



## wwPDB EM Validation Summary Report ⓘ

Feb 25, 2024 – 09:03 AM EST

PDB ID : 6X32  
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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

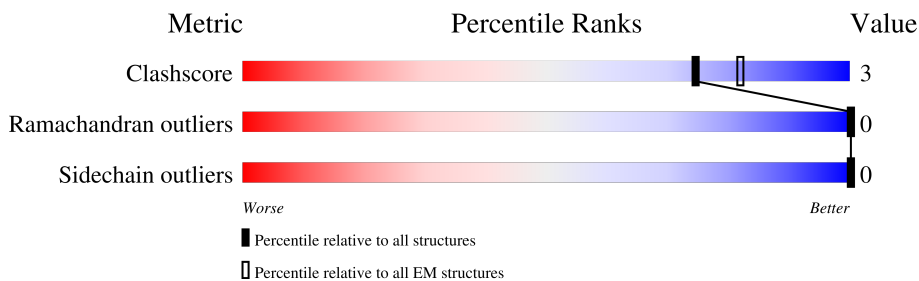
EMDB validation analysis : 0.0.1.dev70  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

# 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.



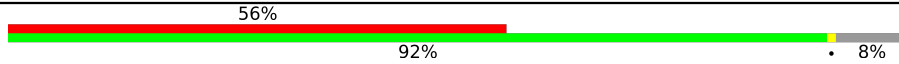
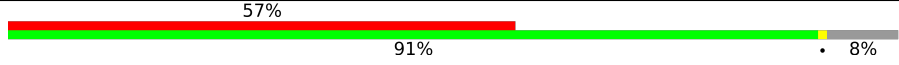
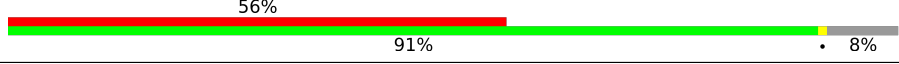
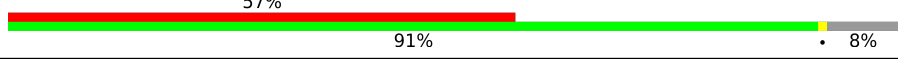
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	110	
1	D	110	
1	G	110	
1	J	110	
2	B	3800	
2	E	3800	
2	H	3800	
2	K	3800	

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Mol	Chain	Length	Quality of chain
3	C	146	 <p>56% 92% 8%</p>
3	F	146	 <p>57% 91% 8%</p>
3	I	146	 <p>56% 91% 8%</p>
3	L	146	 <p>57% 91% 8%</p>

## 2 Entry composition i

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
			Total	C	N	O	S		
1	A	106	742	474	128	136	4	0	0
1	D	106	742	474	128	136	4	0	0
1	G	106	742	474	128	136	4	0	0
1	J	106	742	474	128	136	4	0	0

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
			Total	C	N	O	S		
2	B	3798	27011	17294	4767	4780	170	6	0
2	E	3798	27011	17294	4767	4780	170	6	0
2	H	3798	27011	17294	4767	4780	170	6	0

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

- Molecule 3 is a protein called Calmodulin-1.

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

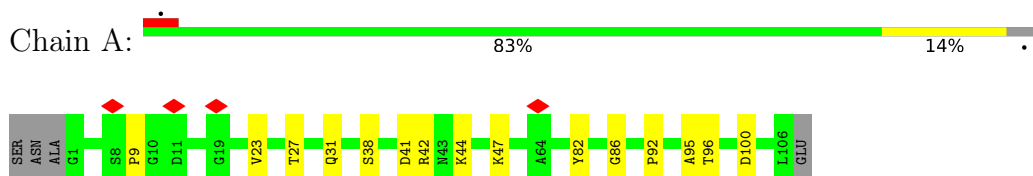
- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

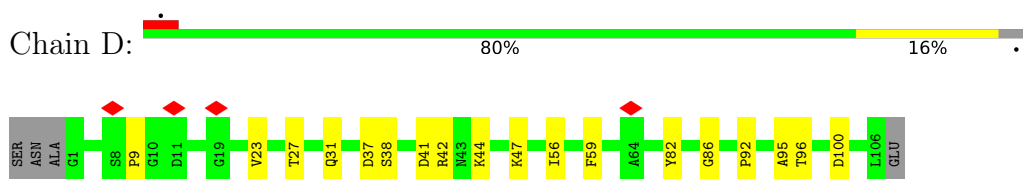
### 3 Residue-property plots

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.

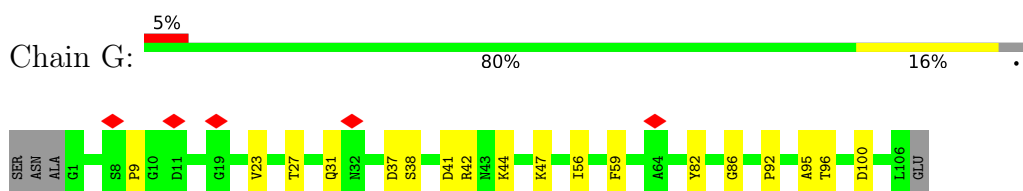
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



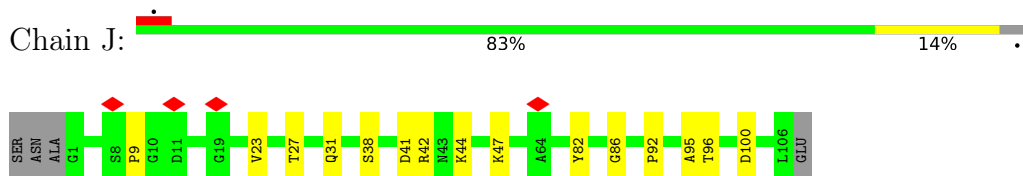
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



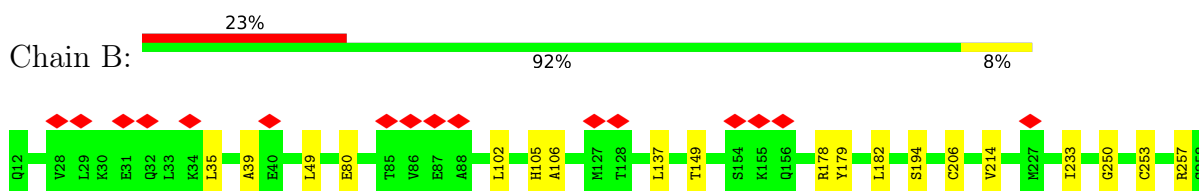
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

