



wwPDB EM Validation Summary Report ⓘ

Nov 9, 2024 – 11:26 AM EST

PDB ID : 5TAY
EMDB ID : EMD-8389
Title : Structure of rabbit RyR1 (ryanodine dataset, class 2)
Authors : Clarke, O.B.; des Georges, A.; Zalk, R.; Marks, A.R.; Hendrickson, W.A.;
Frank, J.
Deposited on : 2016-09-10
Resolution : 4.60 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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

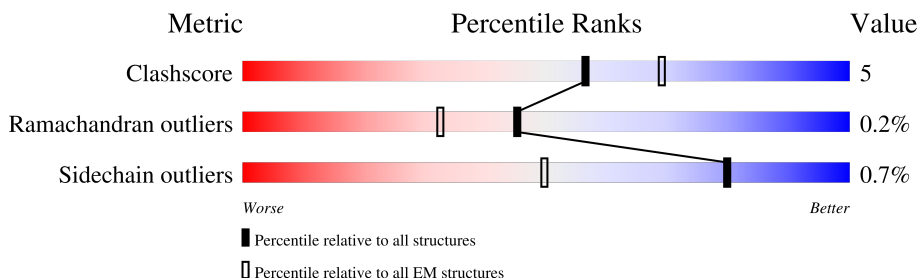
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.60 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	<div> <div>22%</div> <div>89%</div> <div>10%</div> <div>.</div> </div>
1	F	108	<div> <div>22%</div> <div>86%</div> <div>13%</div> <div>.</div> </div>
1	H	108	<div> <div>22%</div> <div>87%</div> <div>12%</div> <div>.</div> </div>
1	J	108	<div> <div>22%</div> <div>86%</div> <div>13%</div> <div>.</div> </div>
2	B	4416	<div> <div>34%</div> <div>84%</div> <div>10%</div> <div>5%</div> </div>
2	E	4416	<div> <div>36%</div> <div>84%</div> <div>10%</div> <div>5%</div> </div>
2	G	4416	<div> <div>34%</div> <div>84%</div> <div>10%</div> <div>5%</div> </div>
2	I	4416	<div> <div>36%</div> <div>85%</div> <div>10%</div> <div>5%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 121276 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	4194	Total	C	N	O	S	0	0
			29499	18686	5228	5428	157		
2	G	4194	Total	C	N	O	S	0	0
			29499	18686	5228	5428	157		
2	I	4194	Total	C	N	O	S	0	0
			29499	18686	5228	5428	157		
2	E	4194	Total	C	N	O	S	0	0
			29499	18686	5228	5428	157		

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

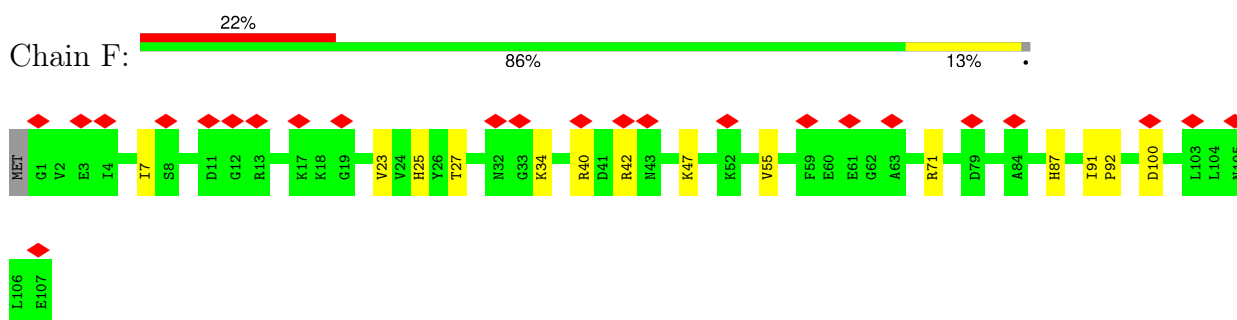
- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

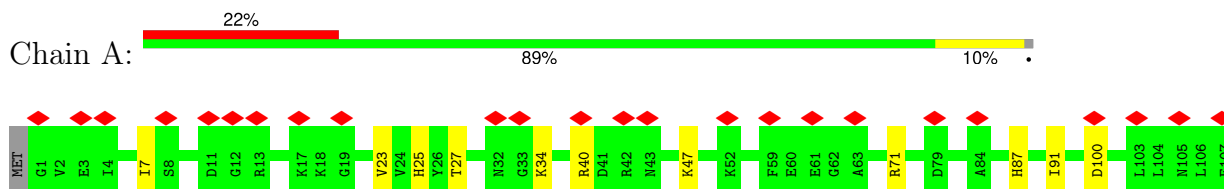
3 Residue-property plots [i](#)

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.

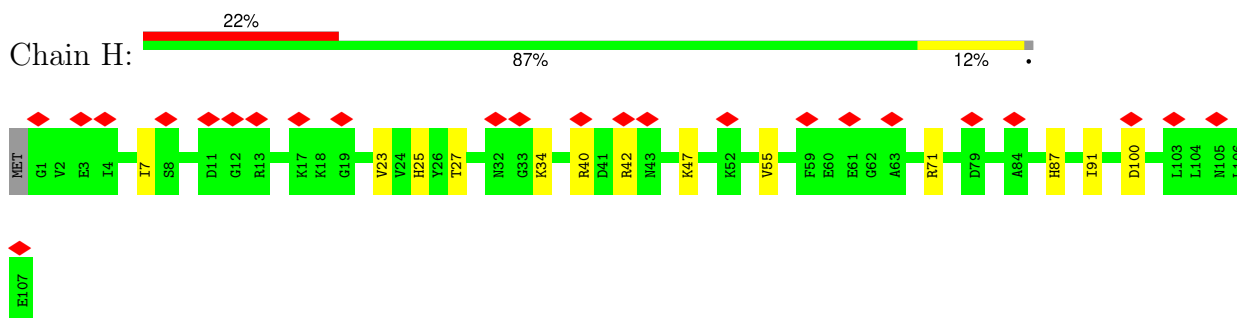
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



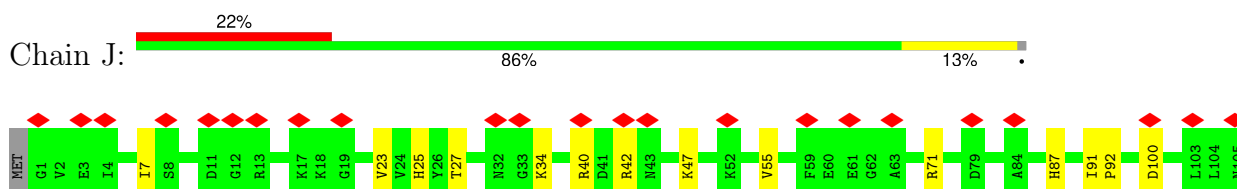
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



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




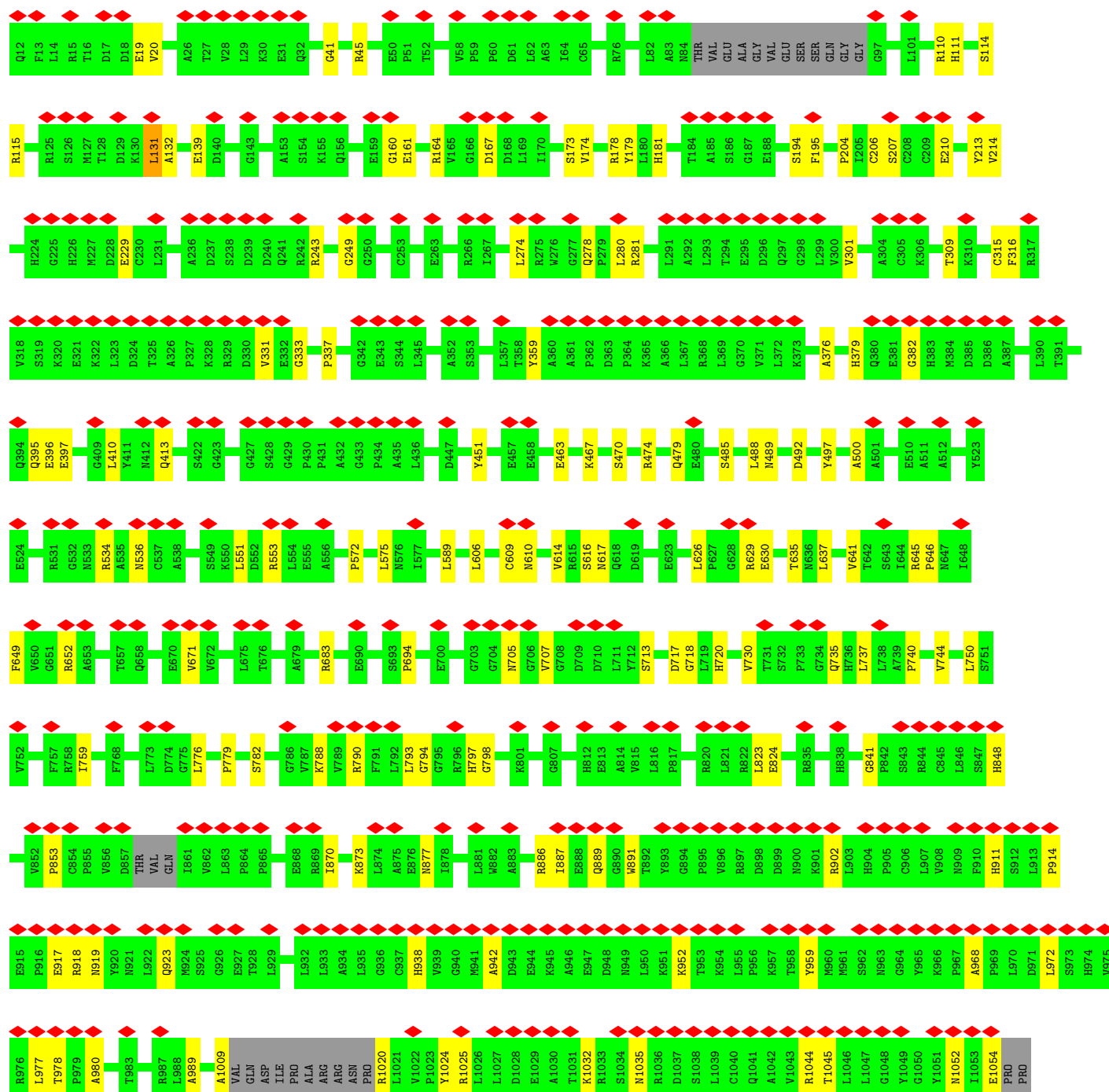
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



