



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 12:32 PM UTC

PDB ID : 5GL1 / pdb_00005gl1
EMDB ID : EMD-9521
Title : Structure of RyR1 in an open state
Authors : Bai, X.C.; Yan, Z.; Wu, J.P.; Yan, N.
Deposited on : 2016-07-07
Resolution : 5.70 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

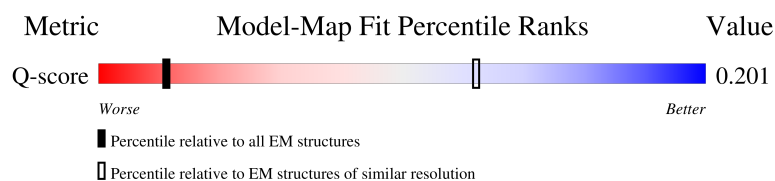
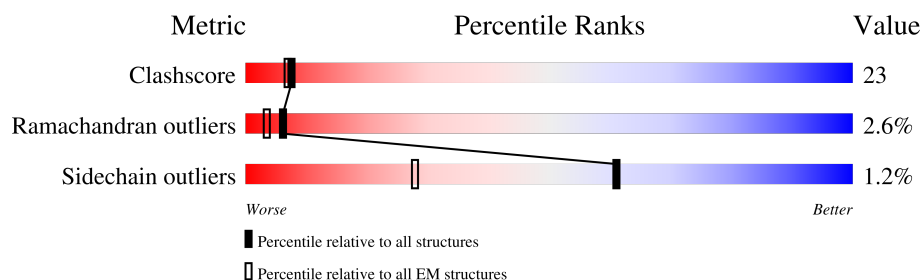
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.70 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	503 (5.20 - 6.20)

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

Mol	Chain	Length	Quality of chain
1	A	5037	
1	C	5037	
1	E	5037	
1	G	5037	

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Mol	Chain	Length	Quality of chain
2	B	108	30% 53% 44% ..
2	D	108	30% 56% 40% ..
2	F	108	30% 56% 41% ..
2	H	108	30% 52% 45% ...

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 110704 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Ryanodine receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3645	Total	C	N	O	S	0	0
			26843	17063	4667	4956	157		
1	C	3645	Total	C	N	O	S	0	0
			26843	17063	4667	4956	157		
1	E	3645	Total	C	N	O	S	0	0
			26843	17063	4667	4956	157		
1	G	3645	Total	C	N	O	S	0	0
			26843	17063	4667	4956	157		

- Molecule 2 is a protein called Peptidyl-prolyl cis-trans isomerase FKBP1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	107	Total	C	N	O	S	0	0
			832	527	146	155	4		
2	D	107	Total	C	N	O	S	0	0
			832	527	146	155	4		
2	F	107	Total	C	N	O	S	0	0
			832	527	146	155	4		
2	H	107	Total	C	N	O	S	0	0
			832	527	146	155	4		

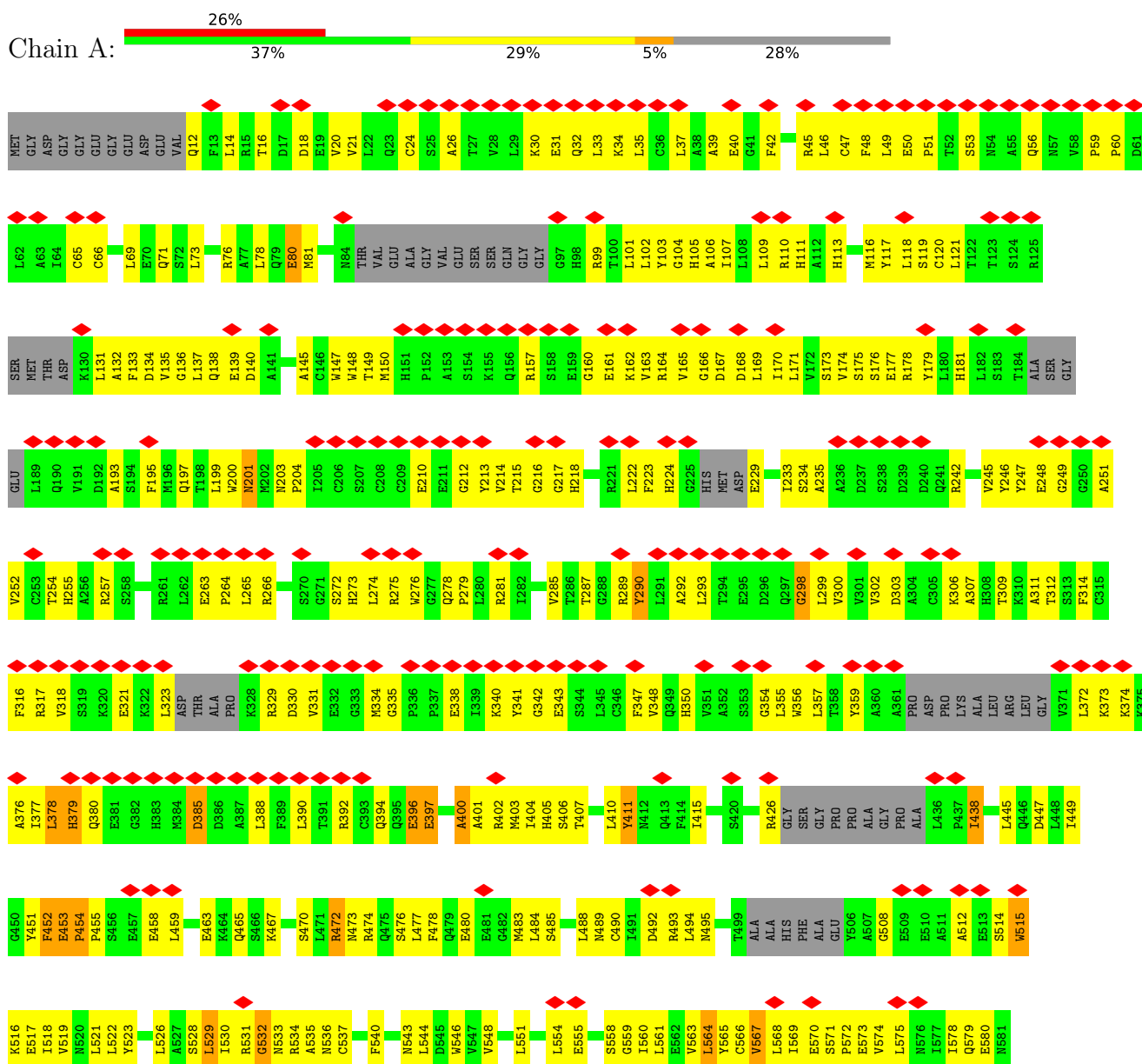
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	Zn	0
			1	1	
3	C	1	Total	Zn	0
			1	1	
3	E	1	Total	Zn	0
			1	1	
3	G	1	Total	Zn	0
			1	1	

