU	N-CA-C	6.12	120.35	108.85
1	A	589	ASN	N-CA-C	-6.08	104.66	111.28
2	B	445	ASN	N-CA-C	-6.06	104.59	111.07
2	B	340	ASP	N-CA-C	6.02	120.62	113.16
2	B	650	PHE	N-CA-C	6.02	117.84	111.28
2	B	569	GLN	N-CA-C	5.92	118.27	108.49
1	A	400	SER	N-CA-C	5.89	117.70	111.28
2	B	130	ILE	N-CA-C	5.88	121.14	112.61
2	B	42	ARG	N-CA-C	-5.88	104.88	111.28
1	A	545	ALA	N-CA-C	-5.84	105.00	111.36
2	B	46	ASN	CA-C-N	5.83	127.13	119.84
2	B	46	ASN	C-N-CA	5.83	127.13	119.84
1	A	438	SER	N-CA-C	5.82	117.43	111.14
2	B	19	GLU	N-CA-C	5.79	117.67	111.36
2	B	256	MET	N-CA-C	-5.79	104.97	111.28
2	B	366	HIS	N-CA-C	5.68	117.47	111.28
2	B	490	ASP	CB-CA-C	-5.67	110.05	116.63
2	B	759	ASN	N-CA-C	5.64	117.43	111.28
1	A	530	LYS	N-CA-C	5.61	117.48	111.36
1	A	594	THR	N-CA-C	5.61	117.40	111.28
1	A	671	MET	N-CA-C	-5.58	105.19	111.28
2	B	276	ALA	N-CA-C	5.53	119.02	111.39
2	B	695	LEU	N-CA-C	-5.52	105.27	111.28
1	A	592	ILE	N-CA-C	-5.51	105.00	110.62
1	A	571	GLU	N-CA-C	5.49	116.65	108.31
2	B	161	ILE	N-CA-C	5.48	116.20	110.62
2	B	295	ILE	N-CA-C	-5.47	105.04	110.62
2	B	542	ASP	N-CA-C	5.46	117.30	108.34
1	A	982	GLN	N-CA-C	5.46	117.23	111.28
1	A	849	GLN	N-CA-C	5.43	117.53	108.02
2	B	490	ASP	N-CA-C	5.41	117.22	108.08
2	B	523	ASN	N-CA-C	-5.38	100.12	108.90
1	A	693	MET	N-CA-C	5.38	117.14	111.28
1	A	847	LEU	N-CA-C	5.37	117.21	111.36
1	A	318	ALA	CA-C-N	5.37	125.00	119.05
1	A	318	ALA	C-N-CA	5.37	125.00	119.05
2	B	857	LYS	N-CA-C	5.36	117.22	109.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	598	GLU	N-CA-C	-5.35	105.45	111.28
2	B	401	GLN	N-CA-C	5.32	117.15	111.36
1	A	341	ASN	N-CA-C	-5.31	104.06	111.39
1	A	959	TYR	N-CA-C	5.30	117.14	111.36
1	A	668	SER	CA-C-N	-5.29	113.28	119.32
1	A	668	SER	C-N-CA	-5.29	113.28	119.32
2	B	38	VAL	N-CA-C	5.28	116.00	110.62
1	A	730	ALA	CA-C-N	5.23	126.68	120.14
1	A	730	ALA	C-N-CA	5.23	126.68	120.14
1	A	685	ASP	N-CA-C	5.20	116.95	111.28
2	B	58	GLY	N-CA-C	5.19	118.96	112.73
1	A	839	LEU	N-CA-C	5.17	116.91	111.28
2	B	87	ALA	N-CA-C	5.16	117.70	110.23
2	B	518	ASP	N-CA-C	5.15	117.69	110.23
1	A	312	LYS	N-CA-C	5.14	116.96	111.36
2	B	686	ILE	N-CA-C	5.12	120.04	112.61
1	A	794	PRO	CA-C-N	5.12	124.43	118.85
1	A	794	PRO	C-N-CA	5.12	124.43	118.85
2	B	21	ALA	N-CA-C	-5.09	105.73	111.28
2	B	806	GLY	N-CA-C	-5.08	108.36	114.66
2	B	384	ASP	N-CA-C	-5.06	105.77	111.28
2	B	521	GLN	N-CA-C	5.06	117.70	109.86
2	B	312	LYS	N-CA-C	-5.04	105.79	111.28

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	2540	0	785	86	0
2	B	3607	0	1177	109	0
3	C	299	0	91	2	0
All	All	6446	0	2053	197	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 23.