L106
E107

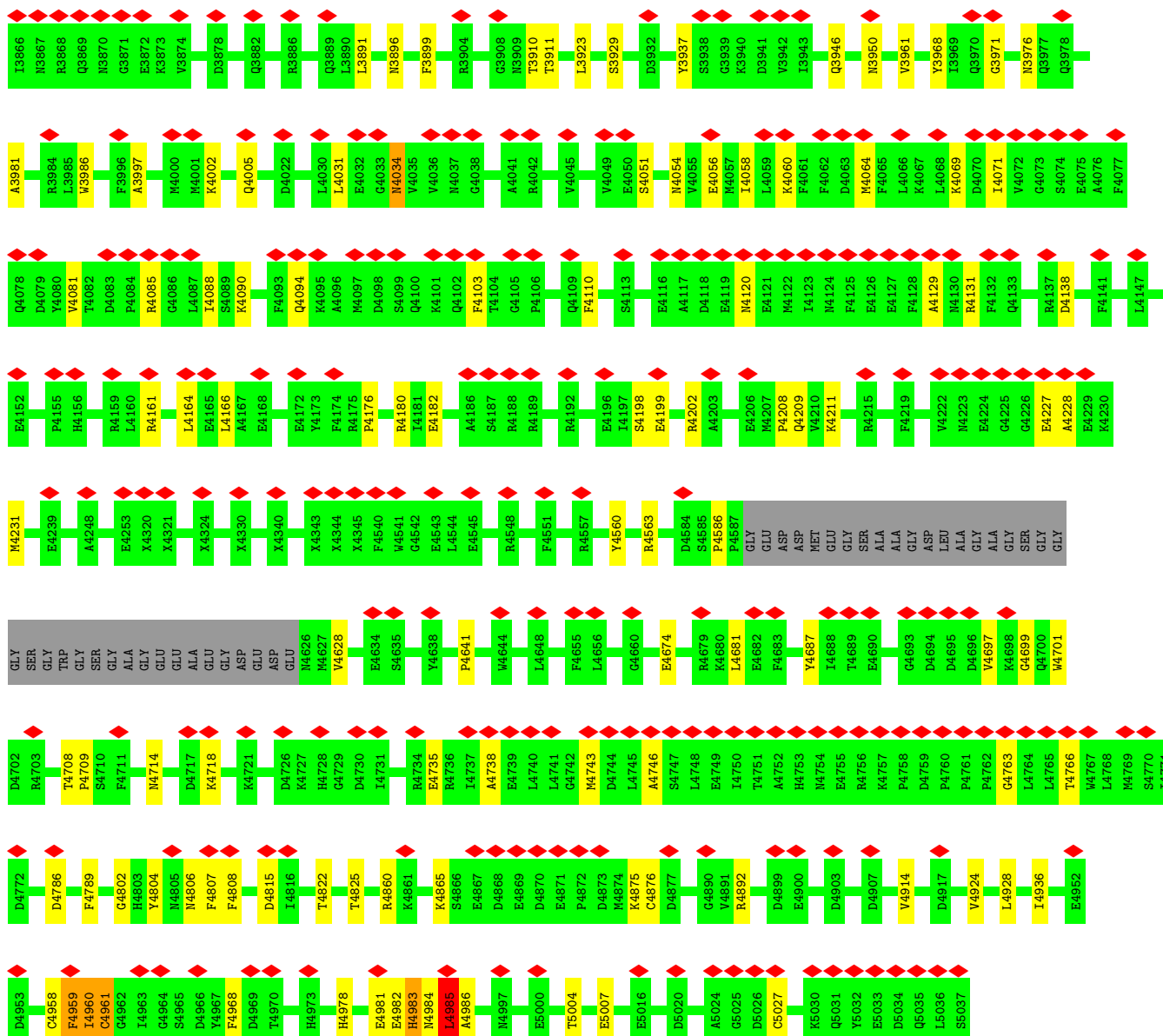
• Molecule 2: Ryanodine receptor 1

Chain B: 

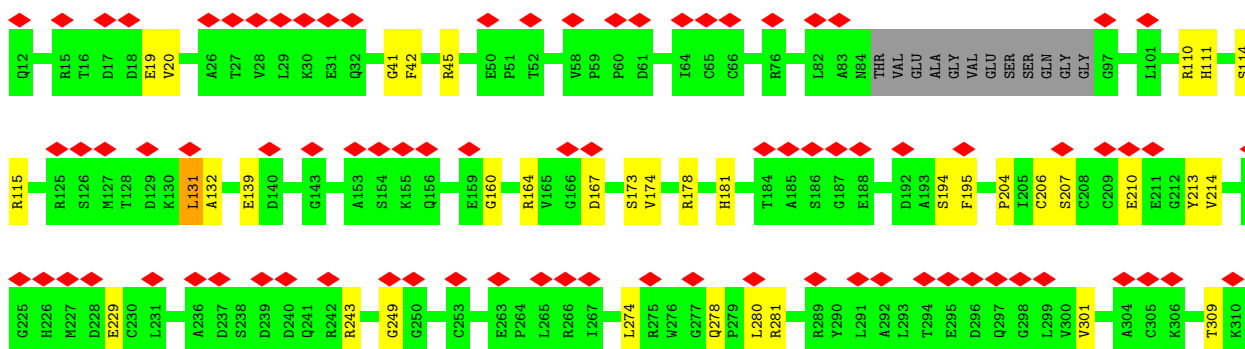
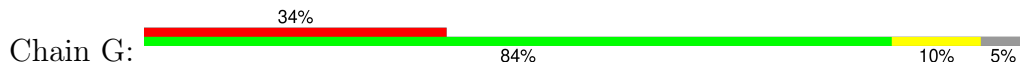


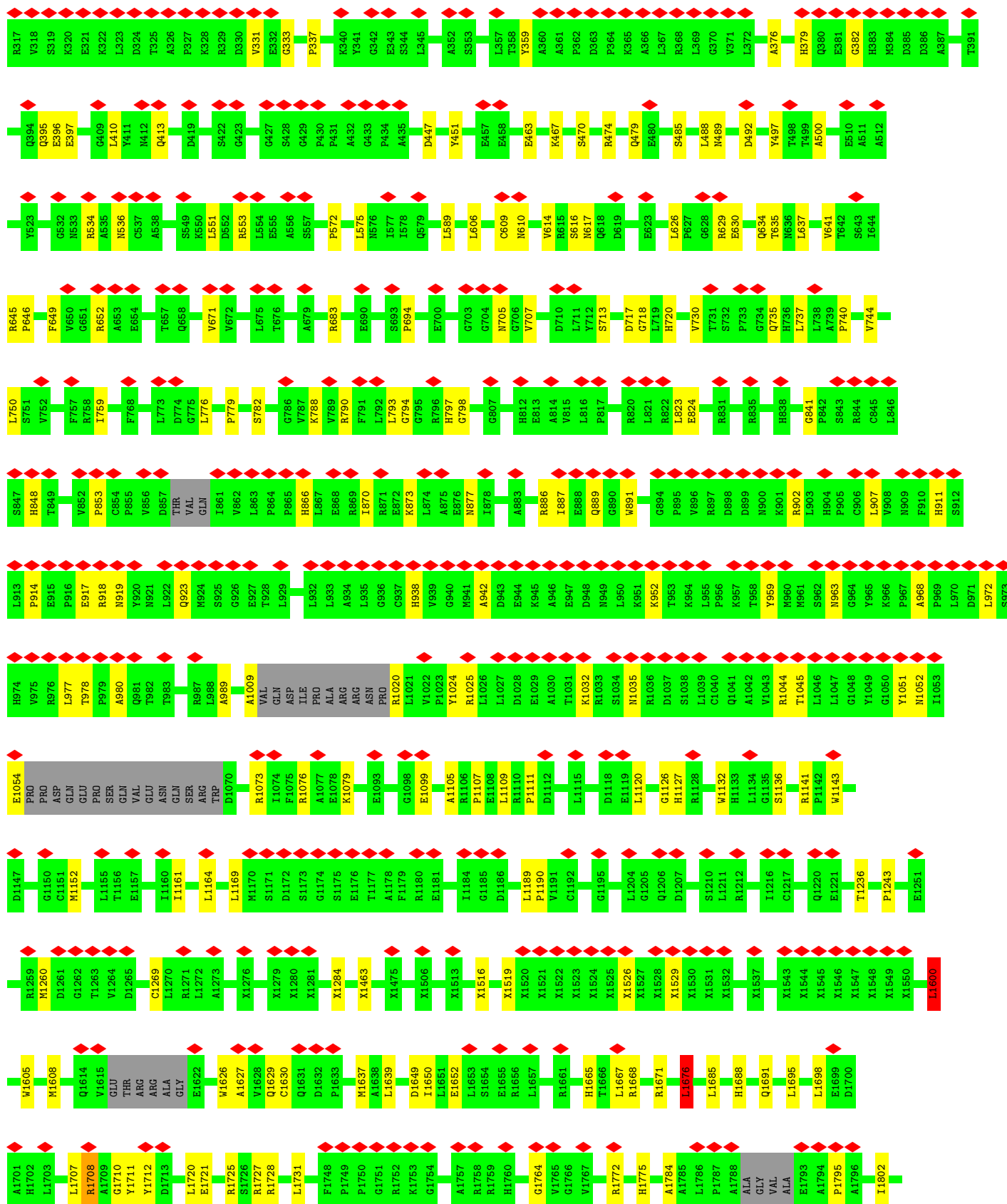
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R2435	P2438	P2439	M2440	H2441	L2442	L2443	Q2444	G2448	I2453	R2454	A2455	V2467	I2470	S2471	L2472	P2473	L2474	P2477	T2478	L2479	X2487	X2512	X2513	X2523	X2531	X2534	X2535	X2536	X2537	X2538	X2561	X2562	X2563	X2568	X2581	X2582	X2583	X2584	X2585	X2598	X2605	X2618										
F2337	F2340	V2341	E2347	E2348	N2349	A2350	N2351	V2352	V2353	L2357	L2358	R2359	F2364	A2367	L2368	E2371	G2372	G2373	S2374	G2375	L2376	L2377	A2378	E2381	D2389	P2390	A2391	P2395	GLY	VAL	ARG	ARG	ASP	ARG	ARG	GLU	HIS	PHE	GLY	GLU	GLU	PRO	X2583	X2584	X2585	X2598	L2429					
K2227	M2228	V2229	S2231	C2232	R2234	Q2247	Y2256	N2260	I2263	G2264	L2265	G2266	Q2267	Q2268	G2269	S2270	T2271	L2272	L2273	A2277	E2285	L2288	A2289	L2290	E2292	Q2293	D2294	L2295	G2304	S2309	C2310	L2314	A2315	Y2318	P2319	D2320	C2326	G2327	R2330	Y2331	L2332	D2333	F2334									
LEU	VAL	LYS	LYS	LYS	GLU	GLU	PRO	GLU	GLU	LEU	PRO	ALA	GLU	K2089	K2090	Q2107	S2122	L2131	G2132	R2140	E2150	L2165	L2166	I2167	Q2173	I2185	N2186	N2187	N2188	N2196	R2199	A2200	N2213	V2214	L2215	G2216	G2217	G2218	E2219	SER	LEU	LEU	LEU	THR	VAL	ARG						
E1997	F1998	P2002	Q2003	E2004	Q2005	L2006	N2007	H2011	F2012	A2016	D2017	E2018	E2019	D2020	C2021	L2023	P2024	I2027	R2028	H2035	L2039	C2042	G2043	T2044	Q2045	L2046	E2047	G2048	GLU	GLU	GLU	PRO	GLU	GLU	THR	SER	LEU	SER	SER	ARG	LEU	ARG	SER	LEU	LEU	THR	VAL	ARG				
GLU	GLU	GLU	LYS	GLU	ASP	ALA	PRO	GLU	GLU	GLU	GLU	ALA	PRO	GLU	GLU	GLU	GLU	L1922	E1923	E1924	Q1928	P1932	E1944	A1960	F1961	A1962	E1963	Y1965	V1966	L1969	Q1973	R1976	L1980	M1981	A1983	F1984	T1985	M1986	S1987	A1988	A1989	E1990	T1991	R1996								
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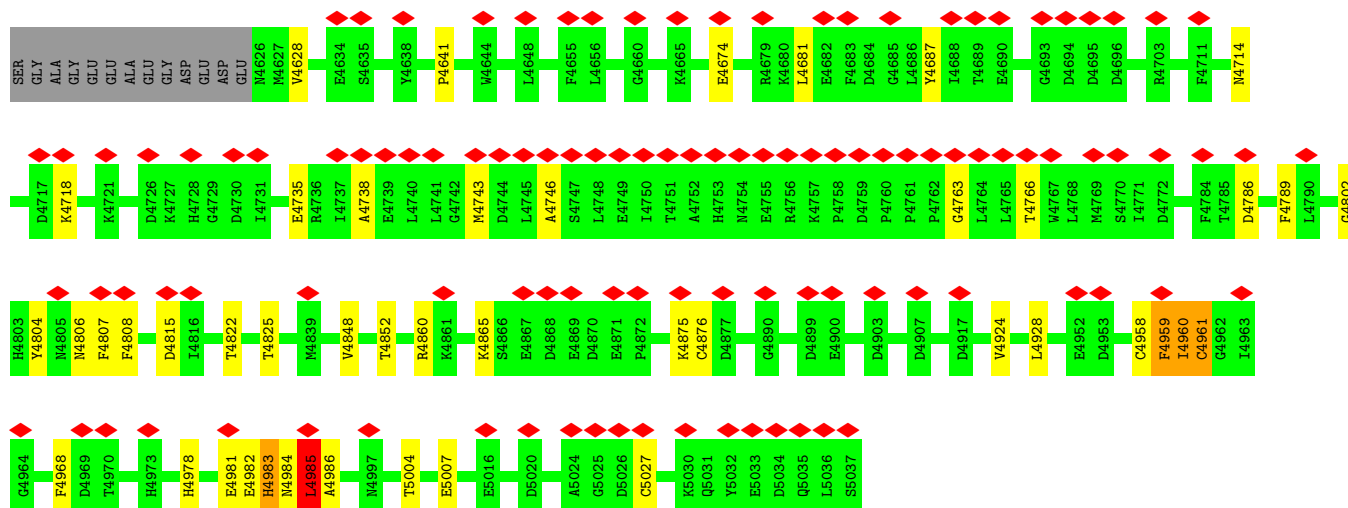
• Molecule 2: Ryanodine receptor 1