3 Residue-property plots

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

• Molecule 1: Ryanodine receptor 1



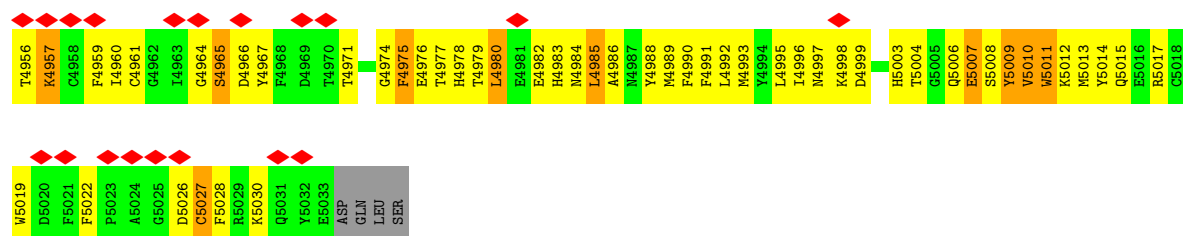




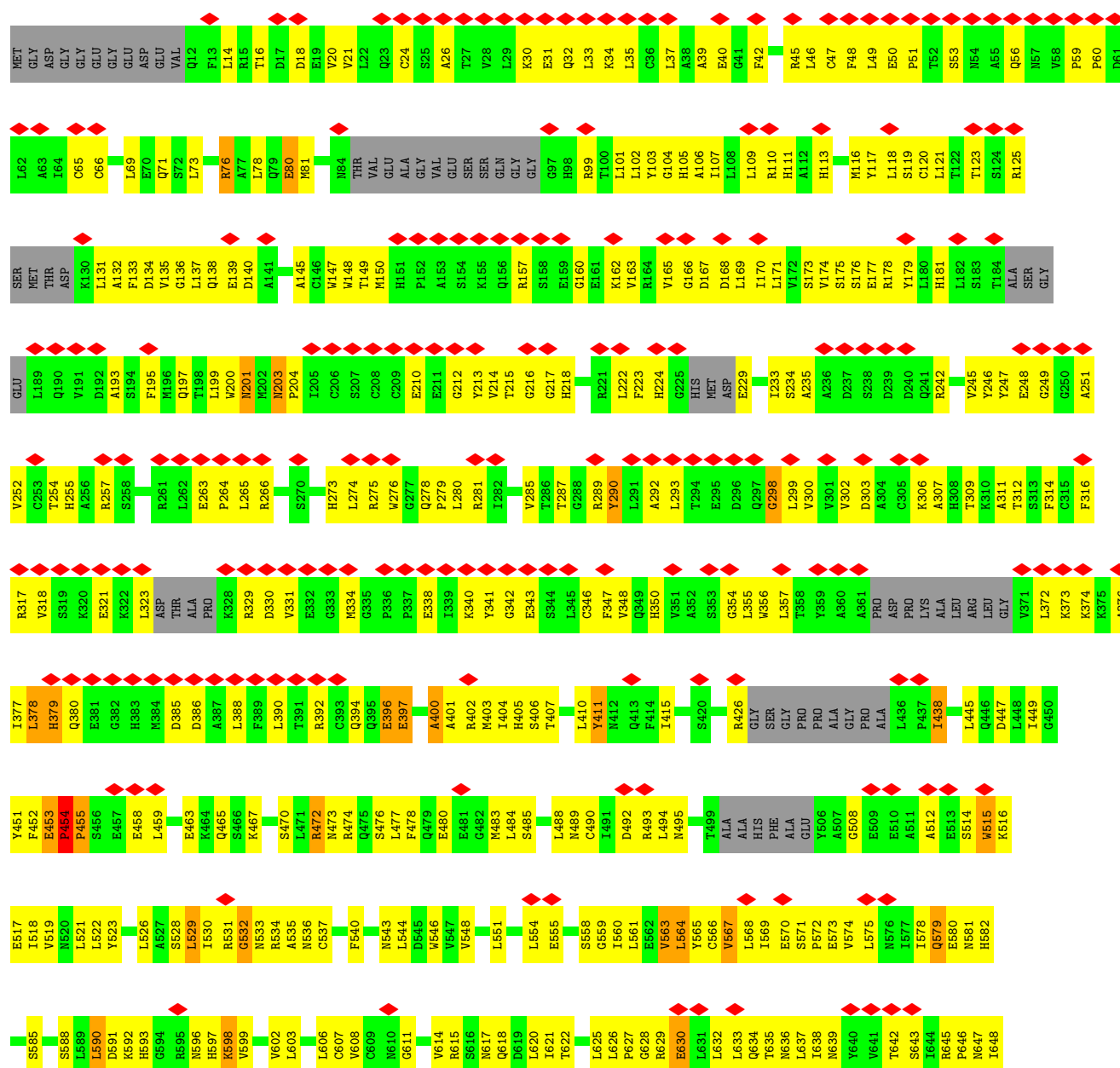
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L3049	V3050	R3051	H3052	R3053	V3054	S3055	L3056	F3057	D3060	A3061	ALA	VAL	VAL	VAL	ASN	GLN	TYR	PHE	THR	ASN	CYS	L3068	H3069	I3070	A3072	R3073	S3074	L3075	D3076	A3077	R3078	T3079	V3080	ASP	K3081	K3082	S3083	G3084	P3085	D3159	D3160	V3161	Q3162	V3163	S3164	C3165	Y3166	R3167	T3168	L3169	C3170	S3171	I3172	S3173	S3174	L3175	G3176	T3177	T3178	LYS																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
F2929	L2930	Q2931	M2932	N2933	Q2934	Y2935	A2936	V2937	T2938	R2939	G2940	LEU	LYS	ASP	MET	ASN	GLN	LEU	THR	ASP	SER	SER	SER	ILE	GLU	LYS	ARG	PHE	PHE	GLY	PHE	LEU	GLN	LEU	ARG	TRP	MET	ASP	ILE	SER	GLN	THR	ALA	THR	GLN	THR	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	

