



## wwPDB EM Validation Summary Report ⓘ

Mar 2, 2024 – 07:20 PM EST

PDB ID : 5TAQ  
EMDB ID : EMD-8382  
Title : Structure of rabbit RyR1 (Caffeine/ATP/Ca<sup>2+</sup> dataset, class 3&4)  
Authors : Clarke, O.B.; des Georges, A.; Zalk, R.; Marks, A.R.; Hendrickson, W.A.;  
Frank, J.  
Deposited on : 2016-09-10  
Resolution : 4.10 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

---

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

EMDB validation analysis : 0.0.1.dev70  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

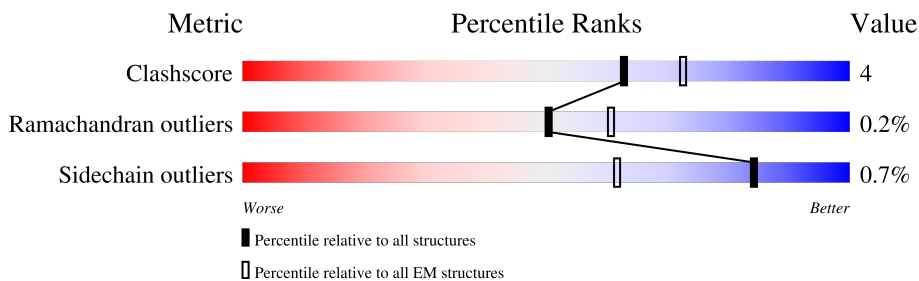
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.10 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	108	
1	F	108	
1	H	108	
1	J	108	
2	B	4416	
2	E	4416	
2	G	4416	
2	I	4416	

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 121456 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

- Molecule 2 is a protein called Ryanodine receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	4194	29499	18686	5228	5428	157	0	0
2	E	4194	29499	18686	5228	5428	157	0	0
2	I	4194	29499	18686	5228	5428	157	0	0
2	G	4194	29499	18686	5228	5428	157	0	0

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula:  $C_{10}H_{16}N_5O_{13}P_3$ ).



Mol	Chain	Residues	Atoms				AltConf
4	B	1	Total	C	N	O	0
			14	8	4	2	
4	E	1	Total	C	N	O	0
			14	8	4	2	
4	I	1	Total	C	N	O	0
			14	8	4	2	
4	G	1	Total	C	N	O	0
			14	8	4	2	

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

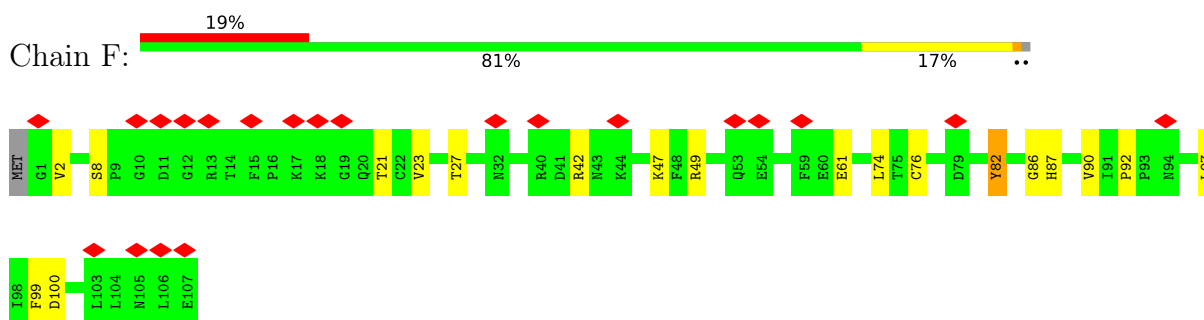
- Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

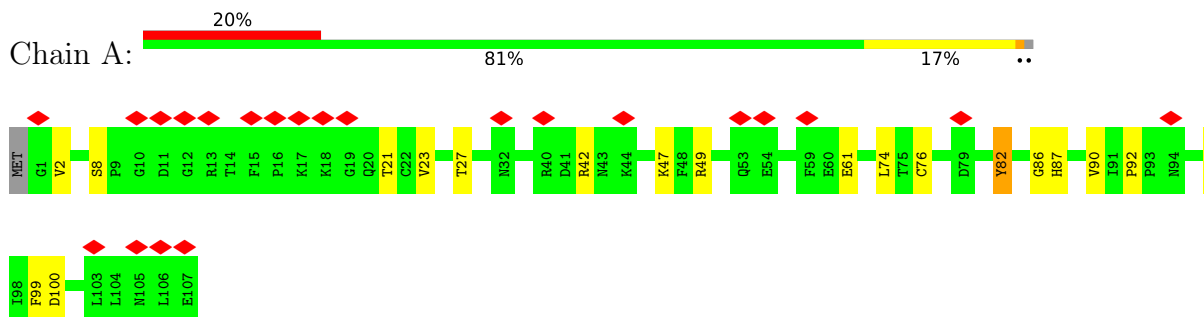
### 3 Residue-property plots [i](#)

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

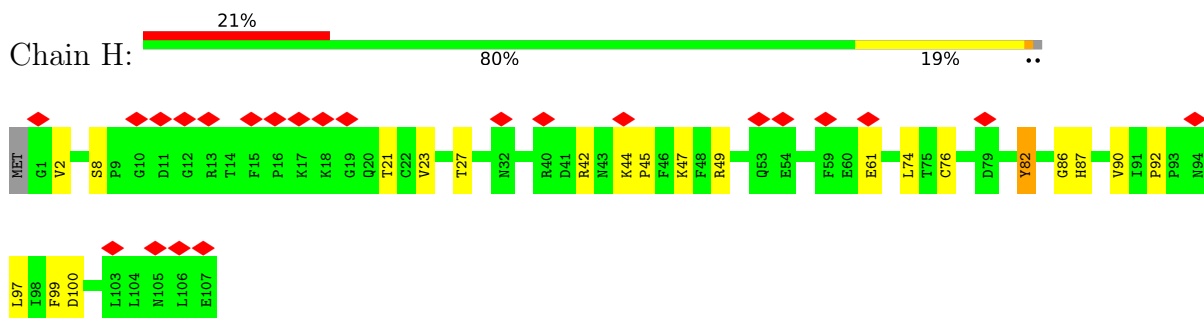
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



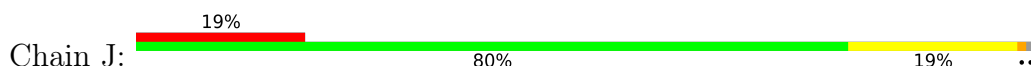
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

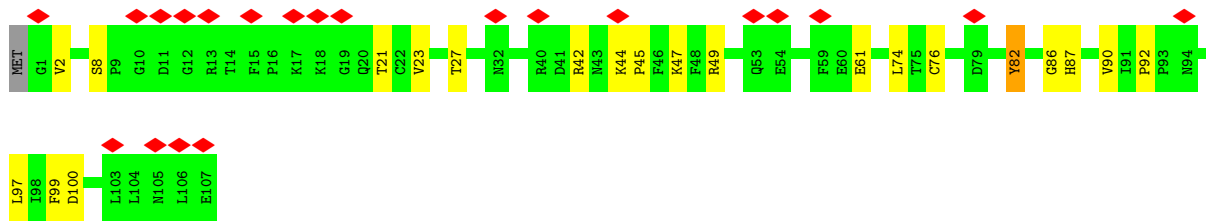


- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

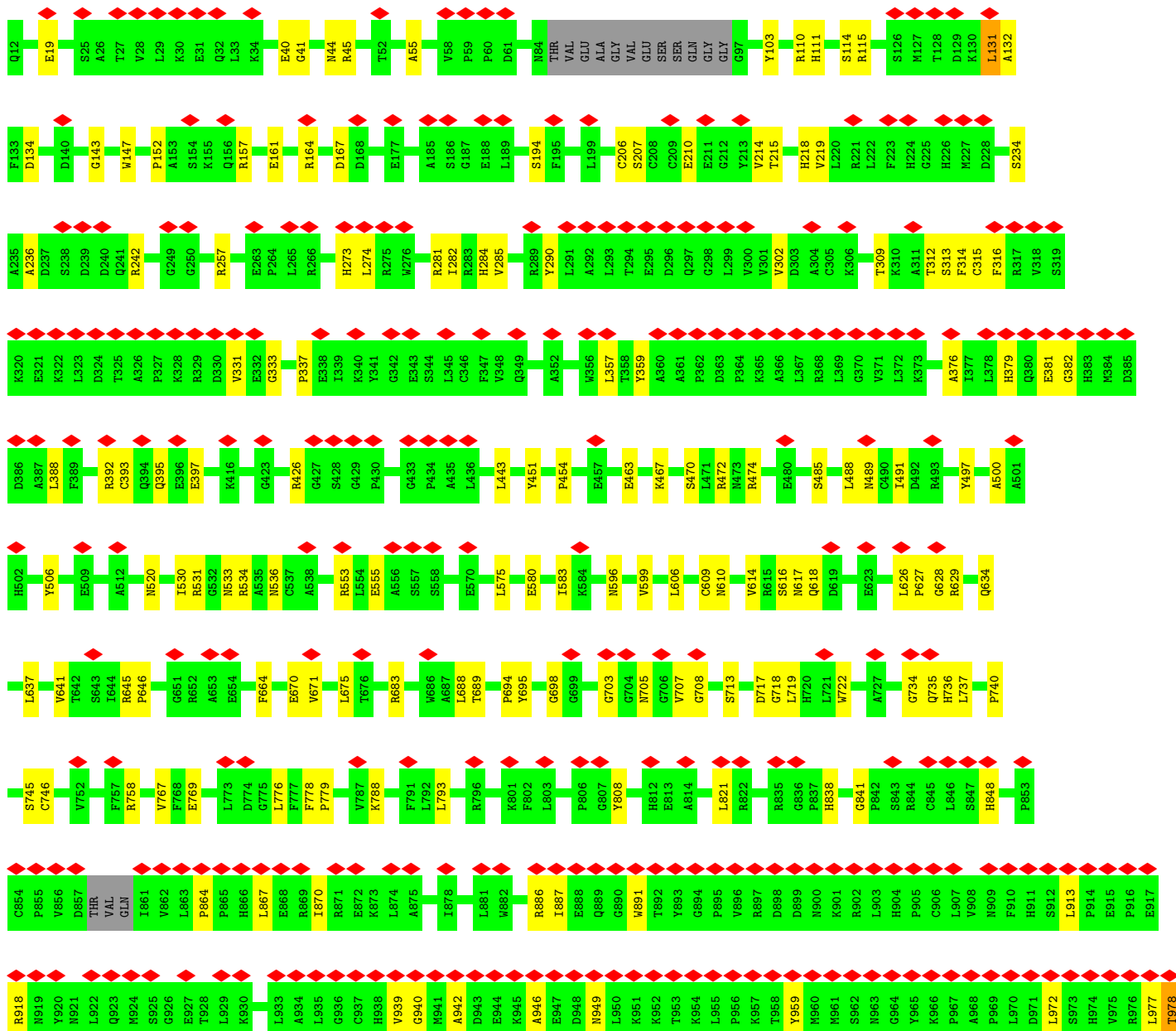
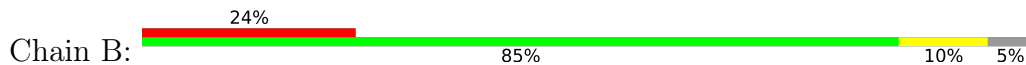


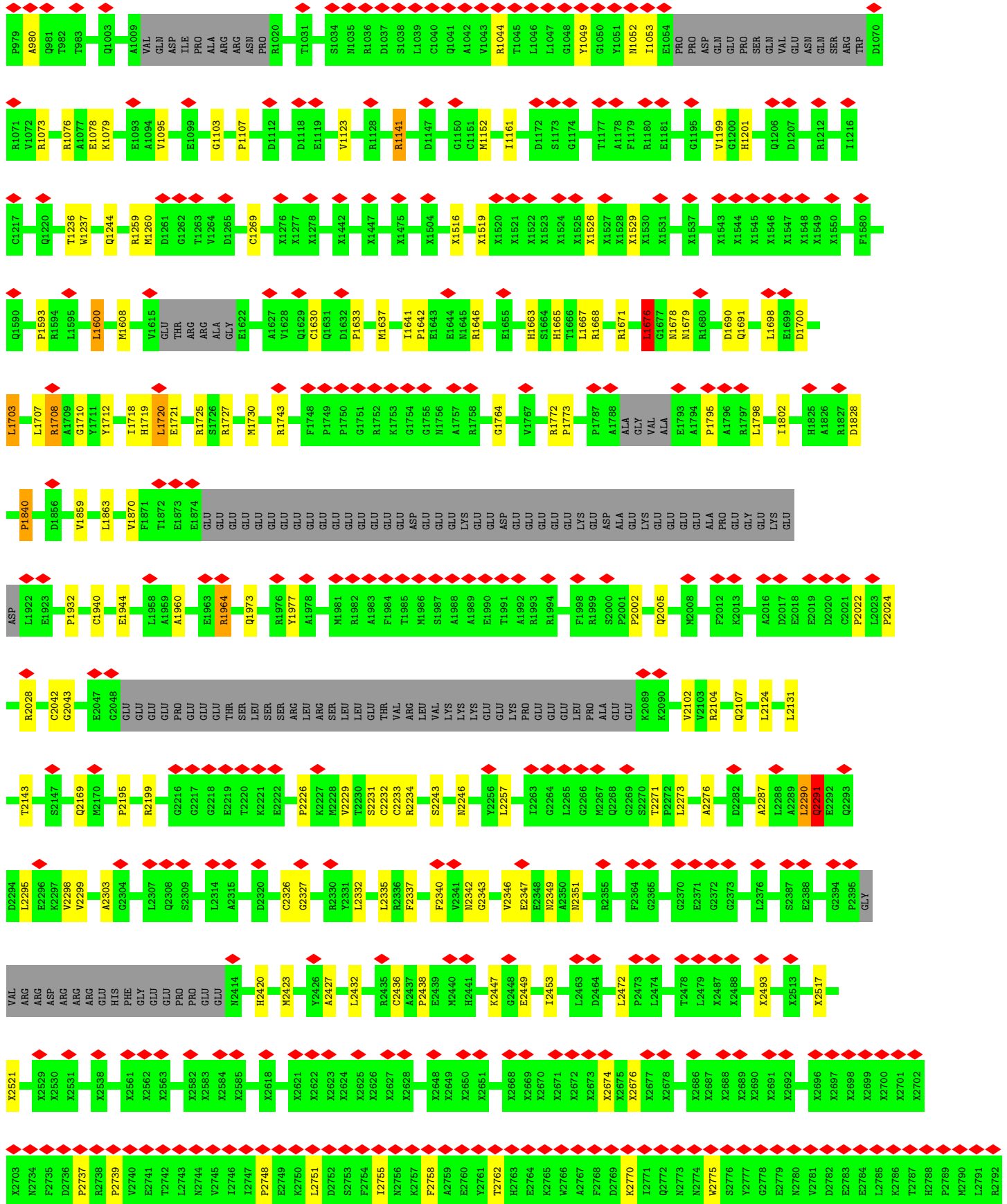
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B





