



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 01:19 PM UTC

PDB ID : 5T9S / pdb_00005t9s
EMDB ID : EMD-8375
Title : Structure of rabbit RyR1 (Ca²⁺-only dataset, class 4)
Authors : Clarke, O.B.; des Georges, A.; Zalk, R.; Marks, A.R.; Hendrickson, W.A.; Frank, J.
Deposited on : 2016-09-09
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:

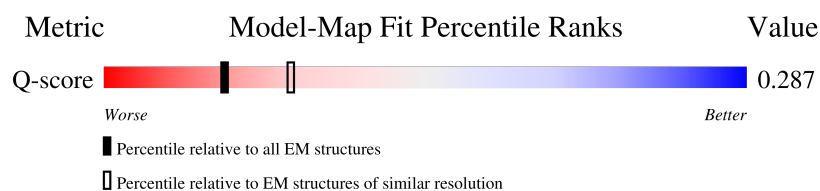
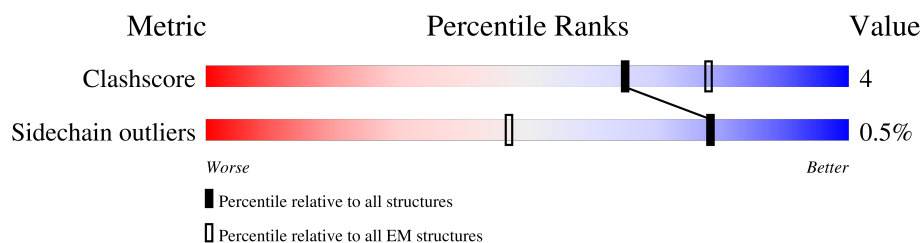
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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



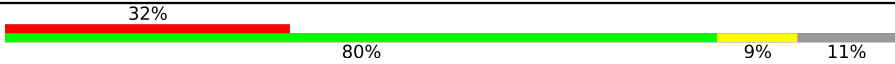
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	5410 (3.70 - 4.70)

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	108	
1	F	108	
1	H	108	
1	J	108	
2	B	4676	

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Mol	Chain	Length	Quality of chain
2	E	4676	
2	G	4676	
2	I	4676	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 120756 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	F	107	Total	C	N	O	S	0	0
			818	516	144	154	4		
1	A	107	Total	C	N	O	S	0	0
			818	516	144	154	4		
1	H	107	Total	C	N	O	S	0	0
			818	516	144	154	4		
1	J	107	Total	C	N	O	S	0	0
			818	516	144	154	4		

- Molecule 2 is a protein called Ryanodine receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	4168	Total	C	N	O	S	0	0
			29369	18608	5202	5402	157		
2	E	4168	Total	C	N	O	S	0	0
			29369	18608	5202	5402	157		
2	I	4168	Total	C	N	O	S	0	0
			29369	18608	5202	5402	157		
2	G	4168	Total	C	N	O	S	0	0
			29369	18608	5202	5402	157		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
3	B	1	Total	Zn	0
			1	1	
3	E	1	Total	Zn	0
			1	1	
3	I	1	Total	Zn	0
			1	1	
3	G	1	Total	Zn	0
			1	1	

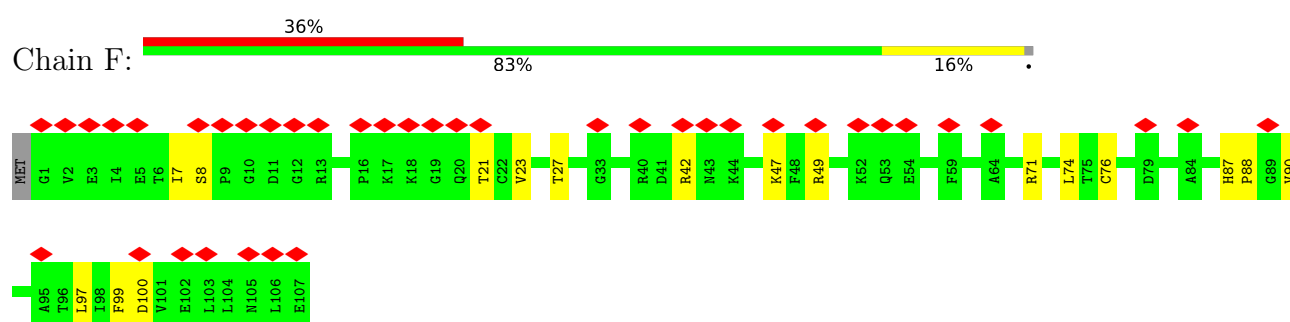
- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
4	B	1	Total 1	Ca 1	0
4	E	1	Total 1	Ca 1	0
4	I	1	Total 1	Ca 1	0
4	G	1	Total 1	Ca 1	0

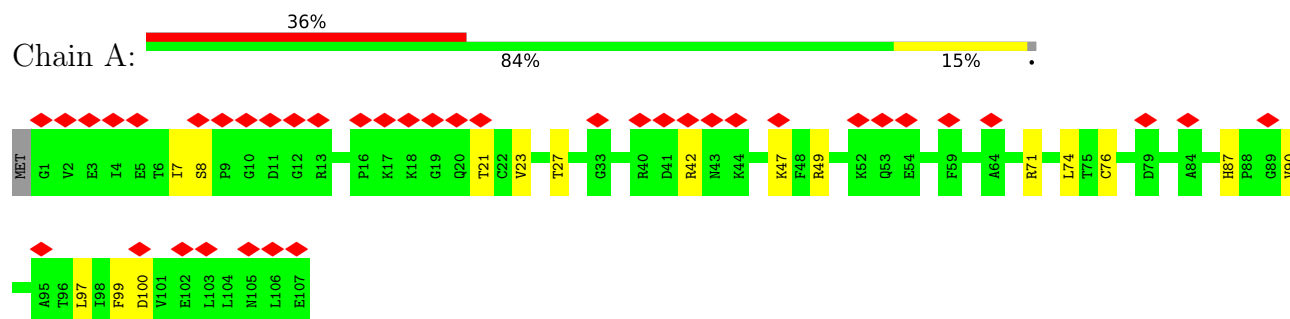
3 Residue-property plots [i](#)

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.

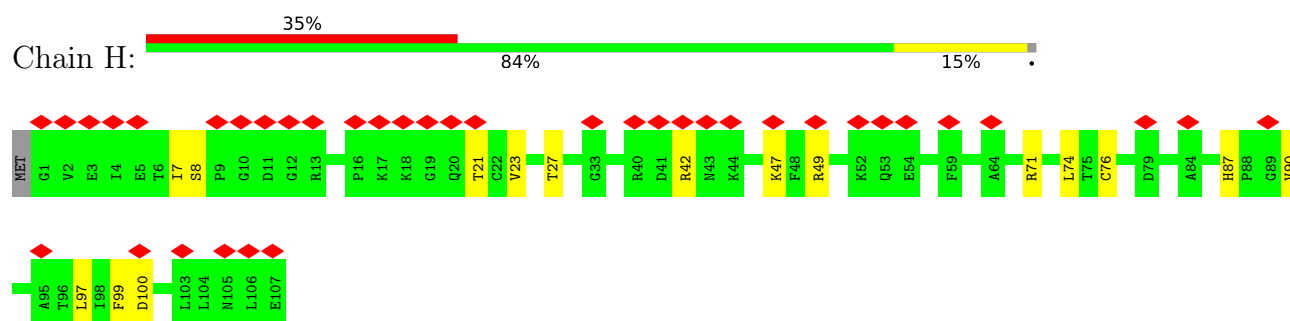
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



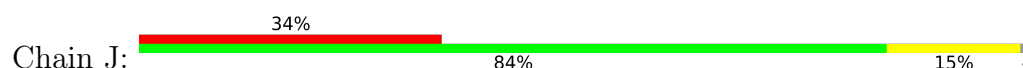
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

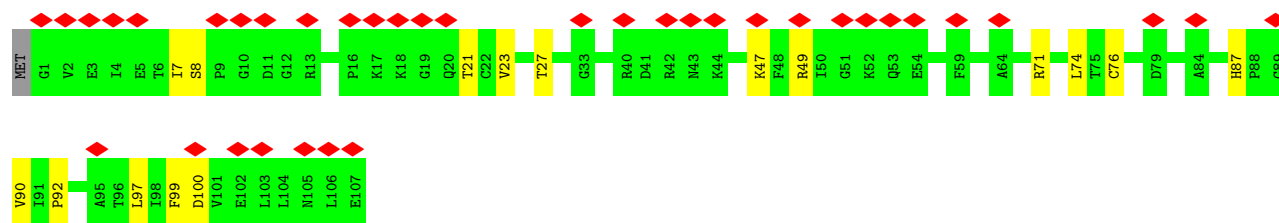


- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

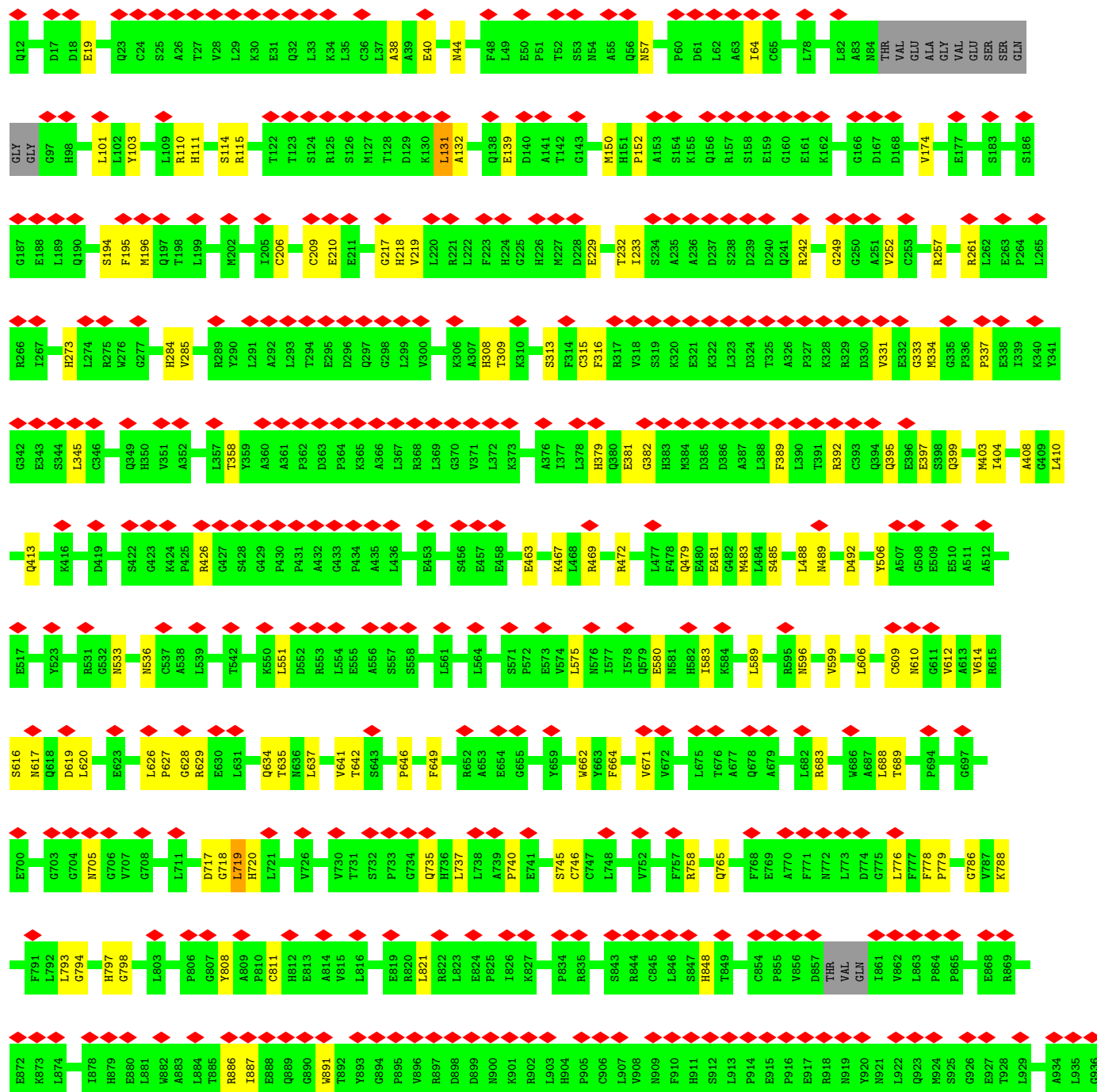
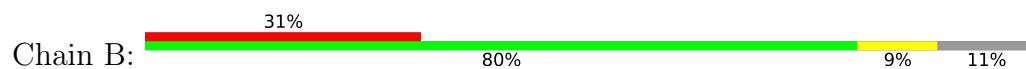