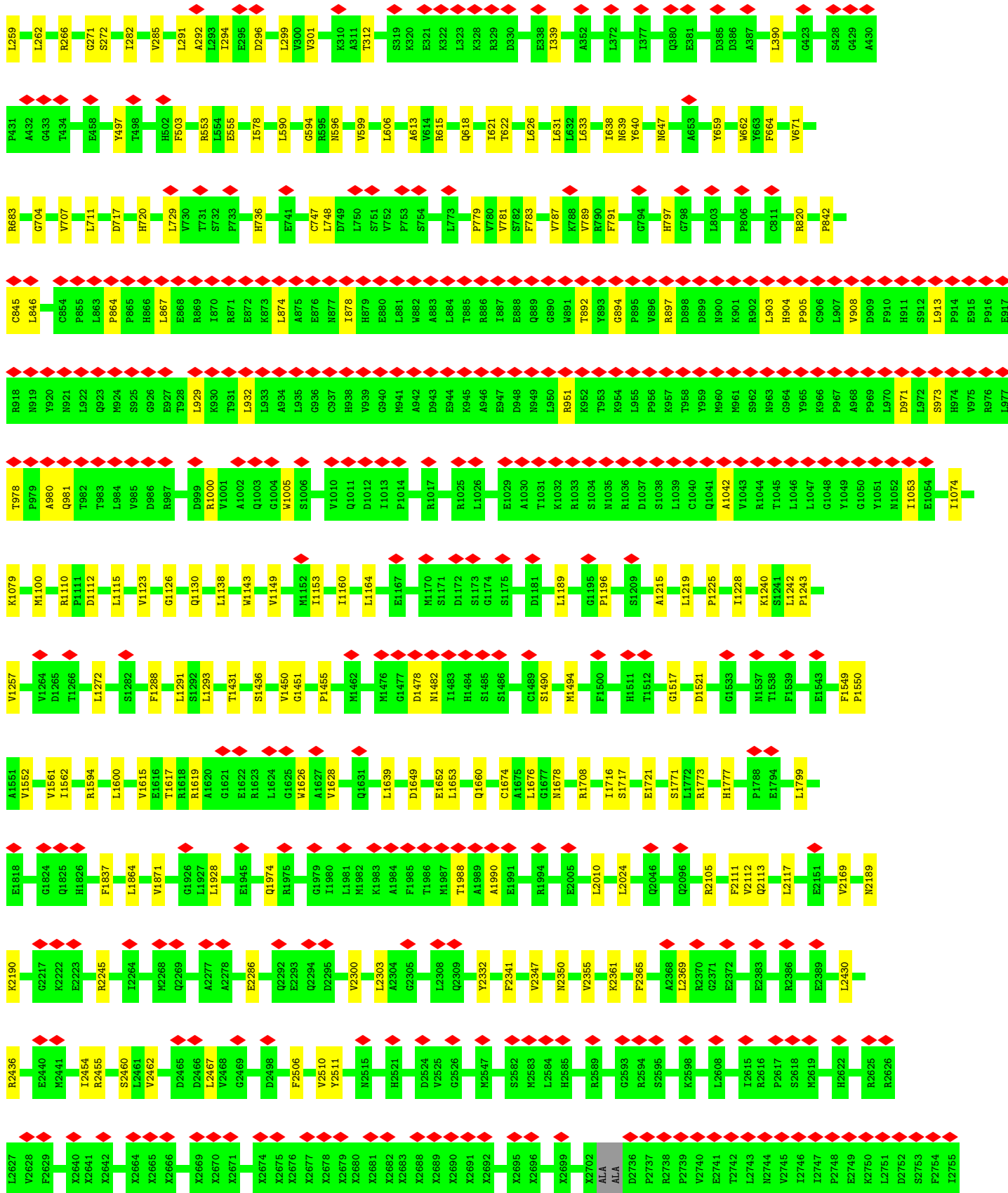


- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



- Molecule 2: Ryanodine Receptor

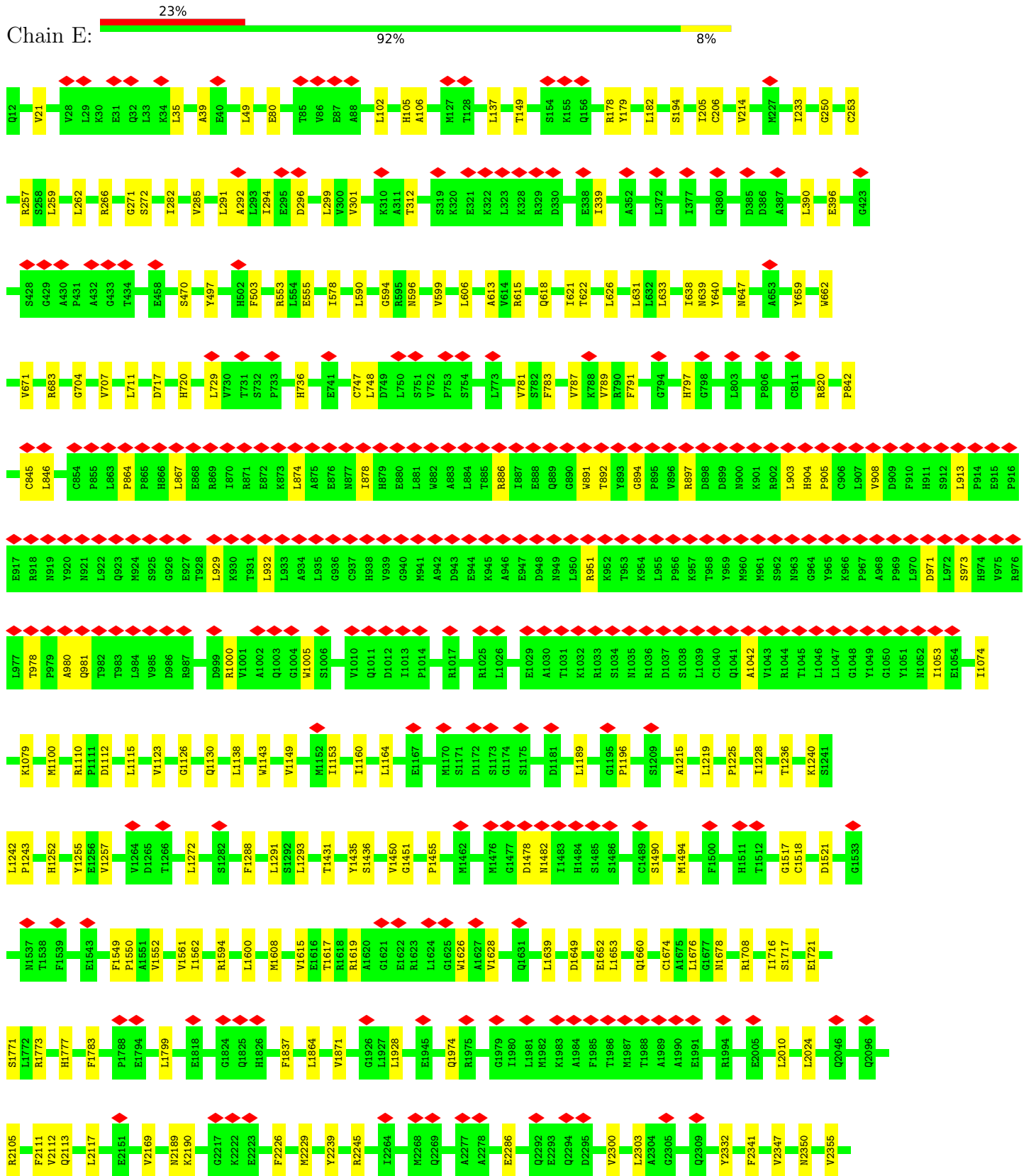


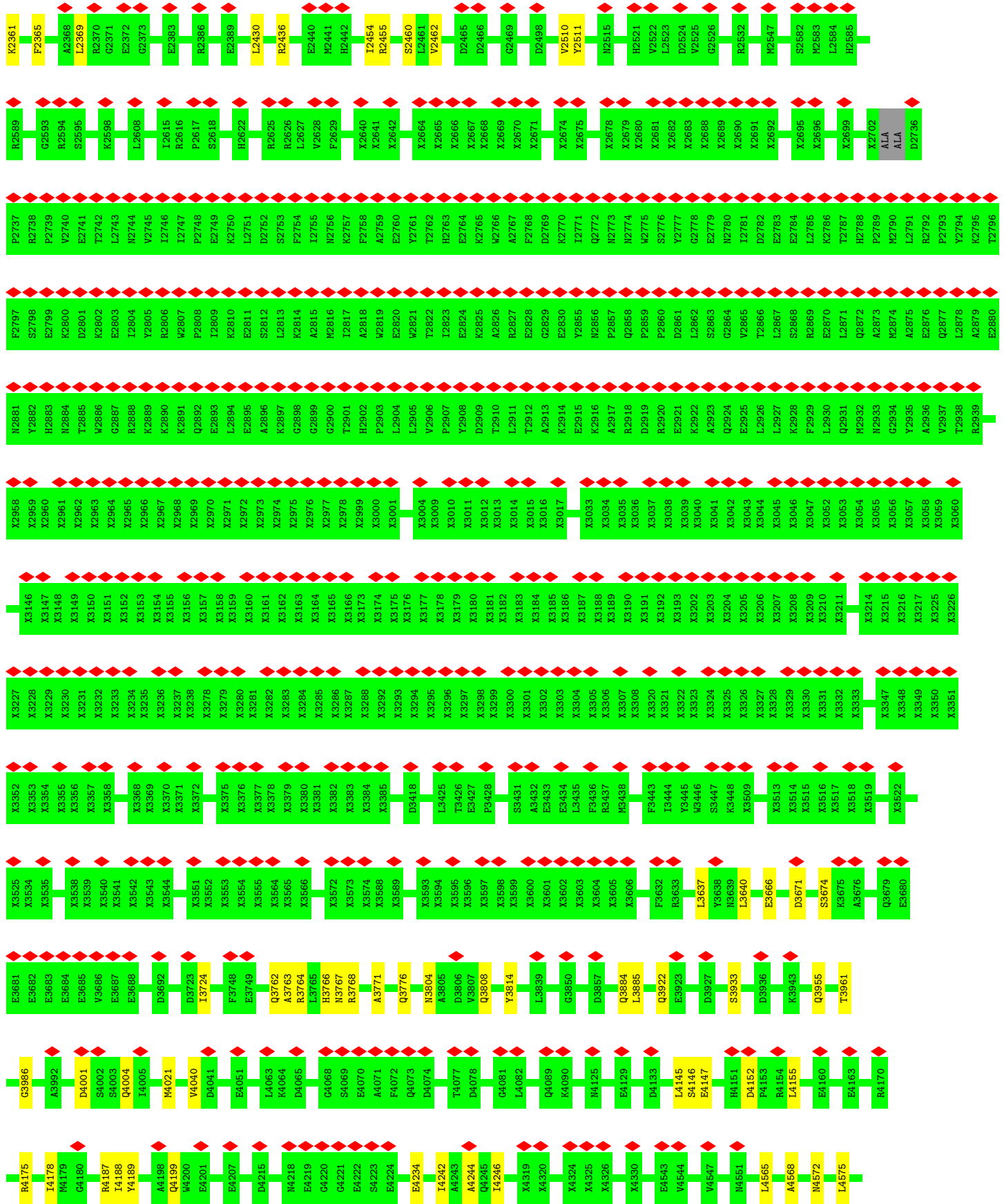


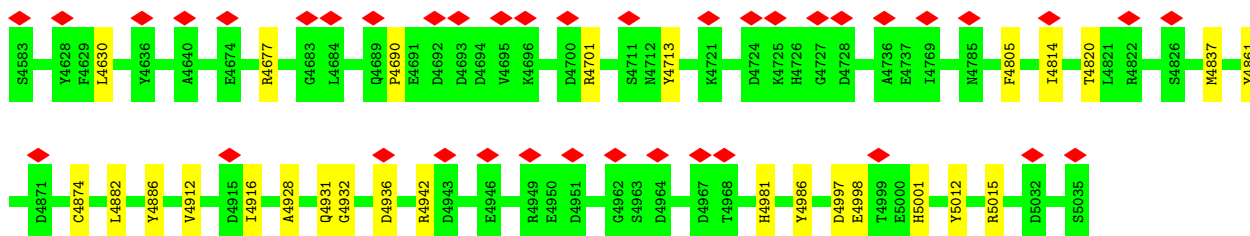
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M2816	L2817	A2818	M2819	E2820	M2821	T2822	L2823	E2824	K2825	A2826	R2827	G2828	E2829	E2830	Y2835	N2836	P2837	R2838	Q2839	P2840	D2841	L2842	S2843	G2844	M2845	D2846	T2847	L2848	P2849	E2850	L2851	M2852	Q2853	N2854	M2855	E2856	Q2857	L2858	M2859	E2860	H2861	Y2862	H2863	M2864	E2865	M2866	L2867	S2868	R2869	E2870	L2871	Q2872	A2873	M2874	A2875	E2876	Q2877	L2878	A2879	E2880	N2881	Y2882	H2883	T2884	M2885	W2886	G2887	R2888	K2889	K2890	K2891	Q2892	E2893	L2894	E2895	K2897	G2898	M2899
G2900	T2901	H2902	P2903	L2904	L2905	V2906	P2907	V2908	D2909	T2910	L2911	T2912	A2913	K2914	E2915	K2916	A2917	R2918	D2919	E2920	R2921	K2922	A2923	Q2924	E2925	L2926	L2927	K2928	P2929	L2930	Q2931	N2932	M2933	G2934	Y2935	A2936	V2937	T2938	R2939	X2958	X2959	X2960	X2961	X2962	X2963	X2964	X2965	X2966	X2967	X2968	X2969	X2970	X2971	X2972	X2973	X2974	X2975																					
X2977	X2978	X2999	X3000	X3001	X3004	X3009	X3010	X3011	X3012	X3013	X3014	X3015	X3016	X3017	X3033	X3034	X3035	X3036	X3037	X3038	X3039	X3040	X3041	X3042	X3043	X3044	X3045	X3046	X3047	X3052	X3053	X3054	X3055	X3056	X3057	X3060	X3146	X3147	X3148	X3149	X3150	X3151	X3152	X3153	X3154	X3155	X3156	X3157	X3158	X3159	X3160	X3161	X3162	X3163	X3164																							
X3165	X3166	X3173	X3174	X3175	X3176	X3177	X3178	X3179	X3180	X3181	X3182	X3183	X3184	X3185	X3188	X3189	X3190	X3191	X3192	X3193	X3202	X3203	X3204	X3205	X3206	X3207	X3208	X3209	X3210	X3211	X3214	X3215	X3216	X3217	X3225	X3226	X3227	X3228	X3229	X3230	X3231	X3232	X3233	X3234	X3235	X3236	X3237	X3238	X3278	X3279	X3280	X3281	X3282	X3283	X3284	X3285	X3286																					
X3287	X3288	X3292	X3293	X3294	X3295	X3296	X3297	X3298	X3299	X3300	X3301	X3302	X3303	X3304	X3305	X3306	X3307	X3308	X3320	X3321	X3322	X3323	X3324	X3325	X3326	X3327	X3328	X3329	X3330	X3331	X3332	X3333	X3347	X3348	X3349	X3350	X3351	X3352	X3353	X3354	X3355	X3356	X3357	X3358	X3368	X3369	X3370	X3371	X3372	X3375	X3376	X3377	X3378	X3379	X3380	X3381																						
