



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 12:02 AM UTC

PDB ID : 5TAZ / pdb_00005taz
EMDB ID : EMD-8390
Title : Structure of rabbit RyR1 (ryanodine dataset, class 3)
Authors : Clarke, O.B.; des Georges, A.; Zalk, R.; Marks, A.R.; Hendrickson, W.A.;
Frank, J.
Deposited on : 2016-09-10
Resolution : 4.30 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:

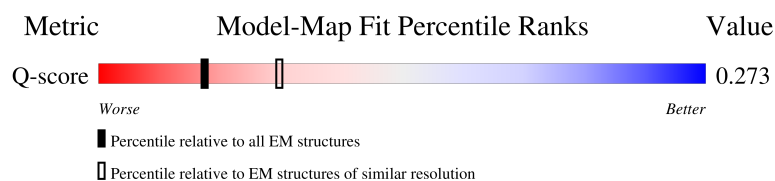
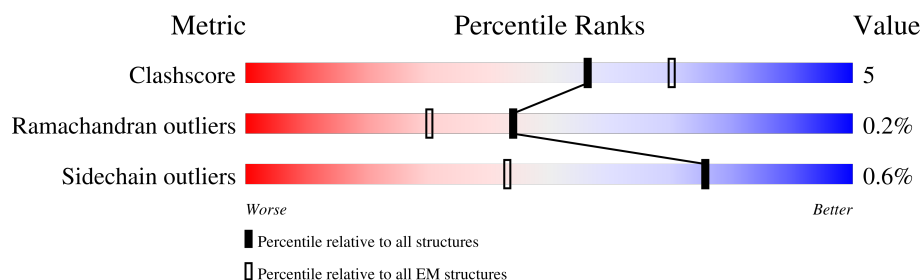
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.30 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	4585 (3.80 - 4.80)

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	 31% 87% 12% .
1	F	108	 31% 89% 10% .
1	H	108	 31% 88% 11% .
1	J	108	 31% 89% 10% .

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Mol	Chain	Length	Quality of chain			
2	B	4416	38% 84% 10% 5%			
2	E	4416	38% 84% 10% 5%			
2	G	4416	38% 84% 10% 5%			
2	I	4416	38% 84% 10% 5%			

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	I	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	E	4194	Total	C	N	O	S	0	0
			29499	18686	5228	5428	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	I	1	Total	Zn	0
			1	1	
3	G	1	Total	Zn	0
			1	1	
3	E	1	Total	Zn	0
			1	1	

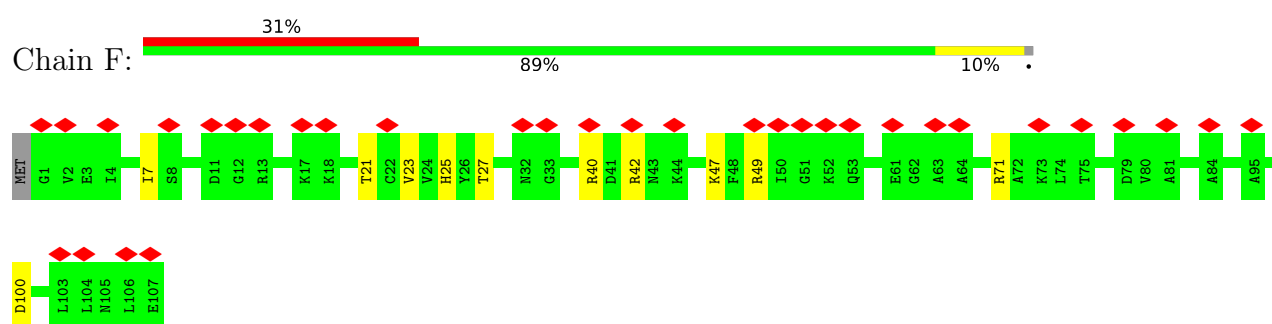
- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

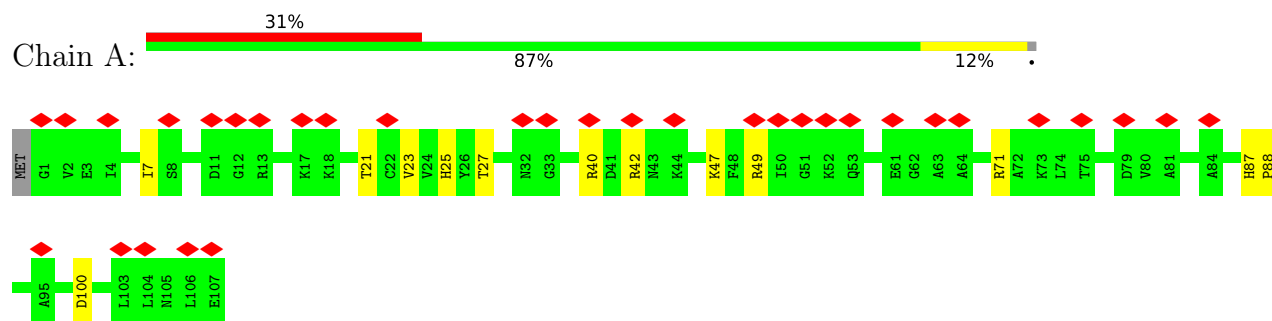
3 Residue-property plots [i](#)

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.

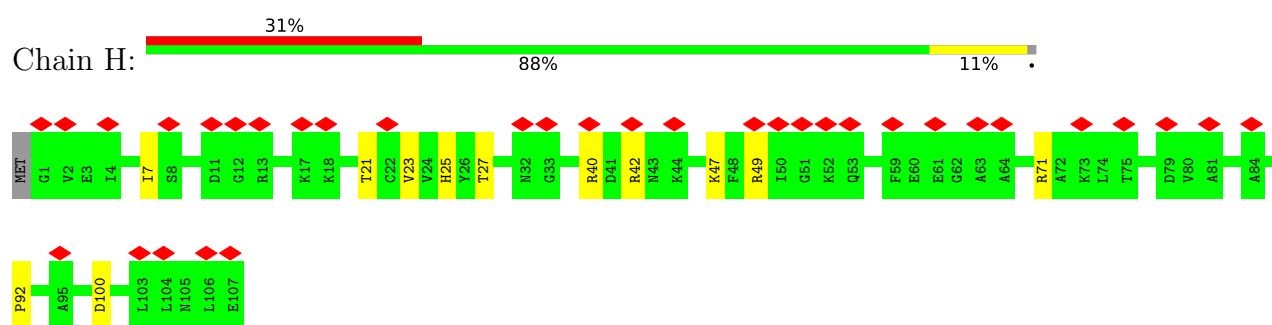
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



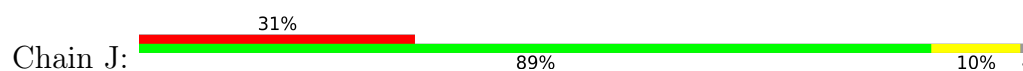
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

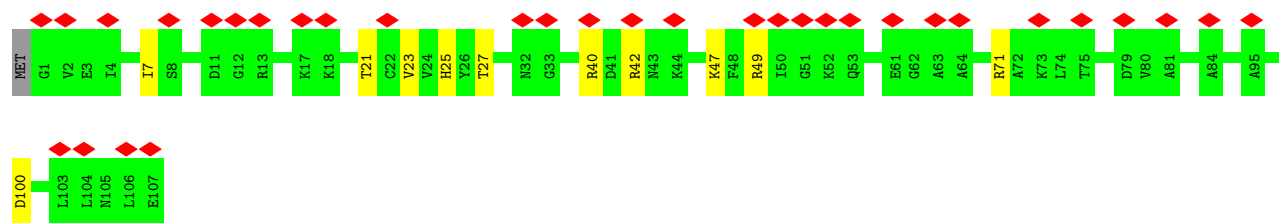


- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



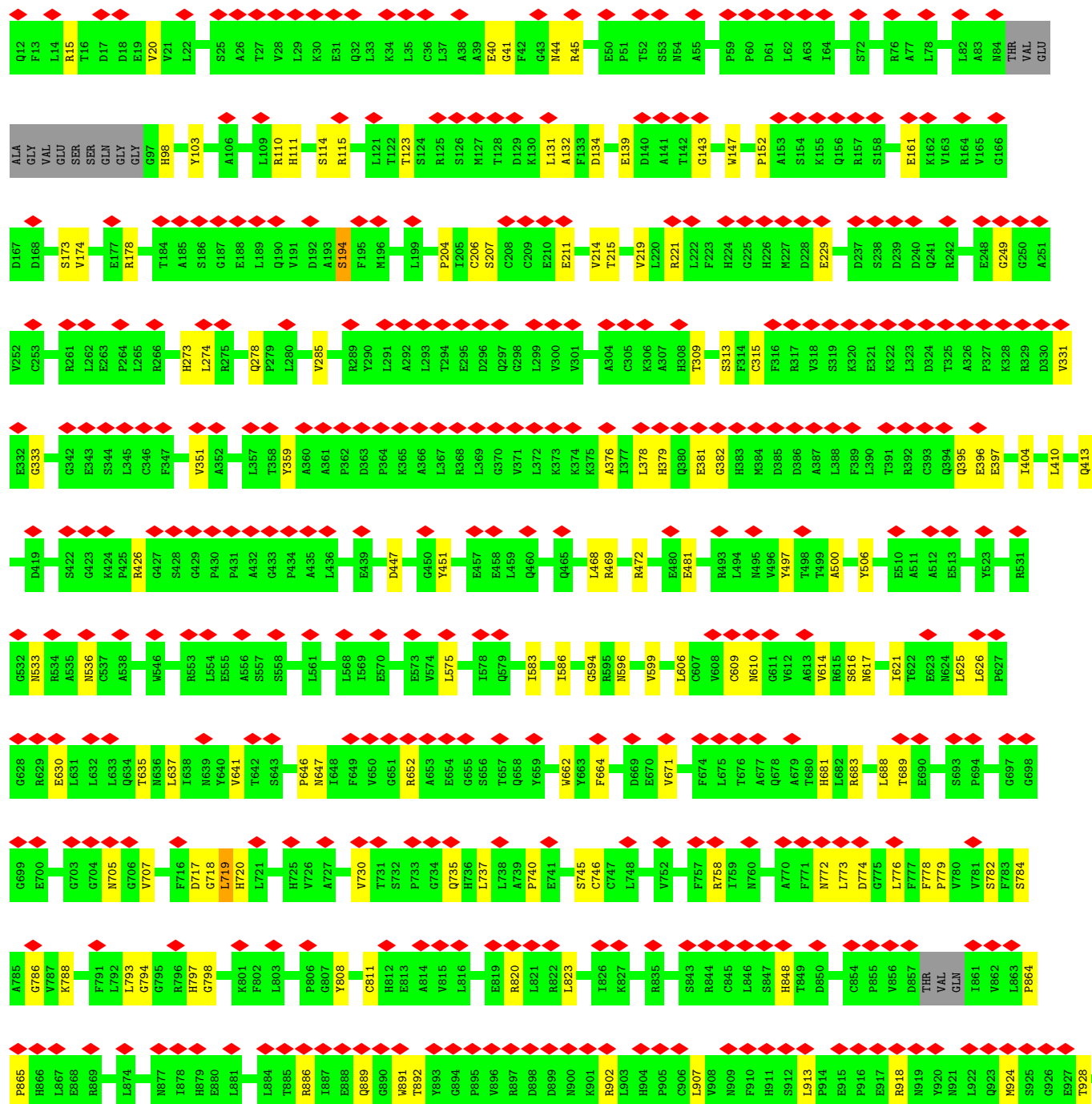
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B





