



## wwPDB EM Validation Summary Report ⓘ

Jan 27, 2022 – 06:21 pm GMT

PDB ID : 7PIM  
EMDB ID : EMD-13442  
Title : Partial structure of tyrosine hydroxylase lacking the first 35 residues in complex with dopamine.  
Authors : Bueno-Carrasco, M.T.; Cuellar, J.; Santiago, C.; Valpuesta, J.M.; Martinez, A.; Flydal, M.I.  
Deposited on : 2021-08-20  
Resolution : 4.60 Å(reported)

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.

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

EMDB validation analysis : 0.0.0.dev97  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.26

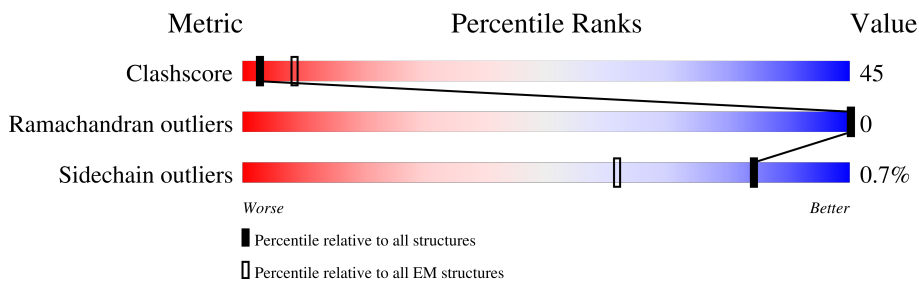
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.60 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  $\geq 3$ , 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	A	335	
1	B	335	
1	D	335	
1	F	335	
2	C	18	
2	E	18	
2	G	18	
2	H	18	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11844 atoms, of which 524 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.

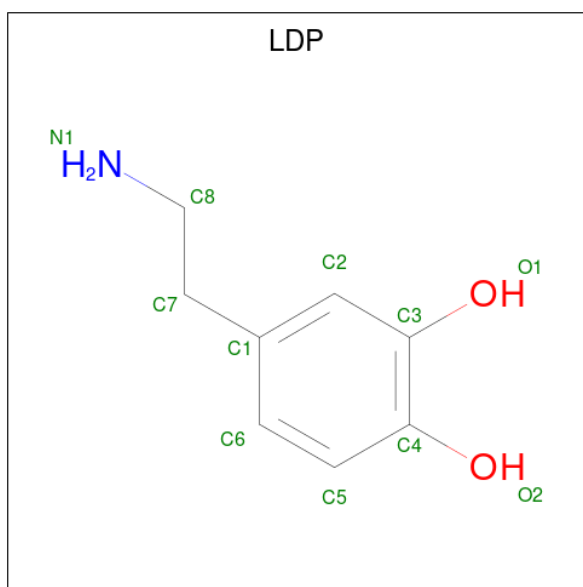
- Molecule 1 is a protein called Tyrosine 3-monooxygenase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	B	335	2688	1712	457	510	9	0	0
1	A	335	2688	1712	457	510	9	0	0
1	D	335	2688	1712	457	510	9	0	0
1	F	335	2688	1712	457	510	9	0	0

- Molecule 2 is a protein called Regulatory domain alpha-helix.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
2	G	18	261	78	131	25	27	0	0
2	C	18	261	78	131	25	27	0	0
2	E	18	261	78	131	25	27	0	0
2	H	18	261	78	131	25	27	0	0

- Molecule 3 is L-DOPAMINE (three-letter code: LDP) (formula:  $C_8H_{11}NO_2$ ).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
3	B	1	11	8	1	2	0
3	A	1	11	8	1	2	0
3	D	1	11	8	1	2	0
3	F	1	11	8	1	2	0

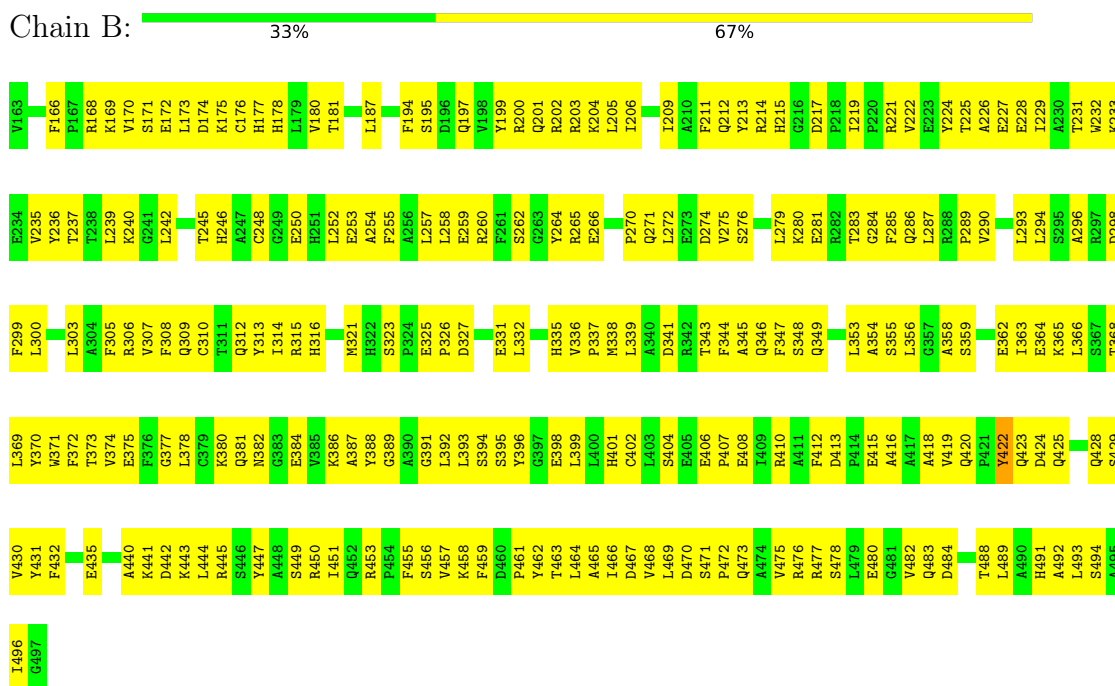
- Molecule 4 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		AltConf
			Total	Fe	
4	B	1	1	1	0
4	A	1	1	1	0
4	D	1	1	1	0
4	F	1	1	1	0

