wwPDB EM Validation Summary Report (i)

Nov 20, 2022 – 06:15 am GMT

PDB ID	:	6I54
EMDB ID	:	EMD-4412
Title	:	Influenza A nucleoprotein docked into 3D helical structure of the wild type ribonucleoprotein complex obtained using cryoEM. Conformation 2.
Authors	:	Coloma, R.; Arranz, R.; de la Rosa-Trevin, J.M.; Sorzano, C.O.S.; Carlero, D.; Ortin, J.; Martin-Benito, J.
Deposited on	:	2018-11-12
Resolution	:	10.00 Å(reported)
Based on initial model	:	2IQH

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

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

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

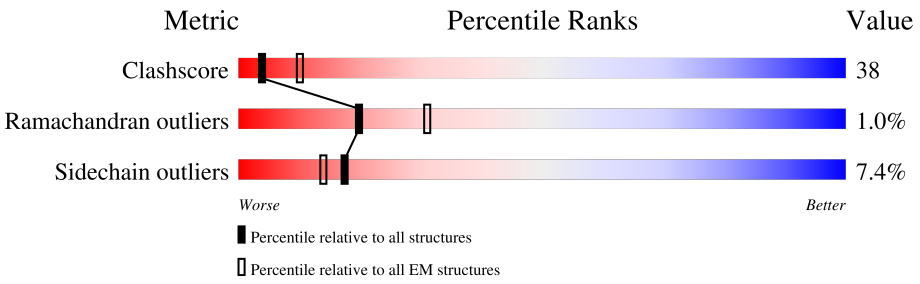
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 10.00 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	382	8% 47% 46% 6%
1	C	382	8% 48% 46% 6%
2	B	19	11% 89%
2	D	19	11% 89%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 6320 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 Nucleoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	382	3012	1871	560	558	23	0	0
1	C	382	3012	1871	560	558	23	0	0

