



## wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 11:59 PM UTC

PDB ID : 7D43 / pdb\_00007d43  
EMDB ID : EMD-30568  
Title : eIF2B-eIF2(aP), aPg complex  
Authors : Kashiwagi, K.; Ito, T.  
Deposited on : 2020-09-22  
Resolution : 4.30 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.

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:

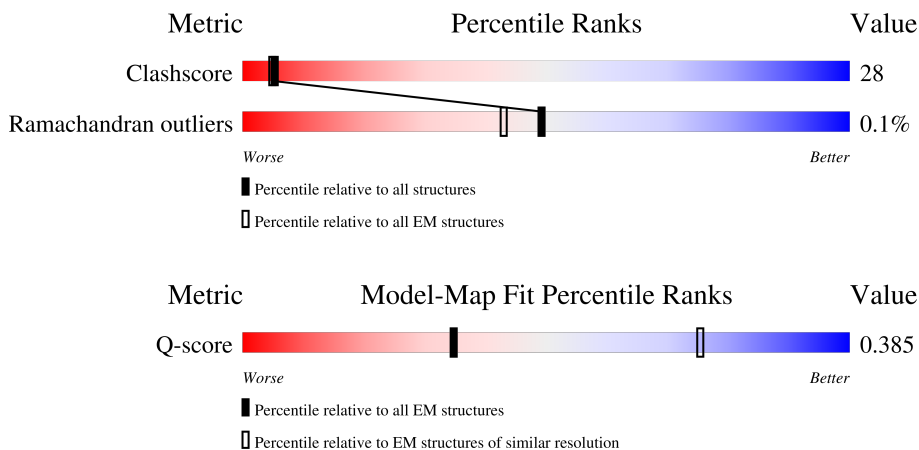
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 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 4.30 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.




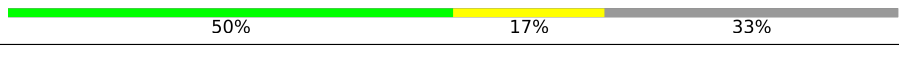

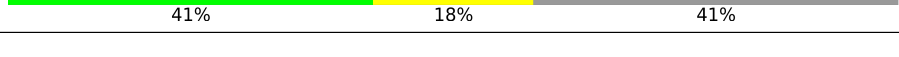
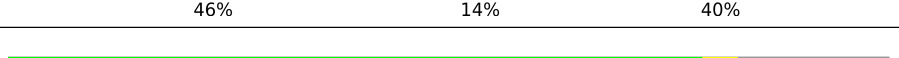
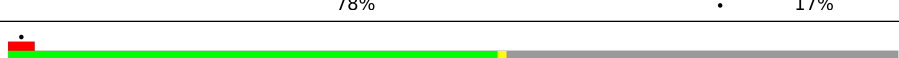
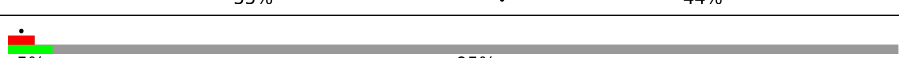
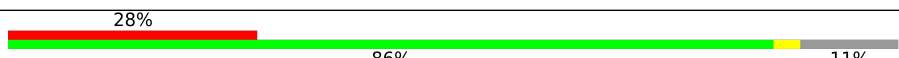
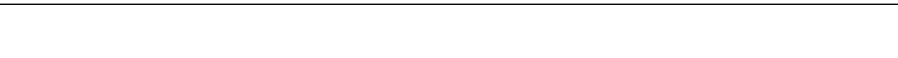
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	4585 ( 3.80 - 4.80 )

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	305	72%	24% .
1	B	305	72%	23% 5%
2	C	351	64%	26% 10%
2	D	351	67%	25% 8%
3	E	452	60%	17% 24%

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Mol	Chain	Length	Quality of chain
3	F	452	 56% 20% 24%
4	G	523	 50% 17% 33%
4	H	523	 50% 17% 33%
5	I	721	 41% 18% 41%
5	J	721	 46% 14% 40%
6	K	315	 78% 17%
6	L	315	 55% 44%
7	M	333	 5% 95%
8	P	472	 28% 86% 11%

## 2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 31009 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 Translation initiation factor eIF-2B subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	293	Total	C	N	O	S	0	0
			2262	1449	377	424	12		
1	B	291	Total	C	N	O	S	0	0
			2249	1442	375	420	12		

- Molecule 2 is a protein called Translation initiation factor eIF-2B subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	C	317	Total	C	N	O	S	0	0
			2476	1565	435	461	15		
2	D	324	Total	C	N	O	S	0	0
			2538	1605	445	473	15		

- Molecule 3 is a protein called Translation initiation factor eIF-2B subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	E	344	Total	C	N	O	S	0	0
			2438	1546	424	453	15		
3	F	343	Total	C	N	O	S	0	0
			2430	1540	423	452	15		

- Molecule 4 is a protein called Translation initiation factor eIF-2B subunit delta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	G	353	Total	C	N	O	S	0	0
			2750	1740	490	506	14		
4	H	353	Total	C	N	O	S	0	0
			2750	1740	490	506	14		

- Molecule 5 is a protein called Translation initiation factor eIF-2B subunit epsilon.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	427	Total	C	N	O	S	0	0
			3358	2115	591	637	15		
5	J	429	Total	C	N	O	S	0	0
			3371	2124	591	641	15		

- Molecule 6 is a protein called Eukaryotic translation initiation factor 2 subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	K	260	Total	C	N	O	P	0	0
			1309	782	262	264	1		
6	L	176	Total	C	N	O	P	0	0
			889	529	179	180	1		

- Molecule 7 is a protein called Eukaryotic translation initiation factor 2 subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	M	16	Total	C	N	O	0	0
			80	48	16	16		

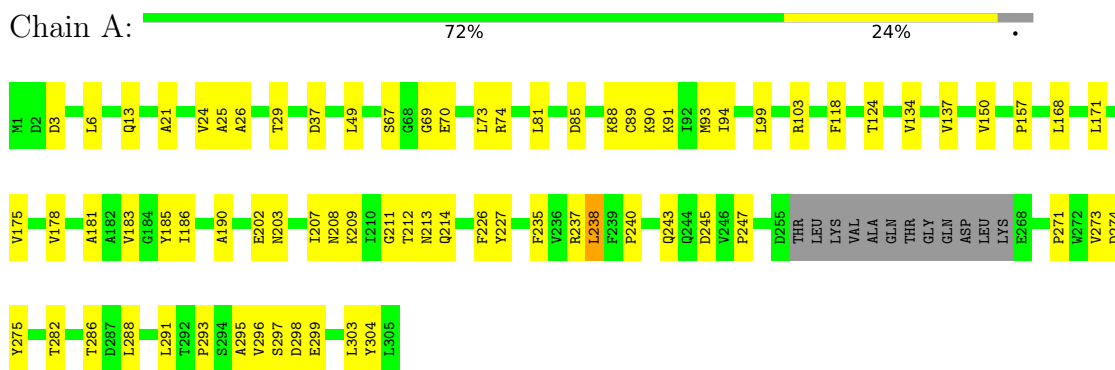
- Molecule 8 is a protein called Eukaryotic translation initiation factor 2 subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	P	421	Total	C	N	O	0	0
			2109	1267	421	421		

