



wwPDB EM Validation Summary Report ⓘ

Feb 25, 2024 – 10:17 AM EST

PDB ID : 7JMJ
EMDB ID : EMD-22396
Title : Functional Pathways of Biomolecules Retrieved from Single-particle Snapshots
- Frame 37 - State 5 (S5)
Authors : Dashti, A.; des Georges, A.; Frank, J.; Ourmazd, A.
Deposited on : 2020-07-31
Resolution : 4.50 Å(reported)
Based on initial model : 5TB4

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

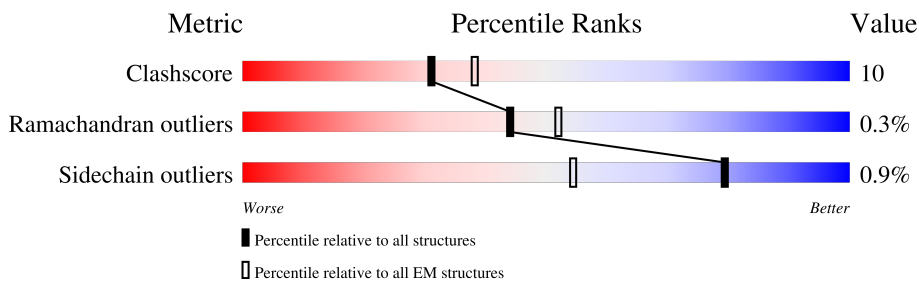
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.50 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 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	107	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">36%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 36%, orange 36%, yellow 70%, green 70%, yellow 80%, grey 80%);"></div> <div style="text-align: center;">70%</div> <div style="text-align: center;">30%</div> </div>
1	F	107	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">52%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 52%, orange 52%, yellow 73%, green 73%, yellow 80%, grey 80%);"></div> <div style="text-align: center;">73%</div> <div style="text-align: center;">27%</div> </div>
1	H	107	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">52%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 52%, orange 52%, yellow 72%, green 72%, yellow 80%, grey 80%);"></div> <div style="text-align: center;">72%</div> <div style="text-align: center;">28%</div> </div>
1	J	107	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">52%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 52%, orange 52%, yellow 72%, green 72%, yellow 80%, grey 80%);"></div> <div style="text-align: center;">72%</div> <div style="text-align: center;">28%</div> </div>
2	B	4687	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">39%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 39%, orange 39%, yellow 70%, green 70%, yellow 80%, grey 80%);"></div> <div style="text-align: center;">70%</div> <div style="text-align: center;">19%</div> <div style="text-align: center;">11%</div> </div>
2	E	4687	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">44%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 44%, orange 44%, yellow 70%, green 70%, yellow 80%, grey 80%);"></div> <div style="text-align: center;">70%</div> <div style="text-align: center;">18%</div> <div style="text-align: center;">11%</div> </div>
2	G	4687	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">49%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 49%, orange 49%, yellow 70%, green 70%, yellow 80%, grey 80%);"></div> <div style="text-align: center;">70%</div> <div style="text-align: center;">19%</div> <div style="text-align: center;">11%</div> </div>
2	I	4687	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">48%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 48%, orange 48%, yellow 70%, green 70%, yellow 80%, grey 80%);"></div> <div style="text-align: center;">70%</div> <div style="text-align: center;">18%</div> <div style="text-align: center;">11%</div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 120756 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Peptidyl-prolyl cis-trans isomerase FKBP1B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	107	818	516	144	154	4	0	0
1	F	107	818	516	144	154	4	0	0
1	H	107	818	516	144	154	4	0	0
1	J	107	818	516	144	154	4	0	0

- Molecule 2 is a protein called ryanodine receptor type 1.

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

- 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	E	1	Total	Zn	0
			1	1	
3	G	1	Total	Zn	0
			1	1	
3	I	1	Total	Zn	0
			1	1	

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca) (labeled as "Ligand of

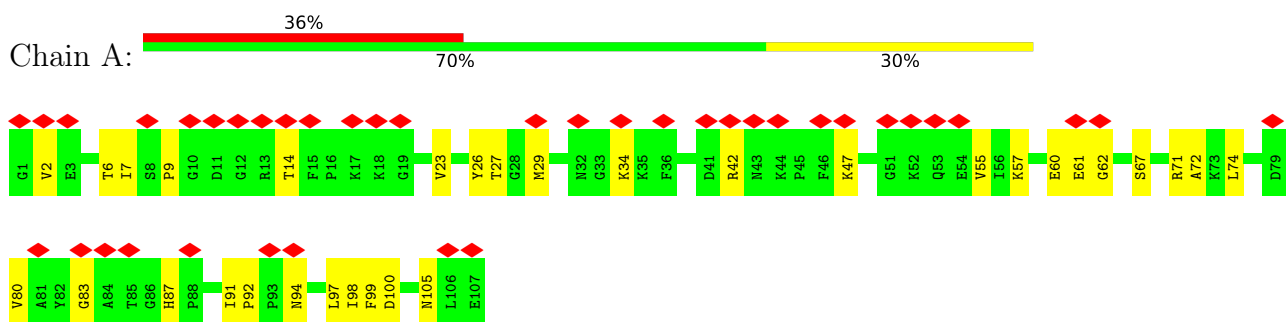
Interest" by depositor).

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

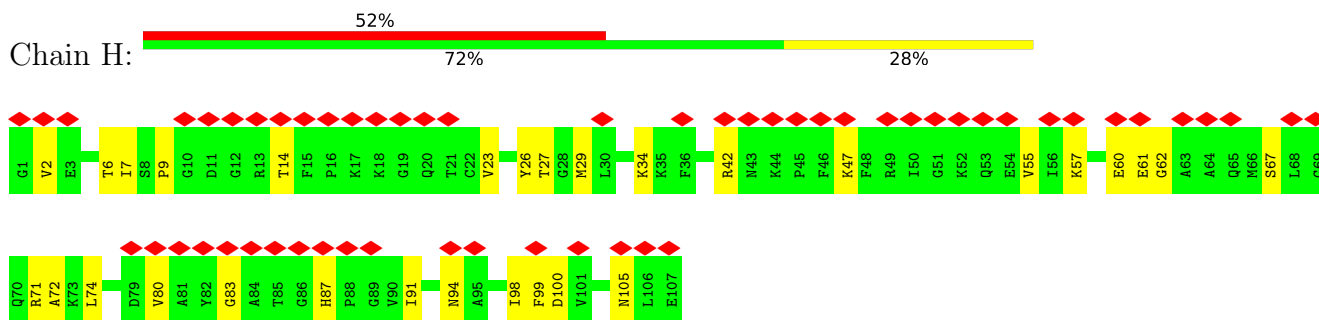
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



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

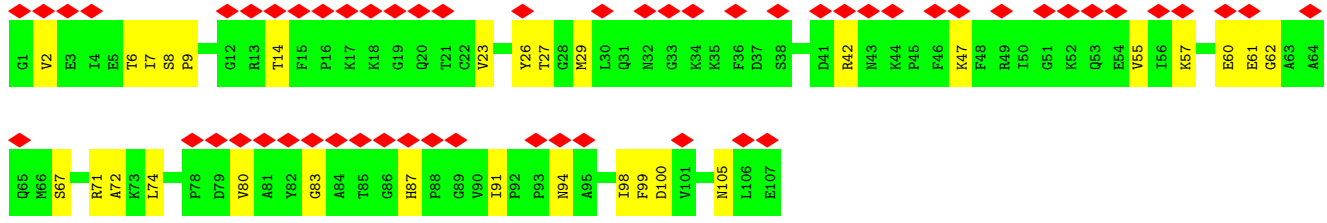


- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

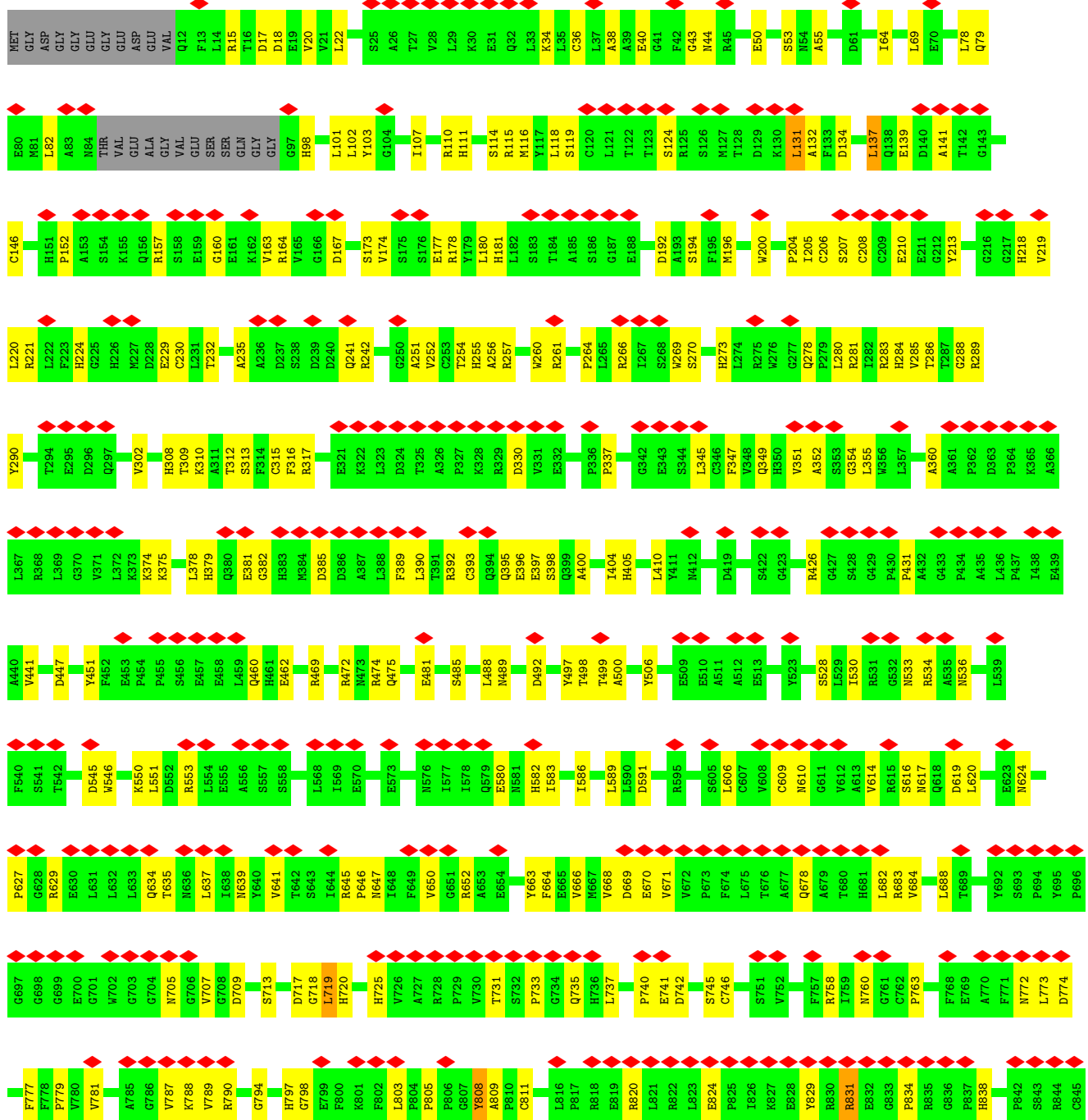


- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

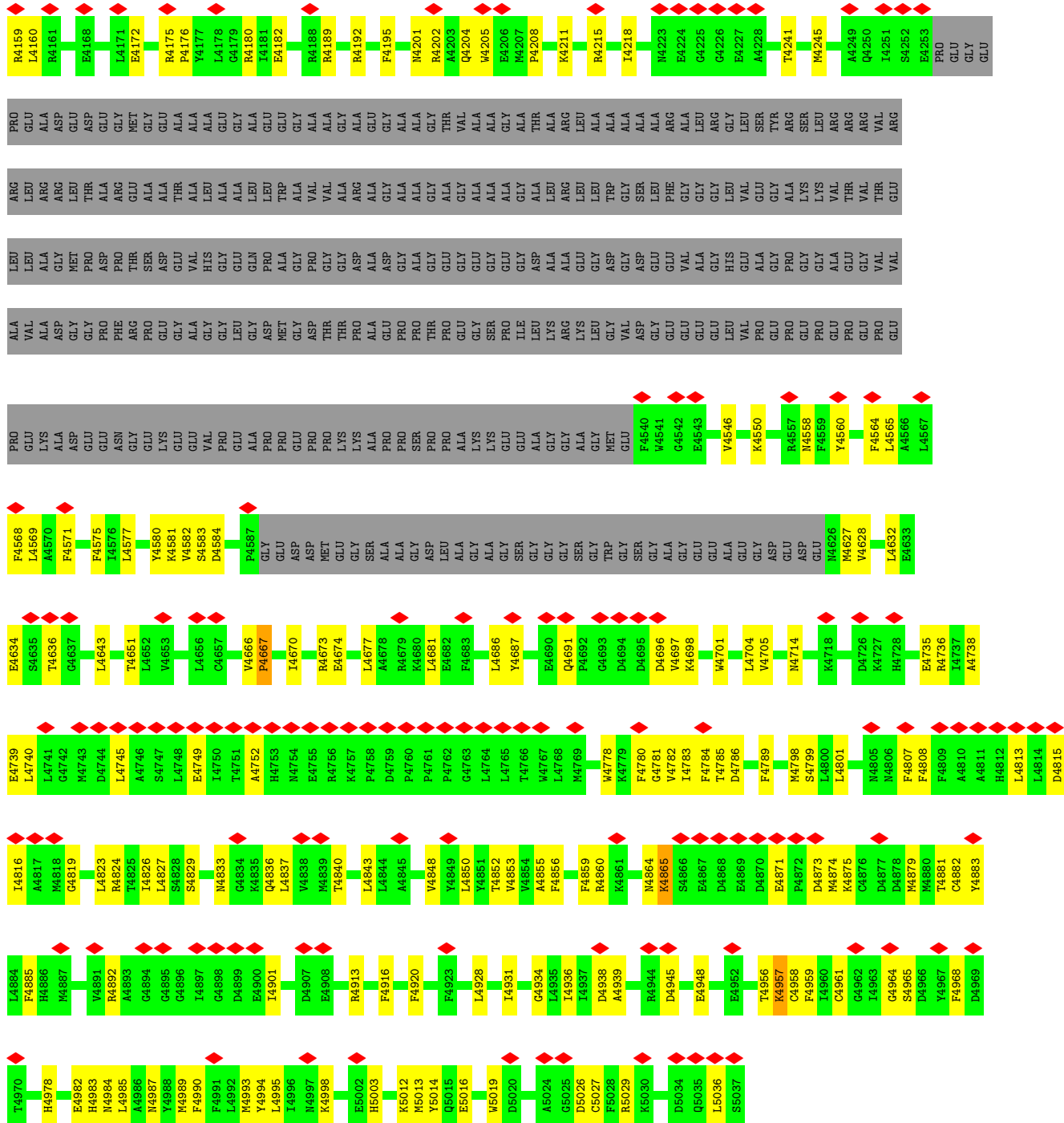




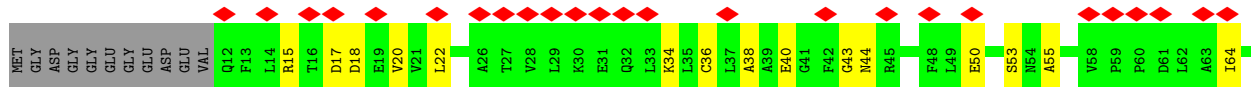
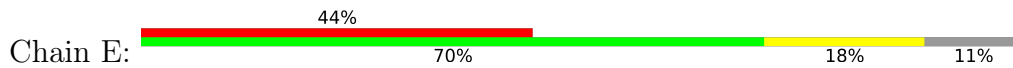
• Molecule 2: ryanodine receptor type 1

