



## wwPDB EM Validation Summary Report ⓘ

Feb 13, 2024 – 12:57 PM EST

PDB ID : 3J5S  
EMDB ID : EMD-5784  
Title : EttA binds to ribosome exit site and regulates translation by restricting ribosome and tRNA dynamics  
Authors : Hashem, Y.  
Deposited on : 2013-11-15  
Resolution : 7.50 Å (reported)  
Based on initial models : 3R8T, 2WDG, 3R8O, 4FIN

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:

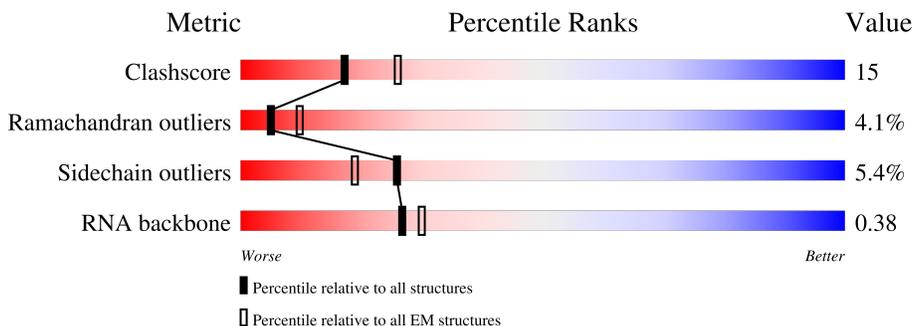
EMDB validation analysis : 0.0.1.dev70  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

# 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 7.50 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
RNA backbone	4643	859

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	B	101	12% (yellow), 13% (orange), 7% (red), 68% (grey)
2	A	360	16% (yellow), 19% (orange), 14% (red), 52% (grey)
3	E	77	5% (red), 40% (yellow), 43% (orange), 17% (red)
4	D	561	18% (red), 65% (green), 25% (yellow), 8% (orange)
5	F	234	5% (red), 64% (green), 29% (yellow), 6% (orange)
6	G	178	6% (red), 71% (green), 22% (yellow), 7% (orange)
7	H	50	12% (red), 74% (green), 18% (yellow), 8% (orange)

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Mol	Chain	Length	Quality of chain
8	I	151	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into four segments: a red segment (23%), a green segment (61%), a yellow segment (30%), and a small orange segment (7%). The percentages are labeled below the bar.</p>

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 15196 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 RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	B	32	687	306	126	223	32	0	0

- Molecule 2 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	A	174	3731	1663	674	1220	174	0	0

- Molecule 3 is a RNA chain called P-site tRNA FMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	E	77	1640	732	297	535	76	0	0

- Molecule 4 is a protein called Energy-dependent translational throttle A (EttA).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	554	4393	2764	781	837	11	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-5	HIS	-	expression tag	UNP P0A9W3
D	-4	HIS	-	expression tag	UNP P0A9W3
D	-3	HIS	-	expression tag	UNP P0A9W3
D	-2	HIS	-	expression tag	UNP P0A9W3
D	-1	HIS	-	expression tag	UNP P0A9W3
D	0	HIS	-	expression tag	UNP P0A9W3

- Molecule 5 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	F	234	1733	1081	315	330	7	0	0

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	G	178	1420	905	251	258	6	0	0

- Molecule 7 is a protein called 50S ribosomal protein L33.

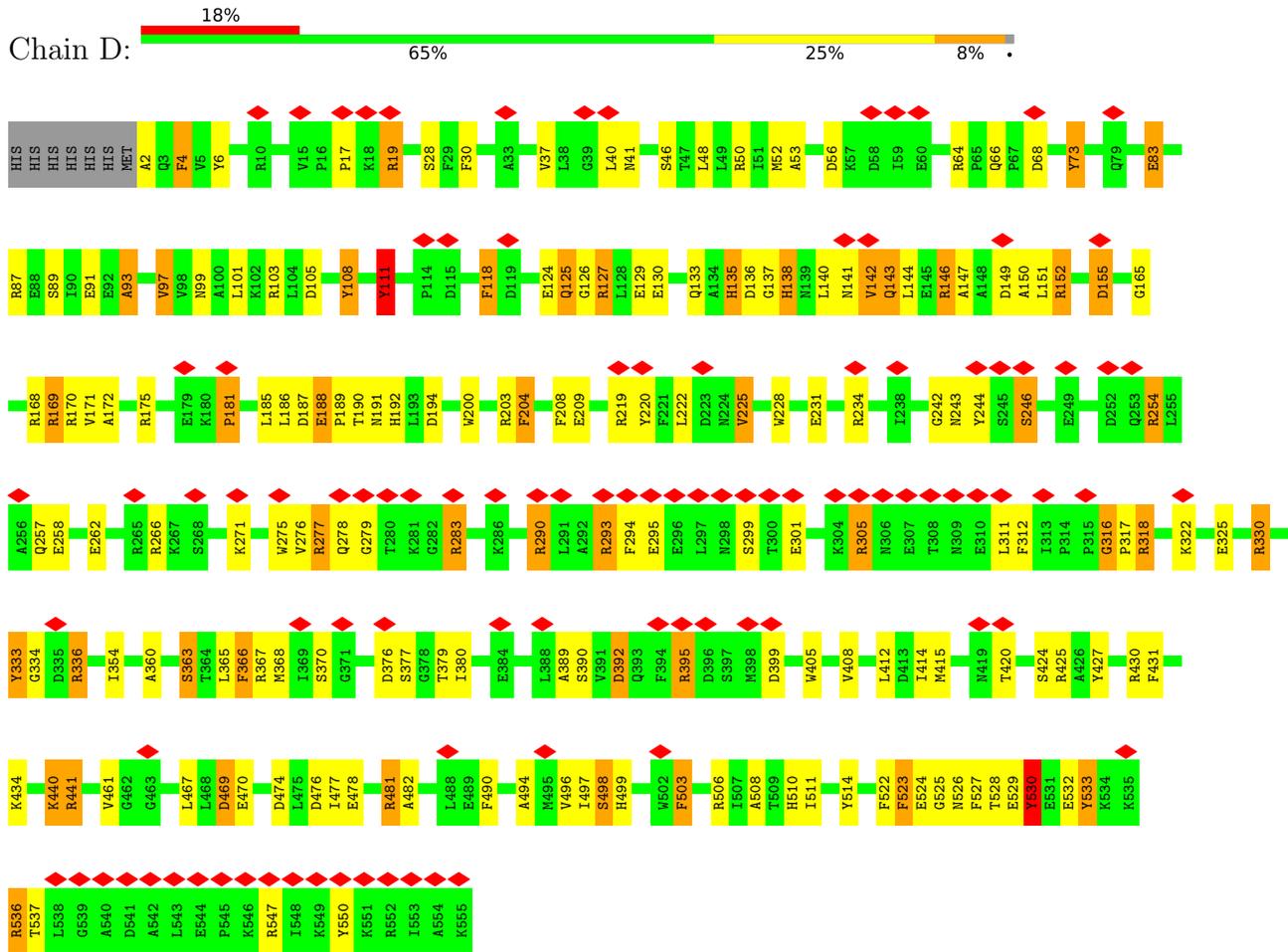
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	H	50	410	263	75	72	0	0

