



## wwPDB EM Validation Summary Report ⓘ

Feb 27, 2025 – 05:13 PM JST

PDB ID : 8YGC  
EMDB ID : EMD-39243  
Title : The Dimer Structure of DSR2-SPR  
Authors : Gao, X.; Zhu, H.; Cui, S.  
Deposited on : 2024-02-26  
Resolution : 4.03 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.dev117  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.41.2

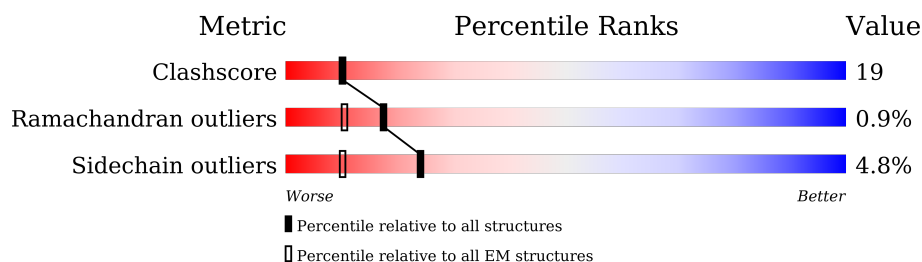
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.03 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	1005	<div> <div>14%</div> <div>67%</div> <div>27%</div> <div>• •</div> </div>
1	B	1005	<div> <div>20%</div> <div>65%</div> <div>31%</div> <div>• •</div> </div>
1	E	1005	<div> <div>25%</div> <div>22%</div> <div>5%</div> <div>72%</div> </div>
1	F	1005	<div> <div>24%</div> <div>18%</div> <div>9%</div> <div>73%</div> </div>
2	C	264	<div> <div>27%</div> <div>27%</div> <div>25%</div> <div>•</div> <div>43%</div> </div>
2	D	264	<div> <div>27%</div> <div>27%</div> <div>26%</div> <div>•</div> <div>43%</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 23242 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 SIR2-like domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	983	Total	C	N	O	S	0	0
			8183	5292	1322	1538	31		
1	B	983	Total	C	N	O	S	0	0
			8183	5292	1322	1538	31		
1	E	277	Total	C	N	O	S	0	0
			2260	1455	367	430	8		
1	F	272	Total	C	N	O	S	0	0
			2220	1432	360	421	7		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	171	ALA	HIS	engineered mutation	UNP D4G637
B	171	ALA	HIS	engineered mutation	UNP D4G637
E	171	ALA	HIS	engineered mutation	UNP D4G637
F	171	ALA	HIS	engineered mutation	UNP D4G637

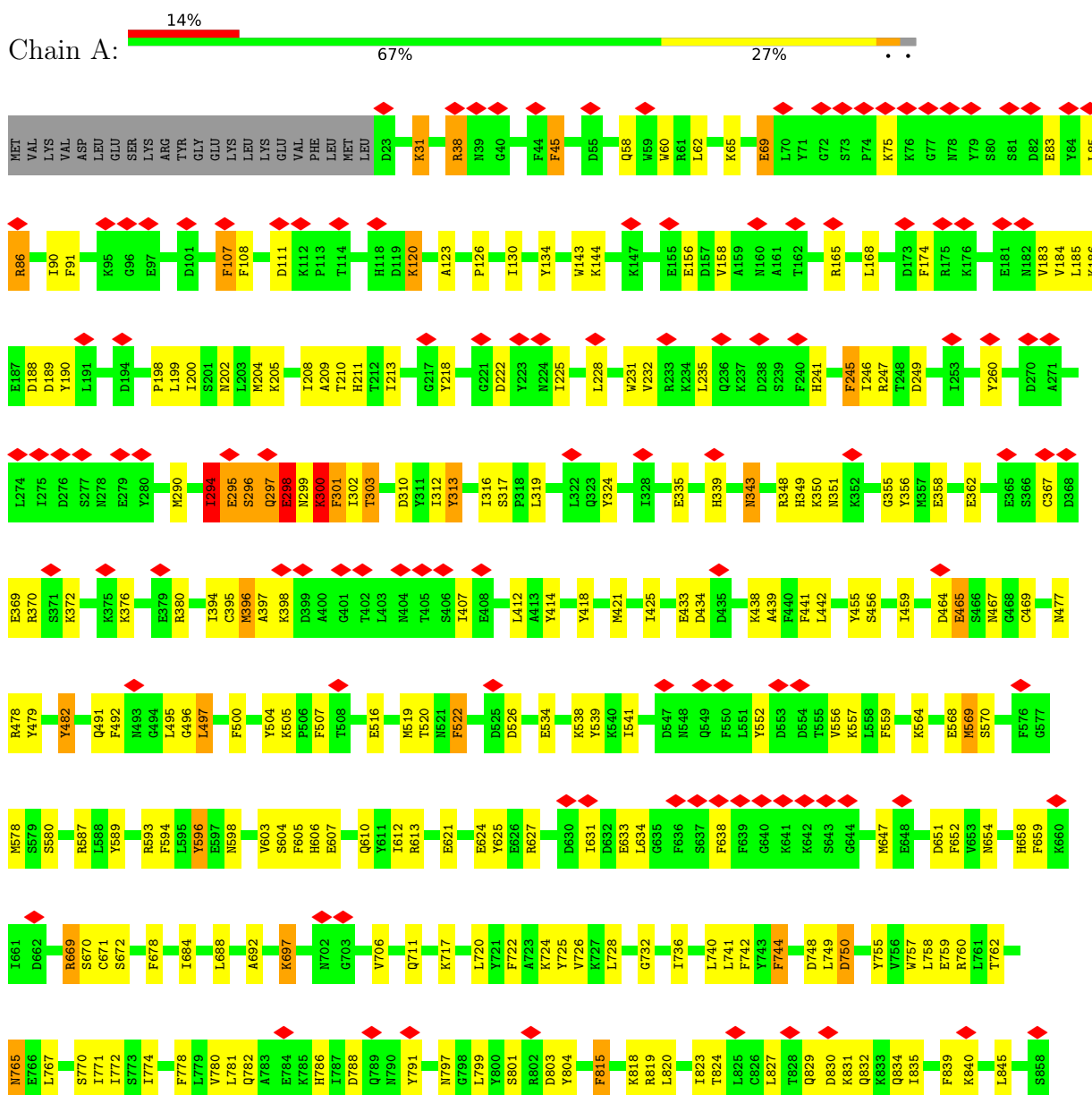
- Molecule 2 is a protein called SPR.

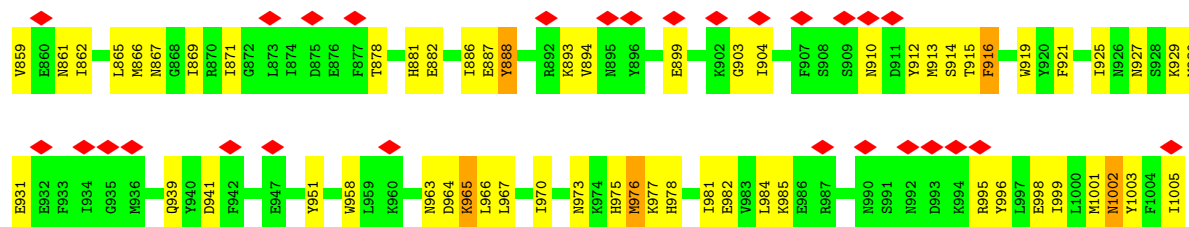
Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	151	Total	C	N	O	S	0	0
			1198	758	189	247	4		
2	D	151	Total	C	N	O	S	0	0
			1198	758	189	247	4		

### 3 Residue-property plots

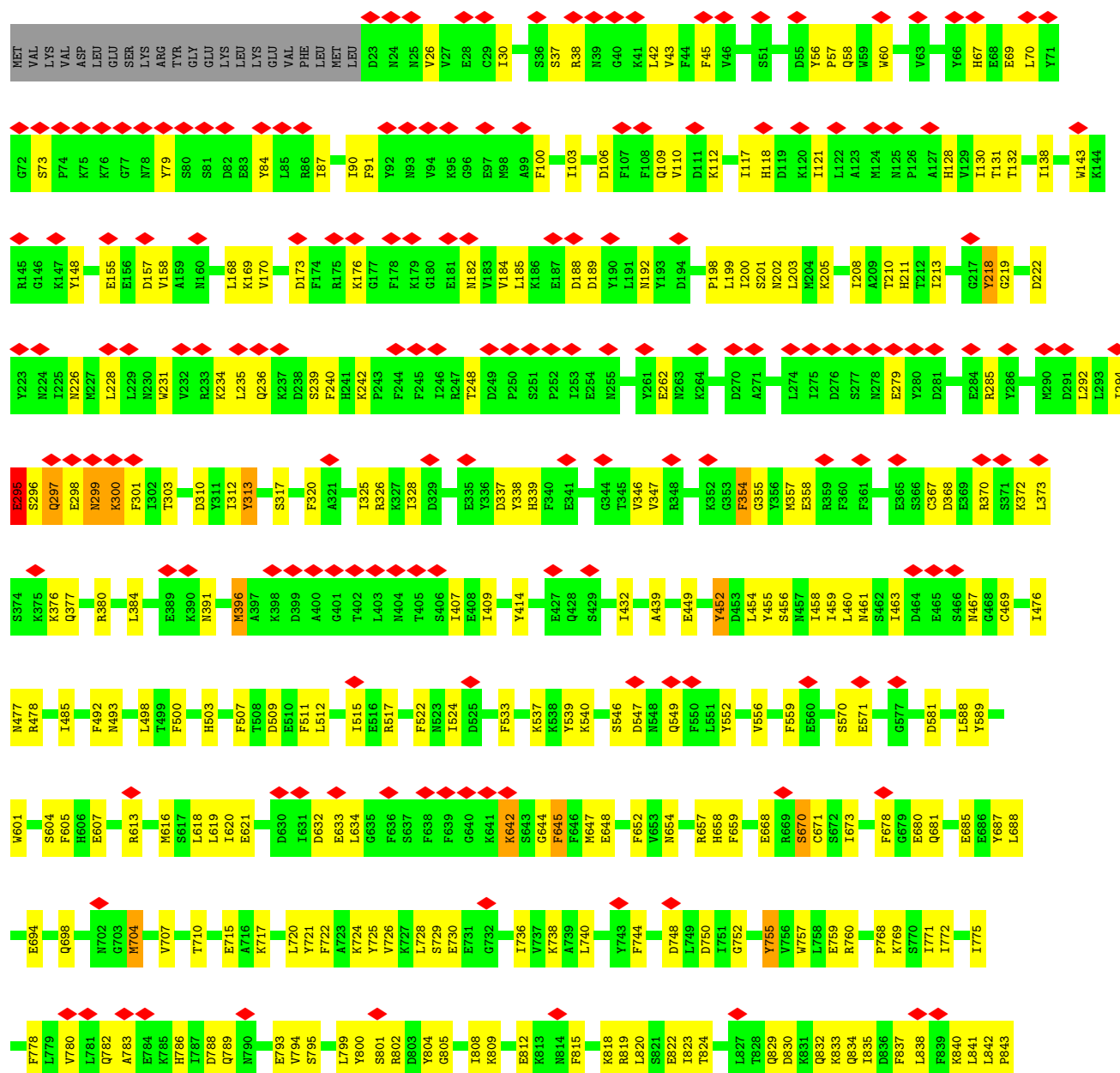
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