All (197) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:780:THR:CA	1:A:830:GLY:HA2	1.54	1.38
1:A:794:PRO:CD	1:A:795:PRO:HD2	1.53	1.36
2:B:323:VAL:N	2:B:324:PRO:HD2	1.57	1.10
1:A:780:THR:CA	1:A:830:GLY:CA	2.31	1.09
2:B:119:ALA:O	2:B:122:PRO:HD2	1.55	1.07
1:A:794:PRO:HD2	1:A:795:PRO:HD2	1.09	1.06
1:A:794:PRO:HG2	1:A:795:PRO:HD3	1.37	1.06
2:B:408:GLN:O	2:B:411:PRO:HG2	1.59	1.03
1:A:794:PRO:CD	1:A:795:PRO:CD	2.40	0.98
1:A:794:PRO:HD2	1:A:795:PRO:CD	1.99	0.91
1:A:794:PRO:CG	1:A:795:PRO:CD	2.49	0.90
2:B:323:VAL:N	2:B:324:PRO:CD	2.37	0.87
2:B:119:ALA:O	2:B:122:PRO:CD	2.23	0.86
1:A:794:PRO:HG2	1:A:795:PRO:CD	2.04	0.85
2:B:408:GLN:C	2:B:411:PRO:HD2	2.04	0.82
2:B:257:GLY:N	2:B:258:PRO:CD	2.46	0.79
2:B:407:ILE:O	2:B:411:PRO:CD	2.32	0.78
1:A:462:PHE:N	1:A:463:PRO:CD	2.48	0.77
1:A:318:ALA:N	1:A:319:PRO:HD2	1.99	0.76
2:B:408:GLN:O	2:B:411:PRO:CG	2.32	0.76
2:B:87:ALA:O	2:B:91:VAL:N	2.20	0.74
1:A:794:PRO:O	1:A:798:PHE:N	2.20	0.74
1:A:794:PRO:N	1:A:795:PRO:HD2	1.97	0.74
1:A:794:PRO:CG	1:A:795:PRO:HD3	2.11	0.73
1:A:696:LEU:O	1:A:700:TYR:N	2.22	0.73
1:A:463:PRO:HB3	1:A:472:MET:O	1.88	0.73
1:A:471:TYR:O	1:A:474:ALA:N	2.23	0.72
2:B:340:ASP:CA	2:B:522:ASN:H	2.03	0.71
2:B:382:TYR:O	2:B:386:ALA:N	2.22	0.71
2:B:444:ILE:O	2:B:448:TYR:N	2.22	0.71
1:A:460:HIS:O	1:A:463:PRO:HD2	1.91	0.71
2:B:319:LEU:O	2:B:323:VAL:N	2.24	0.71
2:B:121:ILE:N	2:B:122:PRO:HD2	2.06	0.70
1:A:561:VAL:O	1:A:565:MET:N	2.25	0.69
2:B:410:MET:N	2:B:411:PRO:HD2	2.08	0.69
2:B:693:MET:O	2:B:697:LEU:N	2.24	0.69
2:B:34:PRO:HG3	2:B:84:ASP:N	2.08	0.68
2:B:256:MET:C	2:B:258:PRO:HD3	2.18	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:629:THR:O	1:A:630:GLN:C	2.36	0.68
2:B:345:CYS:O	2:B:348:ALA:N	2.27	0.68
1:A:337:VAL:O	1:A:341:ASN:N	2.25	0.67
1:A:794:PRO:CG	1:A:795:PRO:HD2	2.10	0.67
2:B:323:VAL:H	2:B:324:PRO:HD2	1.54	0.67
2:B:407:ILE:O	2:B:411:PRO:HD3	1.93	0.67
2:B:544:TYR:N	2:B:545:PRO:HD2	2.10	0.67
2:B:718:GLY:O	2:B:722:LEU:N	2.28	0.66
2:B:686:ILE:N	2:B:687:PRO:HD2	2.11	0.66
2:B:451:PRO:O	2:B:455:CYS:N	2.23	0.66
1:A:711:ASP:O	1:A:716:GLU:N	2.23	0.65
2:B:368:LEU:N	2:B:369:PRO:CD	2.60	0.65
1:A:322:LEU:O	1:A:326:LEU:N	2.29	0.65
1:A:811:GLU:N	1:A:812:PRO:HD2	2.12	0.65
2:B:34:PRO:CG	2:B:84:ASP:H	2.10	0.65
2:B:119:ALA:C	2:B:122:PRO:HD2	2.22	0.64
1:A:471:TYR:O	1:A:472:MET:C	2.37	0.64
1:A:359:CYS:O	1:A:363:SER:N	2.31	0.64
1:A:463:PRO:HA	1:A:472:MET:CA	2.27	0.64
1:A:675:LEU:O	1:A:679:PHE:N	2.27	0.63
2:B:407:ILE:O	2:B:411:PRO:HD2	1.97	0.63
1:A:511:MET:N	1:A:512:PRO:HD2	2.14	0.63
1:A:756:GLN:O	1:A:759:PRO:HD2	1.99	0.62
2:B:322:LEU:C	2:B:324:PRO:HD2	2.22	0.62
2:B:840:ARG:N	2:B:841:PRO:HD2	2.15	0.62
1:A:787:ILE:O	1:A:791:TYR:N	2.31	0.62
2:B:34:PRO:HD3	2:B:85:ALA:H	1.64	0.62
1:A:523:VAL:O	1:A:527:ASN:N	2.31	0.61
1:A:541:PRO:O	1:A:545:ALA:N	2.29	0.61
1:A:590:GLN:O	1:A:594:THR:N	2.32	0.61
1:A:629:THR:O	1:A:632:LEU:N	2.34	0.60
2:B:26:GLU:CA	2:B:53:ALA:CA	2.79	0.60
1:A:561:VAL:O	1:A:564:LYS:N	2.35	0.60
2:B:265:ILE:O	2:B:269:LYS:N	2.32	0.60
2:B:257:GLY:N	2:B:258:PRO:HD2	2.18	0.59
2:B:34:PRO:HG3	2:B:84:ASP:H	1.65	0.59
2:B:368:LEU:N	2:B:369:PRO:HD2	2.18	0.59
2:B:463:GLU:N	2:B:464:PRO:HD2	2.18	0.59
1:A:862:LEU:N	1:A:863:PRO:HD2	2.18	0.59
2:B:408:GLN:O	2:B:411:PRO:CD	2.51	0.59
2:B:692:VAL:O	2:B:696:LEU:N	2.30	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:668:SER:O	1:A:669:PRO:C	2.44	0.57
2:B:712:GLN:O	2:B:716:VAL:N	2.31	0.57
2:B:512:GLU:O	2:B:516:ARG:N	2.37	0.57
2:B:543:CYS:C	2:B:545:PRO:HD2	2.30	0.57
2:B:34:PRO:CG	2:B:84:ASP:N	2.65	0.57
2:B:694:GLN:O	2:B:698:GLU:N	2.29	0.57
2:B:524:LEU:O	2:B:528:ALA:N	2.32	0.56
1:A:723:LYS:O	1:A:727:THR:N	2.38	0.56
2:B:435:ILE:O	2:B:439:LEU:N	2.35	0.56
2:B:493:GLU:N	2:B:494:PRO:HD3	2.18	0.56
2:B:390:PHE:O	2:B:393:ILE:N	2.38	0.56
2:B:27:ARG:O	2:B:31:GLU:N	2.38	0.56
2:B:777:LYS:C	2:B:779:ASP:H	2.14	0.56
2:B:315:ALA:O	2:B:319:LEU:N	2.39	0.55
1:A:542:VAL:O	1:A:546:LEU:N	2.37	0.55
1:A:733:ASP:O	1:A:736:CYS:N	2.38	0.55
1:A:806:PHE:O	1:A:807:PRO:HB2	2.06	0.55
2:B:119:ALA:O	2:B:122:PRO:CG	2.54	0.55
2:B:5:THR:O	2:B:9:LYS:N	2.37	0.54
2:B:179:GLN:O	2:B:183:LYS:N	2.35	0.54
2:B:345:CYS:O	2:B:346:LYS:C	2.50	0.54
