



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 03:31 PM UTC

PDB ID : 8UQ5 / pdb_00008uq5
EMDB ID : EMD-42461
Title : Structure of human RyR2-S2808D in the primed state in the presence of Rapamycin
Authors : Miotto, M.C.; Marks, A.R.
Deposited on : 2023-10-23
Resolution : 3.96 Å(reported)
Based on initial model : 7UA5

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:

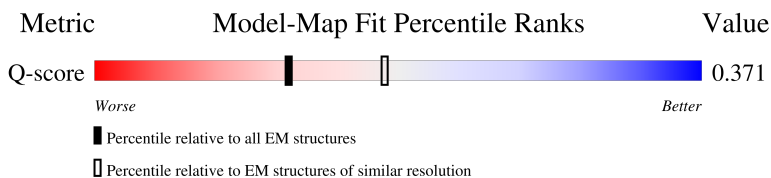
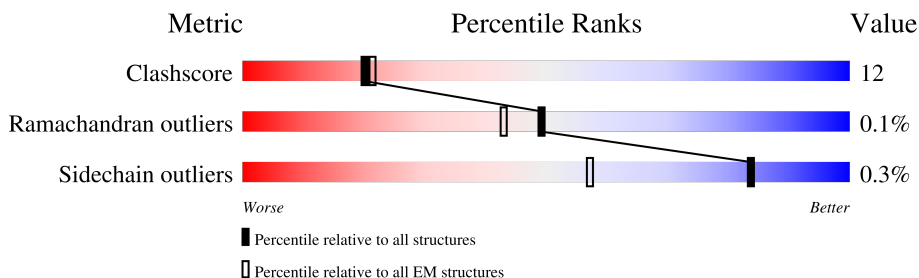
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.96 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	7646 (3.46 - 4.46)

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	4967	
1	B	4967	
1	C	4967	
1	D	4967	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 135336 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Ryanodine receptor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	4224	Total	C	N	O	S	2	0
			33771	21516	5745	6280	230		
1	B	4224	Total	C	N	O	S	2	0
			33771	21516	5745	6280	230		
1	C	4224	Total	C	N	O	S	2	0
			33771	21516	5745	6280	230		
1	D	4224	Total	C	N	O	S	2	0
			33771	21516	5745	6280	230		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2808	ASP	SER	engineered mutation	UNP Q92736
B	2808	ASP	SER	engineered mutation	UNP Q92736
C	2808	ASP	SER	engineered mutation	UNP Q92736
D	2808	ASP	SER	engineered mutation	UNP Q92736

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
2	A	1	Total	Zn	0
			1	1	
2	B	1	Total	Zn	0
			1	1	
2	C	1	Total	Zn	0
			1	1	
2	D	1	Total	Zn	0
			1	1	

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).

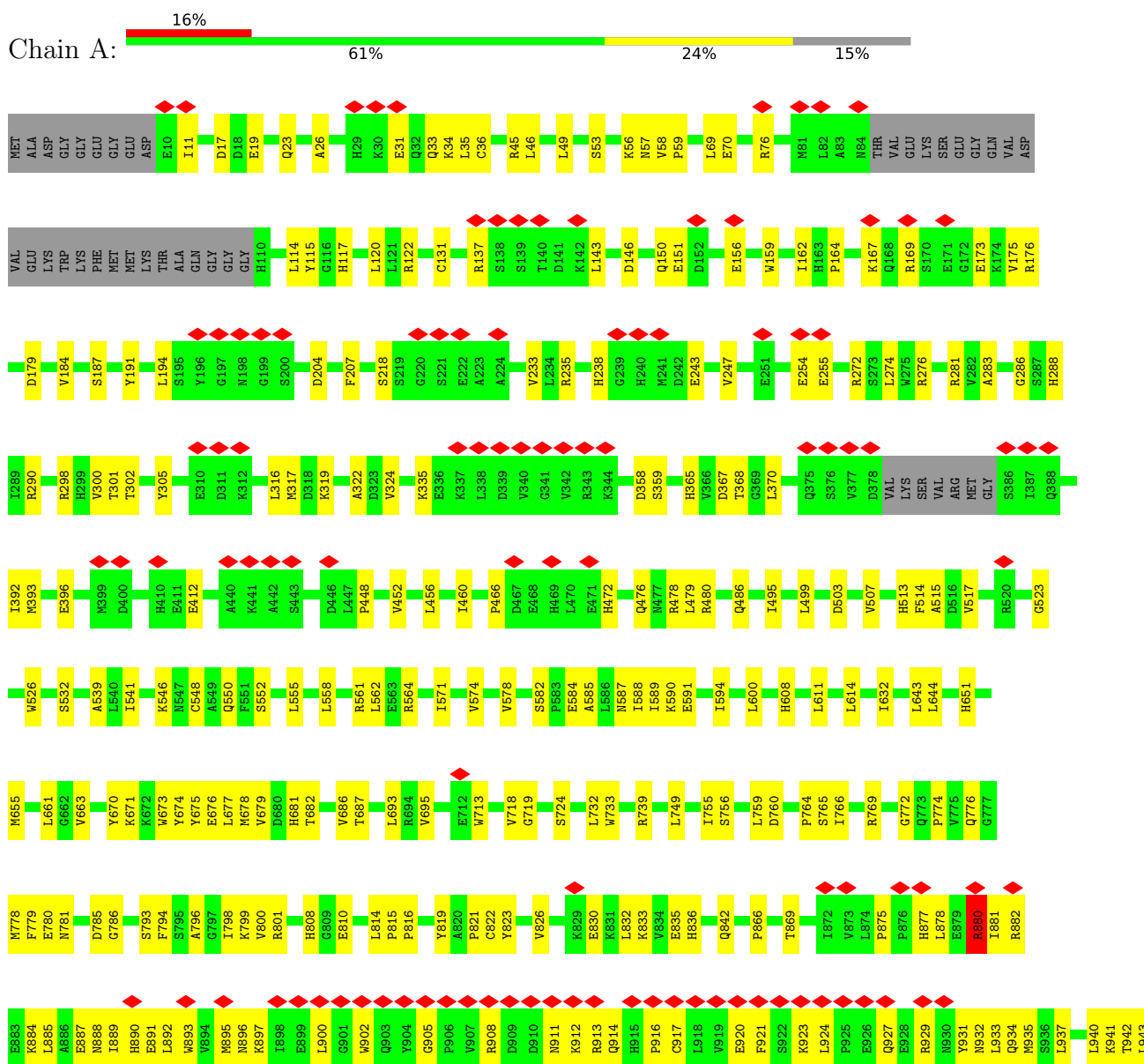


Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total 31	C 10	N 5	O 13	P 3	0
3	A	1	Total 31	C 10	N 5	O 13	P 3	0
3	B	1	Total 31	C 10	N 5	O 13	P 3	0
3	B	1	Total 31	C 10	N 5	O 13	P 3	0
3	C	1	Total 31	C 10	N 5	O 13	P 3	0
3	C	1	Total 31	C 10	N 5	O 13	P 3	0
3	D	1	Total 31	C 10	N 5	O 13	P 3	0
3	D	1	Total 31	C 10	N 5	O 13	P 3	0

3 Residue-property plots

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.