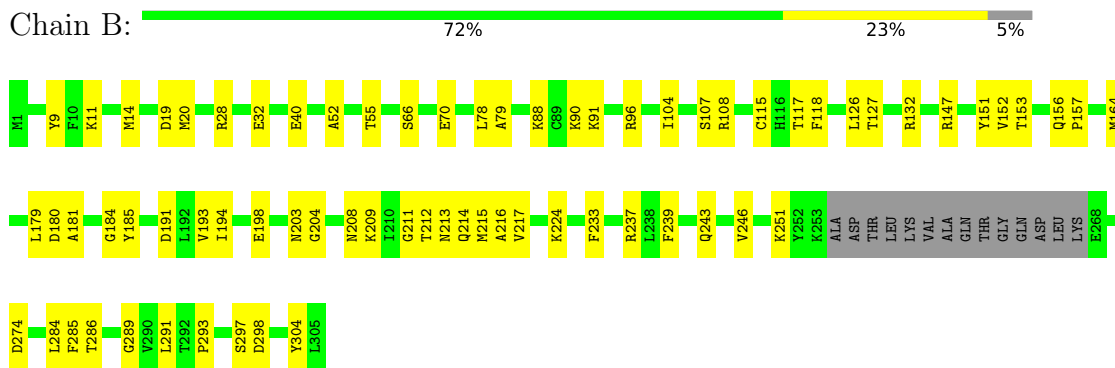
### 3 Residue-property plots [i](#)

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.

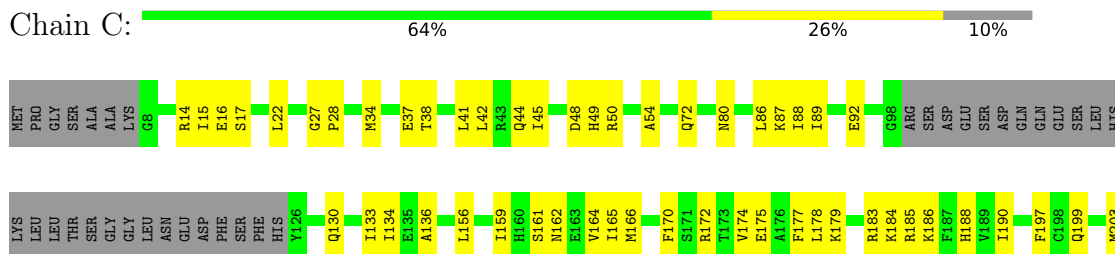
- Molecule 1: Translation initiation factor eIF-2B subunit alpha