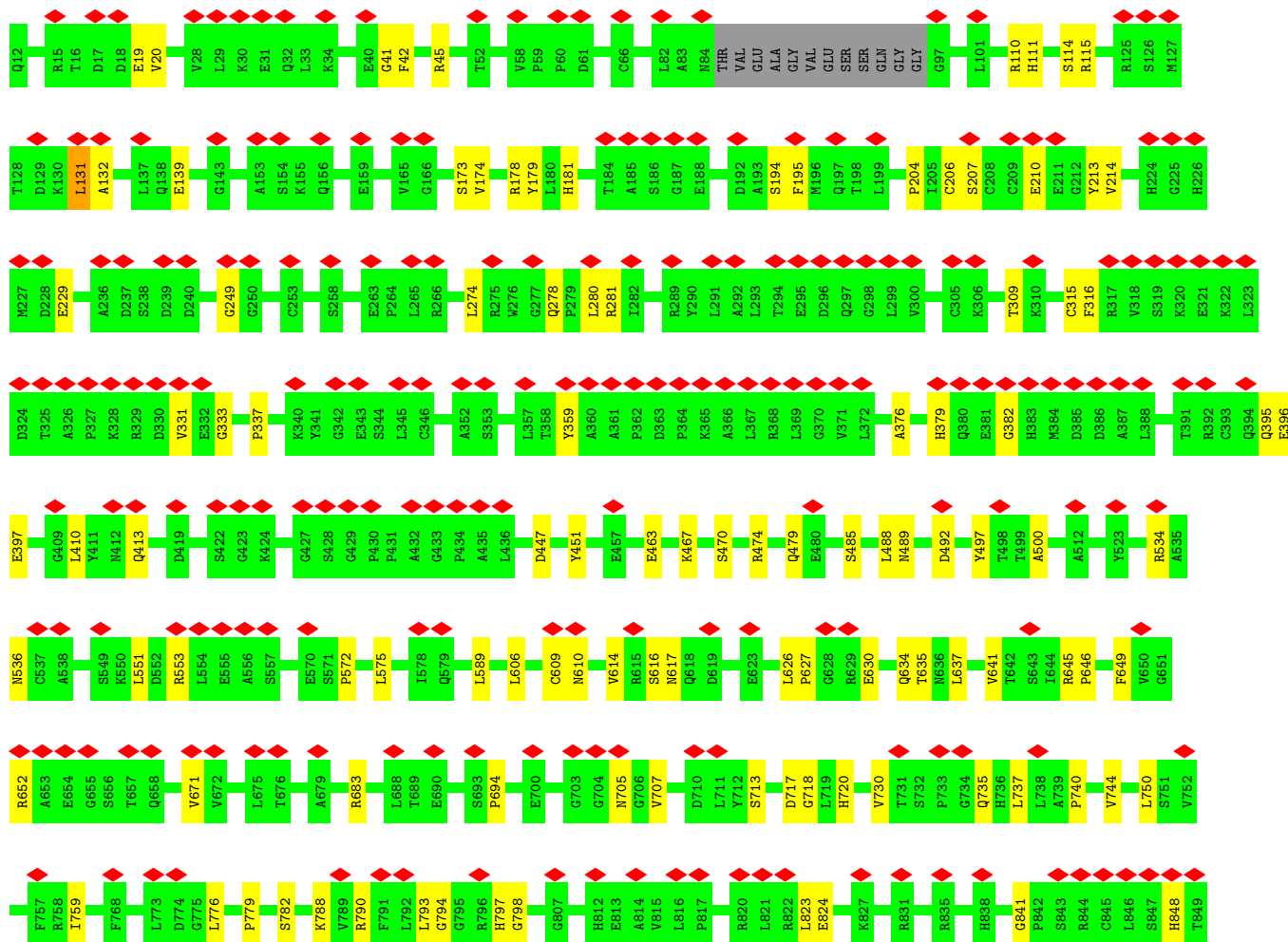
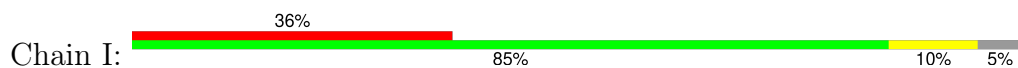




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X4321	E4165	I4088	M4001	K3873	R3762	X3557	X3445	X3163	X3163
X4330	L4166	S4089	K4002	V3874	L3763	X3558	X3449	X3170	X3170
X4338	E4167	K4091	L4003	M3875	Q3766	X3559	X3450	X3171	X3171
X4339	S4169	D4092	L4004	A3876	D3675	X3560	X3451	X3172	X3172
X4340	I4170	F4093	Q4005	D3877	D3676	X3561	X3452	X3173	X3173
X4343	L4171	Q4094	D4022	D3878	L3677	X3562	X3453	X3174	X3174
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X4345	Y4173	A4096	L4031	D3883	G3681	X3564	X3455	X3176	X3176
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SER	K4211	D4127	K4067	S3714	X3589	X3589	X3479	X3207	X3207
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		L4159	D4083	E3747	X3607	X3607	X3495	X3225	X3225
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• Molecule 2: Ryanodine receptor 1



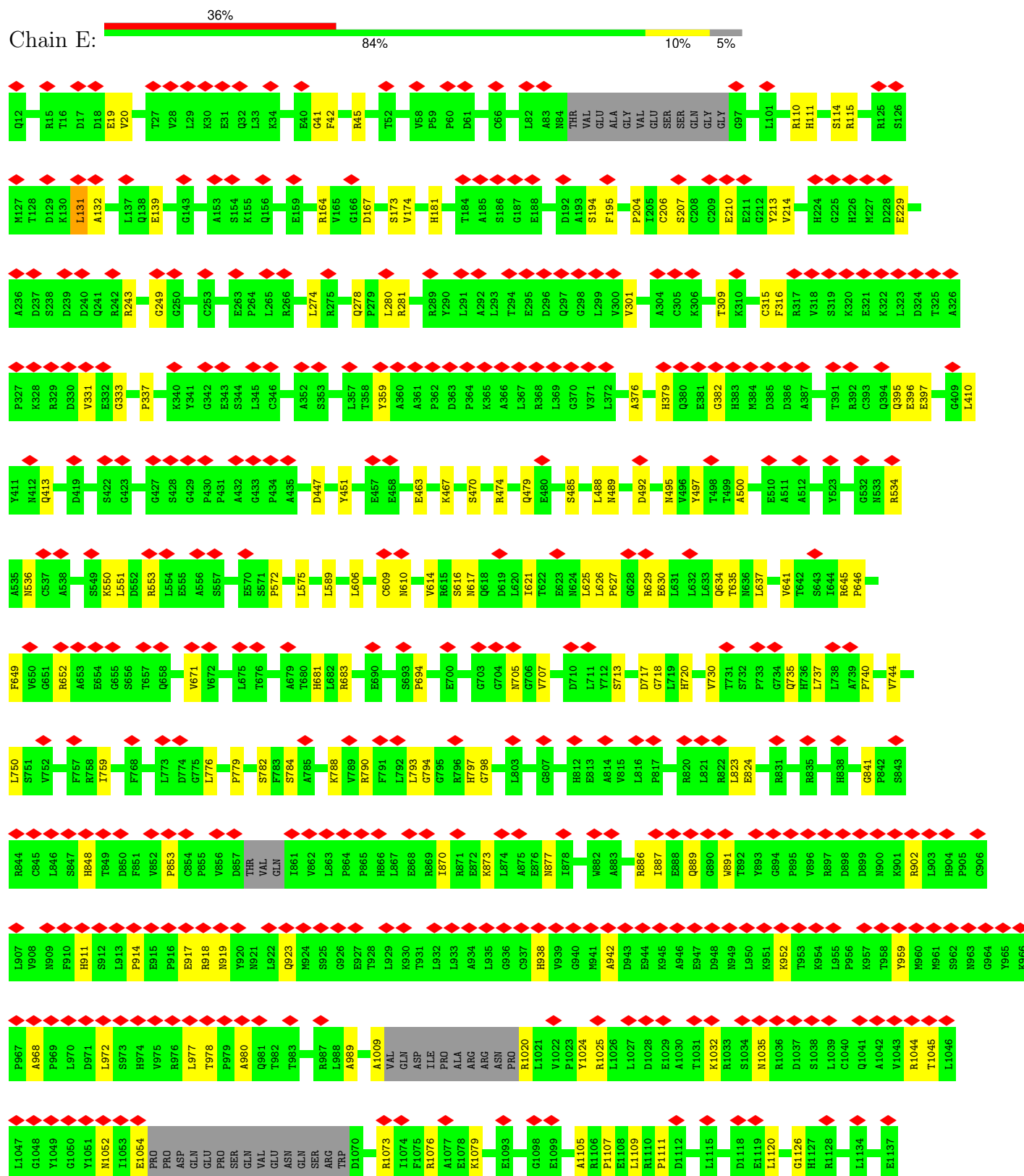
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GLU	LEU	PRO	ALA	GLU	K2089	K2090	Q2107	L2131	R2140	I2144	S2147	E2150	T2167	Q2173	I2185	M2186	N2187	N2188	N2196	Y2318	P2319	D2320	L2321	C2326	G2327	R2330	F2334	F2337	A2338	V2339	F2340	V2341	S2345	V2346	E2347	E2348	V2349	A2350	N2351	V2352	V2353	L2357	C2363																
N2007	H2011	F2012	A2016	D2017	E2018	E2019	D2020	C2021	P2022	L2023	P2024	R2028	H2035	C2042	G2043	I2044	Q2045	L2046	E2047	G2048	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU													
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R3886	L3891	N3896	F3899	G3908	N3909	T3910	T3911	L3923	S3929	D3932	Y3937	S3938	G3939	K3940	D3941	V3942	I3943	Q3946	N3950	V3961	Y3968	I3969	Q3970	Q3971	N3976	Q3977	Q3978	A3981	R3984	L3985	W3986	D3987	F3996	A3997	H3998	M4001	K4002	L4003	A4004	Q4005	D4022																	
R3773	E3777	N3778	V3779	Q3781	S3784	K3787	L3804	L3805	N3809	M3816	L3817	E3825	Q3830	Q3833	L3842	D3843	R3849	Q3850	A3853	E3854	G3855	L3856	G3857	M3858	N3859	N3860	E3861	D3862	G3863	T3864	V3865	I3866	N3867	R3868	A3869	H3869	N3870	G3871	E3872	A3876	D3877	D3878	Q3882	D3883														
B3675	D3676	L3677	A3680	G3681	E3682	Q3683	E3684	E3685	E3686	E3687	E3688	E3689	V3690	E3691	E3692	E3693	R3707	K3713	S3714	K3715	L3716	D3717	M3723	I3728	C3733	H3734	L3735	E3736	E3737	Q3738	Q3739	E3740	N3741	GLY	GLU	ALA	GLU	E3747	E3748	V3749	E3750	V3751	S3752	F3753	E3754	E3759	R3762	Q3766										
X3567	X3568	X3569	X3570	X3571	X3572	X3573	X3574	X3575	X3576	X3577	X3578	X3579	X3580	X3581	X3582	X3583	X3584	X3585	X3586	X3587	X3588	X3589	X3590	X3591	X3592	X3593	X3596	X3597	X3600	X3601	X3604	X3605	X3606	X3607	X3608	X3609	X3610	X3611	X3612	X3613	N3643	L3644	K3658	W3661	L3662	L3663	T3664	E3665	D3666	H3667	S3668	M3673	L3674					
X3464	X3467	X3468	X3511	X3512	X3513	X3514	X3515	X3516	X3517	X3518	X3519	X3520	X3521	X3522	X3523	X3524	X3525	X3526	X3527	X3528	X3529	X3530	X3531	X3532	X3533	X3534	X3535	X3536	X3537	X3538	X3539	X3540	X3541	X3542	X3543	X3544	X3545	X3546	X3547	X3548	X3549	X3550	X3551	X3552	X3553	X3554	X3555	X3556	X3557	X3558	X3559	X3560	X3561	X3562	X3563	X3564	X3565	X3566

