



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 09:42 AM UTC

PDB ID : 5TB2 / pdb_00005tb2
EMDB ID : EMD-8393
Title : Structure of rabbit RyR1 (EGTA-only dataset, class 2)
Authors : Clarke, O.B.; des Georges, A.; Zalk, R.; Marks, A.R.; Hendrickson, W.A.;
Frank, J.
Deposited on : 2016-09-11
Resolution : 4.60 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

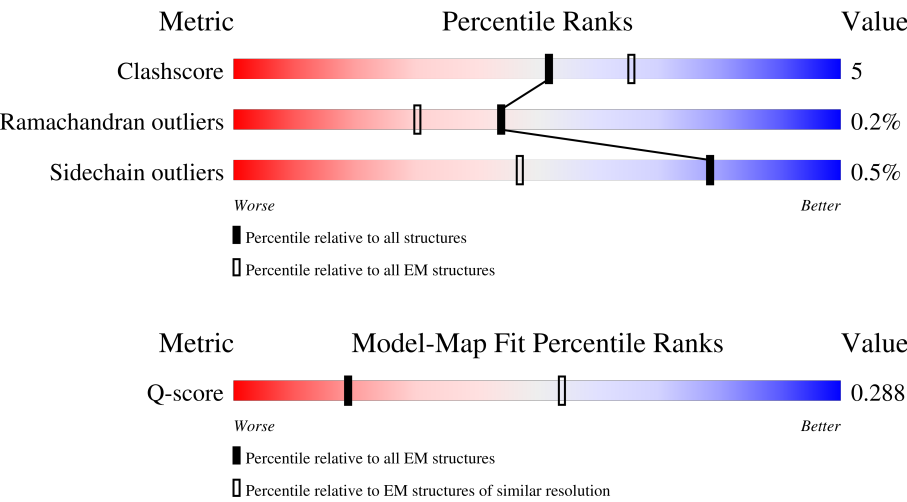
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.60 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2407 (4.10 - 5.10)

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	61% 87%12%
1	F	108	62% 87%12%
1	H	108	61% 85%14%
1	J	108	60% 90%9%

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Mol	Chain	Length	Quality of chain
2	B	4416	51% 84% 11% 5%
2	E	4416	51% 83% 11% 5%
2	G	4416	51% 83% 11% 5%
2	I	4416	52% 84% 11% 5%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 121272 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	E	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		

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

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.

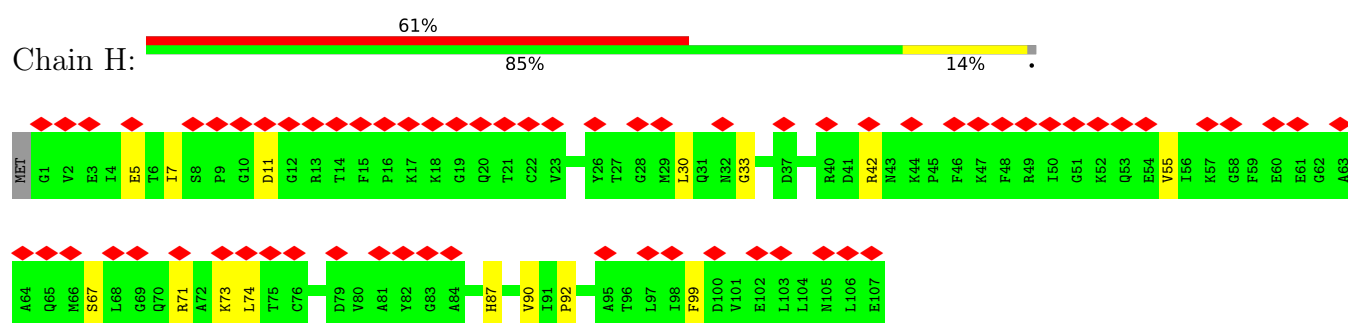
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



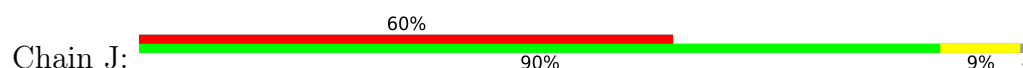
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

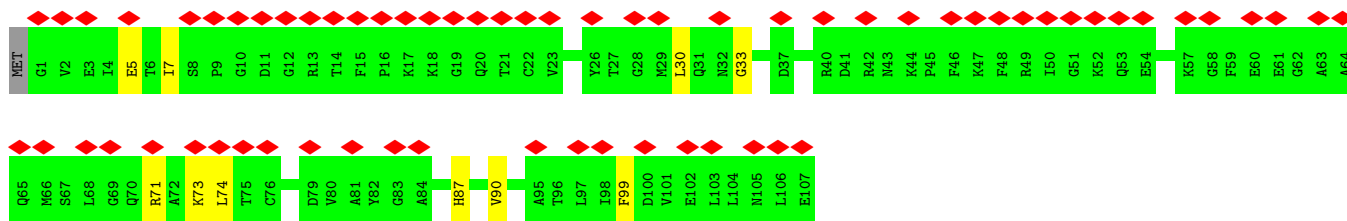


- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

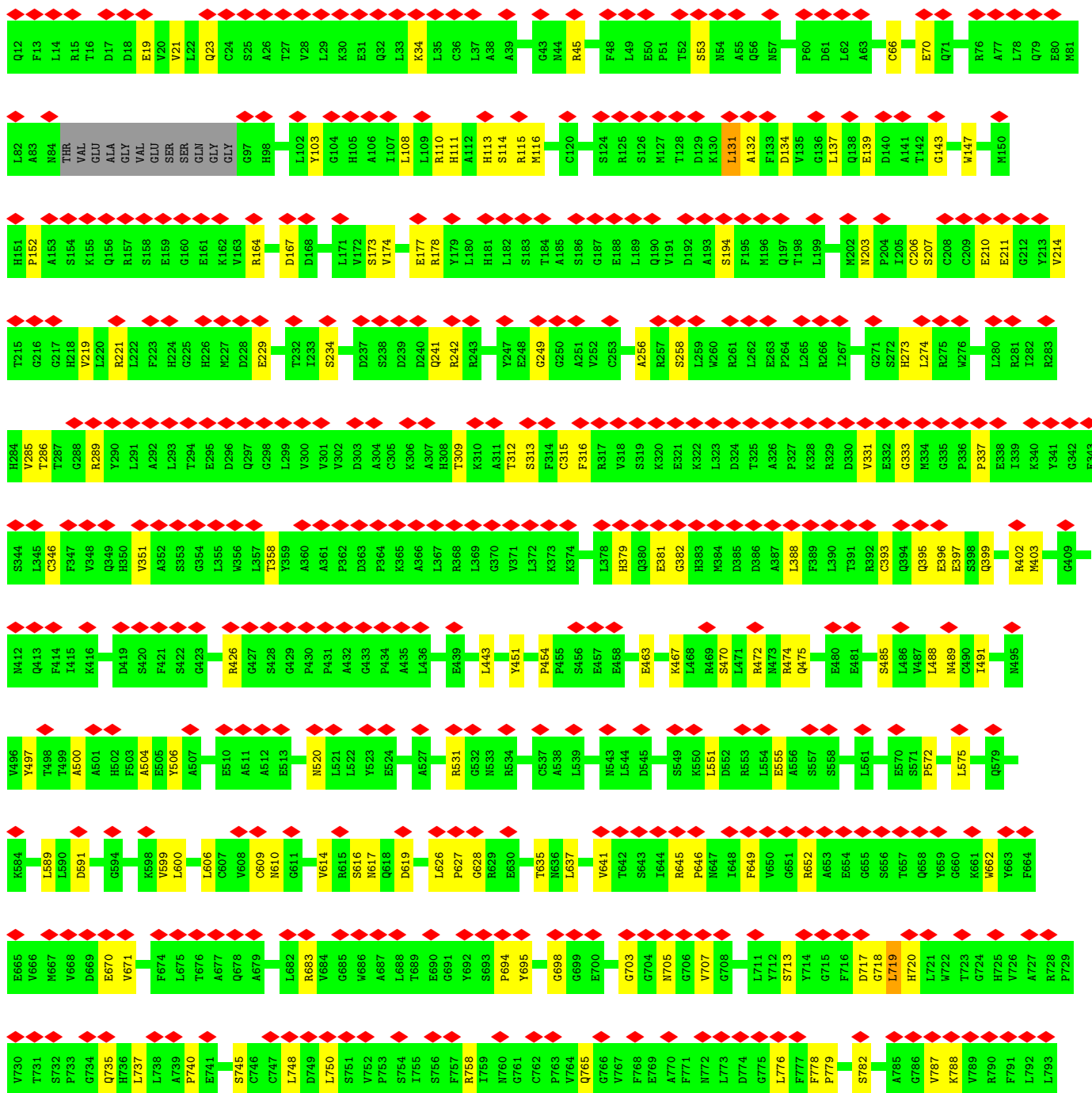
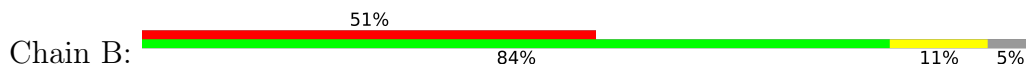


- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B





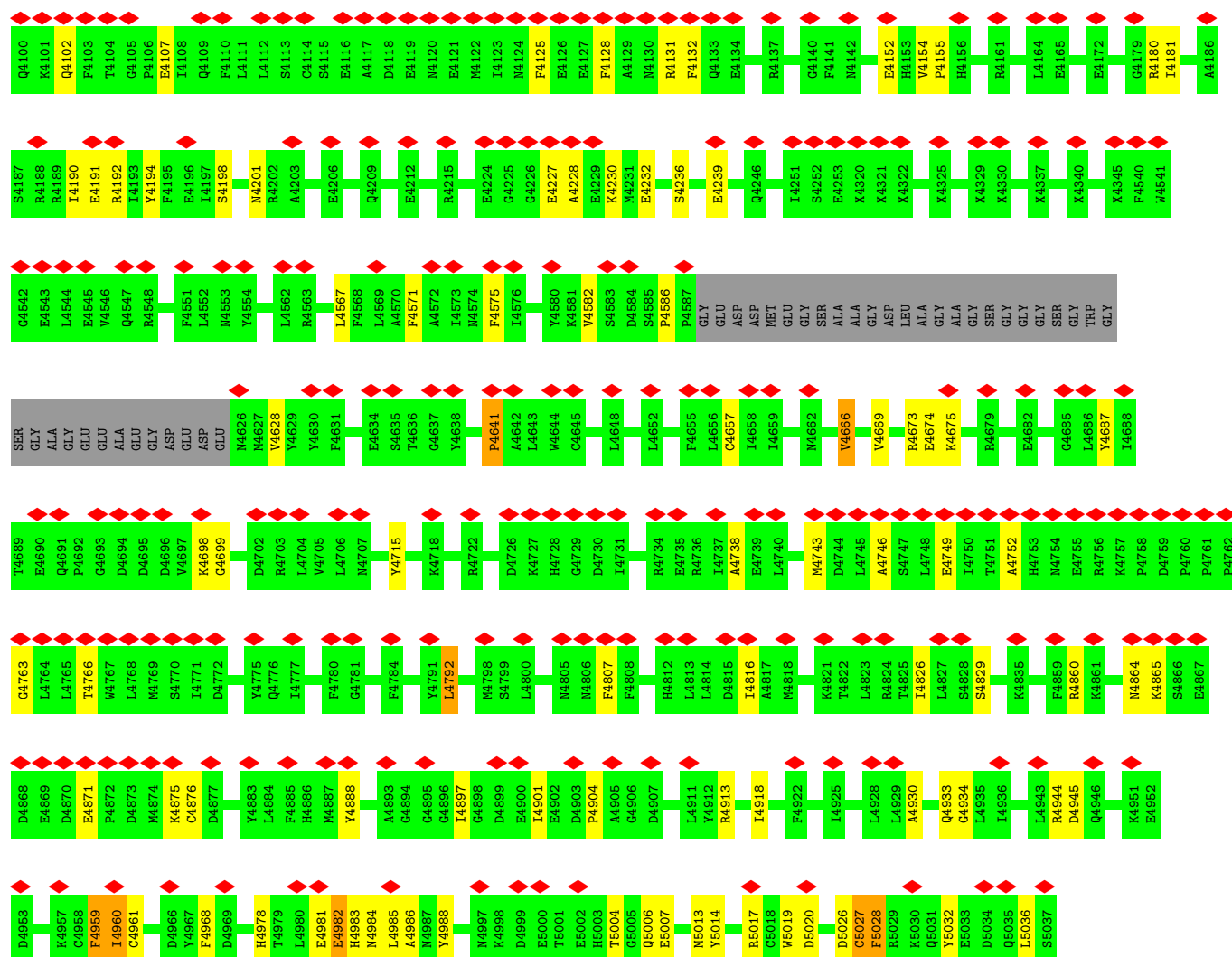
• Molecule 2: Ryanodine receptor 1



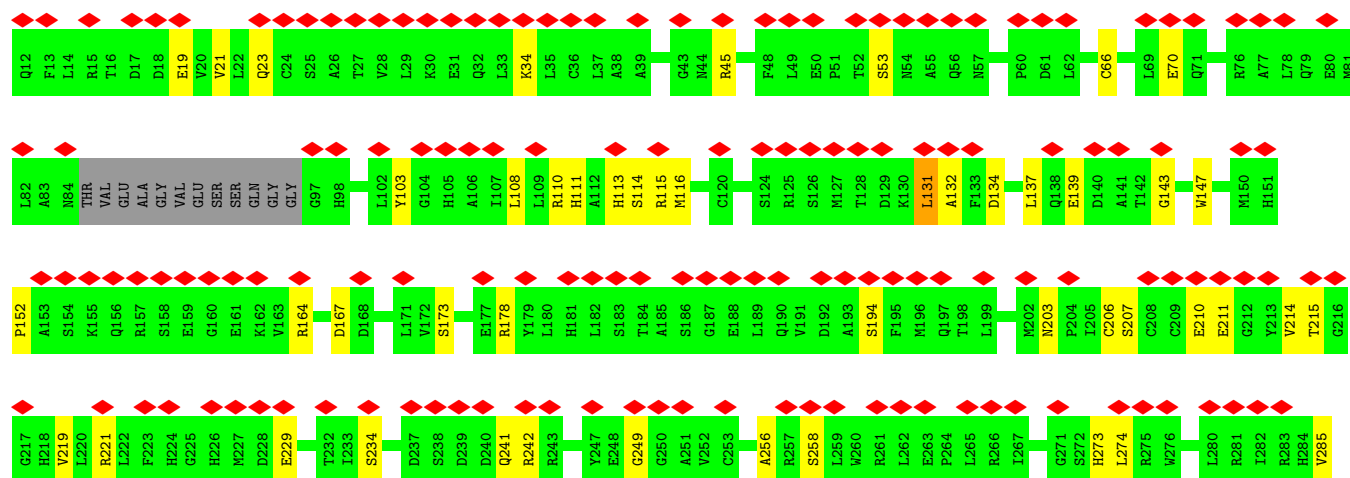
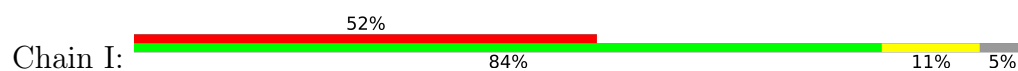


