



wwPDB EM Validation Summary Report ⓘ

Nov 24, 2025 – 01:15 PM EST

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.dev129
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.46

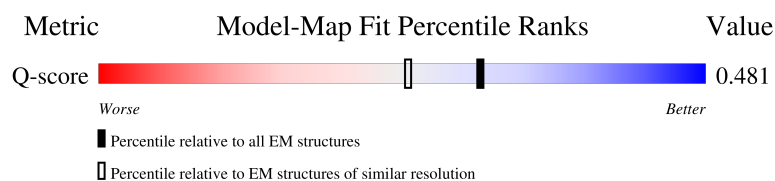
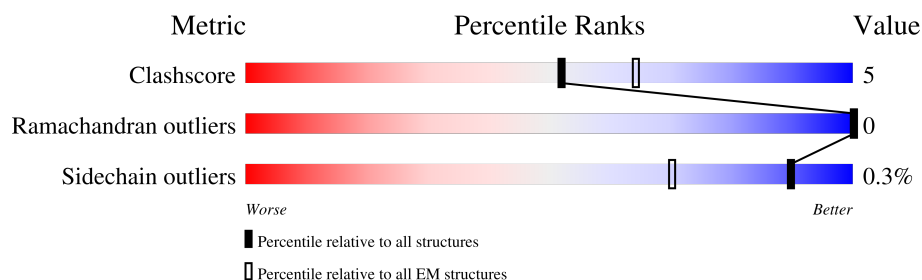
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.11 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	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
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	
1	G	5037	
1	M	5037	
1	S	5037	

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Mol	Chain	Length	Quality of chain
2	B	111	<div><div></div><div>90%</div><div>6%</div><div></div></div>
2	H	111	<div><div></div><div>90%</div><div>6%</div><div></div></div>
2	N	111	<div><div></div><div>90%</div><div>6%</div><div></div></div>
2	T	111	<div><div></div><div>90%</div><div>6%</div><div></div></div>

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	-3	SER	-	expression tag	UNP P68106
B	-2	ASN	-	expression tag	UNP P68106
B	-1	ALA	-	expression tag	UNP P68106
H	-3	SER	-	expression tag	UNP P68106
H	-2	ASN	-	expression tag	UNP P68106
H	-1	ALA	-	expression tag	UNP P68106
N	-3	SER	-	expression tag	UNP P68106
N	-2	ASN	-	expression tag	UNP P68106
N	-1	ALA	-	expression tag	UNP P68106

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Chain	Residue	Modelled	Actual	Comment	Reference
T	-3	SER	-	expression tag	UNP P68106
T	-2	ASN	-	expression tag	UNP P68106
T	-1	ALA	-	expression tag	UNP P68106

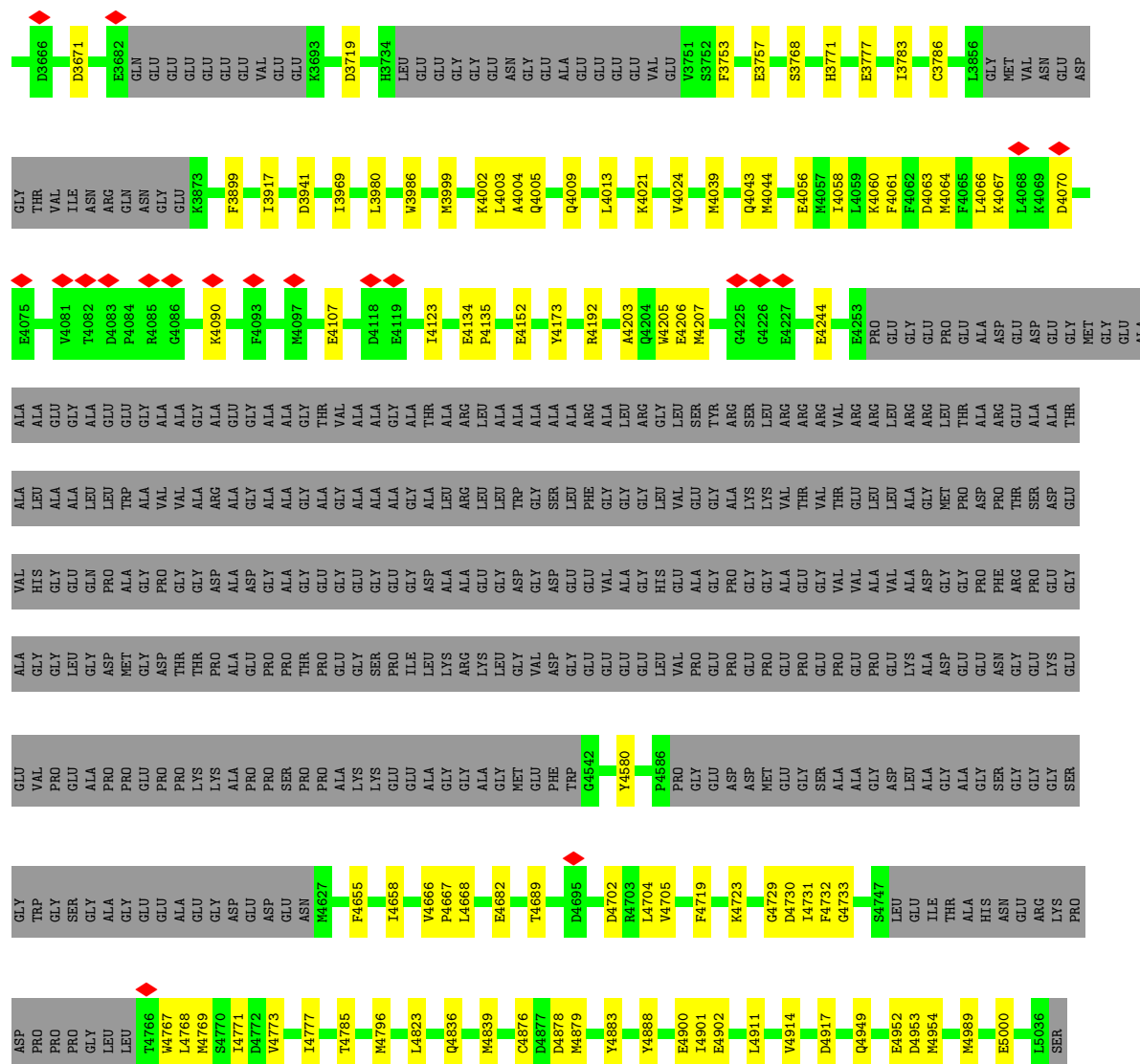
- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

