



## wwPDB EM Validation Summary Report ⓘ

Mar 3, 2025 – 07:21 PM JST

PDB ID : 8X49  
EMDB ID : EMD-38043  
Title : Cryo-EM structure of Ryanodine receptor 1 (100 nM Ca<sup>2+</sup>)  
Authors : Chen, Q.; Hu, H.  
Deposited on : 2023-11-15  
Resolution : 3.40 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

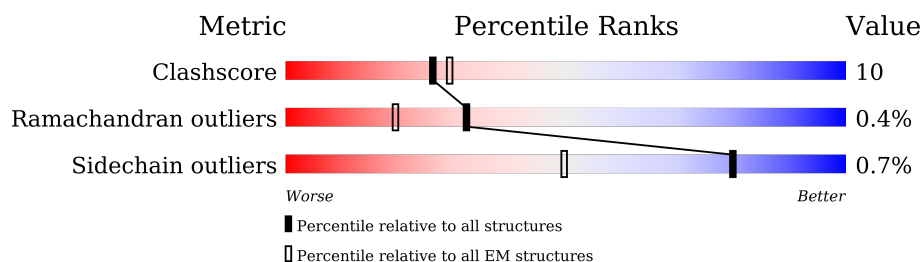
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.40 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	5037	<div> <div>5%</div> <div>63%</div> <div>15%</div> <div>22%</div> </div>
1	B	5037	<div> <div>5%</div> <div>63%</div> <div>15%</div> <div>22%</div> </div>
1	C	5037	<div> <div>5%</div> <div>63%</div> <div>15%</div> <div>22%</div> </div>
1	D	5037	<div> <div>5%</div> <div>63%</div> <div>15%</div> <div>22%</div> </div>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 117356 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 Ryanodine receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3952	Total 29337	C 18674	N 5081	O 5394	S 188	0	0
1	B	3952	Total 29337	C 18674	N 5081	O 5394	S 188	0	0
1	C	3952	Total 29337	C 18674	N 5081	O 5394	S 188	0	0
1	D	3952	Total 29337	C 18674	N 5081	O 5394	S 188	0	0

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
2	A	1	Total 1	Ca 1	0
2	B	1	Total 1	Ca 1	0
2	C	1	Total 1	Ca 1	0
2	D	1	Total 1	Ca 1	0

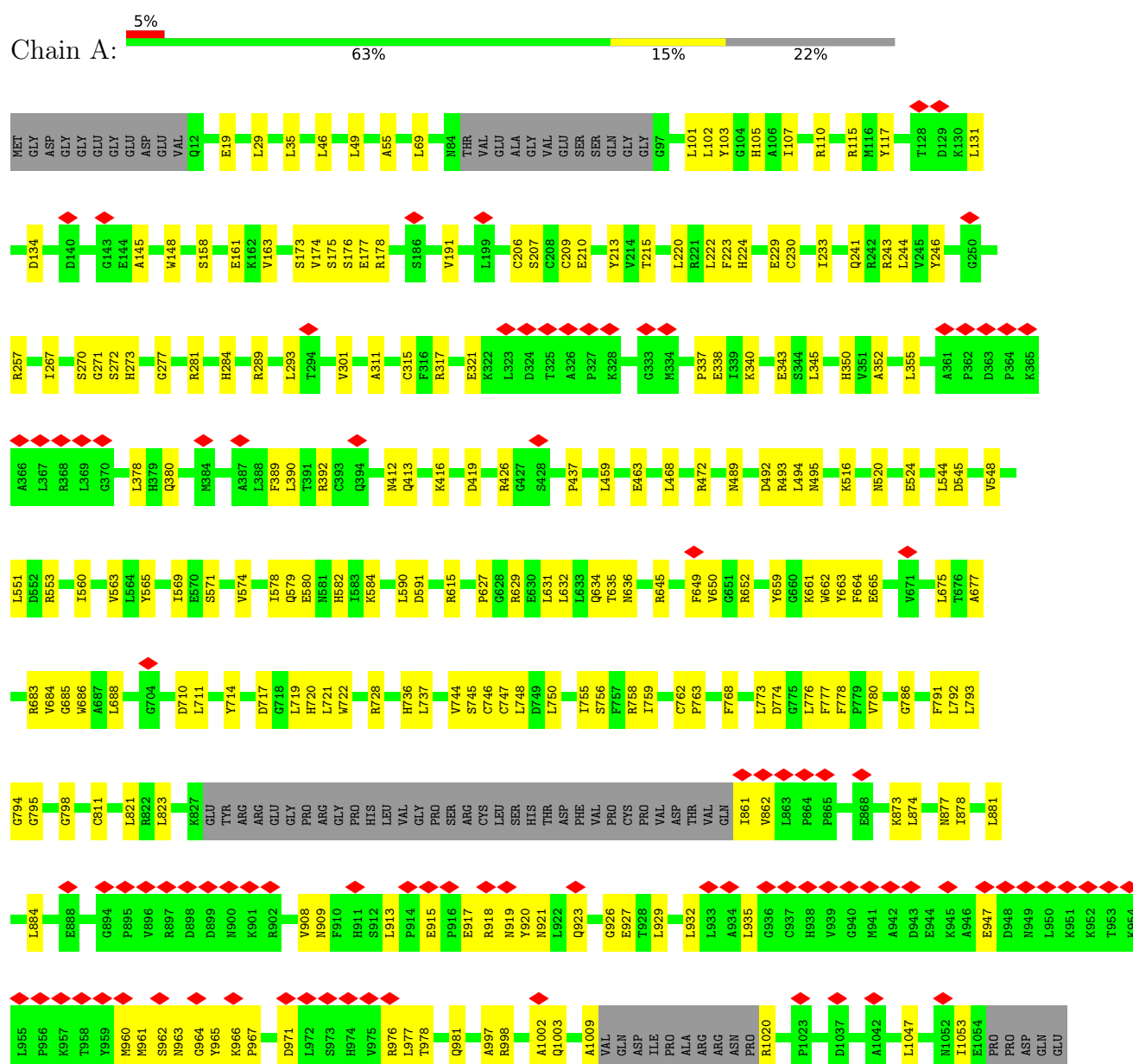
- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total 1	Zn 1	0
3	B	1	Total 1	Zn 1	0
3	C	1	Total 1	Zn 1	0
3	D	1	Total 1	Zn 1	0