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THR	GLU	LYS	LYS	THR	ARG	LYS	ILE	SER	GLN	THR	ALA	GLN	THR	ASP	PRO	ARG	GLU	GLY	Y2855	N2856	P2857	Q2858	P2859	P2860	D2861	L2862	S2863	G2864	V2865	T2866	L2867	S2868	R2869	E2870	L2871	Q2872	A2873	M2874	A2875	E2876	Q2877	L2878	G2879	E2880	N2881	L2882	H2883	N2884	T2885	V2886	Q2887	L2888	K2889	L2890	L2891	Q2892	L2893	E2894																																																																																												
N2774	N2775	S2776	Y2777	G2778	E2779	N2780	V2781	D2782	E2783	E2784	L2785	L2786	L2787	H2788	P2789	N2790	L2791	R2792	P2793	Y2794	L2795	L2796	F2797	S2798	E2799	L2800	D2801	L2802	E2803	L2804	Y2805	L2806	L2807	P2808	L2809	K2810	E2811	S2812	L2813	L2814	A2815	N2816	L2817	L2818	L2819	E2820	N2821	L2822	L2823	E2824	K2825	L2826	A2827	F2828	D2829	E2830	GLU	ARG																																																																																												
X2684	X2685	X2686	X2687	X2688	X2689	X2690	X2691	X2692	X2693	X2694	X2695	X2696	X2697	X2698	X2699	X2700	X2701	X2702	X2703	N2734	F2735	L2736	P2737	R2738	P2739	V2740	E2741	L2742	L2743	L2744	L2745	L2746	L2747	P2748	E2749	K2750	L2751	D2752	S2753	F2754	L2755	N2756	L2757	F2758	A2759	E2760	Y2761	L2762	H2763	E2764	K2765	L2766	A2767	F2768	D2769	K2770	L2771	Q2772	N2773																																																																																											
X2619	X2620	X2621	X2622	X2623	X2624	X2625	X2626	X2627	X2628	X2629	X2630	X2631	X2632	X2633	X2634	X2635	X2636	X2637	X2638	X2639	X2640	X2641	X2642	X2643	X2644	X2645	X2646	X2647	X2648	X2649	X2650	X2651	X2652	X2653	X2654	X2655	X2656	X2657	X2658	X2659	X2660	X2661	X2662	X2663	X2664	X2665	X2666	X2667	X2668	X2669	X2670	X2671	X2672	X2673	X2674	X2675	X2676	X2677	X2678	X2679	X2680	X2681	X2682	X2683																																																																																						
X2524	X2525	X2526	X2527	X2528	X2529	X2530	X2531	X2532	X2533	X2534	X2535	X2536	X2537	X2538	X2539	X2540	X2541	X2542	X2543	X2544	X2545	X2546	X2547	X2548	X2549	X2550	X2551	X2552	X2553	X2554	X2555	X2556	X2557	X2558	X2559	X2560	X2561	X2562	X2563	X2564	X2565	X2566	X2567	X2568	X2569	X2570	X2571	X2572	X2573	X2574	X2575	X2576	X2577	X2578	X2579	X2580	X2581	X2582	X2583	X2584	X2585	X2586	X2587	X2588	X2589	X2590	X2591	X2592	X2593	X2594	X2595	X2596	X2597	X2598	X2599	X2600	X2601	X2602	X2603	X2604	X2605	X2606	X2607	X2608	X2609	X2610	X2611	X2612	X2613	X2614	X2615	X2616	X2617	X2618																																																								
L2432	L2433	G2434	R2435	P2436	H2437	G2438	L2439	R2440	L2441	K2442	G2443	L2444	R2445	L2446	R2447	G2448	L2449	R2450	L2451	R2452	L2453	R2454	A2455	R2456	S2457	L2458	L2459	L2460	L2461	L2462	L2463	L2464	L2465	L2466	L2467	L2468	L2469	L2470	S2471	L2472	L2473	L2474	L2475	L2476	P2477	L2478	L2479	L2480	L2481	L2482	L2483	L2484	L2485	L2486	L2487	L2488	L2489	L2490	L2491	L2492	L2493	L2494	L2495	L2496	L2497	L2498	L2499	L2500	L2501	L2502	L2503	L2504	L2505	L2506	L2507	L2508	L2509	L2510	L2511	L2512	L2513	L2514	L2515	L2516	L2517	L2518	L2519	L2520	L2521	L2522	L2523																																																											
C2363	F2364	G2365	P2366	A2367	L2368	R2369	L2370	E2371	G2372	G2373	S2374	G2375	L2376	L2377	A2378	L2379	T2380	E2381	E2382	A2383	S2384	E2385	D2386	P2387	A2388	L2389	P2390	L2391	L2392	D2393	G2394	P2395	GLY	VAL	ARG	ASP	ARG	ARG	ARG	ARG	GLU	HLIS	PHE	GLY	GLU	GLU	PRO	PRO	GLU	GLU	N2414	R2415	V2416	H2417	L2418	G2419	M2420	L2421	L2422	L2423	L2424	L2425	L2426	L2427	L2428	L2429	L2430	D2431																																																																																		
D2294	L2295	E2296	K2297	Y2301	L2302	A2303	G2304	L2307	L2308	S2309	C2310	P2311	M2312	L2313	L2314	A2315	K2316	G2317	Y2318	P2319	D2320	L2321	G2322	C2323	R2324	L2325	L2326	L2327	L2328	L2329	L2330	L2331	L2332	L2333	F2334	L2335	R2336	F2337	A2338	V2339	F2340	N2341	N2342	G2343	E2344	S2345	V2346	E2347	L2348	N2349	A2350	N2351	R2352	L2353	L2354	L2355	L2356	L2357	L2358	L2359	L2360	P2361	E2362																																																																																							
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E2015	A2016	D2017	E2018	E2019	D2020	C2021	P2022	L2023	D2026	L2027	R2028	Q2029	D2030	L2031	Q2032	D2033	C2042	G2043	I2044	Q2045	L2046	E2047	G2048	GLU	GLU	GLU	GLU	PRO	GLU	GLU	THR	SER	SER	SER	ARG	ARG	LEU	SER	LEU	LEU	THR	THR	VAL	ARG	LEU	VAL	LVS	LVS	GLU	GLU	LVS	PRU	GLU	GLU																																																																																																
GLU	LEU	PRO	ALA	GLU	GLU	K2089	K2090	P2091	Q2092	S2093	R2104	Q2107	F2121	R2126	Q2127	L2131	R2136	R2140	A2141	Y2142	T2143	L2144	S2145	P2146	S2147	E2150	D2151	L2155	L2165	L2166	L2167	M2170	Q2183	M2186	N2187	E2188	K2189	Y2192	Q2193	N2196	E2285	L2286	A2287	L2288	A2200																																																																																																									

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X3547	X3548	X3549	X3550	X3551	X3552	X3553	X3554	X3555	X3556	X3557	X3558	X3559	X3560	X3561	X3562	X3563	X3564	X3565	X3566	X3567	X3568	X3569	X3572	X3573	X3574	X3575	X3576	X3577	X3578	X3579	X3580	X3581	X3582	X3583	X3584	X3585	X3586	X3587	X3588	X3589	X3590	X3591	X3592	X3593	X3597	X3598	X3599	X3600	X3604	X3605	X3606	X3607	X3608	X3609	X3610	X3611			
X3368	X3369	X3370	X3371	X3372	X3373	X3374	X3375	X3376	X3377	X3378	X3379	X3380	X3381	X3382	X3383	X3384	X3385	X3386	X3387	X3388	X3389	X3390	X3391	X3392	X3393	X3394	X3395	X3396	X3397	X3398	X3399	X3400	X3401	X3402	X3403	X3404	X3405	X3406	X3407	X3408	X3409	X3410	X3411	X3412	X3413	X3414	X3415	X3416	X3417	X3420	X3421	X3428	X3429	X3430	X3431	X3432	X3433		
X3306	X3309	X3310	X3311	X3312	X3313	X3314	X3315	X3316	X3317	X3318	X3319	X3320	X3321	X3322	X3323	X3324	X3325	X3326	X3327	X3328	X3329	X3330	X3331	X3332	X3333	X3334	X3335	X3336	X3337	X3338	X3339	X3340	X3341	X3344	X3345	X3346	X3347	X3348	X3349	X3350	X3351	X3352	X3353	X3354	X3355	X3356	X3357	X3358	X3359	X3360	X3361	X3362	X3363	X3364	X3365	X3366	X3367		
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• Molecule 2: Ryanodine receptor 1

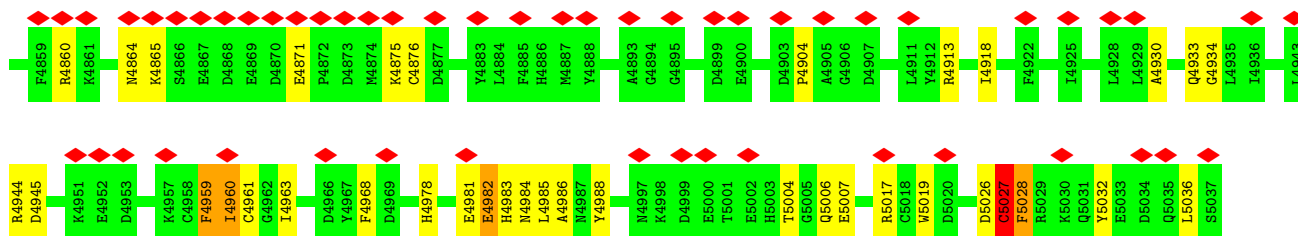


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G1126	PRO	H993	T931		L803	A739	L677	L606	V300	P430	P362	V300
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R1128	VAL	D999	L933		G807	E741	Q678	V608	V302	A432	P364	V302
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R1132	SER	V1001	G937		H812	L748	L682	G611	K306	L436	R368	K306
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F1075	F1075	PRO	E944		R822	S756	G691	P627	F316		L378	F316
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S1174	V1043	V1043	D971		P855	K788	T723	G724	E345		L345	E345
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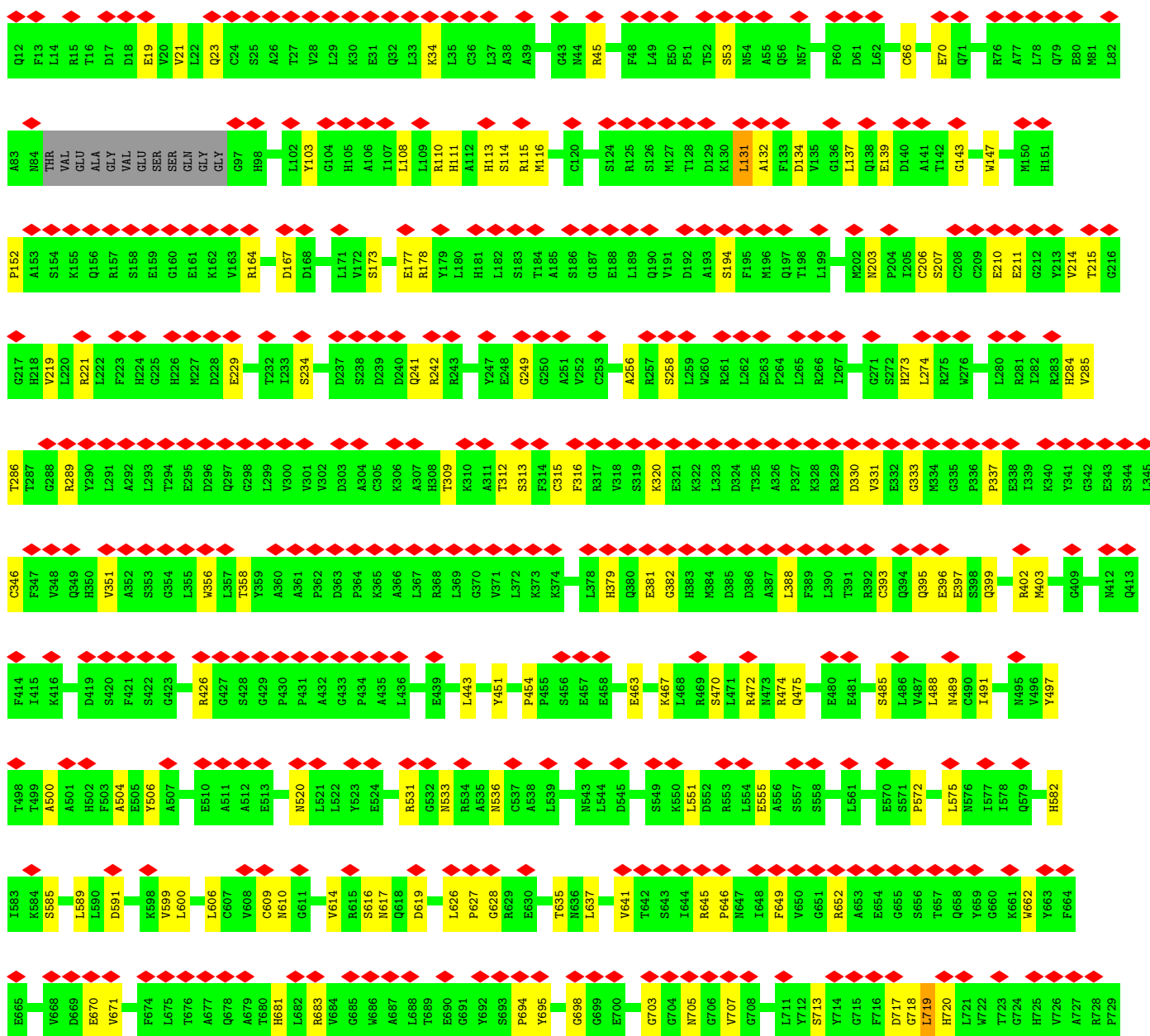
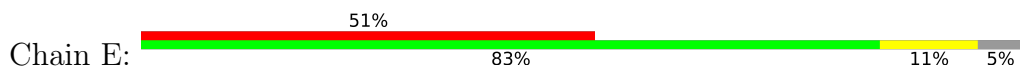