• Molecule 2: Ryanodine receptor 1

Chain E:





L3716	D3717	L3728	C3733	H3734	L3735	E3736	E3737	G3738	G3739	E3740	N3741	GLY	GLU	ALA	GLU	E3747	E3748	V3749	E3750	V3751	S3752	F3753	E3754	E3759	E3760	V3761	T3762	H3763	E3764	W3766	Q3766	R3773	E3777	M3778	V3779	L3780	Q3781	S3784	K3787	I3804	L3805	N3809	M3815	L3817	E3825	Q3830																													
X3592	X3593	X3596	X3597	X3600	X3601	X3604	X3605	X3606	X3607	X3608	X3609	X3610	X3611	X3612	X3613	N3643	L3644	N3643	L3644	N3658	Y3661	I3662	L3663	T3664	E3665	S3667	H3667	S3668	F3669	I3674	D3675	L3676	L3677	A3680	Q3681	E3682	Q3683	E3684	E3685	E3686	E3687	E3688	E3689	V3690	E3691	E3692	K3693	R3707	K3713	S3714	K3715																								
X3529	X3530	X3531	X3532	X3533	X3534	X3535	X3536	X3537	X3538	X3539	X3540	X3541	X3542	X3543	X3544	X3545	X3546	X3547	X3548	X3549	X3550	X3551	X3552	X3553	X3554	X3555	X3556	X3557	X3558	X3559	X3560	X3561	X3562	X3563	X3564	X3565	X3566	X3567	X3568	X3569	X3570		X3574	X3577	X3578	X3579	X3580	X3581	X3582	X3583	X3584	X3585	X3586	X3587	X3588	X3589	X3590	X3591																	
X3417	X3418	X3419	X3420	X3421	X3424	X3425	X3426	X3427	X3428	X3431	X3432	X3433	X3434	X3435	X3436	X3439	X3440	X3441	X3442	X3443	X3446	X3449	X3450	X3451	X3452	X3453	X3454	X3457	X3458	X3463	X3464	X3467	X3468	X3511	X3512	X3513	X3514	X3515	X3516	X3517	X3518	X3519	X3520	X3521	X3522	X3523	X3524	X3525	X3526	X3527	X3528																								
X3292	X3293	X3294	X3295	X3296	X3299	X3300	X3301	X3302	X3303	X3304	X3305	X3306	X3309	X3310	X3311	X3312	X3313	X3314	X3315	X3316	X3317	X3318	X3319	X3320	X3321	X3322	X3325	X3326	X3327	X3328	X3329	X3330	X3331	X3332	X3333	X3334	X3335	X3336	X3337	X3338	X3339	X3340	X3341	X3342	X3345	X3346	X3347	X3348	X3349	X3350	X3351	X3352	X3353	X3354	X3355																				
X3220	X3221	X3224	X3225	X3226	X3227	X3228	X3231	X3232	X3233	X3234	X3235	X3236	X3241	X3242	X3243	X3244	X3245	X3246	X3247	X3248	X3249	X3250	X3251	X3252	X3253	X3254	X3261	X3262	X3263	X3264	X3265	X3266	X3267	X3268	X3269	X3270	X3271	X3272	X3273	X3274	X3275	X3276	X3277	X3278	X3279	X3280	X3281	X3282	X3283	X3284	X3285	X3286	X3287	X3288	X3289	X3290	X3291																		
X3144	X3145	X3146	X3147	X3148	X3151	X3155	X3158	X3159	X3160	X3161	X3162	X3163	X3170	X3171	X3172	X3173	X3174	X3175	X3176	X3177	X3178	X3179	X3180	X3181	X3182	X3185	X3190	X3191	X3192	X3193	X3194	X3195	X3196	X3197	X3200	X3201	X3204	X3207	X3208	X3209	X3210	X3211	X3212	X3213	X3214	X3215	X3216	X3217	X3218	X3219																									
X3002	X3003	X3004	X3005	X3006	X3007	X3008	X3013	X3014	X3015	X3016	X3019	X3020	X3021	X3022	X3023	X3024	X3025	X3029	X3032	X3033	X3034	X3035	X3036	X3037	X3038	X3039	X3040	X3043	X3044	X3045	X3046	X3047	X3048	X3049	X3050	X3051	X3055	X3056	X3057	X3058	X3059	X3062	X3063	X3134	X3135	X3136	X3137	X3138	X3139	X3140	X3141																								
A2917	R2918	D2919	R2920	E2921	K2922	A2923	Q2924	E2925	L2926	L2927	K2928	F2929	L2930	Q2931	M2932	I2933	Q2934	Y2935	A2936	V2937	T2938	R2939	K2942	K2943	X2944	K2945	K2946	K2947	K2948	G2949	K2950	K2952	K2953	K2954	K2955	K2956	K2957	K2958	K2959	K2963	K2964	K2965	K2966	K2967	K2968	K2969	K2970	K2971	K2972	K2973	K2974	K2975	K2976	K2977	K2978	K2979	K2980	K2981	K2982	K2983	K2984	K2985	K2986	K2987	K2988	K2989	K2990	K2991	K2992	K2993	K2994	K2995	K2996	K2997	K2998
P2857	Q2858	P2859	P2860	D2861	L2862	S2863	Q2864	V2865	T2866	L2867	S2868	R2869	E2870	L2871	Q2872	A2873	M2874	A2875	E2876	Q2877	L2878	A2879	E2880	N2881	W2882	H2883	N2884	T2885	W2886	G2887	R2888	K2889	K2890	K2891	Q2892	E2893	L2894	E2895	A2896	K2897	Q2898	G2899	Q2900	T2901	H2902	P2903	GLN	L2904	L2905	V2906	P2907	V2908	D2909	T2910	L2911	T2912	A2913	K2914	E2915	K2916															
F2797	S2798	E2799	K2800	D2801	K2802	E2803	L2804	I2805	R2806	W2807	P2808	L2809	K2810	E2811	S2812	L2813	K2814	A2815	M2816	L2817	A2818	W2819	E2820	W2821	L2822	L2823	E2824	K2825	A2826	R2827	E2828	G2829	GLU	GLU	ARG	THR	GLU	LYS	LYS	THR	ARG	LYS	ILE	SER	GLN	THR	ALA	GLN	THR	TTR	ASP	PRO	ARG	GLU	GLY	Y2855	N2856																		
P2737	R2738	E2739	V2740	E2741	T2742	L2743	H2744	V2745	L2746	W2807	P2808	E2749	K2750	L2751	D2752	S2753	F2754	I2755	N2756	K2757	L2817	F2758	E2759	E2760	Y2761	T2762	H2763	E2764	W2766	A2767	F2768	D2769	K2770	I2771	Q2772	H2773	N2774	W2775	S2776	Y2777	Q2778	E2779	H2780	V2781	D2782	E2783	E2784	L2785	K2786	T2787	H2788	P2789	M2790	L2791	R2792	F2793	Y2794	K2795	T2796																



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	0.133	Depositor
Minimum map value	-0.070	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: ZN, CA

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.30	0/834	0.53	0/1123
1	F	0.30	0/834	0.53	0/1123
1	H	0.30	0/834	0.53	0/1123
1	J	0.30	0/834	0.53	0/1123
2	B	0.30	0/25428	0.54	6/34534 (0.0%)
2	E	0.30	0/25428	0.54	6/34534 (0.0%)
2	G	0.30	0/25428	0.54	6/34534 (0.0%)
2	I	0.30	0/25428	0.54	6/34534 (0.0%)
All	All	0.30	0/105048	0.54	24/142628 (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
2	B	0	11
2	E	0	11
2	G	0	11
2	I	0	11
All	All	0	44

There are no bond length outliers.

