



## wwPDB EM Validation Summary Report ⓘ

Mar 4, 2026 – 09:47 PM UTC

PDB ID : 7PER / pdb\_00007per  
EMDB ID : EMD-12814  
Title : Model of the inner ring of the human nuclear pore complex  
Authors : Schuller, A.P.; Wojtynek, M.; Mankus, D.; Tatli, M.; Kronenberg-Tenga, R.;  
Regmi, S.G.; Dasso, M.; Weis, K.; Medalia, O.; Schwartz, T.U.  
Deposited on : 2021-08-11  
Resolution : 35.00 Å (reported)  
Based on initial model : 5IJN

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

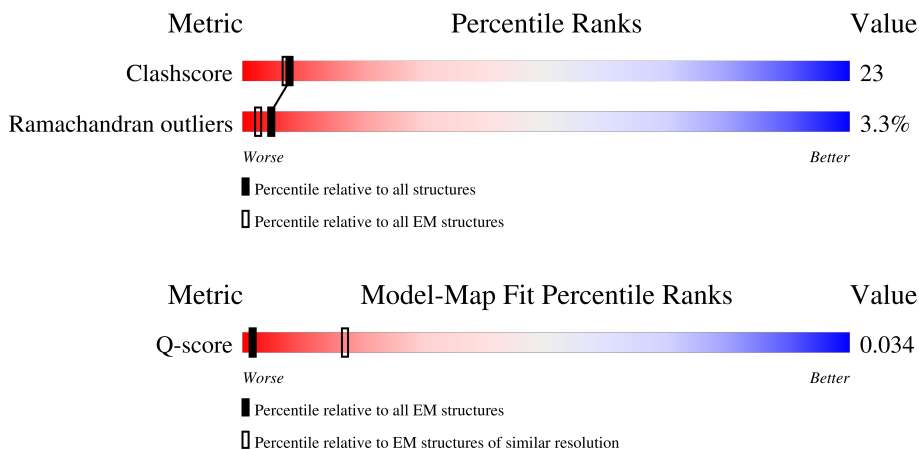
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 35.00 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	-
Q-score	-	25397	12 ( 35.00 - 35.00 )

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  $\geq 3$ , 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	F	507	 33% 21% 7% 5% 34%
1	L	507	 34% 20% 7% 5% 34%
1	R	507	 32% 22% 7% 5% 34%
1	X	507	 35% 20% 7% 5% 34%
2	G	599	 10% 14% 71%

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Mol	Chain	Length	Quality of chain
2	M	599	10% 14% . . 71%
2	S	599	10% 14% . . 71%
2	Y	599	10% 14% . . 71%
3	H	522	11% 16% . . 68%
3	N	522	11% 17% . . 68%
3	T	522	11% 16% . . 68%
3	Z	522	12% 16% . . 68%
4	D	2012	42% 6% . . 49%
4	J	2012	6% 42% 6% . . 49%
4	P	2012	40% 8% . . 49%
4	V	2012	41% 8% . . 49%
5	E	1391	69% 8% . 22%
5	K	1391	68% 8% . 22%
5	Q	1391	69% 8% . 22%
5	W	1391	66% 10% . 22%
6	C	819	56% 13% . 27%
6	I	819	57% 12% . 27%
6	O	819	54% 15% . . 27%
6	U	819	57% 12% . 27%

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 67036 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 Nucleoporin p54.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	F	335	1658	988	335	335	0	0
1	X	335	1658	988	335	335	0	0
1	L	335	1658	988	335	335	0	0
1	R	335	1658	988	335	335	0	0

- Molecule 2 is a protein called Nucleoporin p58/p45.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	G	171	853	511	171	171	0	0
2	Y	171	853	511	171	171	0	0
2	M	171	853	511	171	171	0	0
2	S	171	853	511	171	171	0	0

- Molecule 3 is a protein called Nuclear pore glycoprotein p62.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	H	169	842	504	169	169	0	0
3	Z	169	842	504	169	169	0	0
3	N	169	842	504	169	169	0	0
3	T	169	842	504	169	169	0	0

- Molecule 4 is a protein called Nuclear pore complex protein Nup205.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	P	1028	Total 5094	C 3038	N 1028	O 1028	0	0
4	V	1028	Total 5094	C 3038	N 1028	O 1028	0	0
4	D	1028	Total 5094	C 3038	N 1028	O 1028	0	0
4	J	1028	Total 5094	C 3038	N 1028	O 1028	0	0

- Molecule 5 is a protein called Nuclear pore complex protein Nup155.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	W	1083	Total 5366	C 3200	N 1083	O 1083	0	0
5	K	1083	Total 5366	C 3200	N 1083	O 1083	0	0
5	E	1083	Total 5366	C 3200	N 1083	O 1083	0	0
5	Q	1083	Total 5366	C 3200	N 1083	O 1083	0	0

- Molecule 6 is a protein called Nuclear pore complex protein Nup93.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	C	594	Total 2946	C 1758	N 594	O 594	0	0
6	I	594	Total 2946	C 1758	N 594	O 594	0	0
6	O	594	Total 2946	C 1758	N 594	O 594	0	0
6	U	594	Total 2946	C 1758	N 594	O 594	0	0

