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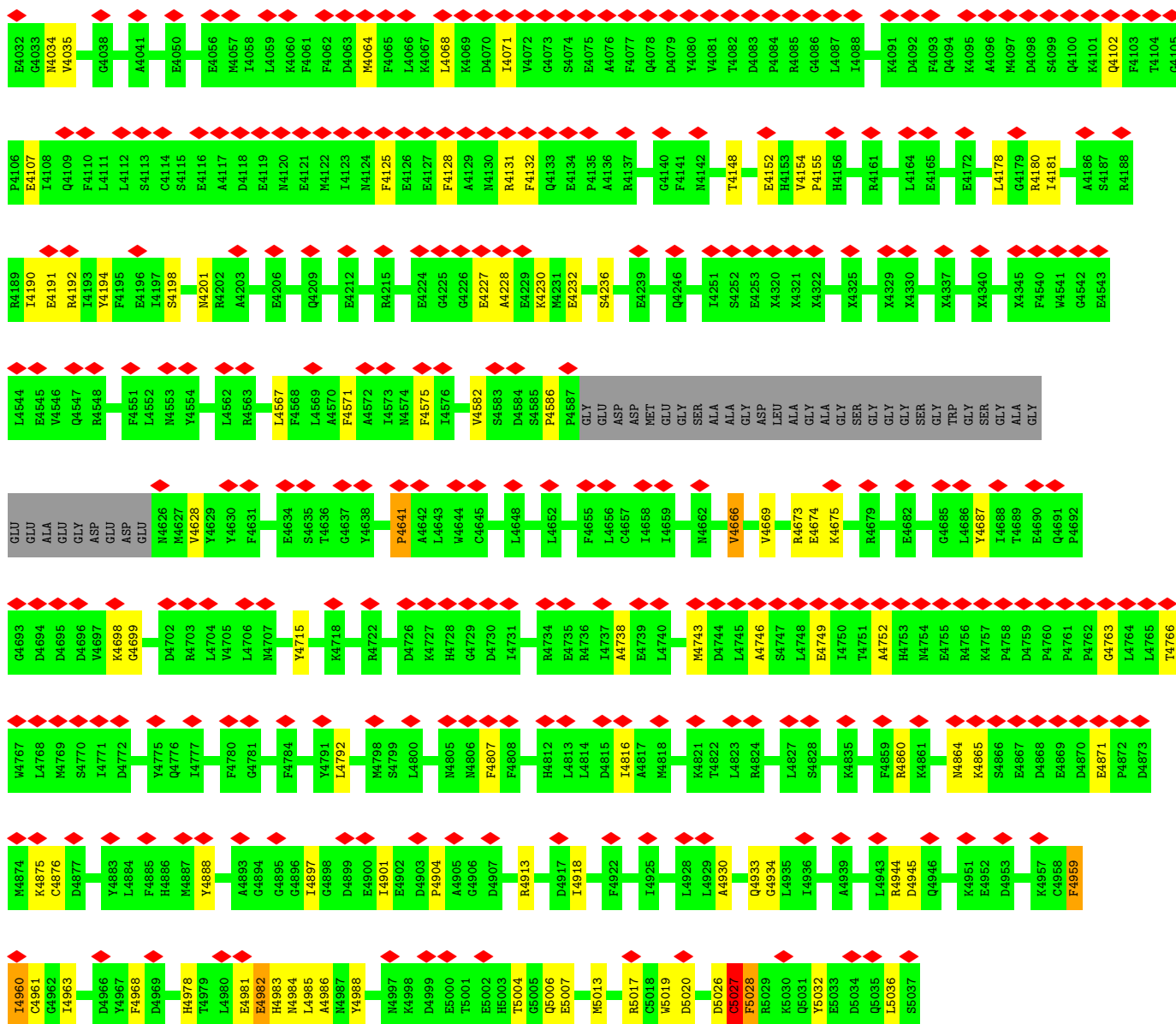
• Molecule 2: Ryanodine receptor 1



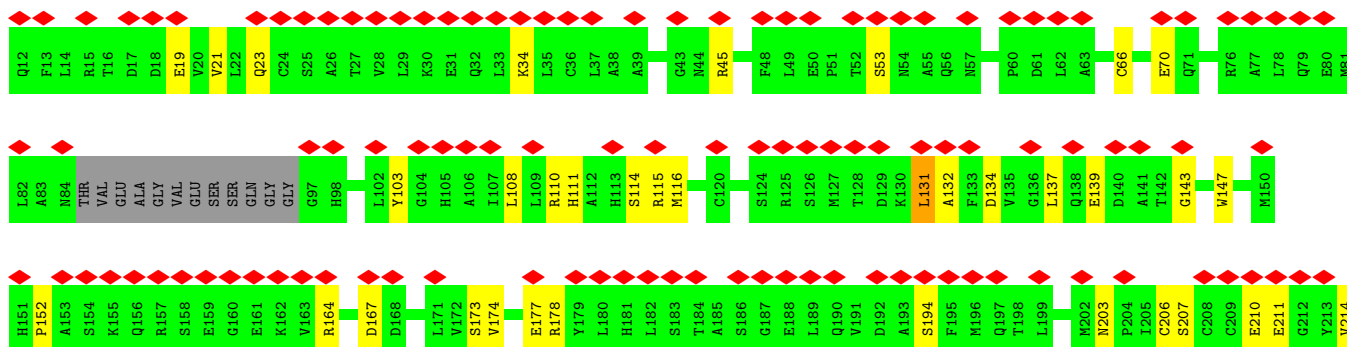
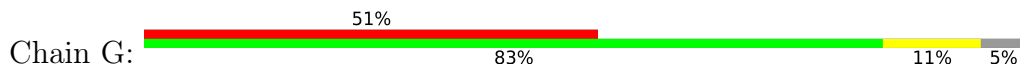


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LYS	Q1949	Q1950	R1954	L1958	A1959	F1961	A1962	E1963	R1964	Y1965	V1966	D1967	Q1970	A1971	N1972	Q1973	R1974	S1975	R1976	Y1977	A1978	L1979	L1980	M1981	R1982	A1983	F1984	L1985	M1986	S1987	A1988	A1989	T1991	A1990	GLY	A1992	L1993	R1994	T1995	R1996	F1997	R1998	R1999	S2000	P2001	P2002	Q2003	E2004	Q2005	L2006	M2007	L2009	L2010	H2011	F2012	K2013																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
LYS	D2014	E2015	A2016	D2017	E2018	D2019	D2020	C2021	P2022	L2023	P2024	E2025	D2026	T2027	R2028	Q2029	D2030	L2031	C2042	G2043	Q2044	Q2045	L2046	E2047	G2048	GLU	GLU	GLU	PRO	GLU	GLU	THR	SER	SER	SER	ARG	LEU	ARG	SER	LEU	THR	VAL	ARG	LEU	VAL	LYS	LYS	LYS	GLU	GLU	GLU	PRO	GLU	GLU																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
LYS	GLU	LEU	PRO	ALA	GLU	K2089	G2090	P2091	Q2092	S2093	R2104	Q2107	F2121	R2126	Q2127	L2131	R2136	R2140	A2141	Y2142	T2143	T2144	S2145	P2146	S2147	E2150	D2151	L2155	L2165	L2166	I2167	M2170	G2183	M2186	N2187	K2188	Y2189	Y2192	Q2193	R2199	A2200	H2204	Q2209	E2210	L2211	E2212	E2213	E2214	E2215	E2216	E2217	E2218	E2219	E2220	E2221	E2222	E2223	E2224	E2225	E2226	E2227	E2228	E2229	E2230	E2231	E2232	E2233	E2234	E2235	E2236	E2237	E2238	E2239	E2240	E2241	E2242	E2243	E2244	E2245	E2246	E2247	E2248	E2249	E2250	E2251	E2252	E2253	E2254	E2255	E2256	E2257	E2258	E2259	E2260	E2261	E2262	E2263	E2264	E2265	E2266	E2267	E2268	E2269	E2270	E2271	E2272	E2273	E2274	E2275	E2276	E2277	E2278	E2279	E2280	E2281	E2282	E2283	E2284	E2285	E2286	E2287	E2288	E2289	E2290	E2291	E2292	E2293	E2294																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
LYS	L2295	E2296	K2297	Y2301	L2302	A2303	Q2304	L2307	Q2308	C2310	P2311	L2312	L2313	L2314	A2315	G2317	P2319	D2320	I2321	C2326	G2327	R2330	L2332	P2333	F2334	L2335	R2336	F2337	K2338	V2339	F2340	V2341	G2342	G2343	E2344	S2345	V2346	E2347	E2348	N2349	A2350	V2351	R2355	L2356	L2357	L2358	R2359	L2360	P2361	E2362	C2363	F2364	G2365	P2366	A2367	L2368	R2369	G2370	E2371	G2372	G2373	S2374	L2375	L2376	L2377	A2378	A2379	I2380	E2381	E2382	A2383	I2384	S2387	E2388	D2389	P2390	A2391	P2392	D2393	G2394	P2395	GLY	VAL	ARG	ARG	ASP	ARG	ARG	ARG	GLU	HIS	PHE	GLY	GLU	GLU	PRO	GLU	GLU	N2414	R2415	V2416	H2417	L2418	G2419	M2423	I2430	D2431																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
LYS	L2432	L2433	G2434	R2435	P2438	H2441	K2447	G2448	L2451	R2452	L2453	A2454	A2455	R2458	S2459	L2460	L2463	L2466	L2469	L2470	S2471	L2472	P2473	L2474	Q2475	L2476	P2477	T2478	L2479	X2487	X2488	X2489	X2490	X2493	X2494	X2495	X2498	X2499	X2500	X2511	X2512	X2513	X2517	X2520	X2521	X2522	X2523	X2524	X2525	X2526	X2527	X2528	X2529	X2530	X2531	X2532	X2533	X2534	X2535	X2536	X2537	X2538	X2539	X2540	X2541	X2542	X2543	X2544	X2545	X2546	X2547	X2548	X2549	X2550	X2551	X2552	X2553	X2554	X2555	X2556	X2557	X2558	X2559	X2560	X2561	X2562	X2563	X2564	X2565	X2566	X2567	X2568	X2569	X2570	X2571	X2572	X2573	X2574	X2575	X2576	X2577	X2578	X2579	X2580	X2581	X2582	X2583	X2584	X2585	X2586	X2587	X2588	X2589	X2590	X2591	X2592	X2593	X2594	X2595	X2596	X2597	X2598	X2599	X2600	X2601	X2602	X2603	X2604	X2605	X2606	X2607	X2608	X2609	X2610	X2611	X2612	X2613	X2614	X2615	X2616	X2617	X2618	X2619	X2620	X2621	X2622	X2623	X2624	X2625	X2626	X2627	X2628	X2629	X2630	X2631	X2632	X2633	X2634	X2635	X2636	X2637	X2638	X2639	X2640	X2641	X2642	X2643	X2644	X2645	X2646	X2647	X2648	X2649	X2650	X2651	X2652	X2653	X2654	X2655	X2656	X2657	X2658	X2659	X2660	X2661	X2662	X2663	X2664	X2665	X2666	X2667	X2668	X2669	X2670	X2671	X2672	X2673	X2674	X2675	X2676	X2677	X2678	X2679	X2680	X2681	X2682	X2683	X2684	X2685	X2686	X2687	X2688	X2689	X2690	X2691	X2692	X2693	X2694	X2695	X2696	X2697	X2698	X2699	X2700	X2701	X2702	X2703	X2704	F2705	D2706	P2707	R2708	P2709	P2710	P2711	P2712	P2713	P2714	P2715	P2716	P2717	P2718	P2719	P2720	P2721	P2722	P2723	P2724	P2725	P2726	P2727	P2728	P2729	P2730	P2731	P2732	P2733	P2734	P2735	P2736	P2737	P2738	P2739	P2740	P2741	P2742	P2743	P2744	P2745	P2746	P2747	P2748	P2749	P2750	P2751	P2752	P2753	P2754	P2755	P2756	P2757	P2758	P2759	P2760	P2761	P2762	P2763	P2764	P2765	P2766	P2767	P2768	P2769	P2770	P2771	P2772	P2773	P2774	P2775	P2776	P2777	P2778	P2779	P2780	P2781	P2782	P2783	P2784	P2785	P2786	P2787	P2788	P2789	P2790	P2791	P2792	P2793	P2794	P2795	P2796	P2797	P2798	P2799	P2800	P2801	P2802	P2803	P2804	P2805	P2806	P2807	P2808	P2809	P2810	P2811	P2812	P2813	P2814	P2815	P2816	P2817	P2818	P2819	P2820	P2821	P2822	P2823	P2824	P2825	P2826	P2827	P2828	P2829	P2830	P2831	P2832	P2833	P2834	P2835	P2836	P2837	P2838	P2839	P2840	P2841	P2842	P2843	P2844	P2845	P2846	P2847	P2848	P2849	P2850	P2851	P2852	P2853	P2854	P2855	P2856	P2857	P2858	P2859	P2860	P2861	P2862	P2863	P2864	P2865	P2866	P2867	P2868	P2869	P2870	P2871	P2872	P2873	P2874	P2875	P2876	P2877	P2878	P2879	P2880	P2881	P2882	P2883	P2884	P2885	P2886	P2887	P2888	P2889	P2890	P2891	P2892	P2893	P2894	P2895	P2896	P2897	P2898	P2899	P2900	P2901	P2902	P2903	P2904	P2905	P2906	P2907	P2908	P2909	P2910	P2911	P2912	P2913	P2914	P2915	P2916	P2917	P2918	P2919	P2920	P2921	P2922	P2923	P2924	P2925	P2926	P2927	P2928	P2929	P2930	P2931	P2932	P2933	P2934	P2935	P2936	P2937	P2938	P2939	P2940	P2941	P2942	P2943	P2944	P2945	P2946	P2947	P2948	P2949	P2950	P2951	P2952	P2953	P2954	P2955	P2956	P2957	P2958	P2959	P2960	P2961	P2962	P2963	P2964	P2965	P2966	P2967	P2968	P2969	P2970	P2971	P2972	P2973	P2974	P2975	P2976	P2977	P2978	P2979	P2980	P2981	P2982	P2983	P2984	P2985	P2986	P2987	P2988	P2989	P2990	P2991	P2992	P2993	P2994	P2995	P2996	P2997	P2998	P2999	P3000	P3001	P3002	P3003	P3004	P3005	P3006	P3007	P3008	P3009	P3010	P3011	P3012	P3013	P3014	P3015	P3016	P3017	P3018	P3019	P3020	P3021	P3022	P3023	P3024	P3025	P3026	P3027	P3028	P3029	P3030	P3031	P3032	P3033	P3034	P3035	P3036	P3037	P3038	P3039	P3040	P3041	P3042	P3043	P3044	P3045	P3046	P3047	P3048	P3049	P3050	P3051	P3052	P3053	P3054	P3055	P3056	P3057	P3058	P3059	P3060	P3061	P3062	P3063	P3064	P3065	P3066	P3067	P3068	P3069	P3070	P3071	P3072	P3073	P3074	P3075	P3076	P3077	P3078	P3079	P3080	P3081	P3082	P3083	P3084	P3085	P3086	P3087	P3088	P3089	P3090	P3091	P3092	P3093	P3094	P3095	P3096	P3097	P3098	P3099	P3100	P3101	P3102	P3103	P3104	P3105	P3106	P3107	P3108	P3109	P3110	P3111	P3112	P3113	P3114	P3115	P3116	P3117	P3118	P3119	P3120	P3121	P3122	P3123	P3124	P3125	P3126	P3127	P3128	P3129	P3130	P3131	P3132	P3133	P3134	P3135	P3136	P3137	P3138	P3139	P3140	P3141	P3142	P3143	P3144	P3145	P3146	P3147	P3148	P3149	P3150	P3151	P3152	P3153	P3154	P3155	P3156	P3157	P3158	P3159	P3160	P3161	P3162	P3163	P3164	P3165	P3166	P3167	P3168	P3169	P3170	P3171	P3172	P3173	P3174	P3175	P3176	P3177	P3178	P3179	P3180	P3181	P3182	P3183	P3184	P3185	P3186	P3187	P3188	P3189	P3190	P3191	P3192	P3193	P3194	P3195	P3196	P3197	P3198	P3199	P3200	P3201	P3202	P3203	P3204	P3205	P3206	P3207	P3208	P3209	P3210	P3211	P3212	P3213	P3214	P3215	P3216	P3217	P3218	P3219	P3220	P3221	P3222	P3223	P3224	P3225	P3226	P3227	P3228	P3229	P3230	P3231	P3232	P3233	P3234	P3235	P3236	P3237	P3238	P3239	P3240	P3241	P3242	P3243	P3244	P3245	P3246	P3247	P3248	P3249	P3250	P3251	P3252	P3253	P3254	P3255	P3256	P3257	P3258	P3259	P3260	P3261	P3262	P3263	P3264	P3265	P3266	P3267	P3268	P3269	P3270	P3271	P3272	P3273	P3274	P3275	P3276	P3277	P3278	P3279	P3280	P3281	P3282	P3283	P3284	P3285	P3286	P3287	P3288	P3289	P3290	P3291	P3292	P3293	P3294	P3295	P3296	P3297	P3298	P3299	P3300	P3301	P3302	P3303	P3304	P3305	P3306	P3307	P3308	P3309	P3310	P3311	P3312	P3313	P3314	P3315	P3316	P3317	P3318	P3319	P3320	P3321	P3322	P3323	P3324	P3325	P3326	P3327	P3328	P3329	P3330	P3331	P3332	P3333	P3334	P3335	P3336	P3337	P3338	P3339	P3340	P3341	P3342	P3343	P3344	P3345	P3346	P3347	P3348	P3349	P3350	P3351	P3352	P3353	P3354	P3355	P3356	P3357	P3358	P3359	P3360	P3361	P3362	P3363	P3364	P3365	P3366	P3367	P3368	P3369	P3370	P3371	P3372	P3373	P3374	P3375	P3376	P3377	P3378	P3379	P3380	P3381	P3382	P3383	P3384	P3385	P3386	P3387	P3388	P3389	P3390	P3391	P3392	P3393	P3394	P3395	P3396	P3397	P3398	P3399	P3400	P3401	P3402	P3403	P3404	P3405	P3406	P3407	P3408	P3409	P3410	P3411	P3412	P3413	P3414	P3415	P3416	P3417	P3418	P3419	P3420	P3421	P3422	P3423	P3424	P3425	P3426	P3427	P3428	P3429	P3430	P3431	P3432	P3433	P3434	P3435	P3436	P3437	P3438	P3439	P3440	P3441	P3442	P3443	P3444	P3445	P3446	P3447	P3448	P3449	P3450	P3451	P3452	P3453	P3454	P3455	P3456	P3457	P3458	P3459	P3460	P3461	P3462	P3463	P3464	P3465	P3466	P3467	P3468	P3469	P3470	P3471	P3472	P3473	P3474