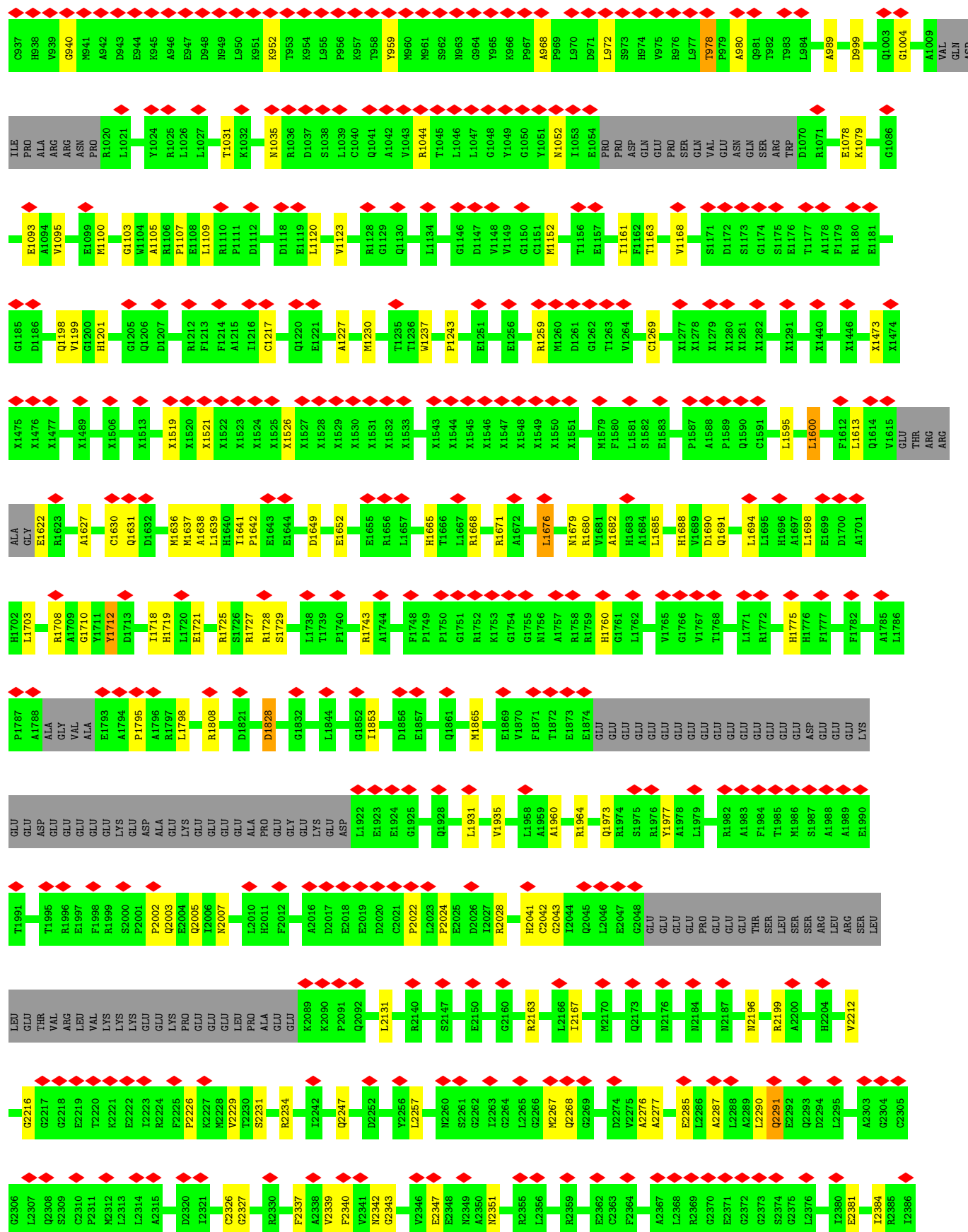
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



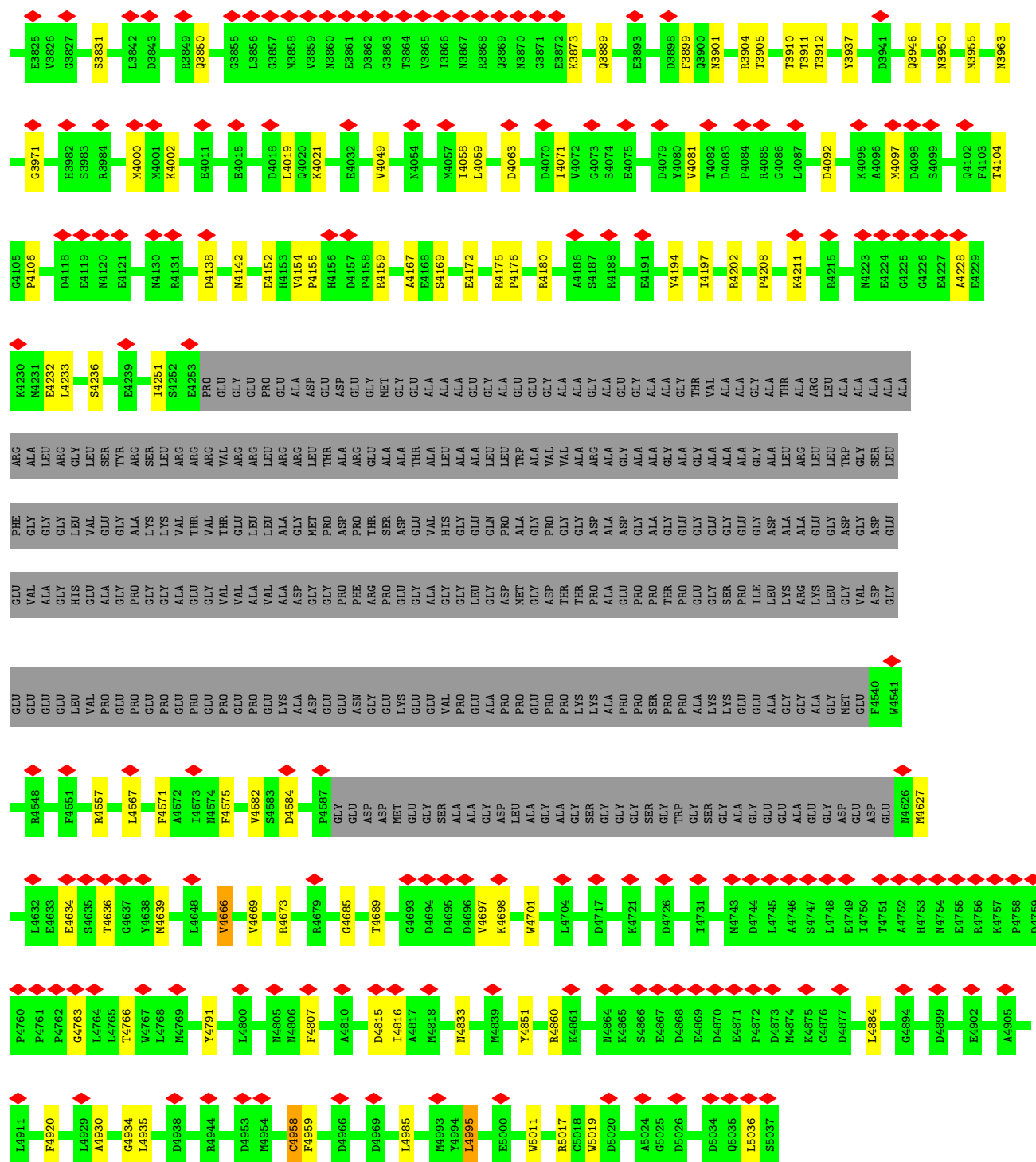


• Molecule 2: Ryanodine receptor 1

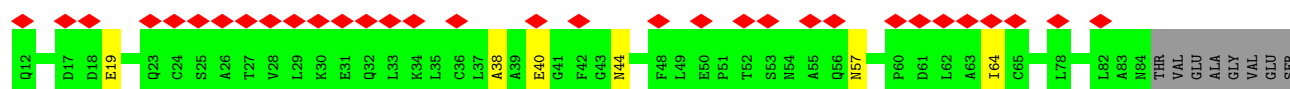
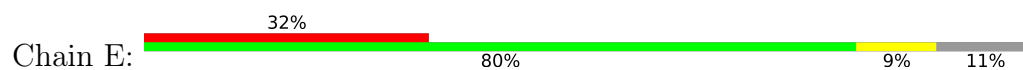