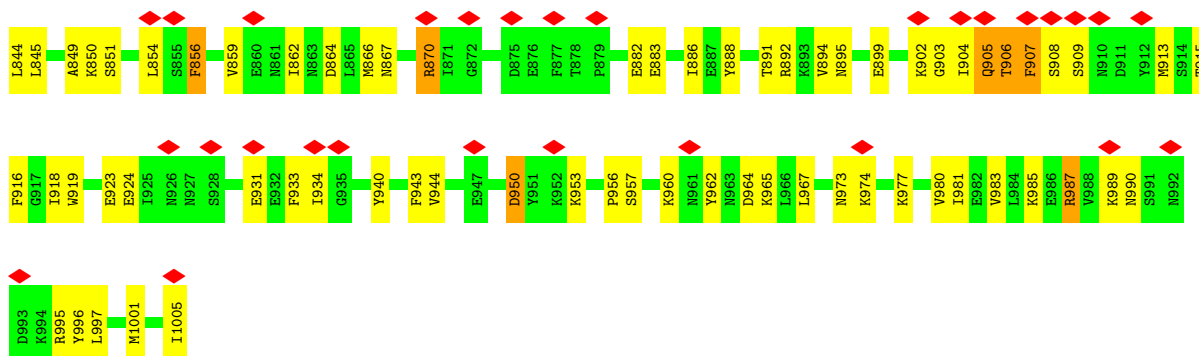
- Molecule 1: SIR2-like domain-containing protein