X3937	S3938	Q3830	K3731	F3640	X3550	X3437	X3371	X3244	X3179	X3041	X2960	K2897
X3938	S3939	Q3833	S3732	L3641	X3551	X3441	X3372	X3245	X3180	X3042	X2961	G2898
X3940	K3941	L3842	C3733	Y3642	X3552	X3442	X3373	X3246	X3181	X3043	X2962	G2899
X3942	V3942	D3843	H3734	N3643	X3553	X3443	X3374	X3247	X3182	X3044	X2963	G2900
X3943	V3943		L3735	L3644	X3554		X3375	X3248	X3183	X3045	X2964	T2901
E3944	E3945		E3736		X3555		X3376	X3249	X3184	X3046	X2965	H2902
E3945			E3737		X3556	X3447	X3377	X3250	X3185	X3047	X2966	F2903
Q3946			G3738	N3651	X3557	X3448	X3378	X3251	X3186	X3048	X2967	L2904
G3947			G3739	F3652	X3558	X3449	X3379	X3252	X3187	X3049	X2968	L2905
G3948			E3740	F3653	X3559	X3450	X3380	X3253	X3188	X3050	X2969	V2906
N3949			N3741	K3658	X3560	X3451	X3381	X3254	X3189			F2907
N3950			GLU	A3659	X3561	X3452	X3382	X3255	X3190	X3053	X2970	V2908
			ALA	A3660	X3562	X3453	X3383	X3256	X3191	X3054	X2971	D2909
			GLU	W3661	X3563	X3454	X3384	X3257	X3192	X3055	X2972	D2910
			GLU	L3662	X3564	X3455	X3385	X3258	X3193	X3056	X2973	T2911
X3953			E3747	L3663	X3565	X3456	X3386	X3259	X3194	X3057	X2974	L2912
V3961			E3748	L3664	X3566	X3457	X3387	X3260	X3195	X3058	X2975	T2913
F3962			V3749	E3665	X3567		X3388	X3261	X3196	X3059	X2976	A2914
N3963			E3750	D3666	X3568	X3463	X3389	X3262	X3197	X3060	X2977	E2915
			V3751	H3667	X3569	X3464	X3390	X3263	X3198	X3061	X2978	K2916
			F3752	S3668		X3467	X3391	X3264	X3199	X3062	X2979	A2917
			F3753	F3669	X3570	X3468	X3392	X3265	X3200	X3063	X2980	D2918
					X3571	X3511	X3393	X3266	X3201	X3064	X2981	D2919
					X3572	X3512	X3394	X3267	X3202	X3065	X2982	E2920
					X3573	X3513	X3395	X3268	X3203	X3066	X2983	E2921
					X3574	X3514	X3396	X3269	X3204	X3067	X2984	K2922
					X3575	X3515	X3397	X3270	X3205	X3068	X2985	A2923
					X3576	X3516	X3398	X3271	X3206	X3069	X2986	Q2924
					X3577	X3517	X3399	X3272	X3207	X3070	X2987	E2925
					X3578	X3518	X3400	X3273	X3208	X3071	X2988	E2926
					X3579	X3519	X3401	X3274	X3209	X3072	X2989	L2927
					X3580	X3520	X3402	X3275	X3210	X3073	X2990	K2928
					X3581	X3521	X3403	X3276	X3211	X3074	X2991	F2929
					X3582	X3522	X3404	X3277	X3212	X3075	X2992	L2930
					X3583		X3405	X3278	X3213	X3076	X2993	Q2931
					X3584		X3406	X3279	X3214	X3077	X2994	H2932
					X3585		X3407	X3280	X3215	X3078	X2995	D2933
					X3586		X3408	X3281	X3216	X3079	X2996	G2934
					X3587		X3409	X3282	X3217	X3080	X2997	V2935
					X3588		X3410	X3283	X3218	X3081	X2998	A2936
					X3589		X3411	X3284	X3219	X3082	X2999	T2937
					X3590		X3412	X3285	X3220	X3083	X3000	T2938
					X3591		X3413	X3286	X3221	X3084	X3001	R2939
					X3592		X3414	X3287	X3222	X3085	X3002	X2942
					X3593		X3415	X3288	X3223	X3086	X3003	K2943
					X3594		X3416	X3289	X3224	X3087	X3004	D2944
					X3595		X3417	X3290	X3225	X3088	X3005	X2945
					X3596		X3418	X3291	X3226	X3089	X3006	X2946
					X3597		X3419	X3292	X3227	X3090	X3007	X2947
					X3598		X3420	X3293	X3228	X3091	X3008	X2948
					X3599		X3421	X3294	X3229	X3092	X3009	X2949
					X3600		X3422	X3295	X3230	X3093	X3010	X2950
					X3601		X3423	X3296	X3231	X3094	X3011	K2951
					X3602		X3424	X3297	X3232	X3095	X3012	X2952
					X3603		X3425	X3298	X3233	X3096	X3013	
					X3604		X3426	X3299	X3234	X3097	X3014	X2955
					X3605		X3427	X3300	X3235	X3098	X3015	X2956
					X3606		X3428	X3301	X3236	X3099	X3016	X2957
					X3607		X3429	X3302	X3237	X3100	X3017	X2958
					X3608		X3430	X3303	X3238	X3101	X3018	
					X3609		X3431	X3304	X3239	X3102	X3019	X2960
					X3610		X3432	X3305	X3240	X3103	X3020	K2961
					X3611		X3433	X3306	X3241	X3104	X3021	X2962
					X3612		X3434	X3307	X3242	X3105	X3022	
					X3613		X3435	X3308	X3243	X3106	X3023	X2963
					T3639		X3436	X3309	X3244	X3107	X3024	X2964
							X3437		X3245	X3108	X3025	X2965
							X3438		X3246	X3109	X3026	
							X3439		X3247	X3110	X3027	X2966
							X3440		X3248	X3111	X3028	X2967
							X3441		X3249	X3112	X3029	X2968
							X3442		X3250	X3113	X3030	X2969
							X3443		X3251	X3114	X3031	X2970
							X3444		X3252	X3115	X3032	X2971
							X3445		X3253	X3116	X3033	X2972
							X3446		X3254	X3117	X3034	X2973
							X3447		X3255	X3118	X3035	X2974
							X3448		X3256	X3119	X3036	X2975
							X3449		X3257	X3120	X3037	X2976
							X3450		X3258	X3121	X3038	X2977
							X3451		X3259	X3122	X3039	X2978
							X3452		X3260	X3123	X3040	X2979
							X3453		X3261	X3124	X3041	X2980
							X3454		X3262	X3125	X3042	X2981
							X3455		X3263	X3126	X3043	X2982
							X3456		X3264	X3127	X3044	X2983
							X3457		X3265	X3128	X3045	X2984
							X3458		X3266	X3129	X3046	X2985
							X3459		X3267	X3130	X3047	X2986
							X3460		X3268	X3131	X3048	X2987
							X3461		X3269	X3132	X3049	X2988
							X3462		X3270	X3133	X3050	X2989
							X3463		X3271	X3134	X3051	X2990
							X3464		X3272	X3135	X3052	X2991
							X3465		X3273	X3136	X3053	X2992
							X3466		X3274	X3137	X3054	X2993
							X3467		X3275	X3138	X3055	X2994
							X3468		X3276	X3139	X3056	X2995
							X3469		X3277	X3140	X3057	X2996
							X3470		X3278	X3141	X3058	X2997
							X3471		X3279	X3142	X3059	X2998
							X3472		X3280	X3143	X3060	X2999
							X3473		X3281	X3144	X3061	X3000
							X3474		X3282	X3145	X3062	X3001
							X3475		X3283	X3146	X3063	X3002
							X3476		X3284	X3147	X3064	X3003
							X3477		X3285	X3148	X3065	X3004
							X3478		X3286	X3149	X3066	X3005
							X3479		X3287	X3150	X3067	X3006
							X3480		X3288	X3151	X3068	X3007
							X3481		X3289	X3152	X3069	X3008
							X3482		X3290	X3153	X3070	X3009
							X3483		X3291	X3154	X3071	X3010
							X3484		X3292	X3155	X3072	X3011
							X3485		X3293	X3156	X3073	X3012
							X3486		X3294	X3157	X3074	X3013
							X3487		X3295	X3158	X3075	X3014
							X3488		X3296	X3159	X3076	X3015
							X3489		X3297	X3160	X3077	X3016
							X3490		X3298	X3161	X3078	X3017
							X3491		X3299	X3162	X3079	X3018
							X3492		X3300	X3163	X3080	X3019
							X3493		X3301	X3164	X3081	X3020
							X3494		X3302	X3165	X3082	X3021
							X3495		X3303	X3166	X3083	X3022
							X3496		X3304	X3167	X3084	X3023
							X3497		X3305	X3168	X3085	X3024
							X3498		X3306	X3169	X3086	X3025
							X3499		X3307	X3170	X3087	X3026
							X3500		X3308	X3171	X3088	X3027
							X3501		X3309	X3172	X3089	X3028
							X3502		X3310	X3173	X3090	X3029
							X3503		X3311	X3174	X3091	X3030
							X3504		X3312	X3175	X3092	X3031
							X3505		X3313	X3176	X3093	X3032
							X3506		X3314	X3177	X3094	X3033
							X3507		X3315	X3178	X3095	X3034
							X35					



