



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 05:51 PM UTC

PDB ID : 5T9R / pdb_00005t9r
EMDB ID : EMD-8374
Title : Structure of rabbit RyR1 (Ca²⁺-only dataset, class 3)
Authors : Clarke, O.B.; des Georges, A.; Zalk, R.; Marks, A.R.; Hendrickson, W.A.; Frank, J.
Deposited on : 2016-09-09
Resolution : 5.80 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

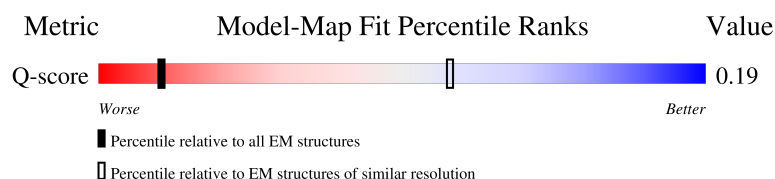
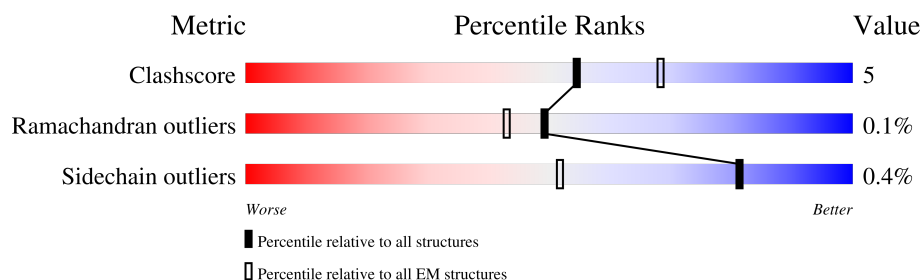
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.80 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.



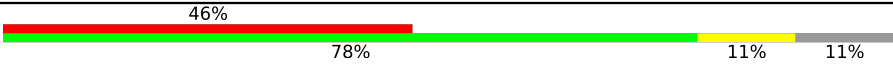
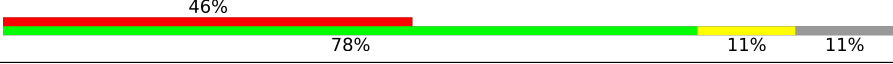
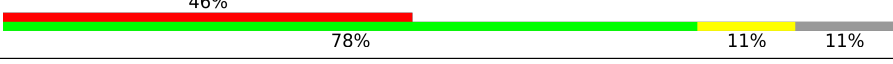
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	511 (5.30 - 6.30)

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	108	60% 80% 19%
1	F	108	56% 80% 19%
1	H	108	57% 81% 18%
1	J	108	57% 81% 18%

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

2 Entry composition

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

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

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

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

- Molecule 2 is a protein called Ryanodine receptor 1.

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

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

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

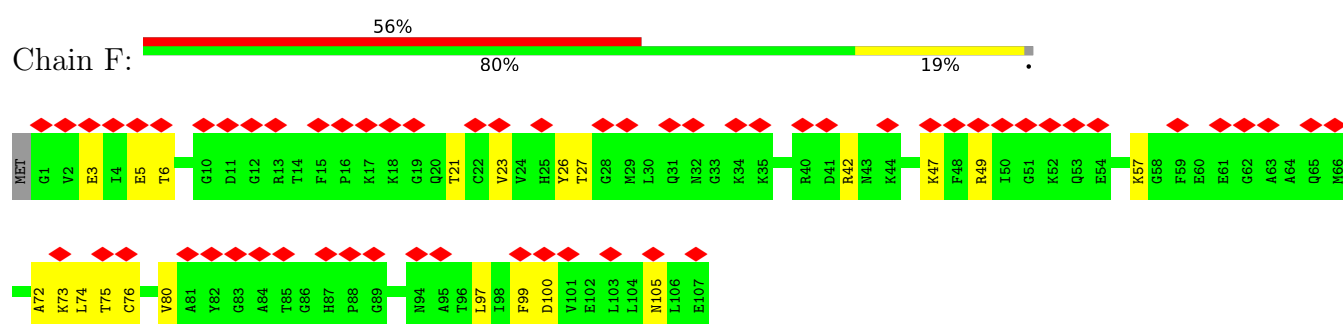
- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

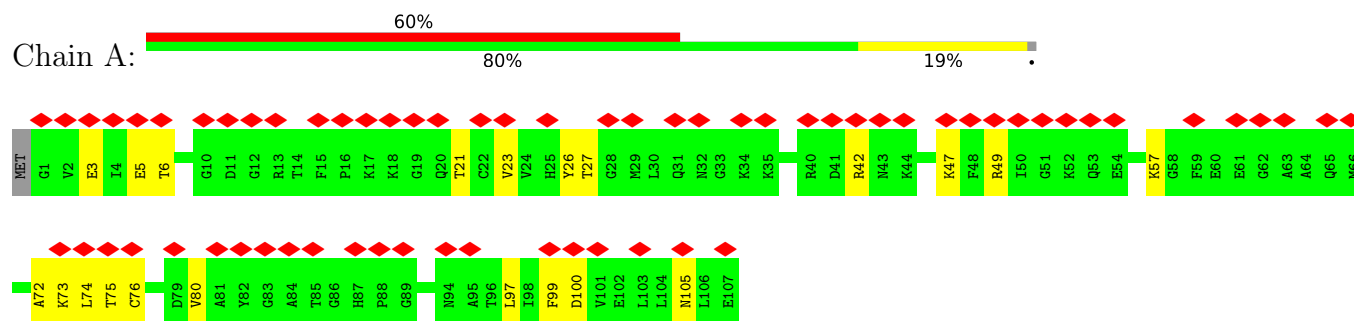
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

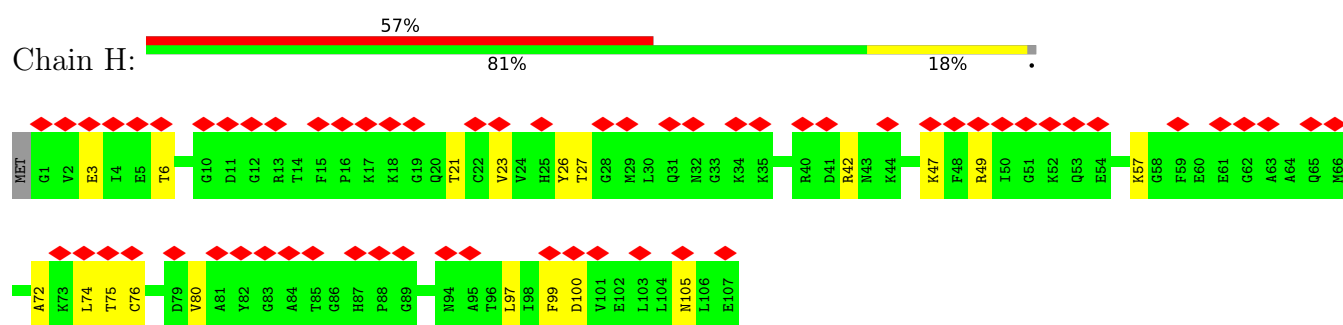
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



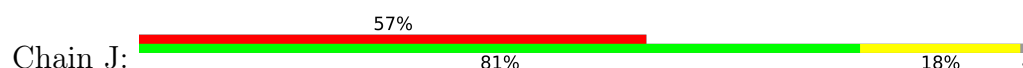
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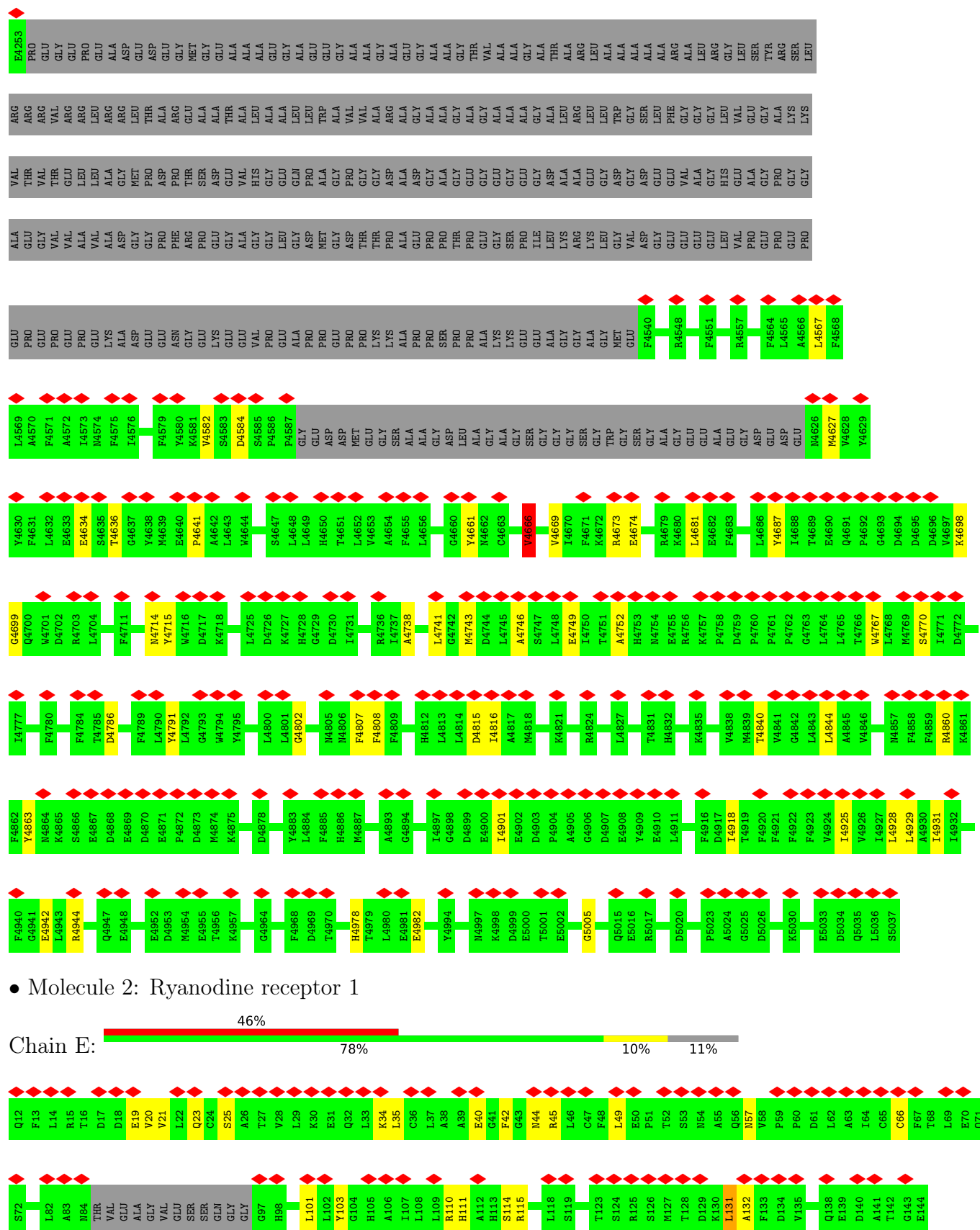