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	131	LEU	CA-CB-CG	7.94	133.56	115.30
2	I	131	LEU	CA-CB-CG	7.93	133.53	115.30
2	B	131	LEU	CA-CB-CG	7.92	133.53	115.30
2	G	131	LEU	CA-CB-CG	7.91	133.49	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	1676	LEU	CA-CB-CG	6.62	130.52	115.30

There are no chirality outliers.

5 of 44 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	139	GLU	Peptide
2	B	1676	LEU	Peptide
2	B	1795	PRO	Peptide
2	B	1828	ASP	Peptide
2	B	694	PRO	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	6	0
1	F	818	0	824	10	0
1	H	818	0	824	9	0
1	J	818	0	824	9	0
2	B	29499	0	24750	264	0
2	E	29499	0	24750	264	0
2	G	29499	0	24750	256	0
2	I	29499	0	24750	256	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	121276	0	102296	1050	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 1050 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:4968:PHE:HE2	2:B:4978:HIS:CE1	1.29	1.49
2:I:4968:PHE:HE2	2:I:4978:HIS:CE1	1.29	1.48
2:E:4968:PHE:HE2	2:E:4978:HIS:CE1	1.29	1.48
2:G:4968:PHE:HE2	2:G:4978:HIS:CE1	1.29	1.48
2:B:4968:PHE:CE2	2:B:4978:HIS:CE1	2.09	1.41

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	105/108 (97%)	93 (89%)	12 (11%)	0	100	100
1	F	105/108 (97%)	93 (89%)	12 (11%)	0	100	100
1	H	105/108 (97%)	93 (89%)	12 (11%)	0	100	100
1	J	105/108 (97%)	93 (89%)	12 (11%)	0	100	100
2	B	3235/4416 (73%)	2892 (89%)	337 (10%)	6 (0%)	44	78
2	E	3235/4416 (73%)	2894 (90%)	335 (10%)	6 (0%)	44	78
2	G	3235/4416 (73%)	2895 (90%)	334 (10%)	6 (0%)	44	78
2	I	3235/4416 (73%)	2891 (89%)	338 (10%)	6 (0%)	44	78
All	All	13360/18096 (74%)	11944 (89%)	1392 (10%)	24 (0%)	45	78

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	1708	ARG
2	G	1708	ARG
2	I	1708	ARG
2	E	1708	ARG

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Mol	Chain	Res	Type
2	E	4985	LEU

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	88/89 (99%)	88 (100%)	0	100	100
1	F	88/89 (99%)	88 (100%)	0	100	100
1	H	88/89 (99%)	88 (100%)	0	100	100
1	J	88/89 (99%)	88 (100%)	0	100	100
2	B	2493/3022 (82%)	2474 (99%)	19 (1%)	79	84
2	E	2493/3022 (82%)	2474 (99%)	19 (1%)	79	84
2	G	2493/3022 (82%)	2474 (99%)	19 (1%)	79	84
2	I	2493/3022 (82%)	2474 (99%)	19 (1%)	79	84
All	All	10324/12444 (83%)	10248 (99%)	76 (1%)	80	87

5 of 76 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	131	LEU
2	E	4131	ARG
2	E	553	ARG
2	E	3663	LEU
2	E	4983	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 148 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	113	HIS
2	E	4120	ASN
2	E	413	GLN
2	E	2041	HIS

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Mol	Chain	Res	Type
2	G	797	HIS

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	14
2	G	14

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Mol	Chain	Number of breaks
2	I	14
2	E	14

The worst 5 of 56 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	4345:UNK	C	4540:PHE	N	73.85
1	G	4345:UNK	C	4540:PHE	N	73.85
1	I	4345:UNK	C	4540:PHE	N	73.85
1	E	4345:UNK	C	4540:PHE	N	73.85
1	B	3613:UNK	C	3639:THR	N	45.57

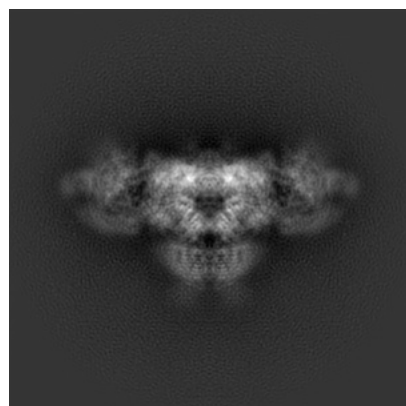
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8389. These allow visual inspection of the internal detail of the map and identification of artifacts.

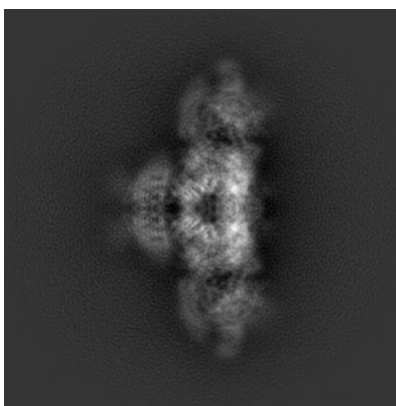
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

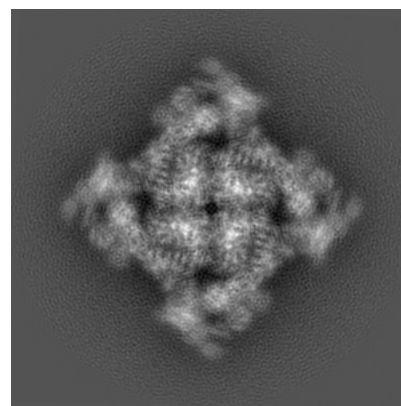
6.1.1 Primary map



X

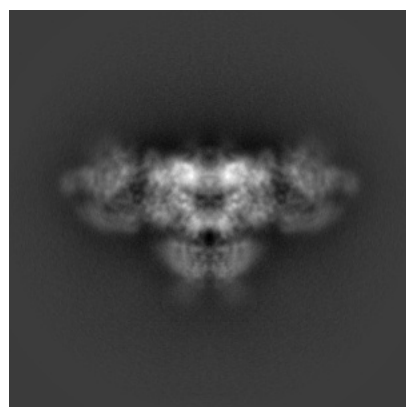


Y

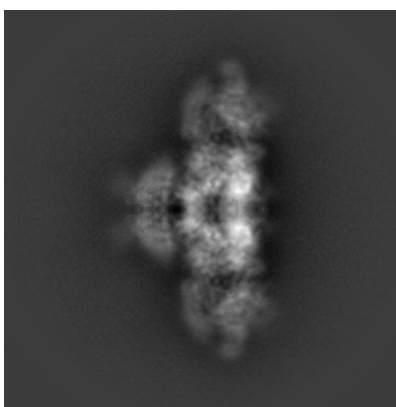


Z

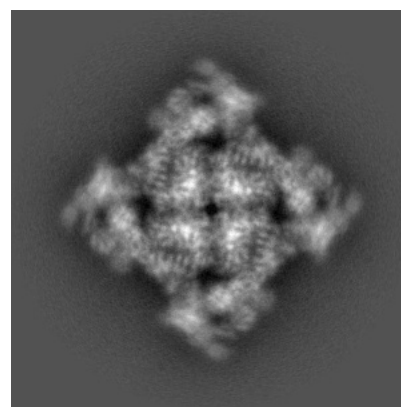
6.1.2 Raw map



X



Y

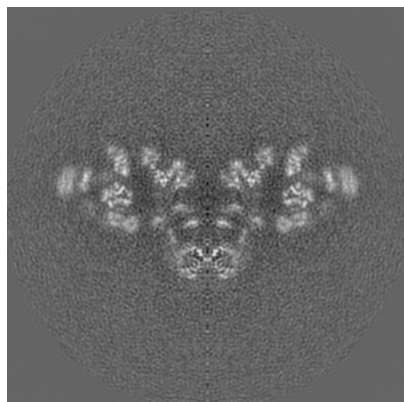


Z

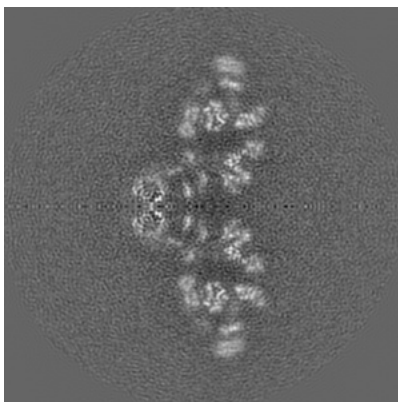
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

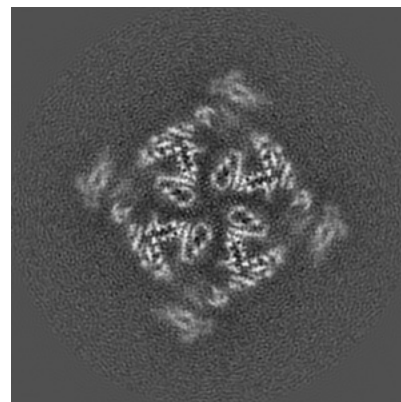
6.2.1 Primary map



X Index: 200

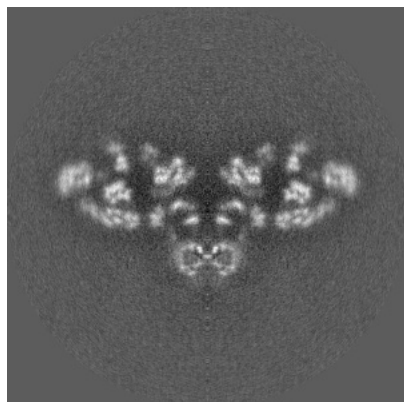


Y Index: 200

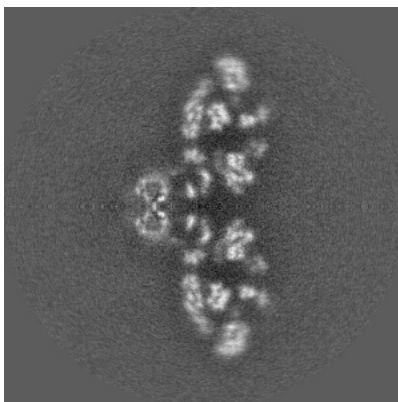


Z Index: 200

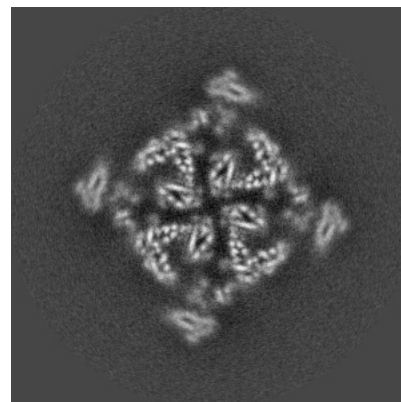
6.2.2 Raw map



X Index: 200



Y Index: 200

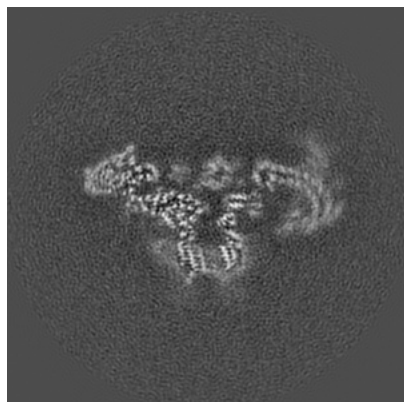


Z Index: 200

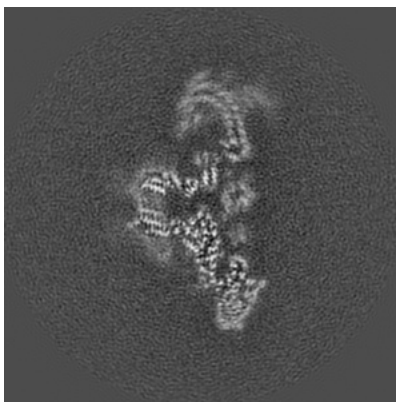
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

