



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 05:50 AM UTC

PDB ID : 9OL6 / pdb_00009ol6
EMDB ID : EMD-70591
Title : Rabbit Ryanodine Receptor 1: DMSO Control Closed Conformation
Authors : Molinarolo, S.M.; Van Petegem, F.
Deposited on : 2025-05-12
Resolution : 3.11 Å(reported)
Based on initial model : 7TZC

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at 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>.

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

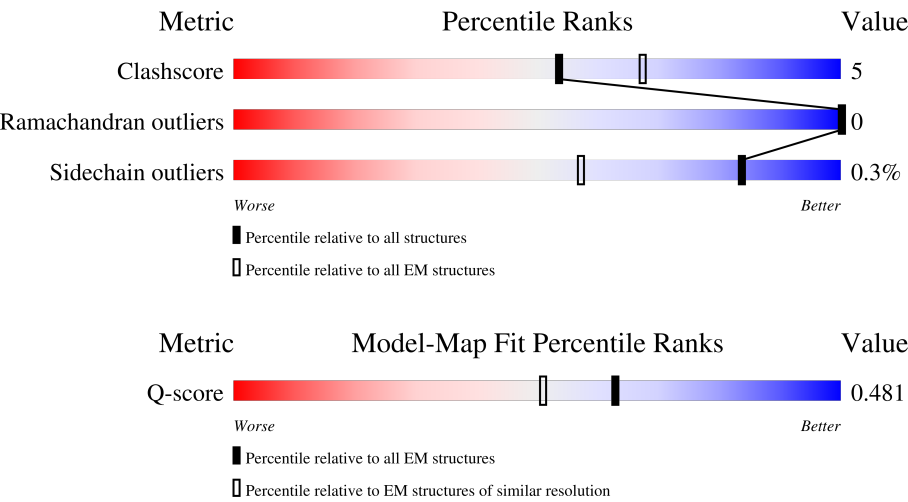
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.11 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.



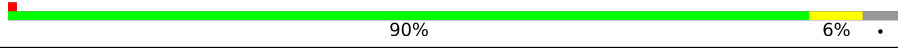
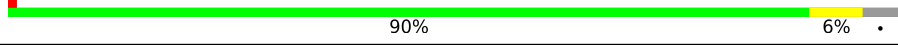
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14465 (2.61 - 3.61)

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 ≥ 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	7% 75% 7% 17%
1	G	5037	7% 76% 7% 17%
1	M	5037	7% 76% 7% 17%
1	S	5037	7% 75% 8% 17%

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Mol	Chain	Length	Quality of chain
2	B	111	 90%6%.
2	H	111	 90%6%.
2	N	111	 90%6%.
2	T	111	 90%6%.

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 133368 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	4185	Total	C	N	O	S	0	0
			32524	20790	5626	5890	218		
1	G	4185	Total	C	N	O	S	0	0
			32524	20790	5626	5890	218		
1	M	4185	Total	C	N	O	S	0	0
			32524	20790	5626	5890	218		
1	S	4185	Total	C	N	O	S	0	0
			32524	20790	5626	5890	218		

- Molecule 2 is a protein called Peptidyl-prolyl cis-trans isomerase FKBP1B.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	107	Total	C	N	O	S	0	0
			816	514	144	154	4		
2	H	107	Total	C	N	O	S	0	0
			816	514	144	154	4		
2	N	107	Total	C	N	O	S	0	0
			816	514	144	154	4		
2	T	107	Total	C	N	O	S	0	0
			816	514	144	154	4		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	SER	-	expression tag	UNP P68106
B	-1	ASN	-	expression tag	UNP P68106
B	0	ALA	-	expression tag	UNP P68106
H	-2	SER	-	expression tag	UNP P68106
H	-1	ASN	-	expression tag	UNP P68106
H	0	ALA	-	expression tag	UNP P68106
N	-2	SER	-	expression tag	UNP P68106
N	-1	ASN	-	expression tag	UNP P68106
N	0	ALA	-	expression tag	UNP P68106

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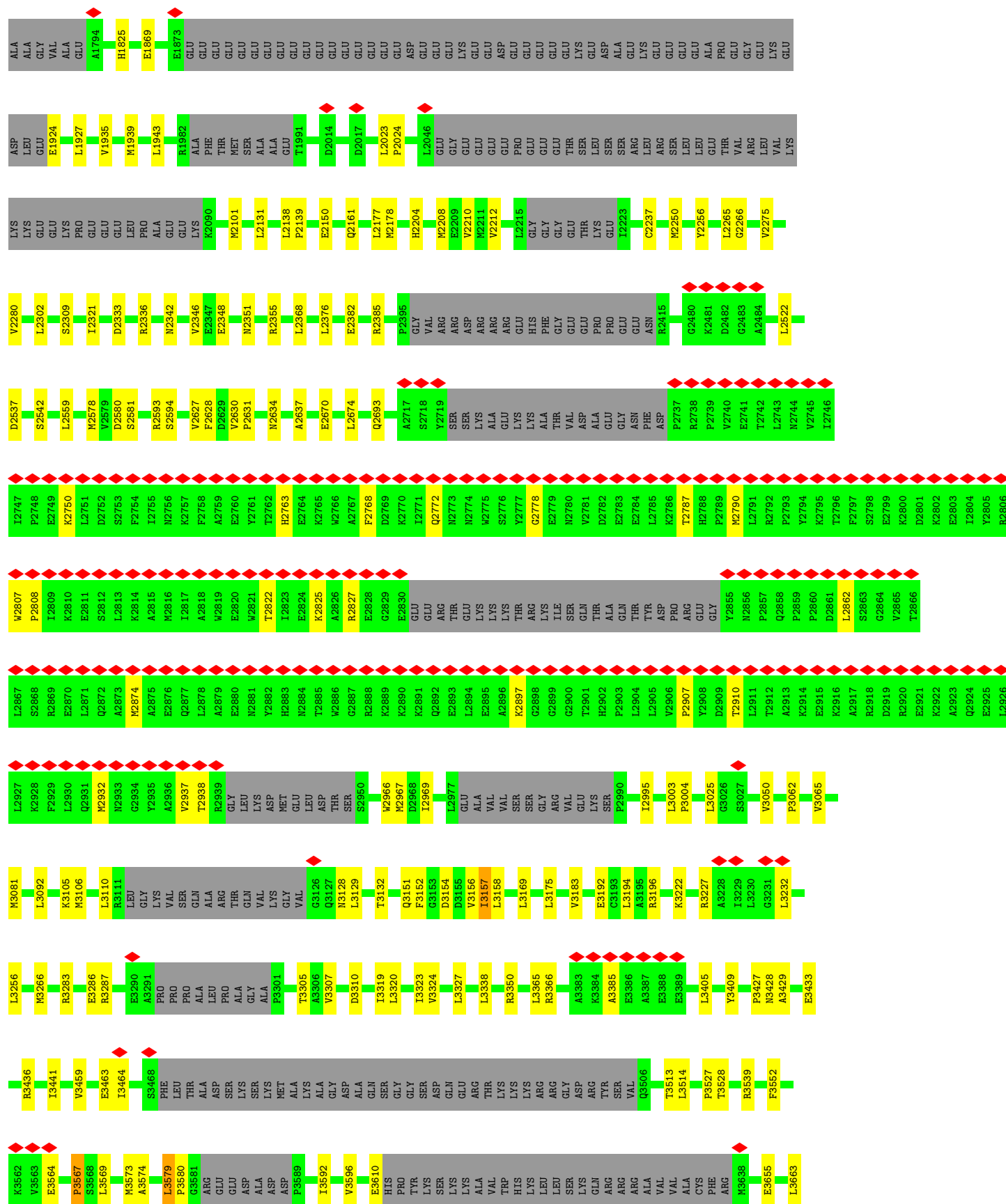
Chain	Residue	Modelled	Actual	Comment	Reference
T	-2	SER	-	expression tag	UNP P68106
T	-1	ASN	-	expression tag	UNP P68106
T	0	ALA	-	expression tag	UNP P68106