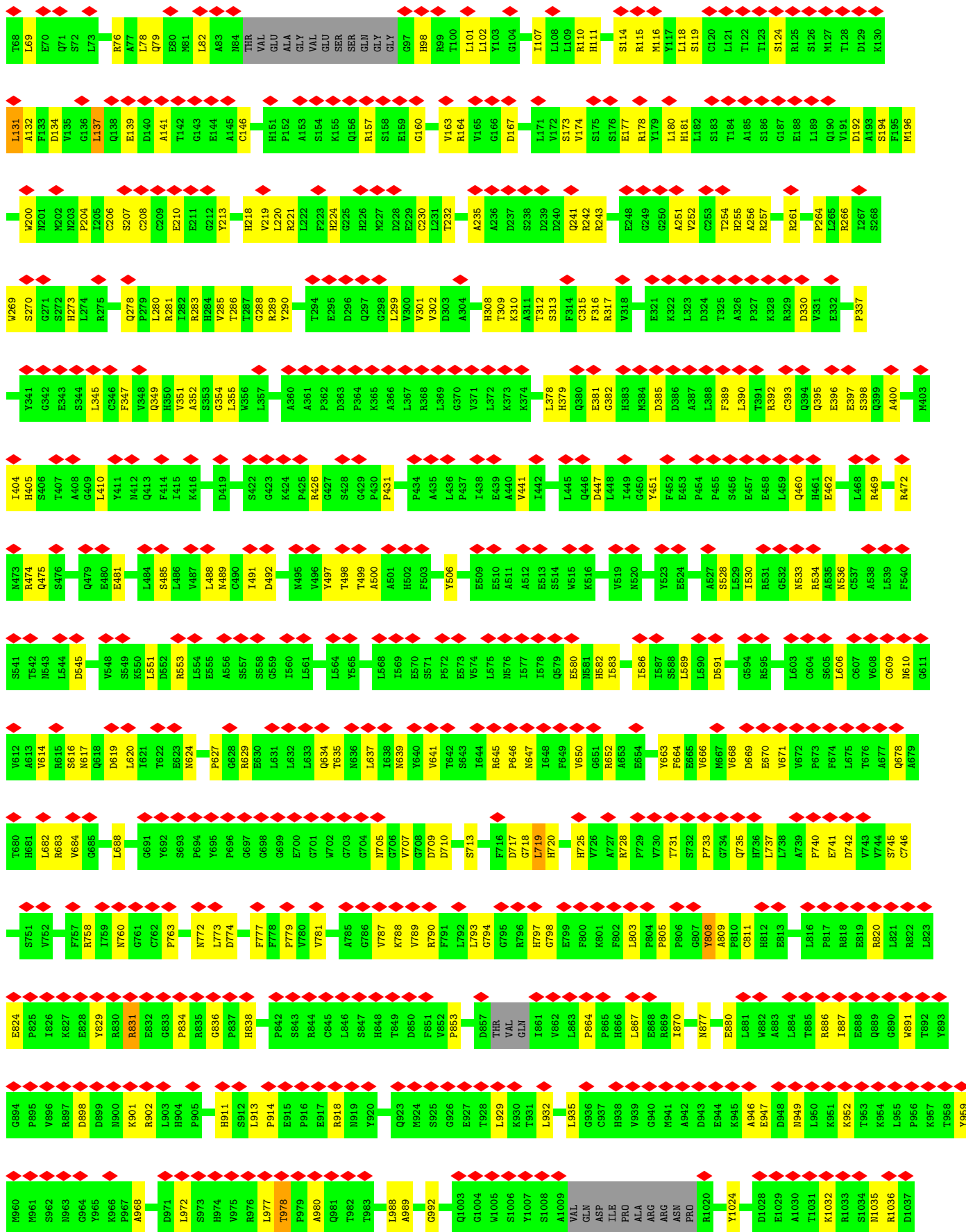


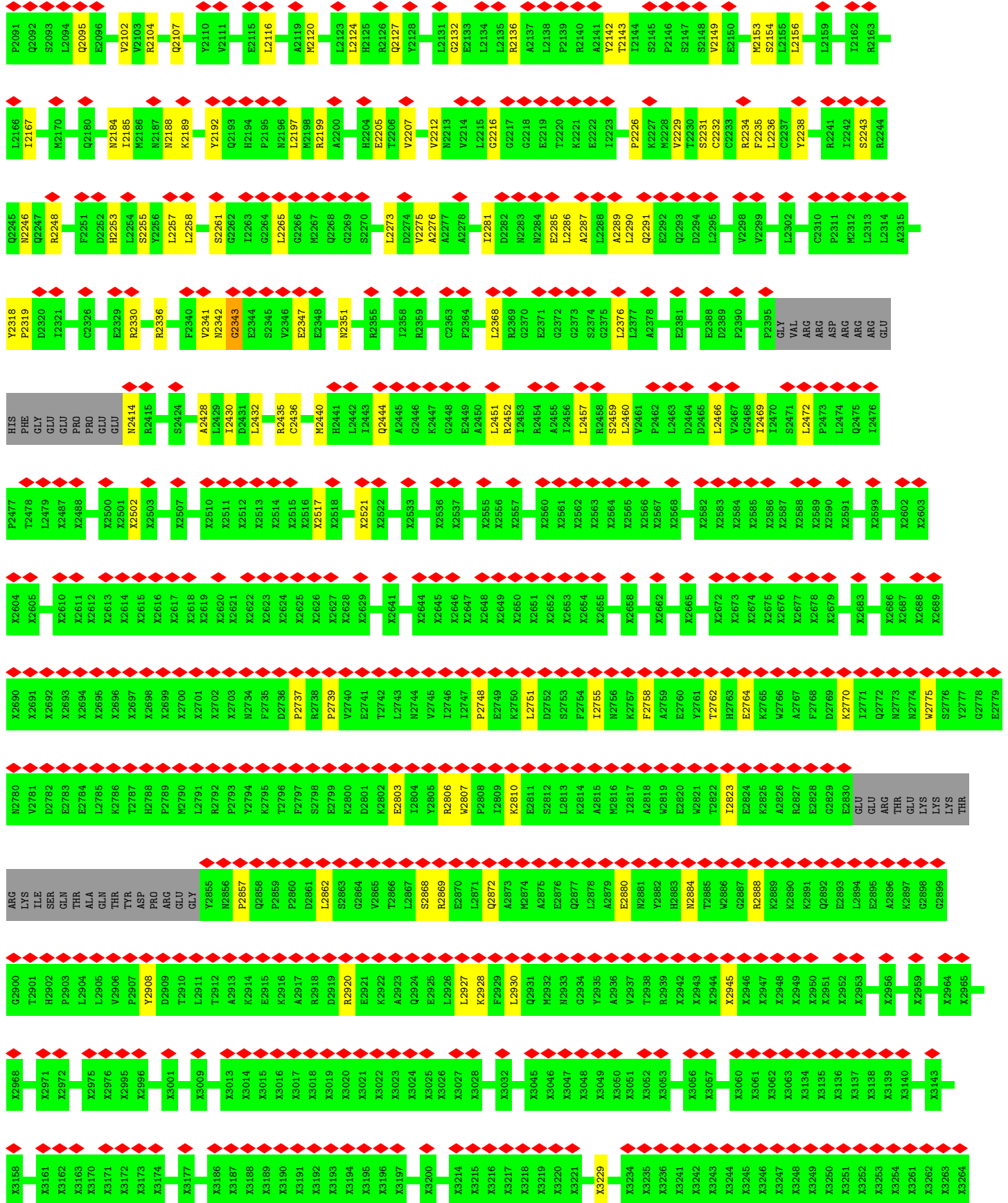
A1959	A1960	F1961	A1962	R1964	Y1965	Q1970	Q1973	Y1977	A1978	L1979	L1980	M1981	R1982	A1983	F1984	T1985	M1986	S1987	A1988	A1989	E1990	T1991	A1992	T1995	R1996	E1997	F1998	R1999	S2000	P2001	P2002	Q2003	E2004	Q2005	T2006	N2007	R2008	H2011	F2012	K2013	A2016	D2017	E2018	E2019	D2020	C2021	P2022	L2023	P2024	I2027	R2028							
L2039	C2042	G2043	I2044	Q2045	L2046	E2047	G2048	GLU	GLU	GLU	GLU	PRO	GLU	GLU	GLU	THR	SER	SER	ARG	LEU	ARG	SER	LEU	LEU	THR	VAL	ARG	LEU	VAL	VAL	LYS	LYS	LYS	GLU	GLU	LYS	PRO	GLU	GLU	K2089	K2090	P2091	Q2092	S2093	L2094	Q2095	V2102	V2103										
R2104	W2105	A2106	Q2107	Y2110	L2116	W2117	R2118	A2119	M2120	L2124	H2125	R2126	Q2127	G2132	L2135	R2136	A2137	L2138	P2139	R2140	A2141	Y2142	T2143	P2146	S2147	F2235	S2148	V2149	M2153	S2154	L2155	L2156	L2159	T2162	R2163	S2164	L2165	L2166	T2167	V2168	Q2169	M2170	N2184	I2185	N2188	K2189	Y2190	F2191	Y2192									
Q2193	H2194	L2197	M2198	R2199	H2204	E2205	T2206	V2207	Y2212	L2215	G2216	G2217	G2218	E2219	T2220	K2221	E2222	I2223	P2226	V2229	T2230	S2231	C2232	C9283	R2284	F2285	L2286	C2287	M2153	S2154	L2155	L2156	L2159	T2162	R2163	S2164	L2165	L2166	T2167	V2168	Q2169	M2170	N2184	I2185	N2188	K2189	Y2190	F2191	Y2192									
L2265	G2266	M2267	Q2268	G2269	S2270	L2273	D2274	V2275	A2276	S2279	V2280	I2281	D2282	N2283	N2284	E2285	L2286	A2287	L2288	A2289	L2290	Q2291	E2292	Q2293	D2294	L2295	E2296	V2299	S2300	A2303	G2304	C2305	G2306	L2307	Q2308	S2309	C2310	P2311	M2312	L2313	L2314	A2315	Y2318	P2319	D2320	I2321	R2330	L2335	R2336	V2341	N2342							
G2343	E2344	S2345	V2346	E2347	E2348	N2351	R2355	L2356	L2357	T2358	R2359	K2360	P2361	E2362	C2363	L2368	R2369	G2370	E2371	G2372	Q2373	Q2374	S2375	L2376	L2377	A2378	E2381	E2382	A2383	T2384	R2385	E2388	D2389	P2390	A2391	P2395	GLY	VAL	ARG	ARG	ASP	ARG	ARG	ARG	GLU	GLU	HIS	PHE	GLY	GLU	PRO	PRO	GLU					
GLU	N2414	A2428	L2429	I2430	L2433	G2434	R2435	C2436	A2437	P2438	E2439	M2440	H2441	Q2444	A2445	G2446	G2448	E2449	A2450	L2451	R2452	A2455	I2456	L2457	R2458	S2459	L2460	V2461	P2462	L2463	D2464	L2466	V2467	G2468	I2469	L2470	S2471	L2472	P2473	L2474	Q2475	I2476	P2477	T2478	L2479	X2487	X2488	X2489	X2490	X2502	X2510							
X2511	X2512	X2513	X2514	X2515	X2516	X2517	X2518	X2519	X2520	X2521	X2522	X2523	X2526	X2529	X2530	X2531	X2532	X2533	X2534	X2535	X2536	X2537	X2551	X2554	X2555	X2556	X2557	X2560	X2561	X2562	X2563	X2564	X2565	X2566	X2567	X2568	X2583	X2584	X2585	X2586	X2597	X2598	X2603	X2604	X2605	X2606	X2610	X2611	X2614									
X2617	X2618	X2619	X2620	X2623	X2624	X2625	X2626	X2627	X2631	X2632	X2635	X2641	X2644	X2645	X2646	X2647	X2648	X2650	X2651	X2652	X2653	X2654	X2655	X2656	X2657	X2658	X2670	X2671	X2672	X2673	X2674	X2675	X2676	X2677	X2683	X2686	X2687	X2688	X2689	X2690	X2691	X2692	X2693	X2694	X2695	X2696	X2697	X2698	X2699									
X2700	X2701	X2702	X2703	M2734	F2735	D2736	P2737	E2738	P2739	V2740	E2741	T2742	L2743	M2744	V2745	I2746	P2748	E2749	R2750	L2751	D2752	S2753	F2754	T2755	M2756	K2757	F2758	A2759	E2760	Y2761	T2762	E2764	K2765	W2766	A2767	F2768	D2769	K2770	I2771	Q2772	M2773	M2774	W2775	S2776	Y2777	G2778	E2779	M2780	V2781	D2782	E2783	E2784	L2785	T2786	H2788	P2789		
M2790	L2791	R2792	P2793	K2795	T2796	F2797	S2798	E2799	K2800	D2801	E2802	E2803	L2804	Y2805	R2806	M2807	P2808	L2809	K2810	E2811	S2812	L2813	R2814	A2815	M2816	L2817	A2818	W2819	E2820	W2821	L2822	L2823	E2824	K2825	A2826	R2827	E2828	G2829	E2830	GLU	ARG	THR	GLU	LYS	LYS	THR	ARG	LYS	ILE	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	M2874	A2875	E2876	Q2877	L2878	A2879	E2880	N2881	Y2882	H2883	N2884	T2885	W2886	G2887	R2888	K2889	K2890	K2891	Q2892	E2893	L2894	E2895	A2896	K2897	G2898	G2899	T2901	H2902	P2903	L2904	L2905	V2906	P2907	Y2908	D2909
T2910	L2911	T2912	A2913	K2914	E2915	A2917	R2918	D2919	R2920	E2921	K2922	A2923	Q2924	E2925	L2926	L2927	K2928	F2929	L2930	Q2931	L2932	M2933	G2934	V2935	A2936	V2937	R2938	T2939	K2942	X2943	X2944	X2945	X2946	X2947	X2948	X2949	X2950	X2951	X2952	X2953	X2954	X2955	X2956	X2959	X2960	X2961	X2965	X2968	X2995	X2996	X2997	X3003	X3004					