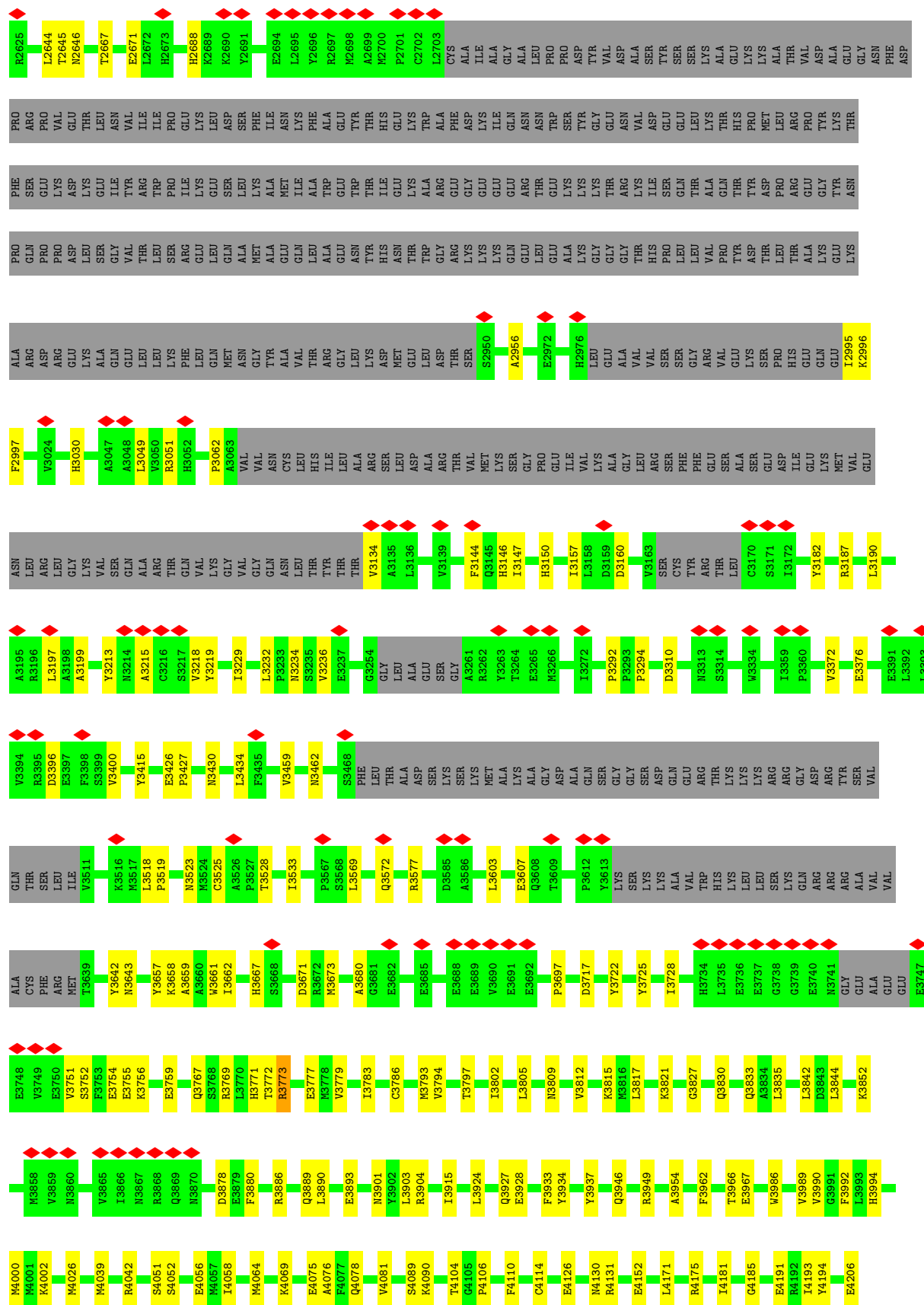
### 3 Residue-property plots

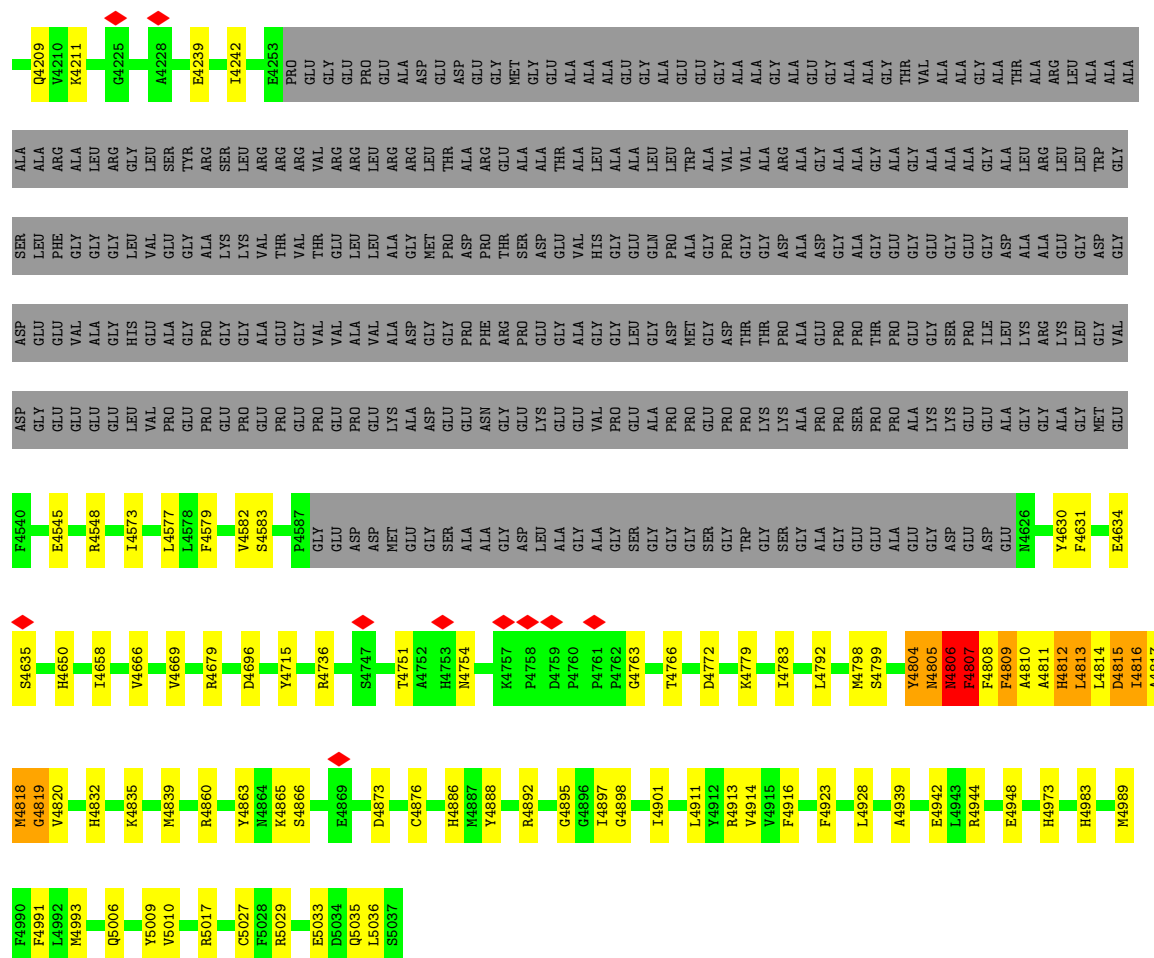
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Ryanodine receptor 1