2:B:410:MET:N	2:B:411:PRO:CD	2.70	0.54
1:A:806:PHE:O	1:A:807:PRO:CB	2.55	0.54
1:A:462:PHE:N	1:A:463:PRO:HD2	2.23	0.54
2:B:389:ALA:O	2:B:392:CYS:N	2.40	0.54
1:A:549:ILE:O	1:A:553:THR:N	2.39	0.54
2:B:408:GLN:O	2:B:411:PRO:HD2	2.07	0.54
1:A:462:PHE:N	1:A:463:PRO:HD3	2.24	0.53
2:B:277:LEU:O	2:B:281:GLU:N	2.40	0.53
2:B:121:ILE:N	2:B:122:PRO:CD	2.71	0.53
2:B:408:GLN:C	2:B:411:PRO:CD	2.78	0.52
1:A:471:TYR:O	1:A:473:ARG:N	2.43	0.52
2:B:21:ALA:O	2:B:24:PHE:N	2.42	0.52
1:A:758:ILE:N	1:A:759:PRO:HD2	2.24	0.52
1:A:439:LEU:CA	1:A:482:TYR:CA	2.88	0.52
2:B:329:THR:C	2:B:331:THR:H	2.18	0.52
1:A:318:ALA:N	1:A:319:PRO:CD	2.71	0.52
1:A:782:CYS:O	1:A:786:ALA:N	2.28	0.52
2:B:493:GLU:N	2:B:494:PRO:CD	2.72	0.52
1:A:610:GLY:O	1:A:611:ILE:C	2.53	0.52
2:B:772:ILE:O	2:B:776:LEU:N	2.22	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:120:GLU:C	2:B:122:PRO:HD2	2.35	0.52
2:B:870:ARG:O	2:B:872:LEU:N	2.43	0.51
1:A:414:PHE:O	1:A:418:ILE:N	2.37	0.51
1:A:561:VAL:O	1:A:562:ILE:C	2.49	0.51
2:B:321:TYR:O	2:B:324:PRO:CG	2.58	0.51
2:B:34:PRO:HG2	2:B:84:ASP:H	1.77	0.50
2:B:674:VAL:C	2:B:676:ASP:H	2.19	0.50
3:C:44:GLY:HA3	3:C:93:PHE:O	2.12	0.50
1:A:668:SER:O	1:A:671:MET:N	2.45	0.50
1:A:414:PHE:O	1:A:415:CYS:C	2.53	0.50
1:A:669:PRO:O	1:A:673:GLN:N	2.42	0.50
1:A:733:ASP:O	1:A:734:ALA:C	2.53	0.50
2:B:362:ASP:C	2:B:365:PRO:HD2	2.37	0.50
2:B:468:SER:O	2:B:472:TRP:N	2.43	0.50
2:B:823:GLY:HA2	2:B:869:LEU:N	2.27	0.50
1:A:736:CYS:O	1:A:737:HIS:C	2.54	0.49
2:B:69:ASP:O	2:B:73:LYS:N	2.40	0.49
1:A:780:THR:CA	1:A:830:GLY:HA3	2.32	0.49
2:B:408:GLN:C	2:B:411:PRO:HG2	2.34	0.49
1:A:460:HIS:C	1:A:463:PRO:HD2	2.36	0.49
2:B:544:TYR:N	2:B:545:PRO:CD	2.75	0.49
1:A:318:ALA:H	1:A:319:PRO:HD2	1.75	0.49
2:B:256:MET:C	2:B:258:PRO:CD	2.81	0.49
2:B:4:ILE:O	2:B:8:GLU:N	2.41	0.48
2:B:711:PRO:O	2:B:715:SER:N	2.38	0.48
1:A:429:LYS:O	1:A:430:ASP:C	2.57	0.48
2:B:321:TYR:O	2:B:324:PRO:HG2	2.13	0.48
1:A:574:THR:N	1:A:575:PRO:HD2	2.27	0.47
2:B:115:GLY:O	2:B:116:ILE:C	2.58	0.47
1:A:355:PHE:N	1:A:356:PRO:CD	2.77	0.47
1:A:548:HIS:O	1:A:552:GLU:N	2.32	0.47
2:B:674:VAL:C	2:B:676:ASP:N	2.71	0.47
1:A:292:PHE:O	1:A:294:LYS:N	2.47	0.47
2:B:34:PRO:CD	2:B:85:ALA:H	2.28	0.47
2:B:483:GLU:O	2:B:487:VAL:N	2.48	0.46
1:A:292:PHE:O	1:A:293:LEU:C	2.58	0.46
1:A:981:THR:O	1:A:985:ASN:N	2.45	0.46
2:B:80:TRP:O	2:B:83:ILE:O	2.33	0.46
2:B:115:GLY:O	2:B:118:CYS:N	2.48	0.46
2:B:381:ARG:O	2:B:385:ALA:N	2.46	0.46
1:A:540:ARG:O	1:A:544:GLN:N	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:560:ASN:O	1:A:563:GLN:N	2.49	0.46
1:A:811:GLU:N	1:A:812:PRO:CD	2.78	0.46
2:B:231:THR:O	2:B:234:ARG:N	2.49	0.45
2:B:408:GLN:C	2:B:411:PRO:CG	2.89	0.45
2:B:763:GLU:O	2:B:766:LEU:N	2.50	0.45
2:B:728:PHE:O	2:B:732:LEU:N	2.46	0.45
3:C:85:LYS:N	3:C:92:SER:O	2.35	0.45
1:A:565:MET:O	1:A:569:TYR:N	2.50	0.45
2:B:867:LYS:O	2:B:871:LYS:N	2.49	0.45
2:B:145:HIS:O	2:B:149:SER:N	2.45	0.44
2:B:403:LYS:N	2:B:404:PRO:HD2	2.32	0.44
2:B:493:GLU:H	2:B:494:PRO:HD3	1.82	0.44
2:B:686:ILE:N	2:B:687:PRO:CD	2.80	0.44
2:B:402:LEU:O	2:B:406:VAL:N	2.40	0.44
1:A:511:MET:N	1:A:512:PRO:CD	2.81	0.44
2:B:389:ALA:O	2:B:390:PHE:C	2.60	0.43
1:A:355:PHE:N	1:A:356:PRO:HD2	2.33	0.43
1:A:511:MET:O	1:A:515:VAL:N	2.49	0.43
2:B:614:MET:O	2:B:618:THR:N	2.44	0.43
2:B:329:THR:C	2:B:331:THR:N	2.77	0.42
2:B:231:THR:O	2:B:232:ARG:C	2.61	0.42
1:A:862:LEU:N	1:A:863:PRO:CD	2.83	0.42
1:A:676:PRO:O	1:A:680:ASP:N	2.36	0.42
1:A:993:GLN:O	1:A:997:THR:N	2.45	0.42
2:B:450:ALA:O	2:B:454:GLN:N	2.45	0.42
2:B:34:PRO:HG3	2:B:85:ALA:H	1.84	0.42
1:A:471:TYR:C	1:A:473:ARG:N	2.78	0.41
1:A:793:SER:N	1:A:794:PRO:HD3	2.35	0.41
2:B:581:GLN:O	2:B:584:LEU:N	2.53	0.41
1:A:461:VAL:C	1:A:463:PRO:HD2	2.46	0.41
1:A:614:THR:O	1:A:615:ILE:C	2.63	0.41
2:B:464:PRO:O	2:B:517:PRO:HG3	2.21	0.41
2:B:840:ARG:N	2:B:841:PRO:CD	2.83	0.40
1:A:805:ARG:CA	1:A:808:ASN:O	2.69	0.40
2:B:418:LYS:O	2:B:419:ASP:C	2.65	0.40
1:A:793:SER:N	1:A:794:PRO:CD	2.85	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	613/1038 (59%)	575 (94%)	30 (5%)	8 (1%)	10 42
2	B	871/876 (99%)	809 (93%)	45 (5%)	17 (2%)	6 31
3	C	72/194 (37%)	71 (99%)	1 (1%)	0	100 100
All	All	1556/2108 (74%)	1455 (94%)	76 (5%)	25 (2%)	10 38