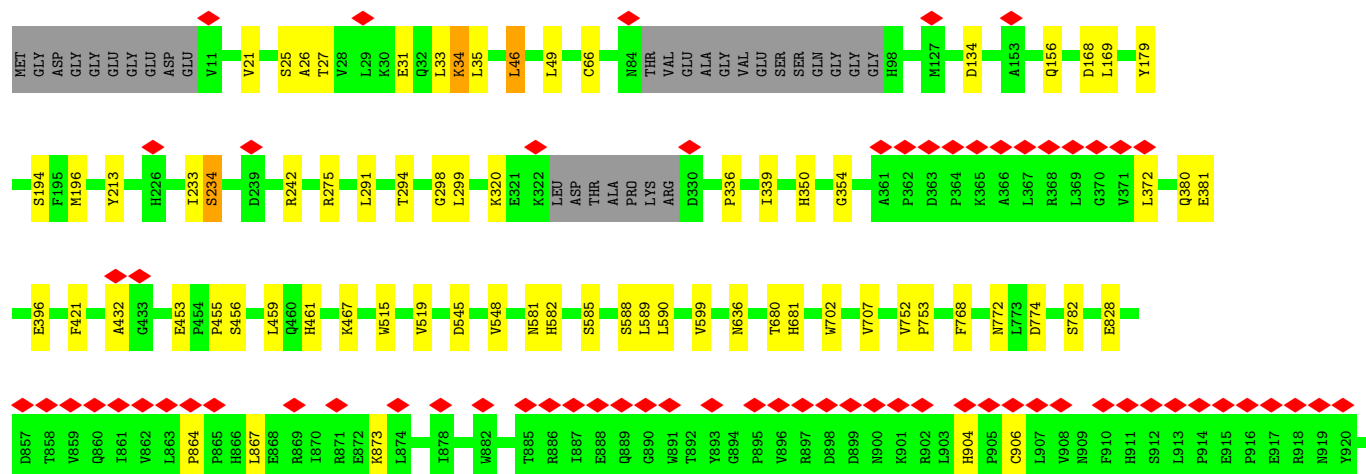
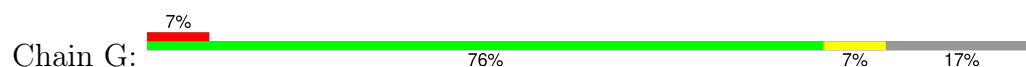
- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