There are 174 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLU	deletion	UNP Q1K9H2
A	?	-	ARG	deletion	UNP Q1K9H2
A	?	-	ARG	deletion	UNP Q1K9H2
A	?	-	ASN	deletion	UNP Q1K9H2
A	?	-	LYS	deletion	UNP Q1K9H2
A	?	-	TYR	deletion	UNP Q1K9H2
A	?	-	LEU	deletion	UNP Q1K9H2
A	?	-	GLU	deletion	UNP Q1K9H2
A	?	-	GLU	deletion	UNP Q1K9H2
A	?	-	HIS	deletion	UNP Q1K9H2
A	?	-	PRO	deletion	UNP Q1K9H2
A	?	-	SER	deletion	UNP Q1K9H2
A	?	-	ALA	deletion	UNP Q1K9H2
A	?	-	GLY	deletion	UNP Q1K9H2
A	?	-	LYS	deletion	UNP Q1K9H2
A	?	-	ASP	deletion	UNP Q1K9H2
A	?	-	PRO	deletion	UNP Q1K9H2
A	?	-	LYS	deletion	UNP Q1K9H2
A	?	-	LYS	deletion	UNP Q1K9H2
A	?	-	ASP	deletion	UNP Q1K9H2
A	?	-	ARG	deletion	UNP Q1K9H2
A	?	-	ASN	deletion	UNP Q1K9H2
A	?	-	PHE	deletion	UNP Q1K9H2
A	?	-	TRP	deletion	UNP Q1K9H2
A	?	-	ARG	deletion	UNP Q1K9H2
A	?	-	GLY	deletion	UNP Q1K9H2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLU	deletion	UNP Q1K9H2
A	?	-	ASN	deletion	UNP Q1K9H2
A	?	-	GLY	deletion	UNP Q1K9H2
A	?	-	ASN	deletion	UNP Q1K9H2
A	?	-	GLN	deletion	UNP Q1K9H2
A	?	-	GLN	deletion	UNP Q1K9H2
A	?	-	ARG	deletion	UNP Q1K9H2
A	?	-	ALA	deletion	UNP Q1K9H2
A	?	-	SER	deletion	UNP Q1K9H2
A	?	-	SER	deletion	UNP Q1K9H2
A	?	-	GLY	deletion	UNP Q1K9H2
A	?	-	GLN	deletion	UNP Q1K9H2
A	?	-	ILE	deletion	UNP Q1K9H2
A	?	-	SER	deletion	UNP Q1K9H2
A	?	-	ILE	deletion	UNP Q1K9H2
A	?	-	GLN	deletion	UNP Q1K9H2
A	?	-	PRO	deletion	UNP Q1K9H2
A	?	-	THR	deletion	UNP Q1K9H2
A	?	-	PHE	deletion	UNP Q1K9H2
A	?	-	SER	deletion	UNP Q1K9H2
A	?	-	VAL	deletion	UNP Q1K9H2
A	?	-	GLN	deletion	UNP Q1K9H2
A	?	-	ARG	deletion	UNP Q1K9H2
A	?	-	ASN	deletion	UNP Q1K9H2
A	?	-	LEU	deletion	UNP Q1K9H2
A	?	-	PRO	deletion	UNP Q1K9H2
A	?	-	PHE	deletion	UNP Q1K9H2
A	?	-	ASP	deletion	UNP Q1K9H2
A	?	-	ARG	deletion	UNP Q1K9H2
A	?	-	PRO	deletion	UNP Q1K9H2
A	?	-	THR	deletion	UNP Q1K9H2
A	?	-	ILE	deletion	UNP Q1K9H2
A	?	-	MET	deletion	UNP Q1K9H2
A	?	-	ALA	deletion	UNP Q1K9H2
A	?	-	ALA	deletion	UNP Q1K9H2
A	?	-	PHE	deletion	UNP Q1K9H2
A	?	-	THR	deletion	UNP Q1K9H2
A	?	-	GLY	deletion	UNP Q1K9H2
A	?	-	ASN	deletion	UNP Q1K9H2
A	?	-	THR	deletion	UNP Q1K9H2
A	?	-	GLU	deletion	UNP Q1K9H2
A	?	-	GLY	deletion	UNP Q1K9H2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ARG	deletion	UNP Q1K9H2
A	?	-	THR	deletion	UNP Q1K9H2
A	?	-	SER	deletion	UNP Q1K9H2
A	?	-	ASP	deletion	UNP Q1K9H2
A	?	-	MET	deletion	UNP Q1K9H2
A	?	-	ARG	deletion	UNP Q1K9H2
A	?	-	THR	deletion	UNP Q1K9H2
A	?	-	GLU	deletion	UNP Q1K9H2
A	?	-	ILE	deletion	UNP Q1K9H2
A	?	-	ILE	deletion	UNP Q1K9H2
A	?	-	ARG	deletion	UNP Q1K9H2
A	?	-	LEU	deletion	UNP Q1K9H2
A	?	-	MET	deletion	UNP Q1K9H2
A	?	-	GLU	deletion	UNP Q1K9H2
A	?	-	SER	deletion	UNP Q1K9H2
A	?	-	ALA	deletion	UNP Q1K9H2
A	?	-	ARG	deletion	UNP Q1K9H2
A	?	-	PRO	deletion	UNP Q1K9H2
A	?	-	GLU	deletion	UNP Q1K9H2
C	?	-	GLU	deletion	UNP Q1K9H2
C	?	-	ARG	deletion	UNP Q1K9H2
C	?	-	ARG	deletion	UNP Q1K9H2
C	?	-	ASN	deletion	UNP Q1K9H2
C	?	-	LYS	deletion	UNP Q1K9H2
C	?	-	TYR	deletion	UNP Q1K9H2
C	?	-	LEU	deletion	UNP Q1K9H2
C	?	-	GLU	deletion	UNP Q1K9H2
C	?	-	GLU	deletion	UNP Q1K9H2
C	?	-	HIS	deletion	UNP Q1K9H2
C	?	-	PRO	deletion	UNP Q1K9H2
C	?	-	SER	deletion	UNP Q1K9H2
C	?	-	ALA	deletion	UNP Q1K9H2
C	?	-	GLY	deletion	UNP Q1K9H2
C	?	-	LYS	deletion	UNP Q1K9H2
C	?	-	ASP	deletion	UNP Q1K9H2
C	?	-	PRO	deletion	UNP Q1K9H2
C	?	-	LYS	deletion	UNP Q1K9H2
C	?	-	LYS	deletion	UNP Q1K9H2
C	?	-	ASP	deletion	UNP Q1K9H2
C	?	-	ARG	deletion	UNP Q1K9H2
C	?	-	ASN	deletion	UNP Q1K9H2
C	?	-	PHE	deletion	UNP Q1K9H2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	TRP	deletion	UNP Q1K9H2
C	?	-	ARG	deletion	UNP Q1K9H2
C	?	-	GLY	deletion	UNP Q1K9H2
C	?	-	GLU	deletion	UNP Q1K9H2
C	?	-	ASN	deletion	UNP Q1K9H2
C	?	-	GLY	deletion	UNP Q1K9H2
C	?	-	ASN	deletion	UNP Q1K9H2
C	?	-	GLN	deletion	UNP Q1K9H2
C	?	-	GLN	deletion	UNP Q1K9H2
C	?	-	ARG	deletion	UNP Q1K9H2
C	?	-	ALA	deletion	UNP Q1K9H2
C	?	-	SER	deletion	UNP Q1K9H2
C	?	-	SER	deletion	UNP Q1K9H2
C	?	-	GLY	deletion	UNP Q1K9H2
C	?	-	GLN	deletion	UNP Q1K9H2
C	?	-	ILE	deletion	UNP Q1K9H2
C	?	-	SER	deletion	UNP Q1K9H2
C	?	-	ILE	deletion	UNP Q1K9H2
C	?	-	GLN	deletion	UNP Q1K9H2
C	?	-	PRO	deletion	UNP Q1K9H2
C	?	-	THR	deletion	UNP Q1K9H2
C	?	-	PHE	deletion	UNP Q1K9H2
C	?	-	SER	deletion	UNP Q1K9H2
C	?	-	VAL	deletion	UNP Q1K9H2
C	?	-	GLN	deletion	UNP Q1K9H2
C	?	-	ARG	deletion	UNP Q1K9H2
C	?	-	ASN	deletion	UNP Q1K9H2
C	?	-	LEU	deletion	UNP Q1K9H2
C	?	-	PRO	deletion	UNP Q1K9H2
C	?	-	PHE	deletion	UNP Q1K9H2
C	?	-	ASP	deletion	UNP Q1K9H2
C	?	-	ARG	deletion	UNP Q1K9H2
C	?	-	PRO	deletion	UNP Q1K9H2
C	?	-	THR	deletion	UNP Q1K9H2
C	?	-	ILE	deletion	UNP Q1K9H2
C	?	-	MET	deletion	UNP Q1K9H2
C	?	-	ALA	deletion	UNP Q1K9H2
C	?	-	ALA	deletion	UNP Q1K9H2
C	?	-	PHE	deletion	UNP Q1K9H2
C	?	-	THR	deletion	UNP Q1K9H2
C	?	-	GLY	deletion	UNP Q1K9H2
C	?	-	ASN	deletion	UNP Q1K9H2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	THR	deletion	UNP Q1K9H2
C	?	-	GLU	deletion	UNP Q1K9H2
C	?	-	GLY	deletion	UNP Q1K9H2
C	?	-	ARG	deletion	UNP Q1K9H2
C	?	-	THR	deletion	UNP Q1K9H2
C	?	-	SER	deletion	UNP Q1K9H2
C	?	-	ASP	deletion	UNP Q1K9H2
C	?	-	MET	deletion	UNP Q1K9H2
C	?	-	ARG	deletion	UNP Q1K9H2
C	?	-	THR	deletion	UNP Q1K9H2
C	?	-	GLU	deletion	UNP Q1K9H2
C	?	-	ILE	deletion	UNP Q1K9H2
C	?	-	ILE	deletion	UNP Q1K9H2
C	?	-	ARG	deletion	UNP Q1K9H2
C	?	-	LEU	deletion	UNP Q1K9H2
C	?	-	MET	deletion	UNP Q1K9H2
C	?	-	GLU	deletion	UNP Q1K9H2
C	?	-	SER	deletion	UNP Q1K9H2
C	?	-	ALA	deletion	UNP Q1K9H2
C	?	-	ARG	deletion	UNP Q1K9H2
C	?	-	PRO	deletion	UNP Q1K9H2
C	?	-	GLU	deletion	UNP Q1K9H2

- Molecule 2 is a protein called Influenza virus nucleoprotein.

