



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2026 – 07:55 PM UTC

PDB ID : 6X32 / pdb_00006x32
EMDB ID : EMD-22015
Title : Wt pig RyR1 in complex with apoCaM, EGTA condition (class 1 and 2, closed)
Authors : Woll, K.W.; Haji-Ghassemi, O.; Van Petegem, F.
Deposited on : 2020-05-21
Resolution : 3.80 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

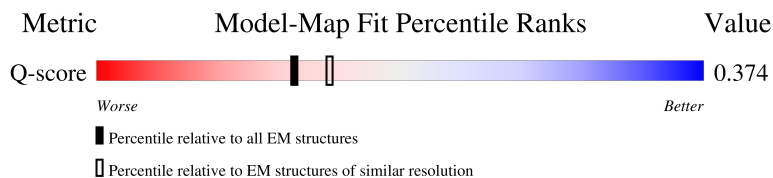
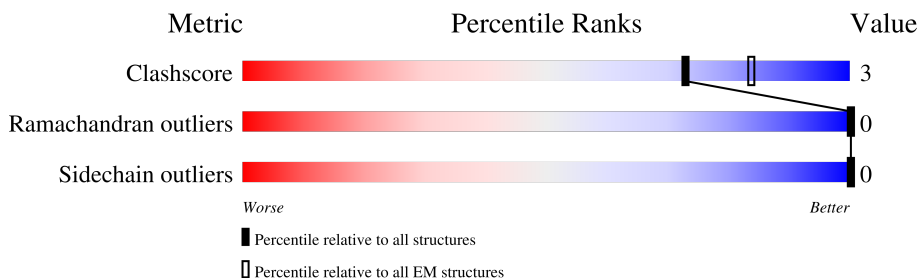
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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	10198 (3.30 - 4.30)

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	110	 81% 15% .
1	D	110	 78% 18% .
1	G	110	 78% 18% .
1	J	110	 81% 15% .

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Mol	Chain	Length	Quality of chain
2	B	3800	
2	E	3800	
2	H	3800	
2	K	3800	
3	C	146	
3	F	146	
3	I	146	
3	L	146	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 114280 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
			742	474	128	136	4		
1	D	106	Total	C	N	O	S	0	0
			742	474	128	136	4		
1	G	106	Total	C	N	O	S	0	0
			742	474	128	136	4		
1	J	106	Total	C	N	O	S	0	0
			742	474	128	136	4		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP P68106
A	-1	ASN	-	expression tag	UNP P68106
A	0	ALA	-	expression tag	UNP P68106
D	-2	SER	-	expression tag	UNP P68106
D	-1	ASN	-	expression tag	UNP P68106
D	0	ALA	-	expression tag	UNP P68106
G	-2	SER	-	expression tag	UNP P68106
G	-1	ASN	-	expression tag	UNP P68106
G	0	ALA	-	expression tag	UNP P68106
J	-2	SER	-	expression tag	UNP P68106
J	-1	ASN	-	expression tag	UNP P68106
J	0	ALA	-	expression tag	UNP P68106

- Molecule 2 is a protein called Ryanodine Receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	3798	Total	C	N	O	S	6	0
			27011	17294	4767	4780	170		
2	E	3798	Total	C	N	O	S	6	0
			27011	17294	4767	4780	170		
2	H	3798	Total	C	N	O	S	6	0
			27011	17294	4767	4780	170		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	K	3798	Total	C	N	O	S	6	0
			27011	17294	4767	4780	170		

- Molecule 3 is a protein called Calmodulin-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	135	Total	C	N	O	S	0	0
			816	505	142	165	4		
3	F	135	Total	C	N	O	S	0	0
			816	505	142	165	4		
3	I	135	Total	C	N	O	S	0	0
			816	505	142	165	4		
3	L	135	Total	C	N	O	S	0	0
			816	505	142	165	4		

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

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

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.

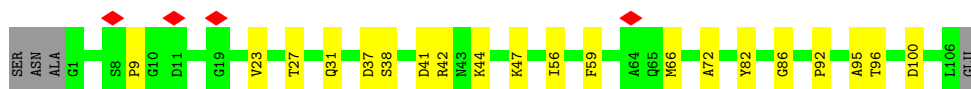
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

Chain A: 



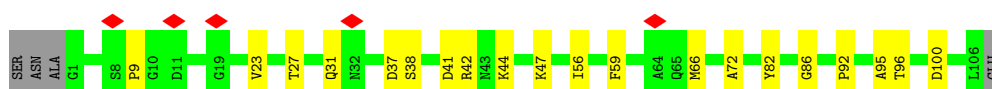
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

Chain D: 



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

Chain G: 

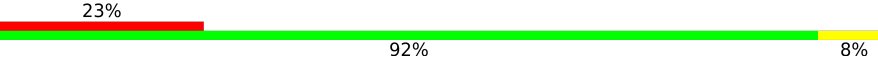


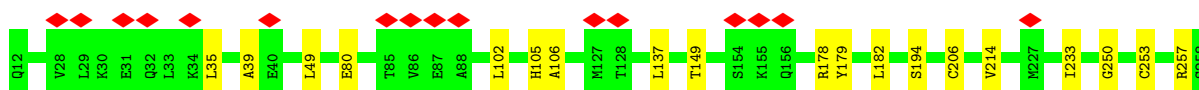
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

Chain J: 



- Molecule 2: Ryanodine Receptor

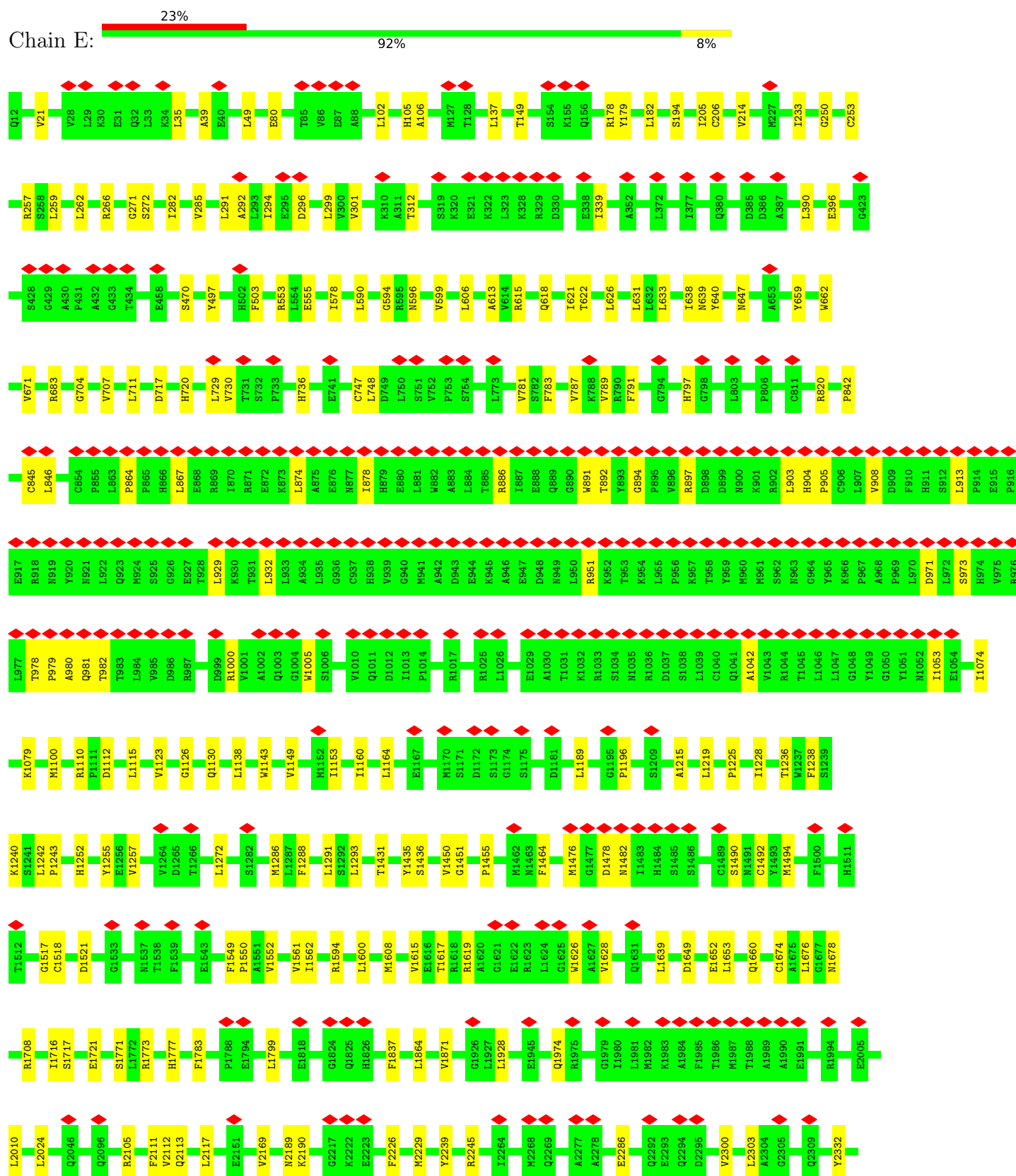
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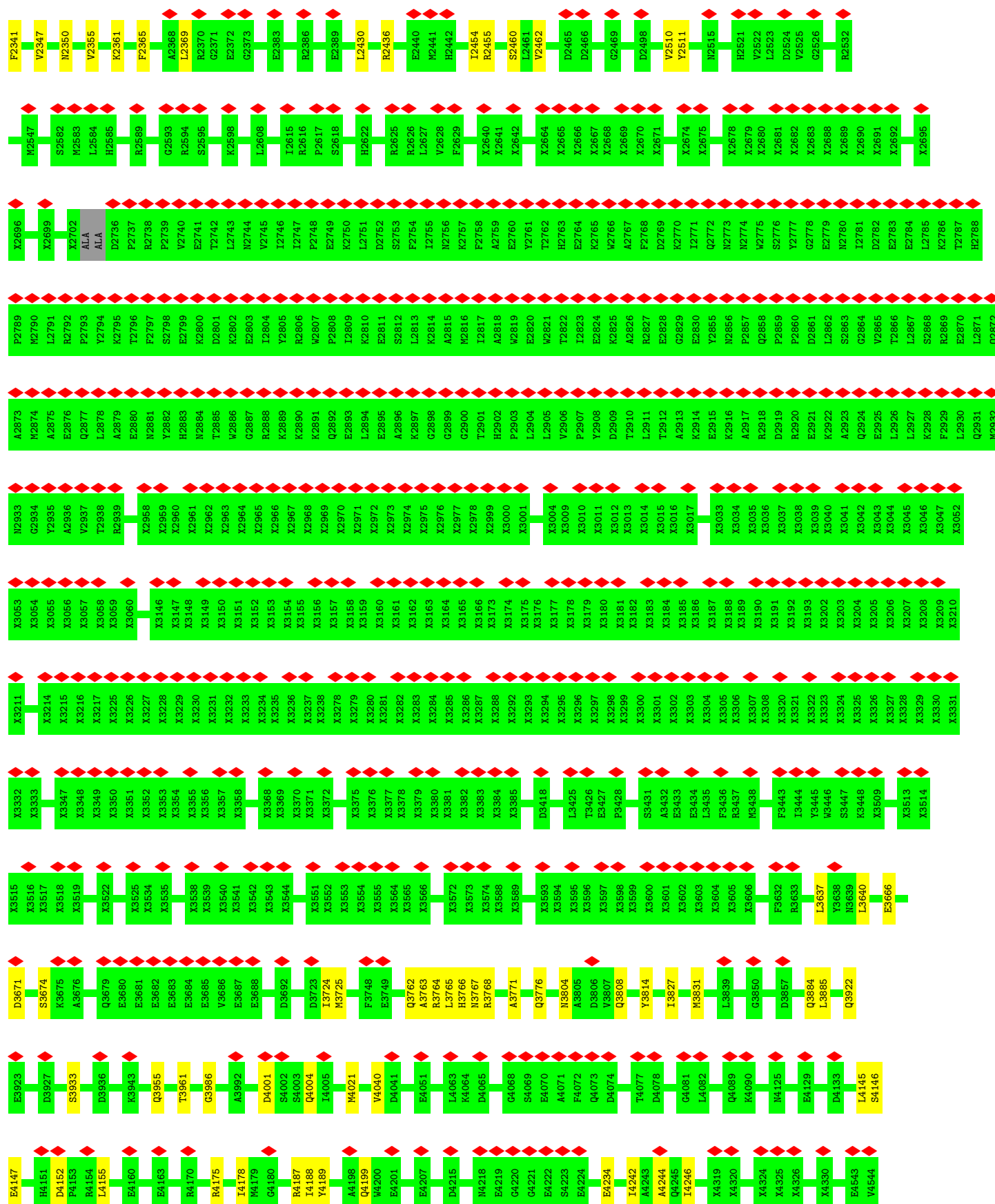