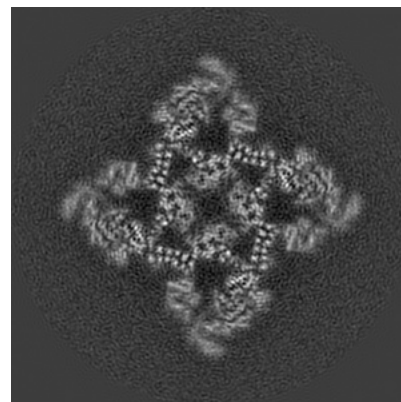
6.3.1 Primary map



X Index: 225

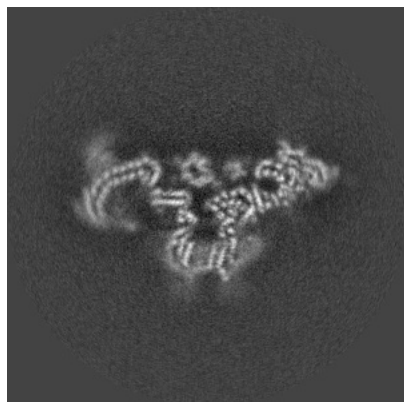


Y Index: 175

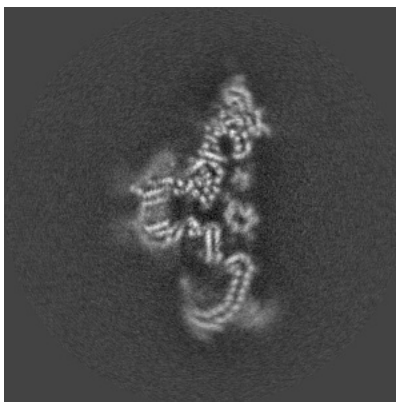


Z Index: 226

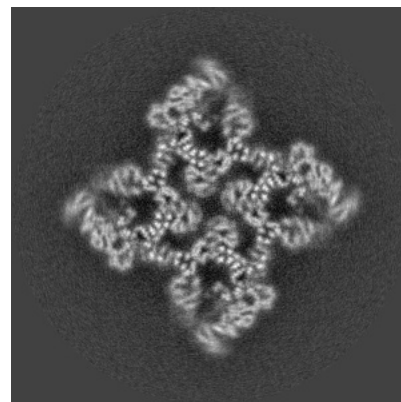
6.3.2 Raw map



X Index: 175



Y Index: 225

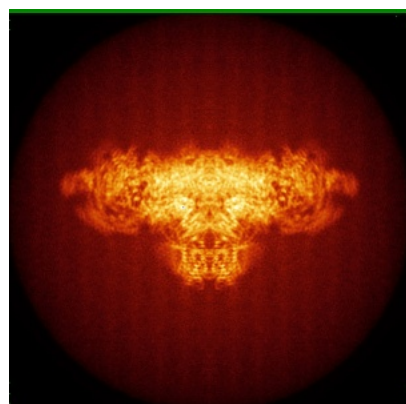


Z Index: 234

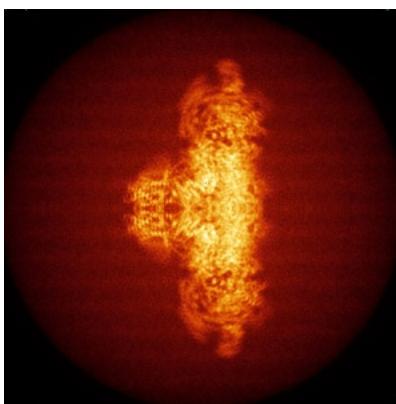
The images above show the largest variance slices of the map in three orthogonal directions.

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

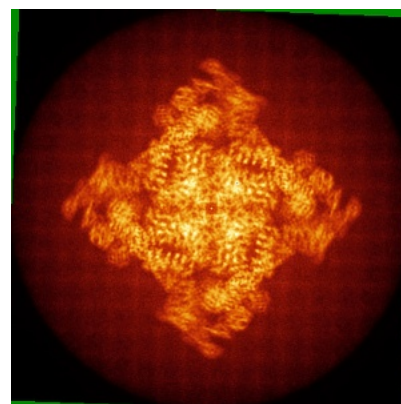
6.4.1 Primary map



X

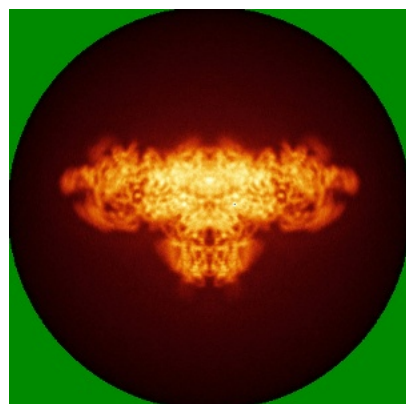


Y

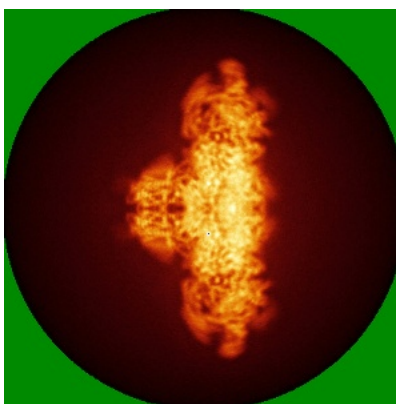


Z

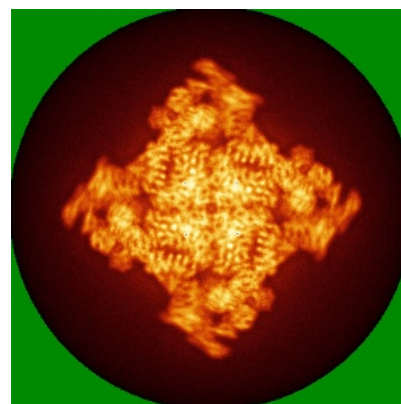
6.4.2 Raw map



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.

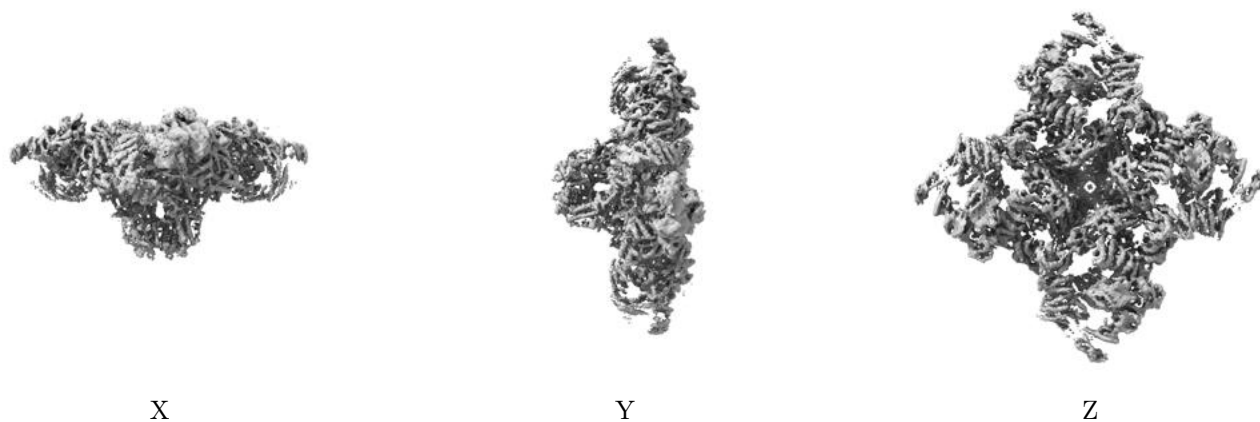
6.5 Orthogonal surface views [i](#)

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.

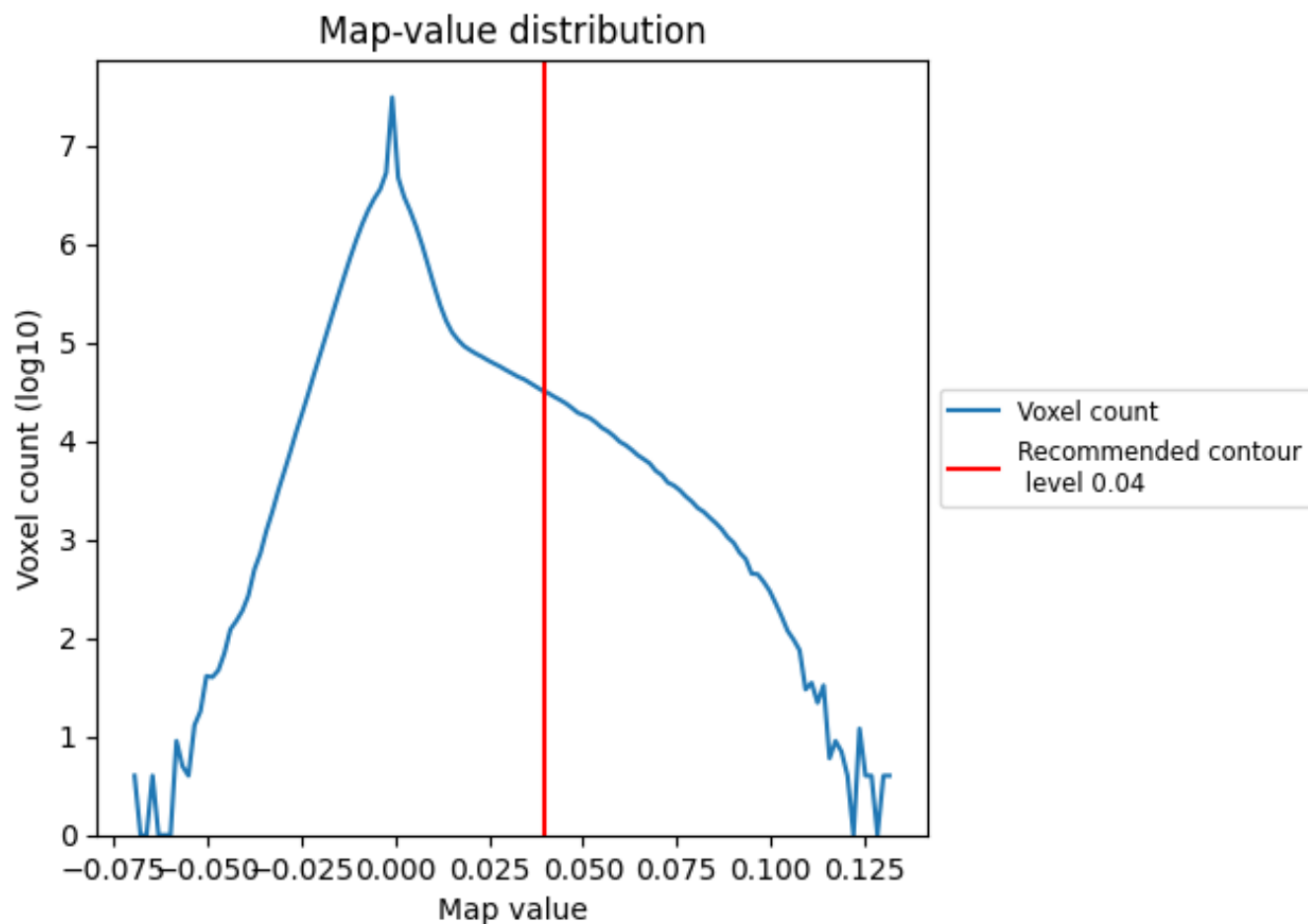
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