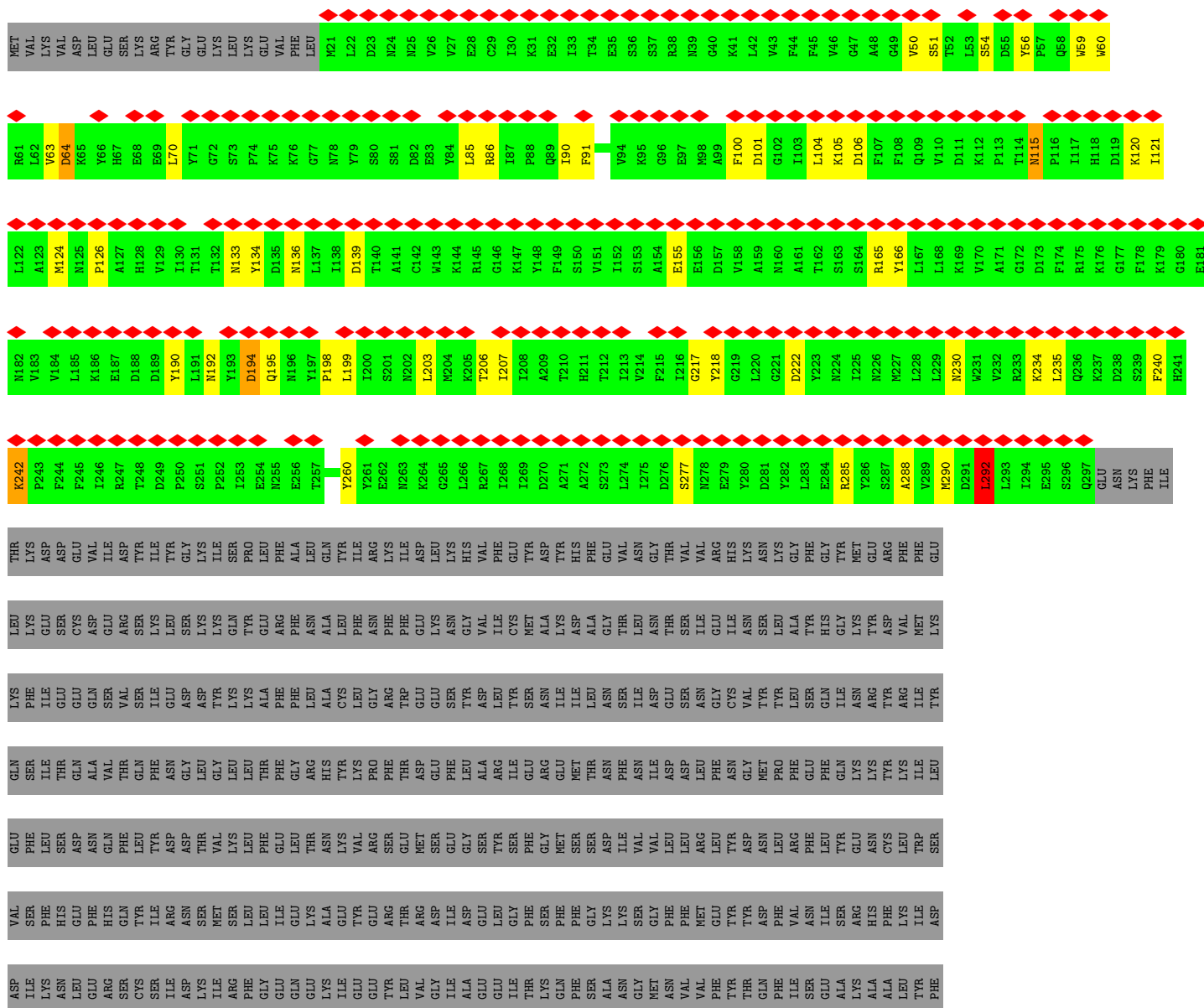


• Molecule 1: SIR2-like domain-containing protein

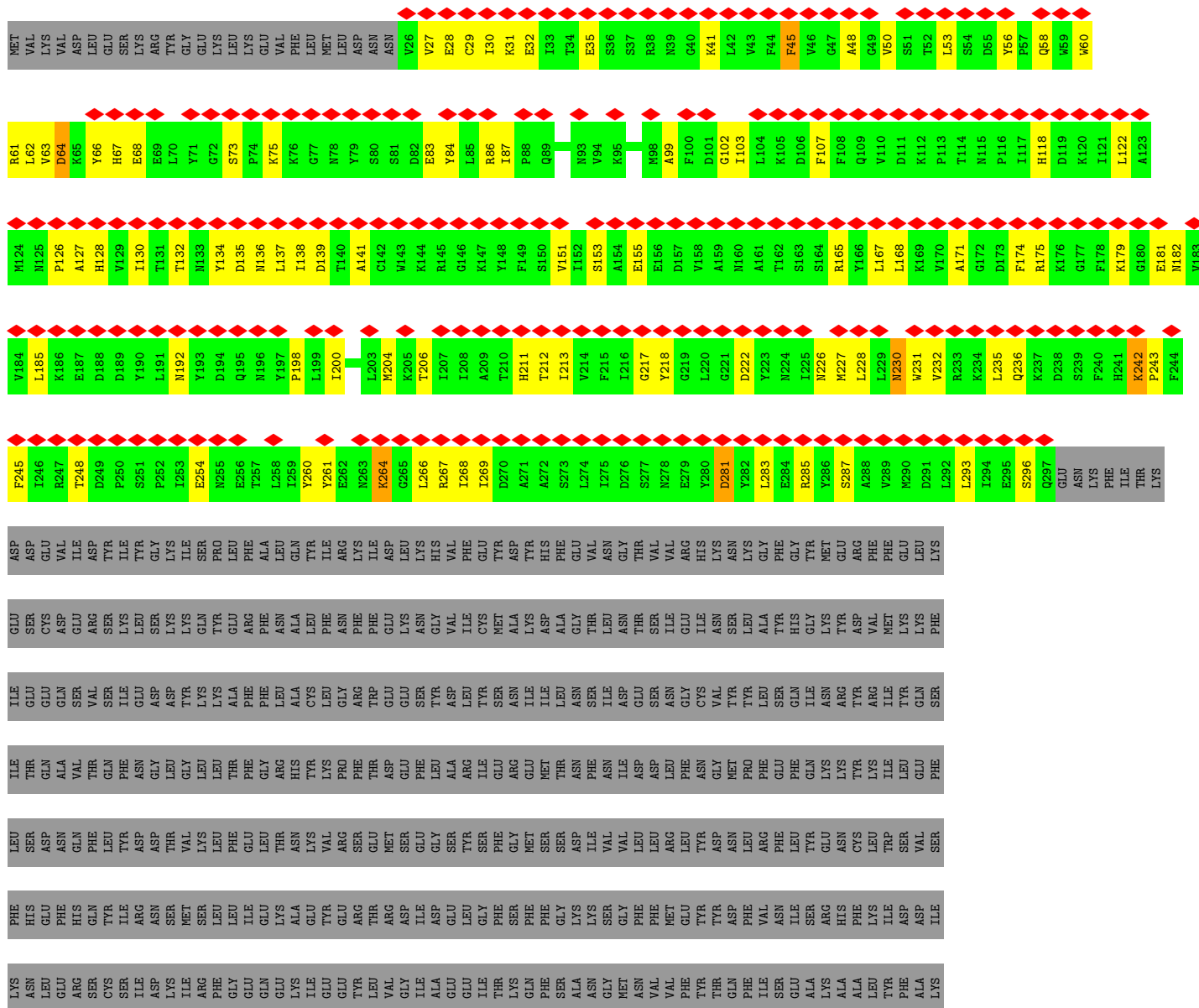




● Molecule 1: SIR2-like domain-containing protein

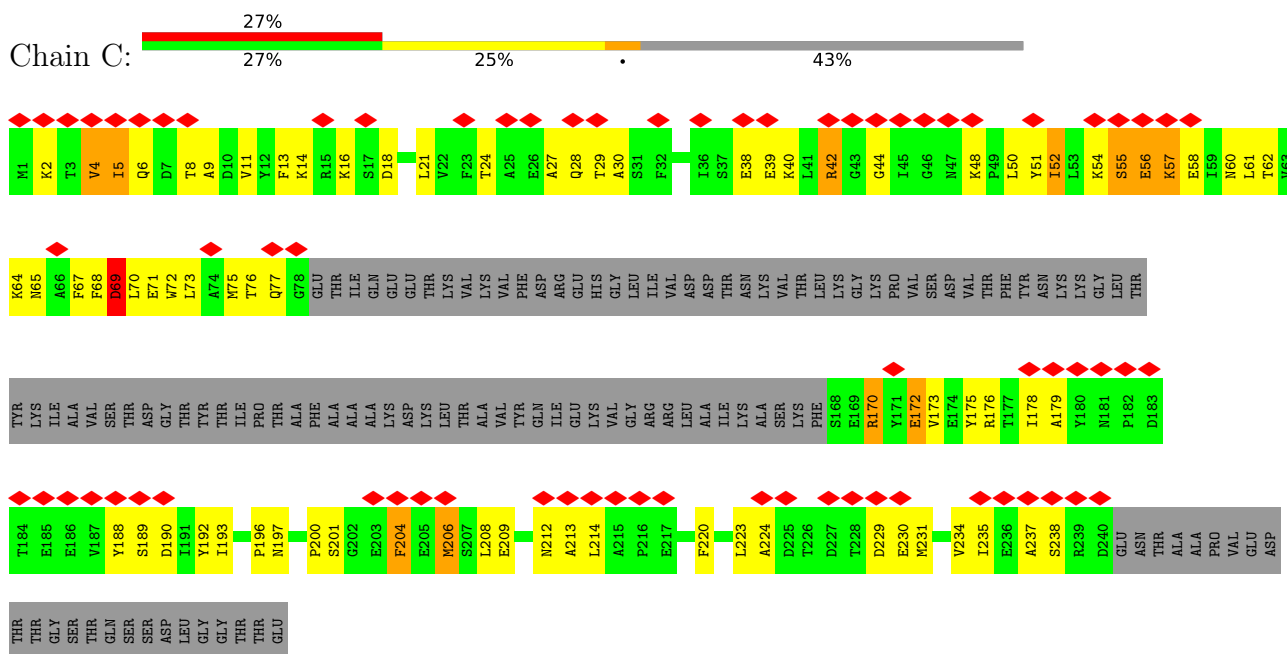


- Molecule 1: SIR2-like domain-containing protein

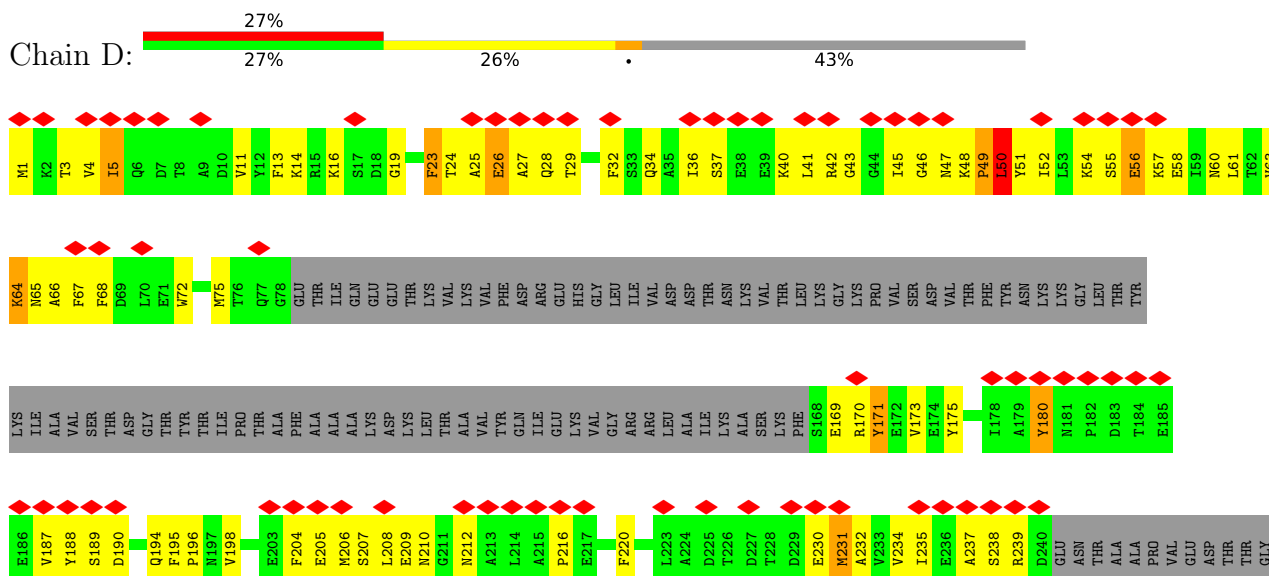


LYS	LEU	THR	GLN	LEU	LYS	THR	VAL	TYR
LEU	LEU	THR	THR	SER	HIS	THR	VAL	VAL
GLY	GLY	SER	SER	ASN	ASP	ASN	ASP	LEU
ILE	ILE	ASN	ASN	LYS	GLN	ASN	GLU	GLU
ALA	ASP	ASP	ASP	SER	TYR	TYR	TYR	GLY
GLY	TYR	TYR	ASP	HIS	SER	SER	GLY	GLY
ASN	ASN	MET	MET	LEU	GLU	VAL	VAL	GLY
HIS	HIS	THR	THR	SER	SER	LYS	LYS	GLY
HIS	HIS	THR	THR	PHE	SER	ASN	VAL	LYS
VAL	VAL	TYR	TYR	GLU	TYR	TYR	ALA	ALA
LEU	LEU	ILE	ILE	ASN	ASP	ASP	GLU	GLU
GLU	GLU	LEU	LEU	ILE	ARG	ILE	ARG	ASP
VAL	VAL	GLU	GLU	ASN	ASP	ASN	LEU	LEU
LYS	LYS	LYS	LYS	ILE	LYS	LYS	LYS	LEU
ASN	ASN	MET	MET	ARG	HIS	PHE	ASP	ASP
SER	SER	GLU	GLU	ILE	ILE	GLY	GLY	GLY
GLY	GLY	ASN	ASN	MET	ASN	ASP	ASP	LYS
VAL	VAL	SER	SER	GLY	ILE	ILE	ASN	ARG
LYS	LYS	LYS	LYS	ILE	ILE	ASP	PHE	TYR
ARG	ARG	GLY	GLY	ASP	GLY	VAL	VAL	VAL
LEU	LEU	ASP	ASP	PHE	ILE	THR	THR	LEU
MET	MET	THR	THR	GLU	SER	PRO	GLU	ARG
ASN	ASN	PHE	PHE	GLU	LEU	GLU	LEU	LEU
TYR	TYR	PHE	PHE	GLU	ILE	THR	THR	THR
PHE	PHE	VAL	VAL	ASP	LEU	THR	CYS	CYS
ILE	ILE	PRO	PRO	ILE	LEU	ASN	ASN	GLU
		GLU	GLU	ILE	LEU	CYS	GLU	GLU
		ASN	ASN	GLU	LEU	THR	PHO	PHO
		PHE	PHE	LEU	GLN	LYS	LYS	LYS
		ASP	ASP	GLU	ASP	SER	SER	SER
		PRO	PRO	TYR	LYS	ILE	ILE	ILE
		TYR	TYR	ARG	GLN	ILE	ILE	ILE
		LYS	LYS	LYS	LYS	SER	SER	SER
		PHE	PHE	VAL	GLN	ILE	ILE	ILE
		ILE	ILE	THR	THR	ASP	ASP	ASP
		VAL	VAL	ILE	PHE	PHE	ASP	PHE
		TRP	TRP	VAL	LEU	LEU	PHE	PHE
		LEU	LEU	GLU	PHE	PHE	LEU	LEU
		LYS	LYS	LYS	LYS	VAL	VAL	VAL
		ASN	ASN	GLU	LEU	LEU	LEU	LEU
		TYR	TYR	LYS	GLN	GLN	GLN	GLN
		ASP	ASP	GLY	PRO	PRO	GLU	GLU
		THR	THR	ILE	THR	THR	ALA	ALA