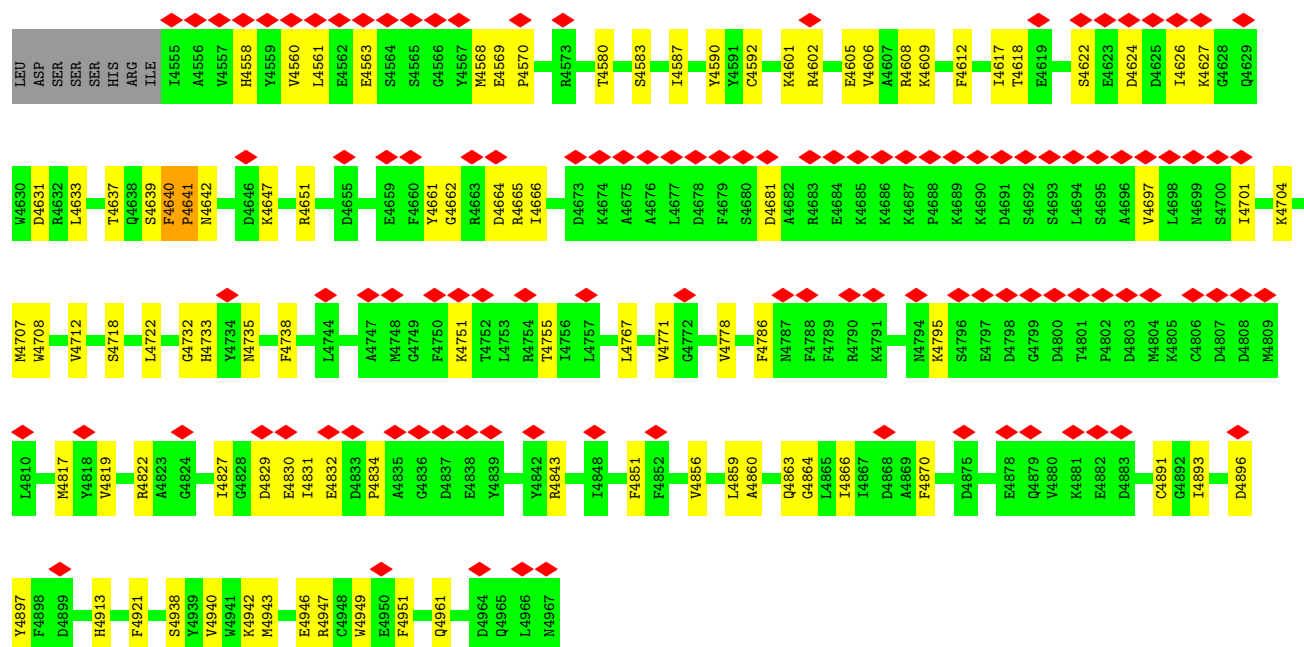
• Molecule 1: Ryanodine receptor 2



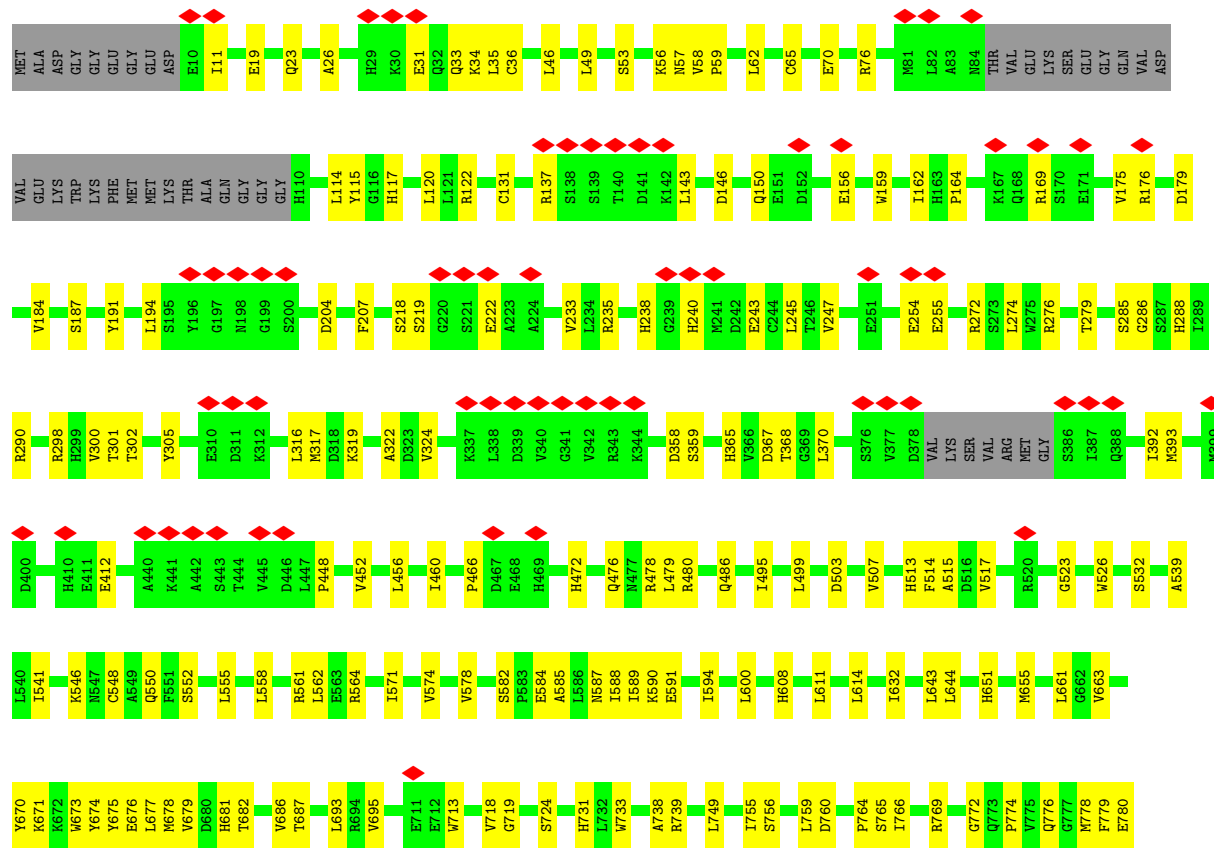








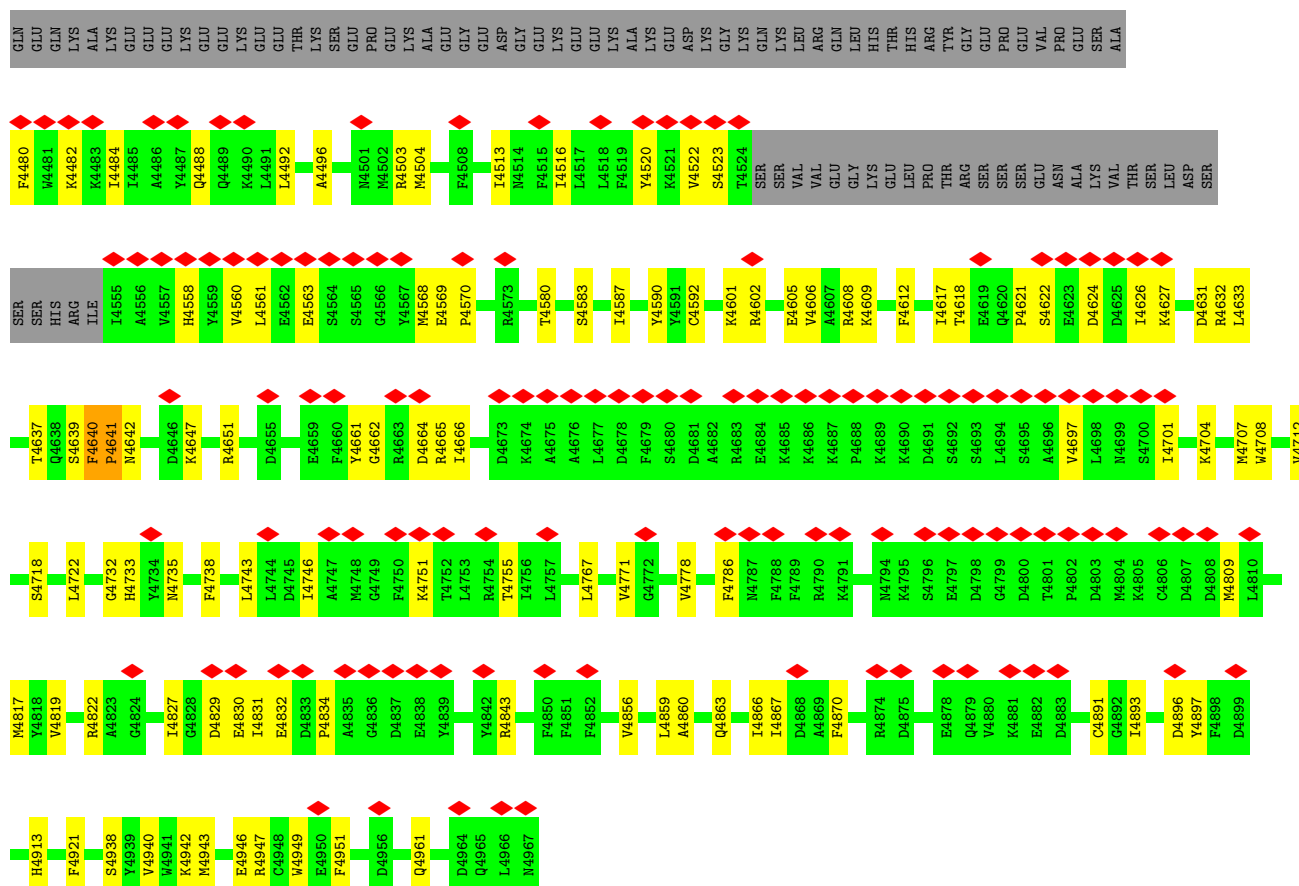
• Molecule 1: Ryanodine receptor 2



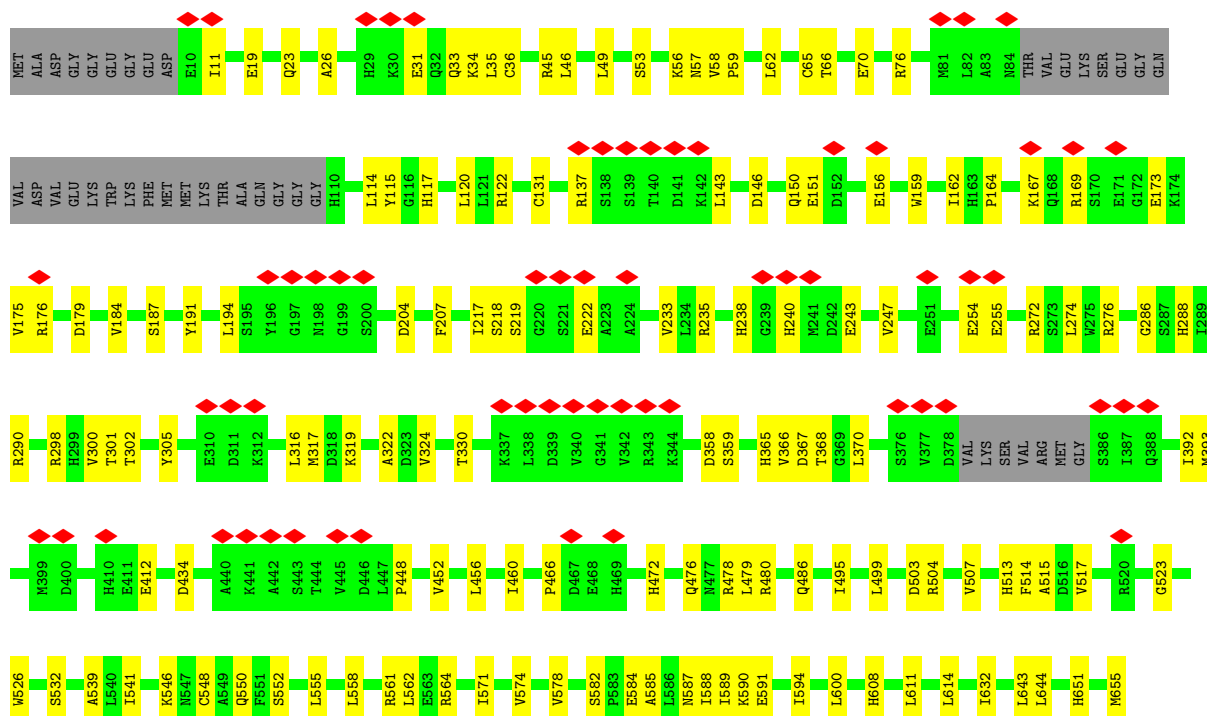


L3140	G3141	T3142	S3145	T3146	V3147	V3148	V3149	V3150	Q3151	Q3152	S3153	A3154	C3158	A3161	F3162	A3163	A3164	A3165	F3166	F3167	V3168	A3169	F3170	L3171	E3172	T3173	H3174	L3175	D3176	K3177	L3178	N3179	I3180	Y3181	S3182	I3183	Y3184	N3185	T3186	K3187	S3188	S3189	R3190	E3191	R3192	A3193	A3194	L3195	S3196	L3197	F3198	T3199	N3200	D3203					
E3073	N3074	L3075	K3076	Q3077	Q3078	Q3079	F3080	T3081	HIS	THR	ARG	ASN	GLN	PRO	K3088	Q3089	V3090	T3091	Q3092	A3093	Y3096	T3097	T3098	V3099	A3100	L3101	L3102	F3103	M3104	L3105	S3106	L3107	L3108	F3109	E3110	H3111	Q3114	H3115	Q3116	F3117	G3118	E3119	L3120	L3121	L3122	L3123	E3124	V3126	Q3127	L3128	E3069	K3070	T3071	M3072	Y3131	R3132	S3136	L3137	
E2935	A2936	H2937	Q2938	Y2939	L2940	E2942	F2943	D2944	G2945	G2946	S2947	R2948	E2949	K2950	G2951	E2952	H2953	F2954	F2955	Y2956	K2961	K2965	V2966	V2967	L2968	P2969	D2972	Q2973	Y2974	F2975	K2976	R2979	F2982	L2983	S2984	A2985	A2986	S2987	R2988	F2989	L3061	D3062	E3066	D3067	L3068	E3069	K3070	T3071	M3072	Y3131	R3132	S3136	L3137						
L2870	P2873	Y2874	Q2875	T2876	L2877	T2878	A2879	K2880	E2881	K2882	A2883	K2884	D2885	R2886	E2887	K2888	A2889	Q2890	D2891	T2892	L2893	K2894	F2895	L2896	Q2897	T2898	N2899	Q2900	Y2901	A2902	R2905	G2906	F2907	K2908	D2909	L2910	E2911	L2912	D2913	T2914	P2915	R2920	F2921	A2922	Y2923	F2925	Q2926	Q2927	Q2928	L2929	S2997	H2998	A2996	S2997	K2999	E3000	K3001	E3002	
ARG	ARG	ILE	ASP	GLN	THR	SER	GLN	VAL	SER	VAL	ASP	ALA	ALA	HIS	G2820	Y2821	S2822	F2823	R2824	A2825	T2826	D2827	M2828	S2829	N2830	T2831	T2832	L2833	S2834	R2835	D2836	L2837	H2838	A2841	E2842	N2843	M2844	A2845	E2846	Y2848	H2849	K2854	K2855	M2858	E2859	L2860	E2861	K2862	K2863	G2864	G2865	G2866	H2867	H2868	P2869				
W2732	S2733	M2734	D2735	K2736	L2737	A2738	N2739	G2740	W2741	T2742	Y2743	G2744	E2745	I2746	Y2747	S2748	S2750	S2751	K2752	V2753	Q2754	P2755	L2756	M2757	K2758	P2759	Y2760	K2761	L2762	G2763	S2764	K2768	E2769	Y2770	Y2771	R2772	W2773	K2776	L2779	M2782	R2788	L2789	E2790	R2793	E2794	A2799	L2800	Y2801	N2802	ARG	THR								
F2662	K2663	L2664	C2668	L2669	S2670	A2673	P2677	Y2680	E2681	E2682	S2683	N2684	Y2685	V2686	S2687	M2688	N2689	E2690	K2691	Q2692	S2693	S2694	C2695	S2696	P2697	D2698	G2699	N2700	F2701	N2702	P2703	Q2704	T2705	V2706	D2707	T2708	K2709	N2710	T2711	T2712	T2713	F2714	E2715	L2716	F2720	L2721	K2723	E2726	H2727	K2731									
M2584	M2585	Q2586	H2587	L2588	L2589	R2590	L2591	R2592	V2593	F2594	H2602	A2603	K2604	M2605	P2606	L2607	K2608	L2609	G2491	T2610	T2611	N2612	R2616	K2619	C2622	L2623	P2624	L2625	G2626	W2627	G2628	N2629	F2630	S2634	E2635	L2638	H2639	L2640	S2641	R2642	K2643	L2644	D2650	A2651	Q2654	K2655	A2656	Y2657	E2658	Q2659	L2661								
F2464	K2465	M2468	F2471	V2475	L2478	E2479	D2482	F2483	L2487	E2488	E2489	V2490	G2491	F2492	A2500	M2512	C2521	L2525	P2526	L2527	L2528	T2529	R2530	L2534	F2535	L2544	L2548	L2549	H2550	T2551	R2554	L2555	S2556	K2557	G2558	C2559	S2560	E2570	L2580	R2581	P2582	S2583																	
N2251	E2252	L2253	A2254	L2255	R2258	D2261	V2265	V2266	C2272	S2276	I2288	G2289	W2290	N2291	P2292	V2293	E2294	G2295	R2297	L2298	A2403	K2413	G2414	L2415	L2302	R2303	L2323	G2332	R2336	G2337	E2338	N2341	G2342	L2343	E2355	R2359	D2360	S2363	P2364	ASN	SER	GLY	SER	SER	LYS	THR													
LEU	ASP	THR	GLU	E2377	E2378	D2379	D2380	H2383	K2384	G2385	N2386	L2387	T2388	F2391	L2395	L2396	D2397	R2401	C2402	A2403	K2413	G2414	L2415	A2416	I2419	L2423	L2426	T2427	P2428	L2429	G2430	D2431	L2432	G2434	V2435	T2436	S2437	L2438	F2440	P2443	E2453	M2456	S2457	A2458															
T2126	E2137	E2138	E2139	K2140	L2141	G2145	I2149	Y2156	Q2157	M2167	N2172	V2176	N2177	V2178	L2179	G2180	G2181	G2182	E2183	S2184	K2185	E2186	T2187	N2192	Y2202	I2206	S2207	R2208	K2214	F2215	Y2220	E2223	V2227	A2230	S2231	P2232	D2241	V2242	K2243	A2244	M2248																		