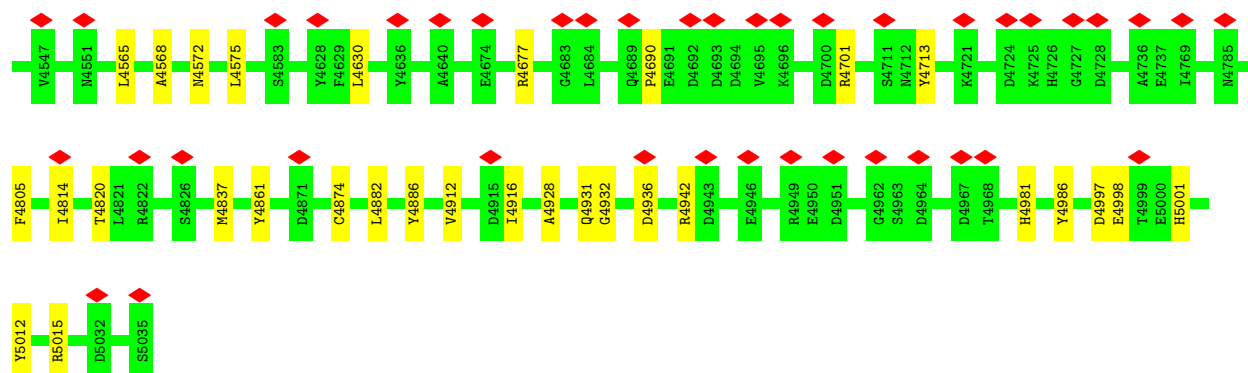


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I4916	E4674	R4187	A4003	M3725	X3551	X3371	X3238	X3155	X2967	K2890	I2746	
Q4931	E4677	Y4189	I4005	S3725	X3552	X3372	X3278	X3156	X2968	K2891	I2747	
D4936	A4021	A4198	M4021	S3747	X3553	X3375	X3279	X3157	X2969	P2892	F2748	
R4942	W4200	W4200	V4040	F3748	X3554	X3376	X3280	X3158	X2970	P2898	E2749	
D4943	E4201	E4201	M4042	E3749	X3555	X3377	X3281	X3159	X2971	K2810	K2750	
E4946	M4202	M4202	M4042	Q3762	X3556	X3378	X3282	X3160	X2972	E2893	L2751	
R4949	E4207	E4207	E4051	R3763	X3572	X3380	X3284	X3161	X2973	E2895	D2752	
E4950	D4215	D4215	L4063	R3764	X3573	X3381	X3285	X3162	X2974	K2896	S2753	
D4951	M4218	M4218	K4064	H3766	X3574	X3382	X3286	X3163	X2975	G2898	F2754	
K4695	E4219	E4219	D4065	N3767	X3588	X3383	X3287	X3164	X2976	G2899	I2755	
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D4700	G4221	G4221	S4069	A3771	X3593	X3385	X3292	X3166	X2978	T2901	K2757	
R4701	E4222	E4222	A4070	M3804	X3594	D3418	X3293	X3174	X2979	H2902	F2758	
S4711	A4071	A4071	F4072	A3805	X3595	L3425	X3294	X3175	X3000	P2903	A2759	
M4712	Q4073	Q4073	Q4073	D3806	X3596	T3426	X3295	X3176	X3001	L2904	E2760	
Y4713	D4074	D4074	D4074	Q3807	X3597	E427	X3296	X3177	X3004	P2905	V2761	
K4721	T4077	T4077	T4077	V3808	X3598	P3428	X3297	X3178	X3009	V2906	I2762	
D4724	D4078	D4078	D4078	M3831	X3599	L3425	X3298	X3179	X3010	P2907	H2763	
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H4726	L4082	L4082	L4082	D3857	X3601	S4431	X3300	X3181	X3012	T2910	K2765	
G4727	Q4089	Q4089	Q4089	D3857	X3602	A4432	X3301	X3182	X3013	T2910	K2766	
D4728	K4090	K4090	K4090	D3857	X3603	E4433	X3302	X3183	X3014	L2911	A2767	
A4736	M4125	M4125	M4125	D3857	X3604	E4434	X3303	X3184	X3015	T2912	F2768	
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I4769	D4133	D4133	D4133	D3857	X3606	F4436	X3305	X3188	X3017	K2914	K2770	
N4785	L4145	L4145	L4145	D3857	X3606	R4437	X3306	X3189	X3017	E2915	I2771	
I4814	E4146	E4146	E4146	D3857	X3606	M4438	X3307	X3190	X3033	A2916	Q2772	
T4820	E4147	E4147	E4147	D3857	X3606	F4438	X3308	X3191	X3034	K2917	Q2773	
L4821	H4151	H4151	H4151	D3857	X3606	I4444	X3320	X3192	X3035	A2918	I2774	
R4822	D4152	D4152	D4152	D3857	X3606	W4445	X3321	X3193	X3036	D2919	W2775	
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D4871	E4160	E4160	E4160	D3857	X3606	X3513	X3325	X3205	X3040	S2863	K2780	
C4874	F4163	F4163	F4163	D3857	X3606	X3514	X3326	X3206	X3042	G2864	I2781	
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Y4886	E4175	E4175	E4175	D3857	X3606	X3516	X3328	X3208	X3044	L2926	D2787	
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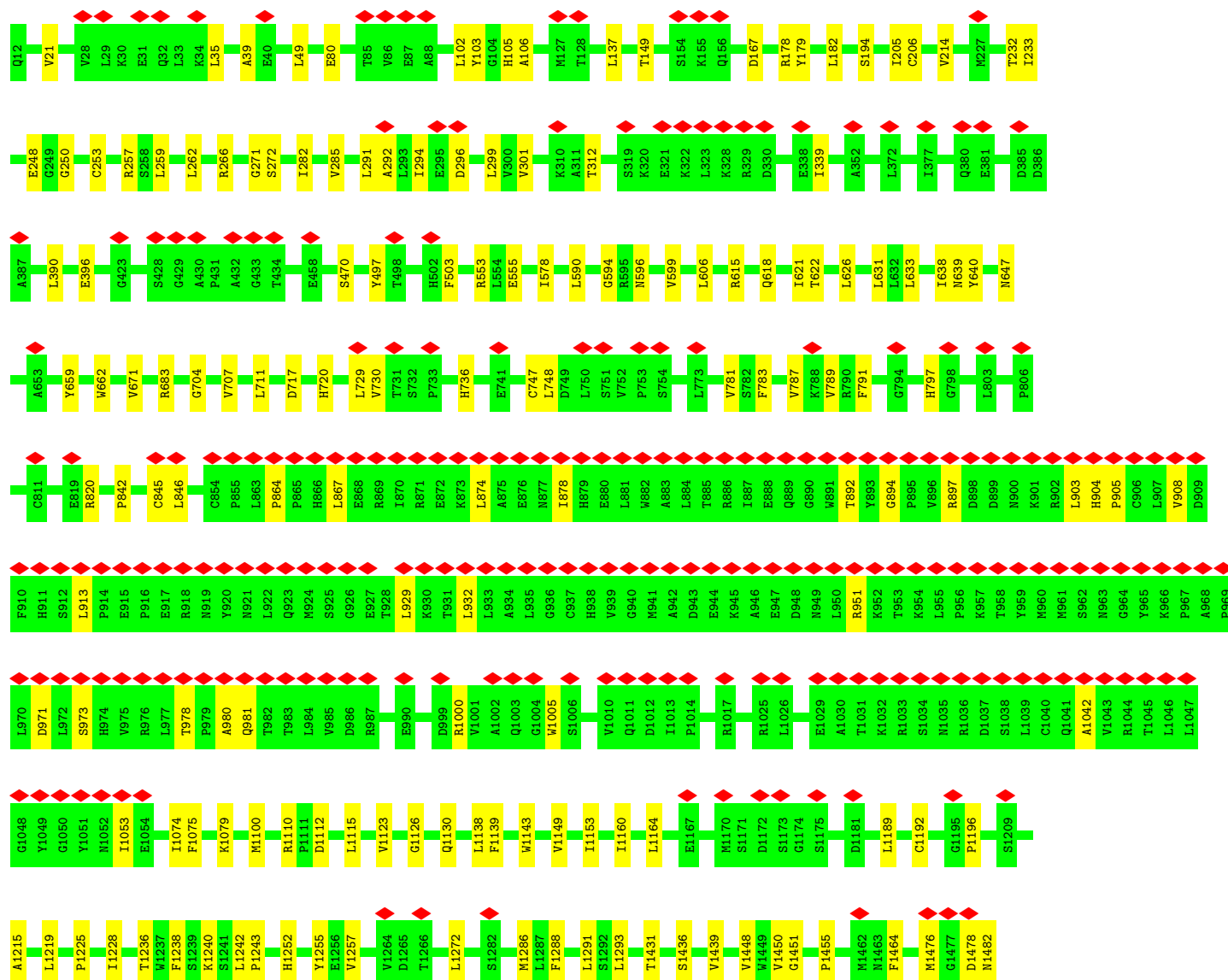
• Molecule 2: Ryanodine Receptor