- Molecule 2: SPR



- Molecule 2: SPR





SER  
THR  
GLN  
SER  
SER  
ASP  
LEU  
GLY  
GLY  
THR  
THR  
GLU

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	23242	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	66	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.312	Depositor
Minimum map value	-0.155	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.1	Depositor
Map size ( $\text{\AA}$ )	381.8, 381.8, 381.8	wwPDB
Map dimensions	460, 460, 460	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.83, 0.83, 0.83	Depositor

## 5 Model quality [i](#)

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.45	0/8374	0.54	1/11280 (0.0%)
1	B	0.43	0/8374	0.53	0/11280
1	E	0.26	0/2314	0.47	1/3136 (0.0%)
1	F	0.30	0/2274	0.52	0/3082
2	C	0.33	0/1218	0.63	0/1645
2	D	0.34	0/1218	0.66	1/1645 (0.1%)
All	All	0.40	0/23772	0.54	3/32068 (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
1	A	0	1
2	C	0	1
2	D	0	2
All	All	0	4

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	50	LEU	CA-CB-CG	7.37	132.24	115.30
1	A	396	MET	CA-CB-CG	5.95	123.42	113.30
1	E	292	LEU	CA-CB-CG	5.92	128.90	115.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	297	GLN	Peptide

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Mol	Chain	Res	Type	Group
2	C	69	ASP	Peptide
2	D	3	THR	Peptide
2	D	64	LYS	Peptide

## 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	8183	0	8009	327	0
1	B	8183	0	8010	322	0
1	E	2260	0	2209	34	0
1	F	2220	0	2173	87	0
2	C	1198	0	1159	83	0
2	D	1198	0	1159	90	0
All	All	23242	0	22719	867	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 19.

The worst 5 of 867 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:965:LYS:NZ	2:D:51:TYR:CZ	1.83	1.45
1:A:965:LYS:NZ	2:D:51:TYR:CE1	1.67	1.41
1:A:965:LYS:CE	2:D:51:TYR:CE1	2.11	1.31
2:D:50:LEU:O	2:D:51:TYR:HD1	1.15	1.28
1:A:866:MET:CE	1:A:912:TYR:CE2	2.25	1.20

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	981/1005 (98%)	918 (94%)	54 (6%)	9 (1%)	14	49
1	B	981/1005 (98%)	921 (94%)	55 (6%)	5 (0%)	25	61
1	E	275/1005 (27%)	267 (97%)	8 (3%)	0	100	100
1	F	270/1005 (27%)	258 (96%)	12 (4%)	0	100	100
2	C	147/264 (56%)	105 (71%)	36 (24%)	6 (4%)	2	21
2	D	147/264 (56%)	105 (71%)	36 (24%)	6 (4%)	2	21
All	All	2801/4548 (62%)	2574 (92%)	201 (7%)	26 (1%)	17	49

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	296	SER
1	A	298	GLU
1	A	303	THR
1	B	905	GLN
1	B	906	THR

### 5.3.2 Protein sidechains ⓘ

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	901/922 (98%)	850 (94%)	51 (6%)	17	41
1	B	901/922 (98%)	871 (97%)	30 (3%)	33	55
1	E	249/922 (27%)	239 (96%)	10 (4%)	27	49
1	F	244/922 (26%)	230 (94%)	14 (6%)	17	41
2	C	130/225 (58%)	121 (93%)	9 (7%)	13	35
2	D	130/225 (58%)	122 (94%)	8 (6%)	15	38
All	All	2555/4138 (62%)	2433 (95%)	122 (5%)	24	45

5 of 122 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	300	LYS
1	F	64	ASP
1	B	748	ASP
1	F	56	TYR
1	F	230	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	226	ASN
1	B	867	ASN
2	D	60	ASN
1	A	339	HIS
1	A	93	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates [i](#)

There are no 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 ⓘ

There are no chain breaks in this entry.

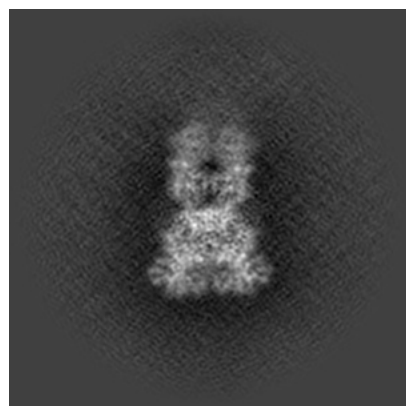
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39243. These allow visual inspection of the internal detail of the map and identification of artifacts.

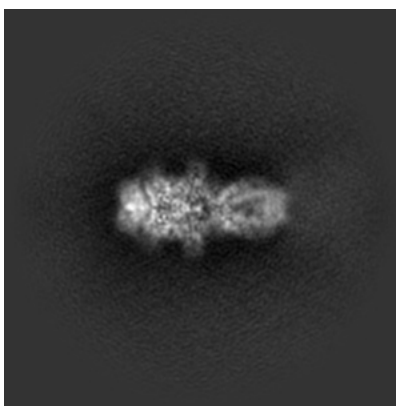
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