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total 1	Ca 1	0
3	G	1	Total 1	Ca 1	0
3	M	1	Total 1	Ca 1	0
3	S	1	Total 1	Ca 1	0

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

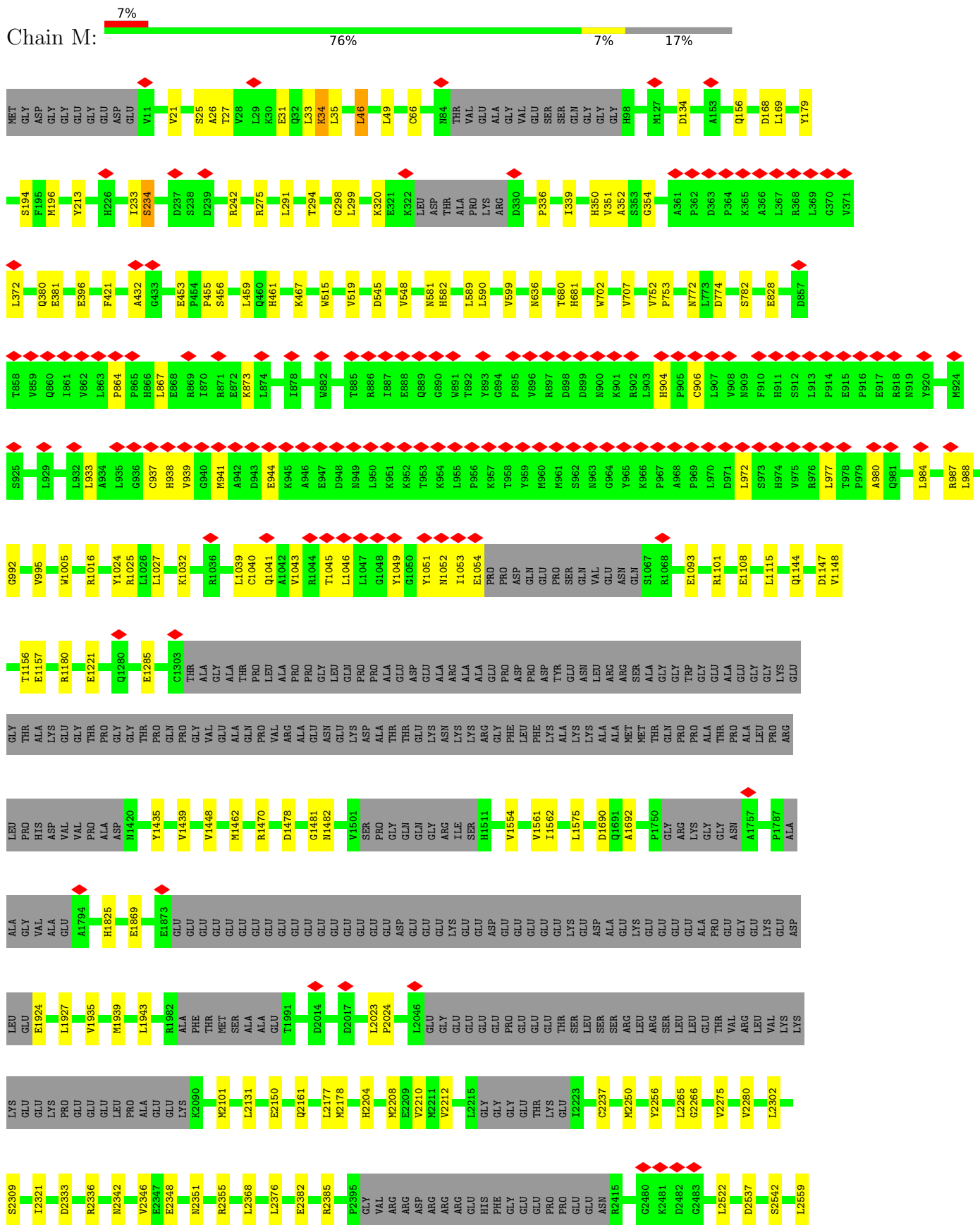
Mol	Chain	Residues	Atoms		AltConf
4	A	1	Total 1	Zn 1	0
4	G	1	Total 1	Zn 1	0
4	M	1	Total 1	Zn 1	0
4	S	1	Total 1	Zn 1	0