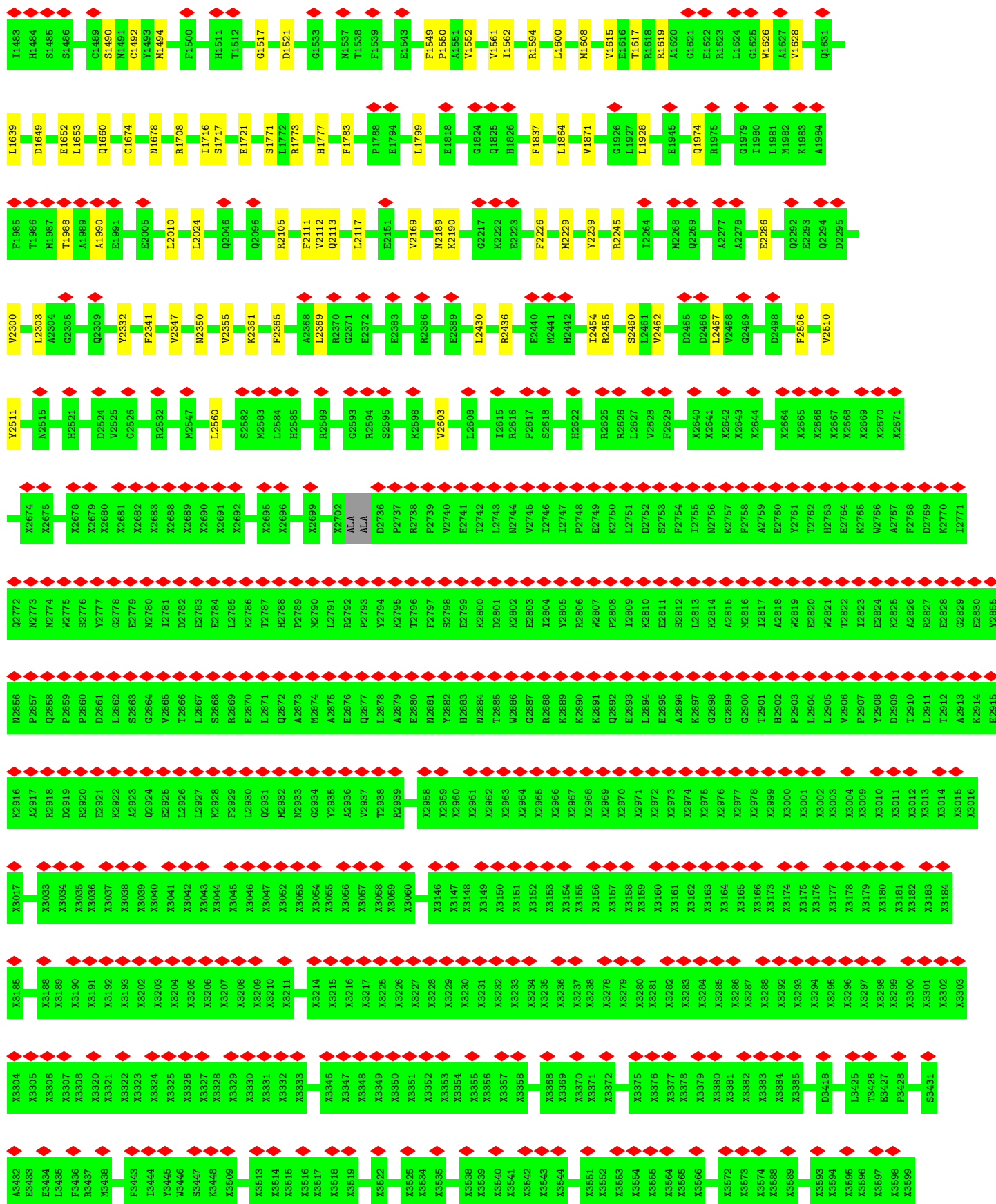


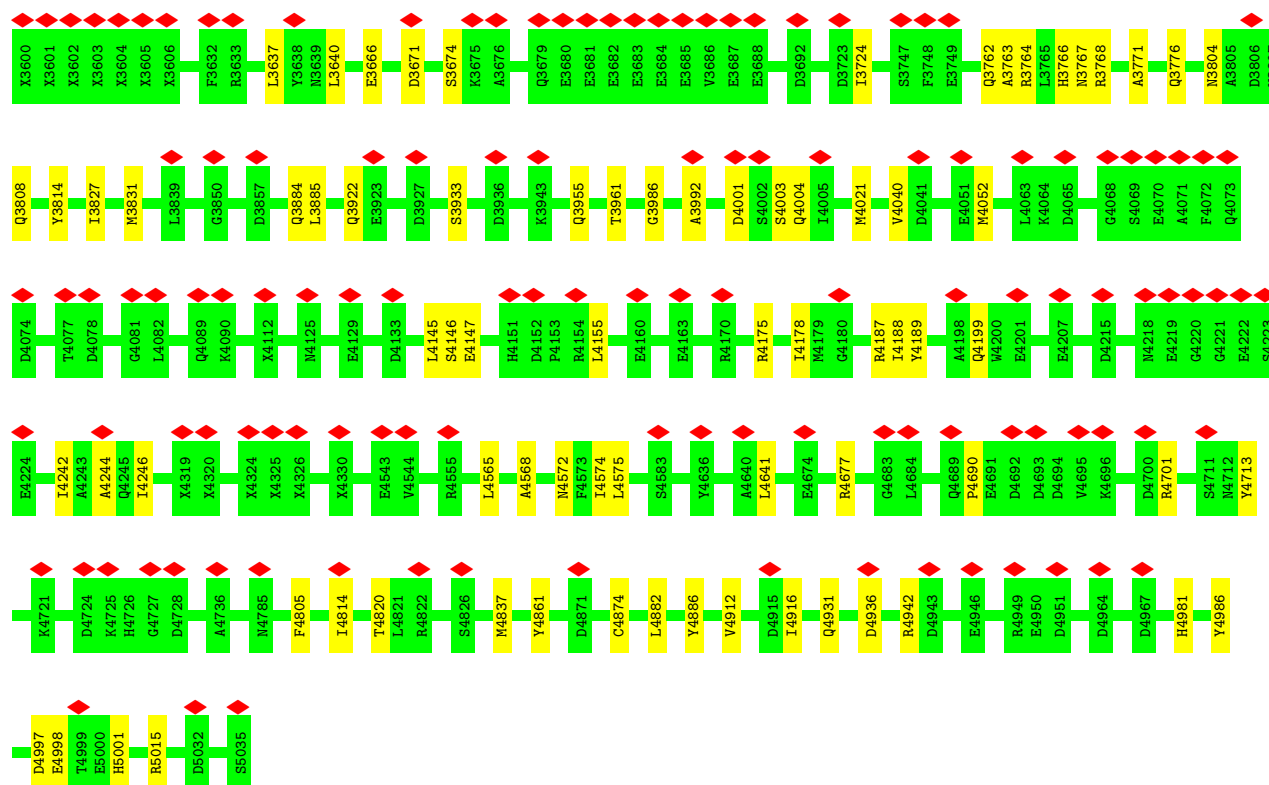




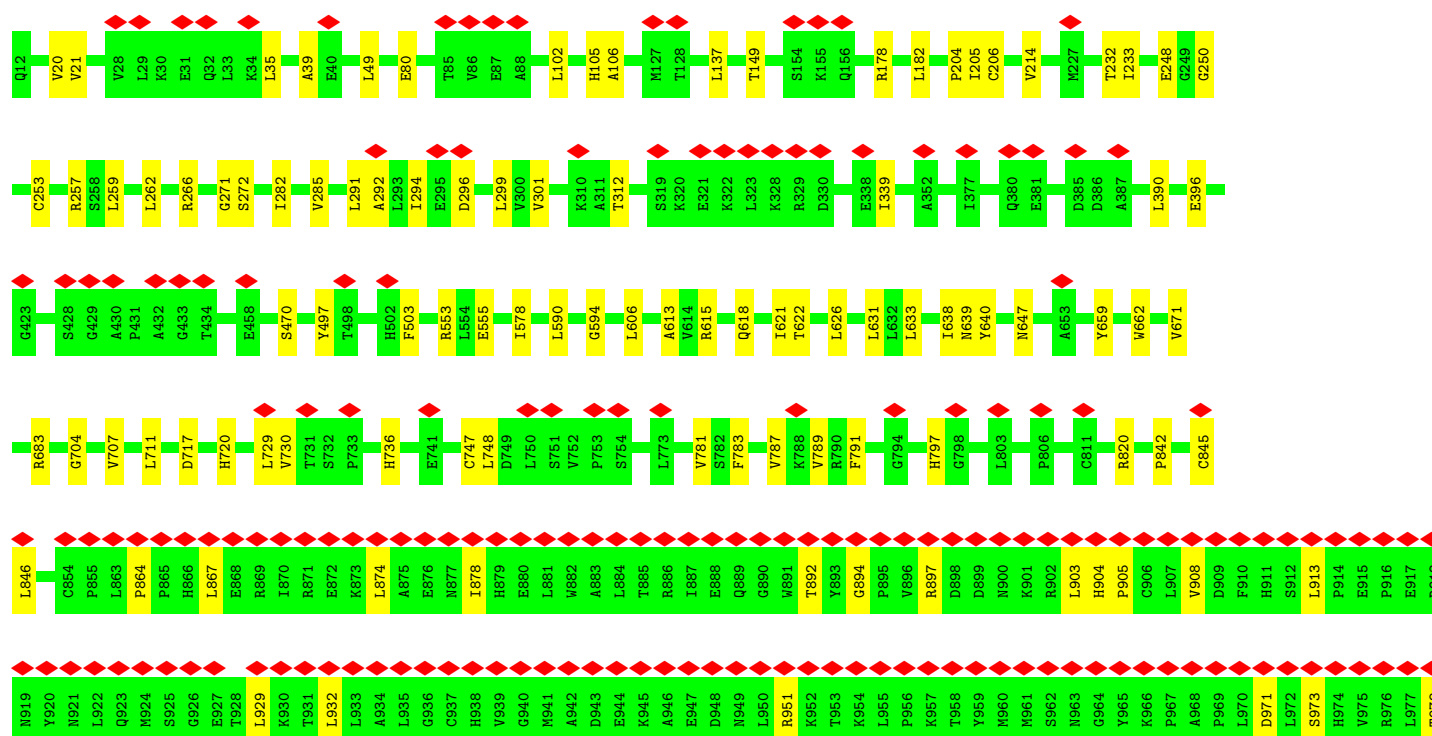