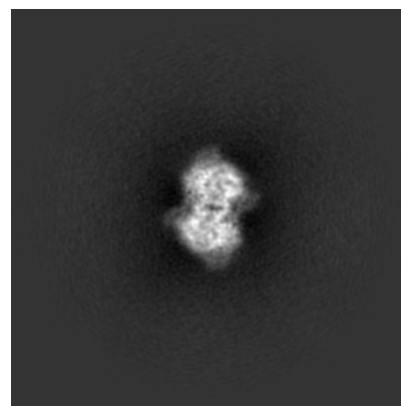
#### 6.1.1 Primary map



X

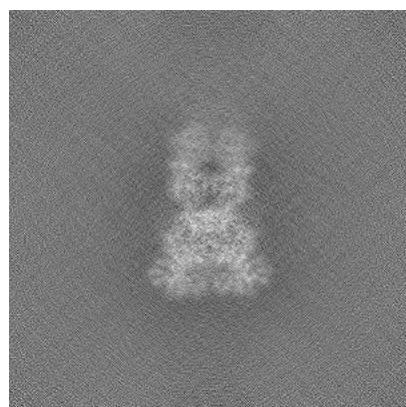


Y

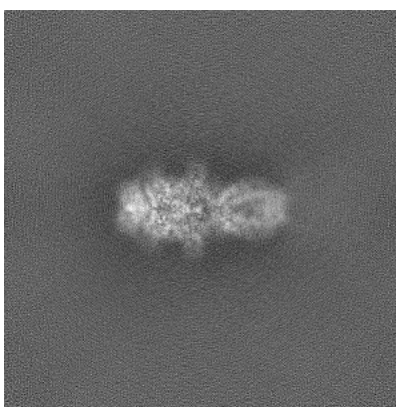


Z

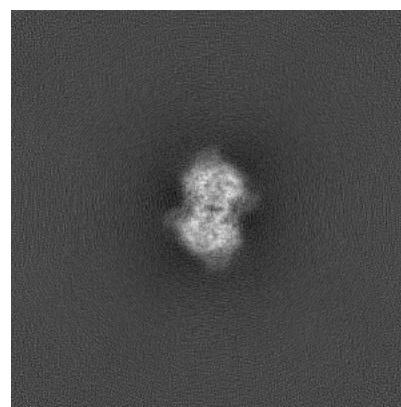
#### 6.1.2 Raw map



X



Y



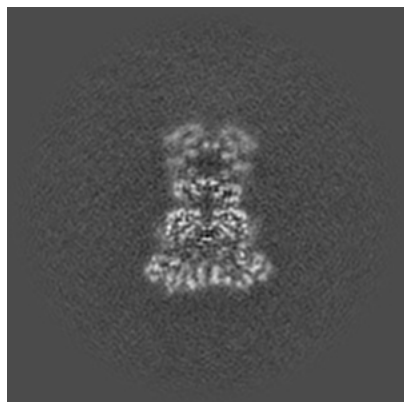
Z

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

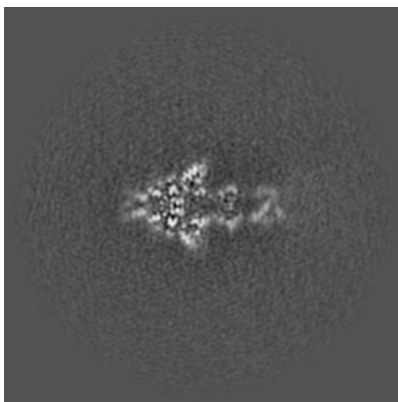


## 6.2 Central slices [i](#)

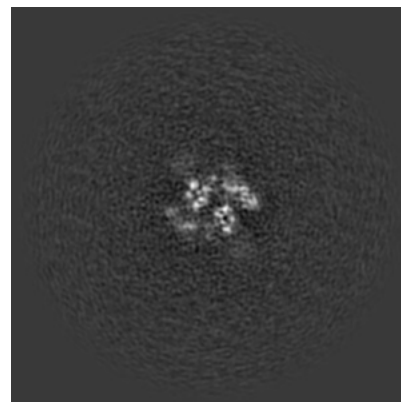
### 6.2.1 Primary map



X Index: 230

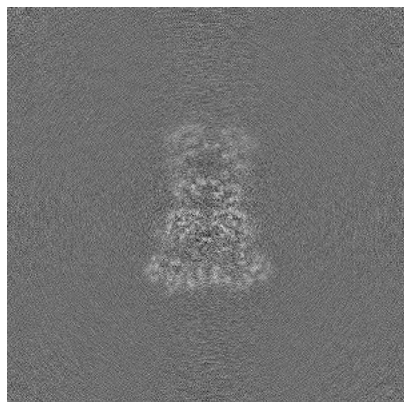


Y Index: 230

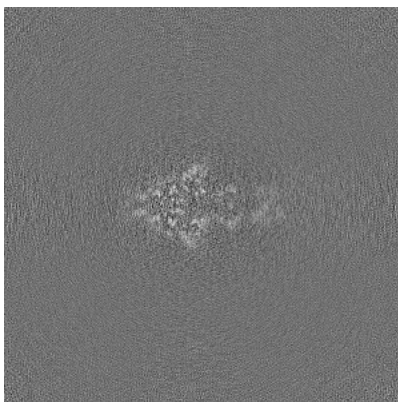


Z Index: 230

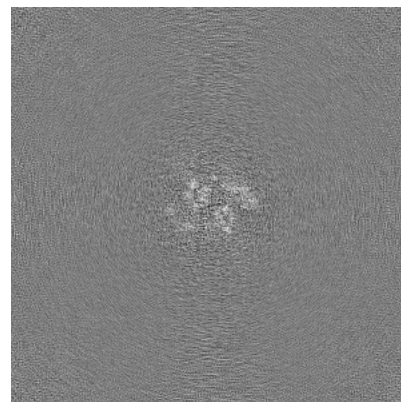
### 6.2.2 Raw map



X Index: 230



Y Index: 230

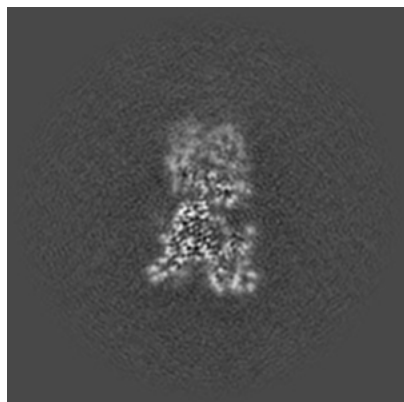


Z Index: 230

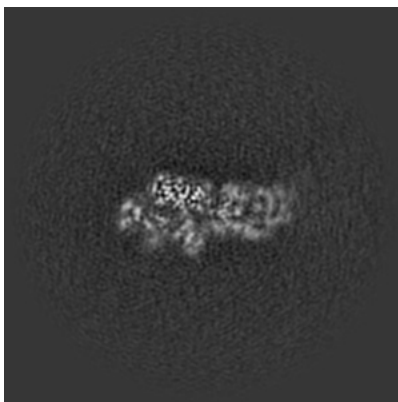
The images above show central slices of the map in three orthogonal directions.

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

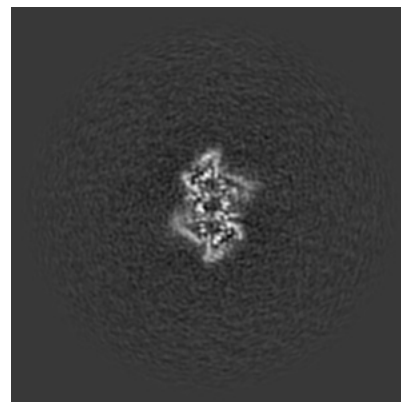
### 6.3.1 Primary map



X Index: 245

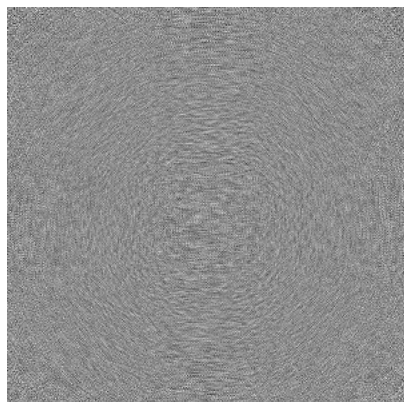


Y Index: 211

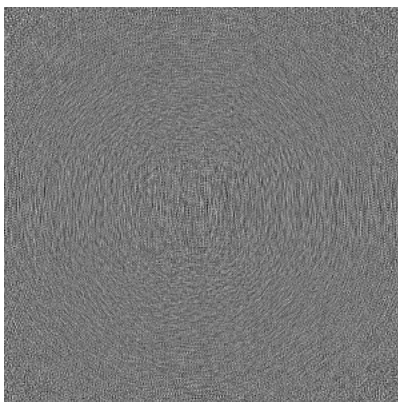


Z Index: 172

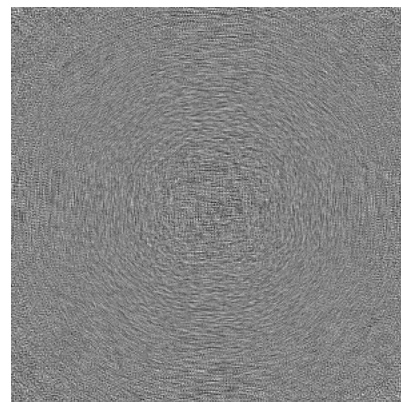
### 6.3.2 Raw map



X Index: 0



Y Index: 0

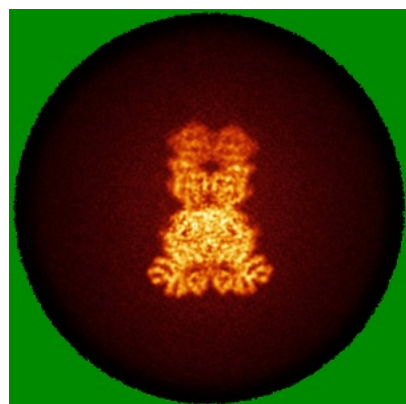


Z Index: 0

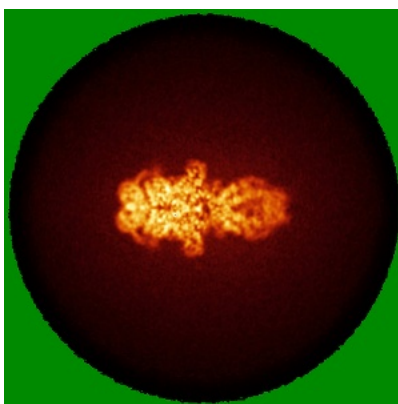
The images above show the largest variance slices of the map in three orthogonal directions.

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

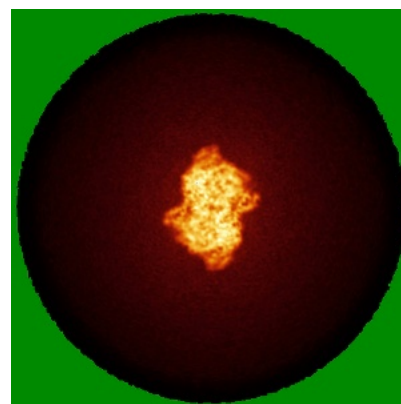
### 6.4.1 Primary map



X

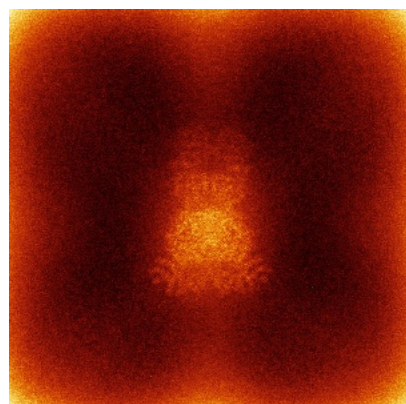


Y

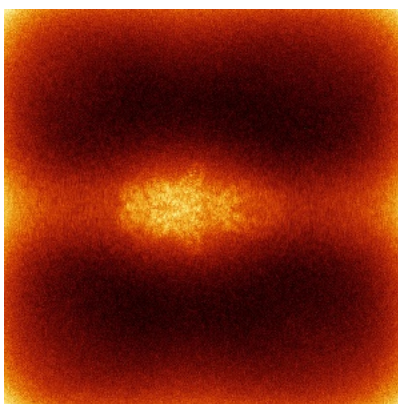


Z

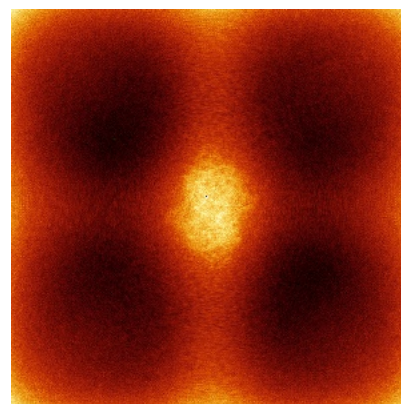
### 6.4.2 Raw map



X



Y

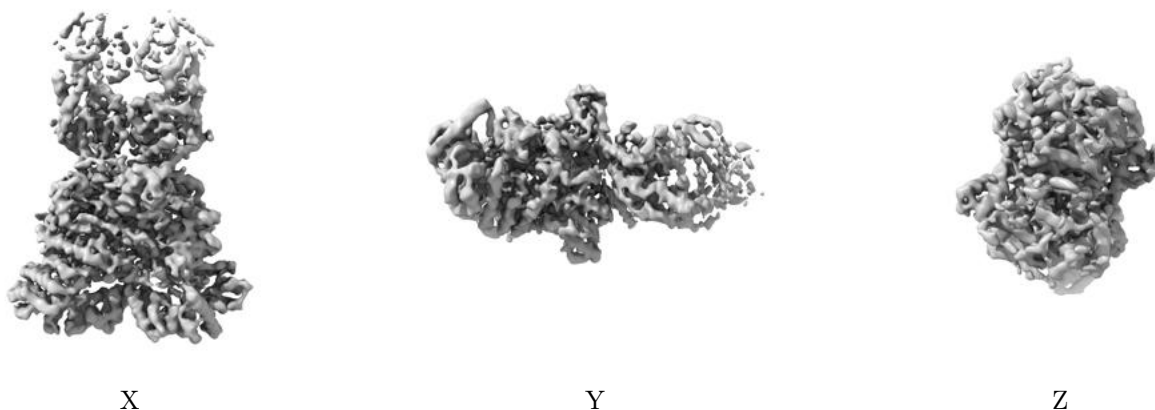


Z

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.