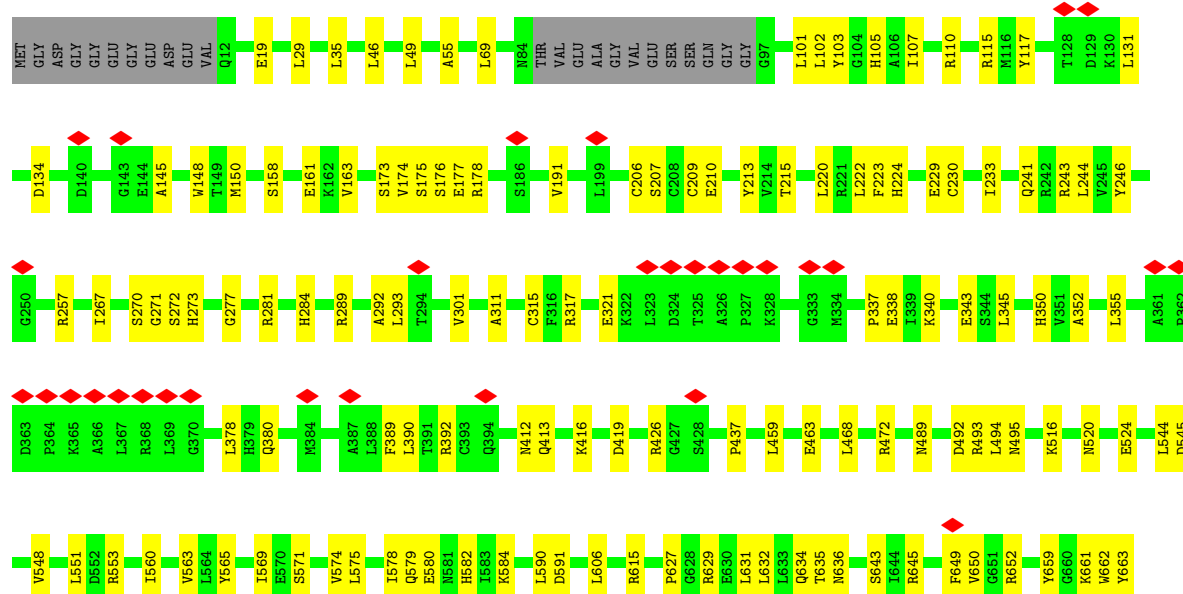








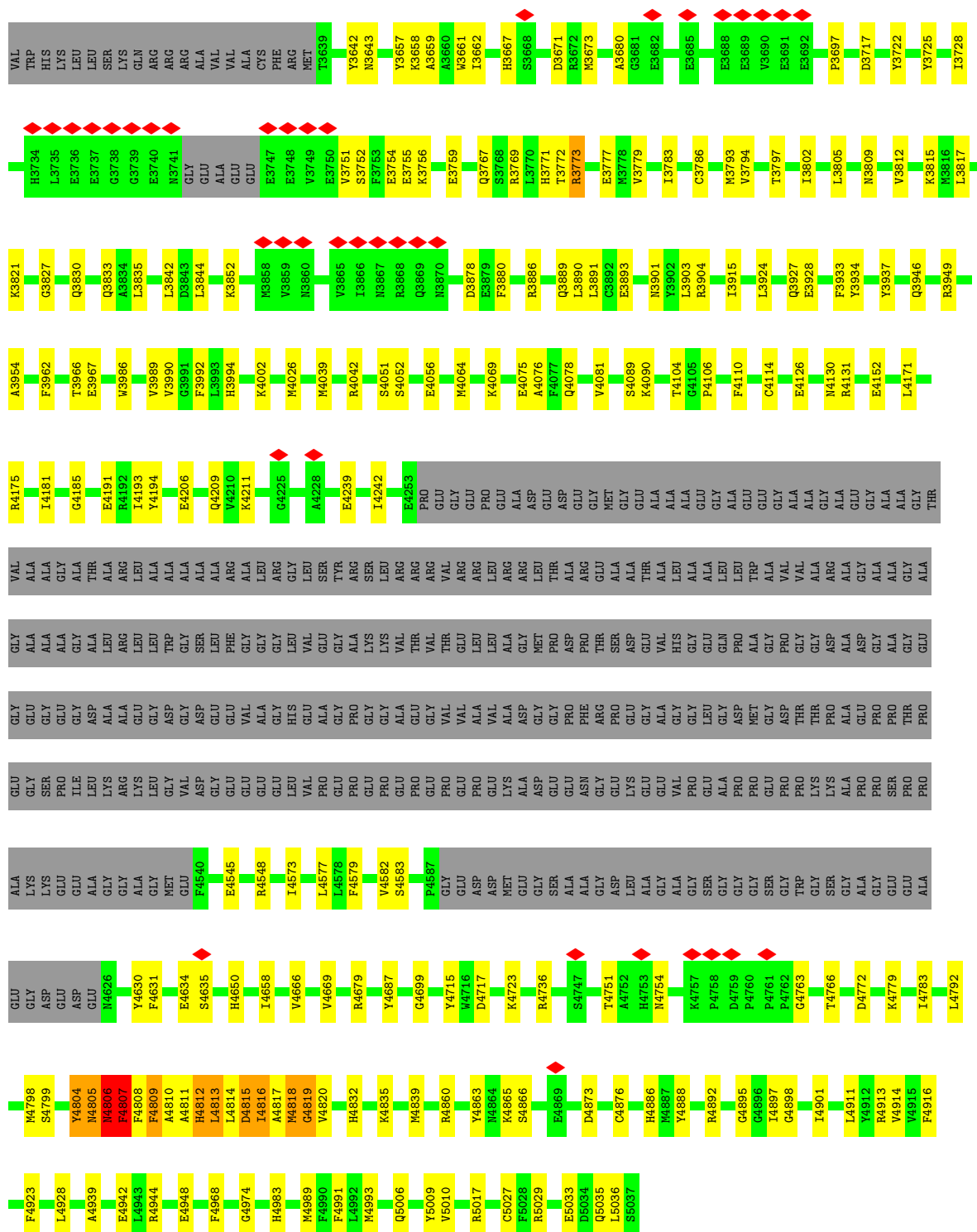
• Molecule 1: Ryanodine receptor 1



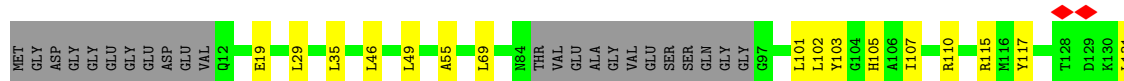


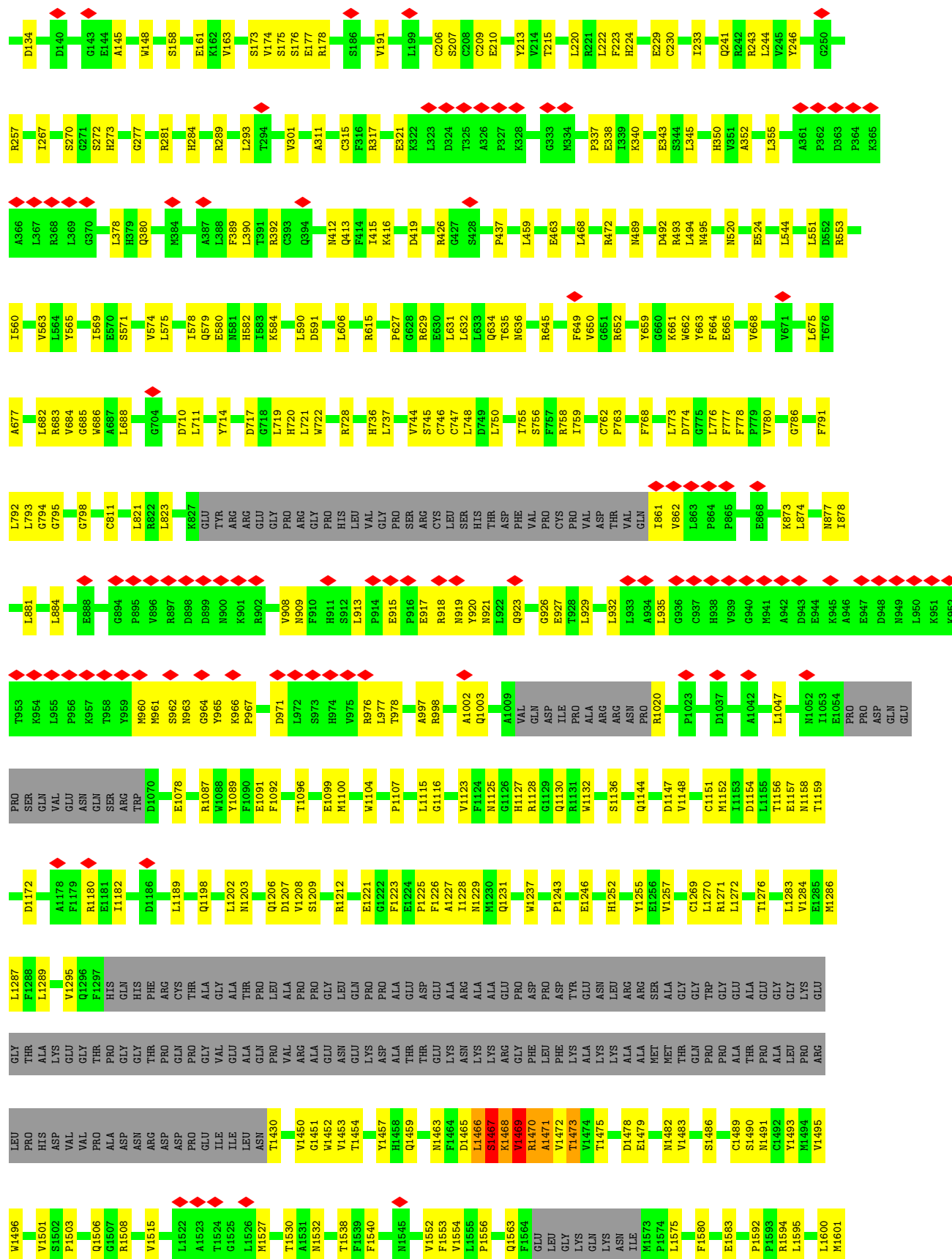






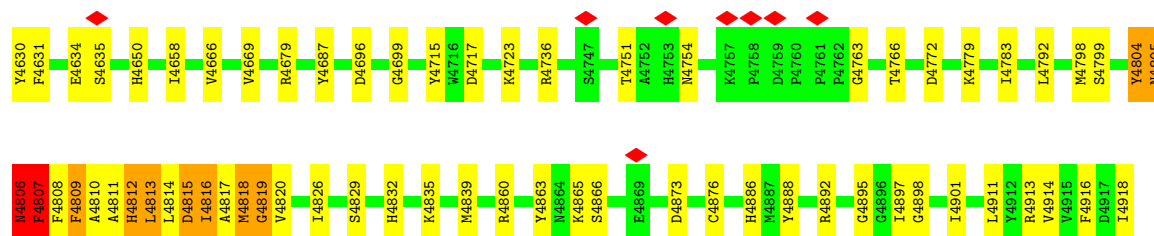
• Molecule 1: Ryanodine receptor 1



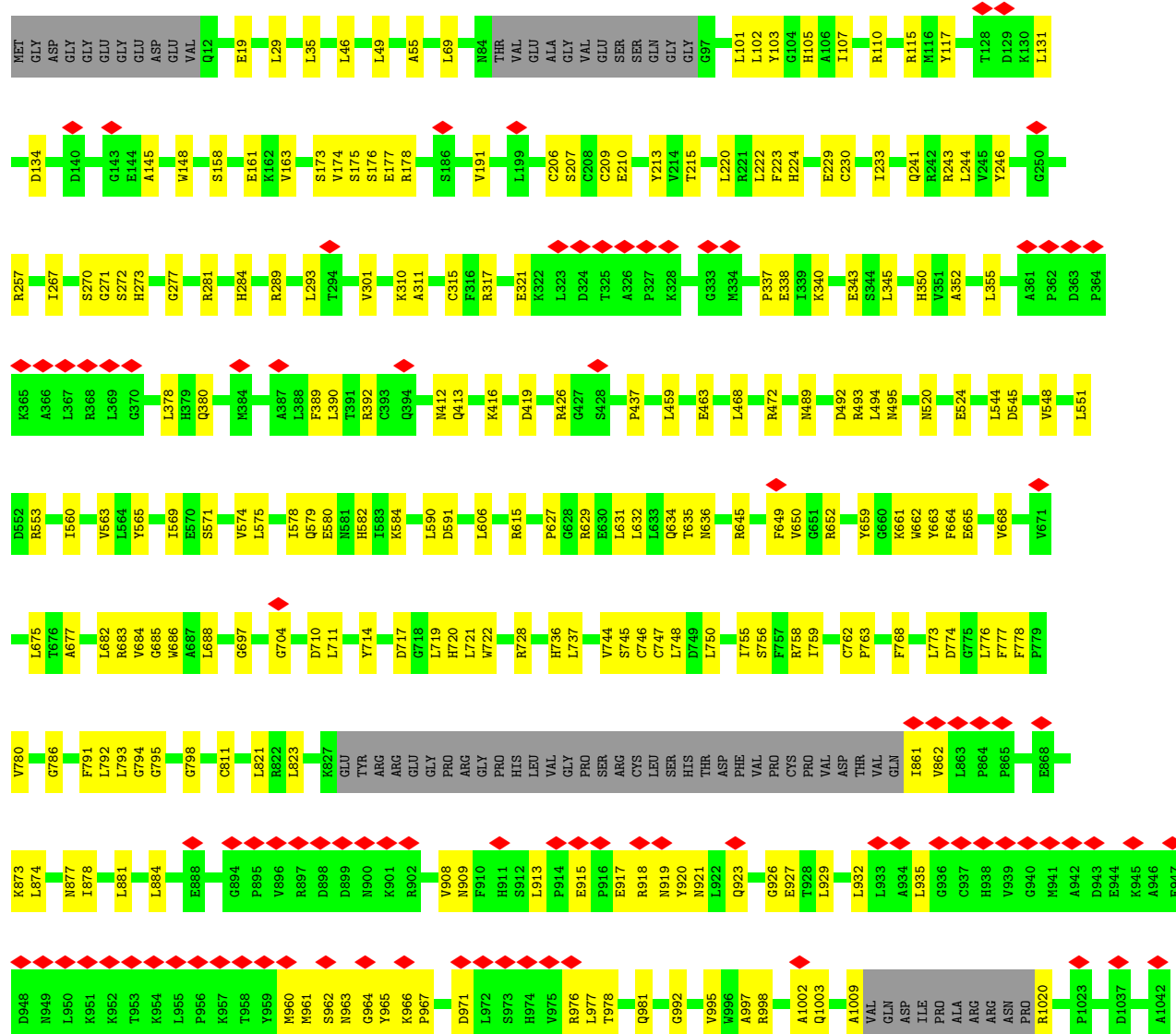








• Molecule 1: Ryanodine receptor 1





A3954	G3827	L3735	HIS	ARG	P3360	R3187	ILE	SER	PRO	GLN	THR	ALA	V2586
F3962	Q3830	E3736	LYS	THR	V3372	L3190	GLU	PRO	TYR	THR	HIS	THR	Y2587
T3966	Q3833	G3738	LYS	LYS	E3376	A3195	VAL	HIS	ASP	MET	ASP	VAL	S2590
E3967	A3834	G3739	LYS	ARG	E3391	R3196	GLN	GLN	PRO	LEU	ALA	ALA	R2591
V3966	L3835	E3740	GLN	ARG	L3392	L3197	ASN	GLU	ARG	ARG	GLY	GLY	Y2613
V3969	L3842	N3741	ARG	GLY	L3393	A3199	LEU	L2995	GLY	TYR	ASN	PHE	P2616
V3989	D3843	GLY	ARG	ASP	L3394	A3199	LEU	R2996	ASN	THR	LYS	ASP	P2616
V3990	L3844	ALA	ARG	ARG	V3394	A3199	GLY	F2997	LYS	THR	LYS	THR	P2616
G3991	K3852	VAL	SER	TYR	R3395	Y3213	LYS	V3024	ALA	PRO	ARG	ARG	R2625
G3992	M3858	VAL	GLN	VAL	D3396	N3214	VAL	A3047	ASP	GLU	SER	PRO	R2625
L3953	V3859	ALA	THR	GLN	E3397	N3214	SER	A3048	ARG	GLU	GLN	PRO	L2644
H3994	N3860	GLU	LYS	LEU	F3398	C3216	ALA	A3049	GLU	ASP	LYS	VAL	T2645
M4000	N3860	V3748	ARG	LEU	S3399	A3217	ARG	L3049	LEU	LYS	LYS	THR	T2645
M4001	N3860	V3749	ILE	ILE	V3400	S3217	THR	R3051	GLN	SER	GLY	LEU	T2667
K4002	E3750	E3750	V3511	V3219	Y3415	Y3219	VAL	H3052	GLU	VAL	TYR	VAL	T2667
V3865	V3751	V3751	K3516	T3229	E3426	T3229	LYS	P3062	LEU	THR	ARG	ILE	E2671
I3866	S3752	S3752	M3517	L3229	E3426	L3229	GLY	A3063	LEU	THR	ARG	ILE	L2672
N3867	F3753	F3753	L3518	L3232	P3427	L3232	VAL	VAL	LYS	THR	PRO	PRO	L2673
E3754	E3754	E3754	P3519	N3234	N3430	N3234	GLN	VAL	GLY	ILE	GLU	GLU	H2688
E3755	K3658	K3658	N3523	S3235	N3430	S3235	ASN	ASN	LEU	GLY	LEU	LEU	R2689
K3756	A3659	A3659	M3524	N3236	L3434	N3236	LEU	LEU	ALA	ASN	SER	ASP	R2690
E3759	A3660	A3660	C3525	V3236	F3435	V3236	THR	ILE	ALA	ALA	LEU	PHE	R2691
E3767	W3661	W3661	A3526	E3237	S3446	E3237	TYR	ILE	GLY	GLY	MET	ASN	R2691
R3769	I3662	I3662	T3528	G3254	H3449	G3254	THR	ALA	VAL	VAL	GLN	ILE	E2694
L3770	H3667	H3667	L3533	GLY	H3449	GLY	THR	ARG	THR	THR	LEU	ALA	L2695
R3771	S3668	S3668	P3567	ALA	V3459	ALA	A3135	SER	ARG	ALA	LEU	TRP	Y2696
L3772	M3673	M3673	T3568	GLU	V3459	GLU	L3136	LEU	GLY	TRP	GLY	ALA	R2697
R3773	A3680	A3680	S3568	SER	N3462	SER	V3139	ASP	GLY	TRP	ASN	THR	Y2698
E3777	E3681	E3681	A3261	GLY	S3468	GLY	F3144	LYS	THR	THR	THR	THR	R2698
R3778	G3681	G3681	R3262	A3261	PHE	R3262	R3145	VAL	GLU	GLY	ALA	ALA	R2697
V3779	E3682	E3682	Y3263	T3264	THR	Y3263	H3146	SER	LEU	GLY	ARG	GLY	Y2698
I3783	E3685	E3685	T3264	M3266	ASP	T3264	I3147	GLY	THR	ARG	GLY	ALA	R2699
C3786	D3585	D3585	E3265	E3266	LYS	E3265	H3150	PRO	SER	LYS	GLY	ALA	Y2700
M3793	A3586	A3586	I3272	I3272	LYS	I3272	P3159	GLU	ASP	LYS	GLY	ALA	F2701
V3794	L3603	L3603	P3292	P3292	MET	P3292	V3163	LEU	MET	GLY	GLY	ILE	C2702
T3797	E3607	E3607	P3293	P3293	ALA	P3293	SER	GLY	THR	GLY	ASP	ALA	L2703
T3802	Q3608	Q3608	L3294	L3294	LYS	L3294	TYR	PRO	ASP	GLY	ASP	ALA	CYS
L3805	T3609	T3609	ALA	ALA	ALA	ALA	CYS	GLY	SER	LYS	ASP	ALA	ILE
L3809	P3612	P3612	D3310	D3310	ASP	D3310	ARG	PRO	LEU	LYS	TYR	VAL	ALA
V3812	Y3613	Y3613	N3313	N3313	GLN	N3313	THR	LEU	GLY	GLY	GLY	GLY	ALA