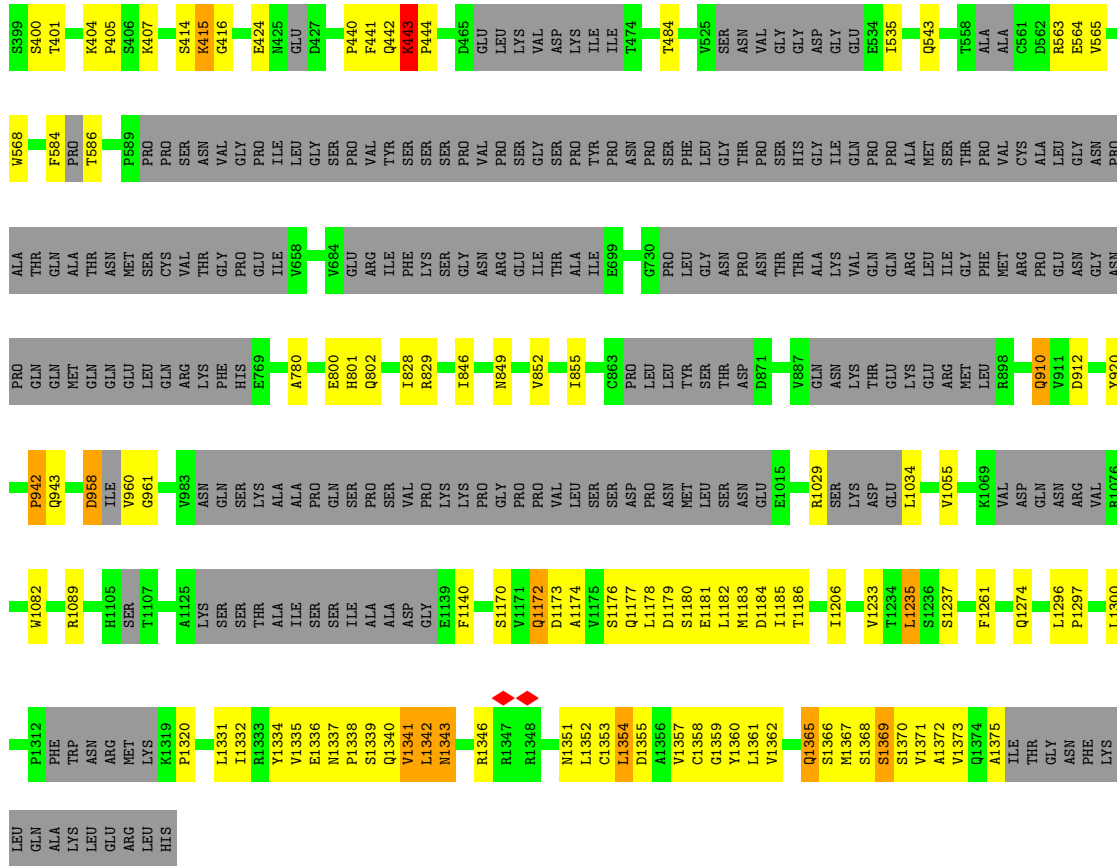




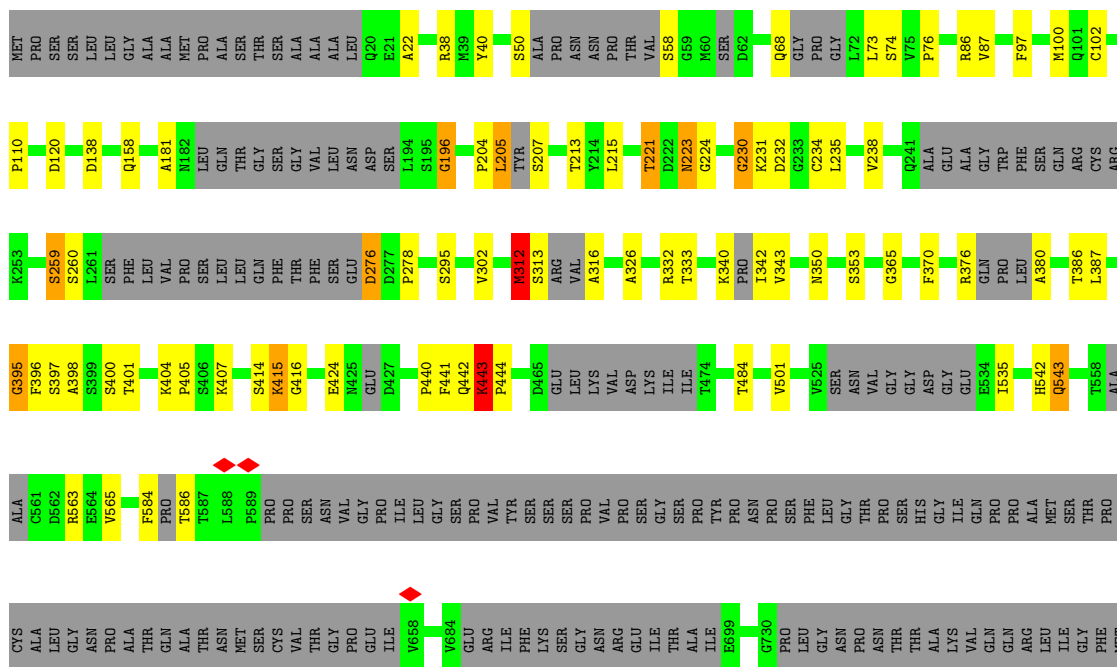






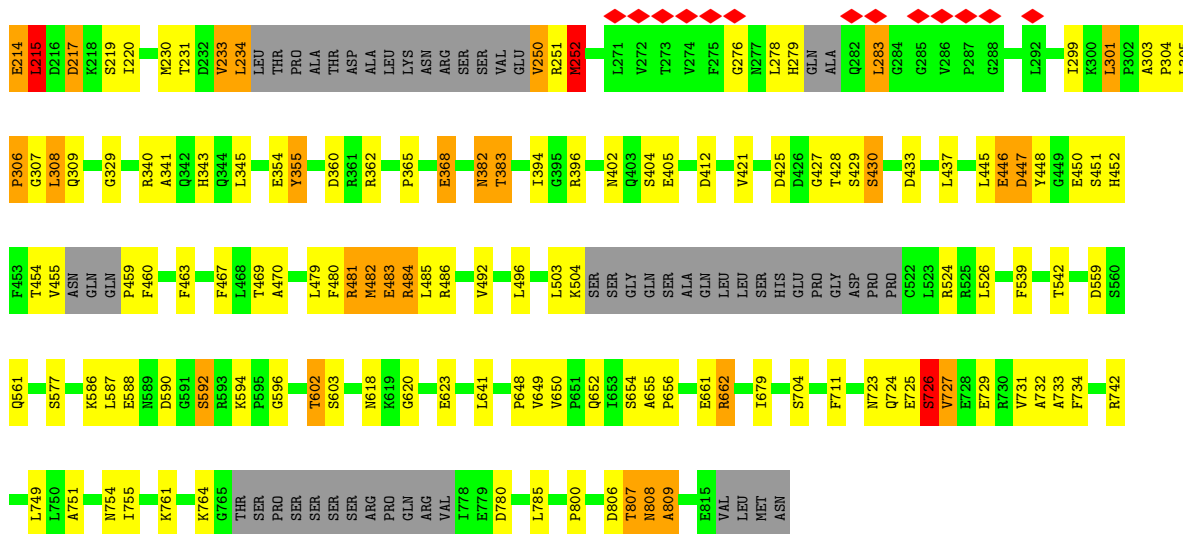


• Molecule 5: Nuclear pore complex protein Nup155

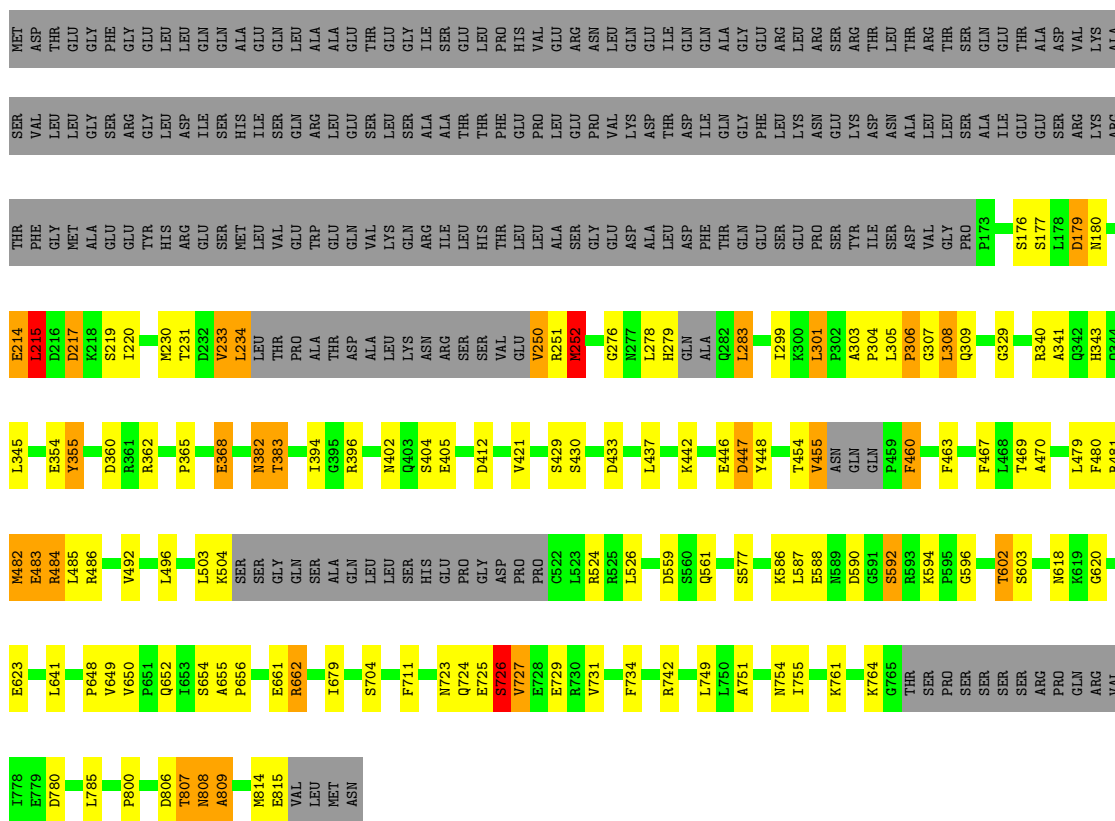




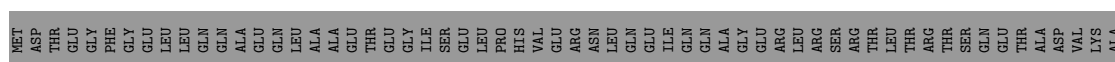


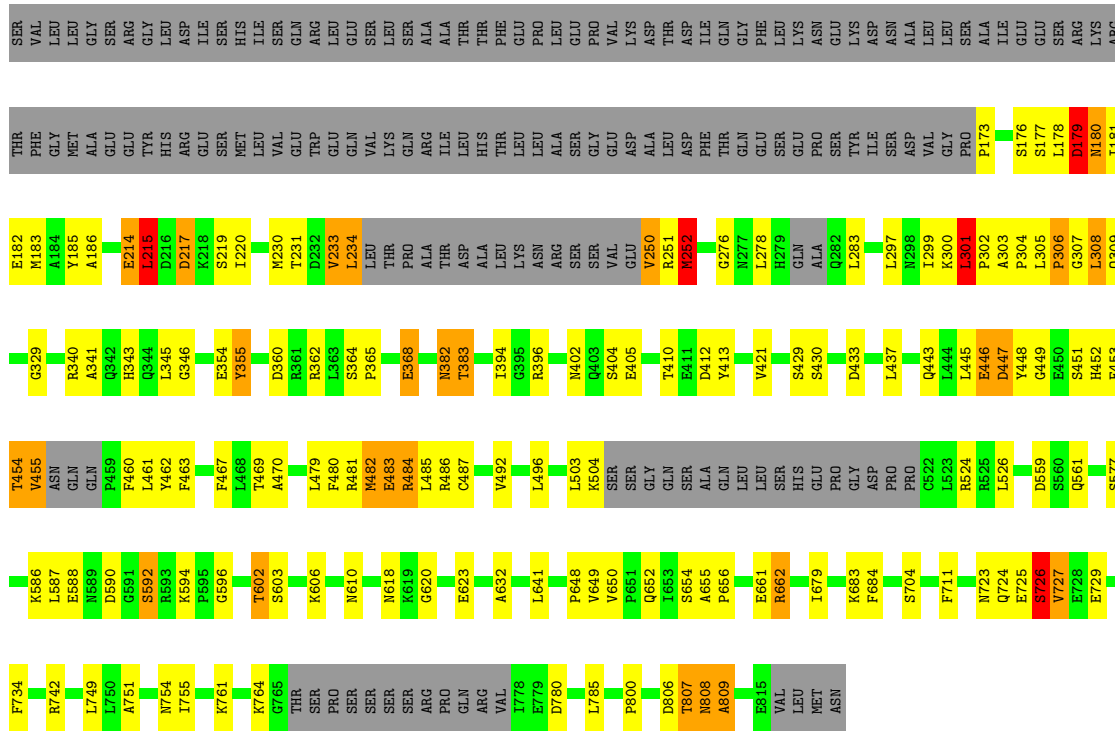


• Molecule 6: Nuclear pore complex protein Nup93

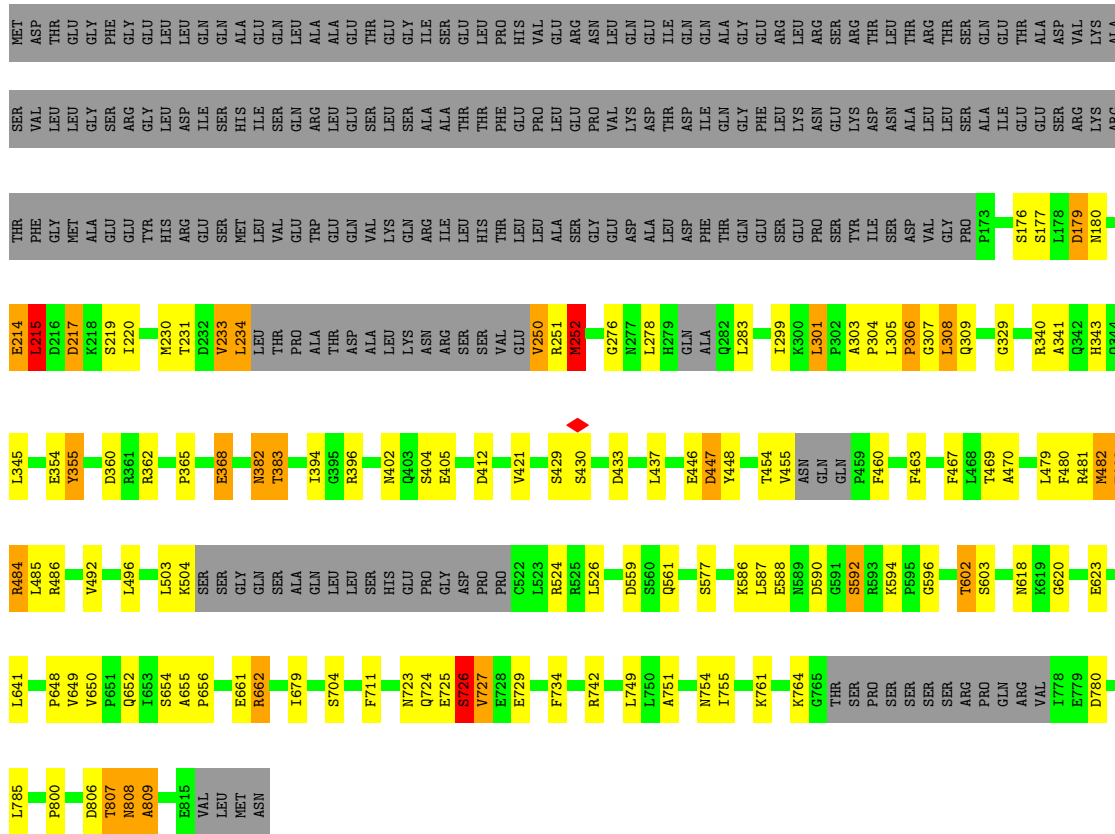


• Molecule 6: Nuclear pore complex protein Nup93





• Molecule 6: Nuclear pore complex protein Nup93



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C8	Depositor
Number of subtomograms used	1252	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	2.4	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.000	Depositor
Minimum map value	0.000	Depositor
Average map value	0.351	Depositor
Map value standard deviation	0.050	Depositor
Recommended contour level	0.44	Depositor
Map size ( $\text{\AA}$ )	2188.8, 2188.8, 2188.8	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	6.84, 6.84, 6.84	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	F	6.00	262/1655 (15.8%)	5.15	365/2302 (15.9%)
1	L	6.00	263/1655 (15.9%)	5.15	364/2302 (15.8%)
1	R	6.01	265/1655 (16.0%)	5.14	363/2302 (15.8%)
1	X	6.00	264/1655 (16.0%)	5.15	364/2302 (15.8%)
2	G	6.74	152/852 (17.8%)	5.80	243/1190 (20.4%)
2	M	6.68	150/852 (17.6%)	5.78	241/1190 (20.3%)
2	S	6.69	153/852 (18.0%)	5.78	243/1190 (20.4%)
2	Y	6.69	151/852 (17.7%)	5.78	242/1190 (20.3%)
3	H	5.53	134/841 (15.9%)	5.00	246/1174 (21.0%)
3	N	5.52	134/841 (15.9%)	5.00	245/1174 (20.9%)
3	T	5.53	133/841 (15.8%)	5.00	249/1174 (21.2%)
3	Z	5.52	134/841 (15.9%)	5.00	245/1174 (20.9%)
4	D	2.04	102/5066 (2.0%)	2.95	284/7020 (4.0%)
4	J	2.04	101/5066 (2.0%)	2.95	285/7020 (4.1%)
4	P	2.04	103/5066 (2.0%)	2.95	288/7020 (4.1%)
4	V	2.04	100/5066 (2.0%)	2.95	287/7020 (4.1%)
5	E	1.56	1/5338 (0.0%)	1.81	94/7399 (1.3%)
5	K	1.56	1/5338 (0.0%)	1.82	94/7399 (1.3%)