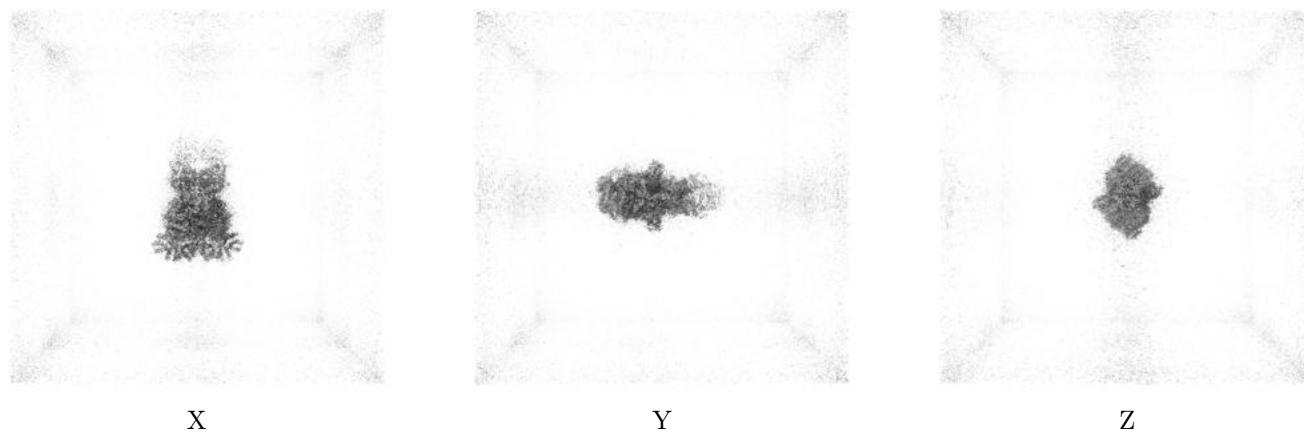
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 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.



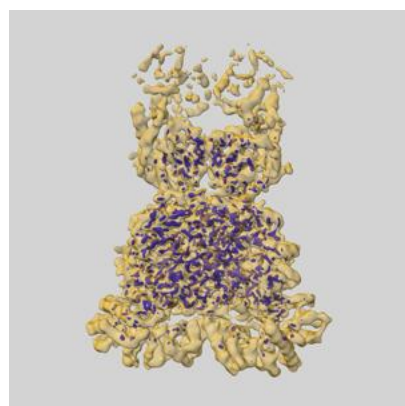
## 6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

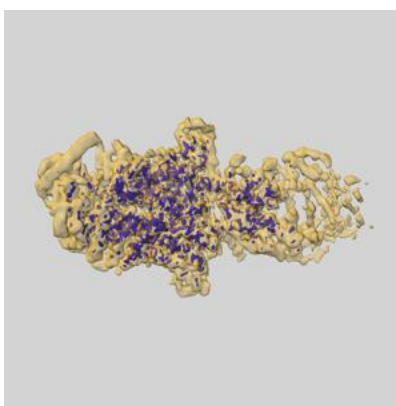
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

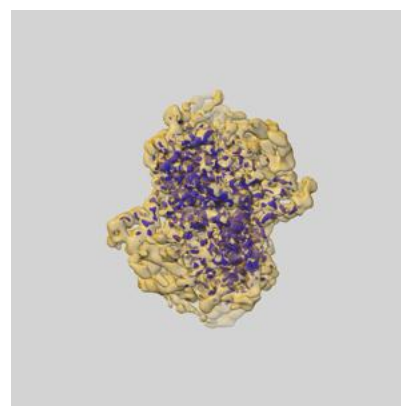
### 6.6.1 emd\_39243\_msk\_1.map [i](#)



X



Y

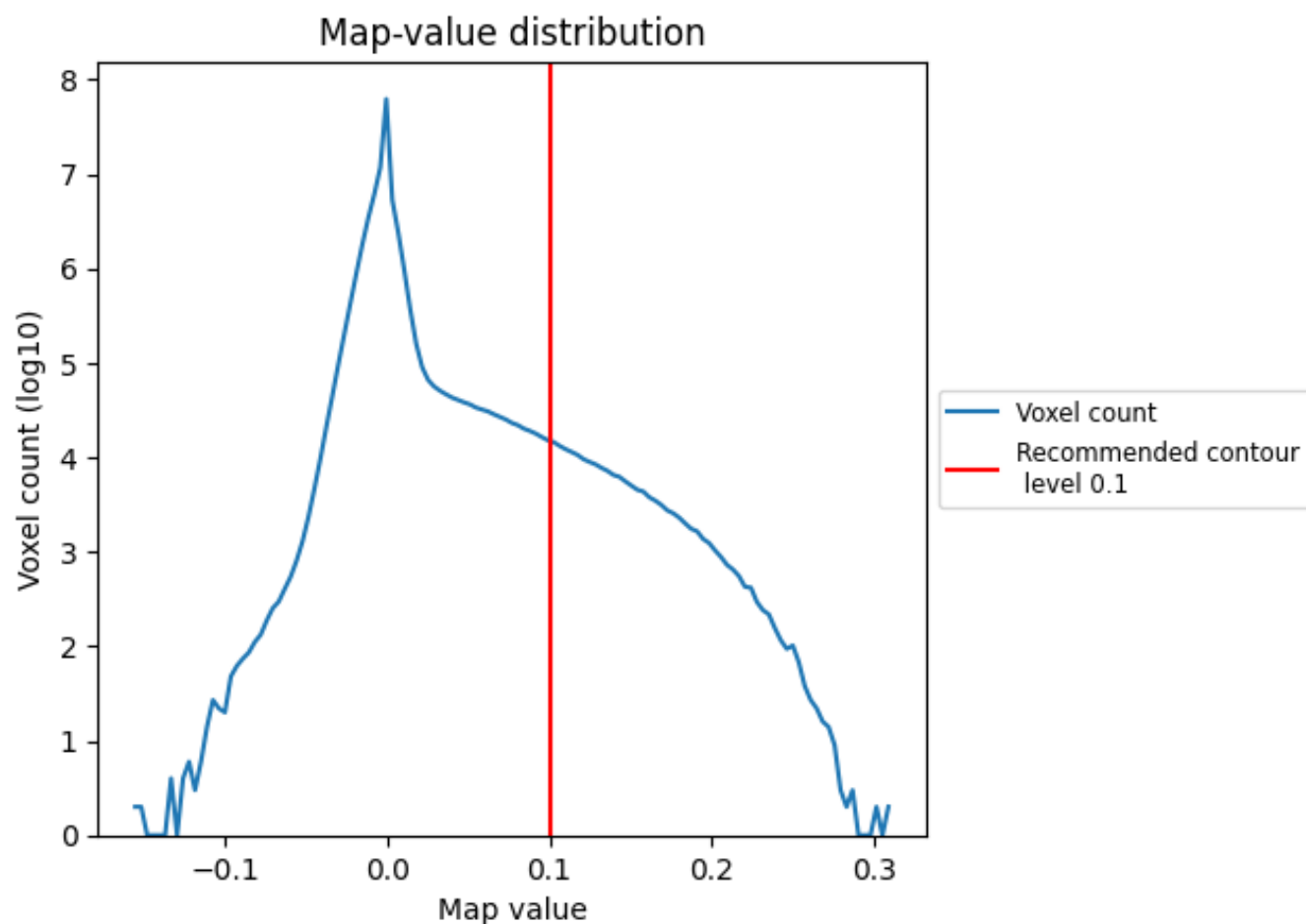


Z

## 7 Map analysis [i](#)

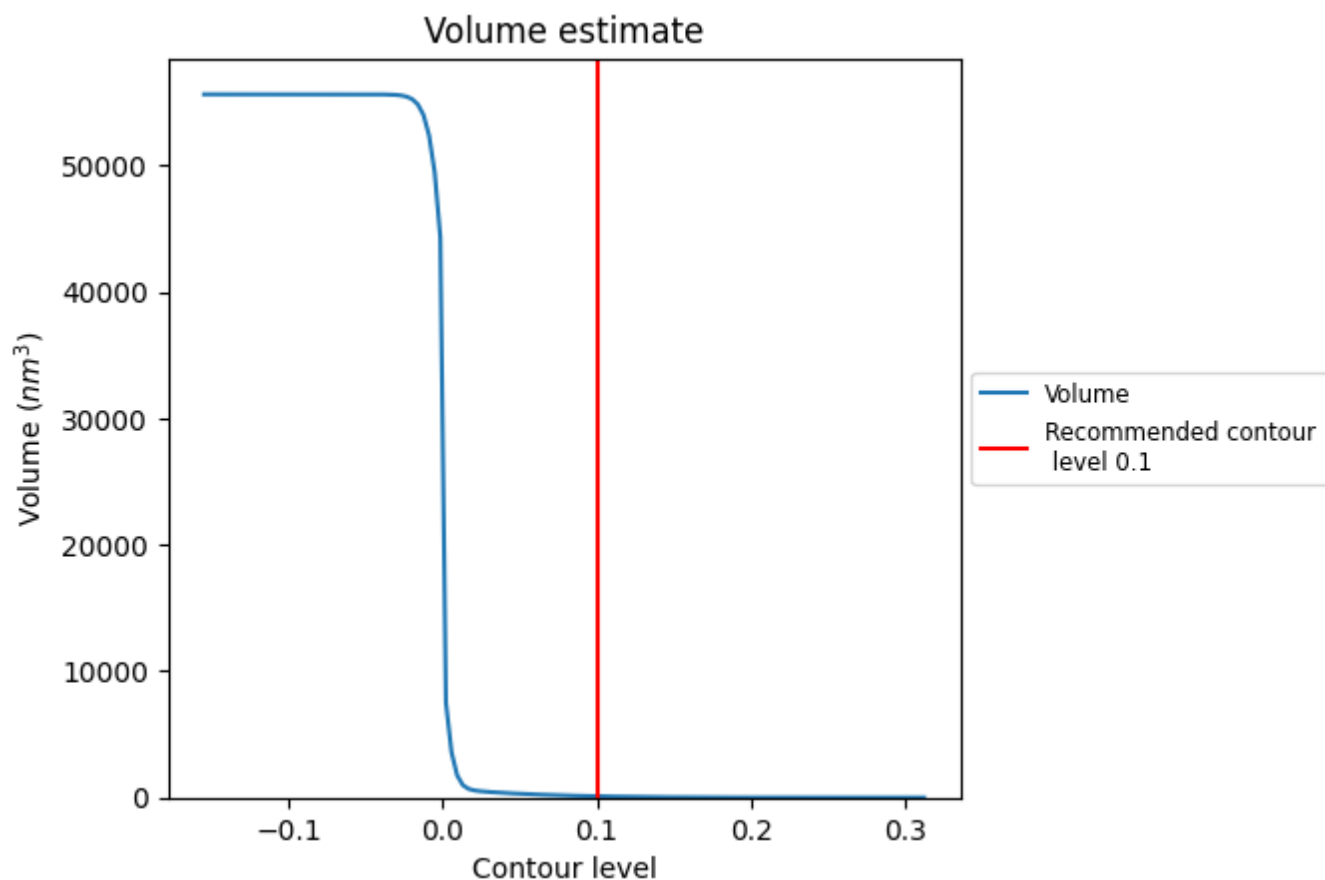
This section contains the results of statistical analysis of the map.