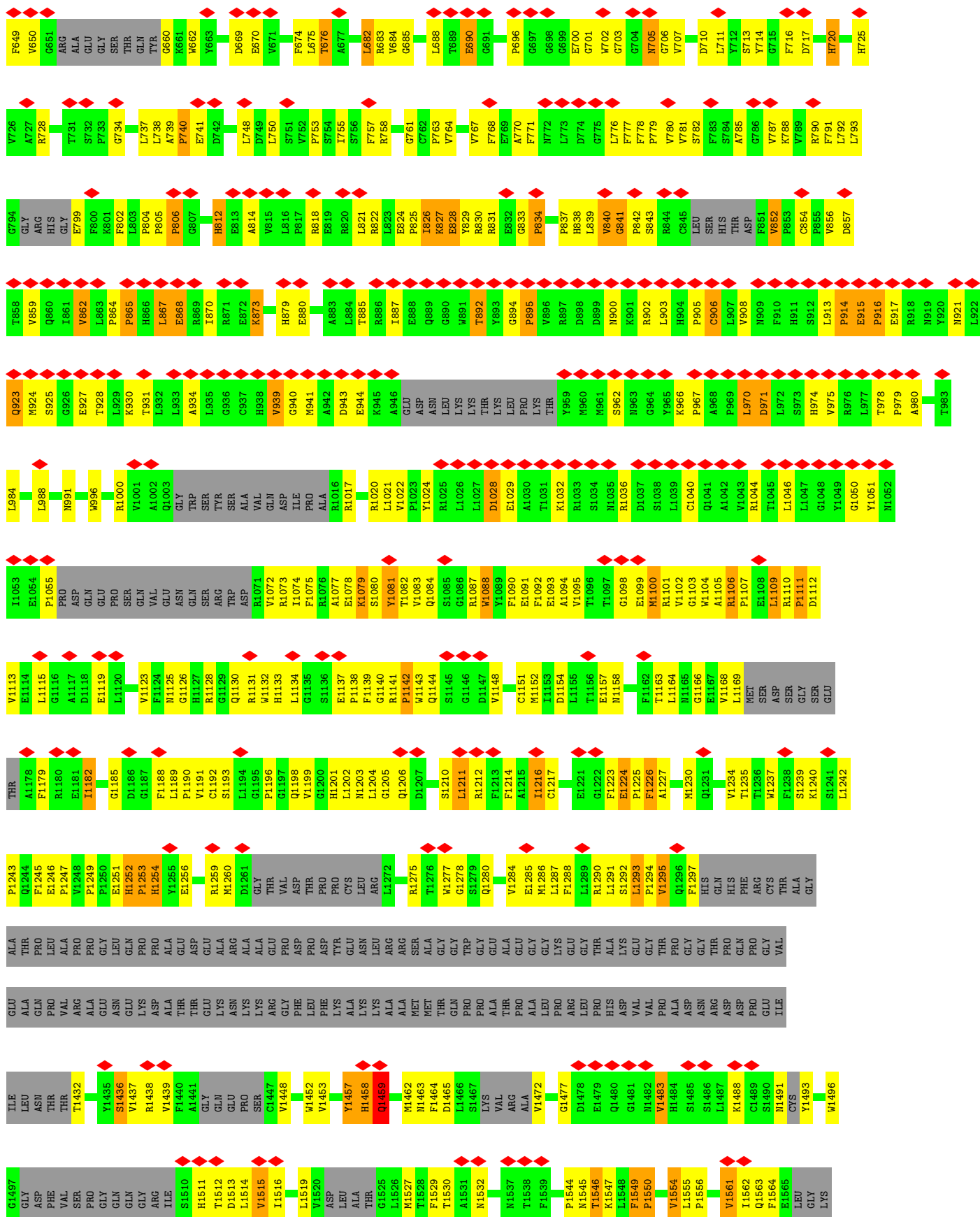






• Molecule 1: Ryanodine receptor 1



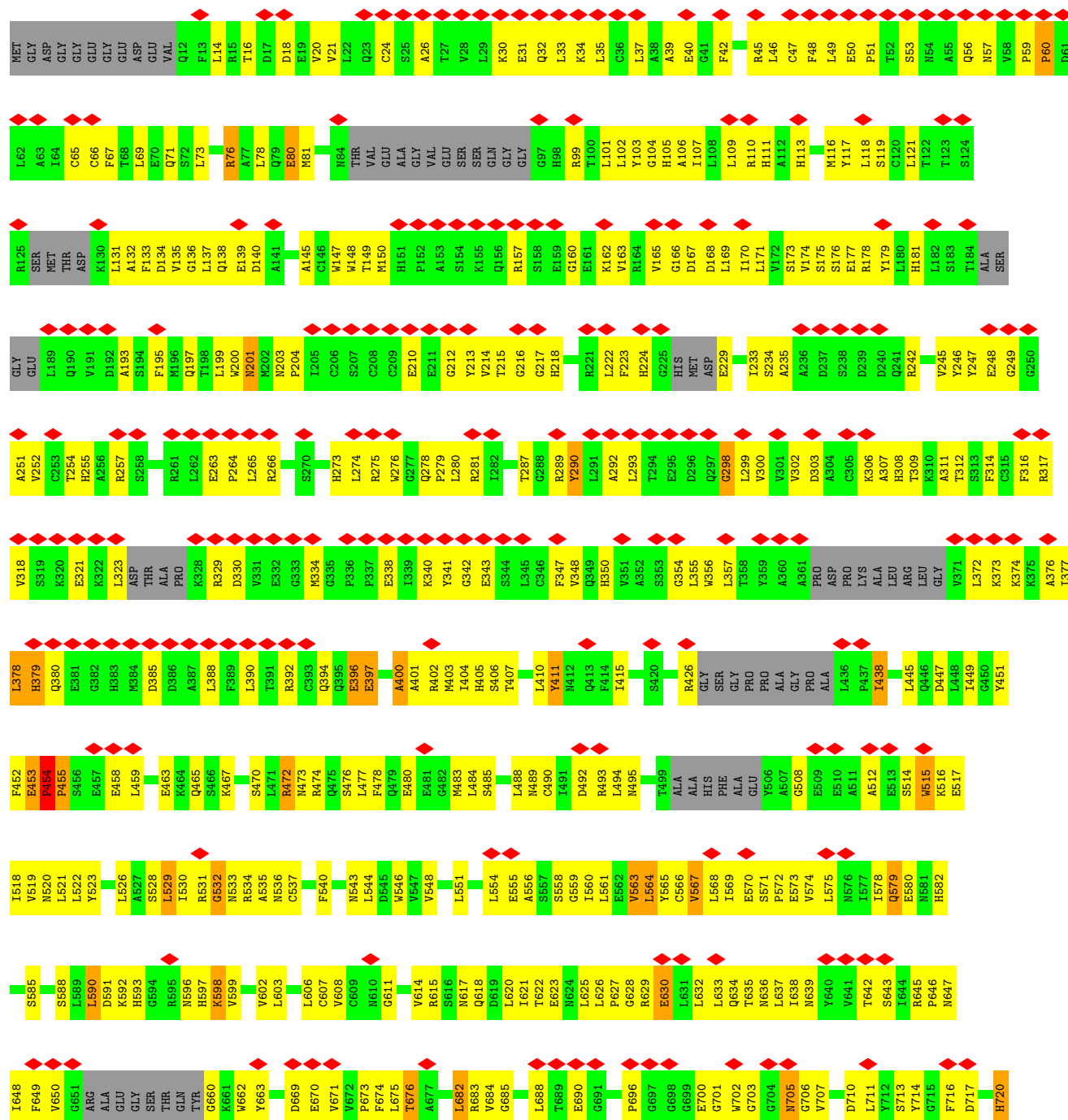




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S3116	GLN	ALA	ARG	THR	GLN	VAL	LYS	VAL	GLY	GLY	ASN	THR	THR	T3132	T3133	L3137	P3138	V3139	L3140	H3146	I3147	Q3151	F3152	GLY	ASP	ASP	VAL	ILE	L3158	D3159	D3160	V3161	Q3162	V3163	S3164	C3165	Y3166	R3167	T3168	L3169	C3170	S3171	I3172	Y3173	S3174	L3175	G3176	T3177	T3178	LYS	ASN	THR	TYR	V3183						
R3053	V3054	S3055	L3056	F3057	D3060	A3061	P3062	ALA	VAL	VAL	ASN	CYS	L3068	H3069	I3070	L3071	A3072	R3073	S3074	L3075	D3076	A3077	R3078	T3079	V3080	M3081	K3082	S3083	G3084	P3085	E3086	I3087	A3090	GLY	LEU	ARG	F3095	F3096	E3097	S3098	A3099	S3100	I3103	E3104	K3105	M3106	V3107	E3108	N3109	L3110	R3111	L3112	G3113	K3114	V3115					