5	Q	1.56	0/5338	1.82	91/7399 (1.2%)
5	W	1.56	0/5338	1.81	91/7399 (1.2%)
6	C	1.58	5/2938 (0.2%)	2.08	119/4086 (2.9%)
6	I	1.58	5/2938 (0.2%)	2.08	116/4086 (2.8%)
6	O	1.58	6/2938 (0.2%)	2.08	116/4086 (2.8%)
6	U	1.58	6/2938 (0.2%)	2.08	117/4086 (2.9%)
All	All	3.14	2625/66760 (3.9%)	3.17	5392/92684 (5.8%)

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	F	7	31

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	L	7	31
1	R	7	31
1	X	7	30
2	G	9	10
2	M	9	10
2	S	9	10
2	Y	9	10
3	H	5	5
3	N	5	5
3	T	5	5
3	Z	5	5
4	D	0	19
4	J	0	20
4	P	0	21
4	V	0	20
5	E	0	1
5	K	0	1
5	Q	0	1
5	W	0	1
All	All	84	267

The worst 5 of 2625 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	Y	379	HIS	CA-C	72.09	2.49	1.52
2	G	379	HIS	CA-C	72.06	2.49	1.52
2	M	379	HIS	CA-C	72.05	2.49	1.52
2	S	379	HIS	CA-C	71.92	2.49	1.52
1	X	453	TYR	CA-C	70.49	2.47	1.52

The worst 5 of 5392 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	341	ALA	CA-C-N	-52.60	63.43	119.19
2	G	341	ALA	C-N-CA	-52.60	63.43	119.19
2	S	341	ALA	CA-C-N	-52.55	63.49	119.19
2	S	341	ALA	C-N-CA	-52.55	63.49	119.19
2	M	341	ALA	CA-C-N	-52.51	63.53	119.19

5 of 84 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	F	305	ASP	CA
1	F	341	ASP	CA
1	F	423	ALA	CA
1	F	454	TYR	CA
1	F	459	LEU	CA

5 of 267 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	393	GLN	Mainchain
1	F	397	ARG	Mainchain
1	F	398	LYS	Peptide,Mainchain
1	F	399	SER	Peptide
1	F	400	GLY	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	F	1658	0	715	195	0
1	L	1658	0	715	165	0
1	R	1658	0	710	243	0
1	X	1658	0	715	163	0
2	G	853	0	384	64	0
2	M	853	0	384	59	0
2	S	853	0	384	60	0
2	Y	853	0	384	58	0
3	H	842	0	365	45	0
3	N	842	0	365	37	0
3	T	842	0	365	40	0
3	Z	842	0	365	39	0
4	D	5094	0	2272	148	0
4	J	5094	0	2271	83	0
4	P	5094	0	2253	360	0
4	V	5094	0	2258	310	0
5	E	5366	0	2365	37	0
5	K	5366	0	2362	71	0
5	Q	5366	0	2365	46	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	W	5366	0	2350	244	0
6	C	2946	0	1307	83	0
