



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 11:49 AM UTC

PDB ID : 5GKY / pdb_00005gky
EMDB ID : EMD-9518
Title : Structure of RyR1 in a closed state (C1 conformer)
Authors : Bai, X.C.; Yan, Z.; Wu, J.P.; Yan, N.
Deposited on : 2016-07-07
Resolution : 3.80 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

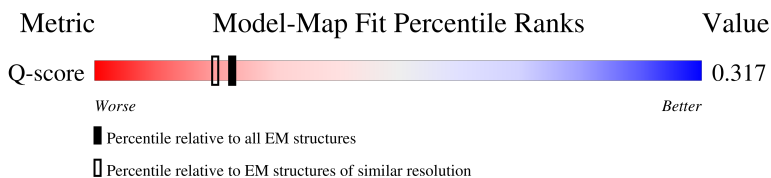
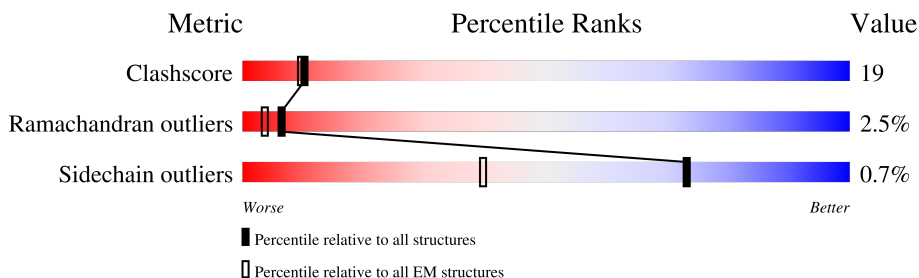
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10198 (3.30 - 4.30)

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

Mol	Chain	Length	Quality of chain
1	A	5037	
1	C	5037	
1	E	5037	
1	G	5037	

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Mol	Chain	Length	Quality of chain
2	B	108	16% 56% 43%
2	D	108	17% 56% 43%
2	F	108	17% 56% 43%
2	H	108	16% 57% 42%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 111036 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 Ryanodine receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3660	Total	C	N	O	S	1	0
			26926	17112	4683	4974	157		
1	C	3660	Total	C	N	O	S	1	0
			26926	17112	4683	4974	157		
1	E	3660	Total	C	N	O	S	1	0
			26926	17112	4683	4974	157		
1	G	3660	Total	C	N	O	S	1	0
			26926	17112	4683	4974	157		

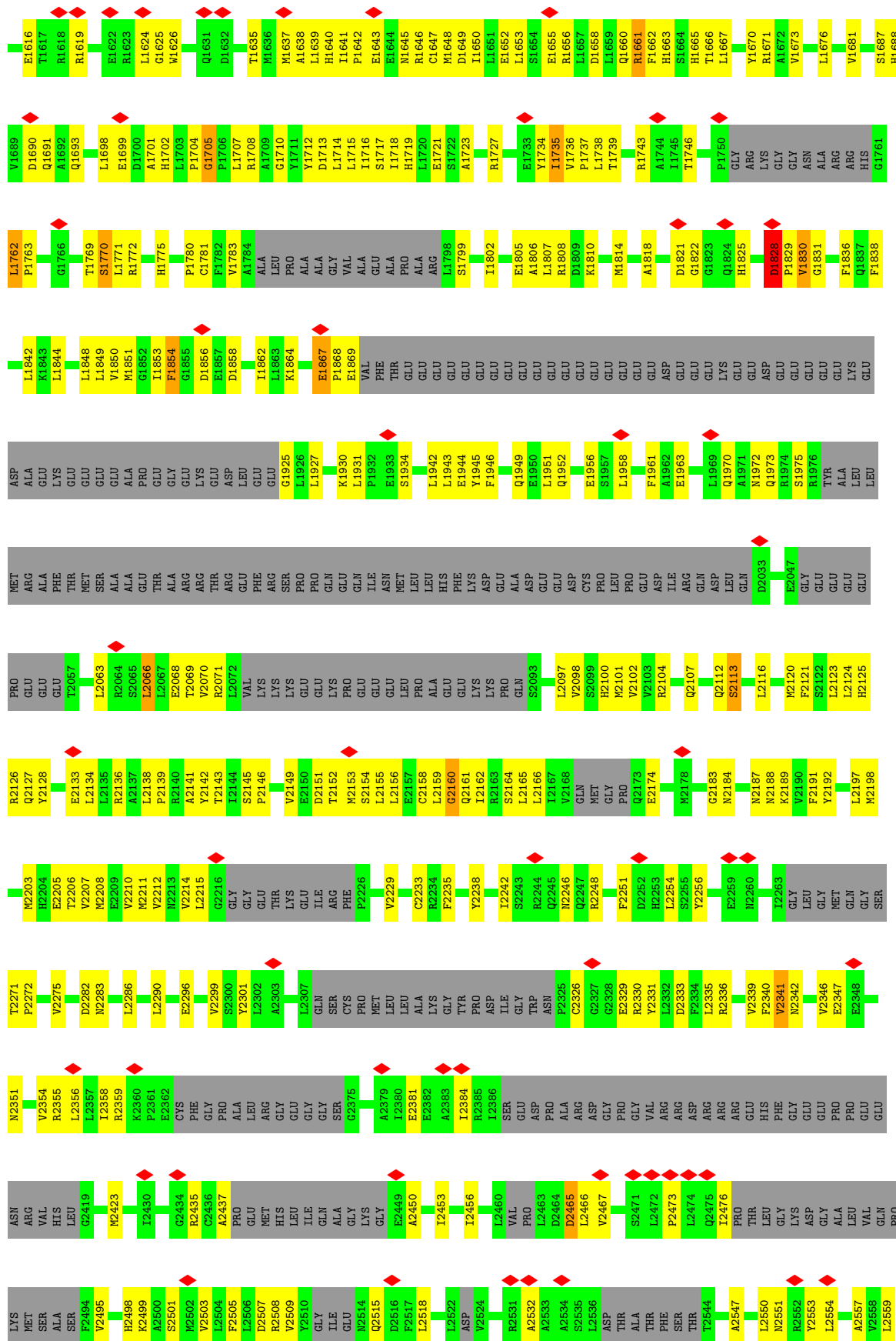
- Molecule 2 is a protein called Peptidyl-prolyl cis-trans isomerase FKBP1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	107	Total	C	N	O	S	0	0
			832	527	146	155	4		
2	D	107	Total	C	N	O	S	0	0
			832	527	146	155	4		
2	F	107	Total	C	N	O	S	0	0
			832	527	146	155	4		
2	H	107	Total	C	N	O	S	0	0
			832	527	146	155	4		

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

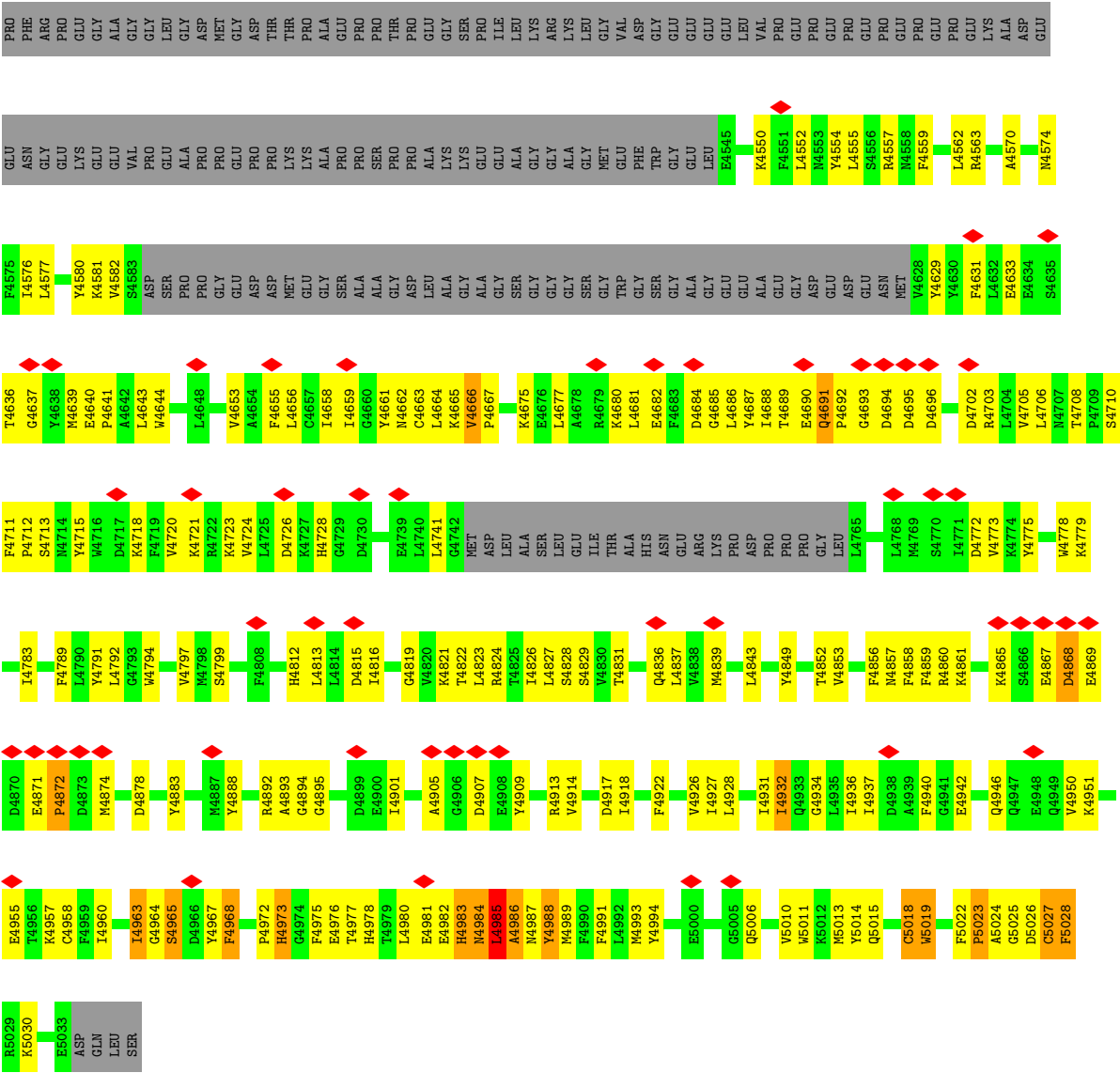
Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	Zn	0
			1	1	
3	C	1	Total	Zn	0
			1	1	
3	E	1	Total	Zn	0
			1	1	
3	G	1	Total	Zn	0
			1	1	