- Molecule 8 is a protein called 30S ribosomal protein S7.

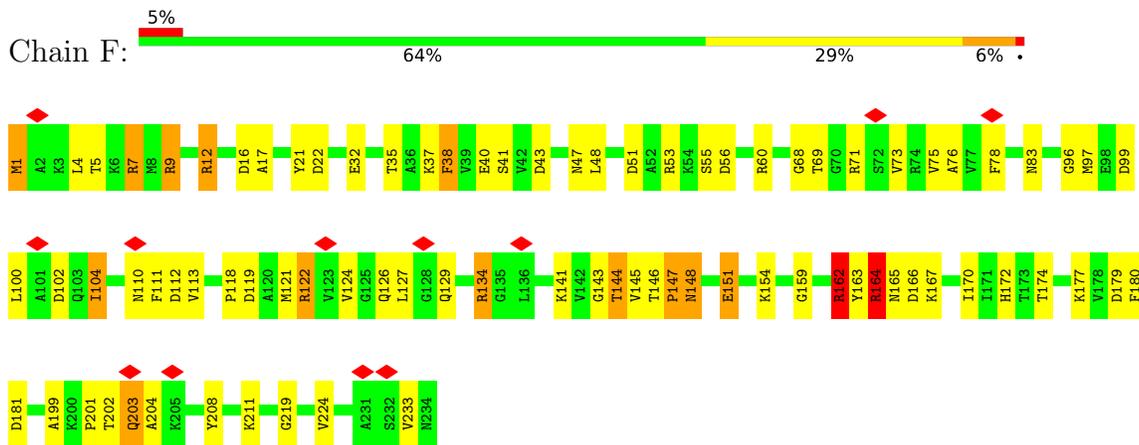
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	I	151	1182	735	227	216	4	0	0



- Molecule 4: Energy-dependent translational throttle A (EttA)

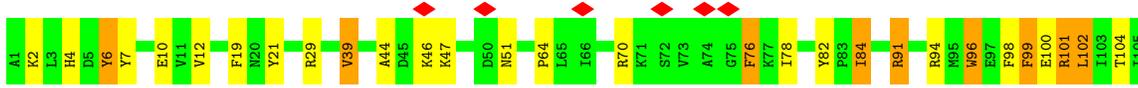


- Molecule 5: 50S ribosomal protein L1

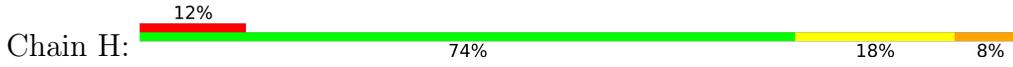


- Molecule 6: 50S ribosomal protein L5

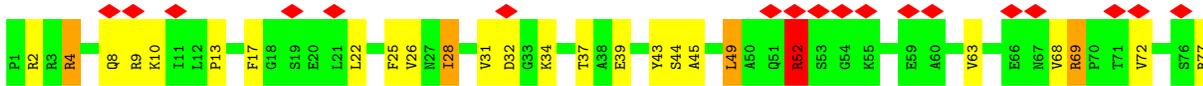




• Molecule 7: 50S ribosomal protein L33



• Molecule 8: 30S ribosomal protein S7



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	39316	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Each micrograph	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	17	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	110637	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor
Maximum map value	338.729	Depositor
Minimum map value	-150.118	Depositor
Average map value	3.621	Depositor
Map value standard deviation	39.948	Depositor
Recommended contour level	80.0	Depositor
Map size ( $\text{\AA}$ )	363.3544, 363.3544, 363.3544	wwPDB
Map dimensions	134, 134, 134	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	2.7116, 2.7116, 2.7116	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	B	3.33	96/766 (12.5%)	3.35	147/1188 (12.4%)
2	A	3.17	486/4174 (11.6%)	3.15	702/6507 (10.8%)
3	E	3.23	213/1832 (11.6%)	3.28	351/2855 (12.3%)
4	D	1.58	22/4474 (0.5%)	2.04	130/6034 (2.2%)
5	F	1.52	5/1748 (0.3%)	1.97	49/2355 (2.1%)
6	G	1.65	8/1444 (0.6%)	2.08	40/1937 (2.1%)
7	H	1.63	2/417 (0.5%)	2.02	11/554 (2.0%)
8	I	1.61	6/1196 (0.5%)	2.31	50/1602 (3.1%)
All	All	2.41	838/16051 (5.2%)	2.65	1480/23032 (6.4%)

