



wwPDB EM Validation Summary Report ⓘ

Oct 20, 2024 – 02:43 PM EDT

PDB ID : 7U9T
EMDB ID : EMD-26408
Title : Structure of PKA phosphorylated human RyR2 in the closed state in the presence of Calmodulin
Authors : Miotto, M.C.; Marks, A.R.
Deposited on : 2022-03-11
Resolution : 2.68 Å(reported)
Based on initial model : 7U9Q

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.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

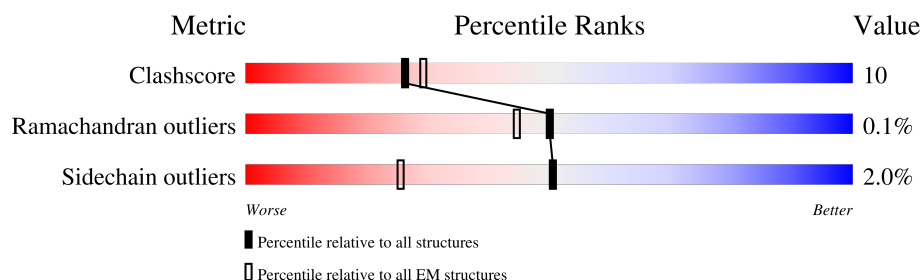
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.68 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	E	108	 66% 30%
1	F	108	 64% 31%
1	G	108	 67% 29%
1	H	108	 65% 31%
2	A	4967	 11% 66% 18% 5%
2	B	4967	 11% 66% 18% 5%
2	C	4967	 11% 66% 18% 5%
2	D	4967	 11% 66% 18% 5%

Continued on next page...

Mol	Chain	Length	Quality of chain
3	I	149	<p>57% 64% 28% 5% 5%</p>
3	J	149	<p>58% 65% 27% 5% 5%</p>
3	K	149	<p>54% 64% 28% 5% 5%</p>
3	L	149	<p>56% 64% 27% 5% 5%</p>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 143236 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	H	107	Total	C	N	O	S	0	0
			818	516	144	154	4		
1	E	107	Total	C	N	O	S	0	0
			818	516	144	154	4		
1	F	107	Total	C	N	O	S	0	0
			818	516	144	154	4		
1	G	107	Total	C	N	O	S	0	0
			818	516	144	154	4		

- Molecule 2 is a protein called Ryanodine receptor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	4229	Total	C	N	O	S	2	0
			33816	21542	5758	6286	230		
2	D	4229	Total	C	N	O	S	2	0
			33816	21542	5758	6286	230		
2	B	4229	Total	C	N	O	S	2	0
			33816	21542	5758	6286	230		
2	C	4229	Total	C	N	O	S	2	0
			33816	21542	5758	6286	230		

- Molecule 3 is a protein called Calmodulin-1.

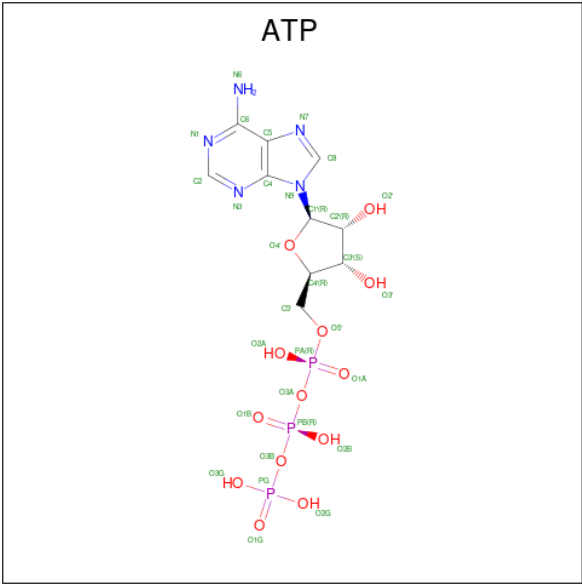
Mol	Chain	Residues	Atoms					AltConf	Trace
3	I	142	Total	C	N	O	S	0	0
			1112	687	181	234	10		
3	J	142	Total	C	N	O	S	0	0
			1112	687	181	234	10		
3	K	142	Total	C	N	O	S	0	0
			1112	687	181	234	10		
3	L	142	Total	C	N	O	S	0	0
			1112	687	181	234	10		

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Inter-

est" by depositor).

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

- Molecule 5 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).



Continued from previous page...

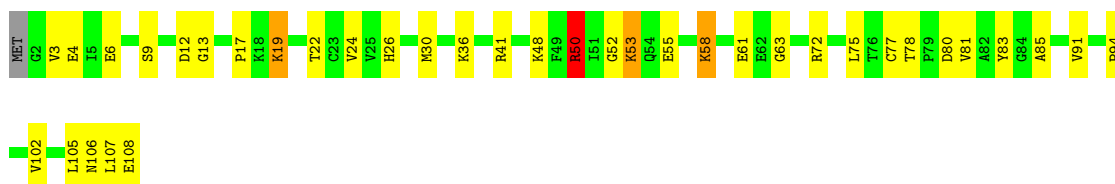
Mol	Chain	Residues	Atoms					AltConf
5	C	1	Total	C	N	O	P	0
			31	10	5	13	3	
5	C	1	Total	C	N	O	P	0
			31	10	5	13	3	

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.

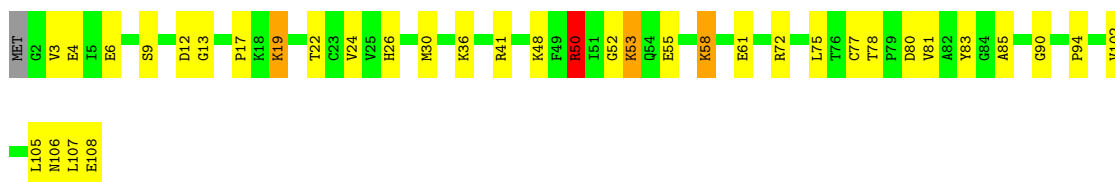
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

Chain H: 



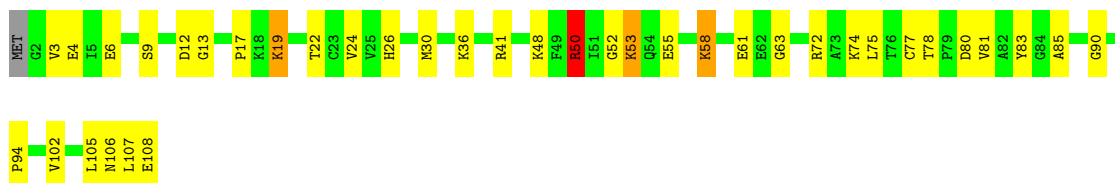
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

Chain E: 



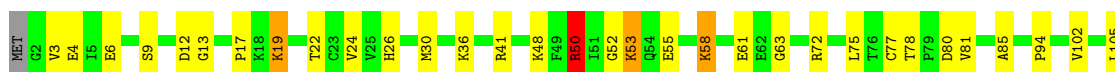
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

Chain F: 



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

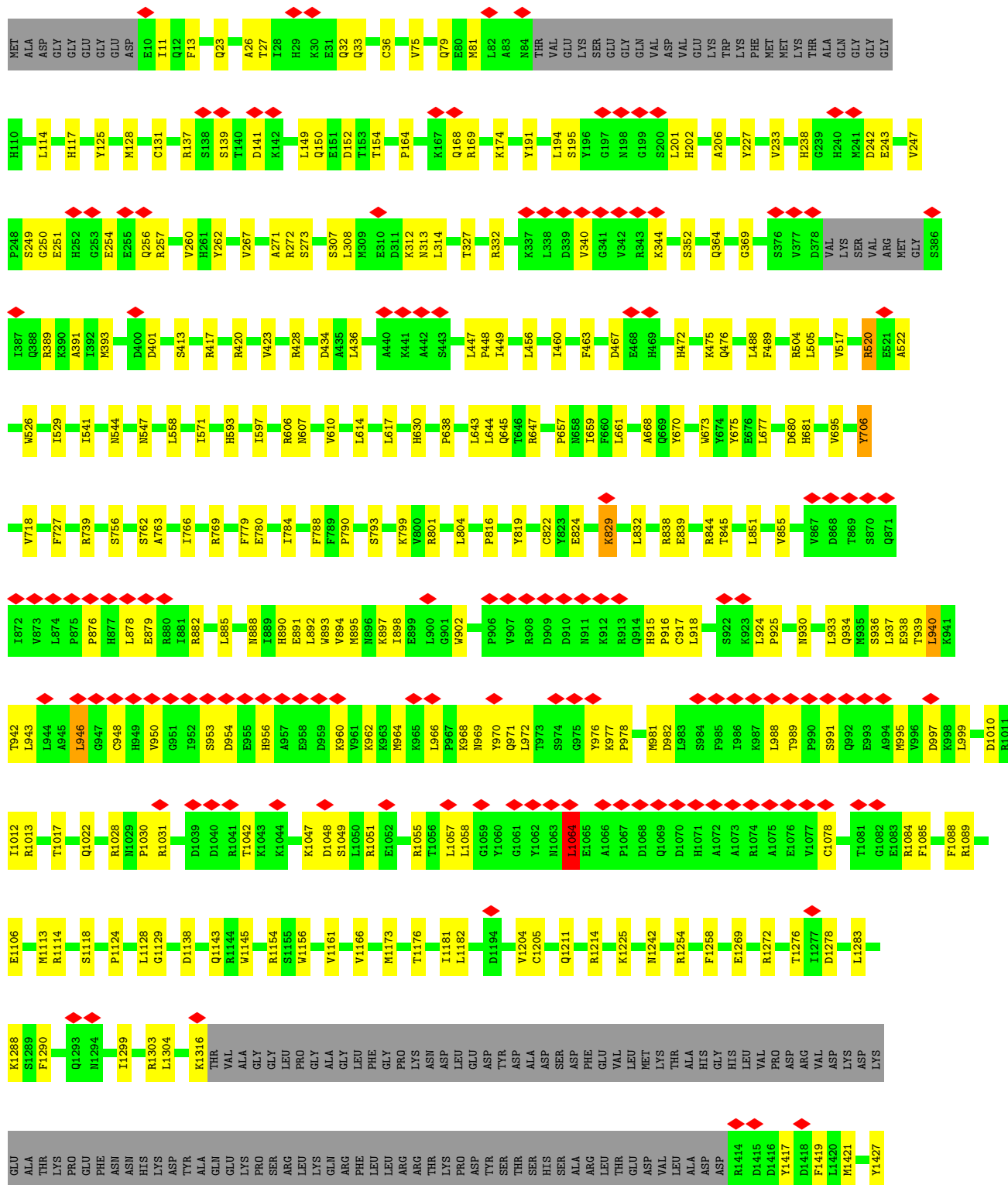
Chain G: 

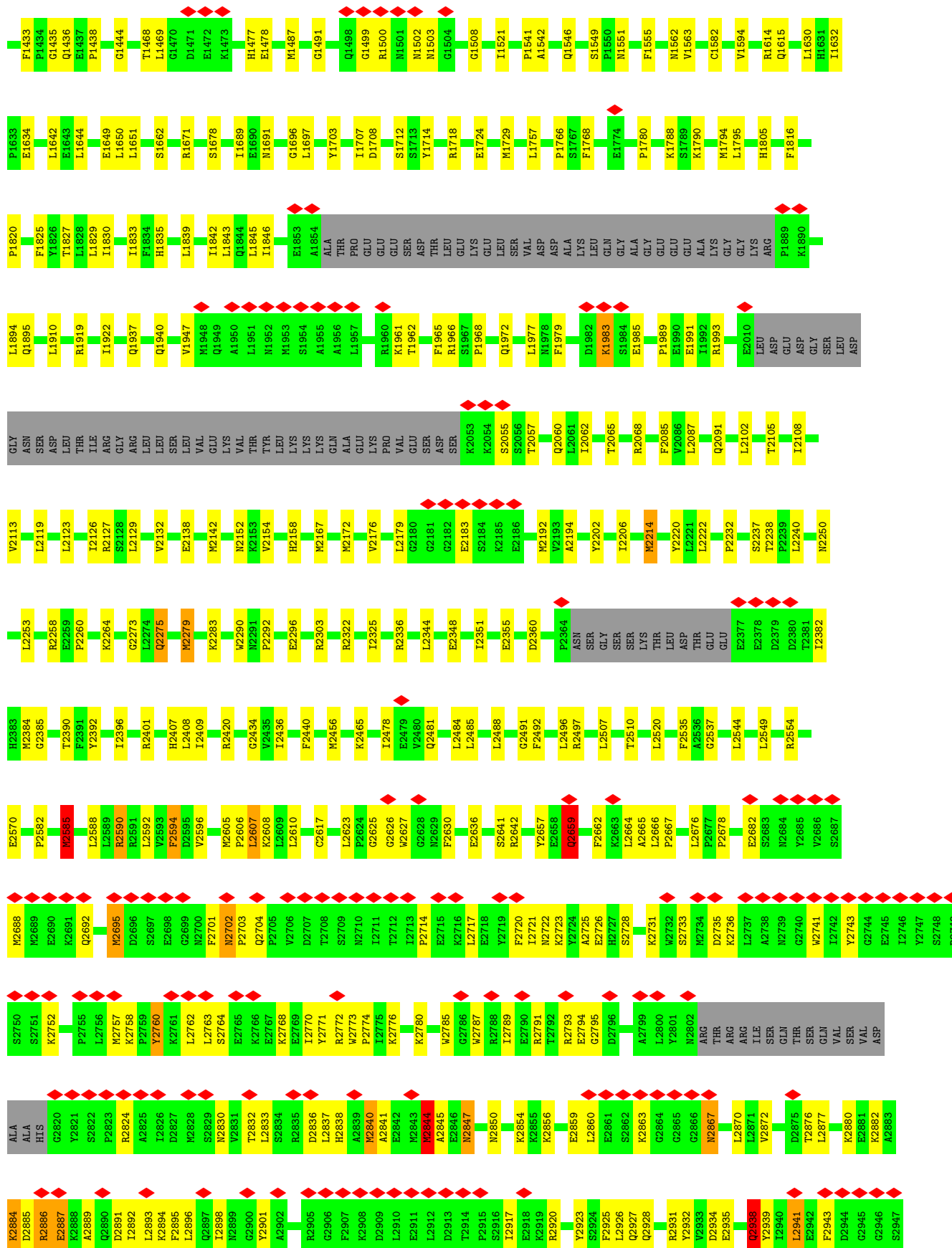


N106
L107
E108

• Molecule 2: Ryanodine receptor 2

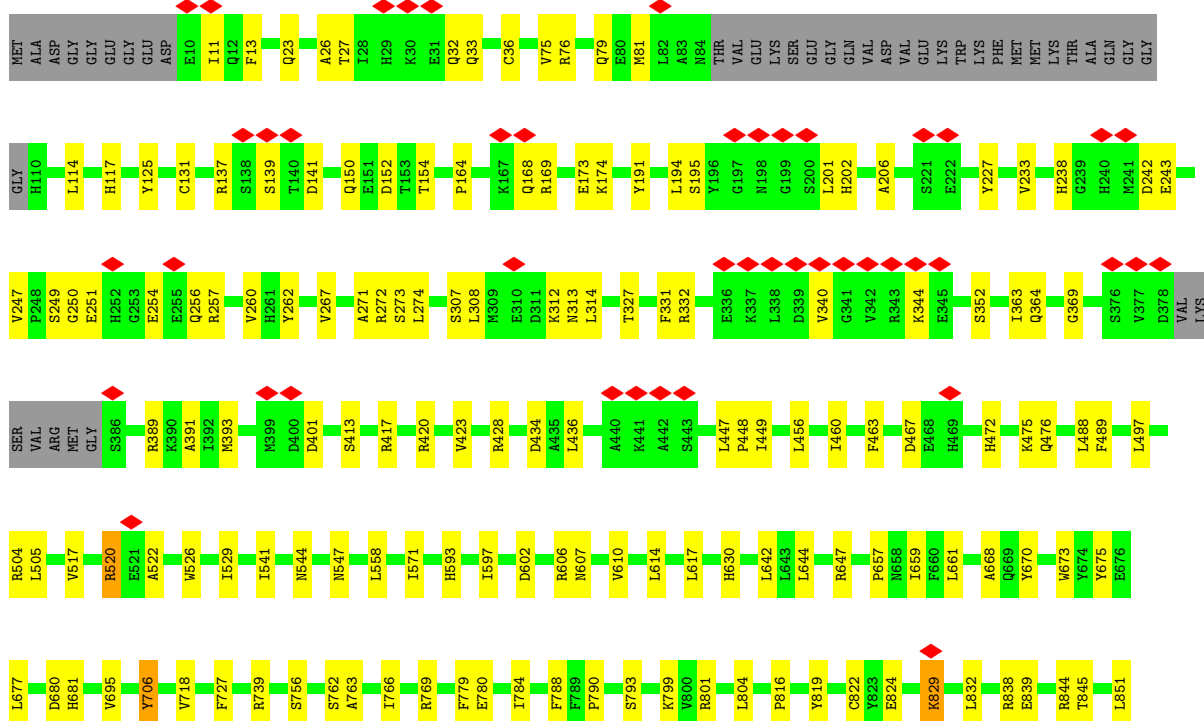
Chain A: 