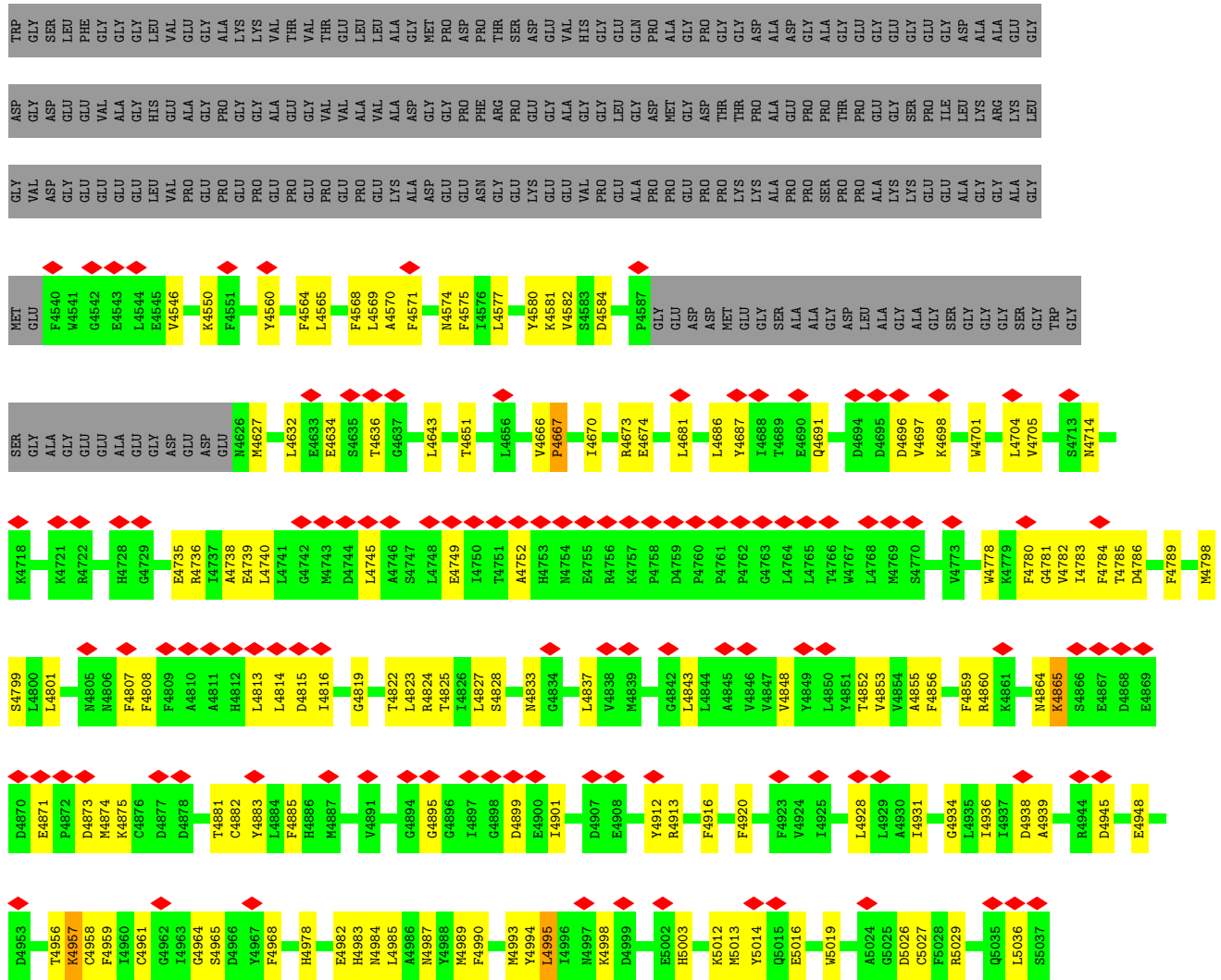
• Molecule 2: ryanodine receptor type 1



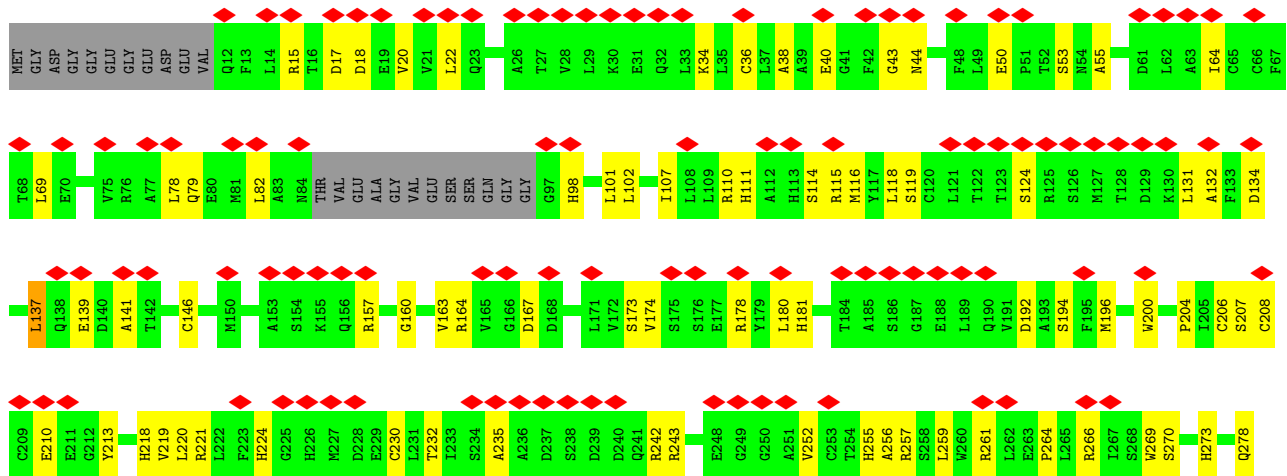


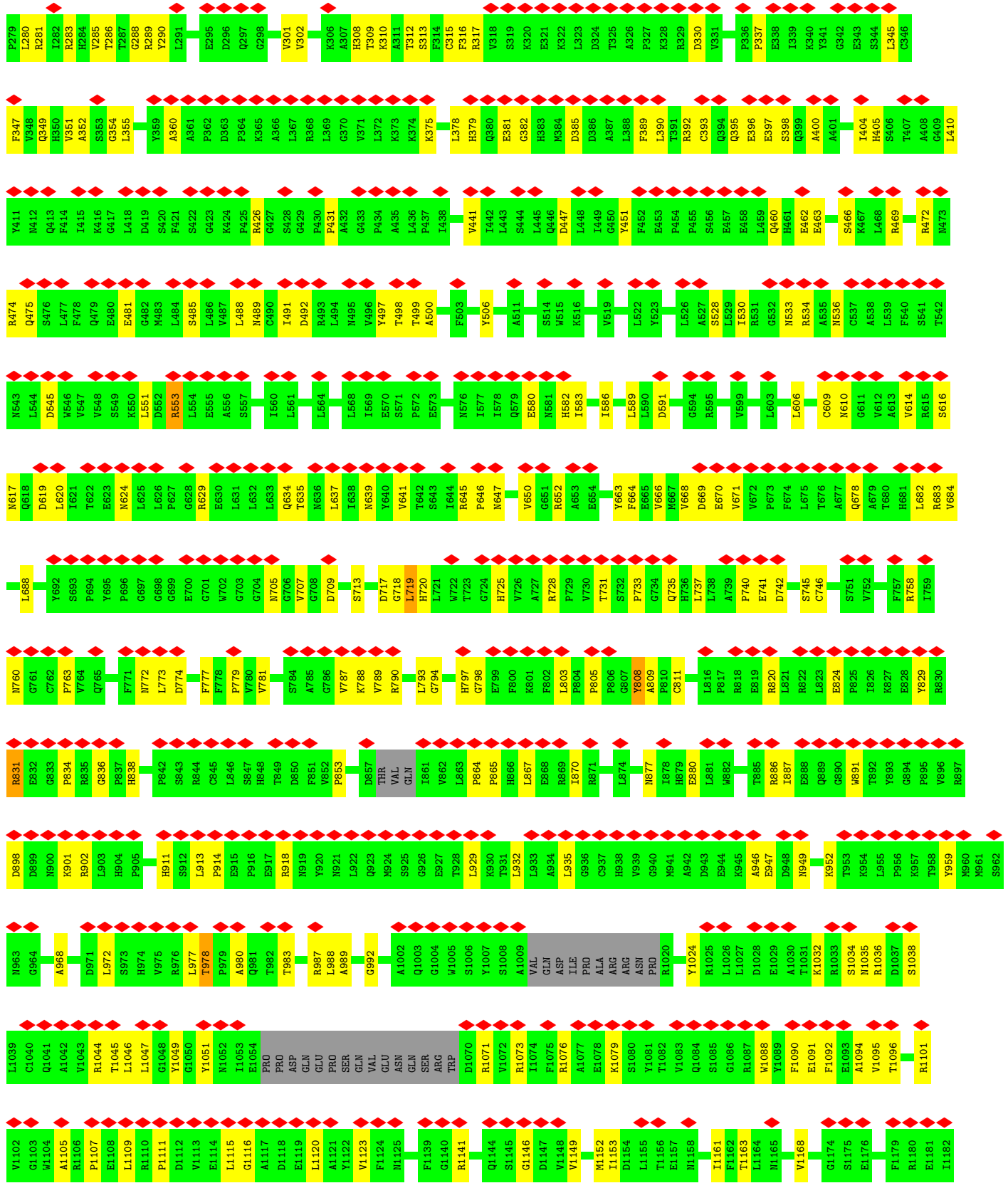


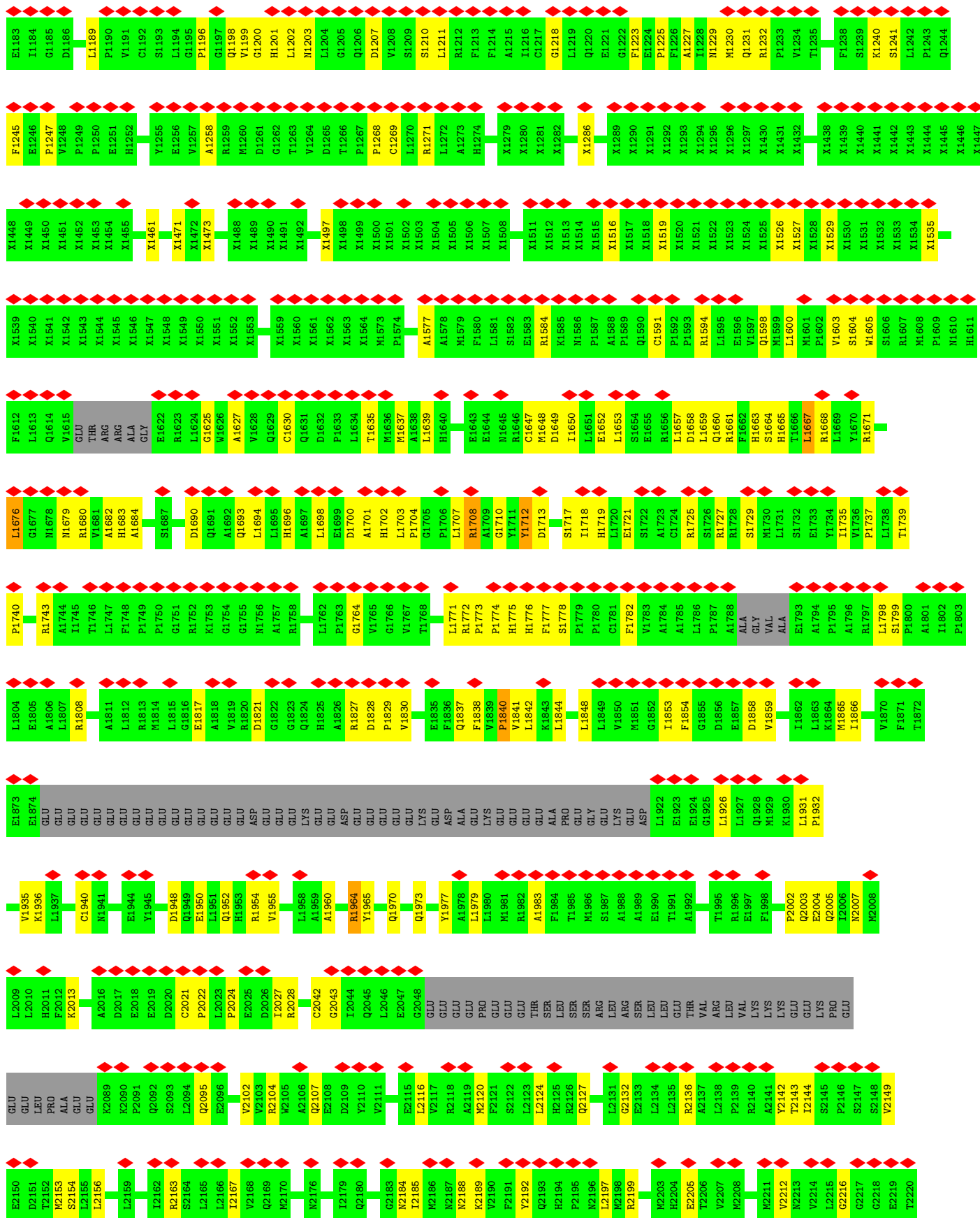
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ALA	M4122	ALA	V4055	G3971	M3875	K3799	C3733	S3668	X3564	X3425	X3347	X3266
ALA	I4123	ALA	E4056	F3972	A3876	K3799	H3734	F3669	X3565	X3426	X3348	X3269
ARG	M4124	ARG	M4057	C3973	D3877	L3800	L3735	E3670	X3566	X3427	X3349	X3270
ALA	F4125	ALA	I4058	T3974	D3878	G3801	E3736	D3671	X3567	X3428	X3350	X3271
LEU	E4126	LEU	L4059	C3977	E3879	I3802	E3737	R3672	X3568	X3429	X3351	X3272
ARG	M4130	ARG	F4062	Q3977	Q3882	S3803	G3738	M3673	X3569	X3430	X3352	X3273
LEU	E4131	LEU	D4063	R3984	D3883	L3805	E3739	I3674	X3570	X3431	X3353	X3274
SER	F4132	SER	M4064	A3988	D3883	L3806	E3740	D3675	X3571	X3432	X3354	X3275
ARG	Q4133	ARG	F4065	A3988	F3885	M3806	E3741	D3676	X3572	X3433	X3355	X3276
SER	E4134	SER	V3989	V3989	F3885	G3807	N3741	D3676	X3573	X3434	X3356	X3277
LEU	R4137	LEU	L4066	R3886	R3886	G3808	GLY	K3679	X3574	X3435	X3357	X3278
ARG	L4068	ARG	K4067	F3887	F3887	ALA	ALA	A3680	X3575	X3436	X3358	X3279
ARG	D4138	ARG	F3992	F3992	Q3889	GLU	GLU	E3682	X3576	X3437	X3359	X3280
ARG	E4253	ARG	D4070	F3996	L3890	K3815	E3747	E3683	X3577	X3464	X3360	X3281
VAL	F4141	VAL	A3997	A3997	E3893	M3816	E3748	Q3683	X3578	X3465	X3361	X3282
ARG	G4073	ARG	H3998	H3998	E3893	L3817	V3749	E3684	X3579	X3466	X3362	X3283
LEU	S4151	LEU	M3999	M3999	E3893	D3818	E3749	E3685	X3580	X3467	X3363	X3284
ARG	E4152	ARG	M4000	M4000	N3896	Y3819	E3750	E3686	X3581	X3468	X3364	X3285
LEU	P4155	LEU	K4001	K4001	F3899	K3823	V3751	E3687	X3582	X3469	X3365	X3286
LEU	R4159	LEU	L4003	L4003	L3903	K3824	SS752	E3688	X3583	X3470	X3366	X3287
THR	L4160	THR	A4004	A4004	R3904	E3825	E3754	E3689	X3584	X3471	X3367	X3288
ALA	F4163	ALA	T3905	T3905	T3905	E3825	E3755	E3690	X3585	X3472	X3368	X3289
ALA	D4083	ALA	Q4009	Q4009	T3910	F3829	E3759	E3691	X3586	X3473	X3369	X3290
GLY	P4084	GLY	I4010	I4010	T3911	K3830	E3759	E3692	X3587	X3474	X3370	X3291
GLY	R4085	GLY	E4011	E4011	T3912	S3831	E3759	K3693	X3588	X3475	X3371	X3292
ALA	I4088	ALA	L4012	L4012	T3912	I3832	K3762	K3694	X3589	X3476	X3372	X3293
ALA	K4091	ALA	L4013	L4013	T3915	Q3833	Y3765	P3697	X3590	X3477	X3373	X3294
LEU	D4092	LEU	K4014	K4014	T3915	L3842	Q3766	L3698	X3591	X3478	X3374	X3295
LEU	D4092	LEU	E4015	E4015	Q3927	D3843	Q3767	H3699	X3592	X3479	X3375	X3296
TRP	L4181	TRP	L4016	L4016	Q3927	L3844	S3768	Q3700	X3593	X3480	X3376	X3297
ALA	E4182	ALA	S3931	S3931	S3931	L3844	R3769	L3701	X3594	X3481	X3377	X3298