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





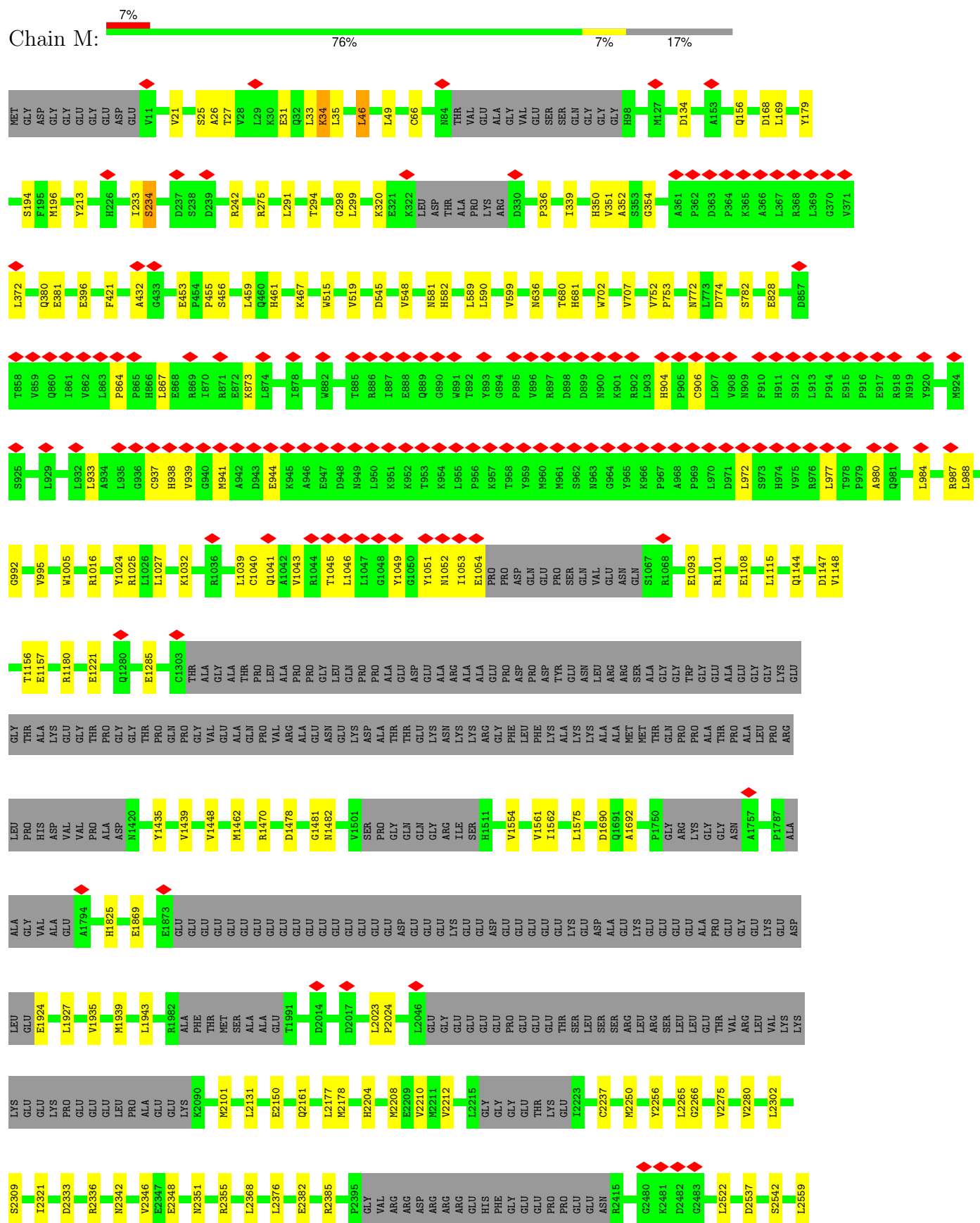
• Molecule 1: Ryanodine receptor 1







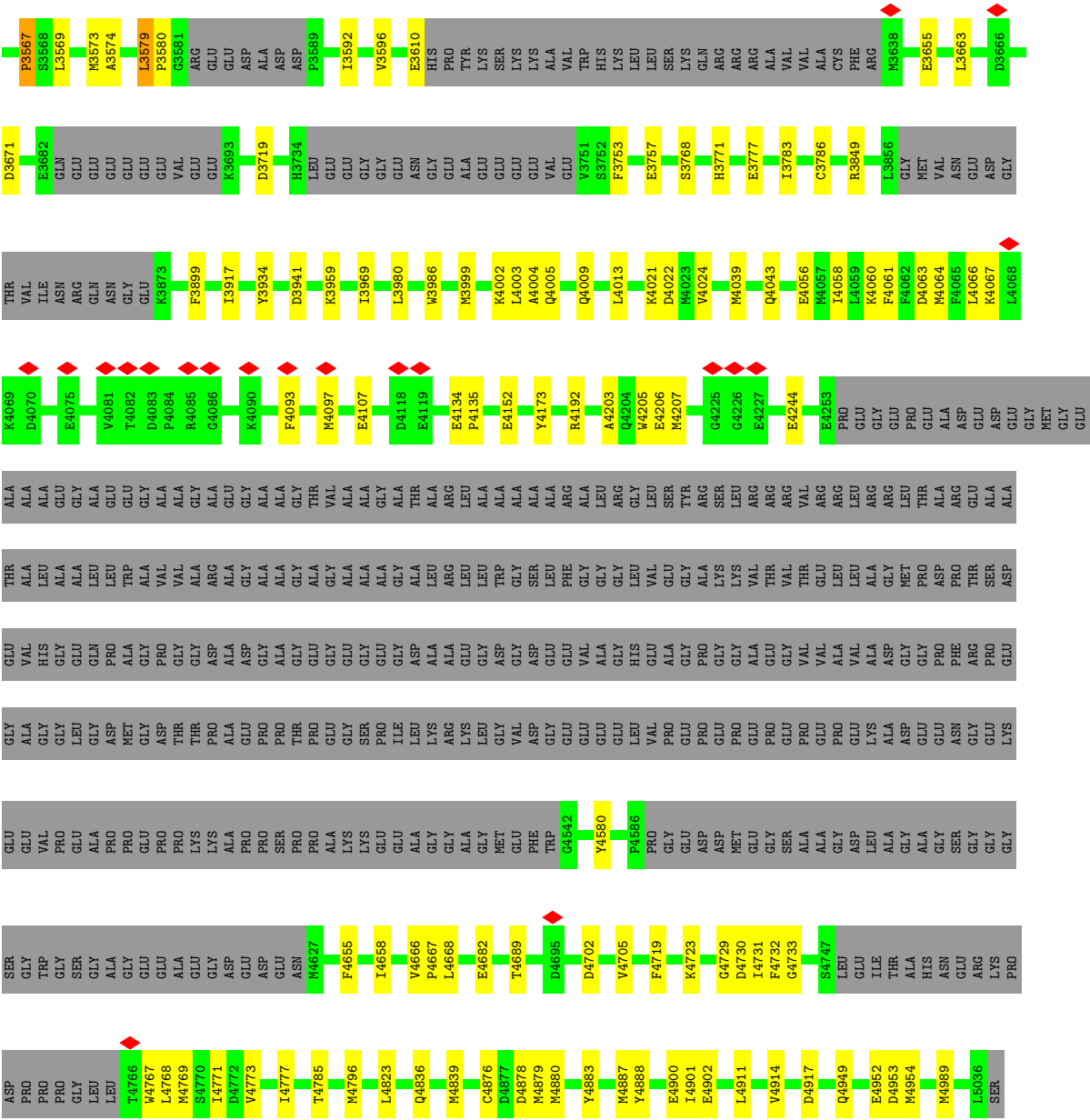
- Molecule 1: Ryanodine receptor 1



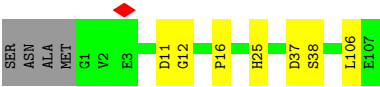
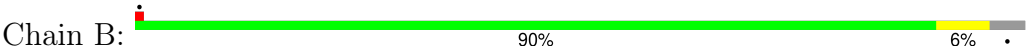
ALA	GLY	GLY	GLU	D4092	K3873	GLU	E286	K3106	M2932	Q2872	S2812	D2752	K2578
ALA	GLY	GLY	GLU	F4093	F3899	GLU	R3287	L3110	N2833	A2873	L2813	S2763	V2579
ALA	GLY	GLY	VAL	M4097	I3917	VAL	A3291	R3111	G2934	M2874	K2814	F2764	D2580
ALA	THR	VAL	GLU	E4107	D3941	GLU	PRO	LEU	Y2835	A2875	A2815	I2765	S2581
ALA	ALA	ALA	GLU	T3969	T3969	GLU	PRO	GLY	Y2836	E2876	M2816	N2766	R2593
ALA	GLY	ALA	ASP	L3980	L3980	GLU	PRO	VAL	V2937	Q2877	L2817	K2767	S2594
ALA	GLY	ALA	ASP	E4118	E4118	GLU	PRO	VAL	T2938	L2878	L2818	F2768	V2627
ALA	GLY	ALA	ASP	E4119	E4119	GLU	PRO	VAL	R2839	A2879	L2819	F2769	F2628
ALA	THR	ALA	ALA	E4134	E4134	GLU	GLY	THR	GLY	E2880	E2820	E2760	D2629
ALA	ALA	ALA	ALA	P4135	P4135	GLU	ALA	ALA	R2839	N2881	W2821	Y2761	V2630
ARG	ARG	ARG	GLU	E4152	E4152	GLU	ALA	THR	ASP	Y2882	W2822	T2762	P2631
LEU	LEU	LEU	GLY	Y4173	Y4173	GLY	VAL	GLN	ASP	H2883	L2823	H2763	N2634
TRP	ALA	ALA	GLY	K4002	K4002	GLU	T3305	LYS	GLY	N2884	E2824	E2764	A2637
ALA	ALA	ALA	ASN	A4004	A4004	GLY	A3306	GLY	LEU	T2885	K2825	K2765	
LEU	ALA	ALA	GLY	Q4005	Q4005	GLY	V3307	VAL	ASP	W2886	A2826	W2766	E2670
PHE	ARG	ARG	PRO	Q4009	Q4009	GLU	D3310	Q3126	THR	Q2887	R2827	A2767	L2674
GLY	ALA	ALA	ALA	W4205	W4205	GLU	I3319	Q3127	GLY	K2888	Q2828	F2768	Q2693
GLY	ALA	ALA	GLY	E4206	E4206	GLU	L3320	N3128	ASP	K2889	Q2829	D2769	
LEU	GLY	GLY	GLY	M4207	M4207	GLY	L3320	L3129	SER	K2890	E2830	K2770	
VAL	LEU	LEU	VAL	K4021	K4021	VAL	I3323	T3132	W2866	K2891	GLU	I2771	A2717
GLU	SER	SER	GLU	V4024	V4024	GLU	L3338	Q3151	M2967	Q2892	ARG	Q2772	S2718
THR	ARG	ARG	THR	E4225	E4225	THR	L3338	F3152	D2968	E2893	THR	N2773	Y2719
VAL	ARG	ARG	VAL	E4226	E4226	THR	L3338	G3153	I2969	N2774	GLU	N2774	SER
VAL	ARG	ARG	VAL	E4227	E4227	THR	R3350	D3154		W2775	LYS	W2775	SER
VAL	ARG	ARG	VAL	E4244	E4244	THR	L3365	R3155		S2776	LYS	S2776	LYS
THR	ARG	ARG	THR	E4253	E4253	THR	R3366	T3157		A2896	ALA	A2896	ALA
THR	ARG	ARG	THR	M4057	M4057	THR	A3383	L3158		G2898	THR	G2778	GLU
GLY	GLY	GLY	GLY	L4058	L4058	THR	K3384	L3169		G2899	LYS	E2779	LYS
GLY	GLY	GLY	GLY	L4059	L4059	THR	A3385	L3175		G2900	ILE	N2780	ALA
GLY	GLY	GLY	GLY	L4060	L4060	THR	A3386	V3183		T2901	GLN	V2781	THR
GLY	GLY	GLY	GLY	L4061	L4061	THR	E3387	E3192		H2902	THR	D2782	VAL
GLY	GLY	GLY	GLY	L4062	L4062	THR	A3388	C3193		P2903	GLN	D2783	ASP
GLY	GLY	GLY	GLY	L4063	L4063	THR	E3389	L3194		L2904	THR	E2784	ALA
GLY	GLY	GLY	GLY	L4064	L4064	THR	L3405	A3195		L2905	TYR	L2785	GLY
GLY	GLY	GLY	GLY	L4065	L4065	THR	Y3409	R3196		V2906	ASP	K2786	ASN
GLY	GLY	GLY	GLY	L4066	L4066	THR	L3409	K3222		P2907	PRO	T2787	PHE
GLY	GLY	GLY	GLY	L4067	L4067	THR	P3407	R3227		Y2908	GLY	H2788	ASP
GLY	GLY	GLY	GLY	L4068	L4068	THR	N3428	A3228		D2909	GLY	P2789	R2738
GLY	GLY	GLY	GLY	L4069	L4069	THR	A3429	I3229		T2910	GLY	M2790	P2739
GLY	GLY	GLY	GLY	L4070	L4070	THR	E3433	L3232		L2911	GLY	L2791	V2740
GLY	GLY	GLY	GLY	E4075	E4075	THR	R3436	L3232		T2912	GLY	R2792	E2741
GLY	GLY	GLY	GLY	V4081	V4081	THR	I3441	L3256		A2913	GLY	R2793	T2742
GLY	GLY	GLY	GLY	T4082	T4082	THR	V3459	K3266		K2914	GLY	Y2794	L2743
GLY	GLY	GLY	GLY	D4083	D4083	THR	E3463	K3283		E2915	GLY	K2795	N2744
GLY	GLY	GLY	GLY	P4084	P4084	THR	I3464			K2916	GLY	T2796	V2745
GLY	GLY	GLY	GLY	R4085	R4085	THR				A2917	GLY	L2797	L2746
GLY	GLY	GLY	GLY	G4086	G4086	THR				R2918	GLY	S2798	I2747
GLY	GLY	GLY	GLY	K4090	K4090	THR				D2919	GLY	E2799	P2748
GLY	GLY	GLY	GLY	K4091	K4091	THR				R2920	GLY	K2800	E2749
GLY	GLY	GLY	GLY			THR				K2921	GLY	K2802	K2750
GLY	GLY	GLY	GLY			THR				K2922	GLY	K2803	L2761
GLY	GLY	GLY	GLY			THR				K2923	GLY	I2804	
GLY	GLY	GLY	GLY			THR				Q2924	GLY	Y2805	
GLY	GLY	GLY	GLY			THR				E2925	GLY	R2806	
GLY	GLY	GLY	GLY			THR				L2926	GLY	R2807	
GLY	GLY	GLY	GLY			THR				L2927	GLY	Y2808	
GLY	GLY	GLY	GLY			THR				K2928	GLY	K2810	
GLY	GLY	GLY	GLY			THR				L2930	GLY	E2811	
GLY	GLY	GLY	GLY			THR				Q2931	GLY		