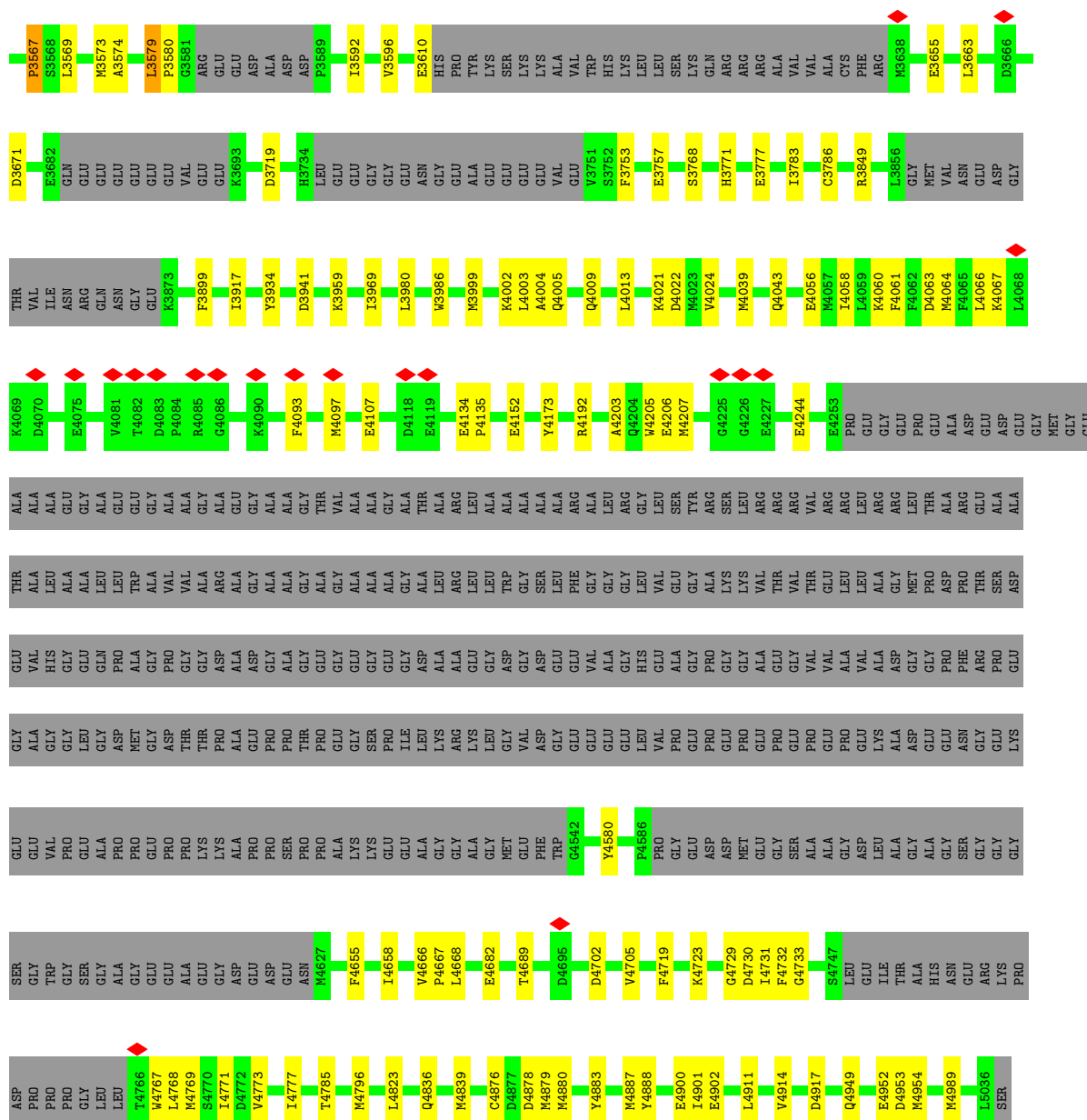
- Molecule 1: Ryanodine receptor 1



ALA	GLY	GLY	GLU	D4092	K3873	GLU	E286	K3106	M2932	Q2872	S2812	K2578
ALA	GLY	GLY	GLU	F4093	F3899	GLU	R3287	L3110	N2833	A2873	L2813	V2579
ALA	GLY	GLY	VAL	M4097	I3917	VAL	A3291	R3111	G2934	M2874	K2814	D2580
ALA	THR	VAL	GLU	E4107	D3941	GLU	PRO	LEU	Y2835	A2875	A2815	S2581
ALA	ALA	ALA	GLU	T3969	T3969	GLU	PRO	GLY	Y2836	E2876	M2816	R2593
ALA	GLY	ALA	ASP	D4118	T3969	GLU	PRO	VAL	V2937	Q2877	L2817	S2594
ALA	GLY	ALA	ASP	E4119	L3980	GLU	PRO	VAL	T2938	L2878	A2818	V2627
ALA	THR	ALA	ASP	E4134	L3980	GLU	PRO	VAL	R2839	A2879	W2819	D2629
ALA	ALA	ALA	P3589	H3734	K3986	GLU	GLY	THR	W2839	E2880	E2820	V2630
ARG	ARG	ALA	T3582	GLU	M3999	GLU	ALA	THR	LEU	Y2882	W2821	P2631
LEU	LEU	ALA	V3596	GLY	K4002	GLY	ALA	GLN	ASP	Y2882	T2822	
LEU	ALA	ALA	E3610	GLY	L4003	GLY	GLY	VAL	MET	H2883	L2823	N2634
TRP	ALA	ALA	HIS	GLY	A4004	GLY	GLY	VAL	GLY	N2884	E2824	A2637
SER	ALA	ALA	VAL	GLY	Q4005	GLY	VAL	VAL	ASP	T2885	K2825	
LEU	ALA	ALA	VAL	GLY	Q4005	GLY	D3310	Q3126	THR	W2886	A2826	E2670
PHE	ARG	ALA	VAL	GLY	Q4009	ALA	GLY	Q3127	SER	Q2887	R2827	L2674
GLY	ALA	ALA	VAL	GLY	W4205	GLU	L3319	N3128	GLU	R2888	Q2828	
GLY	ALA	ALA	VAL	GLY	E4206	GLU	L3320	L3129	W2866	K2889	Q2829	
GLY	ALA	ALA	VAL	GLY	E4207	GLU	L3320	L3129	M2967	K2890	E2830	Q2693
VAL	LEU	VAL	VAL	GLY	K4021	VAL	I3323	T3132	D2968	K2891	GLU	
GLU	SER	SER	VAL	GLY	V4024	GLU	L3338	Q3151	I2969	Q2892	ARG	A2717
GLY	TYR	GLY	THR	GLY	E4225	GLY	L3338	F3152		Q2772	THR	S2718
ALA	ARG	ALA	THR	GLY	E4226	GLY	R3350	G3153		N2773	GLU	Y2719
LYS	SER	LYS	VAL	GLY	E4227	GLY	L3365	D3154		N2774	LYS	SER
LYS	LEU	LYS	VAL	GLY	Q4043	GLY	R3366	R3155		W2775	LYS	SER
VAL	ARG	VAL	VAL	GLY	Q4043	GLY	R3366	R3155		S2776	LYS	LYS
THR	ARG	THR	THR	GLY	E4056	GLY	A3383	L3158		Q2777	THR	ALA
THR	ARG	THR	THR	GLY	M4057	GLY	A3384	L3169		G2778	GLU	GLY
GLY	ARG	GLY	THR	GLY	I4058	GLY	K3384	L3175		E2779	LYS	LYS
LEU	ARG	LEU	ARG	GLY	L4059	GLY	A3385	L3175		N2780	ALA	ALA
LEU	LEU	LEU	SER	GLY	K4060	GLY	E3386	V3183		V2781	THR	ALA
ALA	ARG	ALA	VAL	GLY	F4061	GLY	E3387	E3192		D2782	VAL	ASP
GLY	ARG	GLY	VAL	GLY	D4062	GLY	A3388	C3193		ASP	GLN	ALA
PRO	THR	PRO	VAL	GLY	M4064	GLY	E3389	L3194		E2784	THR	GLU
ASP	ALA	ASP	VAL	GLY	F4065	GLY	L3405	A3195		K2785	GLY	ASN
PRO	ARG	PRO	VAL	GLY	L4066	GLY	Y3409	R3196		K2786	ASP	PHE
THR	GLU	THR	VAL	GLY	K4067	GLY	K3222	K3222		ASP	ARG	ASP
SER	ALA	SER	VAL	GLY	L4068	GLY	P3407	R3227		H2788	GLY	P2737
ASP	ALA	ASP	VAL	GLY	K4069	GLY	N3428	A3228		P2738	ASP	R2738
GLU	THR	GLU	VAL	GLY	D4070	GLY	A3429	I3229		P2739	GLY	P2739
HIS	GLY	HIS	VAL	GLY	E4075	GLY	E3433	L3232		M2790	VAL	V2740
GLY	ALA	GLY	ALA	GLY	E4075	GLY	R3436	L3232		L2791	E2741	E2741
ALA	ALA	ALA	ALA	GLY	V4081	GLY	I3441	L3256		R2792	T2742	T2742
GLN	GLY	GLN	GLY	GLY	T4082	GLY	V3459	M3266		P2793	L2743	L2743
ALA	ALA	ALA	ALA	GLY	D4083	GLY	F3667	K3667		Y2794	N2744	N2744
PRO	ALA	PRO	ALA	GLY	F4084	GLY	S3668	I3569		K2795	V2745	V2745
PRO	GLY	PRO	VAL	GLY	R4085	GLY	L3569	M3266		T2796	L2746	L2746
GLY	VAL	GLY	VAL	GLY	G4086	GLY	M3573	R3283		F2797	I2747	I2747
ASP	ARG	ASP	ARG	ALA	K4090	GLY	A3574	I3464		S2798	P2748	P2748
					K4091	ALA				E2799	E2749	E2749
										K2800	K2750	K2750
										K2802	L2761	L2761
										K2803		
										I2804		
										Y2805		
										R2806		
										W2807		
										P2808		
										K2810		
										E2811		