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S2753	F2754	L2755	N2756	L2757	F2758	A2759	E2760	T2761	T2762	H2763	E2764	L2765	K2766	A2767	F2768	D2769	K2770	L2771	Q2772	N2773	K2774	L2775	S2776	Y2777	G2778	E2779	N2780	L2781	D2782	E2783	E2784	L2785	L2786	T2787	H2788	F2789	N2790	L2791	R2792	P2793	Y2794	K2795	T2796	F2797	L2798	E2799	K2800	D2801	L2802	E2803	L2804	Y2805	R2806	W2807	P2808	K2810	E2811	S2812		
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N2933	G2934	Y2935	A2936	T2937	V2937	R2938	G2940	LEU	LYS	ASP	MET	GLU	GLN	ASP	THR	SER	ILE	GLU	ARG	PHE	ALA	GLY	PHE	LEU	GLN	GLN	LEU	ARG	TRP	MET	ASP	G3027	G3028	G3029	H3030	A3031	S3032	N3033	H3034	E3035	K3036	E3037	M3038	I3039	THR	SER	VAL	GLU	LYS	PRO	HIS	GLU								
GLN	GLU	ILE	LYS	PHE	ALA	LYS	LEU	PRO	ILE	LEU	ASN	TYR	PHE	THR	ASN	HIS	CYS	Y3016	F3017	L3018	S3019	T3020	P3021	A3022	K3023	V3024	L3025	G3026	S3027	G3028	G3029	H3030	A3031	S3032	N3033	K3034	E3035	K3036	E3037	M3038	I3039	THR	SER	VAL	GLU	LYS	PRO	HIS	GLU											