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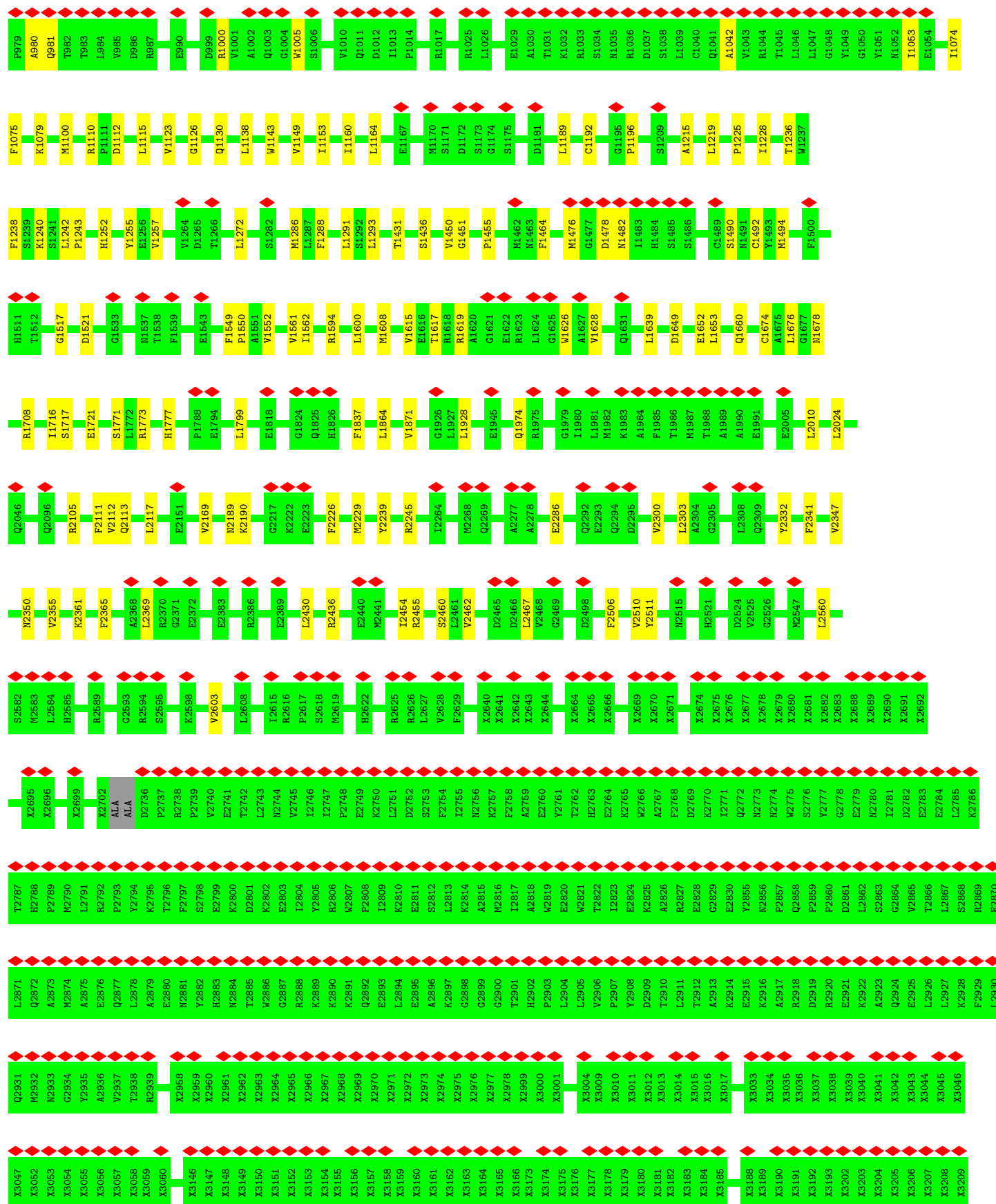