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	B	0	12
2	A	0	84
3	E	0	34
4	D	0	23
5	F	0	9
6	G	0	6
7	H	0	4
8	I	0	6
All	All	0	178

The worst 5 of 838 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	36	A	N9-C4	-18.05	1.27	1.37
1	B	1297	G	N9-C8	15.82	1.49	1.37
2	A	1879	C	N1-C6	14.46	1.45	1.37
1	B	1242	G	C8-N7	-13.58	1.22	1.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1236	A	C5-C4	13.00	1.47	1.38

The worst 5 of 1480 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	I	91	ARG	NE-CZ-NH2	-25.82	107.39	120.30
4	D	430	ARG	NE-CZ-NH1	23.11	131.85	120.30
1	B	1236	A	N1-C6-N6	19.82	130.49	118.60
1	B	1334	G	C5-C6-O6	-18.89	117.27	128.60
1	B	1334	G	N1-C6-O6	17.55	130.43	119.90

There are no chirality outliers.

5 of 178 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	1239	A	Sidechain
1	B	1242	G	Sidechain
1	B	1243	C	Sidechain
1	B	1290	G	Sidechain
1	B	1295	U	Sidechain

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	687	0	342	24	0
2	A	3731	0	1828	67	0
3	E	1640	0	827	29	0
4	D	4393	0	4377	333	0
5	F	1733	0	1824	152	0
6	G	1420	0	1460	10	0
7	H	410	0	440	1	0
8	I	1182	0	1240	124	0
All	All	15196	0	12338	421	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 15.

The worst 5 of 421 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:1240:U:C4	8:I:31:VAL:HG12	1.20	1.68
4:D:108:TYR:HA	5:F:118:PRO:CB	1.17	1.59
4:D:108:TYR:CA	5:F:118:PRO:HB2	1.27	1.57
4:D:108:TYR:CE2	5:F:121:MET:HB3	1.34	1.57
4:D:523:PHE:CD1	8:I:130:LYS:HB2	1.37	1.57

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	
4	D	552/561 (98%)	508 (92%)	27 (5%)	17 (3%)	4	27
5	F	232/234 (99%)	199 (86%)	23 (10%)	10 (4%)	2	22
6	G	176/178 (99%)	138 (78%)	26 (15%)	12 (7%)	1	15
7	H	48/50 (96%)	38 (79%)	9 (19%)	1 (2%)	7	36
8	I	149/151 (99%)	119 (80%)	23 (15%)	7 (5%)	2	21
All	All	1157/1174 (99%)	1002 (87%)	108 (9%)	47 (4%)	5	22

5 of 47 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	83	GLU
4	D	91	GLU
4	D	143	GLN
4	D	317	PRO
6	G	102	LEU

### 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	
4	D	465/472 (98%)	436 (94%)	29 (6%)	18	43
5	F	181/181 (100%)	170 (94%)	11 (6%)	18	44
6	G	149/149 (100%)	143 (96%)	6 (4%)	31	55
7	H	45/45 (100%)	44 (98%)	1 (2%)	52	71
8	I	124/124 (100%)	119 (96%)	5 (4%)	31	55
All	All	964/971 (99%)	912 (95%)	52 (5%)	26	47

5 of 52 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	533	TYR
5	F	69	THR
8	I	49	LEU
5	F	1	MET
5	F	40	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
5	F	172	HIS
7	H	18	HIS
8	I	51	GLN
4	D	257	GLN
4	D	278	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	B	30/101 (29%)	12 (40%)	3 (10%)
2	A	172/360 (47%)	53 (30%)	9 (5%)
3	E	76/77 (98%)	19 (25%)	1 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	278/538 (51%)	84 (30%)	13 (4%)

5 of 84 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	B	1238	A
1	B	1240	U
1	B	1243	C
1	B	1292	G
1	B	1293	C

5 of 13 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	A	2152	G
2	A	2157	G
3	E	9	G
2	A	2159	G
2	A	2172	U

#### 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](#)

There are no chain breaks in this entry.

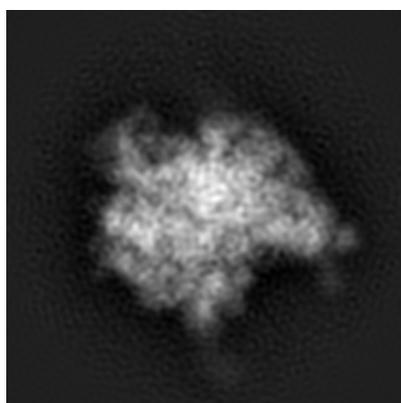
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5784. These allow visual inspection of the internal detail of the map and identification of artifacts.