- Molecule 1: Translation initiation factor eIF-2B subunit alpha

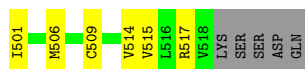


- Molecule 2: Translation initiation factor eIF-2B subunit beta

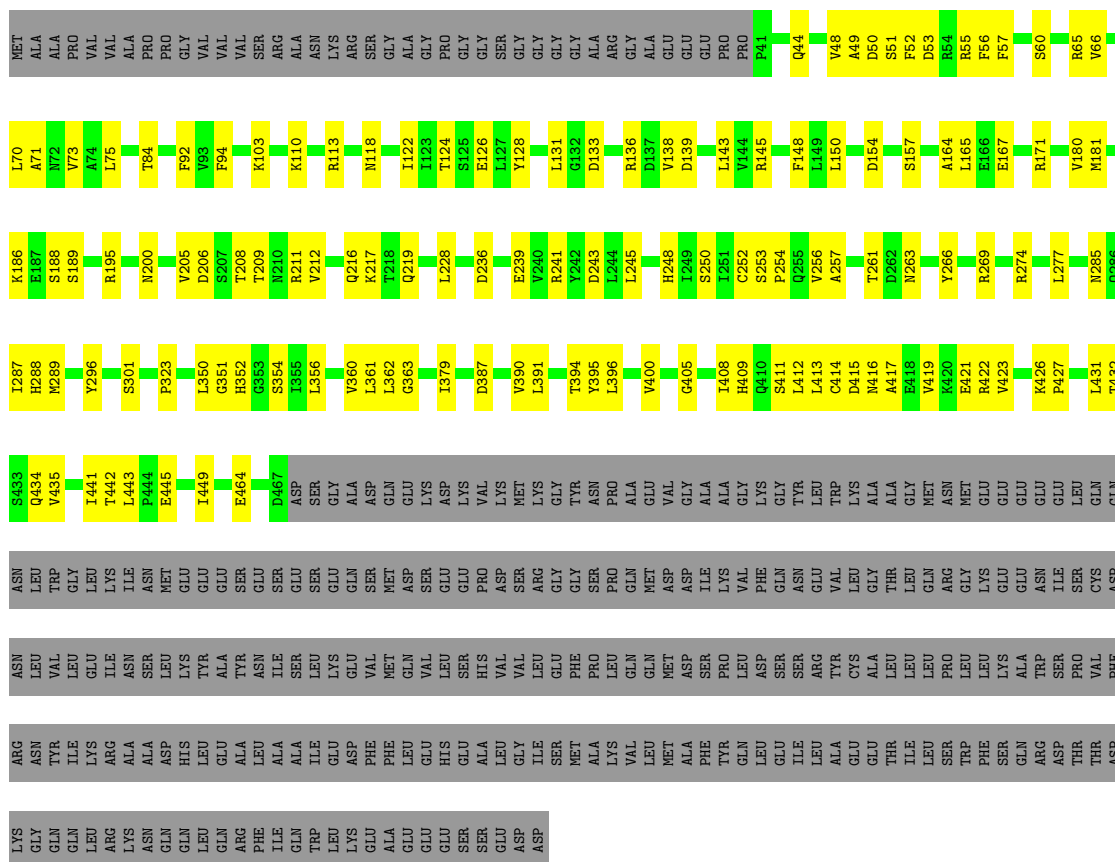




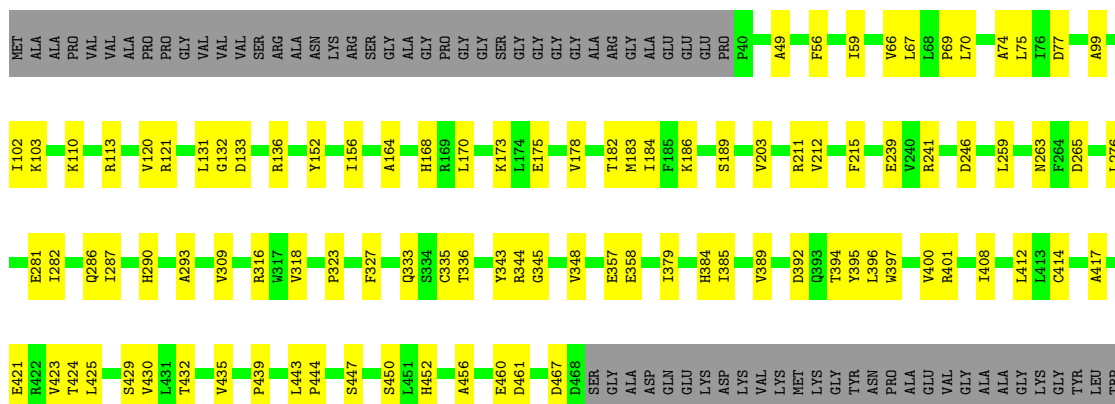




• Molecule 5: Translation initiation factor eIF-2B subunit epsilon



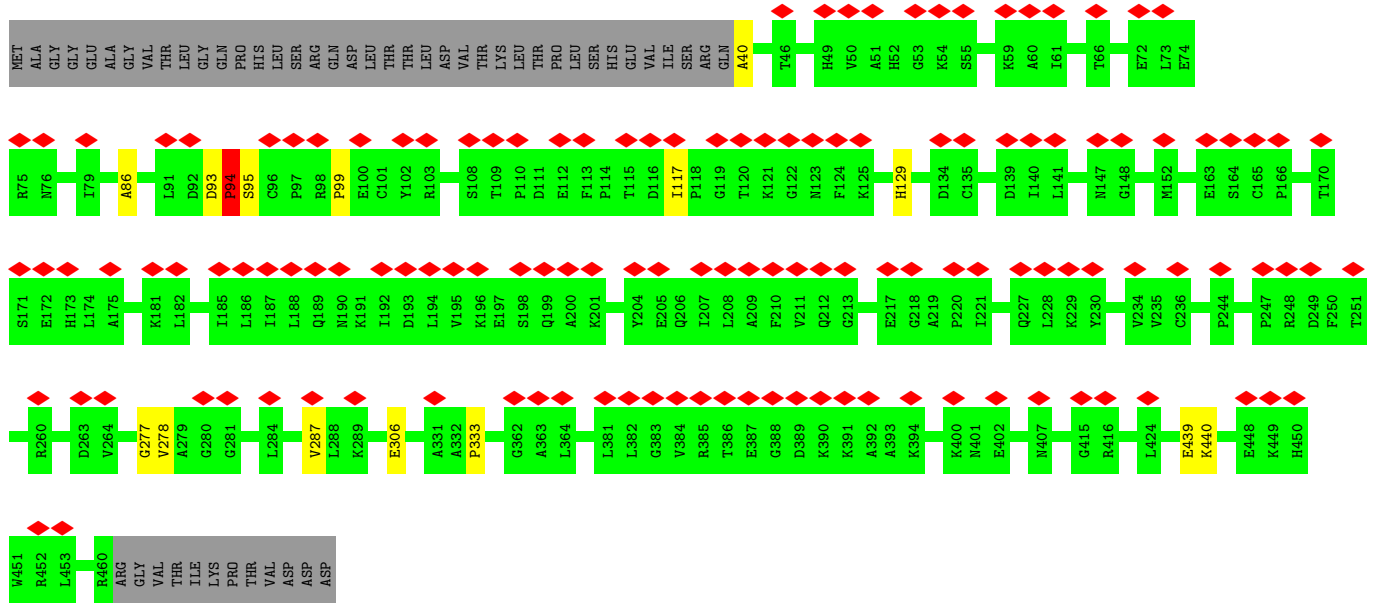
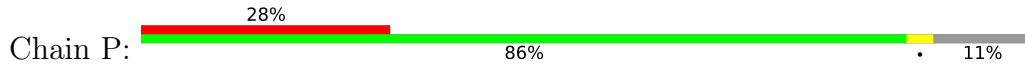
• Molecule 5: Translation initiation factor eIF-2B subunit epsilon





CYS  
GLU  
THR  
CYS  
HIS  
SER  
ARG  
CYS  
VAL  
VAL  
ALA  
SER  
ILE  
LYS  
THR  
GLY  
PHE  
GLN  
ALA  
VAL  
THR  
GLY  
LYS  
ARG  
ALA  
GLN  
LEU  
ARG  
ALA  
ALA  
ASN

• Molecule 8: Eukaryotic translation initiation factor 2 subunit 3



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	66721	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.102	Depositor
Minimum map value	-0.045	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0125	Depositor
Map size ( $\text{\AA}$ )	441.0, 441.0, 441.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.47, 1.47, 1.47	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: SEP

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	0.33	0/2296	0.67	2/3099 (0.1%)
1	B	0.34	0/2283	0.56	0/3081
2	C	0.34	0/2522	0.60	2/3411 (0.1%)
2	D	0.32	0/2587	0.60	0/3498
3	E	0.26	0/2472	0.63	0/3357
3	F	0.26	0/2464	0.59	0/3346
4	G	0.34	0/2802	0.61	0/3809
4	H	0.35	0/2802	0.61	2/3809 (0.1%)
5	I	0.32	0/3427	0.64	0/4662
5	J	0.31	0/3441	0.62	0/4682
6	K	0.22	0/1301	0.58	0/1812
6	L	0.18	0/879	0.52	0/1224
7	M	0.18	0/79	0.56	0/109
8	P	0.33	1/2129 (0.0%)	0.71	6/2973 (0.2%)
All	All	0.31	1/31484 (0.0%)	0.62	12/42872 (0.0%)

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
2	D	0	1
3	E	0	1
4	H	0	1
6	K	0	1
8	P	0	2
All	All	0	6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	P	94	PRO	CA-C	6.90	1.62	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	P	94	PRO	N-CA-C	7.20	127.30	112.47
8	P	439	GLU	N-CA-C	7.04	120.43	110.50
4	H	477	GLN	CA-C-N	6.93	131.78	120.63
4	H	477	GLN	C-N-CA	6.93	131.78	120.63
1	A	238	LEU	CA-C-N	-6.65	116.19	122.37

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	126	TYR	Peptide
3	E	290	TRP	Peptide
4	H	419	GLY	Peptide
6	K	223	MET	Peptide
8	P	94	PRO	Peptide

## 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	A	2262	0	2333	50	0
1	B	2249	0	2324	49	0
2	C	2476	0	2493	62	0
2	D	2538	0	2538	61	0
3	E	2438	0	2208	49	0
3	F	2430	0	2197	64	0
4	G	2750	0	2811	61	0
4	H	2750	0	2811	63	0
5	I	3358	0	3325	81	0
5	J	3371	0	3332	61	0
6	K	1309	0	612	5	0
6	L	889	0	402	1	0
7	M	80	0	31	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	P	2109	0	1073	4	0
All	All	31009	0	28490	572	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 28.