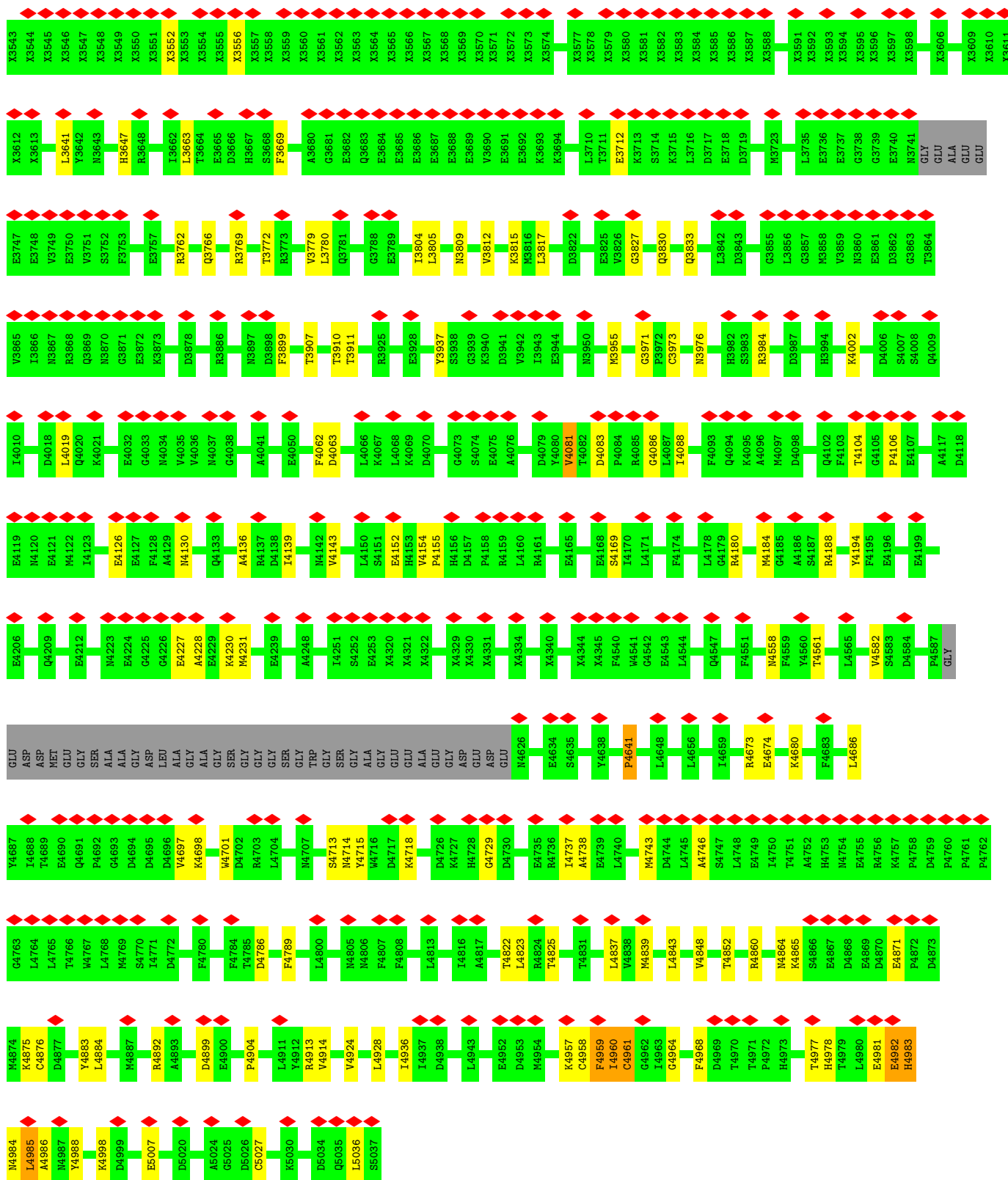
• Molecule 2: Ryanodine receptor 1

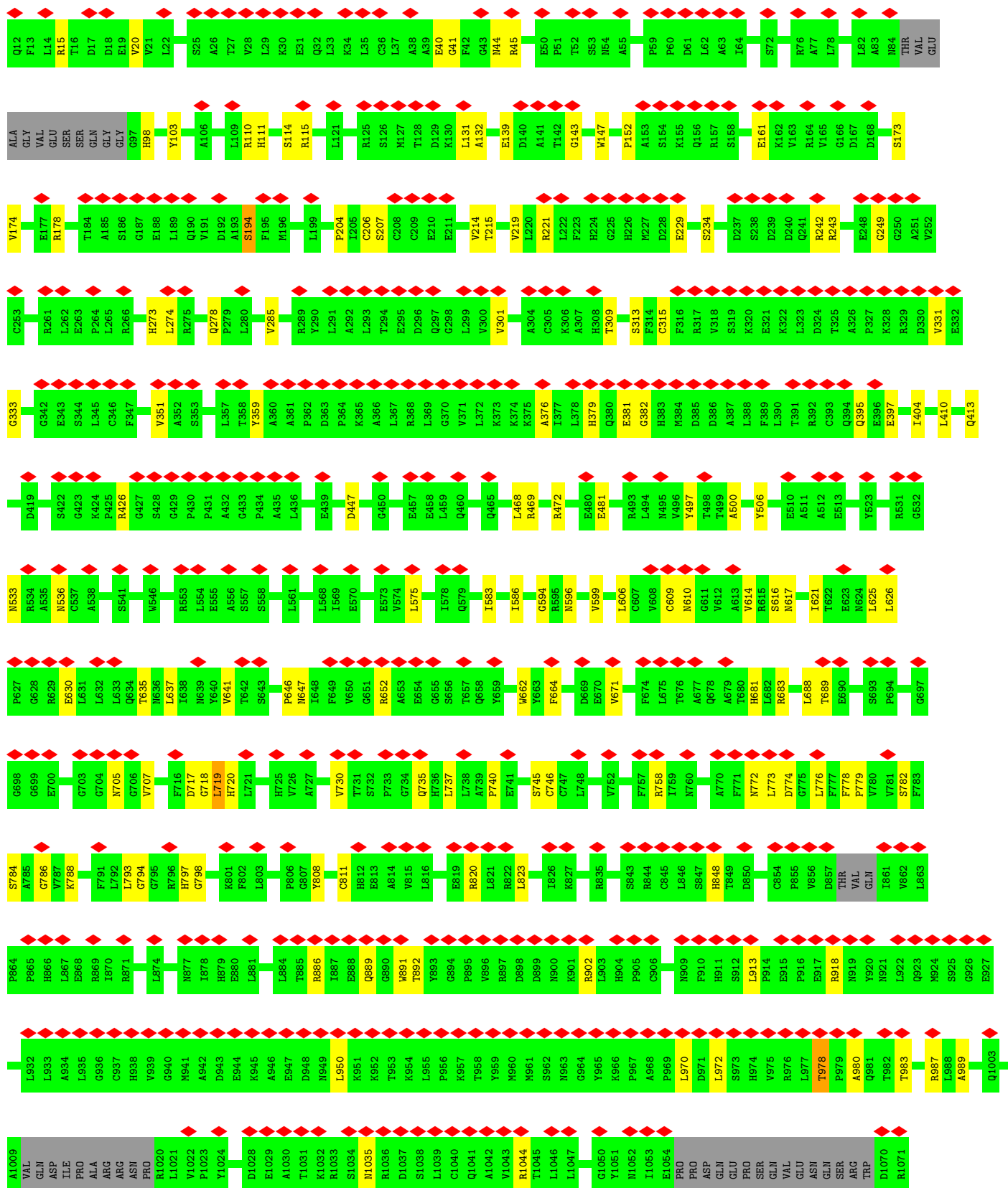
Chain B: 38% 84% 10% 5%





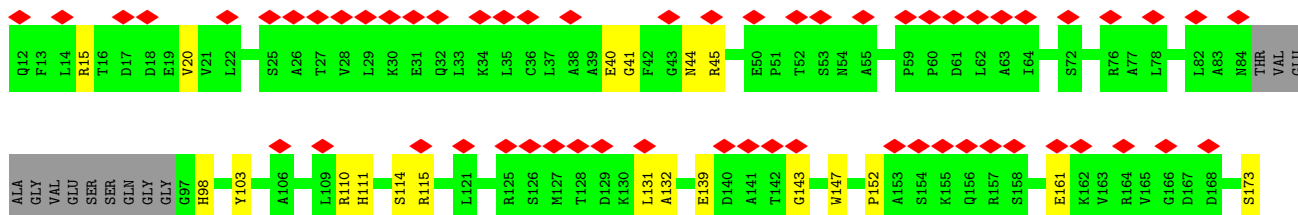
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X3282	X3283	X3284	X3285	X3286	X3287	X3288	X3289	X3290	X3291	X3292	X3293	X3294	X3295	X3296	X3297	X3301	X3302	X3303	X3304	X3311	X3312	X3313	X3314	X3315	X3316	X3317	X3318	X3319	X3320	X3323	X3327	X3331	X3332	X3333	X3334	X3335	X3336	X3337	X3338	X3339	X3340	X3341	X3342	X3343	X3344	X3345	X3346	X3347	X3348	X3349	X3350	X3351	X3352	X3353					
X3211	X3212	X3213	X3214	X3215	X3216	X3217	X3218	X3219	X3220	X3221	X3222	X3223	X3224	X3225	X3226	X3227	X3228	X3229	X3230	X3231	X3232	X3233	X3234	X3235	X3236	X3241	X3242	X3243	X3244	X3245	X3246	X3247	X3248	X3249	X3250	X3251	X3252	X3253	X3254	X3261	X3262	X3263	X3264	X3267	X3268	X3269	X3270	X3271	X3272	X3273	X3274	X3275	X3276	X3277	X3278	X3279	X3280	X3281	
X3045	X3046	X3047	X3048	X3049	X3050	X3057	X3062	X3063	X3134	X3135	X3136	X3137	X3138	X3139	X3142	X3143	X3144	X3148	X3154	X3158	X3159	X3160	X3161	X3162	X3163	X3170	X3171	X3172	X3173	X3174	X3175	X3176	X3177	X3178	X3181	X3190	X3191	X3192	X3193	X3194	X3195	X3196	X3197	X3200	X3201	X3202	X3203	X3204	X3205										
X2943	X2944	X2945	X2946	X2947	X2948	X2949	X2950	X2951	X2952	X2953	X2954	X2963	X2964	X2968	X2969	X2970	X2973	X2974	X2975	X2976	X2995	X2996	X2997	X2998	X2999	X3000	X3001	X3006	X3007	X3008	X3014	X3017	X3021	X3022	X3023	X3027	X3028	X3034	X3035	X3036	X3037	X3038	X3039	X3040	X3041	X3042	X3043	X3044											
E2880	N2881	Y2882	H2883	N2884	T2885	W2886	G2887	R2888	K2889	K2890	K2891	Q2892	E2893	L2894	E2895	A2896	K2897	G2898	G2899	G2900	SER	GLN	THR	ALA	GLN	THR	TYR	ASP	PRO	ARG	GLU	GLY	Y2855	N2856	P2857	Q2858	P2859	P2860	D2861	L2862	S2863	G2864	V2865	T2866	L2867	S2868	R2869	E2870	L2871	Q2872	A2873	N2874	A2875	E2876	Q2877	L2878	A2879		
E2820	W2821	T2822	L2823	E2824	K2825	A2826	R2827	E2828	G2829	E2830	GLU	GLU	ARG	THR	GLU	LYS	LYS	THR	ARG	LYS	ILE	GLN	THR	ALA	GLN	THR	TYR	ASP	PRO	ARG	GLU	GLY	Y2855	N2856	P2857	Q2858	P2859	P2860	D2861	L2862	S2863	G2864	V2865	T2866	L2867	S2868	R2869	E2870	L2871	Q2872	A2873	N2874	A2875	E2876	Q2877	L2878	A2879		
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X2669	X2670	X2671	X2672	X2673	X2674	X2675	X2676	X2677	X2680	X2681	X2682	X2683	X2684	X2685	X2686	X2687	X2688	X2689	X2690	X2691	X2692	X2693	X2694	X2695	X2696	X2697	X2698	X2699	X2700	X2701	X2702	X2703	N2734	F2735	D2736	P2737	R2738	P2739	V2740	E2741	T2742	L2743	N2744	V2745	L2746	L2747	P2748	E2749	L2750	L2751	D2752	S2753	L2754	T2755	N2756	K2757	F2758	A2759	
X2558	X2562	X2563	X2566	X2567	X2571	X2580	X2581	X2582	X2583	X2584	X2585	X2586	X2589	X2596	X2600	X2601	X2612	X2619	X2620	X2621	X2622	X2623	X2624	X2625	X2626	X2627	X2628	X2629	X2630	X2631	X2641	X2649	X2650	X2651	X2652	X2653	X2659	X2663	X2664	X2665	X2666																		
H2441	K2447	G2448	L2451	R2452	I2453	T2456	L2457	R2458	S2459	L2463	D2464	D2465	L2466	I2470	S2471	L2472	P2473	L2474	Q2475	I2476	P2477	L2478	L2479	X2487	X2488	X2489	X2490	X2493	X2494	X2499	X2502	X2513	X2516	X2522	X2523	X2526	X2529	X2530	X2536	X2537	X2538	X2539	X2550																
E2362	A2367	L2368	R2369	G2370	E2371	G2372	G2373	S2374	G2375	L2376	L2377	A2378	A2379	L2380	E2381	L2384	R2385	L2386	S2387	E2388	D2389	P2390	A2391	R2392	D2393	G2394	P2395	GLY	VAL	ARG	ARG	ASP	ARG	ARG	ARG	HIS	PHE	GLY	GLU	GLU	PRO	PRO	GLU	L2414	R2415	H2420	L2430	G2434	R2435	C2436	A2437	P2438							