E3686	E3687	E3688	E3689	V3690	E3691	E3692	K3693	T3711	E3712	K3713	S3714	S3715	L3716	D3717	E3718	D3719	Y3720	E3737	G3738	G3739	E3740	S3741	GLY	GLU	ALA	GLU	E3747	E3748	V3749	E3750	V3751	S3752	F3753	E3754	S3773	M3778	L3779	Q3781	S3784	K3787	G3788	E3789	L3805	N3806	G3807	M3816	L3817	S3822										
X3550	X3556	X3557	X3558	X3559	X3560	X3561	X3562	X3563	X3564	X3565	X3566	X3567	X3568	X3577	X3580	X3581	X3582	X3583	X3584	X3585	X3586	X3587	X3591	X3592	X3609	X3610	X3611	X3612	X3613	T3639	N3643	L3644	P3645	F3653	I3662	E3665	D3666	H3667	S3668	F3669	D3676	K3679	A3680	G3681	E3682	Q3683	E3684	E3685										
X3399	X3400	X3403	X3404	X3409	X3412	X3413	X3417	X3425	X3426	X3427	X3432	X3433	X3434	X3435	X3436	X3452	X3453	X3454	X3455	X3456	X3457	X3464	X3465	X3466	X3467	X3468	X3511	X3512	X3513	X3514	X3515	X3516	X3522	X3529	X3530	X3531	X3532	X3533	X3534	X3539	X3540	X3541	X3542	X3543	X3547	X3548	X3549											
X3320	X3323	X3331	X3332	X3333	X3334	X3335	X3336	X3337	X3338	X3339	X3340	X3341	X3342	X3346	X3347	X3348	X3349	X3352	X3353	X3354	X3355	X3356	X3357	X3358	X3359	X3360	X3361	X3362	X3363	X3364	X3365	X3366	X3369	X3379	X3380	X3381	X3382	X3383	X3384	X3385	X3386	X3387	X3388	X3389	X3390	X3391	X3392	X3393	X3394	X3395	X3396	X3397	X3398					
X3234	X3235	X3236	X3241	X3242	X3245	X3246	X3247	X3250	X3251	X3252	X3253	X3254	X3261	X3262	X3263	X3264	X3265	X3266	X3267	X3268	X3269	X3270	X3271	X3272	X3275	X3276	X3277	X3278	X3281	X3282	X3283	X3284	X3285	X3286	X3287	X3290	X3291	X3292	X3293	X3294	X3295	X3296	X3297	X3298	X3299	X3300	X3301	X3309	X3313	X3314	X3315							
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X2948	X2949	X2950	X2953	X2957	X2965	X2966	X2967	X2968	X2969	X2970	X2971	X2974	X2975	X2976	X2995	X2996	X3001	X3013	X3014	X3021	X3022	X3023	X3024	X3025	X3026	X3027	X3035	X3036	X3040	X3041	X3042	X3043	X3044	X3045	X3046	X3047	X3048	X3049	X3050	X3051	X3052	X3053	X3057	X3058	X3059	X3060	X3061	X3062	X3063									
W2886	G2887	R2888	K2889	K2890	K2891	Q2892	E2893	L2894	E2895	L2896	A2896	K2897	K2898	Q2899	T2901	H2902	P2903	L2904	L2905	V2906	P2907	Y2908	D2909	T2910	T2911	T2912	A2913	K2914	E2915	K2916	A2917	K2918	D2919	R2920	E2921	K2922	Q2924	E2925	L2926	L2927	K2928	F2929	L2930	Q2931	W2932	L2933	Q2934	Y2935	A2936	V2937	T2938	K2939	X2942	X2943	X2944	X2946	X2947	
A2826	R2827	E2828	Q2829	E2830	GLU	GLU	ARG	THR	GLU	LYS	LYS	THR	ARG	LYS	ILE	SER	GLN	THR	ALA	GLN	THR	ASP	PRO	ARG	GLU	GLY	Y2855	N2856	P2857	Q2858	P2859	P2860	D2861	L2862	S2863	G2864	V2865	T2866	L2867	S2868	E2870	L2871	Q2872	M2873	K2874	A2875	E2876	Q2877	L2878	K2879	E2880	N2881	Y2882	H2883	N2884	T2885		
L2479	X2487	X2488	X2493	X2499	X2513	X2514	X2517	X2521	X2531	X2532	X2533	X2534	X2535	X2536	X2537	X2538	X2562	X2563	X2564	X2565	X2580	X2581	X2582	X2583	X2584	X2585	X2586	X2596	X2602	X2613	X2614	X2618	X2619	X2620	X2623	X2624	X2625	X2626	X2627	X2628	X2629	X2650	X2651	X2654														
X2671	X2672	X2673	X2674	X2675	X2676	X2677	X2680	X2686	X2687	X2688	X2689	X2690	X2691	X2692	X2693	X2696	X2697	X2698	X2699	X2700	X2701	X2702	X2703	N2734	P2735	D2736	P2737	P2738	P2739	V2740	E2741	T2742	L2743	N2744	V2745	L2746	L2747	P2748	E2749	K2750	L2751	D2752	S2753	P2754	L2755	N2756	K2757	P2758	A2759	E2760	Y2761	T2762	H2763	E2764	K2765			
W2766	A2767	F2768	D2769	K2770	L2771	Q2772	N2773	W2774	S2775	S2776	Y2777	G2778	E2779	N2780	V2781	D2782	E2783	E2784	L2785	K2786	T2787	H2788	P2789	M2790	L2791	K2792	P2793	Y2794	K2795	L2796	P2797	S2798	E2799	K2800	D2801	K2802	L2804	Y2805	K2806	W2807	P2808	L2809	K2810	E2811	S2812	L2813	K2814	A2815	M2816	L2817	A2818	N2819	E2820	W2821	T2822	L2823	E2824	K2825
R2826	E2827	Q2828	Q2829	E2830	GLU	GLU	ARG	THR	GLU	LYS	LYS	THR	ARG	LYS	ILE	SER	GLN	THR	ALA	GLN	THR	ASP	PRO	ARG	GLU	GLY	Y2855	N2856	P2857	Q2858	P2859	P2860	D2861	L2862	S2863	G2864	V2865	T2866	L2867	S2868	E2870	L2871	Q2872	M2873	K2874	A2875	E2876	Q2877	L2878	K2879	E2880	N2881	Y2882	H2883	N2884	T2885		