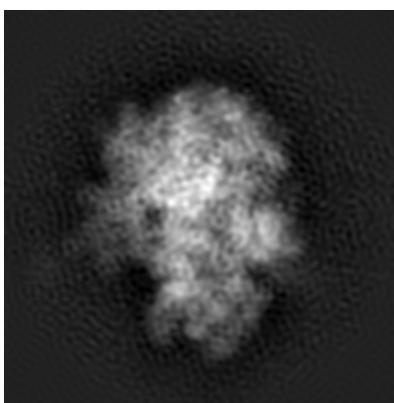
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

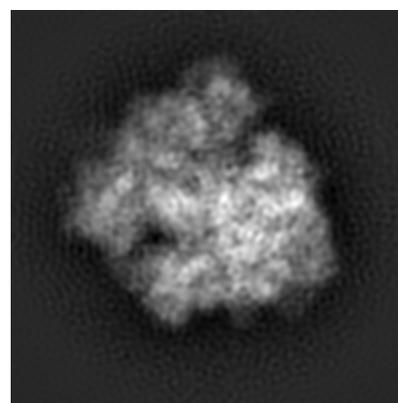
#### 6.1.1 Primary map



X



Y

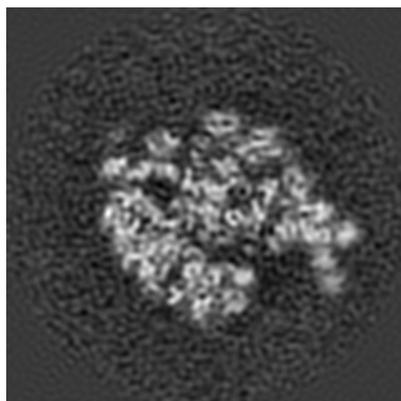


Z

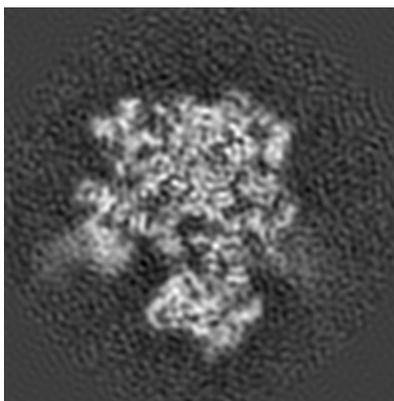
The images above show the map projected in three orthogonal directions.

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

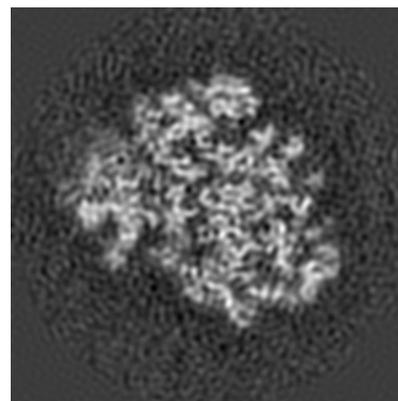
#### 6.2.1 Primary map



X Index: 67



Y Index: 67

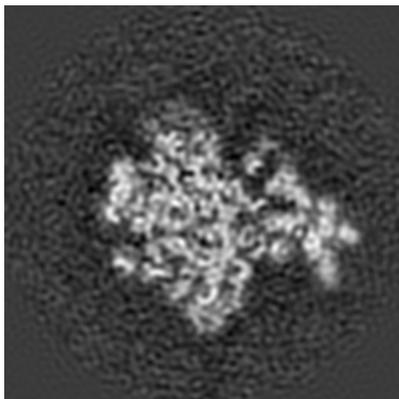


Z Index: 67

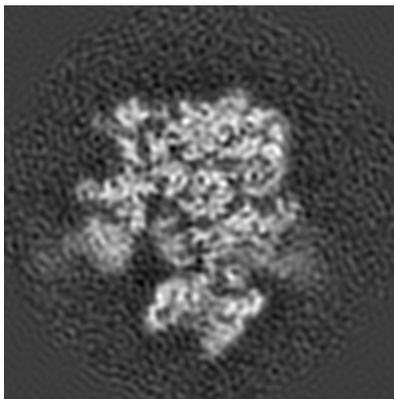
The images above show central slices of the map in three orthogonal directions.

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

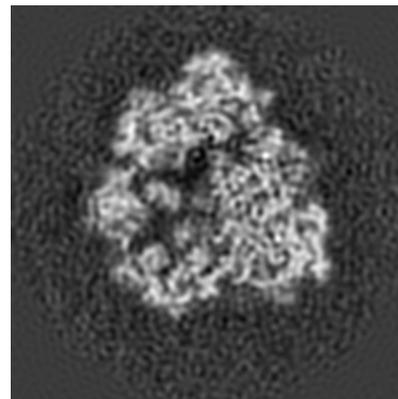
### 6.3.1 Primary map



X Index: 71



Y Index: 69

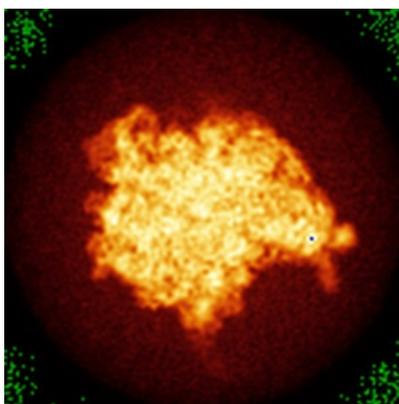


Z Index: 58

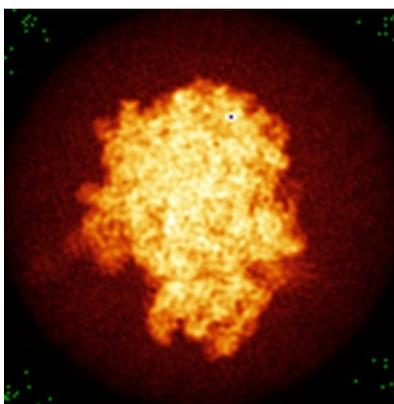
The images above show the largest variance slices of the map in three orthogonal directions.