X3382	X3383	X3384	X3385	D3418	L3425	T3426	E3427	P3428	S3431	E3432	E3433	E3434	F3436	R3437	M3438	F3443	I3444	Y3445	W3446	S3447	K3448	X3449	X3450	X3513	X3514	X3515	X3516	X3517	X3518	X3519	X3522	X3525	X3534	X3535	X3538	X3539	X3540	X3541	X3542	X3543	X3544	X3551	X3552	X3553	X3554	X3555	X3564	X3565	X3566																													
X3572	X3573	X3574	X3588	X3589	X3593	X3594	X3595	X3596	X3597	X3598	X3599	X3600	X3601	X3602	X3603	X3604	X3605	X3606	F3632	R3633	L3637	Y3638	N3639	L3640	E3666	D3671	S3674	K3675	A3676	Q3679	E3680	E3681	E3682	E3683	E3684	E3685	V3686	E3687	E3688	D3692	D3723	L3724	S3747	F3748	E3749	Q3762	A3763	R3764																														
L3785	H3786	R3787	E3788	A3771	N3804	A3805	D3806	Q3808	L3839	G3850	D3857	Q3884	L3885	Q3922	E3923	D3927	S3933	D3936	K3943	Q3955	T3961	W3981	G3986	A3992	D4001	S4002	S4003	Q4004	I4005	M4021	V4040	M4041	M4042	E4051	L4063	R4064	D4065																																									
G4068	S4069	E4070	A4071	F4072	Q4073	D4074	T4077	D4078	G4081	L4082	Q4089	K4090	M4125	E4129	D4133	L4145	S4146	E4147	H4151	D4152	F4153	R4154	L4155	E4160	E4163	R4170	R4175	I4178	M4179	Q4180	R4187	L4188	Y4189	A4198	Q4199	W4200	E4201	M4202	E4207	D4215																																						
M4218	E4219	G4220	G4221	E4222	E4224	E4234	I4242	A4243	A4244	Q4245	L4246	X4317	X4318	X4319	X4320	X4324	X4325	X4326	X4330	E4543	V4544	L4565	A4568	M4572	F4573	L4574	D4582	S4583	L4630	Y4636	A4640	L4641	E4674	R4677	G4683	L4684	Q4689	P4690	E4691	D4692	D4693	D4694																																				
V4695	K4696	D4700	R4701	A4701	S4711	M4712	Y4713	K4721	D4724	K4725	H4726	G4727	D4728	A4736	E4737	I4769	M4785	I4814	T4820	L4821	R4822	S4826	M4837	Y4861	D4871	C4874	L4882	Y4886	V4912	D4915	I4916	Q4931	D4936	R4942	D4943	E4946	R4949	E4950																																								
D4951	D4964	Y4965	F4966	D4967	H4961	Y4986	D4997	E4998	T4999	E5000	H5001	Y5012	R5015	R5027	D5032	S5035																																																														



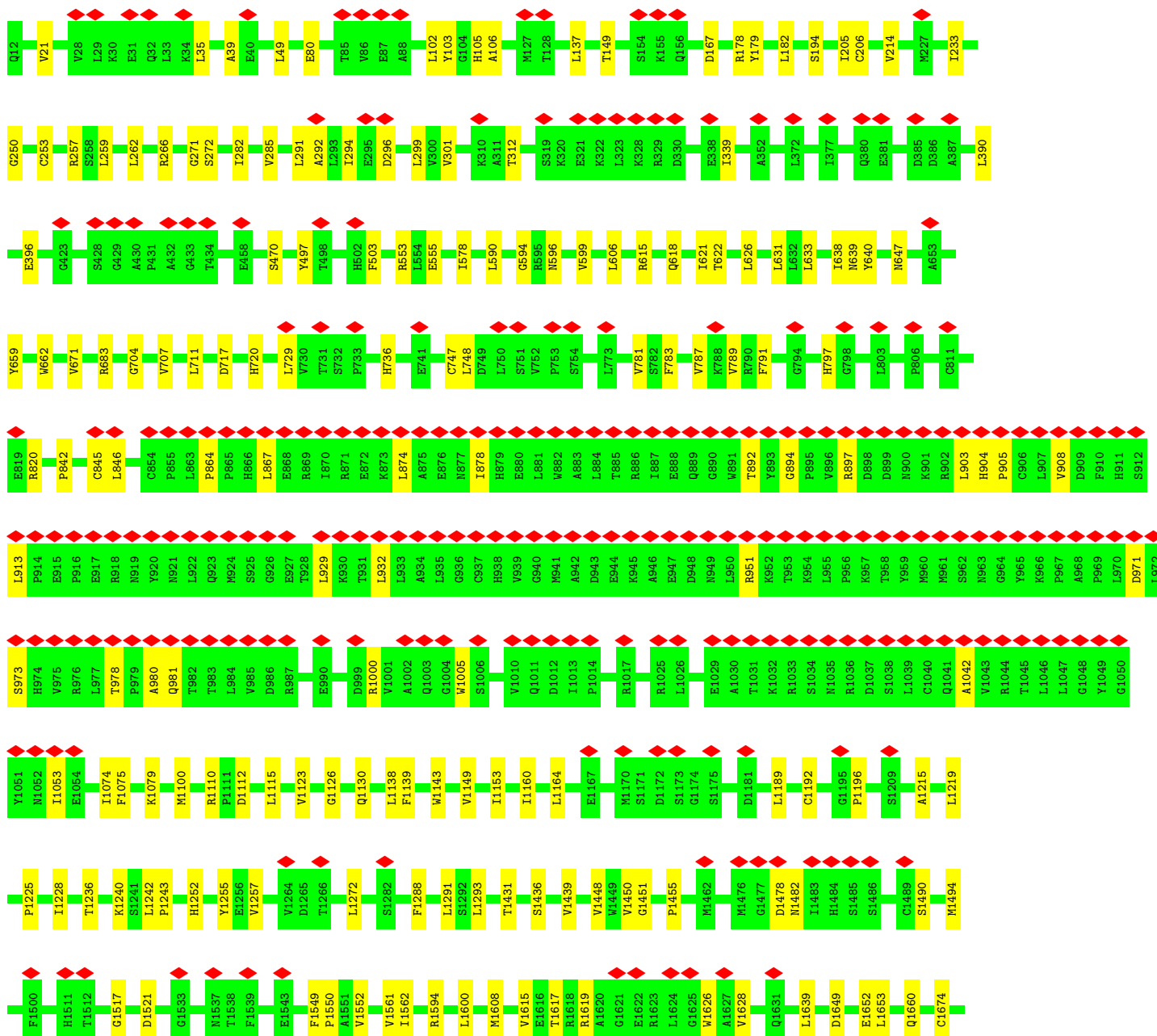
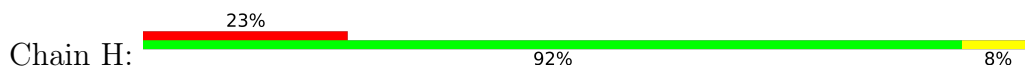
● Molecule 2: Ryanodine Receptor