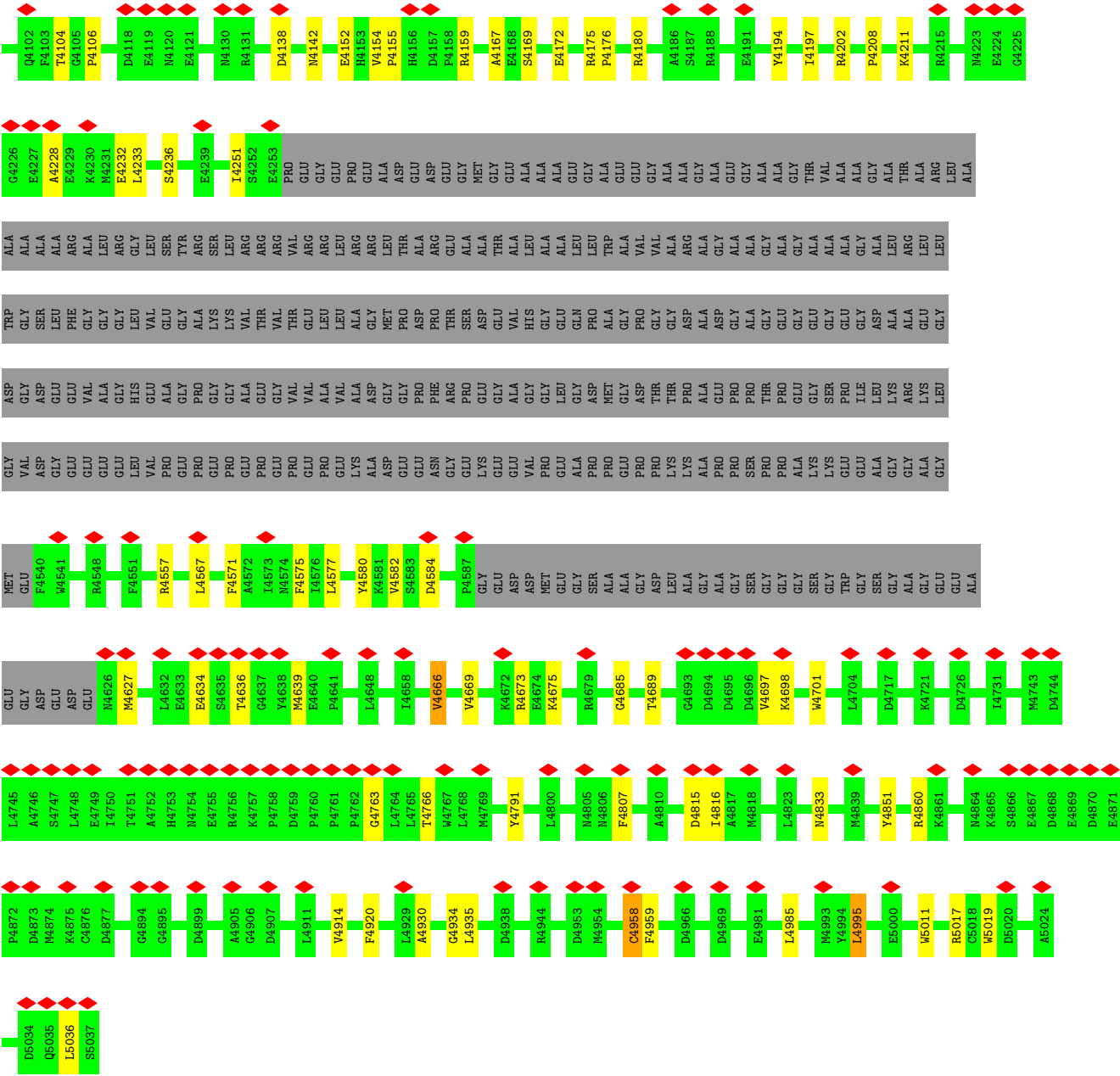
• Molecule 2: Ryanodine receptor 1



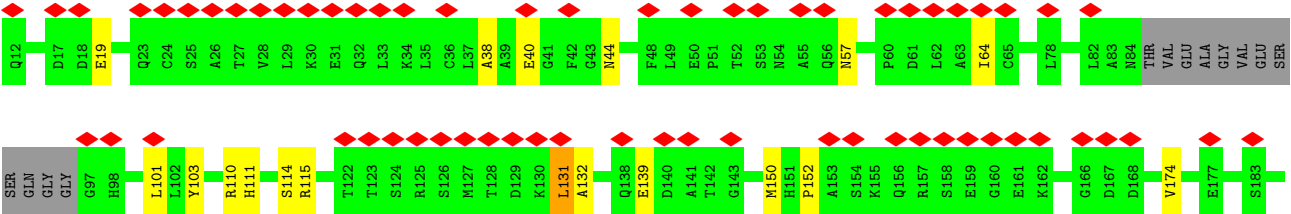
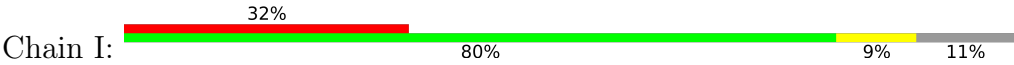
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R266	L267	H273	L274	R275	W276	G277	H284	V285	R289	Y290	L291	A292	L293	T294	E295	D296	Q297	G298	L299	V300	K306	A307	T308	H309	K310	S313	F314	C315	F316	R317	V318	S319	K320	E321	K322	L323	D324	T325	A326	P327	K328	R329	D330	V331	E332	G333	M334	G335	P336	P337	E338	K340	Y341				
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H797	G798	L803	P806	G807	Y808	A809	P810	C811	H812	L719	H720	A814	L816	E819	R820	L821	R822	L823	E824	P825	L826	K827	R835	S843	R844	C845	L846	S847	H848	T849	D850	C854	P855	V856	D857	THR	VAL	GLN	T861	V862	L863	P864	P865	E868	R869	E872	K873	L874	L878	H879							
E880	L881	W882	A883	L884	T885	R886	L887	E888	Q889	G890	W891	T892	Y893	G894	P895	V896	R897	D898	D899	N900	K901	R902	L903	H904	P905	C906	L907	V908	N909	F910	H911	S912	L913	P914	E915	P916	E917	R918	N919	Y920	N921	L922	Q923	M924	S925	G926	T928	L929	L933	A934	L935	C936	C937	H938	V939	G940	M941
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X2654	X2662	X2665	X2669	X2670	X2671	X2672	X2673	X2674	X2675	X2678	X2681	X2682	X2688	X2689	X2690	X2691	X2692	X2693	X2694	X2696	X2572	X2580	X2581	X2582	X2583	X2584	X2585	X2586	X2596	X2602	X2613	X2618	X2619	X2620	X2621	X2622	X2623	X2624	X2625	X2626	X2627	X2628	X2629	X2633	X2640	X2650						
ARG	ASP	ARG	ARG	ARG	GLU	HIS	PHE	GLY	GLU	PRO	PRO	GLU	GLU	N2414	N2415	H2420	G2434	R2435	P2438	E2439	N2440	H2441	L2442	K2447	G2448	E2449	R2452	I2453	L2457	R2458	S2459	L2460	V2461	D2464	D2465	L2466	I2469	I2470	S2471	L2472	P2473	L2474	Q2475	L2476	P2477	T2478	L2479	X2487	X2488	X2489		
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LEU	PRO	ALA	GLU	GLU	K2089	K2090	P2091	Q2092	S2093	L2094	Q2127	L2131	R2140	S2147	E2150	G2160	R2163	L2166	I2167	H2170	Q2173	N2176	N2184	I2185	M2186	N2187	Q2193	N2196	R2199	A2200	H2204	V2212	G2216	G2217	G2218	E2219	T2220	K2221	E2222	I2223	L2234	A2235										
H2011	F2012	A2016	D2017	E2018	E2019	C2020	P2022	L2023	P2024	E2025	D2026	I2027	R2028	H2041	C2042	C2043	I2044	Q2045	L2046	E2047	G2048	GLU	GLU	PRO	GLU	GLU	THR	SER	LEU	SER	SER	SER	ARG	LEU	SER	LEU	LEU	GLU	THR	VAL	ARG	LEU	VAL	LYS	LYS	LYS	GLU	LYS	PRO	GLU	GLU	
ALA	PRO	GLU	GLU	LYS	ASP	L1922	E1923	E1924	G1925	Q1928	L1931	V1935	L1958	A1959	A1960	R1964	Q1973	R1974	S1975	Y1977	A1978	L1979	R1982	A1983	F1984	L1985	M1986	S1987	A1988	A1989	E1990	T1991	R1994	T1995	R1996	E1997	F1998	R1999	S2000	P2001	P2002	Q2003	E2004	Q2005	N2007	L2010						
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		X3611	X3611	X3486	X3408	X3329	X3254	X3096	X2993		
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		X3650	X3650	X3525	X3447	X3368	X3293	X3135	X3032		
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		X3674	X3674	X3549	X3471	X3392	X3317	X3159	X3056		
		X3675	X3675	X3550	X3472	X3393	X3318	X3160	X3057		
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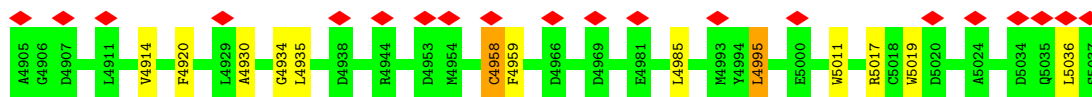
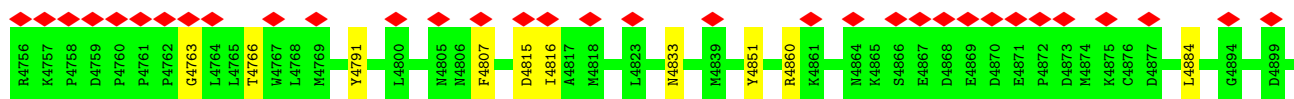
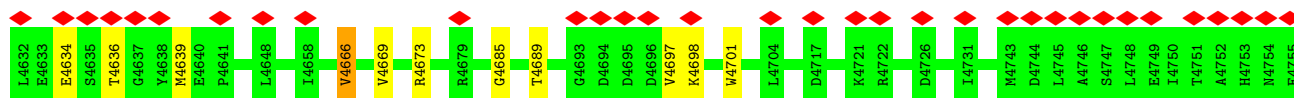
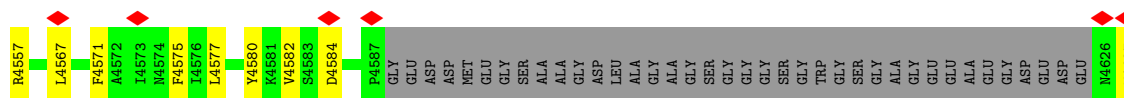
● Molecule 2: Ryanodine receptor 1



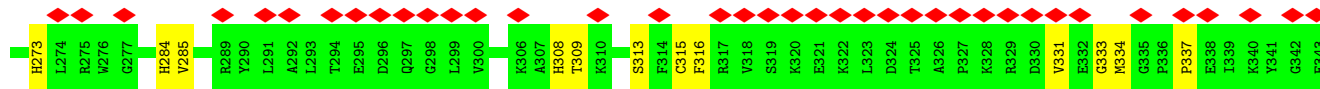
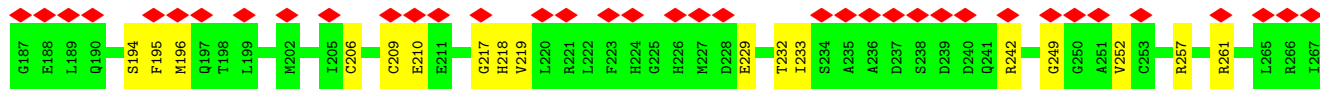
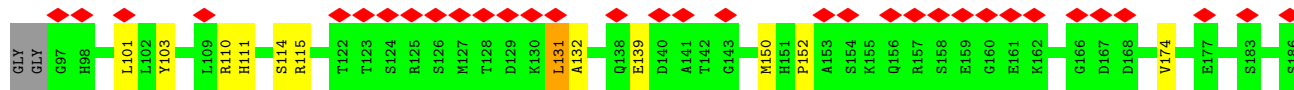
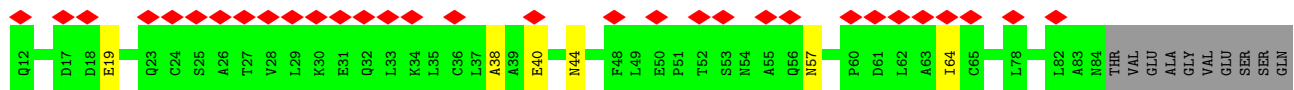
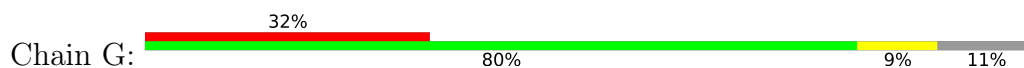


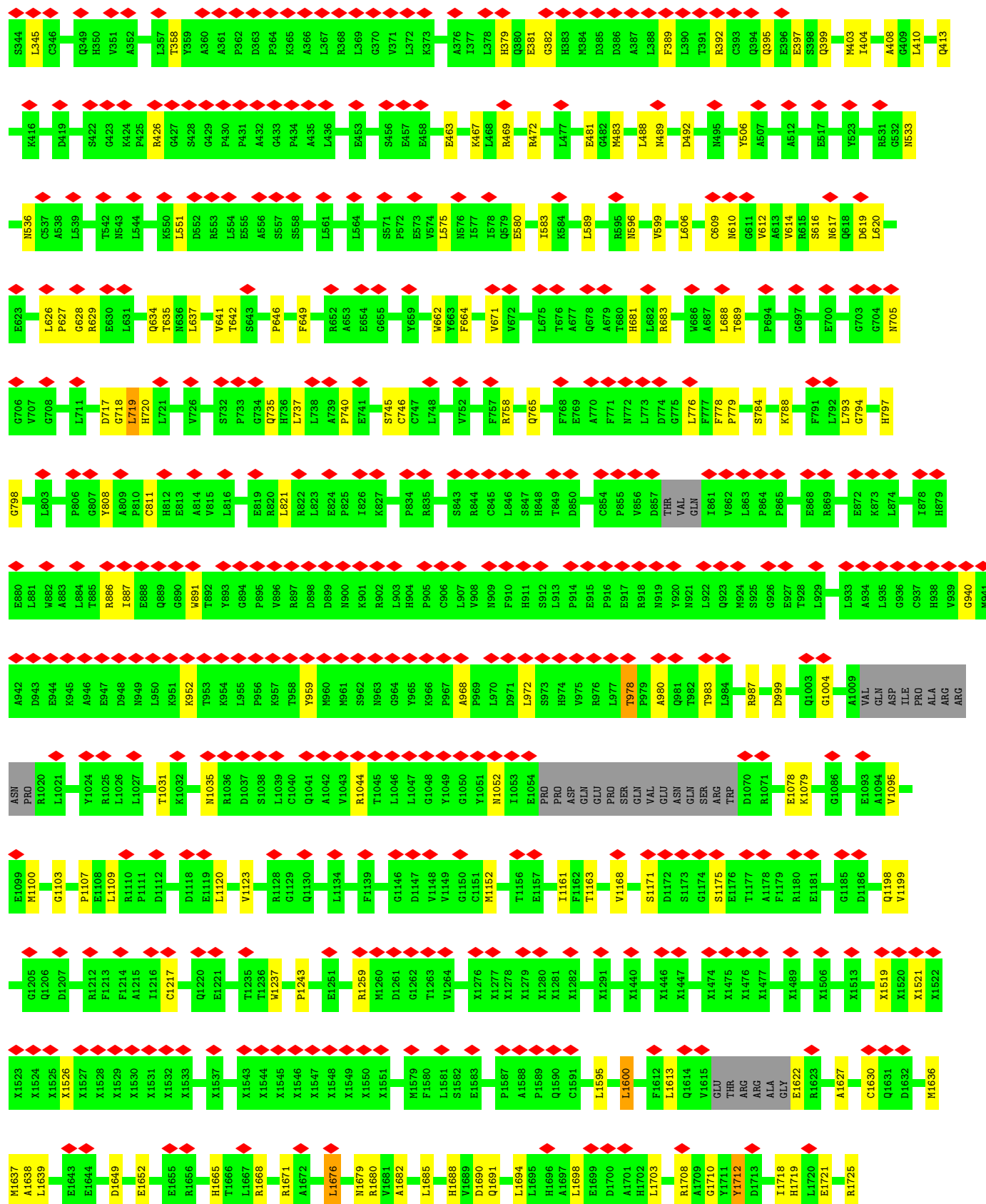


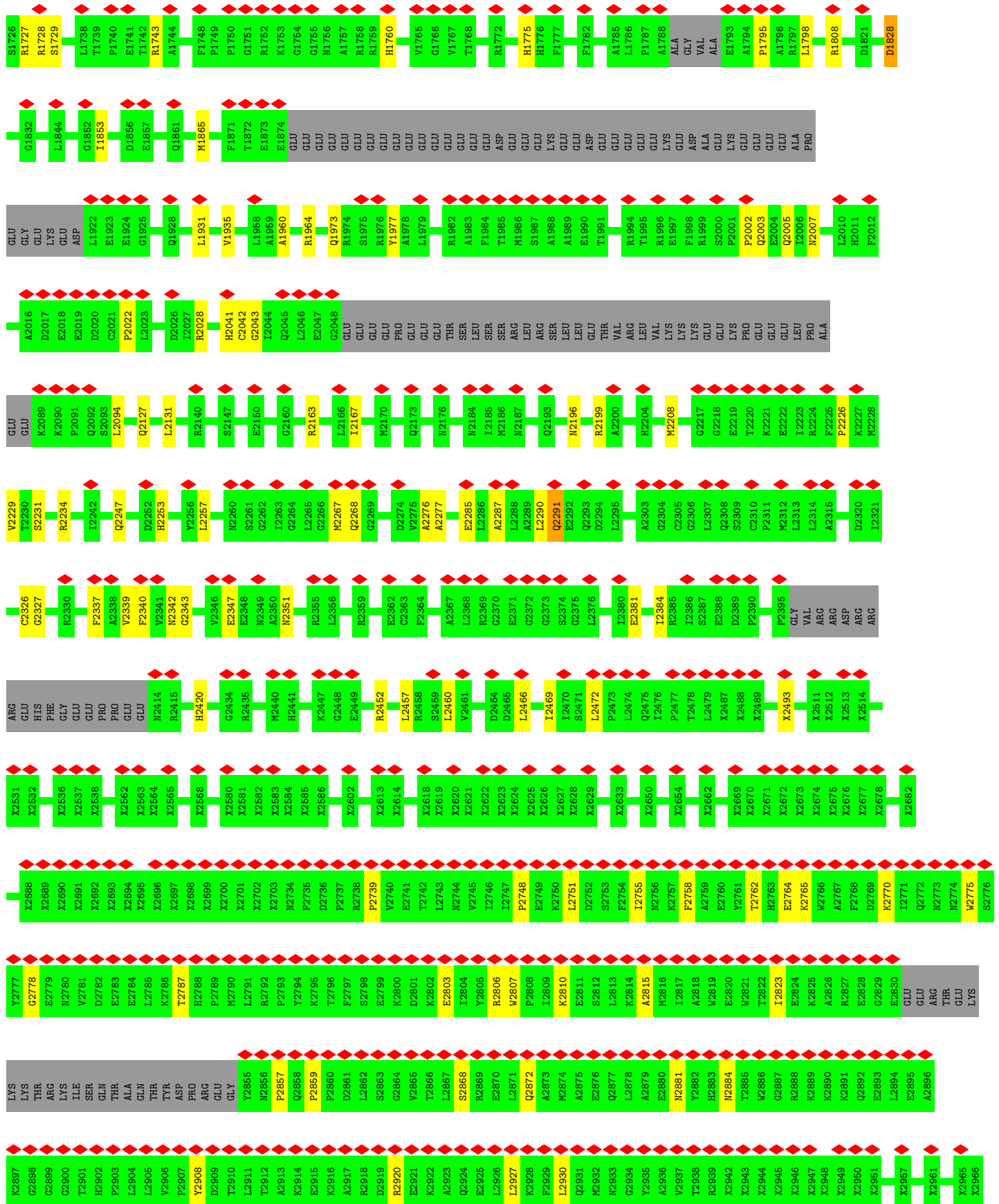
GLU	ARG	THR	GLU	LYS	LYS	LYS	THR	ARG	LYS	ILE	SER	GLN	THR	ALA	GLN	THR	TVR	ASP	PRO	ARG	GLU	GLY																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
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• Molecule 2: Ryanodine receptor 1