The worst 5 of 572 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)
3:F:156:ASP:HA	3:F:171:ALA:O	1.71	0.89
5:J:56:PHE:HB3	5:J:59:ILE:HB	1.55	0.88
3:F:57:ARG:NH2	3:F:64:CYS:SG	2.53	0.81
3:F:236:GLN:HA	3:F:261:LEU:HD21	1.62	0.81
5:I:216:GLN:HA	5:I:274:ARG:HH21	1.44	0.81

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	267/305 (88%)	219 (82%)	48 (18%)	0	100	100
1	B	271/305 (89%)	223 (82%)	48 (18%)	0	100	100
2	C	305/351 (87%)	261 (86%)	44 (14%)	0	100	100
2	D	293/351 (84%)	253 (86%)	40 (14%)	0	100	100
3	E	281/452 (62%)	211 (75%)	70 (25%)	0	100	100
3	F	333/452 (74%)	251 (75%)	82 (25%)	0	100	100
4	G	351/523 (67%)	300 (86%)	51 (14%)	0	100	100
4	H	351/523 (67%)	299 (85%)	51 (14%)	1 (0%)	36	71

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	I	425/721 (59%)	348 (82%)	77 (18%)	0	100	100
5	J	427/721 (59%)	346 (81%)	81 (19%)	0	100	100
6	K	255/315 (81%)	208 (82%)	46 (18%)	1 (0%)	30	66
6	L	173/315 (55%)	148 (86%)	25 (14%)	0	100	100
7	M	14/333 (4%)	13 (93%)	1 (7%)	0	100	100
8	P	419/472 (89%)	316 (75%)	101 (24%)	2 (0%)	24	62
All	All	4165/6139 (68%)	3396 (82%)	765 (18%)	4 (0%)	49	83

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	P	278	VAL
8	P	94	PRO
6	K	60	LYS
4	H	460	PRO

### 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](#)

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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
6	SEP	L	51	6	8,9,10	1.57	1 (12%)	7,12,14	1.55	1 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	SEP	K	51	6	8,9,10	1.62	1 (12%)	7,12,14	1.25	1 (14%)

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
6	SEP	L	51	6	-	6/6/8/10	-
6	SEP	K	51	6	-	2/6/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	K	51	SEP	P-O1P	3.54	1.61	1.50
6	L	51	SEP	P-O1P	3.39	1.61	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	L	51	SEP	OG-CB-CA	3.29	111.34	108.14
6	K	51	SEP	OG-CB-CA	2.54	110.62	108.14

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	K	51	SEP	CA-CB-OG-P
6	L	51	SEP	N-CA-CB-OG
6	L	51	SEP	C-CA-CB-OG
6	L	51	SEP	CA-CB-OG-P
6	L	51	SEP	CB-OG-P-O2P

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

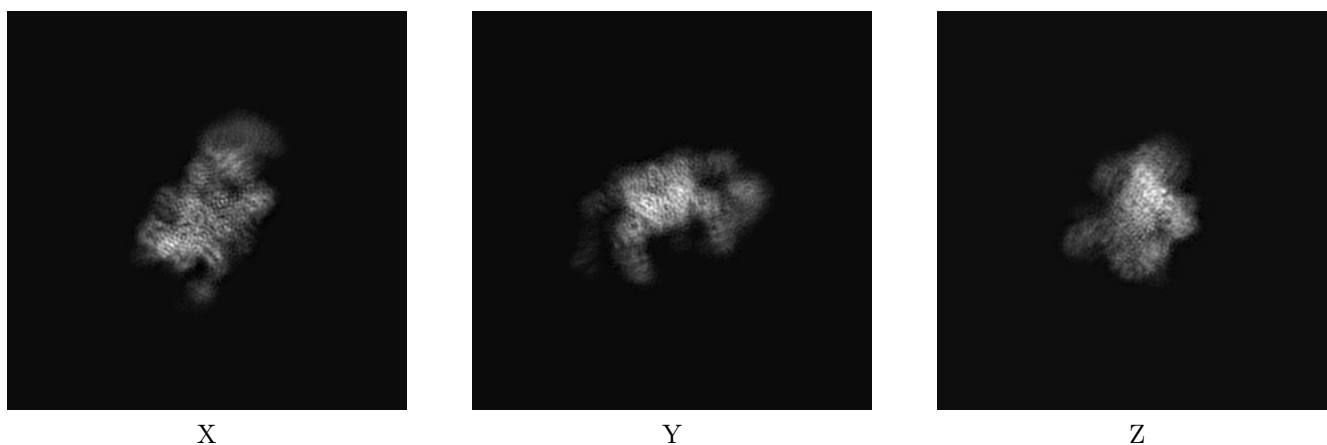
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30568. 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](#)