• Molecule 2: Ryanodine receptor 1

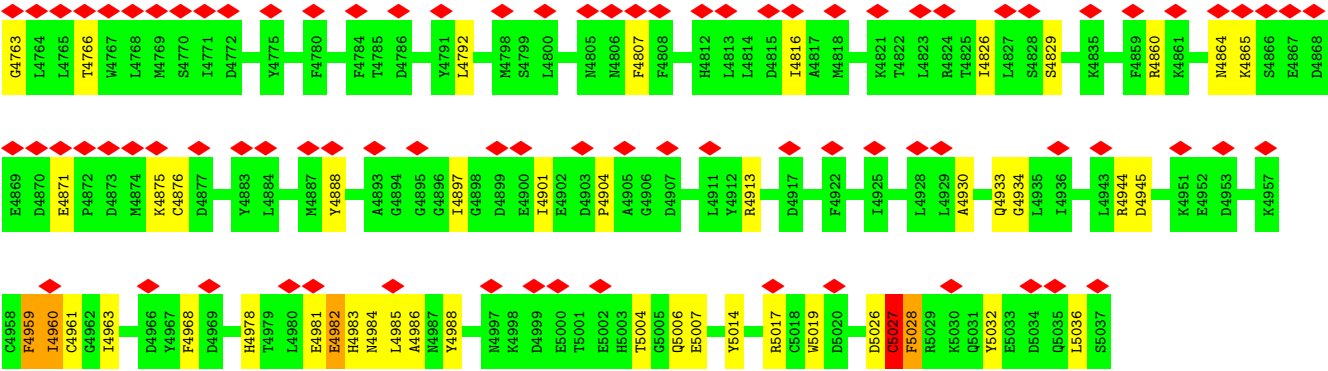


I1053	T983	Q923	L863	G795	T731	V666	K584	V496	M412	S344	H284	T215
E1054	L984	H924	P864	R796	S732	M667		Y497	Q413	L345	V285	G216
PRO	V985	S925	P865		F733	V668	L889	T498	F414	C346	T287	G217
ASP	D986	G926	H866	E799	G734	D669	L589	T499	I415	F347	G288	G218
GLN	R987	E927	L867	F800	Q735	E870	D591	A501	K416	V348	G289	V219
GLU	L988	T928	E868	K901	H736	V671		A500		Q349	R221	L220
PRO	A989		E869	F802	L737					H350	Y290	R221
SER	G992	L929	R869	L803	L738	F674	K598	H502	D419	V351	L291	L222
GLN	H993	K930	T870	A739	A739	L675	V599	F503	S420	A352	A292	F223
VAL	N994	R871	R871	P806	P740	T676	L600	E505	F421	G354	L293	H224
GLU	H994	E872	E872	G807	E741	A677	L606	Y506	G423	G354	T294	G225
ASN	D999	K873	L874	Y808			C607	A507		L355	E295	H227
GLN		R873		A809	S745	Q678	V608	E510	R426	V356	D297	D228
SER	D999	L874			C746	A679	C609	A511	G427	L357	Q296	D228
ARG		A875	E876	H812	C747	L682	N610	A512	S428	T358	G298	E229
TRP	Y1007	E876	N877	E813	L748		G611	E513	G429	Y359	L299	
D1070	S1008	C937	T878	A814	D749	R683	V614		P430	A360	V300	
R1071		H938	L878	V815	L750	G684	R615	N520	P431	A361	V301	T232
V1072	VAL	Y939	H879	L816	S751	V685	S616	L521	A432	P362	V302	I233
R1073	GLN	G940	E880	P817	Y752	G686	N617	L522	D363	D303		S234
I1074	ASP		L881		P753	A687	Q618	Y523	P364	A304		
F1075	ILE	M941	W882	R820	S754	L688	D619	E524	P434	C305		
R1076	ALA	D942	A883	L821	L755	T689			A435	K306		
A1077	ARG	E943	L884	R822	S756	E690	L626	R531	L436	A307		
A1077	ASN	E944	L885	R823	F757	G691	P627	G532		H308		
E1078	ASN	K945	T885	L823	R758	G692	G628	N533	E439	R368		
K1079	PRN	E946	R886	E824		S693	R629	R534	L443	L369		
			T887		I759	S694	E630	A535		K310		
Y1089	L1021	E947	E888	K827	N760	P694		N536		A311		
F1092	V1022	D948	E889	E828	G761	Y695	T635	A538	Y451	T312		
E1093	P1023	N949	Q889	Y829	C762		N636	A538	P454	S313		
A1094	Y1024	G890	C890	R830	P763	G698	L637	L539		F314		
V1095	R951	W891	W891	R831	Y764	G699			P455	C315		
T1096	L1026	T892	T892	E832	Q765	E700	V641	N543	S456	F316		
T1097	L1027	G893	G893	G833	G766			L544	E457	R317		
G1098	D1028	C894	C894	P834	V767	G703	T642	D545	P458	V318		
E1099	K954	P895	P895	R835	F768	G704	S643			H379		
M1100	P956	H896	H896	G836	E769	N705	I644		E463	S319		
	R957	D897	D897	P837	A770	G706	R645	S549	K320	K320		
	T958	R898	R898	H838	F771	V707	P646	K550	E381	E321		
	Y959	D899	D899	L839	N772	G708	N647	L551	G382	R322		
G1103	S1034	N900	N900	S843	D774		I648	D552	H383	L259		
W1104	A1035	K901	K901	R844	G775	L711	F649	R553	K384	V260		
A1105	R1036	S902	S902	C945	G776	Y712	V650	L554	D385	L323		
F1106	D1037	L903	L903	C945	L776	S713	G651	E555	D386	D261		
E1108	S1038	H904	H904	L946	F777	Y714	R652	A556	A387	L262		
L1109	L1039	P905	P905	S947	F778	G715	G652	R474	L388	E263		
R1110	C1040	C906	C906	H848	P779	F716	A653	Q475	F389	P264		
P1111	Q1041	L907	L907	T849		D717	G655		L390	P327		
D1112	A1042	V908	V908	D850	S782	G718	S656	L561	R329	K328		
V1113	V1043	N909	N909	P853	A785	L719	T657	E570	D330	R266		
E1114	R1044	F910	F910	R854	G786	H720	S571	P572	V331	G271		
L1115	T1045	H911	H911	C854	K787	L721	Y659		E332	S272		
G1116	L1046	S912	S912	P855	Y788	W722	G660	L488	G333	H273		
A1117	L1047	L913	L913	V856	H789	T723	K661	M489	K394	L274		
D1118	G1048	P914	P914	D857	R790	G724	W662	I491	E396	R275		
E1119	Y1049	E915	E915	THR	G791	H725	Y663		E397	W276		
L1120	Y1050	P916	P916	VAL	F791	V726	F664		P336			
A1121	N1052	L977	L977	GLN	L792	A727			S398			
Y1122		T978	T978		L793	R728			Q399			
		P979	P979		E917	T729			R402			
		A980	A980		R918				Y403			
		Q981	Q981		N919				G409			
		T982	T982		N921							
					L922							



X3311	X3312	X3313	X3314	X3315	X3316	X3317	X3318	X3319	X3320	X3321	X3324	X3325	X3326	X3327	X3328	X3329	X3330	X3331	X3332	X3333	X3334	X3335	X3336	X3337	X3338	X3339	X3340	X3341	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				
X3245	X3246	X3247	X3248	X3249	X3250	X3251	X3252	X3253	X3254	X3261	X3262	X3263	X3264	X3265	X3266	X3267	X3268	X3269	X3270	X3271	X3272	X3273	X3274	X3275	X3276	X3277	X3278	X3279	X3280	X3281	X3282	X3283	X3284	X3285	X3286	X3287	X3288	X3289	X3290	X3291	X3292	X3293	X3294	X3295	X3296	X3297	X3298	X3299	X3300	X3301	X3302	X3303	X3304	X3305	X3306	X3307	X3308	X3309	X3310		
X3042	X3043	X3044	X3045	X3046	X3047	X3048	X3049	X3050	X3053	X3054	X3055	X3056	X3057	X3058	X3059	X3060	X3061	X3062	X3063	X3134	X3135	X3136	X3137	X3138	X3139	X3140	X3141	X3142	X3143	X3146	X3147	X3148	X3149	X3150	X3151	X3152	X3153	X3154	X3155	X3156	X3157	X3158	X3159	X3160	X3161	X3162	X3163	X3170	X3171	X3172	X3173	X3174	X3175	X3176	X3177	X3178	X3179				
X2961	X2962	X2963	X2964	X2965	X2966	X2967	X2968	X2969	X2970	X2971	X2972	X2973	X2974	X2975	X2976	X2995	X2996	X2997	X2998	X2999	X3000	X3001	X3002	X3003	X3004	X3005	X3006	X3007	X3008	X3009	X3010	X3013	X3014	X3015	X3016	X3017	X3018	X3019	X3020	X3021	X3022	X3023	X3024	X3025	X3026	X3027	X3028	X3029	X3030	X3031	X3032	X3033	X3034	X3035	X3036	X3037	X3038	X3039	X3040	X3041	
G2898	G2899	G2900	T2901	H2902	T2903	L2904	L2905	L2906	T2907	Y2908	D2909	T2910	L2911	T2912	A2913	K2914	E2915	K2916	A2917	D2918	D2919	A2920	E2921	K2922	A2923	Q2924	E2925	L2926	L2927	K2928	F2929	L2930	Q2931	M2932	N2933	G2934	Y2935	A2936	V2937	T2938	R2939	X2942	X2943	X2944	X2945	X2946	X2947	X2948	X2949	X2950	X2951	X2952	X2955	X2956	X2957	X2958	X2959	X2960			
LYS	THR	ARG	ARG	ILE	SER	GLN	THR	ALA	GLN	THR	ASP	ARG	ARG	GLU	GLY	Y2855	N2856	P2857	Q2858	P2859	P2860	D2861	L2862	S2863	G2864	V2865	T2866	L2867	S2868	R2869	E2870	L2871	Q2872	A2873	M2874	E2875	E2876	Q2877	L2878	A2879	E2880	N2881	Y2882	H2883	N2884	T2885	V2886	G2887	R2888	K2889	K2890	K2891	Q2892	E2893	L2894	E2895	A2896	K2897			
G2778	E2779	N2780	V2781	D2782	E2783	E2784	L2785	T2786	T2787	H2788	P2789	L2790	L2791	R2792	P2793	Y2794	T2795	T2796	F2797	S2798	E2799	K2800	D2801	L2802	E2803	L2804	Y2805	R2806	L2807	P2808	L2809	K2810	E2811	S2812	L2813	K2814	A2815	M2816	L2817	A2818	N2819	E2820	W2821	T2822	L2823	E2824	K2825	A2826	R2827	E2828	G2829	E2830	GLU	ARG	THR	GLU	LYS	Y2777			
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	K2750	L2751	D2752	S2753	F2754	T2755	N2756	K2757	P2758	E2759	E2760	Y2761	T2762	H2763	E2764	K2765	W2766	A2767	F2768	D2769	K2770	L2771	Q2772	N2773	W2774	W2775	S2776	Y2777		
X2624	X2625	X2626	X2627	X2628	X2629	X2630	X2631	X2632	X2633	X2634	X2635	X2636	X2637	X2638	X2639	X2640	X2641	X2642	X2643	X2644	X2645	X2646	X2647	X2648	X2649	X2650	X2651	X2652	X2655	X2656	X2657	X2658	X2659	X2660	X2661	X2662	X2663	X2664	X2665	X2666	X2667	X2668	X2669	X2670	X2671	X2672	X2673	X2674	X2675	X2676	X2677	X2678	X2679	X2680	X2681	X2682	X2683	X2684	X2685	X2686	X2687
X2528	X2529	X2532	X2533	X2534	X2535	X2536	X2537	X2538	X2539	X2540	X2558	X2561	X2562	X2563	X2567	X2568	X2569	X2570	X2571	X2577	X2580	X2581	X2582	X2583	X2584	X2585	X2586	X2593	X2596	X2597	X2598	X2599	X2600	X2601	X2602	X2605	X2606	X2611	X2612	X2613	X2614	X2618	X2619	X2620	X2621	X2622	X2623														
P2438	E2439	M2440	H2441	K2447	G2448	L2451	R2452	I2453	R2454	A2455	R2458	S2459	L2460	L2463	L2466	I2469	I2470	S2471	L2472	P2473	Q2475	I2476	P2477	T2478	L2479	X2487	X2488	X2489	X2490	X2493	X2494	X2495	X2498	X2499	X2500	X2511	X2512	X2513	X2517	X2518	X2519	X2520	X2522	X2523	X2524	X2525															
L2368	R2369	G2370	E2371	G2372	G2373	S2374	G2375	L2376	L2377	A2378	A2379	I2380	E2381	E2382	A2383	I2384	S2387	E2388	D2389	P2390	A2391	R2392	D2393	G2394	P2395	GLY	VAL	ARG	ARG	ASP	ARG	ARG	GLU	HIS	PHE	GLY	GLU	GLU	PRO	PRO	GLU	N2414	R2415	V2416	H2417	L2418	G2419	M2423	I2430	L2431	L2432	L2433	G2434	R2435							





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	0.068	Depositor
Minimum map value	-0.038	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.025	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

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	0.20	0/834	0.46	0/1123
1	F	0.20	0/834	0.46	0/1123
1	H	0.20	0/834	0.46	0/1123
1	J	0.20	0/834	0.46	0/1123
2	B	0.23	0/25428	0.53	2/34534 (0.0%)
2	E	0.23	0/25428	0.53	2/34534 (0.0%)
2	G	0.23	0/25428	0.53	2/34534 (0.0%)
2	I	0.23	0/25428	0.53	2/34534 (0.0%)
All	All	0.23	0/105048	0.53	8/142628 (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	17
2	E	0	17
2	G	0	16
2	I	0	16
All	All	0	66

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	5027	CYS	N-CA-C	5.52	117.59	108.49
2	E	5027	CYS	N-CA-C	5.52	117.59	108.49
2	G	5027	CYS	N-CA-C	5.50	117.57	108.49
2	I	5027	CYS	N-CA-C	5.50	117.56	108.49

Continued on next page...