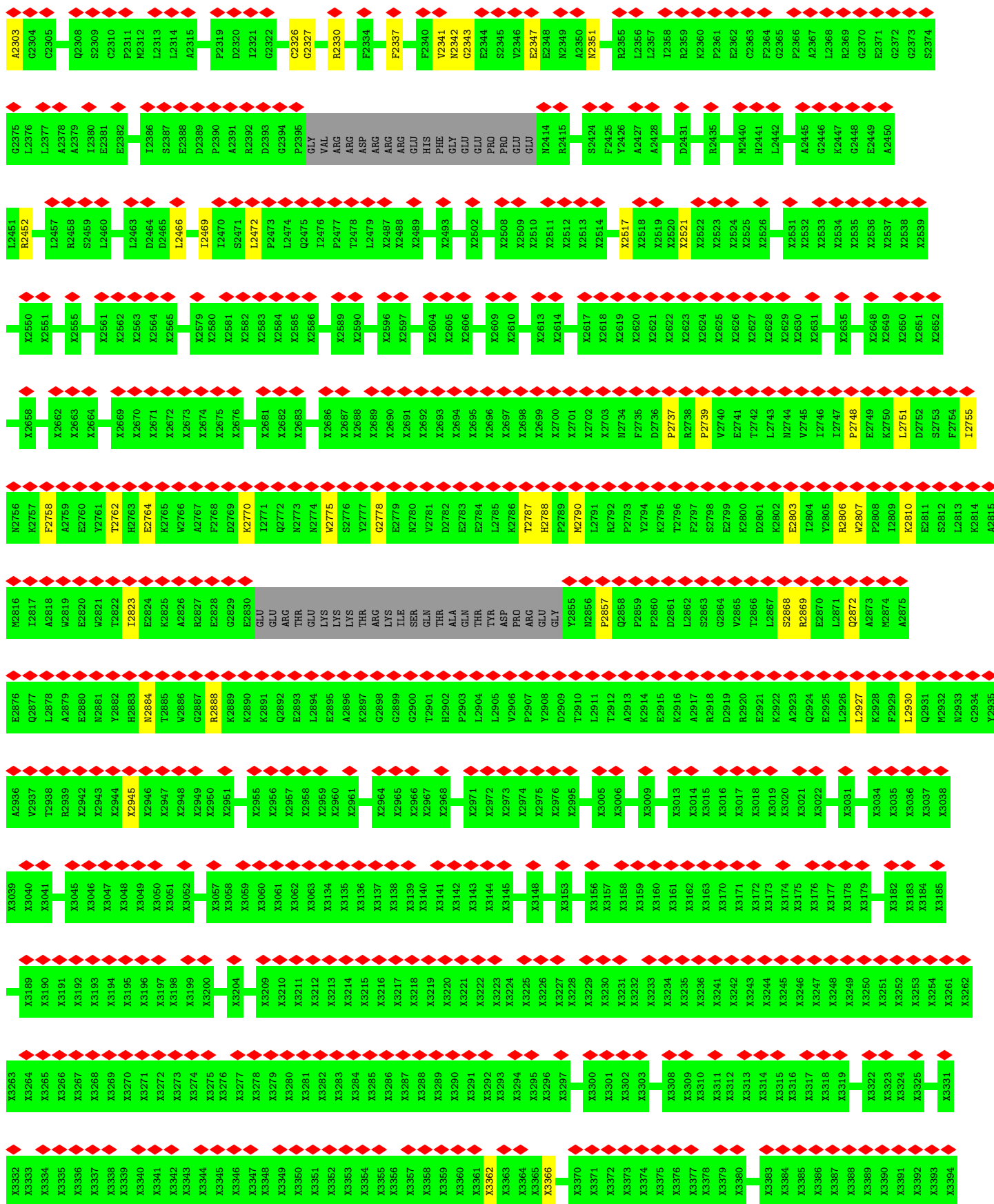
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R2827	E2828	G2829	E2830	GLU	GLU	THR	GLU	LYS	LYS	THR	ARG	LYS	ILE	SER	GLN	THR	ALA	GLN	THR	TVR	ASP	PRO	ARG	GLU	GLY	N2855	N2856	P2857	Q2858	P2859	P2860	P2861	L2862	S2863	G2864	V2865	T2866	L2867	S2868	R2869	E2870	L2871	Q2872	A2873	N2874	E2875	Q2876	Q2877	L2878	E2879	N2881	Y2882	N2883	N2884	T2885	N2886			
K2887	R2888	K2889	K2890	K2891	Q2892	E2893	L2894	E2895	E2896	K2897	G2898	G2899	G2900	T2901	H2902	P2903	L2904	L2905	V2906	P2907	P2908	D2909	T2910	T2911	T2912	A2913	K2914	E2915	E2916	A2917	R2918	D2919	R2920	E2921	K2922	A2923	Q2924	E2925	L2926	L2927	K2928	F2929	L2930	Q2931	N2932	N2933	Q2934	V2935	V2936	V2937	T2938	R2939	X2942	X2943	X2944	X2945	X2946	X2947	X2948
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L2457	R2458	S2459	L2460	L2463	D2464	D2465	L2466	I2470	S2471	L2472	P2473	L2474	Q2475	L2476	P2477	L2478	X2487	X2488	X2489	X2493	X2509	X2510	X2511	X2512	X2513	X2514	X2517	X2518	X2519	X2520	X2521	X2522	X2523	X2524	X2525	X2526	X2531	X2532	X2533	X2534	X2535	X2536	X2537	X2538	X2539	X2550	X2551	X2555	X2561										
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R2827	E2828	G2829	E2830	GLU	GLU	THR	GLU	LYS	LYS	THR	ARG	LYS	ILE	SER	GLN	THR	ALA	GLN	THR	TVR	ASP	PRO	ARG	GLU	GLY	N2855	N2856	P2857	Q2858	P2859	P2860	P2861	L2862	S2863	G2864	V2865	T2866	L2867	S2868	R2869	E2870	L2871	Q2872	A2873	N2874	E2875	Q2876	Q2877	L2878	E2879	N2881	Y2882	N2883	N2884	T2885	N2886			
K2887	R2888	K2889	K2890	K2891	Q2892	E2893	L2894	E2895	E2896	K2897	G2898	G2899	G2900	T2901	H2902	P2903	L2904	L2905	V2906	P2907	P2908	D2909	T2910	T2911	T2912	A2913	K2914	E2915	E2916	A2917	R2918	D2919	R2920	E2921	K2922	A2923	Q2924	E2925	L2926	L2927	K2928	F2929	L2930	Q2931	N2932	N2933	Q2934	V2935	V2936	V2937	T2938	R2939	X2942	X2943	X2944	X2945	X2946	X2947	X2948
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X3051	X3052	X3057	X3058	X3059	X3060	X3061	X3062	X3063	X3134	X3135	X3136	X3137	X3138	X3139	X3140	X3141	X3142	X3143	X3144	X3145	X3148	X3153	X3156	X3157	X3158	X3159	X3160	X3161	X3162	X3163	X3170	X3171	X3172	X3173	X3174	X3175	X3176	X3177	X3178	X3179	X3182	X3183	X3184	X3185	X3189	X3190	X3191	X3192	X3193	X3194	X3195	X3196	X3197				