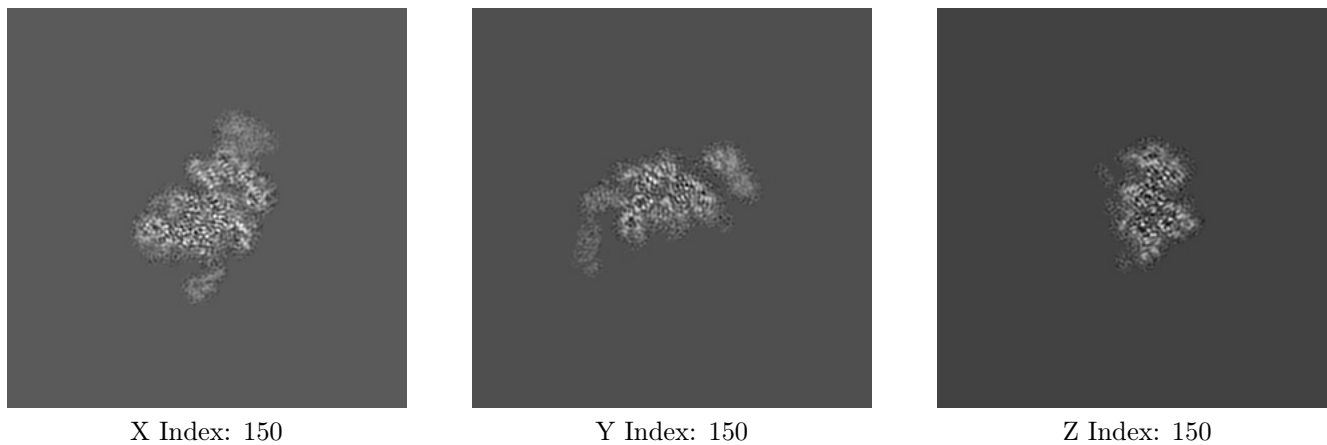
#### 6.1.1 Primary map



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

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

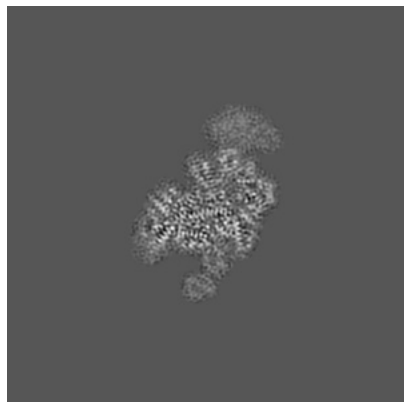
#### 6.2.1 Primary map



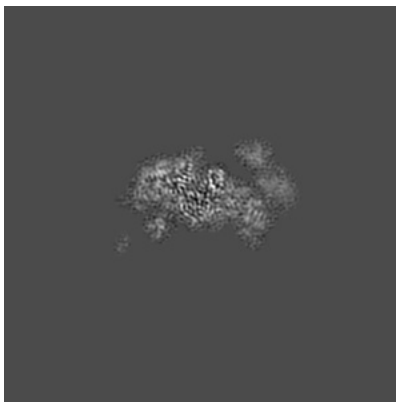
The images above show central slices of the map in three orthogonal directions.

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

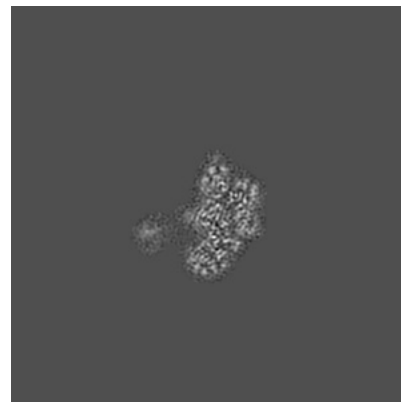
### 6.3.1 Primary map



X Index: 155



Y Index: 158

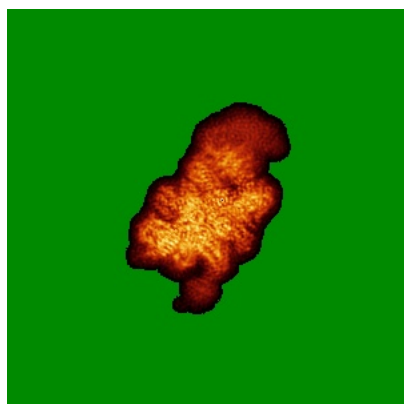


Z Index: 134

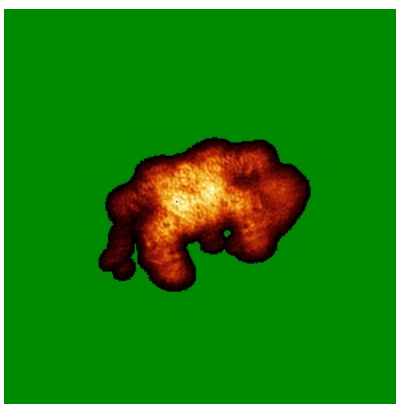
The images above show the largest variance slices of the map in three orthogonal directions.

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

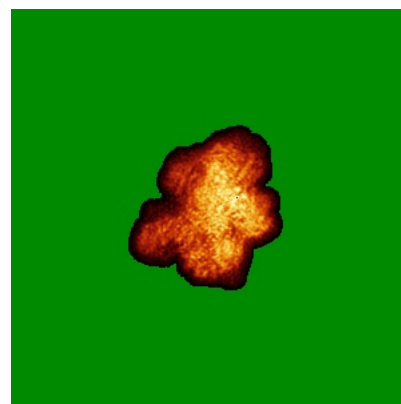
### 6.4.1 Primary map



X



Y

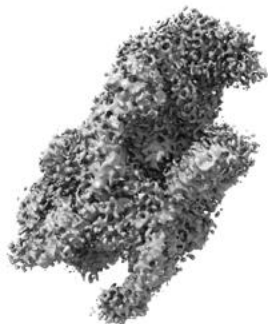


Z

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

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

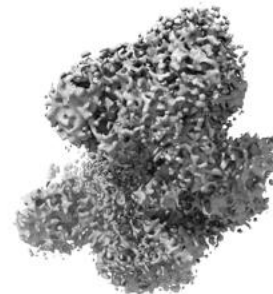
### 6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0125. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