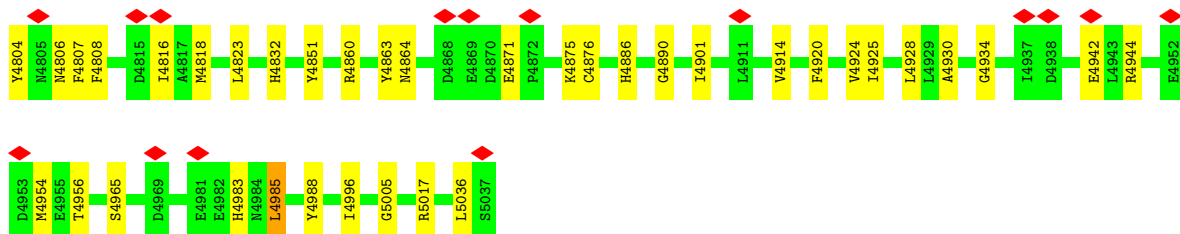
• Molecule 2: Ryanodine receptor 1



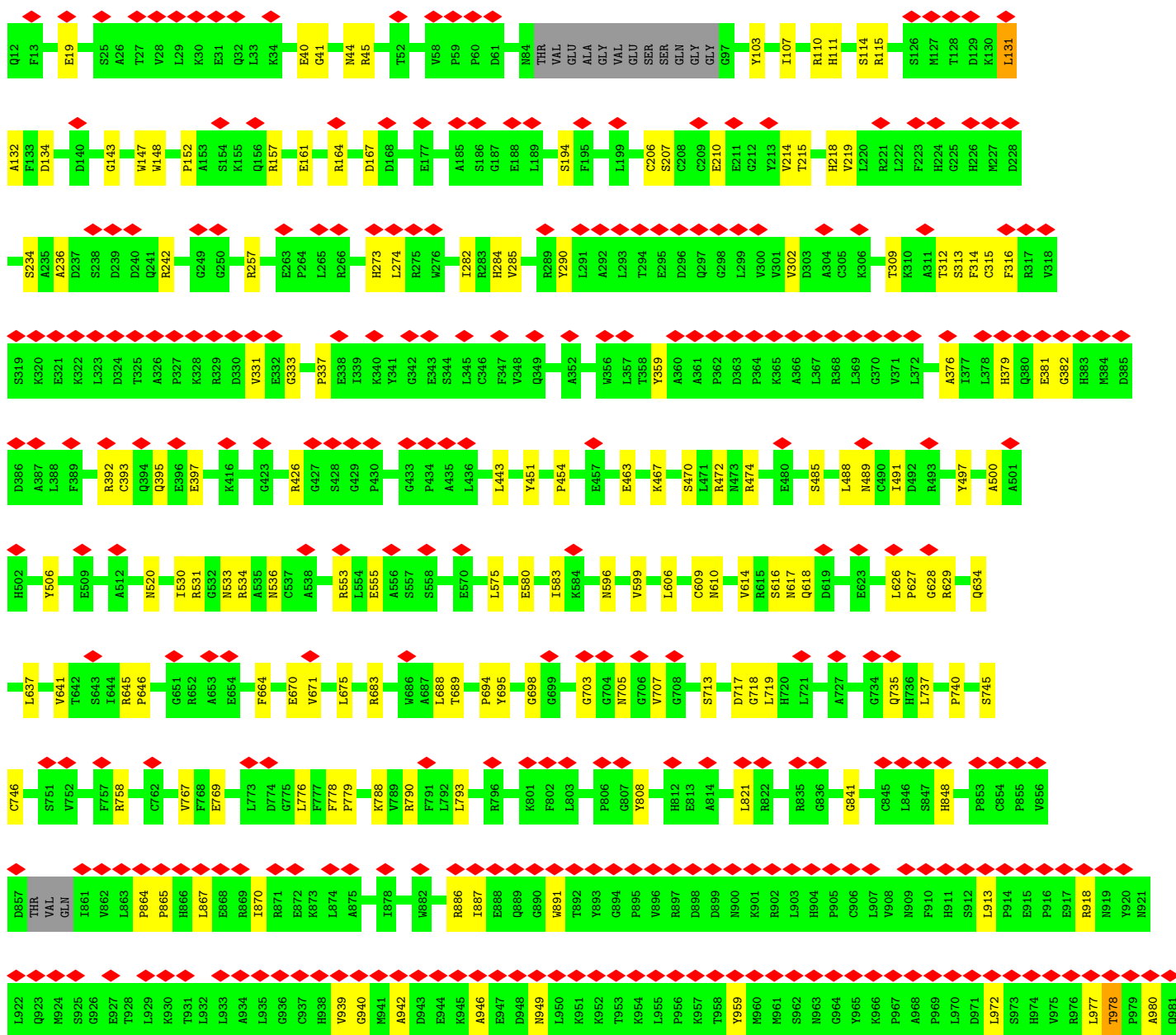
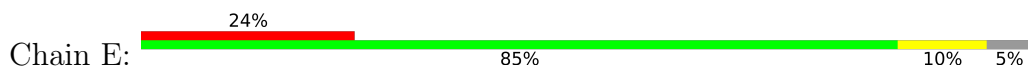




M4639	F4540	D4070	K3815	I3662	X3530	X3378	X3274	X3177	X3010	A2913	GLU
E4640	R4546	D4079	L3842	E3665	X3533	X3381	X3275	X3190	X3019	K2914	GLY
A4642	Y4560	Y4090	D3843	D3666	X3534	X3385	X3276	X3191	X3020	E2915	Y2855
C4645	L4567	D4083	Q3850	H3667	X3540	X3386	X3277	X3192	X3021	K2916	N2856
V4666	A4570	P4084	G3857	S3668	X3543	X3387	X3278	X3193	X3022	R2917	P2857
V4669	M4574	R4085	V3858	K3679	X3544	X3388	X3279	X3194	X3023	R2918	Q2858
R4673	M4582	G4086	N3859	A3680	X3545	X3389	X3280	X3195	D2919	D2920	P2859
E4674	P4587	K4091	E3861	Q3681	X3546	X3390	X3281	X3196	R2921	R2860	P2860
K4680	P4587	K4095	D3862	E3682	X3547	X3391	X3282	X3197	E2922	D2861	D2801
L4686	GLY	A4096	G3863	E3683	X3548	X3392	X3283	L2862	L2862	L2862	L2862
Y4687	GLU	M4097	T3864	E3684	X3549	X3393	X3284	S2863	S2863	G2864	E2803
I4688	ASP	D4098	V3865	E3685	X3550	X3394	X3285	G2864	G2864	G2864	T2804
D4695	ASP	T4104	V3866	E3686	X3553	X3395	X3286	Y2865	Y2865	Y2865	Y2805
D4696	MET	P4106	N3867	E3687	X3554	X3396	X3287	L2867	L2867	L2867	R2806
V4697	GLY	G4105	R3868	E3688	X3555	X3397	X3288	L2868	L2868	L2868	W2807
G4699	GLY	P4106	Q3869	E3689	X3558	X3398	X3289	R2869	R2869	R2869	P2808
Y4715	ALA	N4120	E3691	E3690	X3559	X3399	X3290	E2870	E2870	E2870	L2810
H4728	ALA	M4142	E3692	V3690	X3560	X3400	X3291	L2871	L2871	L2871	E2811
G4729	ALA	V4145	E3693	E3692	X3561	X3401	X3292	Q2872	Q2872	Q2872	S2812
M4743	ASP	E4152	E3712	K3693	X3562	X3402	X3293	M2874	M2874	M2874	L2813
D4744	LEU	E4152	K3713	E3711	X3563	X3403	X3294	G2875	G2875	G2875	L2814
L4745	ALA	E4152	S3714	E3712	X3564	X3404	X3295	A2876	A2876	A2876	A2815
A4746	ALA	P4155	S3715	E3713	X3565	X3405	X3296	E2876	E2876	E2876	M2816
T4751	GLY	H4156	E3714	E3714	X3566	X3406	X3297	Q2877	Q2877	Q2877	M2817
A4752	GLY	P4155	E3715	S3714	X3567	X3407	X3298	L2878	L2878	L2878	L2818
H4753	GLY	H4156	E3716	E3715	X3568	X3408	X3299	E2880	E2880	E2880	W2819
R4756	GLY	Y4173	E3717	E3716	X3569	X3409	X3300	N2881	N2881	N2881	E2820
R4757	GLY	R4180	E3718	E3717	X3570	X3410	X3301	Y2882	Y2882	Y2882	W2821
P4758	GLY	T3919	E3719	E3718	X3576	X3411	X3302	H2883	H2883	H2883	T2822
P4760	GLY	S3929	E3720	E3719	X3580	X3412	X3303	N2884	N2884	N2884	L2823
P4761	GLY	D3932	E3721	E3720	X3581	X3413	X3304	Y2885	Y2885	Y2885	E2824
P4762	GLY	Y3937	E3722	E3721	X3582	X3414	X3305	W2886	W2886	W2886	A2825
G4763	GLY	M3955	E3723	E3722	X3583	X3415	X3306	G2887	G2887	G2887	R2827
L4764	GLY	Q3960	E3724	E3723	X3584	X3416	X3307	R2888	R2888	R2888	E2828
L4765	GLY	G3971	E3725	E3724	X3585	X3417	X3308	K2889	K2889	K2889	G2829
L4766	GLY	R3984	E3726	E3725	X3586	X3418	X3309	L2890	L2890	L2890	E2830
L4767	GLY	K4002	E3727	E3726	X3587	X3419	X3310	K2891	K2891	K2891	GLU
L4768	GLY	Q3960	E3728	E3727	X3588	X3420	X3311	Q2892	Q2892	Q2892	GLU
M4769	GLY	G3971	E3729	E3728	X3589	X3421	X3312	E2893	E2893	E2893	ARG
H4798	GLY	D4046	E3730	E3729	X3590	X3422	X3313	L2894	L2894	L2894	THR
L4801	GLY	D4063	E3731	E3730	X3609	X3423	X3314	E2895	E2895	E2895	LYS
H4803	GLY	L4066	E3732	E3731	X3610	X3424	X3315	A2896	A2896	A2896	LYS
			E3733	E3732	X3611	X3425	X3316	K2897	K2897	K2897	LYS
			Q3781	E3733	X3612	X3426	X3317	G2898	G2898	G2898	THR
			S3784	E3734	X3613	X3427	X3318	G2899	G2899	G2899	ARG
			K3787	E3735	X3614	X3428	X3319	G2900	G2900	G2900	LYS
			L3804	E3736	X3615	X3429	X3320	T2901	T2901	T2901	ILE
			L3805	E3737	X3616	X3430	X3321	G2902	G2902	G2902	SER
			N3809	E3738	X3617	X3431	X3322	H2902	H2902	H2902	THR
				E3739	X3618	X3432	X3323	P2903	P2903	P2903	ALA
				E3740	X3619	X3433	X3324	L2904	L2904	L2904	ALA
				E3741	X3620	X3434	X3325	L2905	L2905	L2905	GLN
				E3742	X3621	X3435	X3326	L2906	L2906	L2906	THR
				E3743	X3622	X3436	X3327	P2907	P2907	P2907	TVR
				E3744	X3623	X3437	X3328	Y2908	Y2908	Y2908	ASP
				E3745	X3624	X3438	X3329	L2910	L2910	L2910	PRO
				E3746	X3625	X3439	X3330	L2911	L2911	L2911	ARG
				E3747	X3626	X3440	X3331	L2912	L2912	L2912	ARG
				E3748	X3627	X3441	X3332				
				E3749	X3628	X3442	X3333				
				E3750	X3629	X3443	X3334				
				E3751	X3630	X3444	X3335				
				E3752	X3631	X3445	X3336				
				E3753	X3632	X3446	X3337				
				E3754	X3633	X3447	X3338				
				E3755	X3634	X3448	X3339				
				E3756	X3635	X3449	X3340				
				E3757	X3636	X3450	X3341				
				E3758	X3637	X3451	X3342				
				E3759	X3638	X3452	X3343				
				E3760	X3639	X3453	X3344				
				E3761	X3640	X3454	X3345				
				E3762	X3641	X3455	X3346				
				E3763	X3642	X3456	X3347				
				E3764	X3643	X3457	X3348				
				E3765	X3644	X3458	X3349				
				E3766	X3645	X3459	X3350				
				E3767	X3646	X3460	X3351				
				E3768	X3647	X3461	X3352				
				E3769	X3648	X3462	X3353				
				E3770	X3649	X3463	X3354				
				E3771	X3650	X3464	X3355				
				E3772	X3651	X3465	X3356				
				E3773	X3652	X3466	X3357				
				E3774	X3653	X3467	X3358				
				E3775	X3654	X3468	X3359				
				E3776	X3655	X3469	X3360				
				E3777	X3656	X3470	X3361				
				E3778	X3657	X3471	X3362				
				E3779	X3658	X3472	X3363				
				E3780	X3659	X3473	X3364				
				E3781	X3660	X3474	X3365				
				E3782	X3661	X3475	X3366				
				E3783	X3662	X3476	X3367				
				E3784	X3663	X3477	X3368				
				E3785	X3664	X3478	X3369				
				E3786	X3665	X3479	X3370				
				E3787	X3666	X3480	X3371				
				E3788	X3667	X3481	X3372				
				E3789	X3668	X3482	X3373				
				E3790	X3669	X3483	X3374				
				E3791	X3670	X3484	X3375				
				E3792	X3671	X3485	X3376				
				E3793	X3672	X3486	X3377				
				E3794	X3673	X3487	X3378				
				E3795	X3674	X3488	X3379				
				E3796	X3675	X3489	X3380				
				E3797	X3676	X3490	X3381				
				E3798	X3677	X3491	X3382				
				E3799	X3678	X3492	X3383				
				E3800	X3679	X3493	X3384				
				E3801	X3680	X3494	X3385				
				E3802	X3681	X3495	X3386				
				E3803	X3682	X3496	X3387				
				E3804	X3683	X3497	X3388				
				E3805	X3684	X3498	X3389				
				E3806	X3685	X3499	X3390				
				E3807	X3686	X3500	X3391				