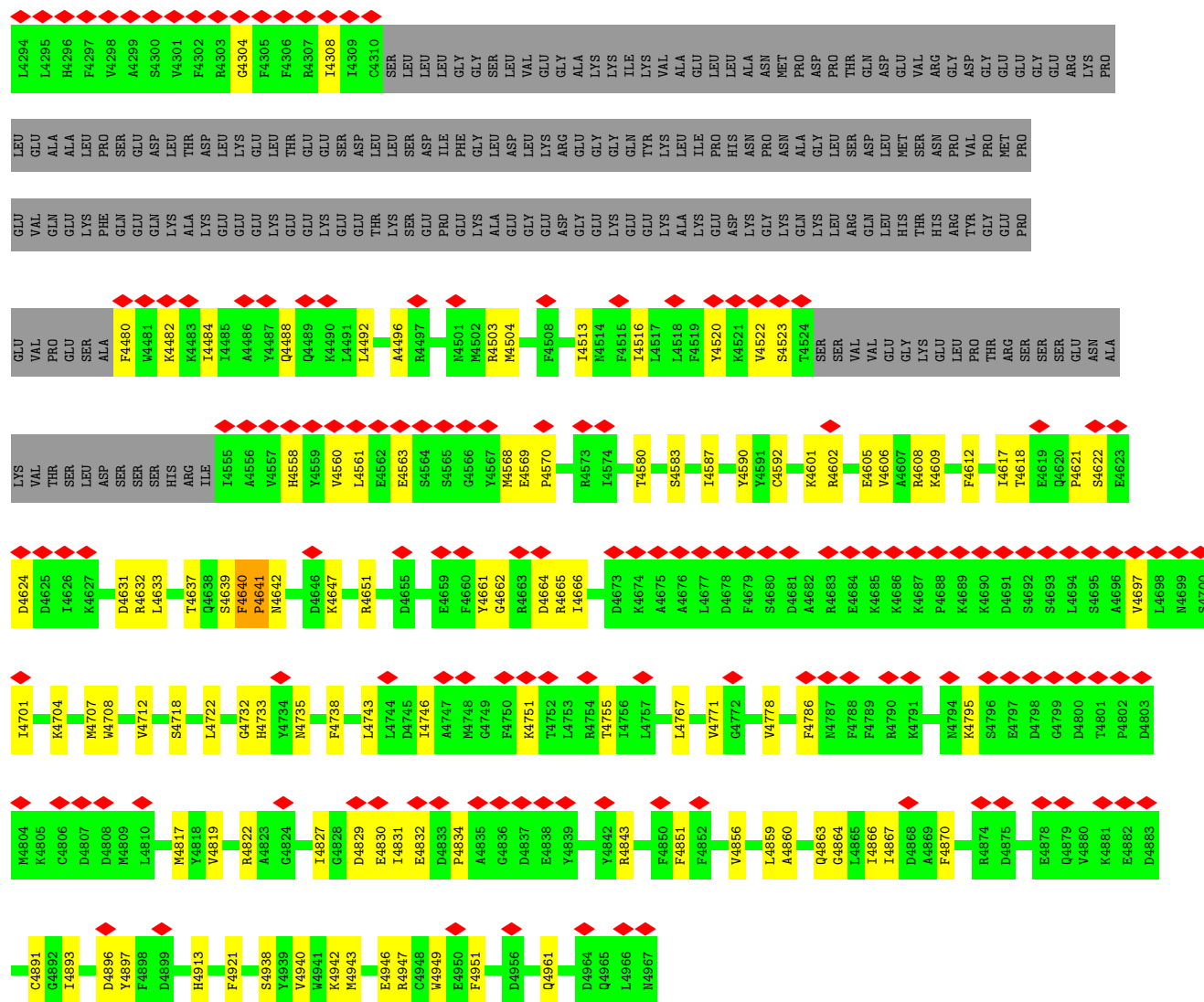
• Molecule 1: Ryanodine receptor 2



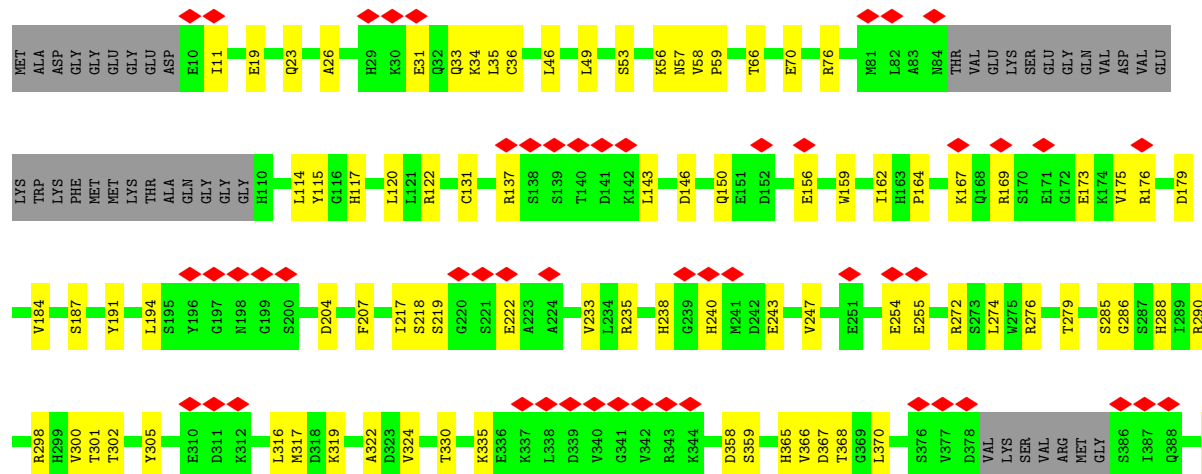


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S2992	G2993	C2994	H2995	A2996	S2997	N2998	K2999	F3000	K3001	K3002	M3003	V3004	T3005	S3006	L3007	F3008	C3009	K3010	V3013	R3016	H3017	R3018	L3019	S3020	N3024	D3025	A3026	T3027	G3028	L3029	V3030	N3031	C3032	L3033	H3034	L3035	L3036	G3037	Q3038	T3039	F3103	K3104	L3105	S3106	S3107	L3108	F3109	E3110	H3111	Q3114	H3115	K3116	F3117	K3118	E3119	D3120	L3121	L3122	L3123																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
Y2923	S2924	F2925	L2926	Q2927	Q2928	S2929	L2929	I2930	R2931	Y2932	V2933	D2934	E2935	A2936	H2937	Q2938	Y2939	T2940	L2941	E2942	F2943	D2944	G2945	G2946	S2947	R2948	G2949	K2950	G2951	E2952	H2953	F2954	P2955	Y2956	K2961	K2965	V2966	V2967	L2968	P2969	D2972	Q2973	Y2974	F2975	R2979	F2982	L2983	S2984	A2985	A2986	S2987	F2988	L2989	C2991																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
R2793	E2794	A2799	L2800	Y2801	R2802	ARG	THR	ARG	THR	ILE	ASP	GLN	THR	SER	GLN	VAL	SER	VAL	ASP	ALA	HIS	G2820	Y2821	S2822	F2823	R2824	A2825	L2826	D2827	M2828	P2755	L2756	K2757	K2758	P2759	Y2760	K2761	R2835	L2836	L2837	H2838	A2841	E2842	M2843	A2844	A2845	E2846	Y2848	H2849	K2854	K2855	M2858	E2859																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
L2860	E2861	S2862	K2863	G2864	G2865	G2866	M2867	H2868	F2869	L2870	P2873	Y2874	D2875	T2876	L2877	T2878	A2879	K2880	E2881	K2882	A2883	K2884	D2885	R2886	E2887	K2888	A2889	K2890	D2891	I2892	L2893	K2894	F2895	L2896	Q2897	I2898	M2899	G2900	Y2901	A2902	R2905	G2906	F2907	K2908	L2909	E2910	L2911	L2912	D2913	T2914	P2915	S2916	I2917	R2920	A2922																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
Y2923	S2924	F2925	L2926	Q2927	Q2928	S2929	L2929	I2930	R2931	Y2932	V2933	D2934	E2935	A2936	H2937	Q2938	Y2939	T2940	L2941	E2942	F2943	D2944	G2945	G2946	S2947	R2948	G2949	K2950	G2951	E2952	H2953	F2954	P2955	Y2956	K2961	K2965	V2966	V2967	L2968	P2969	D2972	Q2973	Y2974	F2975	R2979	F2982	L2983	S2984	A2985	A2986	S2987	F2988	L2989	C2991																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
S2992	G2993	C2994	H2995	A2996	S2997	N2998	K2999	F3000	K3001	K3002	M3003	V3004	T3005	S3006	L3007	F3008	C3009	K3010	V3013	R3016	H3017	R3018	L3019	S3020	N3024	D3025	A3026	T3027	G3028	L3029	V3030	N3031	C3032	L3033	H3034	L3035	L3036	G3037	Q3038	T3039	F3103	K3104	L3105	S3106	S3107	L3108	F3109	E3110	H3111	Q3114	H3115	K3116	F3117	K3118	E3119	D3120	L3121	L3122	L3123																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
E1985	C1986	P1989	E1990	E1991	I1992	L1996	E2010	LEU	ASP	GLU	ASP	GLY	SER	LEU	LEU	ASP	GLY	ASN	ASP	LEU	THR	ILE	ARG	GLY	ARG	LEU	LEU	SER	LEU	VAL	GLU	LYS	VAL	THR	LEU	LYS	LYS	LYS	GLN	ALA	GLU	LYS	PRO	VAL	GLU	SER	ASP	SER	K2053	K2054	S2055	L2061	L2062																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
L2080	L2087	Q2091	G2096	V2099	S2122	L2123	T2126	E2137	E2138	E2139	K2140	L2141	I2149	Y2156	Q2157	M2167	M2172	M2176	N2177	V2178	L2179	G2180	G2181	G2182	E2183	S2184	K2185	E2186	I2187	M2192	Y2202	T2206	S2207	R2208	M2214	F2215	Y2220	E2223	V2227	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	E2295	E2296	E2297	E2298	E2299	E2300	E2301	E2302	E2303	E2304	E2305	E2306	E2307	E2308	E2309	E2310	E2311	E2312	E2313	E2314	E2315	E2316	E2317	E2318	E2319	E2320	E2321	E2322	E2323	E2324	E2325	E2326	E2327	E2328	E2329	E2330	E2331	E2332	E2333	E2334	E2335	E2336	E2337	E2338	E2339	E2340	E2341	E2342	E2343	E2344	E2345	E2346	E2347	E2348	E2349	E2350	E2351	E2352	E2353	E2354	E2355	E2356	E2357	E2358	E2359	E2360	E2361	E2362	E2363	E2364	E2365	E2366	E2367	E2368	E2369	E2370	E2371	E2372	E2373	E2374	E2375	E2376	E2377	E2378	E2379	E2380	E2381	E2382	E2383	E2384	E2385	E2386	E2387	E2388	E2389	E2390	E2391	E2392	E2393	E2394	E2395	E2396	E2397	E2398	E2399	E2400	E2401	E2402	E2403	E2404	E2405	E2406	E2407	E2408	E2409	E2410	E2411	E2412	E2413	E2414	E2415	E2416	E2417	E2418	E2419	E2420	E2421	E2422	E2423	E2424	E2425	E2426	E2427	E2428	E2429	E2430	E2431	E2432	E2433	E2434	E2435	E2436	E2437	E2438	E2439	E2440	E2441	E2442	E2443	E2444	E2445	E2446	E2447	E2448	E2449	E2450	E2451	E2452	E2453	E2454	E2455	E2456	E2457	E2458	E2459	E2460	E2461	E2462	E2463	E2464	E2465	E2466	E2467	E2468	E2469	E2470	E2471	E2472	E2473	E2474	E2475	E2476	E2477	E2478	E2479	E2480	E2481	E2482	E2483	E2484	E2485	E2486	E2487	E2488	E2489	E2490	E2491	E2492	E2493	E2494	E2495	E2496	E2497	E2498	E2499	E2500	E2501	E2502	E2503	E2504	E2505	E2506	E2507	E2508	E2509	E2510	E2511	E2512	E2513	E2514	E2515	E2516	E2517	E2518	E2519	E2520	E2521	E2522	E2523	E2524	E2525	E2526	E2527	E2528	E2529	E2530	E2531	E2532	E2533	E2534	E2535	E2536	E2537	E2538	E2539	E2540	E2541	E2542	E2543	E2544	E2545	E2546	E2547	E2548	E2549	E2550	E2551	E2552	E2553	E2554	E2555	E2556	E2557	E2558	E2559	E2560	E2561	E2562	E2563	E2564	E2565	E2566	E2567	E2568	E2569	E2570	E2571	E2572	E2573	E2574	E2575	E2576	E2577	E2578	E2579	E2580	E2581	E2582	E2583	E2584	E2585	E2586	E2587	E2588	E2589	E2590	E2591	E2592	E2593	E2594	E2595	E2596	E2597	E2598	E2599	E2600	E2601	E2602	E2603	E2604	E2605	E2606	E2607	E2608	E2609	E2610	E2611	E2612	E2613	E2614	E2615	E2616	E2617	E2618	E2619	E2620	E2621	E2622	E2623	E2624	E2625	E2626	E2627	E2628	E2629	E2630	E2631	E2632	E2633	E2634	E2635	E2636	E2637	E2638	E2639	E2640	E2641	E2642	E2643	E2644	E2645	E2646	E2647	E2648	E2649	E2650	E2651	E2652	E2653	E2654	E2655	E2656	E2657	E2658	E2659	E2660	E2661	E2662	E2663	E2664	E2665	E2666	E2667	E2668	E2669	E2670	E2671	E2672	E2673	E2674	E2675	E2676	E2677	E2678	E2679	E2680	E2681	E2682	E2683	E2684	E2685	E2686	E2687	E2688	E2689	E2690	E2691	E2692	E2693	E2694	E2695	E2696	E2697	E2698	E2699	E2700	E2701	E2702	E2703	E2704	E2705	E2706	E2707	E2708	E2709	E2710	E2711	E2712	E2713	E2714	E2715	E2716	E2717	E2718	E2719	E2720	E2721	E2722	E2723	E2724	E2725	E2726	E2727	E2728	E2729	E2730	E2731	E2732	E2733	E2734	E2735	E2736	E2737	E2738	E2739	E2740	E2741	E2742	E2743	E2744	E2745	E2746	E2747	E2748	E2749	E2750	E2751	E2752	E2753	E2754	E2755	E2756	E2757	E2758	E2759	E2760	E2761	E2762	E2763	E2764	E2765	E2766	E2767	E2768	E2769	E2770	E2771	E2772	E2773	E2774	E2775	E2776	E2777	E2778	E2779	E2780	E2781	E2782	E2783	E2784	E2785	E2786	E2787	E2788	E2789	E2790	E2791	E2792	E2793	E2794	E2795	E2796	E2797	E2798	E2799	E2800	E2801	E2802	E2803	E2804	E2805	E2806	E2807	E2808	E2809	E2810	E2811	E2812	E2813	E2814	E2815	E2816	E2817	E2818	E2819	E2820	E2821	E2822	E2823	E2824	E2825	E2826	E2827	E2828	E2829	E2830	E2831	E2832	E2833	E2834	E2835	E2836	E2837	E2838	E2839	E2840	E2841	E2842	E2843	E2844	E2845	E2846	E2847	E2848	E2849	E2850	E2851	E2852	E2853	E2854	E2855	E2856	E2857	E2858	E2859	E2860	E2861	E2862	E2863	E2864	E2865	E2866	E2867	E2868	E2869	E2870	E2871	E2872	E2873	E2874	E2875	E2876	E2877	E2878	E2879	E2880	E2881	E2882	E2883	E2884	E2885	E2886	E2887	E2888	E2889	E2890	E2891	E2892	E2893	E2894	E2895	E2896	E2897	E2898	E2899	E2900	E2901	E2902	E2903	E2904	E2905	E2906	E2907	E2908	E2909	E2910	E2911	E2912	E2913	E2914	E2915	E2916	E2917	E2918	E2919	E2920	E2921	E2922	E2923	E2924	E2925	E2926	E2927	E2928	E2929	E2930	E2931	E2932	E2933	E2934	E2935	E2936	E2937	E2938	E2939	E2940	E2941	E2942	E2943	E2944	E2945	E2946	E2947	E2948	E2949	E2950	E2951	E2952	E2953	E2954	E2955	E2956	E2957	E2958	E2959	E2960	E2961	E2962	E2963	E2964	E2965	E2966	E2967	E2968	E2969	E2970	E2971	E2972	E2973	E2974	E2975	E2976	E2977	E2978	E2979	E2980	E2981	E2982	E2983	E2984	E2985	E2986	E2987	E2988	E2989	E2990	E2991	E2992	E2993	E2994	E2995	E2996	E2997	E2998	E2999	E3000	E3001	E3002	E3003	E3004	E3005	E3006	E3007	E3008	E3009	E3010	E3011	E3012	E3013	E3014	E3015	E3016	E3017	E3018	E3019	E3020	E3021	E3022	E3023	E3024	E3025	E3026	E3027	E3028	E3029	E3030	E3031	E3032	E3033	E3034	E3035	E3036	E3037	E3038	E3039	E3040	E3041	E3042	E3043	E3044	E3045	E3046	E3047	E3048	E3049	E3050	E3051	E3052	E3053	E3054	E3055	E3056	E3057	E3058	E3059	E3060	E3061	E3062	E3063	E3064	E3065	E3066	E3067	E3068	E3069	E3070	E3071	E3072	E3073	E3074	E3075	E3076	E3077	E3078	E3079	E3080	E3081	E3082	E3083	E3084	E3085	E3086	E3087	E3088	E3089	E3090	E3091	E3092	E3093	E3094	E3095	E3096	E3097	E3098	E3099	E3100	E3101	E3102	E3103	E3104	E3105	E3