6	I	2946	0	1306	42	0
6	O	2946	0	1296	197	0
6	U	2946	0	1307	26	0
All	All	67036	0	29563	2196	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.

The worst 5 of 2196 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:G:366:GLU:CB	2:G:366:GLU:CA	1.76	1.63
1:X:451:GLU:CA	1:X:451:GLU:CB	1.77	1.61
1:F:447:VAL:CB	1:F:447:VAL:CA	1.78	1.60
1:R:447:VAL:CA	1:R:447:VAL:CB	1.78	1.60
1:L:454:TYR:CA	1:L:454:TYR:CB	1.77	1.60

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	F	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
1	L	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
1	R	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
1	X	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
2	G	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	3	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	M	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	3	23
2	S	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	2	20
2	Y	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	2	20
3	H	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
3	N	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
3	T	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
3	Z	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
4	D	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
4	J	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
4	P	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
4	V	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
5	E	1027/1391 (74%)	947 (92%)	58 (6%)	22 (2%)	5	30
5	K	1027/1391 (74%)	947 (92%)	58 (6%)	22 (2%)	5	30
5	Q	1027/1391 (74%)	947 (92%)	58 (6%)	22 (2%)	5	30
5	W	1027/1391 (74%)	947 (92%)	58 (6%)	22 (2%)	5	30
6	C	578/819 (71%)	486 (84%)	53 (9%)	39 (7%)	1	12
6	I	578/819 (71%)	486 (84%)	53 (9%)	39 (7%)	1	12
6	O	578/819 (71%)	486 (84%)	52 (9%)	40 (7%)	1	11
6	U	578/819 (71%)	486 (84%)	53 (9%)	39 (7%)	1	12
All	All	12968/23400 (55%)	11776 (91%)	765 (6%)	427 (3%)	5	21