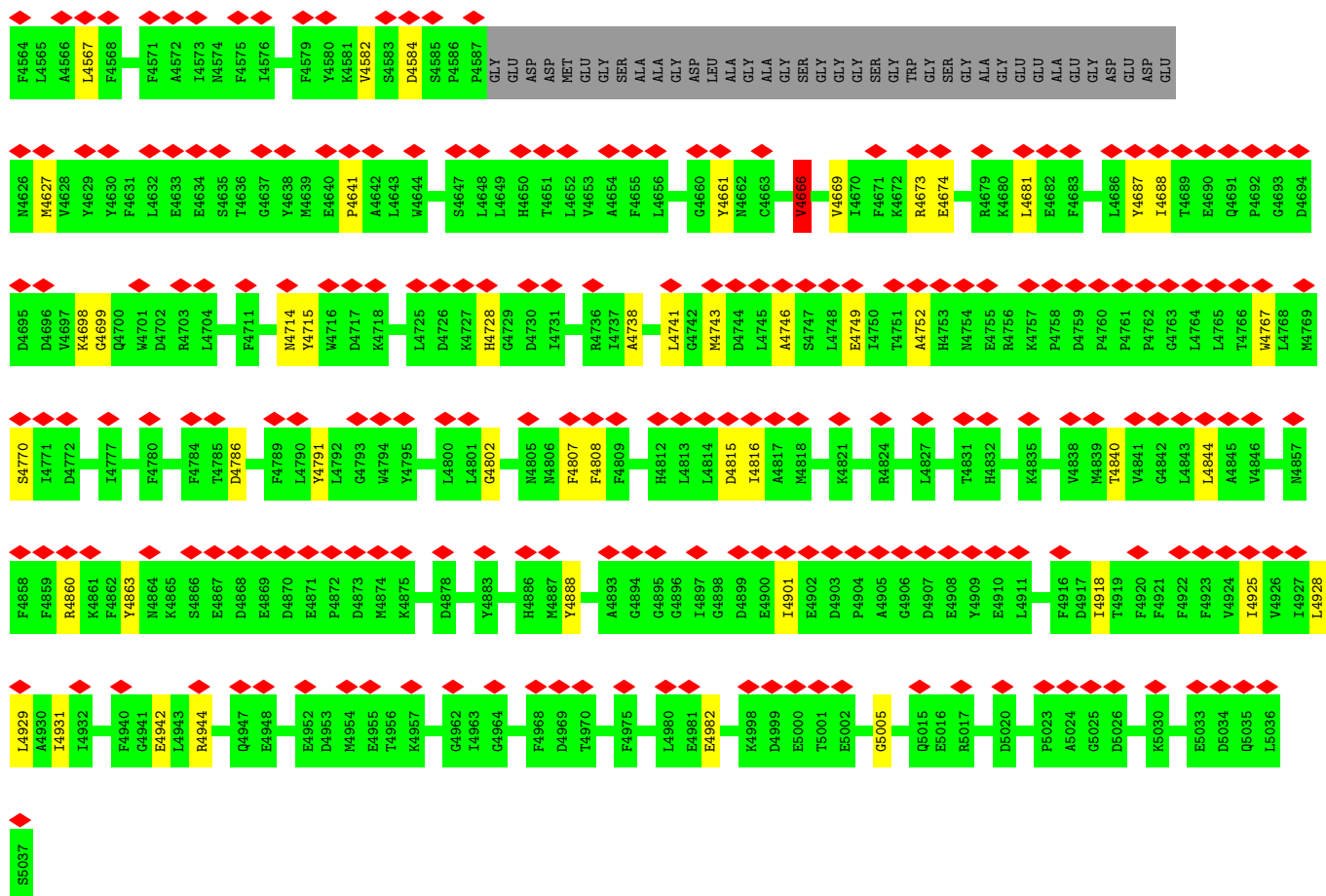






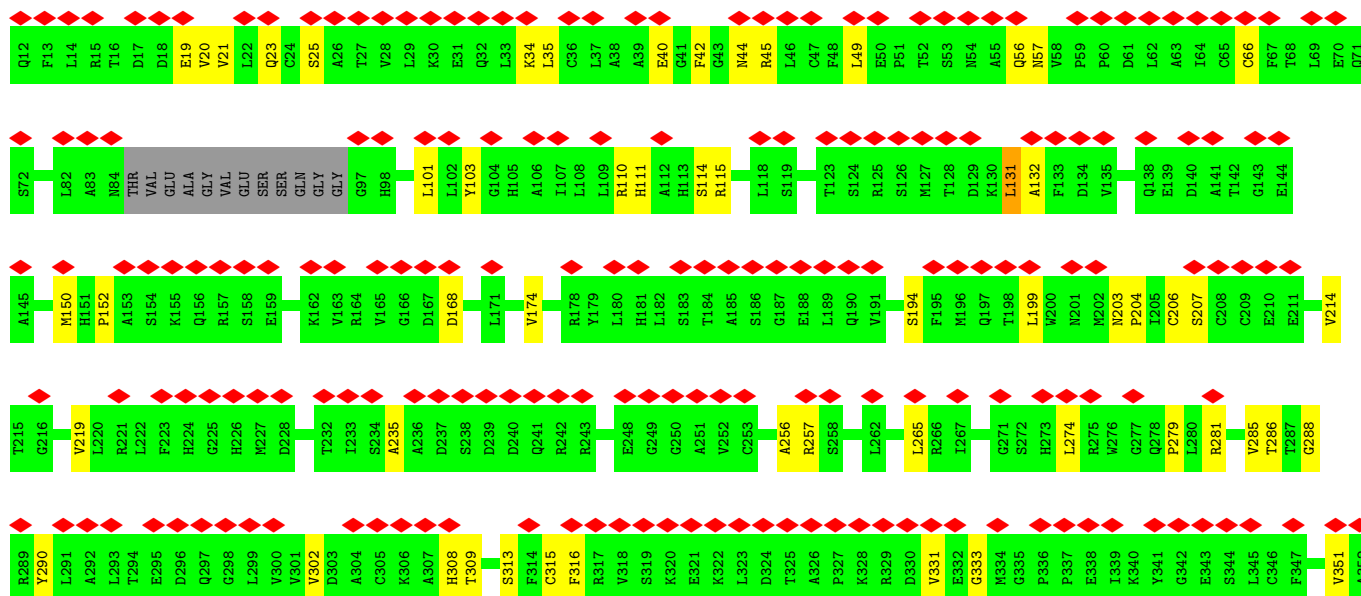


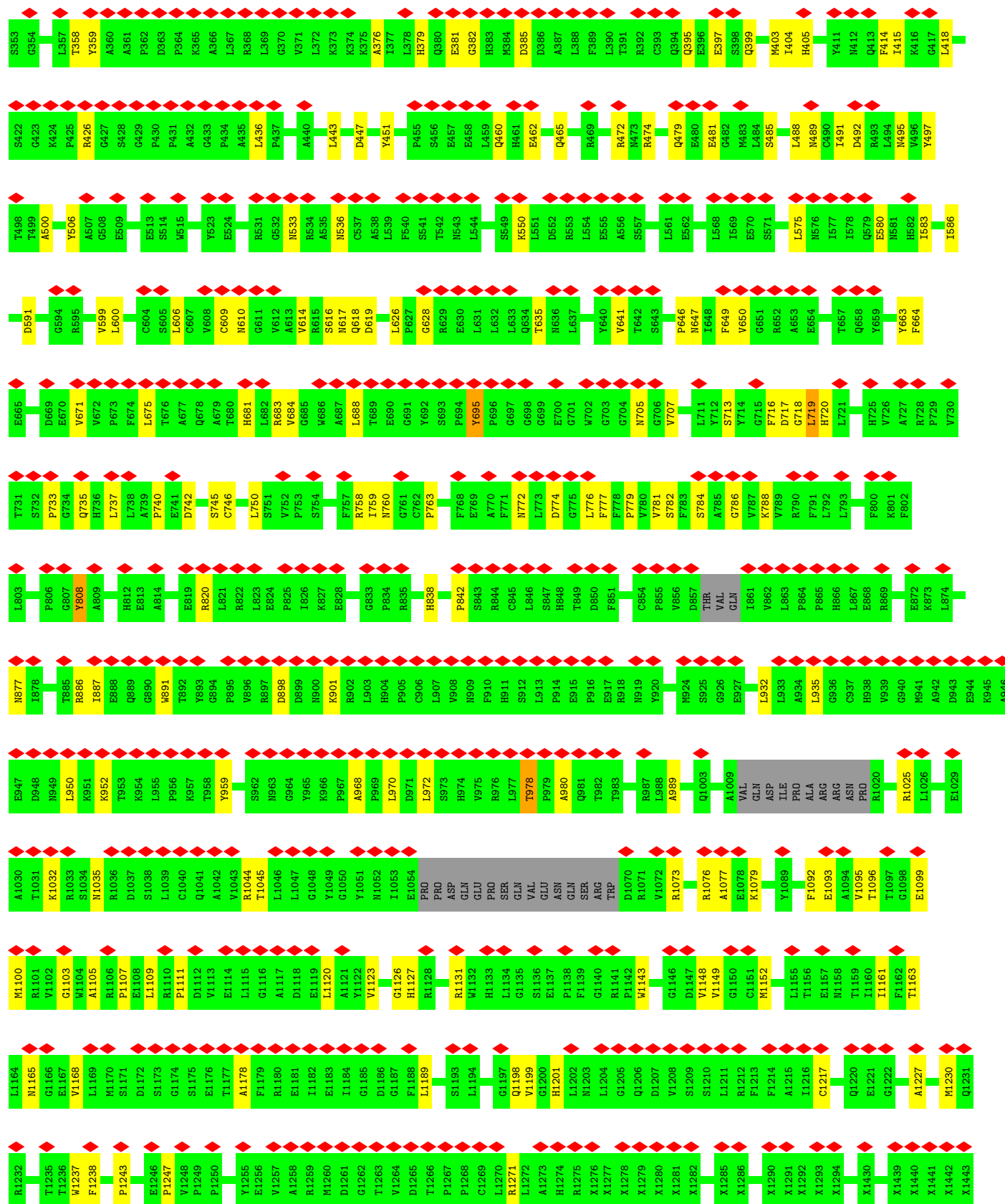


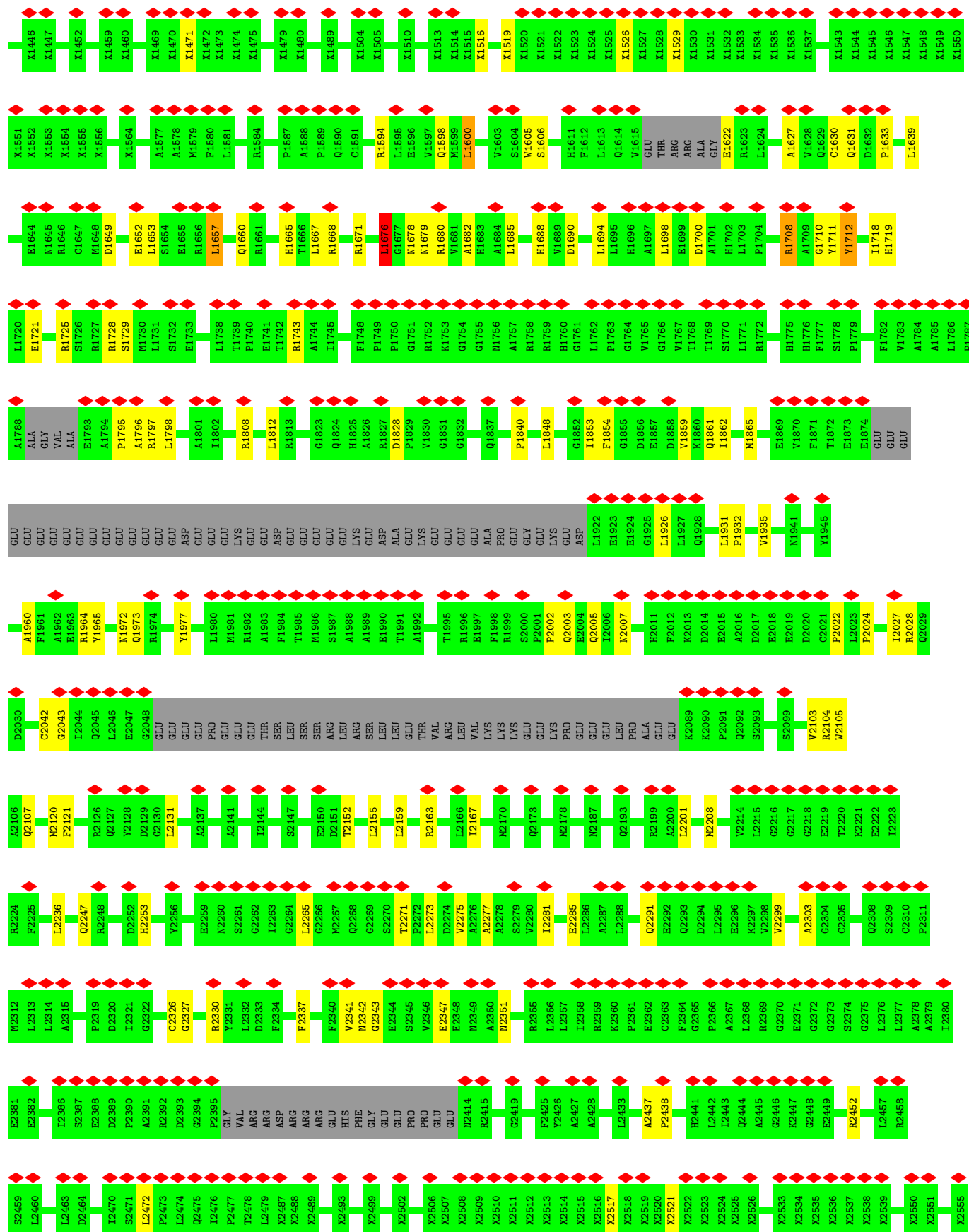


• Molecule 2: Ryanodine receptor 1

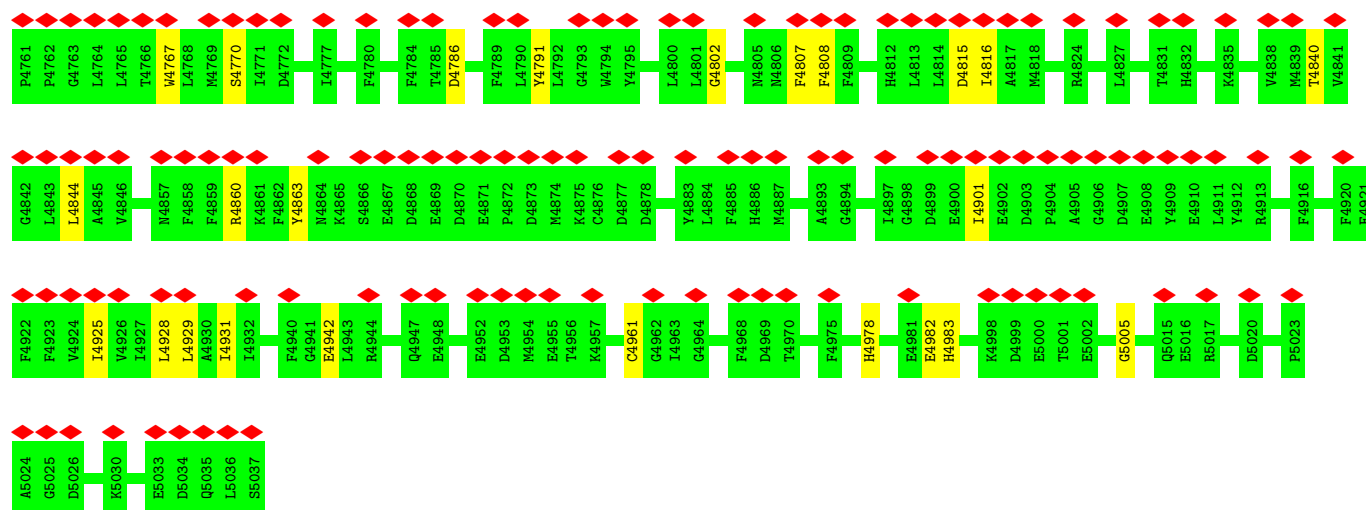
Chain I:



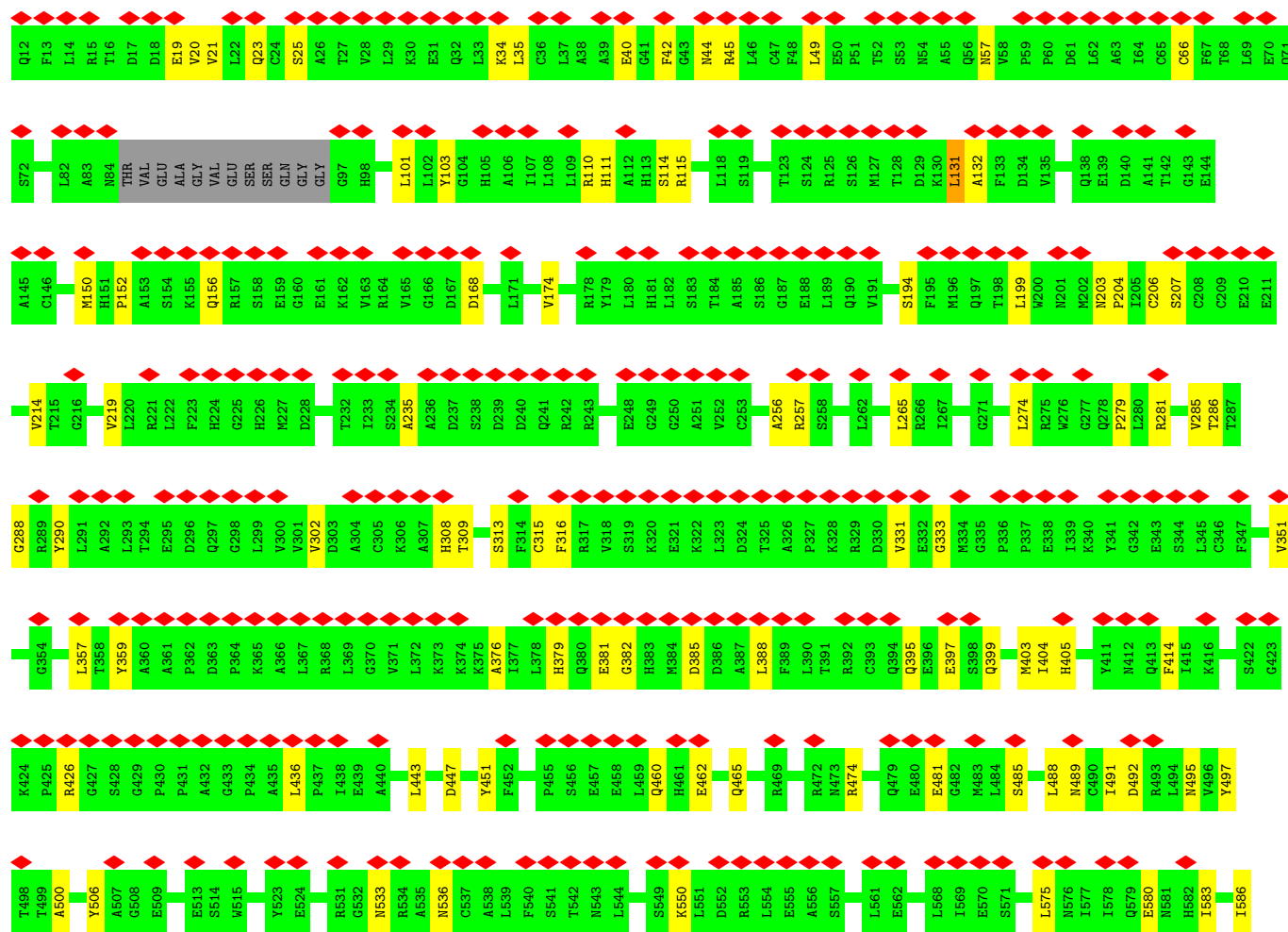
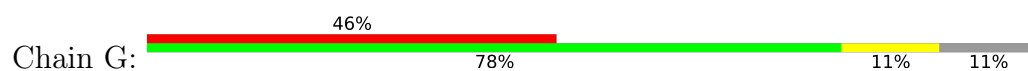