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	131	LEU	CA-CB-CG	5.21	134.52	116.30

There are no chirality outliers.

5 of 66 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	139	GLU	Peptide
2	B	1676	LEU	Peptide
2	B	312	THR	Peptide
2	B	694	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	8	0
1	F	818	0	824	8	0
1	H	818	0	824	9	0
1	J	818	0	824	5	0
2	B	29499	0	24751	296	0
2	E	29499	0	24751	304	0
2	G	29499	0	24751	303	0
2	I	29499	0	24751	296	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
All	All	121272	0	102300	1199	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 1199 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:I:4190:ILE:CD1	2:I:5026:ASP:OD2	1.76	1.33
2:E:4190:ILE:CD1	2:E:5026:ASP:OD2	1.77	1.33
2:G:4190:ILE:CD1	2:G:5026:ASP:OD2	1.77	1.32
2:B:4190:ILE:CD1	2:B:5026:ASP:OD2	1.76	1.31
2:B:4190:ILE:HD11	2:B:5026:ASP:OD2	1.31	1.26

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	105/108 (97%)	93 (89%)	12 (11%)	0	100	100
1	F	105/108 (97%)	93 (89%)	12 (11%)	0	100	100
1	H	105/108 (97%)	93 (89%)	12 (11%)	0	100	100
1	J	105/108 (97%)	93 (89%)	12 (11%)	0	100	100
2	B	3235/4416 (73%)	2892 (89%)	335 (10%)	8 (0%)	43	77
2	E	3235/4416 (73%)	2893 (89%)	334 (10%)	8 (0%)	43	77
2	G	3235/4416 (73%)	2893 (89%)	334 (10%)	8 (0%)	43	77
2	I	3235/4416 (73%)	2891 (89%)	336 (10%)	8 (0%)	43	77
All	All	13360/18096 (74%)	11941 (89%)	1387 (10%)	32 (0%)	44	77

5 of 32 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	5028	PHE
2	I	5028	PHE
2	E	5028	PHE
2	G	5028	PHE
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%)	2481 (100%)	12 (0%)	81	81
2	E	2493/3022 (82%)	2481 (100%)	12 (0%)	81	81
2	G	2493/3022 (82%)	2481 (100%)	12 (0%)	81	81
2	I	2493/3022 (82%)	2481 (100%)	12 (0%)	81	81
All	All	10324/12444 (83%)	10276 (100%)	48 (0%)	78	81

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	1676	LEU
2	E	5027	CYS
2	E	2339	VAL
2	E	4792	LEU
2	G	719	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 236 such sidechains are listed below:

Mol	Chain	Res	Type
2	I	4553	ASN
2	G	4034	ASN
2	E	1702	HIS
2	G	3960	GLN
2	G	1691	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	B	14
2	I	14
2	E	14
2	G	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	73.35
1	I	4345:UNK	C	4540:PHE	N	73.35
1	E	4345:UNK	C	4540:PHE	N	73.35
1	G	4345:UNK	C	4540:PHE	N	73.35

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	3613:UNK	C	3639:THR	N	45.90

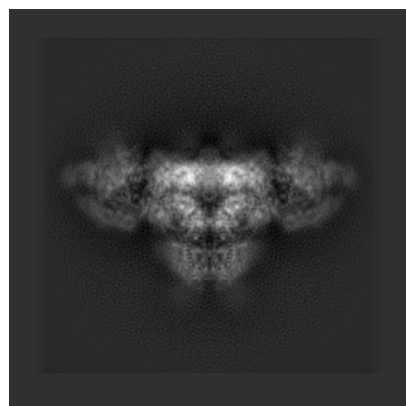
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8393. These allow visual inspection of the internal detail of the map and identification of artifacts.

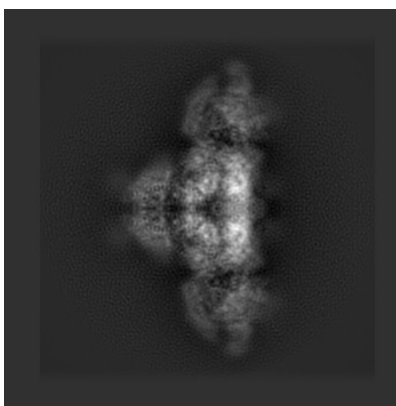
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

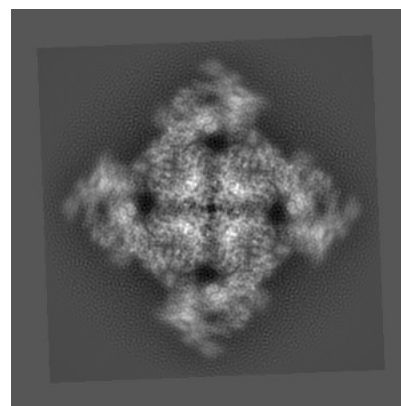
6.1.1 Primary map



X

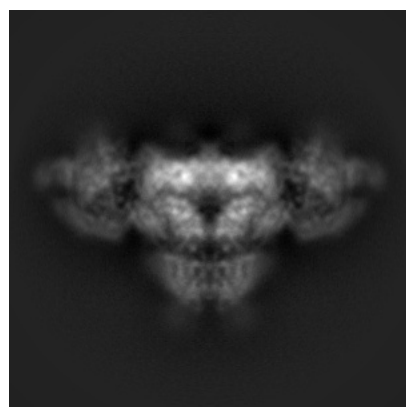


Y

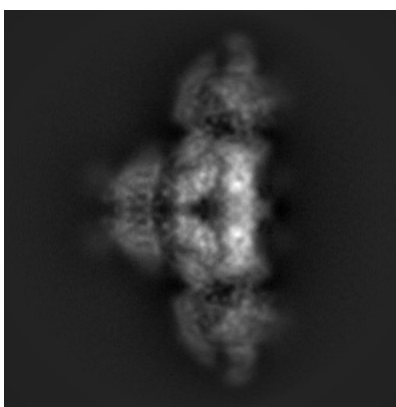


Z

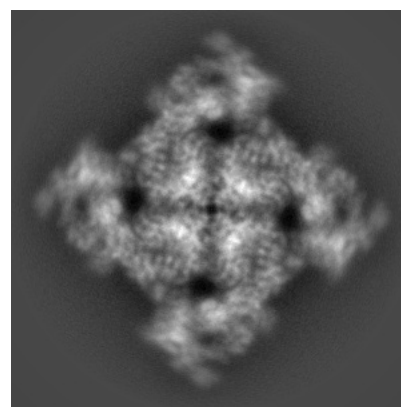
6.1.2 Raw map



X



Y

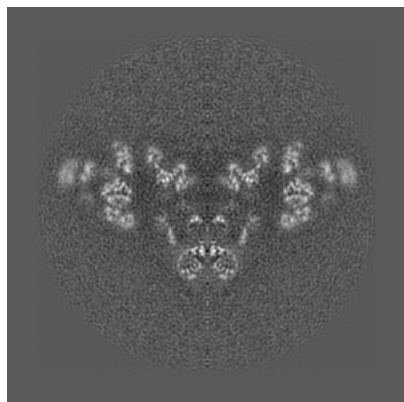


Z

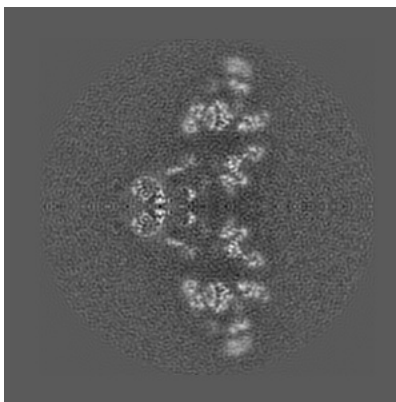
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

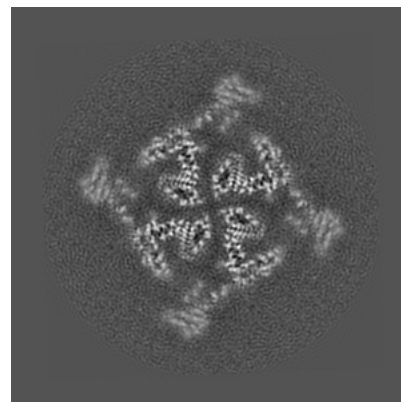
6.2.1 Primary map



X Index: 200

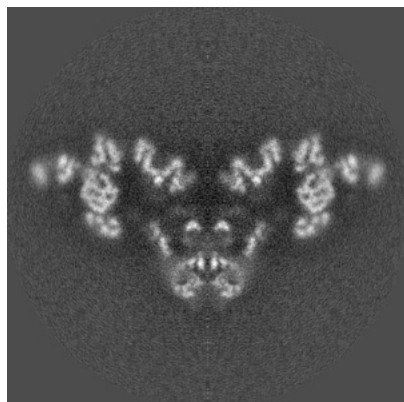


Y Index: 200

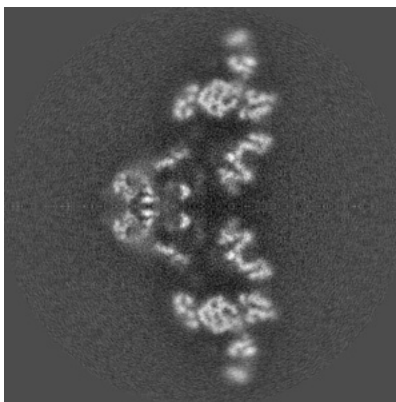


Z Index: 200

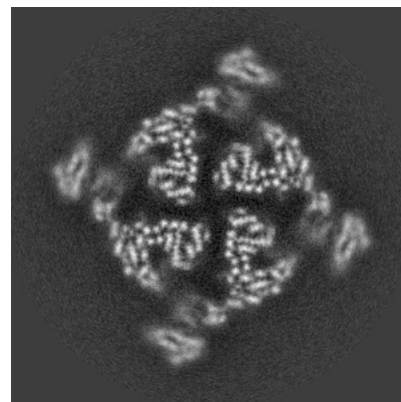
6.2.2 Raw map



X Index: 168



Y Index: 168

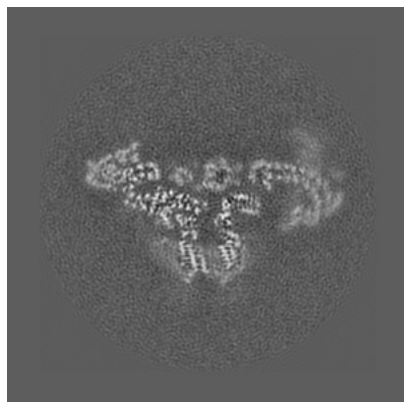


Z Index: 168

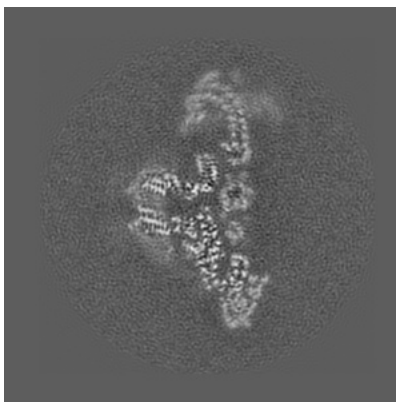
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