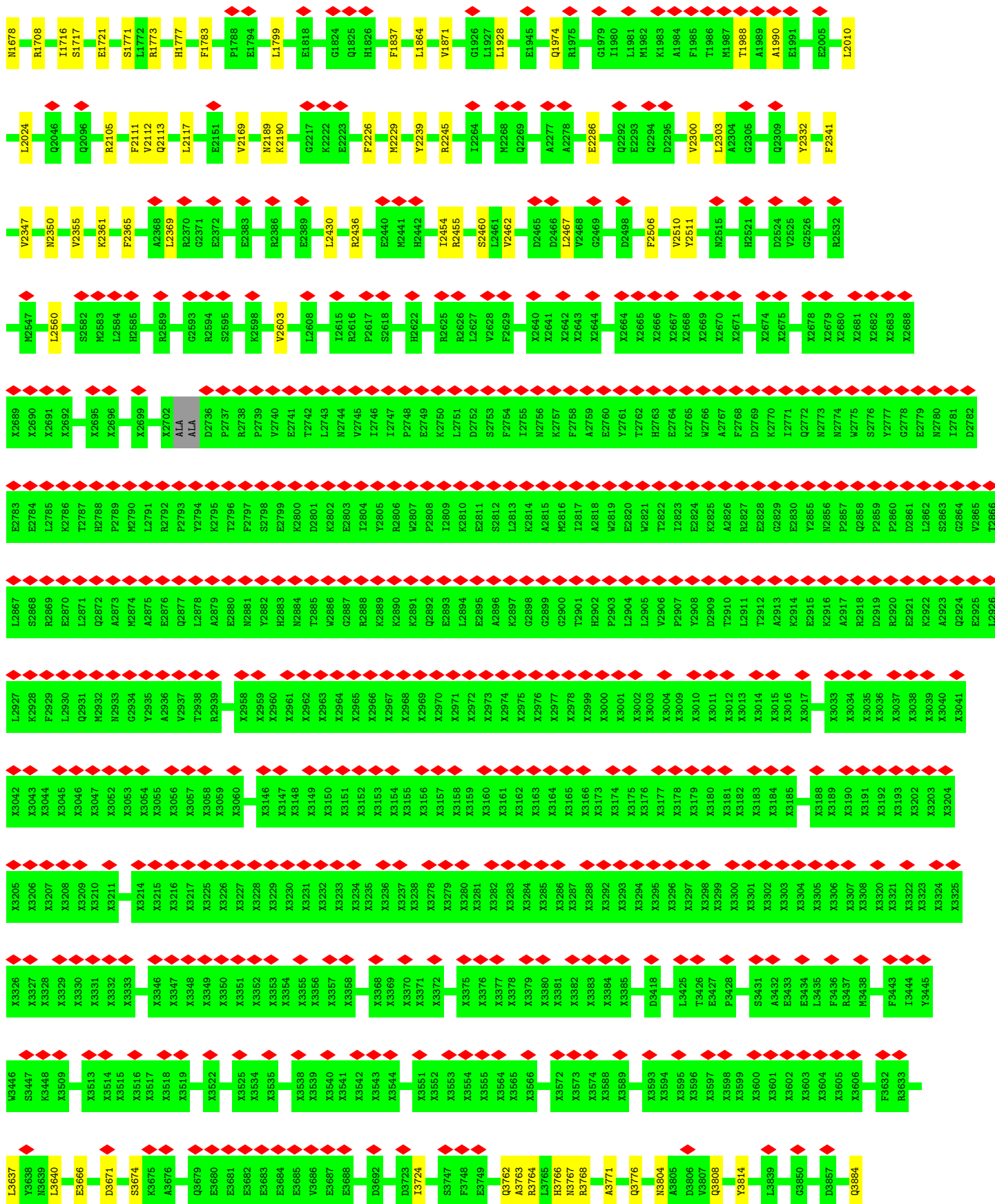


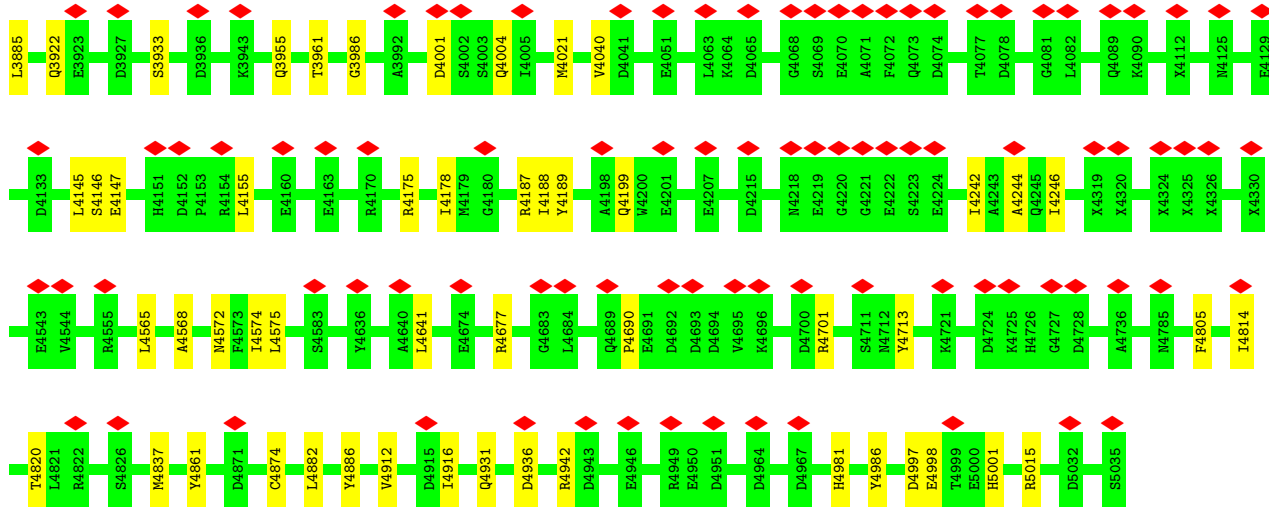




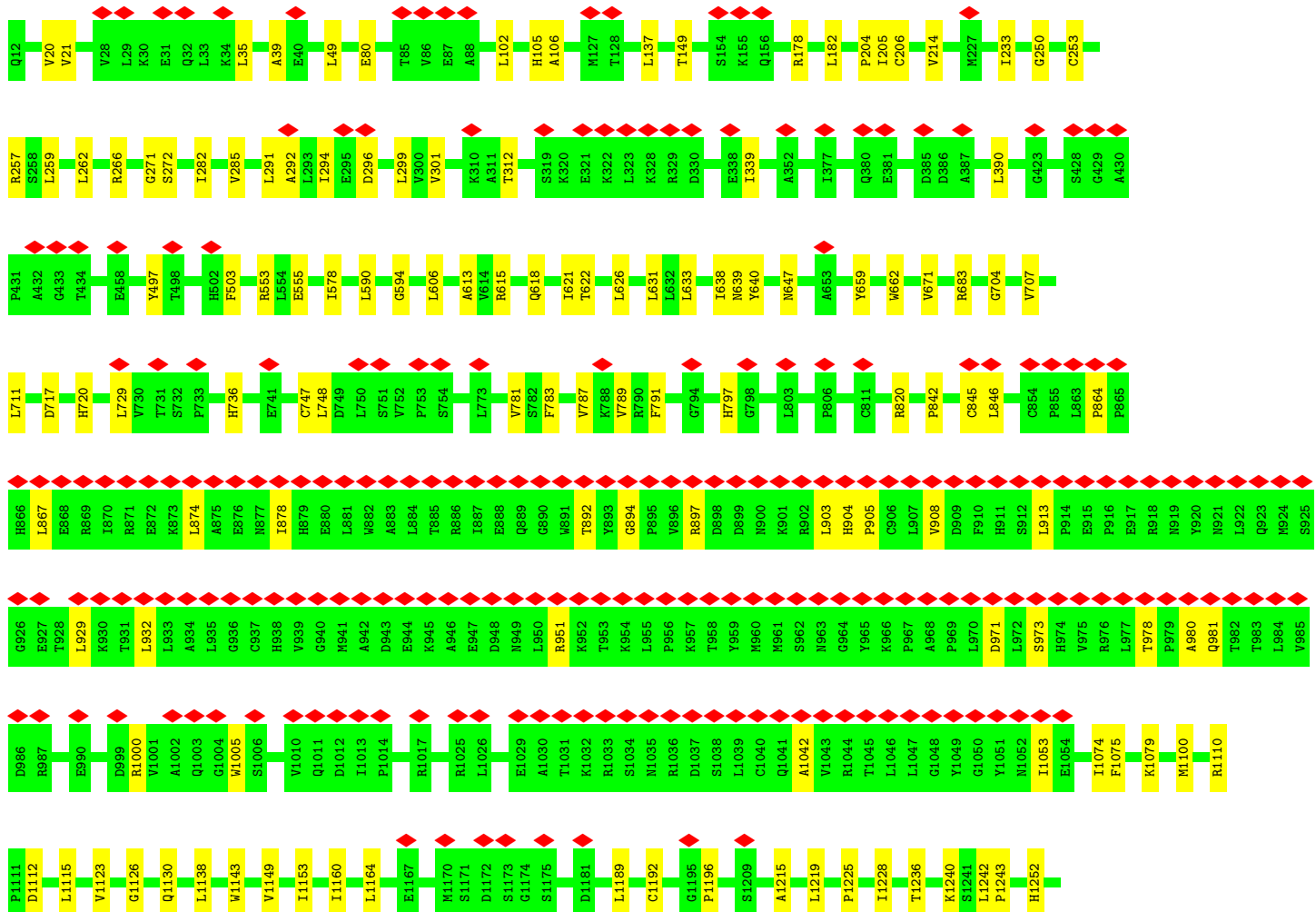
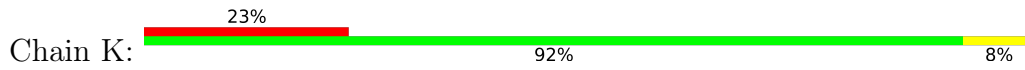
• Molecule 2: Ryanodine Receptor