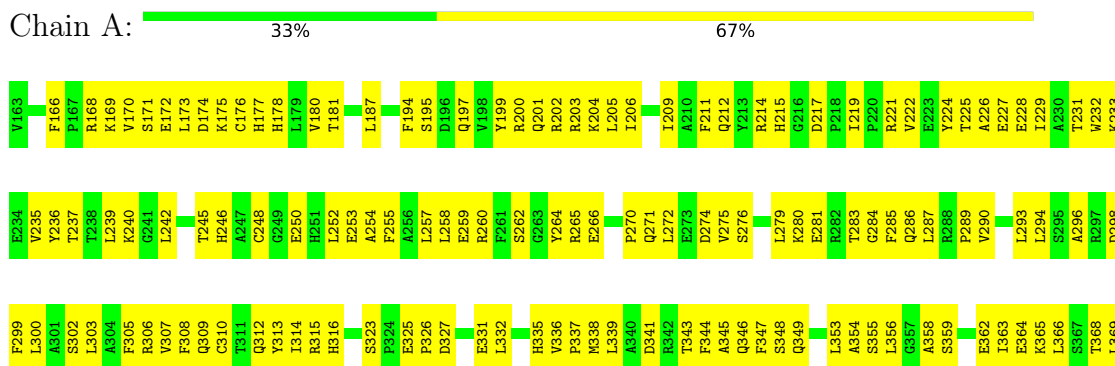
### 3 Residue-property plots i

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: Tyrosine 3-monooxygenase

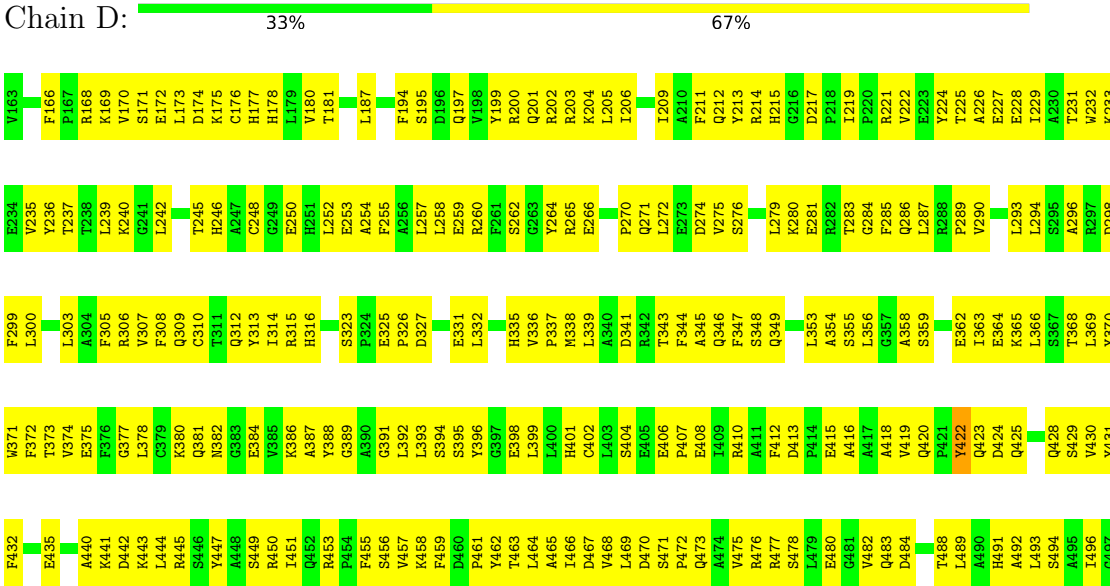


- Molecule 1: Tyrosine 3-monooxygenase

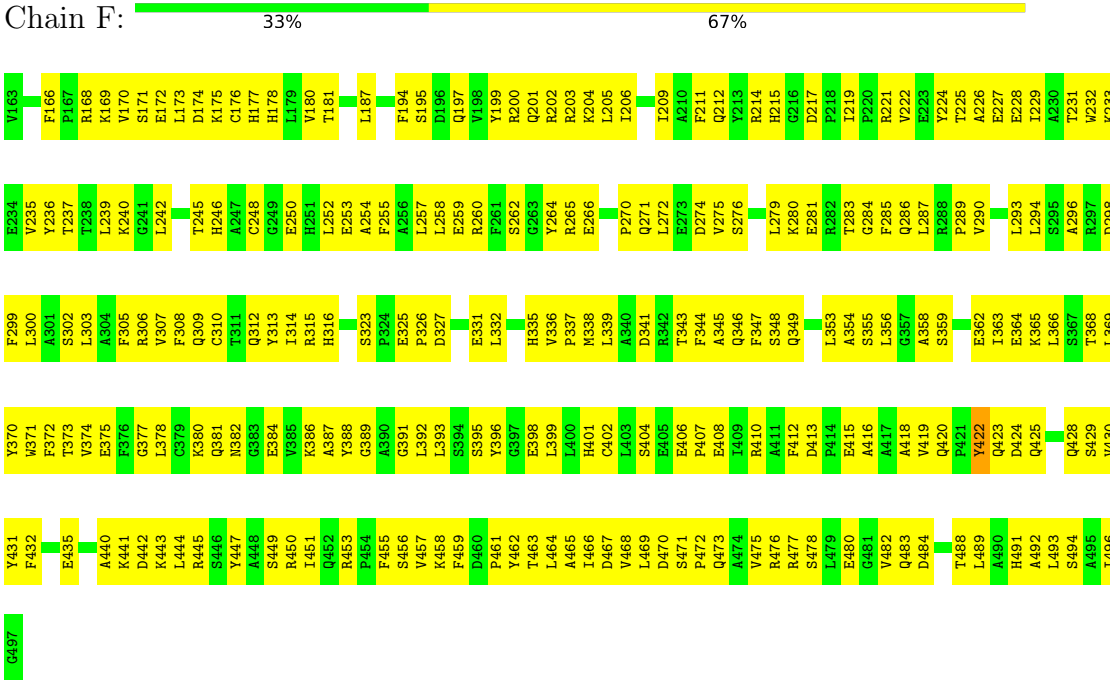


Y370	Y431	Y371	F432	W371	F432	F372	E435	F373	A440	F374	K441	F375	K442	F376	K443	G377	K444	L378	K445	C379	K446	K380	Q381	N382	Y447	G385	A448	E384	S449	V385	R450	K386	I451	A387	Y388	R453	Y389	G389	A390	F455	S456	G391	L392	S195	V457	K458	L393	S394	Q197	F459	D460	S395	P461	Y462	G397	R200	E398	T463	L399	L464	A465	H401	I466	C402	D467	V468	L403	S404	E406	D470	A411	S471	P472	E408	Q473	I409	A474	R410	V475	A412	R477	F412	D478	F414	E415	E480	E416	G481	A417	V482	Q483	A418	V419	D484	Q420	Q421	T488	L489	A490	Q423	H491	D424	A492	Q425	L493	S494	Q428	S429	A495	W232	S496	I496	V430
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