4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	55564	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	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	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.141	Depositor
Minimum map value	-0.064	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	502.0, 502.0, 502.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.255, 1.255, 1.255	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, 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	0.20	0/834	0.45	0/1123
1	F	0.20	0/834	0.45	0/1123
1	H	0.20	0/834	0.45	0/1123
1	J	0.20	0/834	0.45	0/1123
2	B	0.21	0/25428	0.52	5/34534 (0.0%)
2	E	0.21	0/25428	0.52	5/34534 (0.0%)
2	G	0.21	0/25428	0.52	5/34534 (0.0%)
2	I	0.21	0/25428	0.52	5/34534 (0.0%)
All	All	0.21	0/105048	0.52	20/142628 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	F	0	1
1	H	0	1
1	J	0	1
2	B	0	16
2	E	0	16
2	G	0	16
2	I	0	16
All	All	0	68

There are no bond length outliers.

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	1828	ASP	CA-C-N	5.96	125.97	119.89
2	I	1828	ASP	C-N-CA	5.96	125.97	119.89
2	E	1828	ASP	CA-C-N	5.96	125.96	119.89
2	E	1828	ASP	C-N-CA	5.96	125.96	119.89
2	G	1828	ASP	CA-C-N	5.95	125.96	119.89

There are no chirality outliers.

5 of 68 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	8	SER	Peptide
2	B	139	GLU	Peptide
1	F	8	SER	Peptide
1	H	8	SER	Peptide
1	J	8	SER	Peptide

5.2 Too-close contacts

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	818	0	824	8	0
1	F	818	0	824	9	0
1	H	818	0	824	8	0
1	J	818	0	824	9	0
2	B	29369	0	24721	223	0
2	E	29369	0	24721	219	0
2	G	29369	0	24719	217	0
2	I	29369	0	24721	221	0
3	B	1	0	0	0	0
3	E	1	0	0	0	0
3	G	1	0	0	0	0
3	I	1	0	0	0	0
4	B	1	0	0	0	0
4	E	1	0	0	0	0
4	G	1	0	0	0	0
4	I	1	0	0	0	0
All	All	120756	0	102178	898	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 4.

The worst 5 of 898 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:B:426:ARG:HB2	2:B:506:TYR:HA	1.78	0.66
2:I:426:ARG:HB2	2:I:506:TYR:HA	1.78	0.66
2:G:426:ARG:HB2	2:G:506:TYR:HA	1.78	0.66
2:E:426:ARG:HB2	2:E:506:TYR:HA	1.78	0.65
2:B:4860:ARG:HD2	2:E:4582:VAL:HG11	1.77	0.64

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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	88/89 (99%)	88 (100%)	0	100	100
1	F	88/89 (99%)	88 (100%)	0	100	100
1	H	59/89 (66%)	59 (100%)	0	100	100
1	J	71/89 (80%)	71 (100%)	0	100	100
2	B	2486/3202 (78%)	2473 (100%)	13 (0%)	81	81
2	E	2440/3202 (76%)	2428 (100%)	12 (0%)	81	81
2	G	2493/3202 (78%)	2480 (100%)	13 (0%)	81	81
2	I	2467/3202 (77%)	2455 (100%)	12 (0%)	81	81
All	All	10192/13164 (77%)	10142 (100%)	50 (0%)	78	81

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	I	978	THR
2	I	4985	LEU
2	G	4995	LEU
2	I	1676	LEU
2	I	4081	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 206 such sidechains are listed below:

Mol	Chain	Res	Type
2	I	413	GLN
2	I	4037	ASN
2	G	4776	GLN
2	I	765	GLN
2	I	2260	ASN

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	B	12
2	G	12
2	I	12
2	E	12

The worst 5 of 48 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	3613:UNK	C	3639:THR	N	44.23
1	G	3613:UNK	C	3639:THR	N	43.95
1	I	3613:UNK	C	3639:THR	N	43.88
1	E	3613:UNK	C	3639:THR	N	43.84
1	E	3163:UNK	C	3170:UNK	N	16.60

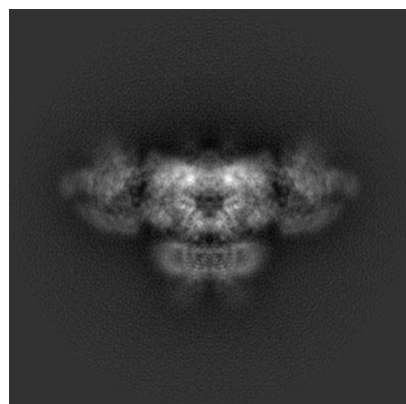
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8375. These allow visual inspection of the internal detail of the map and identification of artifacts.

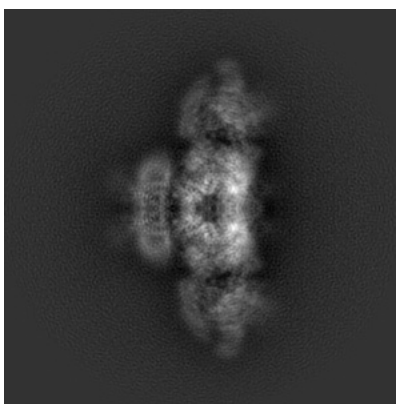
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

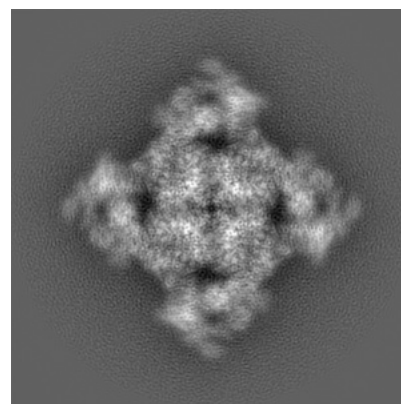
6.1.1 Primary map



X

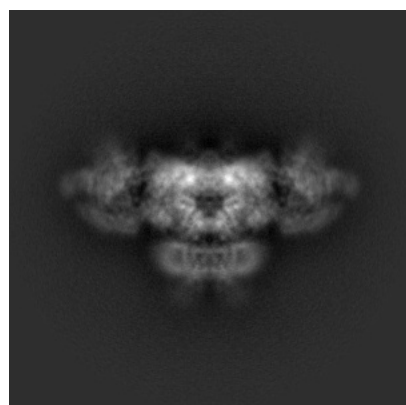


Y

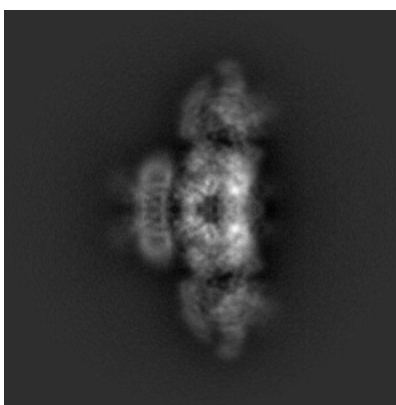


Z

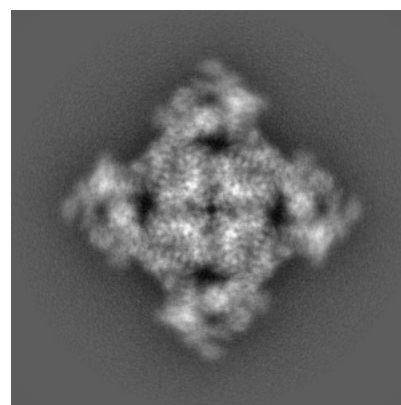
6.1.2 Raw map



X



Y

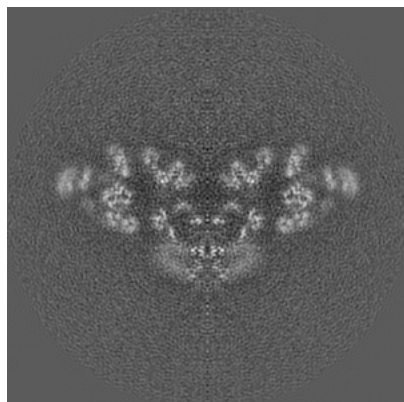


Z

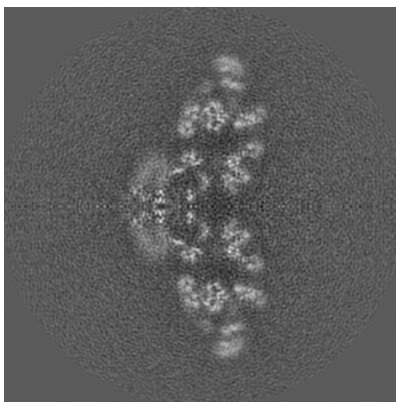
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