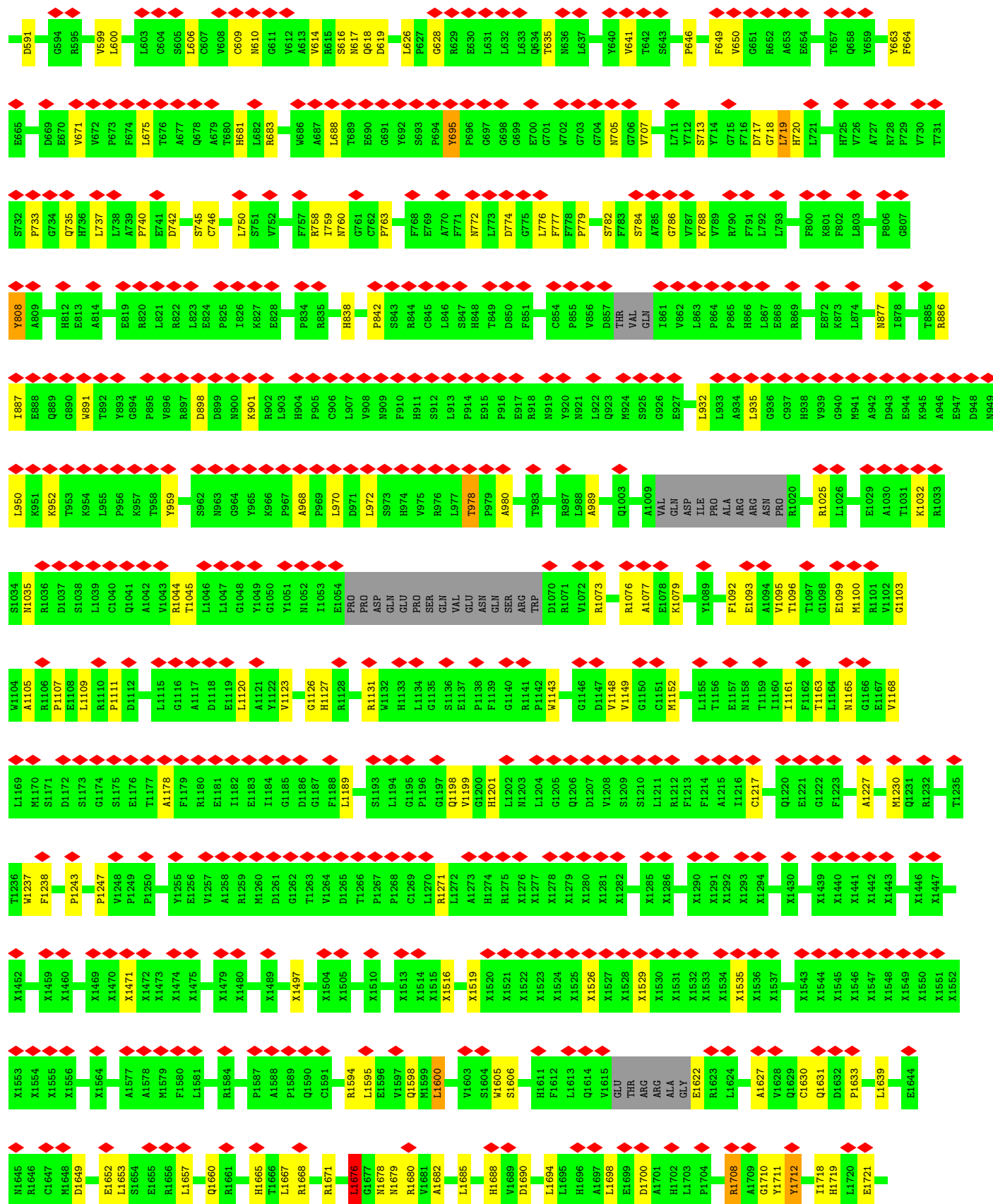






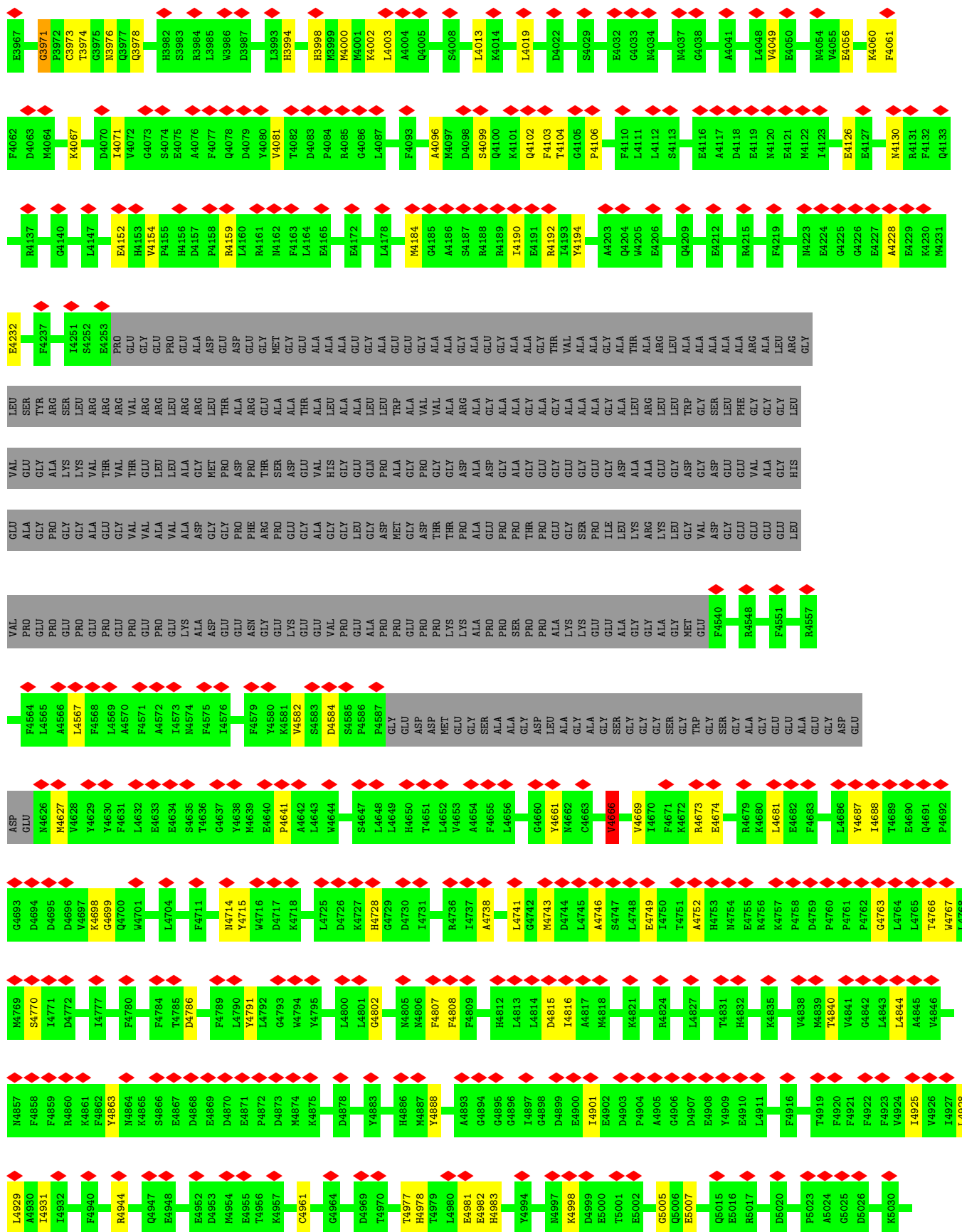
• Molecule 2: Ryanodine receptor 1

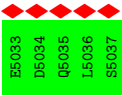




E1793	A1794	P1795	A1796	R1797	L1798	A1801	I1802	P1803	L1804	L1807	R1808	L1812	R1813	G1823	Q1824	H1825	A1826	R1827	D1828	P1829	V1830	G1831	G1832	Q1837	P1840	L1848	G1852	I1853	F1854	G1855	D1856	E1857	D1858	V1859	K1860	Q1861	I1862	M1865	E1869	V1870	F1871	T1872	E1873	E1874	GLU	GLU	GLU	GLU	ALA	GLY	VAL	ALA																																				
GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	ASP	GLU	GLU	GLU	LYS	GLU	ASP	GLU	GLU	GLU	GLU	ASP	GLU	GLU	GLU	GLU	GLU	ALA	GLU	GLY	LYS	ASP	L1922	E1923	E1924	G1925	L1926	L1927	Q1928	L1931	P1932	V1935	M1941	F1945	E1950	L2010	H2011	F2012	K2013	D2014	E2015	A2016	D2017	E2018	E2019	D2020	C2021	P2022																																	
L2023	P2024	I2027	R2028	Q2029	D2030	F2034	L2038	C2042	G2043	I2044	Q2045	L2046	E2047	G2048	GLU	GLU	GLU	PRO	GLU	GLU	THR	SER	LEU	SER	SER	ARG	LEU	LEU	GLU	THR	VAL	ARG	LEU	VAL	LYS	LYS	GLU	PRO	GLU	GLU	LEU	PRO	ALA	GLU	GLU	K2089																																										
K2090	P2091	Q2092	S2093	H2100	R2104	K2105	Q2106	Q2107	A2119	N2120	F2121	R2126	Q2127	Q2128	D2129	L2131	A2137	G2141	G2142	S2147	E2150	D2151	T2152	L2155	L2159	R2163	L2166	I2167	M2170	Q2173	M2178	N2187	N2188	Q2193	A2200	L2201	M2208	V2214	L2215	G2216	G2217	G2218	E2219	T2220	R2221	E2222	F2225	M2228	L2236	Q2247	R2248	D2252	H2253	Y2256	N2260	S2261	G2262	I2263	G2264	L2265	G2266	M2267	Q2268	G2269	S2270	T2271	P2272	L2273	D2274	Y2275	A2276	A2277	A2278	S2279	V2280	I2281	D2282	E2285	L2288	Q2291	E2292	Q2293	D2294	L2295	E2296	K2297	A2303	G2304
C2305	Q2308	S2309	C2310	P2311	M2312	L2313	L2314	A2315	F2319	D2320	I2321	G2322	C2326	Q2327	R2330	F2334	F2337	A2338	V2339	F2340	V2341	N2342	G2343	E2344	S2345	V2346	E2347	E2348	N2349	A2350	N2351	R2355	L2356	L2357	L2358	R2359	K2360	P2361	E2362	C2363	F2364	A2367	L2368	R2369	G2370	E2371	G2372	G2373	S2374	G2375	L2376																																					
L2377	A2378	A2379	I2380	I2386	S2387	E2388	D2389	P2390	A2391	R2392	D2393	G2394	P2395	GLY	VAL	ARG	ASP	ARG	ARG	GLU	HIS	PHE	GLY	GLU	PRO	PRO	GLU	N2414	R2415	V2416	S2424	F2425	Y2426	A2427	A2428	D2431	R2435	C2436	P2437	P2438	E2439	M2440	H2441	L2442	A2445	G2446	T2447	G2448	E2449	A2450																																						
L2451	R2452	L2457	R2458	S2459	L2460	L2463	D2464	D2465	L2466	I2470	S2471	L2472	P2473	L2474	Q2475	I2476	P2477	T2478	L2479	X2487	X2488	X2489	X2493	X2509	X2510	X2511	X2512	X2513	X2514	X2517	X2518	X2519	X2520	X2521	X2522	X2523	X2524	X2525	X2526	X2531	X2532	X2533	X2534	X2535	X2536	X2537	X2538	X2539	X2550	X2551																																						
X2555	X2561	X2562	X2563	X2564	X2565	X2579	X2580	X2581	X2582	X2583	X2584	X2585	X2586	X2589	X2590	X2596	X2597	X2604	X2605	X2606	X2609	X2610	X2613	X2614	X2617	X2618	X2619	X2620	X2621	X2622	X2623	X2624	X2625	X2626	X2627	X2628	X2629	X2630	X2645	X2648	X2649	X2650	X2651	X2652	X2658	X2662	X2663																																									
X2664	X2669	X2670	X2671	X2672	X2673	X2674	X2675	X2676	X2681	X2682	X2683	X2686	X2687	X2688	X2689	X2690	X2691	X2692	X2693	X2694	X2695	X2696	X2697	X2698	X2699	X2700	X2701	X2702	X2703	X2704	X2705	X2706	X2707	X2708	X2709	X2710	X2711	X2712	X2713	X2714	X2715	X2716	X2717	X2718	X2719	X2720	X2721	X2722	X2723	X2724	X2725	X2726	X2727	X2728	X2729	X2730	X2731	X2732	X2733	X2734	X2735	X2736	X2737	X2738	X2739	X2740	X2741	X2742	X2743	X2744	X2745	X2746	X2747	X2748	X2749	X2750	X2751	X2752	X2753	X2754	X2755	X2756	X2757	X2758	X2759	X2760		
X2761	T2762	E2763	E2764	X2765	X2766	X2767	X2768	X2769	X2770	X2771	Q2772	X2773	X2774	X2775	S2776	X2777	X2778	E2779	N2780	X2781	X2782	E2783	E2784	L2785	X2786	T2787	H2788	X2789	X2790	L2791	X2792	X2793	X2794	X2795	X2796	X2797	X2798	X2799	X2800	D2801	X2802	E2803	T2804	X2805	X2806	X2807	X2808	X2809	X2810	E2811	S2812	L2813	X2814	A2815	X2816	X2817	X2818	X2819	E2820																													