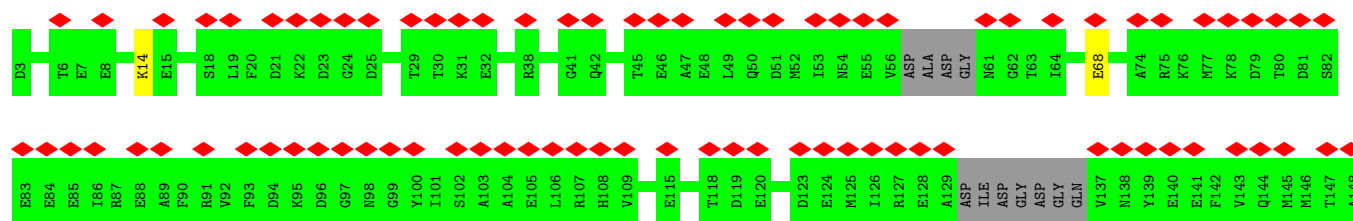




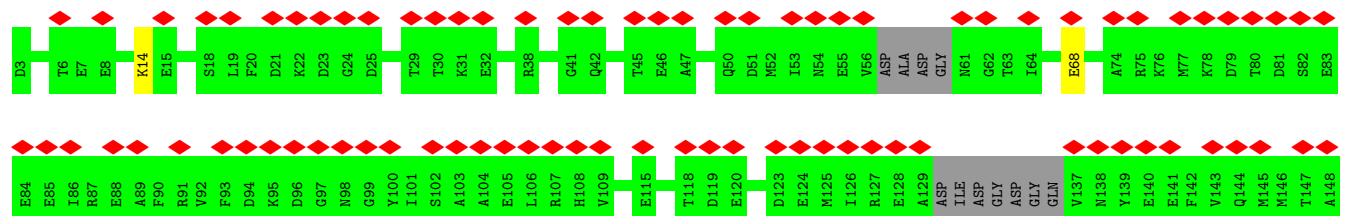
• Molecule 2: Ryanodine Receptor



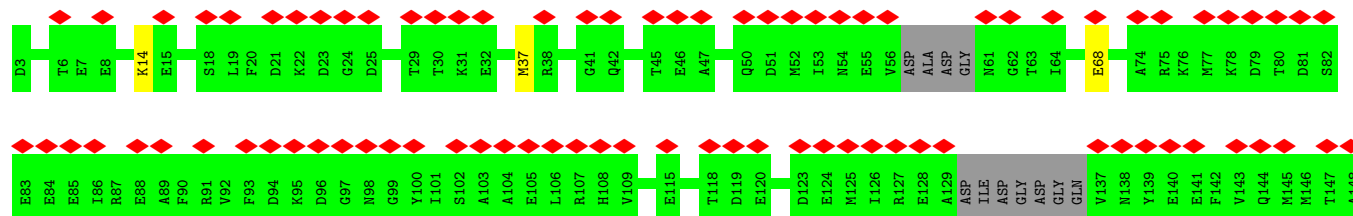
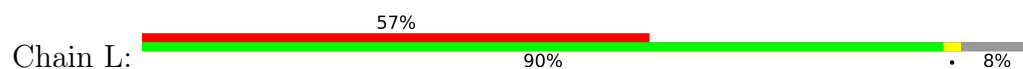




• Molecule 3: Calmodulin-1



• Molecule 3: Calmodulin-1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	44957	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	0.243	Depositor
Minimum map value	-0.195	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	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	0.07	0/758	0.22	0/1033
1	D	0.07	0/758	0.22	0/1033
1	G	0.07	0/758	0.22	0/1033
1	J	0.07	0/758	0.22	0/1033
2	B	0.07	0/25809	0.21	0/35154
2	E	0.07	0/25809	0.21	0/35154
2	H	0.07	0/25809	0.21	0/35154
2	K	0.07	0/25809	0.21	0/35154
3	C	0.06	0/820	0.18	0/1120
3	F	0.06	0/820	0.18	0/1120
3	I	0.06	0/820	0.18	0/1120
3	L	0.06	0/820	0.18	0/1120
All	All	0.07	0/109548	0.21	0/149228

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	742	0	702	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	742	0	702	11	0
1	G	742	0	702	11	0
1	J	742	0	702	9	0
2	B	27011	0	23901	173	0
2	E	27011	0	23901	179	0
2	H	27011	0	23901	181	0
2	K	27011	0	23901	176	0
3	C	816	0	573	1	0
3	F	816	0	573	2	0
3	I	816	0	573	2	0
3	L	816	0	573	3	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	114280	0	100704	716	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 716 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:647:ASN:ND2	2:E:820:ARG:O	2.27	0.67
2:K:647:ASN:ND2	2:K:820:ARG:O	2.27	0.67
2:B:647:ASN:ND2	2:B:820:ARG:O	2.27	0.67
2:H:647:ASN:ND2	2:H:820:ARG:O	2.27	0.66
2:E:1215:ALA:HA	2:E:1219:LEU:HB2	1.81	0.63

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	104/110 (94%)	102 (98%)	2 (2%)	0	100	100
1	D	104/110 (94%)	102 (98%)	2 (2%)	0	100	100
1	G	104/110 (94%)	102 (98%)	2 (2%)	0	100	100
1	J	104/110 (94%)	102 (98%)	2 (2%)	0	100	100
2	B	3382/3800 (89%)	3336 (99%)	46 (1%)	0	100	100
2	E	3382/3800 (89%)	3336 (99%)	46 (1%)	0	100	100
2	H	3382/3800 (89%)	3336 (99%)	46 (1%)	0	100	100
2	K	3382/3800 (89%)	3336 (99%)	46 (1%)	0	100	100
3	C	129/146 (88%)	127 (98%)	2 (2%)	0	100	100
3	F	129/146 (88%)	127 (98%)	2 (2%)	0	100	100
3	I	129/146 (88%)	127 (98%)	2 (2%)	0	100	100
3	L	129/146 (88%)	127 (98%)	2 (2%)	0	100	100
All	All	14460/16224 (89%)	14260 (99%)	200 (1%)	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	71/90 (79%)	71 (100%)	0	100	100
1	D	71/90 (79%)	71 (100%)	0	100	100
1	G	71/90 (79%)	71 (100%)	0	100	100
1	J	71/90 (79%)	71 (100%)	0	100	100
2	B	2373/3010 (79%)	2373 (100%)	0	100	100
2	E	2373/3010 (79%)	2373 (100%)	0	100	100
2	H	2373/3010 (79%)	2373 (100%)	0	100	100
2	K	2373/3010 (79%)	2373 (100%)	0	100	100
3	C	44/125 (35%)	44 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	F	44/125 (35%)	44 (100%)	0	100	100
3	I	44/125 (35%)	44 (100%)	0	100	100
3	L	44/125 (35%)	44 (100%)	0	100	100
All	All	9952/12900 (77%)	9952 (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 80 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	4801	HIS
2	K	2418	HIS
3	I	50	GLN
2	K	1443	GLN
2	K	4196	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	57
2	E	57
2	H	57
2	K	57

The worst 5 of 228 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	4333:UNK	C	4543:GLU	N	53.56
1	E	4333:UNK	C	4543:GLU	N	53.56
1	H	4333:UNK	C	4543:GLU	N	53.56
1	K	4333:UNK	C	4543:GLU	N	53.56
1	B	1054:GLU	C	1071:ARG	N	36.15

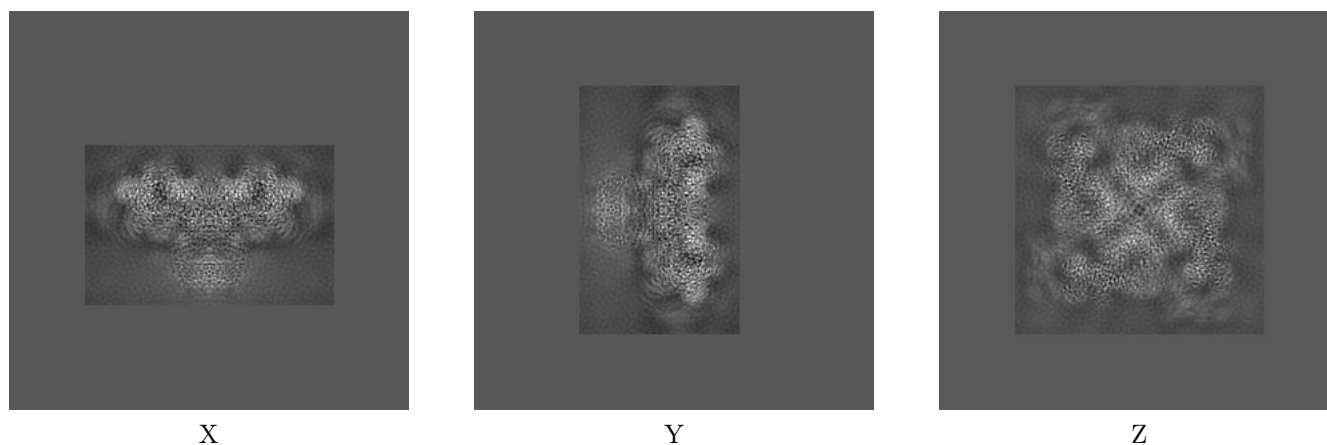
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22015. 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](#)