R3053	V3054	S3055	L3056	F3057	D3060	A3061	P3062	ALA	VAL	VAL	ASN	CYS	L3068	H3069	I3070	L3071	A3072	R3073	S3074	L3075	D3076	A3077	R3078	T3079	V3080	M3081	K3082	S3083	G3084	P3085	E3086	I3087	A3090	GLY	LEU	ARG	F3095	F3096	E3097	S3098	A3099	S3100	I3103	E3104	K3105	M3106	V3107	E3108	N3109	L3110	R3111	L3112	G3113	K3114	V3115					
S3116	GLN	ALA	ARG	THR	GLN	VAL	LYS	VAL	GLY	GLY	ASN	THR	THR	T3132	T3133	L3137	P3138	V3139	L3140	H3146	I3147	Q3151	F3152	GLY	ASP	ASP	VAL	ILE	L3158	D3159	D3160	V3161	Q3162	V3163	S3164	C3165	Y3166	R3167	T3168	L3169	C3170	S3171	I3172	Y3173	S3174	L3175	G3176	T3177	T3178	LYS	ASN	THR	TYR	V3183						
E3184	K3185	L3186	R3187	P3188	A3195	R3196	L3197	A3198	A3199	A3200	MET	PRO	VAL	A3204	F3205	L3206	E3207	P3208	Q3209	L3210	N3211	K3214	A3215	C3216	S3217	VAL	TYR	THR	THR	LYS	SER	PRO	ARG	GLU	ARG	ALA	ILE	GLY	LEU	PRO	ASN	SER	VAL	GLU	GLU	MET	CYS	PRO	ASP	ILE	PRO	VAL	LEU	ASP	ARG	LEU				