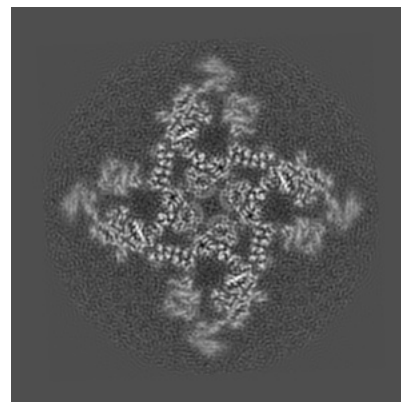
6.3.1 Primary map



X Index: 224

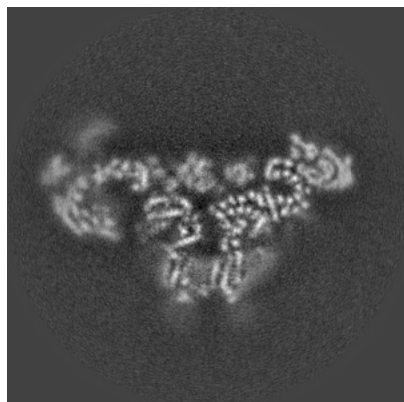


Y Index: 176

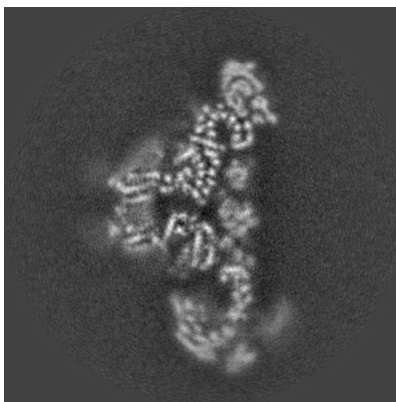


Z Index: 228

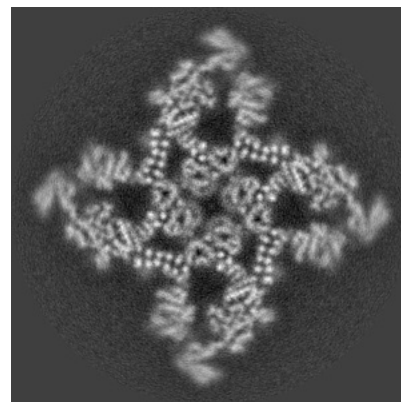
6.3.2 Raw map



X Index: 146



Y Index: 190

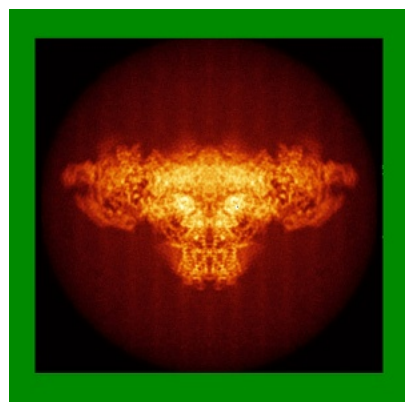


Z Index: 193

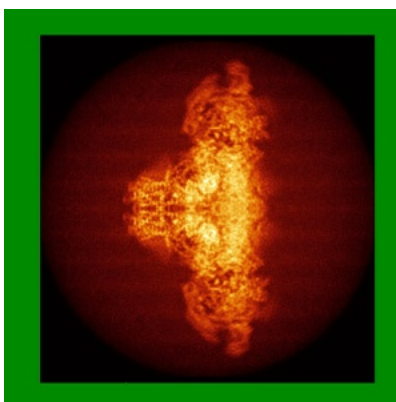
The images above show the largest variance slices of the map in three orthogonal directions.

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

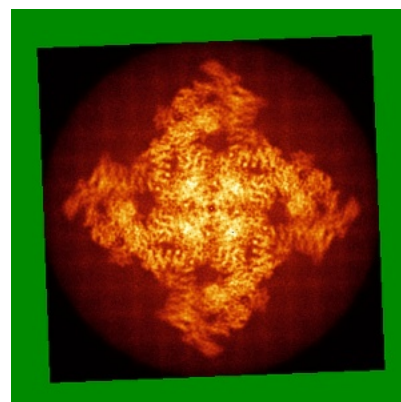
6.4.1 Primary map



X

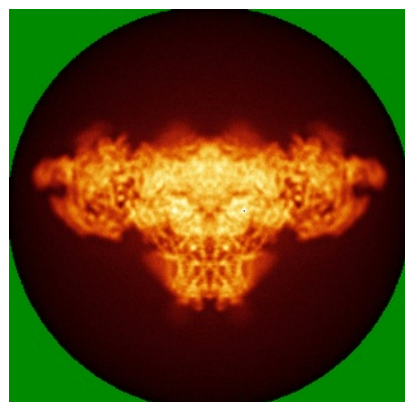


Y

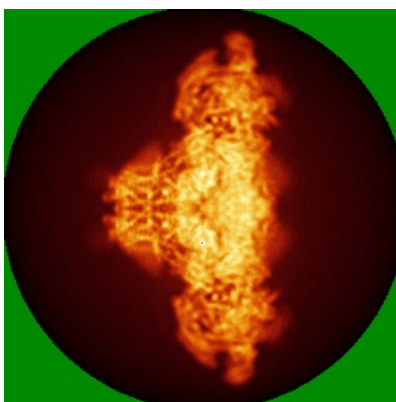


Z

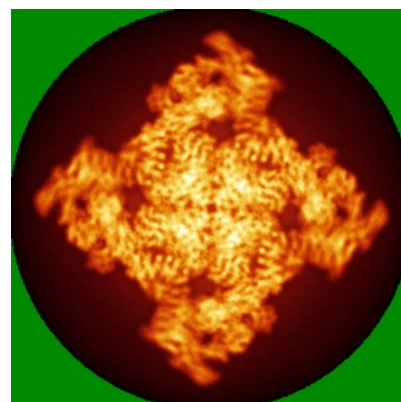
6.4.2 Raw map



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

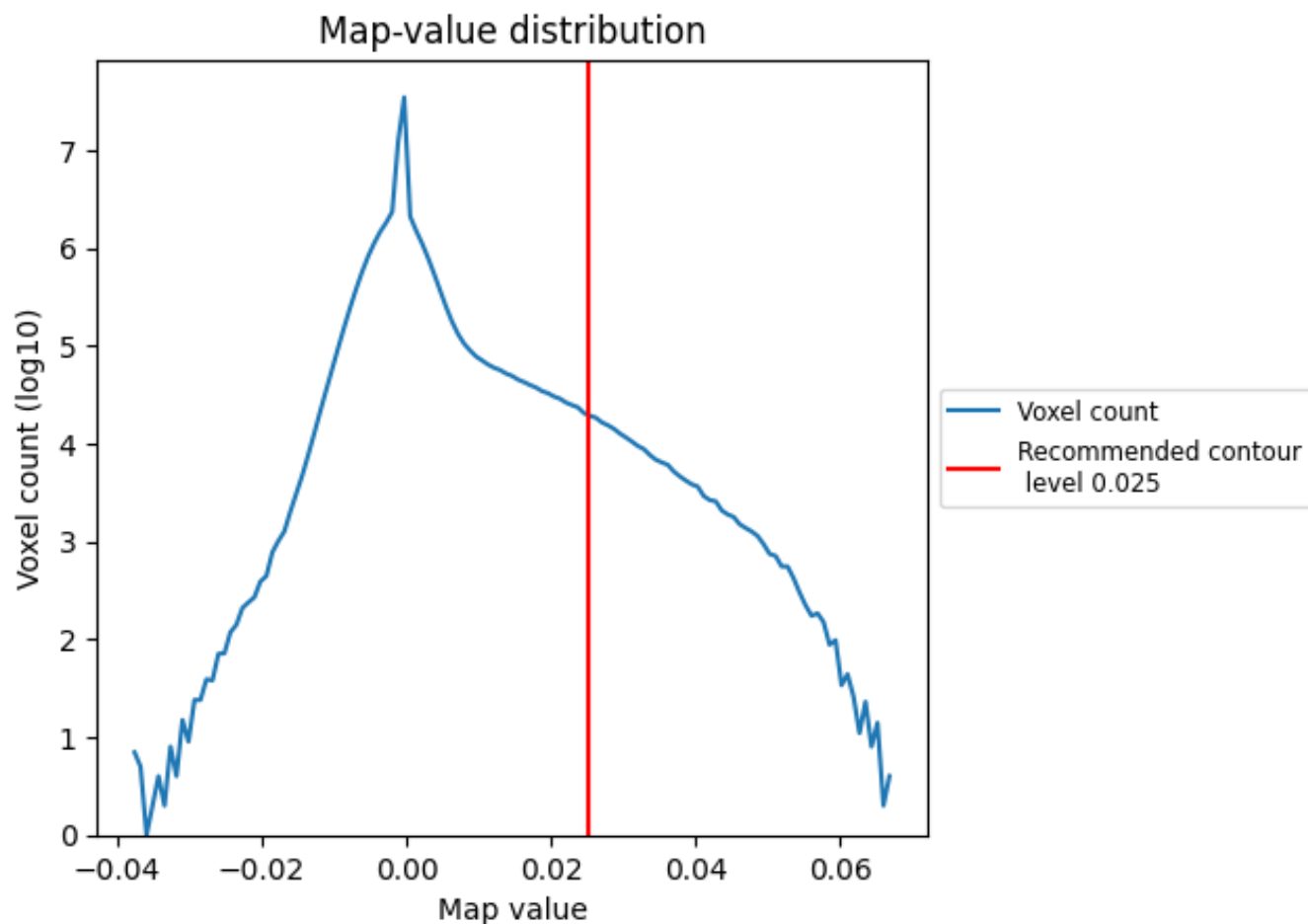
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

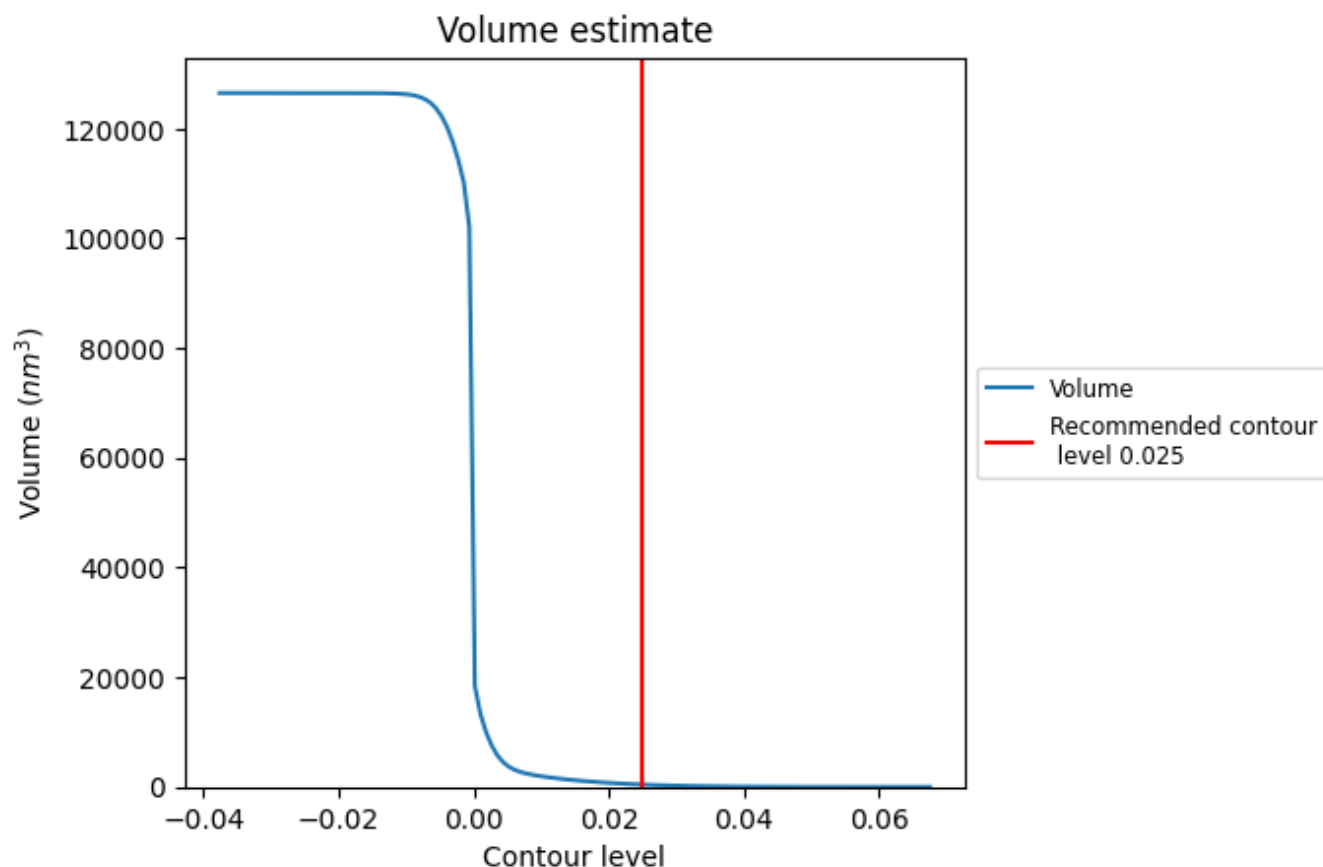
This section contains the results of statistical analysis of the map.

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.