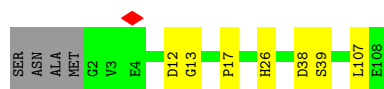






● Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B

Chain B: 90% 6% .



● Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B

Chain H: 90% 6% .



- Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B

Chain N:  90% 6% .



- Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B

Chain T:  90% 6% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	126217	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.269	Depositor
Minimum map value	0.000	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.047	Depositor
Map size (Å)	491.52, 491.52, 491.52	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.96, 0.96, 0.96	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: ZN, CA

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	0.40	0/33267	0.57	15/45152 (0.0%)
1	G	0.40	0/33267	0.57	16/45152 (0.0%)
1	M	0.40	0/33267	0.57	15/45152 (0.0%)
1	S	0.40	0/33267	0.57	16/45152 (0.0%)
2	B	0.77	0/832	0.70	0/1118
2	H	0.77	0/832	0.70	0/1118
2	N	0.78	0/832	0.70	0/1118
2	T	0.78	0/832	0.70	0/1118
All	All	0.41	0/136396	0.58	62/185080 (0.0%)

There are no bond length outliers.

The worst 5 of 62 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	4005	GLN	N-CA-C	-7.38	103.87	113.17
1	G	4005	GLN	N-CA-C	-7.37	103.88	113.17
1	S	4005	GLN	N-CA-C	-7.36	103.90	113.17
1	M	4005	GLN	N-CA-C	-7.34	103.92	113.17
1	G	3157	ILE	CA-C-O	-6.40	117.06	122.63

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	32524	0	31610	354	0
1	G	32524	0	31610	351	0
1	M	32524	0	31610	353	0
1	S	32524	0	31610	358	0
2	B	816	0	815	3	0
2	H	816	0	815	3	0
2	N	816	0	815	3	0
2	T	816	0	815	3	0
3	A	1	0	0	0	0
3	G	1	0	0	0	0
3	M	1	0	0	0	0
3	S	1	0	0	0	0
4	A	1	0	0	0	0
4	G	1	0	0	0	0
4	M	1	0	0	0	0
4	S	1	0	0	0	0
All	All	133368	0	129700	1377	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 5.

The worst 5 of 1377 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:939:VAL:HA	1:A:1053:ILE:HG22	1.36	1.08
1:G:939:VAL:HA	1:G:1053:ILE:HG22	1.36	1.07
1:S:939:VAL:HA	1:S:1053:ILE:HG22	1.35	1.03
1:M:939:VAL:HA	1:M:1053:ILE:HG22	1.36	1.01
1:G:3579:LEU:HD12	1:G:3580:PRO:HD3	1.46	0.97

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	4129/5037 (82%)	4034 (98%)	95 (2%)	0	100	100
1	G	4129/5037 (82%)	4034 (98%)	95 (2%)	0	100	100
1	M	4129/5037 (82%)	4034 (98%)	95 (2%)	0	100	100
1	S	4129/5037 (82%)	4035 (98%)	94 (2%)	0	100	100
2	B	105/111 (95%)	102 (97%)	3 (3%)	0	100	100
2	H	105/111 (95%)	102 (97%)	3 (3%)	0	100	100
2	N	105/111 (95%)	102 (97%)	3 (3%)	0	100	100
2	T	105/111 (95%)	102 (97%)	3 (3%)	0	100	100
All	All	16936/20592 (82%)	16545 (98%)	391 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	3402/4276 (80%)	3393 (100%)	9 (0%)	86	86
1	G	3402/4276 (80%)	3394 (100%)	8 (0%)	87	87
1	M	3402/4276 (80%)	3393 (100%)	9 (0%)	86	86
1	S	3402/4276 (80%)	3394 (100%)	8 (0%)	87	87
2	B	87/91 (96%)	86 (99%)	1 (1%)	65	76
2	H	87/91 (96%)	86 (99%)	1 (1%)	65	76
2	N	87/91 (96%)	86 (99%)	1 (1%)	65	76
2	T	87/91 (96%)	86 (99%)	1 (1%)	65	76
All	All	13956/17468 (80%)	13918 (100%)	38 (0%)	84	86

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	N	26	HIS
1	S	4876	CYS

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Mol	Chain	Res	Type
1	S	34	LYS
1	S	3025	LEU
2	T	26	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 162 such sidechains are listed below:

Mol	Chain	Res	Type
1	M	3994	HIS
1	S	2194	HIS
1	M	4109	GLN
1	S	736	HIS
1	S	2931	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 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.

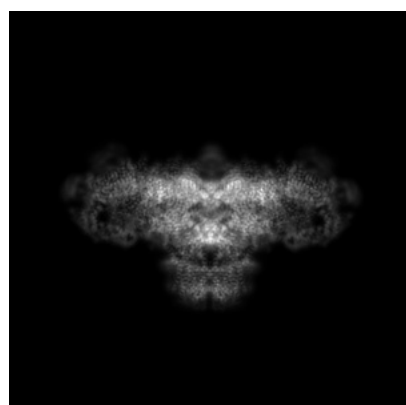
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-70591. These allow visual inspection of the internal detail of the map and identification of artifacts.