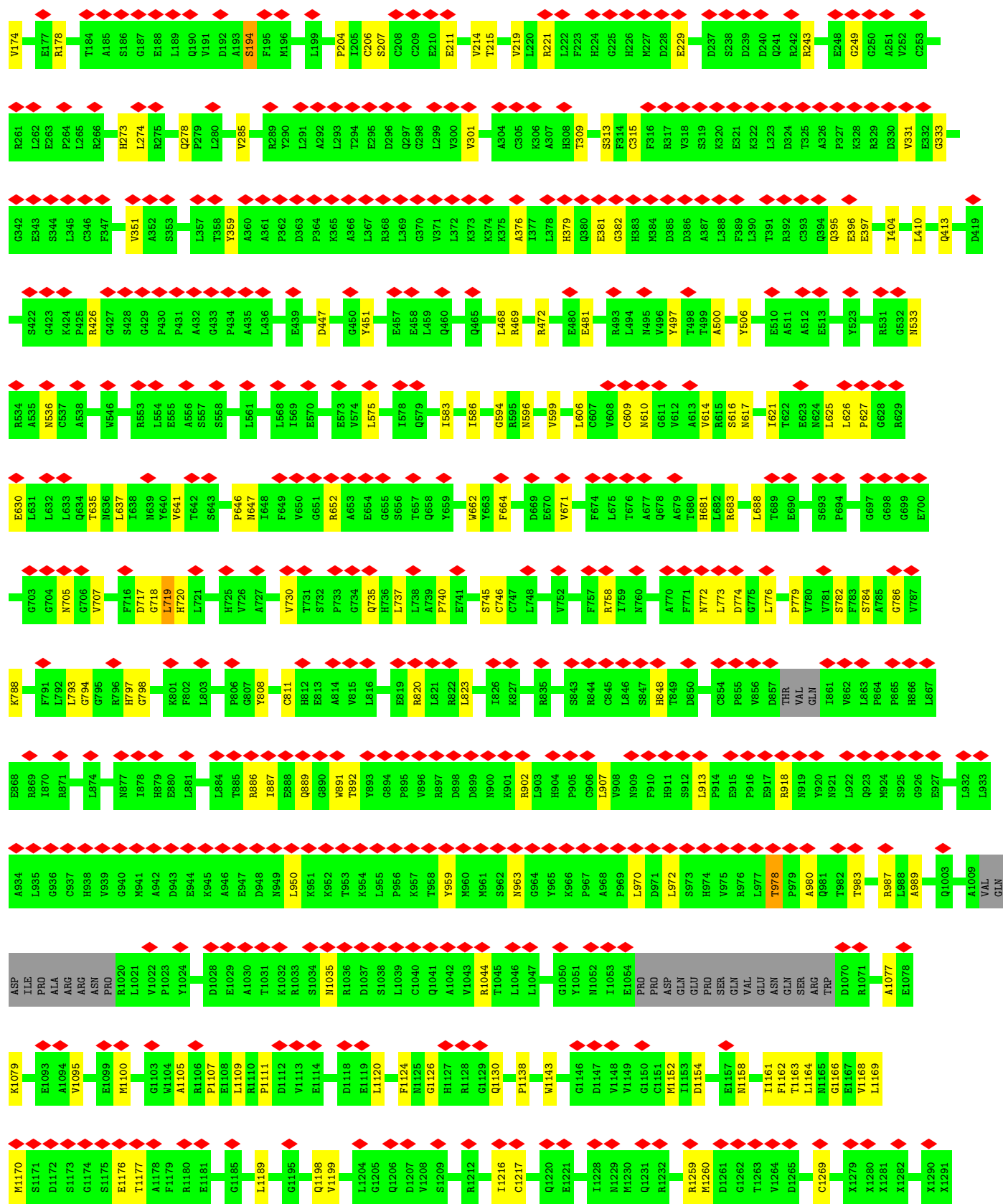


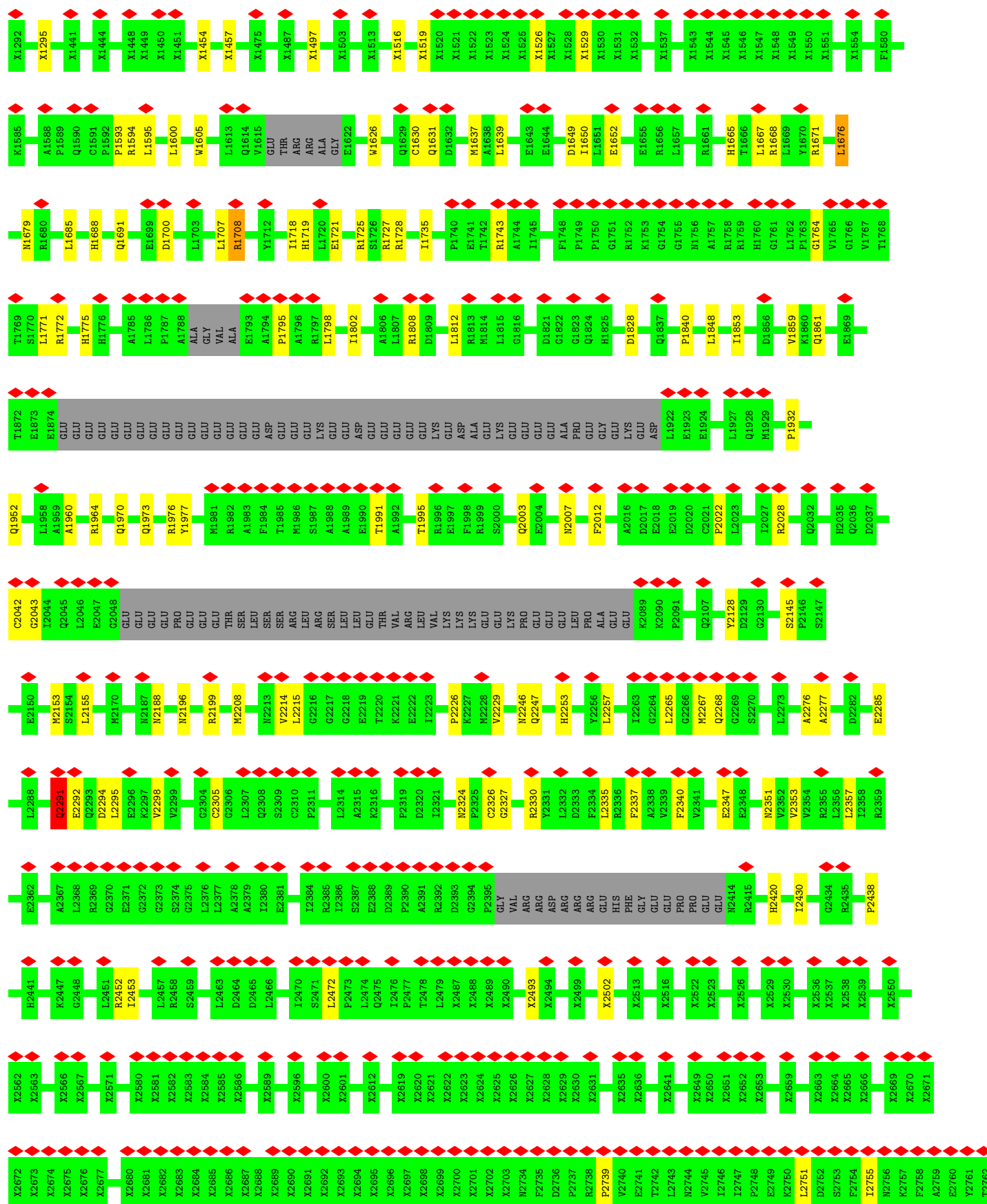


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R2369	Q2370	E2371	Q2372	Q2373	S2374	Q2375	L2376	L2377	A2378	L2379	I2380	E2381	L2384	R2385	I2386	S2387	E2388	D2389	P2390	A2391	R2392	D2393	Q2394	P2395	GLY	VAL	ARG	ARG	ASP	ARG	ARG	GLU	PHE	GLY	PRO	PRO	GLU	N2414	R2415	H2420	Q2434	R2435	P2438	H2441	K2447	G2448	L2451			
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X1280	X1281	X1282	X1290	X1291	X1292	X1295	X1441	X1448	X1451	X1454	X1457	X1475	X1487	X1497	X1503	X1513	X1516	X1519	X1520	X1521	X1522	X1523	X1524	X1525	X1526	X1527	X1528	X1529	X1530	X1531	X1532	X1537	X1543	X1544	X1545	X1546	X1547	X1548	X1549	X1550	X1551	X1554								

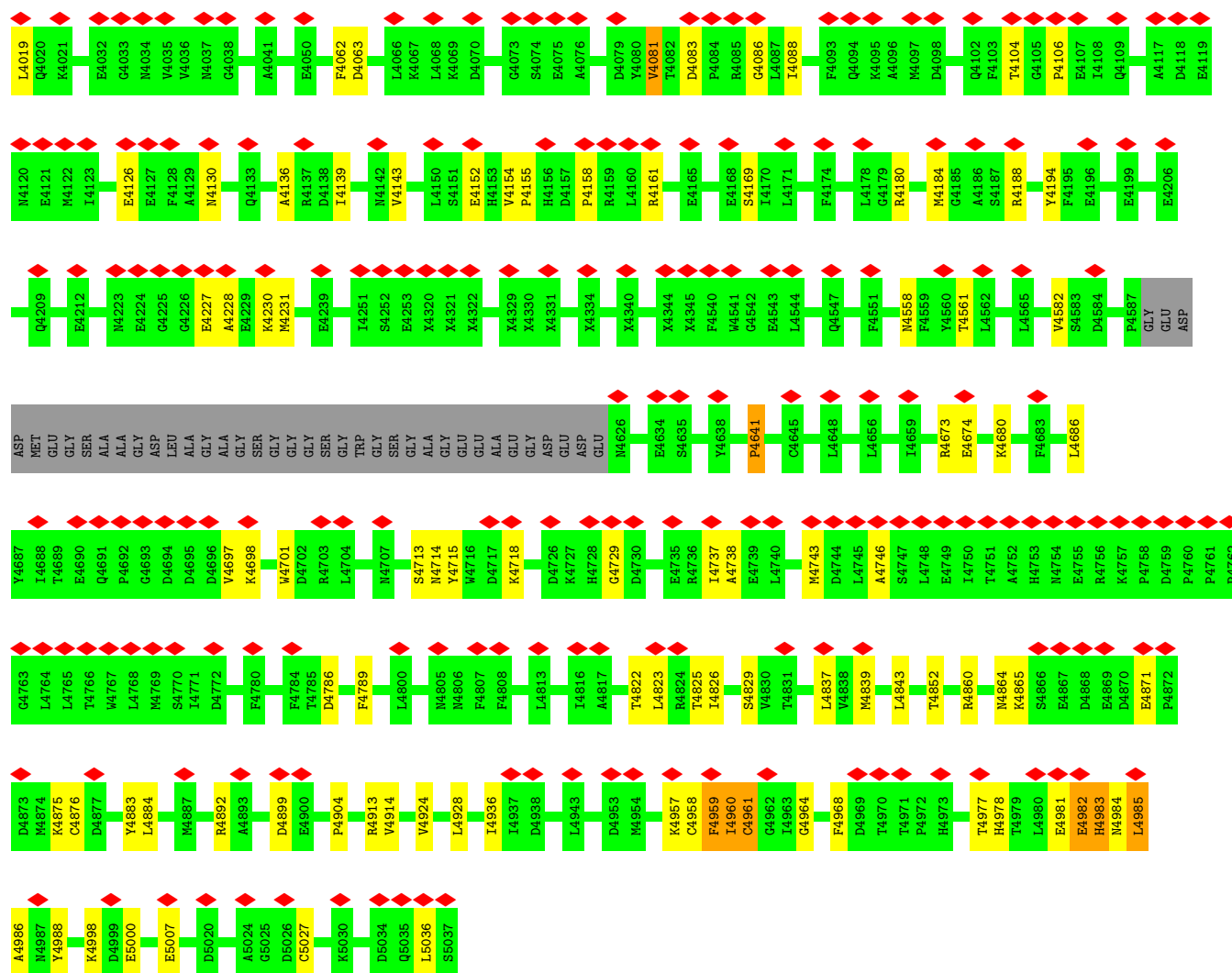




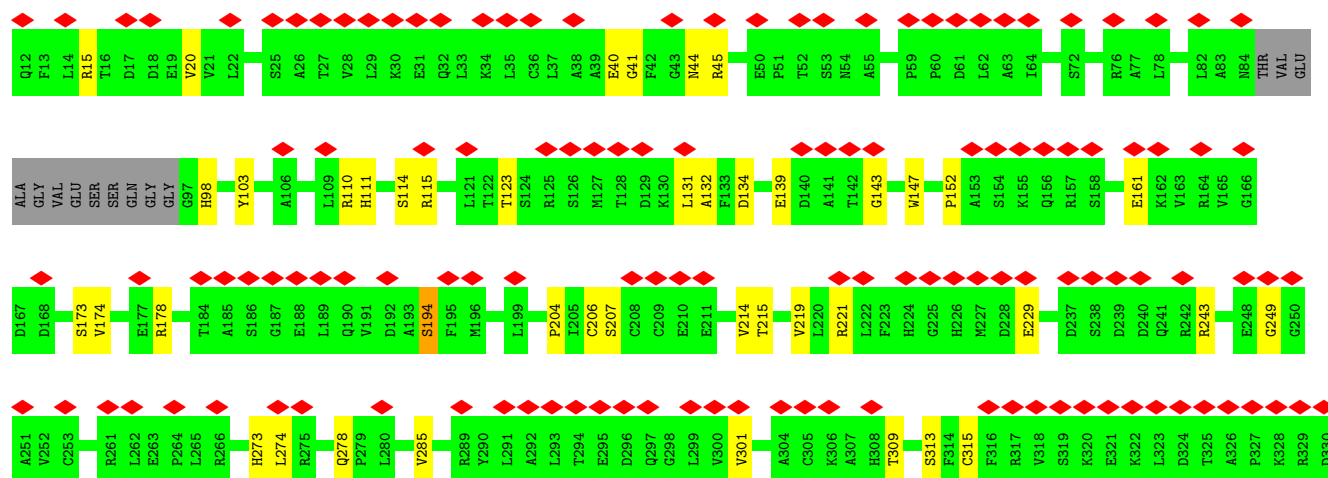
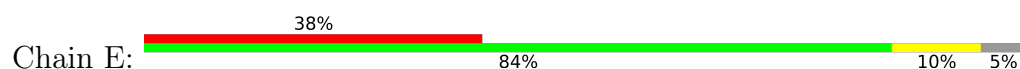