All (25) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	291	VAL
1	A	807	PRO
1	A	974	PRO
2	B	4	ILE
2	B	47	PRO
2	B	105	ARG
2	B	343	ASN
1	A	293	LEU
2	B	275	VAL
2	B	307	PRO
1	A	573	VAL
2	B	440	PRO
2	B	494	PRO
2	B	710	LYS
2	B	871	LYS
2	B	272	ILE
2	B	605	ASP
2	B	724	ILE
1	A	317	ILE
1	A	850	ARG
2	B	163	PRO
1	A	436	ILE
2	B	330	LEU
2	B	378	PRO

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Mol	Chain	Res	Type
2	B	493	GLU

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	21/929 (2%)	21 (100%)	0	100	100
2	B	37/751 (5%)	37 (100%)	0	100	100
3	C	1/158 (1%)	1 (100%)	0	100	100
All	All	59/1838 (3%)	59 (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. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

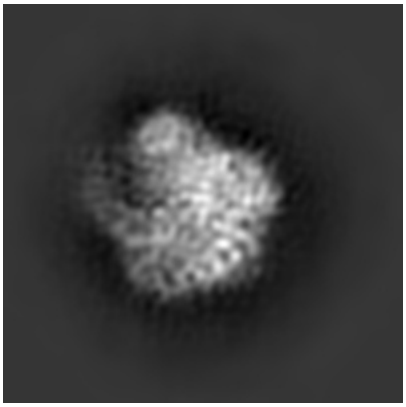
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-0366. These allow visual inspection of the internal detail of the map and identification of artifacts.

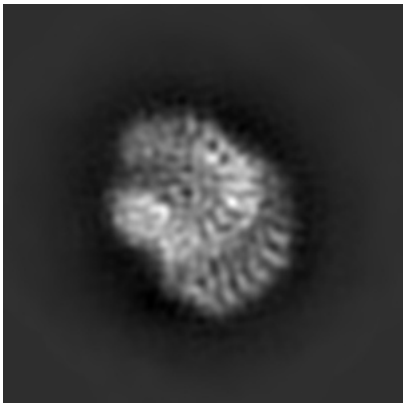
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

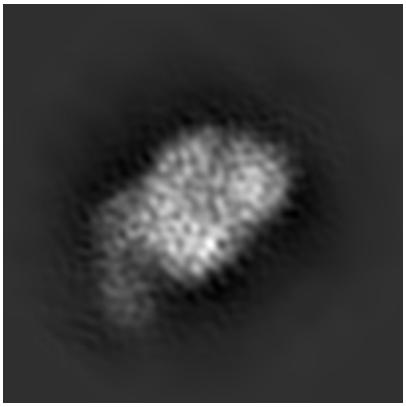
6.1.1 Primary map



X



Y



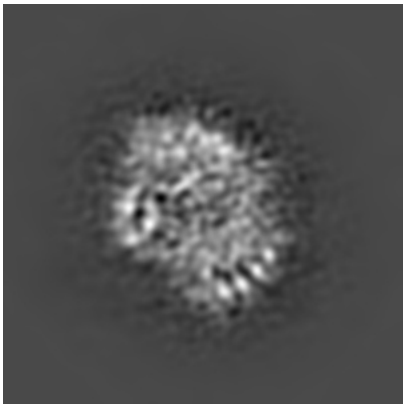
Z

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

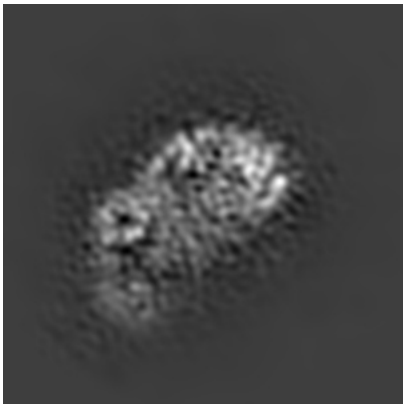
6.2 Central slices

6.2.1 Primary map

X Index: 84



Y Index: 84



Z Index: 84

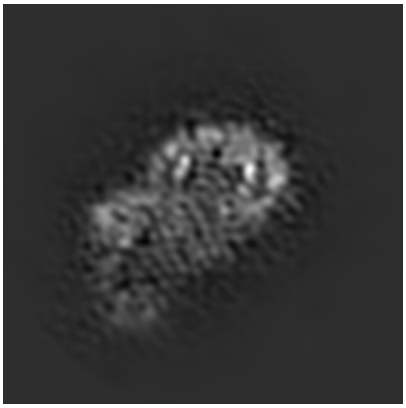
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map