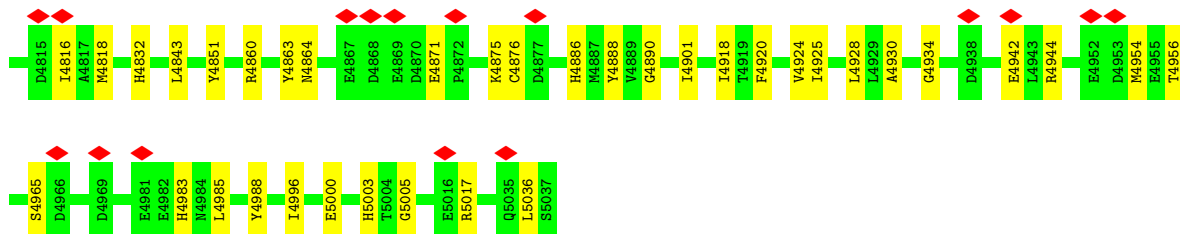


• Molecule 2: Ryanodine receptor 1

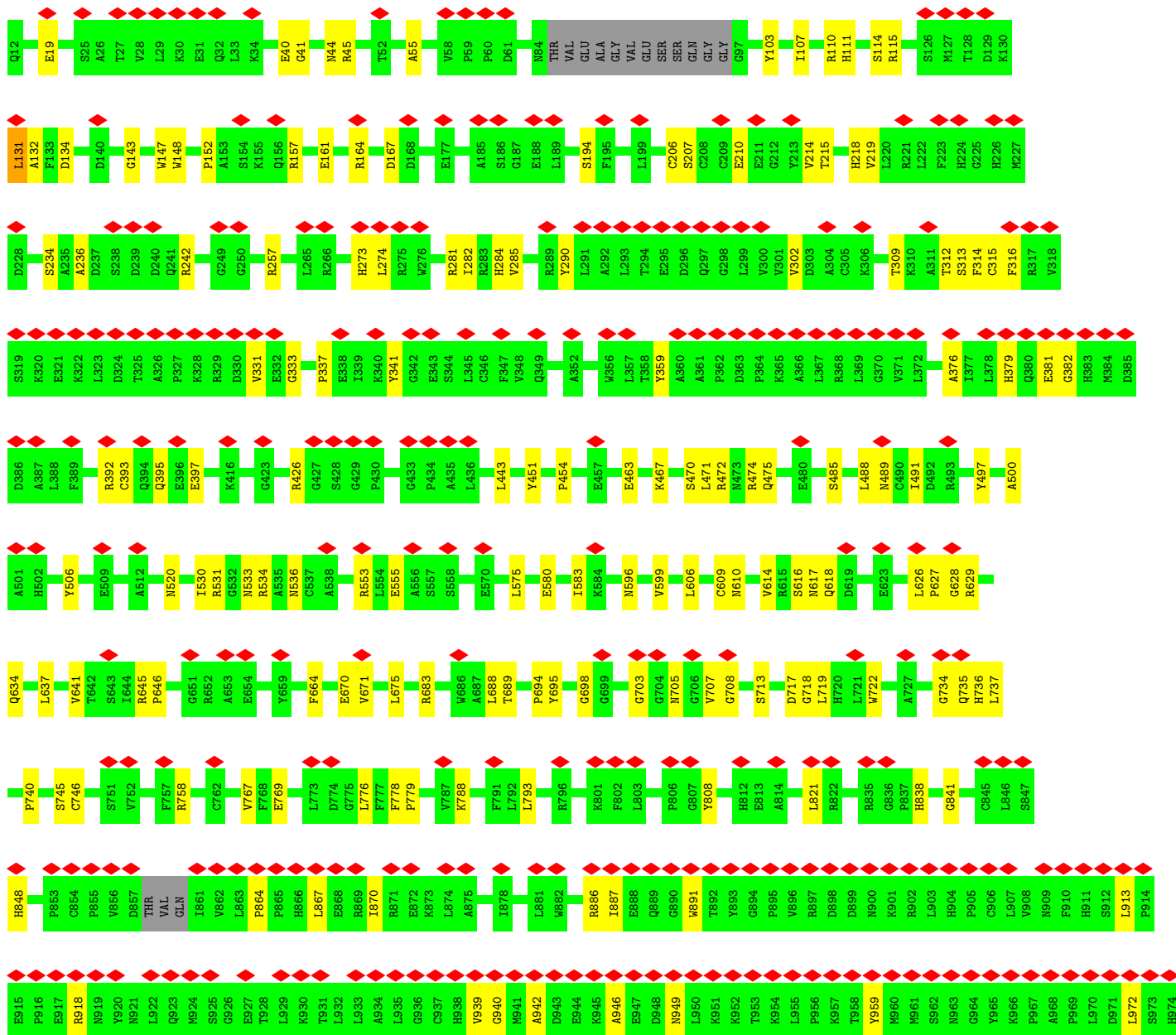
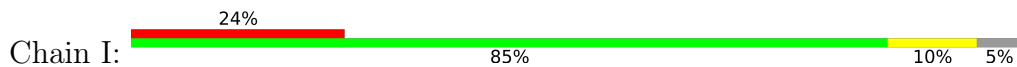


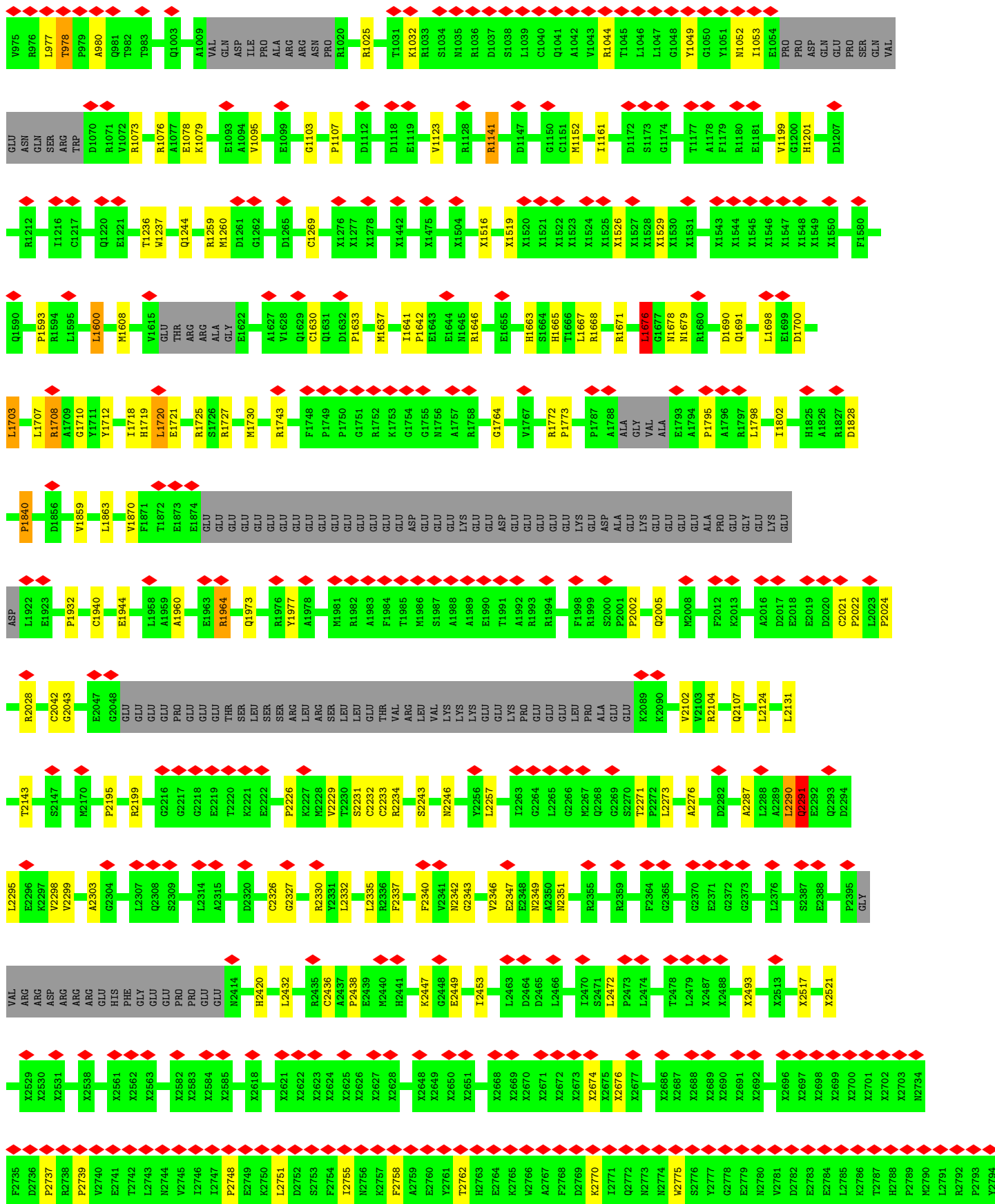


C4645	Y4560	D4070	I3804	X3513	X3369	X3270	X3177	X3019	E2915	Y2855	K2795
Y4666	L4567	D4079	L3805	X3514	X3370	X3271	X3178	X3020	K2916	N2856	T2796
Y4669	A4570	Y4090	X3515	X3520	X3373	X3274	X3179	X3021	A2917	P2857	F2797
R4673	M4574	D4083	X3530	X3534	X3374	X3275	X3190	X3022	R2918	Q2858	S2798
E4674	V4582	P4094	X3534	X3540	X3378	X3276	X3191	X3023	D2919	P2859	E2799
R4675	P4587	R4095	X3540	X3543	X3381	X3277	X3193	X3027	R2920	P2860	K2800
K4680	GLY	D4096	X3544	X3546	X3387	X3278	X3194	X3037	E2921	D2861	D2801
L4686	GLU	K4091	X3546	X3547	X3388	X3281	X3195	X3038	K2922	L2862	K2802
Y4687	ASP	A4097	X3548	X3553	X3385	X3282	X3196	X3039	A2923	S2863	E2803
L4688	MET	A4098	X3549	X3554	X3386	X3284	X3197	X3040	G2924	G2864	T2804
D4694	GLU	D4098	X3549	X3555	X3387	X3285	X3200	X3041	E2925	V2865	Y2805
D4695	GLY	T4104	X3550	X3558	X3388	X3286	X3207	X3042	L2926	T2866	R2806
D4696	ALA	G4105	X3553	X3559	X3389	X3287	X3207	X3043	K2927	L2867	W2807
V4697	ALA	P4106	X3554	X3560	X3390	X3287	X3207	X3044	L2928	S2868	P2808
K4698	GLY	E3861	X3555	X3561	X3391	X3290	X3211	X3045	P2929	R2869	L2809
C4699	ASP	D3862	X3556	X3562	X3392	X3291	X3212	X3046	L2930	E2870	K2810
Y4715	LEU	G3863	X3557	X3563	X3393	X3292	X3213	X3047	Q2931	Q2872	E2811
H4728	ALA	E3864	X3558	X3564	X3394	X3295	X3214	X3048	M2933	A2873	S2812
H4729	ALA	V3865	X3559	X3565	X3395	X3296	X3215	X3049	G2934	A2874	L2813
M4743	GLY	I3866	X3560	X3566	X3396	X3297	X3216	X3050	Y2935	M2875	A2815
D4744	GLY	N3867	X3561	X3567	X3397	X3298	X3217	X3053	V2937	E2876	W2816
L4745	GLY	R3868	X3562	X3568	X3398	X3299	X3218	X3054	Q2938	Q2877	L2817
A4746	GLY	N3870	X3563	X3569	X3399	X3300	X3219	X3055	T2938	L2878	A2818
T4751	GLY	G3871	X3564	X3570	X3400	X3301	X3220	X3056	R2939	A2879	W2819
A4752	SER	E3872	X3565	X3571	X3401	X3302	X3221	X3057	K2942	E2880	E2820
H4753	TRP	K3715	X3566	X3576	X3402	X3323	X3222	X3060	X2943	N2881	W2821
R4756	GLY	E3736	X3567	X3577	X3403	X3324	X3226	X3061	X2944	Y2882	T2822
K4757	GLY	G3737	X3568	X3578	X3404	X3325	X3226	X3062	X2945	H2883	L2823
D4758	ALA	G3738	X3569	X3579	X3405	X3326	X3226	X3063	N2884	N2884	E2824
P4760	GLY	E3740	X3570	X3580	X3409	X3327	X3226	X3064	T2885	T2885	K2825
P4761	GLY	E3741	X3571	X3581	X3410	X3328	X3226	X3065	W2886	W2886	A2826
P4762	GLY	N3741	X3572	X3582	X3411	X3329	X3226	X3066	G2887	R2887	R2827
C4763	GLY	GLY	X3573	X3583	X3412	X3330	X3226	X3067	X2952	X2888	E2828
L4764	GLY	ALA	X3574	X3584	X3413	X3331	X3226	X3068	K2889	K2889	G2829
L4765	GLY	ALA	X3575	X3585	X3414	X3332	X3226	X3069	K2890	K2891	E2830
T4766	GLY	GLU	X3576	X3586	X3415	X3333	X3226	X3070	Q2892	Q2892	GLU
M4767	GLY	E3747	X3577	X3587	X3416	X3334	X3226	X3071	E2893	E2893	ARG
M4768	GLY	V3749	X3578	X3588	X3417	X3335	X3226	X3072	L2894	L2894	THR
M4769	GLY	E3750	X3579	X3589	X3418	X3336	X3226	X3073	E2895	E2895	LYS
M4798	ASP	E3754	X3580	X3590	X3419	X3337	X3226	X3074	K2897	K2897	LYS
L4801	ASP	T3772	X3581	X3609	X3421	X3338	X3226	X3075	G2898	G2898	THR
Y4804	ASP	R3773	X3582	X3610	X3422	X3339	X3226	X3076	G2899	G2899	LYS
M4805	ASP	E3777	X3583	X3611	X3423	X3340	X3226	X3077	SER	SER	ILE
M4806	ASP	M3778	X3584	X3612	X3424	X3341	X3226	X3078	GLN	GLN	SER
F4807	ASP	V3779	X3585	X3613	X3425	X3342	X3226	X3079	THR	THR	GLN
		Q3781	X3586	X3614	X3426	X3343	X3226	X3080	ALA	ALA	ALA
		S3784	X3587	X3615	X3427	X3344	X3226	X3081	THR	THR	THR
		K3787	X3588	X3616	X3428	X3345	X3226	X3082	P2903	P2903	ALA
			X3589	X3617	X3429	X3346	X3226	X3083	L2904	L2904	GLN
			X3590	X3618	X3430	X3347	X3226	X3084	L2905	L2905	TVR
			X3591	X3619	X3431	X3348	X3226	X3085	V2906	V2906	ASP
			X3592	X3620	X3432	X3349	X3226	X3086	P2907	P2907	PRO
			X3593	X3621	X3433	X3350	X3226	X3087	X3004	X3004	ARG
			X3594	X3622	X3434	X3351	X3226	X3088	X3005	X3005	GLU
			X3595	X3623	X3435	X3352	X3226	X3089	X3006	X3006	GLY
			X3596	X3624	X3436	X3353	X3226	X3090			
			X3597	X3625	X3437	X3354	X3226	X3091			
			X3598	X3626	X3438	X3355	X3226	X3092			
			X3599	X3627	X3439	X3356	X3226	X3093			
			X3600	X3628	X3440	X3357	X3226	X3094			
			X3601	X3629	X3441	X3358	X3226	X3095			
			X3602	X3630	X3442	X3359	X3226	X3096			
			X3603	X3631	X3443	X3360	X3226	X3097			
			X3604	X3632	X3444	X3361	X3226	X3098			
			X3605	X3633	X3445	X3362	X3226	X3099			
			X3606	X3634	X3446	X3363	X3226	X3100			
			X3607	X3635	X3447	X3364	X3226	X3101			
			X3608	X3636	X3448	X3365	X3226	X3102			
			X3609	X3637	X3449	X3366	X3226	X3103			
			X3610	X3638	X3450	X3367	X3226	X3104			
			X3611	X3639	X3451	X3368	X3226	X3105			
			X3612	X3640	X3452	X3369	X3226	X3106			
			X3613	X3641	X3453	X3370	X3226	X3107			
			X3614	X3642	X3454	X3371	X3226	X3108			
			X3615	X3643	X3455	X3372	X3226	X3109			
			X3616	X3644	X3456	X3373	X3226	X3110			
			X3617	X3645	X3457	X3374	X3226	X3111			
			X3618	X3646	X3458	X3375	X3226	X3112			
			X3619	X3647	X3459	X3376	X3226	X3113			
			X3620	X3648	X3460	X3377	X3226	X3114			
			X3621	X3649	X3461	X3378	X3226	X3115			
			X3622	X3650	X3462	X3379	X3226	X3116			
			X3623	X3651	X3463	X3380	X3226	X3117			
			X3624	X3652	X3464	X3381	X3226	X3118			
			X3625	X3653	X3465	X3382	X3226	X3119			
			X3626	X3654	X3466	X3383	X3226	X3120			
			X3627	X3655	X3467	X3384	X3226	X3121			
			X3628	X3656	X3468	X3385	X3226	X3122			
			X3629	X3657	X3469	X3386	X3226	X3123			
			X3630	X3658	X3470	X3387	X3226	X3124			
			X3631	X3659	X3471	X3388	X3226	X3125			
			X3632	X3660	X3472	X3389	X3226	X3126			
			X3633	X3661	X3473	X3390	X3226	X3127			
			X3634	X3662	X3474	X3391	X3226	X3128			
			X3635	X3663	X3475	X3392	X3226	X3129			
			X3636	X3664	X3476	X3393	X3226	X3130			
			X3637	X3665	X3477	X3394	X3226	X3131			
			X3638	X3666	X3478	X3395	X3226	X3132			
			X3639	X3667	X3479	X3396	X3226	X3133			
			X3640	X3668	X3480	X3397	X3226	X3134			
			X3641	X3669	X3481	X3398	X3226	X3135			
			X3642	X3670	X3482	X3399	X3226	X3136			
			X3643	X3671	X3483	X3400	X3226	X3137			
			X3644	X3672	X3484	X3401	X3226	X3138			
			X3645	X3673	X3485	X3402	X3226	X3139			
			X3646	X3674	X3486	X3403	X3226	X3140			
			X3647	X3675	X3487	X3404	X3226	X3141			
			X3648	X3676	X3488	X3405	X3226	X3142			
			X3649	X3677	X3489	X3406	X3226	X3143			
			X3650	X3678	X3490	X3407	X3226	X3144			
			X3651	X3679	X3491	X3408	X3226	X3145			
			X3652	X3680	X3492	X3409	X3226	X3146			
			X3653	X3681	X3493	X3410	X3226	X3147			
			X3654	X3682	X3494	X3411	X3226	X3148			
			X3655	X3683	X3495	X3412	X3226	X3149			
			X3656	X3684	X3496	X3413	X3226	X3150			
			X3657	X3685	X3497	X3414	X3226	X3151			
			X3658	X3686	X3498	X3415	X3226	X3152			
			X3659	X3687	X3499	X3416	X3226	X3153			
			X3660	X3688	X3500	X3417	X3226	X3154			
			X3661	X3689	X3501	X3418	X3226	X3155			
			X3662	X3690	X3502	X3419	X3226	X3156			
			X3663	X3691	X3503	X3420	X3226	X3157			
			X3664	X3692	X3504	X3421	X3226	X3158			
			X3665	X3693	X3505	X3422	X3226	X3159			
			X3666	X3694	X3506	X3423	X3226	X3160			
			X3667	X3695	X3507	X3424	X3226	X3161			
			X3668	X3696	X3508	X3425	X3226	X3162			
			X3669	X3697	X3509	X3426	X3226	X3163			
			X3670	X3698	X3510	X3427	X3226	X3164			
			X3671	X3699	X3511	X3428	X3226	X3165			