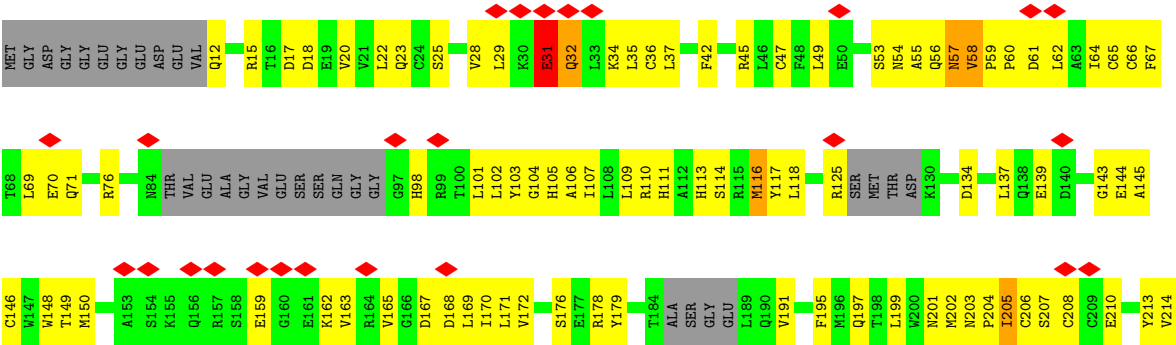


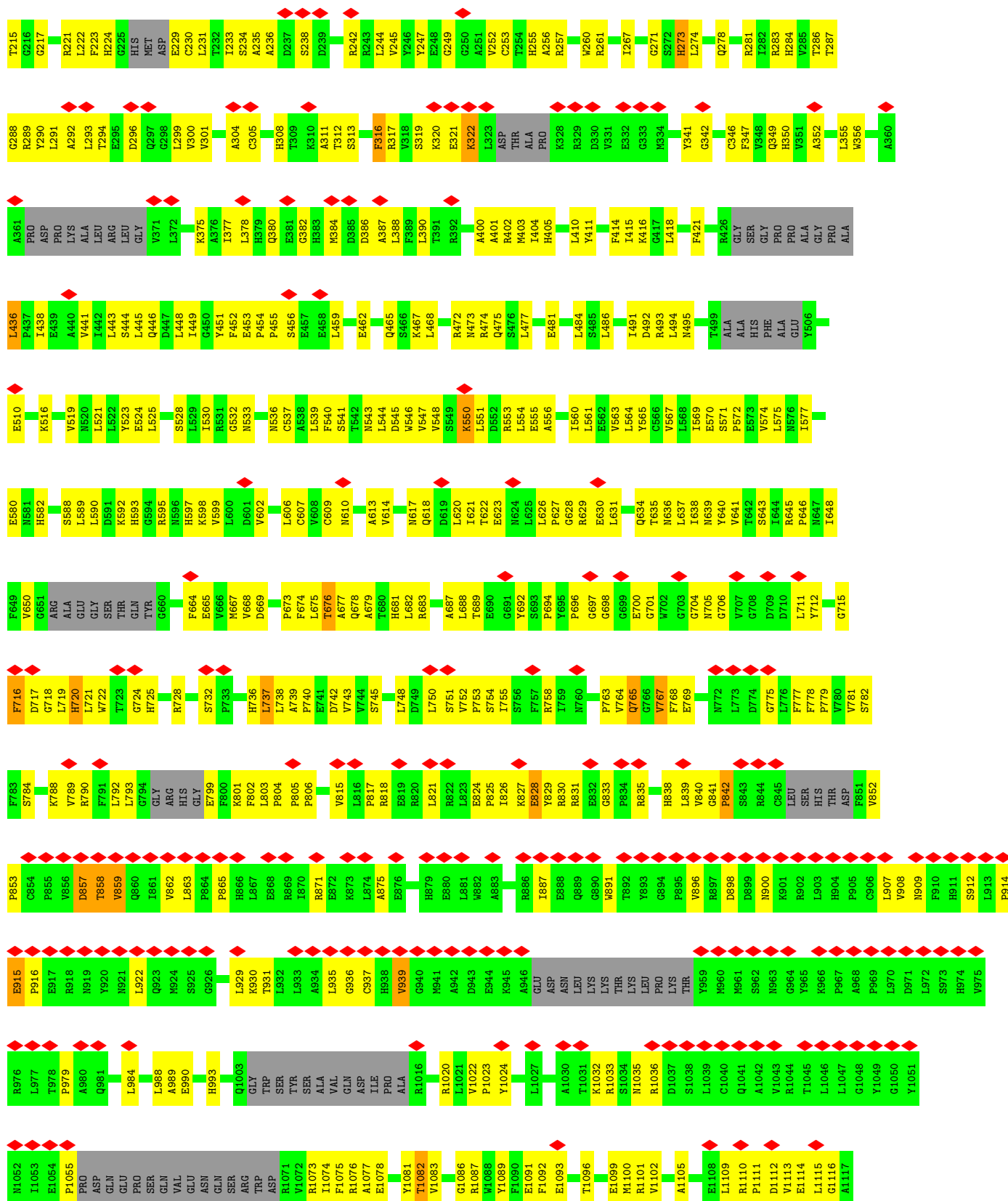






• Molecule 1: Ryanodine receptor 1



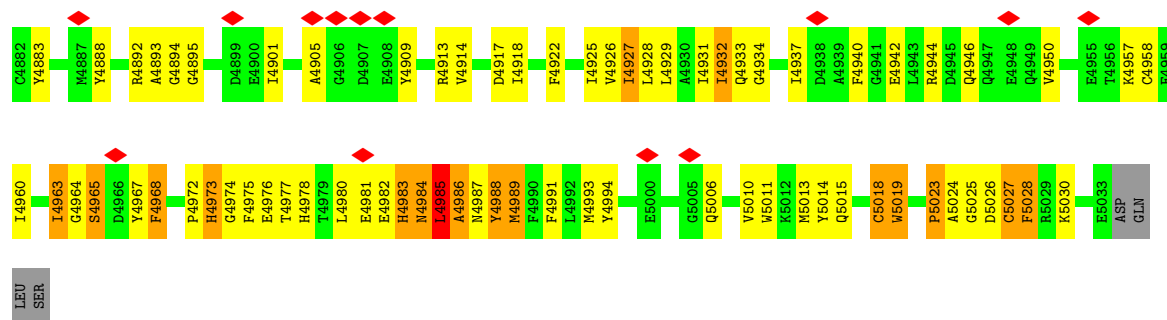




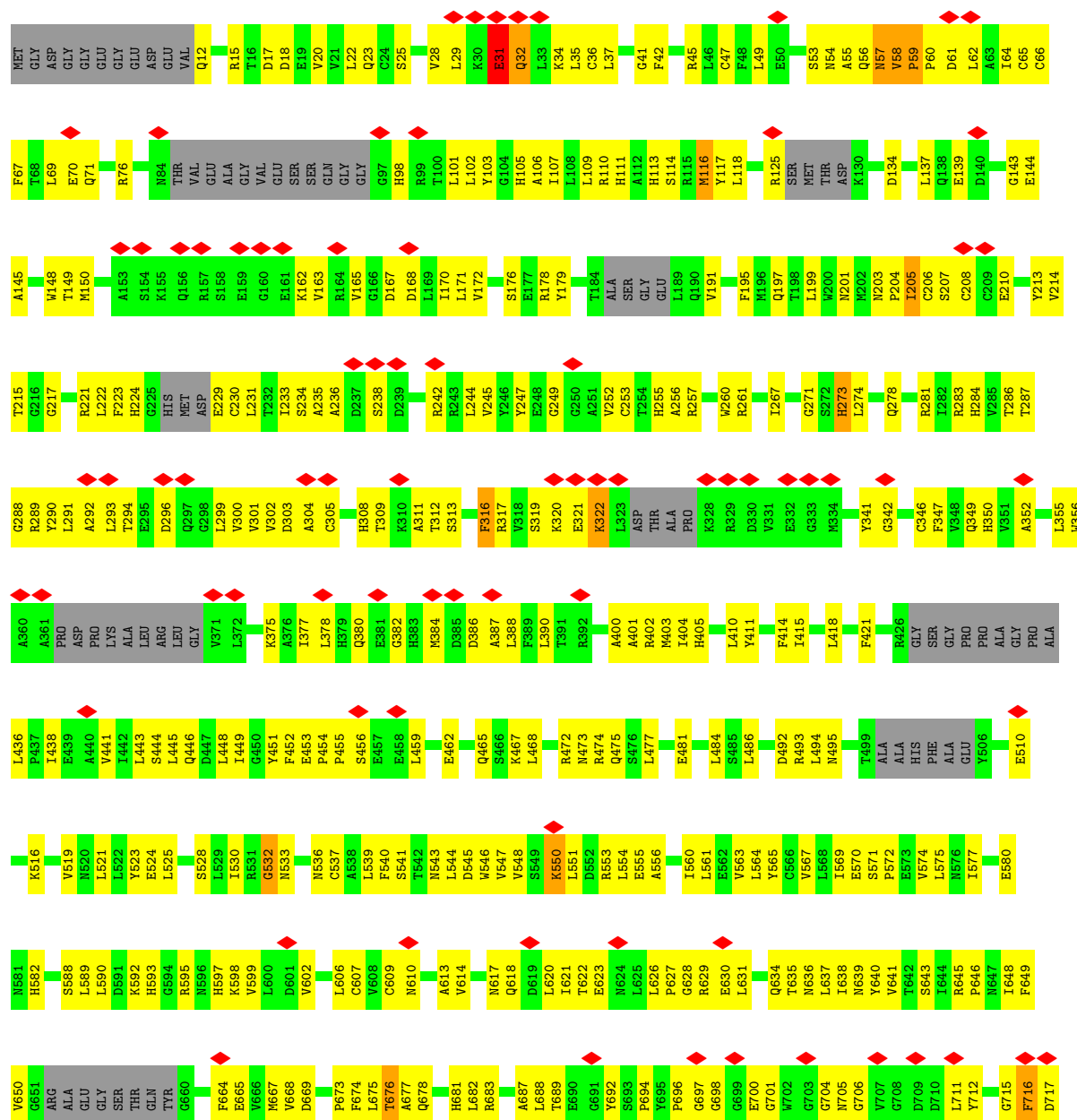
L2063	R2064	S2065	L2066	L2067	E2068	T2069	R2070	R2071	VAL	LYS	LYS	GLU	GLU	LYS	PRO	GLU	GLU	LEU	PRO	ALA	GLU	LYS	LYS	PRO	GLN	S2093	L2094	L2097	V2098	S2099	R2100	R2101	V2102	V2103	R2104	Q2107	S2113	L2116	N2120	F2121	S2122	L2123	L2124	R2125	R2126	Q2127	V2128	E2133	L2134									
L2135	R2136	A2137	L2138	P2139	R2140	A2141	Y2142	T2143	L2144	S2145	P2146	V2149	E2150	D2151	T2152	M2153	L2154	L2155	L2156	E2157	C2158	L2159	G2160	Q2161	I2162	R2163	S2164	L2165	L2166	L2167	V2168	GLN	MET	GLY	PRO	N2187	N2188	K2189	V2190	F2191	Y2192	L2197	M2198	M2203	H2204	E2205	T2206	V2207										
M2208	E2209	V2210	M2211	V2212	R2213	V2214	L2215	Q2216	GLY	GLU	THR	LYS	GLU	ILE	ARG	PHE	P2226	V2229	C2233	R2234	F2235	Y2238	I2242	S2243	R2244	Q2245	Q2246	Q2247	R2248	F2251	D2252	R2253	L2254	S2255	Y2256	E2259	N2260	I2263	GLY	LEU	GLY	MET	GLN	GLY	SER	T2271	P2272	V2275	D2282									
N2283	L2286	L2290	E2296	V2299	Y2300	L2302	A2303	L2307	GLN	SER	CYS	PRO	MET	LEU	LEU	ALA	LYS	GLY	TYR	PRO	ASP	ILE	GLY	TRP	P2325	C2326	G2327	G2328	E2329	R2330	L2331	L2332	D2333	F2334	L2335	R2336	V2339	F2340	V2341	N2342	Y2346	E2347	N2351	V2354	R2355	L2356	L2357											
I2358	R2359	K2360	P2361	E2362	CYS	PHE	GLY	PRO	ALA	ARG	GLY	GLY	GLY	SER	G2375	A2379	I2380	E2381	E2382	A2383	I2384	R2385	I2386	SER	GLU	ASP	PRO	GLY	VAL	ARG	ARG	ARG	ARG	ARG	GLU	HIS	PHE	GLY	GLU	PRO	GLU	GLU	GLY	ASN	ARG	VAL	HIS	LEU	G2419									
N2423	L2430	G2434	R2435	C2436	A2437	PRO	GLU	MET	HIS	LEU	ILE	GLN	ALA	GLY	LYS	GLY	E2449	A2450	I2453	I2456	L2460	VAL	PRO	L2463	D2464	D2465	L2466	V2467	S2471	L2472	P2473	L2474	Q2475	Q2476	PRO	THR	LEU	GLY	LYS	ASP	GLY	GLY	PRO	VAL	GLN	LYS	VAL	GLY	SER	F2494								
V2495	H2498	K2499	A2500	S2501	M2502	L2503	L2504	L2505	L2506	D2507	R2508	V2509	Y2510	ILE	GLY	ILE	Q2514	D2516	F2517	L2518	L2522	ASP	V2524	R2531	A2532	A2533	A2534	S2535	L2536	ASP	THR	ALA	ALA	A2547	L2550	N2551	R2552	Y2553	L2554	A2557	V2558	L2559	P2560	L2561	I2562	THR	LYS	CYS										
ALA	P2567	L2568	G2571	H2574	L2583	H2584	T2585	V2586	TYR	ARG	GLY	LEU	SER	R2591	D2601	A2609	L2611	CYS	ARG	TYR	ILE	R2615	P2616	R2625	L2626	D2629	V2630	P2631	L2632	L2633	N2634	GLU	PHE	ALA	K2638	H2639	P2640	Y2655	C2656	L2657	T2658	G2660	ALA	ASN	PHE	GLY	VAL	S2668										
I2682	L2686	ALA	HIS	LYS	Y2691	A2699	M2700	P2701	C2702	L2703	T2706	A2707	G2708	L2710	P2711	ASP	TYR	VAL	ASP	ALA	LYS	THR	SER	SER	SER	ALA	GLU	LYS	LYS	ALA	VAL	ASP	ALA	GLU	GLY	N2734	F2735	D2736	P2737	R2738	P2739	E2741	T2742	L2743	N2744	V2745	I2746	I2747	P2748	E2749	K2750							
L2751	D2752	S2753	F2754	L2755	R2756	L2757	F2758	A2759	E2760	Y2761	T2762	H2763	E2764	K2765	W2766	A2767	F2768	D2769	K2770	I2771	K2772	N2773	N2774	W2775	S2776	Y2777	G2778	E2779	N2780	F2781	D2782	E2783	E2784	L2785	K2786	T2787	H2788	P2789	M2790	L2791	F2793	Y2794	K2795	L2796	F2797	S2798	E2799	K2800	D2801	K2802	E2803	I2804	Y2805	R2806	W2807	I2809	K2810	
E2811	S2812	L2813	K2814	A2815	M2816	L2817	A2818	W2819	E2820	W2821	T2822	L2823	E2824	K2825	A2826	R2827	G2828	G2829	E2830	GLU	GLU	THR	GLU	LYS	LYS	LYS	THR	ARG	LYS	ILE	SER	GLN	ALA	GLN	THR	Y2849	D2850	P2851	R2852	E2853	G2854	Y2855	N2856	P2857	Q2858	P2859	P2860	D2861	L2862	S2863	G2864	V2865	T2866	L2867	S2868	R2869	E2870	
L2871	Q2872	A2873	M2874	A2875	E2876	Q2877	L2878	A2879	E2880	N2881	Y2882	H2883	N2884	T2885	W2886	R2887	R2888	K2889	K2890	K2891	Q2892	E2893	L2894	E2895	A2896	K2897	G2898	G2899	Q2900	T2901	H2902	P2903	L2904	L2905	V2906	P2907	Y2908	D2909	T2910	L2911	T2912	A2913	K2914	E2915	K2916	A2917	R2918	D2919	E2921	K2922	A2923	Q2924	E2925	L2926	L2927	K2928	F2929	L2930