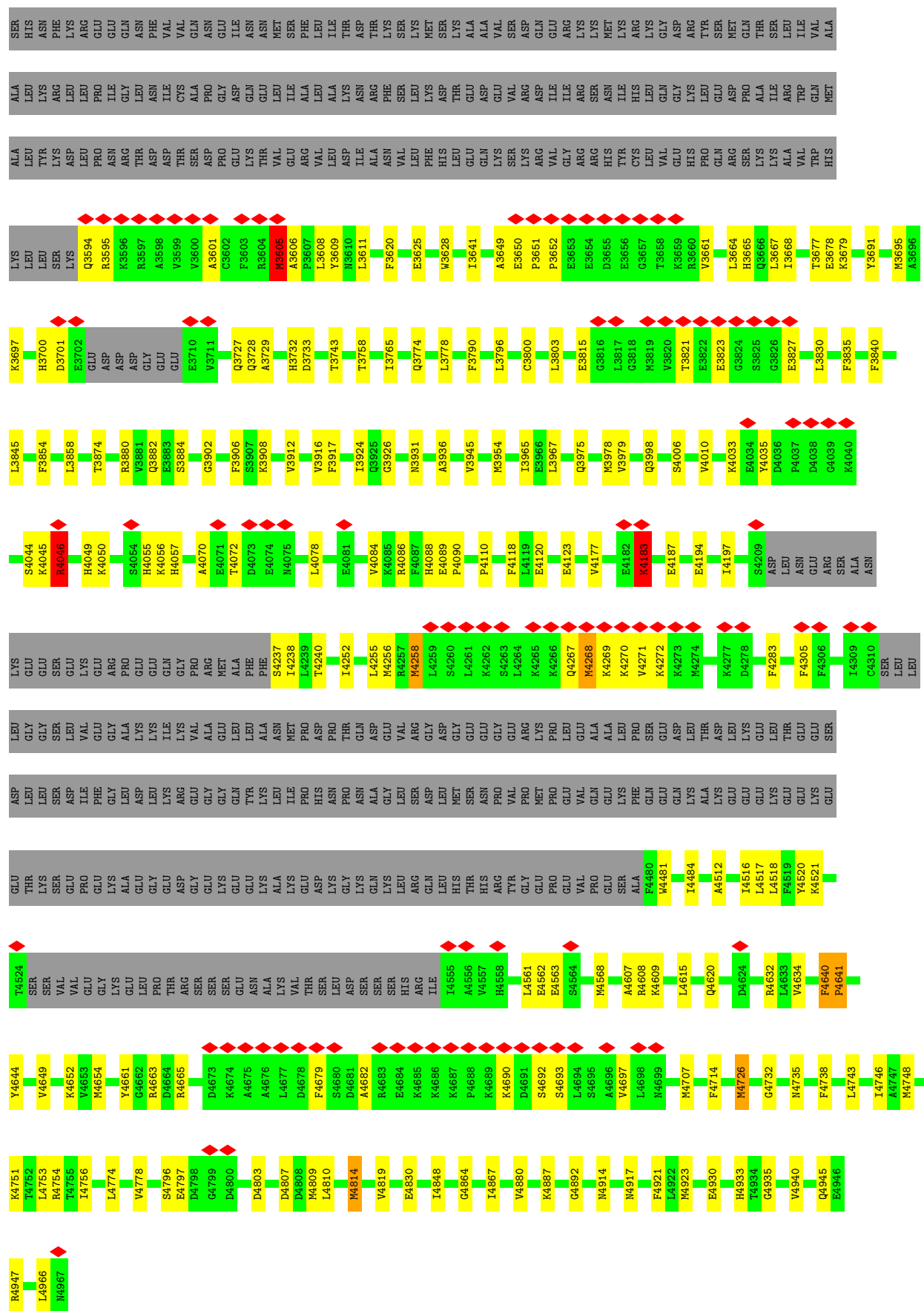
R2948	R2949	R2950	R2951	R2952	R2953	R2954	R2957	R2958	R2959	R2960	R2961	L2968	L2969	L2970	R2979	L2980	L2981	F2982	L2983	S2984	A2985	A2986	S2987	R2988	F2989	L2990	C2991	S2992	G2993	G2994	H2995	N2998	K3001	E3002	K3003	V3004	T3005	S3006	C3009	K3010	L3011	G3012	V3013	L3014	V3015	R3016	H3017	R3018	I3019	S3020	R3024	D3025							
A3026	T3027	S3028	V3030	L3033	H3034	L3036	G3037	Q3038	A3042	R3043	T3044	V3045	M3046	K3047	L3050	E3051	S3052	F3053	K3054	L3057	R3058	A3059	F3060	A3064	L3068	E3069	K3070	T3071	M3072	E3073	N3074	L3075	Q3077	G3078	Q3079	F3080	T3081	HIS	THR	ARG	ASN	GLN	PRO	K3088	G3089	V3090	T3091	Q3092	I3093	I3094									
L3101	L3102	L3103	M3104	L3105	F3109	G3113	Q3114	F3117	G3118	E3119	D3120	L3121	I3122	L3123	V3126	Q3127	S3128	V3129	Y3131	L3134	T3135	S3136	A3139	L3140	G3141	T3142	S3143	K3144	S3145	I3146	Y3147	V3148	E3149	R3150	Q3151	R3152	G3156	F3162	A3163	G3164	A3165	F3166	F3167	V3168	F3170	T3173	H3174	L3175											
D3176	K3177	H3178	N3179	T3180	Y3181	S3182	T3183	Y3184	N3185	T3186	K3187	S3188	S3189	R3190	E3191	R3192	A3193	A3194	L3195	S3196	L3197	T3198	N3199	V3200	V3201	E3202	D3203	V3204	C3205	P3206	N3207	I3208	L3214	K3215	E3216	N3217	I3218	V3219	E3220	L3221	A3222	E3223	S3224	G3225	I3226	R3227	T3228	T3229	Q3230	M3231	P3232	H3233	M3235	E3236	V3237	L3238	L3239		
P3240	K3241	L3242	M3246	S3247	R3248	K3249	W3250	E3251	H3252	G3253	P3254	E3255	L3256	N3257	P3258	E3259	R3260	A3261	E3262	K3263	C3264	C3265	T3266	L3268	N3269	S3270	E3271	H3272	M3273	N3274	T3275	L3276	L3277	G3278	N3279	I3280	L3281	K3282	L3283	I3284	Y3285	N3286	N3287	L3288	G3289	I3290	D3291	E3292	G3293	A3294	W3295	M3296	K3297	R3298	L3299	A3300	V3301		
F3302	S3303	Q3304	F3306	L3307	N3308	K3309	W3310	V3311	K3311	P3312	Q3313	L3314	L3315	K3316	T3317	H3318	F3319	L3320	P3321	L3322	M3323	E3324	K3325	L3326	K3327	K3328	K3329	A3330	A3331	T3332	V3333	V3334	S3335	E3336	E3337	ASP	HIS	LEU	LYS	ALA	LYS	ASN	PHE	GLU	ARG	GLY	ASP	GLU	LEU	LEU	ALA	LYS	ASN	PHE	VAL	VAL			
LEU	ALA	ASP	LEU	ALA	TYR	ALA	PHE	TYR	LEU	LEU	ILE	ARG	PHE	VAL	ASP	TYR	ASN	ALA	ALA	TRP	LEU	LEU	GLY	PRO	GLU	ASN	PRO	GLY	ALA	GLU	PHE	VAL	THR	ILE	SER	ILE	TYR	TRP	SER	LYS	HIS	ALA	LYS	ASN	PHE	GLU	ARG	GLY	ASP	PRO	PRO	ASN	ILE	GLY	LEU	ASN	PHE	VAL	CYS
GLN	ASN	ASP	ILE	ASN	MET	ALA	PHE	ALA	ILE	ASP	THR	ASN	THR	ASP	THR	LYS	SER	VAL	ASP	MET	TYR	ASN	LYS	ALA	ALA	VAL	VAL	ASP	GLN	ASP	GLY	THR	ALA	THR	SER	ILE	VAL	VAL	ALA	LEU	LYS	ASN	PHE	LEU	LEU	ARG	GLY	ASP	PRO	PRO	ASN	ILE	ARG	THR	THR	THR			
ALA	PRO	GLY	ASP	GLN	LEU	ILE	LEU	VAL	LYS	ASP	ASN	ARG	PHE	SER	LEU	LYS	MET	ASP	THR	GLU	GLY	ILE	ARG	GLY	ASN	ILE	HIS	ARG	GLY	LYS	LEU	GLY	LEU	GLU	ASP	PRO	LYS	LYS	ALA	LEU	LEU	TYR	LYS	ASP	LEU	PRO	PRO	ASN	ILE	ARG	THR	THR	THR						
SER	ASP	PRO	GLU	THR	VAL	GLY	THR	VAL	ASP	ILE	ALA	ASN	VAL	VAL	PHE	HIS	LEU	GLY	LEU	ARG	VAL	GLY	ARG	ARG	HIS	TYR	CYS	LEU	VAL	GLY	GLY	ASP	PRO	GLN	LYS	LYS	LYS	LEU	LEU	LEU	SER	LYS	Q3594	K3595	K3596	R3597	A3598	V3599	V3600	A3601									
C3602	F3603	R3604	M3605	A3606	P3607	L3608	Y3609	N3610	L3611	F3620	E3625	W3628	I3641	A3649	E3650	P3651	P3652	E3653	E3654	L3655	E3656	G3657	T3658	K3659	R3660	V3661	L3664	H3665	Q3666	L3667	I3668	T3677	E3678	K3679	Y3691	M3695	A3696	K3697	H3700	D3701	E3702	GLU	ASP	ASP	ASP	GLY	GLU	E3710											
V3711	Q3727	Q3728	A3729	H3732	D3733	T3743	I3744	S3747	T3758	I3765	Q3774	L3778	F3790	L3796	C3800	L3803	E3815	L3816	L3817	G3818	M3819	V3820	T3821	E3822	E3823	G3824	S3825	G3826	E3827	L3830	F3835	F3840	L3845	F3854	L3858	T3874	R3880	V3881																					
Q3882	E3883	S3884	W3890	D3896	G3902	F3906	S3907	K3908	V3912	V3916	F3917	G3926	A3936	V3945	M3954	I3965	Q3975	M3978	V3979	Q3988	S4006	V4010	L4026	D4030	K4033	E4034	Y4035	D4038	G4039	K4040	S4044	K4045	R4046	D4047	F4048	L4049	K4050																						
S4054	H4055	K4056	H4057	A4070	T4072	D4073	D4074	M4075	L4078	E4081	V4084	K4085	R4086	F4087	H4088	E4089	P4090	P4110	F4118	L4119	E4120	E4123	V4177	F4182	K4183	E4187	E4194	P4195	T4196	L4197	M4200	E4208	S4209	ASP	LEU	ASN	GLU	ARG	SER	ALA	ASN	LYS	GLU	GLU	SER														