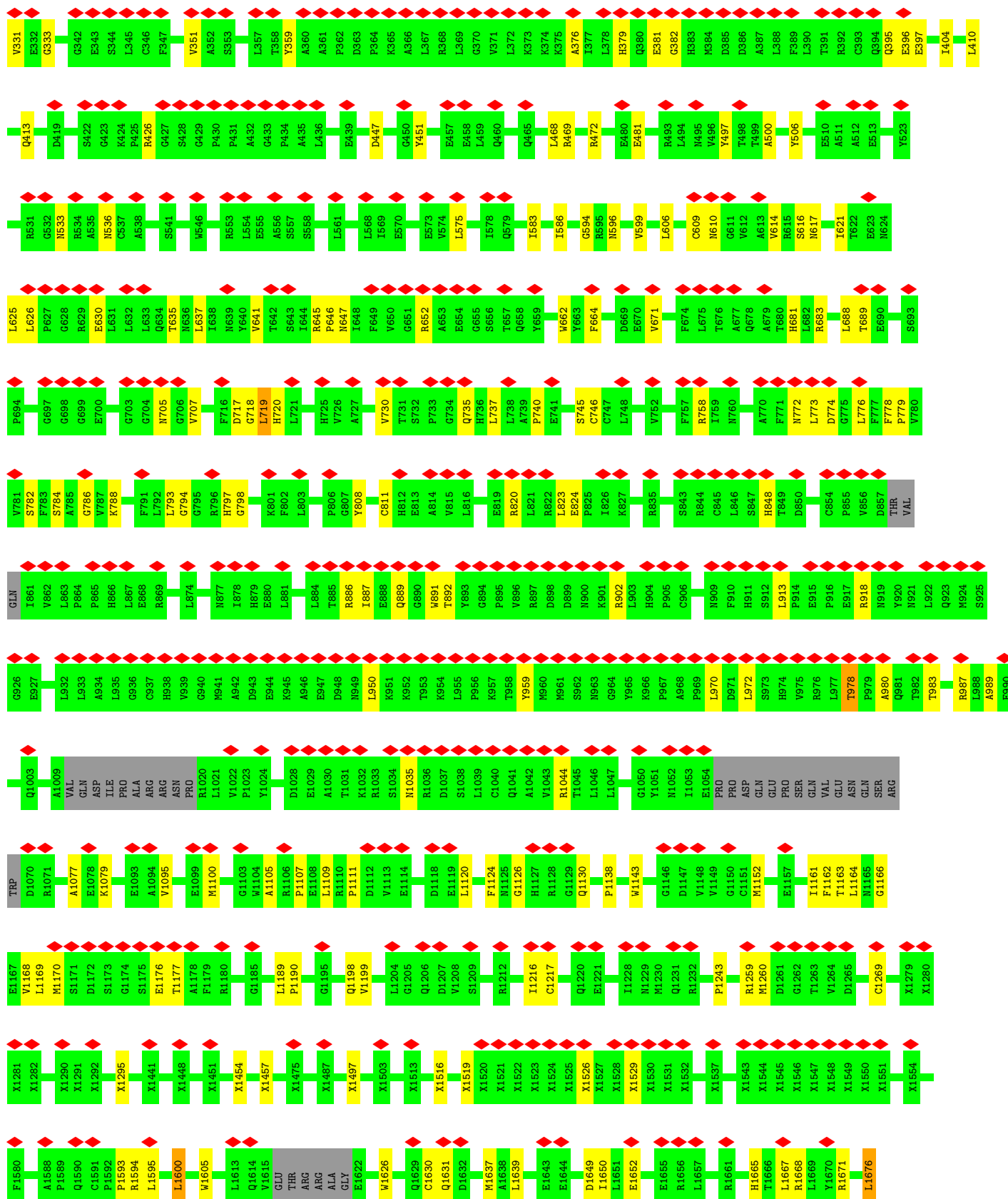


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S3752	F3753	E3757	K3760	Q3761	R3762	Q3766	R3769	T3772	R3773	V3779	L3780	Q3781	G3788	E3789	I3804	L3805	N3809	V3812	K3815	M3816	L3817	D3822	E3825	V3826	G3827	Q3830	Q3833	S3840	V3841	L3842	D3843	G3855	L3856	G3857	M3858	V3859	N3860	E3861	D3862	S4007	S4008	Q4009	D4018																																																				
N3643	H3647	R3648	I3662	L3663	T3664	E3665	D3666	H3667	S3668	F3669	A3680	G3681	E3682	Q3683	E3684	E3685	E3686	E3687	E3688	E3689	V3690	E3691	E3692	K3693	K3694	L3710	T3711	E3712	K3713	S3714	K3715	L3716	D3717	E3718	D3719	M3723	L3735	E3736	E3737	G3738	G3739	E3740	N3741	GLY	GLU	ALA	GLU	E3747	E3748	V3749	E3750	V3751																																											
X3436	X3437	X3441	X3442	X3443	X3446	X3447	X3452	X3453	X3454	X3457	X3463	X3464	X3465	X3466	X3467	X3468	X3469	X3470	X3471	X3472	X3473	X3474	X3475	X3476	X3477	X3478	X3479	X3480	X3481	X3482	X3483	X3484	X3485	X3486	X3487	X3488	X3489	X3490	X3491	X3492	X3493	X3494	X3495	X3496	X3497	X3498	X3499	X3500	X3501	X3502	X3503	X3504	X3505	X3506	X3507	X3508	X3509	X3510	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
X3359	X3360	X3361	X3362	X3363	X3364	X3365	X3366	X3367	X3368	X3369	X3372	X3373	X3374	X3375	X3376	X3377	X3378	X3379	X3380	X3381	X3382	X3383	X3384	X3385	X3388	X3389	X3390	X3391	X3392	X3393	X3394	X3395	X3396	X3397	X3398	X3399	X3400	X3401	X3402	X3405	X3406	X3407	X3408	X3409	X3410	X3411	X3412	X3413	X3414	X3415	X3416	X3423	X3432	X3433																																									
X3285	X3286	X3287	X3288	X3289	X3290	X3291	X3292	X3293	X3294	X3295	X3296	X3297	X3301	X3302	X3303	X3304	X3311	X3312	X3313	X3314	X3315	X3316	X3317	X3318	X3323	X3327	X3331	X3332	X3333	X3334	X3335	X3336	X3337	X3338	X3339	X3340	X3341	X3342	X3343	X3344	X3345	X3346	X3347	X3348	X3349	X3350	X3351	X3352	X3353	X3354	X3355	X3356	X3357	X3358																																									
X3214	X3215	X3216	X3217	X3218	X3219	X3220	X3221	X3222	X3223	X3224	X3225	X3226	X3227	X3228	X3229	X3230	X3231	X3232	X3233	X3234	X3235	X3236	X3241	X3242	X3243	X3244	X3245	X3246	X3247	X3248	X3249	X3250	X3251	X3252	X3253	X3254	X3261	X3262	X3263	X3264	X3267	X3268	X3269	X3270	X3271	X3272	X3273	X3274	X3275	X3276	X3277	X3278	X3279	X3280	X3281	X3282	X3283	X3284																																					
X3048	X3049	X3050	X3057	X3062	X3063	X3134	X3135	X3136	X3137	X3138	X3139	X3142	X3143	X3144	X3146	X3154	X3158	X3159	X3160	X3161	X3162	X3163	X3170	X3171	X3172	X3173	X3174	X3175	X3176	X3177	X3178	X3181	X3190	X3191	X3192	X3193	X3194	X3195	X3196	X3197	X3200	X3201	X3202	X3203	X3204	X3205	X3211	X3212	X3213																																														
X2945	X2946	X2947	X2948	X2949	X2950	X2951	X2952	X2953	X2954	X2962	X2963	X2964	X2968	X2969	X2970	X2973	X2974	X2975	X2976	X2995	X2996	X2997	X2998	X2999	X3000	X3001	X3006	X3007	X3008	X3014	X3017	X3021	X3022	X3023	X3027	X3028	X3034	X3035	X3036	X3037	X3038	X3039	X3040	X3041	X3042	X3043	X3044	X3045	X3046	X3047																																													
H2883	N2884	T2885	W2886	G2887	K2888	K2889	K2890	K2891	Q2892	E2893	L2894	E2895	A2896	K2897	Q2898	G2899	T2901	H2902	P2903	L2904	L2905	V2906	P2907	P2908	D2909	T2910	L2911	T2912	A2913	K2914	E2915	K2916	A2917	R2918	D2919	R2920	E2921	K2922	K2928	F2929	L2930	Q2931	M2932	N2933	Q2934	Y2935	A2936	V2937	T2938	R2939	X2942	X2943	X2944																																										
E2763	E2764	K2765	W2766	A2767	F2768	D2769	K2770	I2771	Q2772	R2773	W2774	W2775	S2776	Y2777	Q2778	E2779	W2780	V2781	D2782	E2783	E2784	L2785	K2786	T2787	H2788	P2789	W2790	L2791	R2792	P2793	W2794	K2795	T2796	F2797	S2798	E2799	K2800	D2801	K2802	E2803	T2804	W2805	R2806	W2807	P2808	L2809	K2810	E2811	S2812	L2813	K2814	A2815	W2816	L2817	A2818	W2819	E2820	W2821	T2822																																				
I2823	E2824	K2825	A2826	R2827	E2828	G2829	E2830	GLU	GLU	ARG	THR	GLY	LYS	LYS	THR	ARG	LYS	ILE	SER	GLN	THR	ALA	GLN	THR	TVR	ASP	PRO	ARG	GLU	GLY	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																																					



