



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 06:20 AM UTC

PDB ID : 6X33 / pdb_00006x33
EMDB ID : EMD-22016
Title : Wt pig RyR1 in complex with apoCaM, EGTA condition (class 3, open)
Authors : Woll, K.W.; Haji-Ghassemi, O.; Van Petegem, F.
Deposited on : 2020-05-21
Resolution : 4.20 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

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

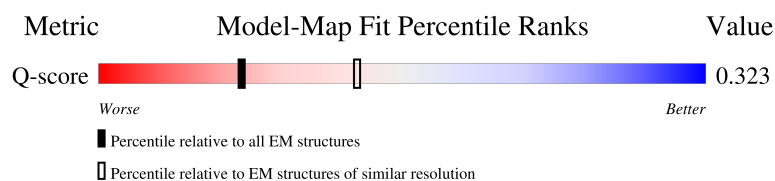
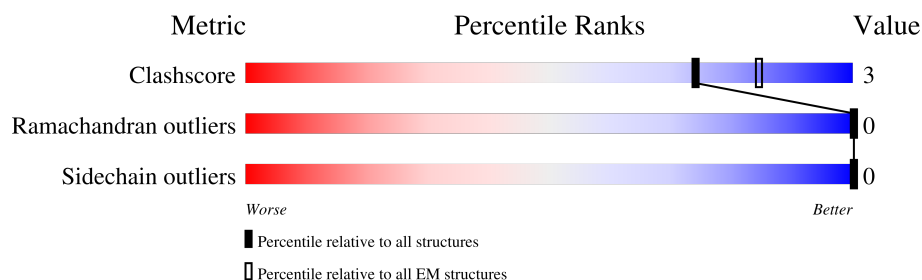
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 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	5410 (3.70 - 4.70)

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	107	19% 89% 10%
1	D	107	19% 89% 10%
1	G	107	20% 89% 10%
1	J	107	19% 89% 10%

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Mol	Chain	Length	Quality of chain
2	B	3816	32% 93% 7%
2	E	3816	32% 93% 7%
2	H	3816	32% 93% 7%
2	K	3816	32% 93% 7%
3	C	148	52% 83% 8% 9%
3	F	148	52% 82% 9% 9%
3	I	148	52% 83% 8% 9%
3	L	148	52% 82% 9% 9%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 112372 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 Peptidyl-prolyl cis-trans isomerase FKBP1B.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	106	Total	C	N	O	S	0	0
			727	460	124	139	4		
1	D	106	Total	C	N	O	S	0	0
			727	460	124	139	4		
1	G	106	Total	C	N	O	S	0	0
			727	460	124	139	4		
1	J	106	Total	C	N	O	S	0	0
			727	460	124	139	4		

- Molecule 2 is a protein called Ryanodine Receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	3816	Total	C	N	O	S	6	0
			26597	17002	4711	4735	149		
2	E	3816	Total	C	N	O	S	6	0
			26597	17002	4711	4735	149		
2	H	3816	Total	C	N	O	S	6	0
			26597	17002	4711	4735	149		
2	K	3816	Total	C	N	O	S	6	0
			26597	17002	4711	4735	149		

- Molecule 3 is a protein called Calmodulin-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	135	Total	C	N	O	S	0	0
			768	477	138	151	2		
3	F	135	Total	C	N	O	S	0	0
			768	477	138	151	2		
3	I	135	Total	C	N	O	S	0	0
			768	477	138	151	2		
3	L	135	Total	C	N	O	S	0	0
			768	477	138	151	2		

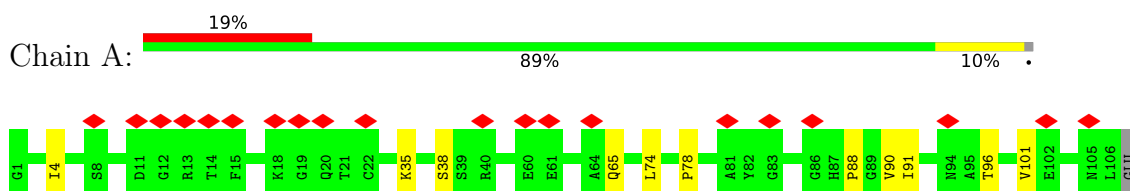
- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
4	B	1	Total 1	Zn 1	0
4	E	1	Total 1	Zn 1	0
4	H	1	Total 1	Zn 1	0
4	K	1	Total 1	Zn 1	0

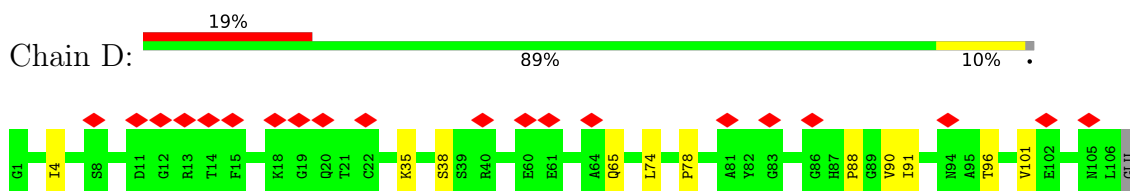
3 Residue-property plots

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.

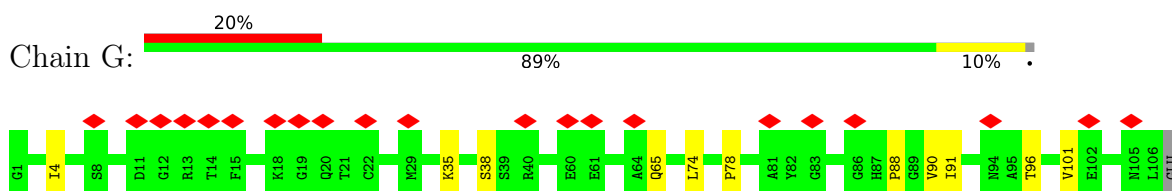
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



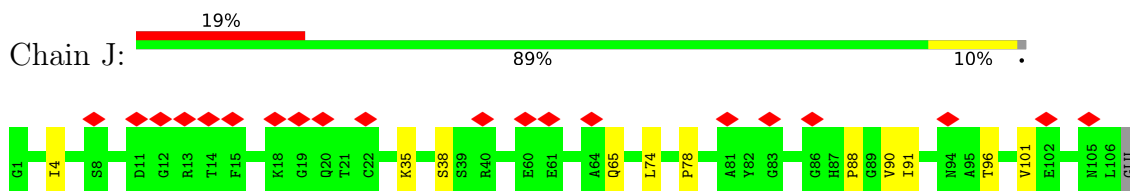
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



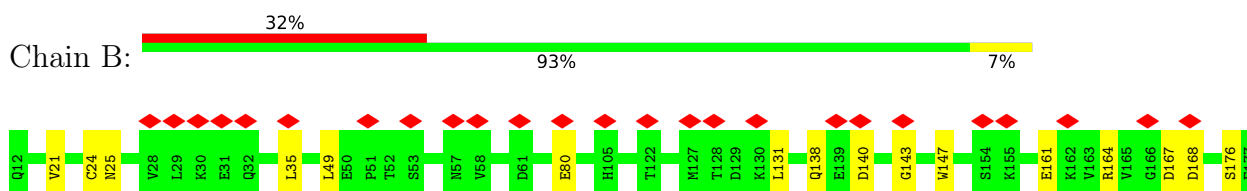
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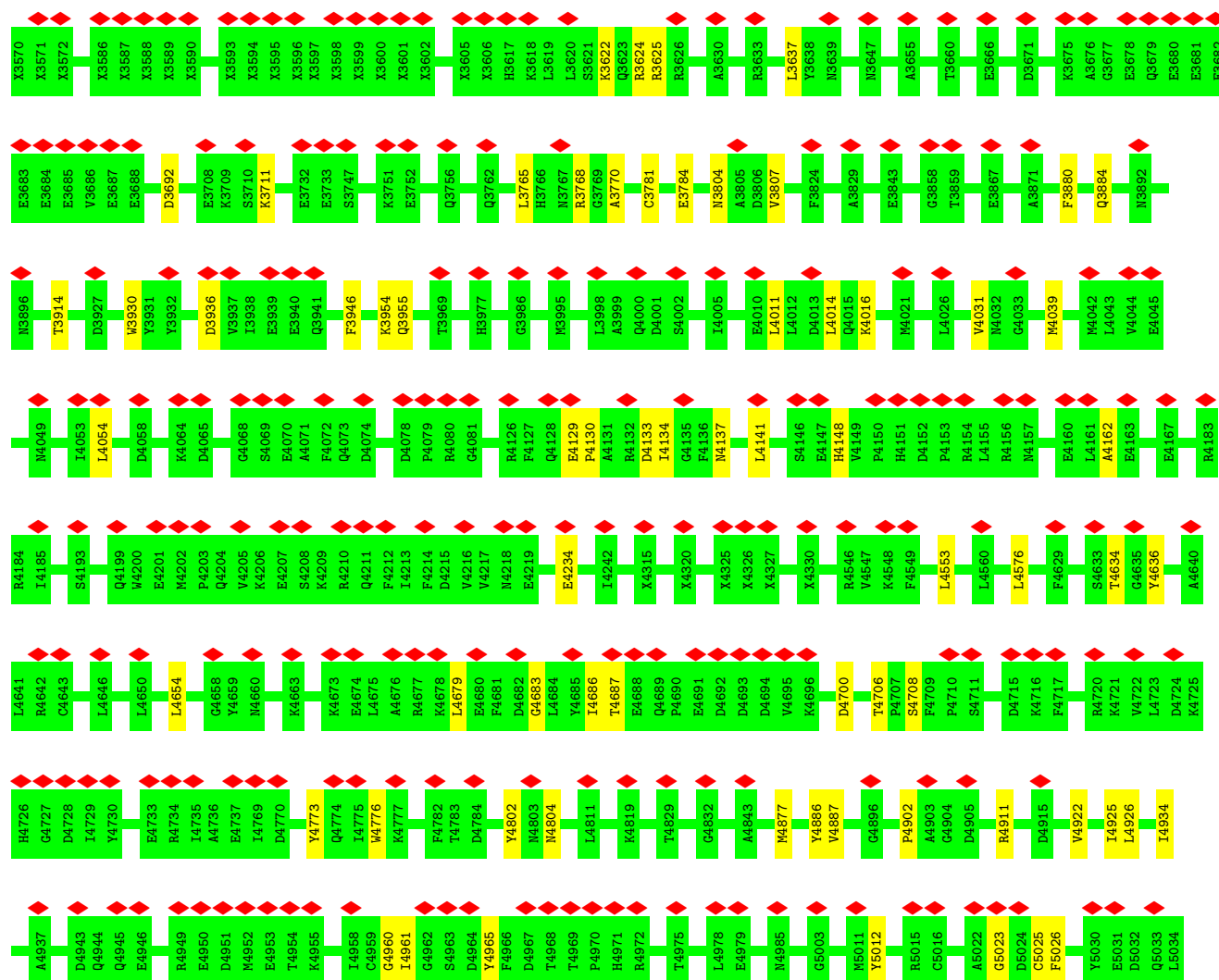