X Index: 76

Y Index: 91

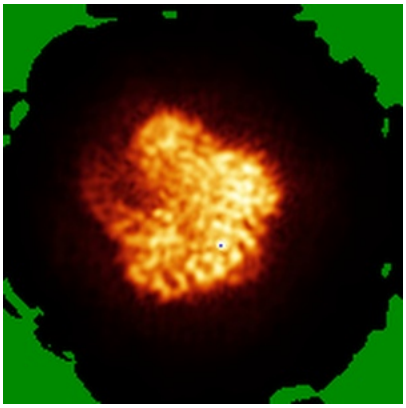


Z Index: 86

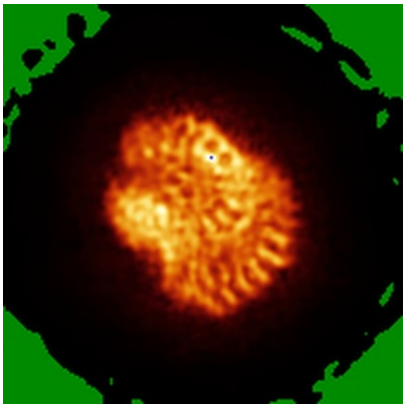
The images above show the largest variance slices of the map in three orthogonal directions.

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

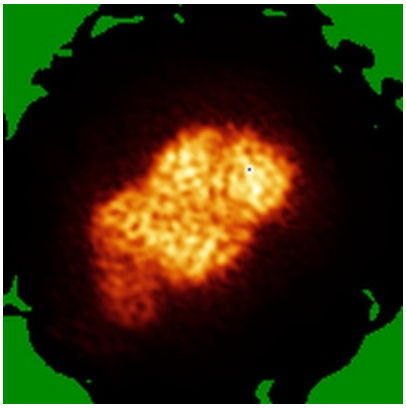
6.4.1 Primary map



X



Y

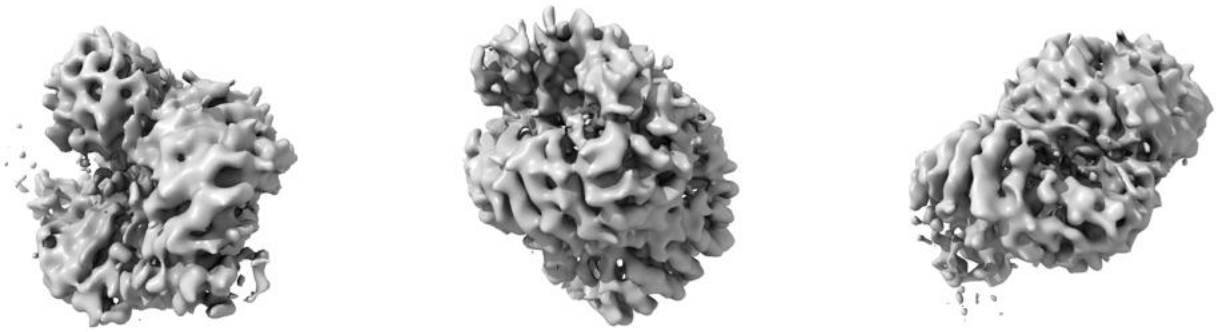


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.0356. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

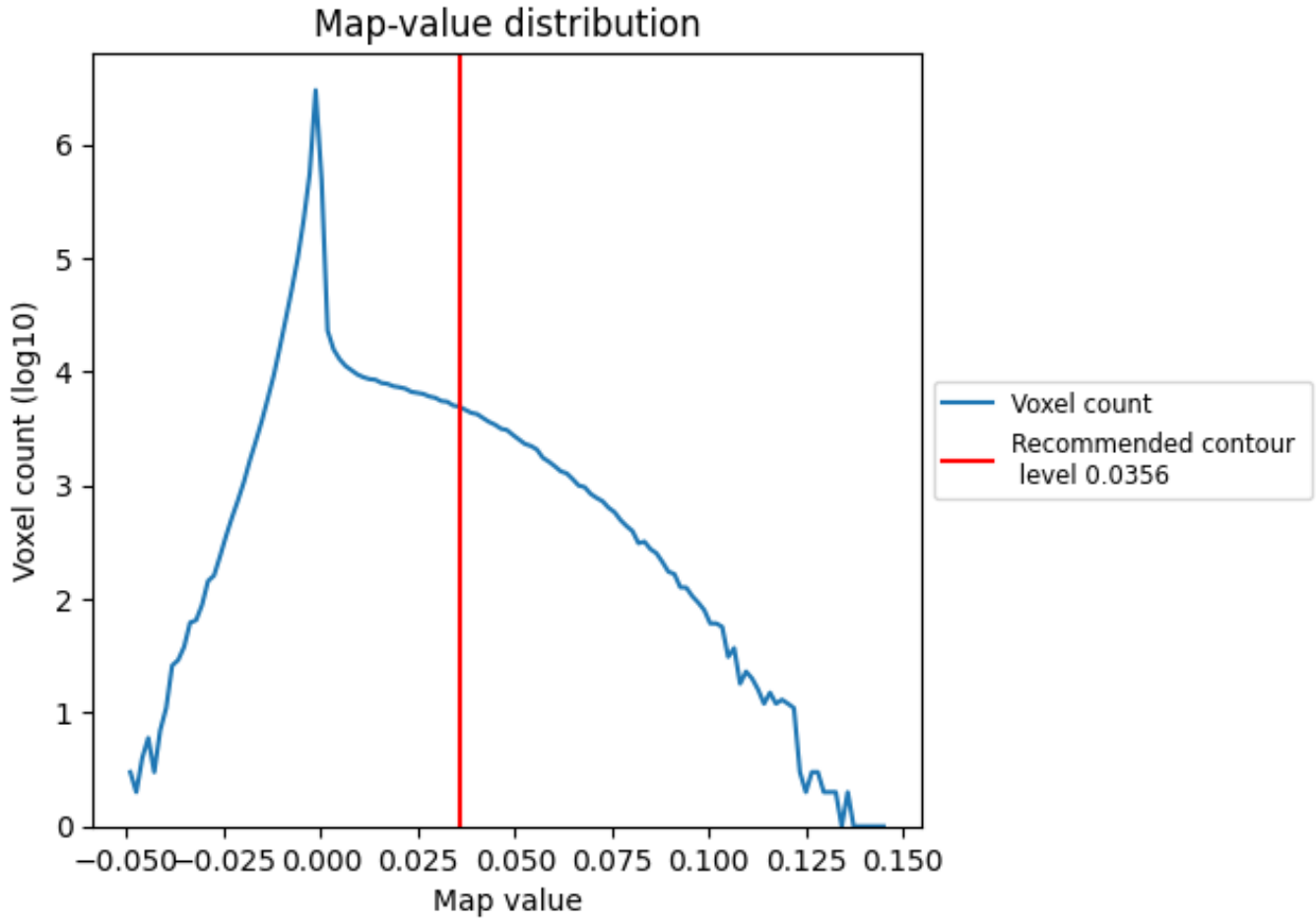
6.6 Mask visualisation (i)