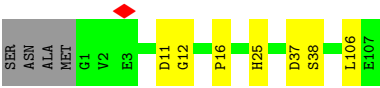
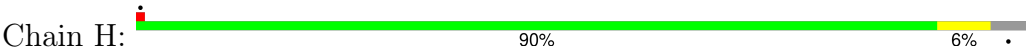




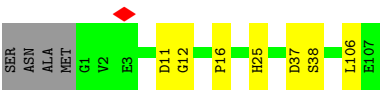
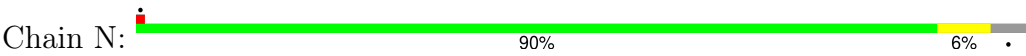
● Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B



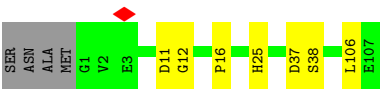
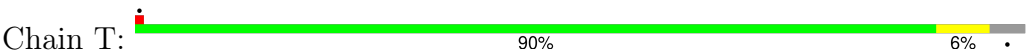
● Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B



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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	818	3	0
2	H	816	0	818	3	0
2	N	816	0	818	3	0
2	T	816	0	818	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	129712	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 ⓘ

5.3.1 Protein backbone ⓘ

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%)	91	95
1	G	3402/4276 (80%)	3394 (100%)	8 (0%)	92	96
1	M	3402/4276 (80%)	3393 (100%)	9 (0%)	91	95
1	S	3402/4276 (80%)	3394 (100%)	8 (0%)	92	96
2	B	87/91 (96%)	86 (99%)	1 (1%)	70	83
2	H	87/91 (96%)	86 (99%)	1 (1%)	70	83
2	N	87/91 (96%)	86 (99%)	1 (1%)	70	83
2	T	87/91 (96%)	86 (99%)	1 (1%)	70	83
All	All	13956/17468 (80%)	13918 (100%)	38 (0%)	90	95

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

Mol	Chain	Res	Type
2	N	25	HIS
1	S	4876	CYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	S	34	LYS
1	S	3025	LEU
2	T	25	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.

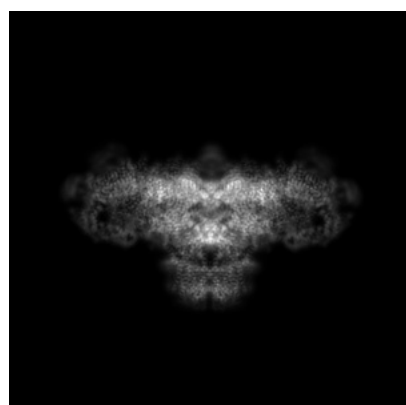
6 Map visualisation [i](#)

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.

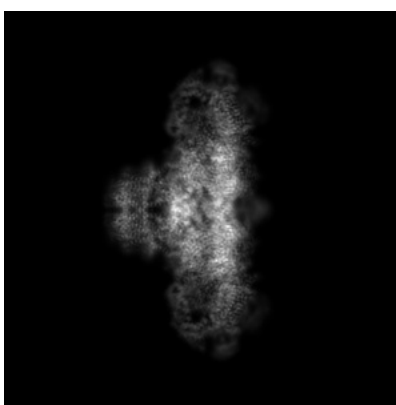
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

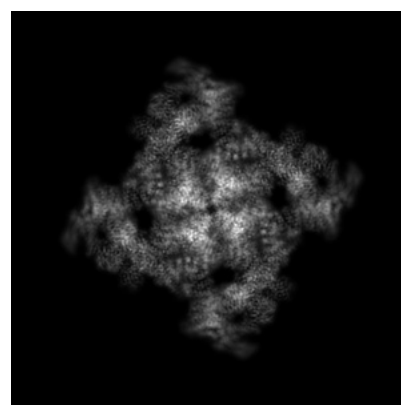
6.1.1 Primary map



X



Y



Z

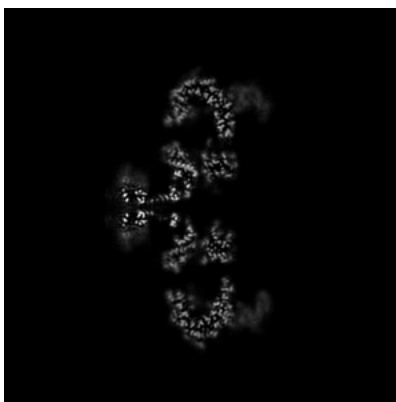
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