- Molecule 2: Ryanodine Receptor

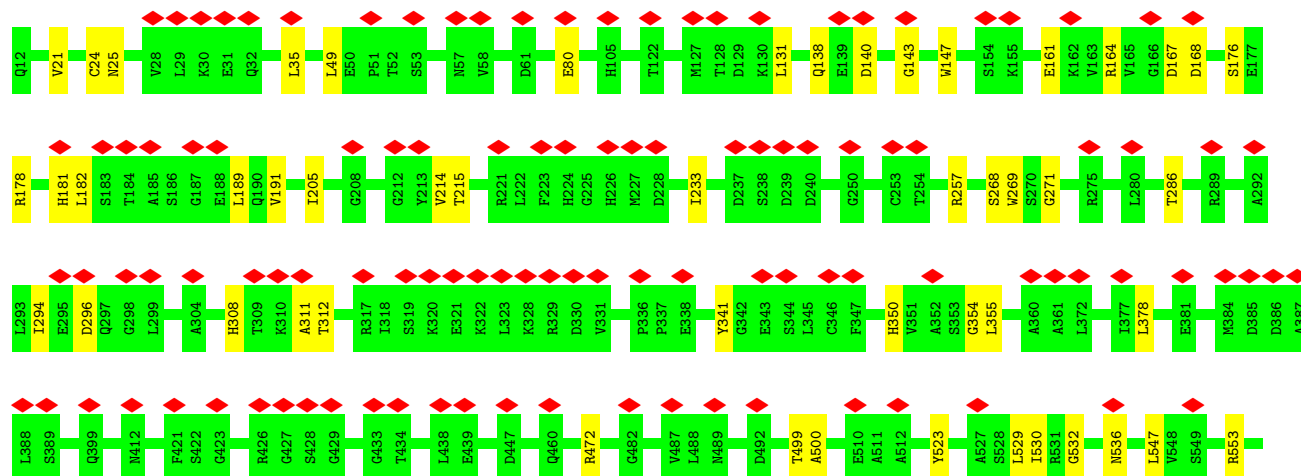
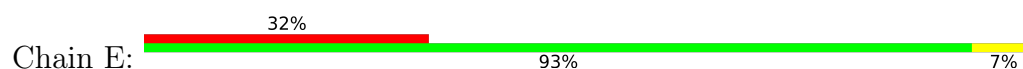


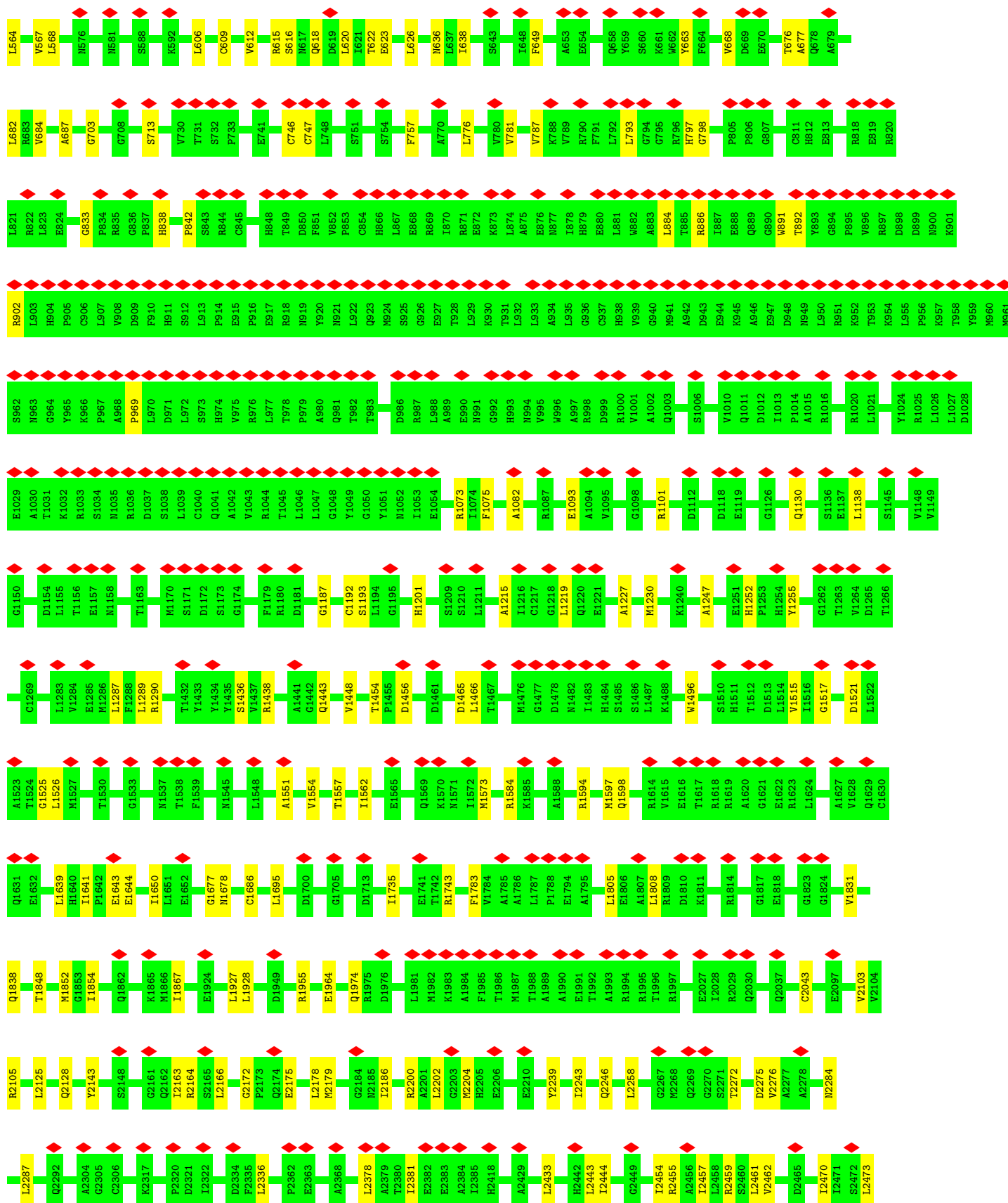


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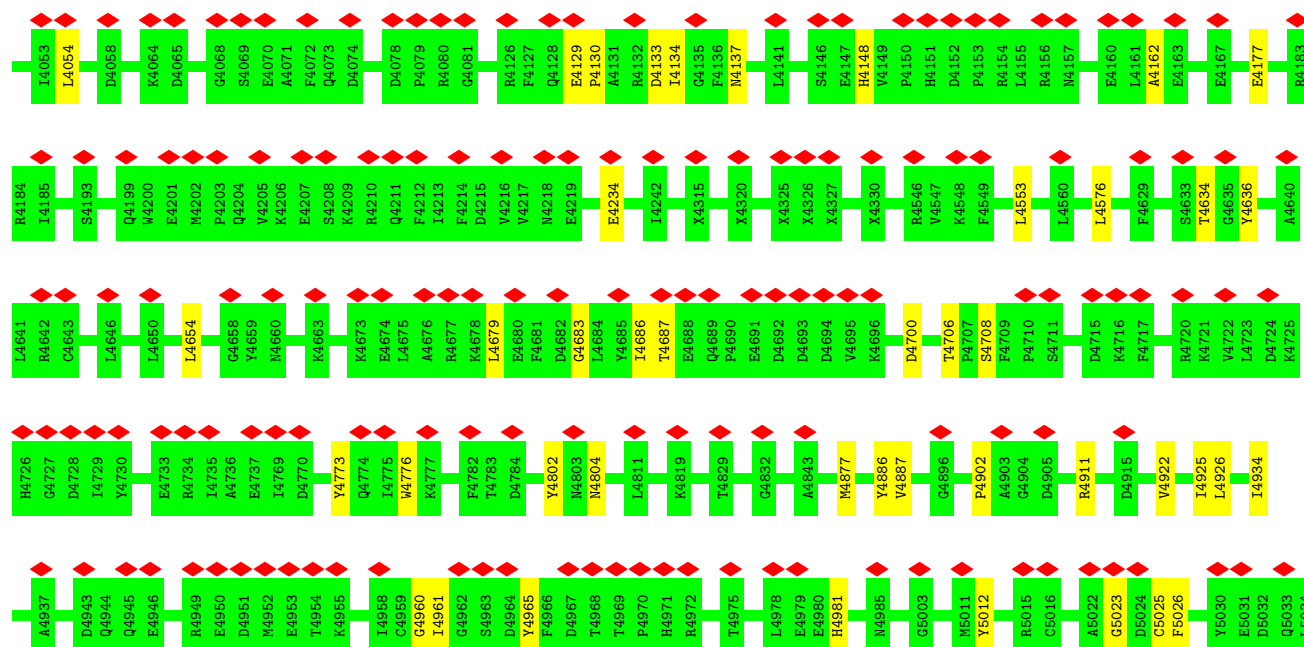