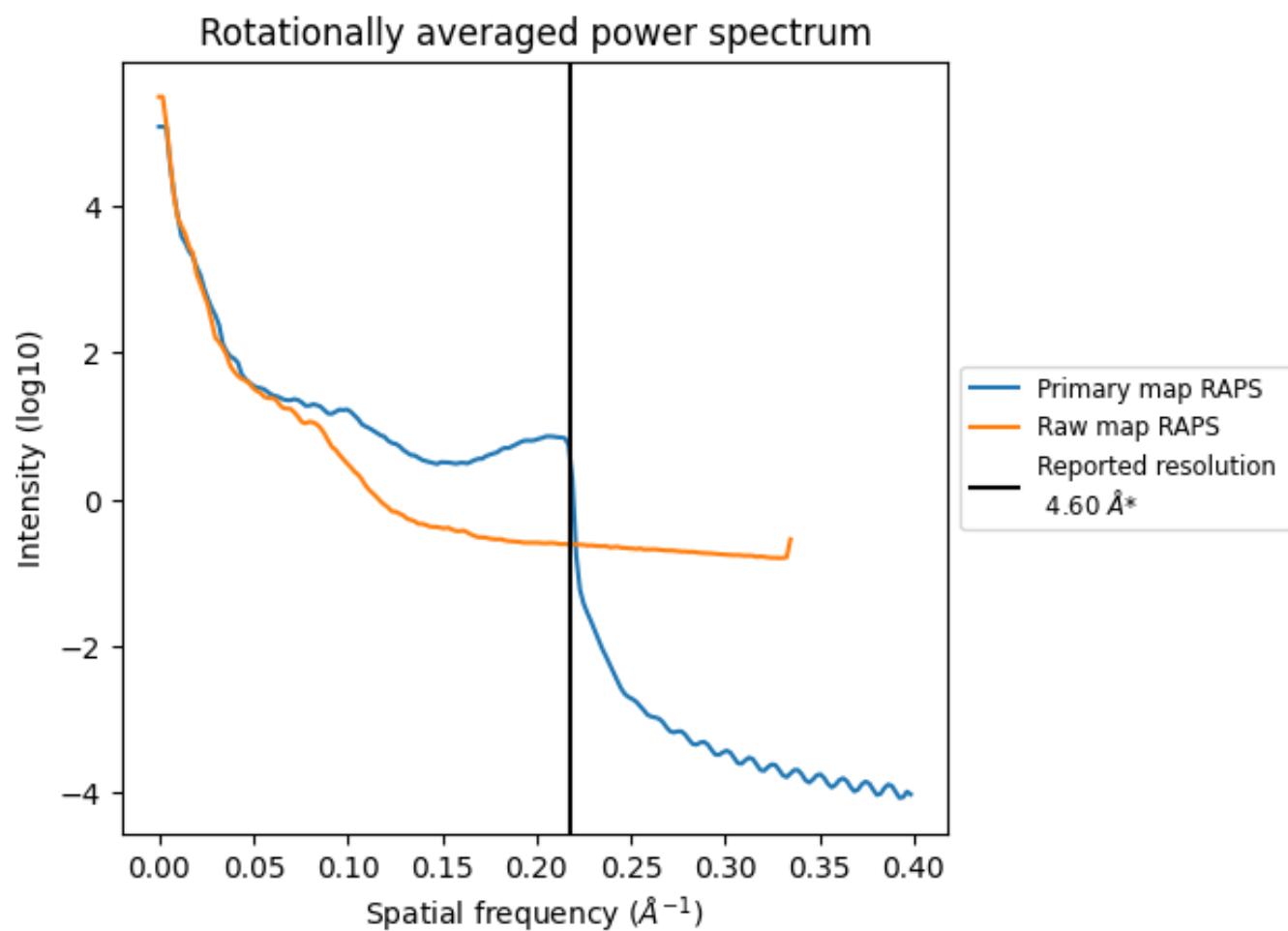
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 431 nm^3 ; this corresponds to an approximate mass of 390 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](#)

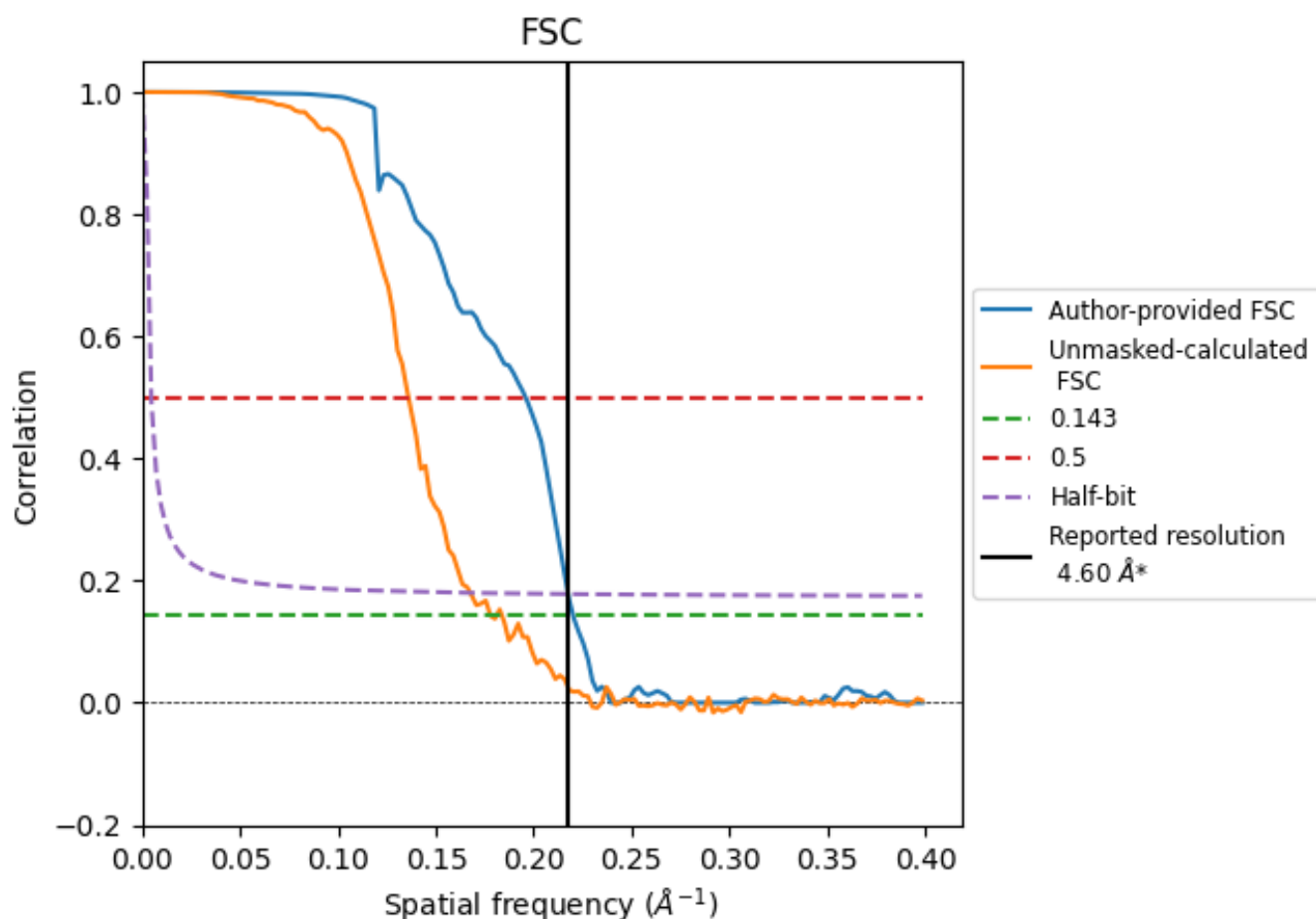


*Reported resolution corresponds to spatial frequency of 0.217 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.217 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.60	-	-
Author-provided FSC curve	4.54	5.11	4.60
Unmasked-calculated*	5.62	7.35	5.97

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

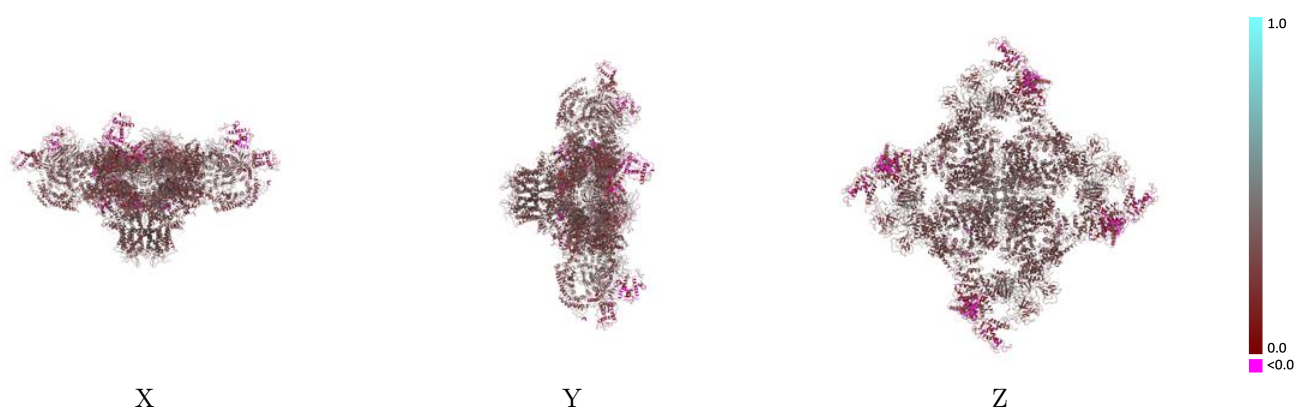
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8393 and PDB model 5TB2. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)

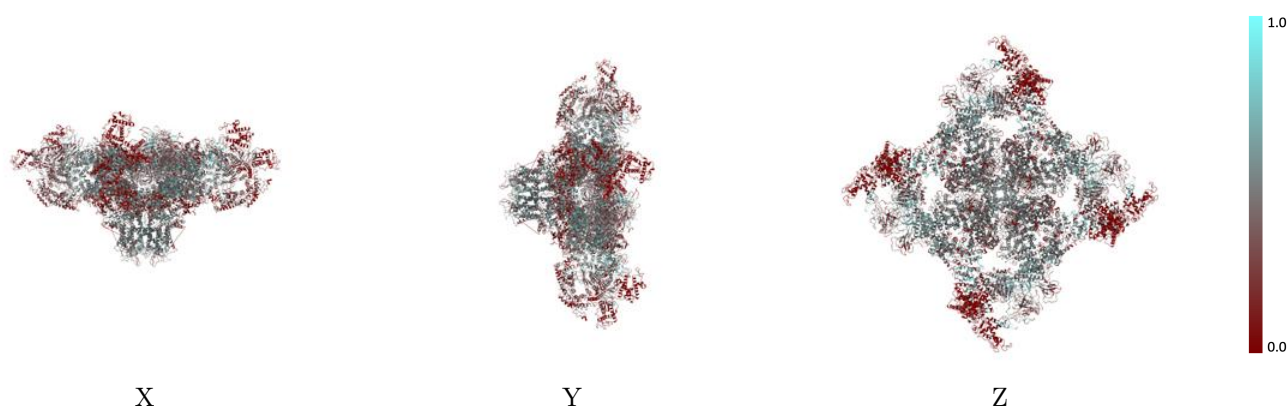
This section was not generated.

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



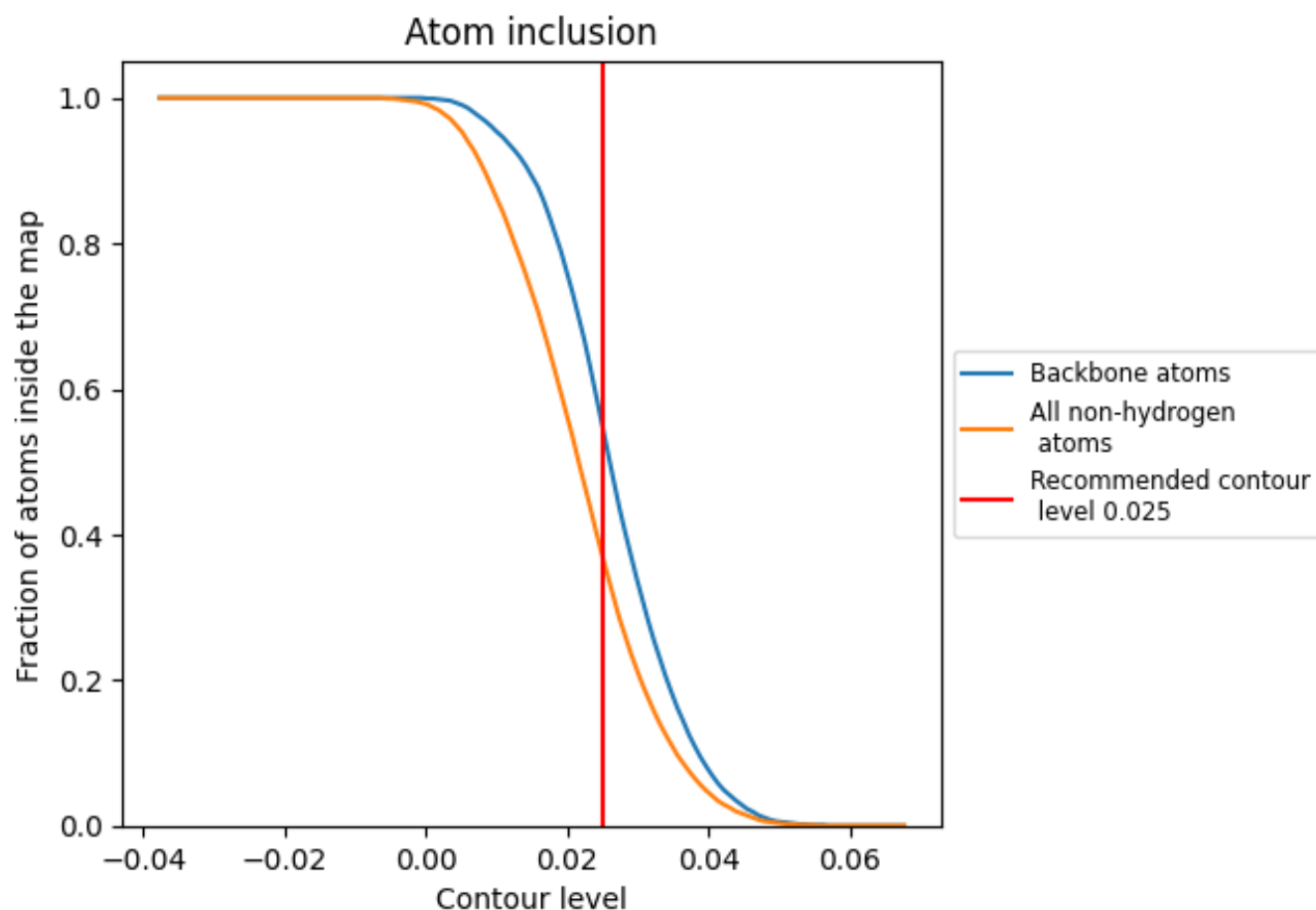
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.025).

9.4 Atom inclusion [i](#)



At the recommended contour level, 55% of all backbone atoms, 37% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3690	0.2880
A	0.3500	0.3000
B	0.3700	0.2880
E	0.3690	0.2880
F	0.3440	0.3030
G	0.3700	0.2880
H	0.3490	0.3040
I	0.3700	0.2870
J	0.3500	0.3030