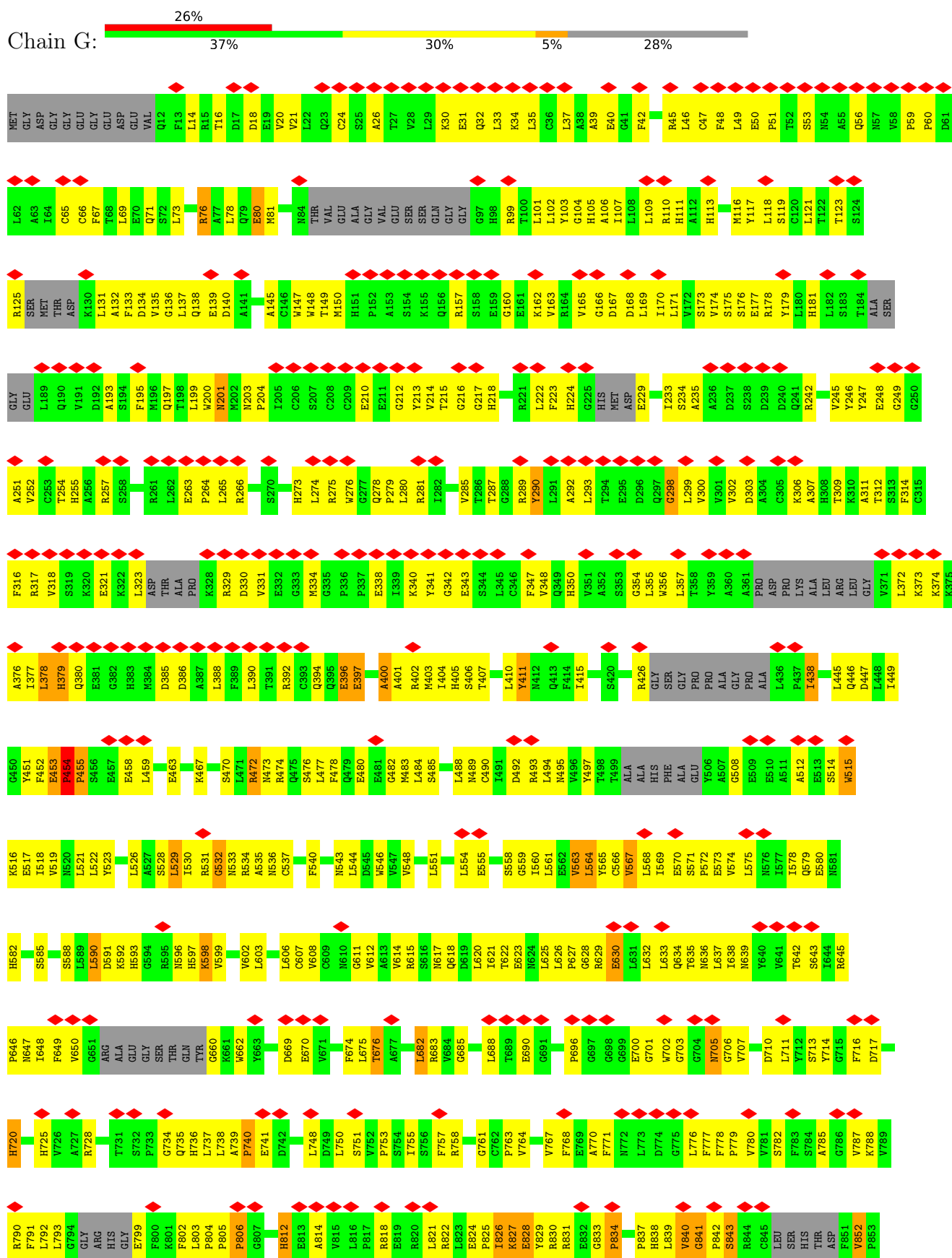




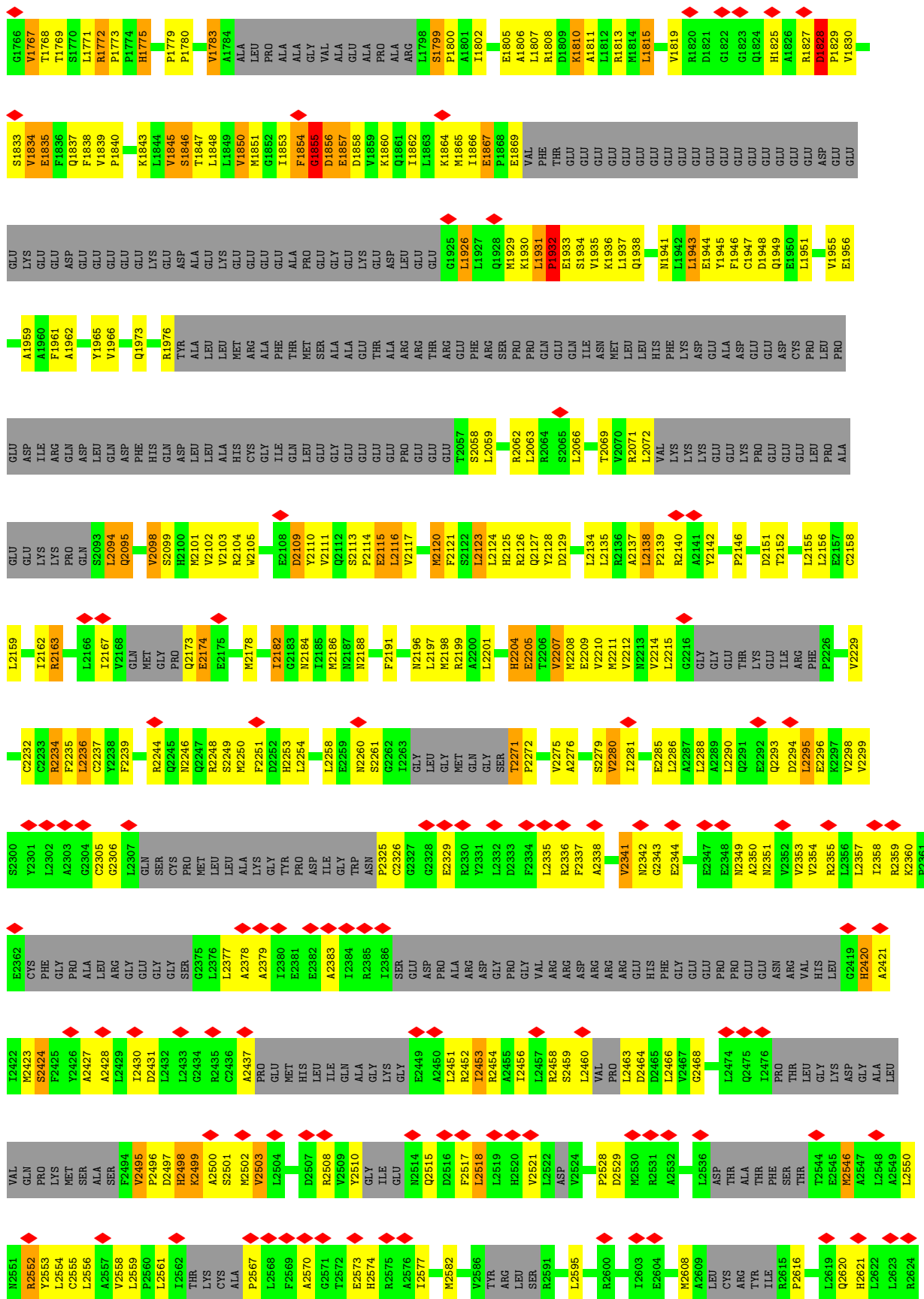


R4131	PHE	L4058	V3989	I3916	R3849	A3775	E3712	CYS	L3514	G3439	E5377	K3313	◆
L4059	GLN	L4060	F3992	I3917	R3849	A3776	K3713	PHE	K3515	E3440	Q3378	SER	◆
F4061	GLU	T3919	L3993	C3918	K3852	E3777	S3714	ARG	K3516	Y3444	L3379	LEU	◆
F4062	GLU	V3920	H3994	T3919	ALA	V3778	K3715	THR	K3517	W3445	R3380	G3317	◆
D4063	GLU	D3921	V3995	V3920	GLU	V3779	L3780	PRO	K3518	S3446	L3381	N3318	◆
M4064	GLY	Q3781	Q3716	Q3781	GLY	Q3716	L3717	LEU	P3519	S3446	E3362	I3319	◆
PHE	GLY	S3784	D3718	S3784	GLY	D3718	E3718	TYR	L3520	K3447	K3383	L3320	◆
L4071	GLY	C3785	D3719	C3785	GLY	D3719	A3724	LEU	G3521	S3448	K3384	R3321	◆
L4072	GLY	C3786	A3724	C3786	GLY	A3724	N3645	ASP	L3522	H3449	A3387	V3324	◆
L4073	GLY	E3789	D3727	E3789	GLY	D3727	N3651	ASP	N3523	N3450	E3388	V3324	◆
L4074	GLY	R3793	I3728	R3793	GLY	I3728	L3654	ASP	C3525	E3455	E3388	N3325	◆
L4075	GLY	V3794	M3729	V3794	GLY	M3729	E3655	PRO	A3526	G3390	E3389	N3326	◆
L4076	GLY	T3797	K3731	T3797	GLY	K3731	A3658	LEU	P3527	N3457	G3390	L3327	◆
L4077	GLY	L3798	S3732	L3798	GLY	S3732	A3659	VAL	THR	N3465	E3391	G3328	◆
L4078	GLY	T3804	C3733	T3804	GLY	C3733	A3660	ASP	ASP	V3394	V3329	I3329	◆
L4079	GLY	N3806	HIS	N3806	GLY	HIS	W3661	ARG	GLN	R3395	D3330	D3330	◆