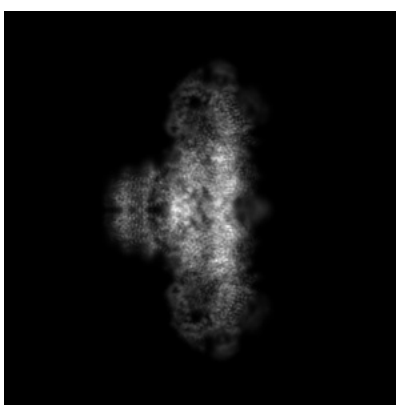
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

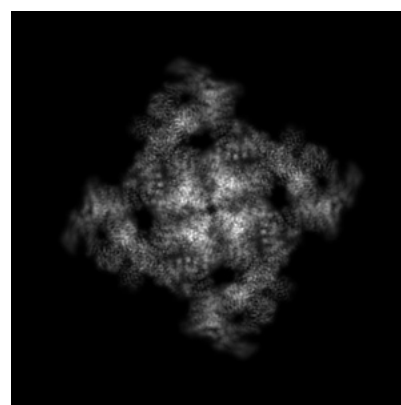
6.1.1 Primary map



X



Y



Z

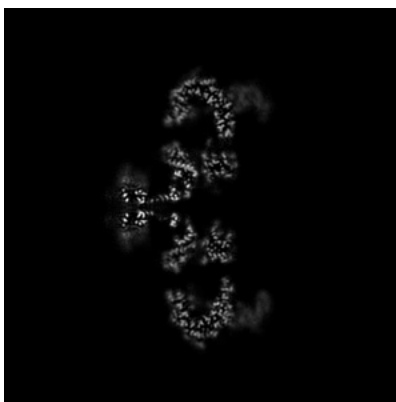
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

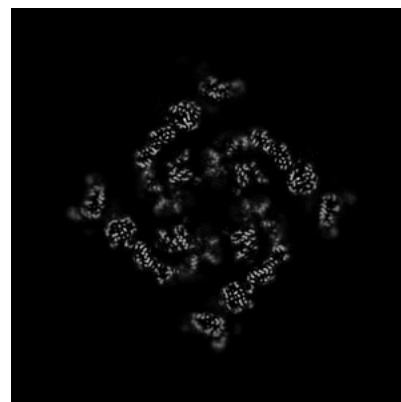
6.2.1 Primary map



X Index: 256



Y Index: 256

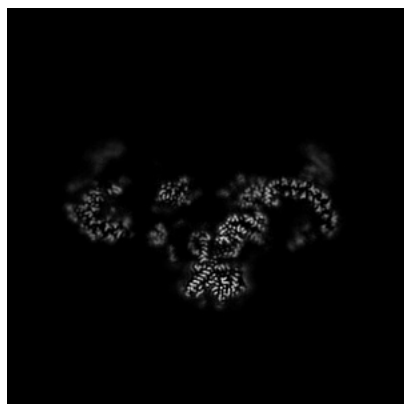


Z Index: 256

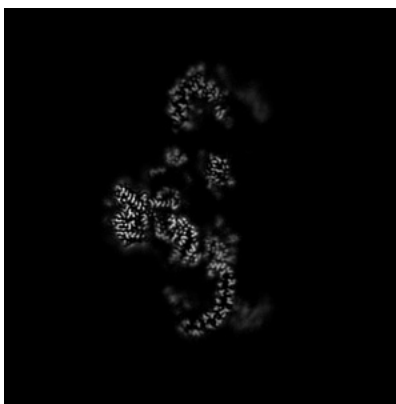
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

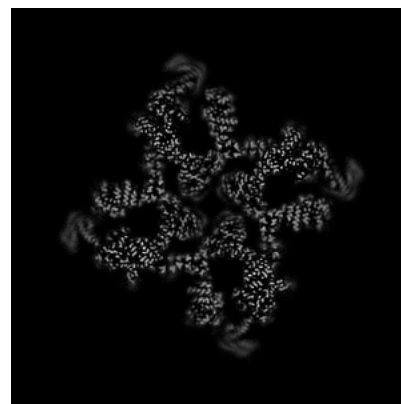
6.3.1 Primary map



X Index: 266



Y Index: 267

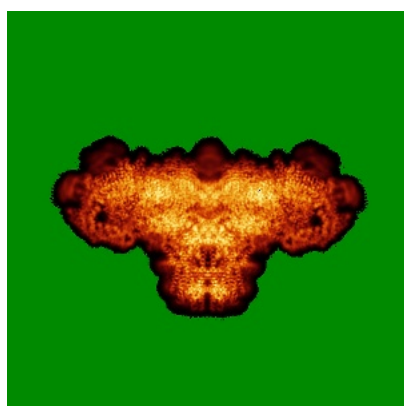


Z Index: 277

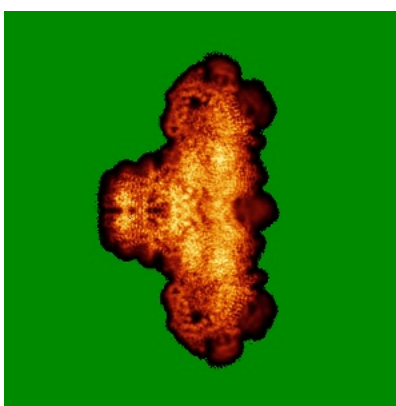
The images above show the largest variance slices of the map in three orthogonal directions.

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

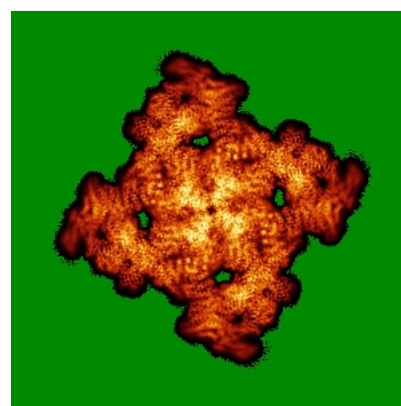
6.4.1 Primary map



X



Y

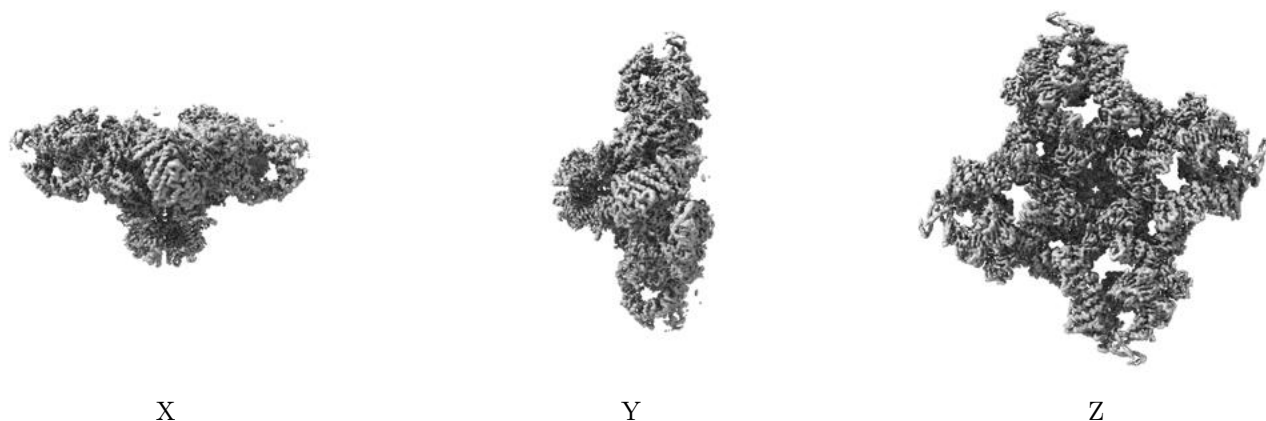


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.047. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