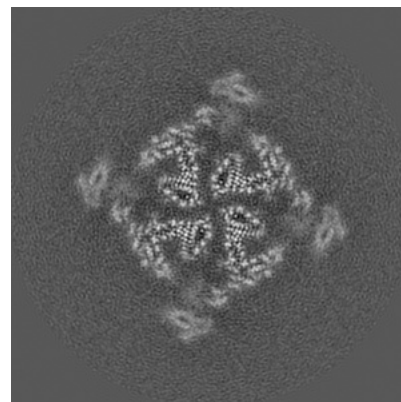
6.2.1 Primary map



X Index: 200

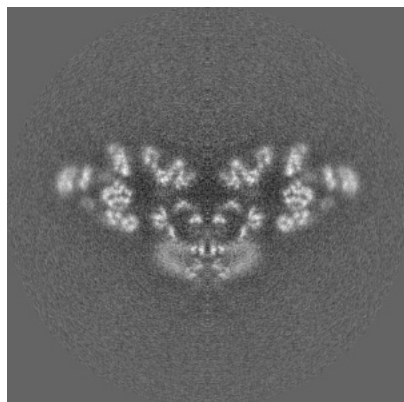


Y Index: 200

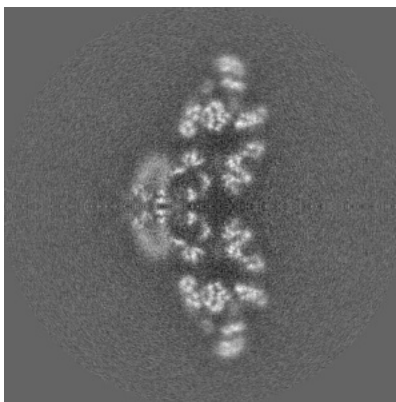


Z Index: 200

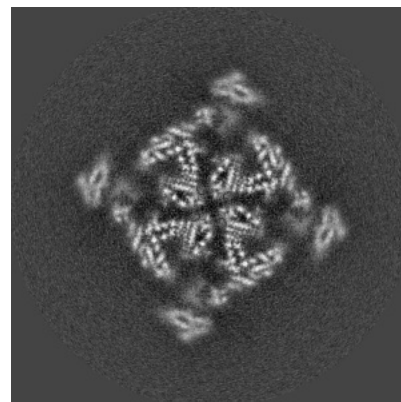
6.2.2 Raw map



X Index: 200



Y Index: 200

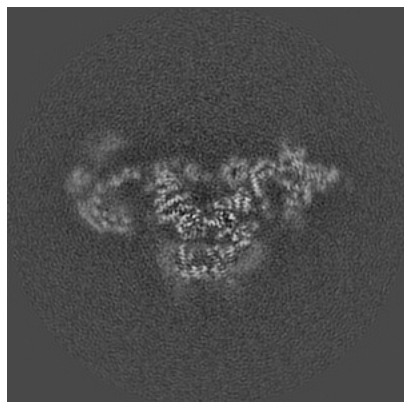


Z Index: 200

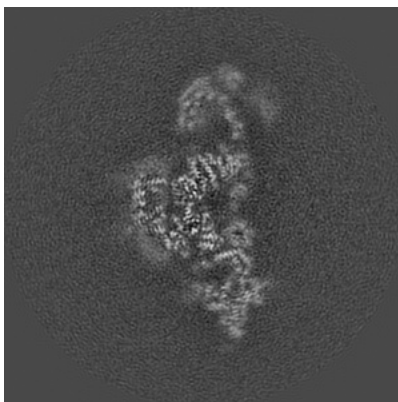
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

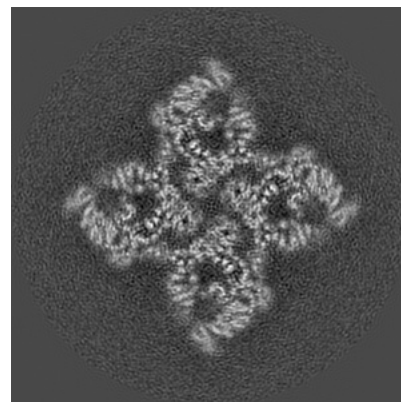
6.3.1 Primary map



X Index: 184

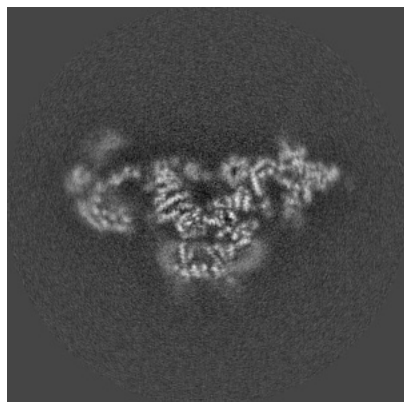


Y Index: 184

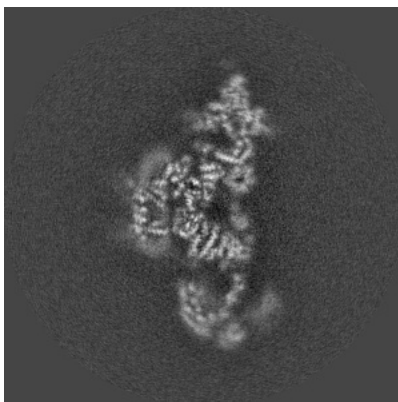


Z Index: 233

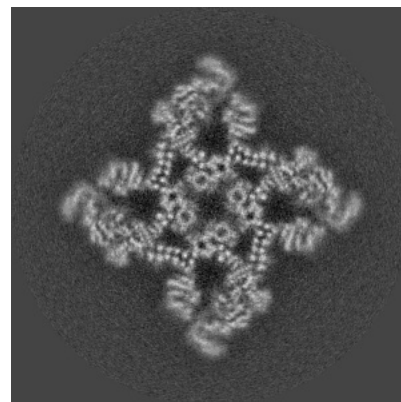
6.3.2 Raw map



X Index: 184



Y Index: 216

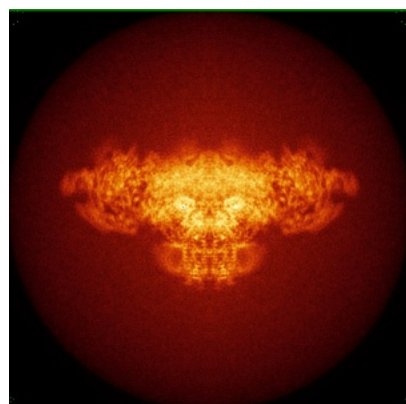


Z Index: 228

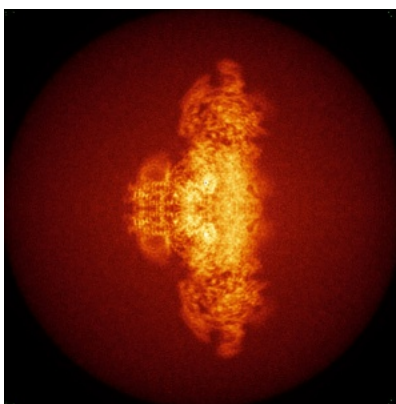
The images above show the largest variance slices of the map in three orthogonal directions.

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

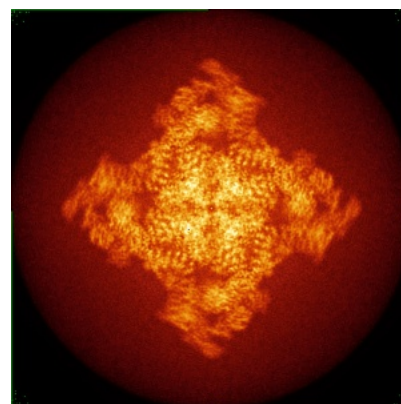
6.4.1 Primary map



X



Y

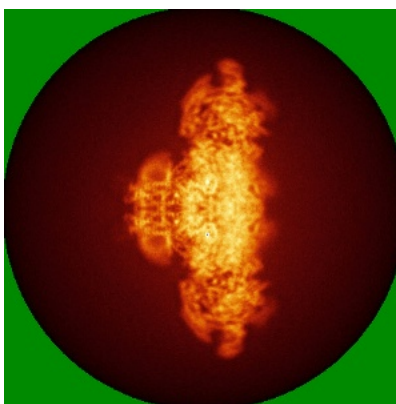


Z

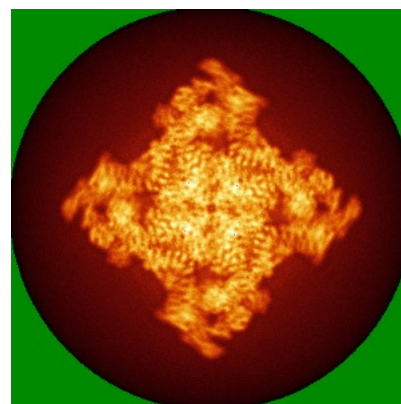
6.4.2 Raw map



X



Y

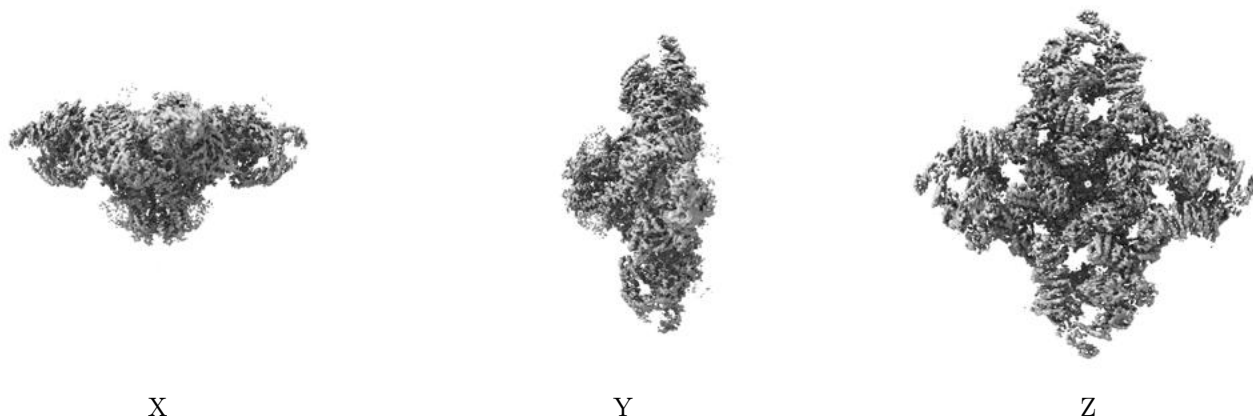


Z

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

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

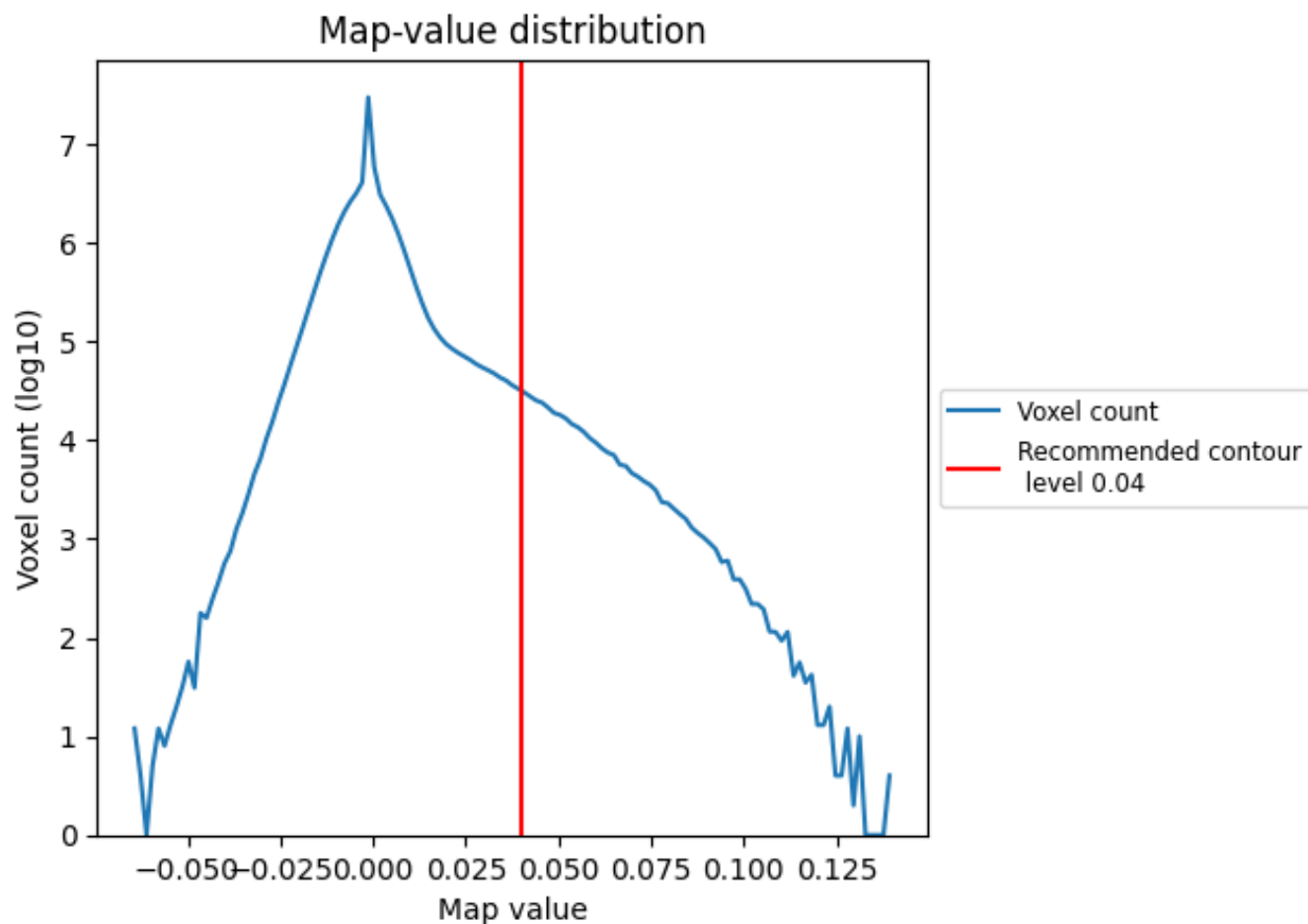
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