VAL	L4182	VAL	D3932	D3932	D3932	M3845	V3702	X3607	X3595	X3482	X3378	X3299
VAL	A4096	VAL	F3933	F3933	F3933	A3846	L3770	X3608	X3596	X3483	X3379	X3300
ALA	A4096	ALA	K4021	K4021	K4021	E3847	H3771	X3609	X3597	X3484	X3380	X3301
ALA	M4097	ALA	V3934	V3934	V3934	F3847	T3772	X3610	X3598	X3485	X3381	X3311
ALA	D4098	ALA	V4024	V4024	V4024	N3851	G3773	X3611	X3599	X3486	X3382	X3312
ALA	S4099	ALA	L4027	L4027	L4027	K3852	G3774	X3612	X3600	X3487	X3383	X3313
ALA	K4101	ALA	L4028	L4028	L4028	A3853	A3775	X3613	X3601	X3488	X3384	X3314
ALA	K4101	ALA	E4032	E4032	E4032	E3854	A3776	X3614	X3602	X3489	X3385	X3315
ALA	Q4102	ALA	G4033	G4033	G4033	G3855	E3777	X3615	X3603	X3490	X3386	X3316
ALA	F4103	ALA	M4034	M4034	M4034	L3856	E3777	X3616	X3604	X3491	X3387	X3317
ALA	T4104	ALA	M4034	M4034	M4034	G3857	M3778	X3617	X3605	X3492	X3388	X3318
ALA	Q4105	ALA	I4040	I4040	I4040	M3857	V3779	X3618	X3606	X3493	X3389	X3319
ALA	P4106	ALA	A4041	A4041	A4041	V3859	L3780	X3619	X3607	X3494	X3390	X3320
ALA	E4107	ALA	M3955	M3955	M3955	V3859	S3714	X3620	X3608	X3495	X3391	X3321
ALA	E4107	ALA	S3956	S3956	S3956	M3860	K3715	X3621	X3609	X3496	X3392	X3322
ALA	I4108	ALA	V3957	V3957	V3957	E3861	L3716	X3622	X3610	X3497	X3393	X3323
ALA	Q4109	ALA	A3958	A3958	A3958	D3862	L3716	X3623	X3611	X3498	X3394	X3324
ALA	F4110	ALA	K3959	K3959	K3959	G3863	D3717	X3624	X3612	X3499	X3395	X3325
ALA	L4111	ALA	T3864	T3864	T3864	E3863	E3718	X3625	X3613	X3500	X3396	X3326
LEU	L4111	LEU	V3865	V3865	V3865	D3718	E3718	X3626	X3614	X3501	X3397	X3327
ARG	E4050	ARG	E4050	E4050	E4050	D3719	N3651	X3627	X3615	X3502	X3398	X3328
LEU	S4051	LEU	S4051	S4051	S4051	Y3720	M3652	X3628	X3616	X3503	X3399	X3329
ALA	E4116	ALA	E4116	E4116	E4116	L3721	F3653	X3629	X3617	X3504	X3400	X3330
ALA	A4117	ALA	L3964	L3964	L3964	L3721	L3644	X3630	X3618	X3505	X3401	X3331
ALA	D4118	ALA	L3966	L3966	L3966	Y3722	P3645	X3631	X3619	X3506	X3402	X3332
LEU	E4119	LEU	T3966	T3966	T3966	M3723	H3647	X3632	X3620	X3507	X3403	X3333
LEU	M4120	LEU	E3967	E3967	E3967	A3724	R3648	X3633	X3621	X3508	X3404	X3334
LEU		LEU				A3725	A3649	X3634	X3622	X3509	X3405	X3335
LEU		LEU				Y3725	C3650	X3635	X3623	X3510	X3406	X3336
LEU		LEU				A3726	N3651	X3636	X3624	X3511	X3407	X3337
LEU		LEU				D3727	M3652	X3637	X3625	X3512	X3408	X3338
LEU		LEU				I3728	F3653	X3638	X3626	X3513	X3409	X3339
LEU		LEU				K3731	K3658	X3639	X3627	X3514	X3410	X3340
LEU		LEU					A3659	X3640	X3628	X3515	X3411	X3341
LEU		LEU					L3662	X3641	X3629	X3516	X3412	X3342
LEU		LEU					L3663	X3642	X3630	X3517	X3413	X3343
LEU		LEU					E3665	X3643	X3631	X3518	X3414	X3344
LEU		LEU					D3666	X3644	X3632	X3519	X3415	X3345