5 of 427 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	148	TRP
1	F	318	ASP
1	F	403	ILE
1	F	405	ALA
1	F	451	GLU

### 5.3.2 Protein sidechains [i](#)

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

### 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	F	5
1	X	5
1	L	5
1	R	5
2	G	3
2	S	3
2	Y	3
2	M	3
3	H	3
3	Z	3
3	N	3
3	T	3
6	C	2
6	I	2
6	O	2
6	U	2

The worst 5 of 52 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	483:GLU	C	484:ARG	N	4.02
1	I	483:GLU	C	484:ARG	N	4.02
1	O	483:GLU	C	484:ARG	N	4.02
1	U	483:GLU	C	484:ARG	N	4.02
1	C	447:ASP	C	448:TYR	N	3.63

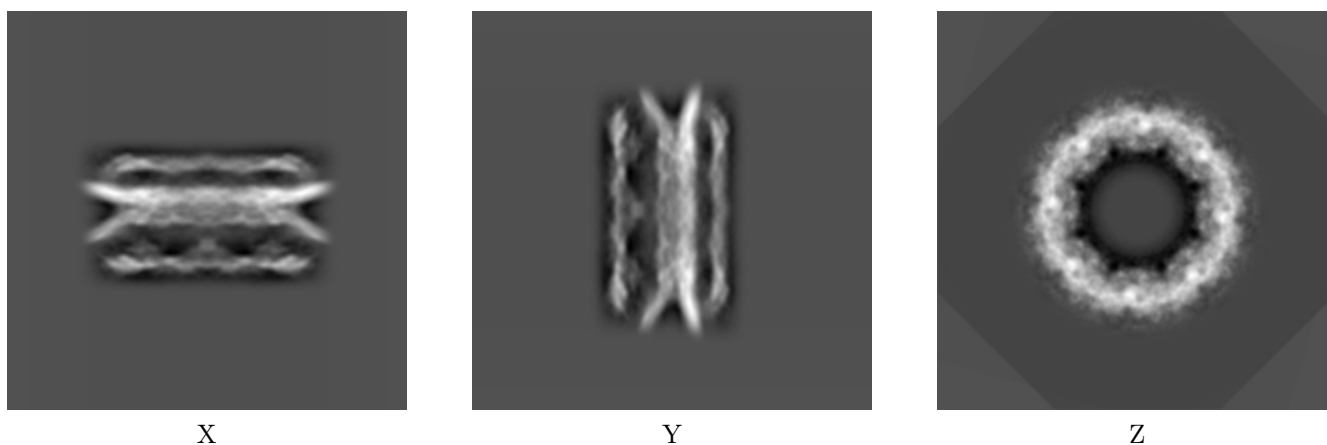
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12814. 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](#)

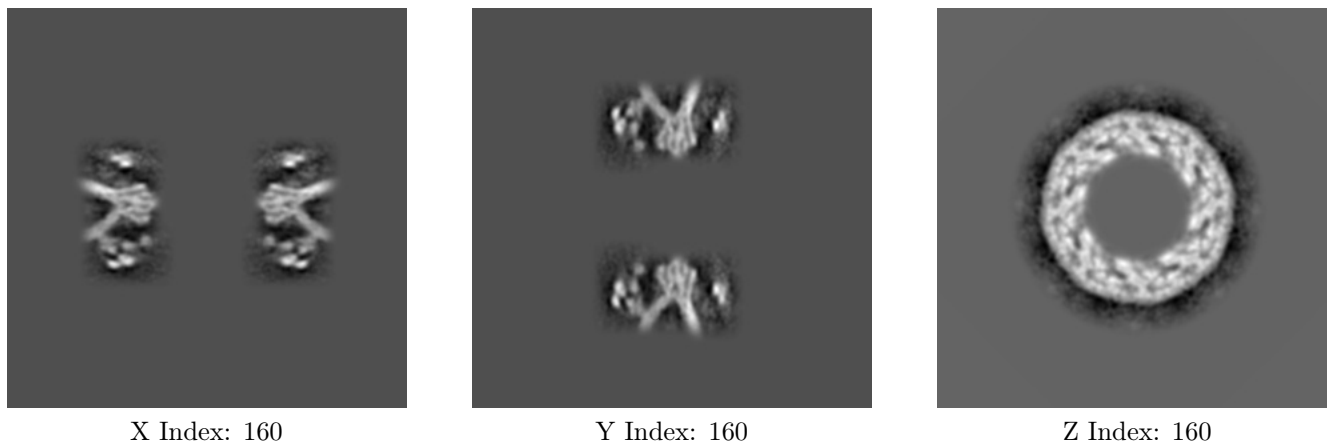
#### 6.1.1 Primary map



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

### 6.2 Central slices [i](#)

#### 6.2.1 Primary map



X Index: 160

Y Index: 160

Z Index: 160

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

## 6.3 Largest variance slices [i](#)

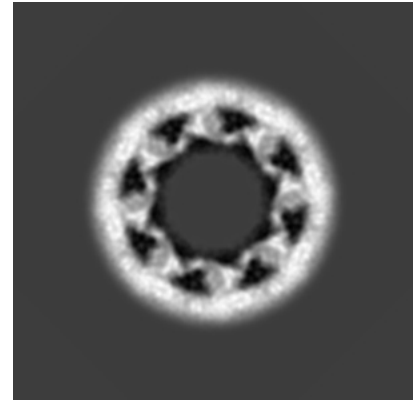
### 6.3.1 Primary map



X Index: 100



Y Index: 220

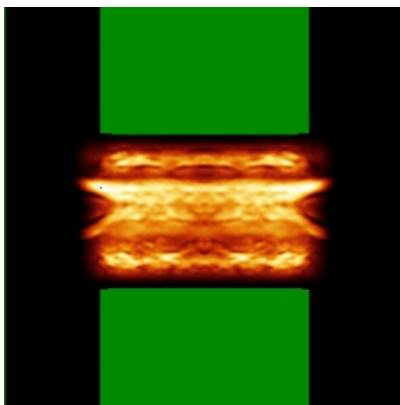


Z Index: 174

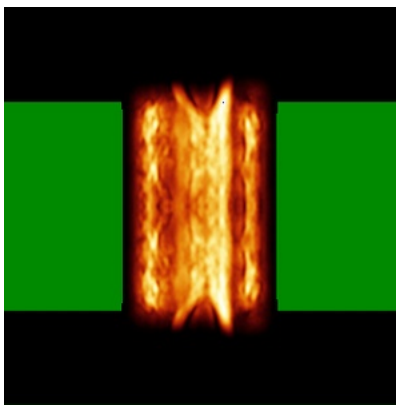
The images above show the largest variance slices of the map in three orthogonal directions.