V3874	V3875	A3876	D3877	D3878	E3879	F3880		D3883	L3884	F3885	F3886	F3887	L3888	Q3889	L3890		N3897	D3898	F3899	Q3900	N3901	V3902	L3903		T3907	Q3908	Q3909	T3910	T3911	T3912	L3913		Y3922		R3925		S3929		D3932		Y3936	T3937	Q3938	Q3939	K3940	D3941	V3942	L3943		N3950		M3955	K3959	Q3960	V3961	F3962	N3963																										
M3782	L3783	S3784		G3788	E3789	T3790		L3805	N3806	F3885	G3807	G3808	K3815	L3816	L3817		K3821	D3822	K3823	K3824	E3825	V3826	G3827	F3828	F3829	Q3830	Q3833	Q3834	L3842	D3843	A3846	R3849	Q3850		A3853	E3854	G3855	L3856	G3857	M3858	V3859	N3860	E3861	D3862	G3863	T3864	V3865	L3866	N3867	K3868	Q3869	N3870	G3871	E3872	K3873																												
H3704	L3710	T3711		S3714	K3715	L3716	D3717	E3718	D3719	V3720		Y3725	A3726	D3727	L3728	A3729	A3730	K3731		L3735	E3736	E3737	G3738	G3739	E3740	M3741	GLY	GLU	ALA	GLY	E3747	E3748	V3749	E3750	V3751	S3752	F3753	E3754	E3755	K3756	E3757	M3758	E3759	Q3760	Q3761		S3768	R3769	L3770	H3771	T3772	R3773		A3776		L3780	Q3781																										
X3527	X3528	X3529	X3530	X3531	X3532	X3533	X3534	X3538	X3539	X3540	X3541	X3542	X3543	X3544	X3545	X3546	X3547	X3548	X3549	X3550	X3551	X3552	X3553	X3554	X3555	X3556	X3557	X3558	X3559	X3560	X3561	X3562	X3563	X3564	X3565	X3566	X3567	X3568	X3569			X3572		X3576	X3577	X3578	X3579	X3580	X3581	X3582	X3583	X3584	X3585	X3586	X3587	X3588	X3589	X3590	X3591																								
X3336	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		X3370	X3371	X3372	X3373	X3374	X3375	X3376	X3377	X3378	X3379	X3380		X3383	X3384	X3385	X3386	X3387	X3388	X3389	X3390	X3391	X3392	X3393	X3394	X3395	X3396	X3397	X3398																								
X3399	X3400	X3401	X3402	X3403	X3404	X3405		X3410	X3411	X3412	X3413	X3414	X3415	X3416	X3417		X3422	X3423		X3430	X3431	X3432	X3433	X3434	X3435	X3436	X3437		X3440	X3441	X3442	X3443	X3444	X3445	X3446	X3447	X3448	X3449	X3450	X3451	X3452		X3458	X3459		X3462	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
X2821	T2822	L2823	E2824	L2825	A2826	R2827	E2828	G2829	E2830	GLU	ARG	THR	GLU	LYS	LYS	LYS	THR	ARG	ILE	SER	GLN	THR	ALA	GLN	THR	TYR	ASP	PRO	ARG	GLU	GLY	Y2855	N2856	P2857	Q2858	P2859	P2860	D2861	L2862	S2863	Q2864	V2865	T2866	L2867	S2868	L2869	E2870	L2871	Q2872	A2873	L2874	E2875	E2876	Q2877	L2878	A2879	E2880																										





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	0.093	Depositor
Minimum map value	-0.044	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.035	Depositor
Map size (Å)	502.0, 502.0, 502.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.255, 1.255, 1.255	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, CA

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.17	0/834	0.44	0/1123
1	F	0.17	0/834	0.44	0/1123
1	H	0.17	0/834	0.44	0/1123
1	J	0.17	0/834	0.44	0/1123
2	B	0.20	1/25428 (0.0%)	0.52	3/34534 (0.0%)
2	E	0.20	1/25428 (0.0%)	0.52	3/34534 (0.0%)
2	G	0.20	1/25428 (0.0%)	0.52	3/34534 (0.0%)
2	I	0.20	1/25428 (0.0%)	0.52	3/34534 (0.0%)
All	All	0.20	4/105048 (0.0%)	0.52	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	14
2	E	0	14
2	G	0	14
2	I	0	14
All	All	0	56

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	695	TYR	C-N	10.84	1.59	1.33
2	I	695	TYR	C-N	10.83	1.59	1.33
2	B	695	TYR	C-N	10.83	1.59	1.33
2	E	695	TYR	C-N	10.83	1.59	1.33

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	4666	VAL	CA-C-N	-7.29	110.73	119.84
2	E	4666	VAL	C-N-CA	-7.29	110.73	119.84
2	B	4666	VAL	CA-C-N	-7.28	110.74	119.84
2	B	4666	VAL	C-N-CA	-7.28	110.74	119.84
2	I	4666	VAL	CA-C-N	-7.27	110.75	119.84

There are no chirality outliers.

5 of 56 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	1676	LEU	Peptide
2	B	1690	ASP	Peptide
2	B	1712	TYR	Peptide
2	B	1795	PRO	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	11	0
1	F	818	0	824	12	0
1	H	818	0	824	10	0
1	J	818	0	824	10	0
2	B	29369	0	24721	275	0
2	E	29369	0	24720	272	0
2	G	29369	0	24720	277	0
2	I	29369	0	24720	277	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	102177	1128	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 1128 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:788:LYS:HG2	2:G:1630:CYS:H	1.52	0.74
2:B:788:LYS:HG2	2:B:1630:CYS:H	1.53	0.72
2:E:788:LYS:HG2	2:E:1630:CYS:H	1.53	0.72
2:I:788:LYS:HG2	2:I:1630:CYS:H	1.53	0.72
2:I:379:HIS:HD2	2:I:382:GLY:H	1.41	0.68

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%)	94 (90%)	11 (10%)	0	100	100
1	F	105/108 (97%)	93 (89%)	12 (11%)	0	100	100
1	H	105/108 (97%)	93 (89%)	12 (11%)	0	100	100
1	J	105/108 (97%)	93 (89%)	12 (11%)	0	100	100
2	B	3235/4676 (69%)	2923 (90%)	308 (10%)	4 (0%)	48	83
2	E	3235/4676 (69%)	2922 (90%)	309 (10%)	4 (0%)	48	83
2	G	3235/4676 (69%)	2922 (90%)	309 (10%)	4 (0%)	48	83
2	I	3235/4676 (69%)	2924 (90%)	307 (10%)	4 (0%)	48	83
All	All	13360/19136 (70%)	12064 (90%)	1280 (10%)	16 (0%)	49	83

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	1708	ARG

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Mol	Chain	Res	Type
2	E	1708	ARG
2	I	1708	ARG
2	G	1708	ARG
2	B	1840	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	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	2493/3202 (78%)	2482 (100%)	11 (0%)	84	84
2	E	2493/3202 (78%)	2482 (100%)	11 (0%)	84	84
2	G	2493/3202 (78%)	2482 (100%)	11 (0%)	84	84
2	I	2493/3202 (78%)	2482 (100%)	11 (0%)	84	84
All	All	10324/13164 (78%)	10280 (100%)	44 (0%)	81	84

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	I	1676	LEU
2	G	719	LEU
2	I	3663	LEU
2	I	4154	VAL
2	G	1600	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 232 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	4864	ASN

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Mol	Chain	Res	Type
2	G	4034	ASN
2	I	1679	ASN
2	G	3960	GLN
2	G	1598	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	12
2	G	12
2	E	12
2	I	12

The worst 5 of 48 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	3613:UNK	C	3639:THR	N	43.37
1	G	3613:UNK	C	3639:THR	N	43.37
1	E	3613:UNK	C	3639:THR	N	43.34
1	I	3613:UNK	C	3639:THR	N	43.32
1	B	3163:UNK	C	3170:UNK	N	16.45

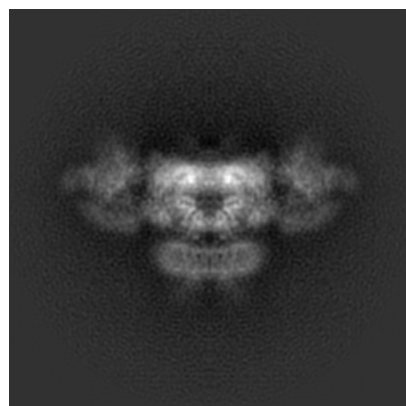
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8374. These allow visual inspection of the internal detail of the map and identification of artifacts.

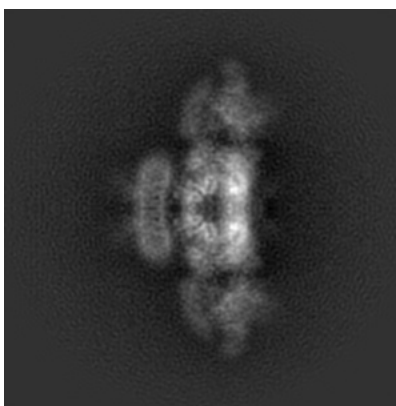
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

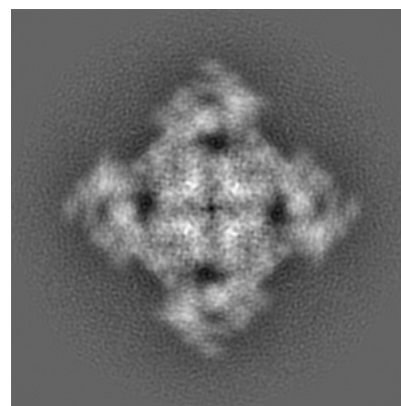
6.1.1 Primary map



X

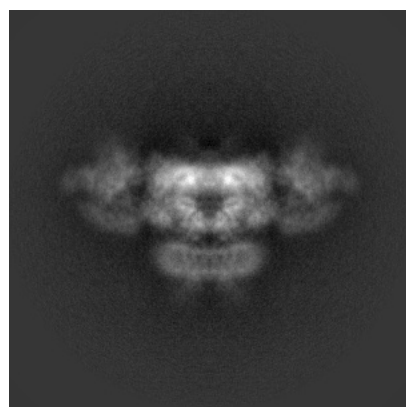


Y

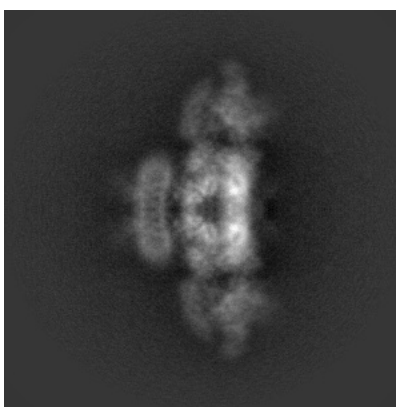


Z

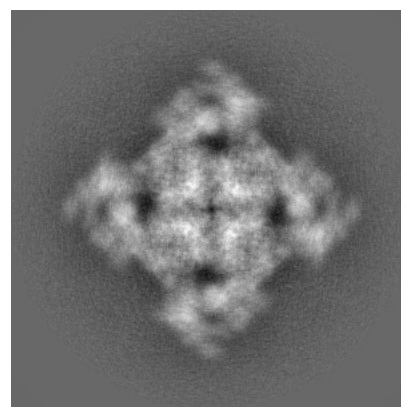
6.1.2 Raw map



X



Y

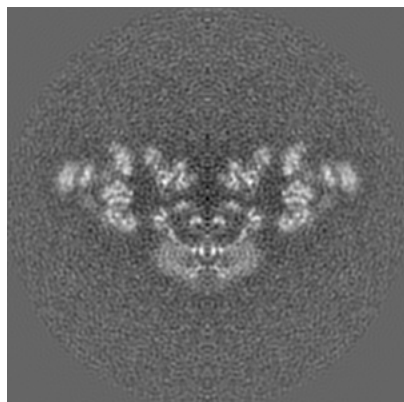


Z

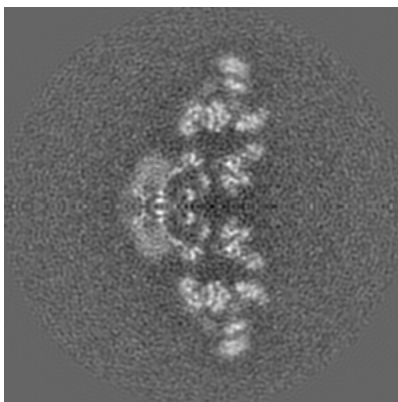
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