Q2931	M2932	N2933	G2934	Y2935	A2936	V2937	T2938	R2939	G2940	LEU	LYS	ASP	MET	GLU	LEU	ASP	THR	SER	ILE	GLU	LYS	ARG	PHE	ALA	PHE	GLY	PHE	LEU	GLN	LEU	LEU	ARG	TRP	ASP	ILE	SER	GLN	GLU	PHE	ILE	ALA	HIS	LEU	GLU	VAL	VAL	SER	SER	GLY	ARG	VAL	GLU	LYS	SER	PRO			

HIS	GLU	GLN	ILE	LYS	PHE	PHE	ALA	LYS	ILE	LEU	LEU	PRO	LEU	LEU	ILE	ASN	GLN	TYR	PHE	THR	ASN	HIS	CYS	LEU	Y3016	F3017	L3018	S3019	T3020	P3021	A3022	H3030	A3031	S3032	M3033	K3036	E3037	M3038	I3039	THR	SER	LEU	F3043	C3044	K3045	P3062	ALA	VAL	VAL	ASN	CYS	L3068	H3069	I3070	L3071	
S3074		R3078		M3081	K3082	S3083	G3084	P3085	E3086	I3087		A3090	GLY	LEU	ASN	ARG	SER		F3095	F3096	E3097	S3098	A3099	S3100	E3101	D3102	I3103		L3110	R3111	L3112	G3113	K3114	V3115	S3116	GLN	ALA	ARG	THR	GLN	VAL	LYS	GLY	VAL	PRO	VAL	ASN	THR	T3132	A3135	P3138	V3139	L3140	T3141	F3144	Q3145
H3146	I3147	A3148	Q3149	H3150	Q3151	F3152	GLY	ASP	ASP	VAL	ILE	L3158	D3159	D3160	S3164	C3170		T3178	LYS	ASN	THR	TYR	V3183	E3184	K3185	P3188	A3189	E3192	C3193	L3194	A3195	R3196	L3197	A3198	A3199	A3200	MET	PRO	VAL	A3204	F3205	L3206	E3207	P3208	Q3209	L3210	N3211	E3212	A3215	C3216	S3217	VAL	TYR	THR		
THR	LYS	SER	PRO	ARG	GLU	ARG	ALA	ILE	LEU	GLY	PRO	ASN	SER	VAL	GLU	GLU	MET	CYS	PRO	ILE	VAL	LEU	ASP	ARG	LEU	GLY	ALA	GLU	SER	GLY	ALA	THR	GLU	MET	PRO	HIS	VAL	ILE	GLU	ILE	T3273	L3274	P3275	M3276	L3277	C3278	S3279	Y3280								
L3281	P3282	R3283	W3284	W3285	E3286	R3287	G3288	E3290	ALA	PRO	P3294	P3297	A3298	G3299	A3300	P3301	P3302	P3303	C3304	T3305	A3306	V3307	T3308	S3309	N3313	SER	LEU	GLY	G3317	N3318	I3319	I3322	V3324	N3325	N3326	I3329	D3330	E3331	A3332	T3333	W3334	M3335	K3336	R3337	L3338	A3339	VAL	PHE	ALA	GLN	PRO	ILE				
V3346	S3347	R3348	A3349	R3350	P3351	E3352	L3353	L3354	H3355	S3356	H3357	F3358	I3359	P3360	T3361	I3362	G3363	ARG	LEU	ARG	K3367	R3368	A3369	G3370	K3371	A3374	Q3378	L3381	E3382	A3383	E3386	A3387	E3388	E3389	G3390	E3391	L3392	L3393	V3394	R3395	D3396	E3397	PHE	SER	VAL	C3402	R3403	D3404	L3405	Y3406	A3407	L3408	Y3409	P3410		
L3411	L3412	I3413	R3414	Y3415	V3416	D3417	N3418	N3419	R3420	A3421	H3422	W3423	L3424	THR	P3427	N3428	A3431	E3432	E3433	L3434	F3435	ARG	MET	V3438	G3439	E3440	I3441	Y3444	W3445	S3446	K3447	S3448	H3449	R3453	E3454	E3455	Q3456	N3457	F3458	N3462	N3465	S3468	F3469	L3470	THR	ALA	ASP	SER	LYS	SER	M3478					
A3479	K3480	A3481	K3482	D3483	A3484	G3487	G3488	S3489	D3490	Q3491	GLU	ARG	T3494	K3495	K3496	K3497	R3498	Y3503	S3504	VAL	GLN	THR	SER	LEU	ILE	VAL	ALA	T3513	L3514	K3515	K3516	M3517	L3518	P3519	I3520	G3521	L3522	N3523	M3524	C3525	A3526	P3527	THR	ASP	GLN	LEU	ILE	MET	LEU	ALA	K3537	T3538	R3539	Y3540	A3541	L3542
K3543	D3544	THR	ASP	GLU	GLU	V3549	R3550	E3551	F3552	L3553	Q3554	N3555	L3559	E3564	G3565	S3566	P3567	S3568	R3570	W3571	Q3572	MET	ALA	LEU	TYR	ARG	GLY	LEU	PRO	GLY	ARG	GLU	ASP	PRO	GLU	LYS	ILE	VAL	ARG	VAL	GLN	VAL	SER	ALA	VAL	LEU	TYR	HIS	LEU	GLU						
GLN	THR	HIS	PRO	TYR	LYS	SER	LYS	ALA	VAL	TRP	HIS	LYS	LEU	SER	LYS	GLN	ARG	ALA	VAL	VAL	ALA	VAL	CYS	PHE	ARG	MET	THR	PRO	LEU	TYR	ASN	P3645	T3646	H3647	R3648	N3651	L3654	E3655	S3656	Y3657	K3658	W3661	T3664	E3665	D3666	H3667	S3668	F3669	E3670	D3671						
R3672	M3673	L3674	D3675	L3676	L3677	A3680	GLY	GLN	GLU	GLU	GLU	GLU	GLU	VAL	GLU	LYS	K3694	P3695	L3698	H3699	L3700	L3701	A3709	L3710	T3711	E3712	K3713	S3714	K3715	L3716	D3717	E3718	Y3722	N3723	A3724	I3728	C3733	HIS	LEU	GLU	GLU	GLY	GLU	ASN	GLY	GLU	ALA	GLU								
GLU	GLU	VAL	E3750	V3751	S3752	F3753	E3754	E3755	Q3767	R3768	R3769	L3770	H3771	T3772	R3773	G3774	A3775	M3778	V3779	L3780	Q3781	M3782	I3783	S3784	S3795	S3796	L3797	L3798	K3799	I3802	L3805	N3806	G3807	G3808	N3809	A3810	E3811	V3812	Q3813	Q3814	K3815	M3816	L3817	D3818	Y3819	L3820	K3821	R3822	K3823	F3828	F3829	L3835				
M3836	C3839	S3840	V3841	L3842	D3843	R3849	A3852	ALA	GLU	GLY	LEU	GLY	MET	VAL	ASN	GLU	ASP	GLY	THR	VAL	ILE	ASN	ARG	GLN	ASN	GLY	GLU	LYS	VAL	MET	ALA	D3877	D3878	E3879	F3880	T3881	Q3882	D3883	L3884	F3885	R3886	F3887	L3888	Q3889	L3890	L3891	C3892	E3893	N3896	N3897	D3898	F3899	Q3900	N3901	Y3902	