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

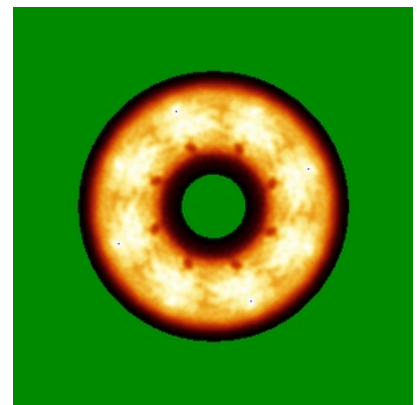
### 6.4.1 Primary map



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



The images above show the 3D surface view of the map at the recommended contour level 0.44. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

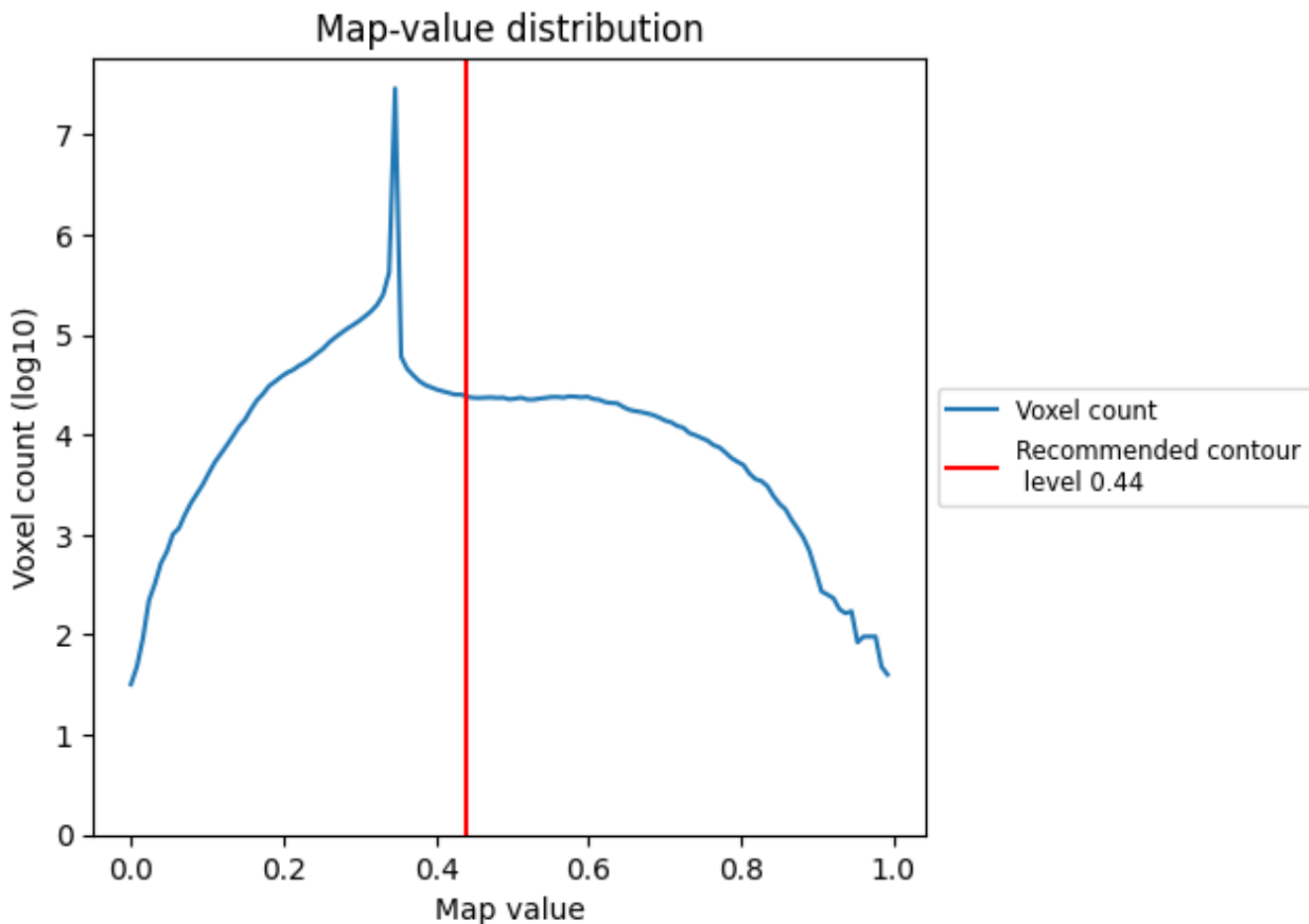
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

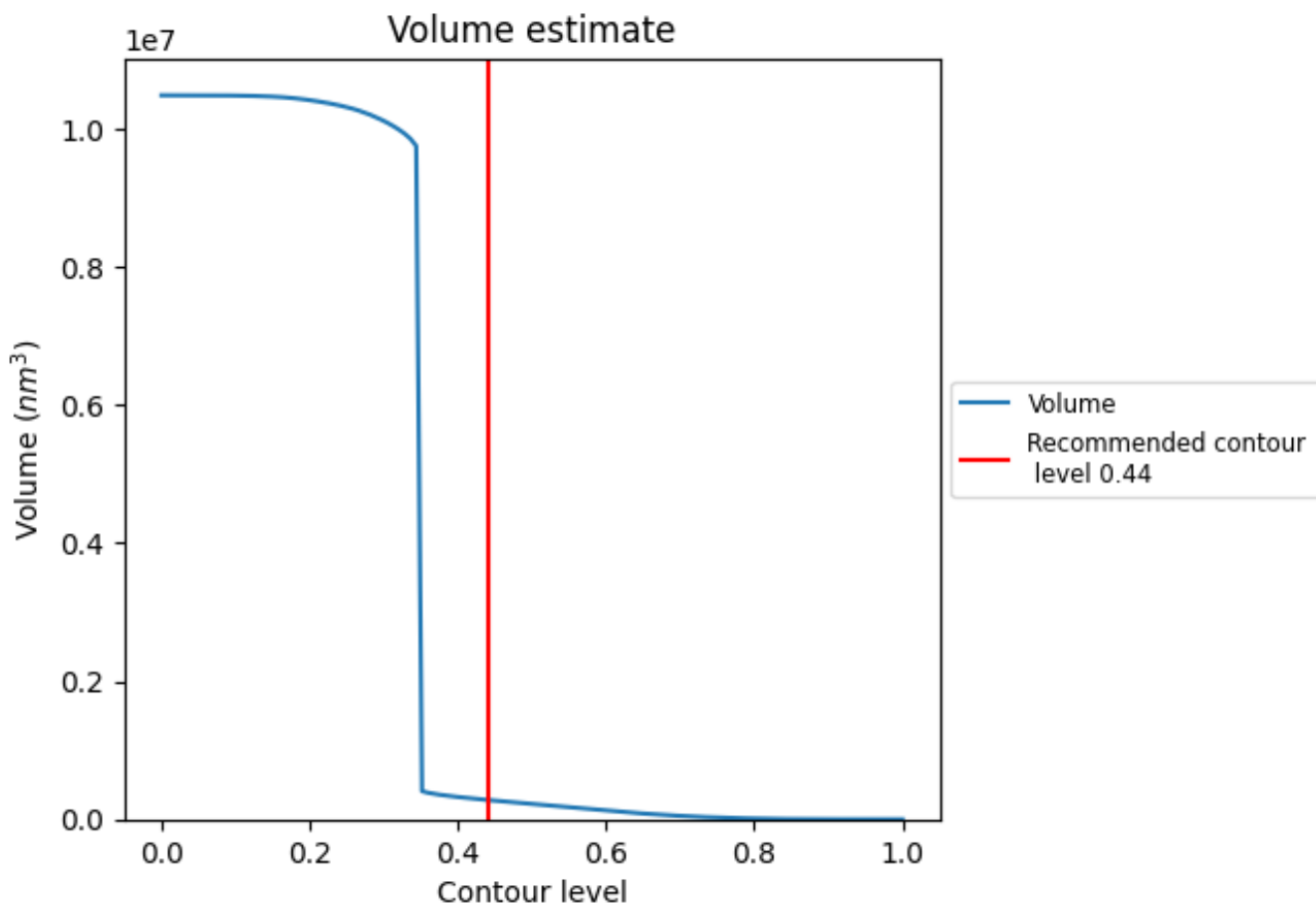
This section contains the results of statistical analysis of the map.