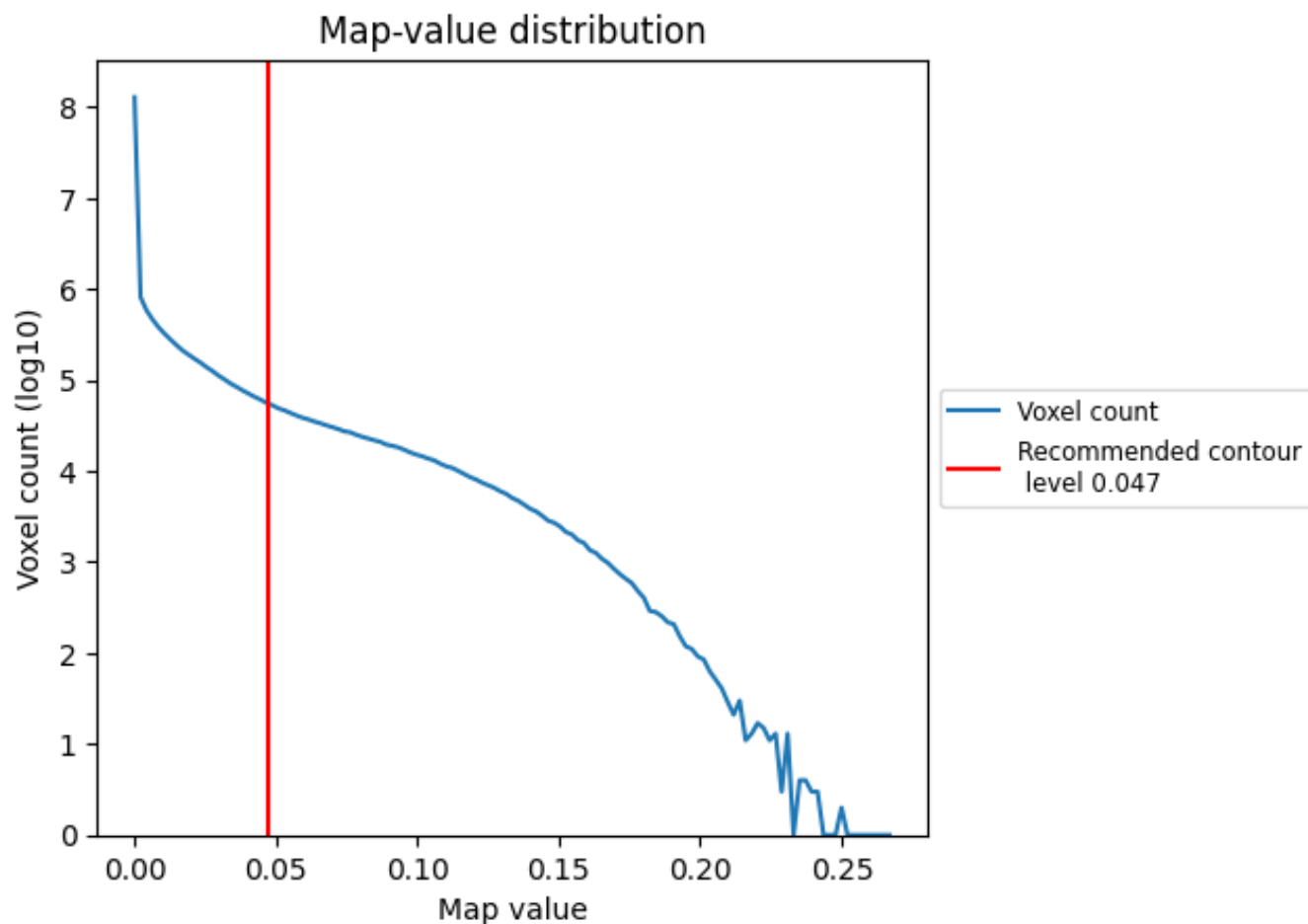
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

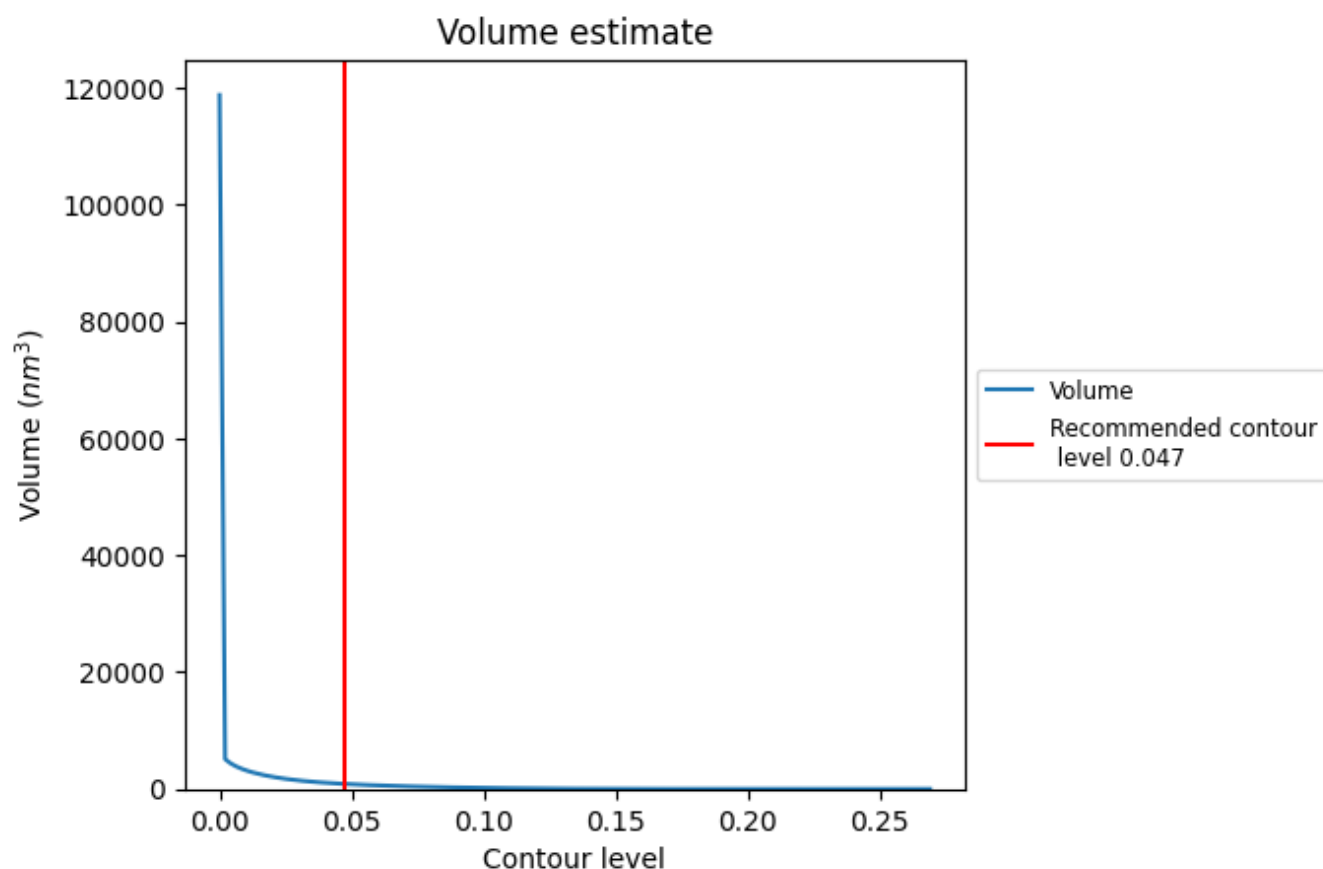
This section contains the results of statistical analysis of the map.