• Molecule 1: Ryanodine receptor 1



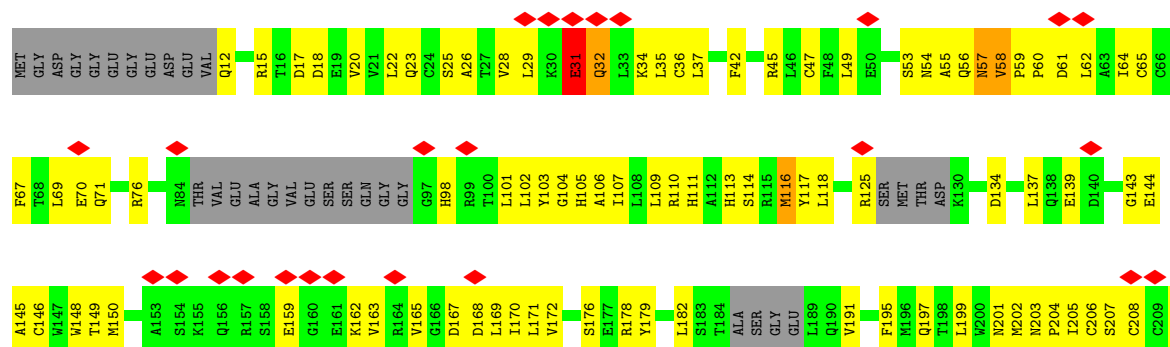


ALA	SER	F2494	V2495	P2496	D2497	H2498	K2499	A2500	N2501	N2502	V2503	L2504	F2505	L2506	D2507	R2508	V2509	G2510	ILE	GLU	N2514	Q2515	D2516	F2517	L2518	L2522	ASP	V2524	R2531	A2532	A2533	A2534	S2535	L2536	ASP	THR	ALA	THR	THR	PHE	SER	THR	T2544	A2547	N2551	R2552	V2553	L2554	A2557	V2558	L2559	P2560	L2561																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
ARG	VAL	HIS	LEU	G2419	T2430	G2434	R2435	C2436	A2437	PRO	GLU	GLU	MET	HIS	LEU	ILE	GLN	ALA	GLY	GLY	LYS	E2449	A2450	I2453	I2456	L2460	VAL	PRO	L2463	D2464	D2465	L2466	V2467	S2471	L2472	P2473	L2474	Q2475	I2476	PRO	THR	LEU	GLY	LYS	ASP	GLY	ALA	LEU	VAL	GLN	PRO	LYS	MET	SER																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
N2351	V2354	R2355	L2356	L2357	R2358	R2359	K2360	P2361	E2362	CYS	PHE	GLY	PRO	ALA	LEU	ILE	ARG	GLY	GLY	GLY	GLY	SER	G2375	A2379	A2383	L2384	R2385	L2386	SER	GLU	ASP	PRO	ALA	ARG	ASP	GLY	PRO	GLY	VAL	ARG	L2332	D2333	F2334	R2335	R2336	V2339	F2340	N2341	N2342	V2346	E2347	E2348																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
N2198	M2203	H2204	E2205	T2206	V2207	M2208	E2209	M2210	M2211	V2212	N2213	V2214	L2215	G2216	GLY	GLY	THR	LYS	GLU	ILE	ARG	PHE	F2226	V2229	C2233	R2234	F2235	Y2238	T2242	S2243	R2244	Q2245	N2246	Q2247	R2248	F2251	D2252	H2253	L2254	S2255	Y2256	E2259	N2260	L2263	GLY	LEU	GLY	MET	GLN	GLY																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
H2125	R2126	Q2127	Y2128	E2133	L2134	L2135	R2136	A2137	S2138	P2139	R2140	A2141	Y2142	T2143	S2144	Q2145	P2146	V2149	E2150	D2151	T2152	M2153	L2155	L2156	E2157	C2158	L2159	Q2160	Q2161	L2162	R2163	S2164	L2165	L2166	T2167	V2168	GLN	MET	GLY	PRO	Q2173	E2174	M2178	G2183	N2184	N2187	K2188	L2189	V2190	F2191	Y2192	L2197																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
GLU	PRO	GLU	GLU	T2057	L2063	R2064	S2065	L2066	L2067	E2068	T2069	R2070	R2071	L2072	VAL	LYS	LYS	LYS	GLU	GLU	LYS	PRO	GLN	GLN	ILE	ASN	MET	LEU	PRO	ALA	GLU	LYS	PRO	GLN	S2093	L2097	V2098	S2099	H2100	M2101	V2102	V2103	R2104	Q2107	Q2112	S2113	L2116	M2120	F2121	S2122	L2123	L2124																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
LEU	MET	ARG	ALA	PHE	THR	MET	SER	ALA	ALA	GLU	THR	ALA	ARG	ARG	THR	ARG	PHE	SER	PRO	PRO	GLN	GLN	ILE	ASN	MET	LEU	LEU	HIS	PHE	ASP	LYS	ASP	GLU	ALA	ASP	GLU	Q1949	E1950	L1951	Q1952	E1956	S1957	L1958	F1961	L1969	Q1970	A1971	N1972	Q1973	R1974	S1975	R1976	TYR	ALA	LEU																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
F1836	Q1837	F1838	L1842	L1843	L1844	L1848	L1849	V1850	M1851	G1852	F1853	G1855	D1856	E1857	D1858	I1862	L1863	K1864	E1867	P1868	E1869	VAL	PHE	THR	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	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	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	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	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	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	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	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	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	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	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	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	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	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	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	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	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	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	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	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	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	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	GLU	GLU	GLU	GLU	GLU	GLU