- Molecule 2: Ryanodine receptor 2



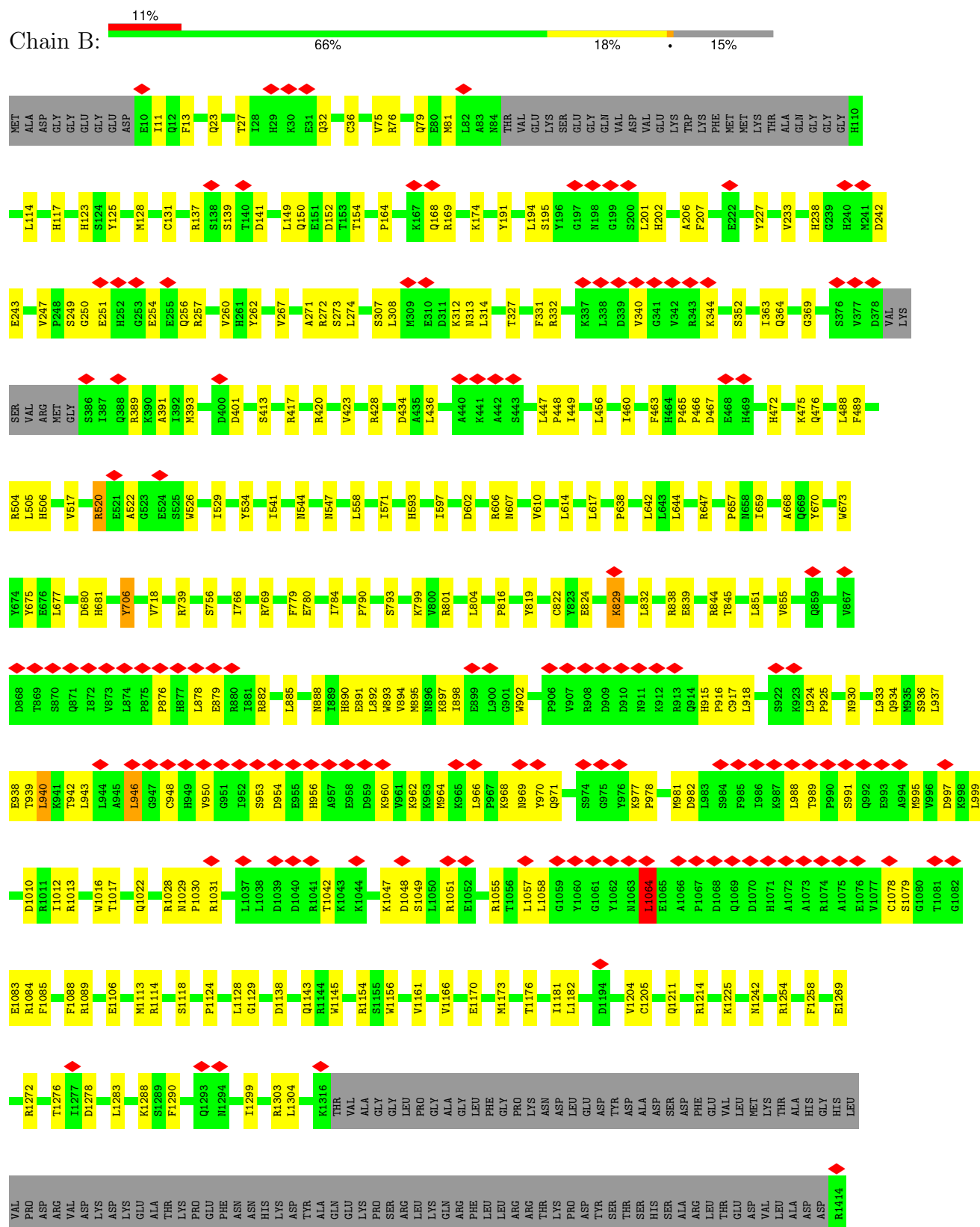


SER	GLY	L2926	L2860	R2793	W2727	L2507	GLY
GLU	SER	Q2927	E2861	E2794	S2728	T2510	SER
ALA	SER	Q2928	S2862	G2795	D2729	L2520	LYS
LEU	THR	R2931	K2863	A2799	K2731	F2535	THR
LEU	THR	Y2932	Y2932	L2800	S2733	A2536	LEU
TLE	ASP	V2933	G2864	Y2801	W2734	G2537	ASP
LEU	ASP	E2935	G2866	N2802	K2735	L2544	GLU
ASP	ASP	Q2938	N2867	ARG	D2736	E2377	E2377
M3296	GLU	Y2939	L2870	THR	L2737	E2378	E2378
PHE	THR	I2940	L2871	ARG	A2738	D2379	D2379
THR	THR	E2942	V2872	ILE	N2739	D2380	D2380
THR	THR	L2941	F2873	SER	G2740	D2381	D2381
LEU	ALA	F2943	D2875	GLN	E2882	I2382	I2382
ALA	ASP	D2944	T2876	THR	S2883	K2383	K2383
LEU	LEU	G2945	T2877	GLN	M2884	H2384	H2384
LEU	LEU	G2946	L2877	SER	Y2885	G2385	G2385
LEU	LEU	G2947	K2880	VAL	V2886	T2390	T2390
LEU	LEU	R2948	K2881	ASP	V2887	F2391	F2391
LEU	LEU	G2949	K2882	ALA	S2887	Y2392	Y2392
LEU	LEU	K2950	K2883	ALA	M2888	I2396	I2396
LEU	LEU	G2951	K2884	HIS	M2889	R2401	R2401
LEU	LEU	G2952	K2885	G2820	E2890	H2407	H2407
LEU	LEU	H2953	K2886	Y2821	V2891	L2408	L2408
LEU	LEU	F2954	E2887	S2822	K2692	I2409	I2409
LEU	LEU	E2957	K2888	S2823	S2693	R2420	R2420
LEU	LEU	E2957	K2889	R2824	S2694	G2434	G2434
LEU	LEU	E2957	K2890	A2825	M2695	P2606	P2606
LEU	LEU	E2957	K2891	L2826	D2696	W2435	W2435
LEU	LEU	E2957	K2892	A2826	S2697	K2436	K2436
LEU	LEU	E2957	K2893	L2826	E2698	L2440	L2440
LEU	LEU	E2957	K2894	L2826	D2699	M2456	M2456
LEU	LEU	E2957	K2895	L2826	S2699	K2465	K2465
LEU	LEU	E2957	K2896	L2826	E2699	I2478	I2478
LEU	LEU	E2957	K2897	L2826	D2701	E2479	E2479
LEU	LEU	E2957	K2898	L2826	N2700	W2480	W2480
LEU	LEU	E2957	K2899	L2826	S2701	Q2481	Q2481
LEU	LEU	E2957	K2900	L2826	N2702	L2484	L2484
LEU	LEU	E2957	K2901	L2826	P2703	L2485	L2485
LEU	LEU	E2957	K2902	L2826	Q2704	L2488	L2488
LEU	LEU	E2957	K2903	L2826	P2705	G2491	G2491
LEU	LEU	E2957	K2904	L2826	V2706	F2492	F2492
LEU	LEU	E2957	K2905	L2826	D2707	L2496	L2496
LEU	LEU	E2957	K2906	L2826	G2625	R2497	R2497
LEU	LEU	E2957	K2907	L2826	W2627		
LEU	LEU	E2957	K2908	L2826	T2708		
LEU	LEU	E2957	K2909	L2826	S2709		
LEU	LEU	E2957	K2910	L2826	N2710		
LEU	LEU	E2957	K2911	L2826	I2711		
LEU	LEU	E2957	K2912	L2826	T2712		
LEU	LEU	E2957	K2913	L2826	I2713		
LEU	LEU	E2957	K2914	L2826	P2714		
LEU	LEU	E2957	K2915	L2826	L2717		
LEU	LEU	E2957	K2916	L2826	E2718		
LEU	LEU	E2957	K2917	L2826	Y2719		
LEU	LEU	E2957	K2918	L2826	F2720		
LEU	LEU	E2957	K2919	L2826	I2721		
LEU	LEU	E2957	K2920	L2826	N2722		
LEU	LEU	E2957	K2921	L2826	K2723		
LEU	LEU	E2957	K2922	L2826	Y2724		
LEU	LEU	E2957	K2923	L2826	A2725		
LEU	LEU	E2957	K2924	L2826	E2726		
LEU	LEU	E2957	K2925	L2826			
LEU	LEU	E2957	K2926	L2826			
LEU	LEU	E2957	K2927	L2826			
LEU	LEU	E2957	K2928	L2826			
LEU	LEU	E2957	K2929	L2826			
LEU	LEU	E2957	K2930	L2826			
LEU	LEU	E2957	K2931	L2826			
LEU	LEU	E2957	K2932	L2826			
LEU	LEU	E2957	K2933	L2826			
LEU	LEU	E2957	K2934	L2826			
LEU	LEU	E2957	K2935	L2826			
LEU	LEU	E2957	K2936	L2826			
LEU	LEU	E2957	K2937	L2826			
LEU	LEU	E2957	K2938	L2826			
LEU	LEU	E2957	K2939	L2826			
LEU	LEU	E2957	K2940	L2826			
LEU	LEU	E2957	K2941	L2826			
LEU	LEU	E2957	K2942	L2826			
LEU	LEU	E2957	K2943	L2826			
LEU	LEU	E2957	K2944	L2826			
LEU	LEU	E2957	K2945	L2826			
LEU	LEU	E2957	K2946	L2826			
LEU	LEU	E2957	K2947	L2826			
LEU	LEU	E2957	K2948	L2826			
LEU	LEU	E2957	K2949	L2826			
LEU	LEU	E2957	K2950	L2826			
LEU	LEU	E2957	K2951	L2826			
LEU	LEU	E2957	K2952	L2826			
LEU	LEU	E2957	K2953	L2826			
LEU	LEU	E2957	K2954	L2826			
LEU	LEU	E2957	K2955	L2826			
LEU	LEU	E2957	K2956	L2826			
LEU	LEU	E2957	K2957	L2826			
LEU	LEU	E2957	K2958	L2826			
LEU	LEU	E2957	K2959	L2826			
LEU	LEU	E2957	K2960	L2826			
LEU	LEU	E2957	K2961	L2826			
LEU	LEU	E2957	K2962	L2826			
LEU	LEU	E2957	K2963	L2826			
LEU	LEU	E2957	K2964	L2826			
LEU	LEU	E2957	K2965	L2826			
LEU	LEU	E2957	K2966	L2826			
LEU	LEU	E2957	K2967	L2826			
LEU	LEU	E2957	K2968	L2826			
LEU	LEU	E2957	K2969	L2826			
LEU	LEU	E2957	K2970	L2826			
LEU	LEU	E2957	K2971	L2826			
LEU	LEU	E2957	K2972	L2826			
LEU	LEU	E2957	K2973	L2826			
LEU	LEU	E2957	K2974	L2826			
LEU	LEU	E2957	K2975	L2826			
LEU	LEU	E2957	K2976	L2826			
LEU	LEU	E2957	K2977	L2826			
LEU	LEU	E2957	K2978	L2826			
LEU	LEU	E2957	K2979	L2826			
LEU	LEU	E2957	K2980	L2826			
LEU	LEU	E2957	K2981	L2826			
LEU	LEU	E2957	K2982	L2826			
LEU	LEU	E2957	K2983	L2826			
LEU	LEU	E2957	K2984	L2826			
LEU	LEU	E2957	K2985	L2826			
LEU	LEU	E2957	K2986	L2826			
LEU	LEU	E2957	K2987	L2826			
LEU	LEU	E2957	K2988	L2826			
LEU	LEU	E2957	K2989	L2826			
LEU	LEU	E2957	K2990	L2826			
LEU	LEU	E2957	K2991	L2826			
LEU	LEU	E2957	K2992	L2826			
LEU	LEU	E2957	K2993	L2826			
LEU	LEU	E2957	K2994	L2826			
LEU	LEU	E2957	K2995	L2826			
LEU	LEU	E2957	K2996	L2826			
LEU	LEU	E2957	K2997	L2826			
LEU	LEU	E2957	K2998	L2826			
LEU	LEU	E2957	K2999	L2826			
LEU	LEU	E2957	K3000	L2826			
LEU	LEU	E2957	K3001	L2826			
LEU	LEU	E2957	K3002	L2826			
LEU	LEU	E2957	K3003	L2826			
LEU	LEU	E2957	K3004	L2826			
LEU	LEU	E2957	K3005	L2826			
LEU	LEU	E2957	K3006	L2826			
LEU	LEU	E2957	K3007	L2826			
LEU	LEU	E2957	K3008	L2826			
LEU	LEU	E2957	K3009	L2826			
LEU	LEU	E2957	K3010	L2826			
LEU	LEU	E2957	K3011	L2826			
LEU	LEU	E2957	K3012	L2826			
LEU	LEU	E2957	K3013	L2826			
LEU	LEU	E2957	K3014	L2826			
LEU	LEU	E2957	K3015	L2826			
LEU	LEU	E2957	K3016	L2826			
LEU	LEU	E2957	K3017	L2826			
LEU	LEU	E2957	K3018	L2826			
LEU	LEU	E2957	K3019	L2826			
LEU	LEU	E2957	K3020	L2826			
LEU	LEU	E2957	K3021	L2826			
LEU	LEU	E2957	K3022	L2826			
LEU	LEU	E2957	K3023	L2826			
LEU	LEU	E2957	K3024	L2826			
LEU	LEU	E2957	K3025	L2826			
LEU	LEU	E2957	K3026	L2826			
LEU	LEU	E2957	K3027	L2826			
LEU	LEU	E2957	K3028	L2826			
LEU	LEU	E2957	K3029	L2826			
LEU	LEU	E2957	K3030	L2826			
LEU	LEU	E2957	K3031	L2826			
LEU	LEU	E2957	K3032	L2826			
LEU	LEU	E2957	K3033	L2826			
LEU	LEU	E2957	K3034	L2826			
LEU	LEU	E2957	K3035	L2826			
LEU	LEU	E2957	K3036	L2826			
LEU	LEU	E2957	K3037	L2826			
LEU	LEU	E2957	K3038	L2826			
LEU	LEU	E2957	K3039	L2826			
LEU	LEU	E2957	K3040	L2826			
LEU	LEU	E2957	K3041	L2826			
LEU	LEU	E2957	K3042	L2826			
LEU	LEU	E2957	K3043	L2826			
LEU	LEU	E2957	K3044	L2826			
LEU	LEU	E2957	K3045	L2826			
LEU	LEU	E2957	K3046	L2826			
LEU	LEU	E2957	K3047	L2826			
LEU	LEU	E2957	K3048	L2826			
LEU	LEU	E2957	K3049	L2826			
LEU	LEU	E2957	K3050	L2826			
LEU	LEU	E2957	K3051	L2826			
LEU	LEU	E2957	K3052	L2826			
LEU	LEU	E2957	K3053	L2826			
LEU	LEU	E2957	K3054	L2826			
LEU	LEU	E2957	K3055	L2826			
LEU	LEU	E2957	K3056	L2826			
LEU	LEU	E2957	K3057	L2826			
LEU	LEU	E2957	K3058	L2826			
LEU	LEU	E2957	K3059	L2826			
LEU	LEU	E2957	K3060	L2826			
LEU	LEU	E2957	K3061	L2826			
LEU	LEU	E2957	K3062	L2826			
LEU	LEU	E2957	K3063	L2826			
LEU	LEU	E2957	K3064	L2826			
LEU	LEU	E2957	K3065	L2826			
LEU	LEU	E2957	K3066	L2826			



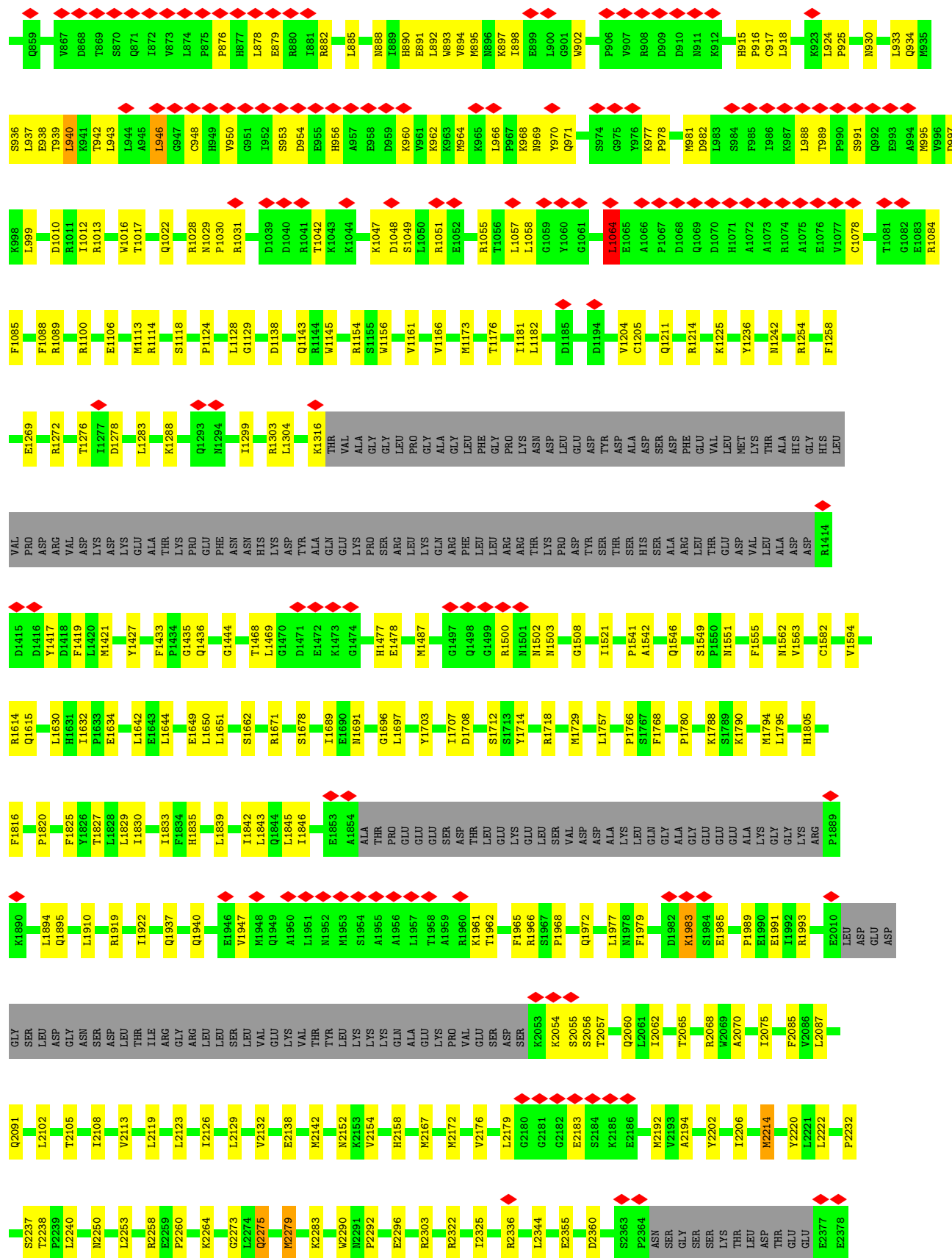
• Molecule 2: Ryanodine receptor 2

Chain B:





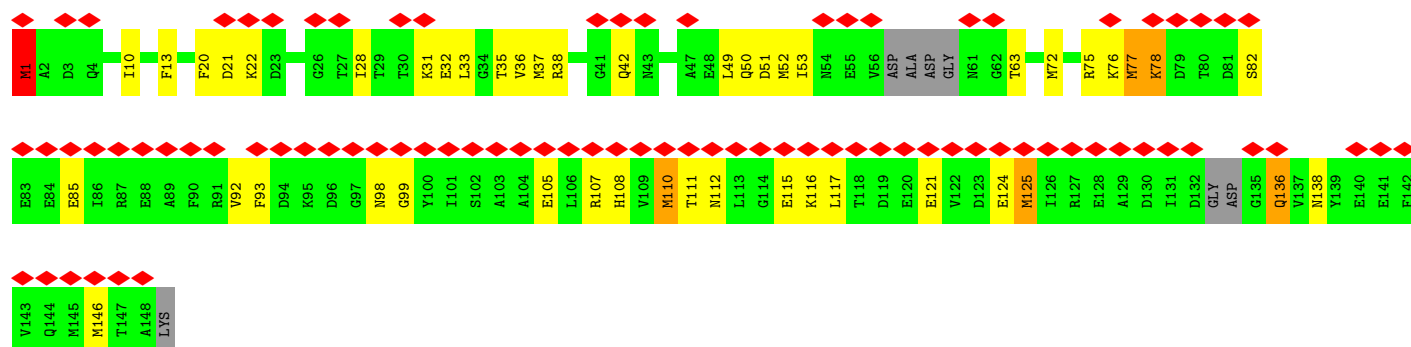




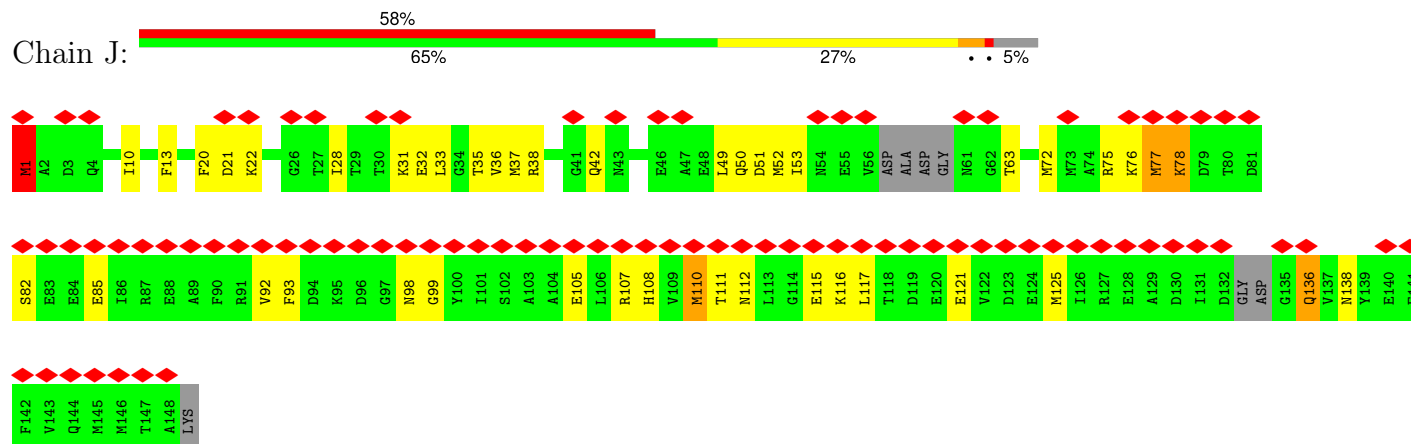
LEU	D2379	L2676	G2740	ILE	P2869	E2935	G3012	F3080	A3165	T3229	G3293	G3293	LEU
LEU	D2380	P2677	W2741	SER	L2870	Q2938	V3013	T3081	F3166	Q3230	A3294	A3294	LEU
ILE	T2381	P2678	I2742	THR	L2871	Q2939	L3014	THR	P3167	Q3231	W3295	W3295	ILE
ASP	H2383	R2564	Y2743	SER	D2875	L2941	R3016	ARG	A3169	P3232	M3296	M3296	ASP
PHE	M2384	E2570	G2744	GLN	T2876	E2942	R3018	ASN	F3170	P3233	K3297	K3297	GLU
THR	G2385	P2582	E2745	VAL	L2877	F2943	L3019	GLN	L3171	E3234	R3298	R3298	THR
THR	T2390	P2582	I2746	VAL	K2880	D2944	S3020	PRO	E3172	M3235	A3300	A3300	THR
LEU	F2391	M2585	Y2747	ASP	E2881	G2945	S3021	K3088	H3173	E3236	V3301	V3301	LEU
ASP	Y2392	L2588	D2748	ALA	K2882	G2946	L3021	Q3092	L3175	V3237	F3302	F3302	ASP
ASP	I2396	L2588	S2749	ALA	A2883	S2947	H3024	V3090	L3175	L3238	S3303	S3303	ASP
ALA	R2401	R2590	D2750	HIS	D2884	R2948	D3025	T3091	D3176	P3240	Q3304	Q3304	LEU
ALA	R2401	R2590	S2751	HIS	D2885	G2949	A3026	Q3092	K3177	M3241	G3304	G3304	ALA
THR	H2407	L2592	K2752	G2820	E2886	S2947	S3027	L3101	H3178	L3242	I3306	I3306	THR
THR	L2408	V2593	P2755	G2821	E2887	R2948	D3028	L3102	I3179	M3246	P3307	P3307	PHE
THR	I2409	F2594	L2756	Y2821	E2888	R2949	T3027	L3103	I3180	S3247	T3307	T3307	PHE
THR	R2420	D2595	K2761	P2823	A2889	G2949	S3028	L3104	S3182	R3248	N3308	N3308	THR
THR	R2420	D2596	P2755	P2823	Q2890	G2945	L3033	L3105	I3183	W3249	P3309	P3309	THR
THR	R2420	D2596	L2756	R2824	Q2891	G2946	L3034	F3109	H3184	W3250	V3310	V3310	THR
THR	R2420	D2596	K2757	A2825	D2891	G2946	H3035	Q3114	T3185	E3251	K3311	K3311	THR
THR	R2420	D2596	K2758	I2826	L2892	G2946	I3036	Q3114	T3186	H3252	P3312	P3312	THR
THR	R2420	D2596	P2759	M2828	L2893	G2946	L3037	F3117	T3187	G3253	Q3313	Q3313	THR
THR	R2420	D2596	Y2760	M2829	K2894	G2946	G3037	Q3117	K3187	P3254	Q3314	Q3314	THR
THR	R2420	D2596	K2761	N2830	F2895	G2946	Q3038	Q3117	S3188	E3255	L3314	L3314	THR
THR	R2420	D2596	L2762	V2831	Q2897	G2946	A3042	G3118	R3189	N3256	L3315	L3315	THR
THR	R2420	D2596	S2764	L2832	L2898	G2946	R3043	G3119	R3190	K3257	K3316	K3316	THR
THR	R2420	D2596	E2765	L2833	L2898	G2946	F3044	L3120	E3191	P3258	L3317	L3317	THR
THR	R2420	D2596	K2766	S2834	Y2901	G2946	K3046	L3121	A3193	R3259	H3318	H3318	THR
THR	R2420	D2596	E2767	D2836	A2902	G2946	K3047	L3122	A3194	R3260	F3319	F3319	THR
THR	R2420	D2596	K2768	R2837	L2902	G2946	L3050	L3123	L3195	A3261	L3320	L3320	THR
THR	R2420	D2596	E2769	H2838	R2905	G2946	L3051	V3126	L3196	E3262	P3321	P3321	THR
THR	R2420	D2596	L2770	L2839	G2906	G2946	E3051	Q3127	S3196	K3263	L3322	L3322	THR
THR	R2420	D2596	R2771	A2839	F2907	G2946	S3052	Q3127	L3197	R3264	M3323	M3323	THR
THR	R2420	D2596	R2772	A2841	K2908	G2946	F3053	Y3131	L3198	C3263	G3324	G3324	THR
THR	R2420	D2596	W2773	E2842	D2909	G2946	K3054	Y3131	T3199	C3265	K3325	K3325	THR
THR	R2420	D2596	L2775	M2843	L2910	G2946	L3057	L3134	M3200	T3266	L3326	L3326	THR
THR	R2420	D2596	K2776	K2844	E2911	G2946	R3058	T3135	E3202	A3267	L3327	L3327	THR
THR	R2420	D2596	K2776	A2845	E2912	G2946	A3059	S3136	E3203	L3268	L3328	L3328	THR
THR	R2420	D2596	K2780	E2846	D2913	G2946	F3060	A3139	D3203	S3270	K3328	K3328	THR
THR	R2420	D2596	W2785	N2847	T2914	G2946	A3064	G3141	C3205	F3271	A3330	A3330	THR
THR	R2420	D2596	G2786	H2849	S2916	G2946	A3065	T3142	P3206	H3272	A3331	A3331	THR
THR	R2420	D2596	W2787	N2850	L2917	G2946	E3066	G3143	M3207	M3273	L3332	L3332	THR
THR	R2420	D2596	K2788	K2854	K2918	G2946	E3067	S3144	L3214	L3276	V3334	V3334	THR
THR	R2420	D2596	L2789	K2855	E2918	G2946	D3067	T3145	E3216	N3279	S3335	S3335	THR
THR	R2420	D2596	E2790	K2856	T2919	G2946	L3068	S3146	E3217	L3280	E3336	E3336	THR
THR	R2420	D2596	R2791	K2857	K2920	G2946	E3069	T3147	I3218	L3281	E3337	E3337	THR
THR	R2420	D2596	T2792	M2858	V2923	G2946	K3070	V3148	F3219	K3283	ASP	ASP	THR
THR	R2420	D2596	R2793	E2859	S2924	G2946	T3071	E3149	V3219	L3283	HIS	HIS	THR
THR	R2420	D2596	E2795	L2860	F2925	G2946	E3073	E3149	S3219	T3284	LEU	LEU	THR
THR	R2420	D2596	D2786	S2861	Q2927	G2946	N3074	Q3151	L3221	Y3285	LYS	LYS	THR
THR	R2420	D2596	K2789	S2862	Q2928	G2946	L3075	R3152	A3222	N3286	ALA	ALA	THR
THR	R2420	D2596	A2799	K2863	T2931	G2946	K3076	R3156	E3223	L3287	GLU	GLU	THR
THR	R2420	D2596	L2800	G2864	Y2932	G2946	Q3077	G3156	S3224	L3288	ALA	ALA	THR
THR	R2420	D2596	Y2801	G2865	V2933	G2946	G3078	G3156	G3225	G3289	ARG	ARG	THR
THR	R2420	D2596	N2802	G2866	D2934	G2946	Q3079	F3162	I3226	E3291	GLY	GLY	THR
THR	R2420	D2596	ARG	N2867	K3010	G2946	G3079	F3162	R3227	T3290	ASP	ASP	THR
THR	R2420	D2596	THR	H2868	L3011	G2946	G3079	F3162	Y3228	E3292	SER	SER	THR
THR	R2420	D2596	ARG	H2868	L3011	G2946	G3079	F3162	Y3228	E3292	GLU	GLU	THR
THR	R2420	D2596	ARG	H2868	L3011	G2946	G3079	F3162	Y3228	E3292	ALA	ALA	THR

- Molecule 3: Calmodulin-1

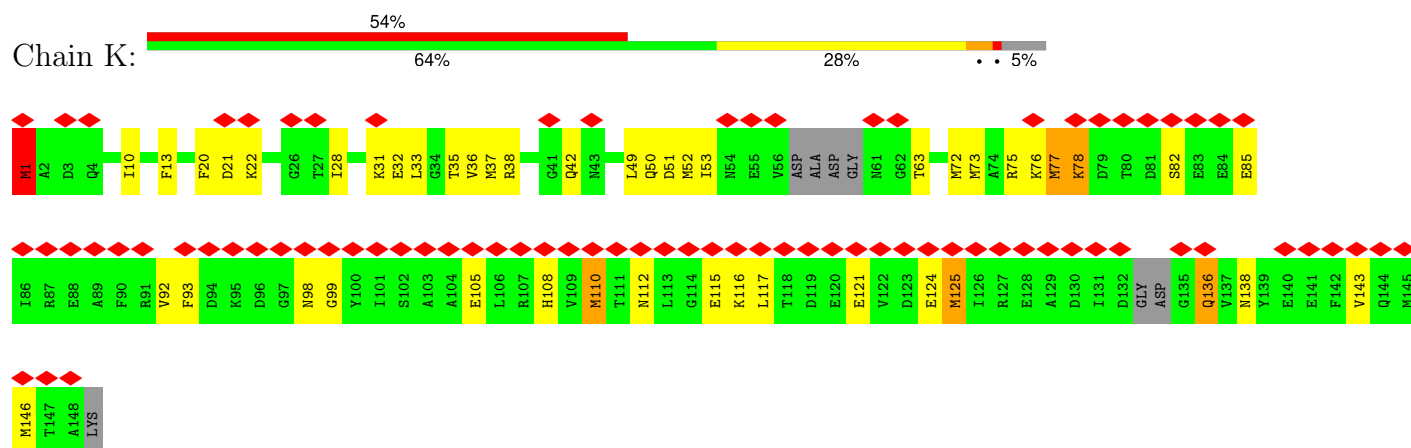




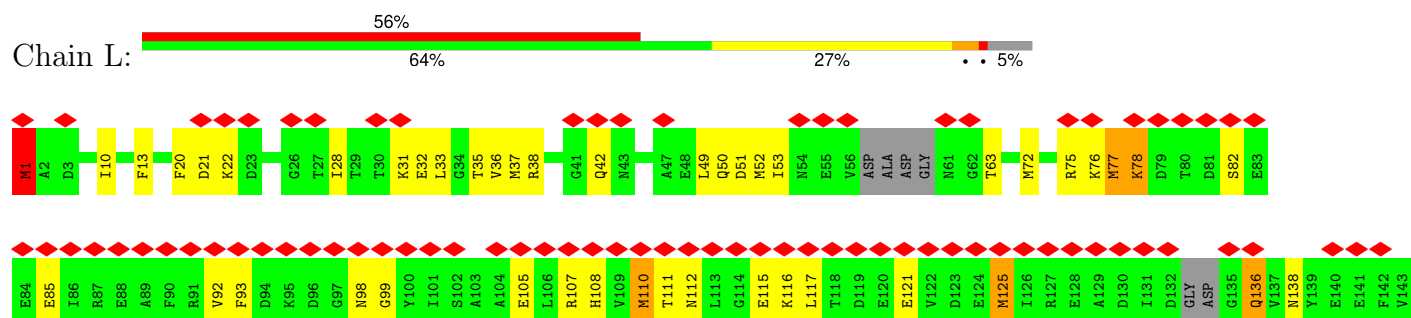
• Molecule 3: Calmodulin-1



• Molecule 3: Calmodulin-1



• Molecule 3: Calmodulin-1



Q144	M145	M146	T147	A148	LYS
------	------	------	------	------	-----

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	38187	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)	400	Depositor
Maximum defocus (nm)	1200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.728	Depositor
Minimum map value	-0.012	Depositor
Average map value	0.015	Depositor
Map value standard deviation	0.035	Depositor
Recommended contour level	0.14	Depositor
Map size (\AA)	425.984, 425.984, 425.984	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.832, 0.832, 0.832	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, 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	E	0.32	0/834	0.67	1/1123 (0.1%)
1	F	0.32	0/834	0.66	1/1123 (0.1%)
1	G	0.32	0/834	0.67	1/1123 (0.1%)
1	H	0.32	0/834	0.66	1/1123 (0.1%)
2	A	0.27	0/34556	0.53	23/46672 (0.0%)
2	B	0.27	0/34556	0.53	23/46672 (0.0%)
2	C	0.27	0/34556	0.53	23/46672 (0.0%)
2	D	0.27	0/34556	0.53	23/46672 (0.0%)
3	I	0.28	0/1122	0.75	7/1504 (0.5%)
3	J	0.28	0/1122	0.75	6/1504 (0.4%)
3	K	0.28	0/1122	0.75	7/1504 (0.5%)
3	L	0.28	0/1122	0.75	7/1504 (0.5%)
All	All	0.27	0/146048	0.54	123/197196 (0.1%)

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	A	0	4
2	B	0	4
2	C	0	4
2	D	0	4
All	All	0	16

There are no bond length outliers.

The worst 5 of 123 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2659	GLN	CA-CB-CG	9.01	133.23	113.40
2	B	2659	GLN	CA-CB-CG	9.00	133.21	113.40
2	A	2659	GLN	CA-CB-CG	8.99	133.19	113.40
2	C	2659	GLN	CA-CB-CG	8.99	133.18	113.40
2	C	2840	MET	CB-CG-SD	8.84	138.93	112.40

There are no chirality outliers.