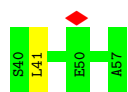
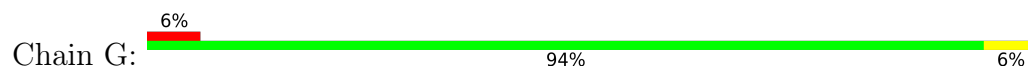
● Molecule 1: Tyrosine 3-monooxygenase



● Molecule 1: Tyrosine 3-monooxygenase



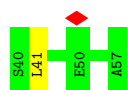
- Molecule 2: Regulatory domain alpha-helix



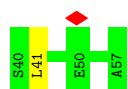
- Molecule 2: Regulatory domain alpha-helix



- Molecule 2: Regulatory domain alpha-helix



- Molecule 2: Regulatory domain alpha-helix



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	152128	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	30	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.061	Depositor
Minimum map value	-0.027	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0042	Depositor
Map size ( $\text{\AA}$ )	171.52, 171.52, 171.52	wwPDB
Map dimensions	160, 160, 160	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.072, 1.072, 1.072	Depositor



## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FE, LDP

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	0.24	0/2758	0.44	0/3740
1	B	0.24	0/2758	0.44	0/3740
1	D	0.24	0/2758	0.44	0/3740
1	F	0.24	0/2758	0.44	0/3740
2	C	0.22	0/129	0.51	0/172
2	E	0.23	0/129	0.50	0/172
2	G	0.23	0/129	0.49	0/172
2	H	0.23	0/129	0.50	0/172
All	All	0.24	0/11548	0.44	0/15648

There are no bond length outliers.

There are no bond angle outliers.

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	2688	0	2590	253	0
1	B	2688	0	2590	255	0
1	D	2688	0	2590	253	0
1	F	2688	0	2590	253	0
2	C	130	131	131	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	130	131	131	0	0
2	G	130	131	131	0	0
2	H	130	131	131	0	0
3	A	11	0	9	4	0
3	B	11	0	9	5	0
3	D	11	0	9	5	0
3	F	11	0	9	4	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	D	1	0	0	0	0
4	F	1	0	0	0	0
All	All	11320	524	10920	968	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 45.

The worst 5 of 968 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:326:PRO:HG3	3:A:501:LDP:H2	1.36	1.04
1:F:326:PRO:HG3	3:F:501:LDP:H2	1.36	1.04
1:B:206:ILE:HD12	1:B:312:GLN:HB2	1.38	1.02
1:D:206:ILE:HD12	1:D:312:GLN:HB2	1.38	1.02
1:B:326:PRO:HG3	3:B:501:LDP:H2	1.36	1.02

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	333/335 (99%)	326 (98%)	7 (2%)	0	<b>100</b> <b>100</b>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	333/335 (99%)	326 (98%)	7 (2%)	0	100	100
1	D	333/335 (99%)	326 (98%)	7 (2%)	0	100	100
1	F	333/335 (99%)	326 (98%)	7 (2%)	0	100	100
2	C	16/18 (89%)	16 (100%)	0	0	100	100
2	E	16/18 (89%)	16 (100%)	0	0	100	100
2	G	16/18 (89%)	16 (100%)	0	0	100	100
2	H	16/18 (89%)	16 (100%)	0	0	100	100
All	All	1396/1412 (99%)	1368 (98%)	28 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	288/288 (100%)	287 (100%)	1 (0%)	92	95
1	B	288/288 (100%)	287 (100%)	1 (0%)	92	95
1	D	288/288 (100%)	287 (100%)	1 (0%)	92	95
1	F	288/288 (100%)	287 (100%)	1 (0%)	92	95
2	C	11/11 (100%)	10 (91%)	1 (9%)	9	31
2	E	11/11 (100%)	10 (91%)	1 (9%)	9	31
2	G	11/11 (100%)	10 (91%)	1 (9%)	9	31
2	H	11/11 (100%)	10 (91%)	1 (9%)	9	31
All	All	1196/1196 (100%)	1188 (99%)	8 (1%)	84	90

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	41	LEU
1	F	422	TYR

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Mol	Chain	Res	Type
1	D	422	TYR
2	C	41	LEU
2	E	41	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	420	GLN
1	F	381	GLN
1	D	381	GLN
1	A	420	GLN
1	D	420	GLN

### 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](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	LDP	A	501	4	10,11,11	0.97	2 (20%)	13,14,14	0.62	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	LDP	D	501	4	10,11,11	0.98	2 (20%)	13,14,14	0.61	0
3	LDP	F	501	4	10,11,11	0.97	2 (20%)	13,14,14	0.62	0
3	LDP	B	501	4	10,11,11	0.97	2 (20%)	13,14,14	0.62	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	LDP	A	501	4	-	2/3/3/3	0/1/1/1
3	LDP	D	501	4	-	2/3/3/3	0/1/1/1
3	LDP	F	501	4	-	2/3/3/3	0/1/1/1
3	LDP	B	501	4	-	2/3/3/3	0/1/1/1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	501	LDP	O2-C4	2.07	1.40	1.36
3	F	501	LDP	O2-C4	2.07	1.40	1.36
3	D	501	LDP	O2-C4	2.06	1.40	1.36
3	D	501	LDP	O1-C3	2.06	1.40	1.36
3	B	501	LDP	O2-C4	2.04	1.40	1.36

There are no bond angle outliers.

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	501	LDP	C2-C1-C7-C8
3	A	501	LDP	C2-C1-C7-C8
3	D	501	LDP	C2-C1-C7-C8
3	F	501	LDP	C2-C1-C7-C8
3	B	501	LDP	C6-C1-C7-C8

There are no ring outliers.

4 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	501	LDP	4	0
3	D	501	LDP	5	0
3	F	501	LDP	4	0
3	B	501	LDP	5	0

## 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.

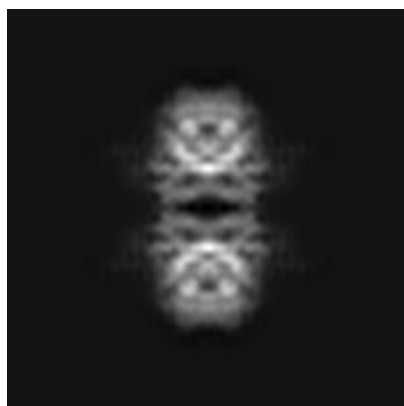
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13442. These allow visual inspection of the internal detail of the map and identification of artifacts.