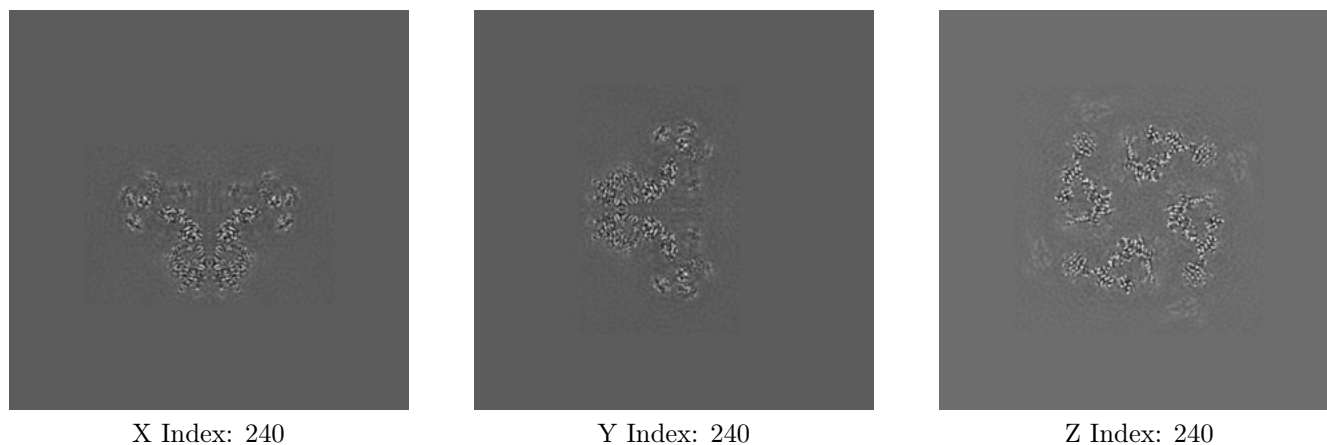
6.1.1 Primary map



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

6.2 Central slices [i](#)

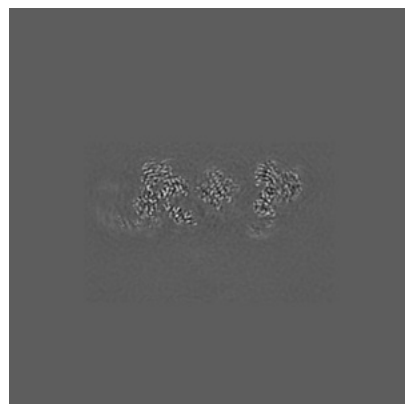
6.2.1 Primary map



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

6.3 Largest variance slices [i](#)

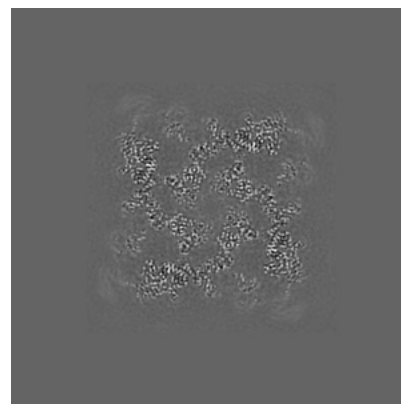
6.3.1 Primary map



X Index: 311



Y Index: 311

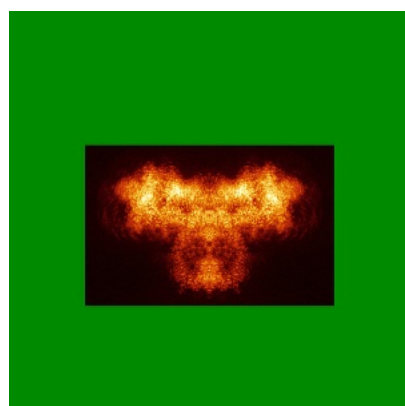


Z Index: 258

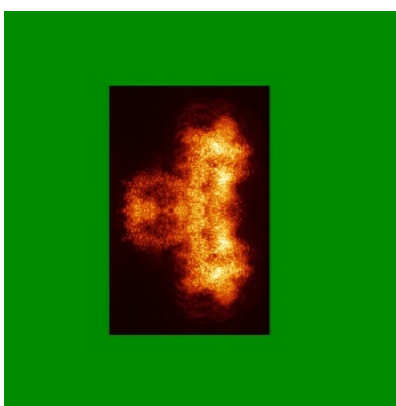
The images above show the largest variance slices of the map in three orthogonal directions.

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

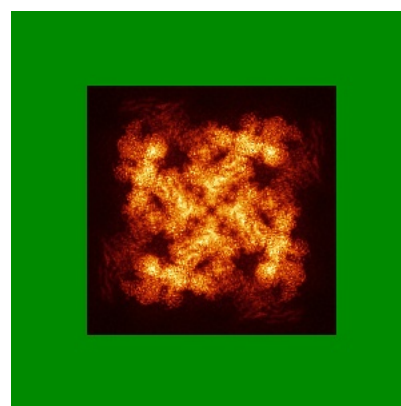
6.4.1 Primary map



X



Y

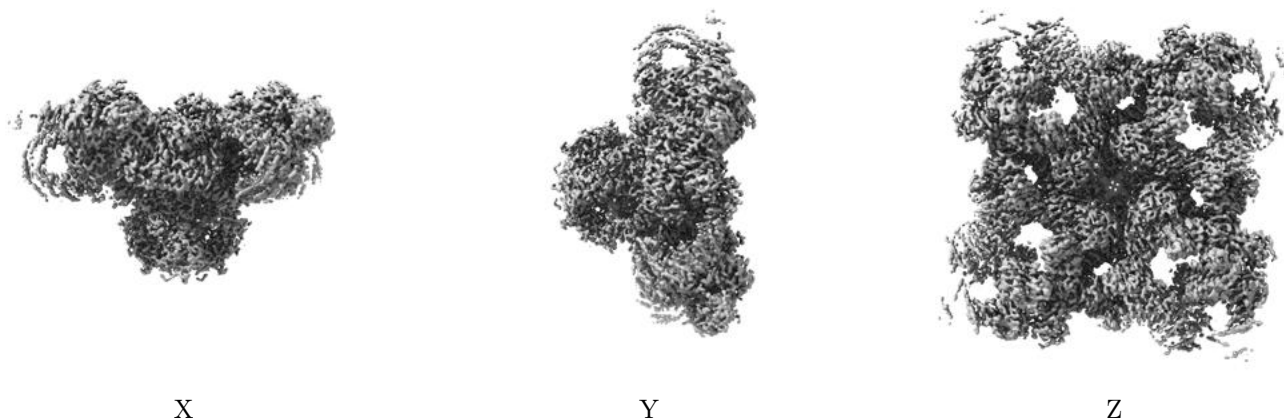


Z

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.

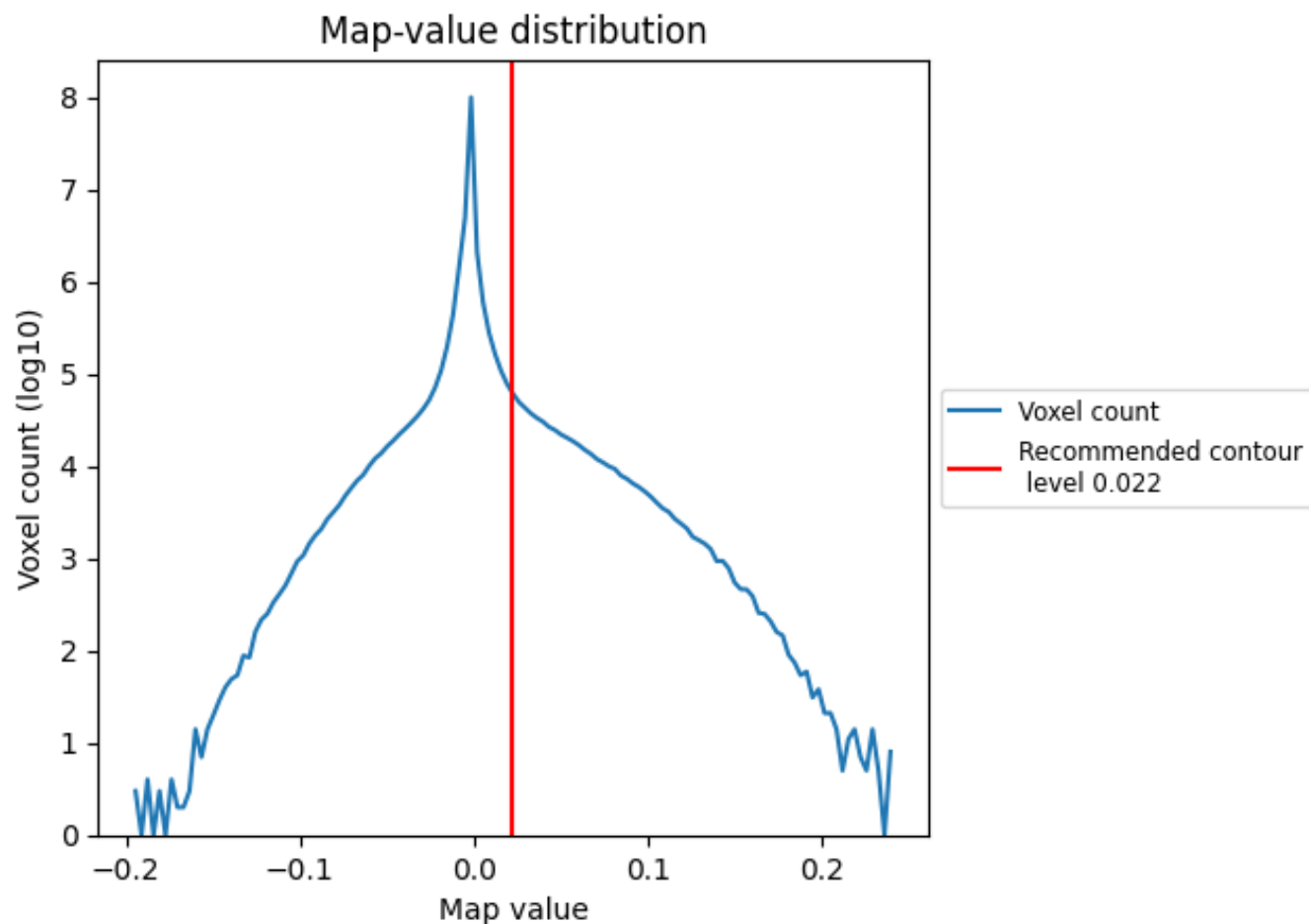
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