5 of 16 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	2886	ARG	Sidechain
2	A	2995	HIS	Peptide
2	A	4640	PHE	Peptide
2	A	520	ARG	Sidechain
2	D	520	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	E	818	0	821	26	0
1	F	818	0	821	29	0
1	G	818	0	821	25	0
1	H	818	0	821	27	0
2	A	33816	0	33507	667	0
2	B	33816	0	33507	664	0
2	C	33816	0	33507	666	0
2	D	33816	0	33507	675	0
3	I	1112	0	1053	31	0
3	J	1112	0	1053	27	0
3	K	1112	0	1053	28	0
3	L	1112	0	1053	30	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	62	0	24	0	0
5	B	62	0	24	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C	62	0	24	0	0
5	D	62	0	24	0	0
All	All	143236	0	141620	2829	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

The worst 5 of 2829 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:A:2841:ALA:HA	2:A:2844:MET:HG3	1.35	1.09
2:B:2841:ALA:HA	2:B:2844:MET:HG3	1.35	1.08
2:C:2841:ALA:HA	2:C:2844:MET:HG3	1.34	1.06
2:D:2841:ALA:HA	2:D:2844:MET:HG3	1.35	1.04
1:F:50:ARG:HH11	1:F:50:ARG:HB2	1.34	0.93

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	E	105/108 (97%)	101 (96%)	4 (4%)	0	100	100
1	F	105/108 (97%)	101 (96%)	4 (4%)	0	100	100
1	G	105/108 (97%)	101 (96%)	4 (4%)	0	100	100
1	H	105/108 (97%)	101 (96%)	4 (4%)	0	100	100
2	A	4203/4967 (85%)	4057 (96%)	144 (3%)	2 (0%)	100	100
2	B	4203/4967 (85%)	4057 (96%)	144 (3%)	2 (0%)	100	100
2	C	4203/4967 (85%)	4057 (96%)	144 (3%)	2 (0%)	100	100
2	D	4203/4967 (85%)	4057 (96%)	144 (3%)	2 (0%)	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	I	136/149 (91%)	126 (93%)	9 (7%)	1 (1%)	19	38
3	J	136/149 (91%)	126 (93%)	9 (7%)	1 (1%)	19	38
3	K	136/149 (91%)	126 (93%)	9 (7%)	1 (1%)	19	38
3	L	136/149 (91%)	126 (93%)	9 (7%)	1 (1%)	19	38
All	All	17776/20896 (85%)	17136 (96%)	628 (4%)	12 (0%)	50	71

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	2988	ARG
2	A	4641	PRO
2	D	2988	ARG
2	D	4641	PRO
2	B	2988	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	E	88/89 (99%)	81 (92%)	7 (8%)	10	22
1	F	88/89 (99%)	81 (92%)	7 (8%)	10	22
1	G	88/89 (99%)	81 (92%)	7 (8%)	10	22
1	H	88/89 (99%)	81 (92%)	7 (8%)	10	22
2	A	3712/4358 (85%)	3646 (98%)	66 (2%)	54	78
2	B	3712/4358 (85%)	3646 (98%)	66 (2%)	54	78
2	C	3712/4358 (85%)	3646 (98%)	66 (2%)	54	78
2	D	3712/4358 (85%)	3646 (98%)	66 (2%)	54	78
3	I	119/127 (94%)	111 (93%)	8 (7%)	13	30
3	J	119/127 (94%)	111 (93%)	8 (7%)	13	30
3	K	119/127 (94%)	111 (93%)	8 (7%)	13	30
3	L	119/127 (94%)	111 (93%)	8 (7%)	13	30

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	15676/18296 (86%)	15352 (98%)	324 (2%)	50 74

5 of 324 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	4726	MET
2	C	3296	MET
2	C	829	LYS
2	C	2838[A]	HIS
3	J	1	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	2702	ASN
2	C	2217	HIS
2	B	2702	ASN
2	B	2217	HIS
2	C	1905	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 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
5	ATP	B	5003	-	28,33,33	0.62	0	34,52,52	0.58	1 (2%)
5	ATP	C	5003	-	28,33,33	0.63	0	34,52,52	0.59	1 (2%)
5	ATP	C	5002	-	28,33,33	0.63	0	34,52,52	0.66	1 (2%)
5	ATP	B	5002	-	28,33,33	0.62	0	34,52,52	0.66	1 (2%)
5	ATP	D	5003	-	28,33,33	0.63	0	34,52,52	0.58	1 (2%)
5	ATP	A	5003	-	28,33,33	0.64	0	34,52,52	0.58	1 (2%)
5	ATP	A	5002	-	28,33,33	0.64	0	34,52,52	0.66	1 (2%)
5	ATP	D	5002	-	28,33,33	0.63	0	34,52,52	0.66	1 (2%)

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
5	ATP	B	5003	-	-	9/18/38/38	0/3/3/3
5	ATP	C	5003	-	-	9/18/38/38	0/3/3/3
5	ATP	C	5002	-	-	11/18/38/38	0/3/3/3
5	ATP	B	5002	-	-	11/18/38/38	0/3/3/3
5	ATP	D	5003	-	-	9/18/38/38	0/3/3/3
5	ATP	A	5003	-	-	9/18/38/38	0/3/3/3
5	ATP	A	5002	-	-	11/18/38/38	0/3/3/3
5	ATP	D	5002	-	-	11/18/38/38	0/3/3/3

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(°)
5	C	5003	ATP	C5-C6-N6	2.34	123.88	120.31
5	D	5002	ATP	C5-C6-N6	2.34	123.87	120.31
5	A	5003	ATP	C5-C6-N6	2.33	123.86	120.31
5	A	5002	ATP	C5-C6-N6	2.32	123.85	120.31
5	C	5002	ATP	C5-C6-N6	2.32	123.85	120.31

There are no chirality outliers.

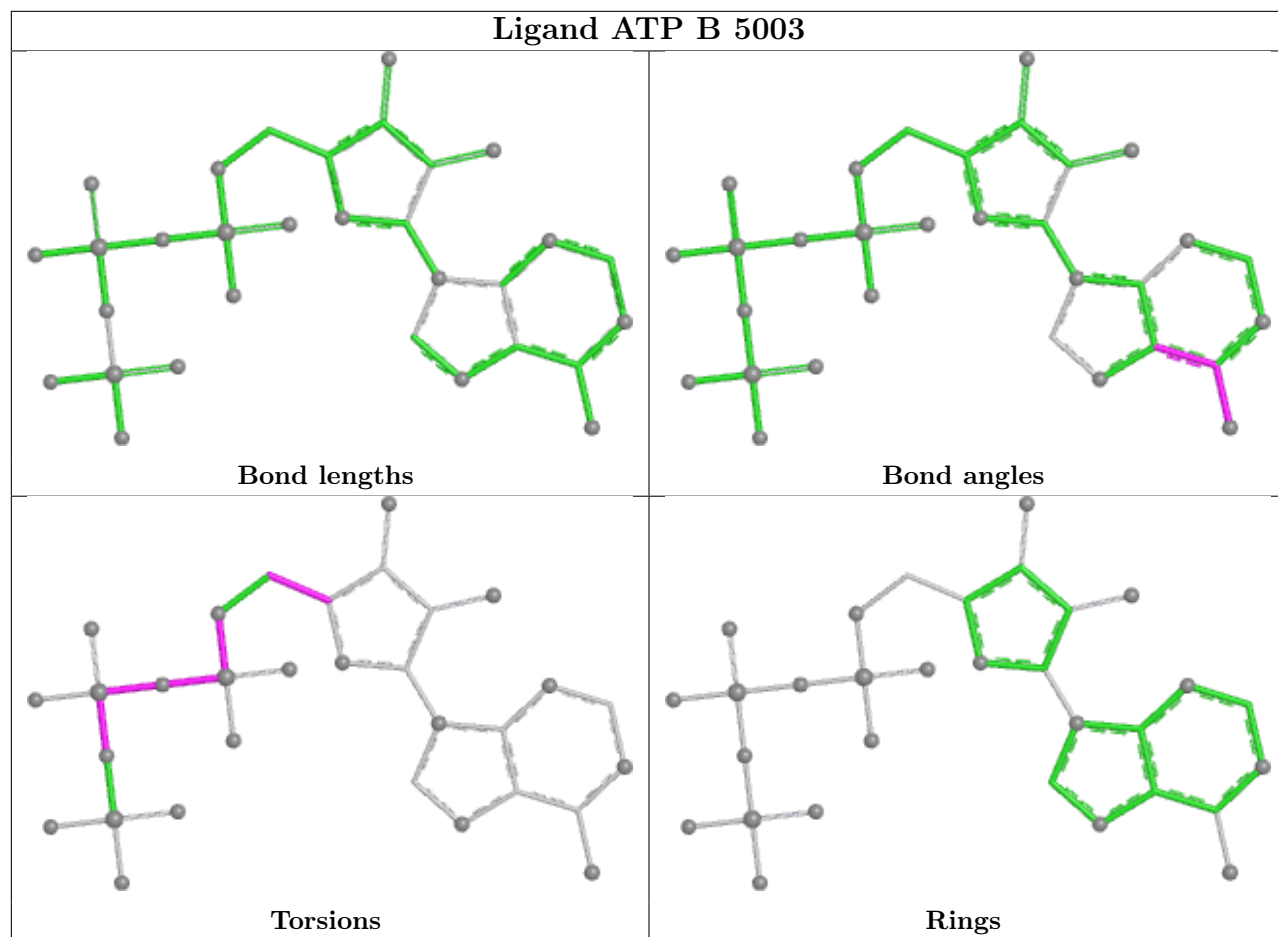
5 of 80 torsion outliers are listed below:

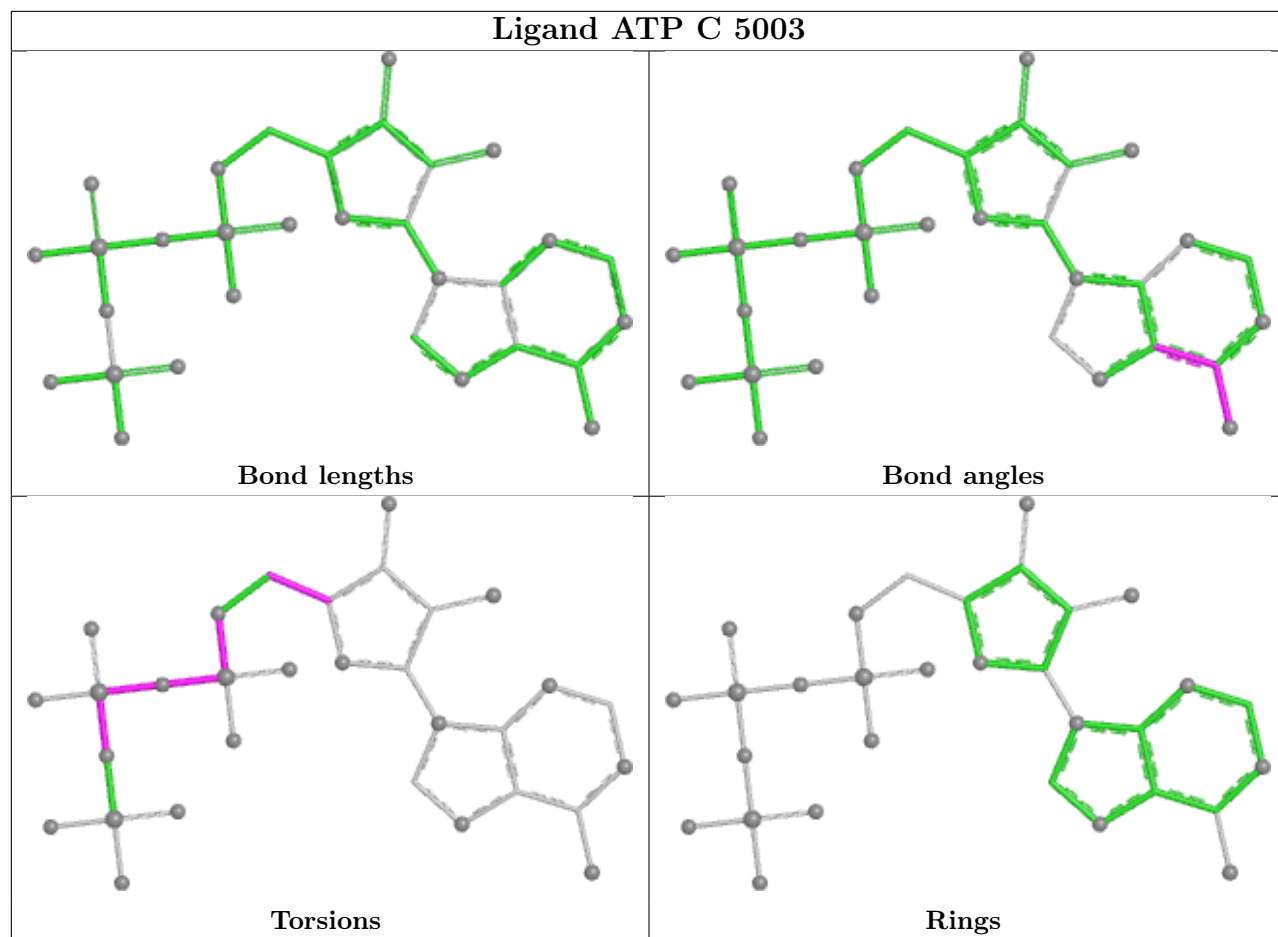
Mol	Chain	Res	Type	Atoms
5	A	5002	ATP	PB-O3B-PG-O3G
5	A	5002	ATP	C5'-O5'-PA-O1A
5	A	5002	ATP	C5'-O5'-PA-O2A
5	A	5002	ATP	C5'-O5'-PA-O3A
5	A	5002	ATP	O4'-C4'-C5'-O5'

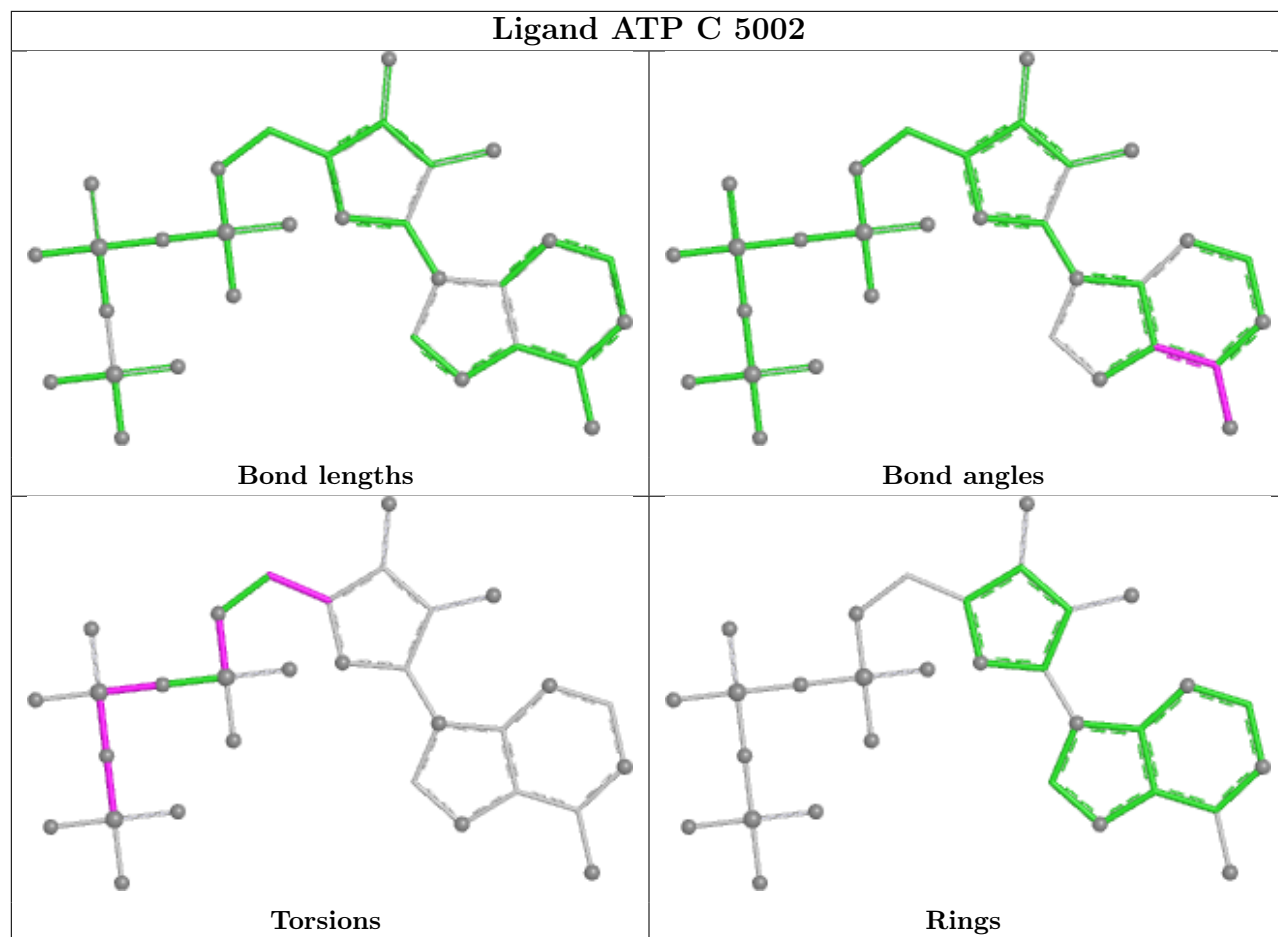
There are no ring outliers.