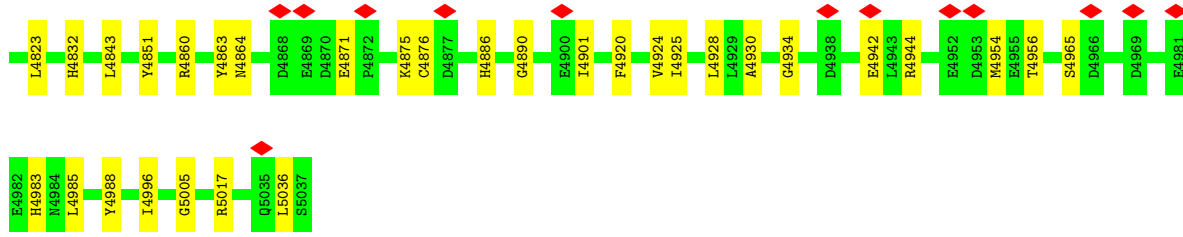


• Molecule 2: Ryanodine receptor 1

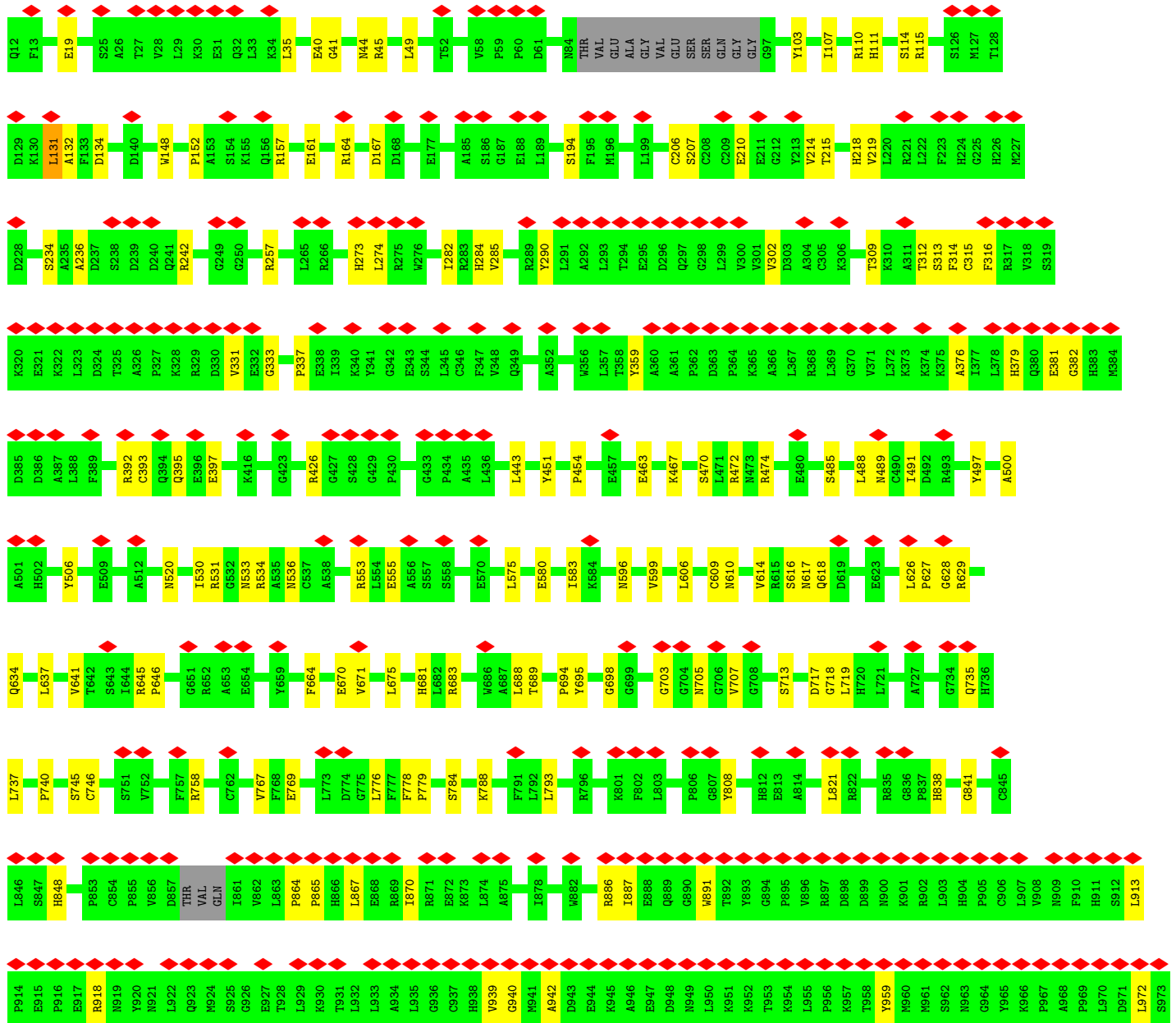
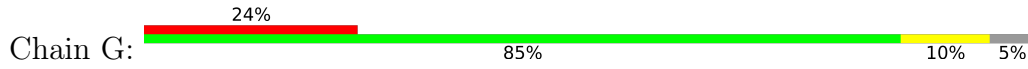




K2795	K2796	F2797	S2798	E2799	K2800	D2801	K2802	E2803	L2804	V2805	R2806	W2807	P2808	L2809	K2810	E2811	S2812	L2813	K2814	A2815	M2816	L2817	A2818	W2819	E2820	W2821	T2822	L2823	E2824	K2825	A2826	R2827	E2828	G2829	E2830	GLU	ARG	THR	GLU	LYS	LYS	LYS	THR	ARG	LYS	ILE	SER	GLN	THR	ALA	GLN	THR	TVR	ASP	PRO	ARG	GLU	GLY	
Y2855	N2856	P2857	Q2858	P2859	P2860	D2861	L2862	S2863	G2864	V2865	T2866	L2867	S2868	R2869	E2870	L2871	Q2872	A2873	M2874	A2875	E2876	Q2877	L2878	A2879	E2880	N2881	Y2882	H2883	N2884	T2885	W2886	G2887	R2888	K2889	K2890	K2891	Q2892	E2893	L2894	E2895	A2896	K2897	G2898	G2899	G2900	T2901	H2902	P2903	L2904	L2905	V2906	P2907	Y2908	D2909	T2910	L2911	L2912	A2913	K2914
E2915	K2916	A2917	R2918	D2919	R2920	E2921	K2922	A2923	Q2924	E2925	L2926	L2927	K2928	F2929	L2930	Q2931	M2932	M2933	G2934	Y2935	A2936	V2937	T2938	R2939	K2942	K2943	K2944	K2945	K2946	K2947	K2948	K2949	X2952	X2957	X2962	X2965	X2966	X2967	X2968	X2969	X2970	X2971	X2972	X2973	X2974	X2975	X2976	X2995	X2996	X2997	X3003	X3004	X3005	X3006					
X3010	X3019	X3020	X3021	X3022	X3023	X3027	X3037	X3038	X3039	X3040	X3041	X3042	X3043	X3044	X3045	X3046	X3047	X3048	X3049	X3050	X3053	X3054	X3055	X3060	X3061	X3062	X3063	X3134	X3135	X3136	X3137	X3138	X3142	X3143	X3144	X3153	X3154	X3155	X3156	X3157	X3158	X3159	X3160	X3161	X3162	X3163	X3170	X3171	X3172	X3173	X3174								
X3177	X3178	X3179	X3190	X3191	X3192	X3193	X3194	X3195	X3196	X3197	X3200	X3207	X3211	X3212	X3213	X3214	X3215	X3216	X3217	X3218	X3219	X3220	X3221	X3222	X3230	X3231	X3232	X3233	X3234	X3235	X3236	X3241	X3242	X3243	X3244	X3245	X3246	X3247	X3248	X3249	X3250	X3251	X3252	X3253	X3254	X3261	X3262	X3263	X3267	X3268	X3269	X3270							
X3271	X3274	X3275	X3276	X3277	X3278	X3279	X3280	X3281	X3284	X3285	X3286	X3287	X3290	X3291	X3292	X3295	X3296	X3313	X3314	X3318	X3330	X3331	X3332	X3333	X3334	X3335	X3336	X3337	X3338	X3339	X3340	X3341	X3342	X3348	X3349	X3350	X3351	X3352	X3358	X3359	X3360	X3361	X3362	X3365	X3366	X3369	X3370												
X3373	X3374	X3378	X3381	X3385	X3386	X3387	X3388	X3389	X3390	X3391	X3392	X3393	X3394	X3395	X3396	X3397	X3398	X3399	X3400	X3401	X3402	X3403	X3404	X3405	X3409	X3410	X3411	X3412	X3413	X3414	X3421	X3433	X3436	X3441	X3452	X3453	X3454	X3455	X3456	X3464	X3467	X3468	X3511	X3512	X3513	X3514	X3515												
X3520	X3530	X3533	X3534	X3540	X3543	X3544	X3545	X3546	X3547	X3548	X3549	X3550	X3553	X3554	X3558	X3559	X3560	X3561	X3562	X3563	X3564	X3565	X3566	X3567	X3568	X3576	X3580	X3581	X3582	X3583	X3584	X3586	X3587	X3588	X3589	X3609	X3610	X3611	X3612	X3613	N3643	N3651	S3656	Y3657	K3658														
K3661	L3662	E3665	D3666	H3667	S3668	G3681	E3682	Q3683	E3684	E3685	E3686	E3687	E3688	E3689	E3690	E3691	E3692	K3693	E3712	K3713	S3714	K3715	E3736	E3737	G3738	G3739	E3740	N3741	GLY	GLU	ALA	GLU	GLU	E3747	E3748	V3749	E3750	E3754	T3772	R3773	E3777	M3778	L3780	Q3781	S3784	K3787	L3804	L3805											
N3809	K3815	L3842	D3843	Q3850	G3857	M3858	V3859	N3860	T3862	G3863	T3864	V3865	I3866	N3867	R3868	Q3869	N3870	G3871	E3872	K3873	D3878	Q3889	N3896	S3929	Y3937	M3955	Q3960	E3967	G3971	R3984	K4002	L4019	E4032	G4033	M4034	L4046	L4066																						
D4070	D4079	Y4080	D4083	P4084	R4085	G4086	A4096	M4097	D4098	T4104	G4105	P4106	M4120	E4152	P4155	H4156	Y4173	R4180	A4186	S4187	R4188	Q4209	R4215	G4226	E4227	A4228	E4232	L4233	S4236	X4321	X4322	F4540	R4548	Y4560	L4567	A4570	M4574																						
V4582	P4587	GLY	ASP	ASP	MET	GLU	GLY	SER	ALA	ALA	ASP	LEU	ALA	GLY	GLY	GLY	TRP	GLY	SER	GLY	ALA	GLY	GLU	GLU	GLU	GLU	GLU	ASP	ASP	GLU	M4626	S4635	T4636	G4637	M4639	E4640	P4641	A4642	C4645	V4666	Y4669	N4806	F4807	F4808	D4815	L4816	A4817	R4818											
E4674	K4680	L4686	Y4687	I4688	D4694	D4695	D4696	V4697	K4698	G4699	Y4715	H4728	G4729	H4743	D4744	L4745	A4746	T4751	A4752	H4753	M4754	E4755	R4756	K4757	P4758	D4759	P4760	P4761	P4762	O4763	L4764	L4765	T4766	W4767	L4768	W4769	M4798	L4801	G4802	H4803	Y4804	N4805	F4807	F4808	D4815	L4816	A4817	R4818											



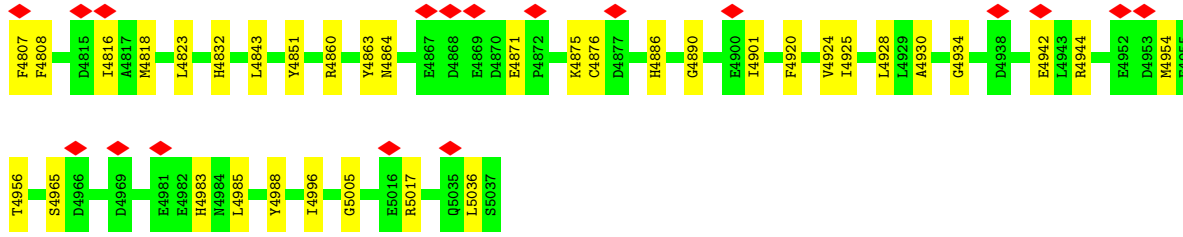
• Molecule 2: Ryanodine receptor 1











## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	55564	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.114	Depositor
Minimum map value	-0.070	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.025	Depositor
Map size (Å)	502.0, 502.0, 502.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.255, 1.255, 1.255	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA, CFF, 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	0.32	0/834	0.54	0/1123
1	F	0.32	0/834	0.54	0/1123
1	H	0.32	0/834	0.54	0/1123
1	J	0.32	0/834	0.54	0/1123
2	B	0.32	0/25428	0.57	13/34534 (0.0%)
2	E	0.32	0/25428	0.57	13/34534 (0.0%)
2	G	0.32	0/25428	0.57	13/34534 (0.0%)
2	I	0.32	0/25428	0.57	13/34534 (0.0%)
All	All	0.32	0/105048	0.57	52/142628 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	F	0	2
1	H	0	2
1	J	0	2
2	B	0	18
2	E	0	18
2	G	0	18
2	I	0	18
All	All	0	80

There are no bond length outliers.

The worst 5 of 52 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	131	LEU	CA-CB-CG	8.14	134.03	115.30
2	B	131	LEU	CA-CB-CG	8.13	134.00	115.30
2	E	131	LEU	CA-CB-CG	8.13	134.00	115.30
2	I	131	LEU	CA-CB-CG	8.13	134.00	115.30
2	E	4639	MET	C-N-CA	6.84	138.79	121.70

There are no chirality outliers.