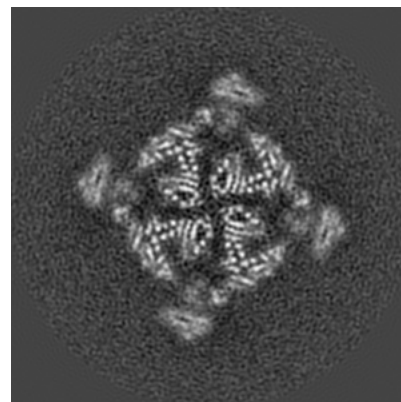
6.2.1 Primary map



X Index: 200

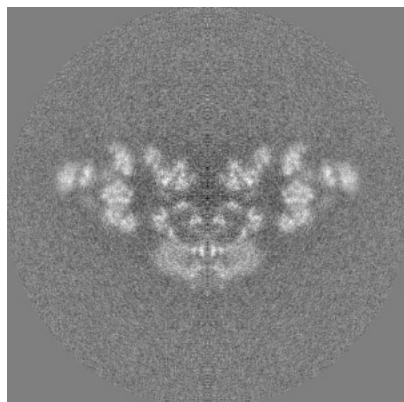


Y Index: 200

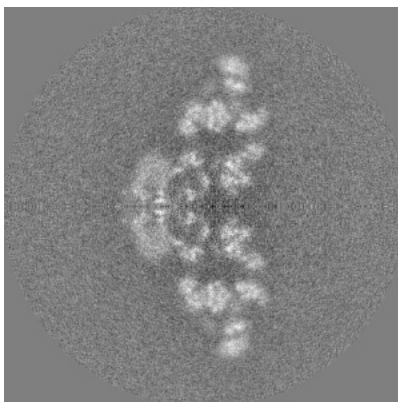


Z Index: 200

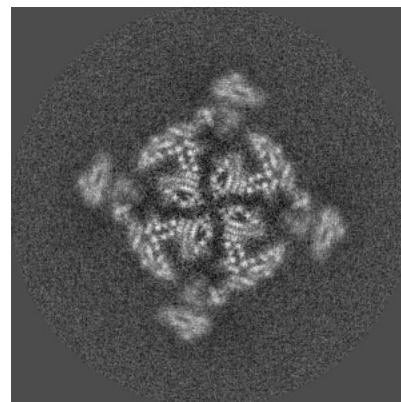
6.2.2 Raw map



X Index: 200



Y Index: 200

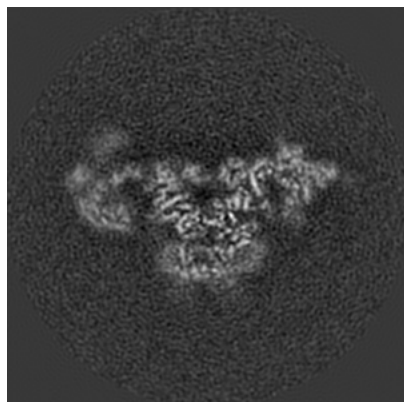


Z Index: 200

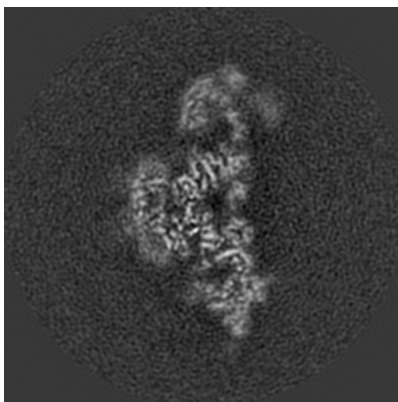
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

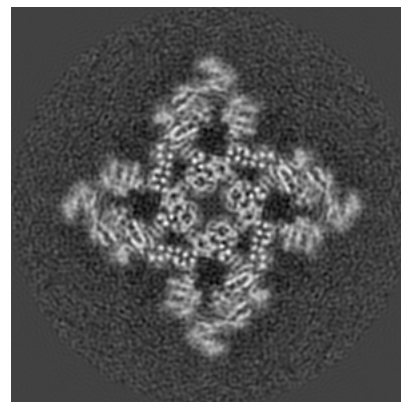
6.3.1 Primary map



X Index: 184

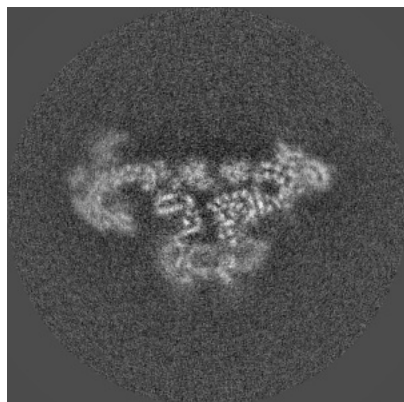


Y Index: 184

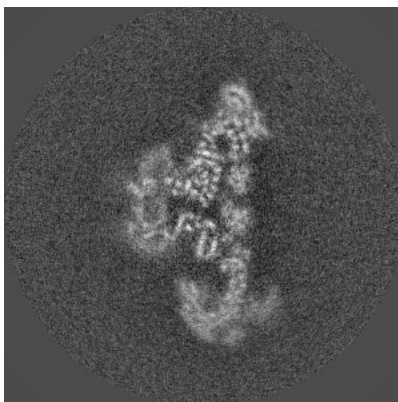


Z Index: 227

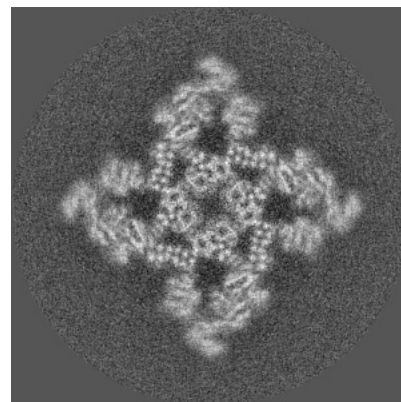
6.3.2 Raw map



X Index: 179



Y Index: 221

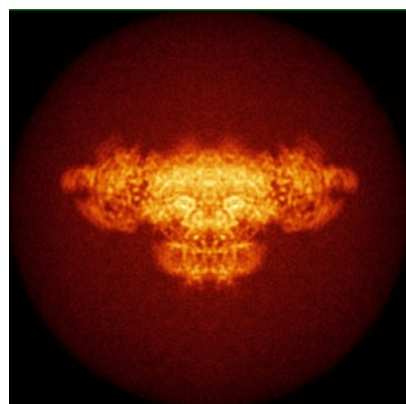


Z Index: 227

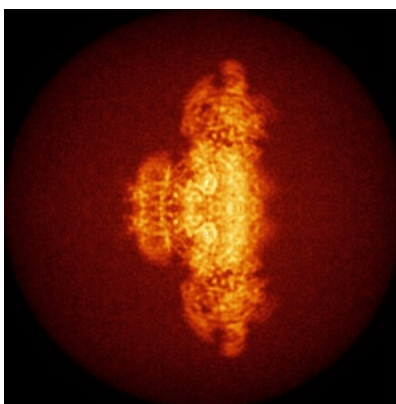
The images above show the largest variance slices of the map in three orthogonal directions.

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

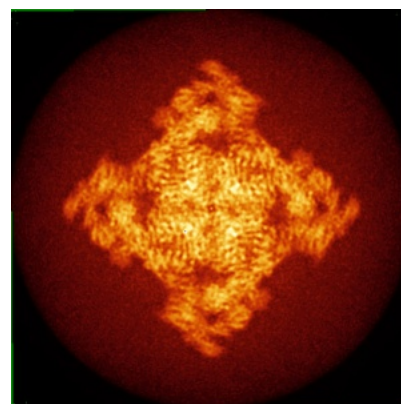
6.4.1 Primary map



X

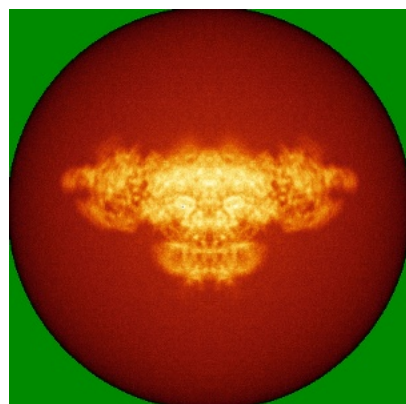


Y

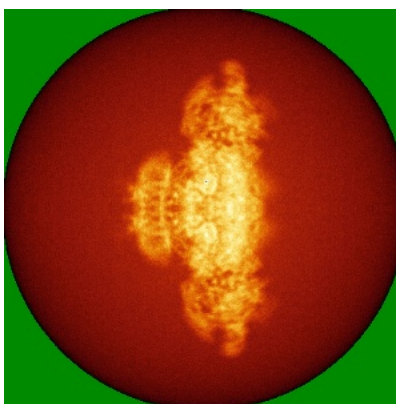


Z

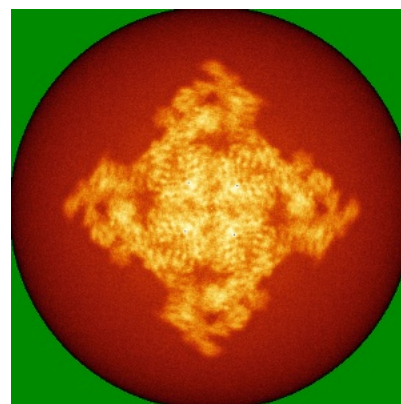
6.4.2 Raw map



X



Y

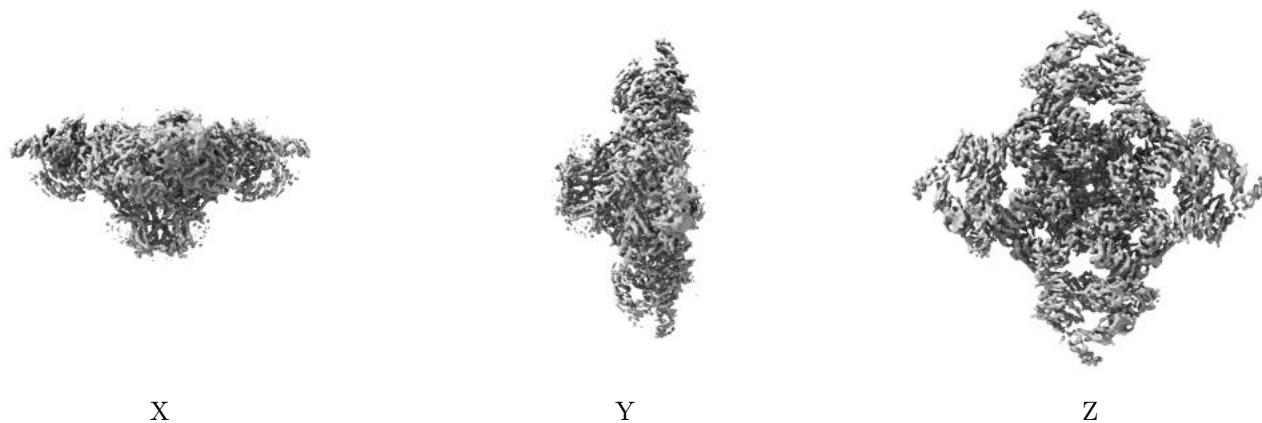


Z

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.

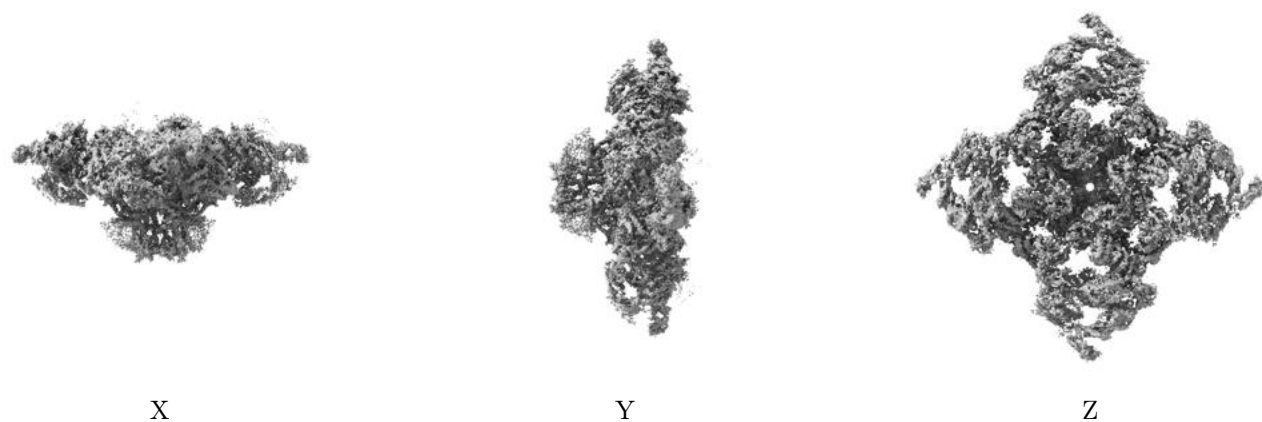
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.035. 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.