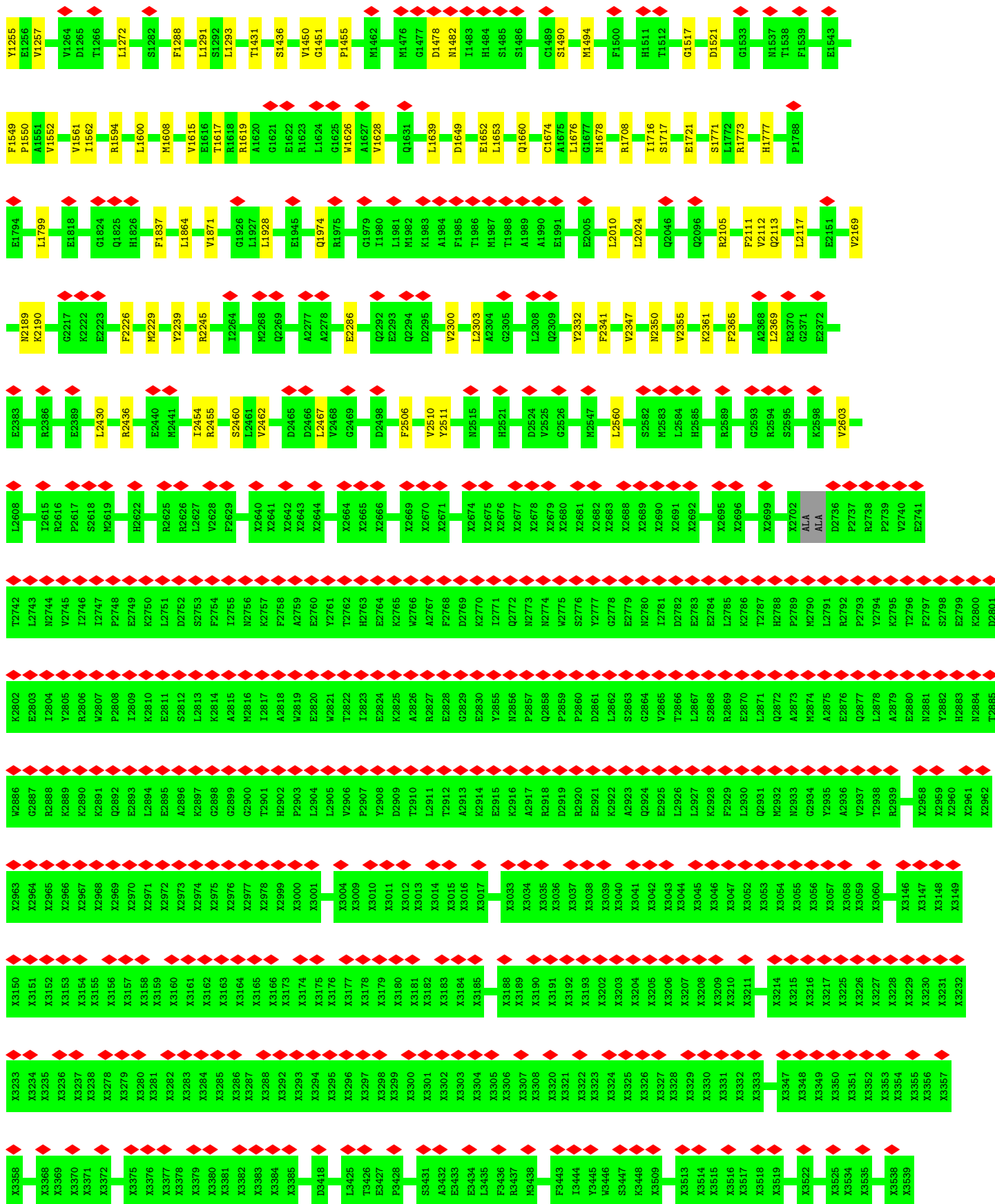


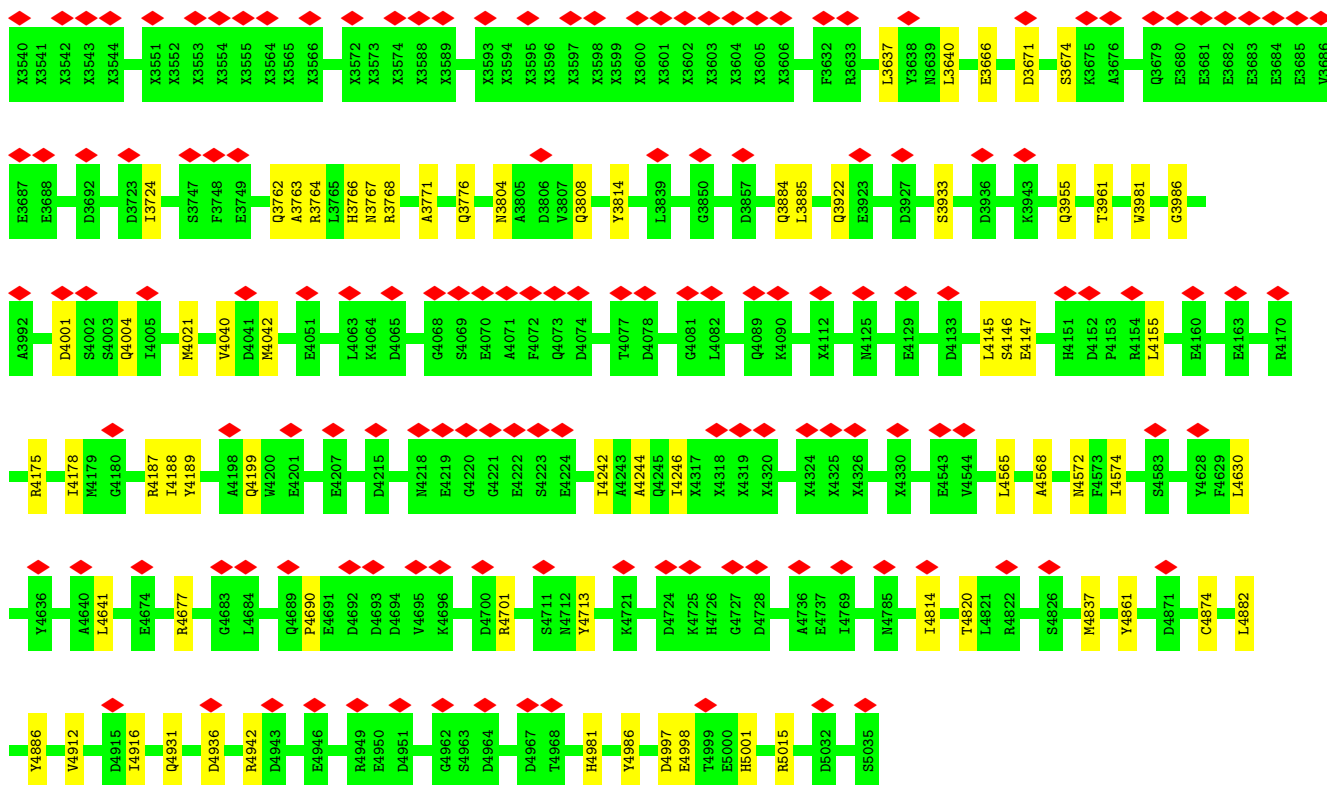




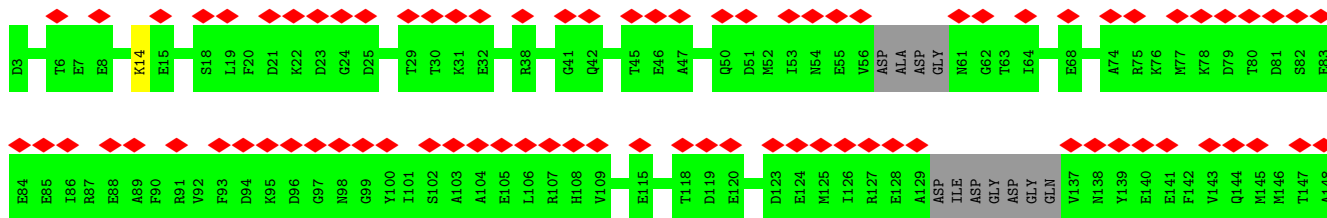
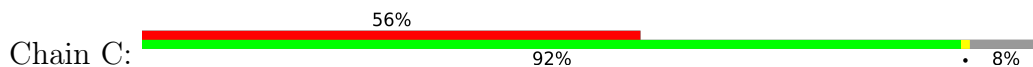
• Molecule 2: Ryanodine Receptor



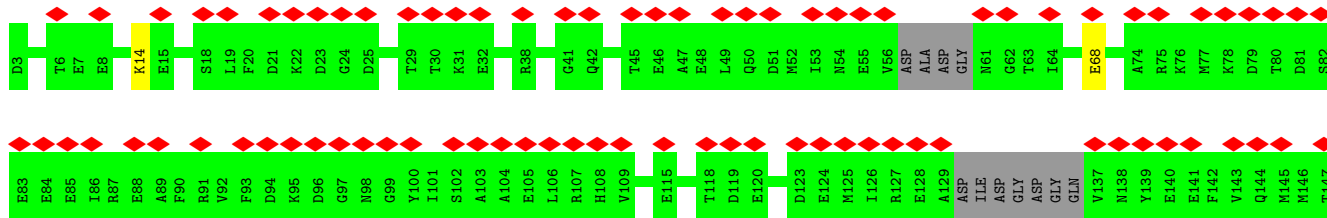
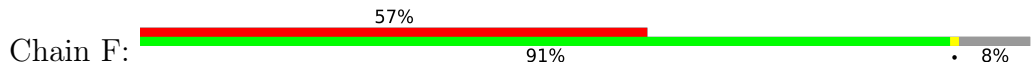




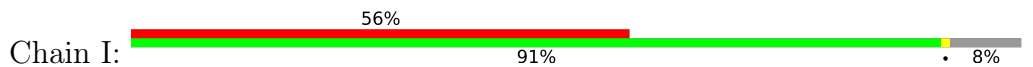
• Molecule 3: Calmodulin-1

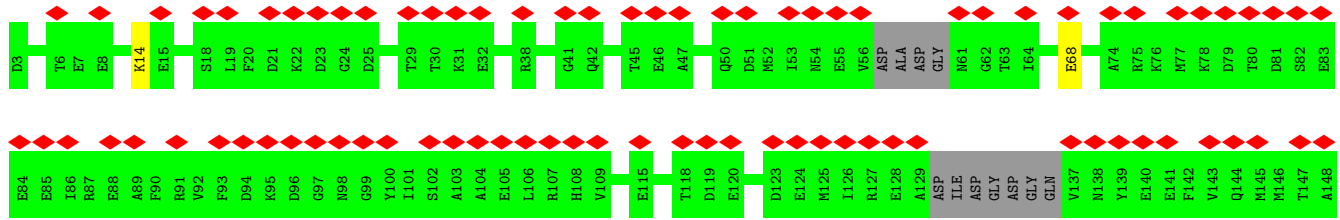


• Molecule 3: Calmodulin-1

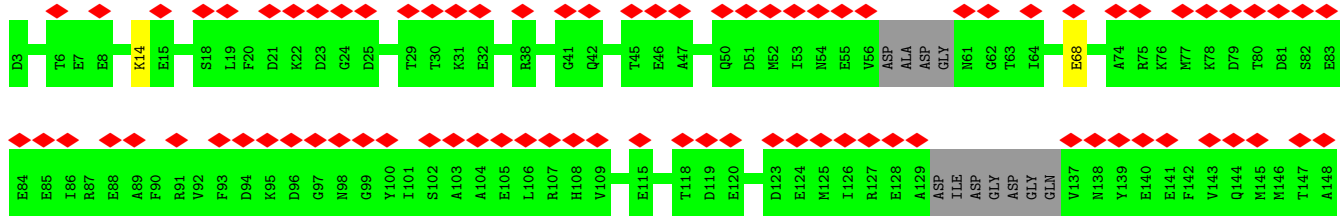
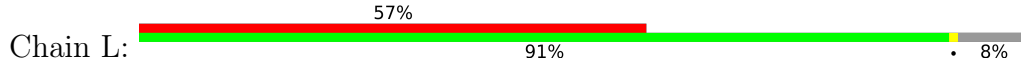


• Molecule 3: Calmodulin-1





• Molecule 3: Calmodulin-1





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, 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	0.25	0/758	0.43	0/1033
1	D	0.25	0/758	0.43	0/1033
1	G	0.25	0/758	0.43	0/1033
1	J	0.25	0/758	0.43	0/1033
2	B	0.23	0/25809	0.37	0/35154
2	E	0.23	0/25809	0.37	0/35154
2	H	0.23	0/25809	0.37	0/35154
2	K	0.23	0/25809	0.37	0/35154
3	C	0.24	0/820	0.37	0/1120
3	F	0.24	0/820	0.37	0/1120
3	I	0.24	0/820	0.37	0/1120
3	L	0.24	0/820	0.37	0/1120
All	All	0.23	0/109548	0.37	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	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	742	0	702	10	0
1	G	742	0	702	10	0
1	J	742	0	702	8	0
2	B	27011	0	23901	165	0
2	E	27011	0	23901	171	0
2	H	27011	0	23901	173	0
2	K	27011	0	23901	169	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	2	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	680	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 680 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 [i](#)