5 of 80 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	8	SER	Peptide
1	A	82	TYR	Peptide
1	F	8	SER	Peptide
1	F	82	TYR	Peptide
1	H	8	SER	Peptide

## 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	818	0	824	10	0
1	F	818	0	824	10	0
1	H	818	0	824	11	0
1	J	818	0	824	11	0
2	B	29499	0	24752	242	0
2	E	29499	0	24752	242	0
2	G	29499	0	24752	241	0
2	I	29499	0	24752	243	0
3	B	31	0	12	1	0
3	E	31	0	12	0	0
3	G	31	0	12	0	0
3	I	31	0	12	0	0
4	B	14	0	10	1	0
4	E	14	0	10	1	0
4	G	14	0	10	1	0
4	I	14	0	10	1	0
5	B	1	0	0	0	0
5	E	1	0	0	0	0

*Continued on next page...*

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	G	1	0	0	0	0
5	I	1	0	0	0	0
6	B	1	0	0	0	0
6	E	1	0	0	0	0
6	G	1	0	0	0	0
6	I	1	0	0	0	0
All	All	121456	0	102392	986	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 4.

The worst 5 of 986 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:646:PRO:HD2	2:G:779:PRO:HB2	1.73	0.70
2:I:379:HIS:HD2	2:I:382:GLY:H	1.40	0.69
2:G:379:HIS:HD2	2:G:382:GLY:H	1.40	0.69
2:B:646:PRO:HD2	2:B:779:PRO:HB2	1.73	0.69
2:G:641:VAL:HG21	2:G:705:ASN:HA	1.75	0.69

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	105/108 (97%)	94 (90%)	11 (10%)	0	100	100
1	F	105/108 (97%)	93 (89%)	12 (11%)	0	100	100
1	H	105/108 (97%)	94 (90%)	11 (10%)	0	100	100
1	J	105/108 (97%)	93 (89%)	12 (11%)	0	100	100
2	B	3235/4416 (73%)	2877 (89%)	352 (11%)	6 (0%)	47	80

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	E	3235/4416 (73%)	2878 (89%)	351 (11%)	6 (0%)	47	80
2	G	3235/4416 (73%)	2877 (89%)	352 (11%)	6 (0%)	47	80
2	I	3235/4416 (73%)	2878 (89%)	351 (11%)	6 (0%)	47	80
All	All	13360/18096 (74%)	11884 (89%)	1452 (11%)	24 (0%)	50	80

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	1708	ARG
2	B	1840	PRO
2	B	1932	PRO
2	B	4641	PRO
2	E	1708	ARG

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	88/89 (99%)	88 (100%)	0	100	100
1	F	88/89 (99%)	88 (100%)	0	100	100
1	H	88/89 (99%)	88 (100%)	0	100	100
1	J	88/89 (99%)	88 (100%)	0	100	100
2	B	2493/3022 (82%)	2476 (99%)	17 (1%)	84	90
2	E	2493/3022 (82%)	2476 (99%)	17 (1%)	84	90
2	G	2493/3022 (82%)	2476 (99%)	17 (1%)	84	90
2	I	2493/3022 (82%)	2476 (99%)	17 (1%)	84	90
All	All	10324/12444 (83%)	10256 (99%)	68 (1%)	84	90

5 of 68 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	G	1600	LEU

Continued on next page...



*Continued from previous page...*

Mol	Chain	Res	Type
2	G	1964	ARG
2	G	4120	ASN
2	E	1676	LEU
2	E	1600	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 156 such sidechains are listed below:

Mol	Chain	Res	Type
2	I	4691	GLN
2	G	3771	HIS
2	G	111	HIS
2	G	949	ASN
2	G	4120	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 8 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	B	5101	-	26,33,33	0.87	1 (3%)	31,52,52	1.57	5 (16%)
3	ATP	I	5101	-	26,33,33	0.88	1 (3%)	31,52,52	1.55	5 (16%)
4	CFF	I	5102	-	8,15,15	2.53	3 (37%)	8,23,23	1.19	1 (12%)
4	CFF	B	5102	-	8,15,15	2.52	3 (37%)	8,23,23	1.19	1 (12%)
4	CFF	G	5102	-	8,15,15	2.53	4 (50%)	8,23,23	1.19	1 (12%)
3	ATP	E	5101	-	26,33,33	0.87	1 (3%)	31,52,52	1.54	5 (16%)
3	ATP	G	5101	-	26,33,33	0.87	1 (3%)	31,52,52	1.54	5 (16%)
4	CFF	E	5102	-	8,15,15	2.53	3 (37%)	8,23,23	1.20	1 (12%)

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	B	5101	-	-	4/18/38/38	0/3/3/3
3	ATP	I	5101	-	-	4/18/38/38	0/3/3/3
4	CFF	I	5102	-	-	-	0/2/2/2
4	CFF	B	5102	-	-	-	0/2/2/2
4	CFF	G	5102	-	-	-	0/2/2/2
3	ATP	E	5101	-	-	4/18/38/38	0/3/3/3
3	ATP	G	5101	-	-	4/18/38/38	0/3/3/3
4	CFF	E	5102	-	-	-	0/2/2/2

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	5102	CFF	C6-N1	-4.46	1.31	1.38
4	I	5102	CFF	C6-N1	-4.46	1.31	1.38
4	G	5102	CFF	C6-N1	-4.44	1.31	1.38
4	B	5102	CFF	C6-N1	-4.43	1.31	1.38
4	E	5102	CFF	C5-C4	-4.41	1.33	1.39

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	5101	ATP	PB-O3B-PG	-3.54	120.69	132.83
3	E	5101	ATP	PB-O3B-PG	-3.53	120.71	132.83
3	G	5101	ATP	PB-O3B-PG	-3.51	120.77	132.83

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	5101	ATP	PB-O3B-PG	-3.51	120.80	132.83
3	E	5101	ATP	PA-O3A-PB	-3.35	121.34	132.83

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

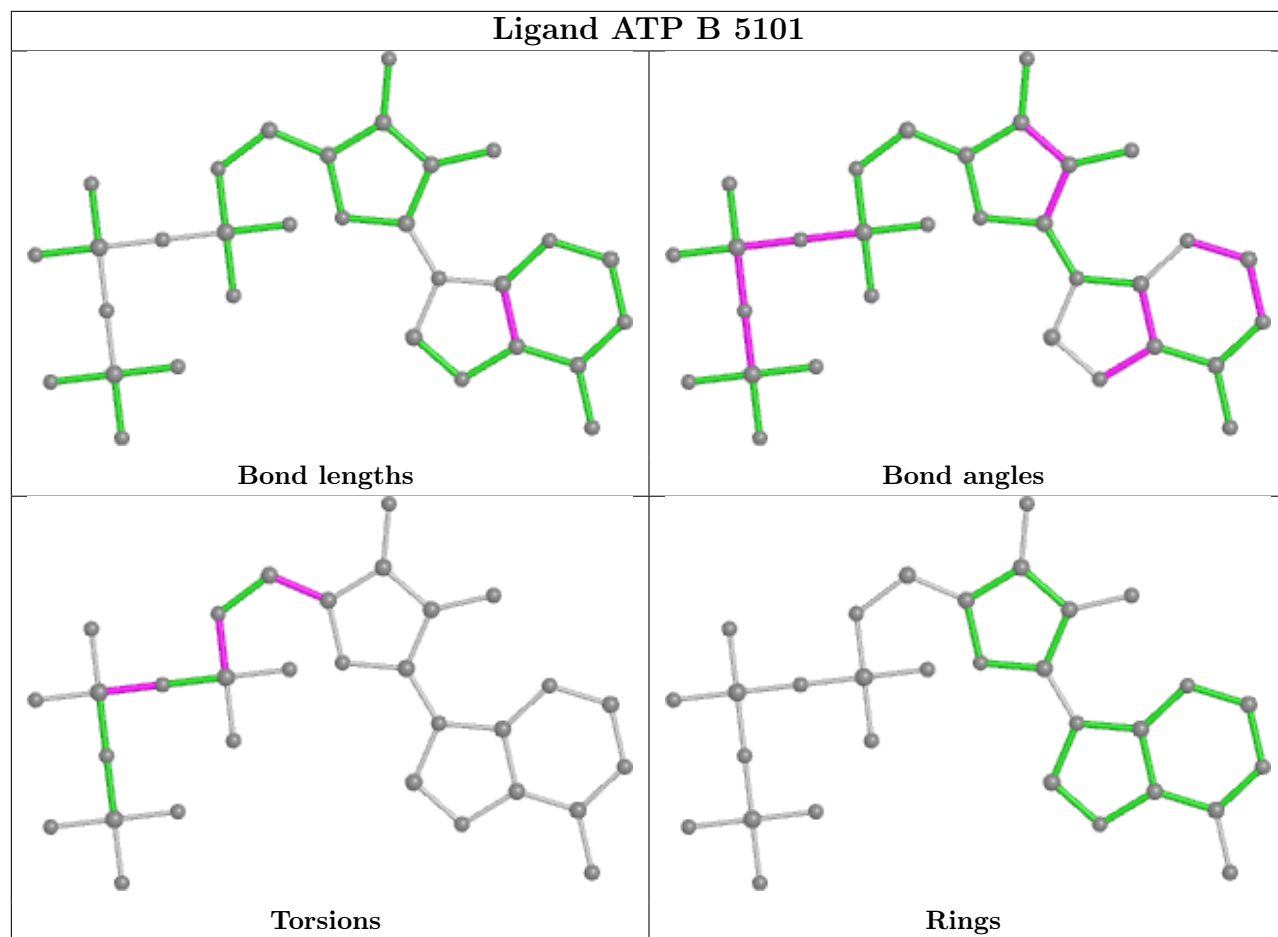
Mol	Chain	Res	Type	Atoms
3	B	5101	ATP	C5'-O5'-PA-O1A
3	E	5101	ATP	C5'-O5'-PA-O1A
3	I	5101	ATP	C5'-O5'-PA-O1A
3	G	5101	ATP	C5'-O5'-PA-O1A
3	B	5101	ATP	PA-O3A-PB-O1B

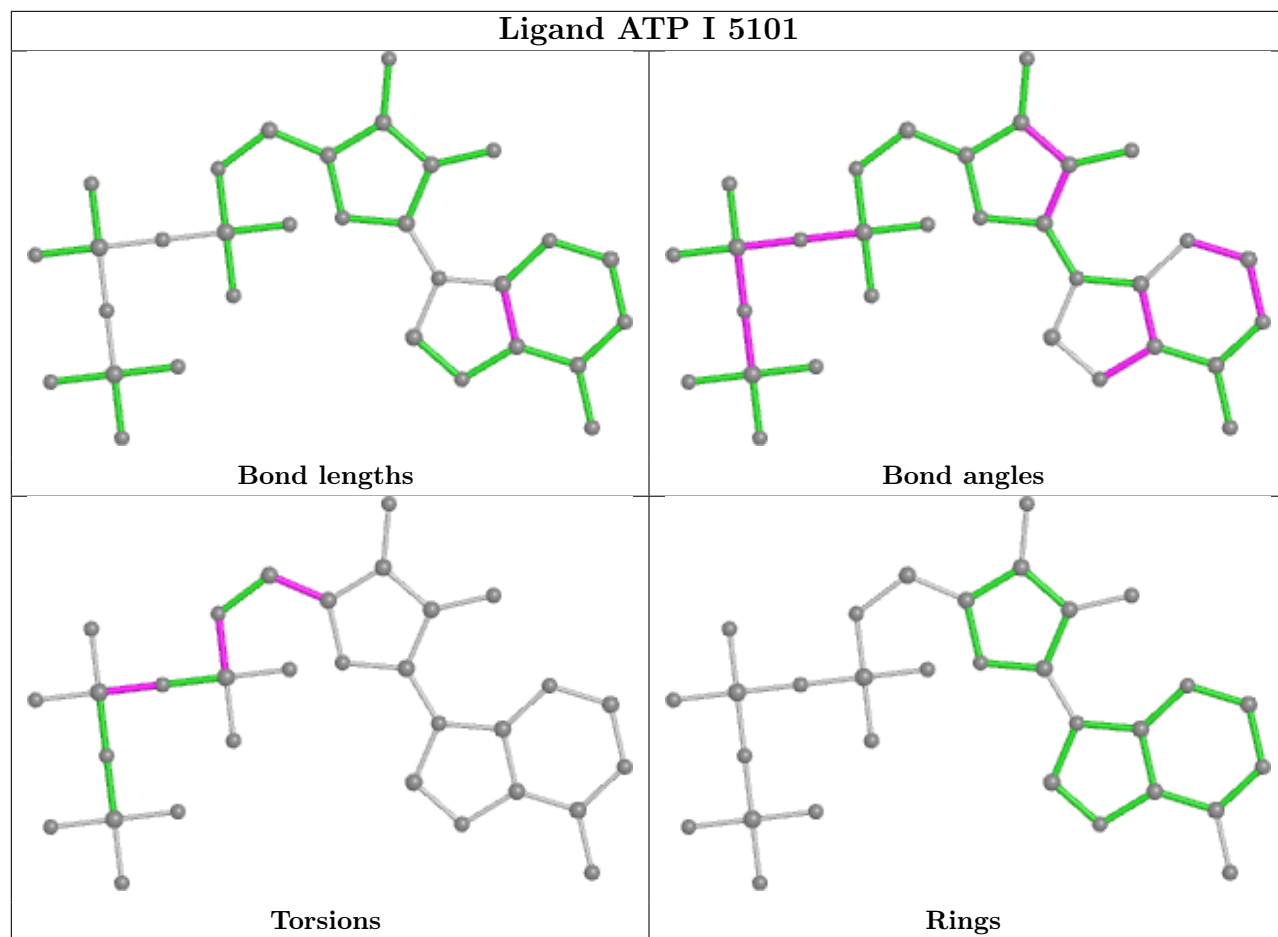
There are no ring outliers.