K3815	LYS	LYS	S3314	S3314	SER	S3314	LEU	VAL	VAL	THR	THR	THR	ALA
M3816	SER	SER	G3317	G3317	GLY	G3317	GLY	GLY	VAL	GLY	GLY	GLY	ALA
L3817	LYS	LYS	L3320	L3320	GLY	L3320	ARG	ARG	VAL	GLY	GLY	GLY	ALA
V3821	ALA	ALA	H3334	H3334	ASP	H3334	THR	PHE	SER	THR	THR	THR	ALA
H3734	TRP	TRP	I3359	I3359	GLU	I3359	E3182	GLU	GLY	VAL	VAL	VAL	ALA
							E3184	ASP	GLU	GLY	GLY	GLY	ALA
													LYS





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	183859	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 ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	4.737	Depositor
Minimum map value	-2.523	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.130	Depositor
Recommended contour level	0.466	Depositor
Map size (Å)	516.72003, 516.72003, 516.72003	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0765, 1.0765, 1.0765	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: CA, ZN

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	0.30	0/29956	0.47	0/40772
1	B	0.30	0/29956	0.47	0/40772
1	C	0.30	0/29956	0.47	0/40772
1	D	0.30	0/29956	0.47	0/40772
All	All	0.30	0/119824	0.47	0/163088

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	29337	0	27528	579	0
1	B	29337	0	27528	585	0
1	C	29337	0	27528	579	0
1	D	29337	0	27528	580	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
All	All	117356	0	110112	2250	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 10.

The worst 5 of 2250 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:C:1965:TYR:CE2	1:C:1969:LEU:HD11	2.12	0.85
1:D:1965:TYR:CE2	1:D:1969:LEU:HD11	2.12	0.84
1:B:1965:TYR:CE2	1:B:1969:LEU:HD11	2.12	0.84
1:A:1965:TYR:CE2	1:A:1969:LEU:HD11	2.12	0.84
1:C:3990:VAL:HG23	1:C:4051:SER:HB3	1.61	0.82

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	3906/5037 (78%)	3513 (90%)	376 (10%)	17 (0%)	30	60
1	B	3906/5037 (78%)	3513 (90%)	376 (10%)	17 (0%)	30	60
1	C	3906/5037 (78%)	3513 (90%)	376 (10%)	17 (0%)	30	60
1	D	3906/5037 (78%)	3513 (90%)	376 (10%)	17 (0%)	30	60
All	All	15624/20148 (78%)	14052 (90%)	1504 (10%)	68 (0%)	32	60

5 of 68 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1469	VAL
1	A	1470	ARG
1	A	1472	VAL
1	A	1836	PHE
1	B	1469	VAL

### 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	2885/4276 (68%)	2865 (99%)	20 (1%)	81	88
1	B	2885/4276 (68%)	2865 (99%)	20 (1%)	81	88
1	C	2885/4276 (68%)	2865 (99%)	20 (1%)	81	88
1	D	2885/4276 (68%)	2865 (99%)	20 (1%)	81	88
All	All	11540/17104 (68%)	11460 (99%)	80 (1%)	80	88

5 of 80 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	4813	LEU
1	D	1843	LYS
1	C	4818	MET
1	D	1468	LYS
1	D	4806	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 58 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	4201	ASN
1	D	4094	GLN
1	C	3572	GLN
1	D	3998	HIS
1	D	3430	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](#)

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

### 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.

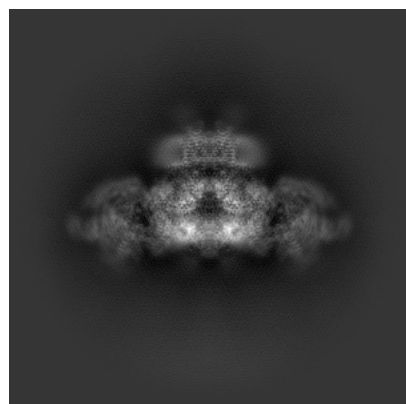
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38043. These allow visual inspection of the internal detail of the map and identification of artifacts.

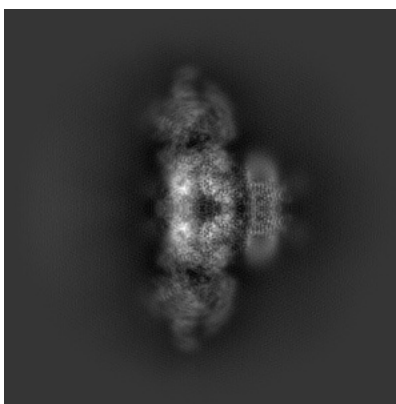
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