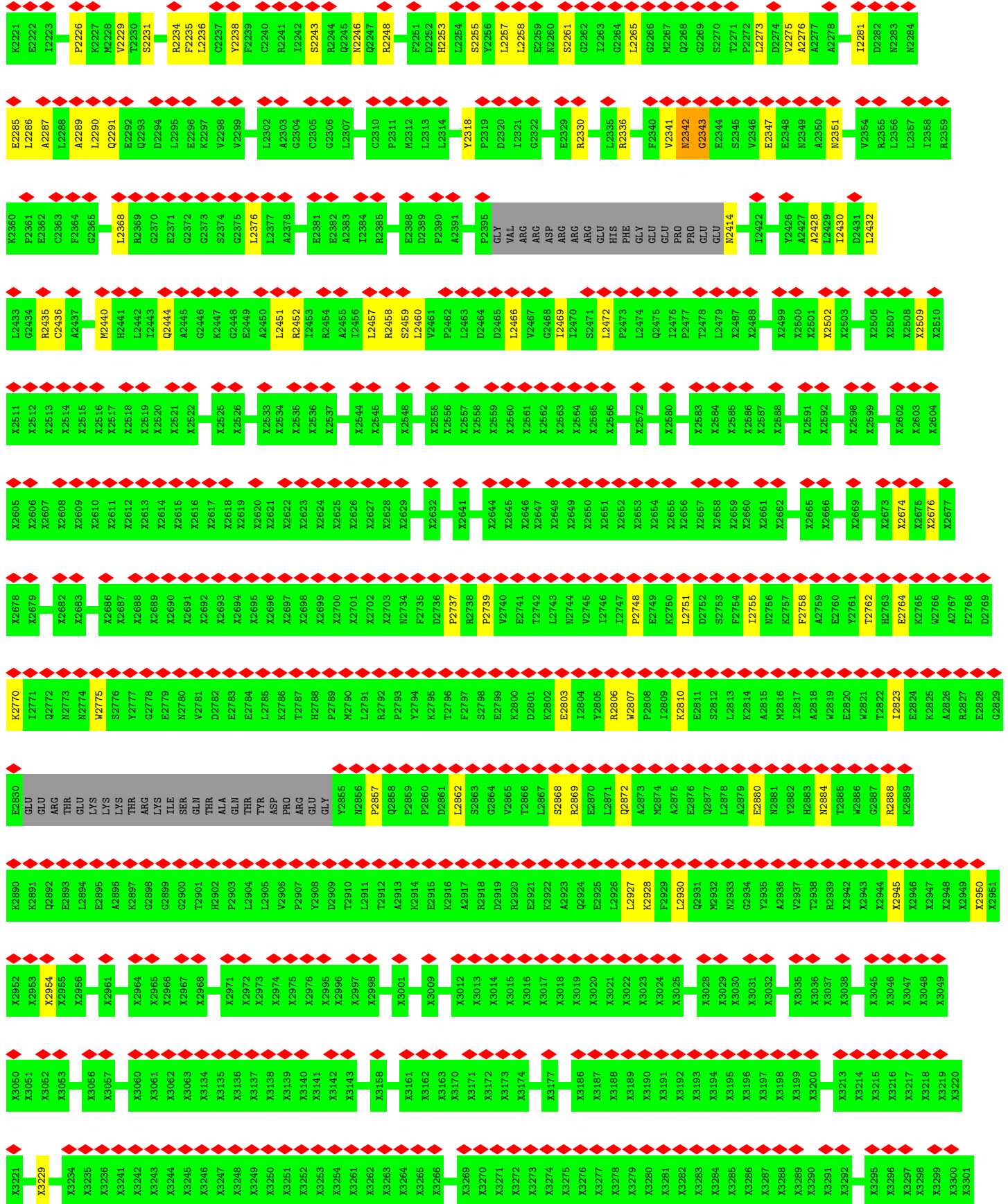


• Molecule 2: ryanodine receptor type 1

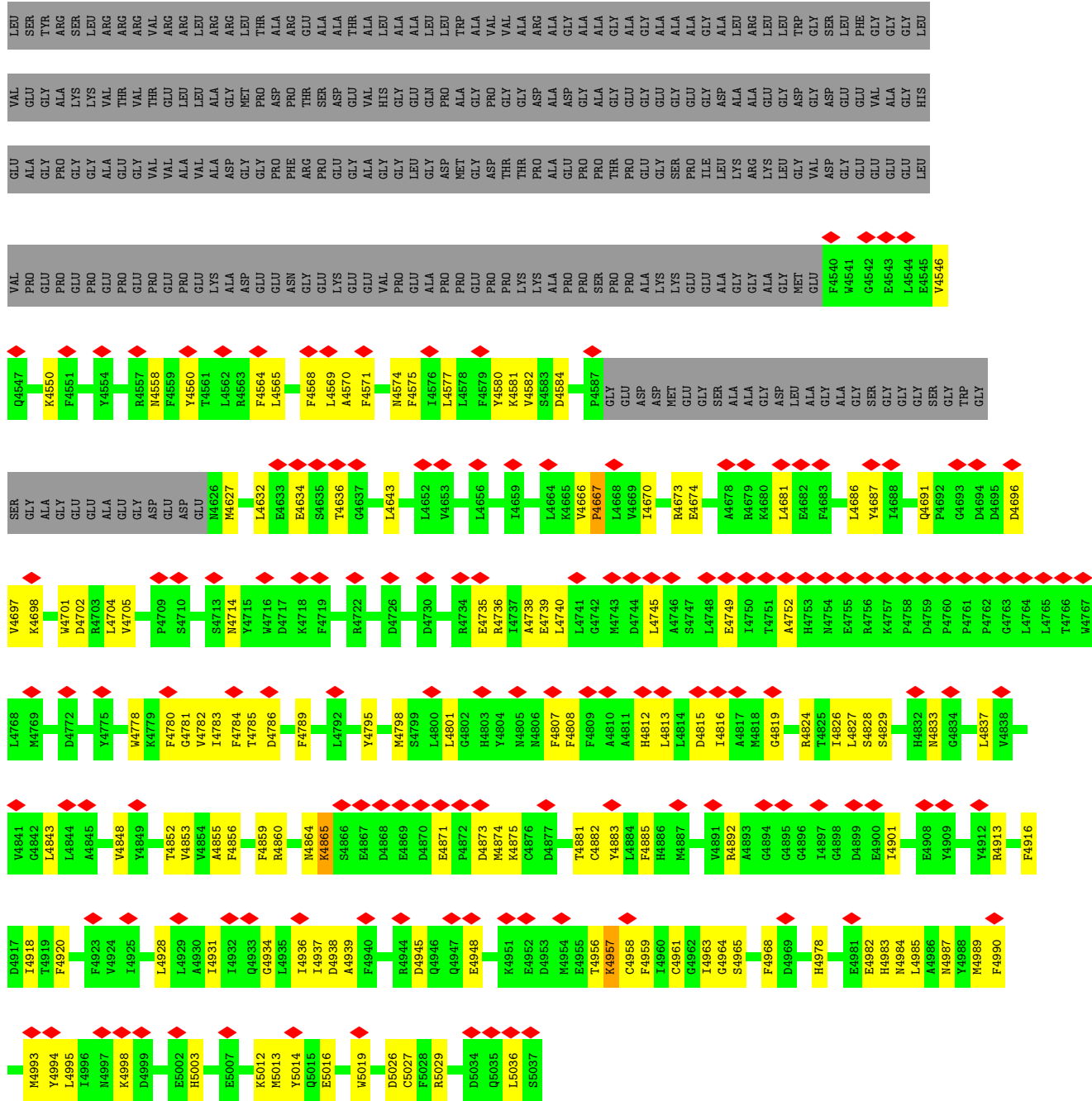








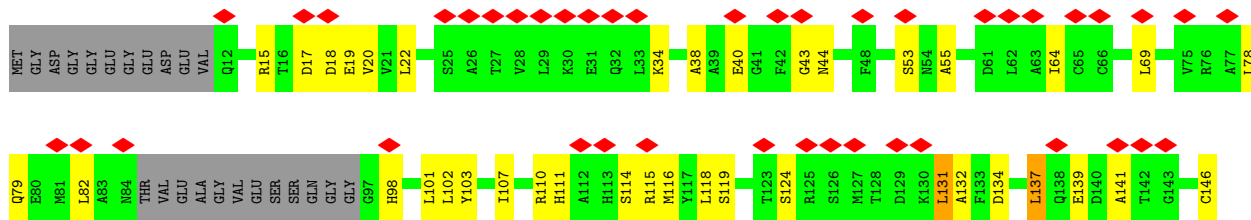
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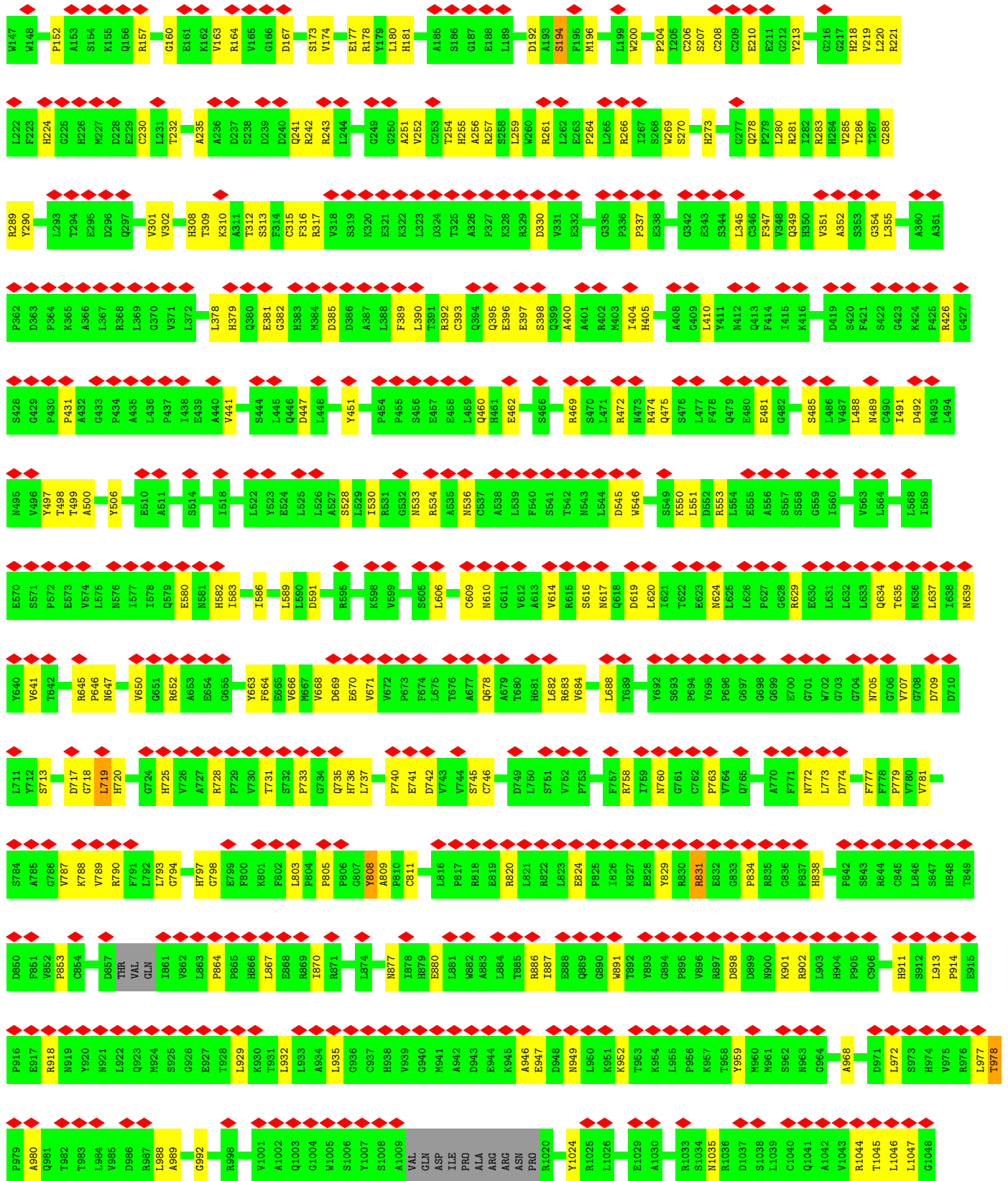


● Molecule 2: ryanodine receptor type 1



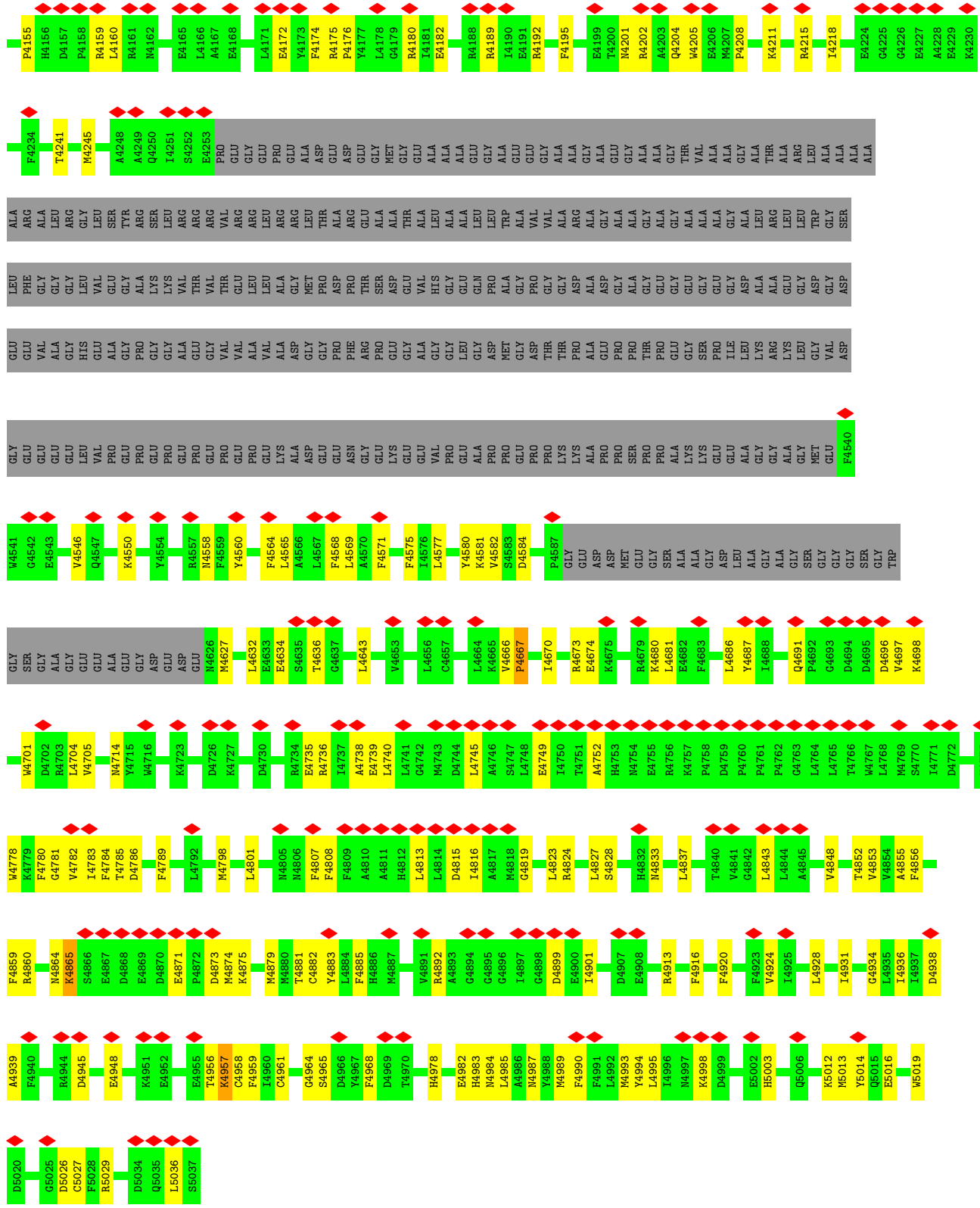
Chain I:





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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	L2927	K2928	F2929	L2930	Q2931	M2932	N2933	G2934	Y2935	A2936	V2937	T2938	R2939	X2942	X2943	X2945	X2946	X2947	X2948	X2949	X2950	X2951	X2952	X2953	X2954	X2955	X2956	X2961	X2964	X2965	X2968			
IIE	SER	GLN	THR	ALA	GLN	THR	TYR	ASP	PRD	ARG	GLU	GLY	Y2855	M2856	P2857	Q2858	P2859	P2860	D2861	L2862	S2863	G2864	V2865	L2866	S2868	R2869	E2870	L2871	Q2872	A2873	M2874	A2875	E2876	Q2877	L2878	A2879	E2880	M2881	Y2882	H2883	N2884	T2885	G2886	R2888	K2889	K2890	K2891	Q2892	E2893	L2894	E2895	A2896	K2897	G2898	G2899	G2900	T2901	
D2782	E2783	E2784	L2785	K2786	T2787	H2788	P2789	M2790	L2791	K2792	P2793	Y2794	K2795	T2796	F2797	E2798	S2799	K2800	D2801	E2802	L2803	I2804	Y2805	K2806	W2807	P2808	I2809	K2810	E2811	S2812	L2813	K2814	K2815	L2816	I2817	A2818	W2819	E2820	W2821	L2822	I2823	E2824	K2825	A2826	R2827	E2828	K2829	E2830	GLU	ARG	THR	GLU	LYS	LYS	THR	ARG	LYS	
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G2372	G2373	S2374	G2375	L2376	L2377	A2378	E2381	E2382	A2383	I2384	R2385	E2388	D2389	P2390	A2391	R2392	P2395	GLY	VAL	ARG	ARG	ASP	ARG	ARG	GLU	HIS	PHE	GLY	GLU	GLU	M2341	N2342	G2343	E2344	S2345	S2346	E2347	E2348	M2349	A2350	M2351	V2354	R2355	L2356	L2357	L2358	R2359	K2360	P2361	E2362	C2363	F2364	L2368	R2369	G2370	E2371		
E2296	K2297	V2298	S2300	Y2301	L2302	A2303	C2305	G2306	L2307	M2312	L2313	L2314	A2315	Y2318	P2319	D2320	L2321	G2322	R2330	M2331	L2332	L2335	R2336	F2340	W2341	N2342	G2343	E2344	S2345	S2346	E2347	E2348	M2349	A2350	M2351	V2354	R2355	L2356	L2357	L2358	R2359	K2360	P2361	E2362	C2363	F2364	L2368	R2369	G2370	E2371								
R2234	F2235	L2236	C2237	V2238	P2239	C2240	R2241	L2242	S2243	R2244	Q2245	M2246	E2247	R2248	F2251	D2252	H2253	L2254	S2255	Y2256	L2257	L2258	E2259	M2260	N2261	S2261	G2262	I2263	G2264	L2265	G2266	M2267	G2268	G2269	S2270	T2271	L2272	L2273	D2274	V2275	A2276	S2279	V2280	L2281	D2282	M2283	N2284	E2285	R2286	F2287	L2288	A2289	L2290	Q2291	E2292	C2293	D2294	L2295
L2166	L2167	V2168	Q2169	M2170	G2171	P2172	N2176	I2179	Q2180	N2184	L2185	M2186	N2187	N2188	K2189	V2190	F2191	Y2192	Q2193	H2194	P2195	N2196	L2197	M2198	R2199	M2203	H2204	E2205	L2206	V2207	G2208	M2211	N2212	N2213	V2214	L2215	G2216	G2217	G2218	E2219	T2220	K2221	E2222	L2223	R2224	F2225	P2226	K2227	M2228	T2229	S2231	C2232	C2233					
V2102	R2103	R2104	W2105	A2106	Q2107	V2110	V2111	Q2112	S2113	P2114	E2115	L2116	W2117	R2118	A2119	R2120	F2121	S2122	L2123	L2124	H2125	R2126	Q2127	V2128	D2129	G2130	L2131	G2132	L2135	R2136	A2137	L2138	P2139	R2140	A2141	L2142	L2143	L2144	S2145	P2146	S2147	S2148	V2149	T2152	L2153	S2154	L2155	L2156	L2159	L2162	R2163	S2164	L2165					