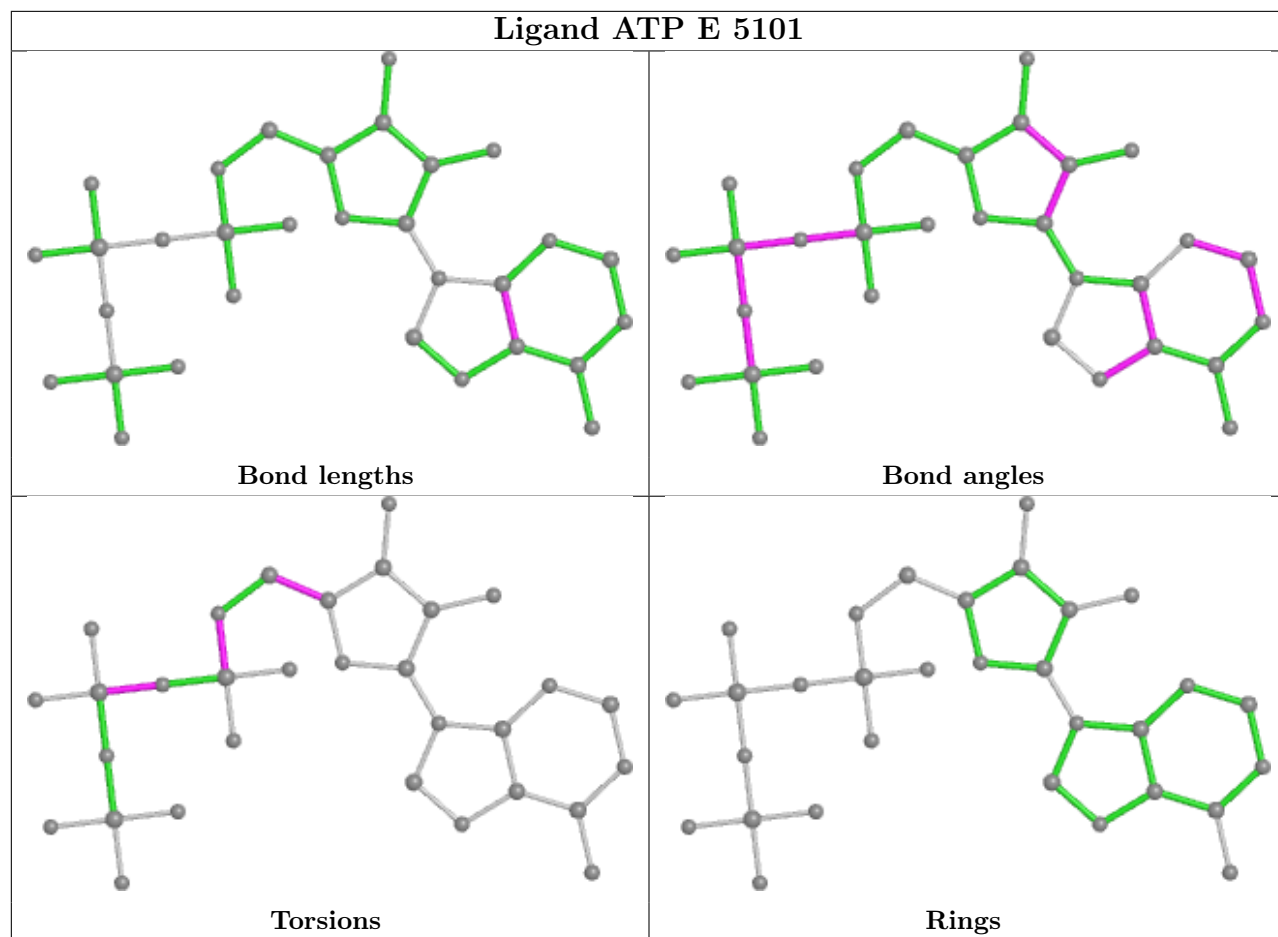
5 monomers are involved in 5 short contacts:

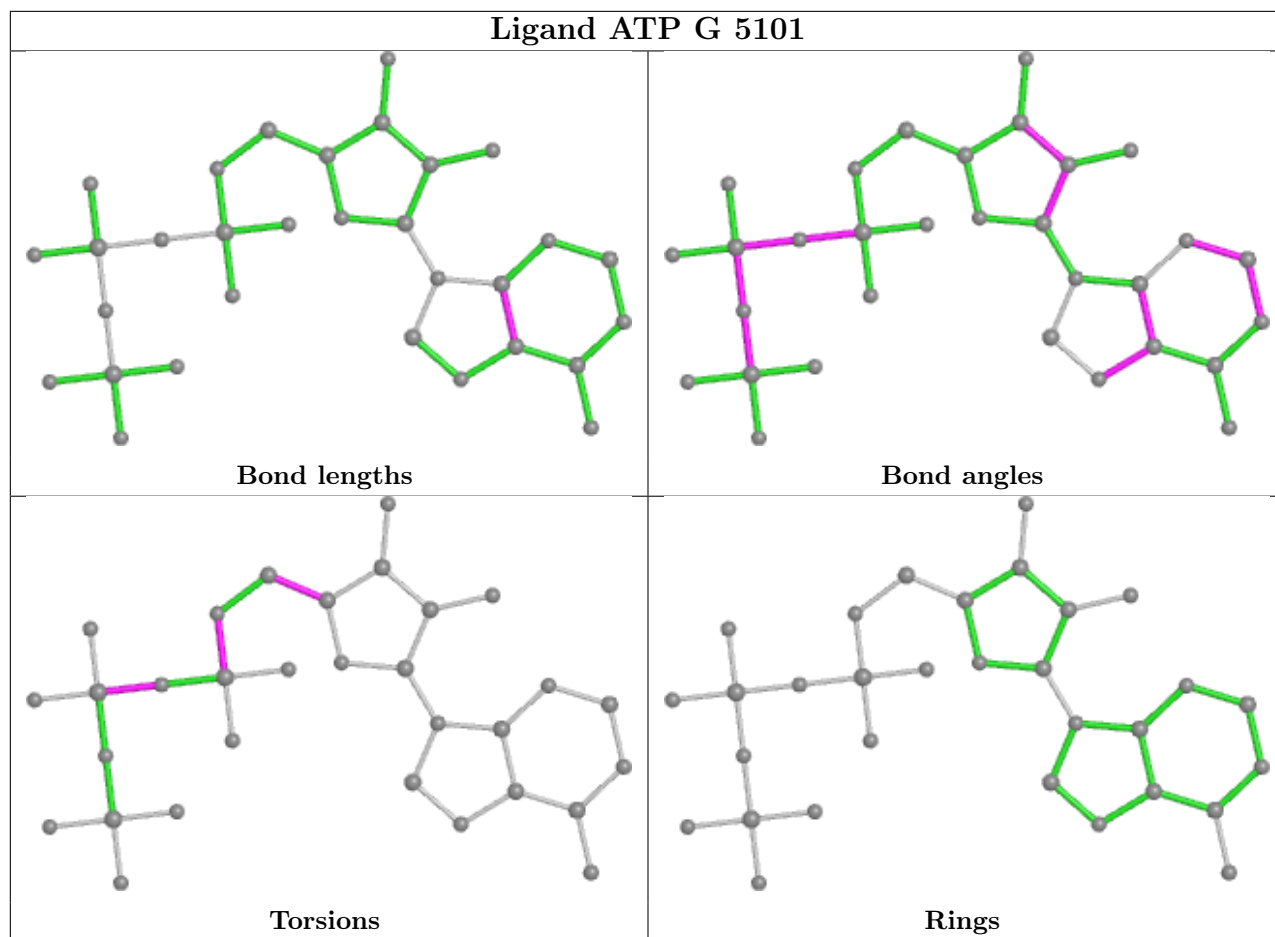
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	5101	ATP	1	0
4	I	5102	CFF	1	0
4	B	5102	CFF	1	0
4	G	5102	CFF	1	0
4	E	5102	CFF	1	0

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	E	14
2	B	14
2	I	14
2	G	14

The worst 5 of 56 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	4345:UNK	C	4540:PHE	N	72.62
1	B	4345:UNK	C	4540:PHE	N	72.61

*Continued on next page...*

*Continued from previous page...*

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	I	4345:UNK	C	4540:PHE	N	72.60
1	G	4345:UNK	C	4540:PHE	N	72.60
1	E	3613:UNK	C	3639:THR	N	43.07



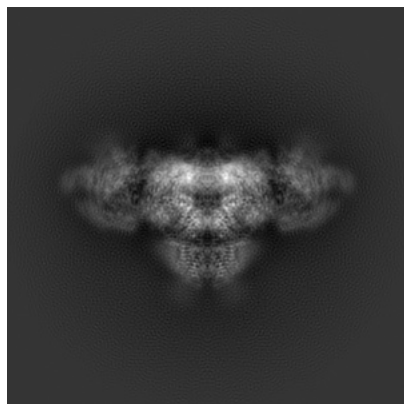
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8382. These allow visual inspection of the internal detail of the map and identification of artifacts.

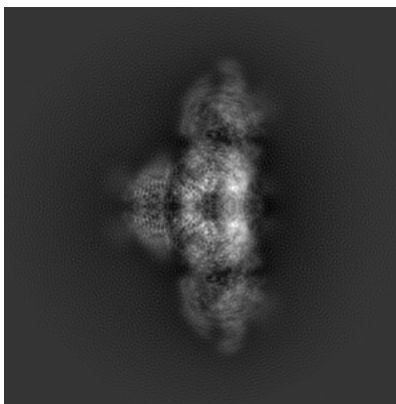
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

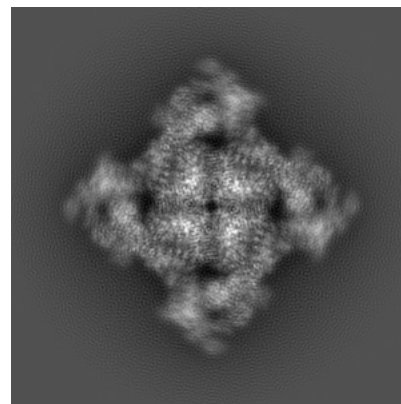
#### 6.1.1 Primary map



X

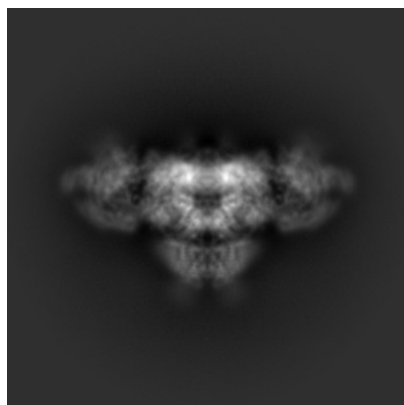


Y

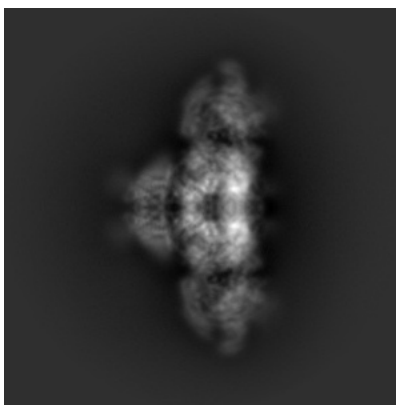


Z

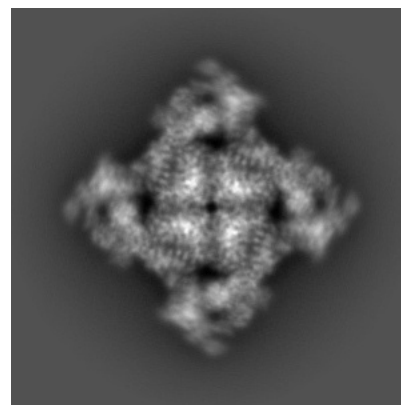
#### 6.1.2 Raw map



X



Y

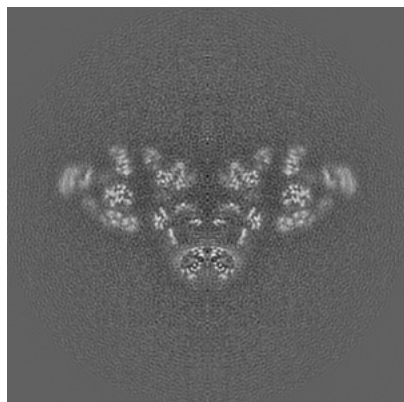


Z

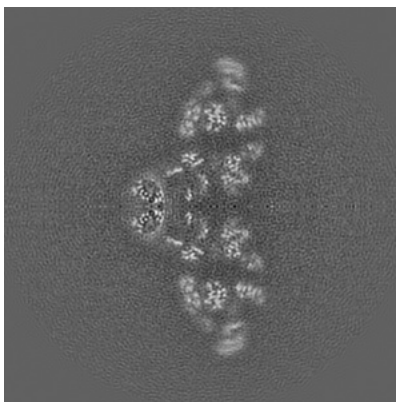
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

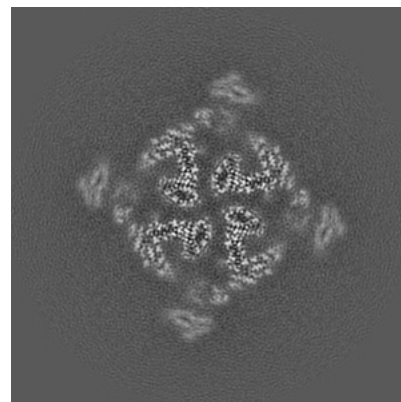
### 6.2.1 Primary map



X Index: 200

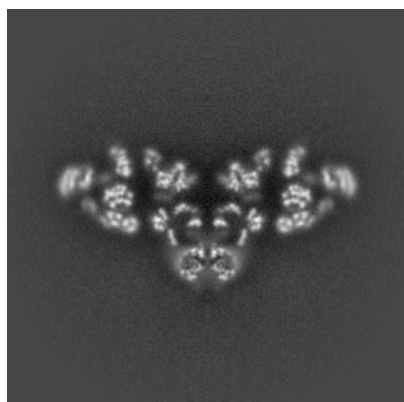


Y Index: 200

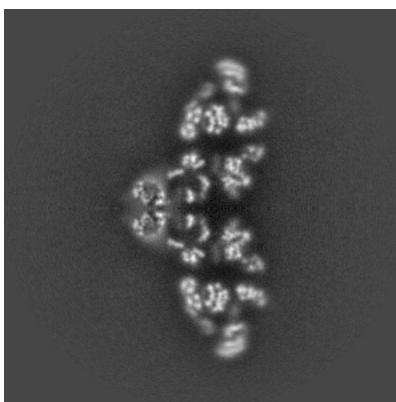


Z Index: 200

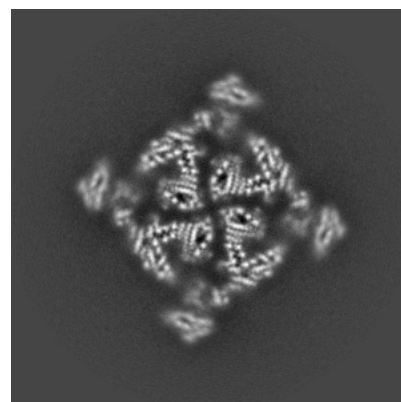
### 6.2.2 Raw map



X Index: 200



Y Index: 200

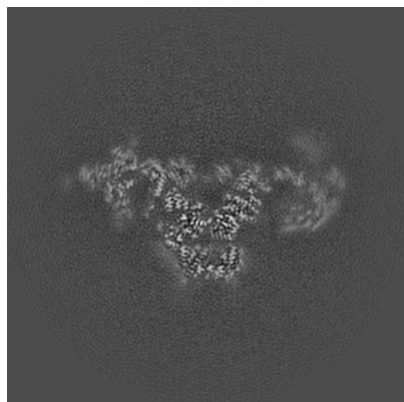


Z Index: 200

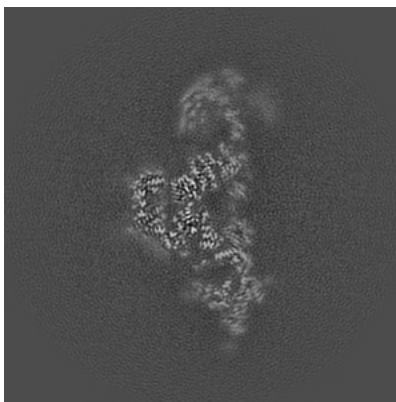
The images above show central slices of the map in three orthogonal directions.