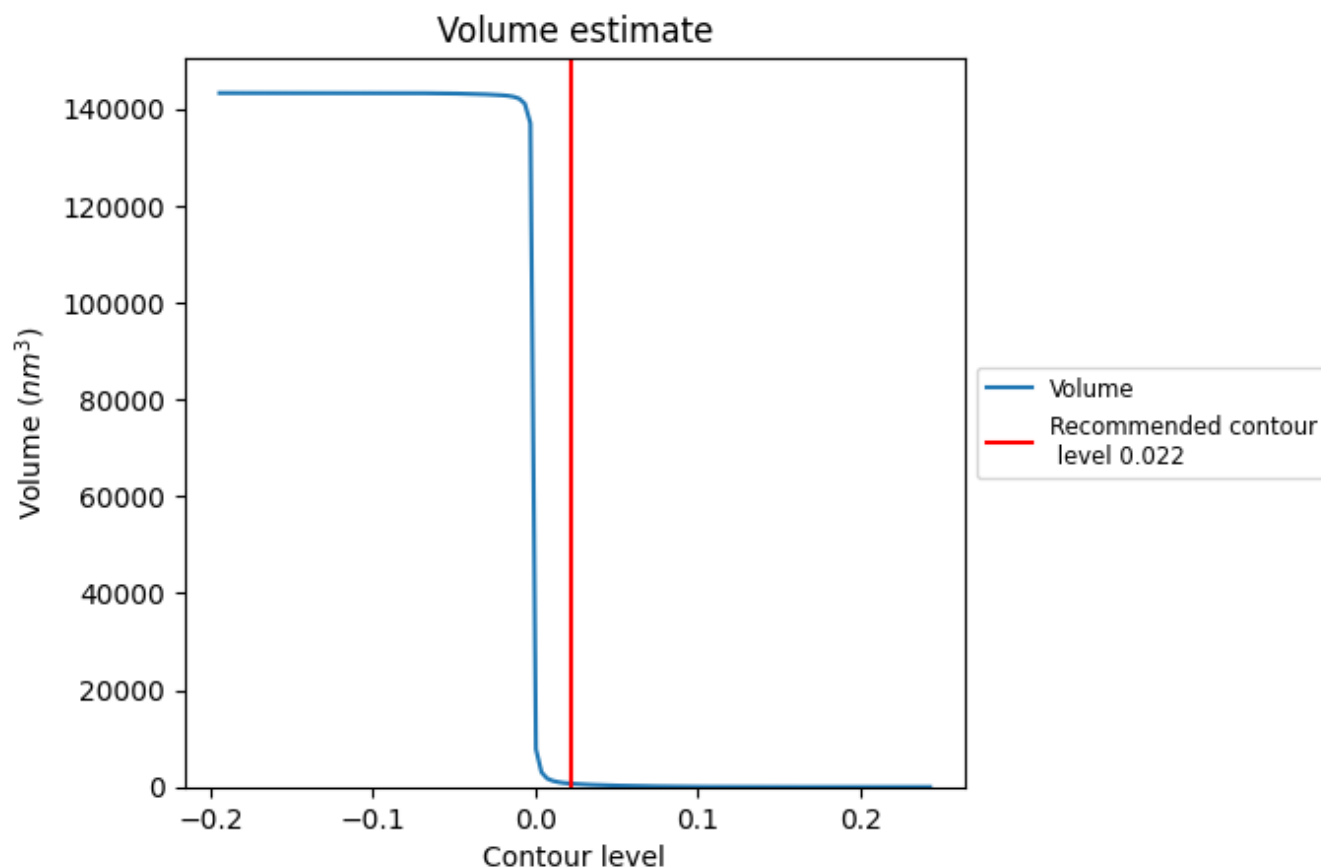
This section contains the results of statistical analysis of the map.

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.

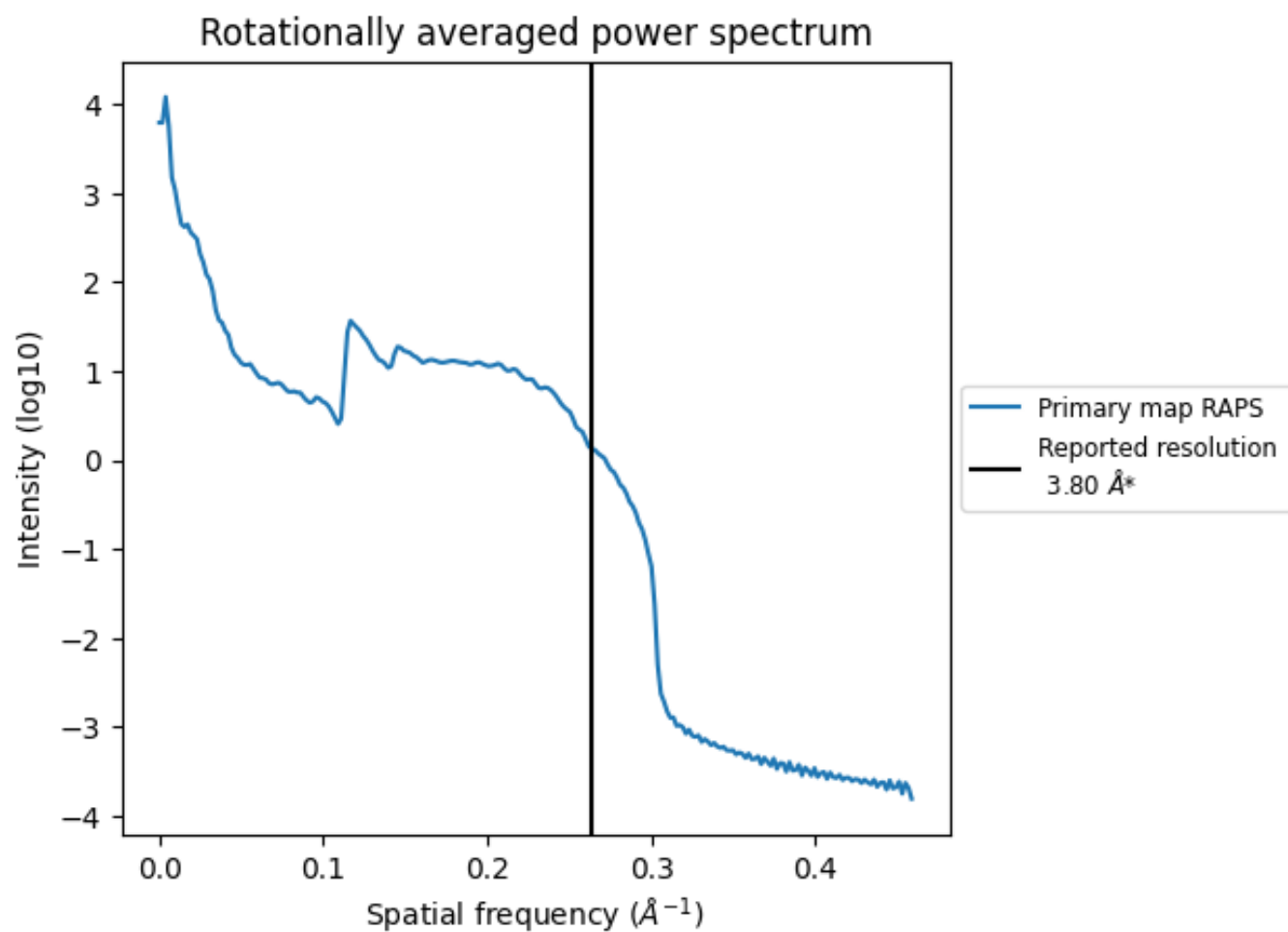
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 692 nm³; this corresponds to an approximate mass of 625 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 0.263 Å⁻¹