### 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.

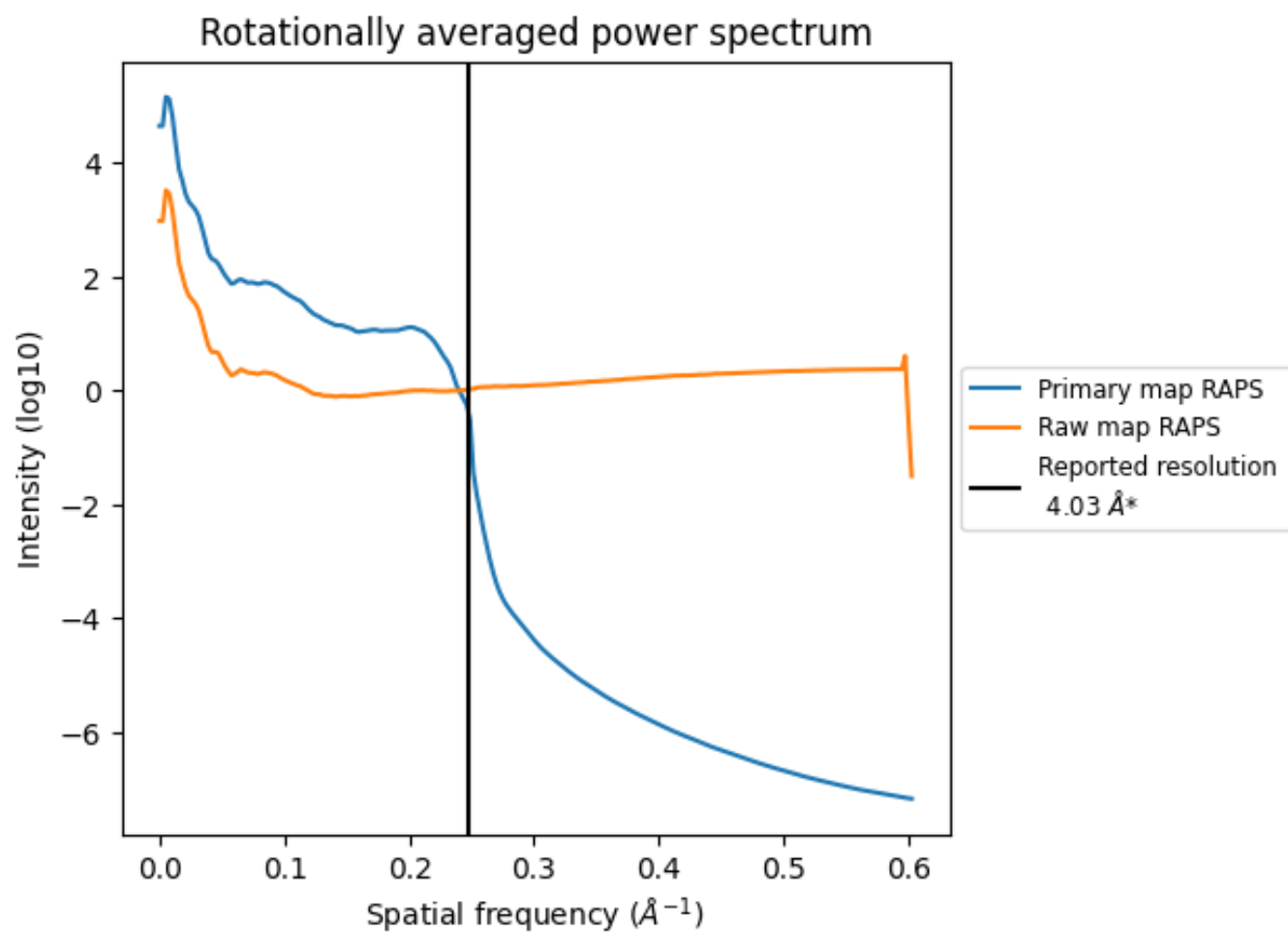
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 103  $\text{nm}^3$ ; this corresponds to an approximate mass of 93 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 ⓘ



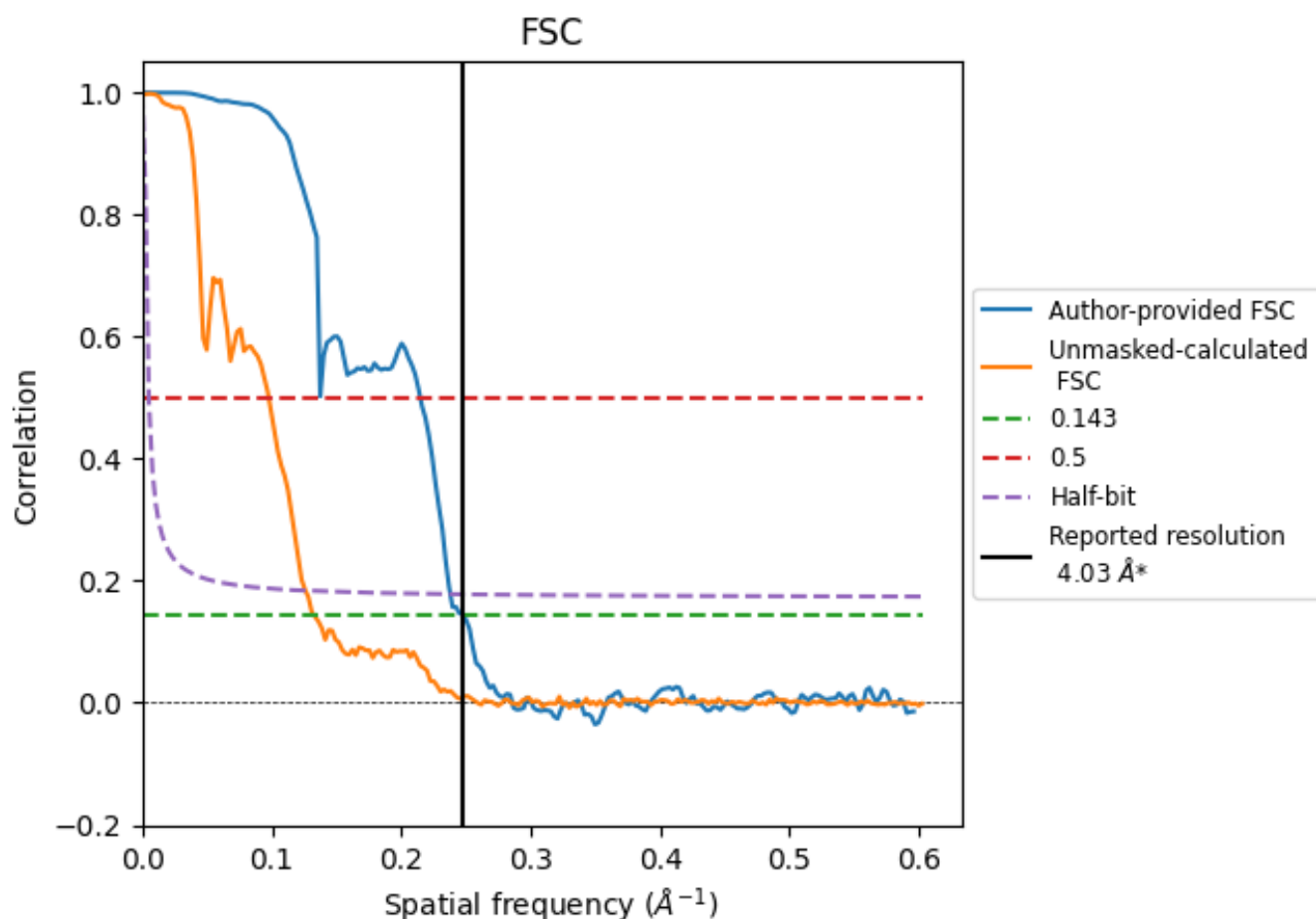
\*Reported resolution corresponds to spatial frequency of 0.248 Å<sup>-1</sup>