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

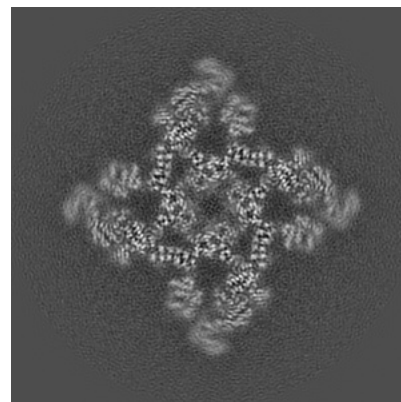
### 6.3.1 Primary map



X Index: 216

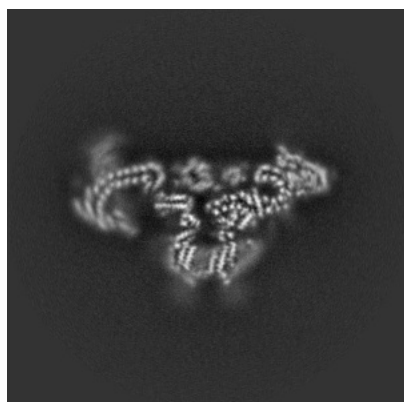


Y Index: 184

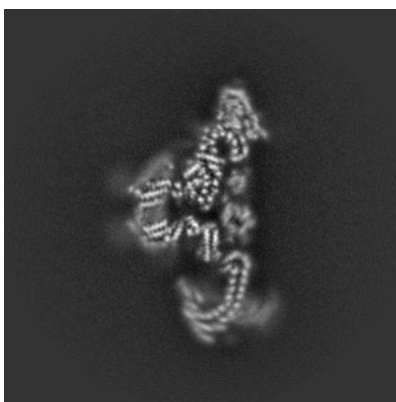


Z Index: 226

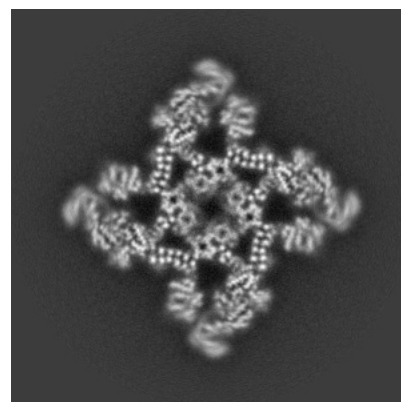
### 6.3.2 Raw map



X Index: 176



Y Index: 224

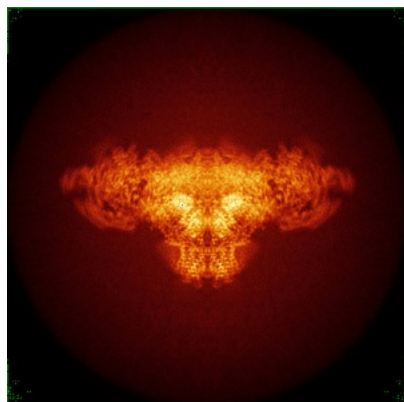


Z Index: 227

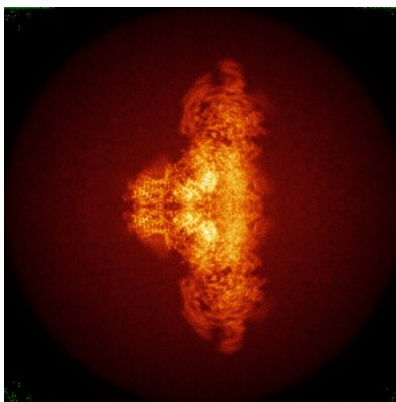
The images above show the largest variance slices of the map in three orthogonal directions.

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

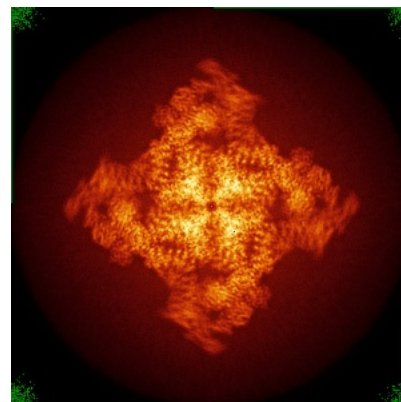
### 6.4.1 Primary map



X

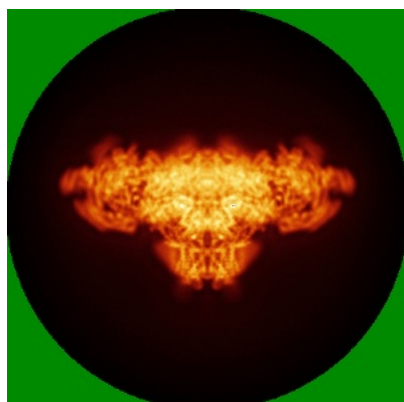


Y

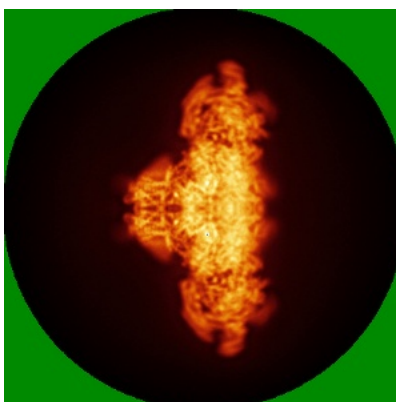


Z

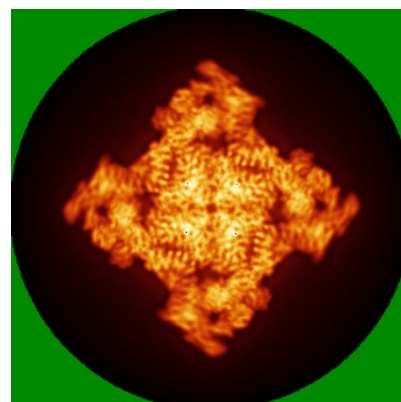
### 6.4.2 Raw map



X



Y

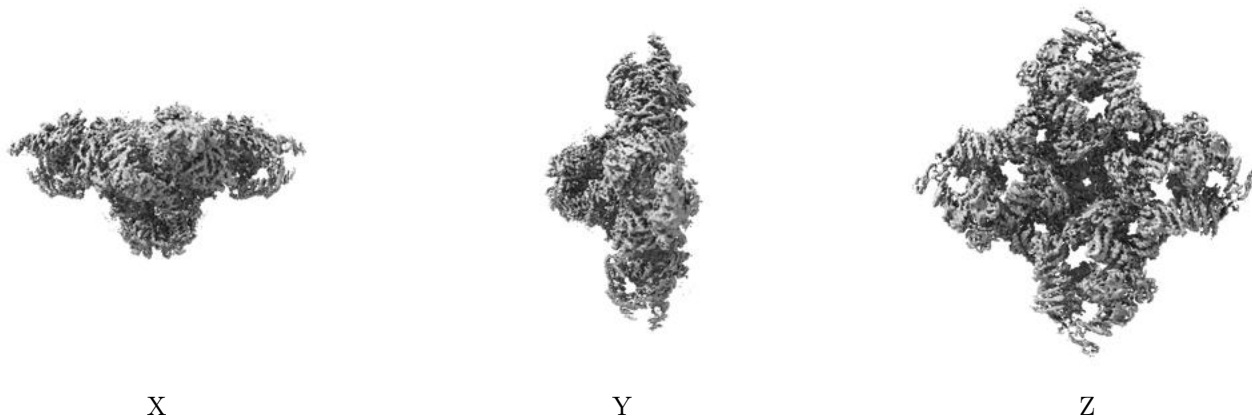


Z

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

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

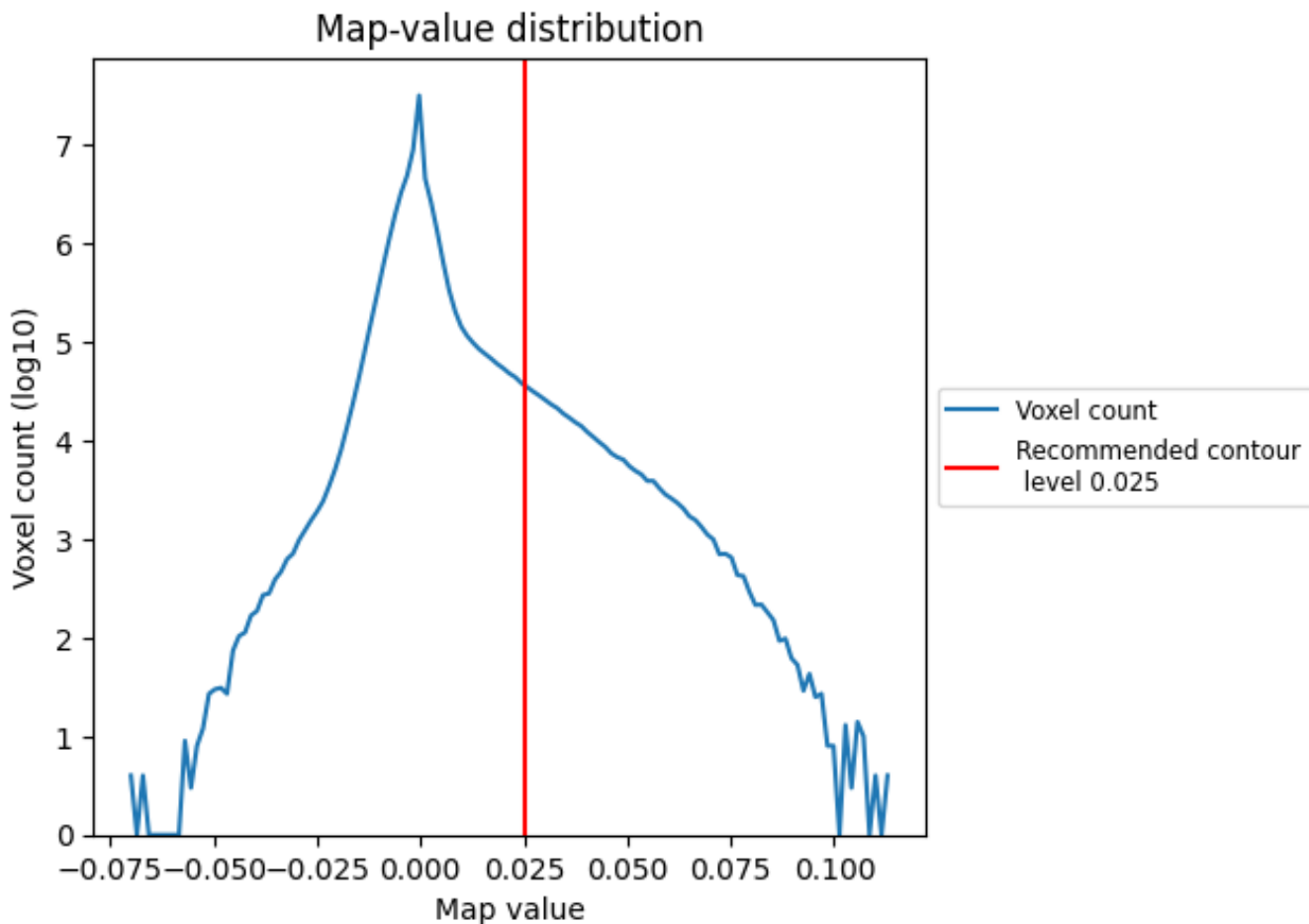
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

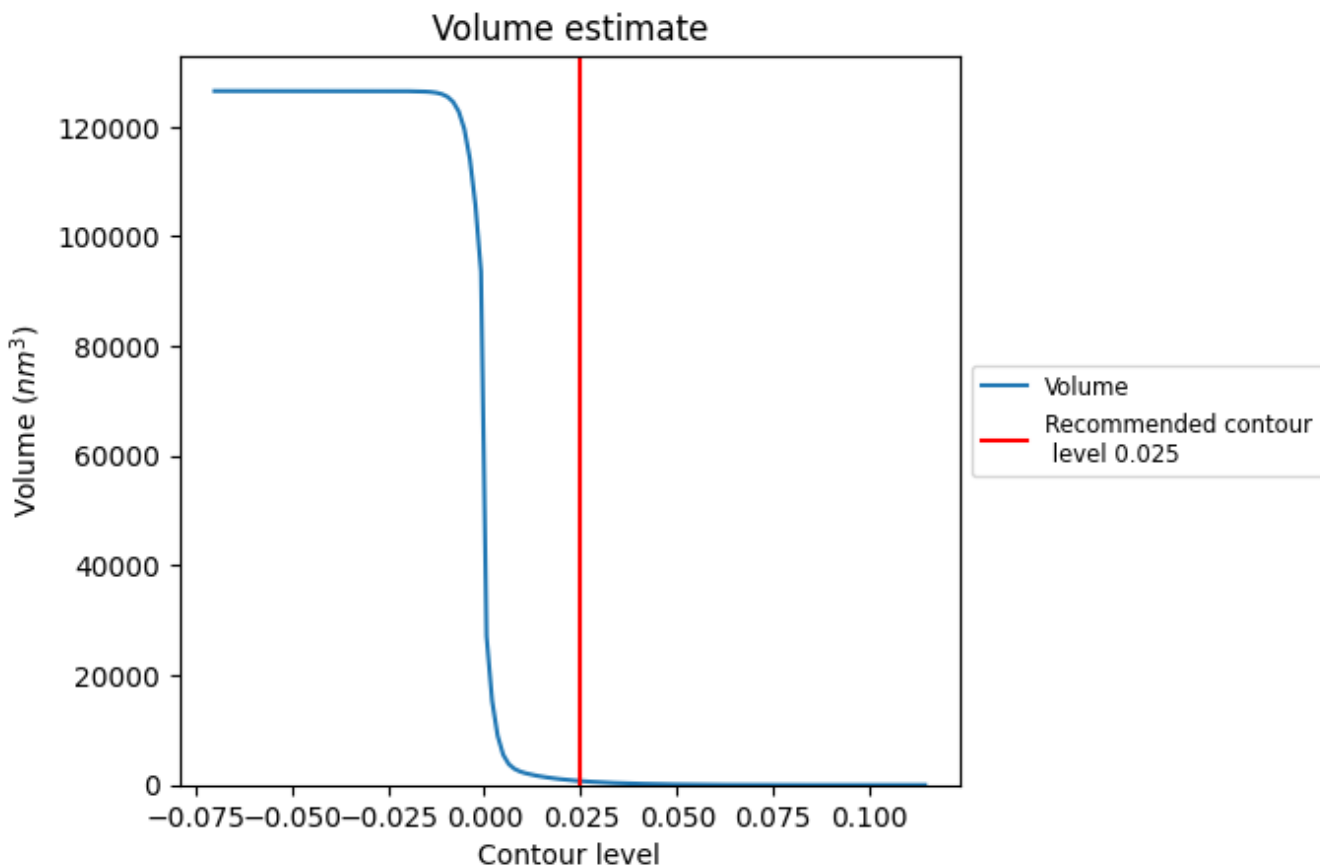
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

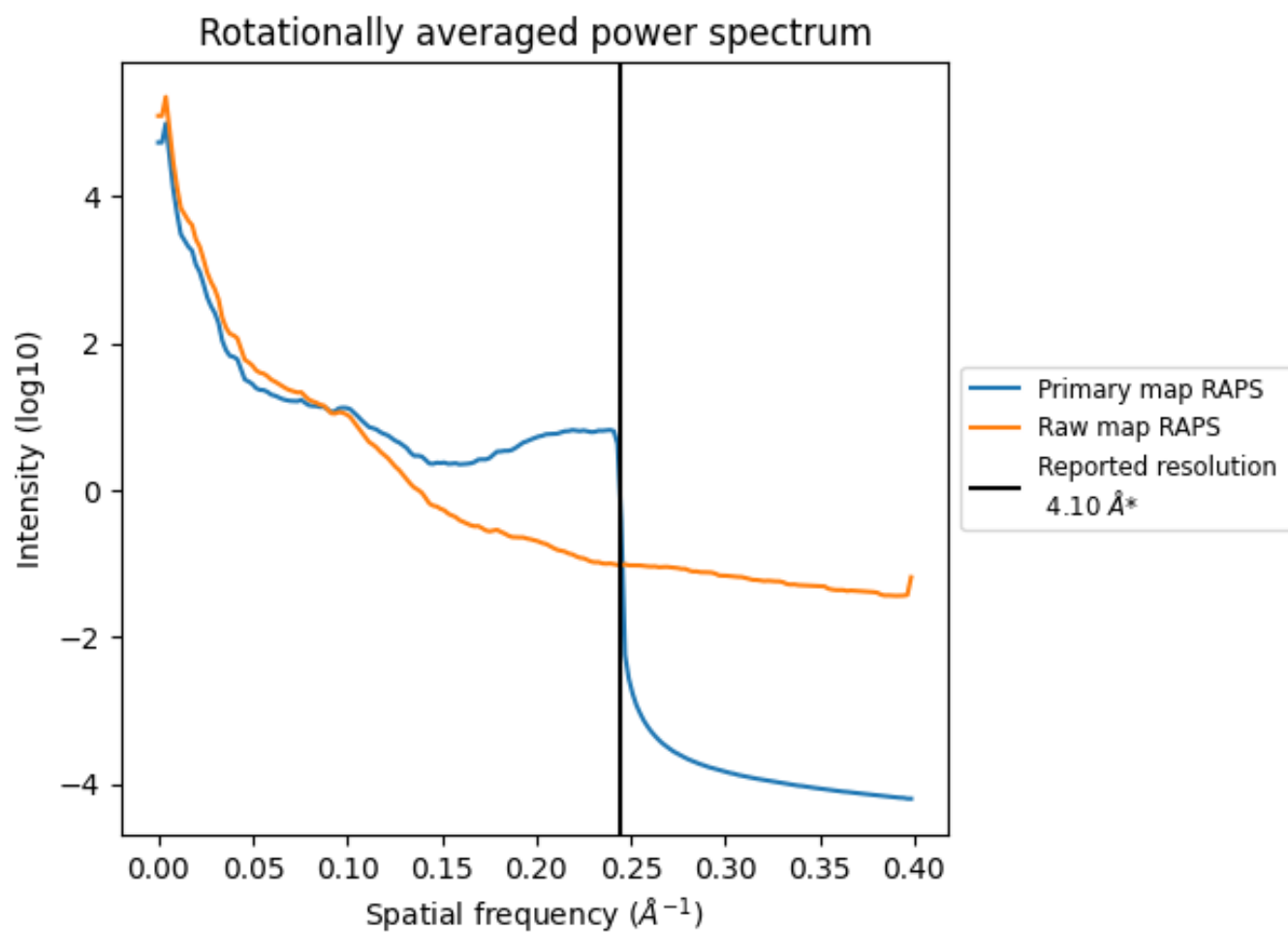
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 713  $\text{nm}^3$ ; this corresponds to an approximate mass of 644 kDa.