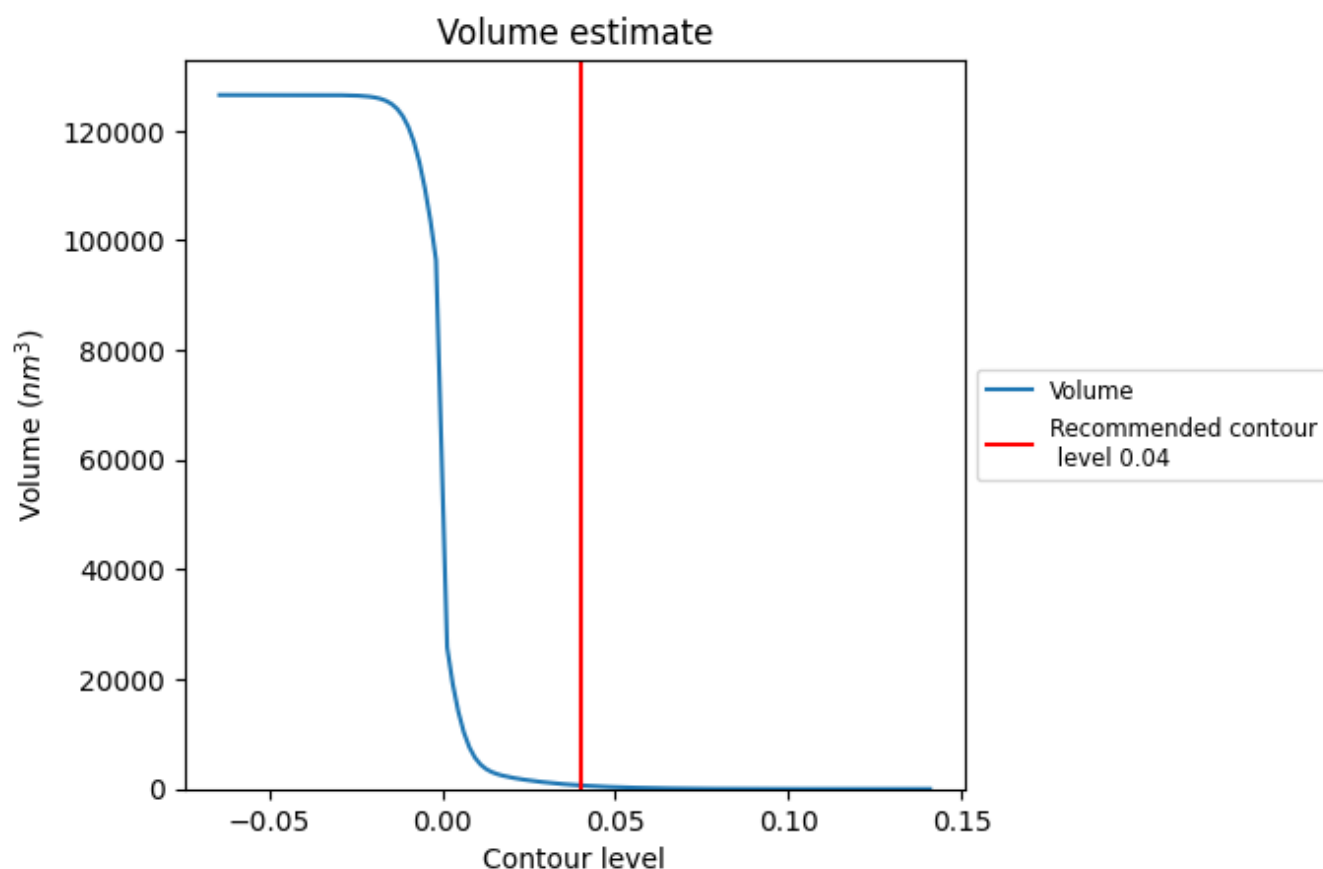
This section contains the results of statistical analysis of the map.

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.

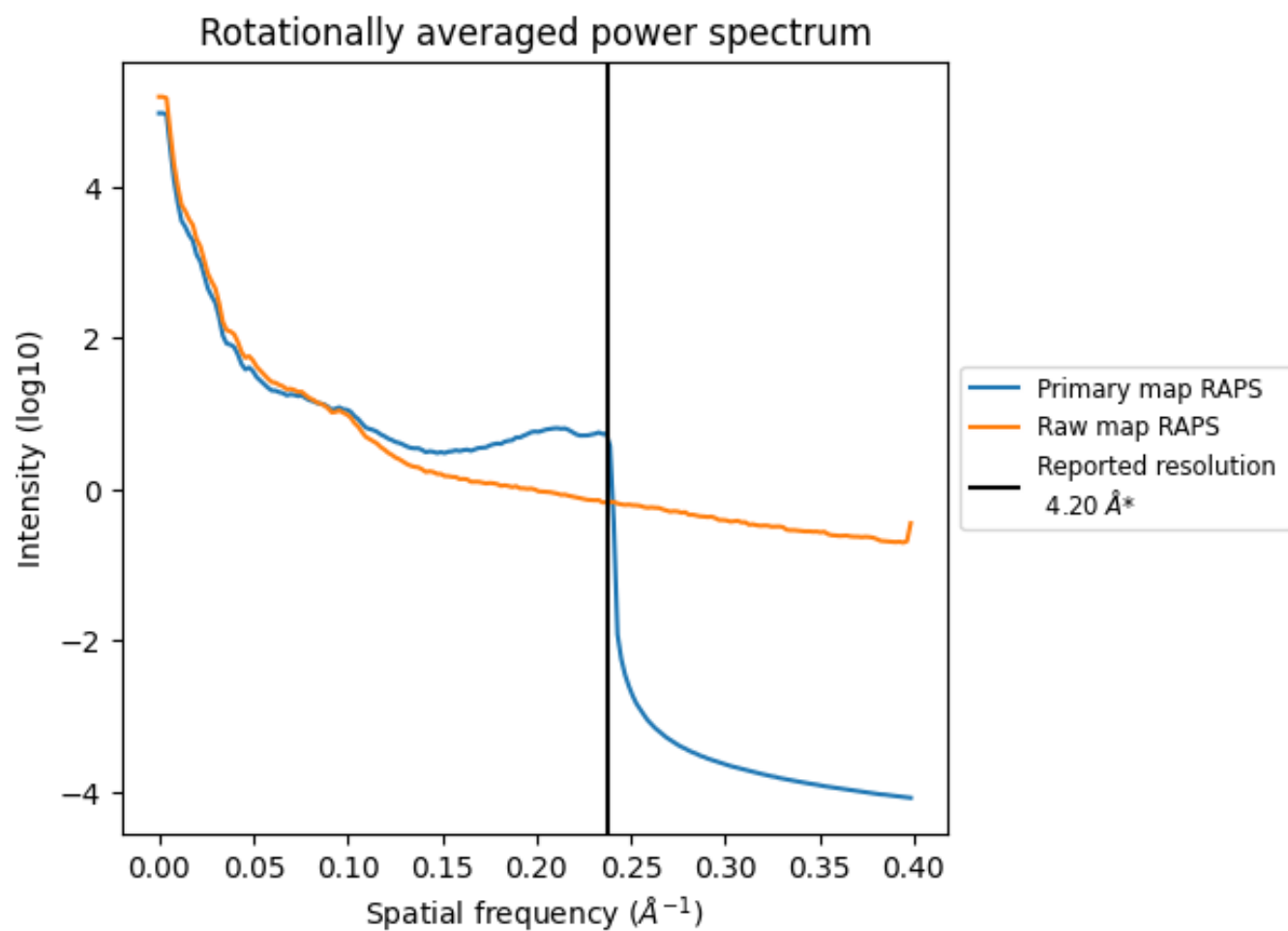
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 651 nm^3 ; this corresponds to an approximate mass of 588 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 ⓘ