• Molecule 2: Ryanodine Receptor

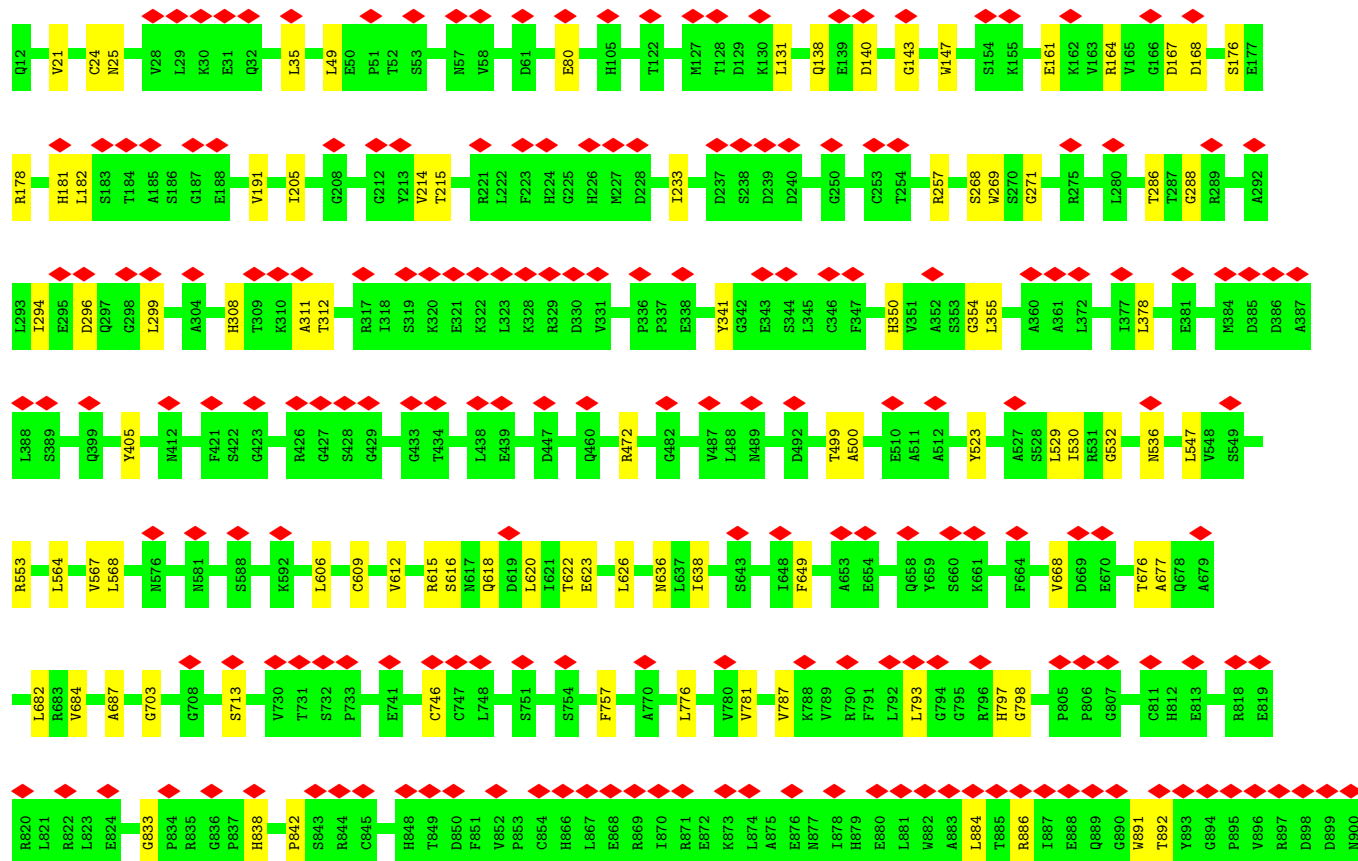




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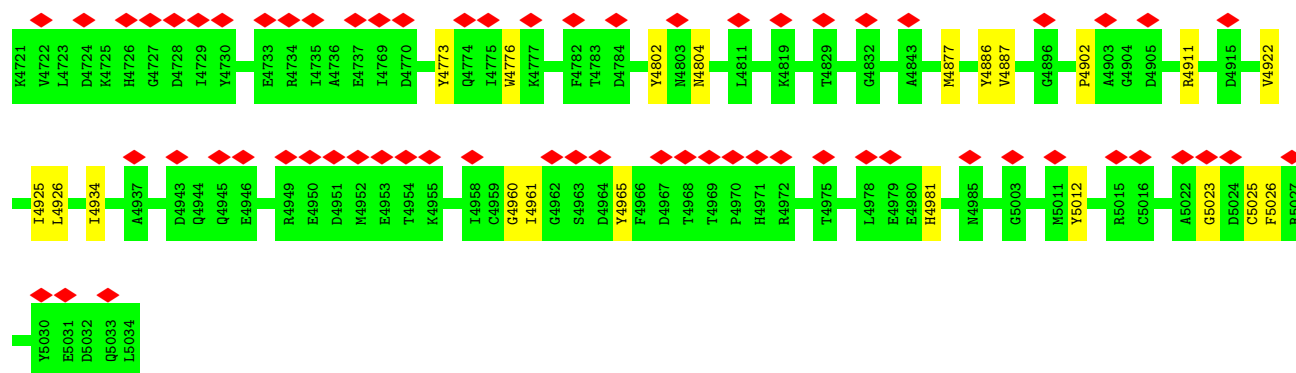


• Molecule 2: Ryanodine Receptor

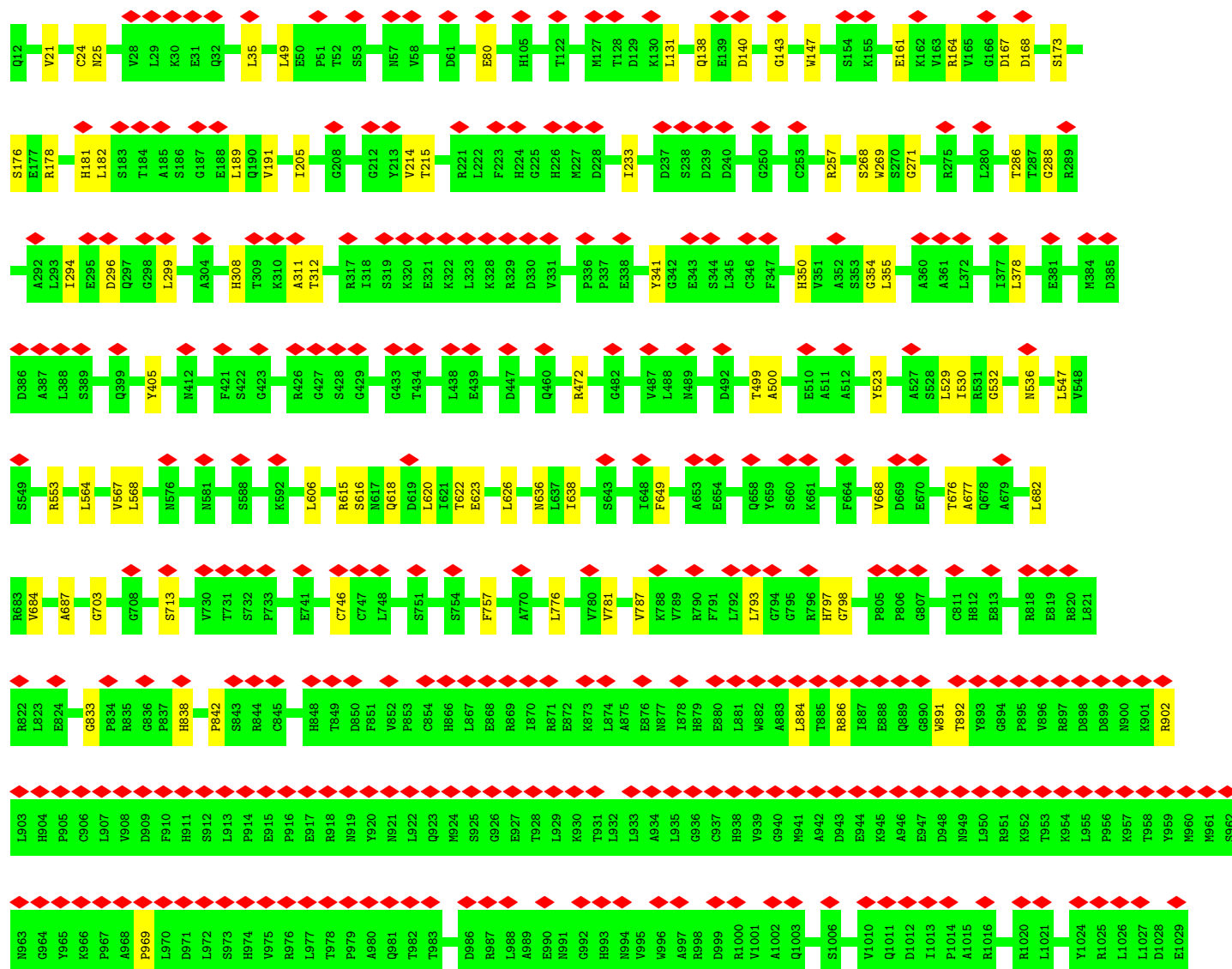


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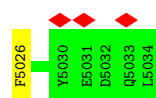