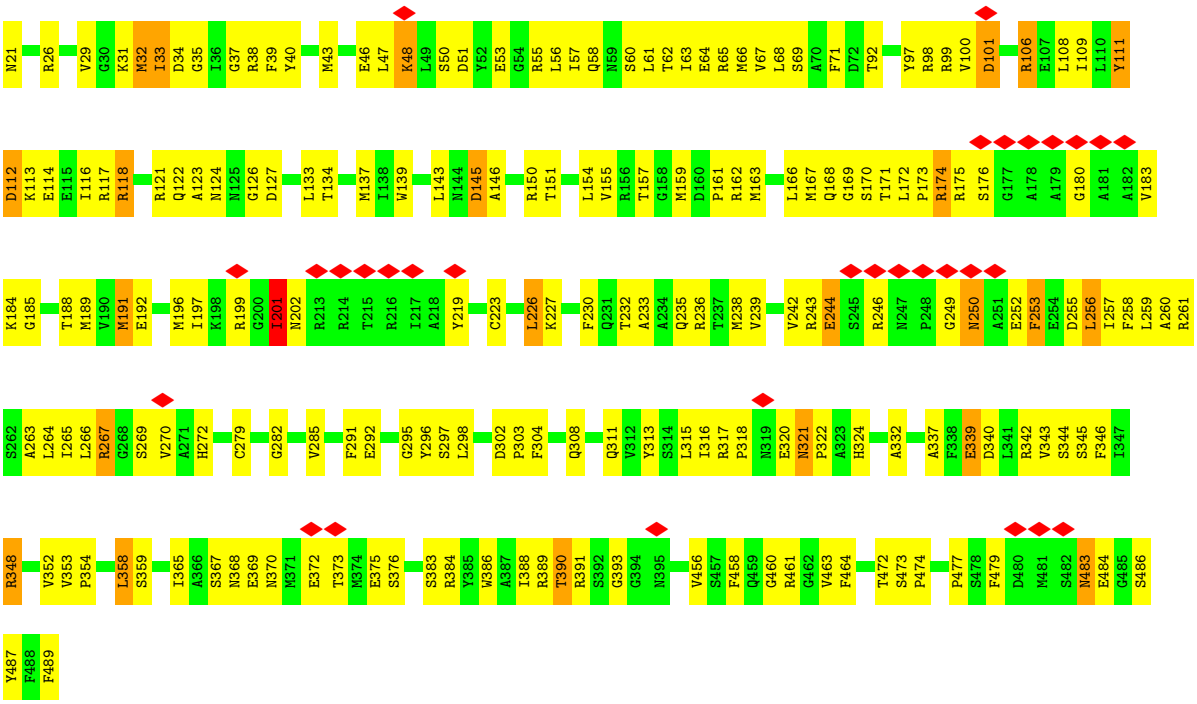
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	B	19	148	94	26	28	0	0
			Total	C	N	O		
2	D	19	148	94	26	28	0	0

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.

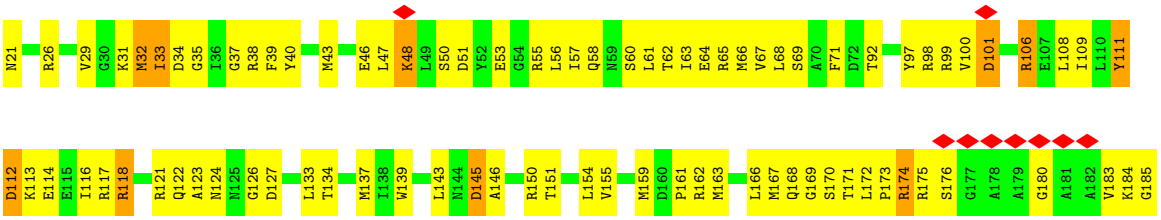
- Molecule 1: Nucleoprotein

Chain A:



- Molecule 1: Nucleoprotein

Chain C:



T188 M189 V190 M191 E192 M196 I197 K198 R199 G200 I201 N202 R213 R214 T215 R216 I217 A218 Y219 E220 R221 W222 C223 N224 I225 L226 K227 F230 Q231 T232 A233 A234 Q235 R236 T237 M238 V239 V242 R243 E244 S245 R246 N247 P248 G249 N250 A251 E252 F253 E254 D255 L256 I257 F258 L259 A260

R261 S262 A263 L264 I265 L266 R267 G268 S269 V270 A271 H272 C279 G282 V285 F291 E292 G295 Y296 S297 L298 D302 P303 F304 Q308 Q311 W312 Y313 S314 L315 I316 R317 P318 N319 E320 N321 P322 A323 H324 A332 A337 F338 E339 D340 L341 R342 V343 S344 S345 F346

I347 R348 V352 V353 P354 L358 S359 I365 A366 S367 N368 E369 N370 M371 E372 T373 M374 E375 S376 S383 R384 Y385 W386 R389 T390 R391 S392 G393 G394 N395 V456 S457 F458 Q459 G460 R461 G462 V463 F464 T472 P477 S478 F479 D480 M481 S482 N483 E484 G485 S486 Y487 F488

F489

- Molecule 2: Influenza virus nucleoprotein

Chain B: 11% 89%

S402 S403 G404 Q405 I406 S407 I408 Q409 P410 T411 F412 S413 V414 Q415 R416 N417 L418 P419 F420

- Molecule 2: Influenza virus nucleoprotein

Chain D: 11% 89%

S402 S403 G404 Q405 I406 S407 I408 Q409 P410 T411 F412 S413 V414 Q415 R416 N417 L418 P419 F420

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-68.33°, rise=34.47 Å, axial sym=D1	Depositor
Number of segments used	4806	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.093	Depositor
Minimum map value	-0.052	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.044	Depositor
Map size (Å)	271.2, 271.2, 271.2	wwPDB
Map dimensions	120, 120, 120	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.26, 2.26, 2.26	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	0.93	1/3060 (0.0%)	0.91	6/4112 (0.1%)
1	C	0.93	1/3060 (0.0%)	0.91	6/4112 (0.1%)
2	B	0.88	0/151	0.94	0/204
2	D	0.88	0/151	0.94	0/204
All	All	0.93	2/6422 (0.0%)	0.92	12/8632 (0.1%)