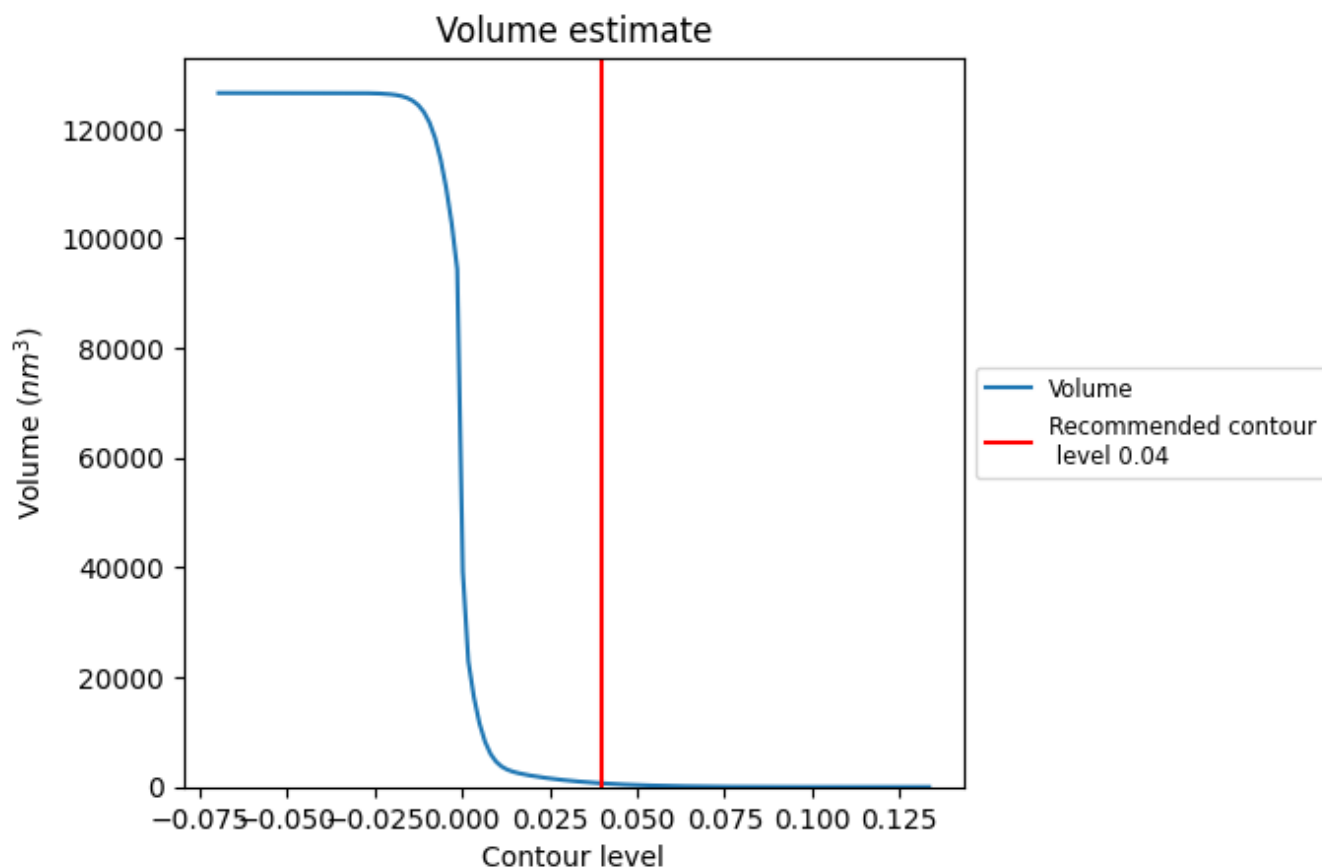
This section contains the results of statistical analysis of the map.

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.

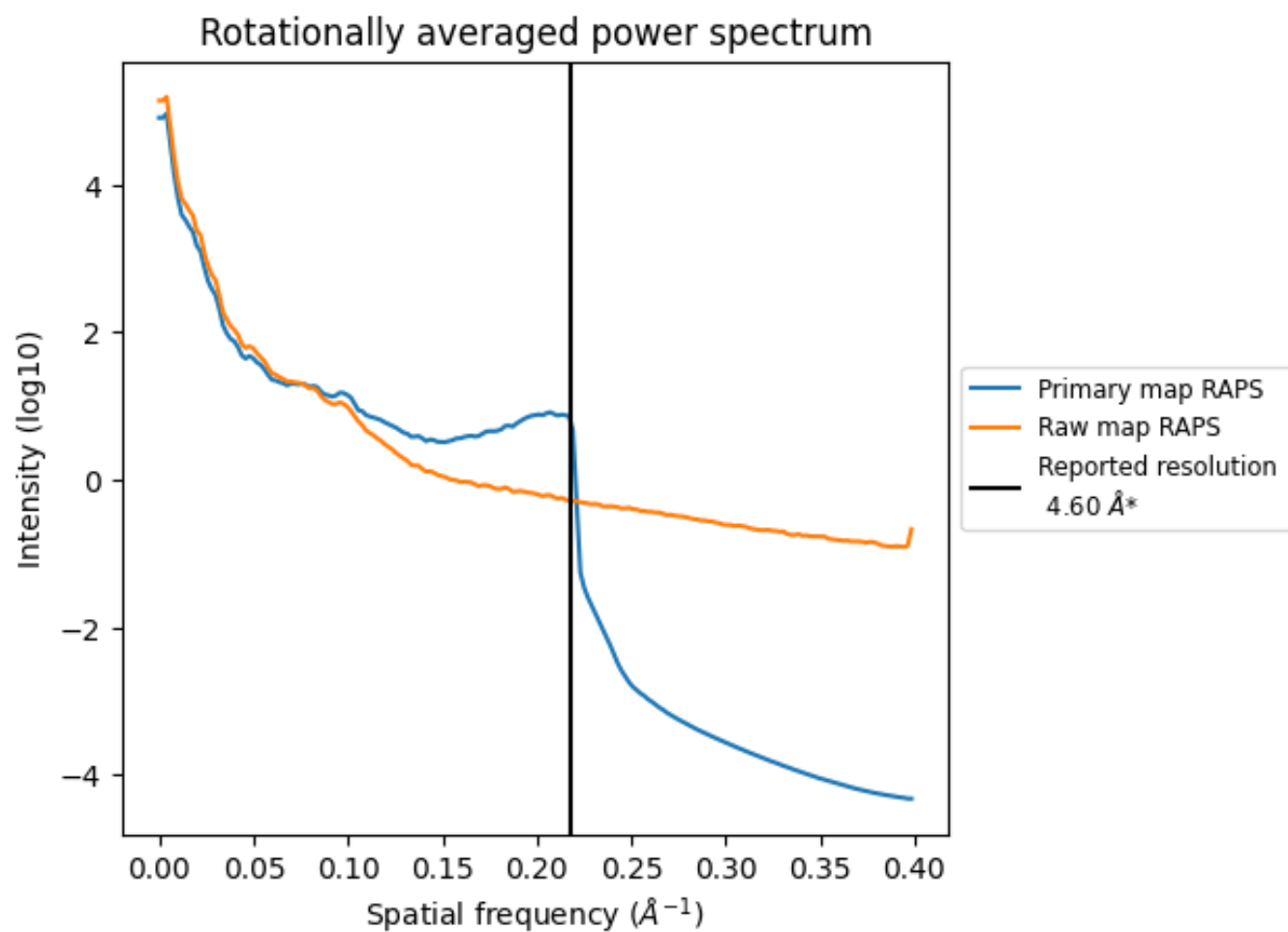
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 666 nm³; this corresponds to an approximate mass of 601 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 ⓘ