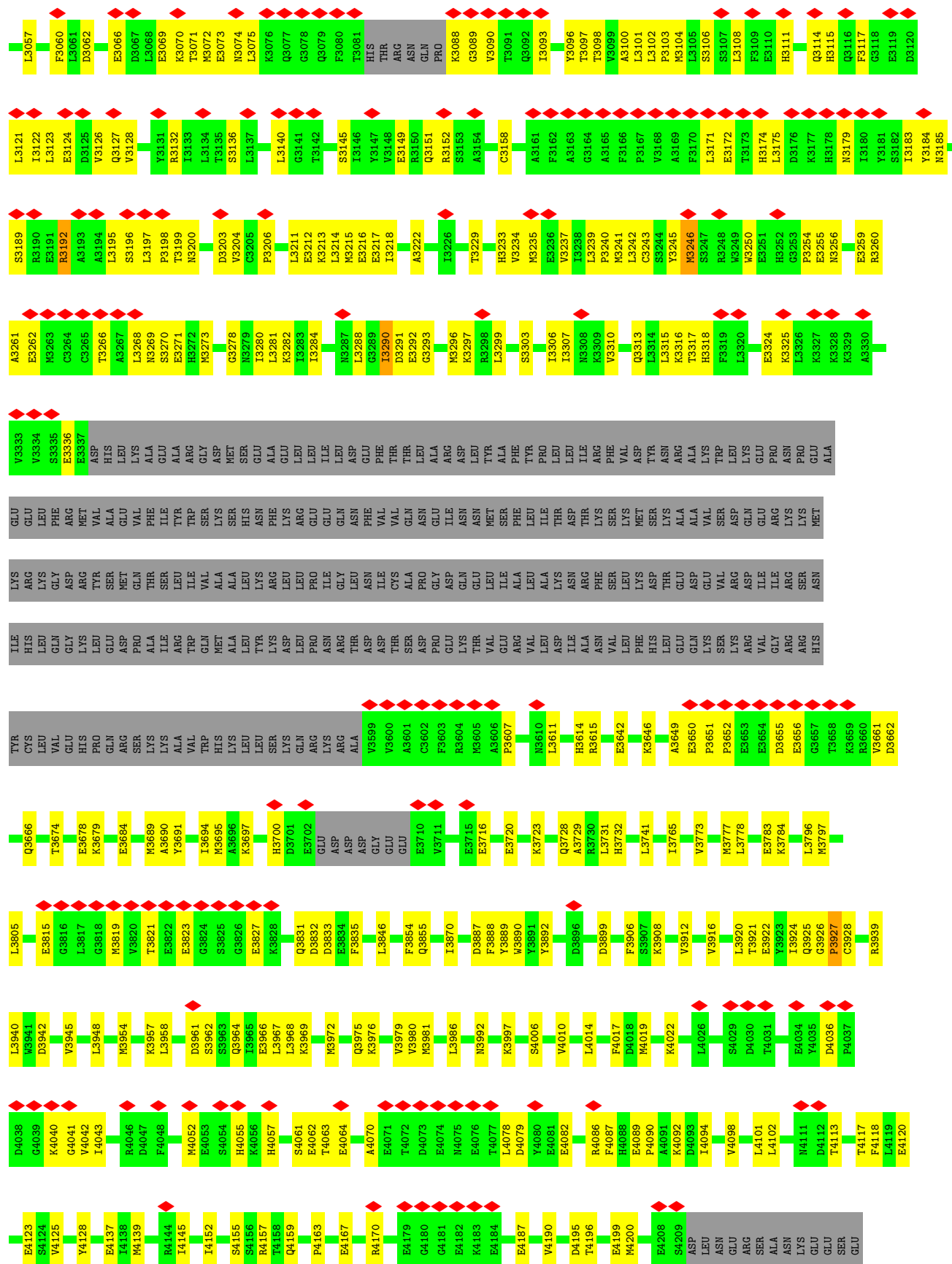


• Molecule 1: Ryanodine receptor 2









E4378	S4795	S4692	K4609	GLU	ARG	SER	ARG	F4283
E4379	S4796	S4693	F4612	LEU	GLN	ASP	GLY	F4284
V4380	E4797	L4694		THR	HIS	LEU	GLY	S4285
K4881	D4798	S4695	L4617	ARG	THR	SER	GLY	S4286
E4882	G4799	A4696	T4618	SER	HIS	ASN	GLY	Y4287
D4883	D4800	V4697	E4619	SER	ARG	PRO	GLY	W4288
	T4801	L4698	Q4620	SER	TYR	VAL	GLU	S4289
C4891	P4802	M4699	P4621	GLY	GLY	PRO	ARG	F4291
G4892	D4803	S4700	S4622	ASN	GLY	MET	GLY	I4290
I4893	M4804	I4701	E4623	ALA	PRO	PRO	PRO	F4292
D4896	C4806	K4704	D4624	VAL	VAL	VAL	GLY	M4292
Y4897	D4807	V4705	D4625	THR	PRO	GLN	ALA	T4293
D4899	D4808	W4707	L4626	SER	GLY	GLY	ALA	L4294
		W4708	K4627	ASP	ALA	PHE	LEU	L4295
	M4817	V4712	D4631	SER	F4480	GLN	SER	H4296
	V4819	S4718	R4632	SER	W4481	GLN	GLY	F4297
			L4633	HIS	K4482	LYS	ASP	T4298
			T4637	ARG	K4483	THR	LEU	V4241
				ILE	I4484	LYS	ASP	A4299
					I4555	GLY	LEU	S4300
					A4556	GLU	LEU	V4301
					V4557	GLY	GLY	F4302
					H4558	LYS	LEU	R4303
					Y4559	GLU	THR	G4304
					V4560	GLY	GLY	F4305
					L4561	GLU	ASP	A4247
					E4562	THR	LEU	R4307
					E4563	LYS	LEU	I4308
					E4564	SER	ASP	I4309
					S4565	GLU	ASP	C4310
					F4660	PRO	ILE	SER
					Y4661	GLY	PHE	LEU
					G4662	ALA	GLY	LEU
					R4663	GLY	LEU	LEU
					D4664	GLY	ASP	GLY
					R4665	GLY	GLY	GLY
					I4666	ASP	LEU	SER
						P4570	ARG	LEU
							GLY	VAL
							GLY	L4261
							GLY	L4262
							GLN	S4263
							TYR	LYS
							ALA	L4264
							ALA	LYS
							ILE	LYS
							VAL	VAL
							ASP	ALA
							ASN	GLY
							PRO	LEU
							ASN	LEU
							GLN	K4270
							ALA	ALA
							GLY	V4271
							ASN	K4272
							MET	PRO
							ASP	K4273
							THR	M4274
							PRO	T4275
							GLN	V4276
							ASP	K4277
							GLY	D4278
							VAL	M4279
								V4280
								T4281
								M4282

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	18232	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	58	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.473	Depositor
Minimum map value	-0.016	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.12	Depositor
Map size (Å)	424.96, 424.96, 424.96	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.15	0/34511	0.43	7/46614 (0.0%)
1	B	0.15	0/34511	0.43	7/46614 (0.0%)
1	C	0.15	0/34511	0.43	7/46614 (0.0%)
1	D	0.15	0/34511	0.43	7/46614 (0.0%)
All	All	0.15	0/138044	0.43	28/186456 (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
1	A	0	3
1	B	0	3
1	C	0	3
1	D	0	3
All	All	0	12

There are no bond length outliers.

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	1948	MET	CB-CG-SD	7.13	134.09	112.70
1	B	1948	MET	CB-CG-SD	7.12	134.07	112.70
1	C	1948	MET	CB-CG-SD	7.12	134.07	112.70
1	A	1948	MET	CB-CG-SD	7.12	134.06	112.70
1	D	880	ARG	N-CA-CB	7.09	120.51	109.94

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	3192	ARG	Sidechain
1	A	4640	PHE	Peptide
1	A	880	ARG	Sidechain
1	B	3192	ARG	Sidechain
1	B	880	ARG	Sidechain

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	33771	0	33455	844	0
1	B	33771	0	33455	838	0
1	C	33771	0	33455	848	0
1	D	33771	0	33455	853	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	62	0	24	1	0
3	B	62	0	24	2	0
3	C	62	0	24	1	0
3	D	62	0	24	1	0
All	All	135336	0	133916	3298	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 12.

The worst 5 of 3298 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:4891:CYS:SG	1:B:4913:HIS:CE1	2.51	1.04
1:A:4891:CYS:SG	1:A:4913:HIS:CE1	2.51	1.02
1:D:4891:CYS:SG	1:D:4913:HIS:CE1	2.51	1.00
1:C:4891:CYS:SG	1:C:4913:HIS:CE1	2.51	1.00
1:C:3101:LEU:HA	1:C:3104:MET:HE2	1.49	0.94

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	4198/4967 (84%)	4085 (97%)	109 (3%)	4 (0%)	48	81
1	B	4198/4967 (84%)	4085 (97%)	109 (3%)	4 (0%)	48	81
1	C	4198/4967 (84%)	4085 (97%)	109 (3%)	4 (0%)	48	81
1	D	4198/4967 (84%)	4084 (97%)	110 (3%)	4 (0%)	48	81
All	All	16792/19868 (84%)	16339 (97%)	437 (3%)	16 (0%)	49	81

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2770	ILE
1	A	3927	PRO
1	A	4641	PRO
1	B	2770	ILE
1	B	3927	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	3434/4358 (79%)	3424 (100%)	10 (0%)	86	85
1	B	3708/4358 (85%)	3697 (100%)	11 (0%)	86	85
1	C	3708/4358 (85%)	3697 (100%)	11 (0%)	86	85
1	D	3708/4358 (85%)	3697 (100%)	11 (0%)	86	85
All	All	14558/17432 (84%)	14515 (100%)	43 (0%)	84	85

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	3121	LEU
1	D	1421	MET
1	C	3246	MET
1	D	880	ARG
1	D	1948	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 243 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	4961	GLN
1	D	3304	GLN
1	C	2316	ASN
1	D	3274	ASN
1	D	4636	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	ATP	A	5002	-	32,33,33	0.25	0	48,52,52	0.29	0
3	ATP	D	5002	-	32,33,33	0.25	0	48,52,52	0.29	0
3	ATP	D	5003	-	32,33,33	0.25	0	48,52,52	0.27	0
3	ATP	C	5002	-	32,33,33	0.25	0	48,52,52	0.29	0
3	ATP	C	5003	-	32,33,33	0.25	0	48,52,52	0.27	0
3	ATP	B	5002	-	32,33,33	0.26	0	48,52,52	0.29	0
3	ATP	B	5003	-	32,33,33	0.25	0	48,52,52	0.27	0
3	ATP	A	5003	-	32,33,33	0.25	0	48,52,52	0.27	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ATP	A	5002	-	-	6/22/38/38	0/3/3/3
3	ATP	D	5002	-	-	6/22/38/38	0/3/3/3
3	ATP	D	5003	-	-	9/22/38/38	0/3/3/3
3	ATP	C	5002	-	-	6/22/38/38	0/3/3/3
3	ATP	C	5003	-	-	9/22/38/38	0/3/3/3
3	ATP	B	5002	-	-	6/22/38/38	0/3/3/3
3	ATP	B	5003	-	-	9/22/38/38	0/3/3/3
3	ATP	A	5003	-	-	9/22/38/38	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 60 torsion outliers are listed below:

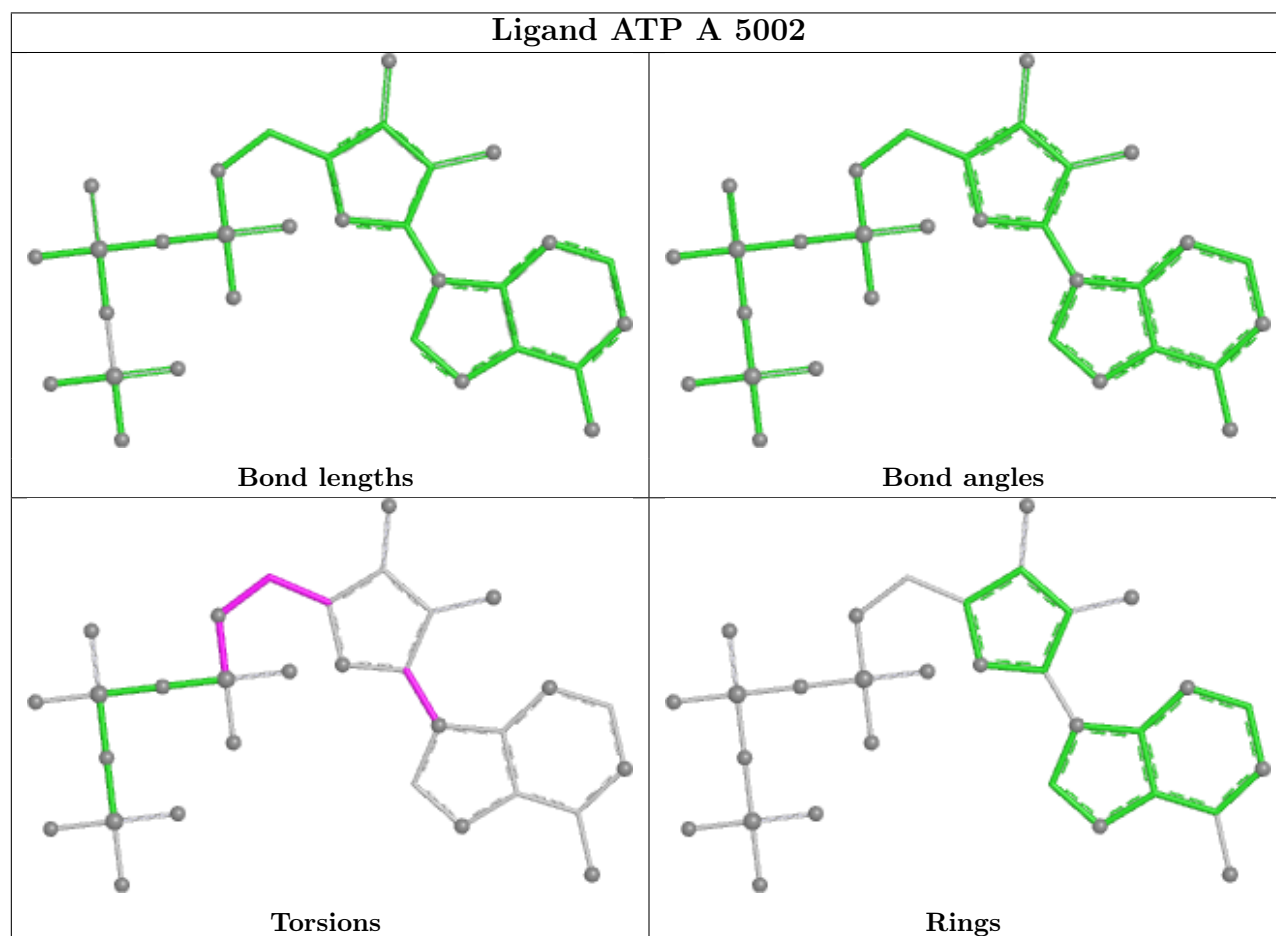
Mol	Chain	Res	Type	Atoms
3	A	5002	ATP	O4'-C4'-C5'-O5'
3	A	5002	ATP	C3'-C4'-C5'-O5'
3	A	5003	ATP	O4'-C4'-C5'-O5'
3	B	5002	ATP	O4'-C4'-C5'-O5'
3	B	5002	ATP	C3'-C4'-C5'-O5'