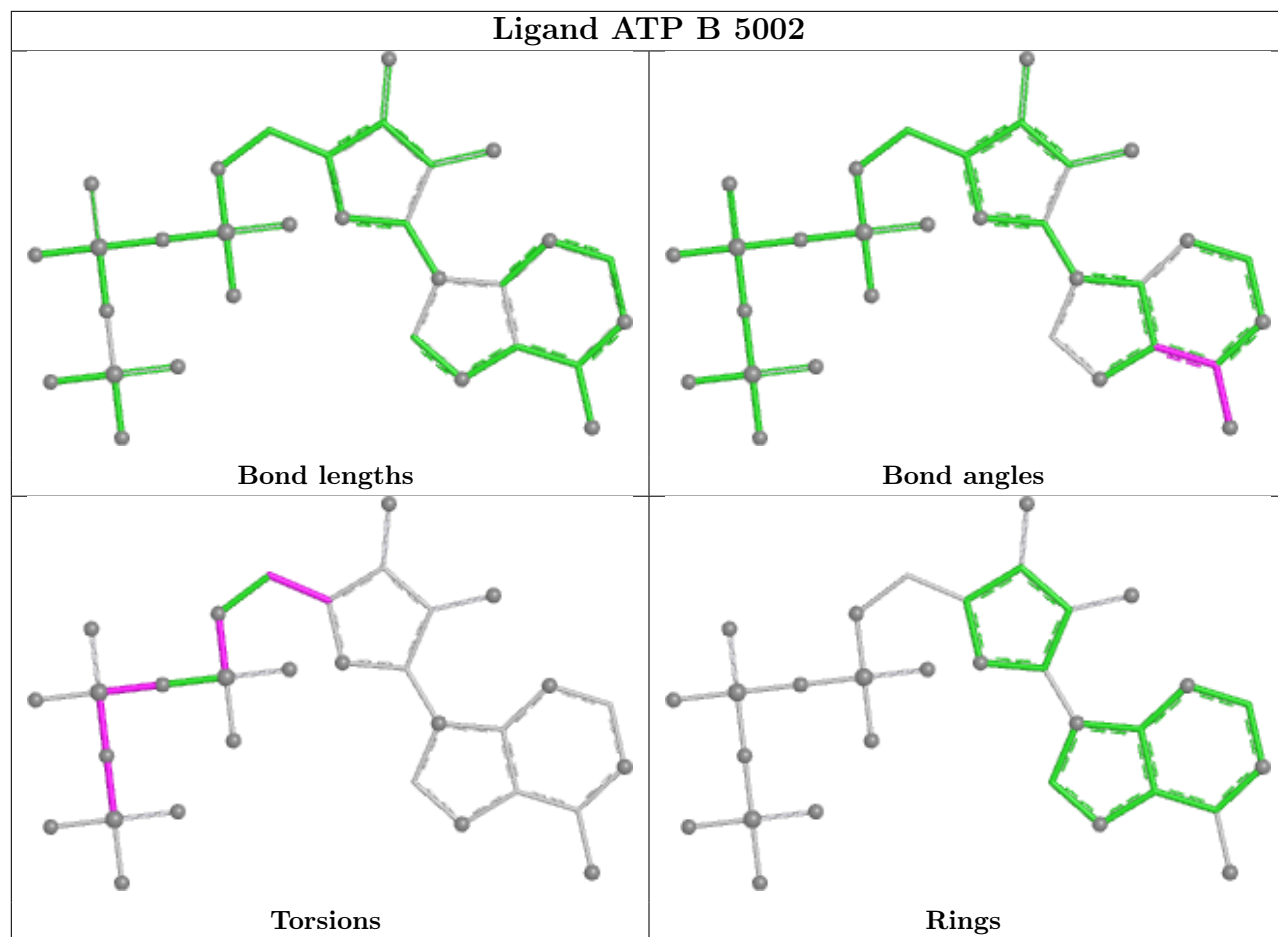
No monomer is involved in short contacts.

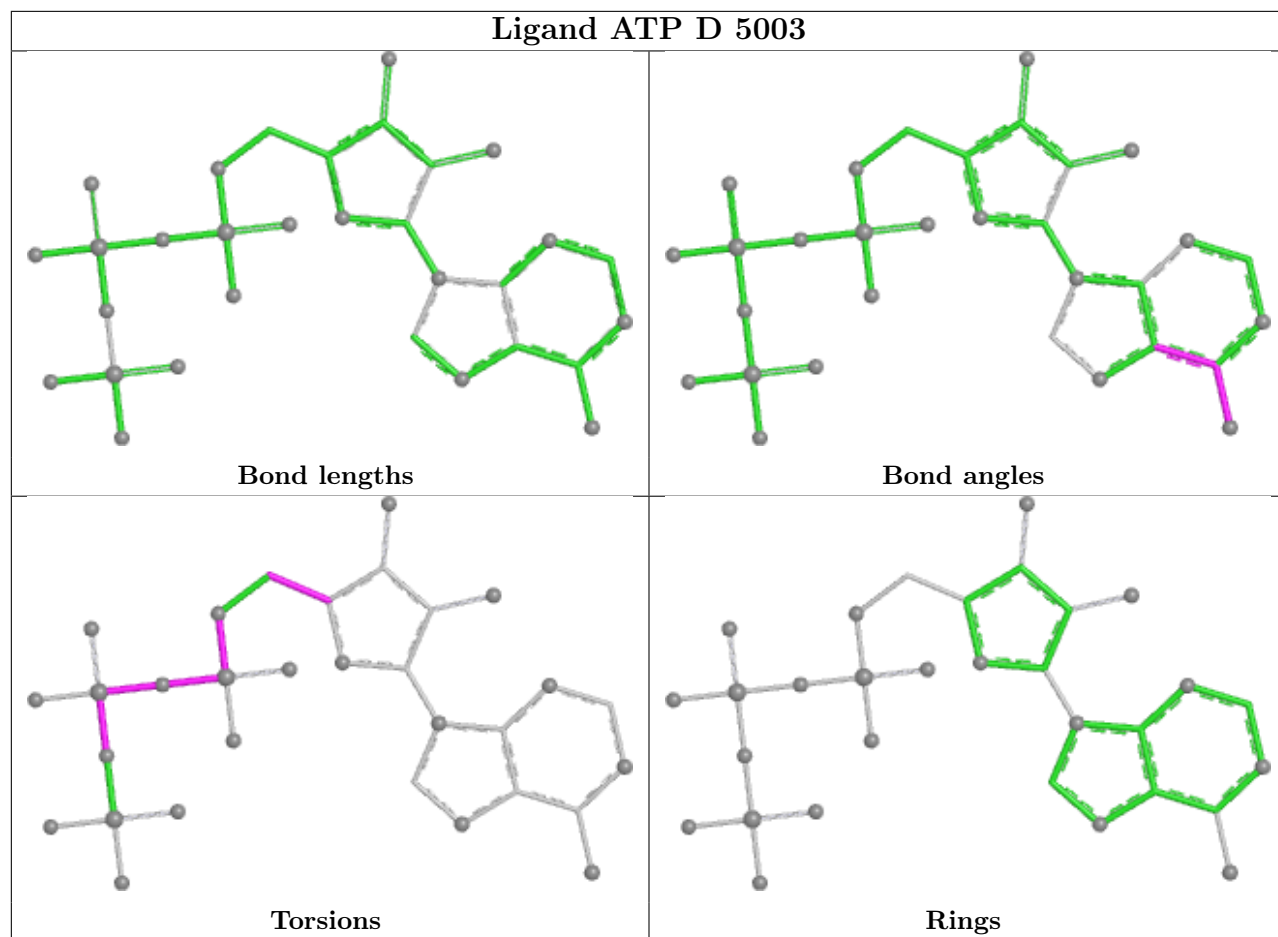
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