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	1
1	C	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	201	ILE	C-N	-5.22	1.22	1.34
1	C	201	ILE	C-N	-5.15	1.22	1.34

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	201	ILE	O-C-N	-6.21	112.76	122.70
1	A	201	ILE	O-C-N	-6.18	112.81	122.70
1	A	358	LEU	CB-CG-CD2	-5.70	101.30	111.00
1	C	358	LEU	CB-CG-CD2	-5.69	101.33	111.00
1	C	66	MET	CG-SD-CE	5.51	109.02	100.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	201	ILE	Mainchain
1	C	201	ILE	Mainchain

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	3012	0	3007	229	0
1	C	3012	0	3007	228	0
2	B	148	0	146	36	0
2	D	148	0	146	33	0
All	All	6320	0	6306	476	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 38.

The worst 5 of 476 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:111:TYR:HB3	1:A:116:ILE:HD11	1.47	0.96
1:A:483:ASN:H	1:A:483:ASN:HD22	1.09	0.96
1:C:483:ASN:HD22	1:C:483:ASN:H	1.09	0.96
1:C:111:TYR:HB3	1:C:116:ILE:HD11	1.46	0.95
1:C:189:MET:HE1	1:C:192:GLU:OE1	1.66	0.95

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	374/382 (98%)	324 (87%)	46 (12%)	4 (1%)	14	52
1	C	374/382 (98%)	324 (87%)	46 (12%)	4 (1%)	14	52
2	B	17/19 (90%)	15 (88%)	2 (12%)	0	100	100
2	D	17/19 (90%)	15 (88%)	2 (12%)	0	100	100
All	All	782/802 (98%)	678 (87%)	96 (12%)	8 (1%)	20	55

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	233	ALA
1	A	472	THR
1	C	233	ALA
1	C	472	THR
1	A	101	ASP

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	322/322 (100%)	297 (92%)	25 (8%)	12	36
1	C	322/322 (100%)	297 (92%)	25 (8%)	12	36
2	B	18/18 (100%)	18 (100%)	0	100	100
2	D	18/18 (100%)	18 (100%)	0	100	100
All	All	680/680 (100%)	630 (93%)	50 (7%)	17	38

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	48	LYS
1	C	174	ARG
1	C	484	GLU

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Continued from previous page...

Mol	Chain	Res	Type
1	C	106	ARG
1	C	112	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	319	ASN
1	C	368	ASN
1	C	324	HIS
1	C	370	ASN
1	A	368	ASN

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 monosaccharides 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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	3
1	C	3

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	202:ASN	C	213:ARG	N	14.50
1	C	202:ASN	C	213:ARG	N	14.50
1	A	72:ASP	C	92:THR	N	10.26
1	C	72:ASP	C	92:THR	N	10.26
1	A	396:THR	C	455:ASP	N	9.84

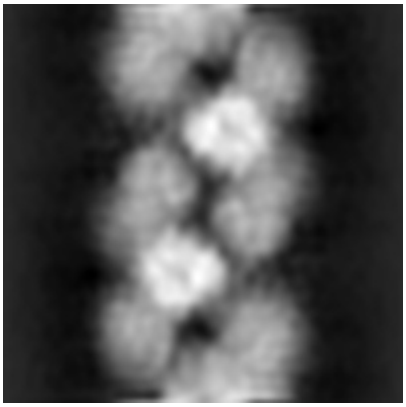
6 Map visualisation (i)

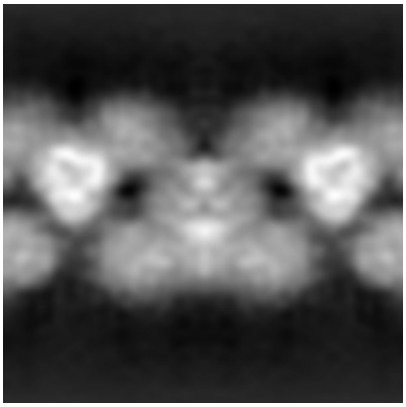
This section contains visualisations of the EMDB entry EMD-4412. These allow visual inspection of the internal detail of the map and identification of artifacts.

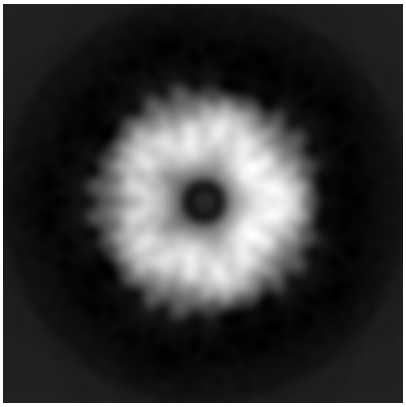
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

6.1.1 Primary map


X

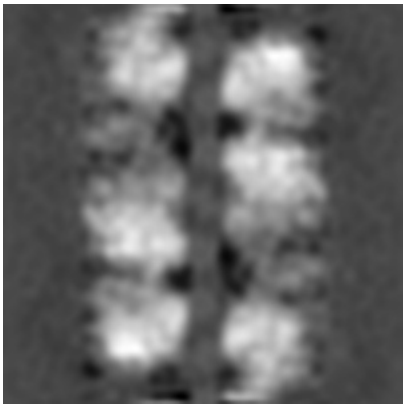

Y

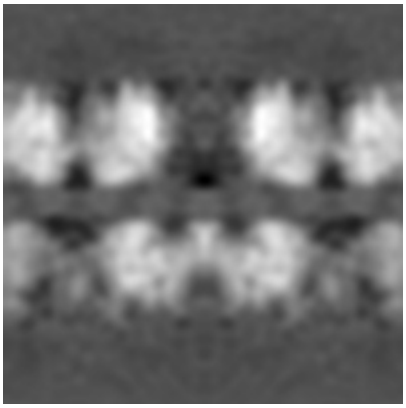

Z

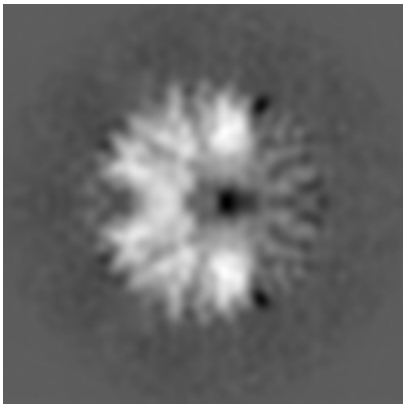
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