X3135	X3136	X3137	X3138	X3139	X3140	X3141	X3142	X3143	X3146	X3162	X3163	X3170	X3171	X3172	X3173	X3174	X3183	X3184	X3185	X3186	X3187	X3188	X3189	X3190	X3191	X3192	X3193	X3194	X3195	X3196	X3197	X3198	X3199	X3200	X3201	X3202	X3205	X3206	X3209	X3210	X3214	X3217	X3218	X3219	X3220	X3221	X3222	X3223	X3226	X3229							
X3230	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	X3295	X3296	X3297	X3301	X3302	X3307	X3308	X3309	X3310		
X3311	X3312	X3313	X3314	X3315	X3316	X3317	X3318	X3319	X3320	X3321	X3322	X3323	X3324	X3325	X3326	X3330	X3331	X3332	X3337	X3338	X3339	X3340	X3341	X3342	X3343	X3344	X3345	X3346	X3347	X3348	X3349	X3350	X3351	X3352	X3353	X3354	X3355	X3356	X3357	X3358	X3359	X3360	X3361	X3362	X3363	X3364	X3365	X3366	X3367	X3368	X3369	X3370	X3371	X3372	X3373	X3377	X3378
X3379	X3380	X3383	X3384	X3385	X3386	X3387	X3388	X3389	X3390	X3391	X3392	X3393	X3394	X3395	X3396	X3397	X3398	X3407	X3411	X3412	X3413	X3414	X3415	X3416	X3417	X3418	X3419	X3420	X3421	X3422	X3423	X3424	X3425	X3426	X3427	X3428	X3429	X3430	X3431	X3432	X3433	X3434	X3435	X3436	X3437	X3438	X3441	X3444	X3445	X3446	X3447	X3448	X3453				
X3462	X3463	X3464	X3465	X3466	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	X3539	X3540	X3543	X3544	X3547	X3552	X3556	X3557	X3558	X3559	X3560	X3561	X3562	X3563	X3564	X3565	X3566	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	X3602	X3603	X3604	X3605	X3606	X3607	X3608	X3609	X3610	X3611	X3612	X3613	X3642	X3643	X3644	X3645	X3648	X3649	X3650	X3651	X3652	X3655	X3657	X3658	X3659	X3660	X3661	X3662	X3663	X3664	X3665	X3666	X3667	X3668	X3669	X3670	
M3673	I3674	D3675	D3676	A3680	G3681	E3682	Q3683	E3684	E3685	E3686	E3687	E3688	E3689	V3690	E3691	E3692	K3694	P3695	L3698	H3699	Q3700	L3701	L3702	L3703	H3704	F3705	S3706	R3707	T3708	A3709	L3710	L3711	E3712	K3713	S3714	L3715	D3717	E3718	D3719	Y3720	M3723	A3724	Y3725	A3726	D3727	L3728	M3729	A3730	K3731	S3732	C3733	H3734	L3735	E3736			
E3737	G3738	G3739	E3740	M3741	GLY	ALA	GLU	GLU	E3747	E3748	V3749	E3750	E3751	S3752	F3753	E3754	E3755	K3756	E3759	K3760	L3763	L3764	Y3765	Q3766	Q3767	S3768	R3769	L3770	H3771	T3772	G3773	G3774	A3775	A3776	V3779	L3780	Q3781	M3782	L3783	S3784	A3785	C3786	K3787	G3788	E3789	T3790	C3791	A3792	M3793	V3794	S3795	L3798	K3799				
I3802	S3803	L3804	L3805	N3806	G3807	G3808	N3809	K3815	M3816	L3817	L3820	K3821	K3824	E3825	F3829	Q3830	S3831	Q3833	M3836	Q3837	T3838	C3839	L3842	D3843	L3844	N3845	A3846	F3847	E3848	R3849	Q3850	N3851	A3852	A3853	E3854	G3855	L3856	G3857	M3858	V3859	N3860	E3861	D3862	G3863	T3864	V3865	I3866	N3867	Q3868	N3870	G3871						
E3872	K3873	V3874	D3877	D3878	T3881	Q3882	F3885	L3888	Q3889	L3890	E3893	N3896	M3897	D3898	F3899	L3903	R3904	T3905	Q3906	T3907	G3908	N3909	T3910	T3911	L3912	I3913	M3914	I3915	I3916	I3917	V3920	D3921	Y3922	L3923	L3924	R3925	L3926	Q3927	E3928	S3931	D3932	F3933	Y3934	W3935	Y3936	Y3937	S3938	G3939	K3940	D3941							
V3942	K3948	R3949	N3950	F3951	A3954	M3955	S3956	A3958	K3959	F3962	S3964	L3965	T3966	E3967	Y3968	I3969	Q3970	G3971	P3972	C3973	T3974	Q3977	Q3978	A3981	H3982	S3983	R3984	D3987	V3990	G3991	F3992	L3993	H3994	V3995	F3996	A3997	H3998	R3999	M4000	M4001	K4002	L4003	A4004	Q4005	S4008	Q4009	I4010	E4011	L4012								
L4013	K4014	E4015	L4016	L4017	D4018	L4019	Q4020	K4021	V4024	L4027	L4028	S4029	L4030	M4034	N4037	I4040	A4041	R4042	Q4043	M4044	V4045	L4108	Q4109	F4110	L4111	L4112	S4113	A4117	D4118	F4119	N4120	F4121	L4122	L4123	L4124	F4061	F4062	D4063	M4064	F4065	K4067	L4068	K4069	D4070	G4073	S4074	E4075	A4076	D4079	Y4080							
V4081	T4082	D4083	F4084	R4085	I4088	K4091	D4092	F4093	Q4094	K4095	A4096	M4097	D4098	S4099	Q4100	K4101	Q4102	F4103	T4104	O4105	F4106	E4107	Q4108	F4109	L4110	L4111	L4112	S4113	A4117	D4118	F4119	N4120	F4121	L4122	L4123	L4124	F4061	F4062	D4063	M4064	F4065	K4067	L4068	K4069	D4070	G4073	S4074	E4075	A4076	D4079	Y4080						



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	791956	Depositor
Resolution determination method	OTHER	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	0.466	Depositor
Minimum map value	-0.266	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.16	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 [i](#)

5.1 Standard geometry [i](#)

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	0.37	0/834	0.61	0/1123
1	F	0.37	0/834	0.61	0/1123
1	H	0.37	0/834	0.61	0/1123
1	J	0.37	0/834	0.61	0/1123
2	B	0.40	0/25428	0.61	5/34534 (0.0%)
2	E	0.40	0/25428	0.61	5/34534 (0.0%)
2	G	0.40	0/25428	0.61	5/34534 (0.0%)
2	I	0.40	0/25428	0.61	5/34534 (0.0%)
All	All	0.40	0/105048	0.61	20/142628 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	19
2	E	0	19
2	G	0	19
2	I	0	20
All	All	0	77

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	4985	LEU	CA-CB-CG	6.40	130.01	115.30
2	B	4985	LEU	CA-CB-CG	6.39	130.00	115.30
2	I	719	LEU	CA-CB-CG	6.39	130.00	115.30
2	B	719	LEU	CA-CB-CG	6.38	129.99	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	719	LEU	CA-CB-CG	6.38	129.97	115.30

There are no chirality outliers.

5 of 77 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	137	LEU	Peptide
2	B	1676	LEU	Peptide
2	B	1690	ASP	Peptide
2	B	1712	TYR	Peptide
2	B	808	TYR	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	818	0	824	21	0
1	F	818	0	824	19	0
1	H	818	0	824	19	0
1	J	818	0	824	20	0
2	B	29369	0	24716	533	0
2	E	29369	0	24712	519	0
2	G	29369	0	24713	531	0
2	I	29369	0	24713	522	0
3	B	1	0	0	0	0
3	E	1	0	0	0	0
3	G	1	0	0	0	0
3	I	1	0	0	0	0
4	B	1	0	0	0	0
4	E	1	0	0	0	0
4	G	1	0	0	0	0
4	I	1	0	0	0	0
All	All	120756	0	102150	2154	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 10.

The worst 5 of 2154 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:G:4860:ARG:HD2	2:I:4582:VAL:HG11	1.65	0.79
2:B:853:PRO:HB3	2:B:1024:TYR:H	1.51	0.76
2:B:379:HIS:HD2	2:B:382:GLY:H	1.35	0.75
2:I:853:PRO:HB3	2:I:1024:TYR:H	1.51	0.75
2:E:853:PRO:HB3	2:E:1024:TYR:H	1.51	0.75

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	105/107 (98%)	95 (90%)	10 (10%)	0	100	100
1	F	105/107 (98%)	95 (90%)	10 (10%)	0	100	100
1	H	105/107 (98%)	95 (90%)	10 (10%)	0	100	100
1	J	105/107 (98%)	95 (90%)	10 (10%)	0	100	100
2	B	3235/4687 (69%)	2859 (88%)	367 (11%)	9 (0%)	41	76
2	E	3235/4687 (69%)	2860 (88%)	367 (11%)	8 (0%)	47	81
2	G	3235/4687 (69%)	2859 (88%)	367 (11%)	9 (0%)	41	76
2	I	3235/4687 (69%)	2860 (88%)	366 (11%)	9 (0%)	41	76
All	All	13360/19176 (70%)	11818 (88%)	1507 (11%)	35 (0%)	44	76

5 of 35 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	3772	THR
2	B	4667	PRO
2	E	3772	THR
2	E	4667	PRO

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Mol	Chain	Res	Type
2	G	3772	THR

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	88/88 (100%)	88 (100%)	0	100	100
1	F	88/88 (100%)	88 (100%)	0	100	100
1	H	88/88 (100%)	88 (100%)	0	100	100
1	J	88/88 (100%)	88 (100%)	0	100	100
2	B	2493/3209 (78%)	2469 (99%)	24 (1%)	76	86
2	E	2493/3209 (78%)	2469 (99%)	24 (1%)	76	86
2	G	2493/3209 (78%)	2469 (99%)	24 (1%)	76	86
2	I	2493/3209 (78%)	2469 (99%)	24 (1%)	76	86
All	All	10324/13188 (78%)	10228 (99%)	96 (1%)	79	87

5 of 96 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	G	3663	LEU
2	G	4995	LEU
2	G	3805	LEU
2	G	4180	ARG
2	I	688	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 169 such sidechains are listed below:

Mol	Chain	Res	Type
2	G	3978	GLN
2	I	1598	GLN
2	G	4120	ASN
2	I	218	HIS

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Mol	Chain	Res	Type
2	I	2005	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 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	G	12
2	I	12

Continued on next page...

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Mol	Chain	Number of breaks
2	B	12
2	E	12

The worst 5 of 48 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	G	3613:UNK	C	3639:THR	N	44.11
1	I	3613:UNK	C	3639:THR	N	44.00
1	B	3613:UNK	C	3639:THR	N	43.94
1	E	3613:UNK	C	3639:THR	N	43.92
1	B	3163:UNK	C	3170:UNK	N	16.36

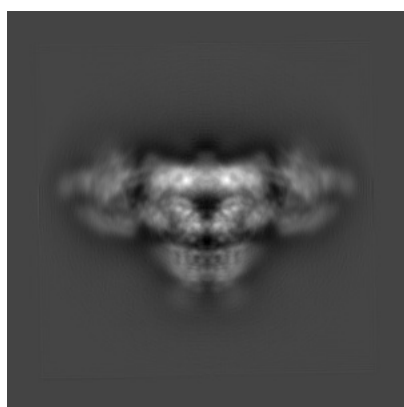
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22396. These allow visual inspection of the internal detail of the map and identification of artifacts.