## 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 0.248  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

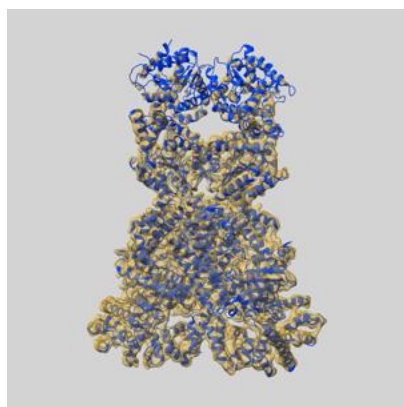
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.03	-	-
Author-provided FSC curve	4.03	4.66	4.20
Unmasked-calculated*	7.53	10.24	7.93

\*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 7.53 differs from the reported value 4.03 by more than 10 %

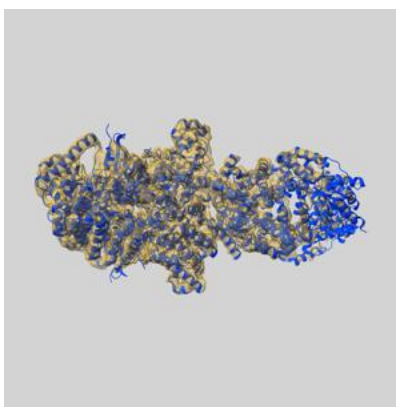
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-39243 and PDB model 8YGC. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

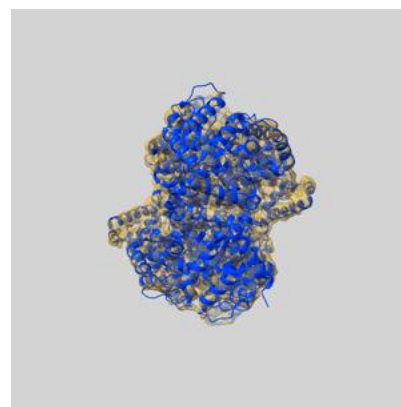
### 9.1 Map-model overlay [i](#)



X



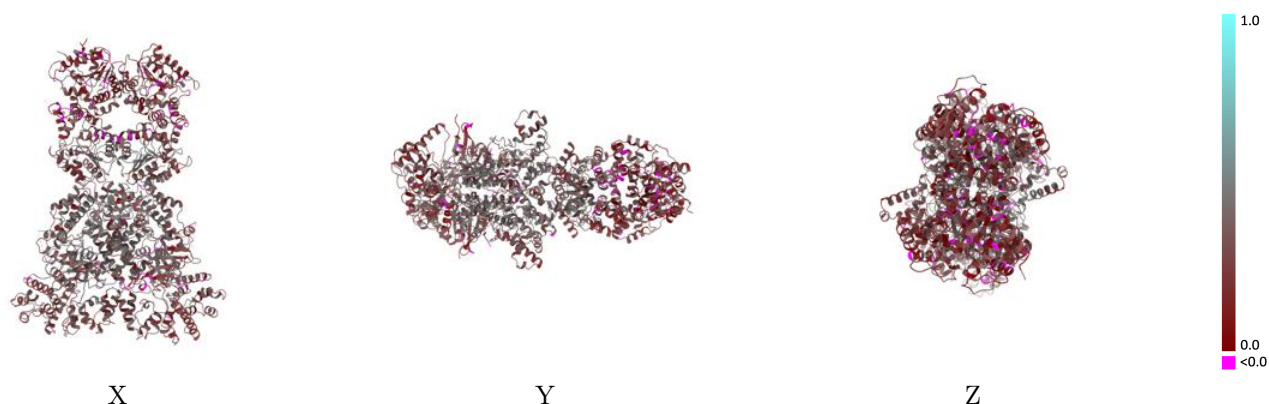
Y



Z

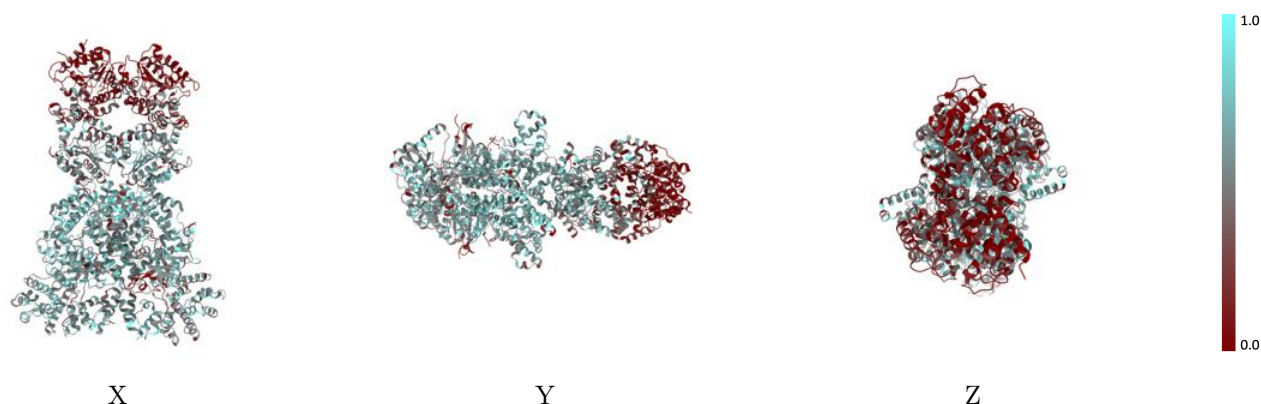
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



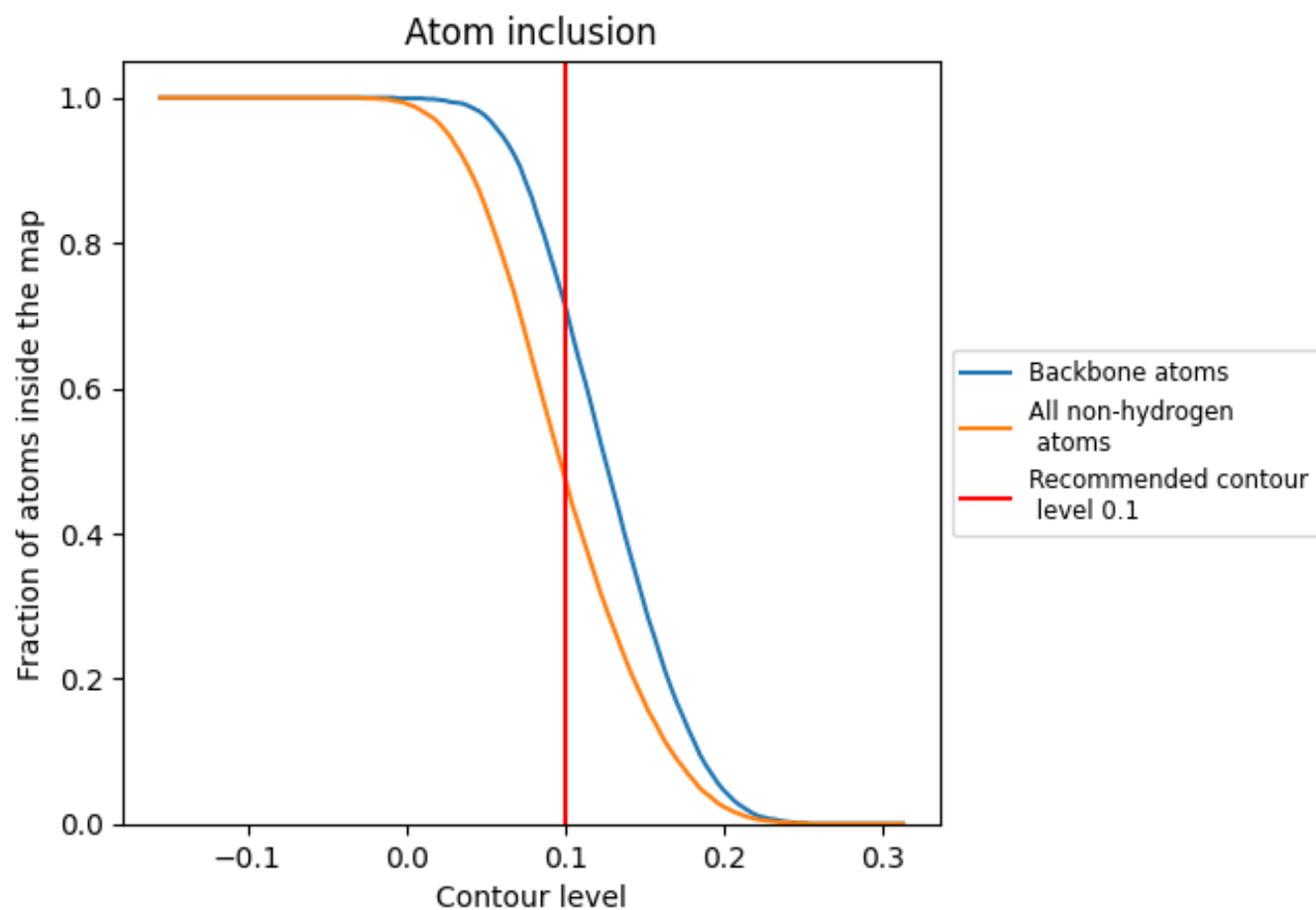
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 47% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.4730	<div></div> 0.3080
A	<div></div> 0.5940	<div></div> 0.3500
B	<div></div> 0.5610	<div></div> 0.3310
C	<div></div> 0.3900	<div></div> 0.2760
D	<div></div> 0.4030	<div></div> 0.2780
E	<div></div> 0.1260	<div></div> 0.1960
F	<div></div> 0.1390	<div></div> 0.2200

1.0  
0.0  
-0.0