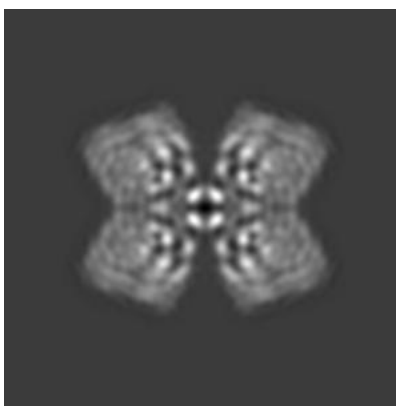
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

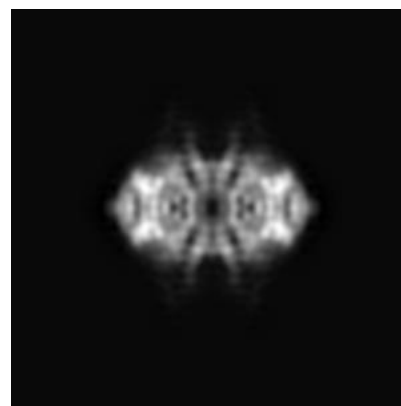
#### 6.1.1 Primary map



X

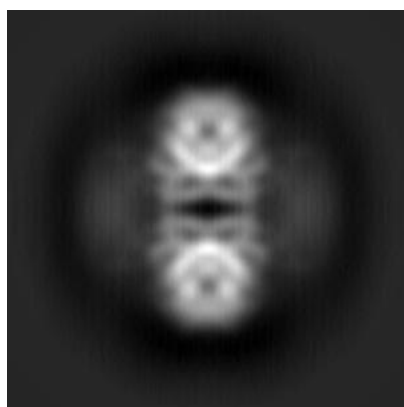


Y

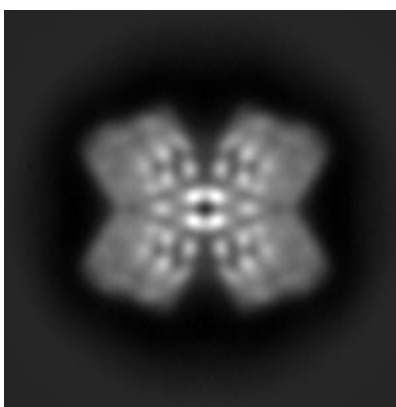


Z

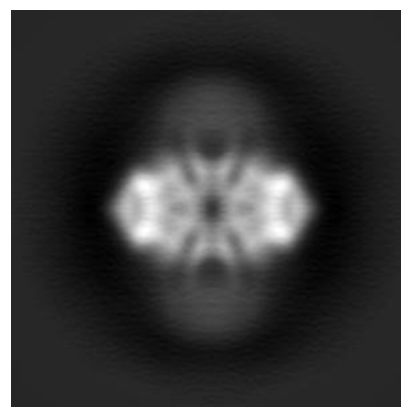
#### 6.1.2 Raw map



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: 80

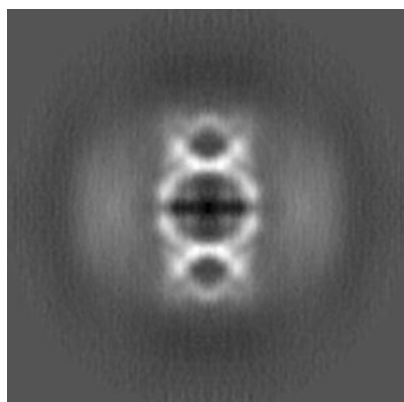


Y Index: 80

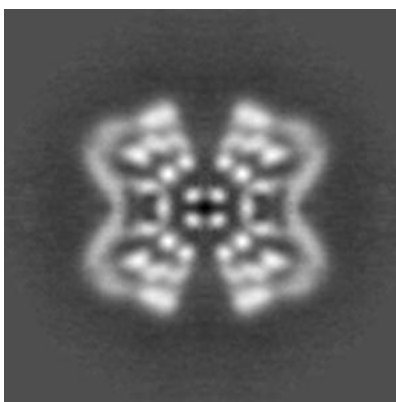


Z Index: 80

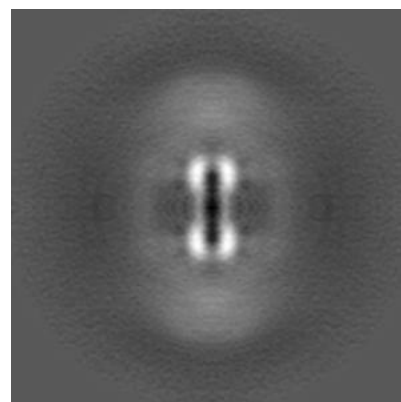
### 6.2.2 Raw map



X Index: 80



Y Index: 80



Z Index: 80

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



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