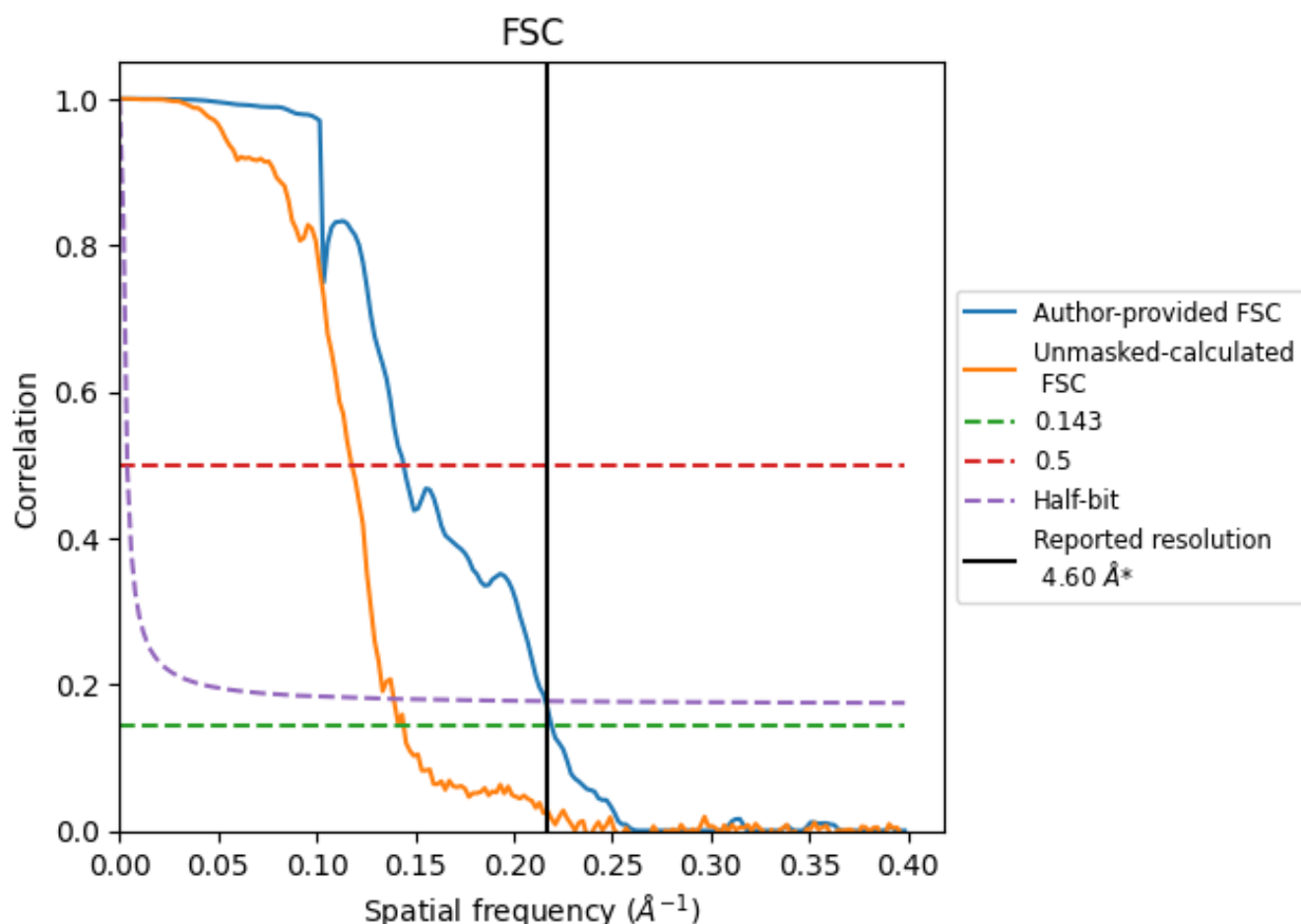


*Reported resolution corresponds to spatial frequency of 0.217 Å⁻¹

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 0.217 Å⁻¹

8.2 Resolution estimates [i](#)

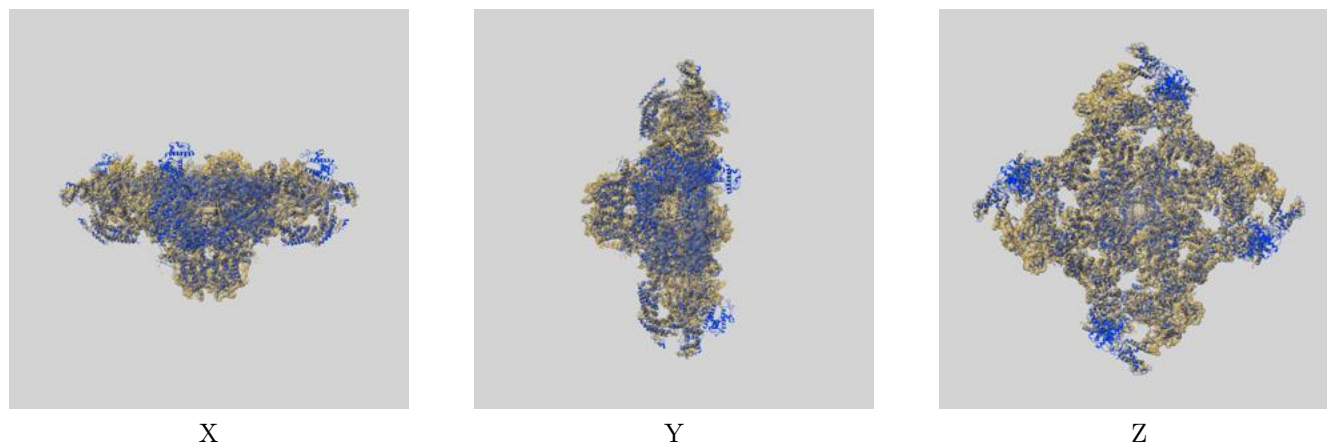
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.60	-	-
Author-provided FSC curve	4.56	6.94	4.63
Unmasked-calculated*	6.93	8.49	7.18

*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 6.93 differs from the reported value 4.6 by more than 10 %

9 Map-model fit [i](#)

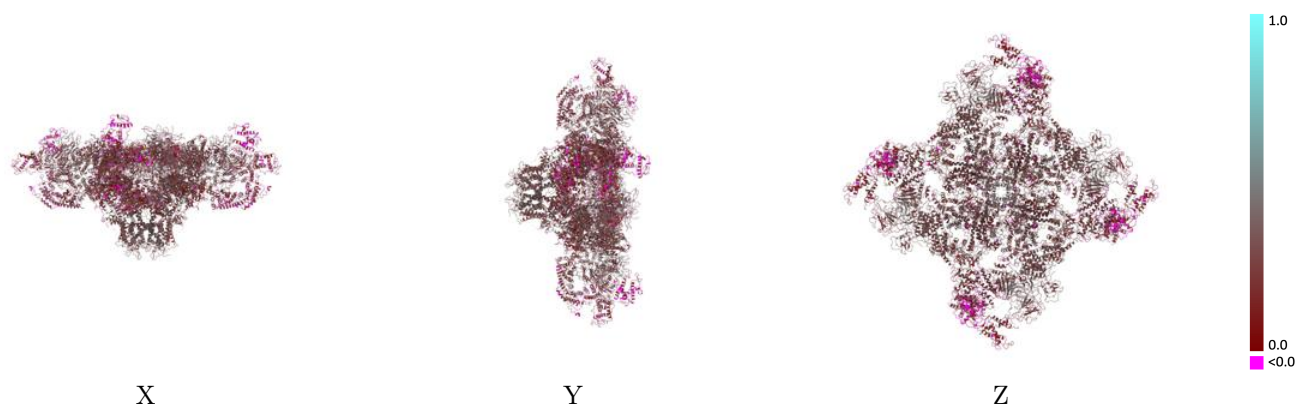
This section contains information regarding the fit between EMDB map EMD-8389 and PDB model 5TAY. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)



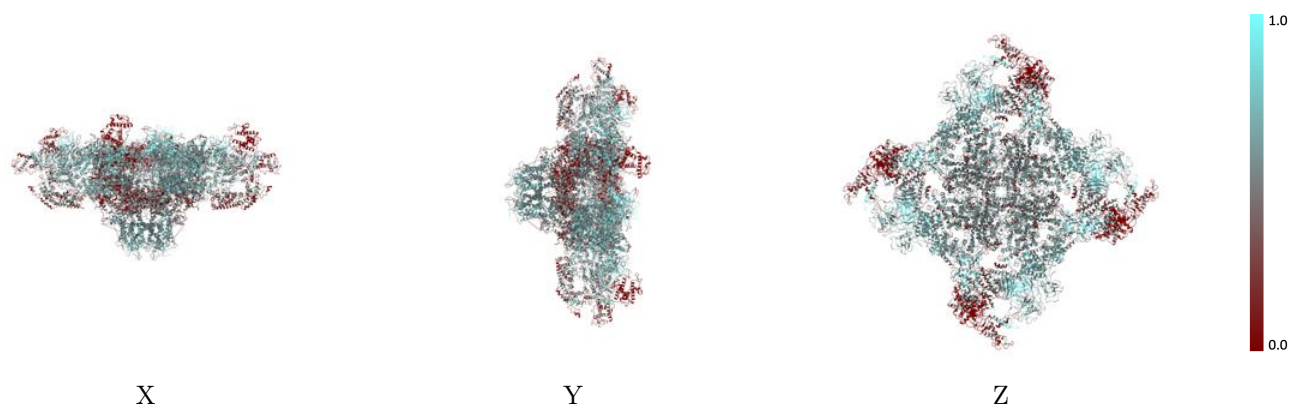
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



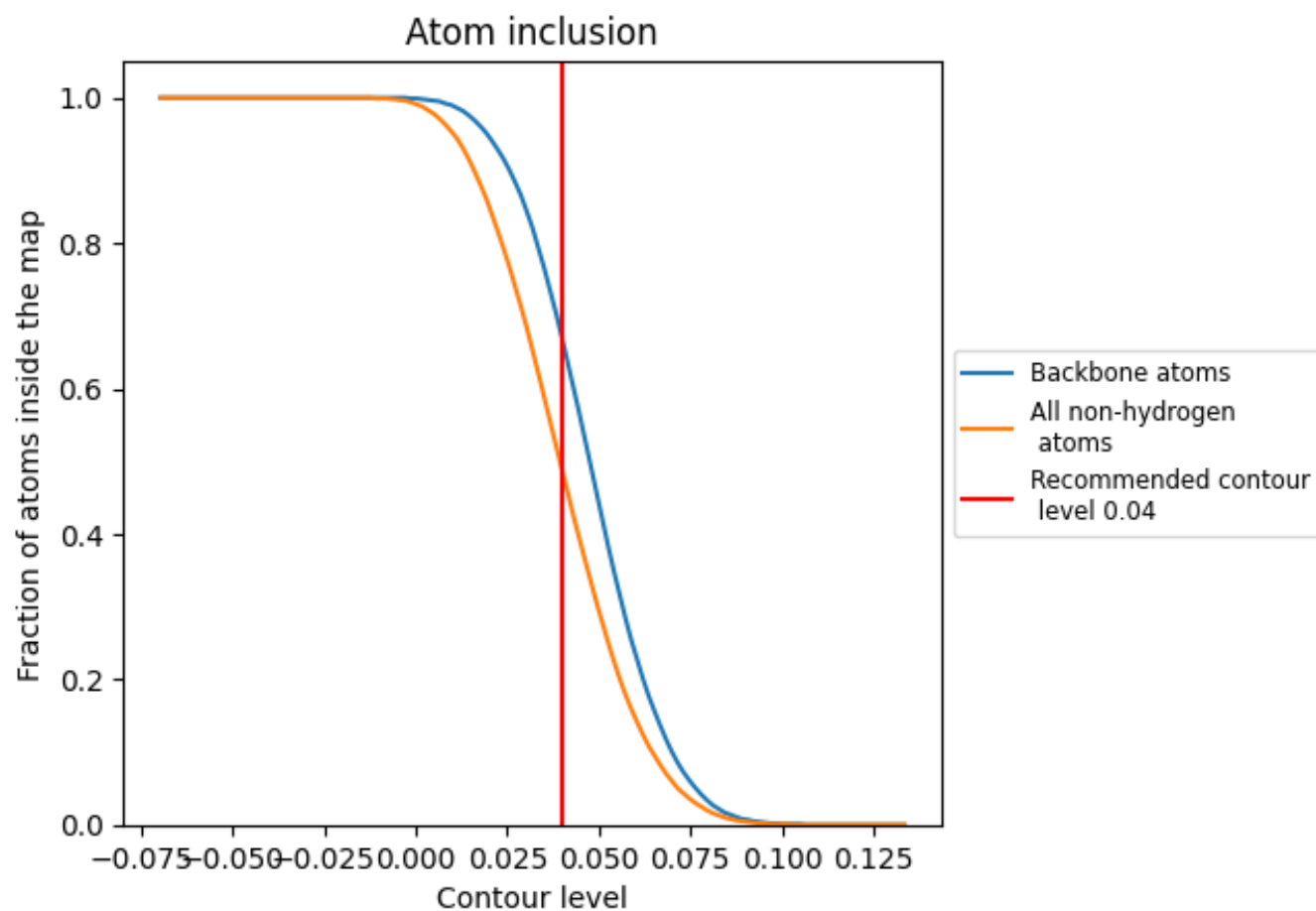
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 49% 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	<div></div> 0.4870	<div></div> 0.2640
A	<div></div> 0.5660	<div></div> 0.3270
B	<div></div> 0.4910	<div></div> 0.2670
E	<div></div> 0.4800	<div></div> 0.2570
F	<div></div> 0.5670	<div></div> 0.3310
G	<div></div> 0.4890	<div></div> 0.2650
H	<div></div> 0.5670	<div></div> 0.3300
I	<div></div> 0.4810	<div></div> 0.2590
J	<div></div> 0.5650	<div></div> 0.3280

1.0

0.0

<0.0