L4080	GLY	N3807	LEU	N3807	GLY	LEU	I3662	ARG	ASP	F3469	E3331	E3331	◆
L4081	GLY	C3807	GLU	C3807	GLY	GLU	L3663	VAL	LEU	L3470	A3332	A3332	◆
L4082	GLY	G3808	GLY	G3808	GLY	GLY	T3664	VAL	MET	THR	T3333	T3333	◆
L4083	GLY	N3809	GLY	N3809	GLY	GLY	E3665	VAL	LEU	ALA	W3334	W3334	◆
L4084	GLY	N3810	GLY	N3810	GLY	GLY	D3666	SER	ALA	SER	N3335	N3335	◆
L4085	GLY	A3811	GLY	A3811	GLY	GLY	H3667	VAL	ALA	VAL	L3338	L3338	◆
L4086	GLY	V3812	GLY	V3812	GLY	GLY	S3668	VAL	VAL	SER	A3339	A3339	◆
L4087	GLY	Q3813	ALA	Q3813	GLY	ALA	F3669	TYR	TYR	LYS	PHE	VAL	◆
L4088	GLY	Q3814	GLU	Q3814	GLY	GLU	E3670	LEU	LEU	M3478	R3403	R3403	◆
L4089	GLY	N3815	GLU	N3815	GLY	GLU	I3674	LEU	GLU	A3479	D3404	D3404	◆
L4090	GLY	K3816	GLU	K3816	GLY	GLU	D3675	GLN	L3542	K3480	L3405	L3405	◆
L4091	GLY	D3817	GLU	D3817	GLY	GLU	D3676	THR	K3543	A3481	A3407	PRO	◆
L4092	GLY	V3819	VAL	V3819	GLY	VAL	L3677	GLU	D3544	C3482	L3408	ILE	◆
L4093	GLY	L3820	E3750	L3820	GLY	E3750	V3751	HIS	THR	D3483	Y3409	V3346	◆
L4094	GLY	K3821	V3751	K3821	GLY	V3751	S3678	PRO	ASP	A3484	P3410	S3347	◆
L4095	GLY	F3822	F3752	F3822	GLY	F3752	K3679	TYR	GLU	Q3485	R3411	R3347	◆
L4096	GLY	K3823	F3753	K3823	GLY	F3753	A3680	SER	GLY	S3486	L3412	R3349	◆
L4097	GLY	E3824	E3754	E3824	GLY	E3754	GLY	LYS	V3549	G3487	I3413	R3350	◆