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

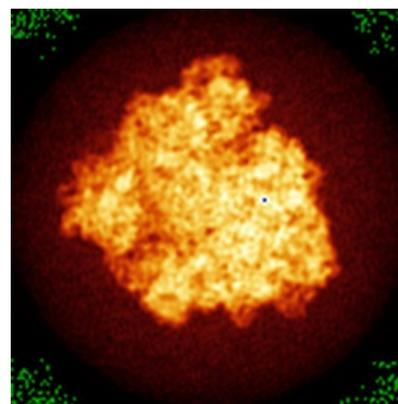
### 6.4.1 Primary map



X



Y

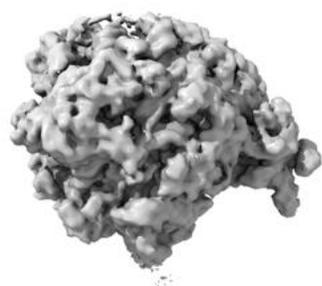


Z

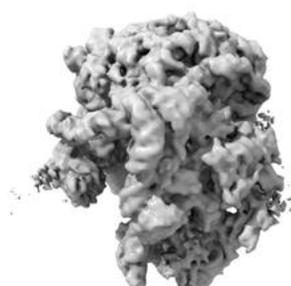
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 6.5 Orthogonal surface views [i](#)

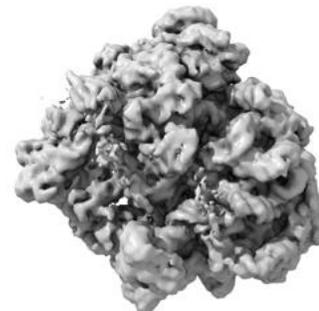
### 6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 80.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

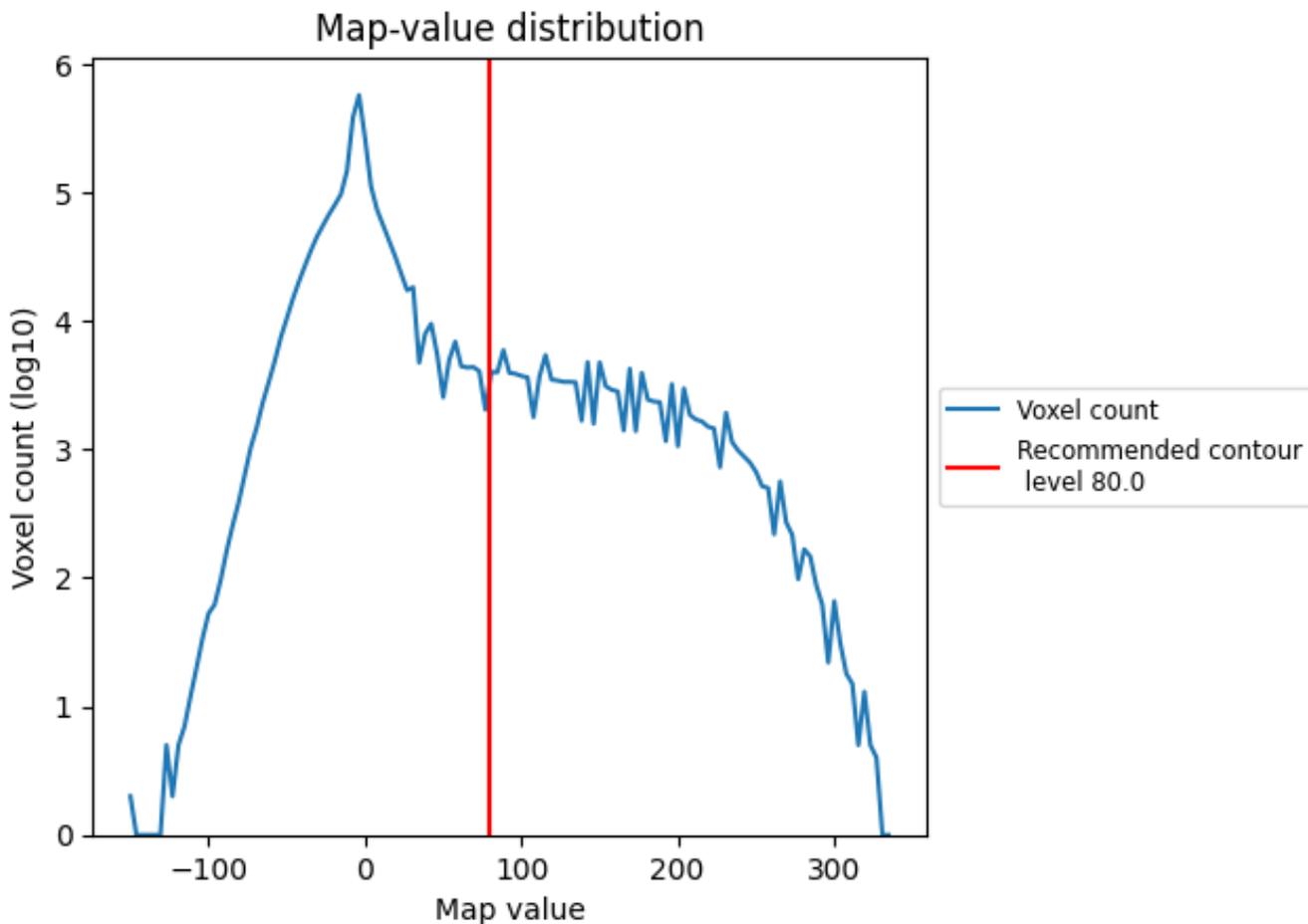
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