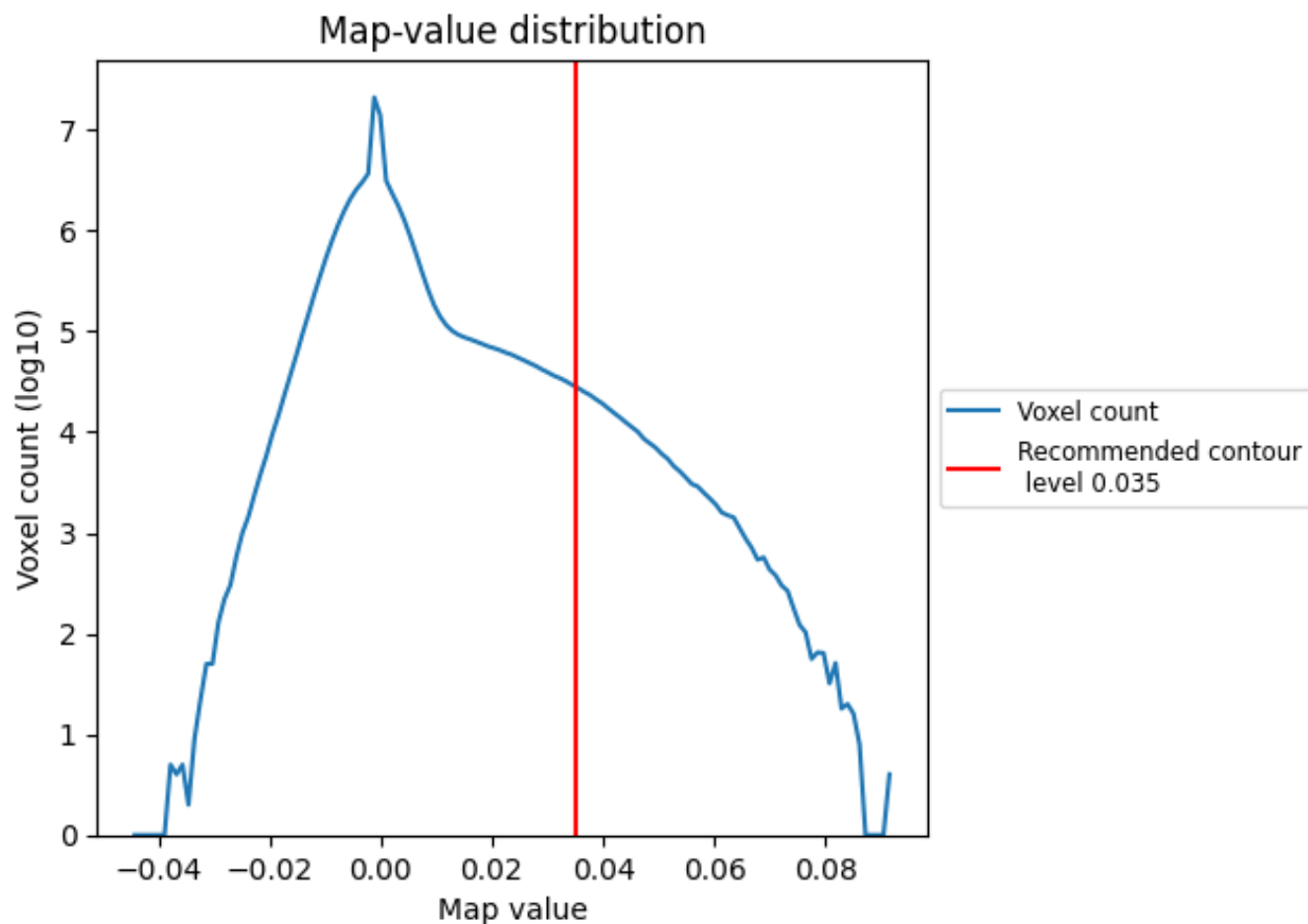
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

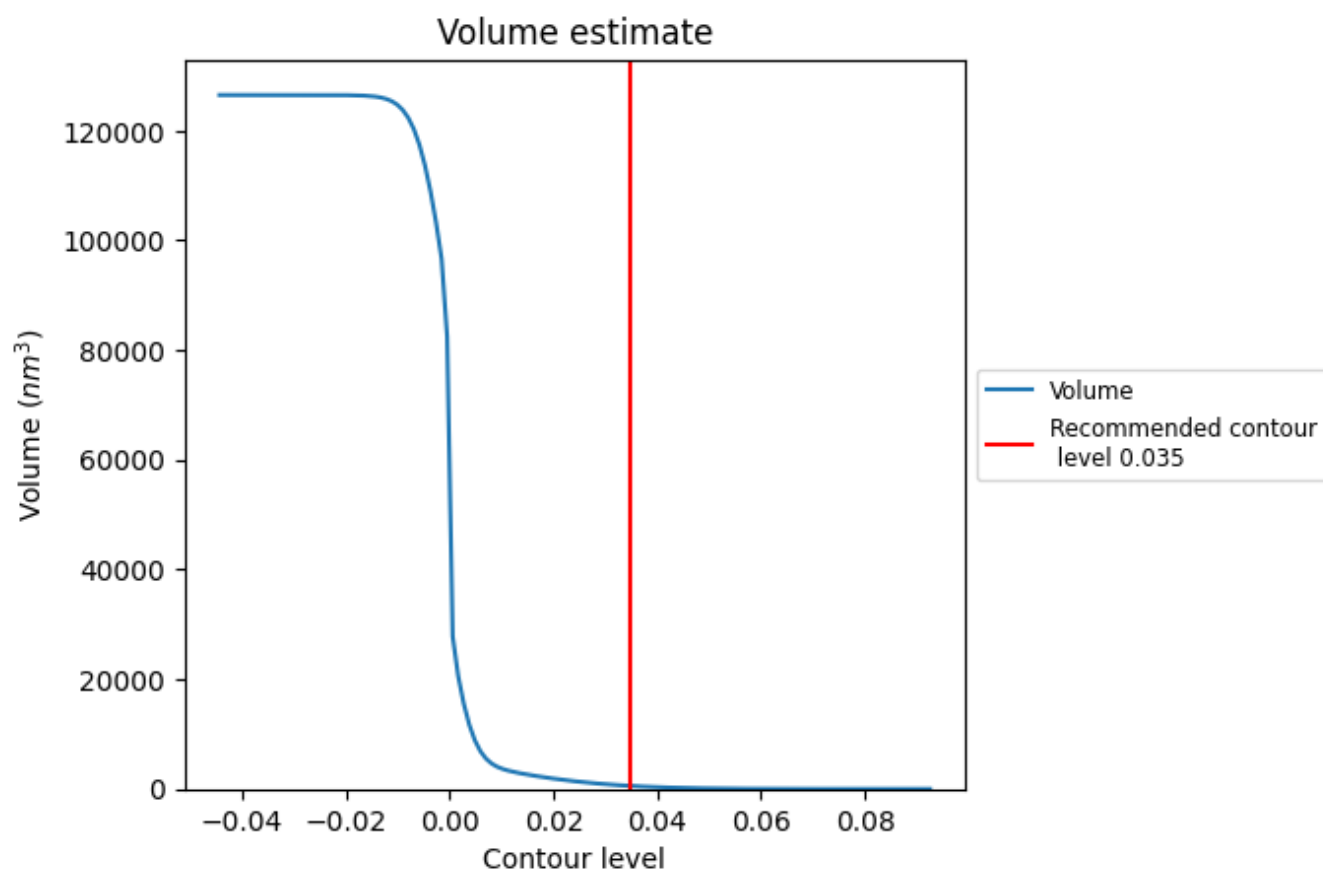
This section contains the results of statistical analysis of the map.

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.

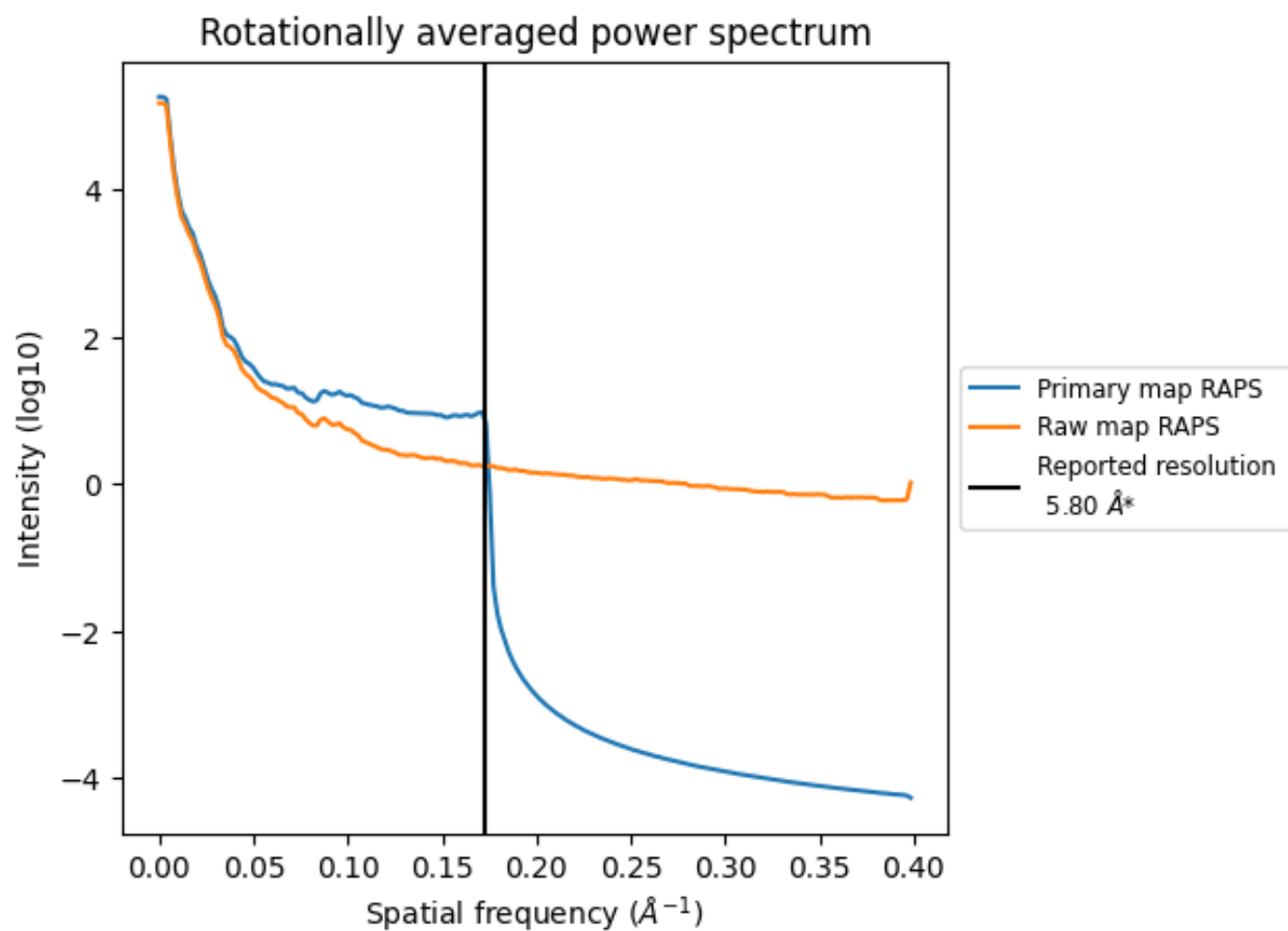
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 553 nm^3 ; this corresponds to an approximate mass of 500 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 ⓘ