• Molecule 2: Ryanodine Receptor

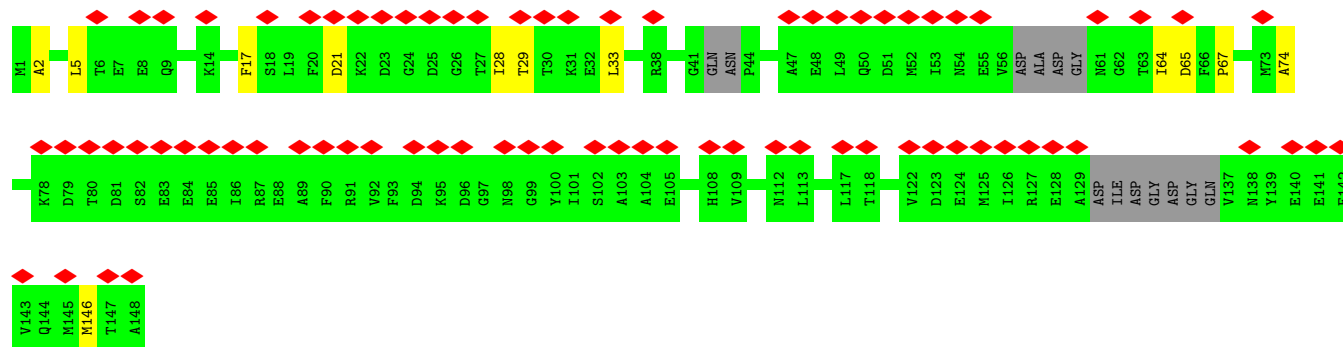
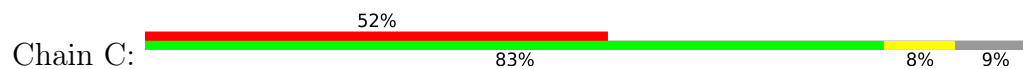




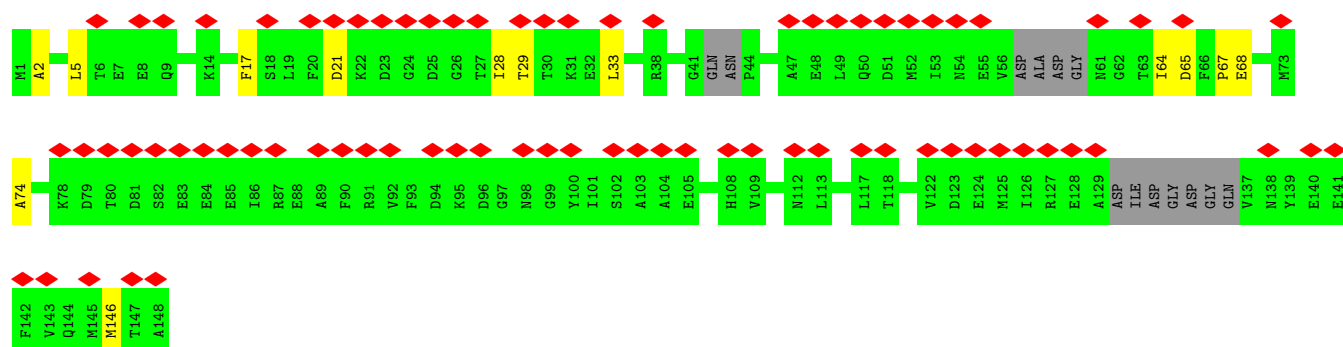
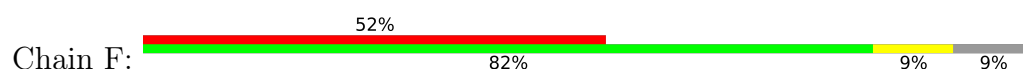
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	D4915	L4576	L4161	M4039	E3867	T3660	X3537	X3383	X3270	X3190	X3027
	D4915	L4576	L4161	M4039	A3871	X3666	X3538	X3384	X3271	X3191	X3028
	D4915	L4576	L4161	M4039	F3880	E3675	X3539	X3385	X3272	X3192	X3029
	D4915	L4576	L4161	M4039	F3880	A3676	X3540	X3386	X3273	X3193	X3030
	D4915	L4576	L4161	M4039	F3880	E3677	X3541	X3387	X3274	X3194	X3031
	D4915	L4576	L4161	M4039	F3880	E3677	X3542	X3388	X3275	X3195	X3032
	D4915	L4576	L4161	M4039	F3880	E3677	X3543	X3389	X3276	X3196	X3033
	D4915	L4576	L4161	M4039	F3880	E3677	X3544	X3390	X3277	X3197	X3034
	D4915	L4576	L4161	M4039	F3880	E3677	X3545	X3391	X3278	X3198	X3035
	D4915	L4576	L4161	M4039	F3880	E3677	X3546	X3392	X3279	X3199	X3036
	D4915	L4576	L4161	M4039	F3880	E3677	X3547	X3393	X3280	X3200	X3037
	D4915	L4576	L4161	M4039	F3880	E3677	X3548	X3394	X3281	X3201	X3038
	D4915	L4576	L4161	M4039	F3880	E3677	X3549	X3395	X3282	X3202	X3039
	D4915	L4576	L4161	M4039	F3880	E3677	X3550	X3396	X3283	X3203	X3040
	D4915	L4576	L4161	M4039	F3880	E3677	X3551	X3397	X3284	X3204	X3041
	D4915	L4576	L4161	M4039	F3880	E3677	X3552	X3398	X3285	X3205	X3042
	D4915	L4576	L4161	M4039	F3880	E3677	X3553	X3399	X3286	X3206	X3043
	D4915	L4576	L4161	M4039	F3880	E3677	X3554	X3400	X3287	X3207	X3044
	D4915	L4576	L4161	M4039	F3880	E3677	X3555	X3401	X3288	X3208	X3045
	D4915	L4576	L4161	M4039	F3880	E3677	X3556	X3402	X3289	X3209	X3046
	D4915	L4576	L4161	M4039	F3880	E3677	X3557	X3403	X3290	X3210	X3047
	D4915	L4576	L4161	M4039	F3880	E3677	X3558	X3404	X3291	X3211	X3048
	D4915	L4576	L4161	M4039	F3880	E3677	X3559	X3405	X3292	X3212	X3049
	D4915	L4576	L4161	M4039	F3880	E3677	X3560	X3406	X3293	X3213	X3050
	D4915	L4576	L4161	M4039	F3880	E3677	X3561	X3407	X3294	X3214	X3051
	D4915	L4576	L4161	M4039	F3880	E3677	X3562	X3408	X3295	X3215	X3052
	D4915	L4576	L4161	M4039	F3880	E3677	X3563	X3409	X3296	X3216	X3053
	D4915	L4576	L4161	M4039	F3880	E3677	X3564	X3410	X3297	X3217	X3054
	D4915	L4576	L4161	M4039	F3880	E3677	X3565	X3411	X3298	X3218	X3055
	D4915	L4576	L4161	M4039	F3880	E3677	X3566	X3412	X3299	X3219	X3056
	D4915	L4576	L4161	M4039	F3880	E3677	X3567	X3413	X3300	X3220	X3057
	D4915	L4576	L4161	M4039	F3880	E3677	X3568	X3414	X3301	X3221	X3058
	D4915	L4576	L4161	M4039	F3880	E3677	X3569	X3415	X3302	X3222	X3059
	D4915	L4576	L4161	M4039	F3880	E3677	X3570	X3416	X3303	X3223	X3060
	D4915	L4576	L4161	M4039	F3880	E3677	X3571	X3417	X3304	X3224	X3061
	D4915	L4576	L4161	M4039	F3880	E3677	X3572	X3418	X3305	X3225	X3062
	D4915	L4576	L4161	M4039	F3880	E3677	X3573	X3419	X3306	X3226	X3063
	D4915	L4576	L4161	M4039	F3880	E3677	X3574	X3420	X3307	X3227	X3064
	D4915	L4576	L4161	M4039	F3880	E3677	X3575	X3421	X3308	X3228	X3065
	D4915	L4576	L4161	M4039	F3880	E3677	X3576	X3422	X3309	X3229	X3066
	D4915	L4576	L4161	M4039	F3880	E3677	X3577	X3423	X3310	X3230	X3067
	D4915	L4576	L4161	M4039	F3880	E3677	X3578	X3424	X3311	X3231	X3068
	D4915	L4576	L4161	M4039	F3880	E3677	X3579	X3425	X3312	X3232	X3069
	D4915	L4576	L4161	M4039	F3880	E3677	X3580	X3426	X3313	X3233	X3070
	D4915	L4576	L4161	M4039	F3880	E3677	X3581	X3427	X3314	X3234	X3071
	D4915	L4576	L4161	M4039	F3880	E3677	X3582	X3428	X3315	X3235	X3072
	D4915	L4576	L4161	M4039	F3880	E3677	X3583	X3429	X3316	X3236	X3073
	D4915	L4576	L4161	M4039	F3880	E3677	X3584	X3430	X3317	X3237	X3074
	D4915	L4576	L4161	M4039	F3880	E3677	X3585	X3431	X3318	X3238	X3075
	D4915	L4576	L4161	M4039	F3880	E3677	X3586	X3432	X3319	X3239	X3076
	D4915	L4576	L4161	M4039	F3880	E3677	X3587	X3433	X3320	X3240	X3077
	D4915	L4576	L4161	M4039	F3880	E3677	X3588	X3434	X3321	X3241	X3078
	D4915	L4576	L4161	M4039	F3880	E3677	X3589	X3435	X3322	X3242	X3079
	D4915	L4576	L4161	M4039	F3880	E3677	X3590	X3436	X3323	X3243	X3080
	D4915	L4576	L4161	M4039	F3880	E3677	X3591	X3437	X3324	X3244	X3081
	D4915	L4576	L4161	M4039	F3880	E3677	X3592	X3438	X3325	X3245	X3082
	D4915	L4576	L4161	M4039	F3880	E3677	X3593	X3439	X3326	X3246	X3083
	D4915	L4576	L4161	M4039	F3880	E3677	X3594	X3440	X3327	X3247	X3084
	D4915	L4576	L4161	M4039	F3880	E3677	X3595	X3441	X3328	X3248	X3085
	D4915	L4576	L4161	M4039	F3880	E3677	X3596	X3442	X3329	X3249	X3086
	D4915	L4576	L4161	M4039	F3880	E3677	X3597	X3443	X3330	X3250	X3087
	D4915	L4576	L4161	M4039	F3880	E3677	X3598	X3444	X3331	X3251	X3088
	D4915	L4576	L4161	M4039	F3880	E3677	X3599	X3445	X3332	X3252	X3089
	D4915	L4576	L4161	M4039	F3880	E3677	X3600	X3446	X3333	X3253	X3090
	D4915	L4576	L4161	M4039	F3880	E3677	X3601	X3447	X3334</		