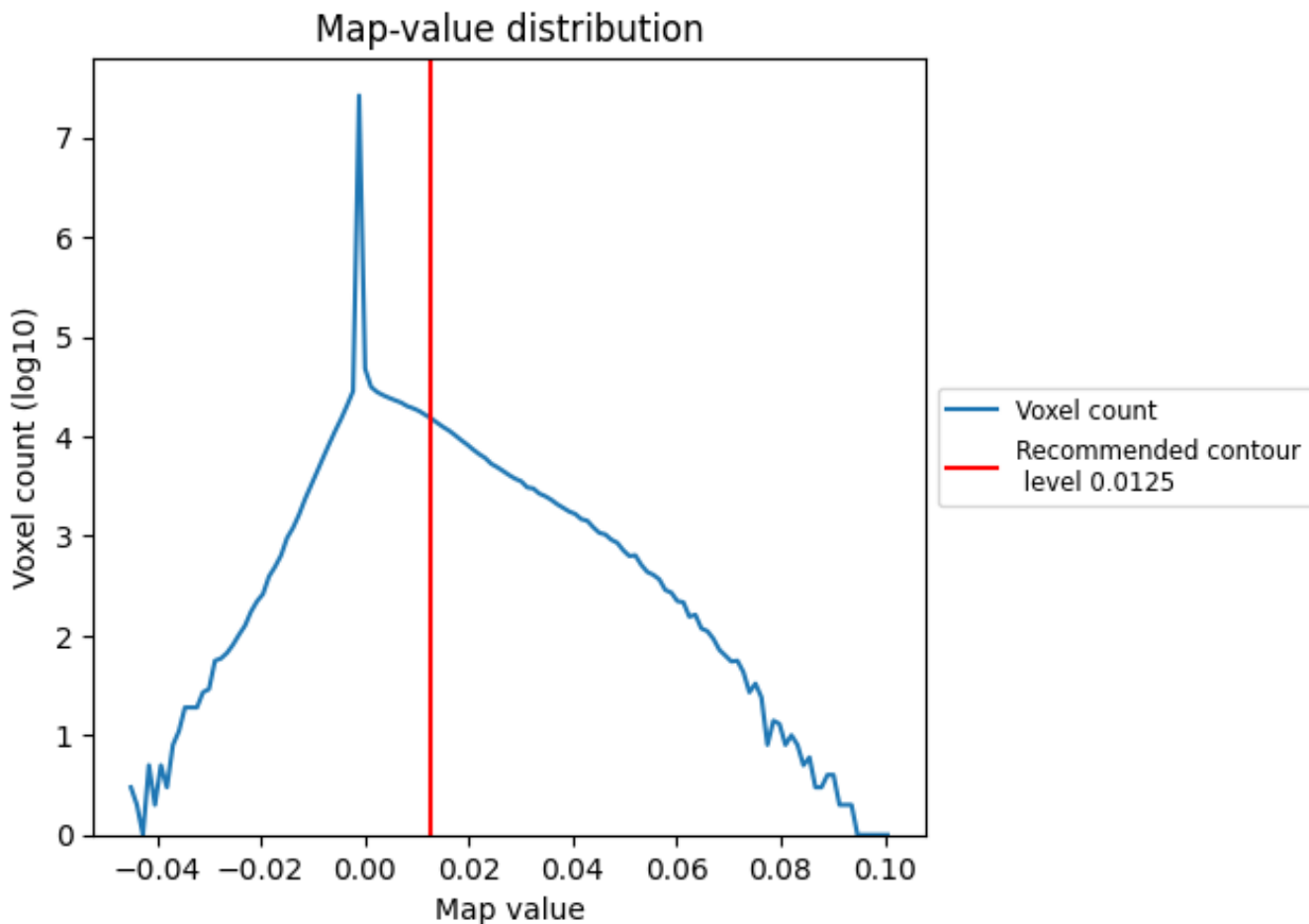
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

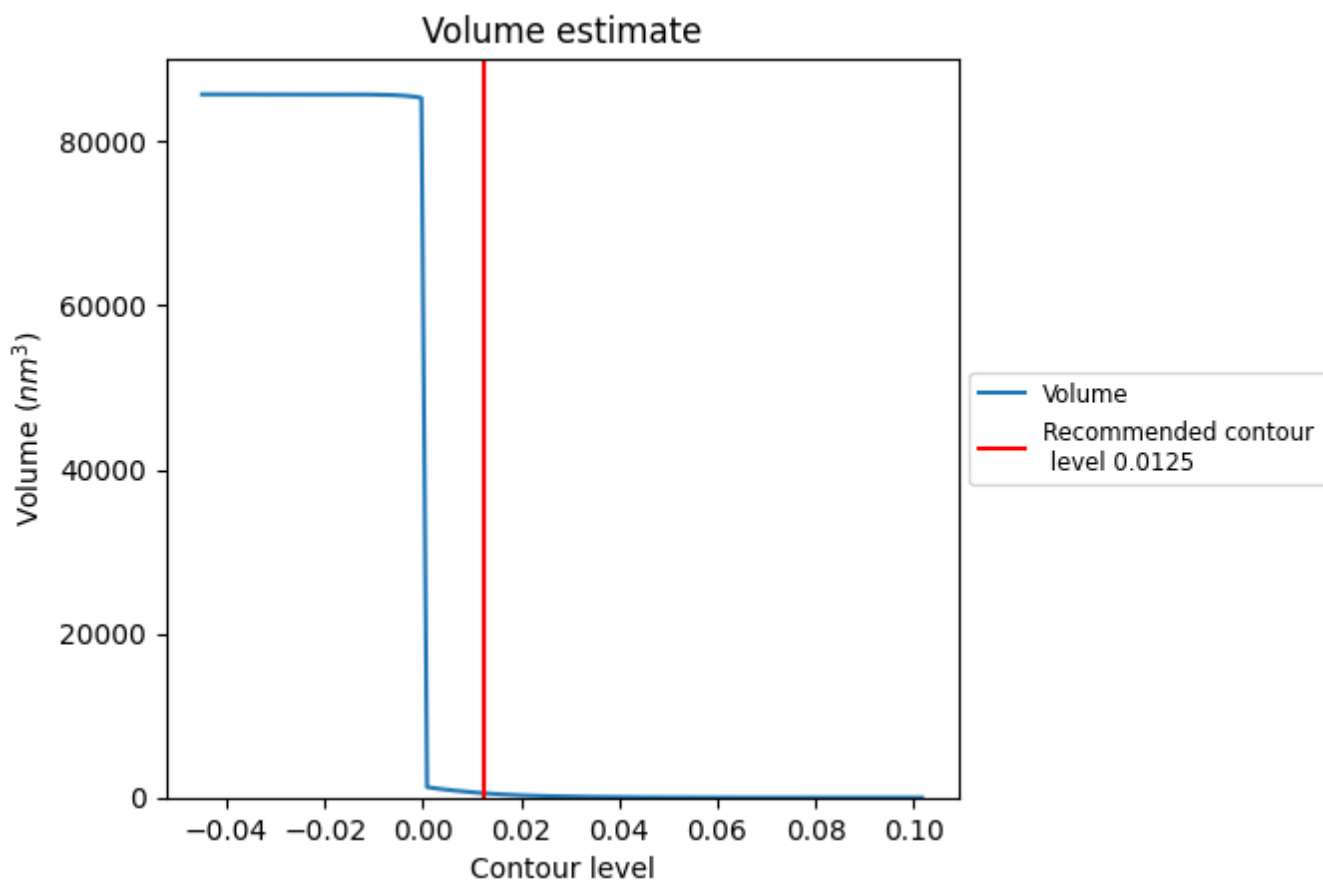
This section contains the results of statistical analysis of the map.