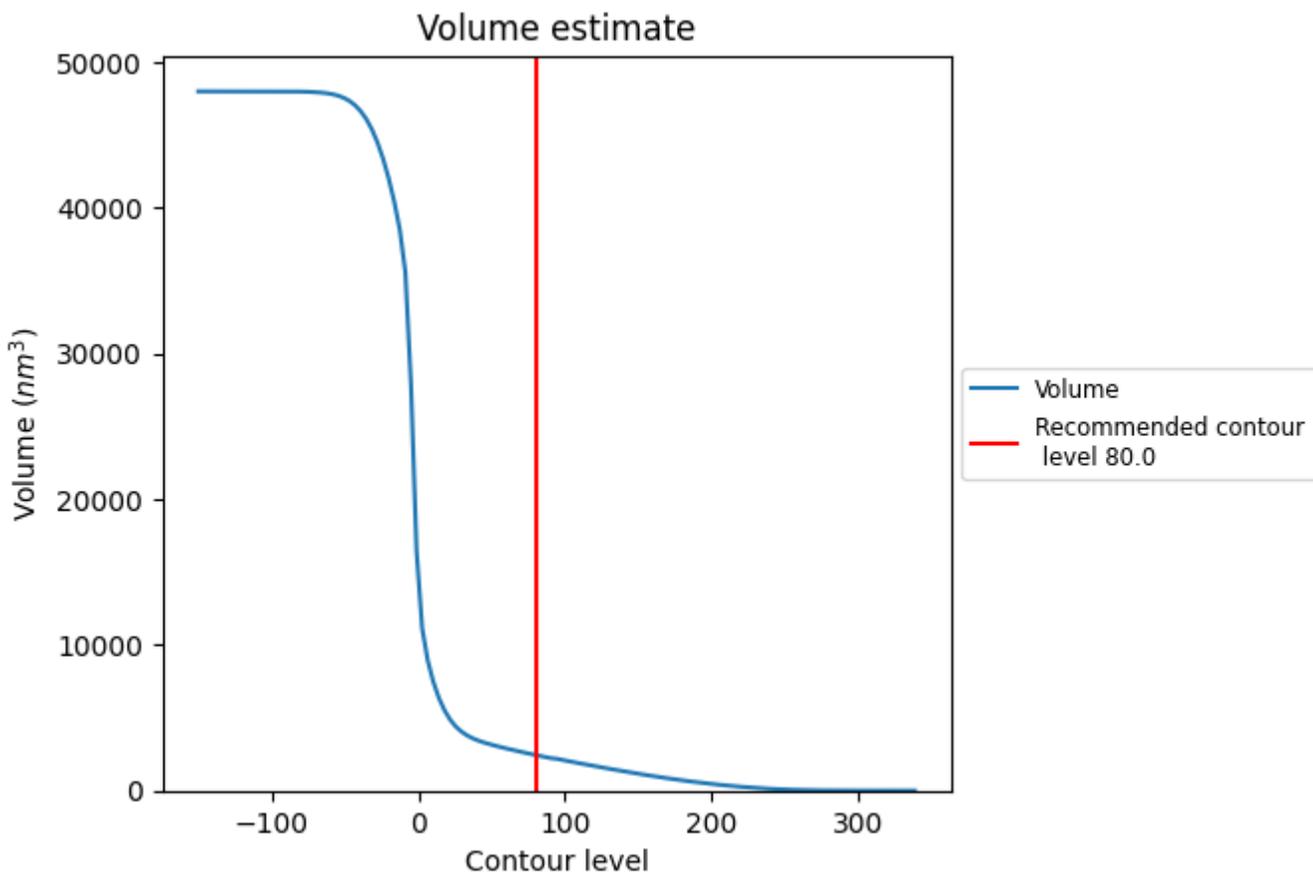
This section contains the results of statistical analysis of the map.

### 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.

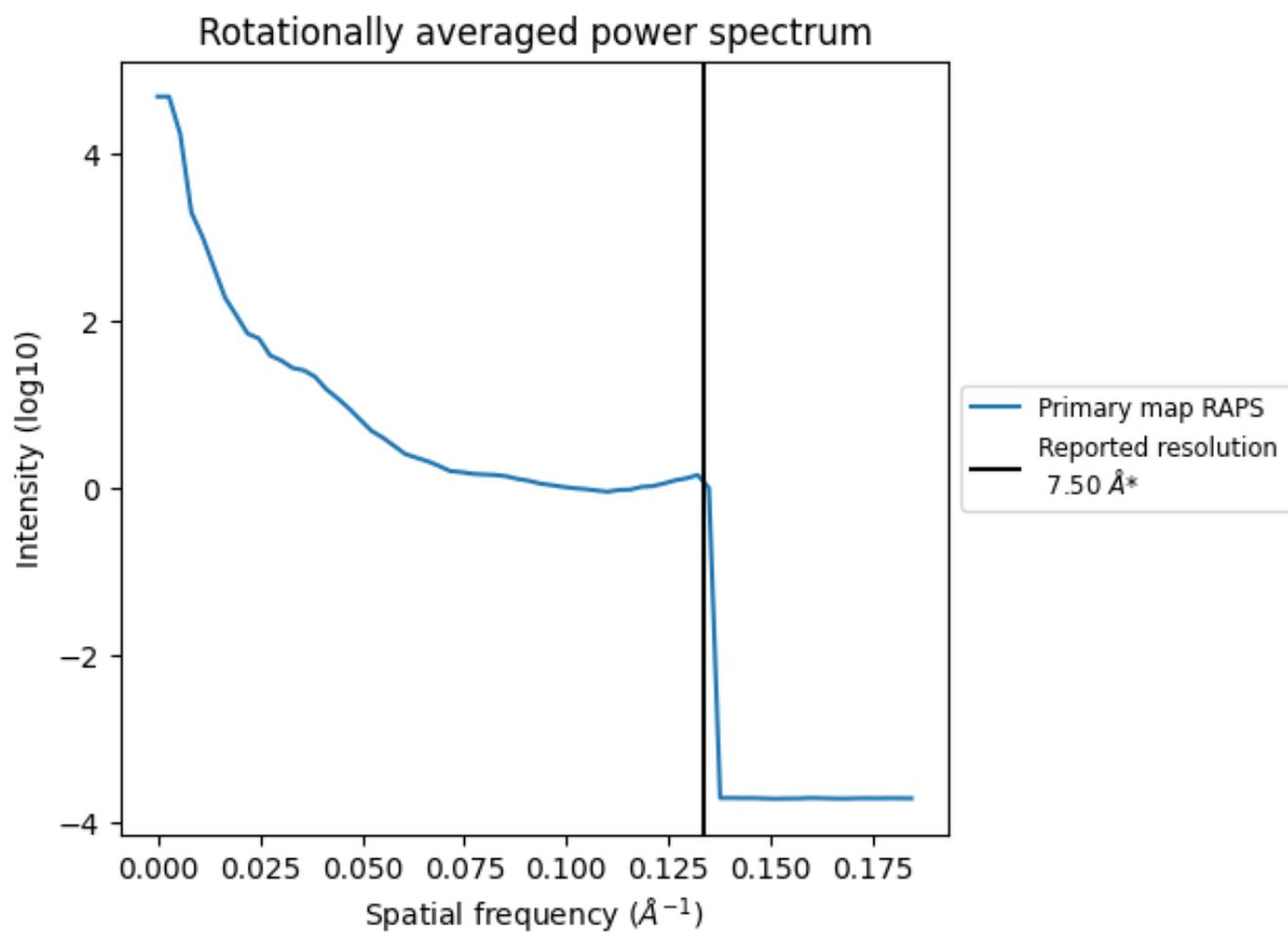
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2444 nm<sup>3</sup>; this corresponds to an approximate mass of 2208 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 0.133 Å<sup>-1</sup>