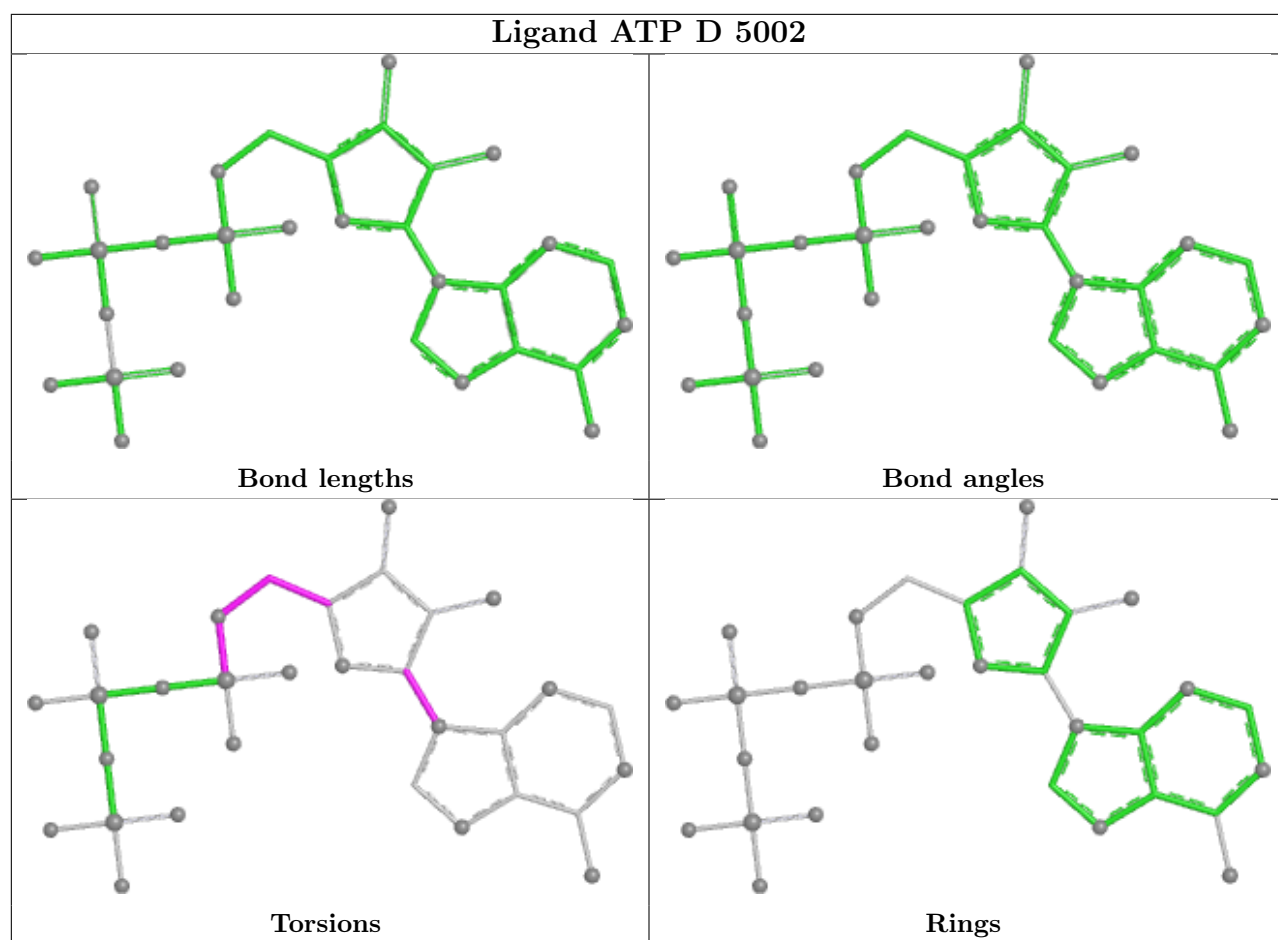
There are no ring outliers.

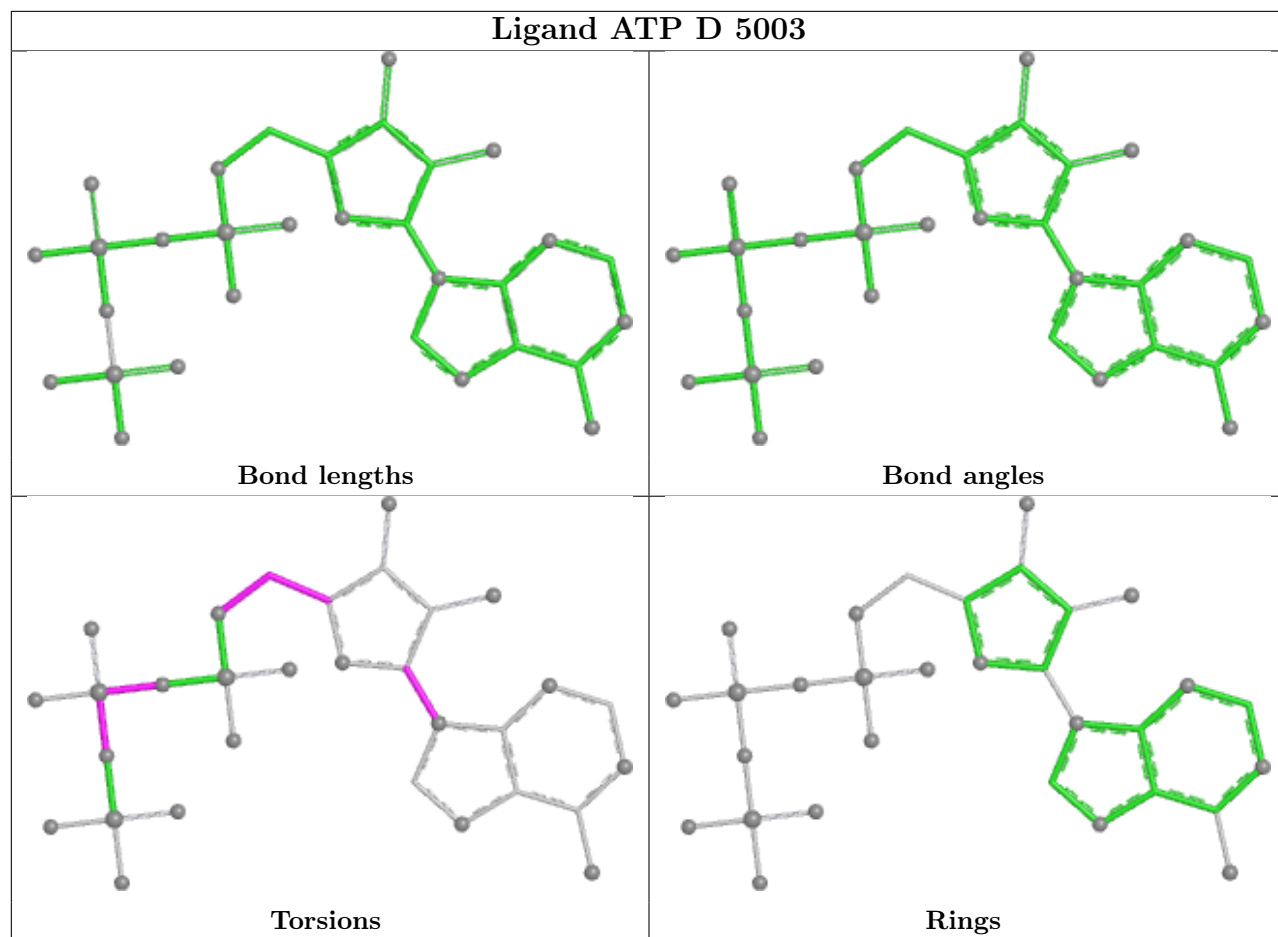
4 monomers are involved in 5 short contacts:

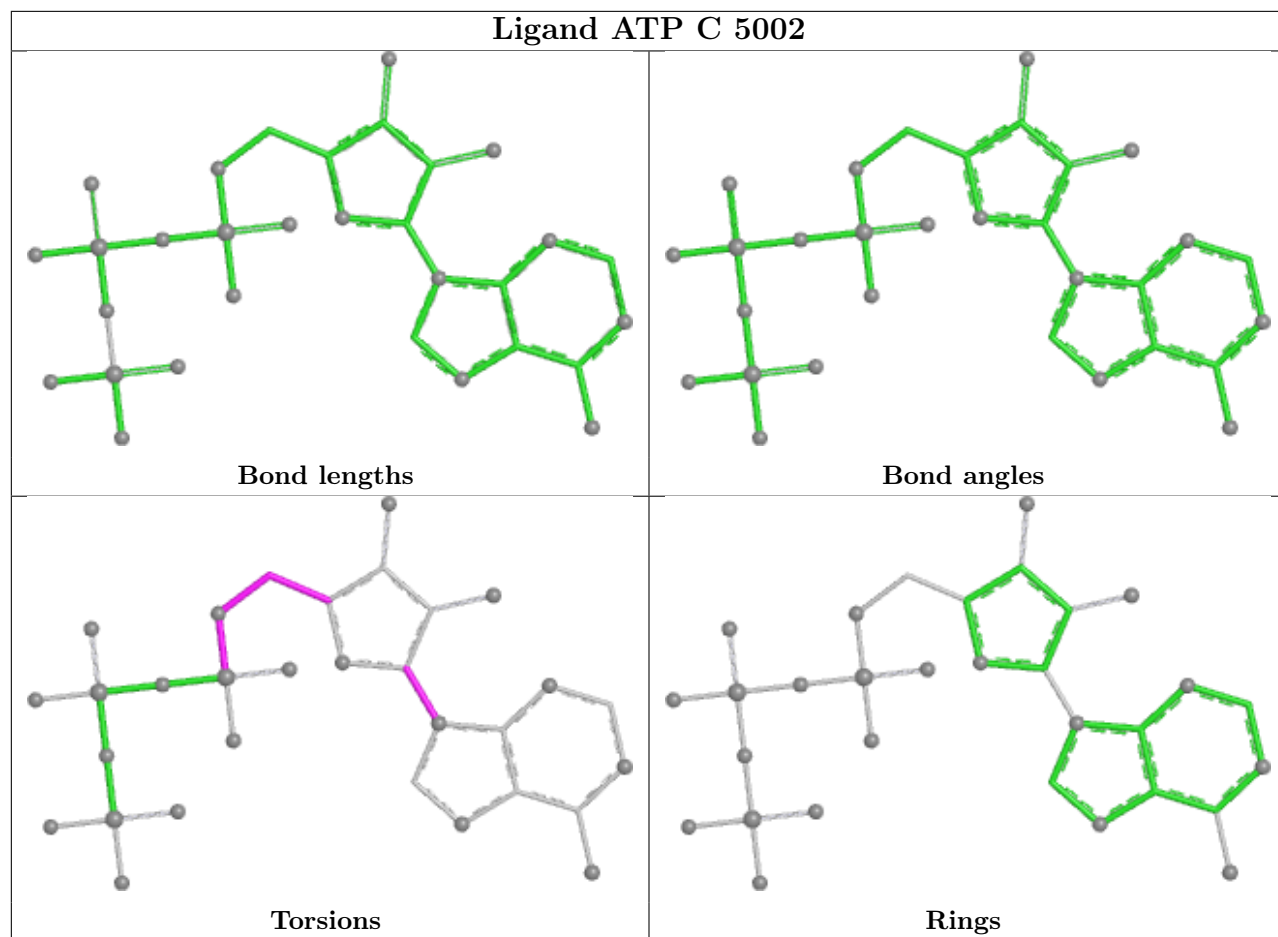
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	5003	ATP	1	0
3	C	5003	ATP	1	0
3	B	5003	ATP	2	0
3	A	5003	ATP	1	0