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. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	3955	GLN
2	B	4199	GLN
2	E	3955	GLN
2	H	3955	GLN
2	K	3955	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 monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

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

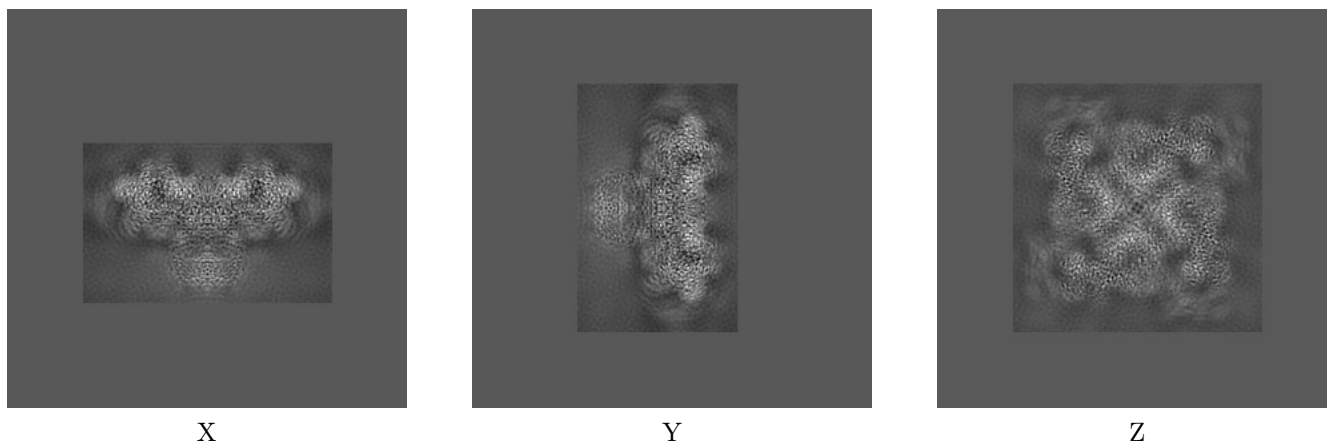
## 6 Map visualisation [i](#)

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](#)

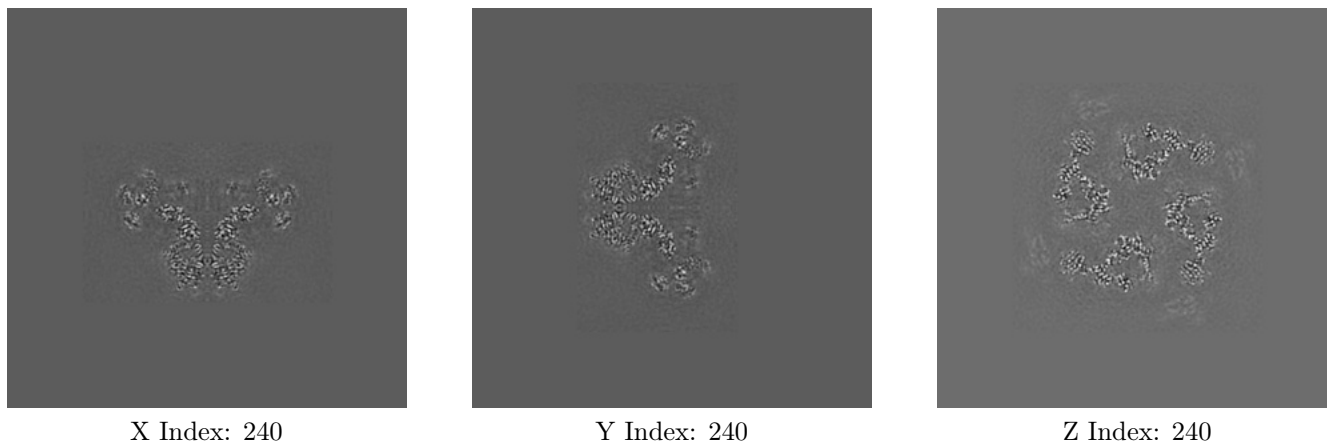
#### 6.1.1 Primary map



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

### 6.2 Central slices [i](#)

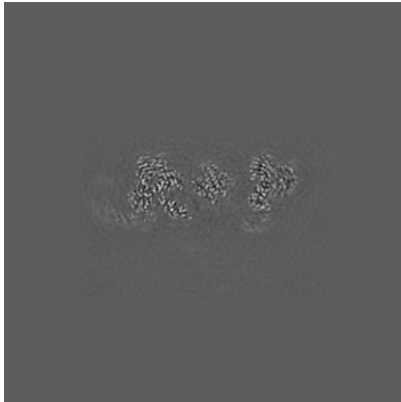
#### 6.2.1 Primary map



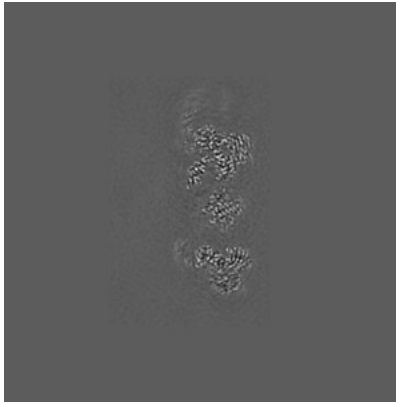
The images above show central slices of the map in three orthogonal directions.

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

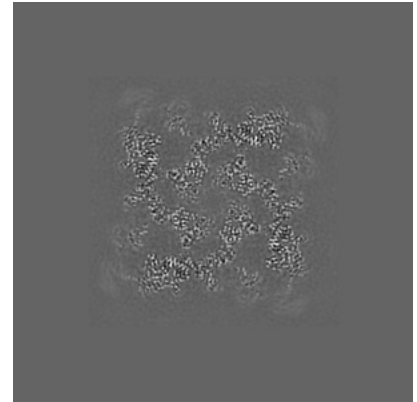
### 6.3.1 Primary map



X Index: 311



Y Index: 311

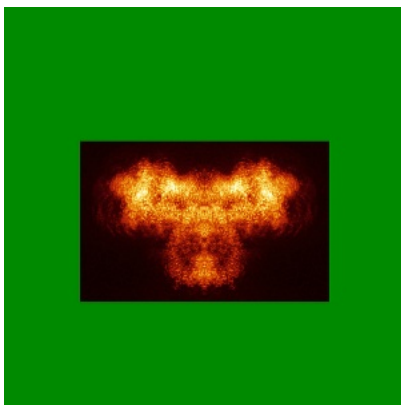


Z Index: 258

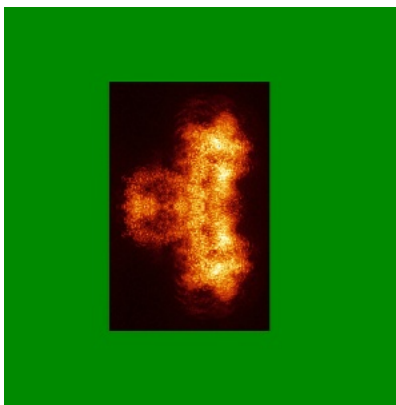
The images above show the largest variance slices of the map in three orthogonal directions.

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

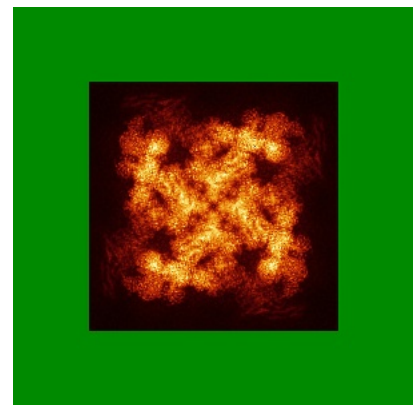
### 6.4.1 Primary map



X



Y



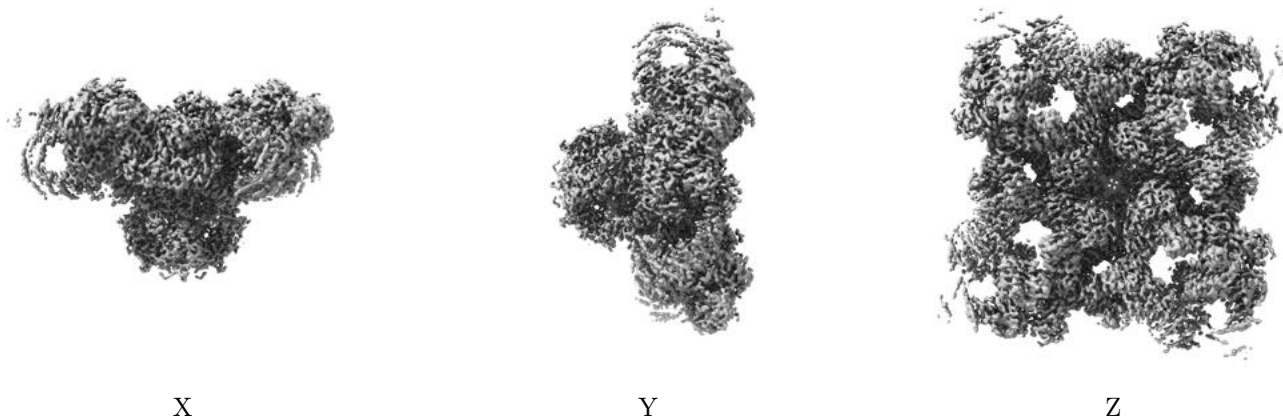
Z

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.