A3407	L3408	P3409	L3410	L3411	L3412	L3413	L3414	L3415	L3416	L3417	L3418	L3419	L3420	L3421	L3422	L3423	L3424	THR	P3427	N3428	A3431	E3432	E3433	L3434	F3435	ARG	MET	V3436	G3439	E3440	I3441	Y3444	W3445	S3446	K3447	H3448	R3453	E3454	E3455	Q3456	N3457	F3458	N3462	N3465	S3468	F3469	L3470	THR	ALA	ASP	SER																																																								
ALA	GLN	PRO	ILE	V3346	S3347	R3348	A3349	R3350	P3351	E3352	L3353	L3354	H3355	S3356	H3357	F3358	W3423	P3360	T3361	I3362	G3363	ARG	LEU	ARG	K3367	R3368	A3369	G3370	K3371	A3374	Q3378	L3381	E3382	A3383	E3386	A3387	E3388	E3389	G3390	E3391	L3392	L3393	V3394	R3395	D3396	E3397	PHE	SER	VAL	LEU	C3402	R3403	L3404	L3405	Y3406																																																				
T3141	F3144	Q3145	H3146	I3147	Q3148	Q3149	H3150	Q3151	Q3152	GLY	ASP	ASP	VAL	ILE	L3158	D3159	D3160	S3164	C3170	L3178	LYS	ASN	THR	TYR	V3183	E3184	K3185	P3188	A3189	E3192	C3193	L3194	A3195	R3196	L3197	A3198	A3199	MET	PRO	VAL	A3204	F3205	L3206	E3207	P3208	Q3209	L3210	N3211	E3212	A3215	C3216																																																								
H3069	I3070	L3071	S3074	R3078	M3081	K3082	S3083	G3084	P3085	E3086	I3087	A3090	GLY	LEU	ARG	SER	F3095	F3096	E3097	S3098	A3099	S3100	E3101	D3102	I3103	L3110	R3111	L3112	G3113	K3114	V3115	S3116	GLN	ALA	ARG	THR	GLN	VAL	LYS	GLY	VAL	GLY	GLN	ASN	LEU	THR	T3132	A3135	P3138	V3139	L3140																																																								
GLU	LYS	SER	PRO	HIS	GLU	GLN	GLU	ILE	PHE	PHE	ALA	LYS	ILE	LEU	PRO	ILE	ASN	GLN	THR	THR	CYS	LEU	Y3016	F3017	L3018	S3019	T3020	P3021	A3022	H3030	A3031	S3032	N3033	K3036	E3037	N3038	I3039	THR	SER	LEU	F3043	C3044	K3045	P3062	ALA	VAL	VAL	ASN	CYS	L3068																																																									
L2927	K2928	F2929	L2930	Q2931	Q2932	N2933	G2934	Y2935	A2936	V2937	T2938	R2939	G2940	LEU	LYS	ASP	GLU	MET	GLU	LEU	ASP	THR	SER	ILE	GLU	K2889	K2890	K2891	Q2892	E2893	L2894	E2895	A2896	K2897	G2898	G2899	G2900	T2901	H2902	P2903	L2904	L2905	V2906	P2907	Y2908	D2909	T2910	L2911	T2912	A2913	K2914	E2915	K2916	A2917	R2918	D2919	R2920	E2921	K2922	A2923	Q2924	E2925	L2926																																												
L2867	S2868	R2869	E2870	L2871	Q2872	A2873	M2874	A2875	E2876	Q2877	L2878	A2879	E2880	N2881	Y2882	H2883	M2884	T2885	W2886	G2887	R2888	K2889	K2890	GLU	GLU	ARG	THR	THR	GLU	THR	LYS	LYS	LYS	THR	ARG	LYS	ILE	GLN	ALA	THR	Y2849	D2850	P2851	R2852	E2853	G2854	N2855	P2857	Q2858	P2859	L2860	K2861	L2862	S2863	V2865	T2866																																																			
W2807	P2808	I2809	K2810	E2811	S2812	L2813	K2814	A2815	N2816	I2817	A2818	W2819	E2820	W2821	T2822	L2823	E2824	K2825	A2826	R2827	E2828	G2829	E2830	GLU	GLU	ARG	THR	THR	GLU	LYS	LYS	LYS	LYS	THR	ARG	LYS	THR	ARG	LYS	THR	LYS	GLU	LYS	E2779	E2780	Y2781	D2782	VAL	ASP	ALA	GLU	GLY	N2734	F2735	D2736	P2737	R2738	P2739	V2740	E2741	T2742	L2743	N2744	V2745	I2746																																										
VAL	T2667	S2668	I2682	L2686	ALA	HIS	HIS	LYS	LYS	Y2691	A2699	M2700	P2701	C2702	L2703	I2706	A2707	G2708	A2709	L2710	P2711	P2712	ASP	TYR	VAL	ASP	ALA	ALA	SER	TYR	SER	SER	LYS	LYS	ALA	GLU	LYS	LYS	ALA	LYS	LYS	THR	VAL	THR	ALA	ASP	GLU	GLY	N2754	F2755	D2756	P2757	R2758	A2759	E2760	Y2761	T2762	H2763	E2764	K2765	W2766	A2767	P2768	D2769	K2770	I2771	Q2772	N2773	N2774	W2775	S2776	Y2777	Q2778	E2779	N2780	Y2781	D2782	THR	VAL	ASP	ALA	GLU	GLY	N2784	D2785	K2786	T2787	H2788	P2789	M2790	L2791	R2792	N2793	P2793	Y2794	K2795	L2796	P2797	S2798	E2799	K2800	D2801	K2802	E2803	I2804	Y2805	R2806
T2562	THR	LYS	CYS	ALA	P2567	L2568	G2571	H2574	L2583	H2584	T2585	V2586	TYR	ARG	LEU	SER	R2591	D2601	A2609	LEU	CYS	ARG	TYR	ILE	R2615	P2616	R2625	L2626	D2629	V2630	P2631	L2632	L2633	K2634	GLU	PHE	ALA	K2638	M2639	P2640	Y2655	C2656	L2657	P2658	T2659	G2660	TRP	ALA	ASN	PHE	GLY																																																								



- Molecule 1: Ryanodine receptor 1



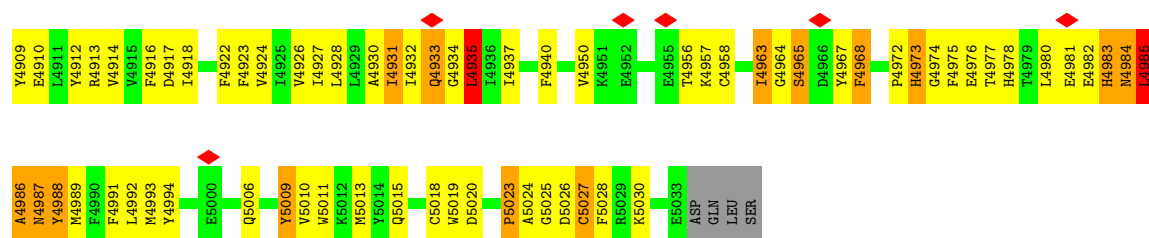




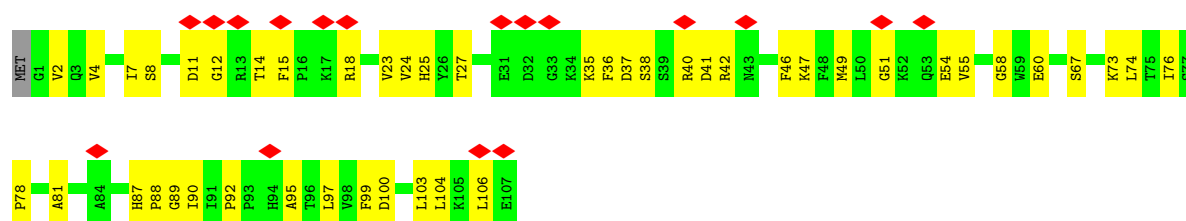




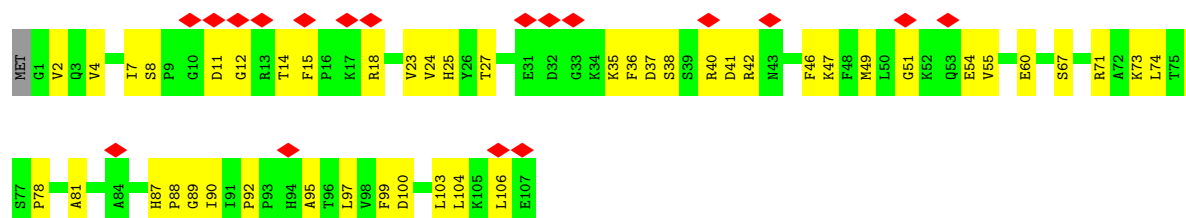




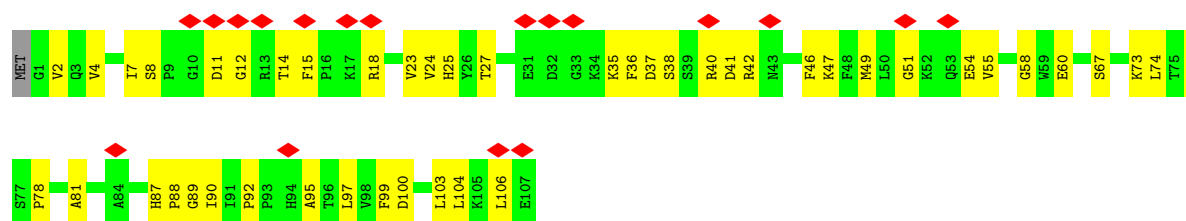
• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A



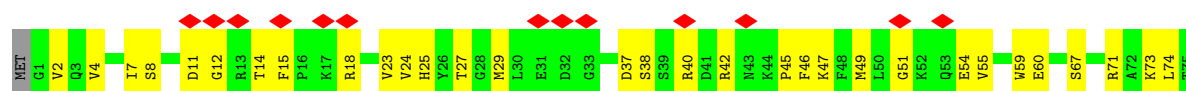
• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A

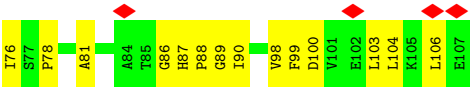


• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A



• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	119000	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.382	Depositor
Minimum map value	-0.148	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.085	Depositor
Map size (Å)	482.40002, 482.40002, 482.40002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.34, 1.34, 1.34	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

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	1.08	60/27395 (0.2%)	1.09	104/37119 (0.3%)
1	C	1.08	59/27395 (0.2%)	1.09	107/37119 (0.3%)
1	E	1.08	59/27395 (0.2%)	1.09	106/37119 (0.3%)
1	G	1.08	56/27395 (0.2%)	1.09	107/37119 (0.3%)
2	B	0.86	0/851	0.94	0/1146
2	D	0.86	0/851	0.94	0/1146
2	F	0.86	0/851	0.94	0/1146
2	H	0.88	1/851 (0.1%)	0.94	0/1146
All	All	1.07	235/112984 (0.2%)	1.09	424/153060 (0.3%)

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	17
1	C	0	17
1	E	0	17
1	G	0	16
All	All	0	67

The worst 5 of 235 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2853	GLU	CD-OE1	10.54	1.45	1.25
1	E	2853	GLU	CD-OE1	10.51	1.45	1.25
1	G	2853	GLU	CD-OE1	10.28	1.44	1.25
1	C	2853	GLU	CD-OE1	10.19	1.44	1.25
1	A	4181	ILE	CA-C	-8.29	1.45	1.52

The worst 5 of 424 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	915	GLU	CA-C-N	14.52	137.99	119.84
1	C	915	GLU	C-N-CA	14.52	137.99	119.84
1	G	915	GLU	CA-C-N	14.40	137.84	119.84
1	G	915	GLU	C-N-CA	14.40	137.84	119.84
1	E	915	GLU	CA-C-N	14.39	137.83	119.84

There are no chirality outliers.

5 of 67 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1187	GLY	Mainchain
1	A	31	GLU	Mainchain,Peptide
1	A	322	LYS	Peptide
1	A	841	GLY	Mainchain,Peptide
1	A	857	ASP	Mainchain,Peptide

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	26926	0	24467	1033	0
1	C	26926	0	24467	1049	0
1	E	26926	0	24467	1036	0
1	G	26926	0	24467	986	0
2	B	832	0	831	41	0
2	D	832	0	831	41	0
2	F	832	0	831	41	0
2	H	832	0	831	39	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
3	E	1	0	0	0	0
3	G	1	0	0	0	0
All	All	111036	0	101192	4067	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 19.