6.2.1 Primary map


X Index: 60

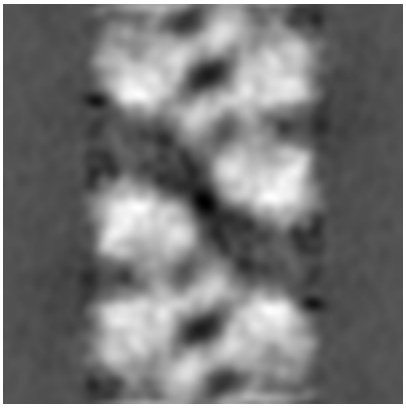

Y Index: 60


Z Index: 60

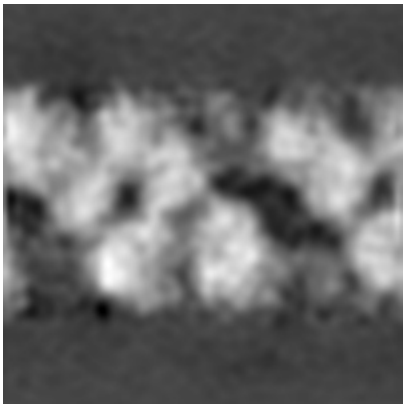
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

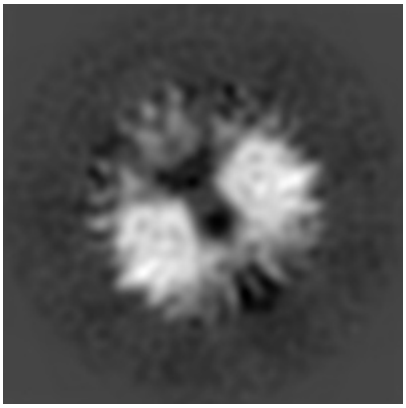
6.3.1 Primary map



X Index: 67



Y Index: 50

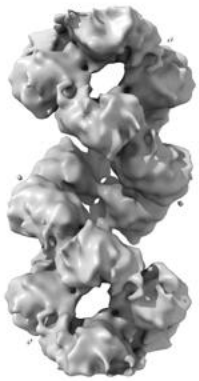


Z Index: 114

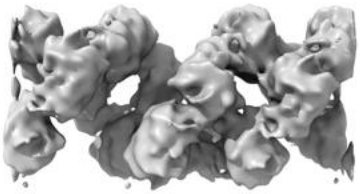
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

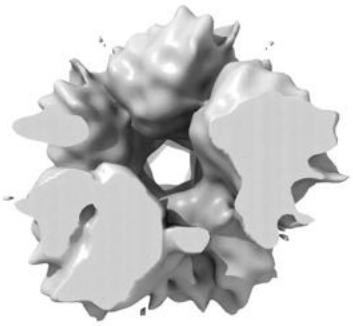
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.044. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

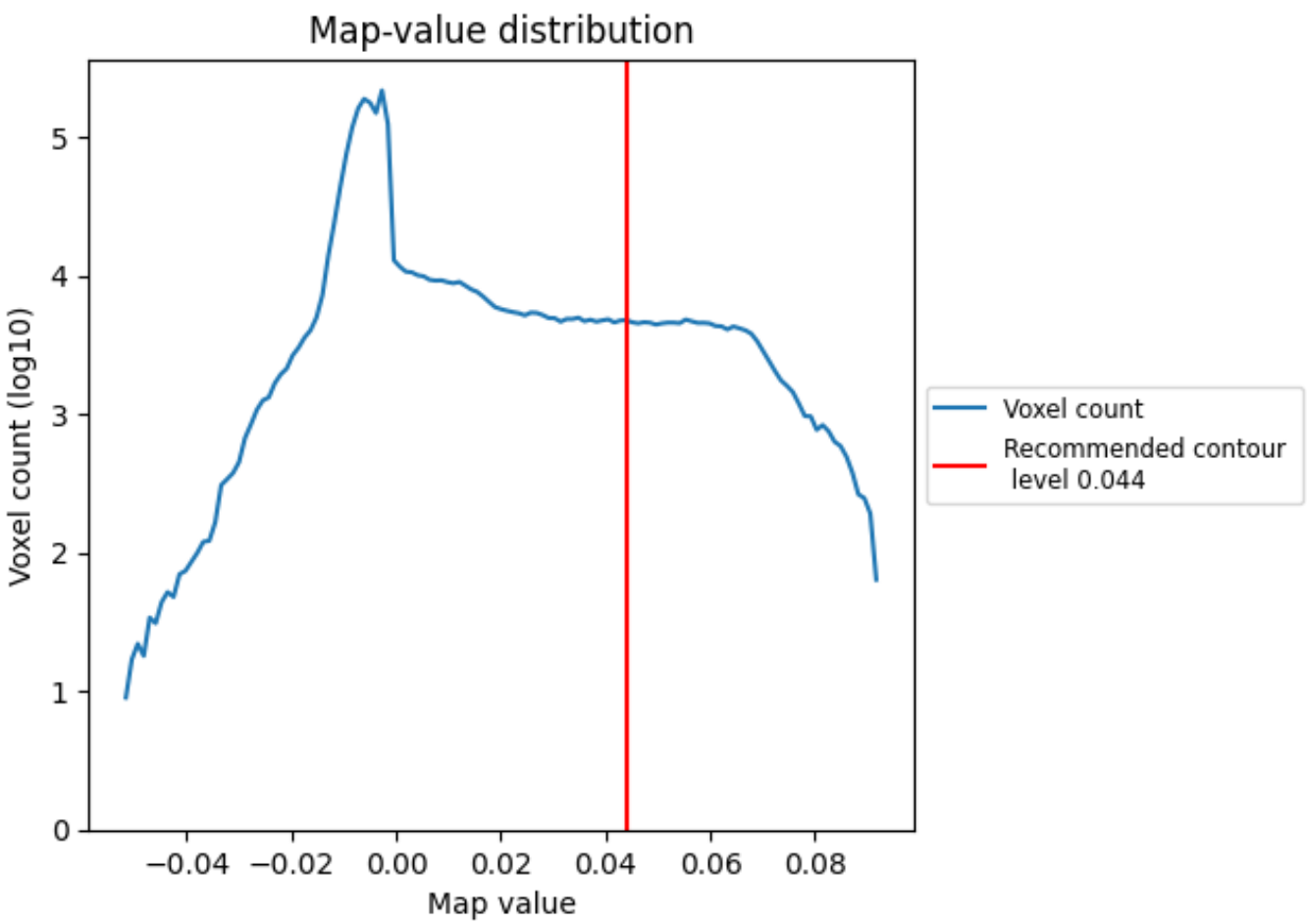
6.5 Mask visualisation (i)