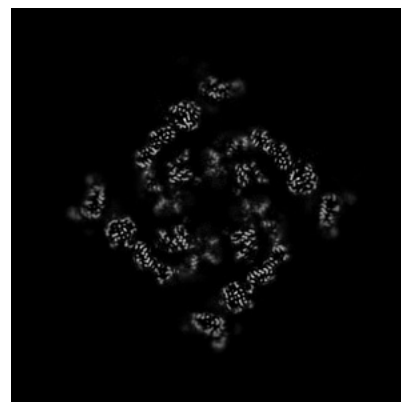
6.2.1 Primary map



X Index: 256



Y Index: 256

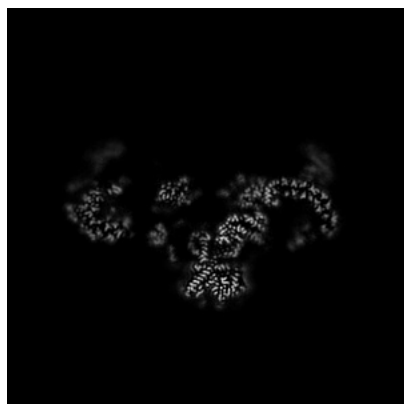


Z Index: 256

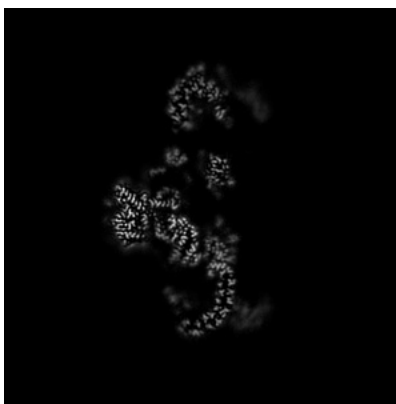
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

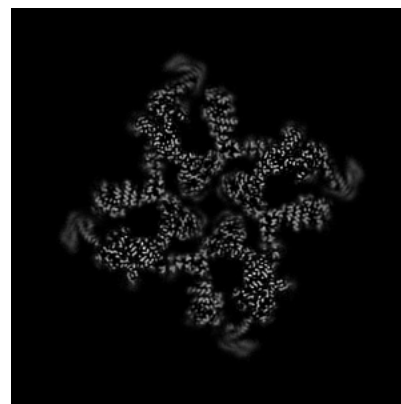
6.3.1 Primary map



X Index: 266



Y Index: 267

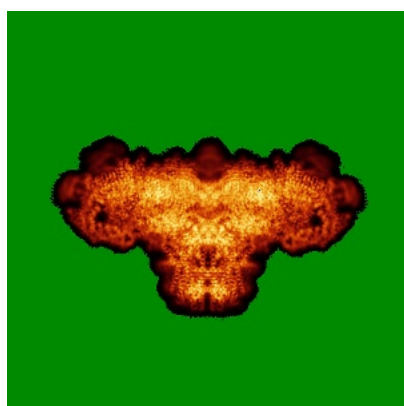


Z Index: 277

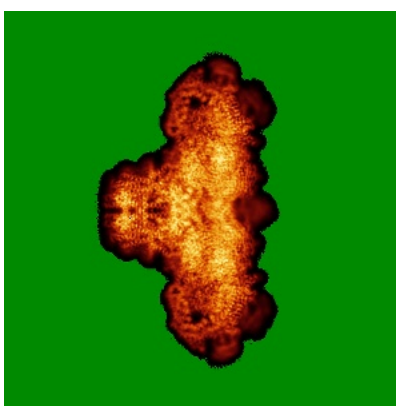
The images above show the largest variance slices of the map in three orthogonal directions.

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

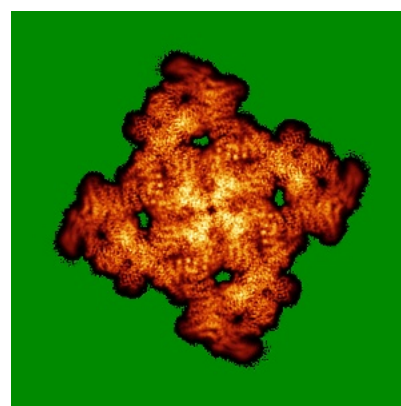
6.4.1 Primary map



X



Y

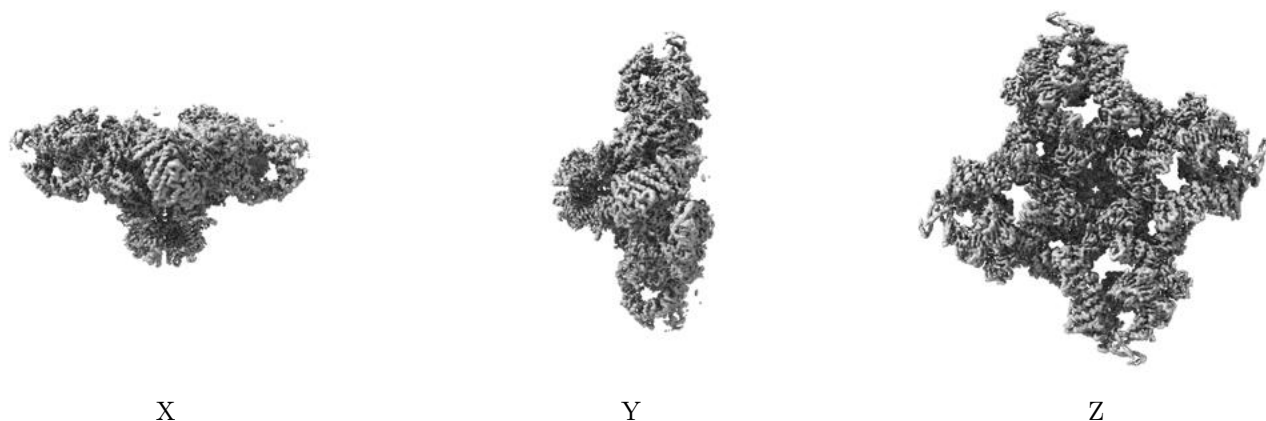


Z

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.