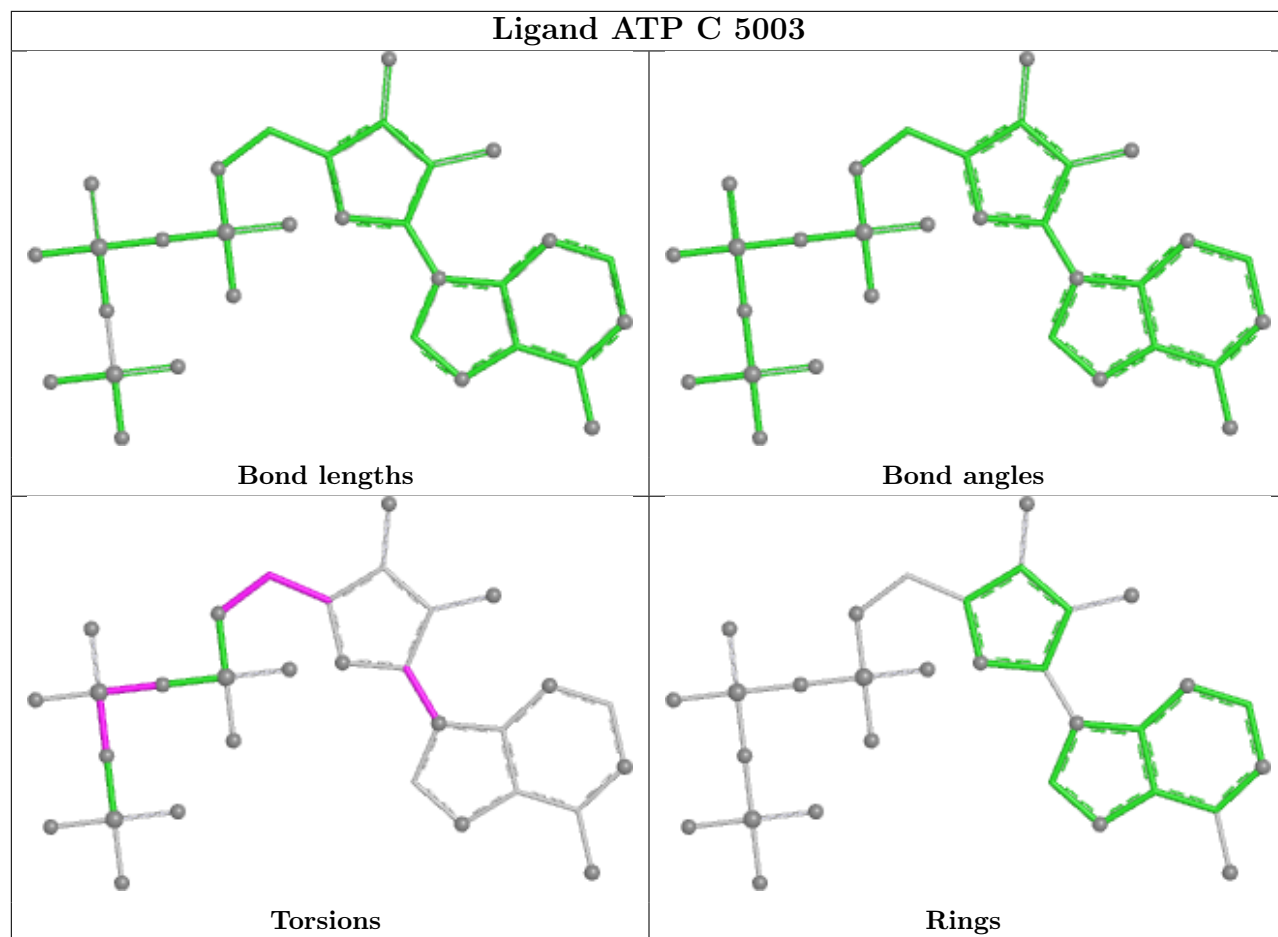
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

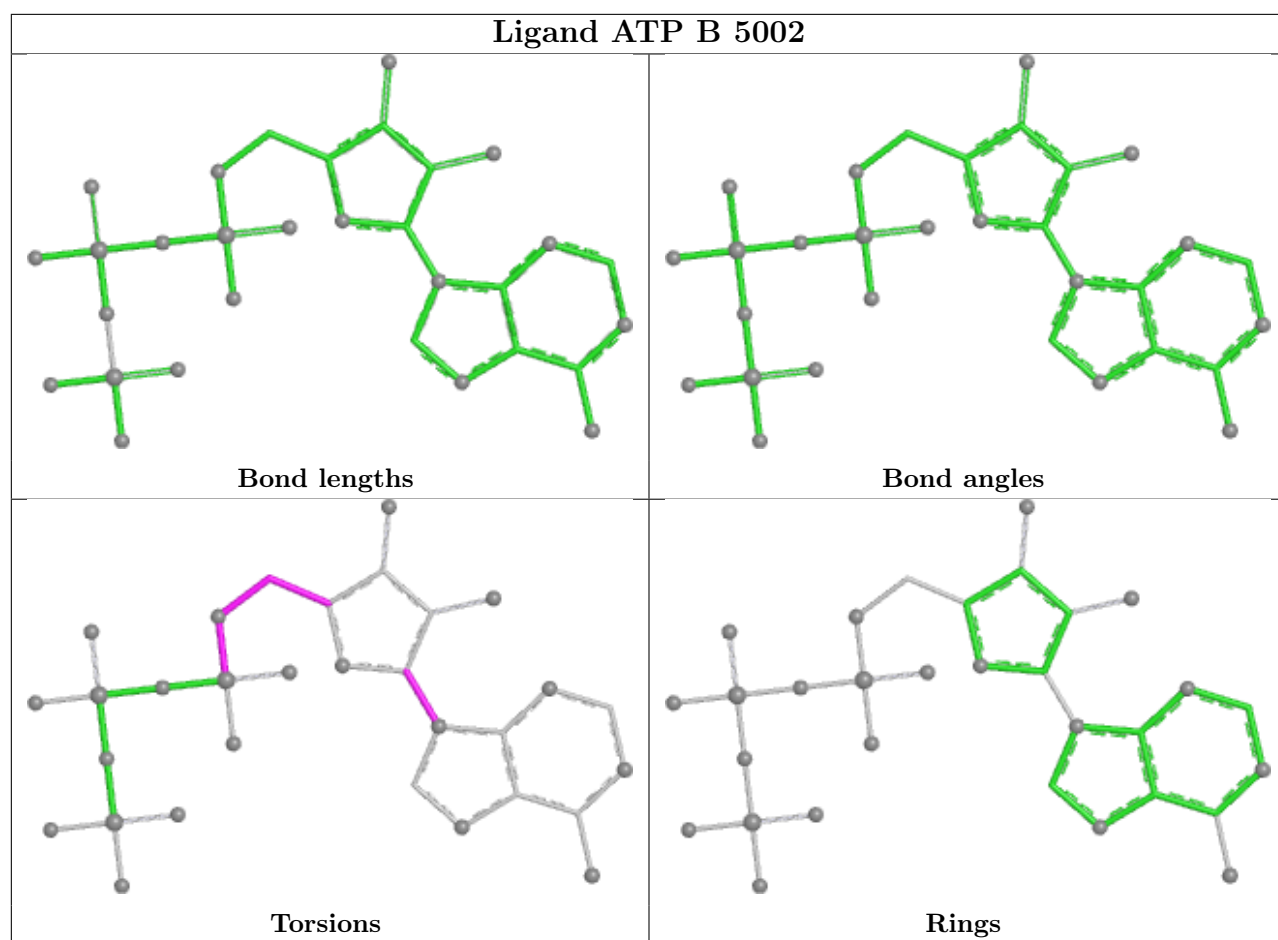


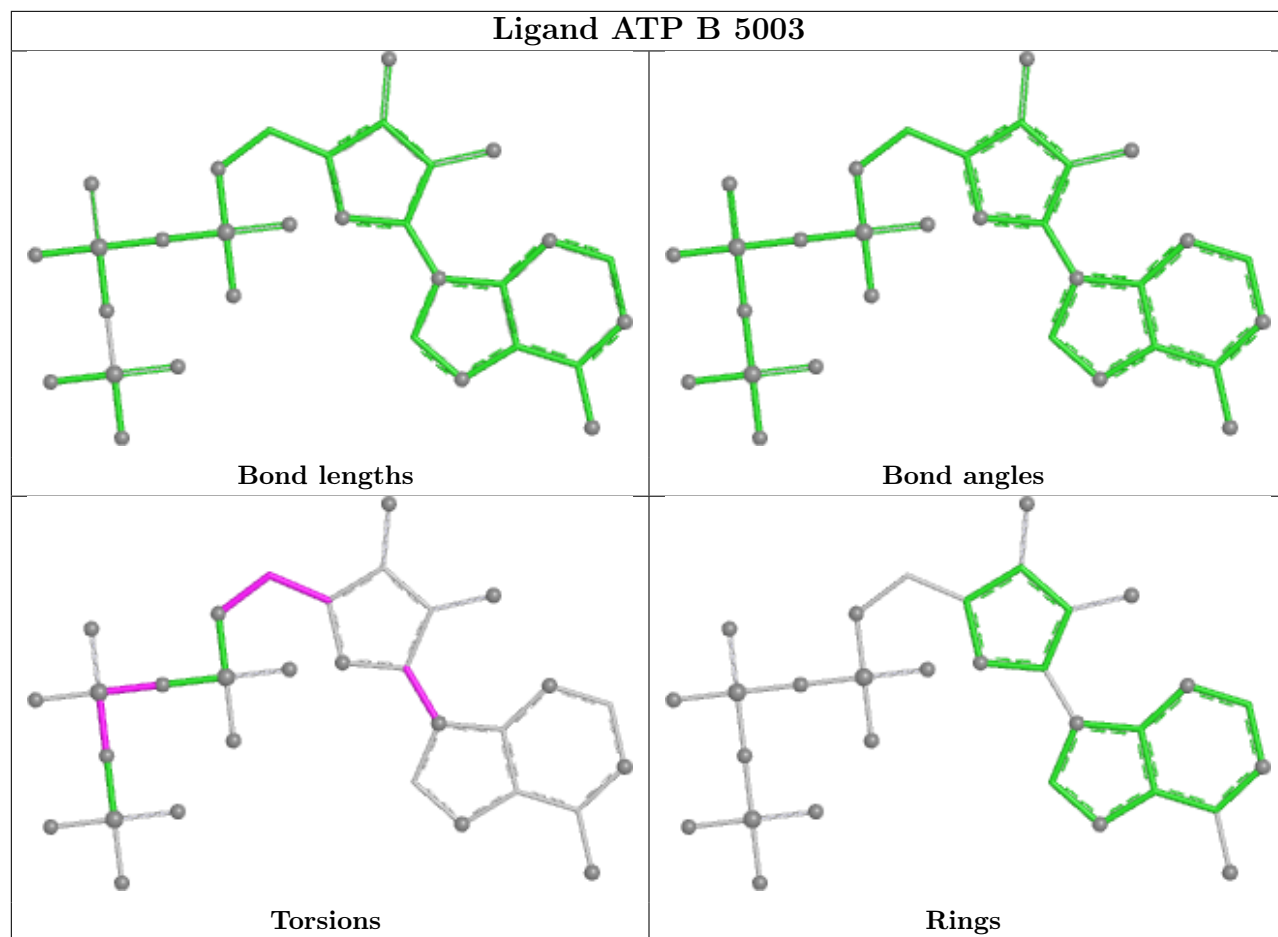


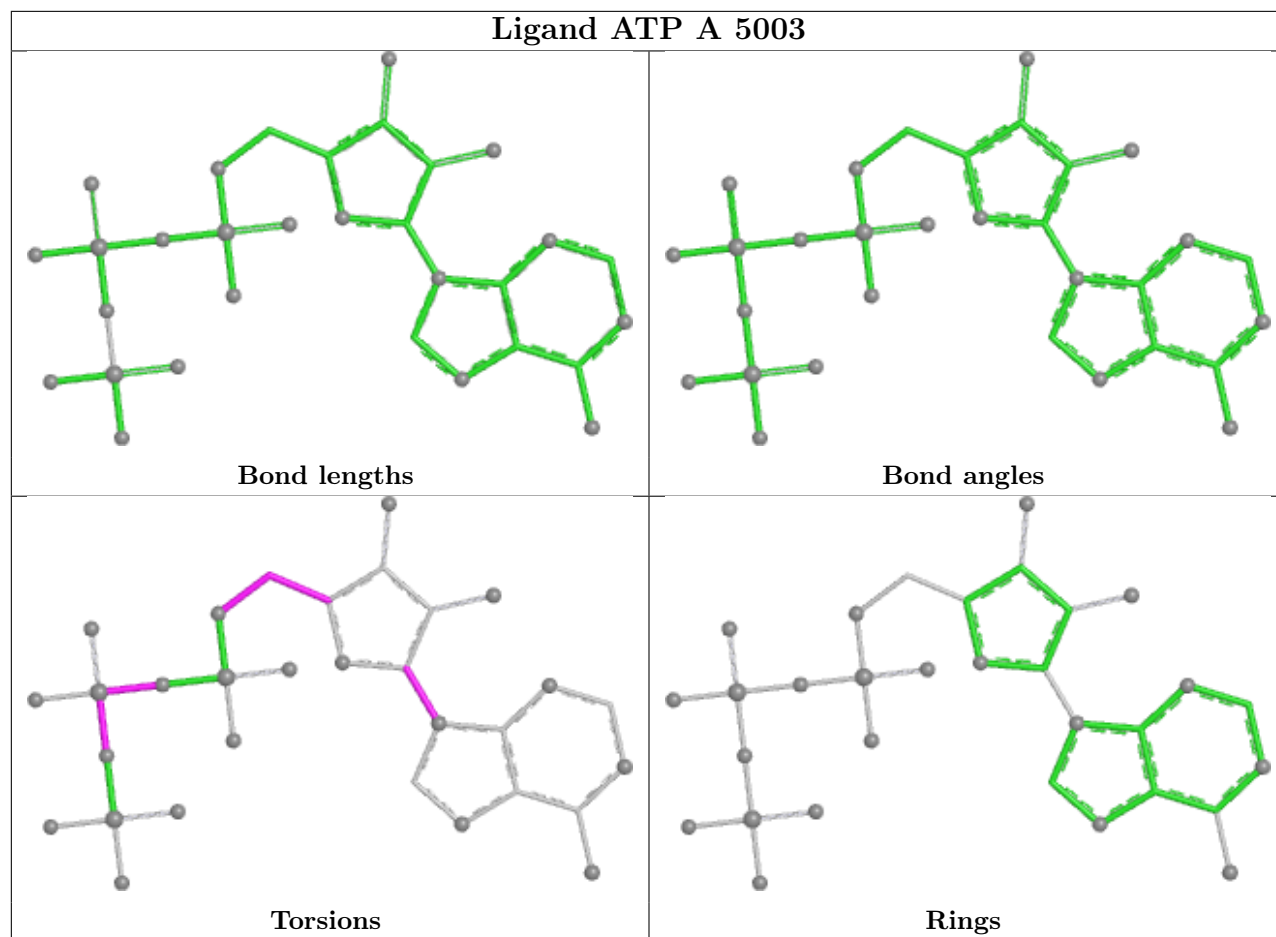












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

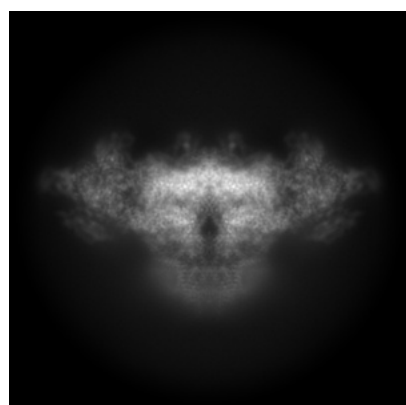
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42461. These allow visual inspection of the internal detail of the map and identification of artifacts.