### 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.

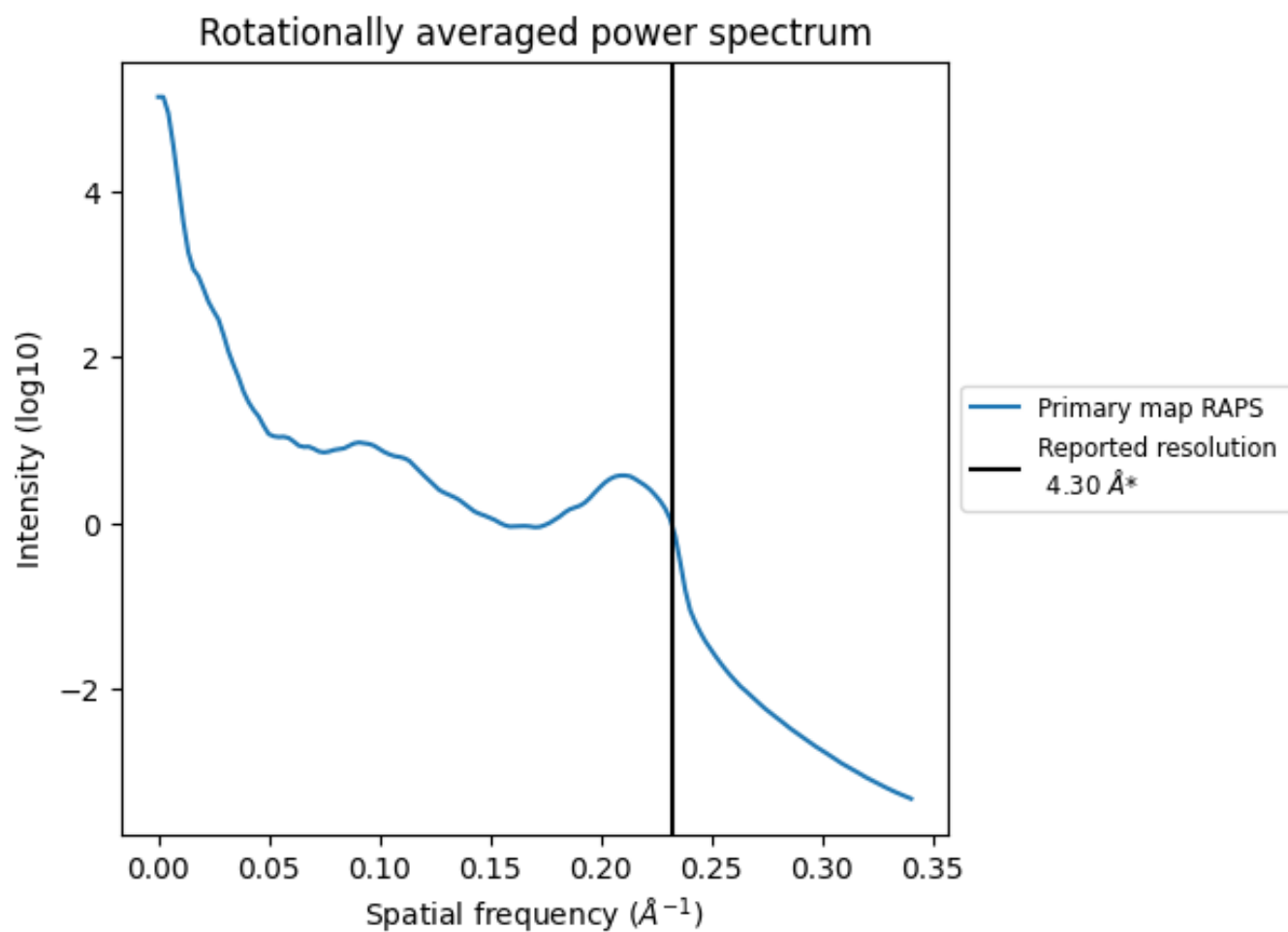
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 525 nm<sup>3</sup>; this corresponds to an approximate mass of 475 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  $0.233 \text{\AA}^{-1}$

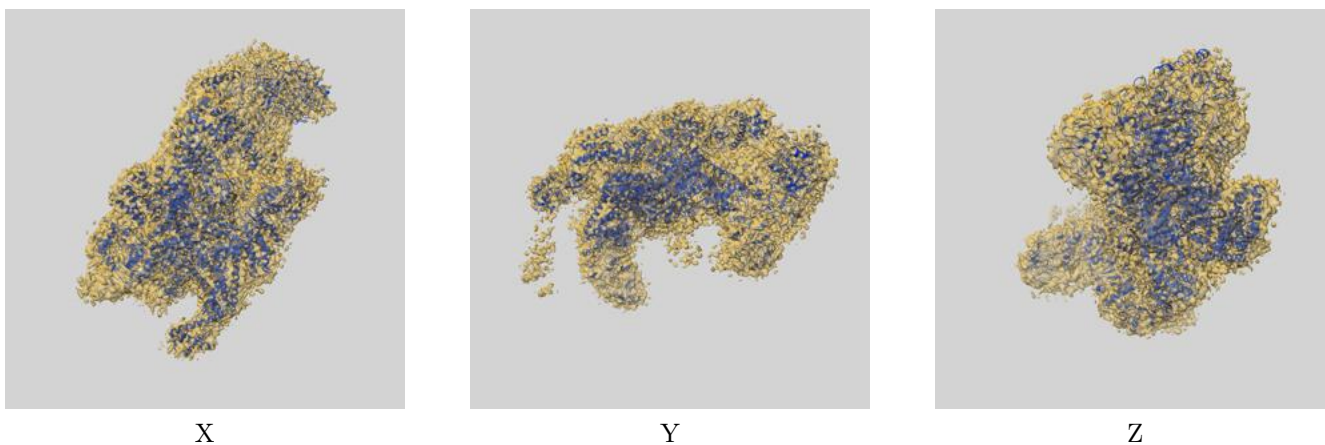
## 8 Fourier-Shell correlation

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

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

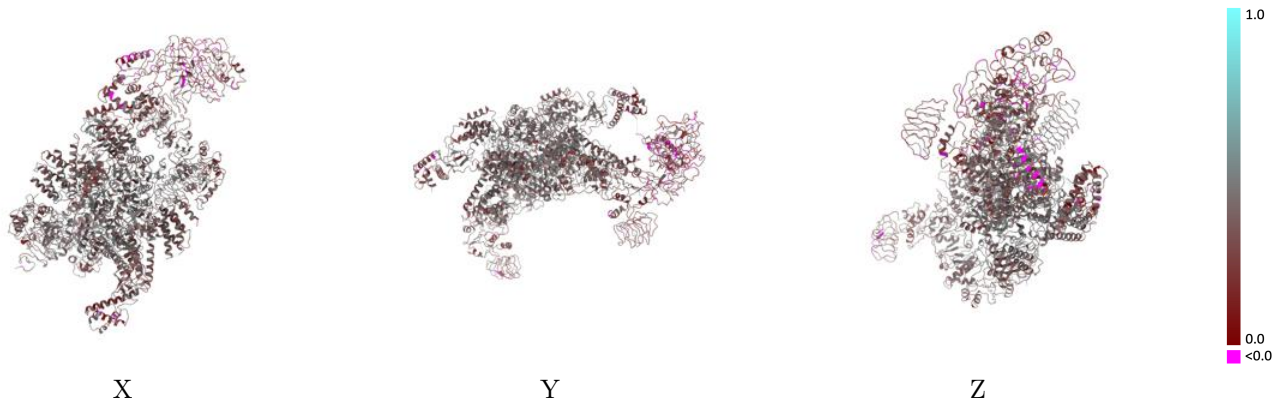
This section contains information regarding the fit between EMDB map EMD-30568 and PDB model 7D43. Per-residue inclusion information can be found in section 3 on page 6.