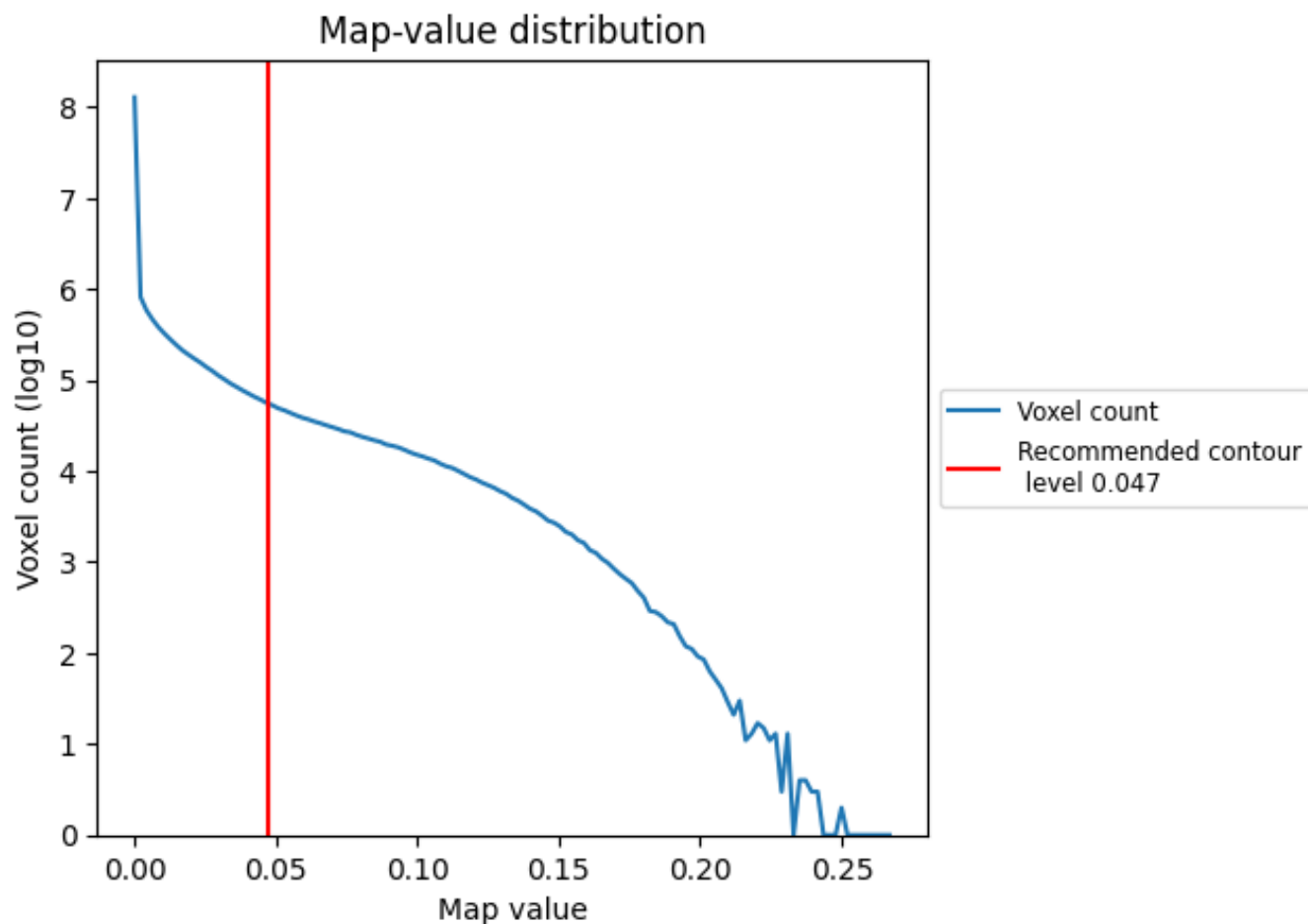
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

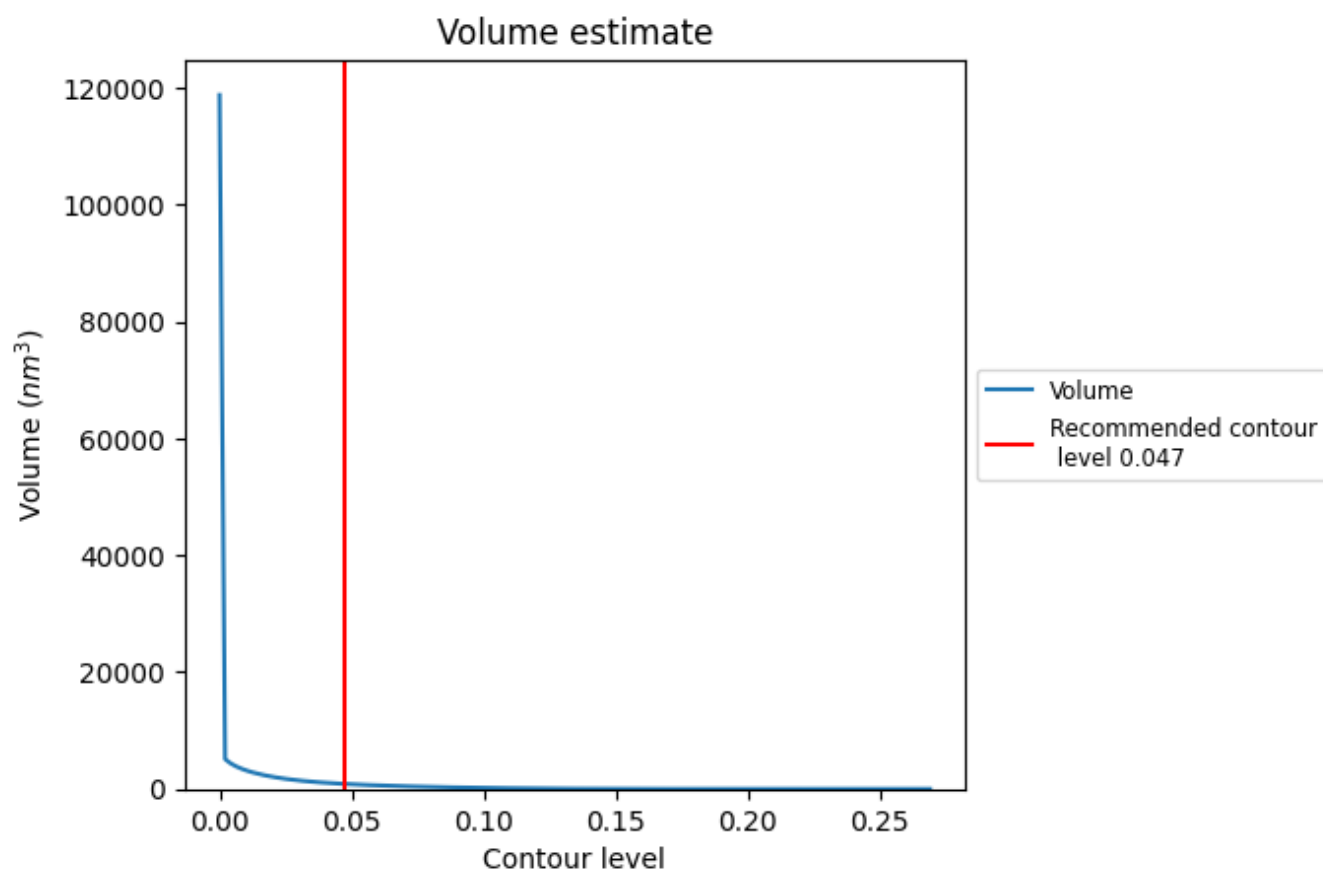
This section contains the results of statistical analysis of the map.