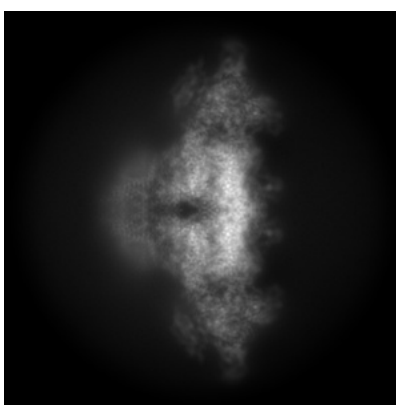
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

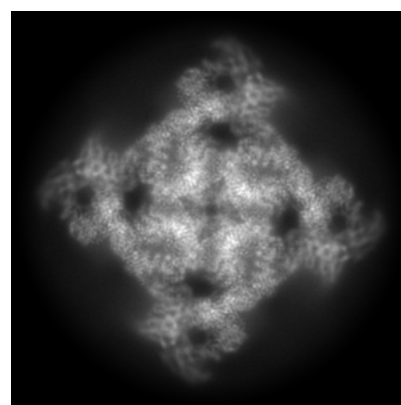
6.1.1 Primary map



X



Y

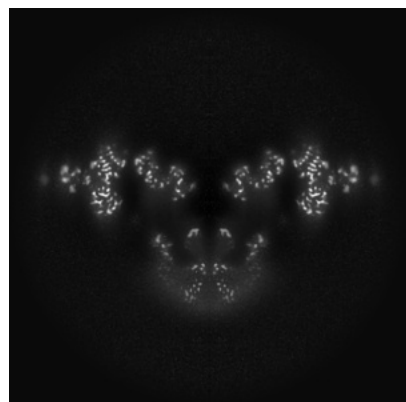


Z

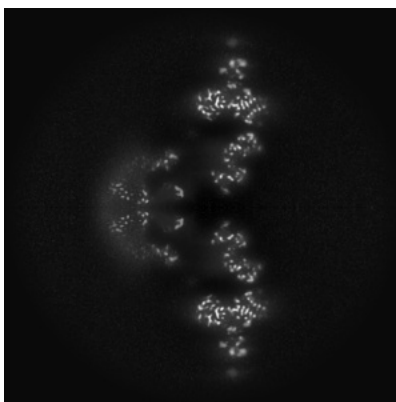
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

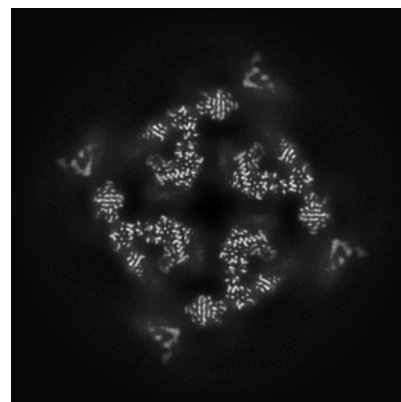
6.2.1 Primary map



X Index: 256



Y Index: 256

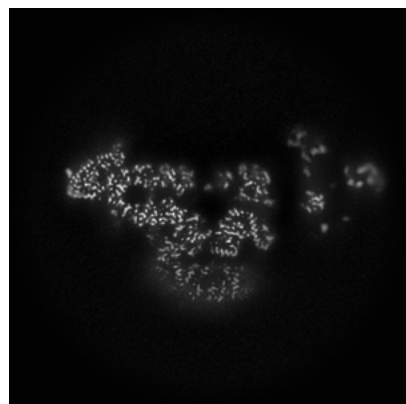


Z Index: 256

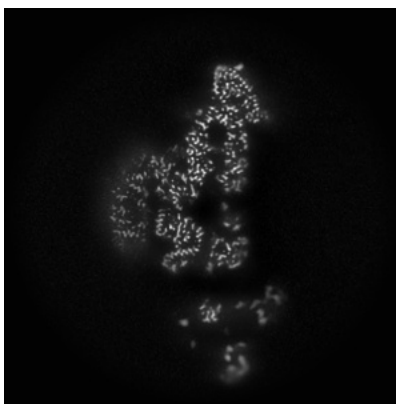
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

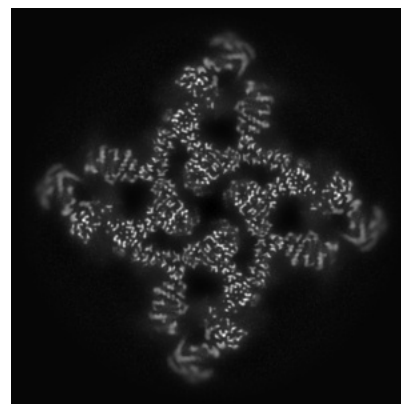
6.3.1 Primary map



X Index: 279



Y Index: 279



Z Index: 289

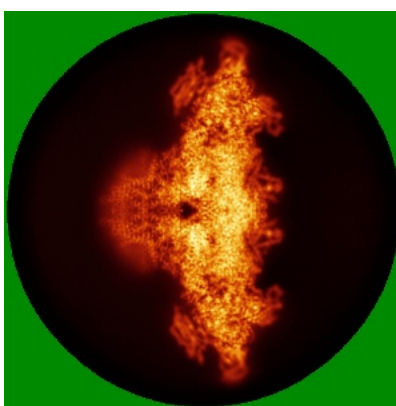
The images above show the largest variance slices of the map in three orthogonal directions.

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

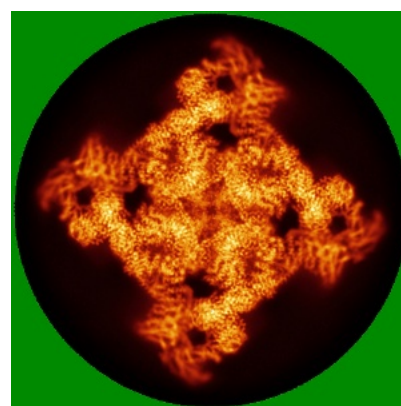
6.4.1 Primary map



X



Y

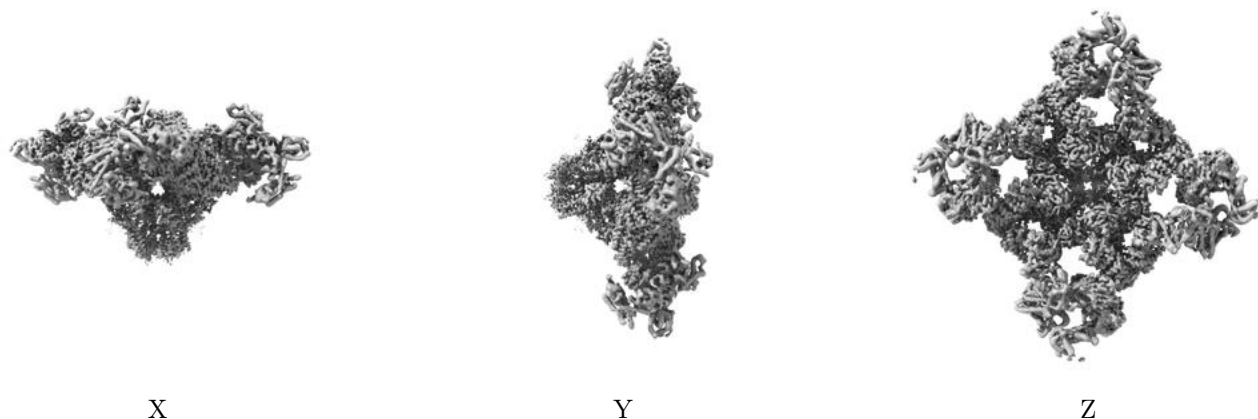


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.12. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

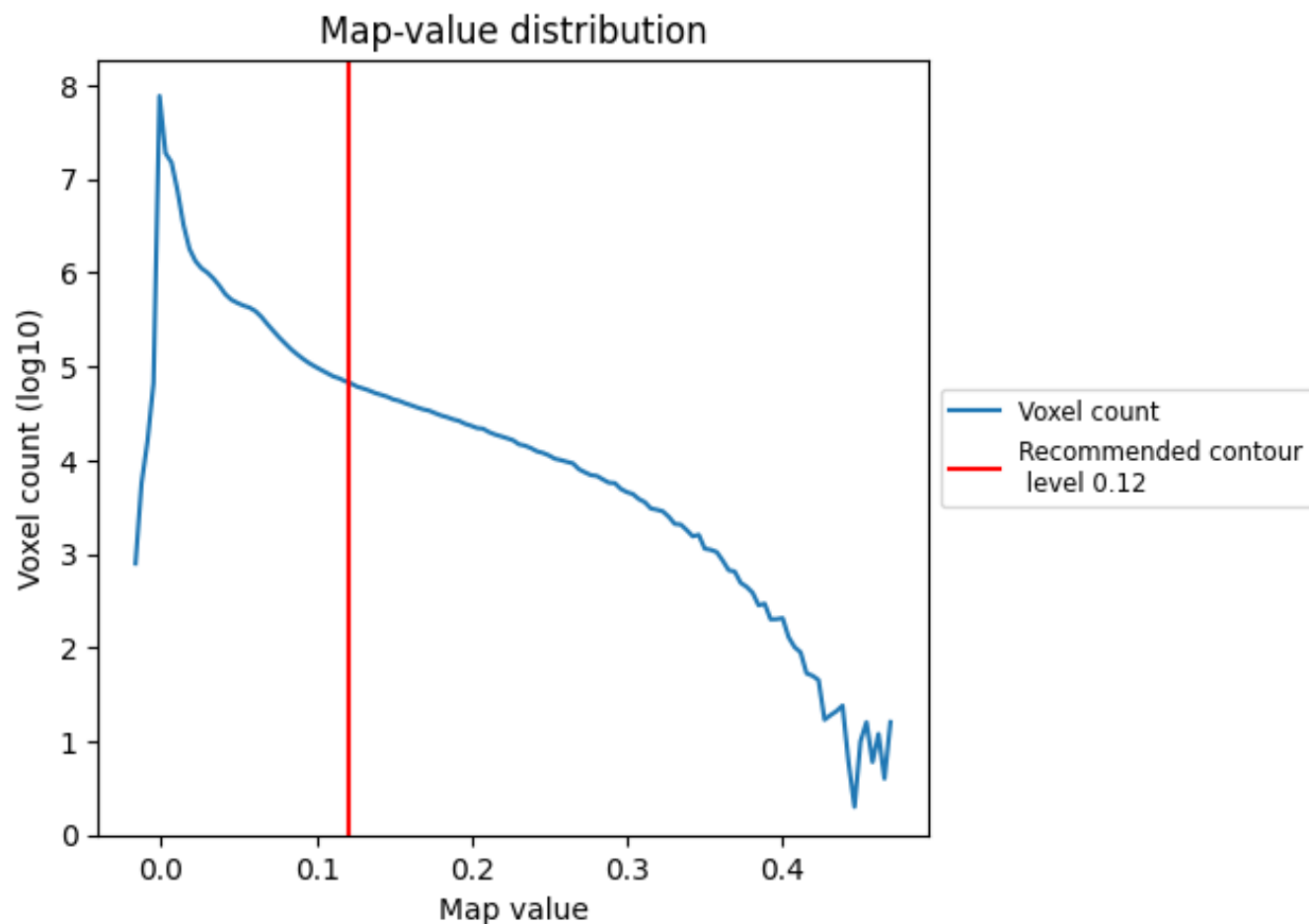
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

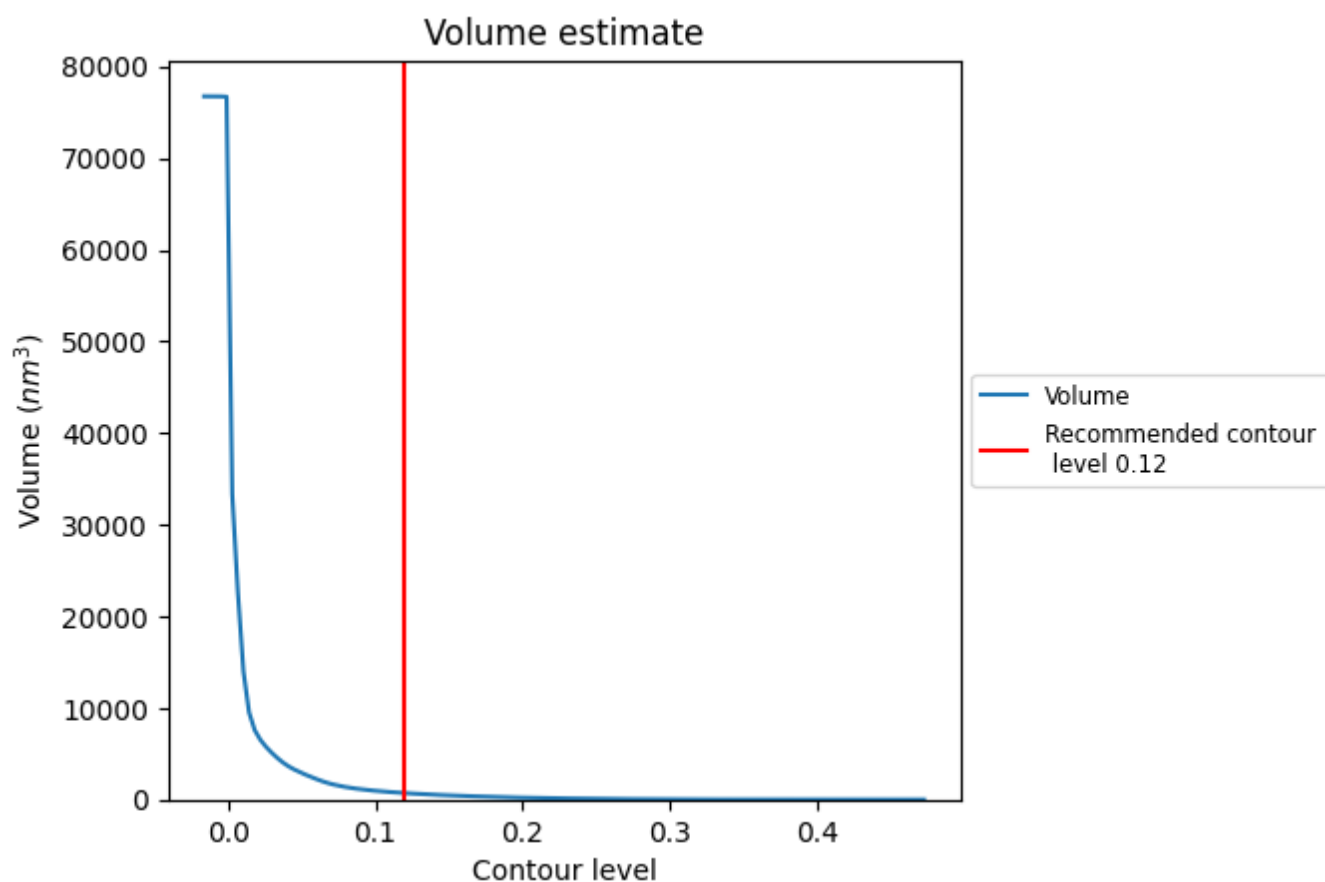
This section contains the results of statistical analysis of the map.