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



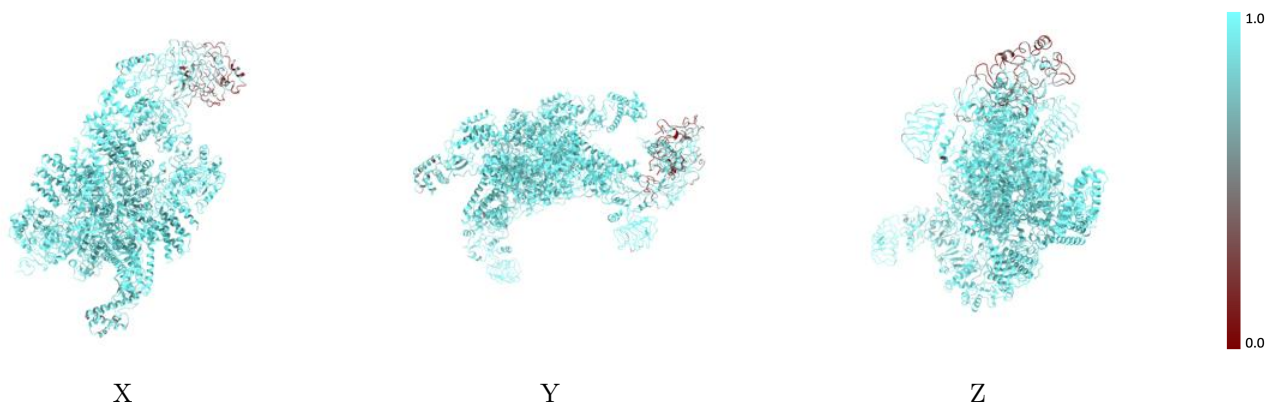
The images above show the 3D surface view of the map at the recommended contour level 0.0125 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



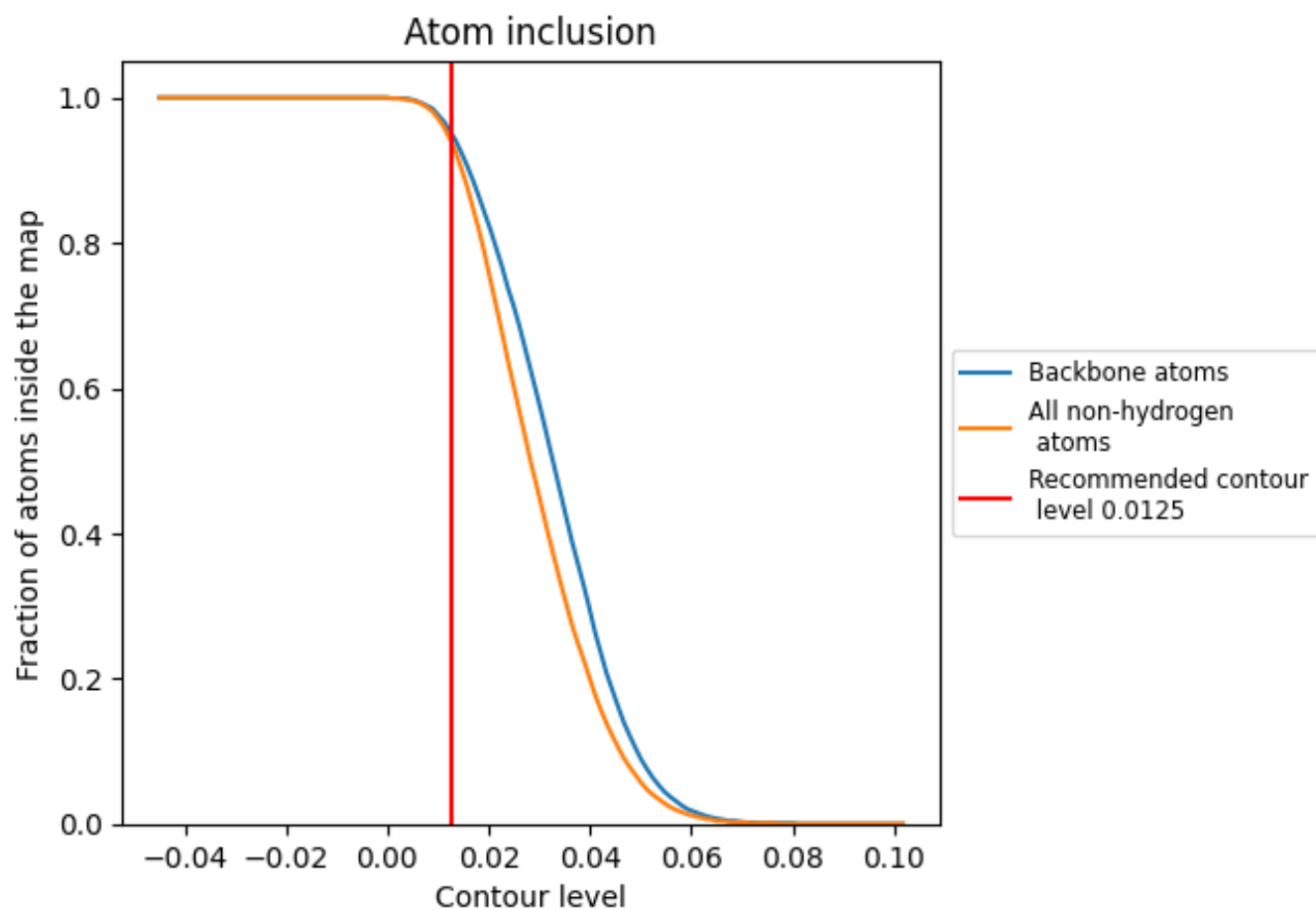
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0125).































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 94% 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 (0.0125) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9410	 0.3850
A	 0.9750	 0.4160
B	 0.9770	 0.4110
C	 0.9680	 0.4230
D	 0.9690	 0.4250
E	 0.9540	 0.3370
F	 0.9600	 0.3340
G	 0.9650	 0.4100
H	 0.9660	 0.4230
I	 0.9640	 0.4030
J	 0.9750	 0.4030
K	 0.9680	 0.3230
L	 0.8570	 0.3500
M	 0.3750	 0.3070
P	 0.6540	 0.2620