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

7 Map analysis

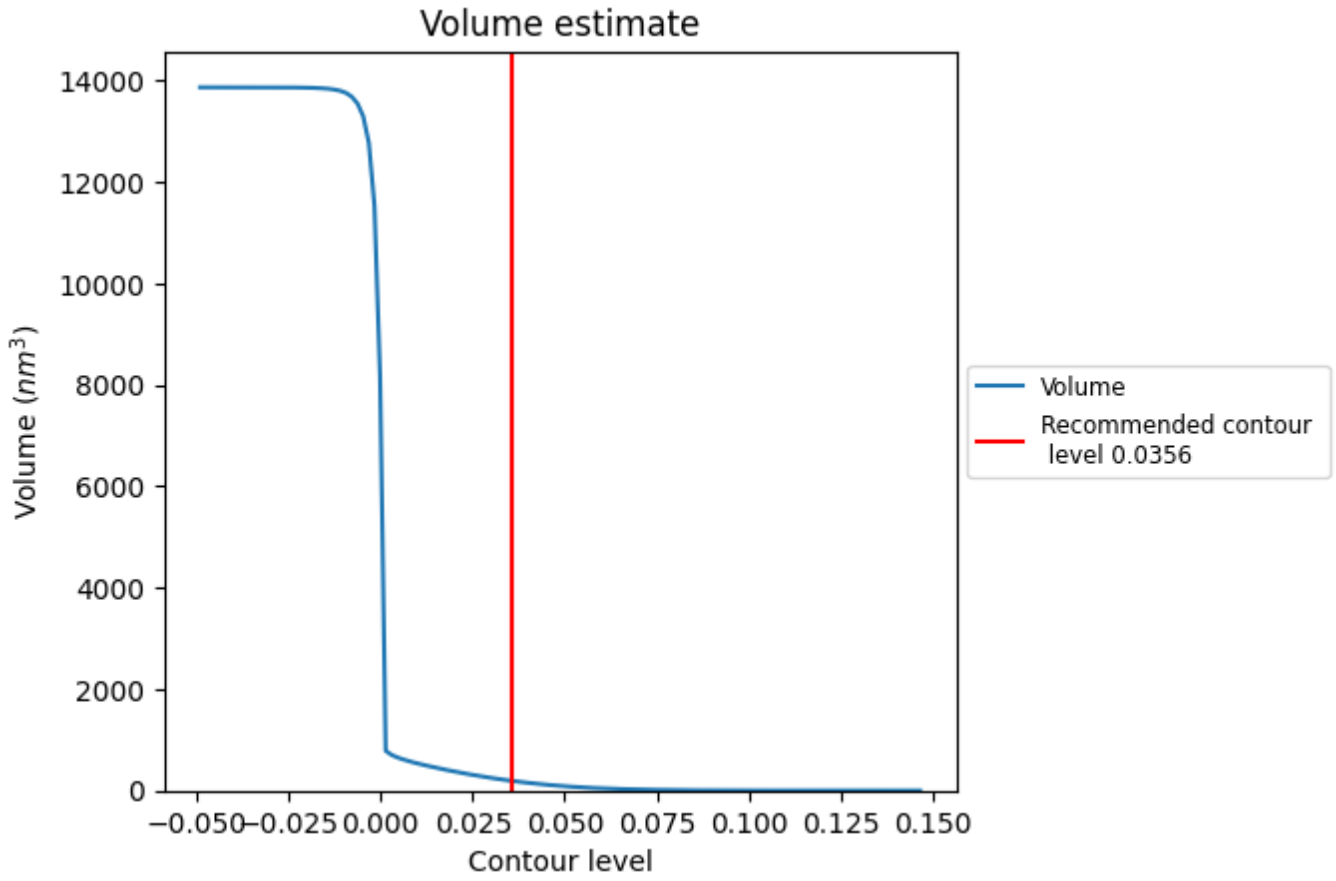
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