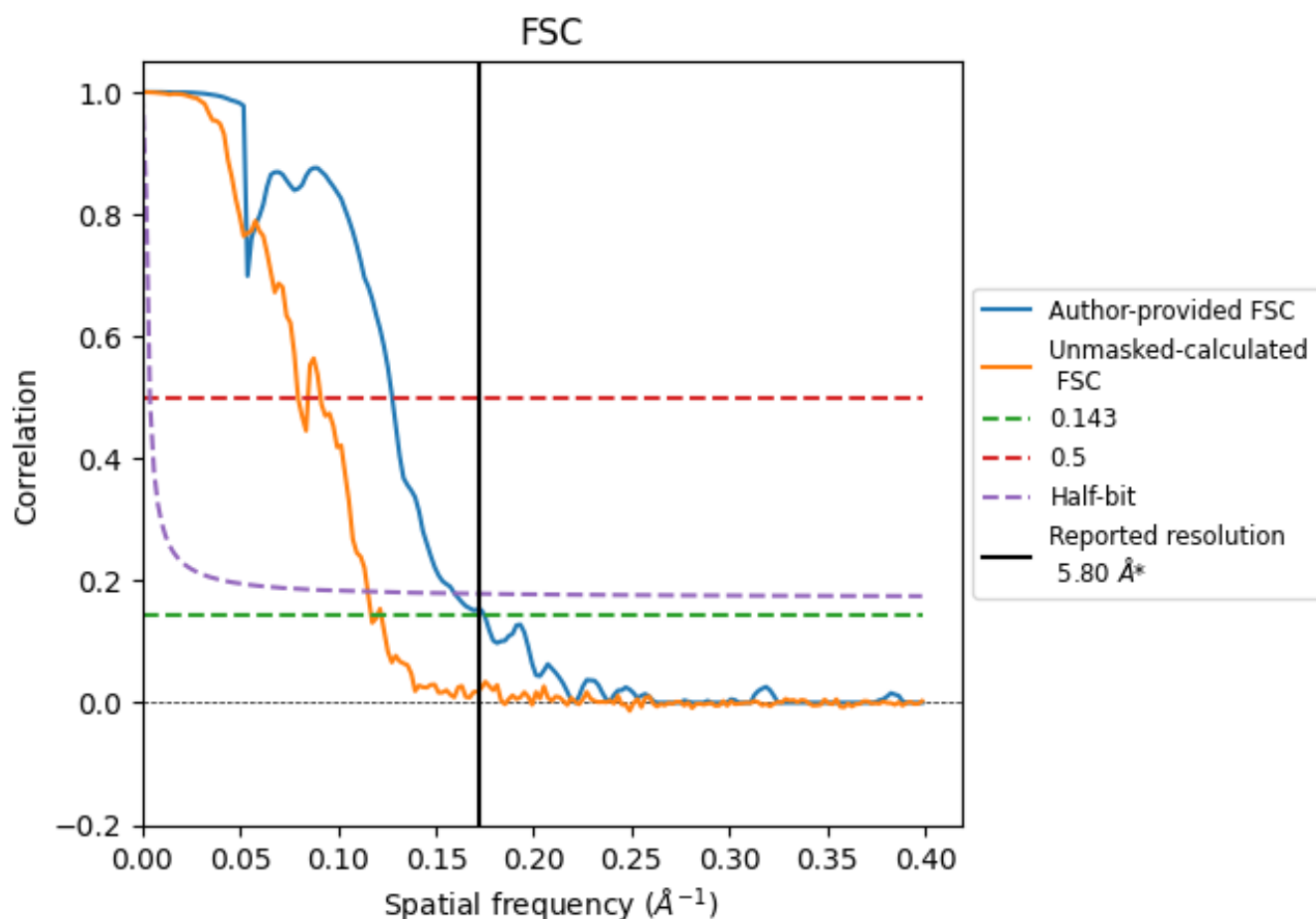


*Reported resolution corresponds to spatial frequency of 0.172 $\text{\AA}^{-1}$

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 $0.172 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

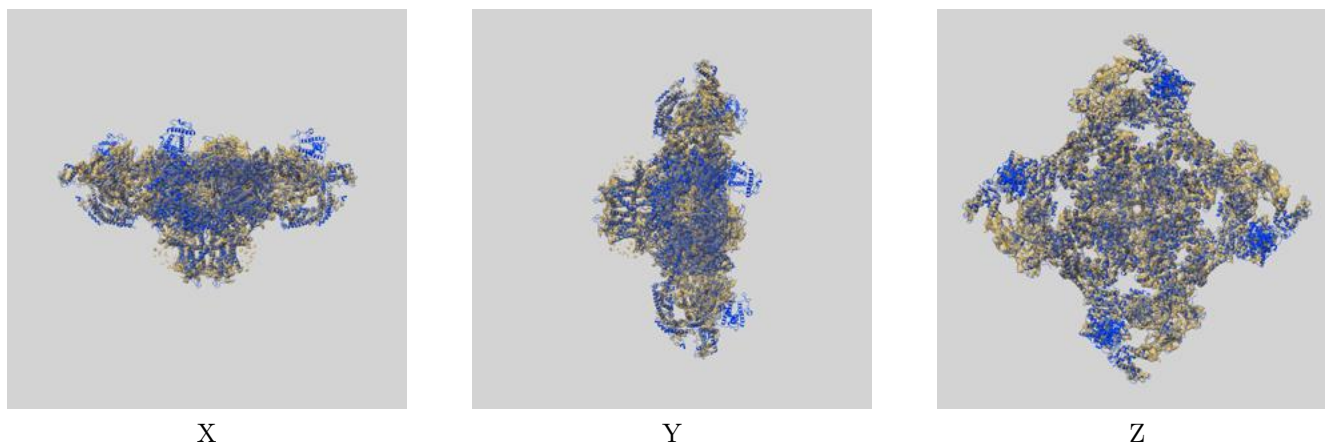
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.80	-	-
Author-provided FSC curve	5.72	7.83	6.27
Unmasked-calculated*	8.55	12.56	8.67

*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 8.55 differs from the reported value 5.8 by more than 10 %

9 Map-model fit [i](#)

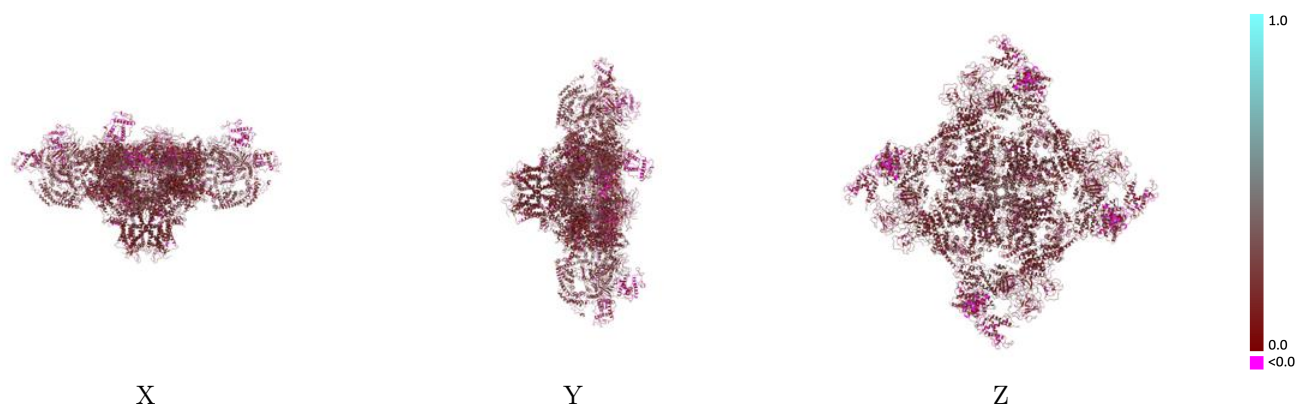
This section contains information regarding the fit between EMDB map EMD-8374 and PDB model 5T9R. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



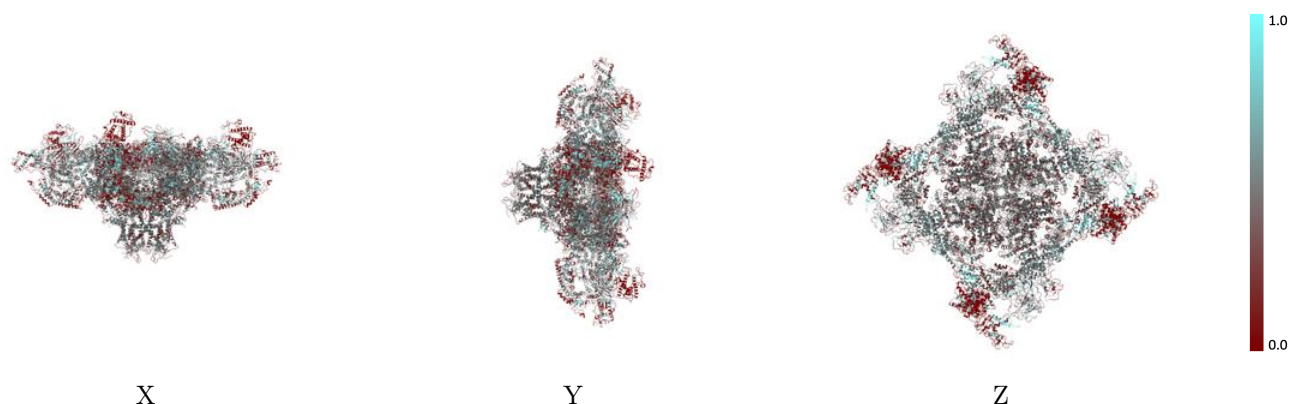
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



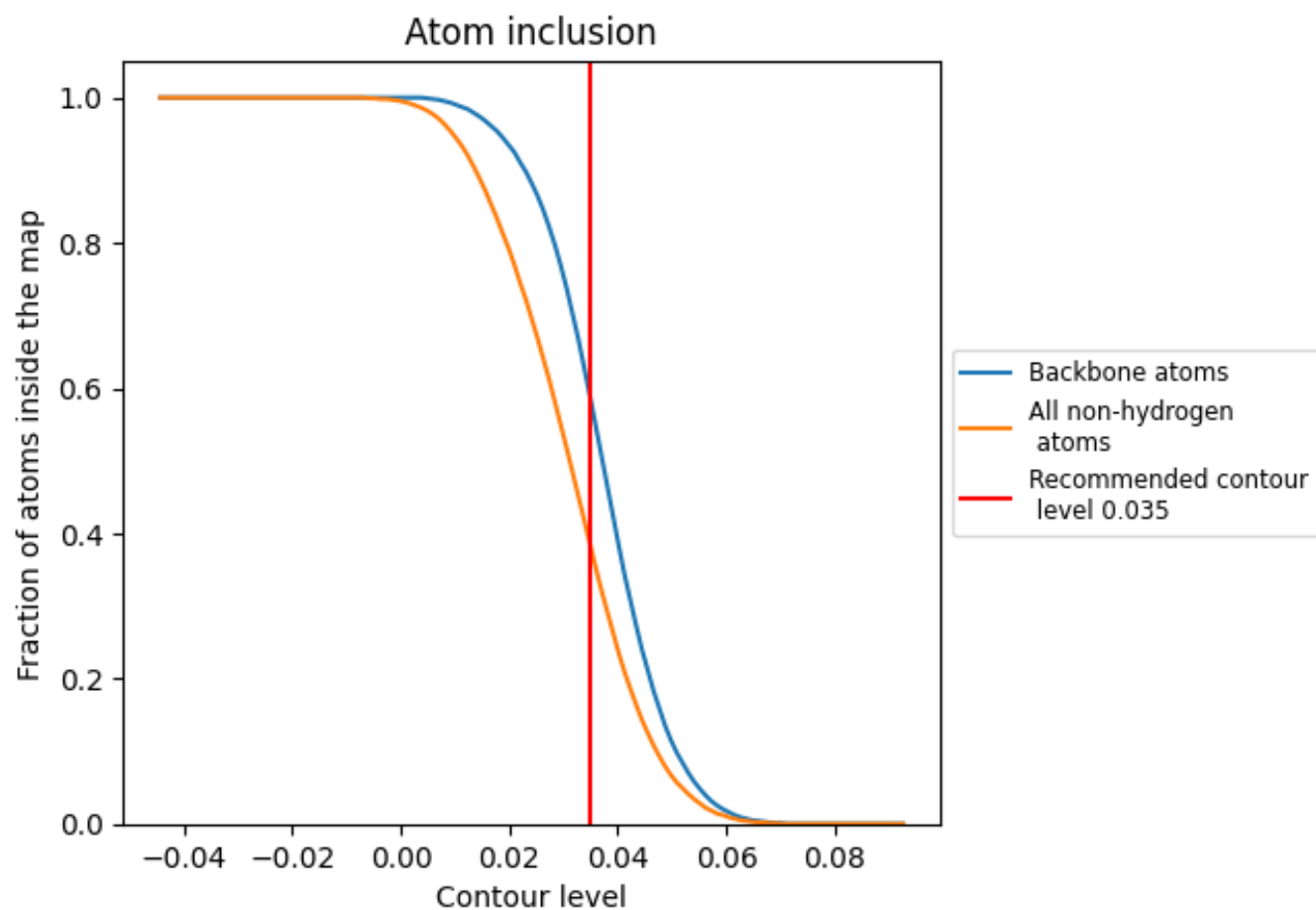
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.035).

9.4 Atom inclusion [i](#)



At the recommended contour level, 58% of all backbone atoms, 38% 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 (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3810	0.1900
A	0.3330	0.1720
B	0.3830	0.1910
E	0.3820	0.1910
F	0.3350	0.1750
G	0.3830	0.1900
H	0.3360	0.1740
I	0.3820	0.1910
J	0.3350	0.1740

1.0

0.0

<0.0