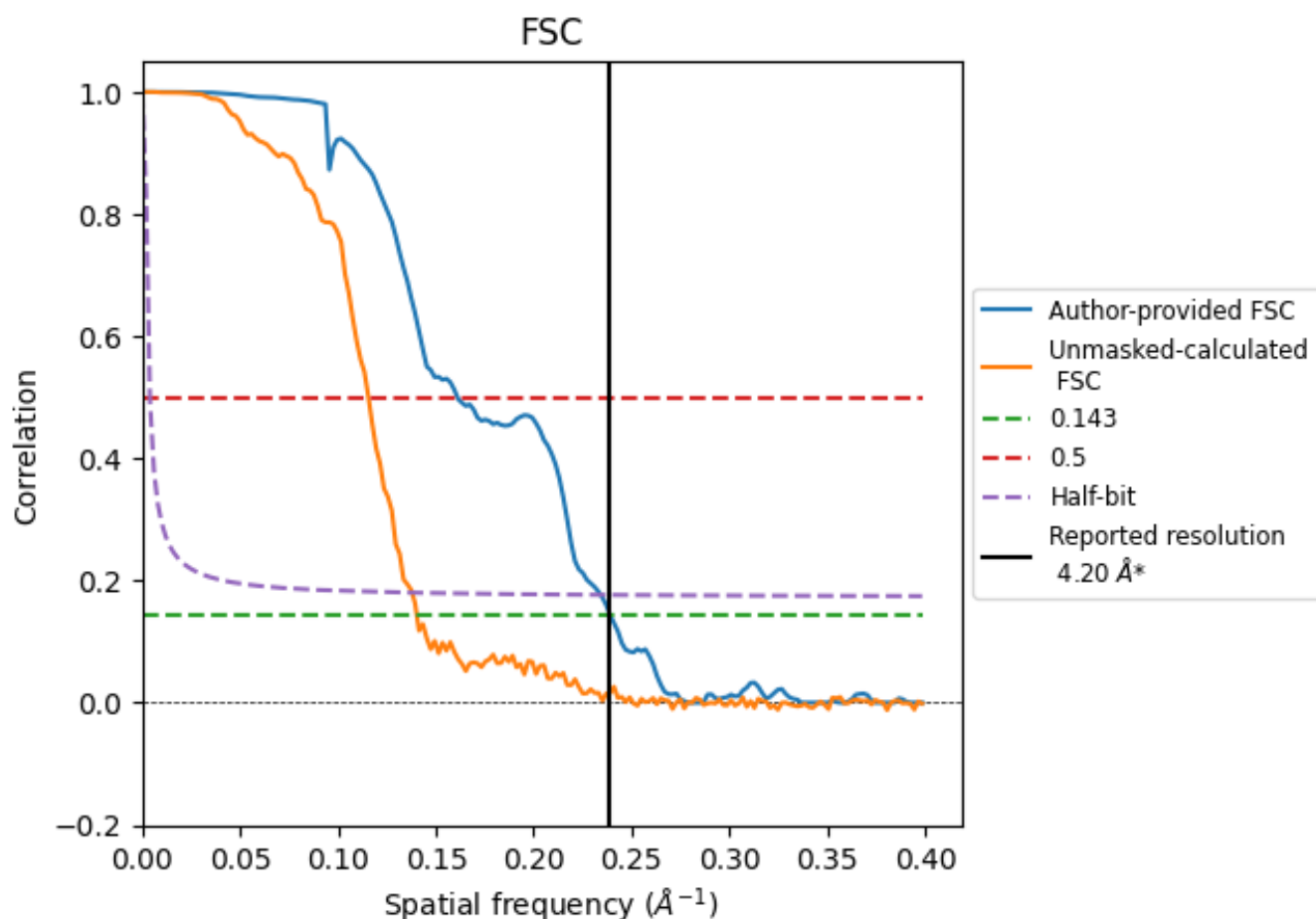


*Reported resolution corresponds to spatial frequency of 0.238 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.238 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

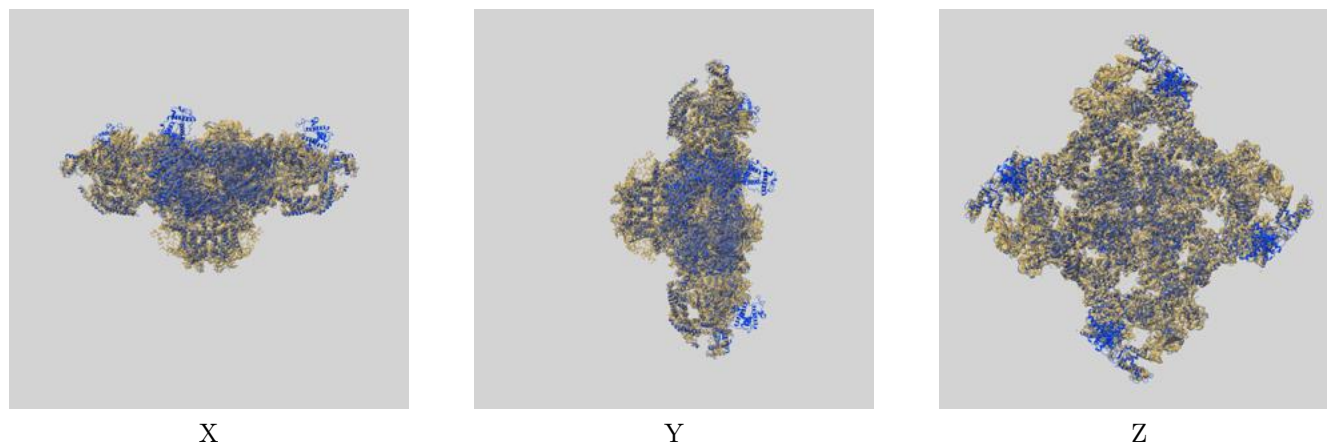
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.20	-	-
Author-provided FSC curve	4.18	6.21	4.27
Unmasked-calculated*	7.13	8.65	7.26

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.13 differs from the reported value 4.2 by more than 10 %

9 Map-model fit [i](#)

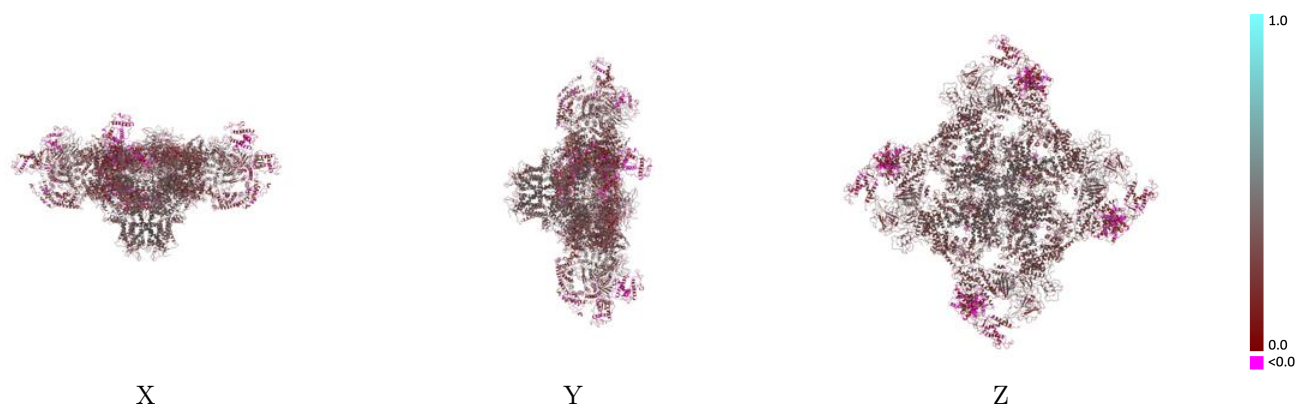
This section contains information regarding the fit between EMDB map EMD-8375 and PDB model 5T9S. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



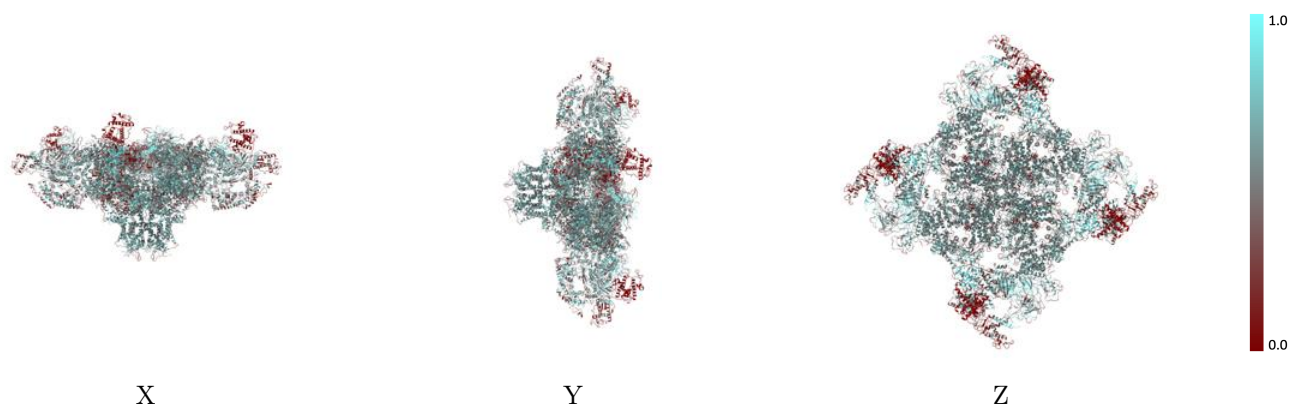
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



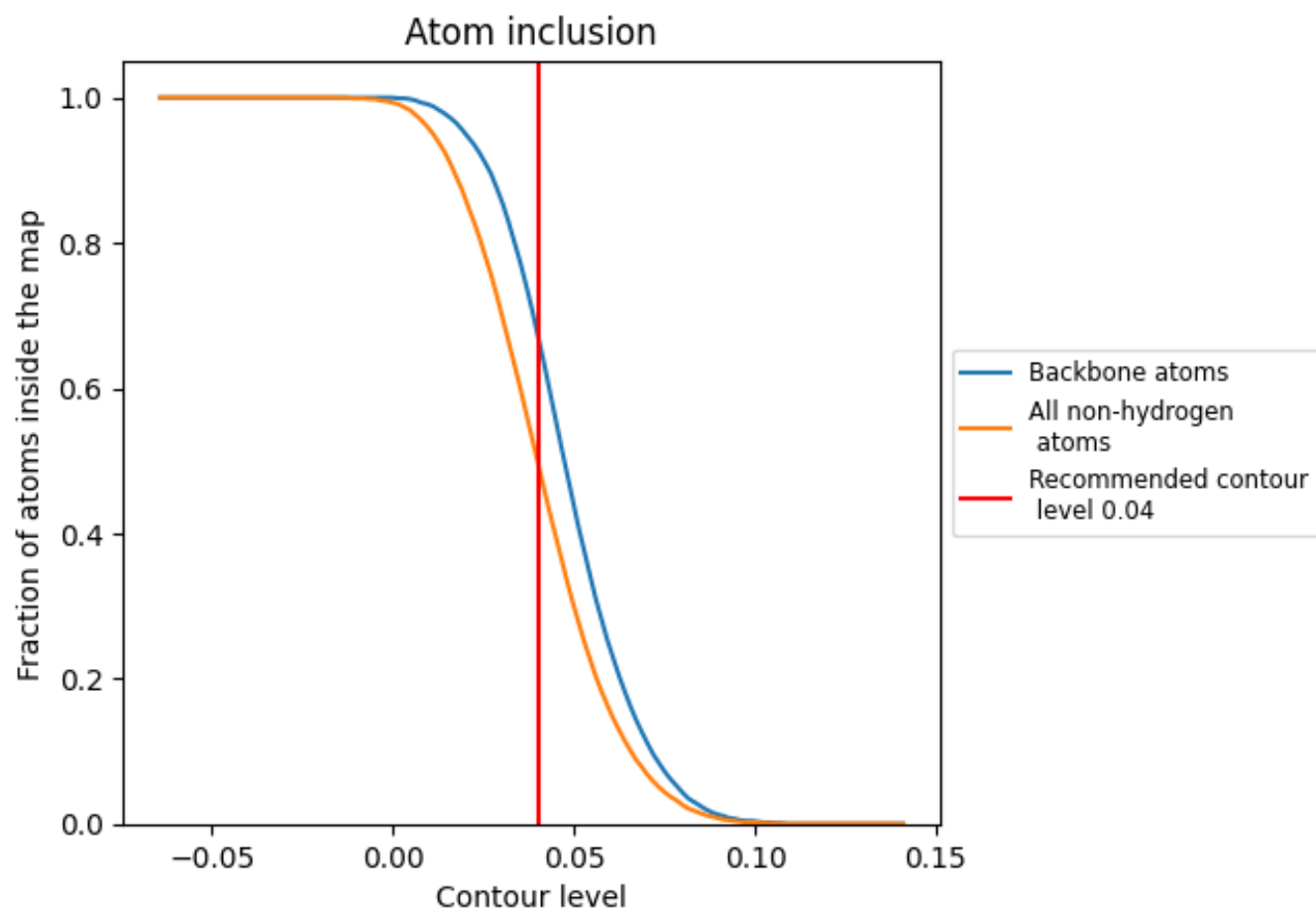
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 67% of all backbone atoms, 50% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4980	0.2870
A	0.4780	0.3000
B	0.5030	0.2900
E	0.4950	0.2850
F	0.4780	0.3050
G	0.5000	0.2870
H	0.4840	0.3060
I	0.4950	0.2850
J	0.4840	0.2990

1.0

0.0

<0.0