• Molecule 2: Ryanodine receptor 1







N2884	X2946	X3049	X3215	X3286	X3360	X3436	X3548	N3643	V3749	V3865	K4021	N4122
T2885	X2947	X3050	X3216	X3287	X3361	X3437	X3549	H3647	E3750	I3866	E4032	I4123
G2886	X2948	X3057	X3217	X3288	X3362	X3441	X3550	R3648	V3751	N3867	G4033	E4126
G2887	X2949	X3062	X3218	X3289	X3363	X3442	X3551	I3652	S3752	R3868	N4034	E4127
R2888	X2950	X3063	X3219	X3290	X3364	X3443	X3552	L3653	F3753	Q3869	V4035	F4128
R2889	X2951	X3064	X3220	X3291	X3365	X3444	X3553	L3654	E3757	N3870	V4036	A4129
R2890	X2952	X3065	X3221	X3292	X3366	X3445	X3554	L3655	E3761	G3871	N4037	N4130
R2891	X2953	X3066	X3222	X3293	X3367	X3446	X3555	D3656	K3760	E3872	G4038	D4133
Q2892	X2954	X3067	X3223	X3294	X3368	X3447	X3556	F3659	R3762	K3873	A4041	A4136
E2893	X2955	X3068	X3224	X3295	X3369	X3448	X3557	D3676	Q3766	D3878	E4050	A4137
L2894	X2956	X3069	X3225	X3296	X3370	X3449	X3558	A3680	T3772	N3886	F4062	D4138
E2895	X2957	X3070	X3226	X3297	X3371	X3450	X3559	G3681	R3773	D3887	D4063	I4139
R2896	X2958	X3071	X3227	X3298	X3372	X3451	X3560	E3682	V3779	N3888	L4066	N4142
K2897	X2959	X3072	X3228	X3299	X3373	X3452	X3561	Q3683	Q3781	F3899	K4067	V4143
L2898	X2960	X3073	X3229	X3300	X3374	X3453	X3562	E3684	L3780	T3910	L4068	L4150
E2899	X2961	X3074	X3230	X3301	X3375	X3454	X3563	E3685	Q3788	T3911	S4151	S4151
G2900	X2962	X3075	X3231	X3302	X3376	X3455	X3564	E3686	E3789	R3925	K4069	E4152
K2901	X2963	X3076	X3232	X3303	X3377	X3456	X3565	E3687	G3789	E3928	D4070	V4153
H2902	X2964	X3077	X3233	X3304	X3378	X3457	X3566	E3688	L3804	Y3937	G4073	L4154
P2903	X2965	X3078	X3234	X3305	X3379	X3458	X3567	E3689	L3805	S3938	S4074	V4155
L2904	X2966	X3079	X3235	X3306	X3380	X3459	X3568	V3690	N3809	G3939	K4075	H4156
L2905	X2967	X3080	X3236	X3307	X3381	X3460	X3569	E3691	V3812	K3940	S4076	P4157
V2906	X2968	X3081	X3237	X3308	X3382	X3461	X3570	E3692	K3815	V3942	A4076	R4158
P2907	X2969	X3082	X3238	X3309	X3383	X3462	X3571	K3694	G3816	T3943	D4079	R4159
L2908	X2970	X3083	X3239	X3310	X3384	X3463	X3572	P3695	L3817	E3944	Y4080	L4160
P2909	X2971	X3084	X3240	X3311	X3385	X3464	X3573	L3710	D3822	N3950	Y4081	R4161
T2910	X2972	X3085	X3241	X3312	X3386	X3465	X3574	E3712	E3825	M3955	T4082	E4165
L2911	X2973	X3086	X3242	X3313	X3387	X3466	X3575	K3711	V3826	G3971	P4084	E4168
T2912	X2974	X3087	X3243	X3314	X3388	X3467	X3576	K3712	G3827	P3972	R4085	S4169
A2913	X2975	X3088	X3244	X3315	X3389	X3468	X3577	S3714	G3827	C3973	G4086	L4170
K2914	X2976	X3089	X3245	X3316	X3390	X3469	X3578	K3715	Q3830	N3976	Q4094	L4171
E2915	X2977	X3090	X3246	X3317	X3391	X3470	X3579	L3716	Q3833	H3982	K4095	F4174
L2916	X2978	X3091	X3247	X3318	X3392	X3471	X3580	E3718	L3842	S3983	M4097	L4178
A2917	X2979	X3092	X3248	X3319	X3393	X3472	X3581	D3719	D3843	R3984	D4098	G4179
R2918	X2980	X3093	X3249	X3320	X3394	X3473	X3582	M3723	G3855	H3994	F4102	L4180
D2919	X2981	X3094	X3250	X3321	X3395	X3474	X3583	L3735	L3856	K4002	Q4103	G4185
R2920	X2982	X3095	X3251	X3322	X3396	X3475	X3584	E3736	G3857	D4006	F4104	S4186
E2921	X2983	X3096	X3252	X3323	X3397	X3476	X3585	E3737	K3858	S4007	T4104	S4187
K2922	X2984	X3097	X3253	X3324	X3398	X3477	X3586	G3738	N3859	L4008	G4105	R4188
A2923	X2985	X3098	X3254	X3325	X3399	X3478	X3587	G3739	V3860	E4107	P4106	Y4194
Q2924	X2986	X3099	X3255	X3326	X3400	X3479	X3588	E3740	N3861	I4108	E4109	F4195
E2925	X2987	X3100	X3256	X3327	X3401	X3480	X3589	N3741	E3862	Q4009	Q4117	E4196
L2926	X2988	X3101	X3257	X3328	X3402	X3481	X3590	GLY	G3863	D4018	A4117	E4206
L2927	X2989	X3102	X3258	X3329	X3403	X3482	X3591	ALA	G3864	L4019	D4118	Q4209
L2928	X2990	X3103	X3259	X3330	X3404	X3483	X3592	GLU	T3864	Q4020	E4119	
F2929	X2991	X3104	X3260	X3331	X3405	X3484	X3593	X3610			N4120	
L2930	X2992	X3105	X3261	X3332	X3406	X3485	X3594	X3611			E4121	
Q2931	X2993	X3106	X3262	X3333	X3407	X3486	X3595	X3612				
R2932	X2994	X3107	X3263	X3334	X3408	X3487	X3596	X3613				
G2933	X2995	X3108	X3264	X3335	X3409	X3488	X3597	X3614				
G2934	X2996	X3109	X3265	X3336	X3410	X3489	X3598	X3615				
Y2935	X2997	X3110	X3266	X3337	X3411	X3490	X3599	X3616				
L2936	X2998	X3111	X3267	X3338	X3412	X3491	X3600	X3617				
L2937	X2999	X3112	X3268	X3339	X3413	X3492	X3601	X3618				
L2938	X3000	X3113	X3269	X3340	X3414	X3493	X3602	X3619				
L2939	X3001	X3114	X3270	X3341	X3415	X3494	X3603	X3620				
F2940	X3002	X3115	X3271	X3342	X3416	X3495	X3604	X3621				
X3003	X3003	X3116	X3272	X3343	X3417	X3496	X3605	X3622				
X3004	X3004	X3117	X3273	X3344	X3418	X3497	X3606	X3623				
X3005	X3005	X3118	X3274	X3345	X3419	X3498	X3607	X3624				
X3006	X3006	X3119	X3275	X3346	X3420	X3499	X3608	X3625				
X3007	X3007	X3120	X3276	X3347	X3421	X3500	X3609	X3626				
X3008	X3008	X3121	X3277	X3348	X3422	X3501	X3610	X3627				
X3009	X3009	X3122	X3278	X3349	X3423	X3502	X3611	X3628				
X3010	X3010	X3123	X3279	X3350	X3424	X3503	X3612	X3629				
X3011	X3011	X3124	X3280	X3351	X3425	X3504	X3613	X3630				
X3012	X3012	X3125	X3281	X3352	X3426	X3505	X3614	X3631				
X3013	X3013	X3126	X3282	X3353	X3427	X3506	X3615	X3632				
X3014	X3014	X3127	X3283	X3354	X3428	X3507	X3616	X3633				
X3015	X3015	X3128	X3284	X3355	X3429	X3508	X3617	X3634				
X3016	X3016	X3129	X3285	X3356	X3430	X3509	X3618	X3635				
X3017	X3017	X3130	X3286	X3357	X3431	X3510	X3619	X3636				
X3018	X3018	X3131	X3287	X3358	X3432	X3511	X3620	X3637				
X3019	X3019	X3132	X3288	X3359	X3433	X3512	X3621	X3638				
X3020	X3020	X3133	X3289	X3360	X3434	X3513	X3622	X3639				
X3021	X3021	X3134	X3290	X3361	X3435	X3514	X3623	X3640				
X3022	X3022	X3135	X3291	X3362	X3436	X3515	X3624	X3641				
X3023	X3023	X3136	X3292	X3363	X3437	X3516	X3625	X3642				
X3024	X3024	X3137	X3293	X3364	X3438	X3517	X3626	X3643				
X3025	X3025	X3138	X3294	X3365	X3439	X3518	X3627	X3644				
X3026	X3026	X3139	X3295	X3366	X3440	X3519	X3628	X3645				
X3027	X3027	X3140	X3296	X3367	X3441	X3520	X3629	X3646				
X3028	X3028	X3141	X3297	X3368	X3442	X3521	X3630	X3647				
X3029	X3029	X3142	X3298	X3369	X3443	X3522	X3631	X3648				
X3030	X3030	X3143	X3299	X3370	X3444	X3523	X3632	X3649				
X3031	X3031	X3144	X3300	X3371	X3445	X3524	X3633	X3650				
X3032	X3032	X3145	X3301	X3372	X3446	X3525	X3634	X3651				
X3033	X3033	X3146	X3302	X3373	X3447	X3526	X3635	X3652				
X3034	X3034	X3147	X3303	X3374	X3448	X3527	X3636	X3653				
X3035	X3035	X3148	X3304	X3375	X3449	X3528	X3637	X3654				
X3036	X3036	X3149	X3305	X3376	X3450	X3529	X3638	X3655				
X3037	X3037	X3150	X3306	X3377	X3451	X3530	X3639	X3656				
X3038	X3038	X3151	X3307	X3378	X3452	X3531	X3640	X3657				
X3039	X3039	X3152	X3308	X3379	X3453	X3532	X3641	X3658				
X3040	X3040	X3153	X3309	X3380	X3454	X3533	X3642	X3659				
X3041	X3041	X3154	X3310	X3381	X3455	X3534	X3643	X3660				
X3042	X3042	X3155	X3311	X3382	X3456	X3535	X3644	X3661				
X3043	X3043	X3156	X3312	X3383	X3457	X3536	X3645	X3662				
X3044	X3044	X3157	X3313	X3384	X3458	X3537	X3646	X3663				
X3045	X3045	X3158	X3314	X3385	X3459	X3538	X3647	X3664				
X3046	X3046	X3159	X3315	X3386	X3460	X3539	X3648	X3665				
X3047	X3047	X3160	X3316	X3387	X3461	X3540	X3649	X3666				
X3048	X3048	X3161	X3317	X3388	X3462	X3541	X3650	X3667				
X3049	X3049	X3162	X3318	X3389	X3463	X3542	X3651	X3668				
X3050	X3050	X3163	X3319	X3390	X3464	X3543	X3652	X3669				
X3051	X3051	X3164	X3320	X3391	X3465	X3544	X3653	X3670				
X3052	X3052	X3165	X3321	X3392	X3466	X3545	X3654	X3671				
X3053	X3053	X3166	X3322	X3393	X3467	X3546	X3655	X3672				
X3054	X3054	X3167	X3323	X3394	X3468	X3547	X3656	X3673				
X3055	X3055	X3168	X3324	X3395	X3469	X3548	X3657	X3674				
X3056	X3056	X3169	X3325	X3396	X3470	X3549	X3658	X3675				
X3057	X3057	X3170	X3326	X3397	X3471	X3550	X3659	X3676				
X3058	X3058</											



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	0.147	Depositor
Minimum map value	-0.068	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.05	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	0.19	0/834	0.48	0/1123
1	F	0.19	0/834	0.48	0/1123
1	H	0.19	0/834	0.48	0/1123
1	J	0.19	0/834	0.48	0/1123
2	B	0.20	0/25428	0.51	3/34534 (0.0%)
2	E	0.20	0/25428	0.51	3/34534 (0.0%)
2	G	0.20	0/25428	0.51	3/34534 (0.0%)
2	I	0.20	0/25428	0.51	3/34534 (0.0%)
All	All	0.20	0/105048	0.51	12/142628 (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 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	4960	ILE	N-CA-C	-6.71	105.30	111.67
2	B	4960	ILE	N-CA-C	-6.68	105.33	111.67
2	I	4960	ILE	N-CA-C	-6.68	105.33	111.67
2	E	4960	ILE	N-CA-C	-6.68	105.33	111.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2291	GLN	CA-C-N	5.70	132.43	121.54

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	194	SER	Peptide
2	B	808	TYR	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	7	0
1	F	818	0	824	6	0
1	H	818	0	824	7	0
1	J	818	0	824	6	0
2	B	29499	0	24749	274	0
2	E	29499	0	24749	272	0
2	G	29499	0	24749	275	0
2	I	29499	0	24748	272	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	102291	1086	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 1086 close contacts within the same asymmetric unit are listed below, sorted by

their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:4968:PHE:CE2	2:E:4978:HIS:CE1	2.18	1.32
2:B:4968:PHE:CE2	2:B:4978:HIS:CE1	2.18	1.32
2:I:4968:PHE:CE2	2:I:4978:HIS:CE1	2.18	1.30
2:G:4968:PHE:CE2	2:G:4978:HIS:CE1	2.18	1.30
2:B:4968:PHE:HE2	2:B:4978:HIS:CE1	1.67	1.02

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%)	94 (90%)	11 (10%)	0	100	100
1	H	105/108 (97%)	94 (90%)	11 (10%)	0	100	100
1	J	105/108 (97%)	94 (90%)	11 (10%)	0	100	100
2	B	3235/4416 (73%)	2899 (90%)	330 (10%)	6 (0%)	43	77
2	E	3235/4416 (73%)	2900 (90%)	329 (10%)	6 (0%)	43	77
2	G	3235/4416 (73%)	2900 (90%)	329 (10%)	6 (0%)	43	77
2	I	3235/4416 (73%)	2899 (90%)	330 (10%)	6 (0%)	43	77
All	All	13360/18096 (74%)	11973 (90%)	1363 (10%)	24 (0%)	44	77

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	4985	LEU
2	I	4985	LEU
2	G	4985	LEU
2	E	4985	LEU

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Mol	Chain	Res	Type
2	B	1708	ARG

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%)	2478 (99%)	15 (1%)	78	80
2	E	2493/3022 (82%)	2478 (99%)	15 (1%)	78	80
2	G	2493/3022 (82%)	2478 (99%)	15 (1%)	78	80
2	I	2493/3022 (82%)	2478 (99%)	15 (1%)	78	80
All	All	10324/12444 (83%)	10264 (99%)	60 (1%)	76	80

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	I	4982	GLU
2	E	4959	PHE
2	G	1676	LEU
2	E	4154	VAL
2	E	4983	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 234 such sidechains are listed below:

Mol	Chain	Res	Type
2	I	4102	GLN
2	E	3994	HIS
2	G	1691	GLN
2	E	3960	GLN

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Mol	Chain	Res	Type
2	E	1691	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no 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	I	14

Continued on next page...

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Mol	Chain	Number of breaks
2	G	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	73.83
1	I	4345:UNK	C	4540:PHE	N	73.83
1	G	4345:UNK	C	4540:PHE	N	73.83
1	E	4345:UNK	C	4540:PHE	N	73.83
1	B	3613:UNK	C	3639:THR	N	45.16

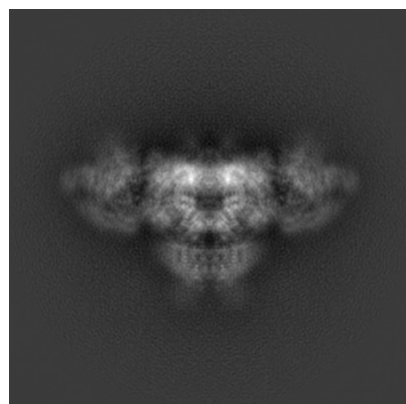
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8390. These allow visual inspection of the internal detail of the map and identification of artifacts.