The worst 5 of 4067 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)
1:G:1808:ARG:NH1	1:G:1858:ASP:OD2	1.79	1.16
1:E:1808:ARG:NH1	1:E:1858:ASP:OD2	1.79	1.16
1:C:1808:ARG:NH1	1:C:1858:ASP:OD2	1.79	1.15
1:A:1808:ARG:NH1	1:A:1858:ASP:OD2	1.79	1.14
1:A:1243:PRO:HD2	1:A:1458:HIS:HB3	1.20	1.10

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	3499/5037 (70%)	3211 (92%)	199 (6%)	89 (2%)	4	28
1	C	3499/5037 (70%)	3211 (92%)	201 (6%)	87 (2%)	4	28
1	E	3499/5037 (70%)	3211 (92%)	199 (6%)	89 (2%)	4	28
1	G	3499/5037 (70%)	3211 (92%)	199 (6%)	89 (2%)	4	28
2	B	105/108 (97%)	97 (92%)	8 (8%)	0	100	100
2	D	105/108 (97%)	97 (92%)	8 (8%)	0	100	100
2	F	105/108 (97%)	97 (92%)	8 (8%)	0	100	100
2	H	105/108 (97%)	97 (92%)	7 (7%)	1 (1%)	12	43
All	All	14416/20580 (70%)	13232 (92%)	829 (6%)	355 (2%)	6	28

5 of 355 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	55	ALA
1	A	737	LEU
1	A	858	THR

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Mol	Chain	Res	Type
1	A	896	VAL
1	A	916	PRO

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	2503/4276 (58%)	2484 (99%)	19 (1%)	73	76
1	C	2504/4276 (59%)	2485 (99%)	19 (1%)	73	76
1	E	2504/4276 (59%)	2486 (99%)	18 (1%)	76	77
1	G	2502/4276 (58%)	2485 (99%)	17 (1%)	76	77
2	B	89/90 (99%)	89 (100%)	0	100	100
2	D	89/90 (99%)	89 (100%)	0	100	100
2	F	89/90 (99%)	89 (100%)	0	100	100
2	H	89/90 (99%)	89 (100%)	0	100	100
All	All	10369/17464 (59%)	10296 (99%)	73 (1%)	73	77

5 of 73 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	380	GLN
1	G	4935	LEU
1	G	806	PRO
1	G	1055	PRO
1	C	862	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 220 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	413	GLN
1	E	3699	HIS
2	H	87	HIS

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Mol	Chain	Res	Type
1	G	3699	HIS
1	E	582	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 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](#)

There are no chain breaks in this entry.

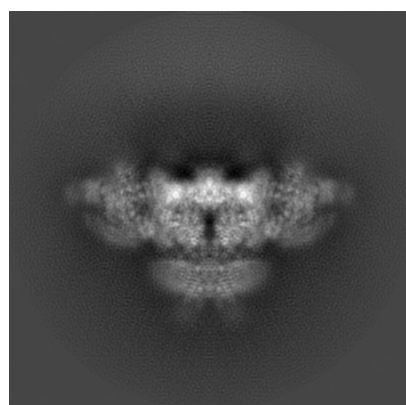
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9518. These allow visual inspection of the internal detail of the map and identification of artifacts.

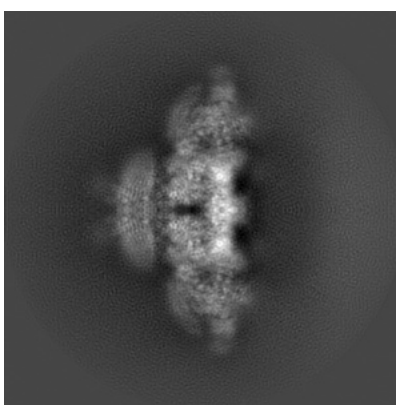
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

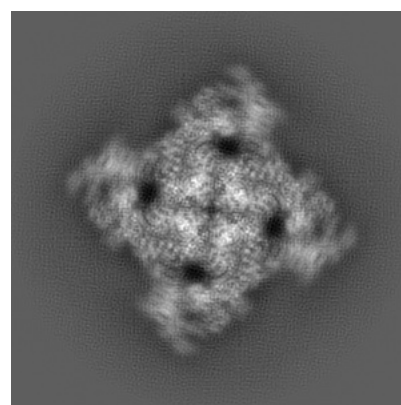
6.1.1 Primary map



X



Y

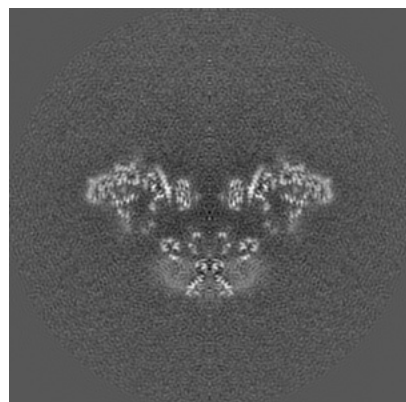


Z

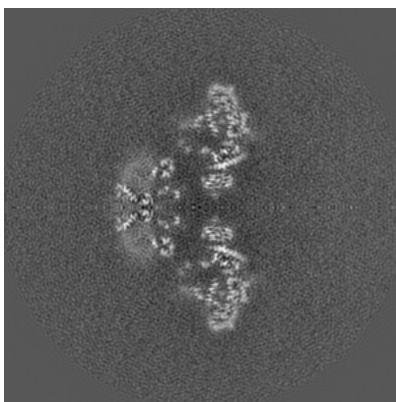
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

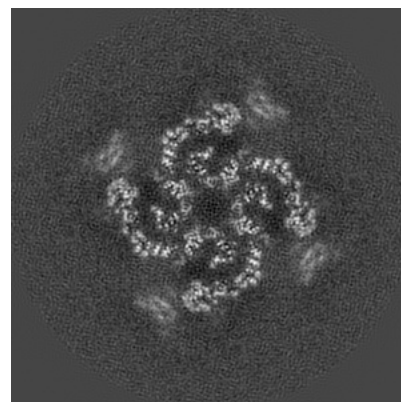
6.2.1 Primary map



X Index: 180



Y Index: 180

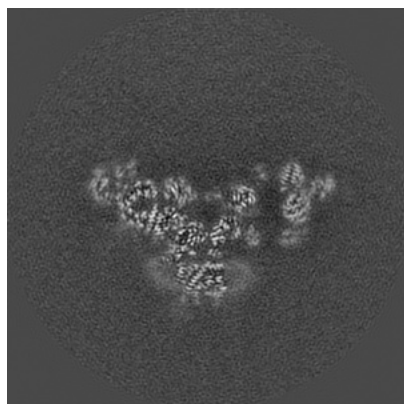


Z Index: 180

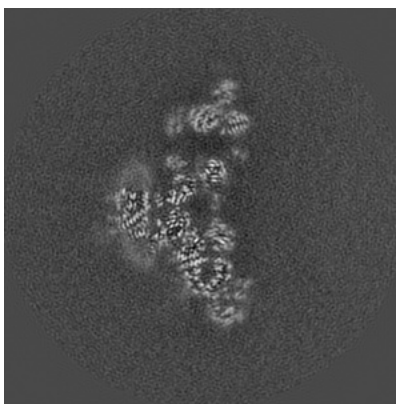
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

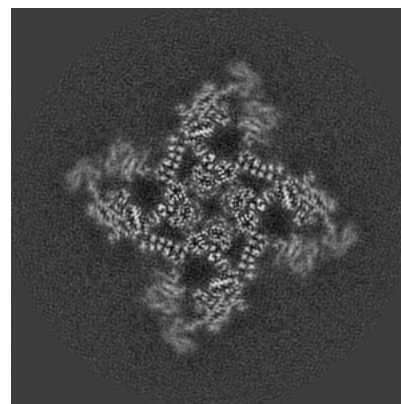
6.3.1 Primary map



X Index: 191



Y Index: 169

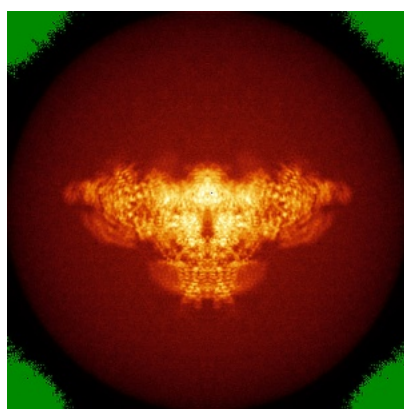


Z Index: 190

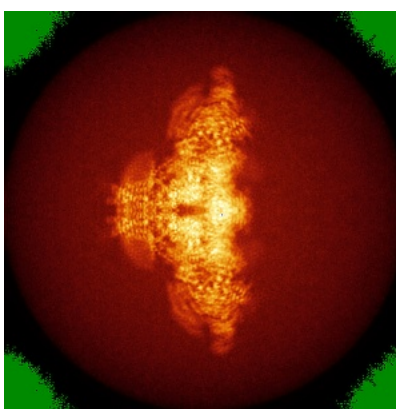
The images above show the largest variance slices of the map in three orthogonal directions.