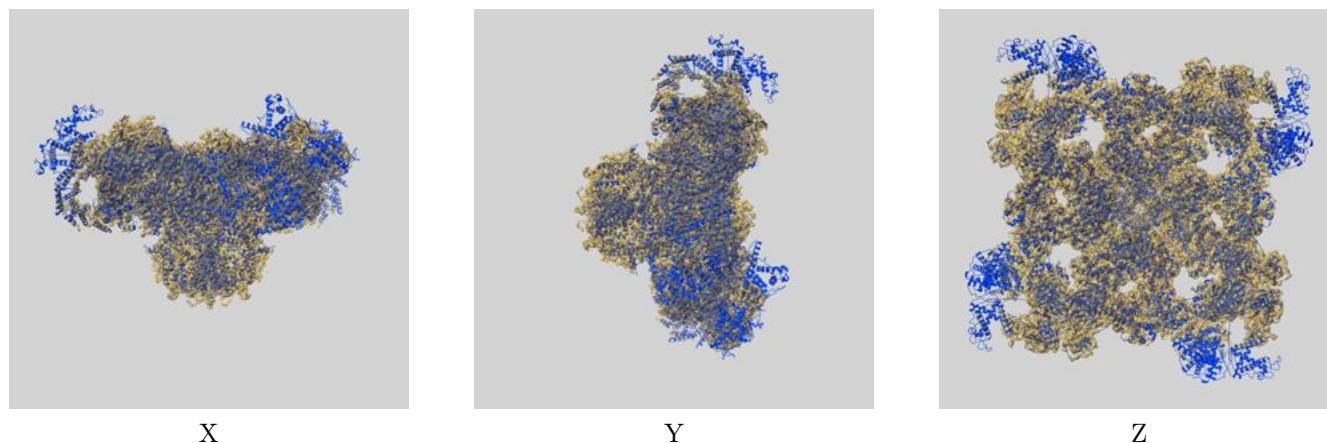
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

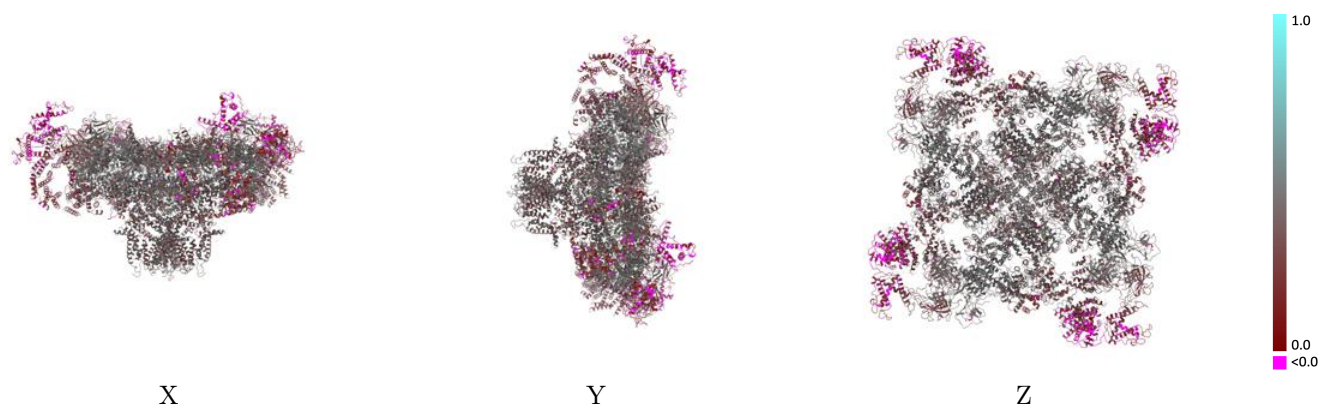
This section contains information regarding the fit between EMDB map EMD-22015 and PDB model 6X32. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



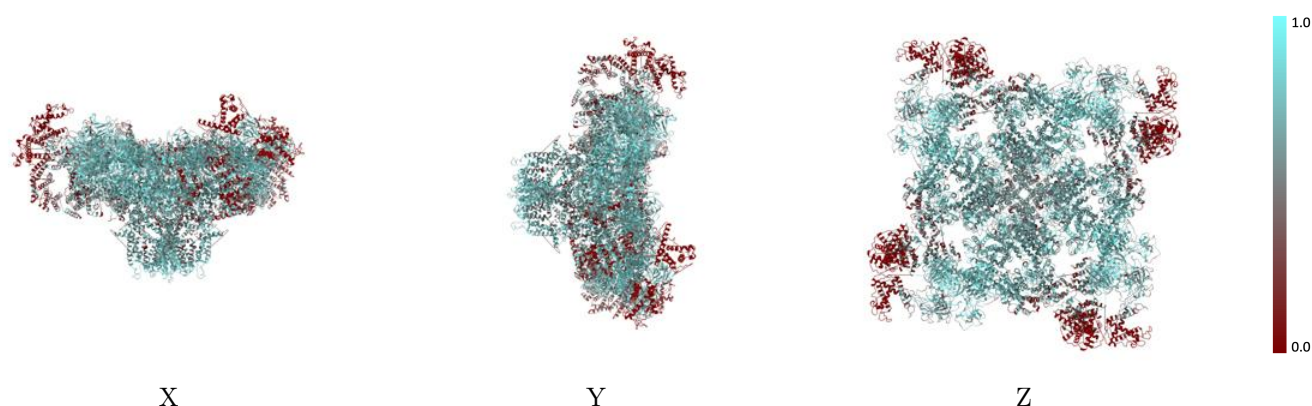
The images above show the 3D surface view of the map at the recommended contour level 0.022 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



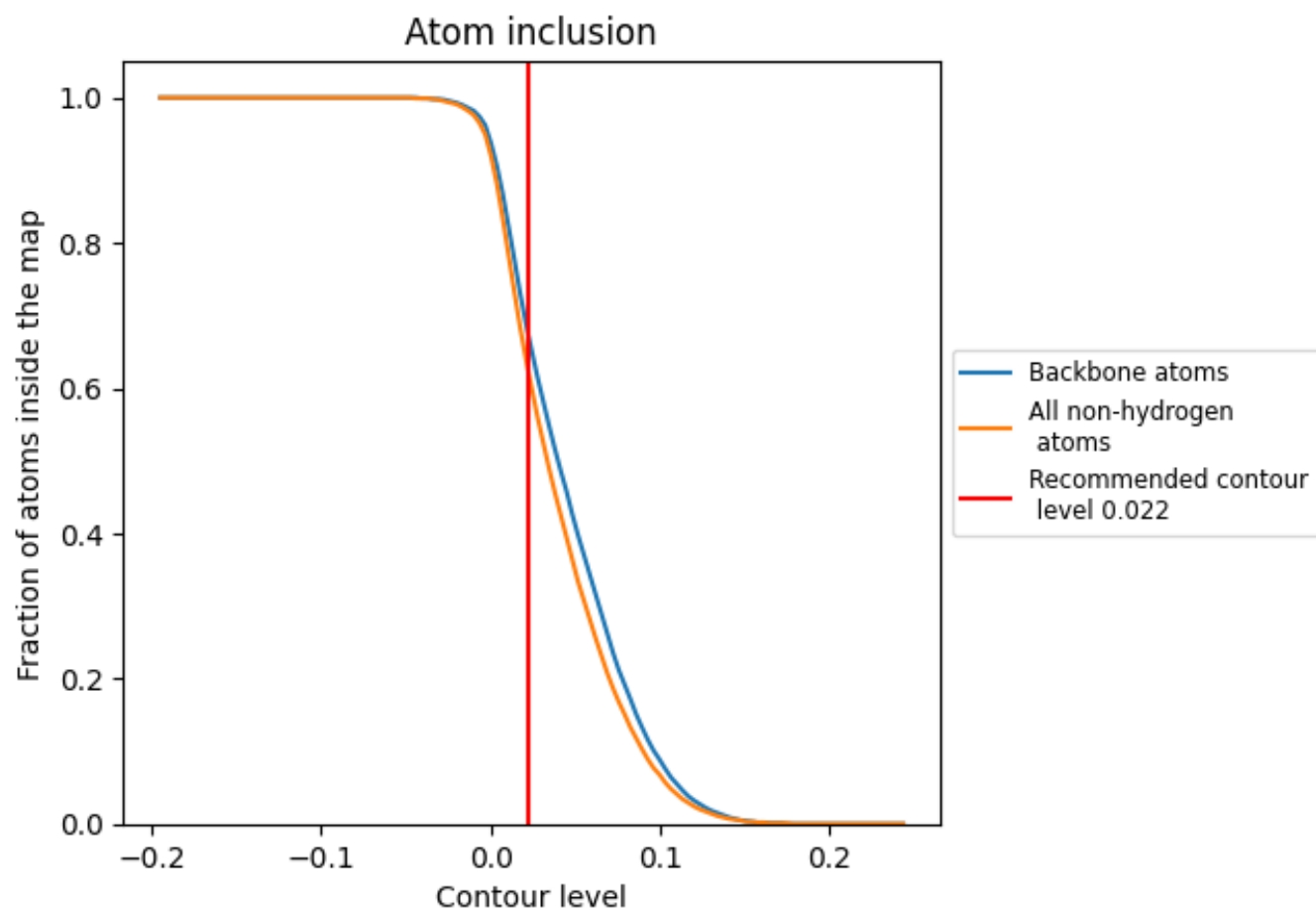
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.4 Atom inclusion ⓘ



At the recommended contour level, 68% of all backbone atoms, 63% 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	0.6270	0.3740
A	0.7080	0.4070
B	0.6330	0.3770
C	0.3970	0.2520
D	0.7050	0.4060
E	0.6320	0.3770
F	0.3960	0.2510
G	0.7050	0.4060
H	0.6310	0.3760
I	0.3960	0.2540
J	0.7080	0.4040
K	0.6320	0.3760
L	0.3920	0.2510

1.0

0.0

<0.0