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.

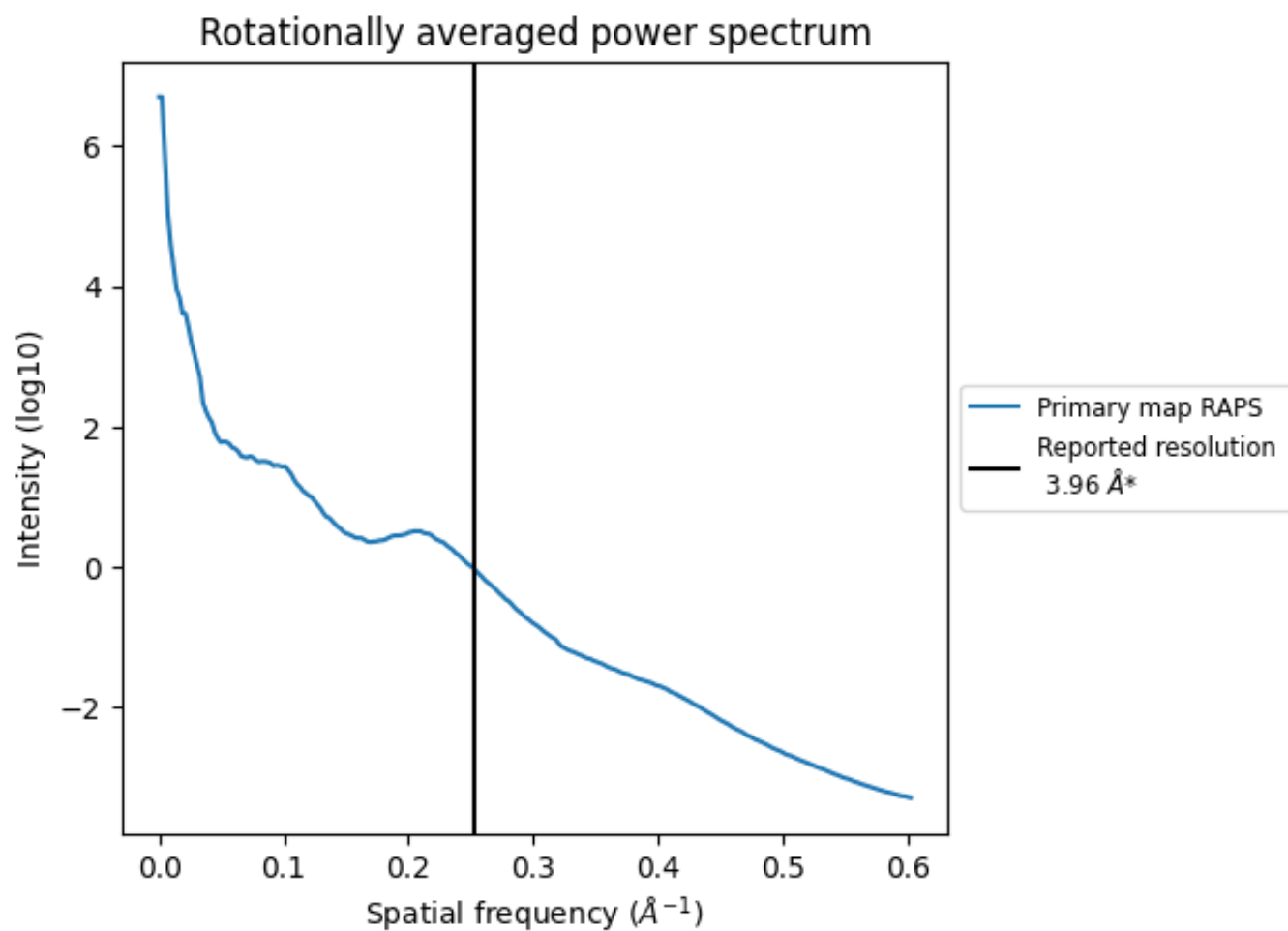
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 708 nm^3 ; this corresponds to an approximate mass of 640 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 0.253 Å⁻¹

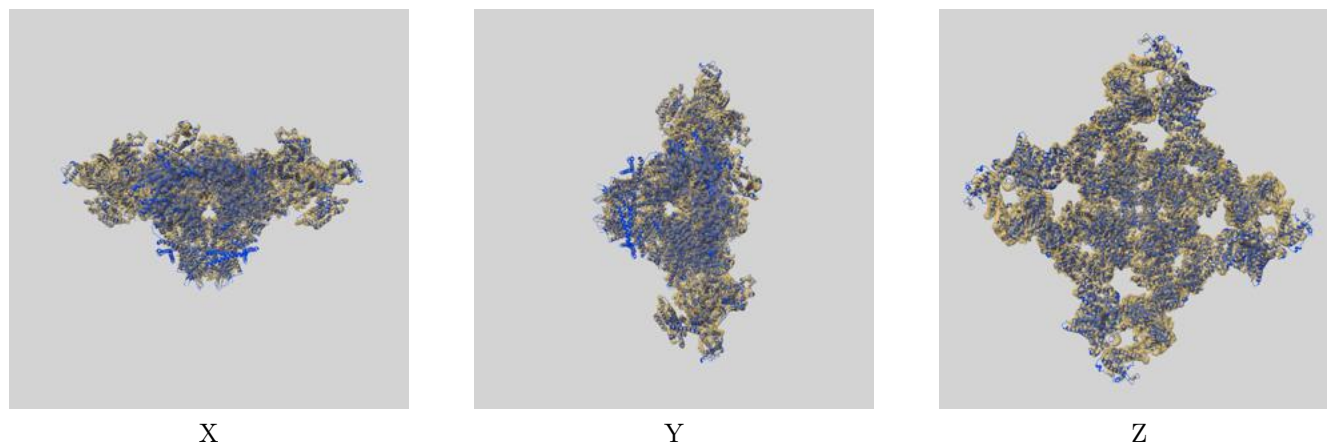
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

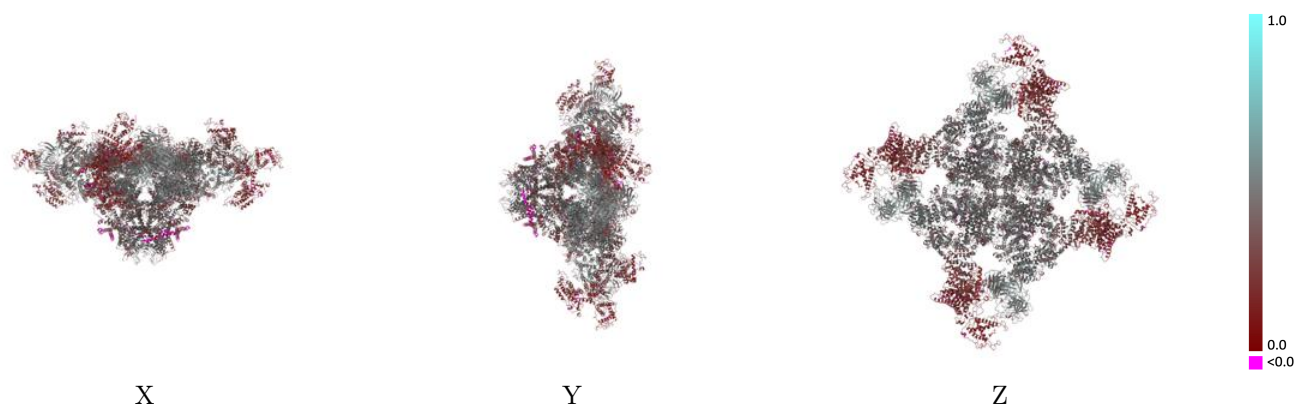
This section contains information regarding the fit between EMDB map EMD-42461 and PDB model 8UQ5. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



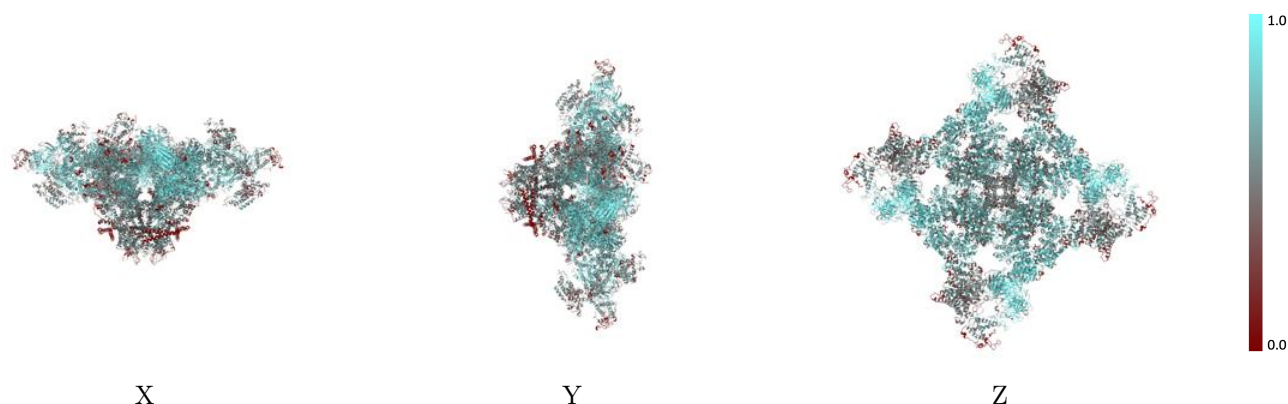
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



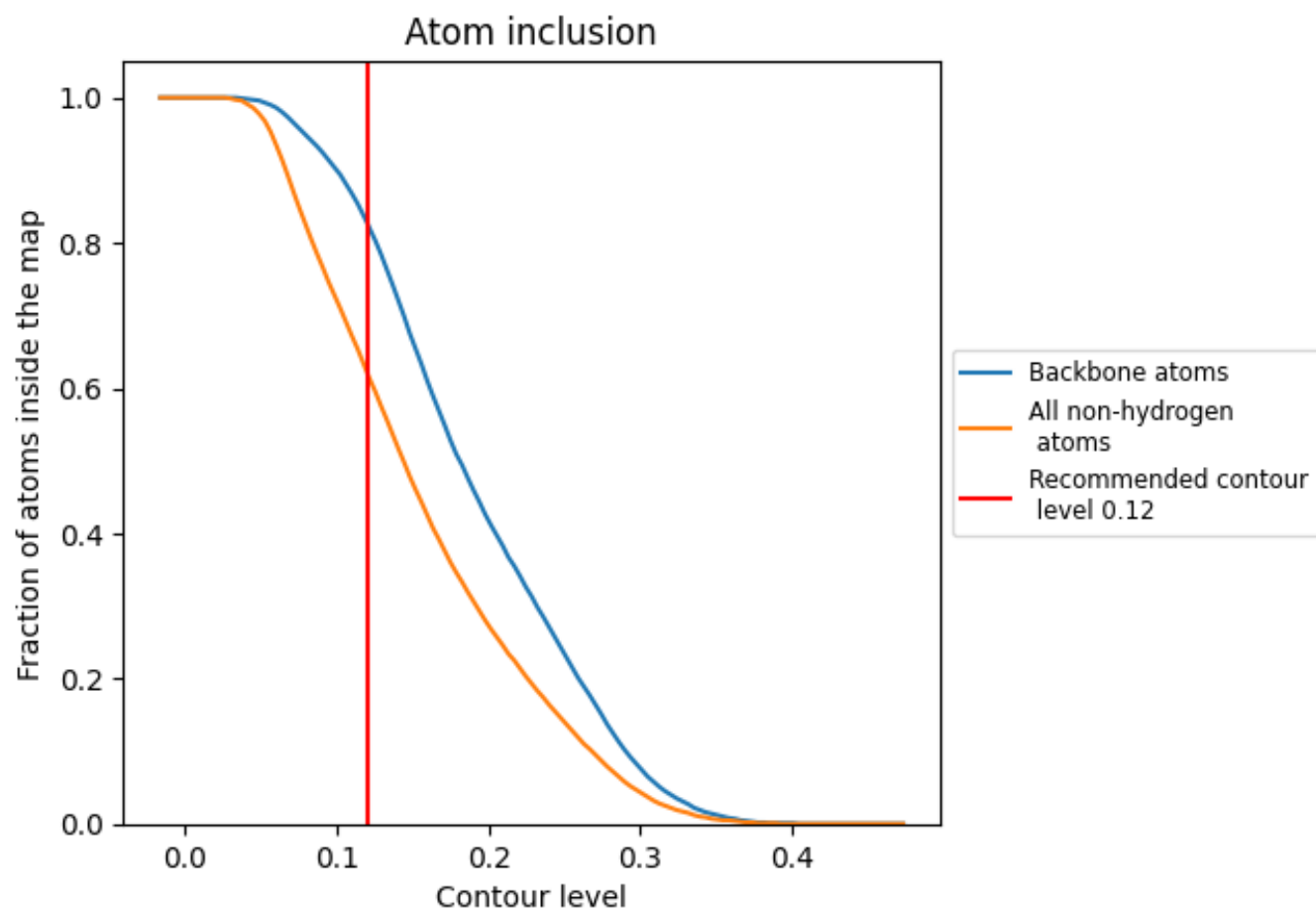
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.12).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 62% 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 (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6210	0.3710
A	0.6200	0.3710
B	0.6220	0.3710
C	0.6220	0.3710
D	0.6210	0.3720