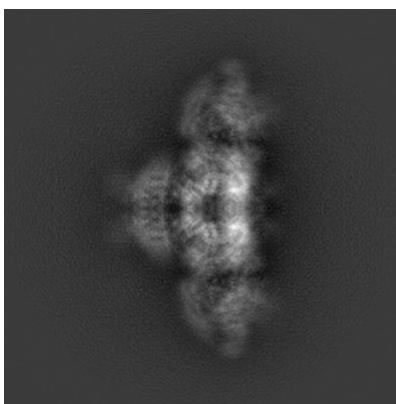
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

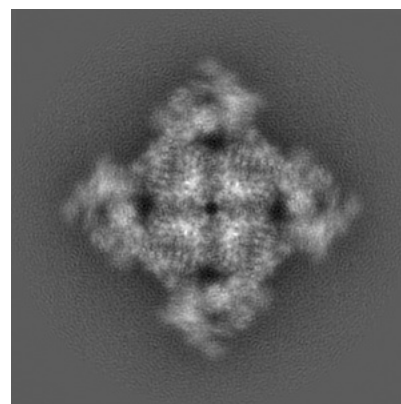
6.1.1 Primary map



X

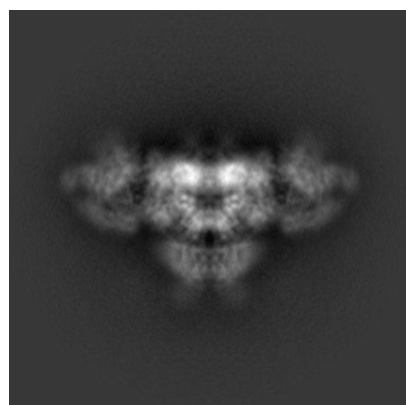


Y

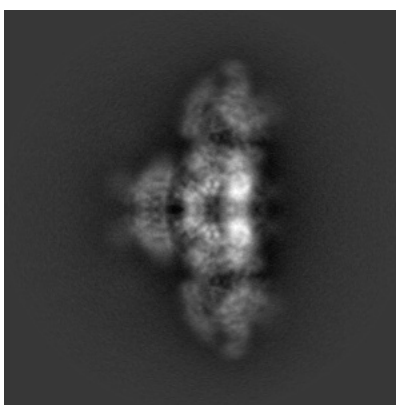


Z

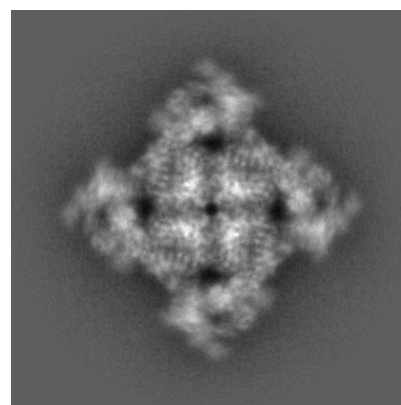
6.1.2 Raw map



X



Y



Z

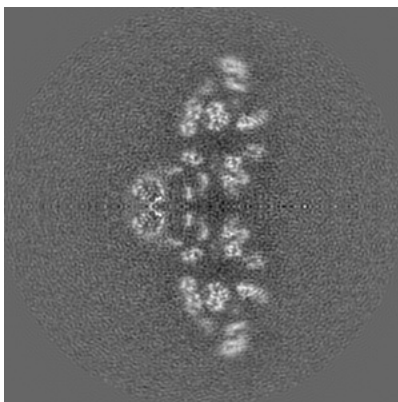
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

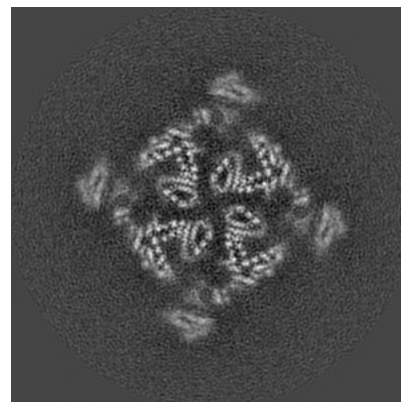
6.2.1 Primary map



X Index: 200

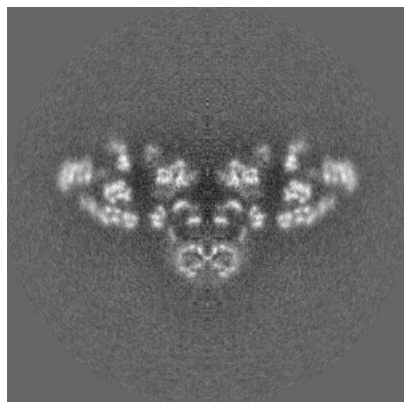


Y Index: 200

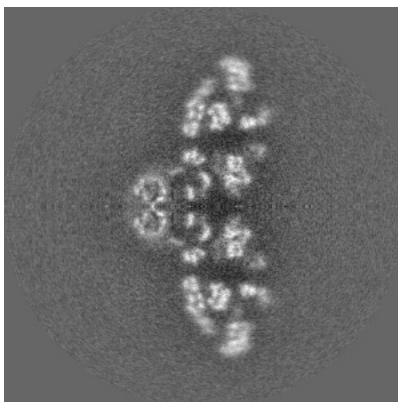


Z Index: 200

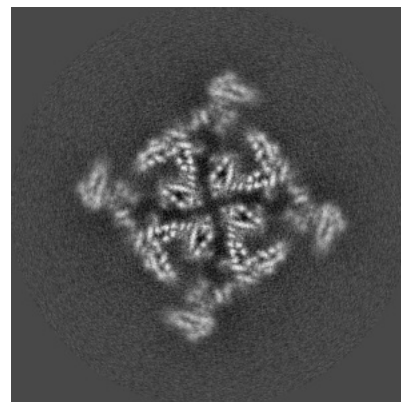
6.2.2 Raw map



X Index: 200



Y Index: 200

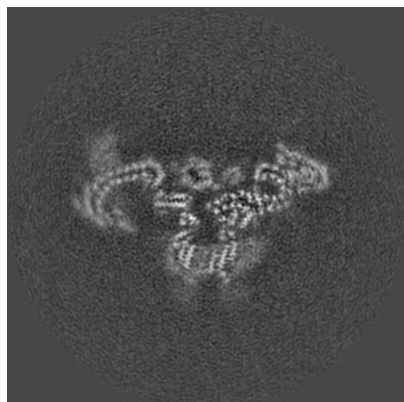


Z Index: 200

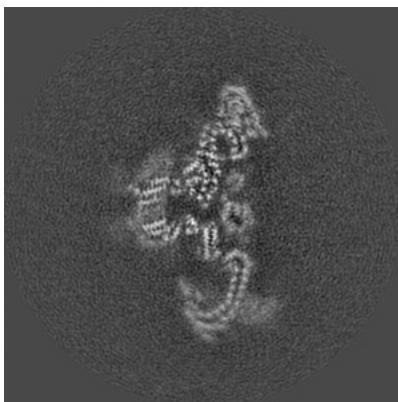
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

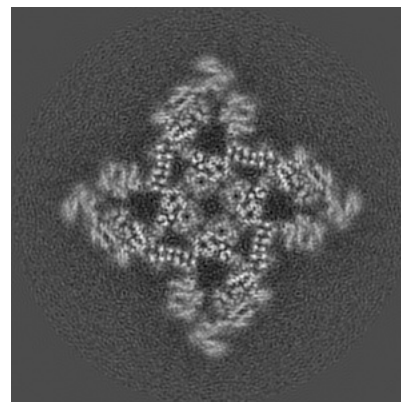
6.3.1 Primary map



X Index: 175

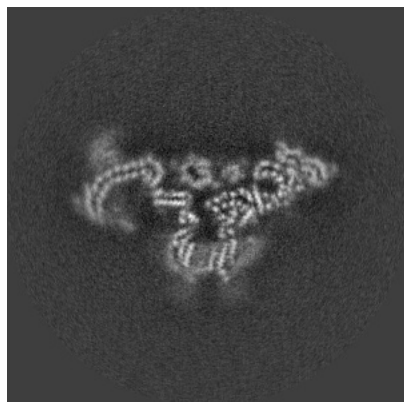


Y Index: 225

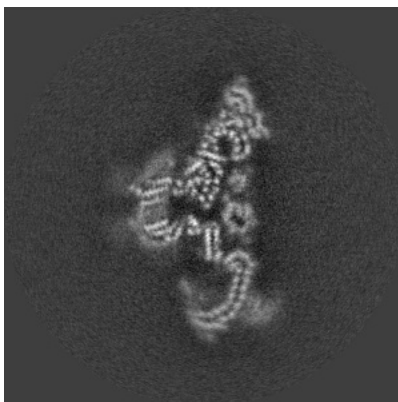


Z Index: 227

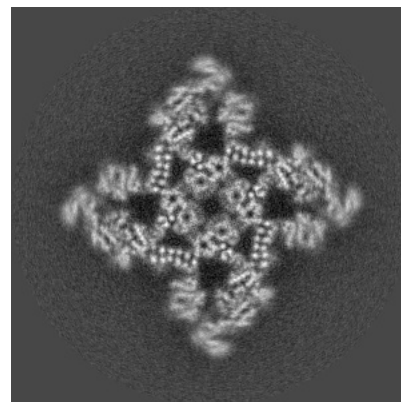
6.3.2 Raw map



X Index: 175



Y Index: 225

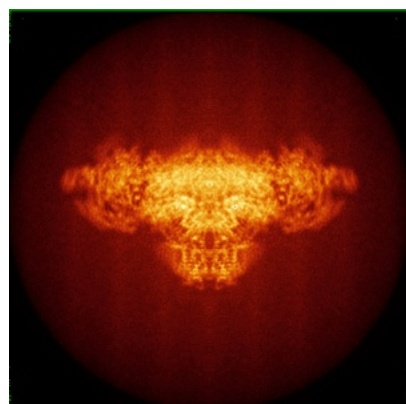


Z Index: 229

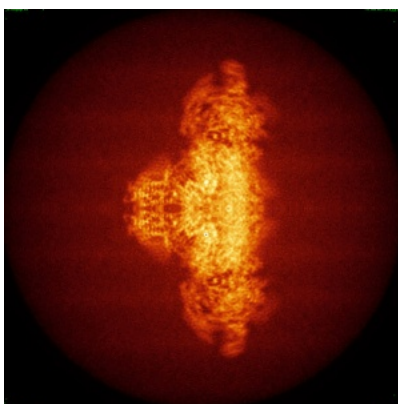
The images above show the largest variance slices of the map in three orthogonal directions.

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

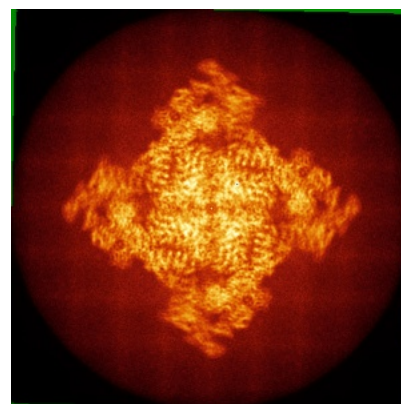
6.4.1 Primary map



X

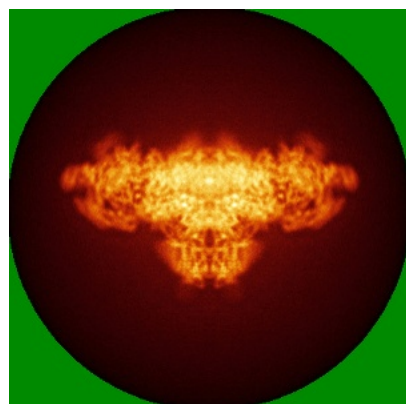


Y

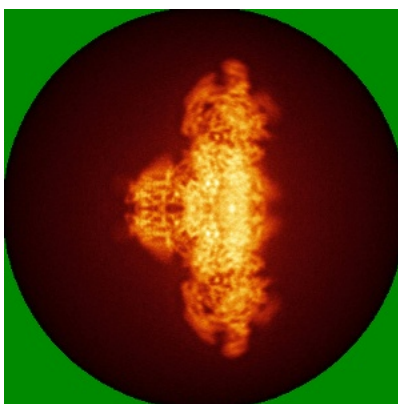


Z

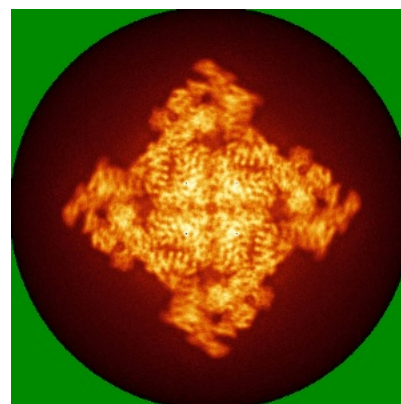
6.4.2 Raw map



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.