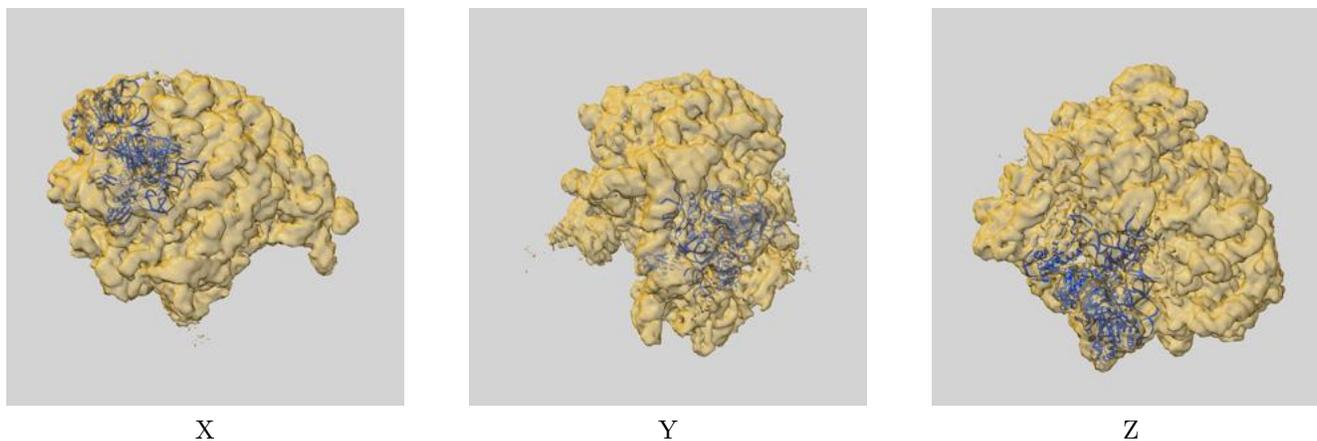
## 8 Fourier-Shell correlation

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

## 9 Map-model fit [i](#)

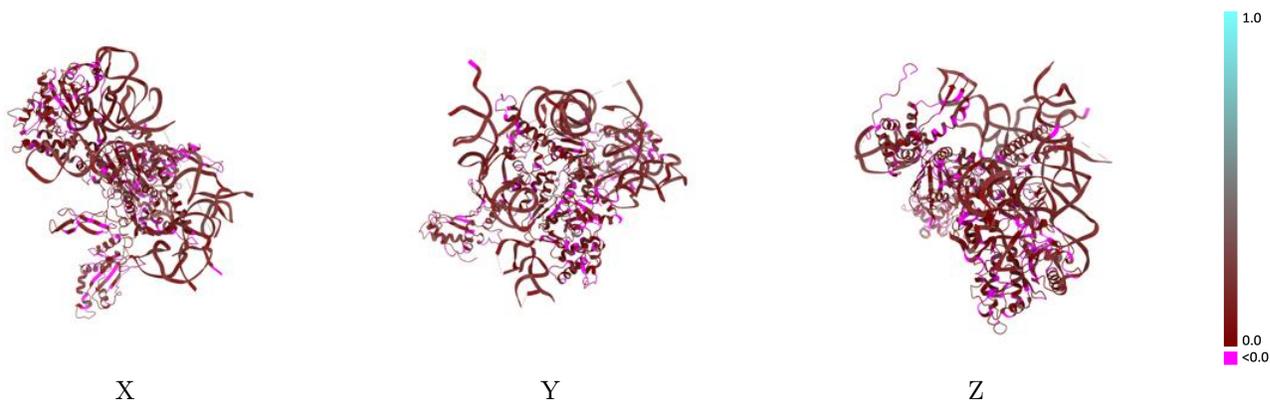
This section contains information regarding the fit between EMDB map EMD-5784 and PDB model 3J5S. Per-residue inclusion information can be found in section 3 on page 6.