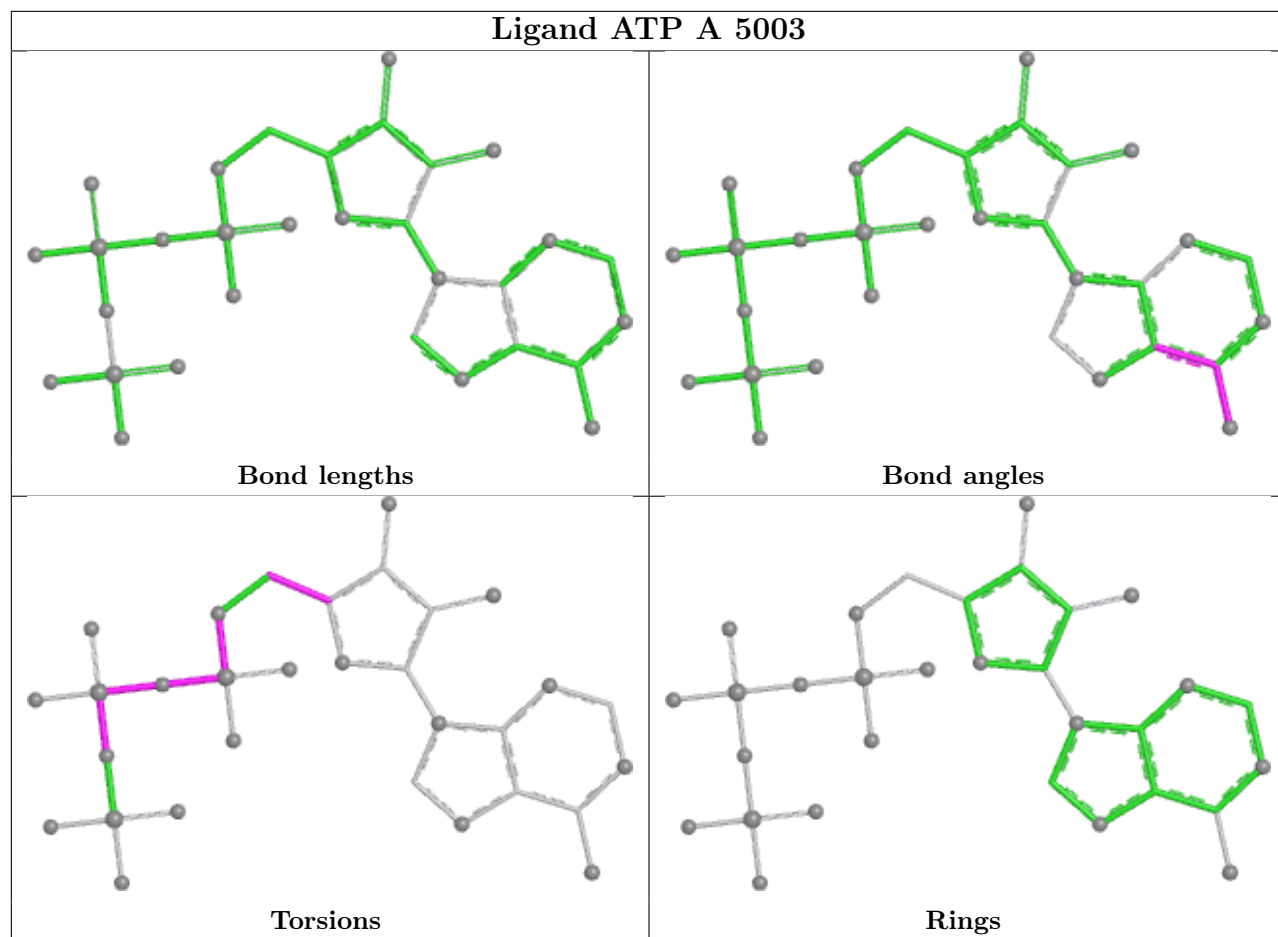


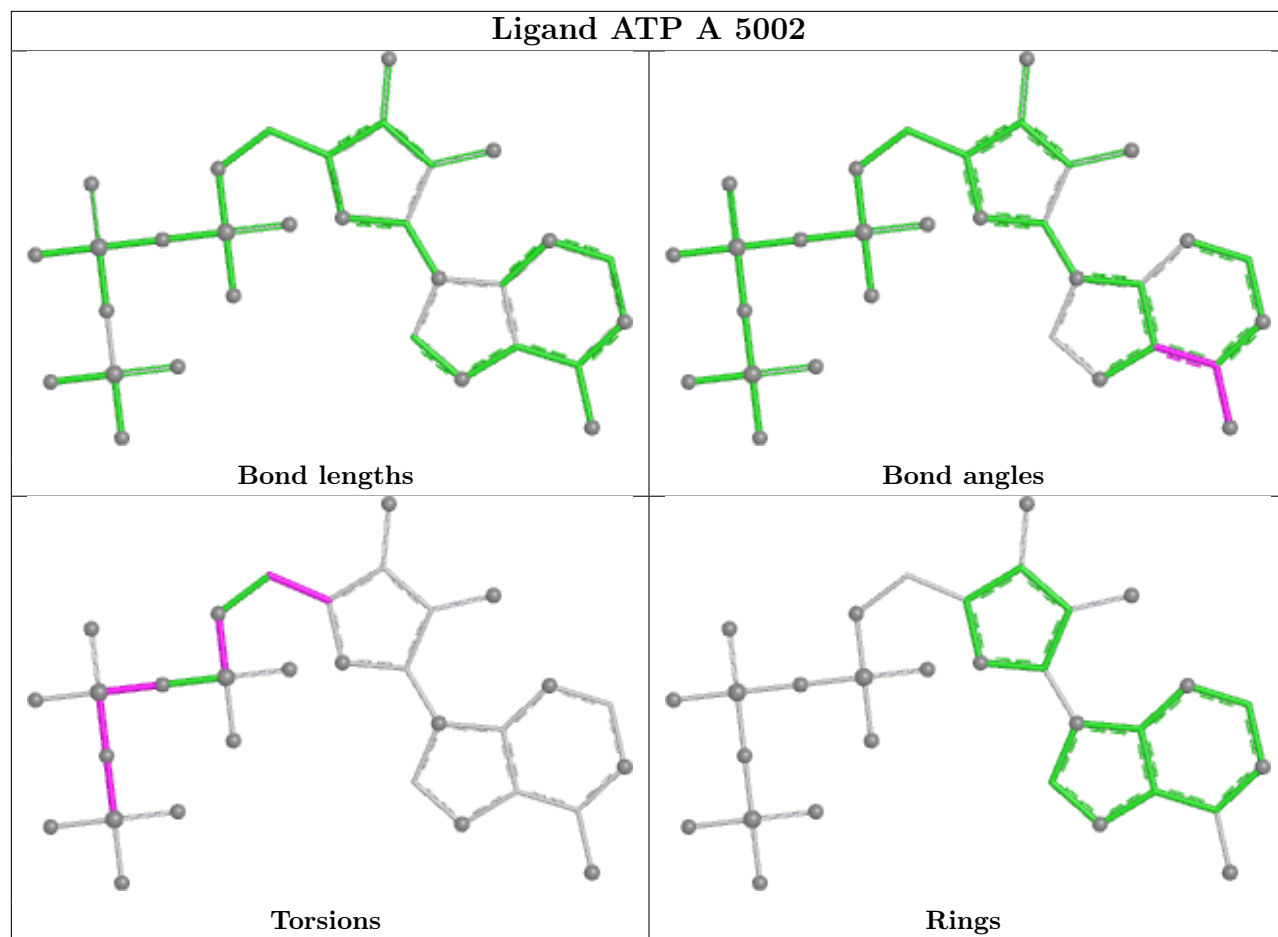


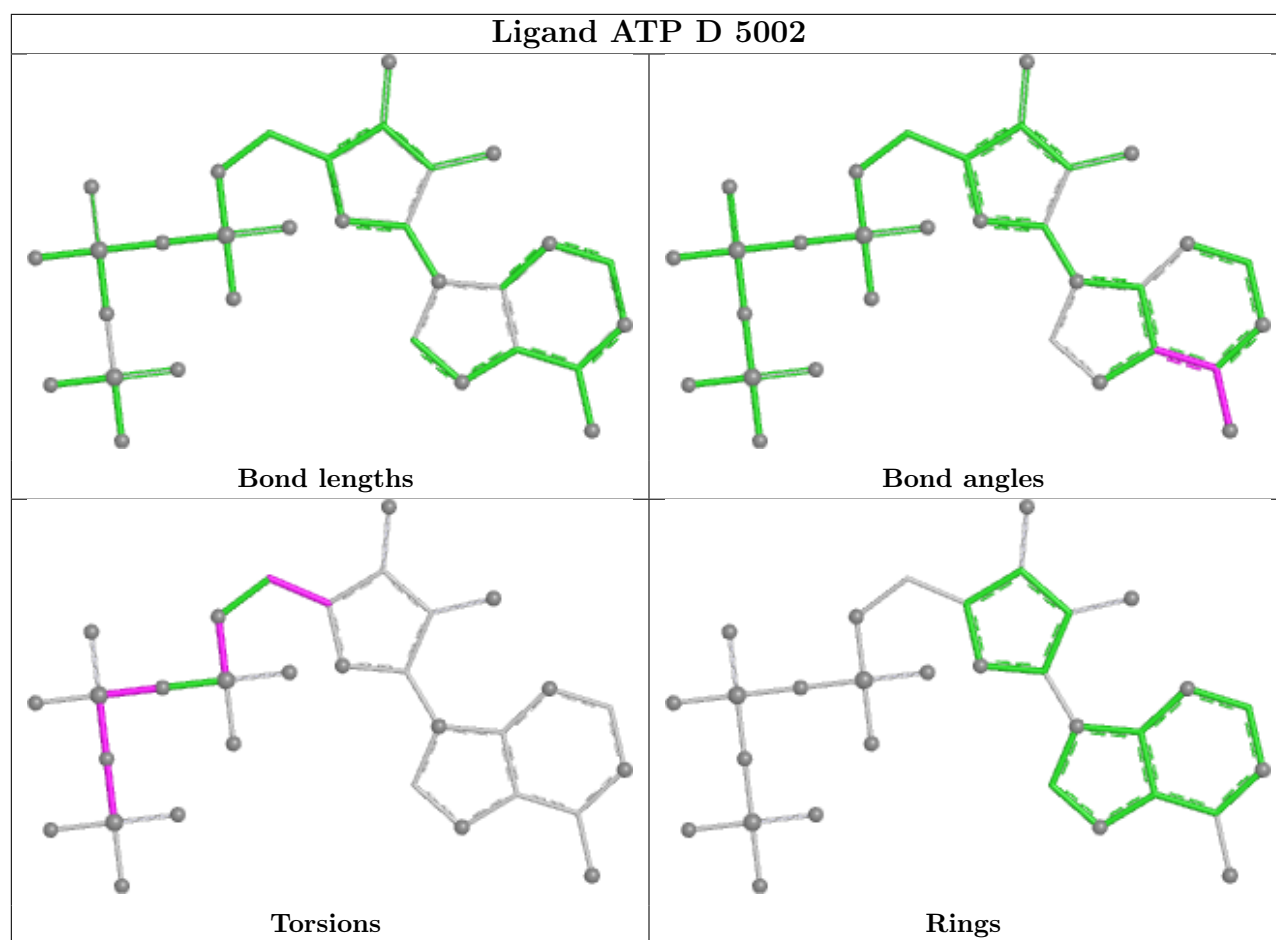












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

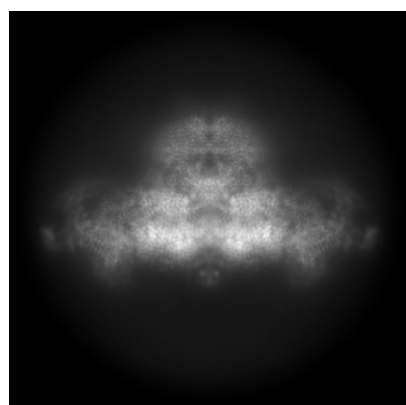
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26408. These allow visual inspection of the internal detail of the map and identification of artifacts.

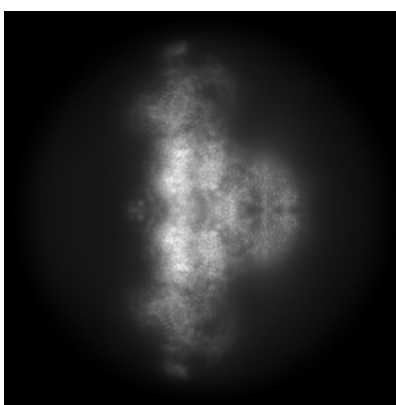
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

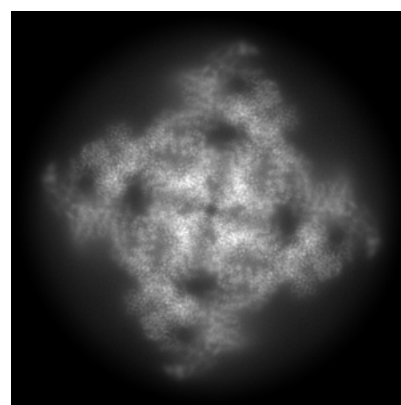
6.1.1 Primary map



X



Y

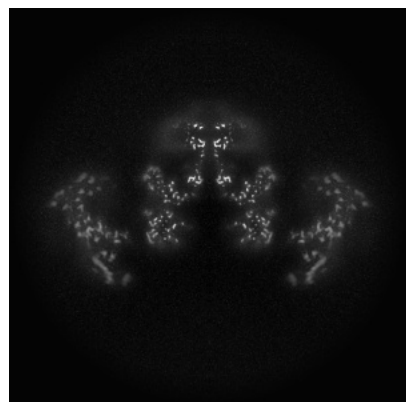


Z

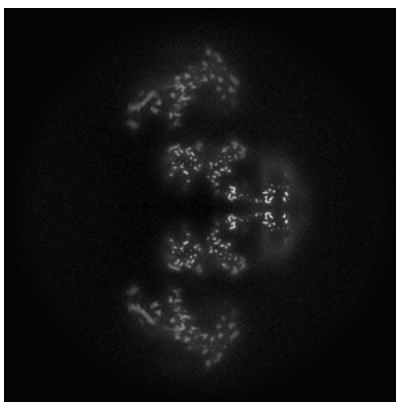
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

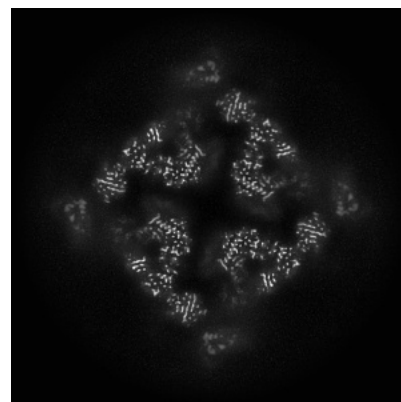
6.2.1 Primary map



X Index: 256



Y Index: 256

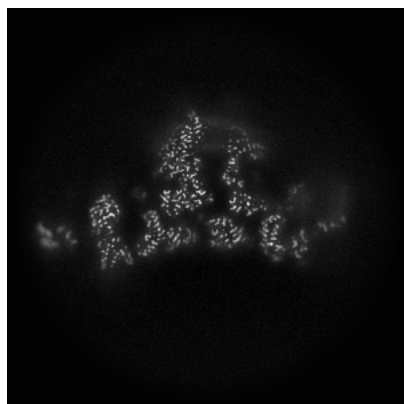


Z Index: 256

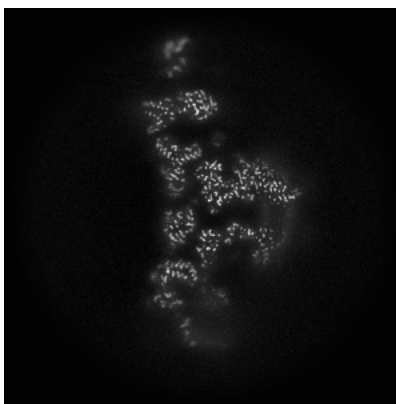
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

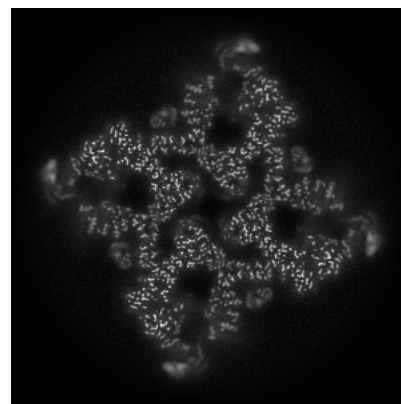
6.3.1 Primary map



X Index: 220



Y Index: 220

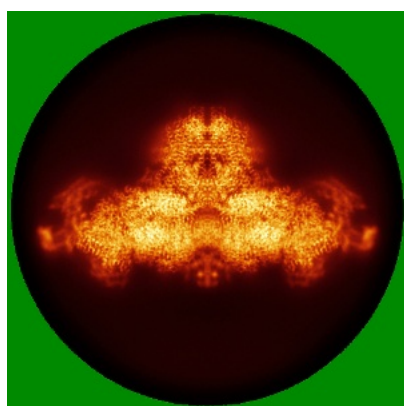


Z Index: 223

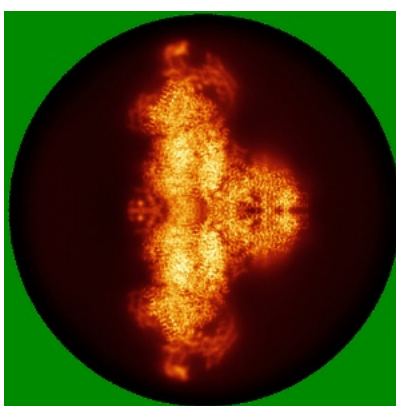
The images above show the largest variance slices of the map in three orthogonal directions.

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

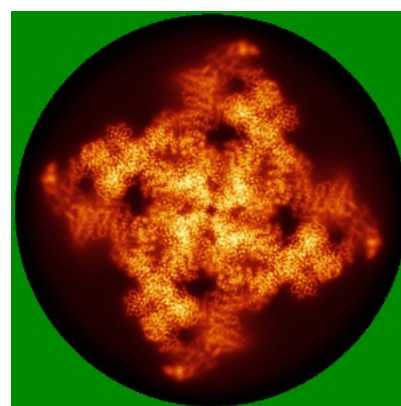
6.4.1 Primary map



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

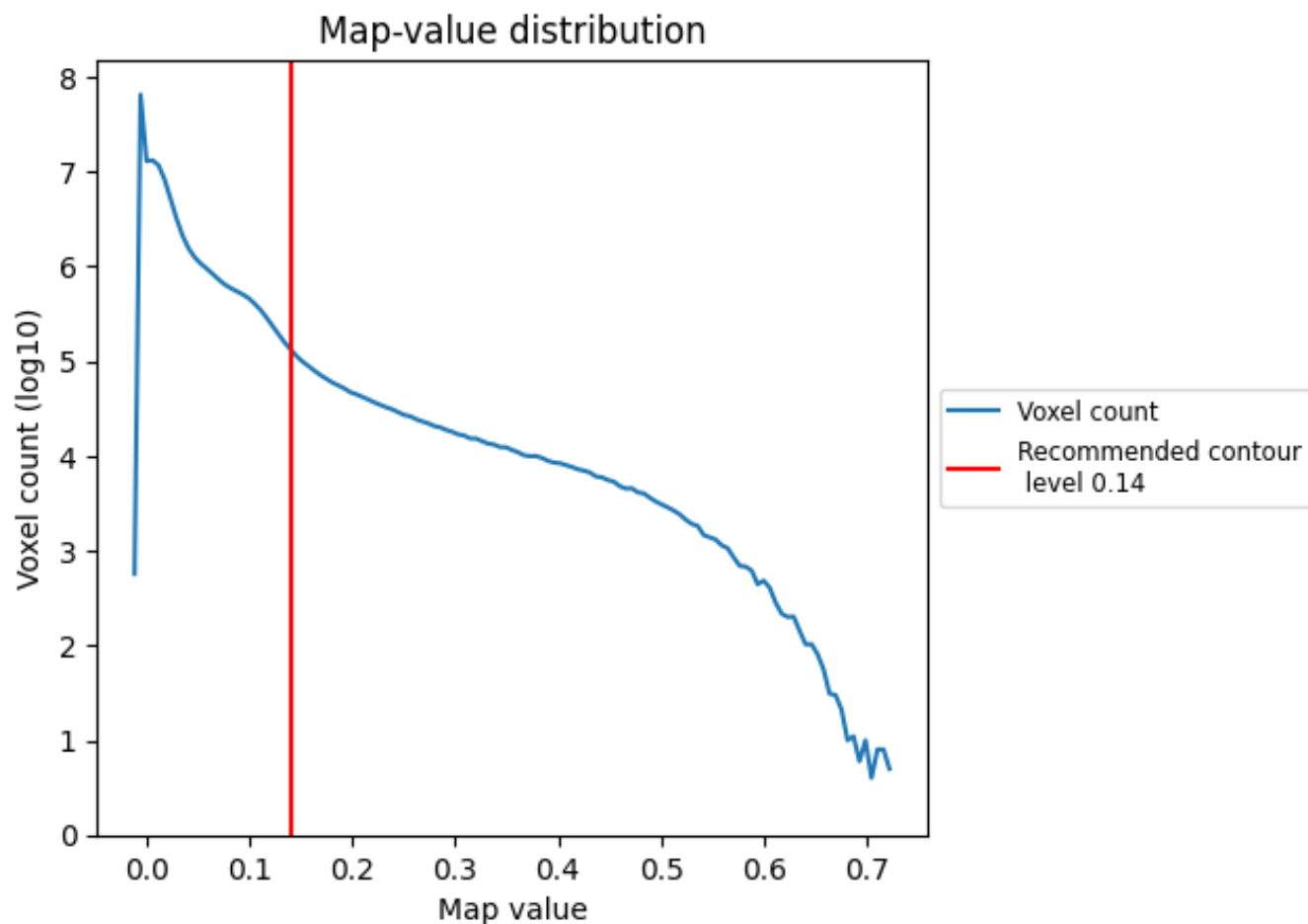
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

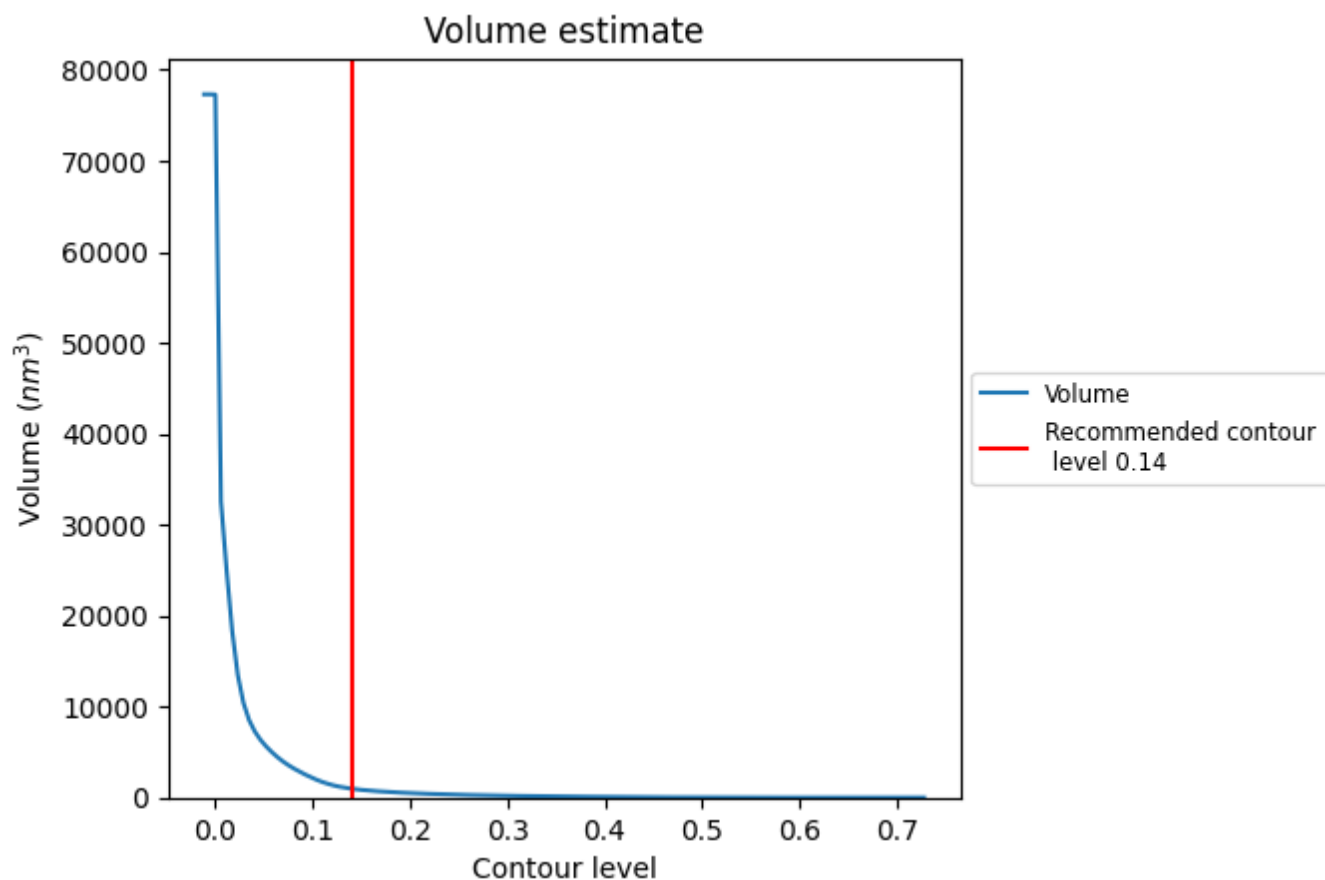
This section contains the results of statistical analysis of the map.