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.

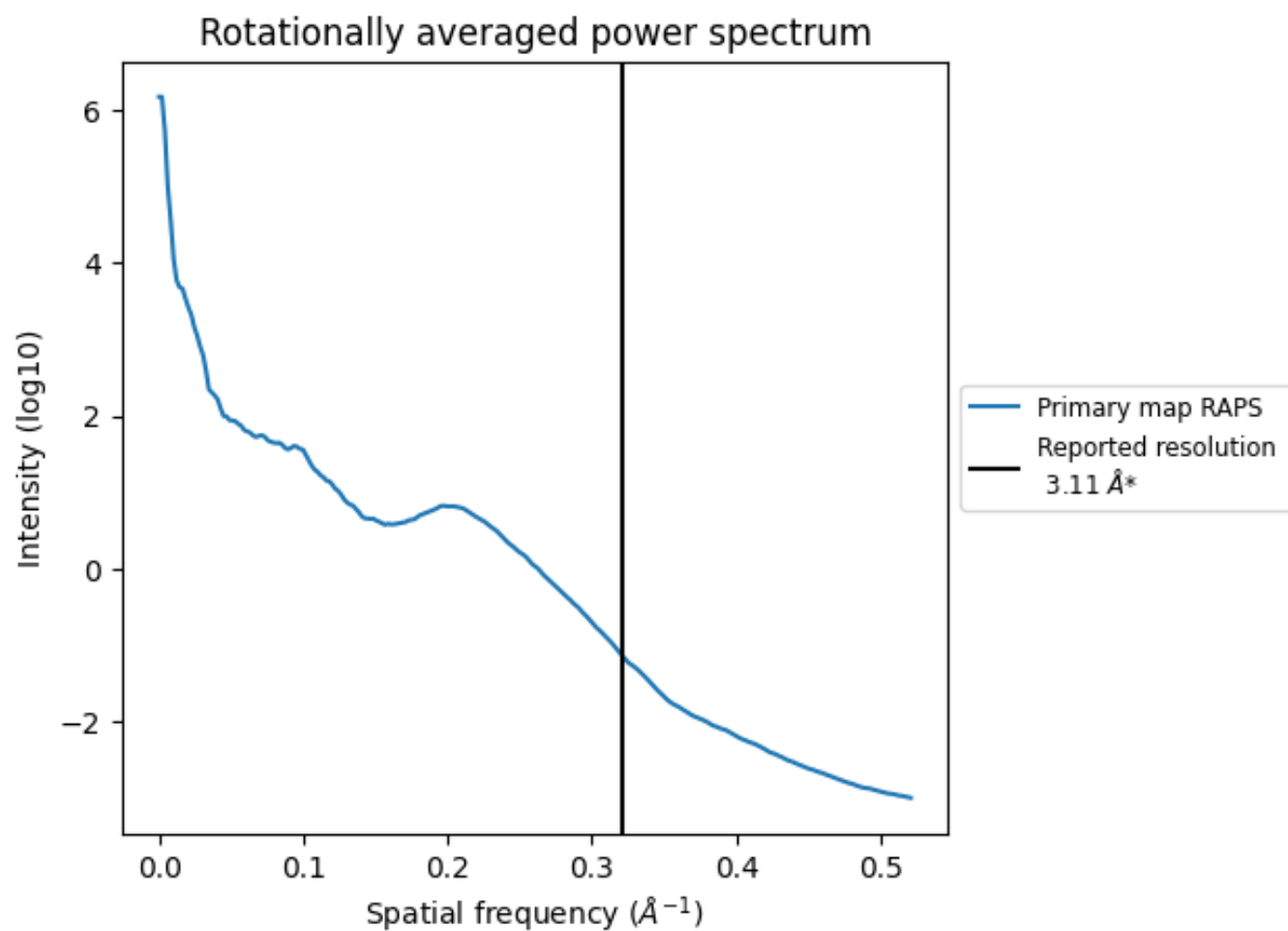
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 871 nm^3 ; this corresponds to an approximate mass of 787 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 0.322 Å⁻¹

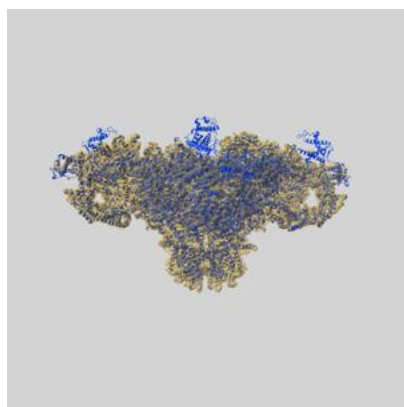
8 Fourier-Shell correlation

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

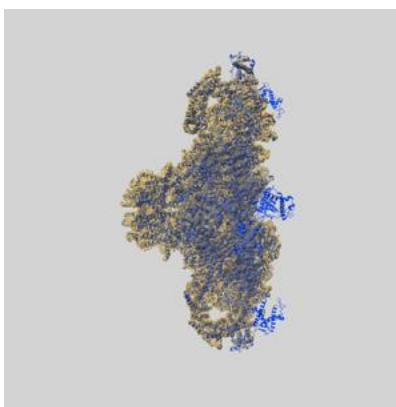
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-70591 and PDB model 9OL6. Per-residue inclusion information can be found in section [3](#) on page [6](#).

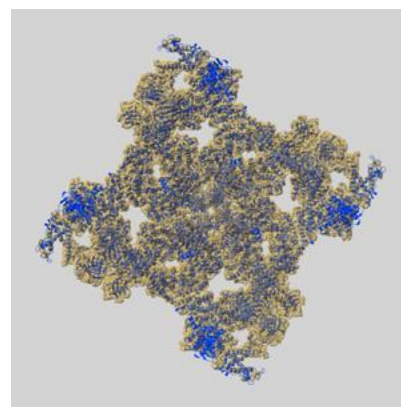
9.1 Map-model overlay [i](#)