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



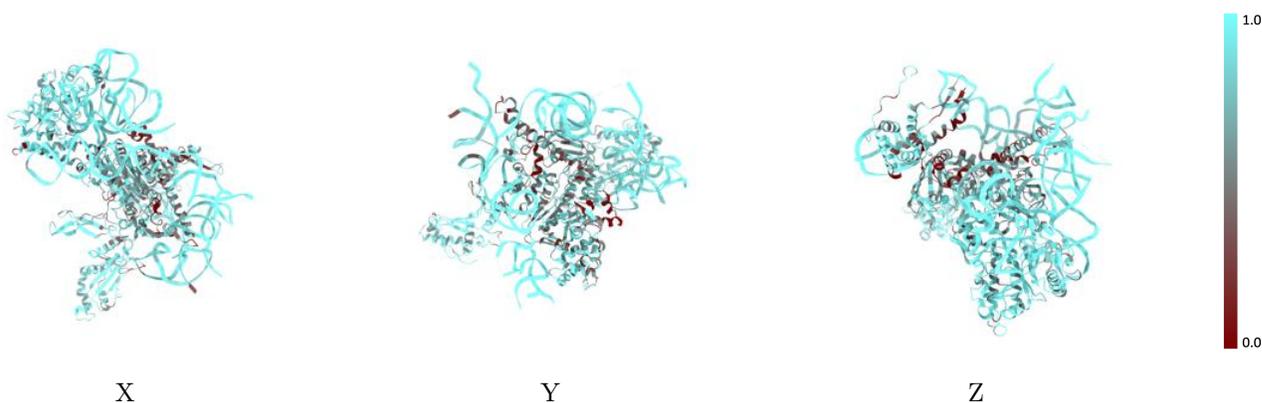
The images above show the 3D surface view of the map at the recommended contour level 80.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



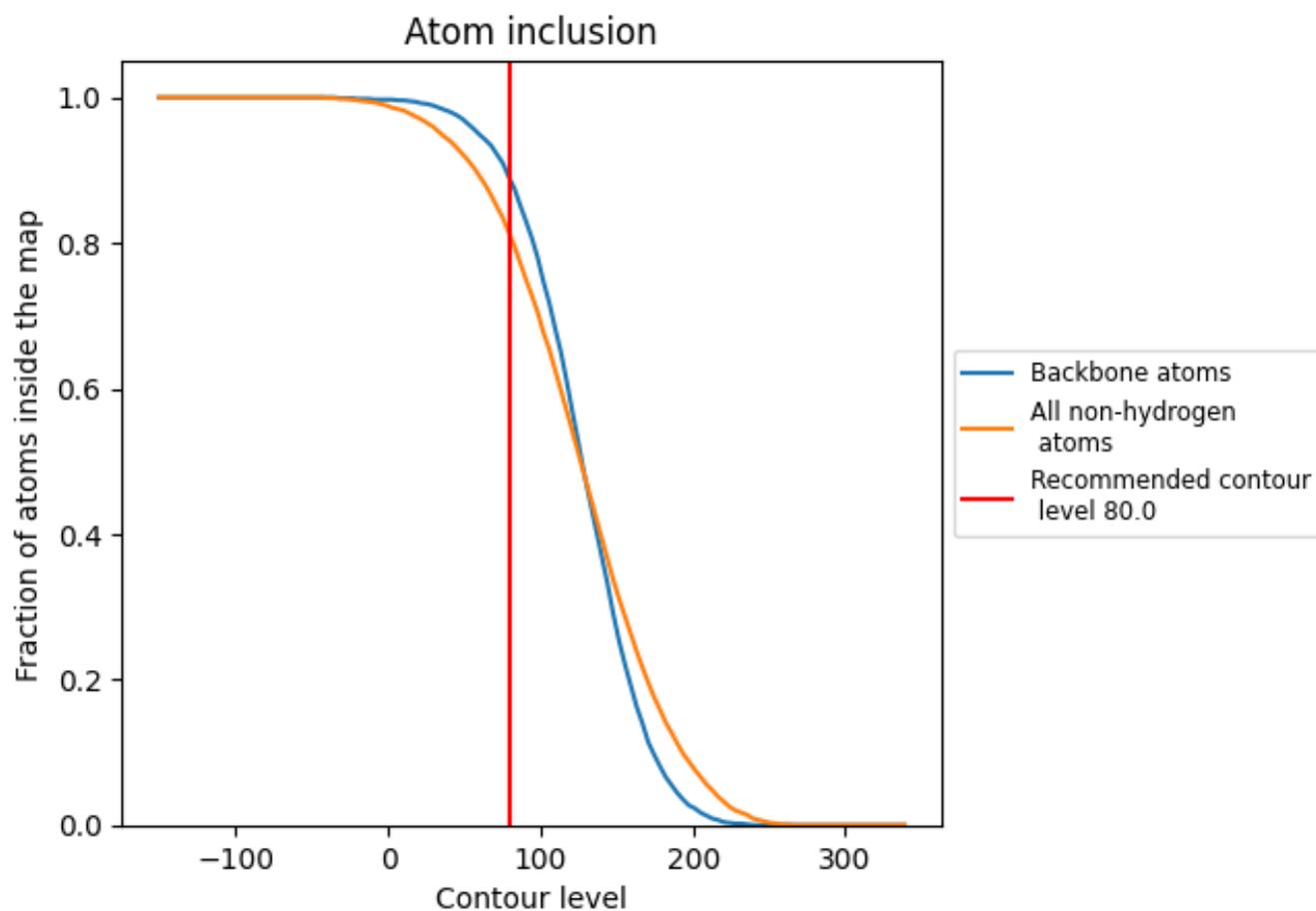
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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 (80.0).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 81% 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 (80.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8110	 0.1220
A	 0.9550	 0.1600
B	 0.9880	 0.1690
D	 0.6450	 0.1120
E	 0.8680	 0.1700
F	 0.8670	 0.0700
G	 0.8440	 0.0980
H	 0.7710	 0.0940
I	 0.6640	 0.0650