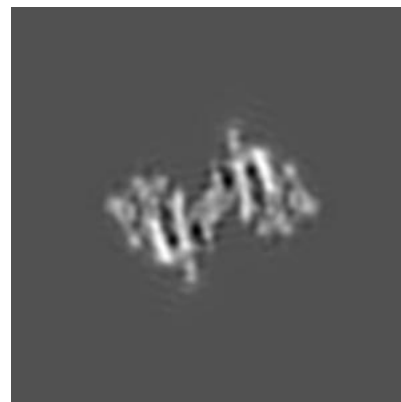
### 6.3.1 Primary map



X Index: 66

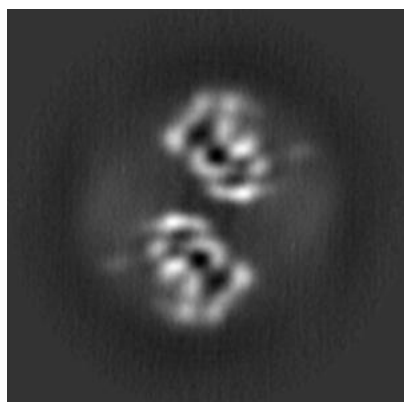


Y Index: 91

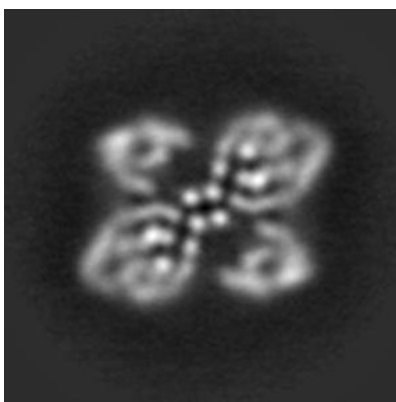


Z Index: 64

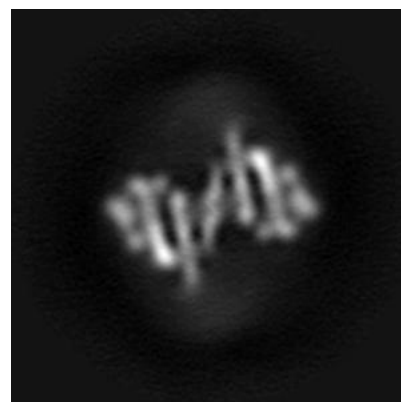
### 6.3.2 Raw map



X Index: 65



Y Index: 71

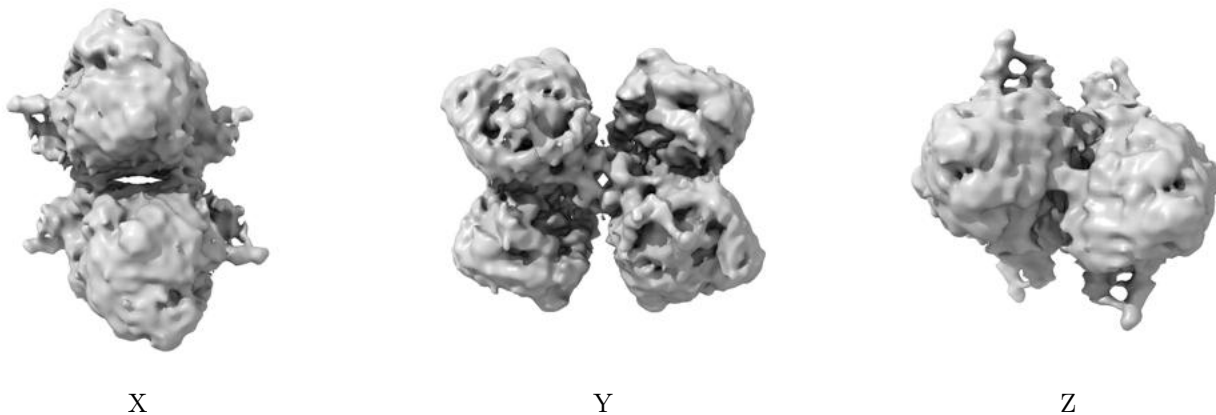


Z Index: 64

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

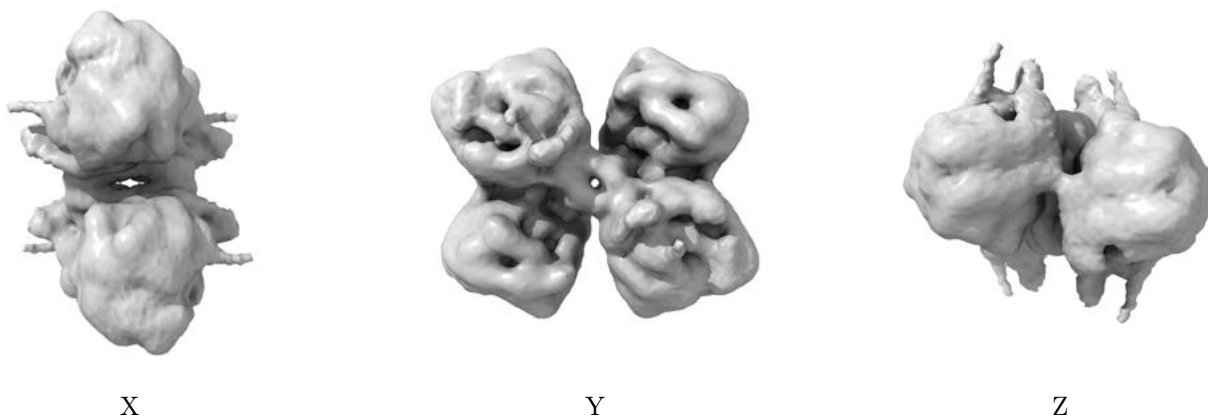
## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0042. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.4.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

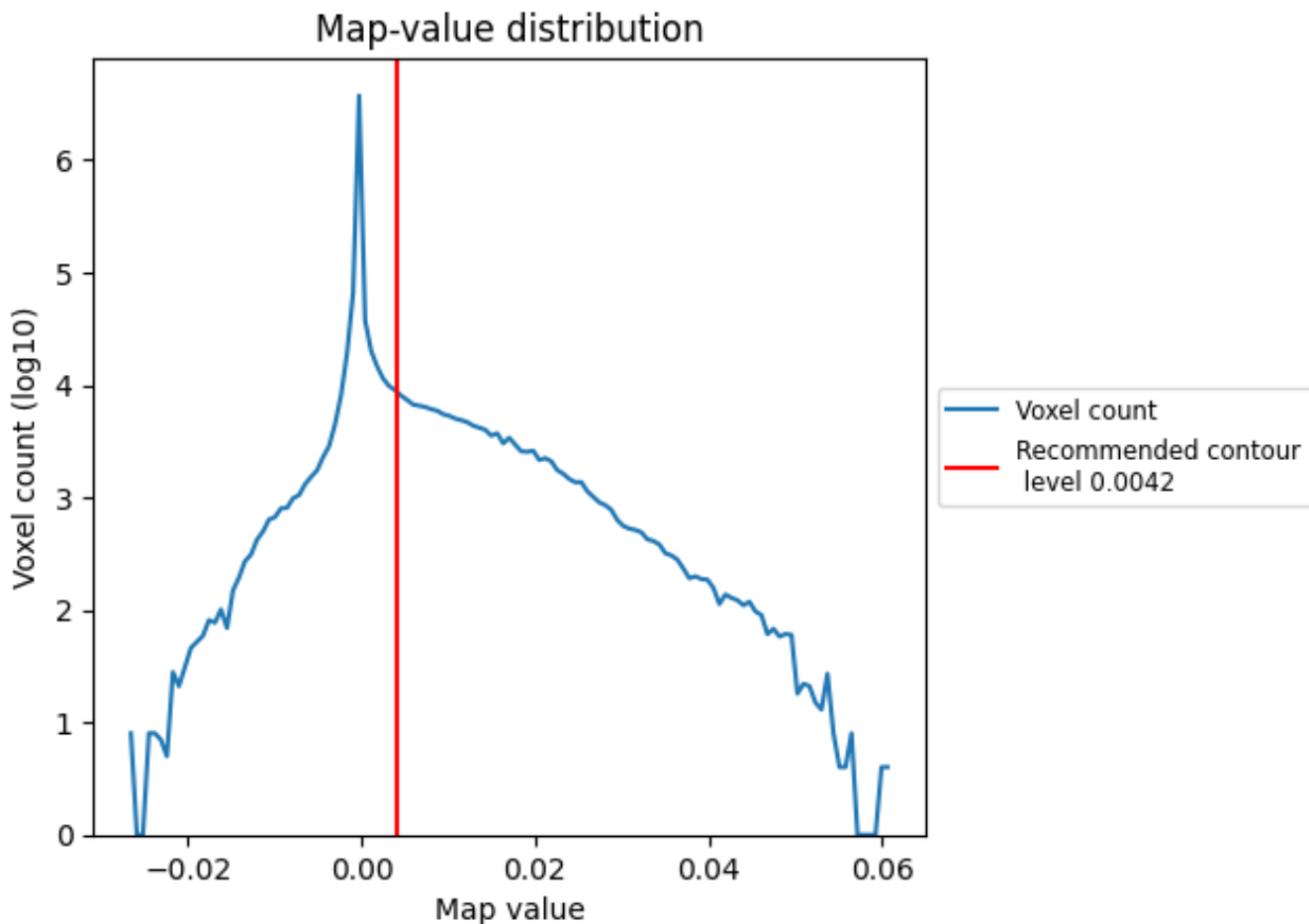
## 6.5 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