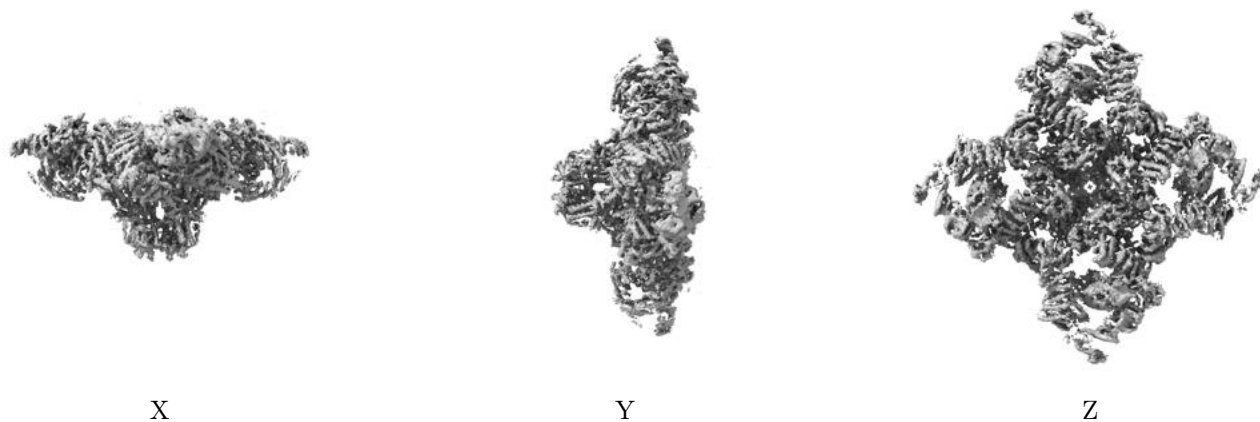
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.05. 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.

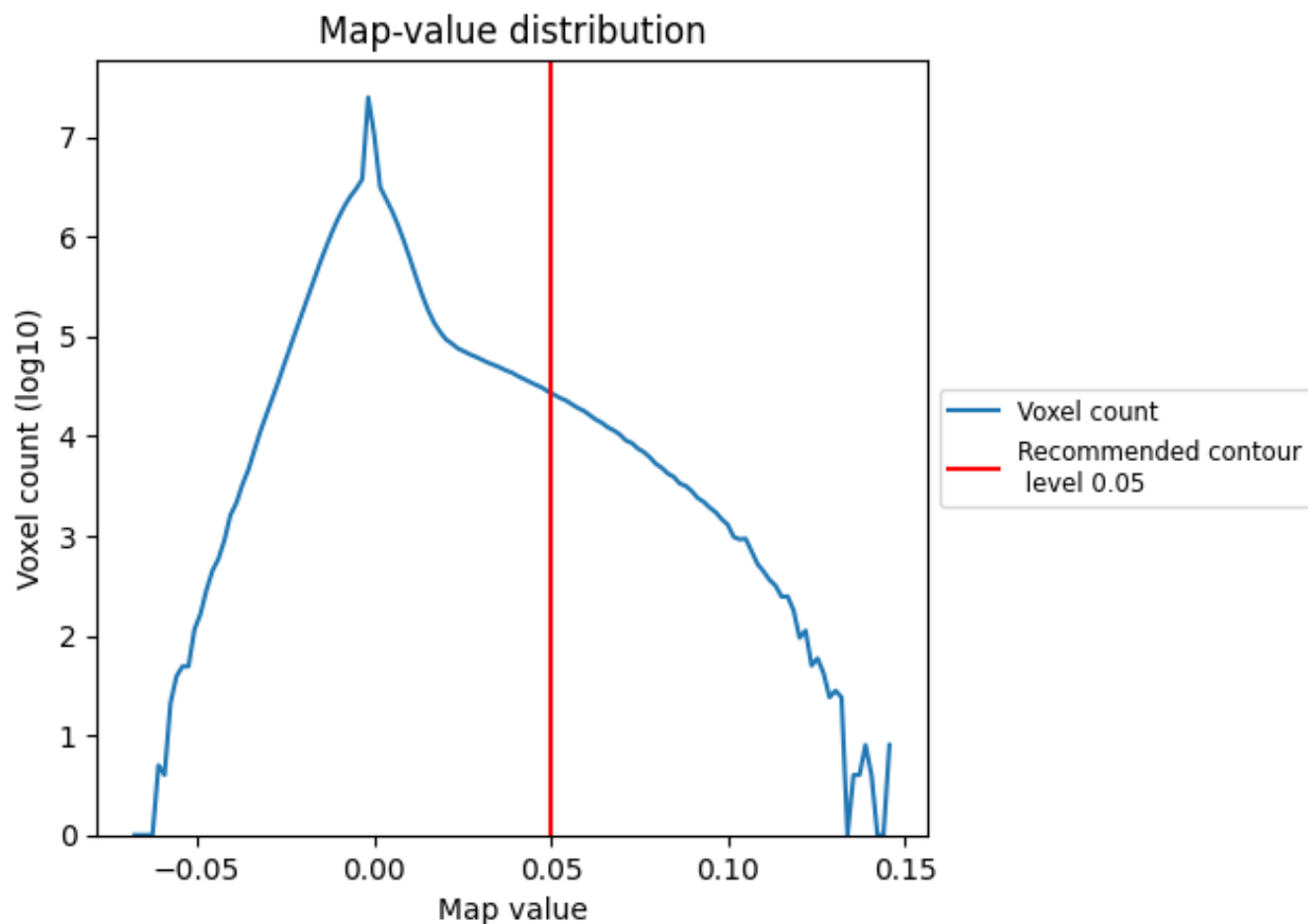
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

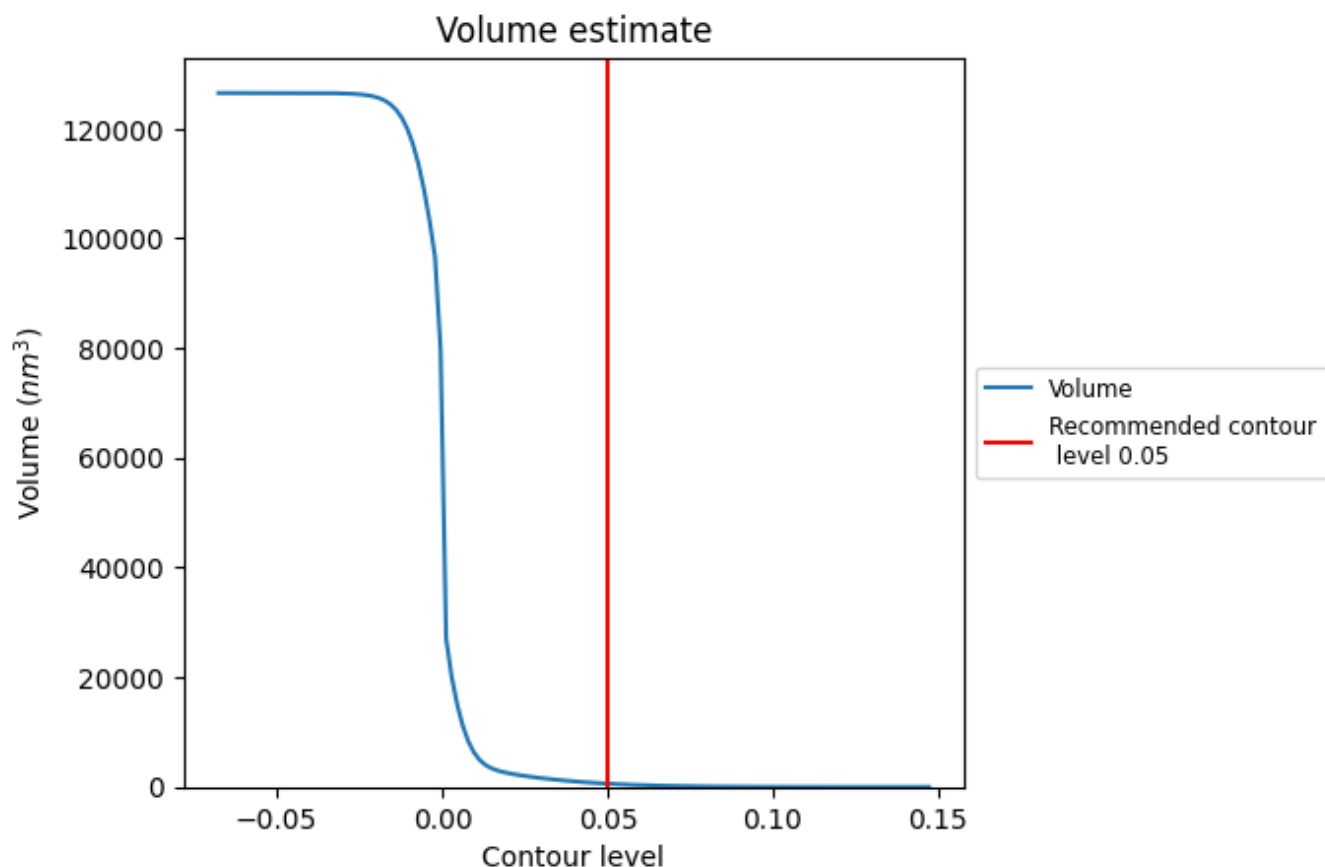
This section contains the results of statistical analysis of the map.

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.

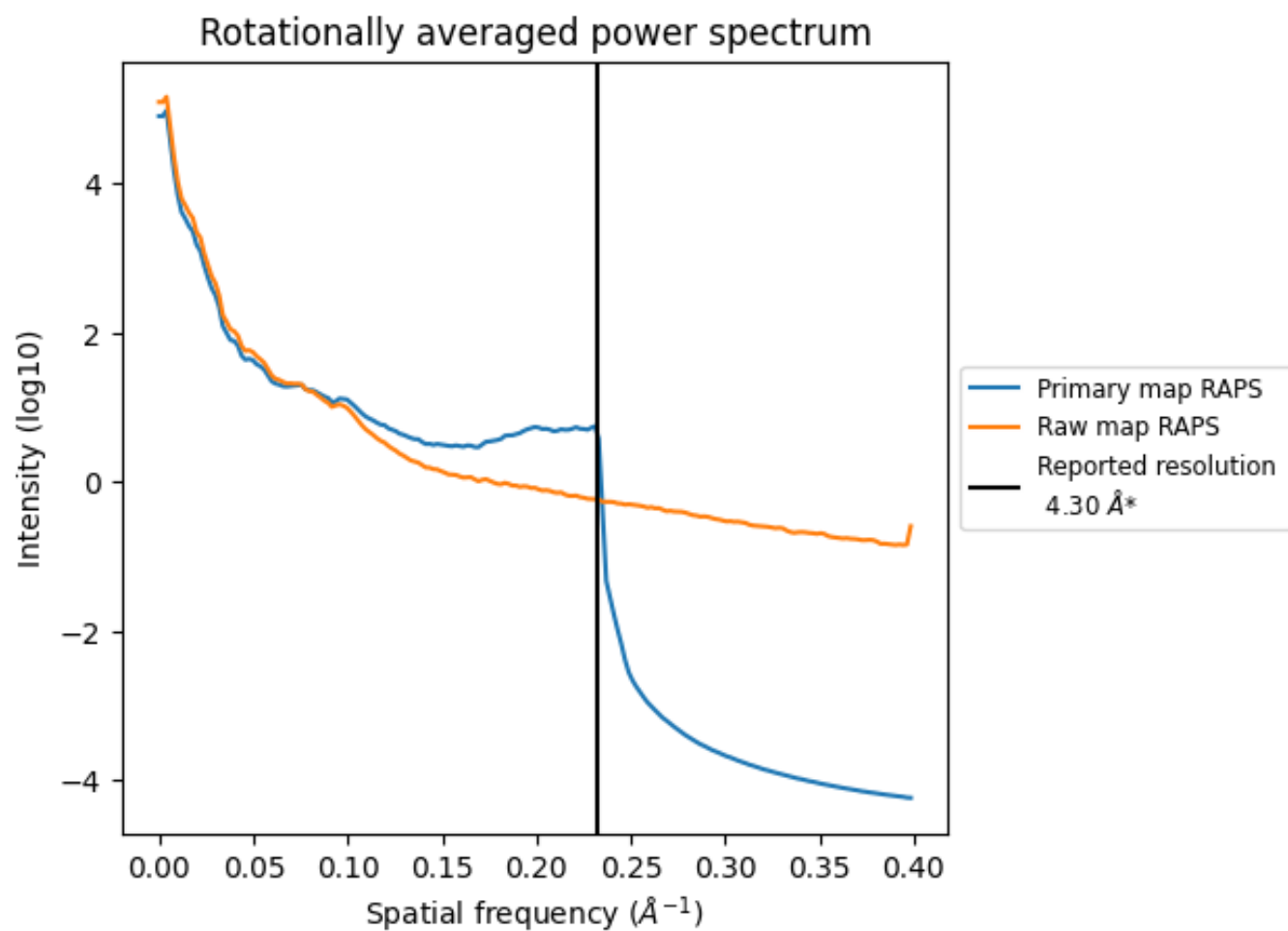
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 603 nm^3 ; this corresponds to an approximate mass of 545 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 ⓘ