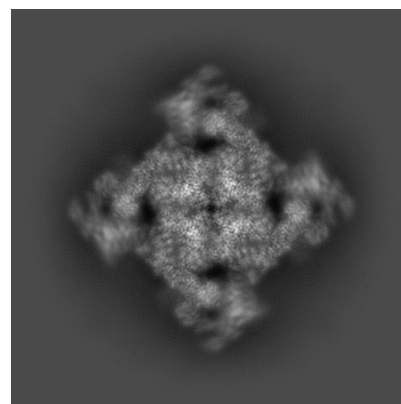
#### 6.1.1 Primary map



X

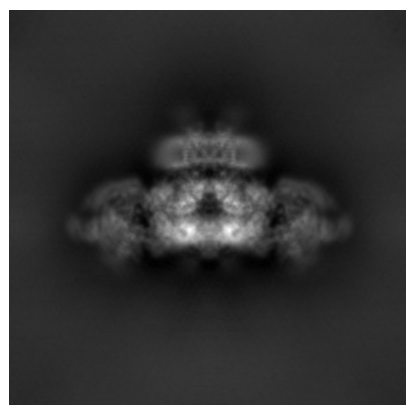


Y

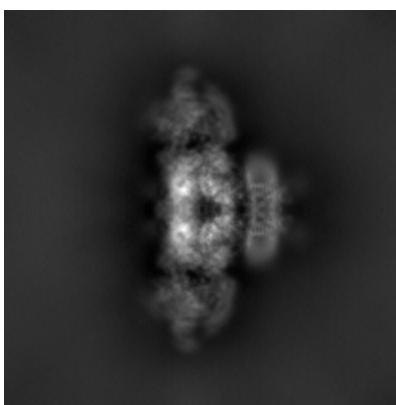


Z

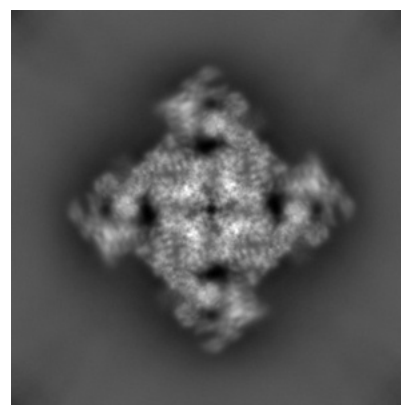
#### 6.1.2 Raw map



X



Y

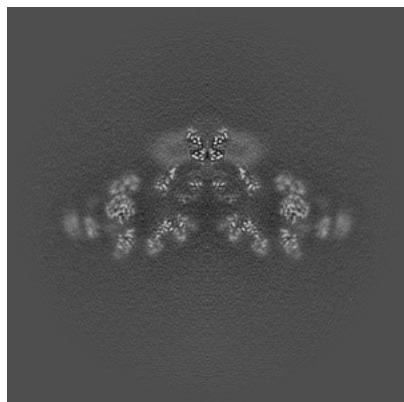


Z

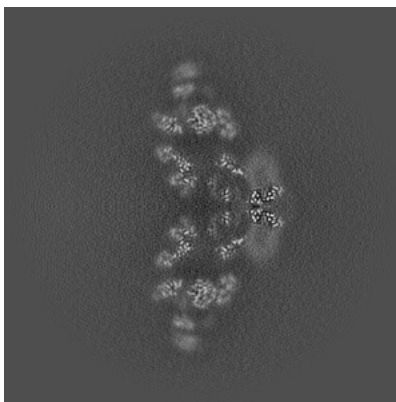
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

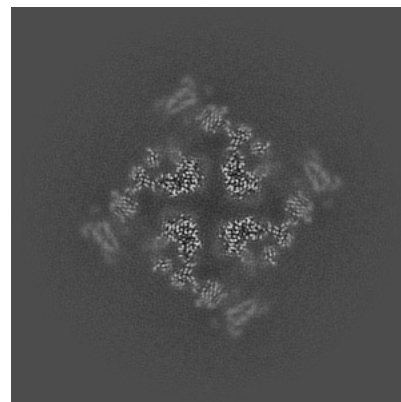
### 6.2.1 Primary map



X Index: 240

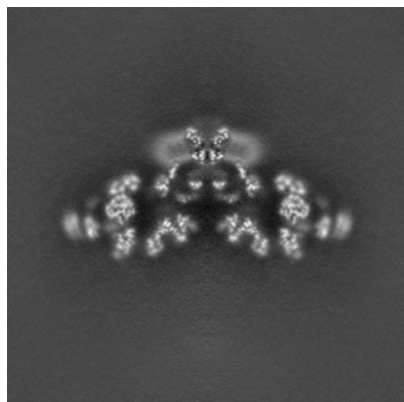


Y Index: 240

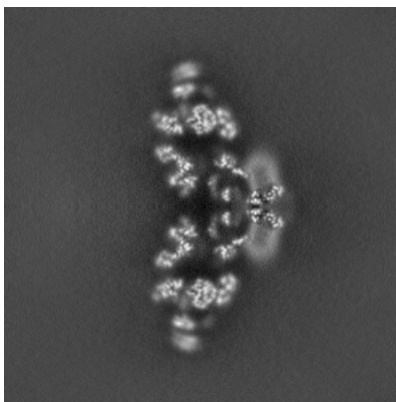


Z Index: 240

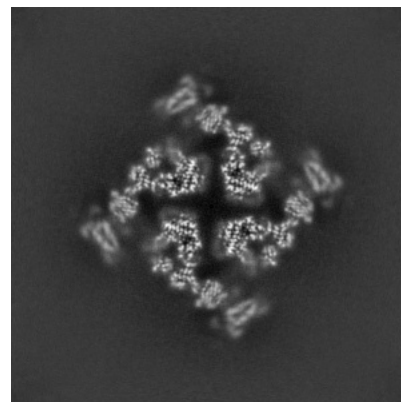
### 6.2.2 Raw map



X Index: 240



Y Index: 240



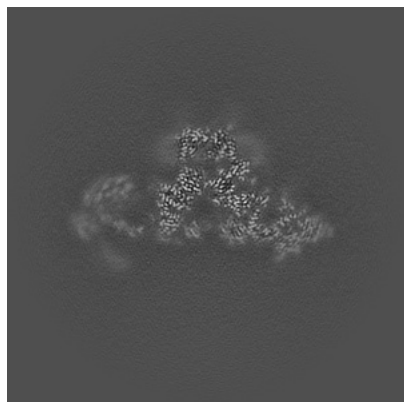
Z Index: 240

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

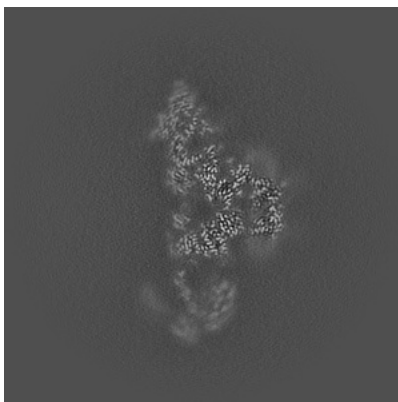


## 6.3 Largest variance slices [i](#)

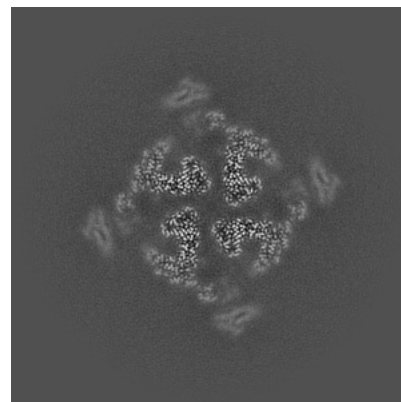
### 6.3.1 Primary map



X Index: 259

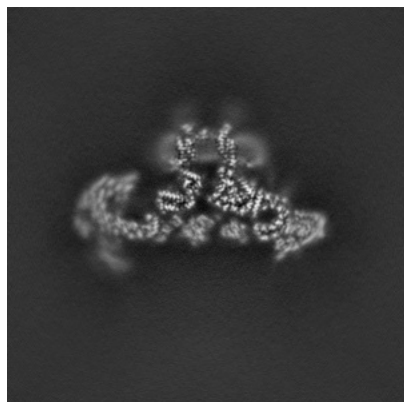


Y Index: 221

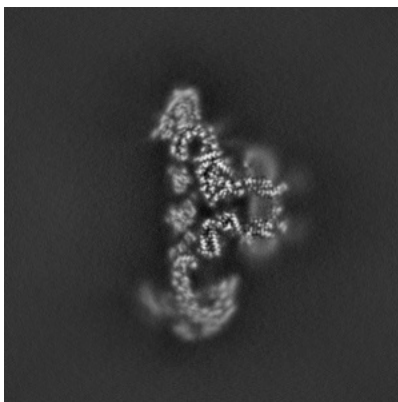


Z Index: 248

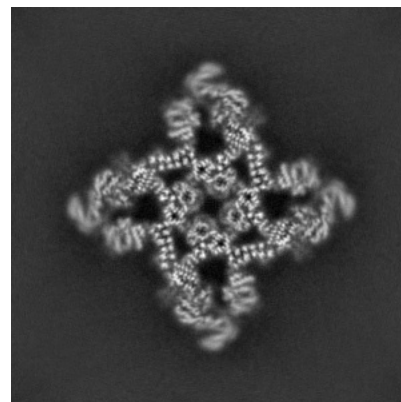
### 6.3.2 Raw map



X Index: 265



Y Index: 215

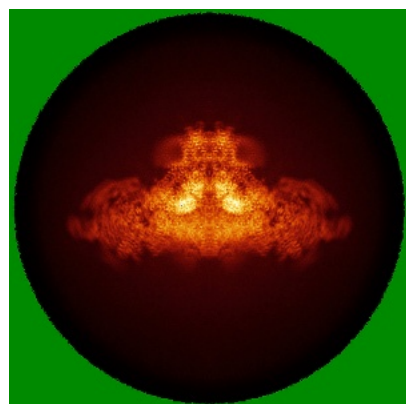


Z Index: 218

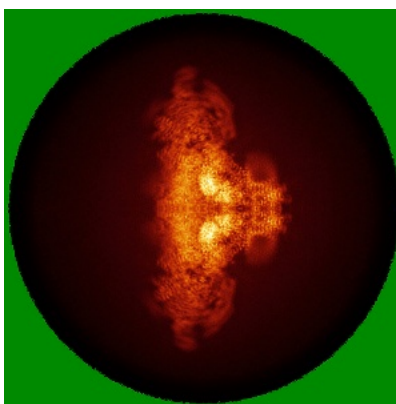
The images above show the largest variance slices of the map in three orthogonal directions.