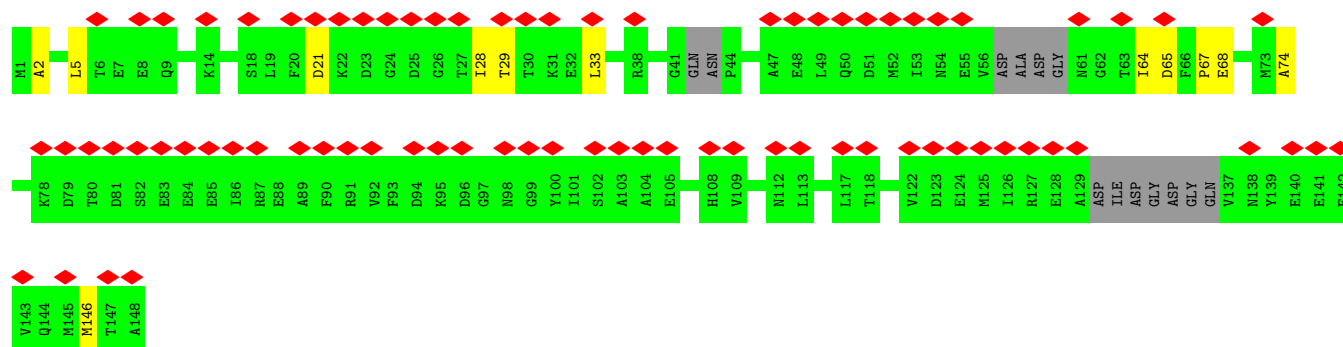
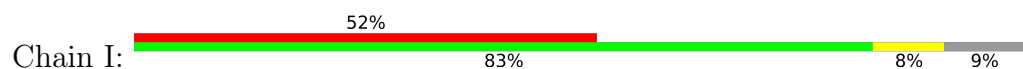
• Molecule 3: Calmodulin-1



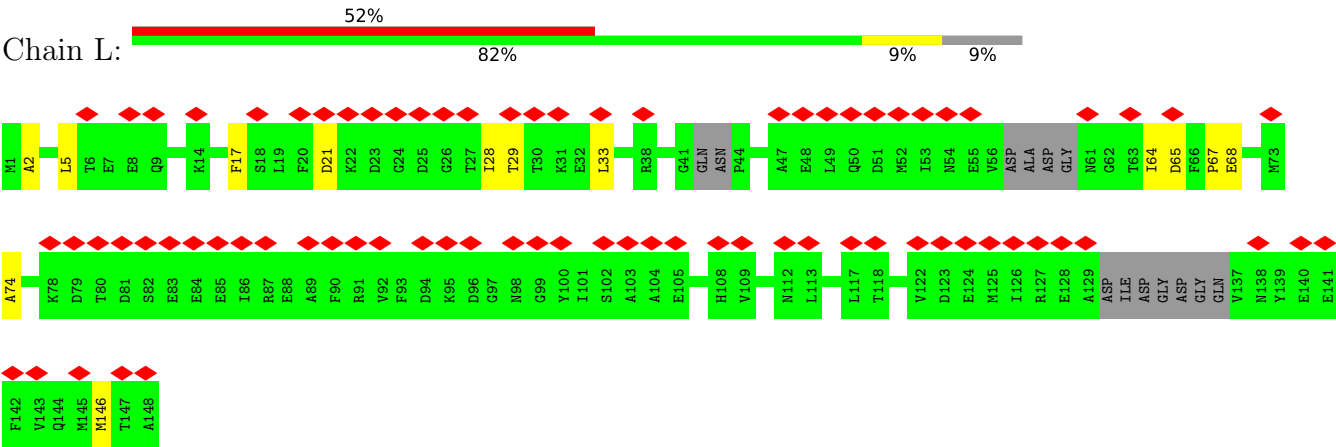
• Molecule 3: Calmodulin-1



• Molecule 3: Calmodulin-1



• Molecule 3: Calmodulin-1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	25122	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.173	Depositor
Minimum map value	-0.136	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.022	Depositor
Map size ($\text{\AA}$)	523.2, 523.2, 523.2	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.09, 1.09, 1.09	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

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	0.09	0/743	0.25	0/1014
1	D	0.09	0/743	0.25	0/1014
1	G	0.09	0/743	0.25	0/1014
1	J	0.09	0/743	0.25	0/1014
2	B	0.07	0/25353	0.21	0/34606
2	E	0.07	0/25353	0.21	0/34606
2	H	0.07	0/25353	0.21	0/34606
2	K	0.07	0/25353	0.21	0/34606
3	C	0.08	0/772	0.22	0/1059
3	F	0.08	0/772	0.22	0/1059
3	I	0.08	0/772	0.22	0/1059
3	L	0.08	0/772	0.22	0/1059
All	All	0.07	0/107472	0.22	0/146716

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	727	0	651	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	727	0	651	8	0
1	G	727	0	651	8	0
1	J	727	0	651	8	0
2	B	26597	0	22867	162	0
2	E	26597	0	22867	157	0
2	H	26597	0	22867	160	0
2	K	26597	0	22867	164	0
3	C	768	0	486	8	0
3	F	768	0	486	9	0
3	I	768	0	486	8	0
3	L	768	0	486	9	0
4	B	1	0	0	0	0
4	E	1	0	0	0	0
4	H	1	0	0	0	0
4	K	1	0	0	0	0
All	All	112372	0	96016	674	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 3.

The worst 5 of 674 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)
2:E:886:ARG:HB2	2:E:891:TRP:HB2	1.73	0.71
2:B:886:ARG:HB2	2:B:891:TRP:HB2	1.73	0.71
2:H:886:ARG:HB2	2:H:891:TRP:HB2	1.73	0.71
2:K:886:ARG:HB2	2:K:891:TRP:HB2	1.73	0.71
2:E:4706:THR:HG21	2:E:4773:TYR:HB2	1.74	0.70

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	104/107 (97%)	98 (94%)	6 (6%)	0	100	100
1	D	104/107 (97%)	98 (94%)	6 (6%)	0	100	100
1	G	104/107 (97%)	98 (94%)	6 (6%)	0	100	100
1	J	104/107 (97%)	98 (94%)	6 (6%)	0	100	100
2	B	3396/3816 (89%)	3335 (98%)	61 (2%)	0	100	100
2	E	3396/3816 (89%)	3335 (98%)	61 (2%)	0	100	100
2	H	3396/3816 (89%)	3335 (98%)	61 (2%)	0	100	100
2	K	3396/3816 (89%)	3335 (98%)	61 (2%)	0	100	100
3	C	127/148 (86%)	124 (98%)	3 (2%)	0	100	100
3	F	127/148 (86%)	124 (98%)	3 (2%)	0	100	100
3	I	127/148 (86%)	124 (98%)	3 (2%)	0	100	100
3	L	127/148 (86%)	124 (98%)	3 (2%)	0	100	100
All	All	14508/16284 (89%)	14228 (98%)	280 (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	66/88 (75%)	66 (100%)	0	100	100
1	D	66/88 (75%)	66 (100%)	0	100	100
1	G	66/88 (75%)	66 (100%)	0	100	100
1	J	66/88 (75%)	66 (100%)	0	100	100
2	B	2222/3025 (74%)	2222 (100%)	0	100	100
2	E	2222/3025 (74%)	2222 (100%)	0	100	100
2	H	2222/3025 (74%)	2222 (100%)	0	100	100
2	K	2222/3025 (74%)	2222 (100%)	0	100	100
3	C	29/126 (23%)	29 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	F	29/126 (23%)	29 (100%)	0	100	100
3	I	29/126 (23%)	29 (100%)	0	100	100
3	L	29/126 (23%)	29 (100%)	0	100	100
All	All	9268/12956 (72%)	9268 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 103 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	991	ASN
2	H	3972	GLN
2	K	4196	ASN
2	H	1198	GLN
2	H	2214	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 4 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	B	56
2	E	56
2	H	56
2	K	56

The worst 5 of 224 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	4331:UNK	C	4543:GLU	N	51.24
1	E	4331:UNK	C	4543:GLU	N	51.24
1	H	4331:UNK	C	4543:GLU	N	51.24
1	K	4331:UNK	C	4543:GLU	N	51.24
1	B	1054:GLU	C	1071:ARG	N	36.98

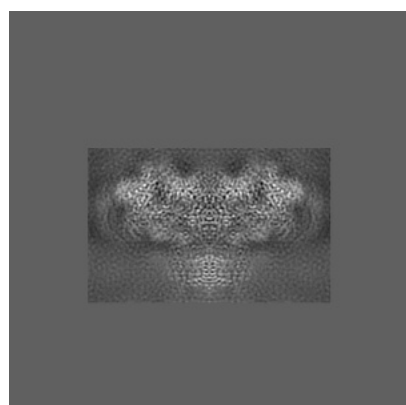
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22016. These allow visual inspection of the internal detail of the map and identification of artifacts.