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.

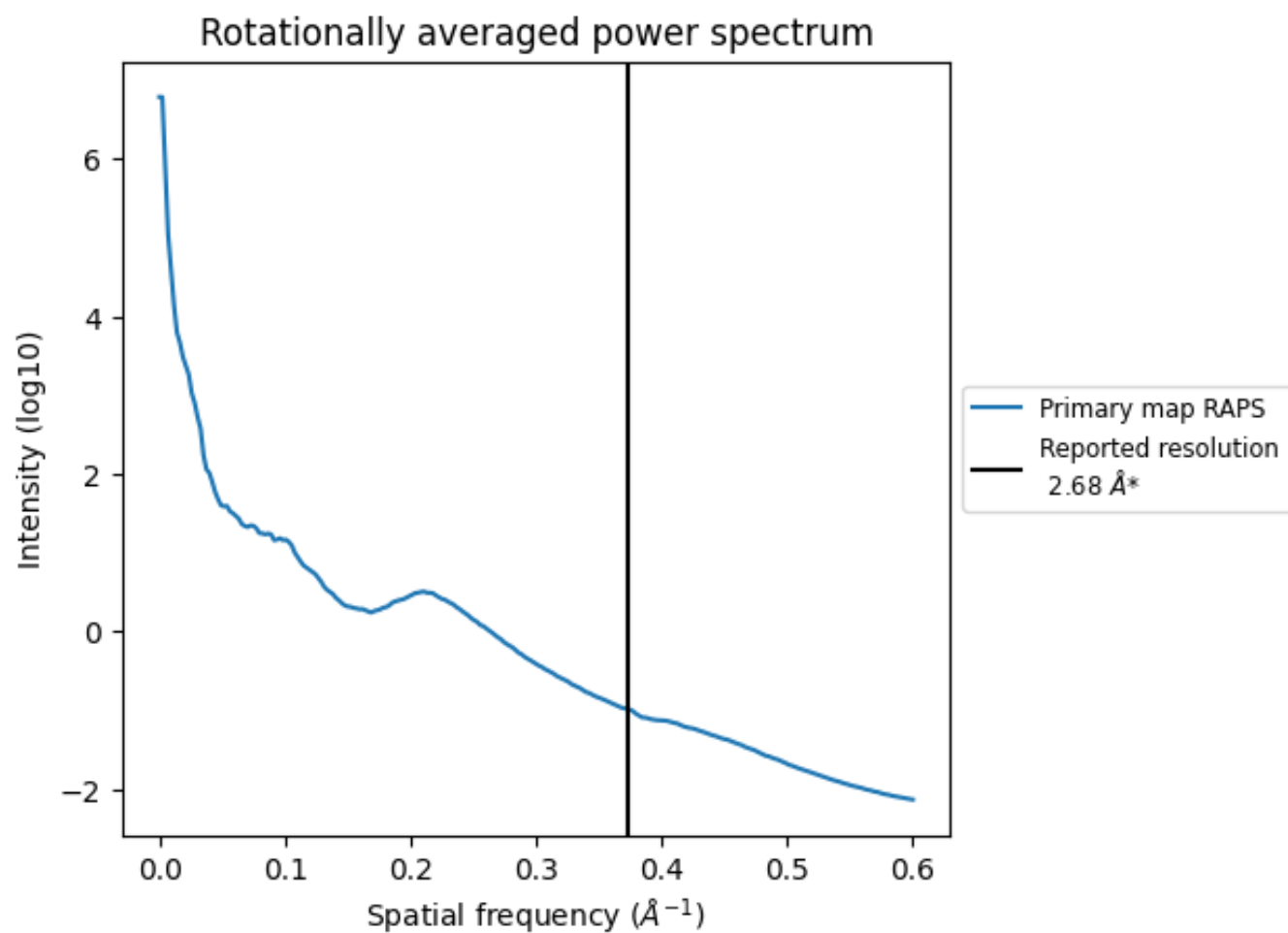
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 973 nm³; this corresponds to an approximate mass of 879 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 0.373 Å⁻¹

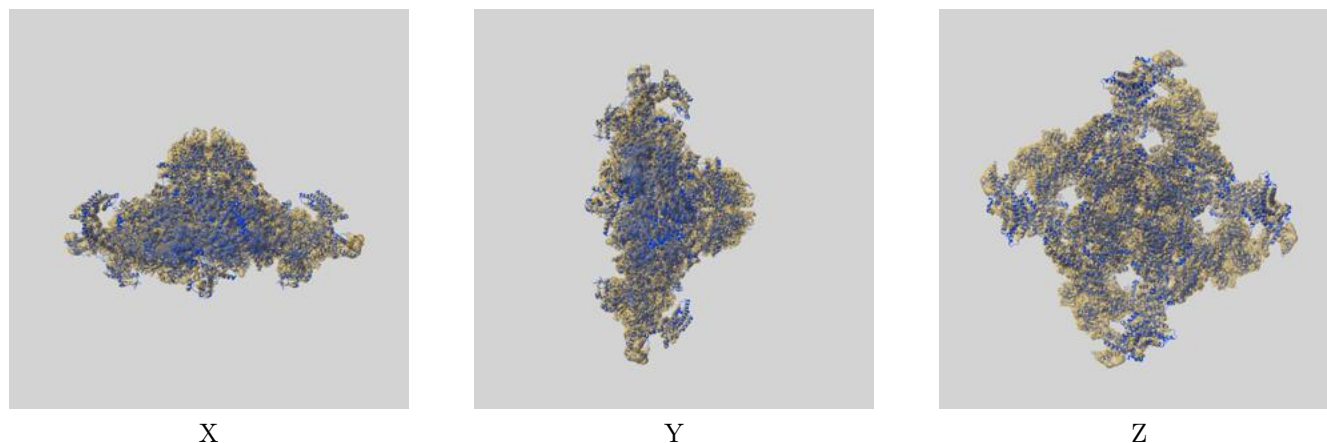
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

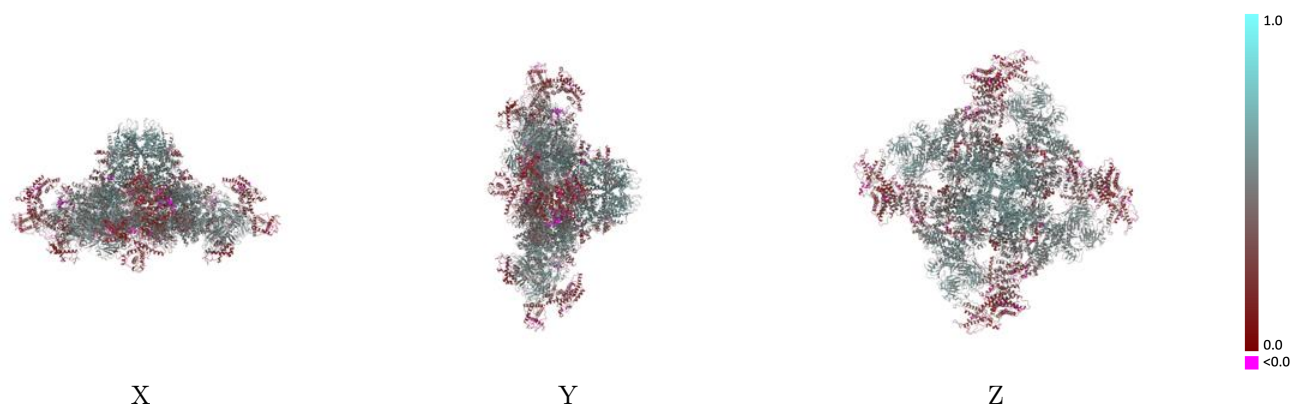
This section contains information regarding the fit between EMDB map EMD-26408 and PDB model 7U9T. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



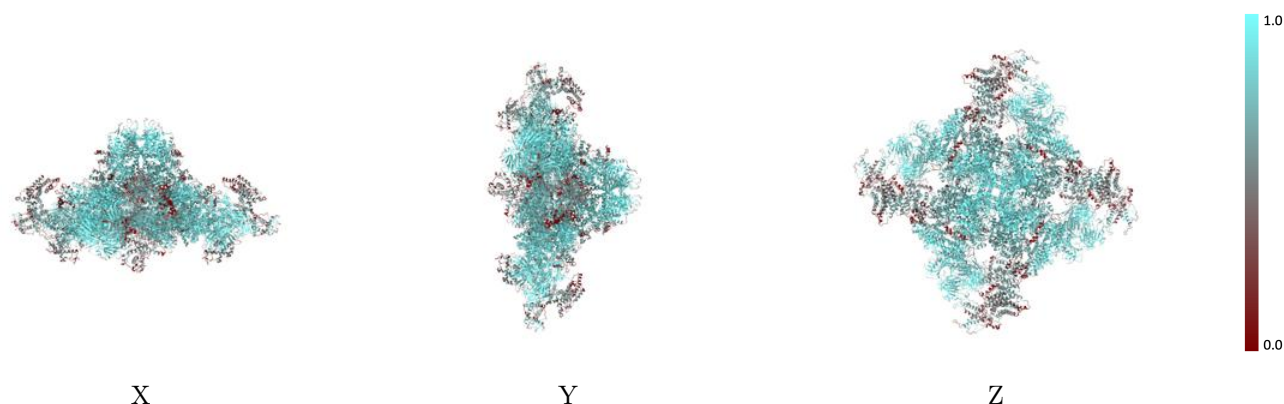
The images above show the 3D surface view of the map at the recommended contour level 0.14 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



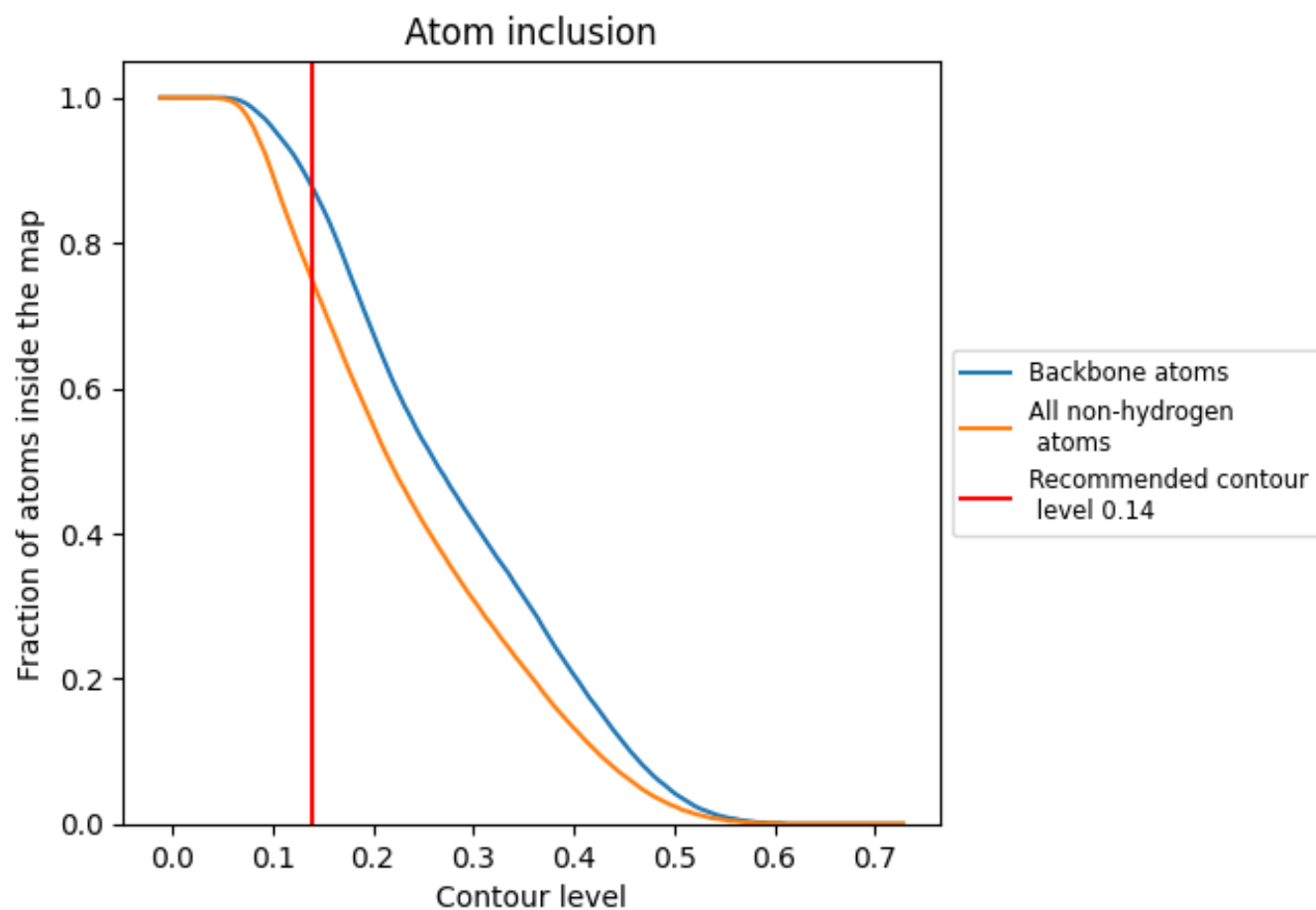
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.14).

9.4 Atom inclusion ⓘ



At the recommended contour level, 88% of all backbone atoms, 75% 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 (0.14) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7470	<div></div> 0.4270
A	<div></div> 0.7580	<div></div> 0.4290
B	<div></div> 0.7570	<div></div> 0.4370
C	<div></div> 0.7560	<div></div> 0.4270
D	<div></div> 0.7570	<div></div> 0.4350
E	<div></div> 0.8940	<div></div> 0.5320
F	<div></div> 0.8900	<div></div> 0.5210
G	<div></div> 0.9020	<div></div> 0.5370
H	<div></div> 0.9130	<div></div> 0.5530
I	<div></div> 0.3320	<div></div> 0.1940
J	<div></div> 0.3090	<div></div> 0.1570
K	<div></div> 0.3330	<div></div> 0.1800
L	<div></div> 0.3360	<div></div> 0.1990

1.0

0.0

<0.0