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

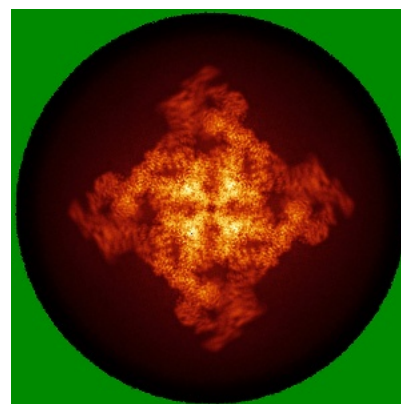
### 6.4.1 Primary map



X

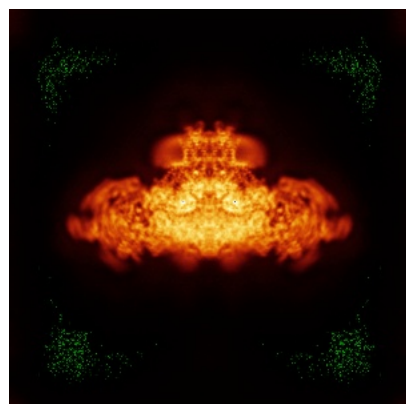


Y

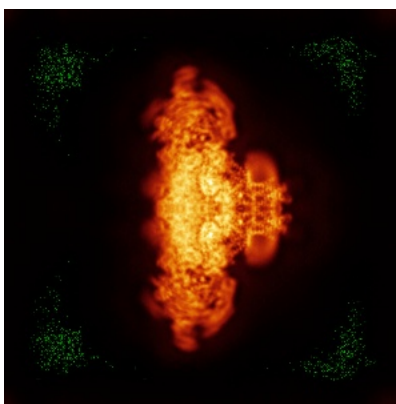


Z

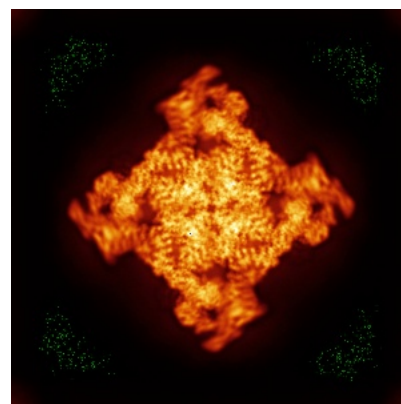
### 6.4.2 Raw map



X



Y

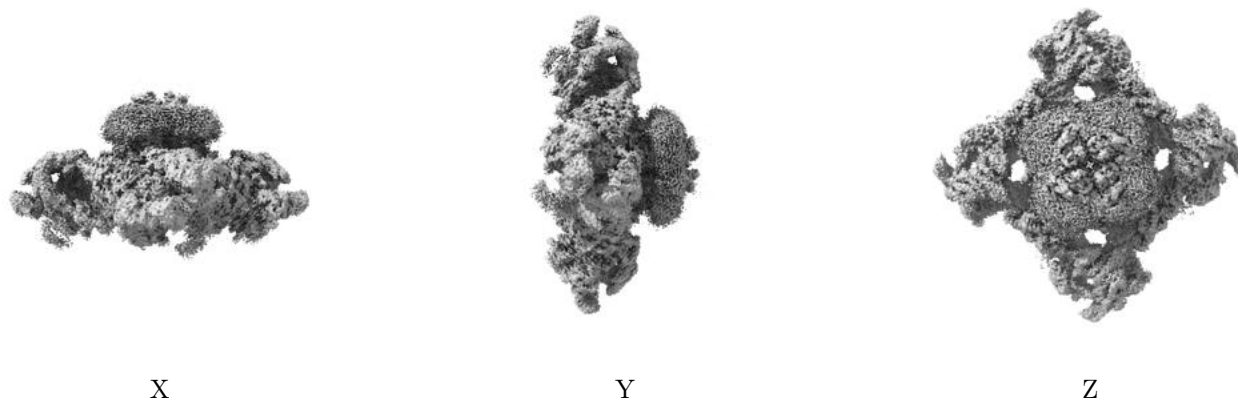


Z

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.

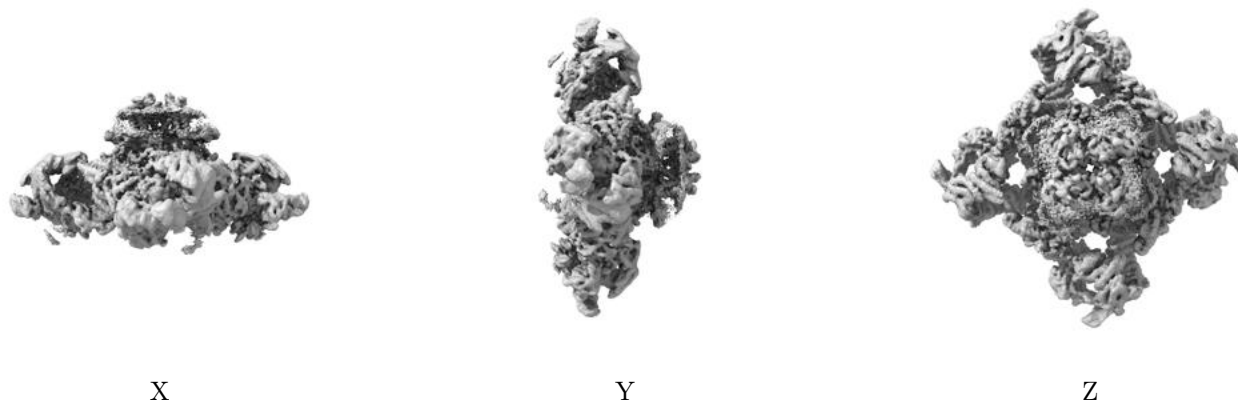
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.466. 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.

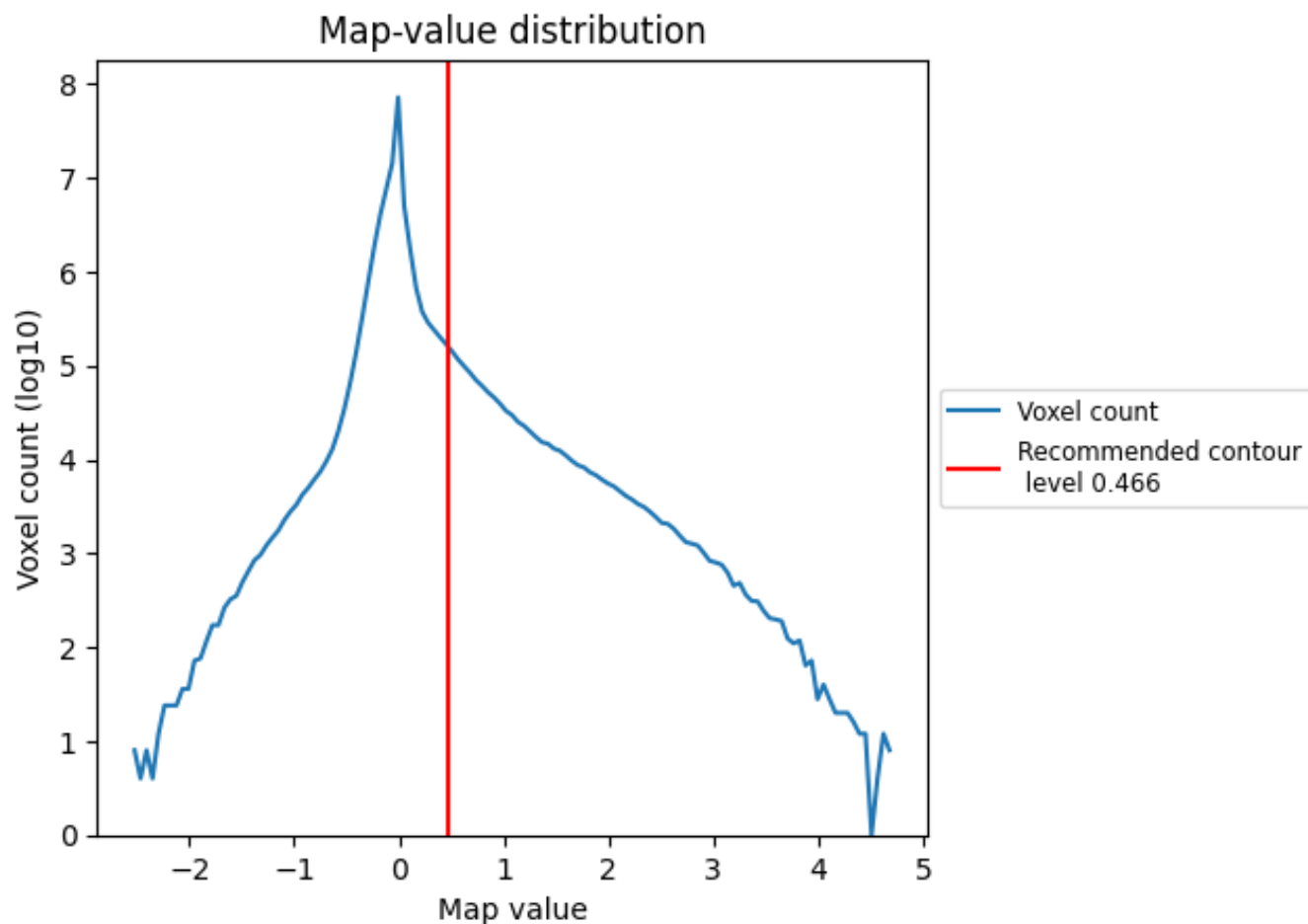
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