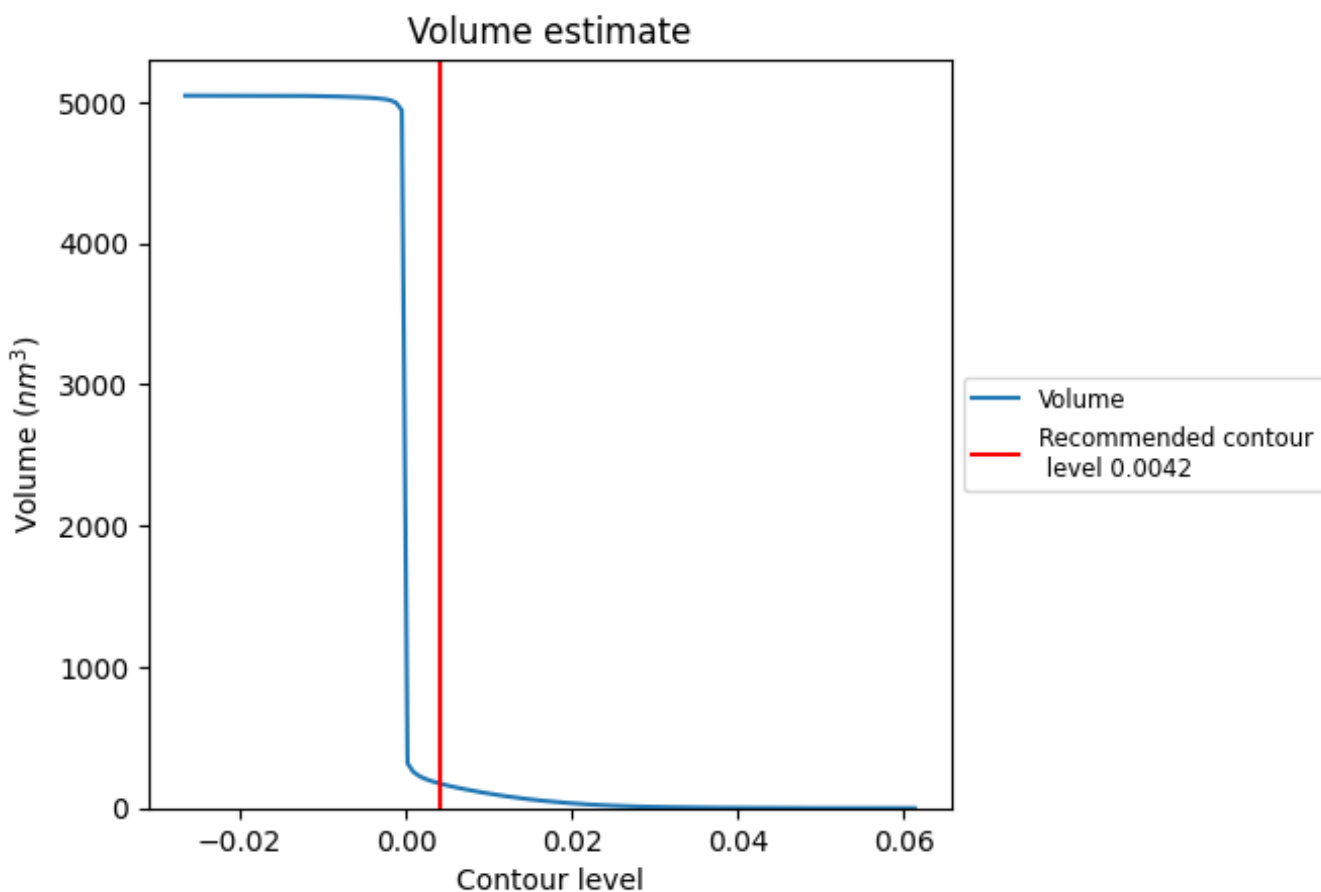
This section contains the results of statistical analysis of the map.