### 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.

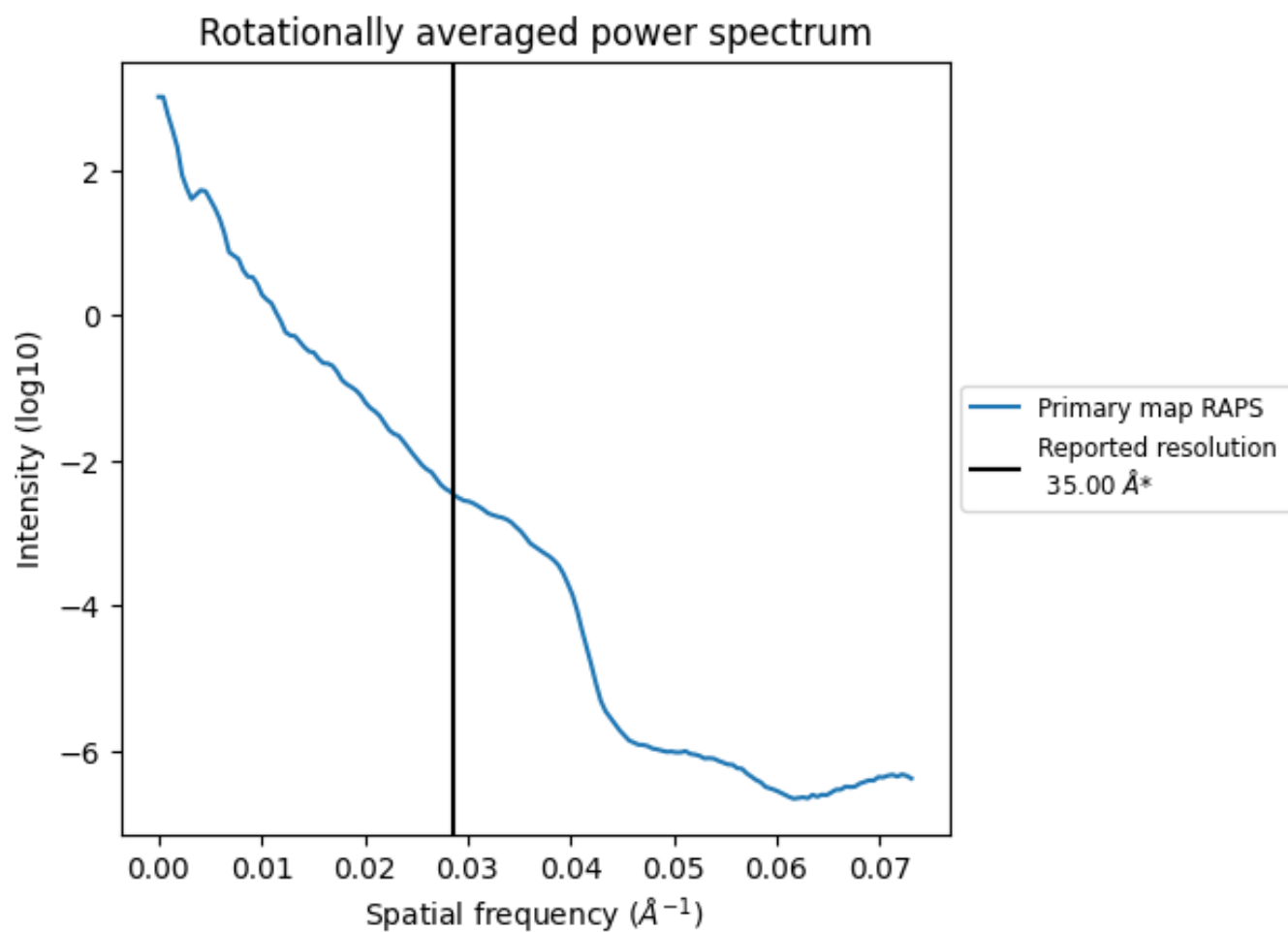
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 280168 nm<sup>3</sup>; this corresponds to an approximate mass of 253083 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 0.029 Å<sup>-1</sup>

## 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-12814 and PDB model 7PER. Per-residue inclusion information can be found in section 3 on page 6.