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

### 7.3 Rotationally averaged power spectrum i



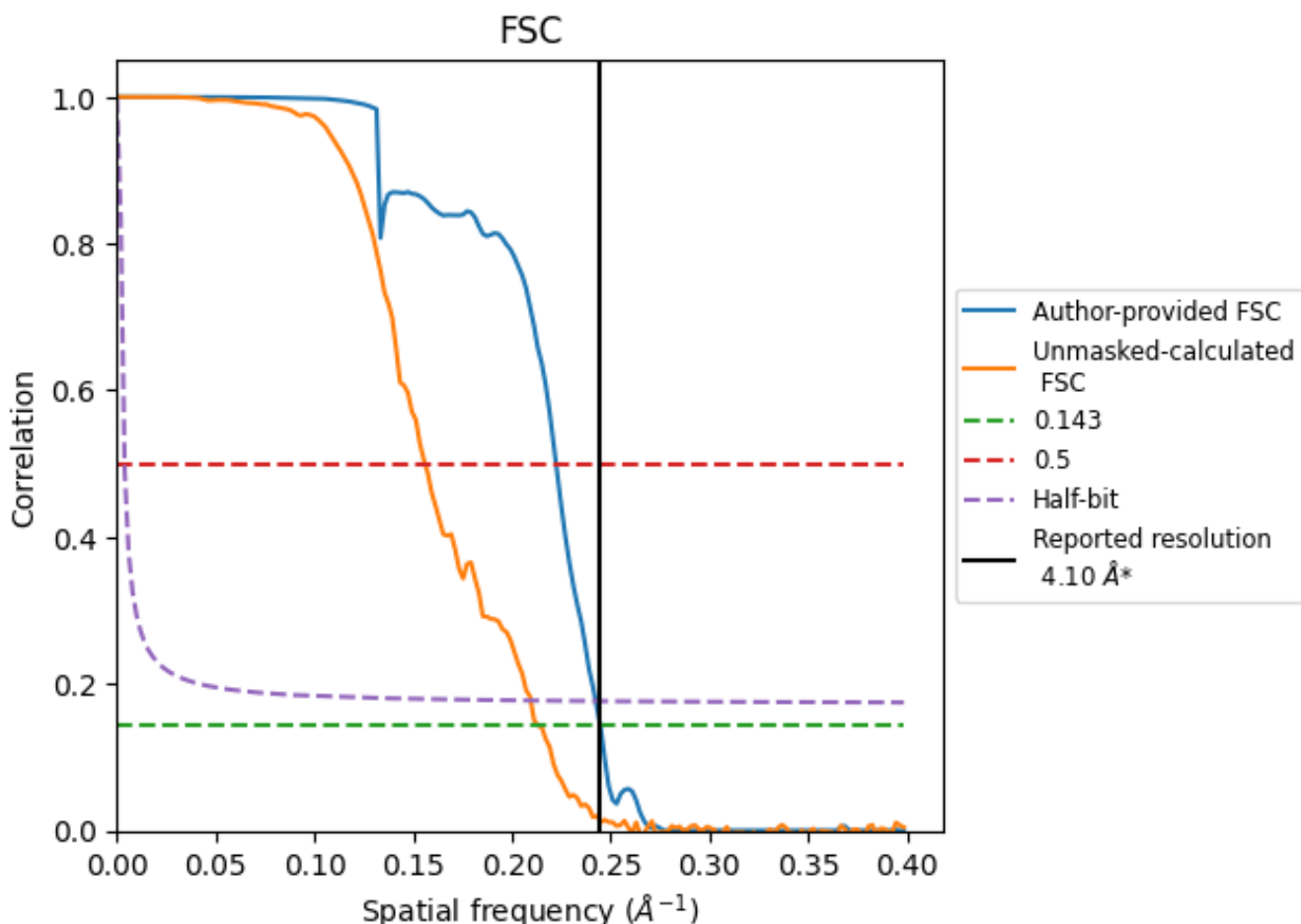
\*Reported resolution corresponds to spatial frequency of 0.244 Å<sup>-1</sup>



## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.244 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

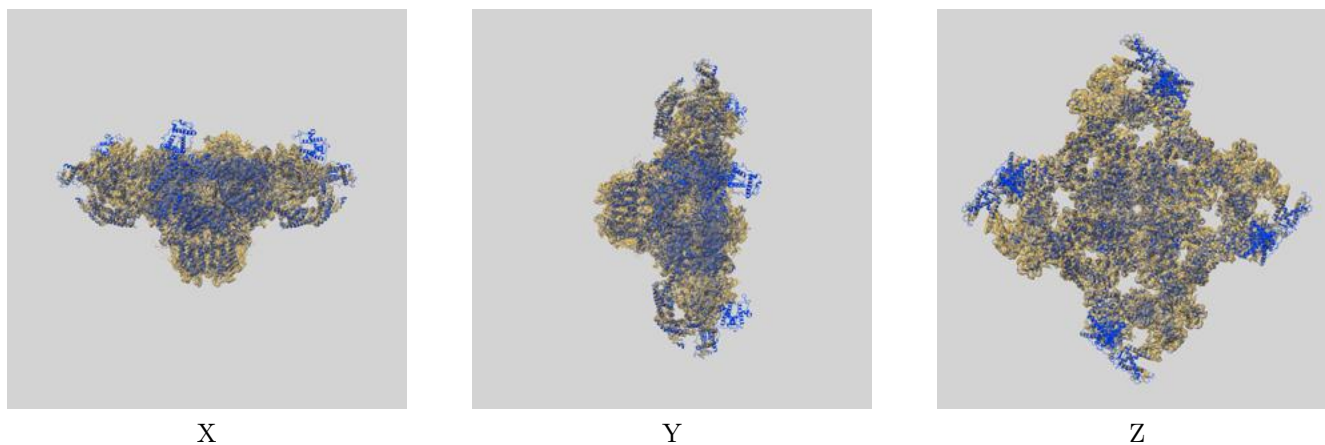
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	4.08	4.50	4.13
Unmasked-calculated*	4.69	6.41	4.77

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.69 differs from the reported value 4.1 by more than 10 %

## 9 Map-model fit [i](#)

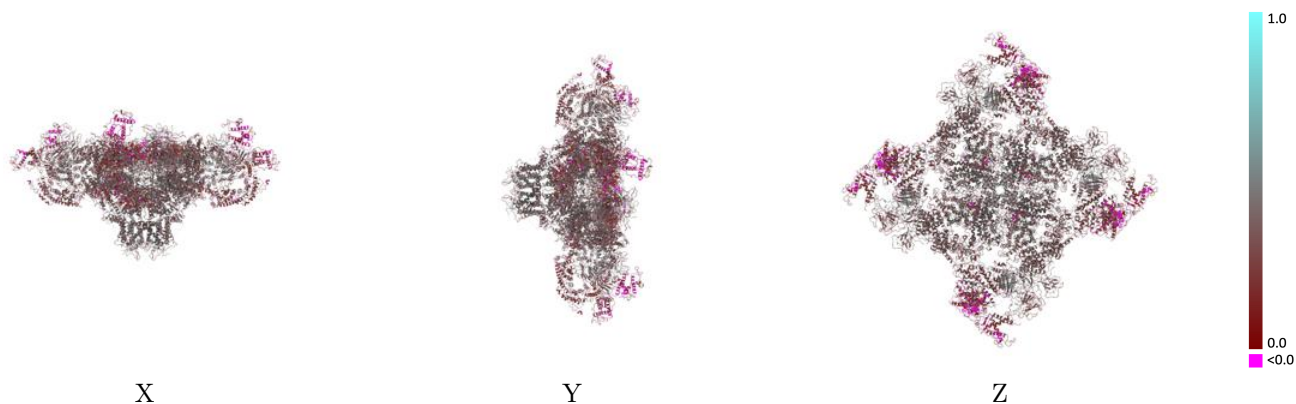
This section contains information regarding the fit between EMDB map EMD-8382 and PDB model 5TAQ. Per-residue inclusion information can be found in section 3 on page 6.

### 9.1 Map-model overlay [i](#)



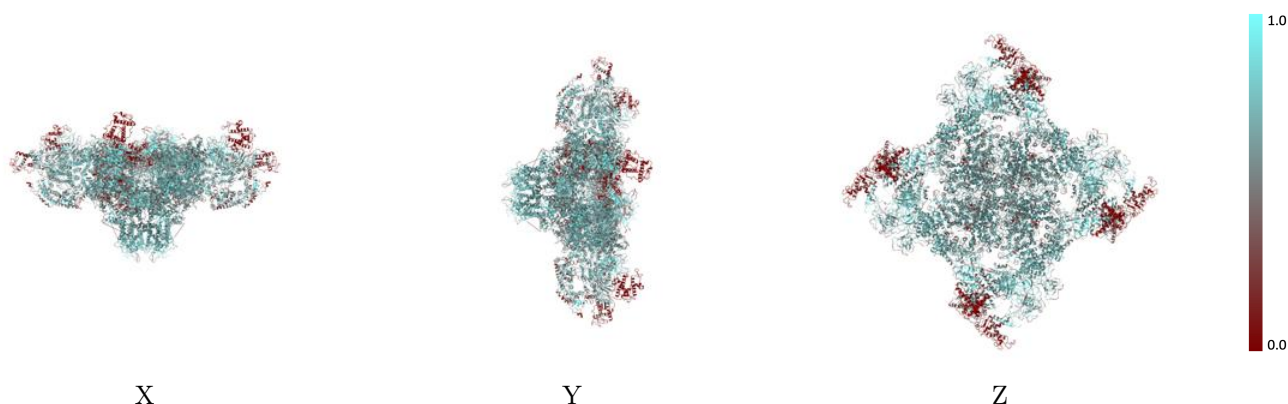
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



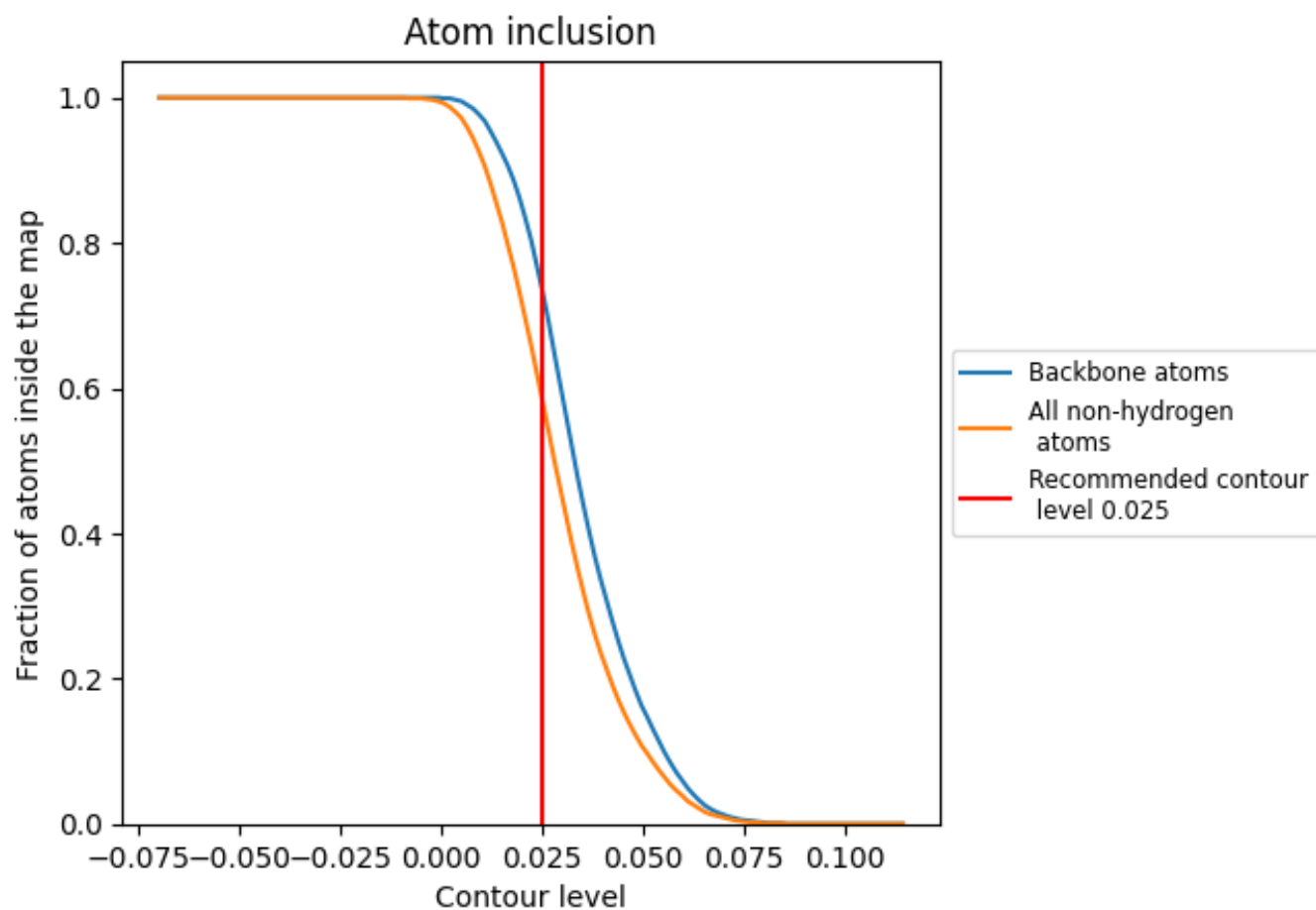
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



















## 9.4 Atom inclusion [i](#)



At the recommended contour level, 73% of all backbone atoms, 58% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5830	 0.3350
A	 0.5570	 0.3500
B	 0.5830	 0.3340
E	 0.5840	 0.3340
F	 0.5600	 0.3560
G	 0.5840	 0.3350
H	 0.5560	 0.3530
I	 0.5840	 0.3350
J	 0.5620	 0.3490