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

7 Map analysis (i)

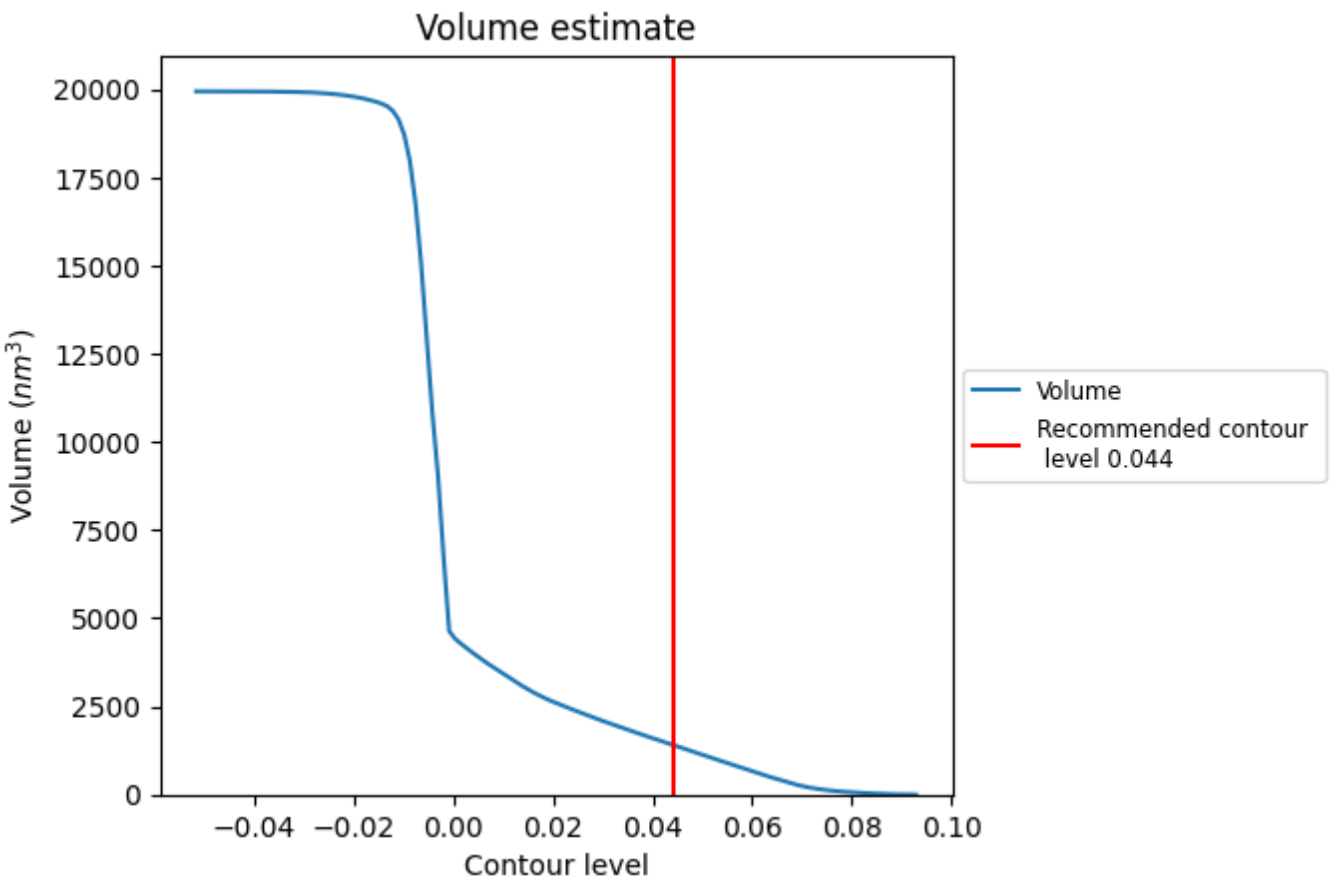
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