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.

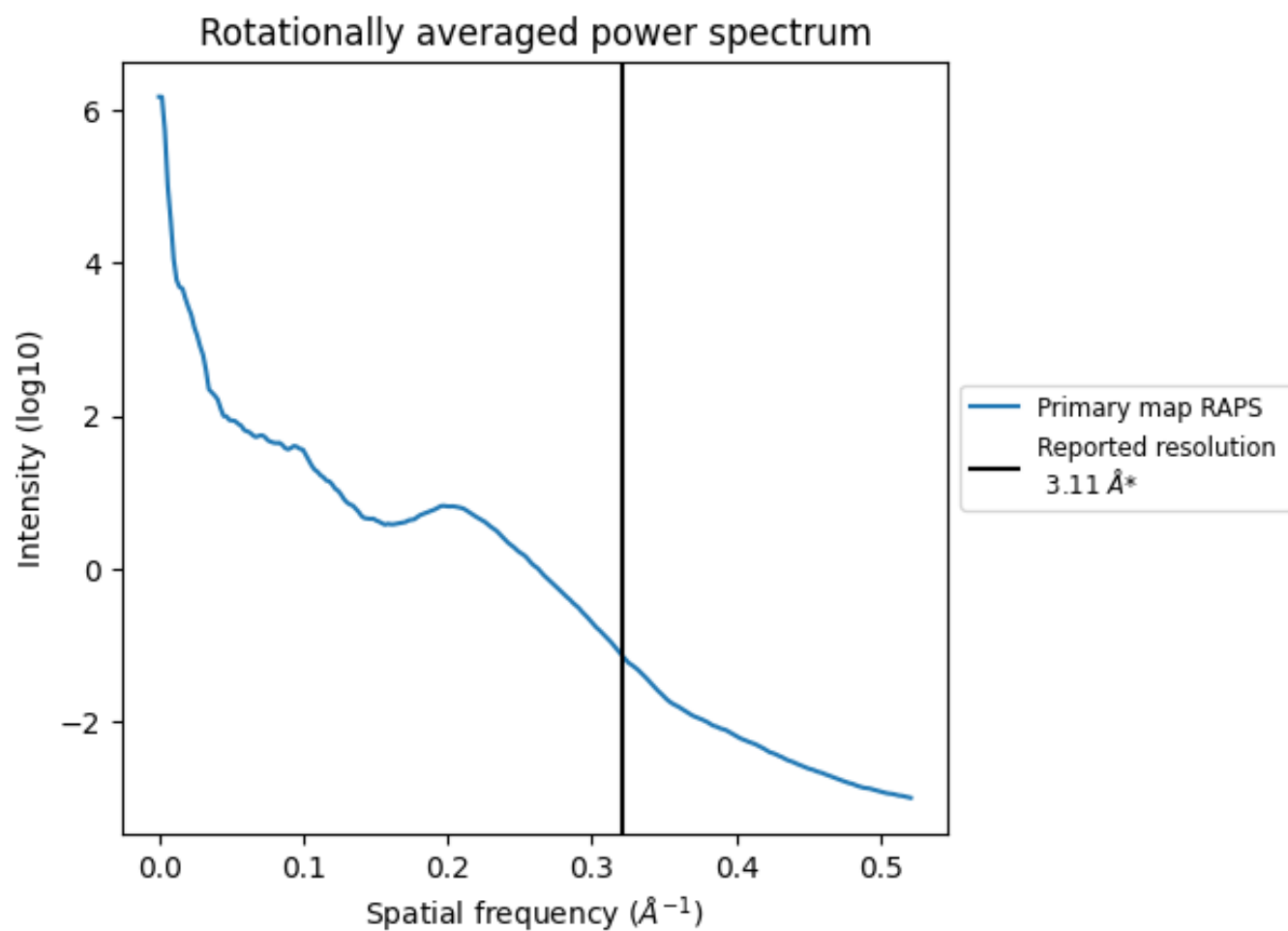
7.2 Volume estimate [i](#)



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

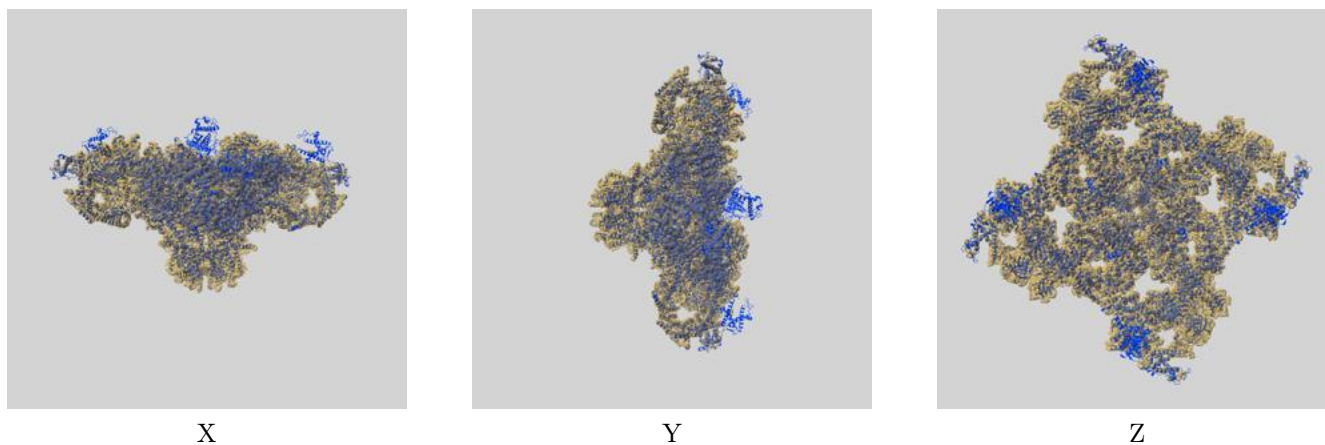
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

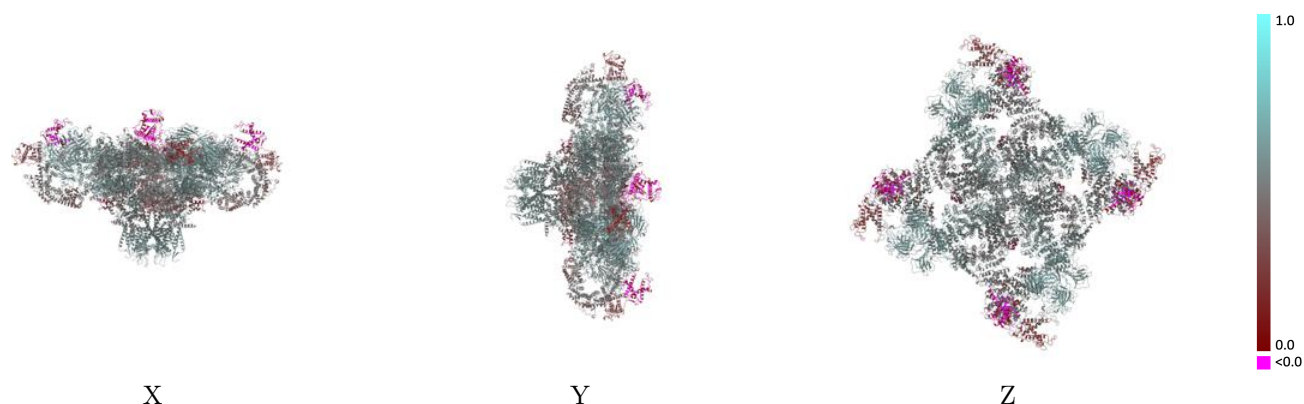
This section contains information regarding the fit between EMDB map EMD-70591 and PDB model 9OL6. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