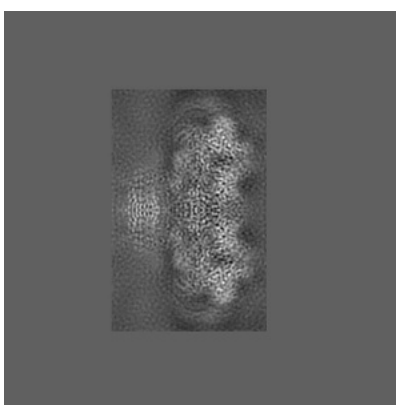
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

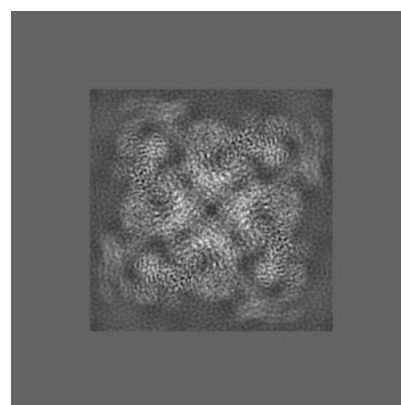
6.1.1 Primary map



X



Y

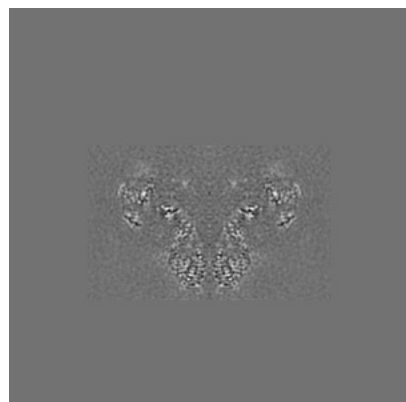


Z

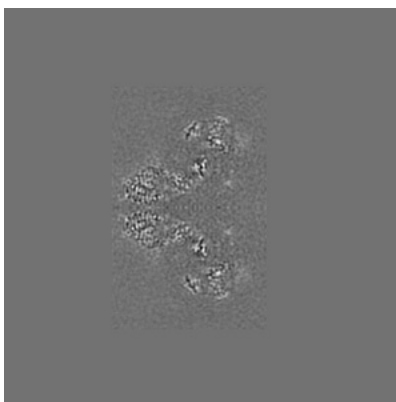
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

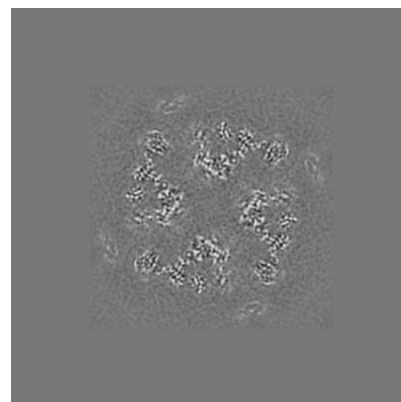
6.2.1 Primary map



X Index: 240



Y Index: 240

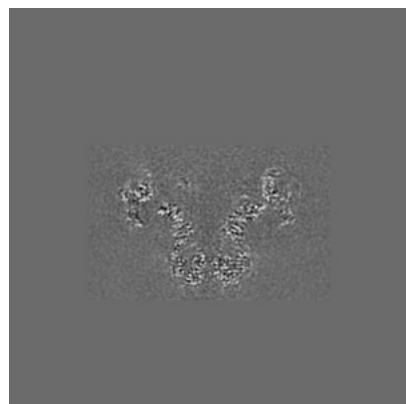


Z Index: 240

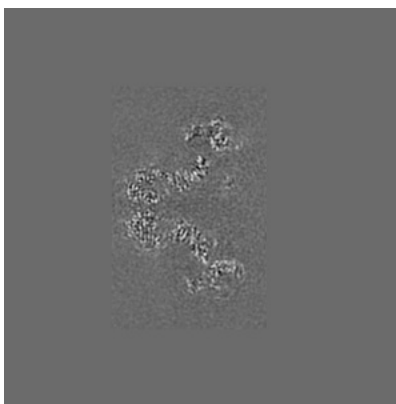
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

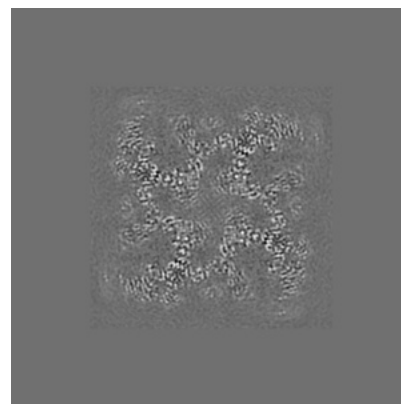
6.3.1 Primary map



X Index: 236



Y Index: 236

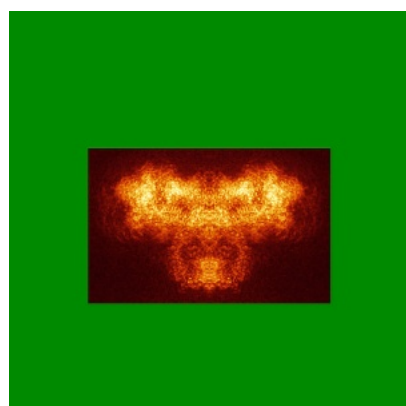


Z Index: 265

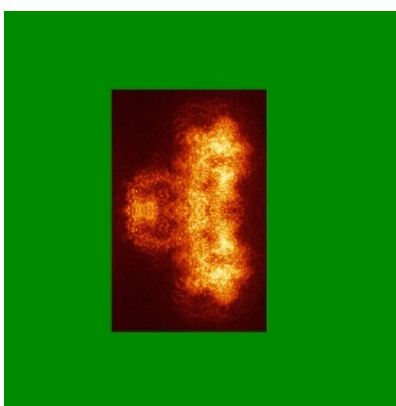
The images above show the largest variance slices of the map in three orthogonal directions.

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

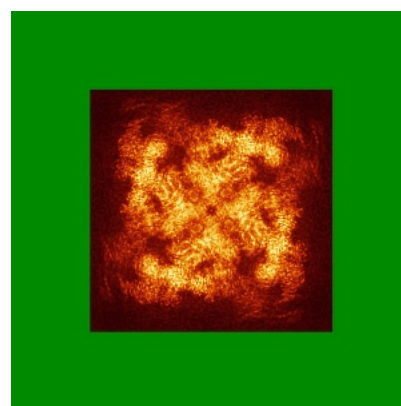
6.4.1 Primary map



X



Y

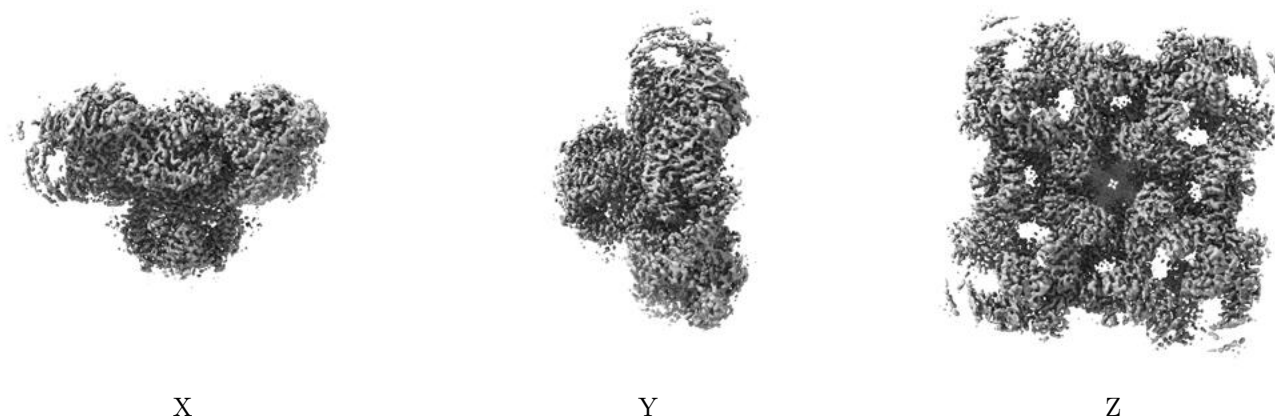


Z

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 0.022. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