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

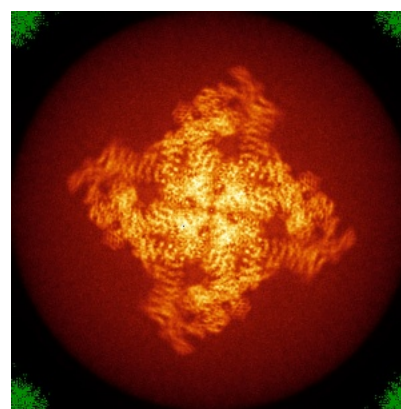
6.4.1 Primary map



X



Y

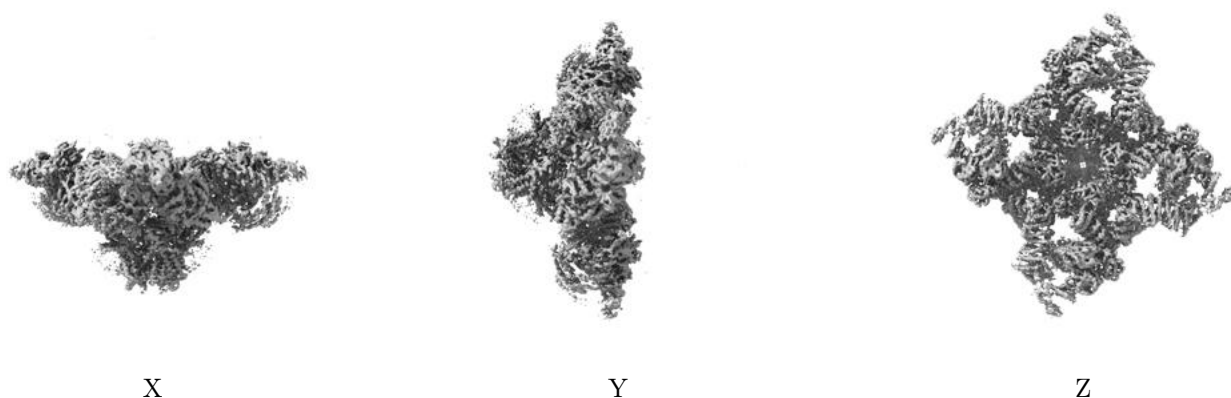


Z

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

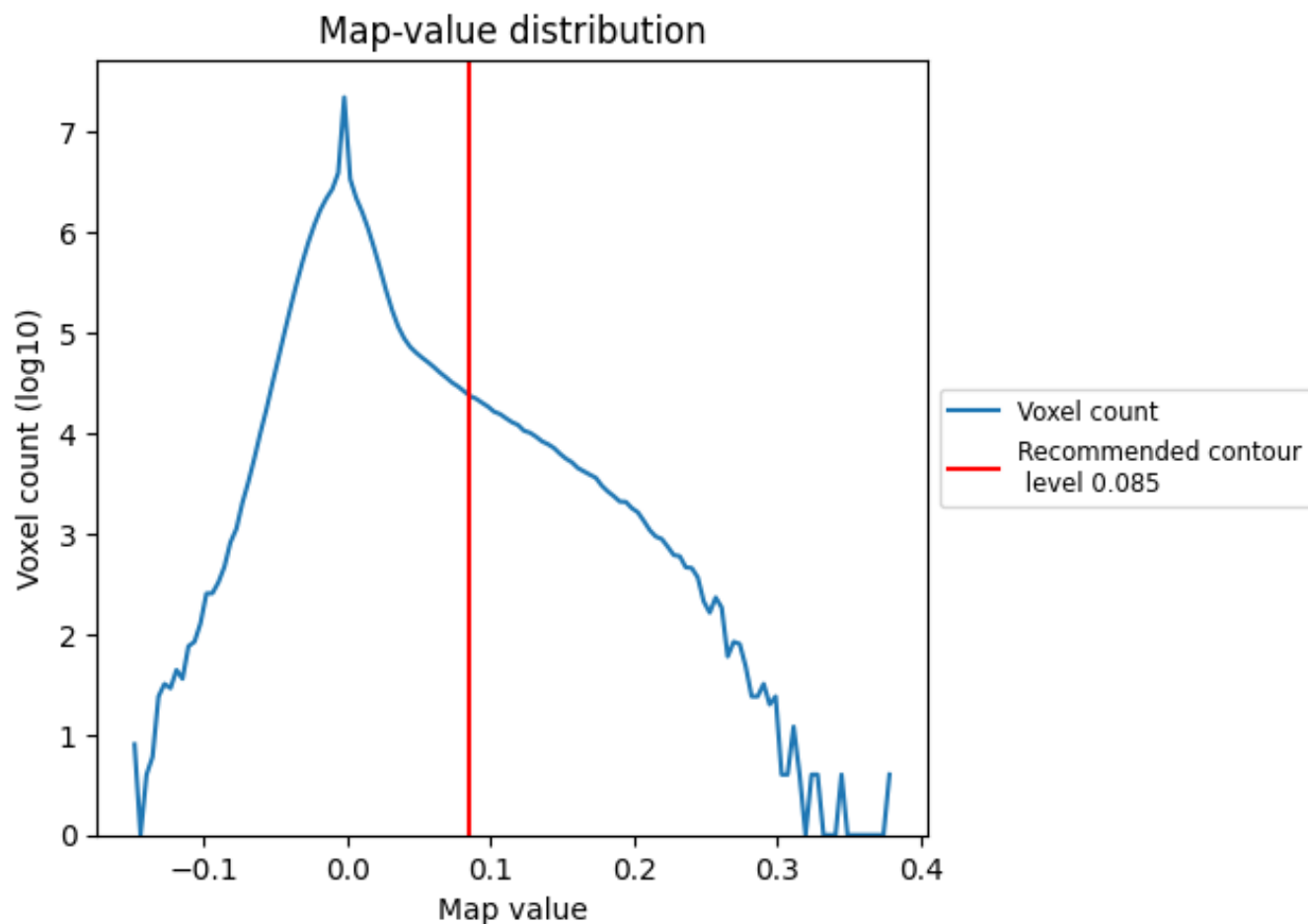
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

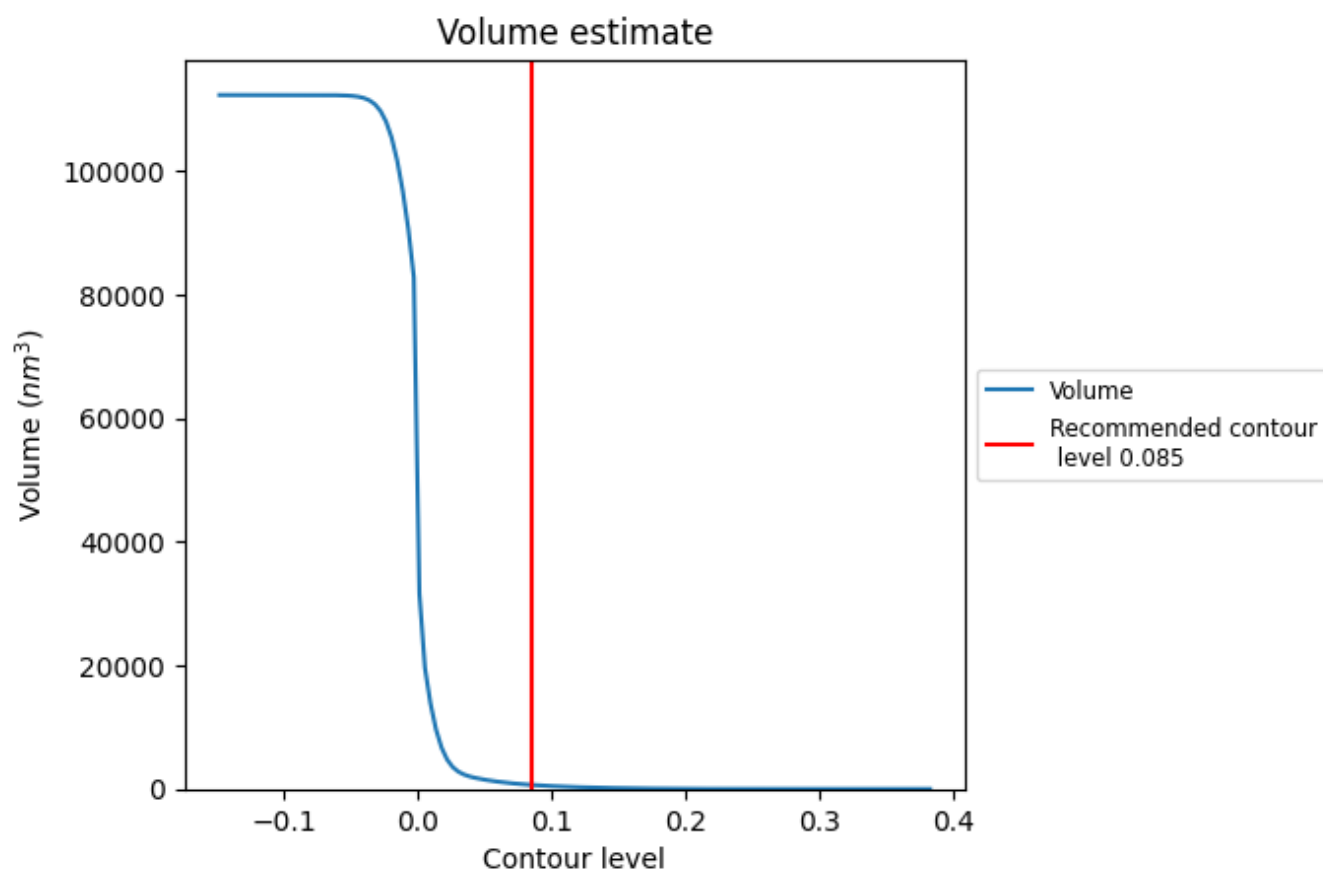
This section contains the results of statistical analysis of the map.

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.

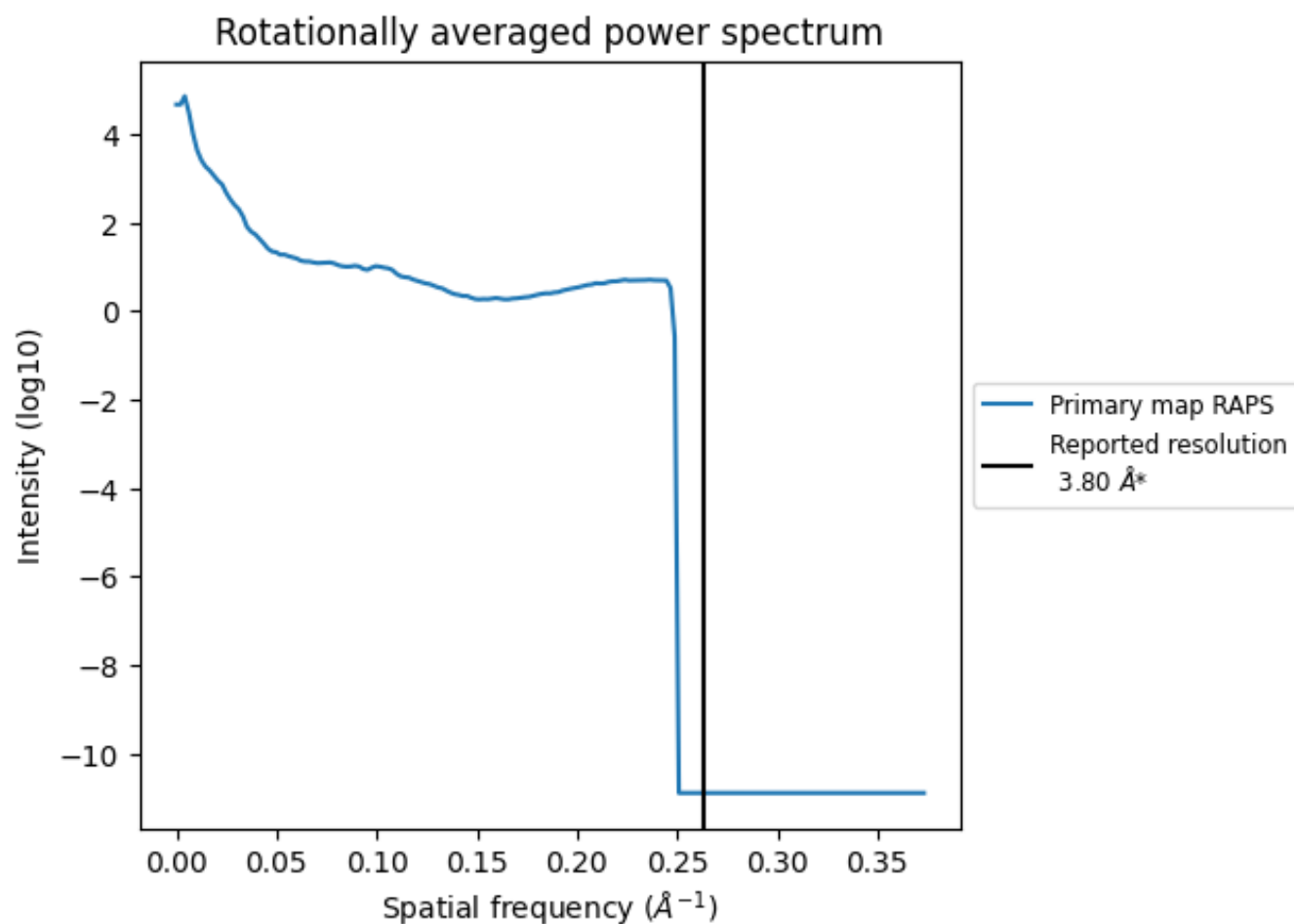
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 655 nm³; this corresponds to an approximate mass of 591 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