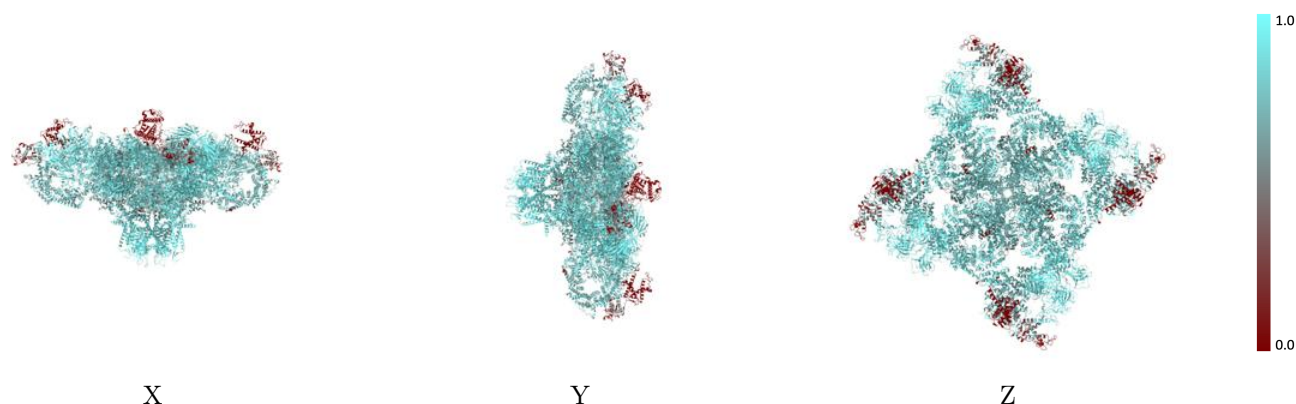
The images above show the 3D surface view of the map at the recommended contour level 0.047 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



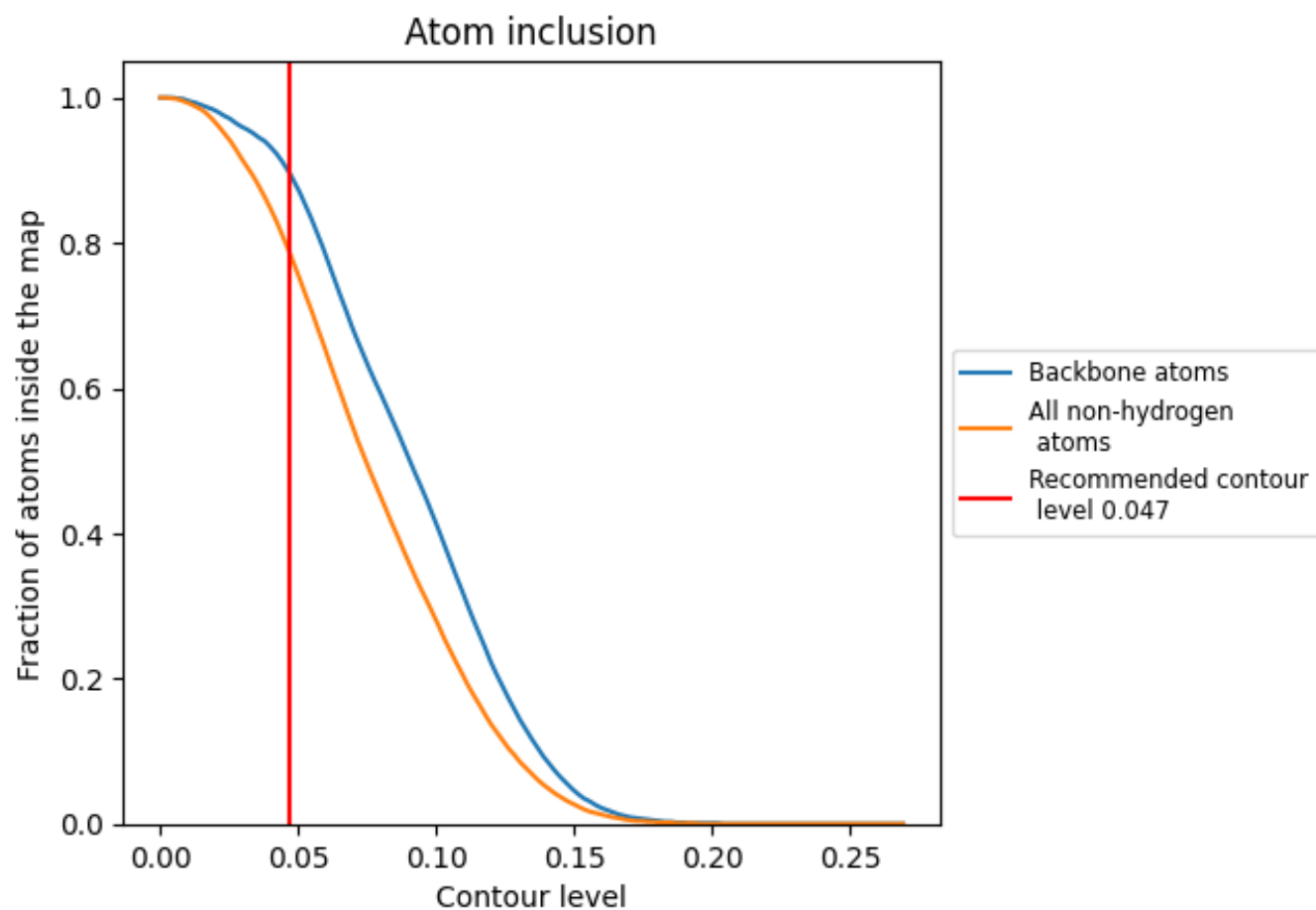
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	<div><div></div></div> 0.7850	<div><div></div></div> 0.4810
A	<div><div></div></div> 0.7820	<div><div></div></div> 0.4790
B	<div><div></div></div> 0.8660	<div><div></div></div> 0.5590
G	<div><div></div></div> 0.7830	<div><div></div></div> 0.4800
H	<div><div></div></div> 0.8690	<div><div></div></div> 0.5620
M	<div><div></div></div> 0.7830	<div><div></div></div> 0.4800
N	<div><div></div></div> 0.8690	<div><div></div></div> 0.5600
S	<div><div></div></div> 0.7820	<div><div></div></div> 0.4790
T	<div><div></div></div> 0.8680	<div><div></div></div> 0.5630

1.0

0.0

<0.0