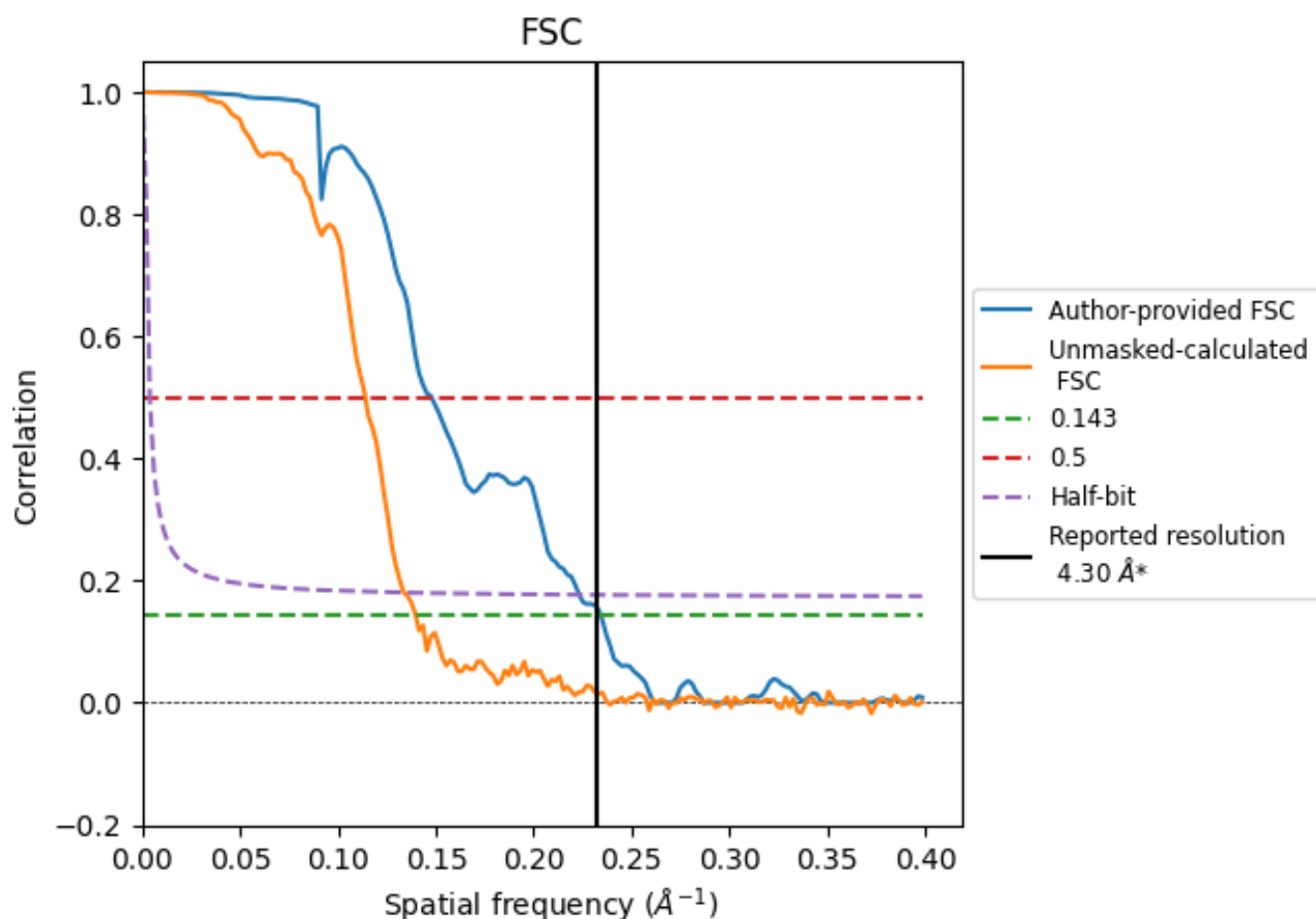


*Reported resolution corresponds to spatial frequency of 0.233 Å⁻¹

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 $0.233 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

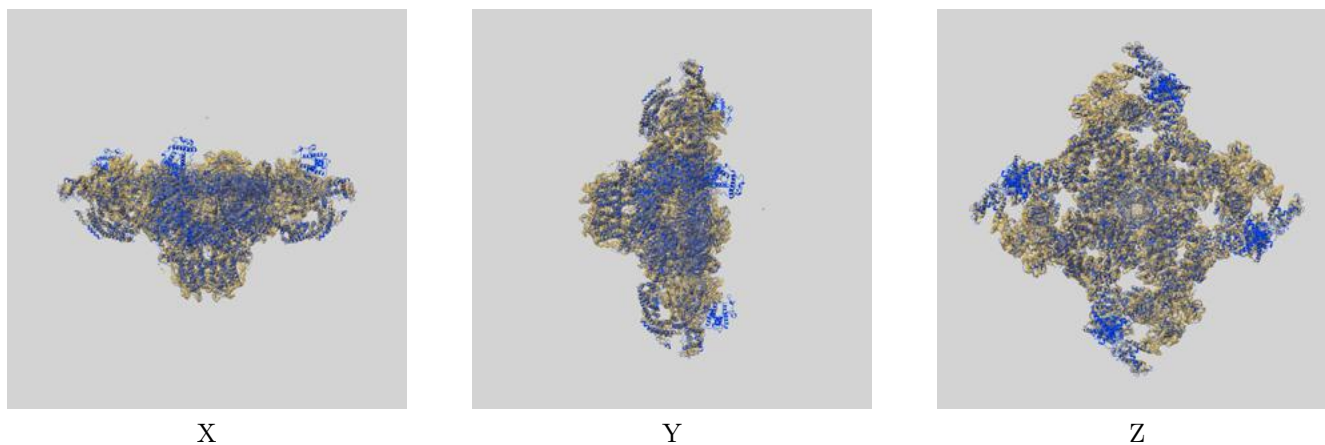
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.30	-	-
Author-provided FSC curve	4.27	6.77	4.48
Unmasked-calculated*	7.16	8.77	7.49

*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 7.16 differs from the reported value 4.3 by more than 10 %

9 Map-model fit [i](#)

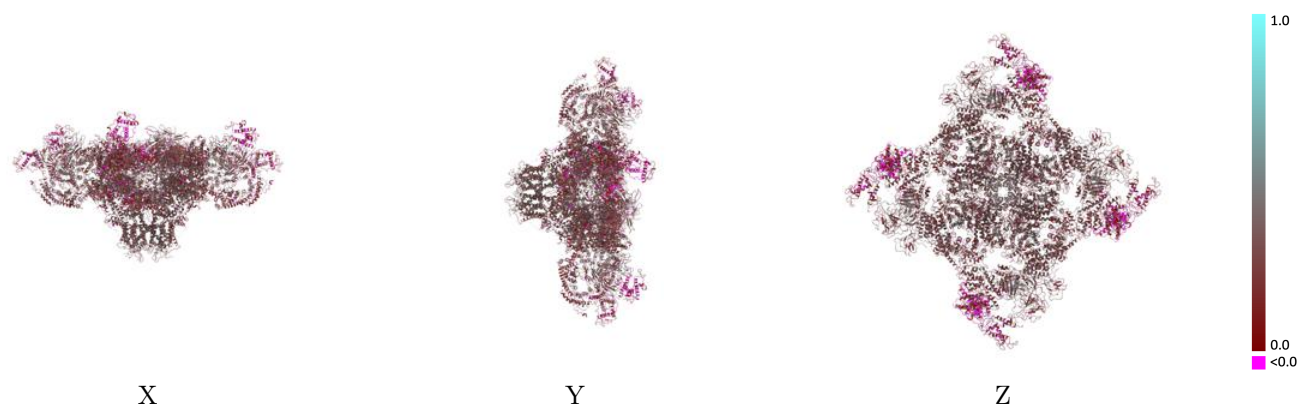
This section contains information regarding the fit between EMDB map EMD-8390 and PDB model 5TAZ. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



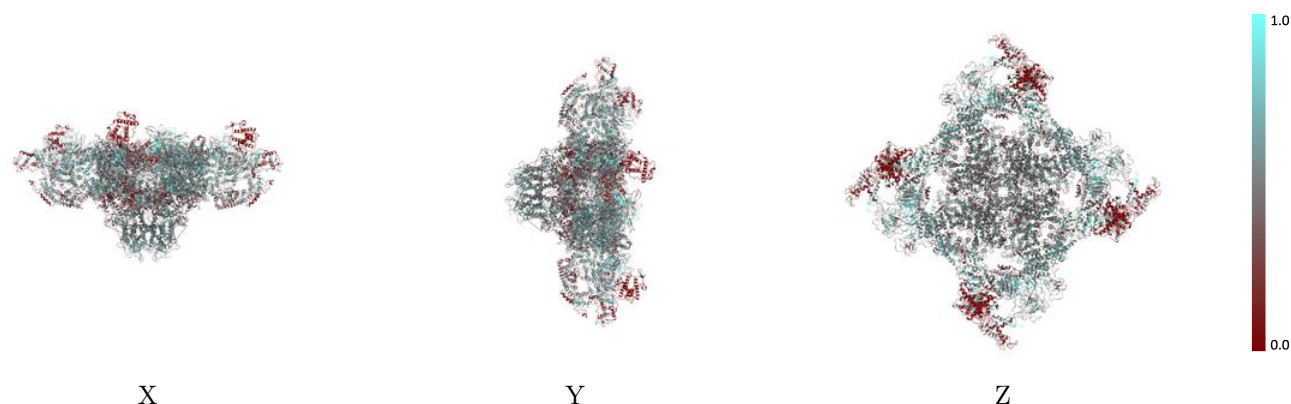
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



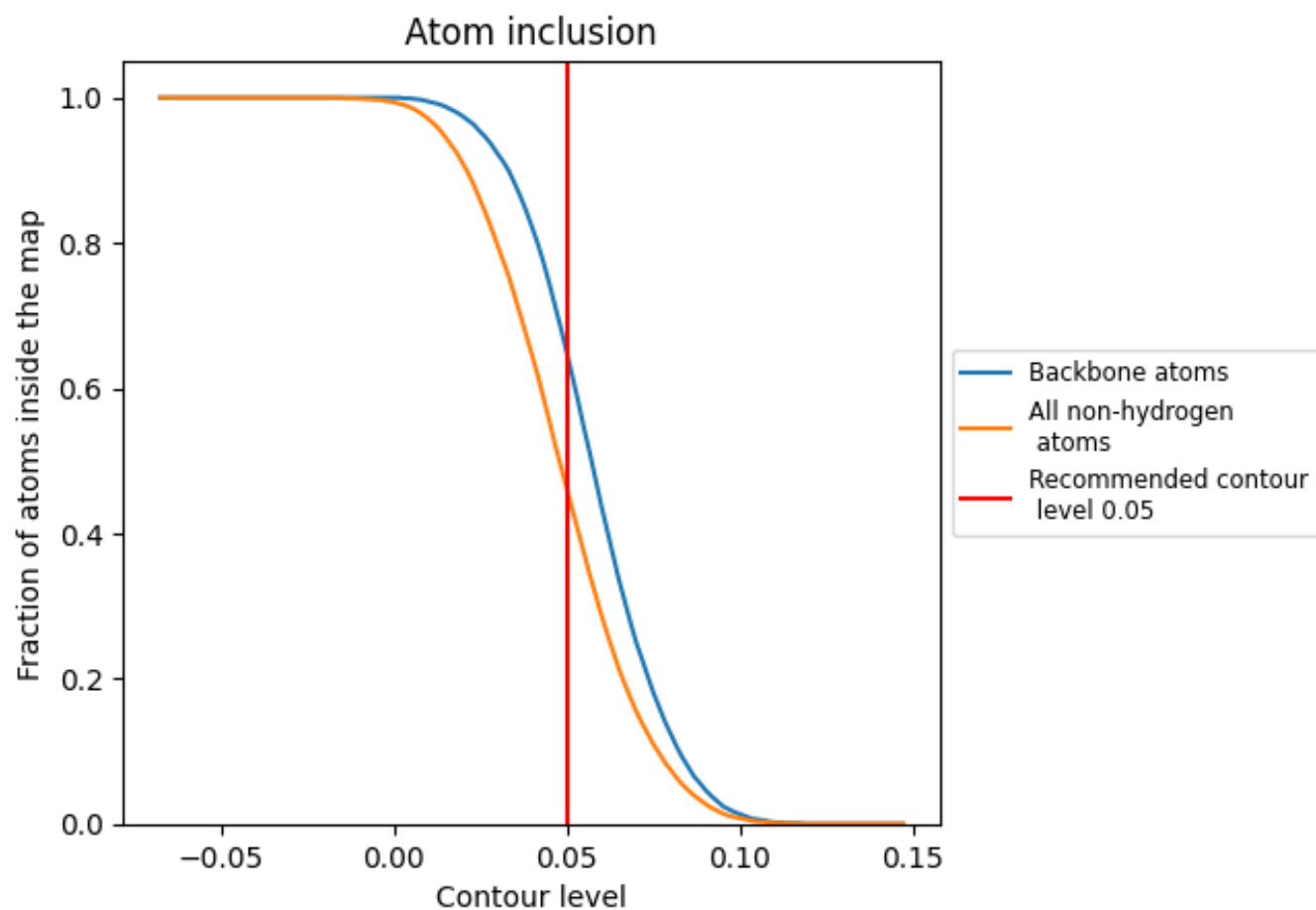
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 46% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4620	0.2730
A	0.4880	0.2880
B	0.4610	0.2730
E	0.4610	0.2730
F	0.4860	0.2930
G	0.4610	0.2730
H	0.4850	0.2930
I	0.4610	0.2730
J	0.4910	0.2910

1.0

0.0

<0.0