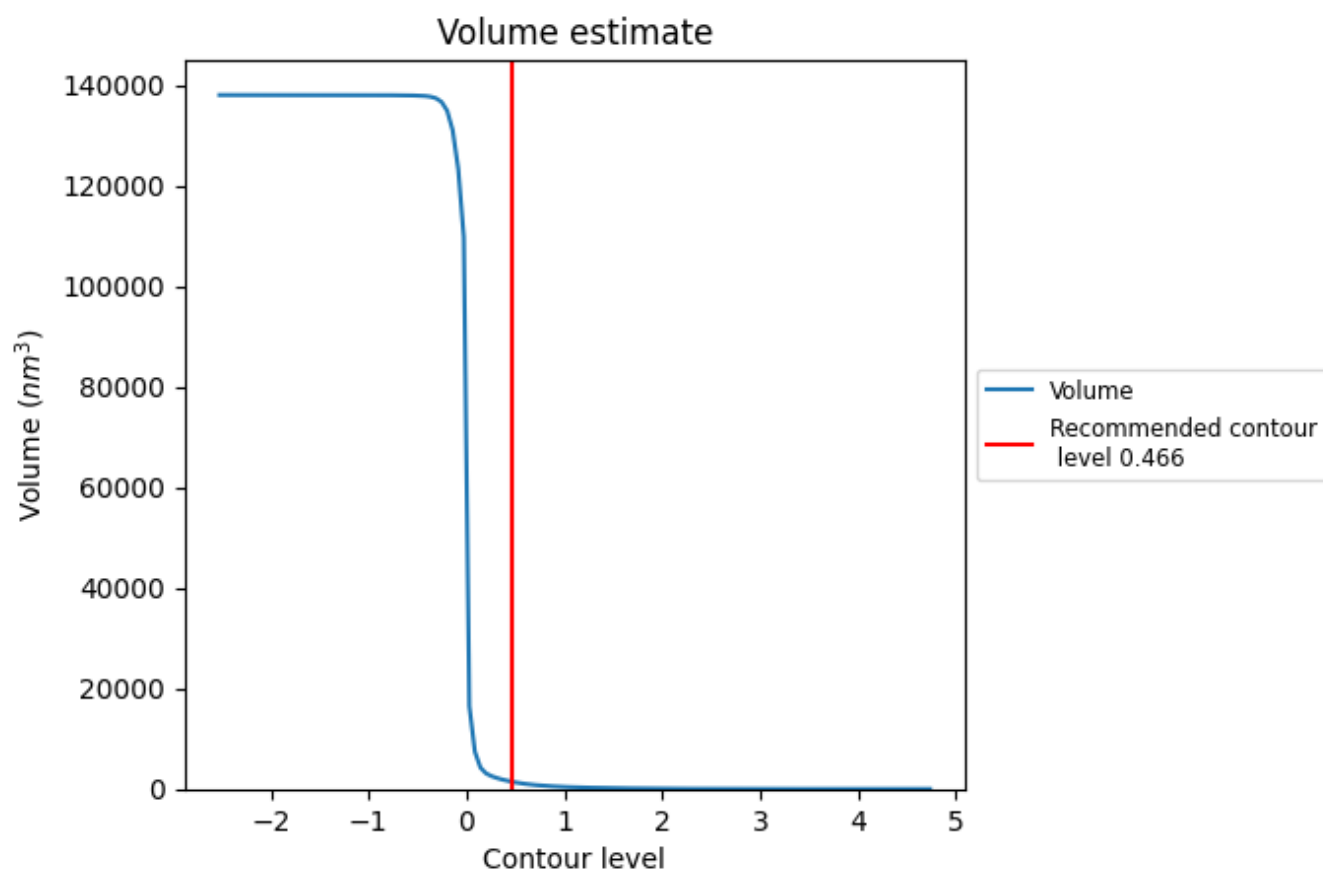
This section contains the results of statistical analysis of the map.

### 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.

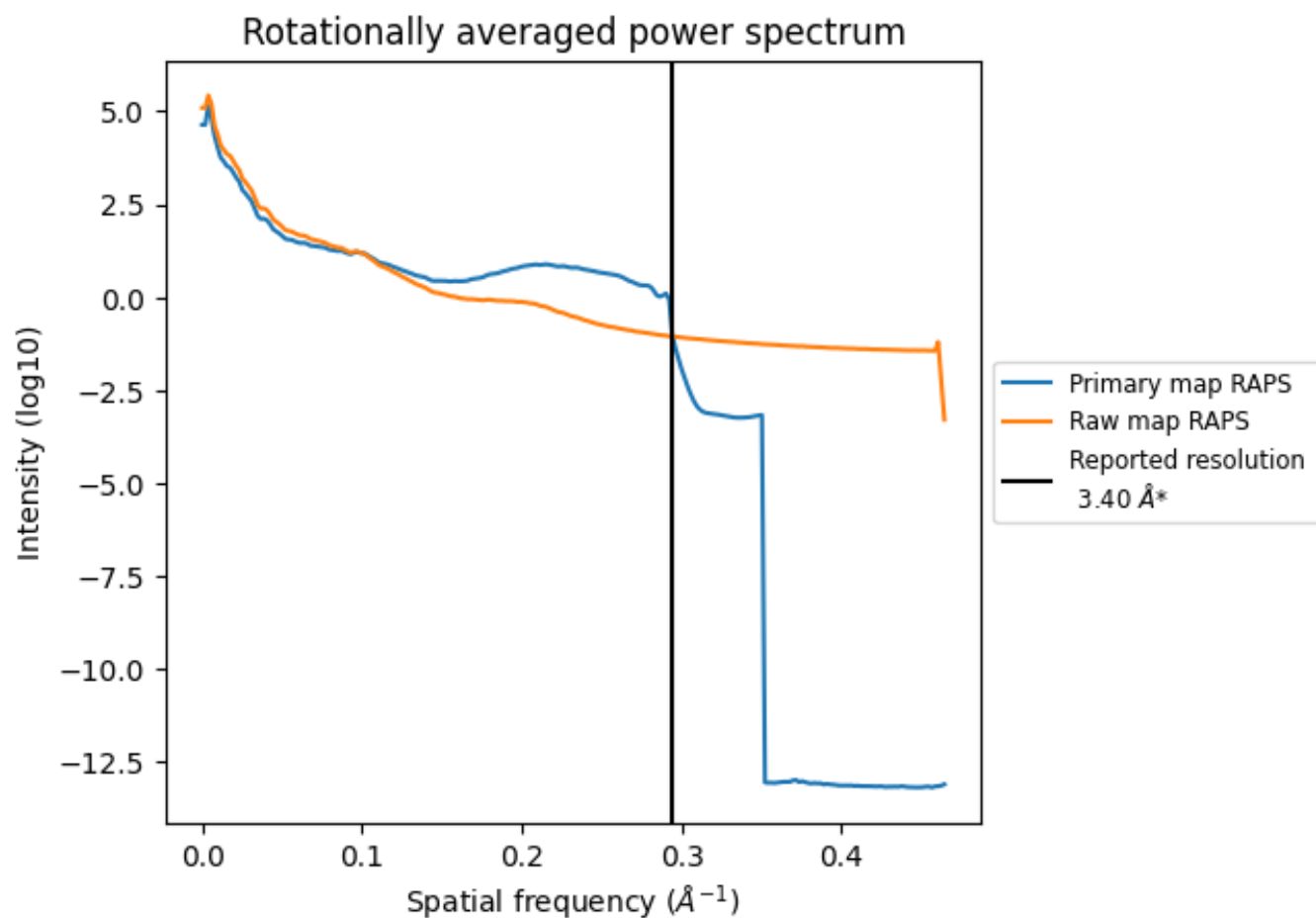
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1425 nm<sup>3</sup>; this corresponds to an approximate mass of 1287 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 ⓘ

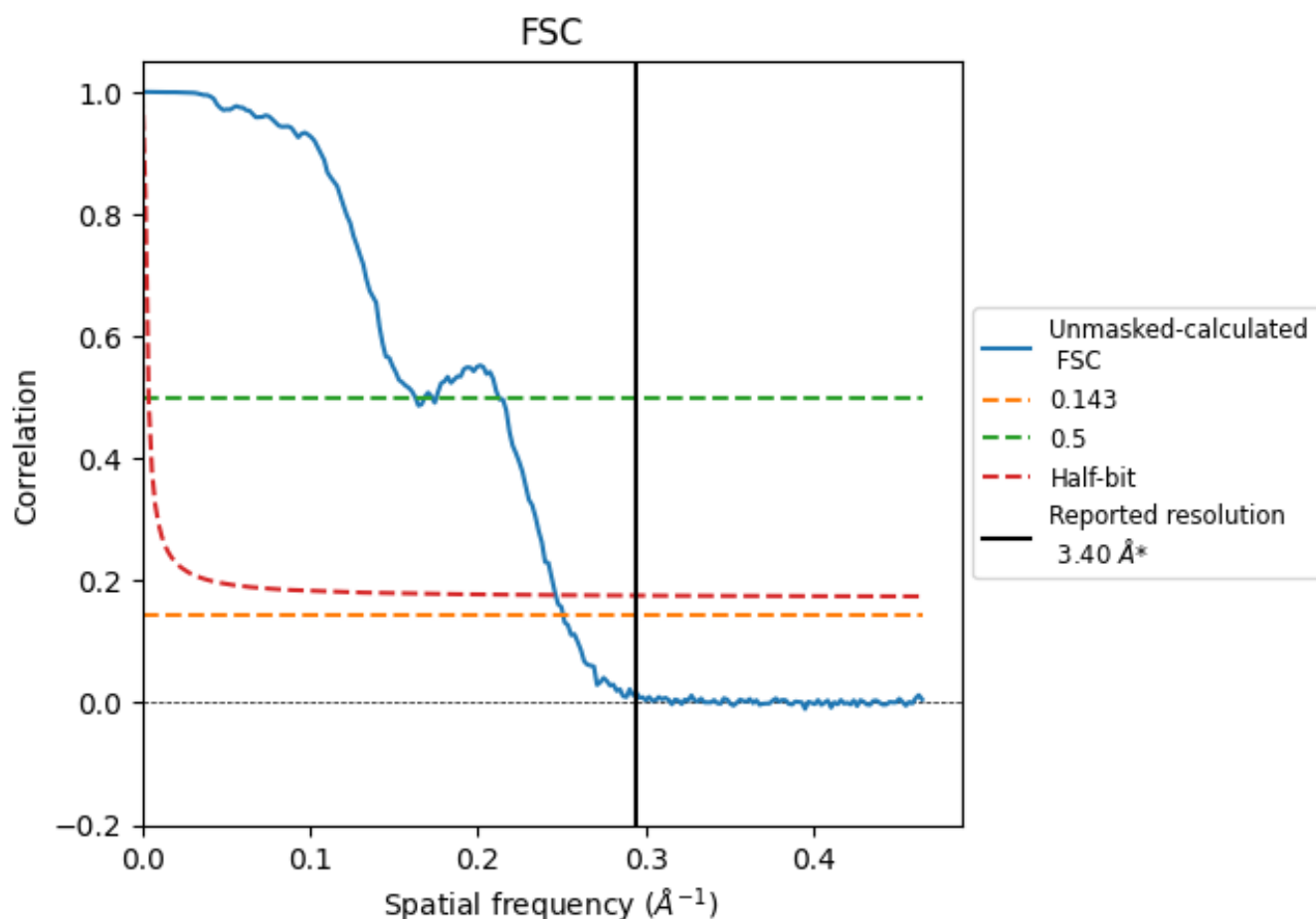


\*Reported resolution corresponds to spatial frequency of 0.294 Å<sup>-1</sup>

## 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 0.294 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	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.99	6.15	4.06