### 9.1 Map-model overlays

#### 9.1.1 Map-model overlay [i](#)

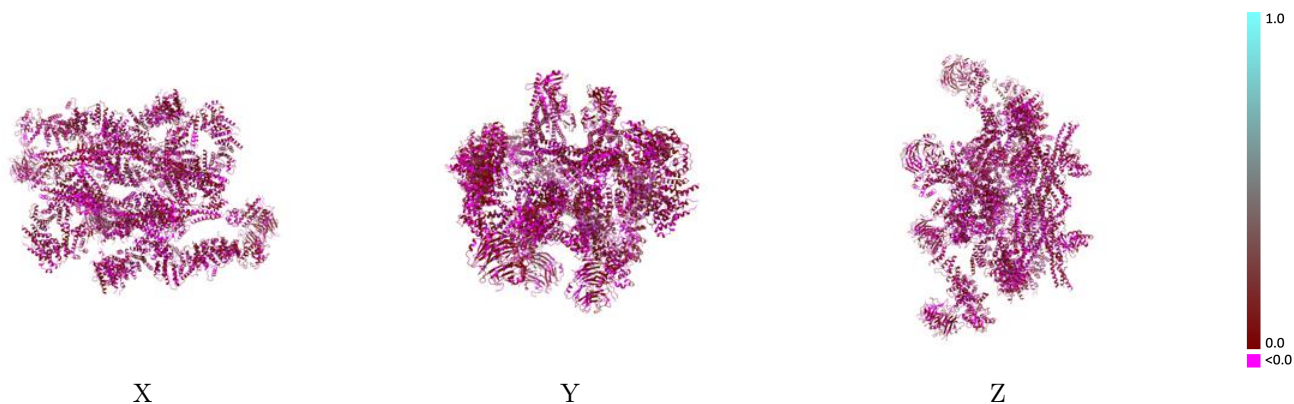


#### 9.1.2 Map-model assembly overlay [i](#)



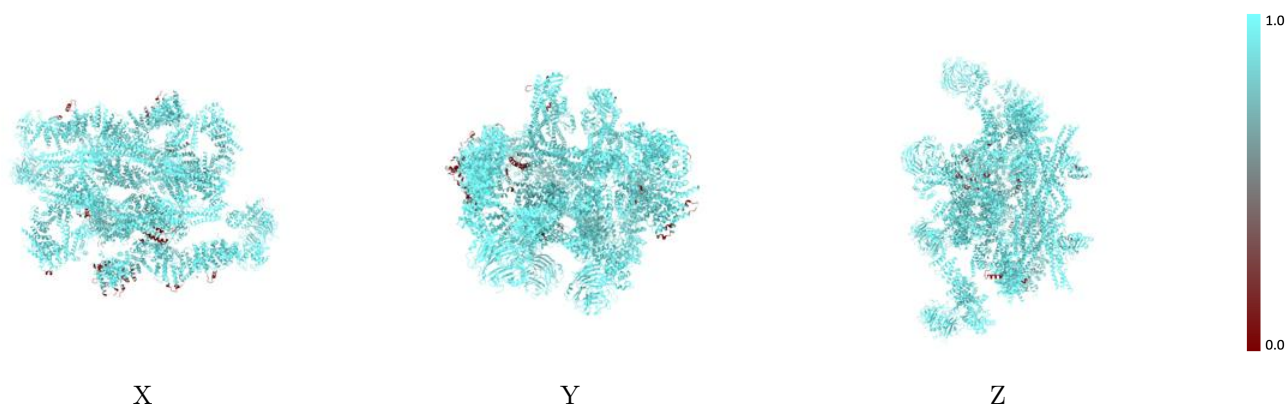
The images above show the 3D surface view of the map at the recommended contour level 0.44 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



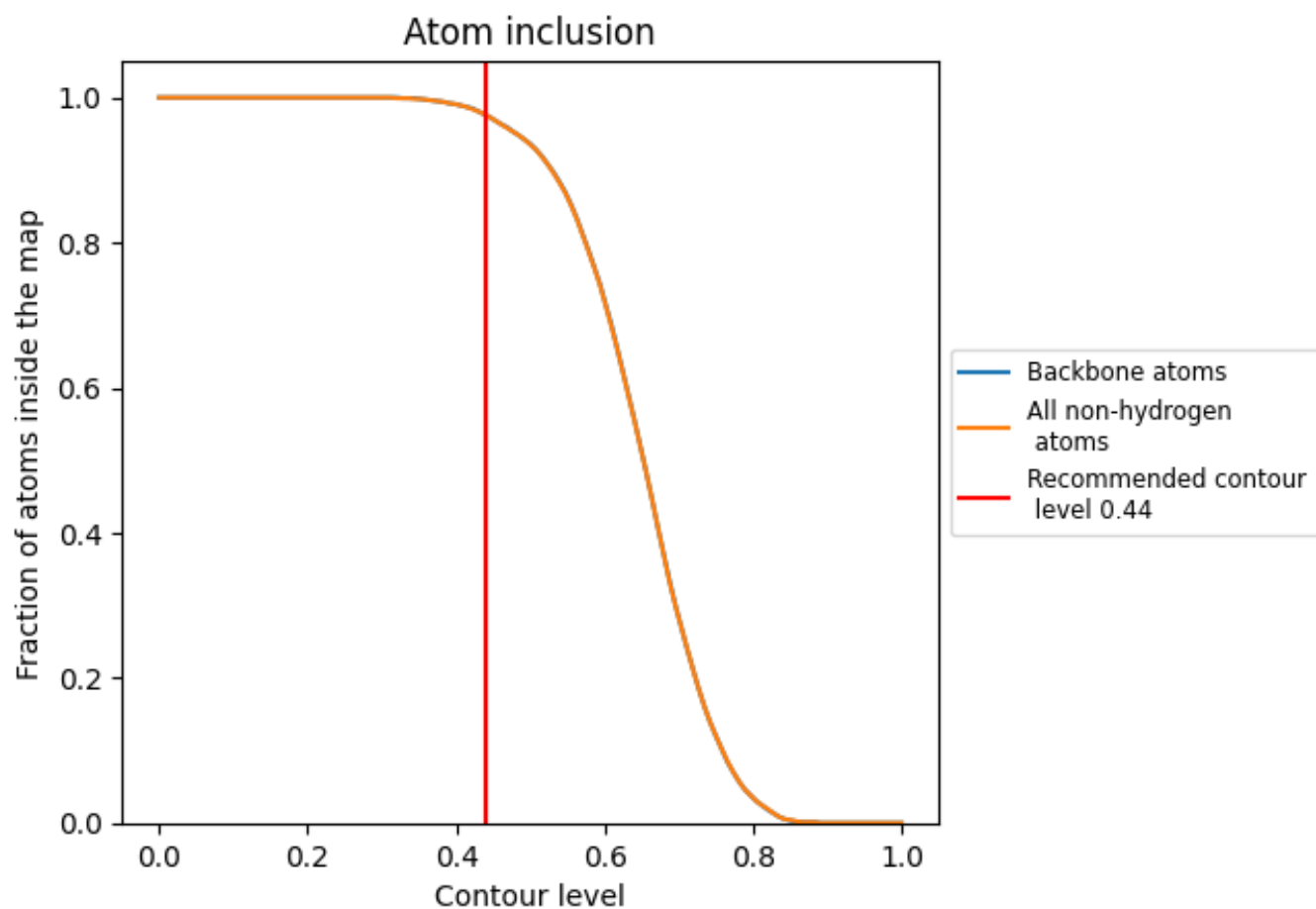
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.44).



















































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% 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 (0.44) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9760	 0.0340
C	 0.9770	 0.0310
D	 0.9850	 0.0360
E	 1.0000	 0.0310
F	 0.9600	 0.0070
G	 0.9980	 0.0190
H	 1.0000	 0.0000
I	 0.9990	 0.0460
J	 0.8800	 0.0370
K	 0.9770	 0.0300
L	 0.9040	 0.0160
M	 0.9190	 -0.0030
N	 0.9810	 0.0550
O	 1.0000	 0.0250
P	 0.9990	 0.0450
Q	 0.9920	 0.0430
R	 0.9930	 0.0330
S	 1.0000	 0.0350
T	 1.0000	 0.0340
U	 0.9980	 0.0350
V	 0.9320	 0.0440
W	 0.9990	 0.0320
X	 0.9920	 0.0320
Y	 1.0000	 0.0160
Z	 1.0000	 0.0670