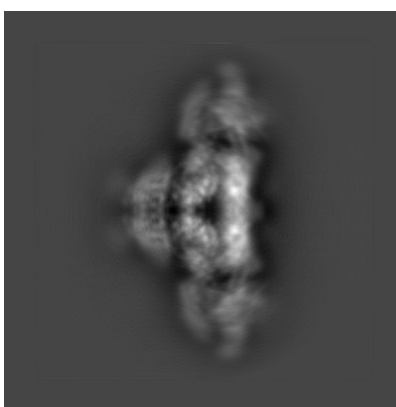
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

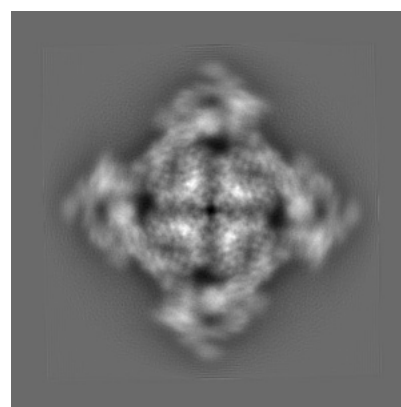
6.1.1 Primary map



X



Y

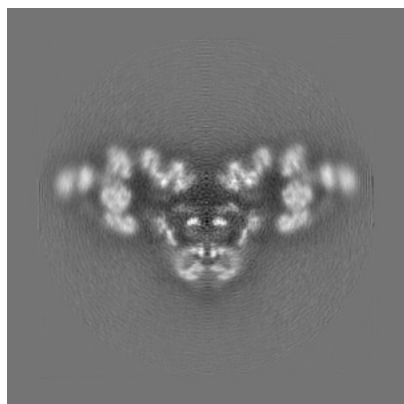


Z

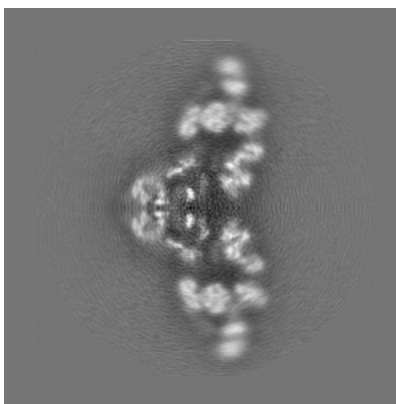
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

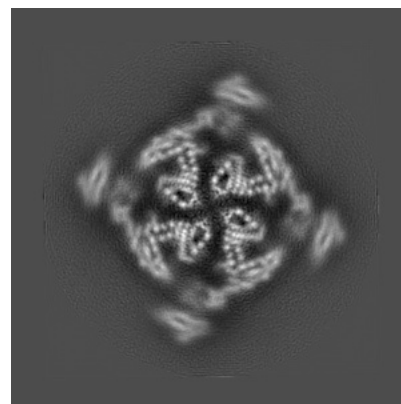
6.2.1 Primary map



X Index: 200



Y Index: 200

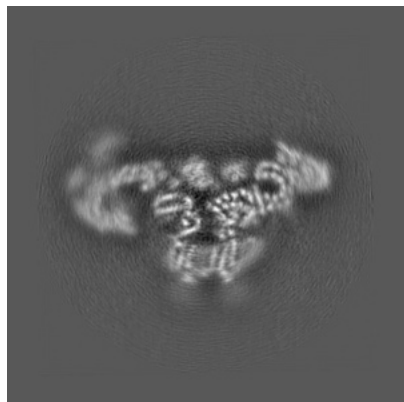


Z Index: 200

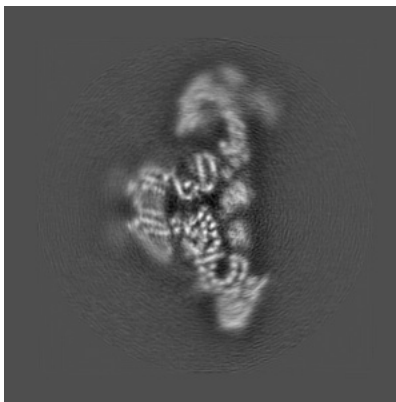
The images above show central slices of the map in three orthogonal directions.

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

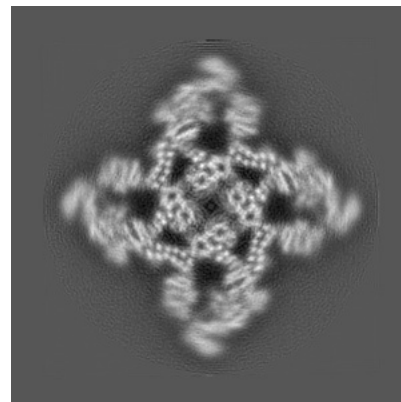
6.3.1 Primary map



X Index: 177



Y Index: 177



Z Index: 227

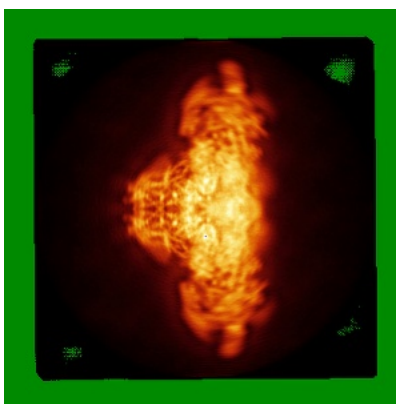
The images above show the largest variance slices of the map in three orthogonal directions.

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

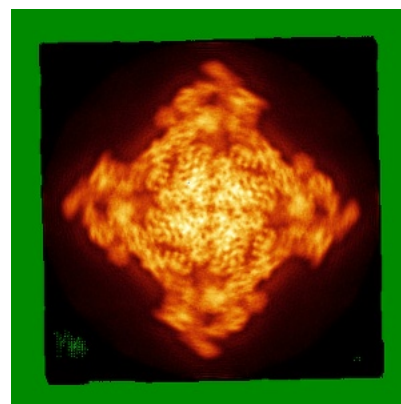
6.4.1 Primary map



X



Y

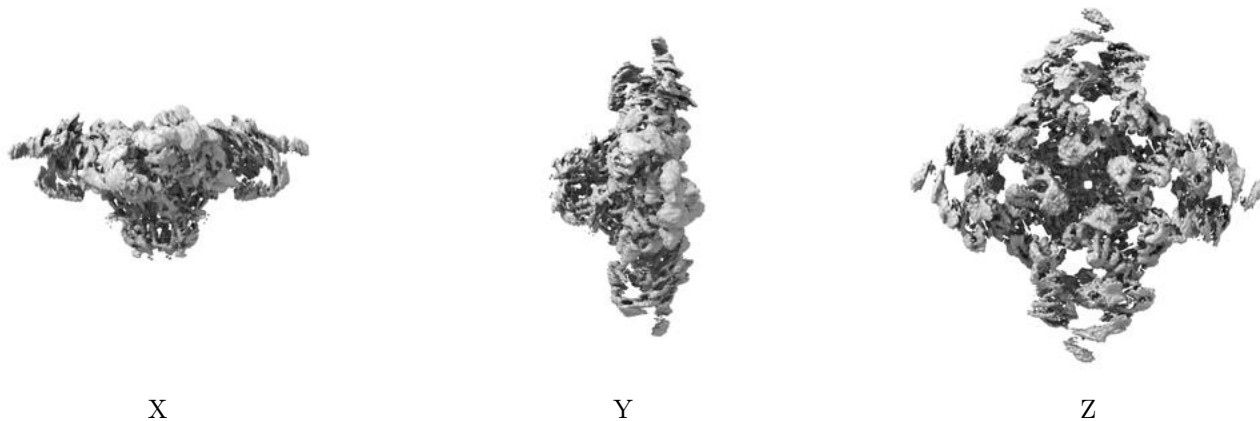


Z

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

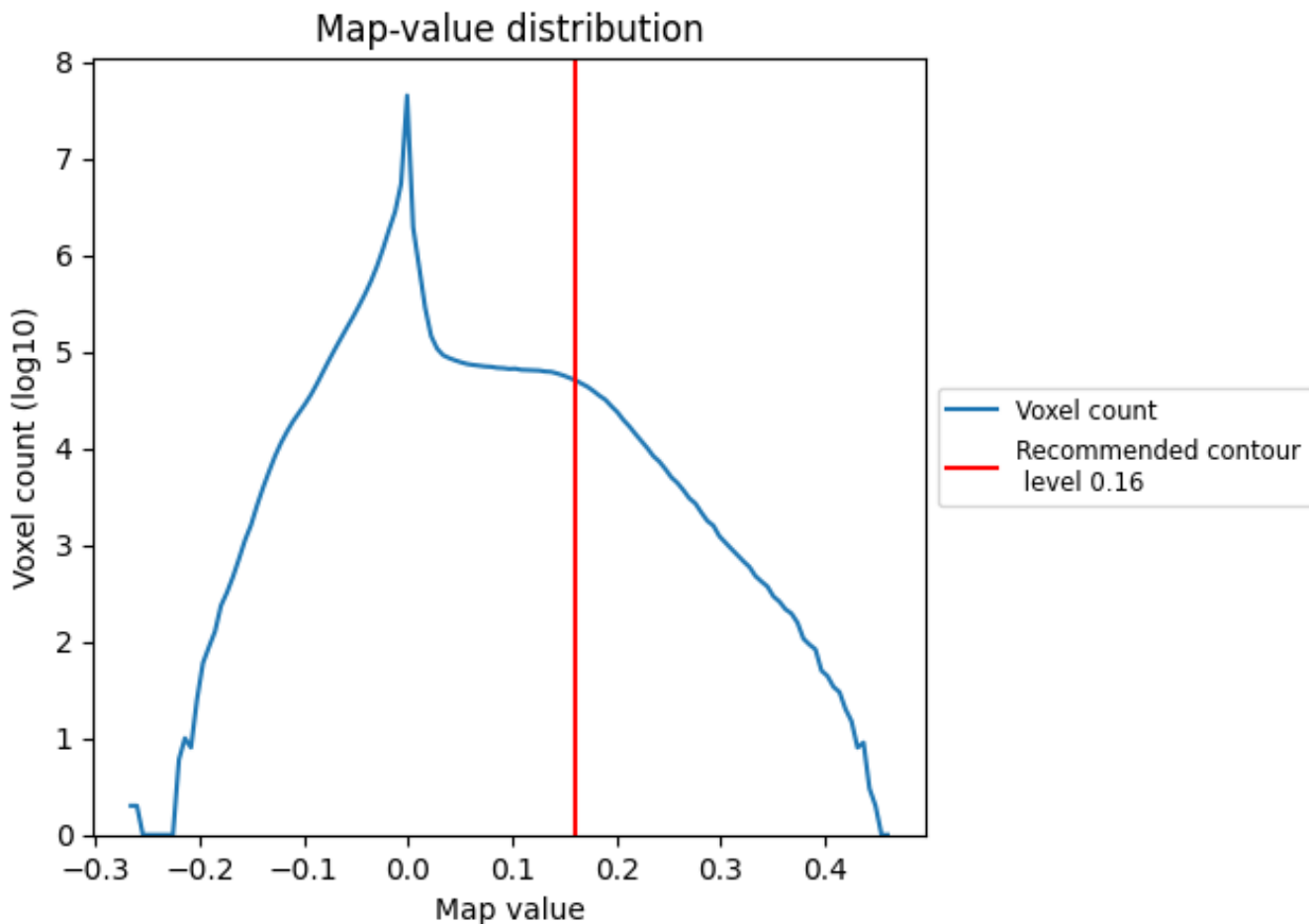
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

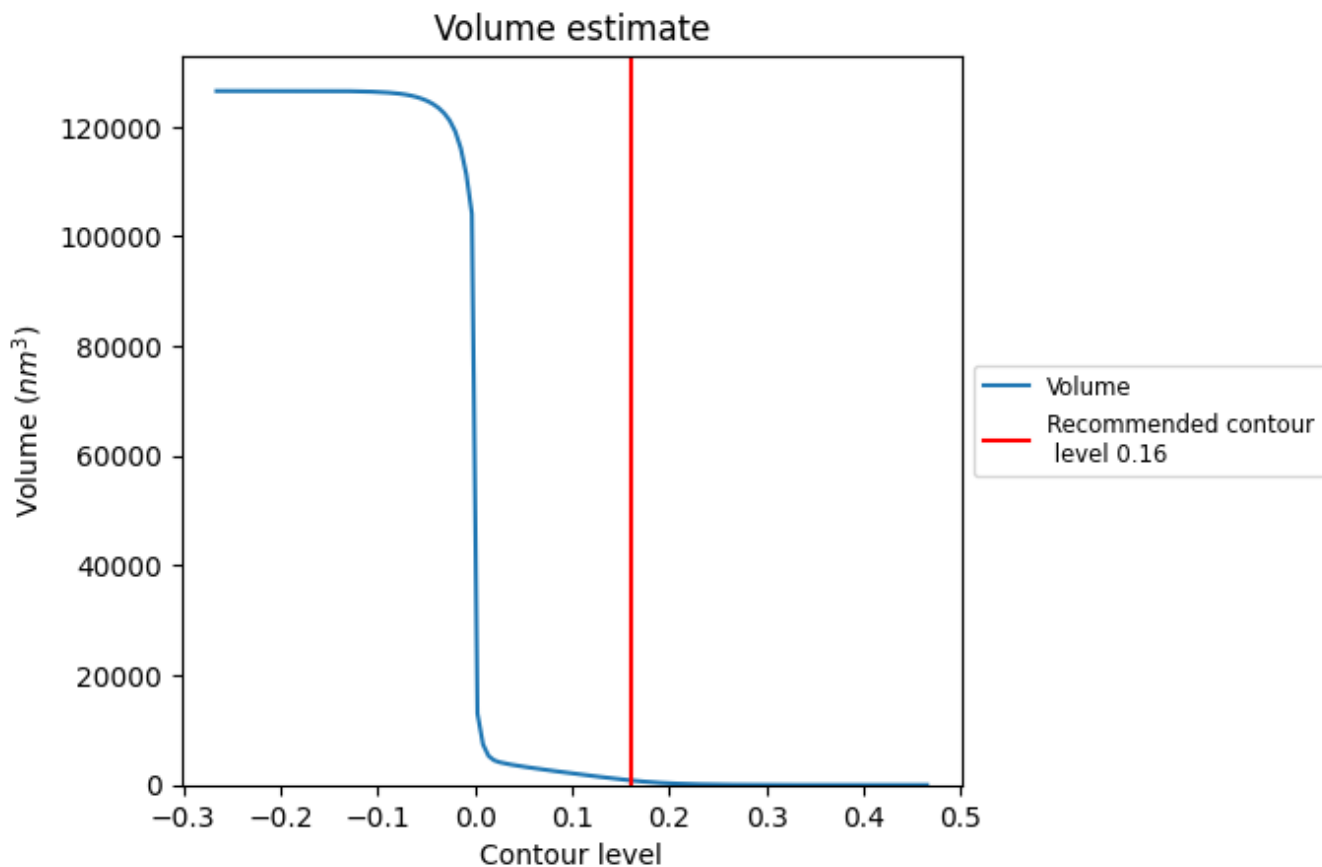
This section contains the results of statistical analysis of the map.