### 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.

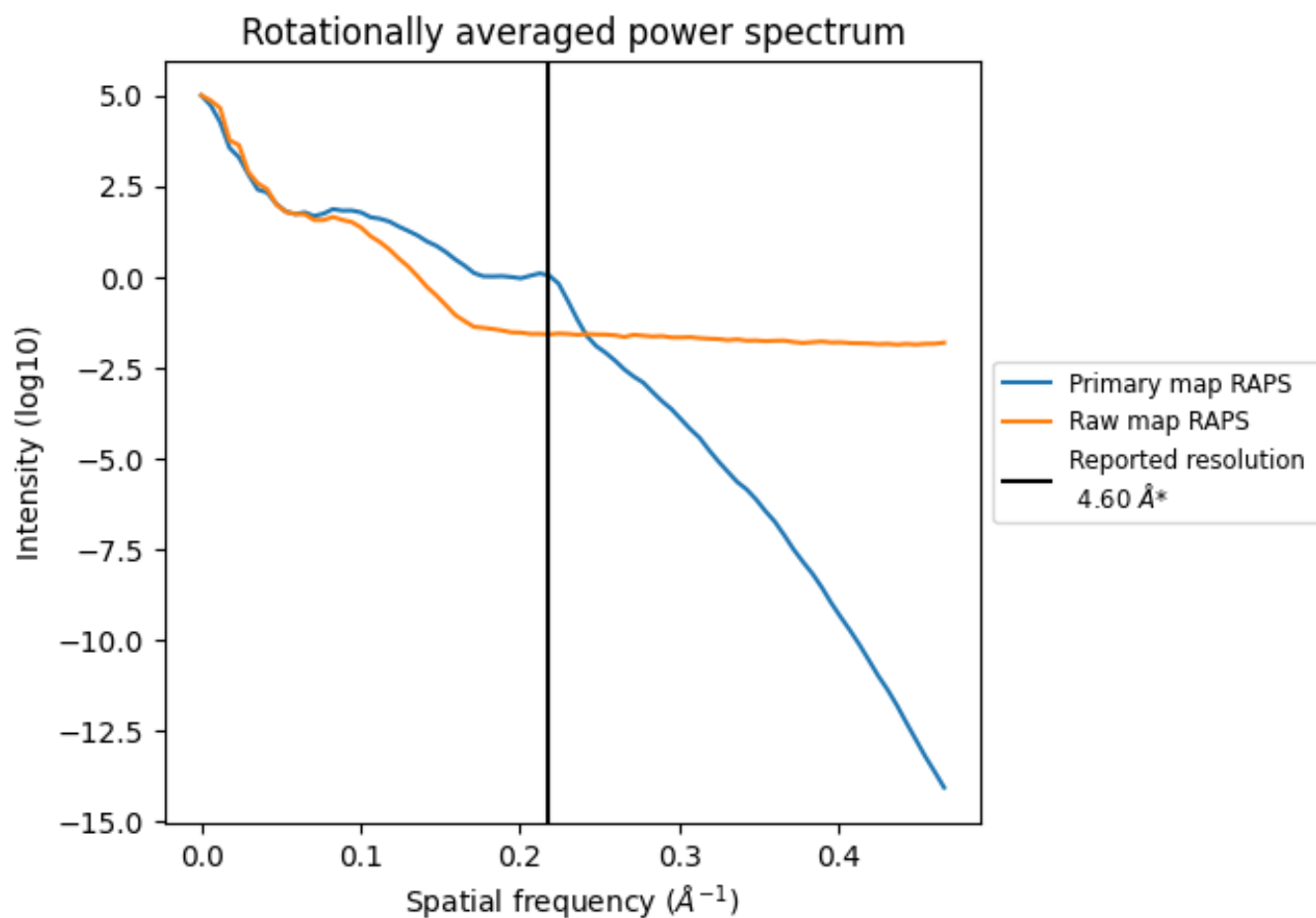
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is  $173 \text{ nm}^3$ ; this corresponds to an approximate mass of 156 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](#)

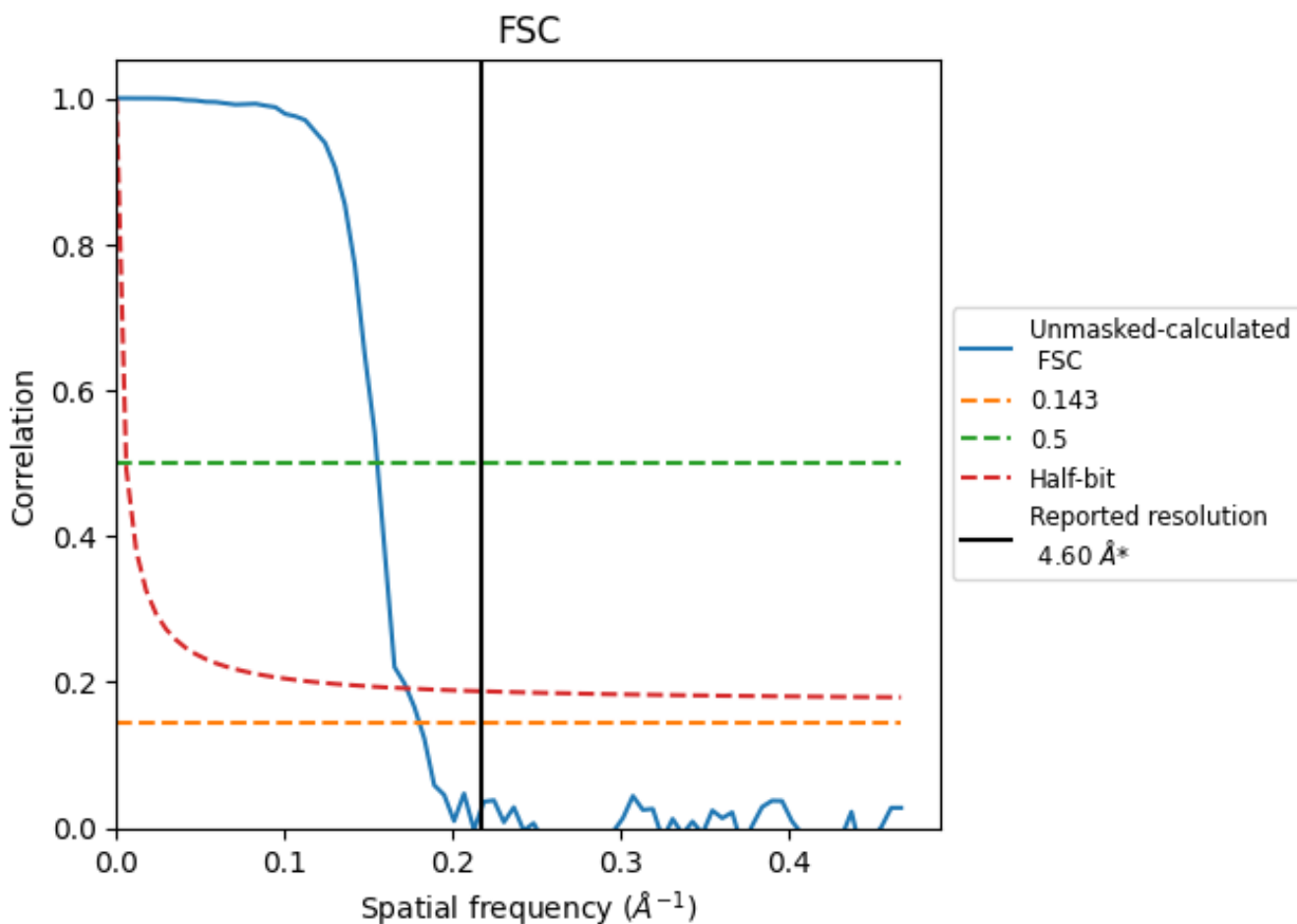


\*Reported resolution corresponds to spatial frequency of 0.217 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.217 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