X



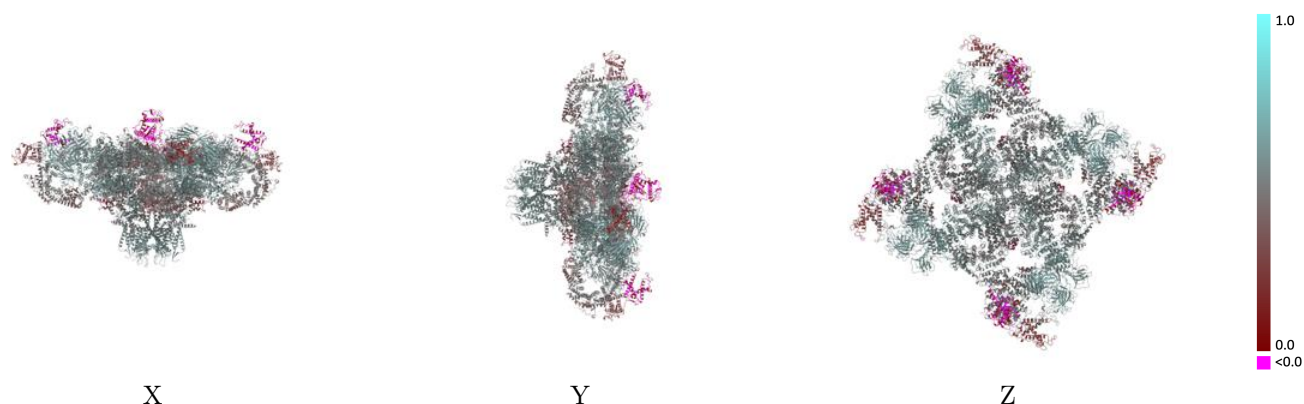
Y



Z

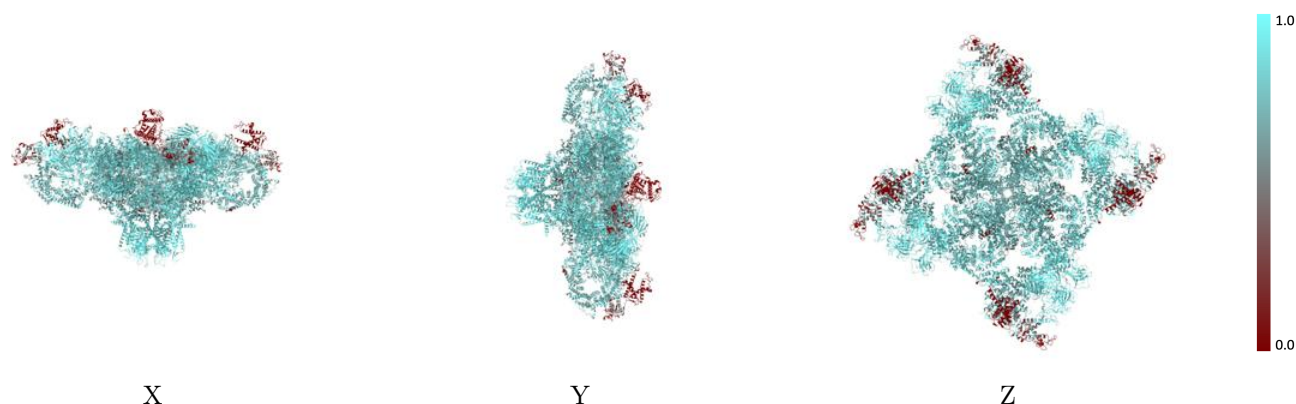
The images above show the 3D surface view of the map at the recommended contour level 0.047 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



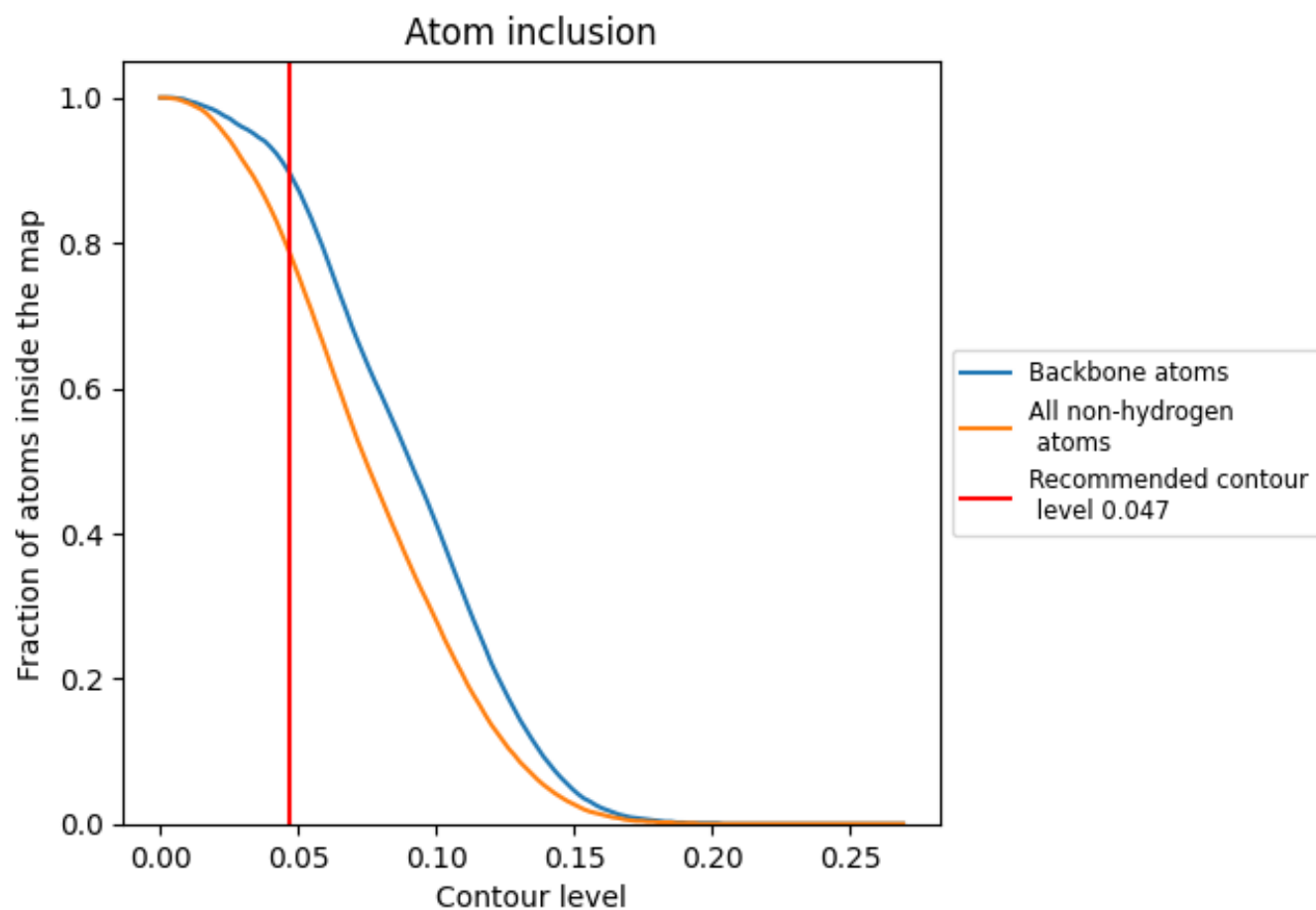
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.047).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 78% 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 (0.047) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7850	0.4810
A	0.7820	0.4790
B	0.8660	0.5590
G	0.7830	0.4800
H	0.8690	0.5620
M	0.7830	0.4800
N	0.8690	0.5600
S	0.7820	0.4790
T	0.8680	0.5630