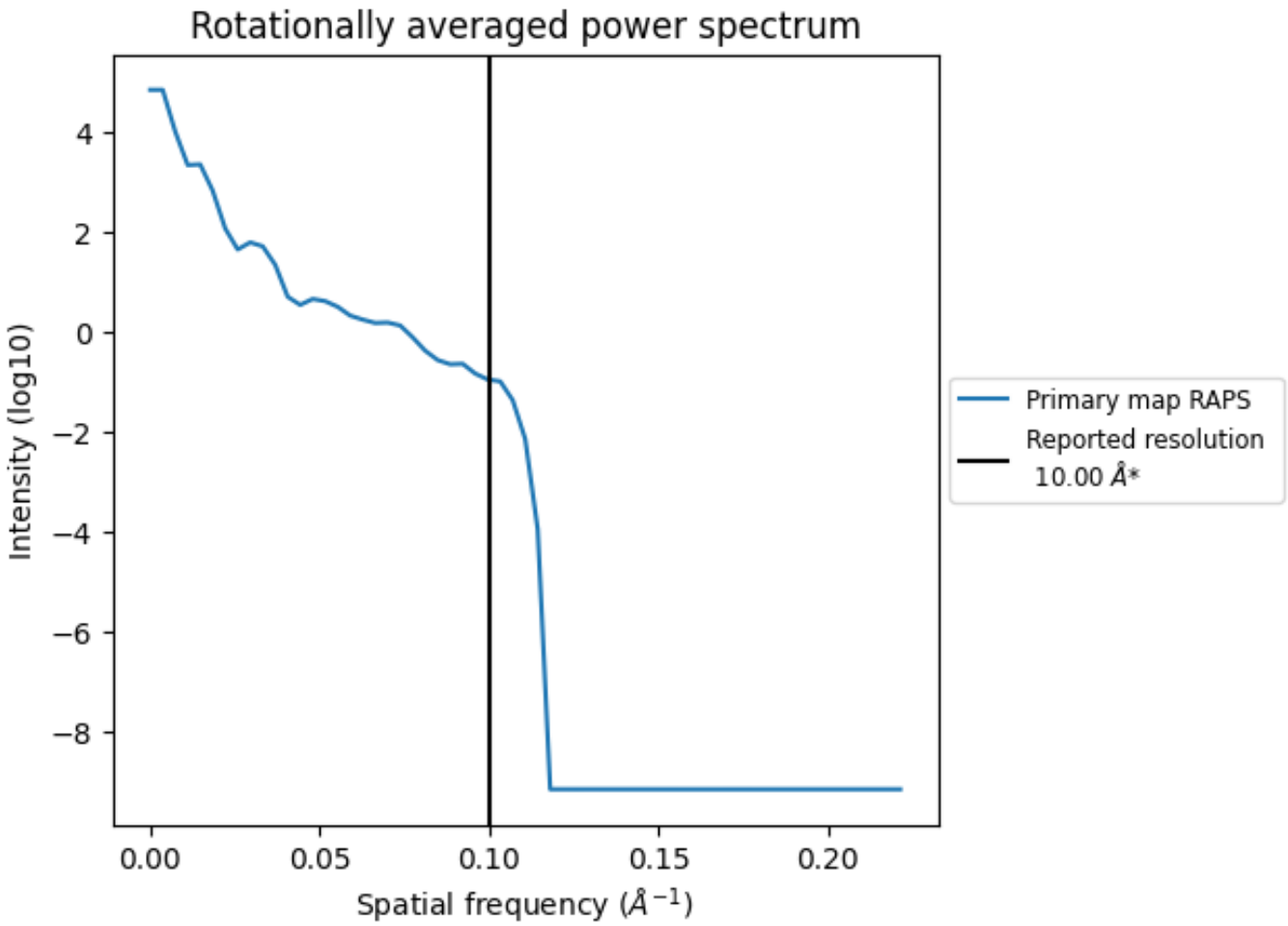
7.2 Volume estimate (i)



The volume at the recommended contour level is 1406 nm^3; this corresponds to an approximate mass of 1270 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 0.100 Å^{-1}

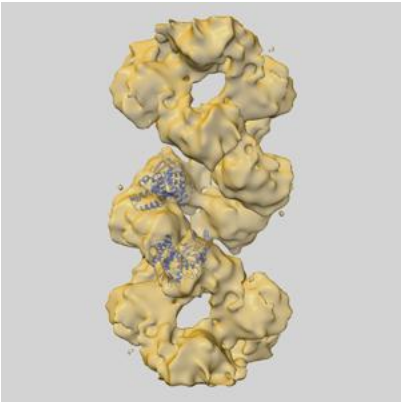
8 Fourier-Shell correlation (i)

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

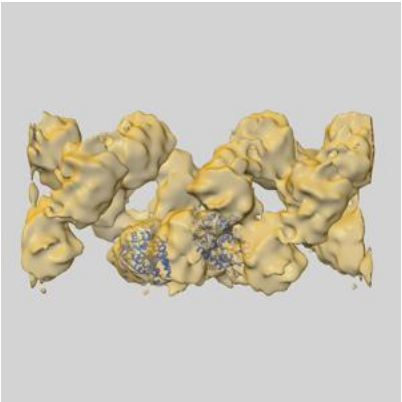
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-4412 and PDB model 6I54. Per-residue inclusion information can be found in section 3 on page 8.

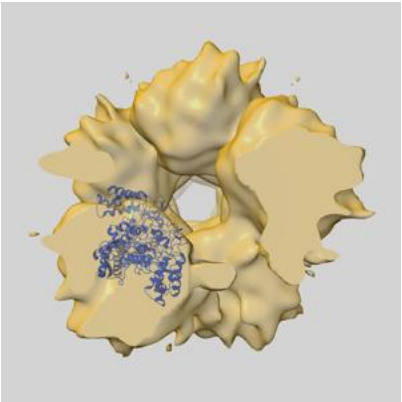
9.1 Map-model overlay (i)



X



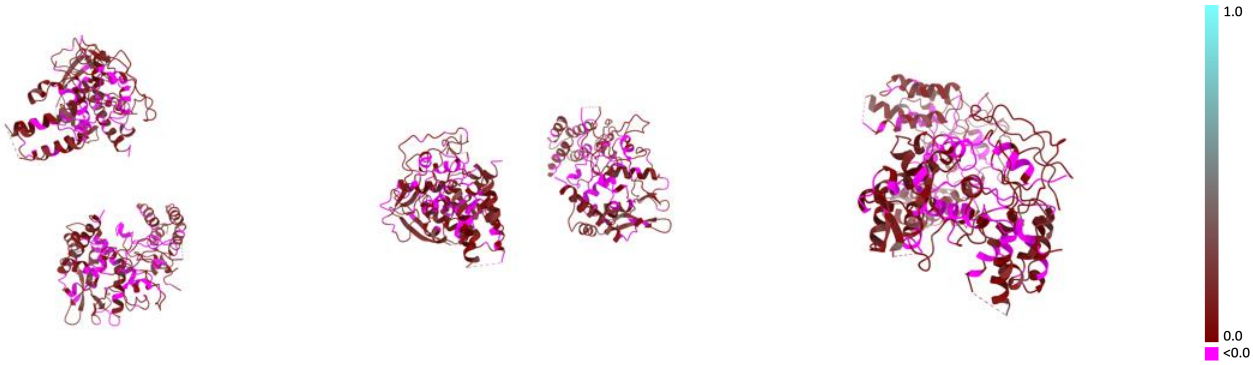
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.044 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.