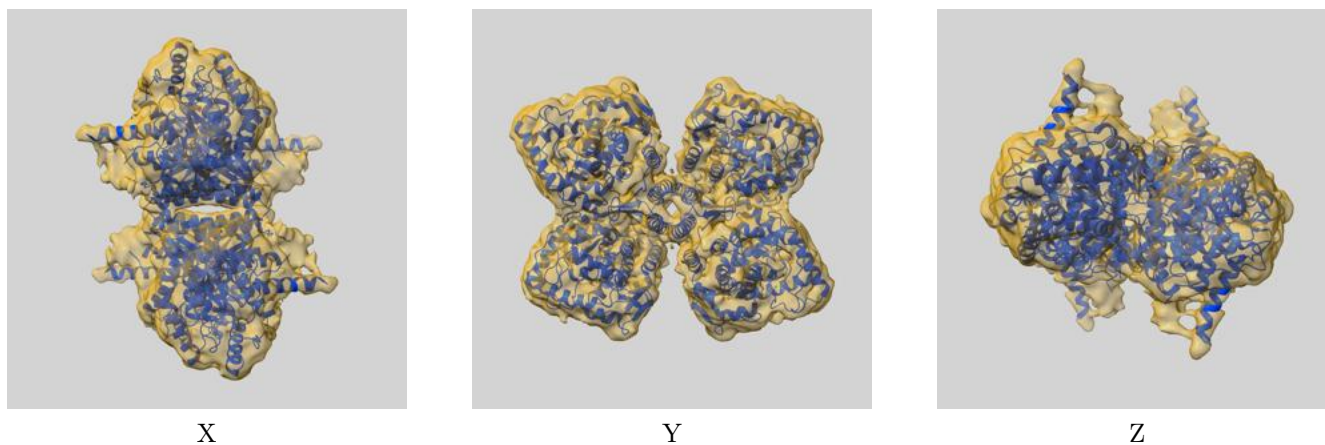
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.55	6.45	5.80

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.55 differs from the reported value 4.6 by more than 10 %

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

This section contains information regarding the fit between EMDB map EMD-13442 and PDB model 7PIM. Per-residue inclusion information can be found in section 3 on page 5.

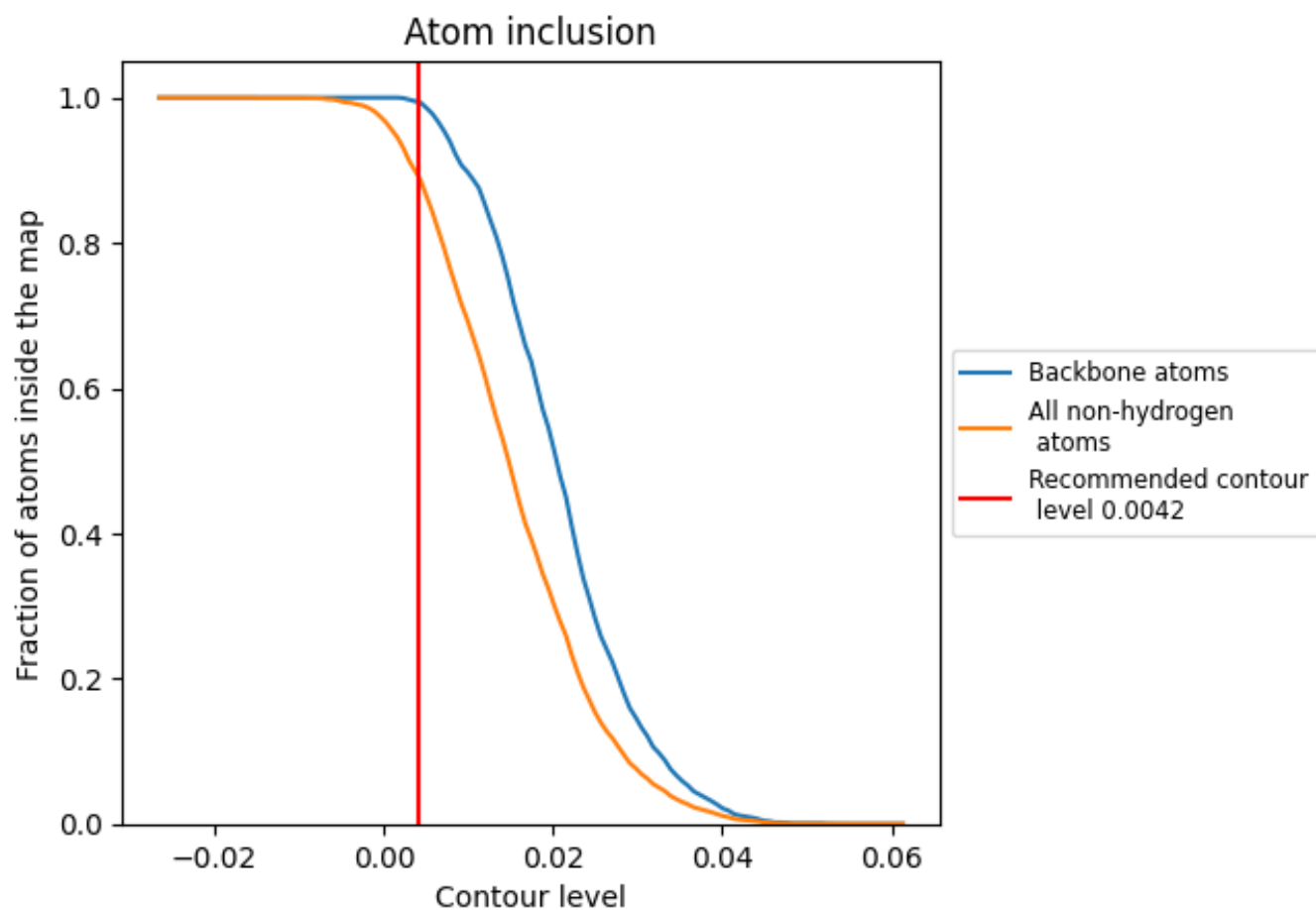
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.0042 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 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 89% of all non-hydrogen atoms, are inside the map.