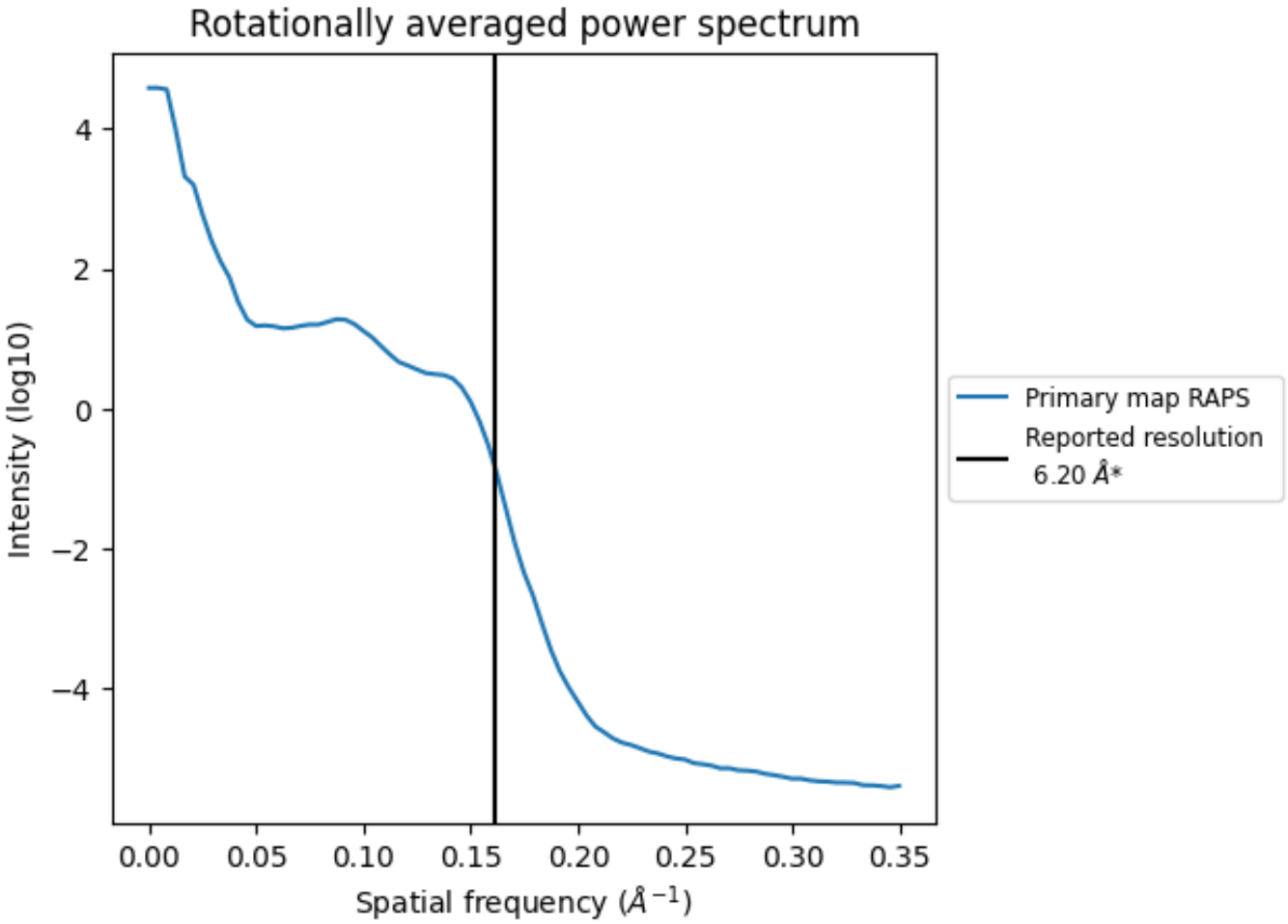
7.2 Volume estimate (i)



The volume at the recommended contour level is 192 nm^3; this corresponds to an approximate mass of 173 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.161 Å^{-1}

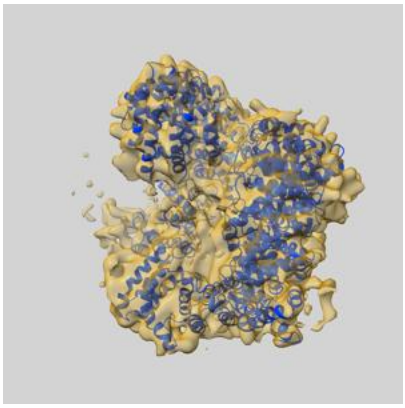
8 Fourier-Shell correlation (i)

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

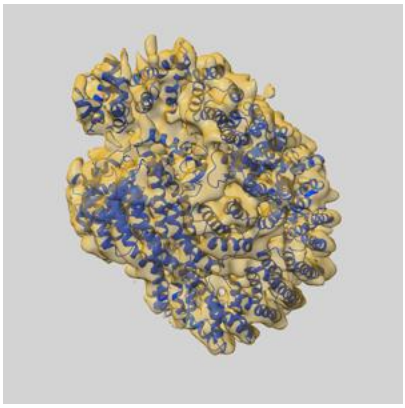
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-0366 and PDB model 6N88. Per-residue inclusion information can be found in section 3 on page 4.

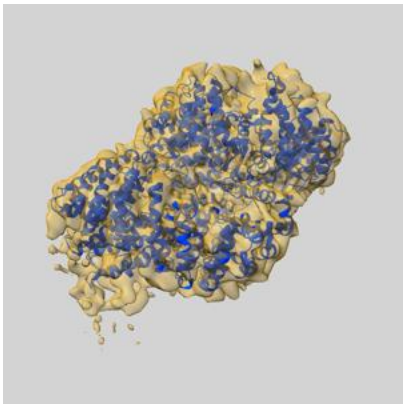
9.1 Map-model overlay



X



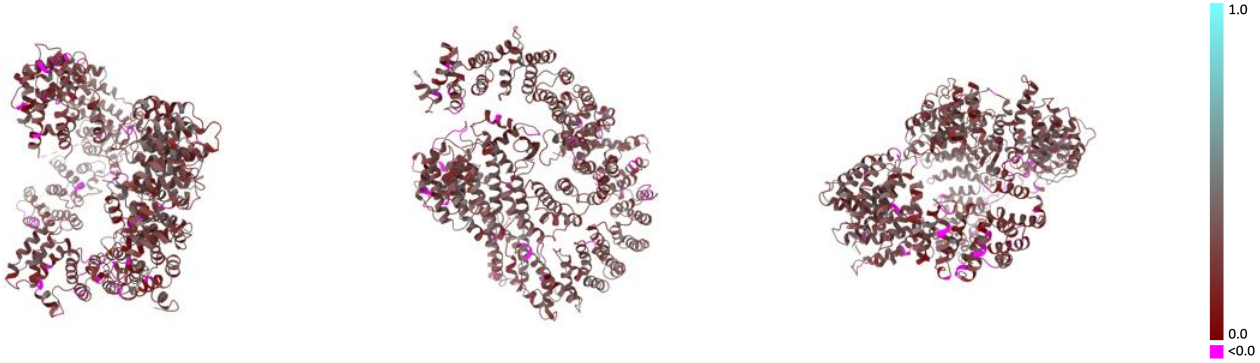
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0356 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