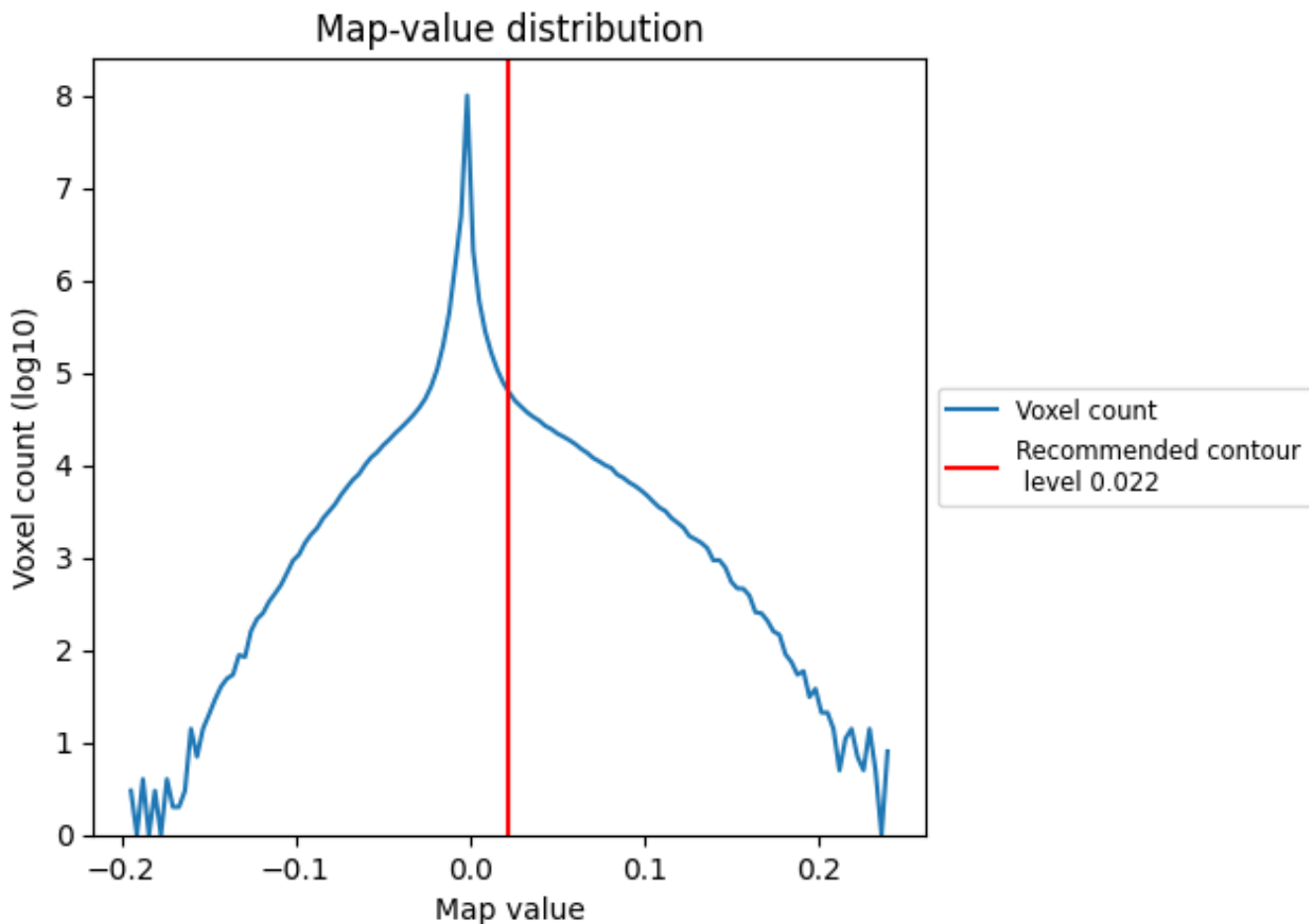
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

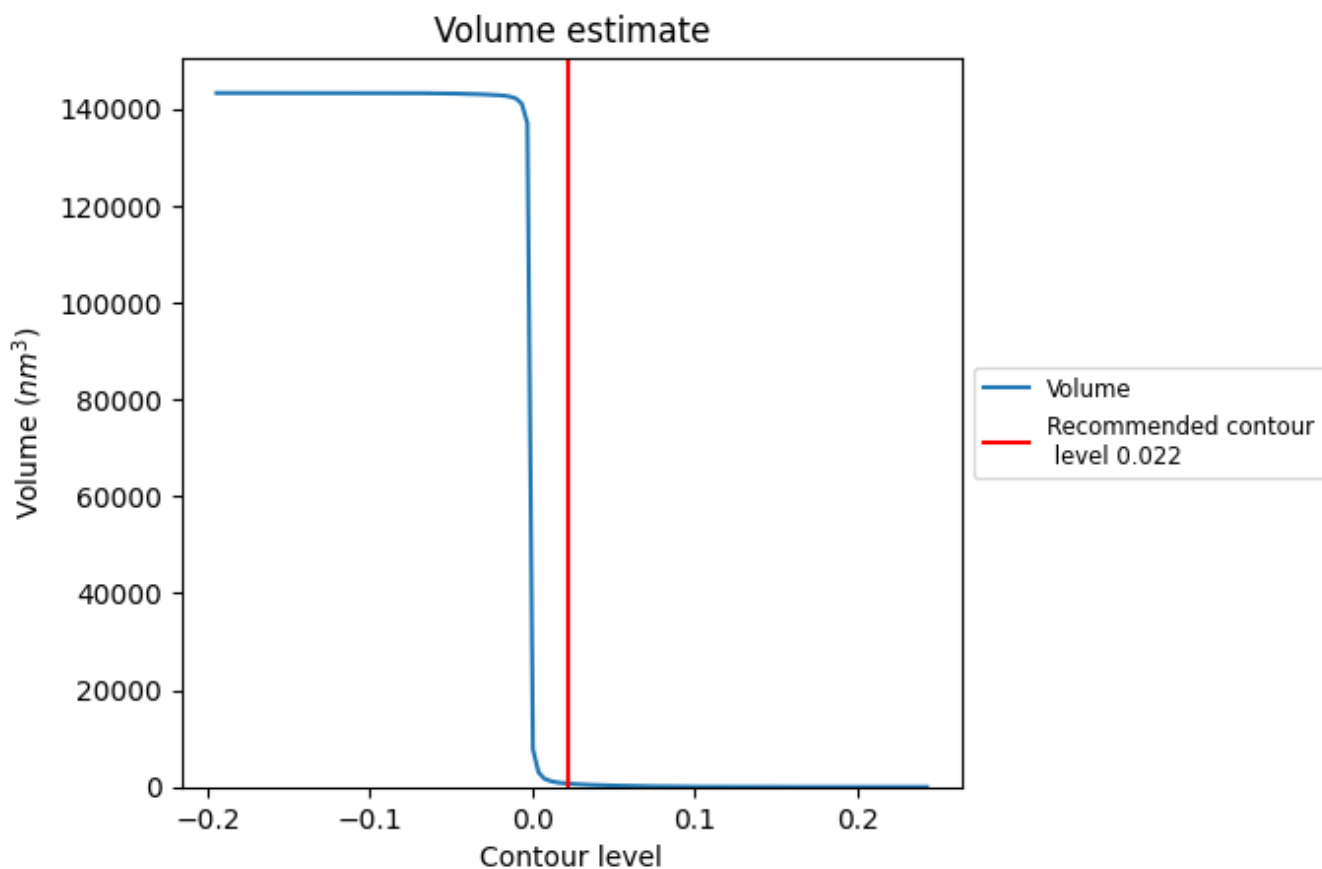
This section contains the results of statistical analysis of the map.

### 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.

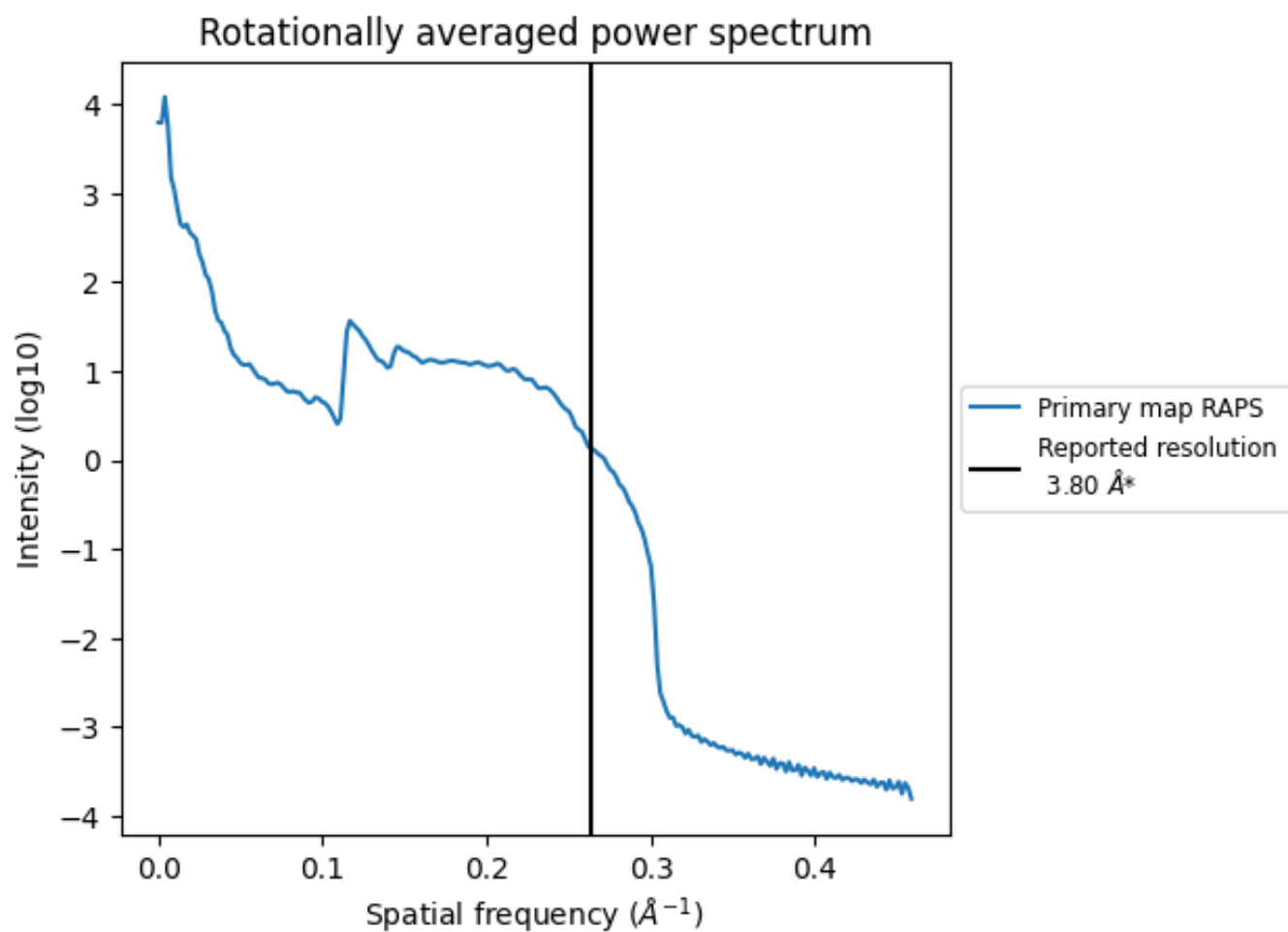
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 692 nm<sup>3</sup>; 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 [i](#)