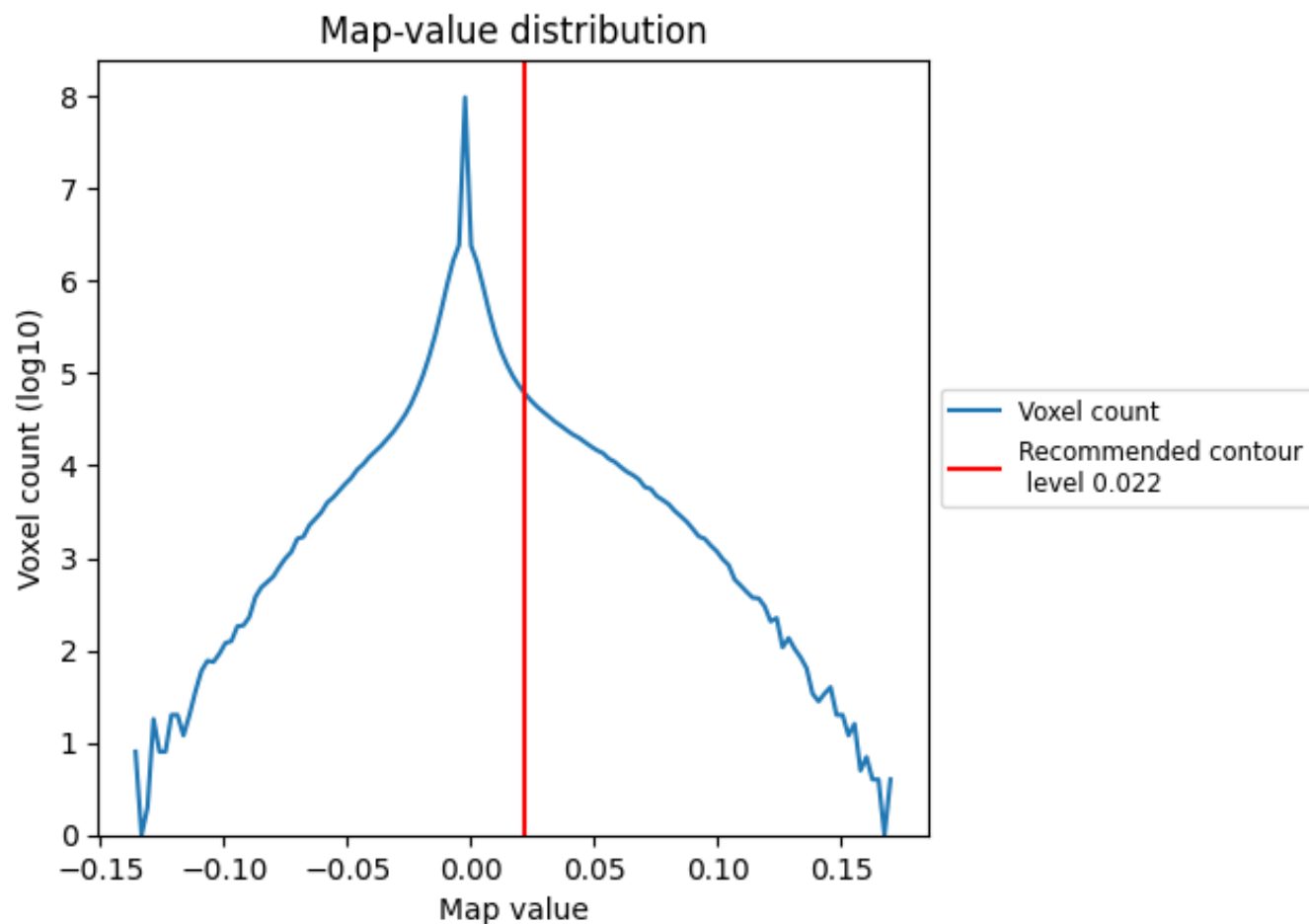
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

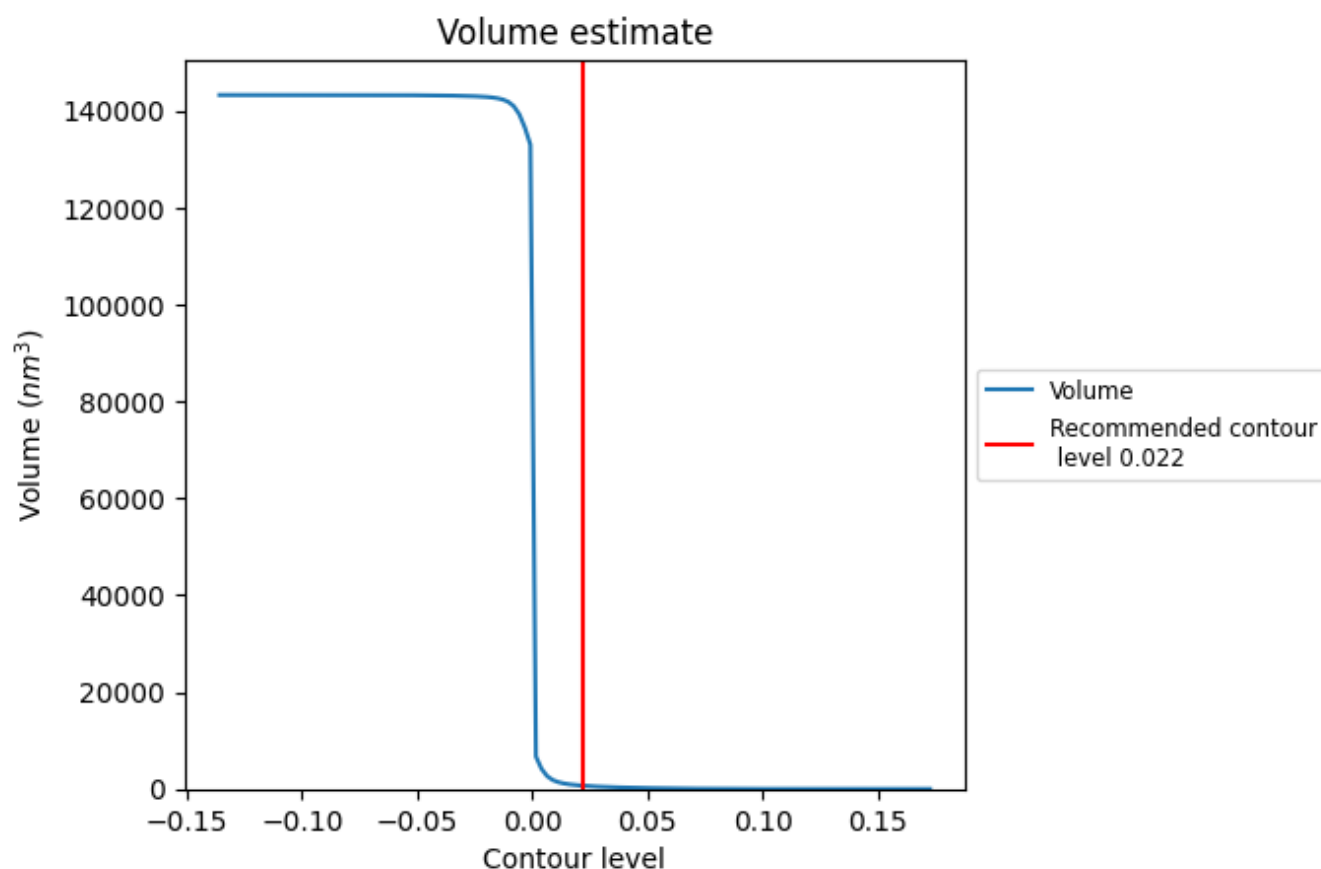
This section contains the results of statistical analysis of the map.

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.

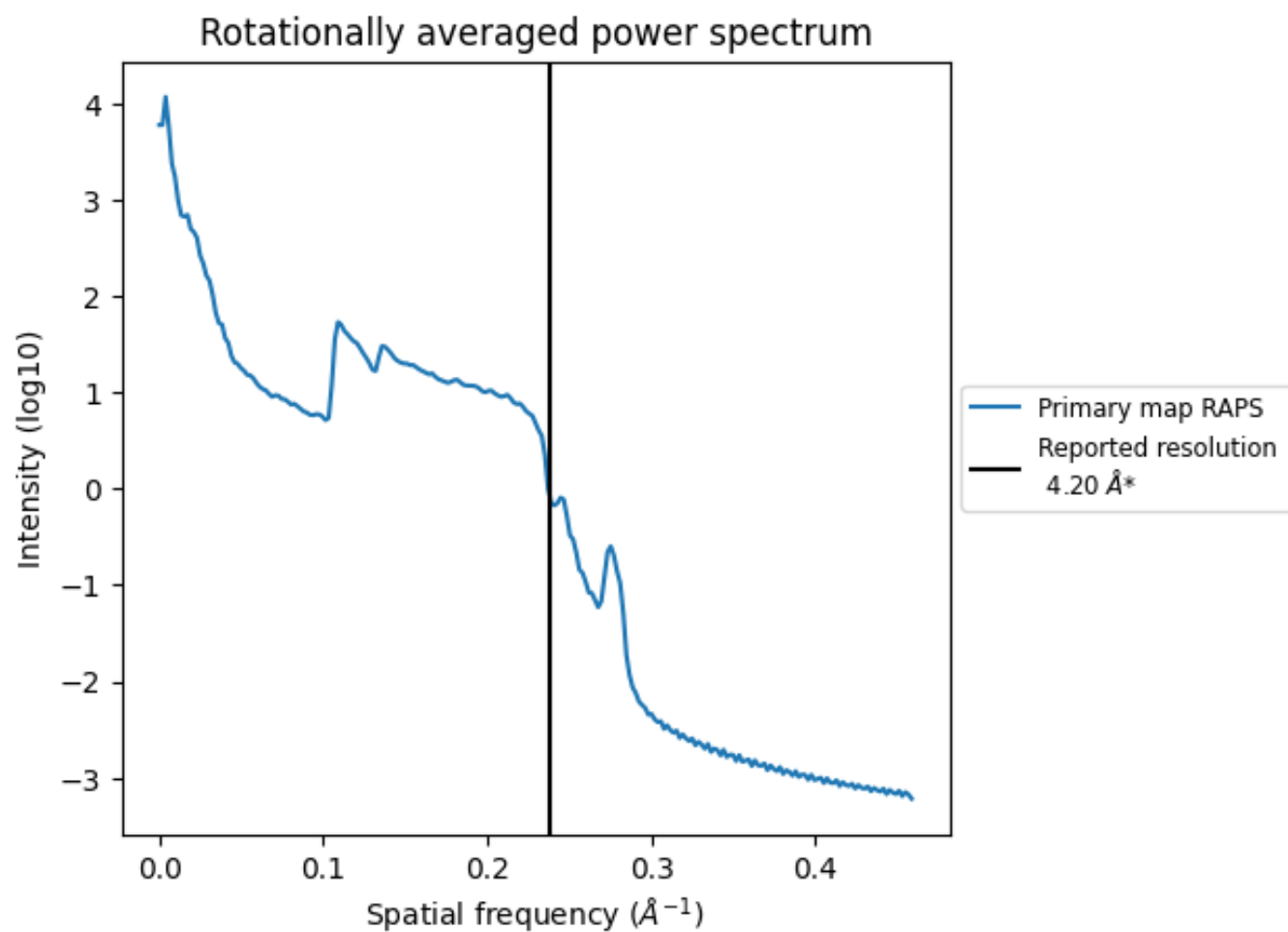
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 672 nm³; this corresponds to an approximate mass of 607 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 0.238 Å⁻¹