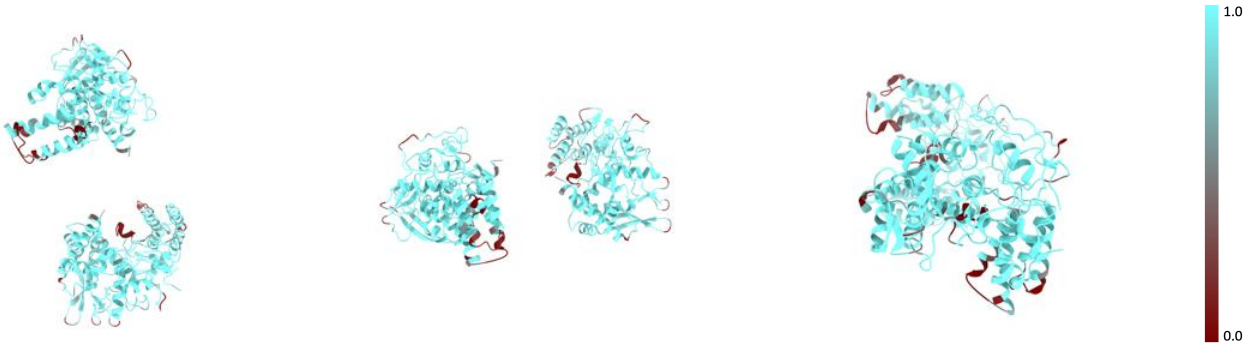
9.2 Q-score mapped to coordinate model (i)



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.

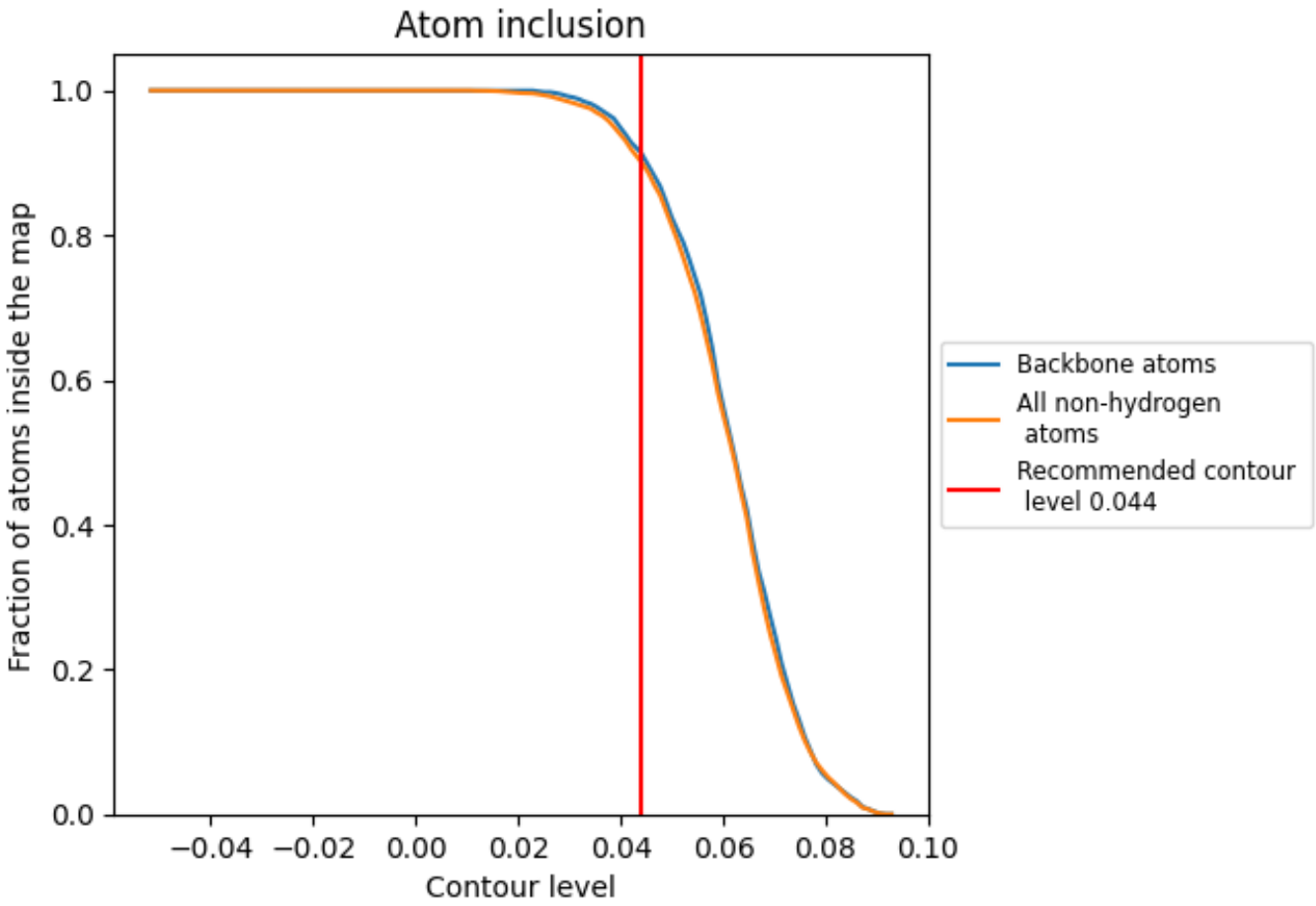
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.044).

9.4 Atom inclusion (i)



At the recommended contour level, 91% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.044) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9018	0.0530
A	0.8971	0.0510
B	0.9932	0.1020
C	0.8974	0.0500
D	0.9932	0.1010