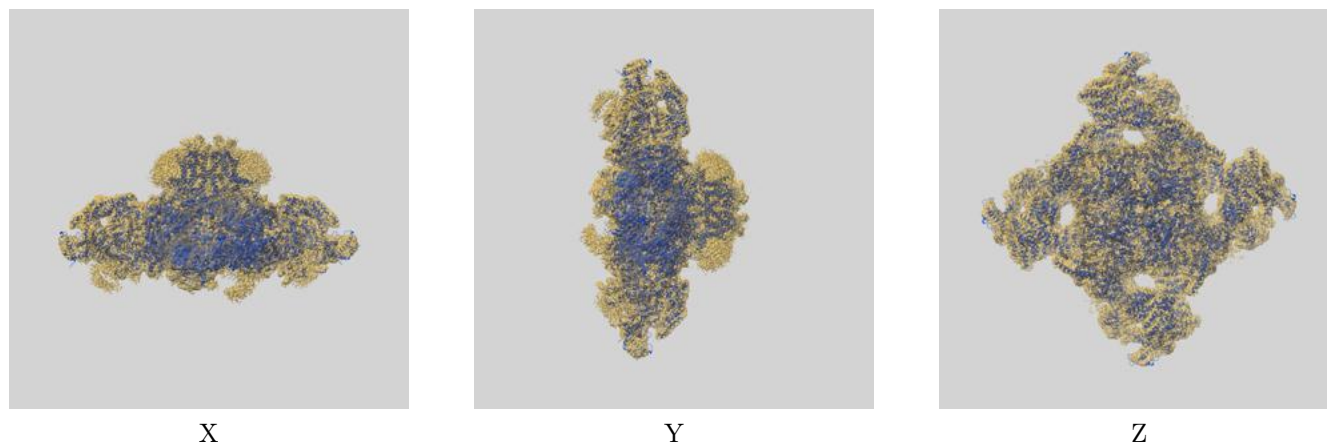
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.99 differs from the reported value 3.4 by more than 10 %



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

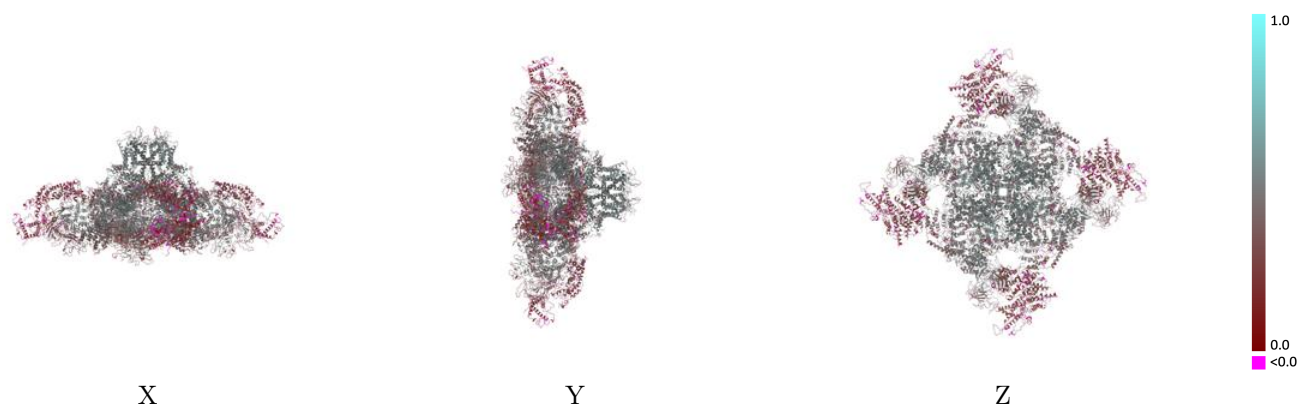
This section contains information regarding the fit between EMDB map EMD-38043 and PDB model 8X49. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

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



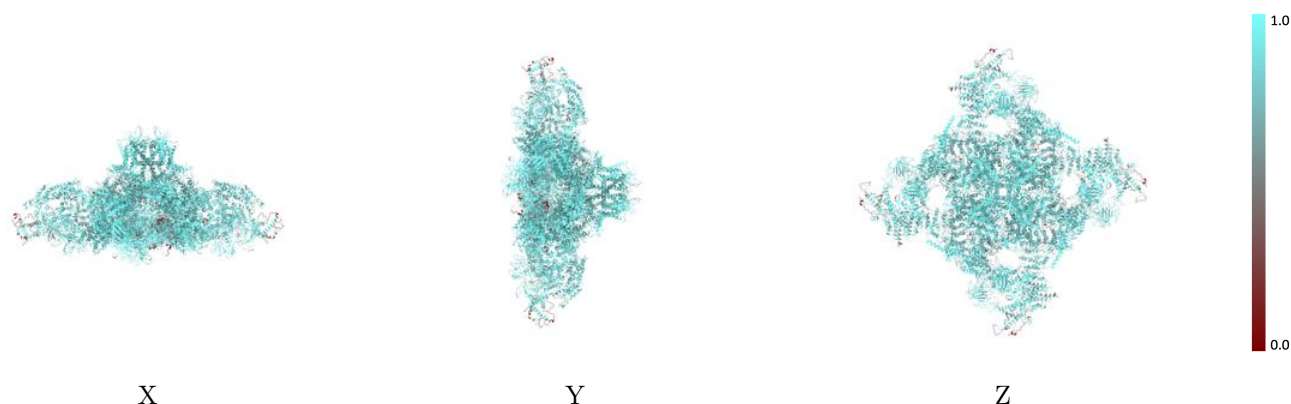
The images above show the 3D surface view of the map at the recommended contour level 0.466 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



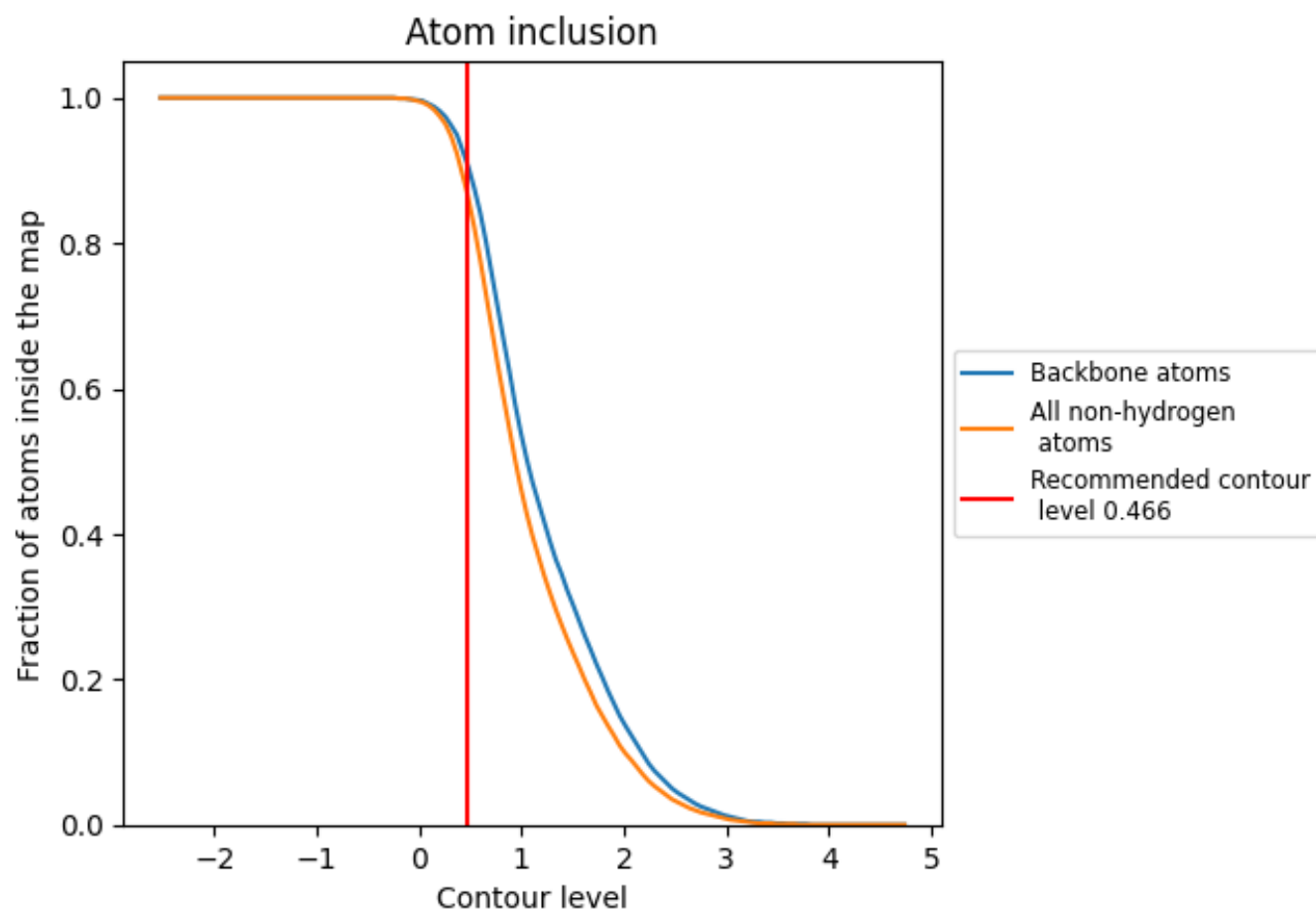
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.466).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 87% 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 (0.466) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8710	<div></div> 0.3900
A	<div></div> 0.8710	<div></div> 0.3900
B	<div></div> 0.8710	<div></div> 0.3900
C	<div></div> 0.8710	<div></div> 0.3900
D	<div></div> 0.8710	<div></div> 0.3900