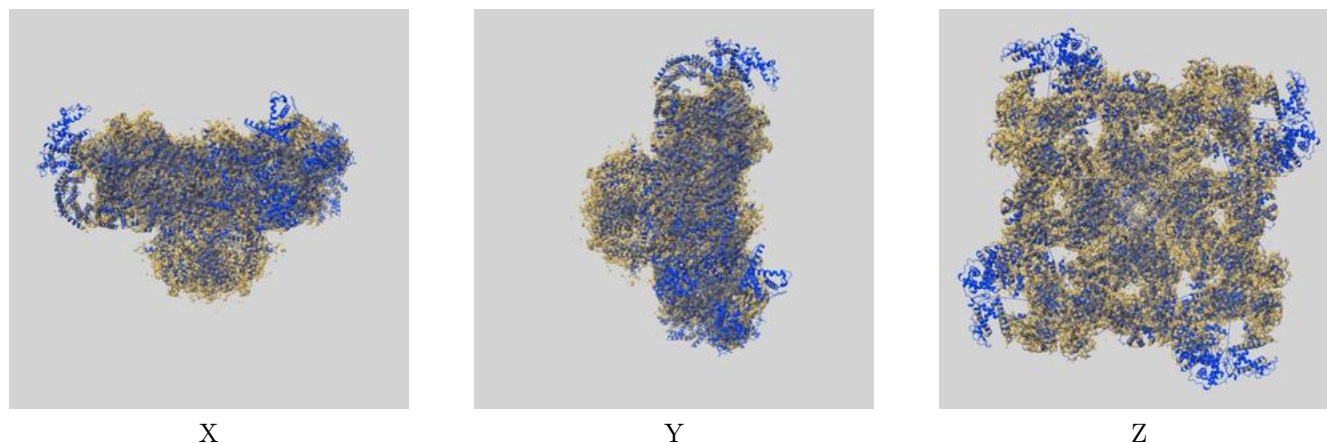
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

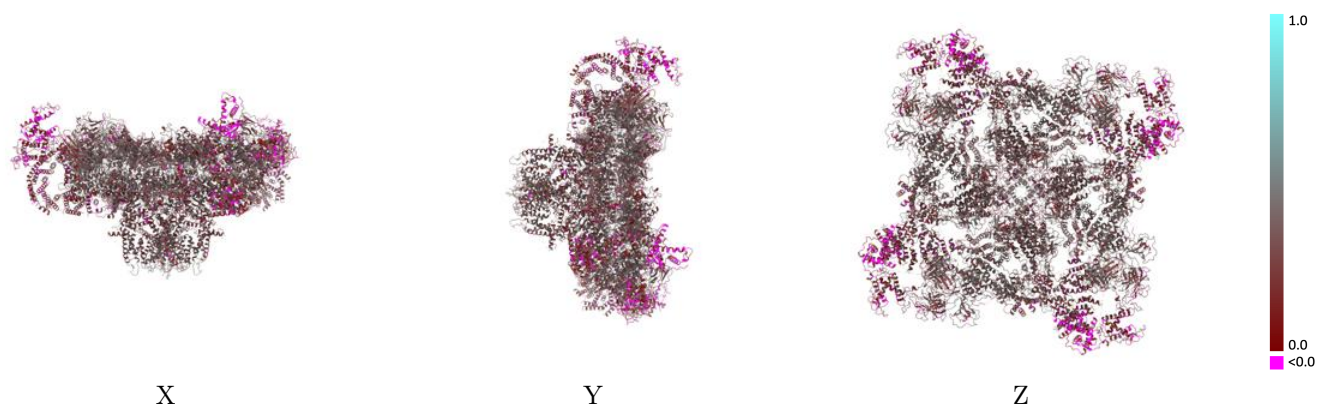
This section contains information regarding the fit between EMDB map EMD-22016 and PDB model 6X33. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



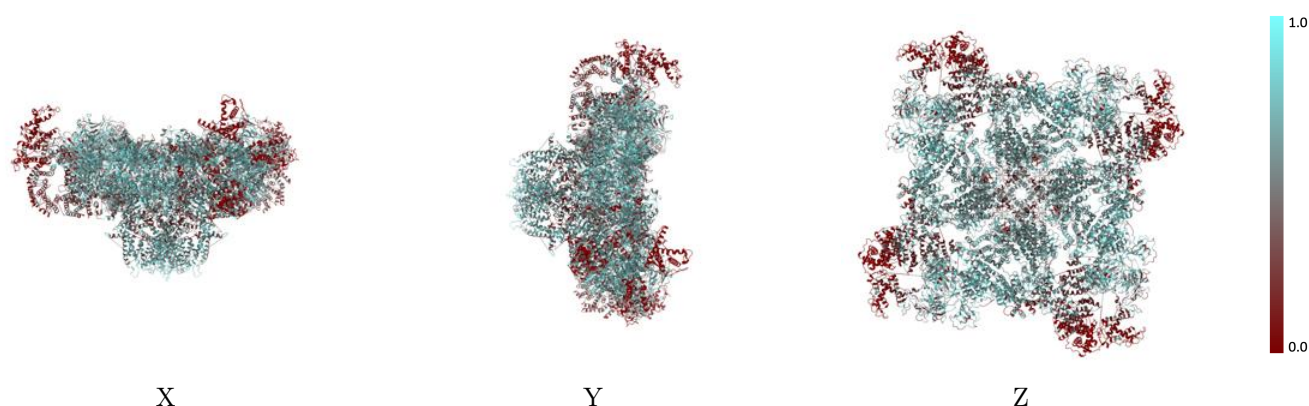
The images above show the 3D surface view of the map at the recommended contour level 0.022 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



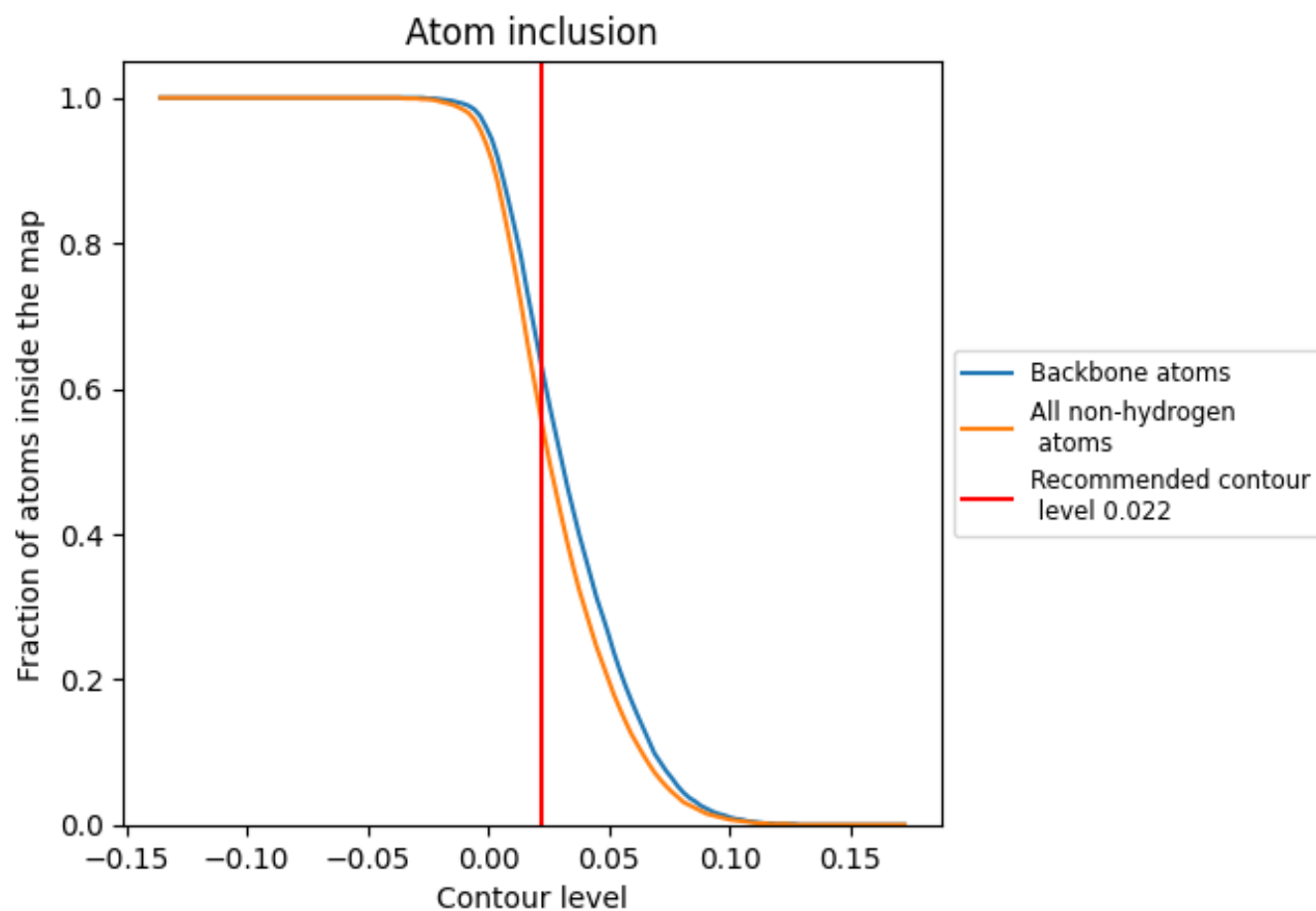
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.022).

9.4 Atom inclusion [i](#)



At the recommended contour level, 63% of all backbone atoms, 56% 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 (0.022) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5580	0.3230
A	0.6020	0.3810
B	0.5610	0.3230
C	0.4110	0.2760
D	0.6020	0.3780
E	0.5610	0.3230
F	0.4110	0.2740
G	0.6010	0.3780
H	0.5610	0.3230
I	0.4110	0.2720
J	0.6020	0.3790
K	0.5620	0.3220
L	0.4110	0.2750

1.0

0.0

<0.0