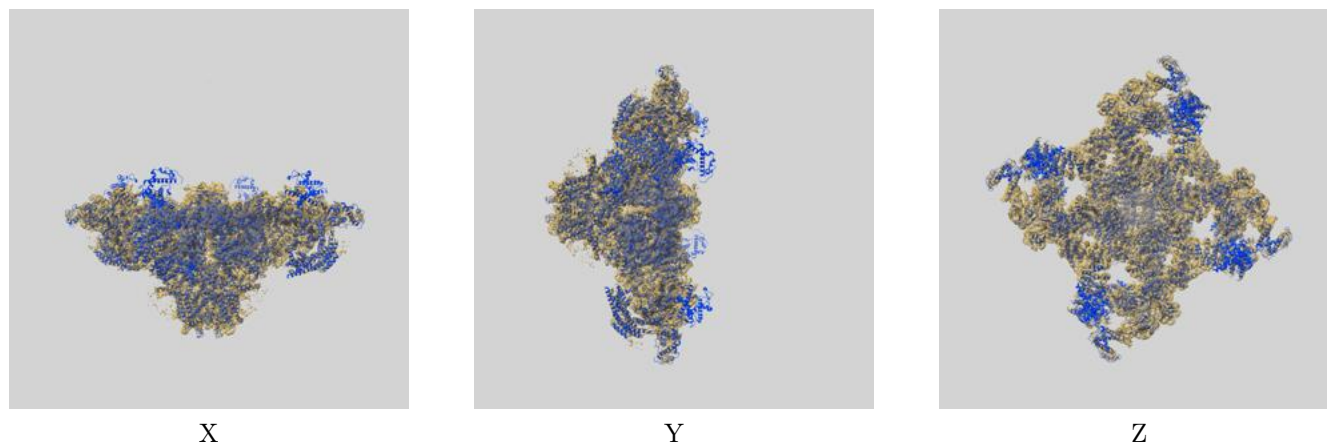
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

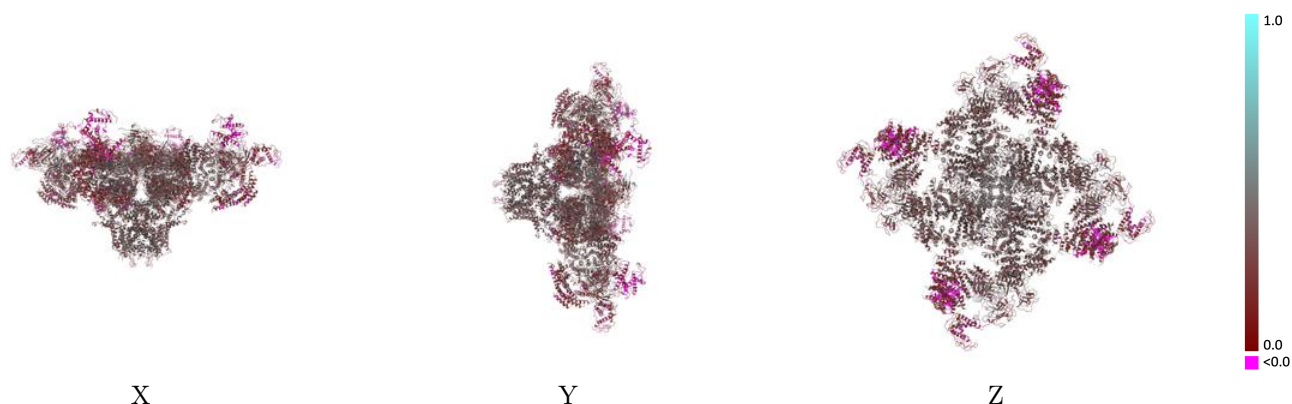
This section contains information regarding the fit between EMDB map EMD-9518 and PDB model 5GKY. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



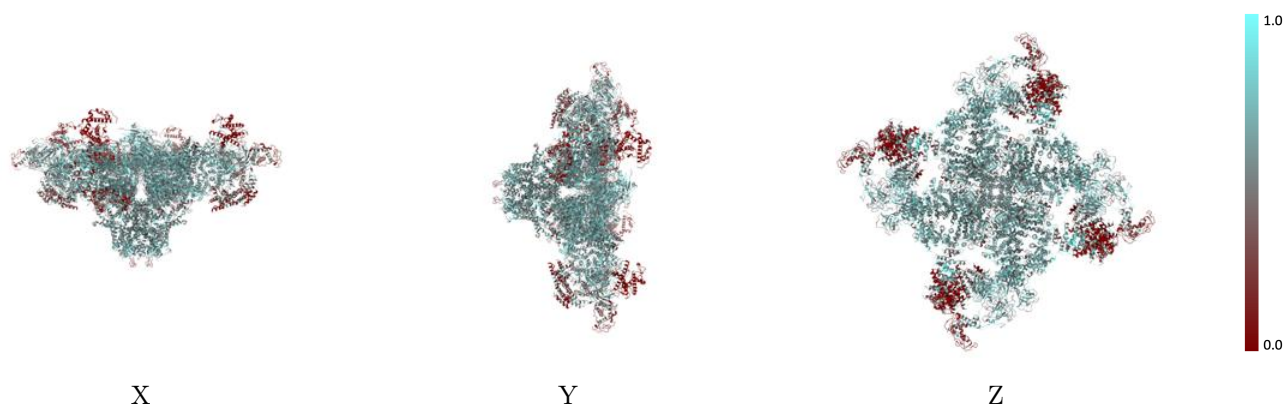
The images above show the 3D surface view of the map at the recommended contour level 0.085 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



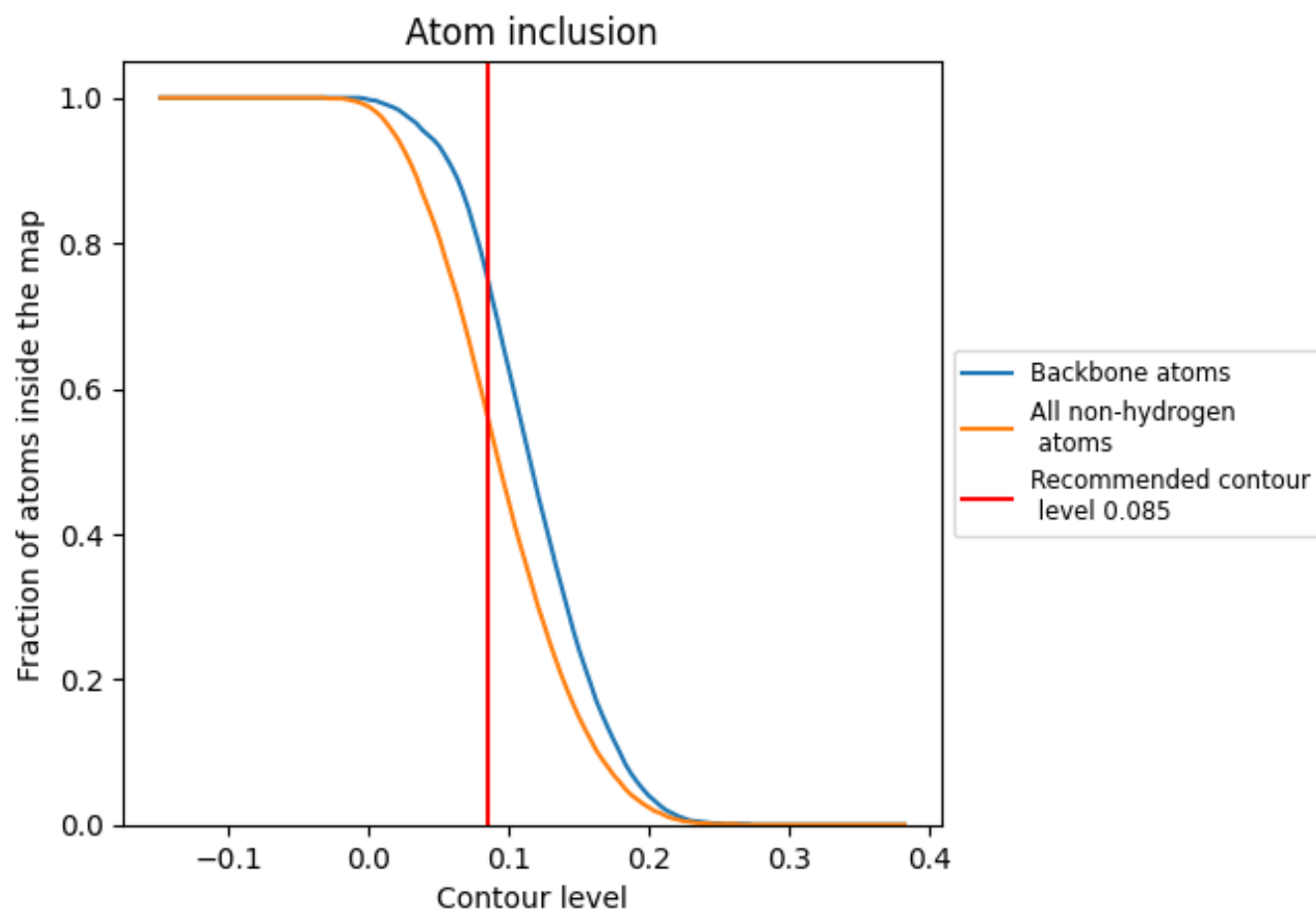
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.085).

9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 56% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.085) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5630	0.3170
A	0.5630	0.3160
B	0.5760	0.3340
C	0.5630	0.3160
D	0.5760	0.3310
E	0.5630	0.3160
F	0.5740	0.3290
G	0.5630	0.3170
H	0.5740	0.3370

1.0

0.0

<0.0