\*Reported resolution corresponds to spatial frequency of 0.263 Å<sup>-1</sup>

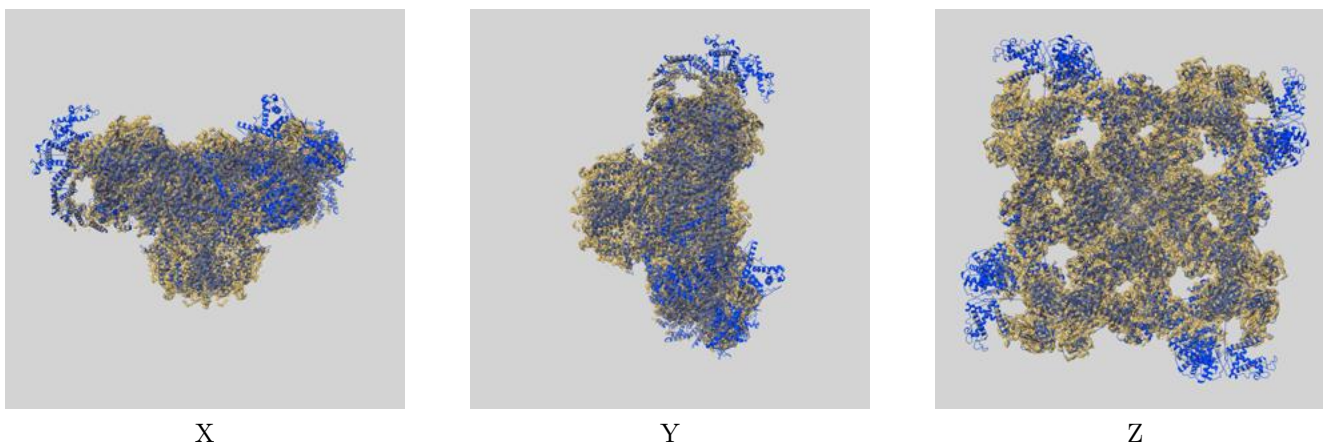
## 8 Fourier-Shell correlation

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

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

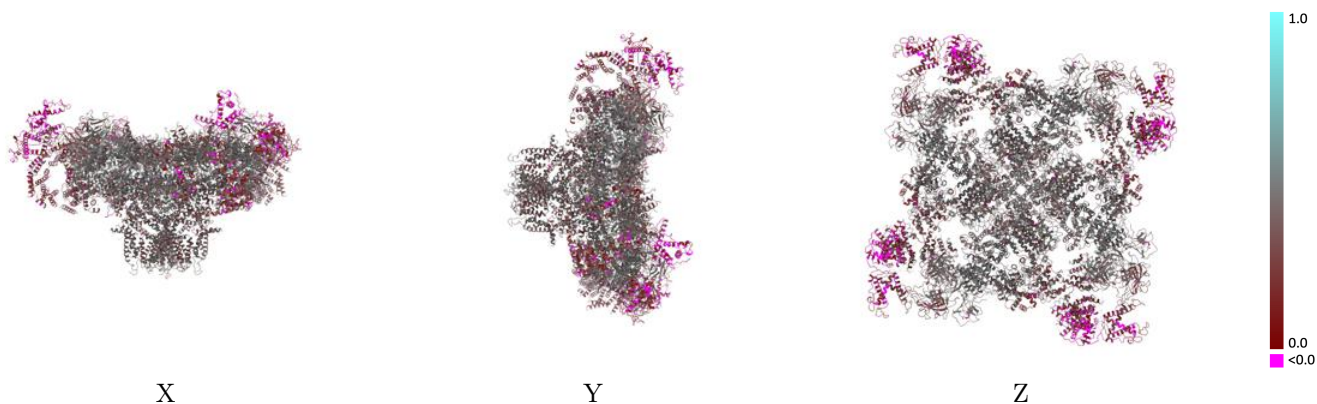
This section contains information regarding the fit between EMDB map EMD-22015 and PDB model 6X32. Per-residue inclusion information can be found in section 3 on page 6.

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



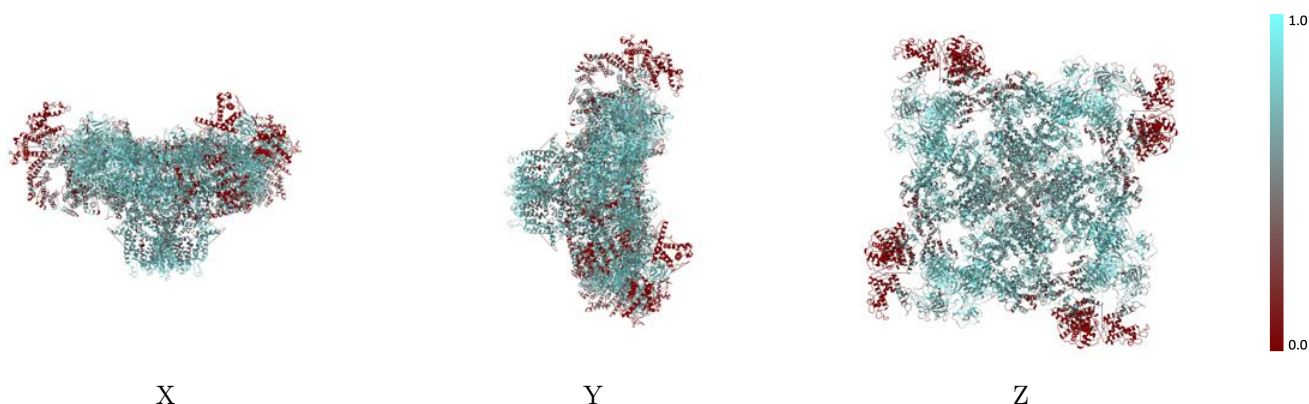
The images above show the 3D surface view of the map at the recommended contour level 0.022 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



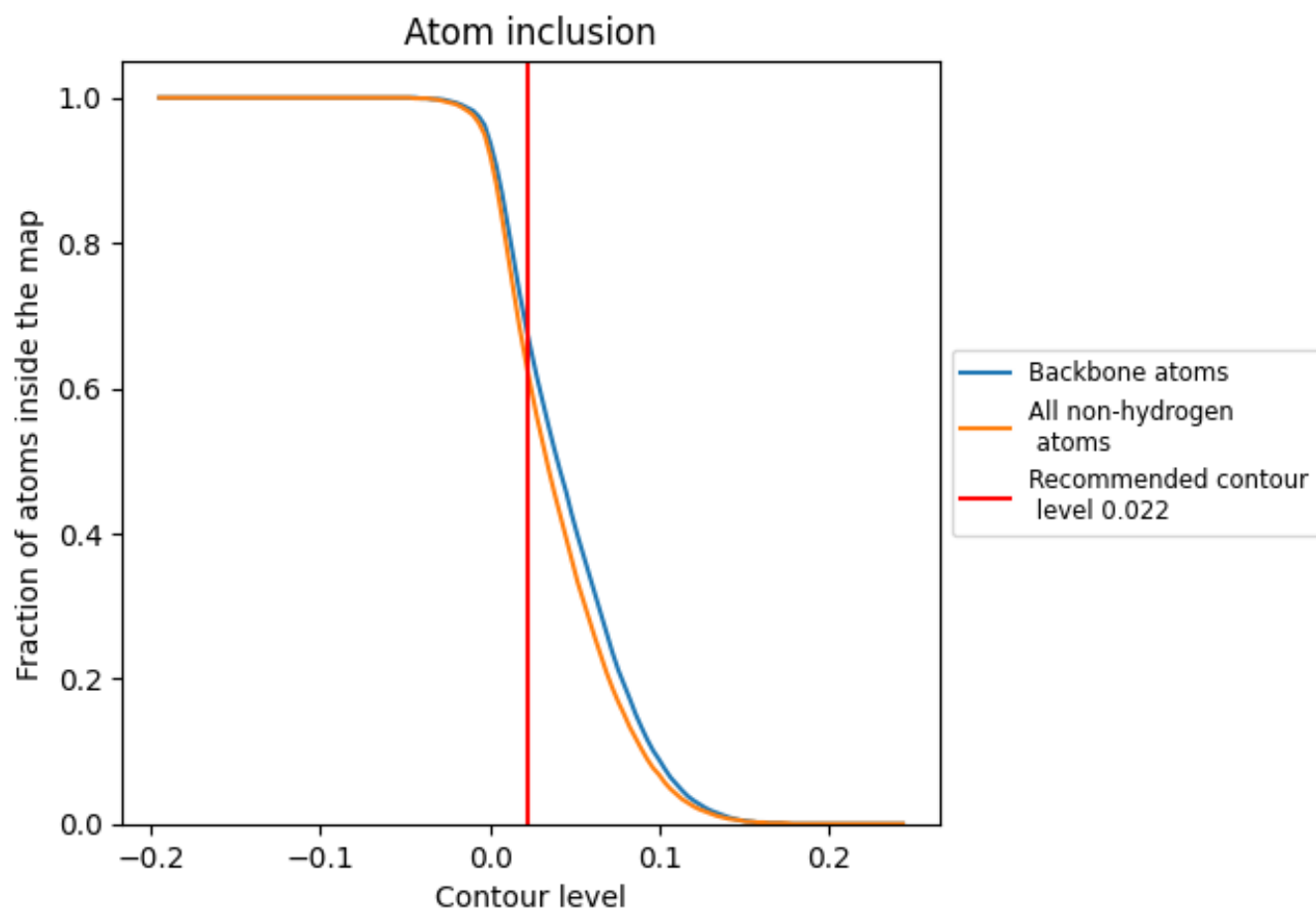
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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





























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 [i](#)

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