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.

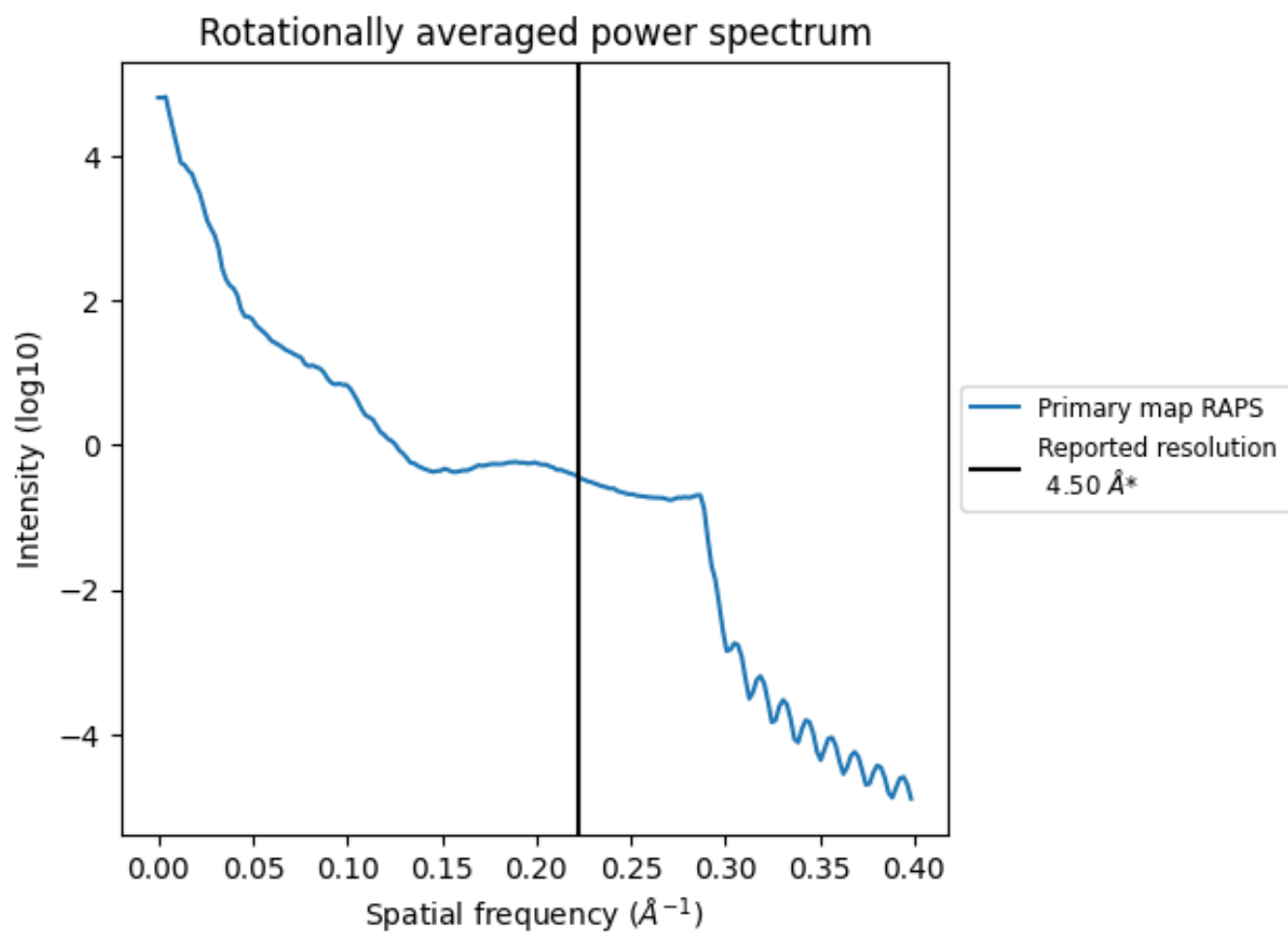
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 846 nm³; this corresponds to an approximate mass of 764 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.222\AA^{-1}

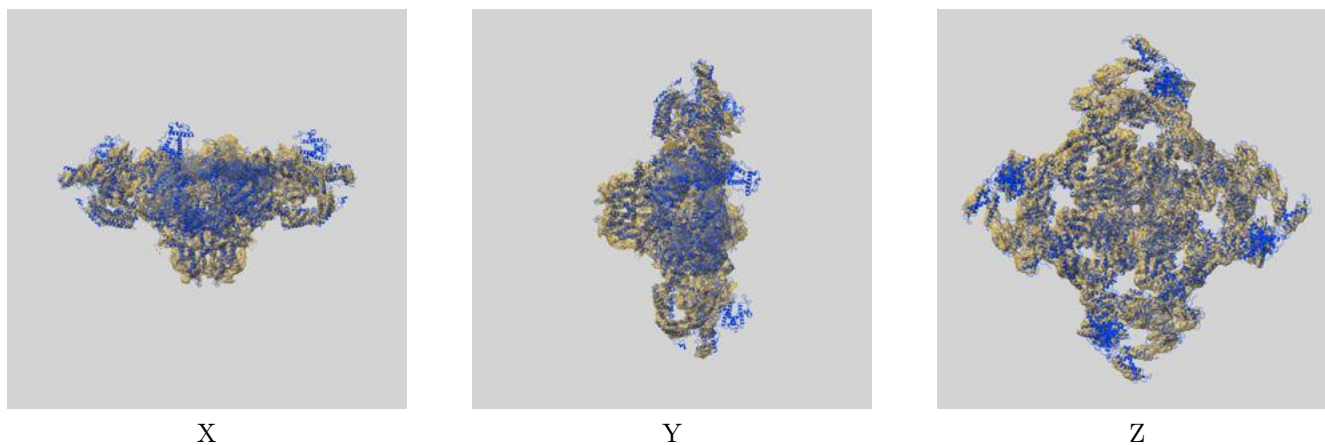
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

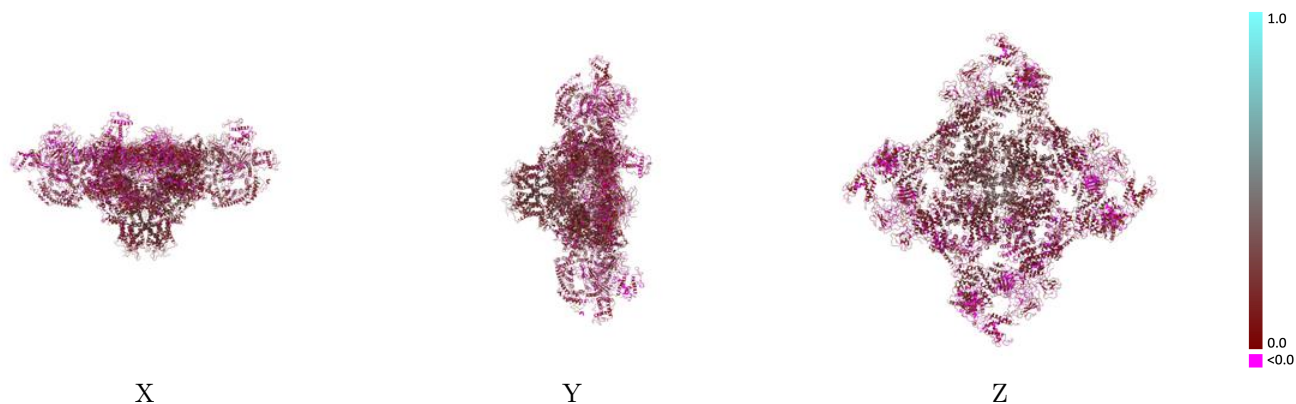
This section contains information regarding the fit between EMDB map EMD-22396 and PDB model 7JMJ. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



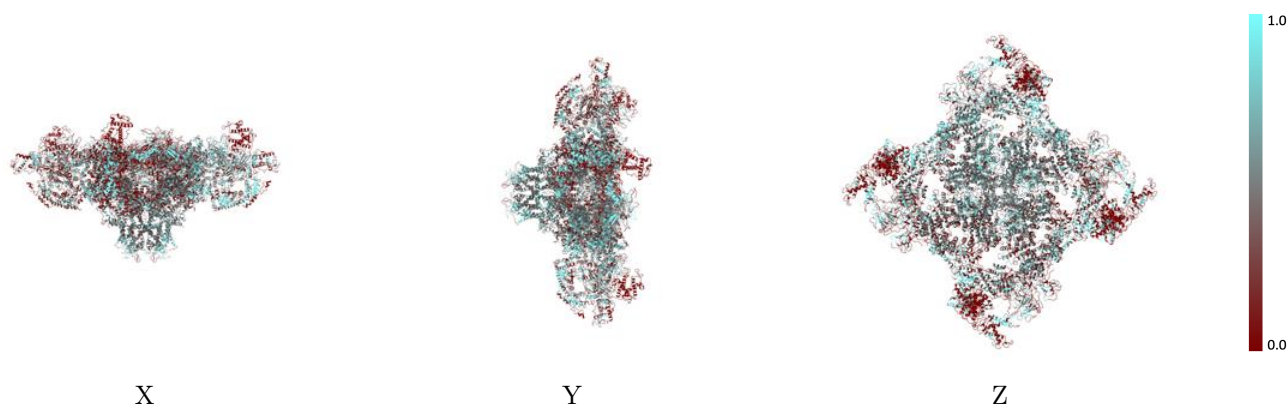
The images above show the 3D surface view of the map at the recommended contour level 0.16 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



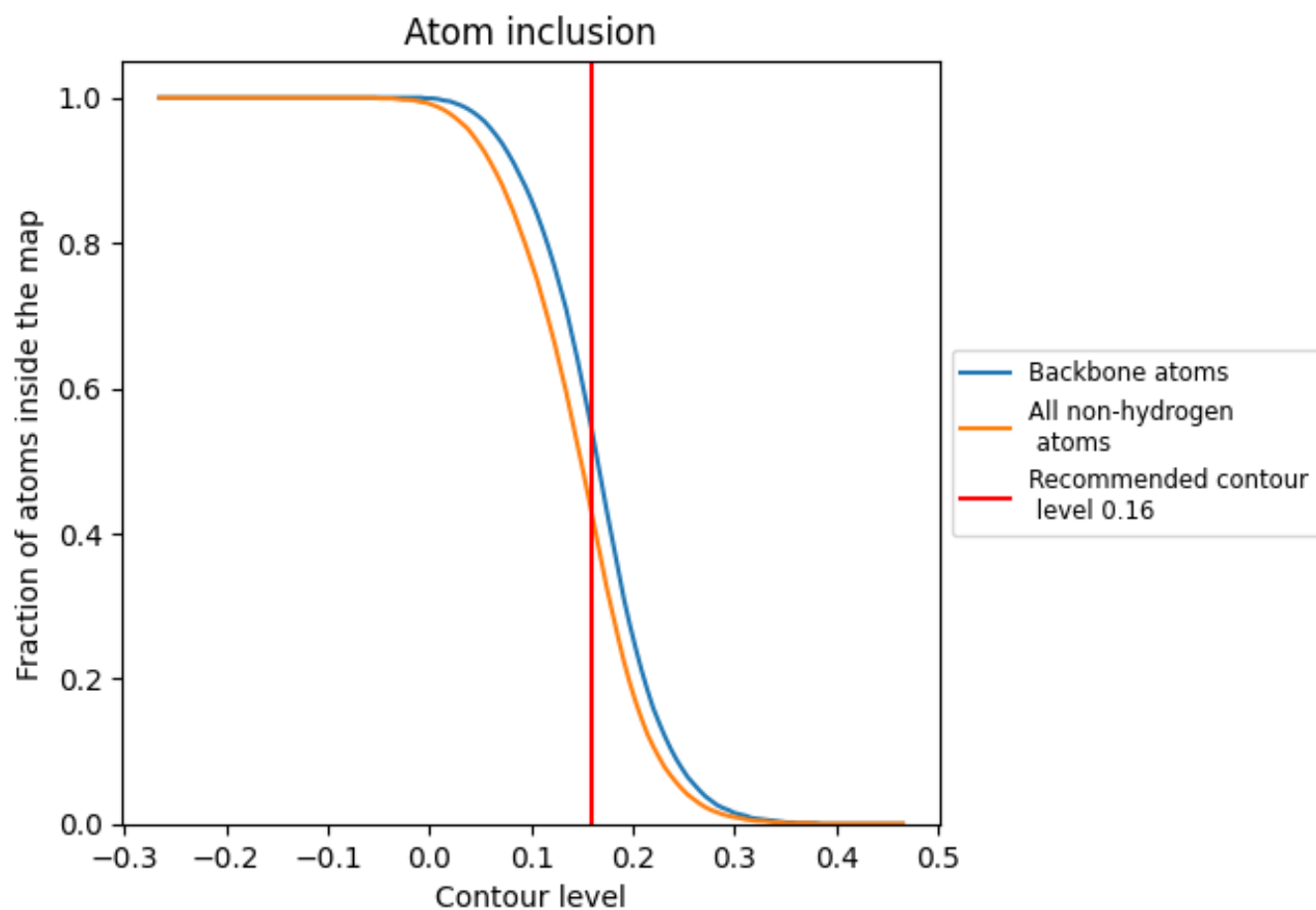
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.16).



















9.4 Atom inclusion [i](#)



At the recommended contour level, 54% of all backbone atoms, 42% 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 (0.16) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4250	 0.1330
A	 0.4530	 0.1410
B	 0.4630	 0.1670
E	 0.4320	 0.1360
F	 0.4260	 0.1110
G	 0.3980	 0.1060
H	 0.3920	 0.1210
I	 0.4060	 0.1230
J	 0.4020	 0.1150