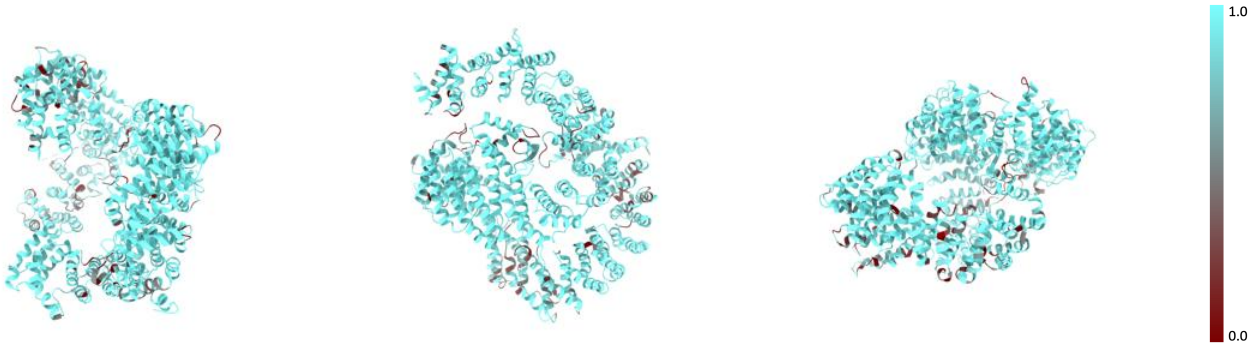
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

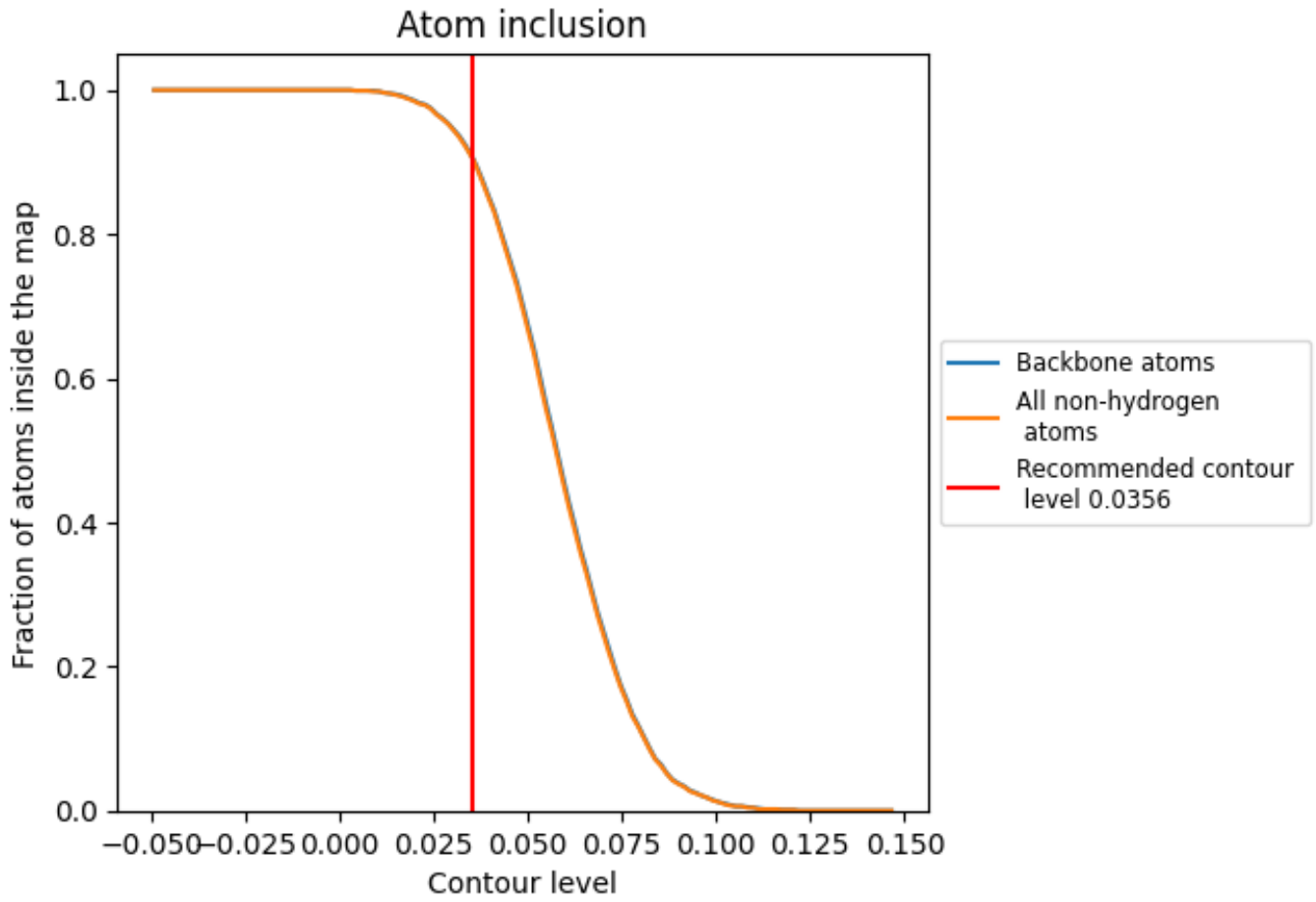
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0356).

9.4 Atom inclusion (i)



At the recommended contour level, 90% of all backbone atoms, 90% 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 (0.0356) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9030	0.2630
A	0.8530	0.2450
B	0.9410	0.2770
C	0.8560	0.2430