L4098	GLY	E3825	K3756	E3825	GLY	K3756	R3550	LYS	R3550	G3488	R3414	P3351	◆
L4099	GLY	E3826	M3758	E3826	GLY	M3758	E3551	VAL	E3552	S3489	Y3415	E3352	◆
L4100	GLY	C3827	F3759	C3827	GLY	F3759	L3553	TRP	L3553	D3490	V3416	L3353	◆
L4101	GLY	F3828	K3760	F3828	GLY	K3760	Q3554	HIS	GLU	Q3491	D3417	L3354	◆
L4102	GLY	F3829	Q3761	F3829	GLY	Q3761	N3555	LYS	GLU	ARG	N3418	H3355	◆
L4103	GLY	T3832	R3762	T3832	GLY	R3762	N3556	LEU	ARG	T3494	N3419	S3356	◆
L4104	GLY	Q3833	L3763	Q3833	GLY	L3763	L3557	SER	VAL	K3495	R3420	H3357	◆
L4105	GLY	L3834	L3764	L3834	GLY	L3764	H3558	GLN	K3496	H3422	F3359	I3359	◆
L4106	GLY	R3835	Y3765	R3835	GLY	Y3765	L3559	ARG	K3497	W3423	P3360	P3360	◆
L4107	GLY	N3836	Q3766	N3836	GLY	Q3766	Q3560	ARG	D3501	THR	T3361	T3361	◆
L4108	GLY	Q3837	Q3767	Q3837	GLY	Q3767	K3561	ALA	R3502	GLU	I3362	I3362	◆
L4109	GLY	T3905	R3769	T3905	GLY	R3769	L3701	VAL	VAL	Y3503	ARG	G3363	◆
L4110	GLY	T3906	H3771	T3906	GLY	H3771	V3702	VAL	G3565	N3428	P3427	ARG	◆
L4111	GLY	Y3902	R3772	Y3902	GLY	R3772	H3704	ALA	S3566	LEU	N3429	LEU	◆
L4112	GLY	T3905	R3773	T3905	GLY	R3773	F3705	VAL	G3567	THR	A3431	ARG	◆
L4113	GLY	Q3906	G3774	Q3906	GLY	G3774		VAL	S3568	SER	R3367	R3367	◆
L4114	GLY	T3907		T3907	GLY			THR	L3569	LEU	R3368	R3368	◆
L4115	GLY	Q3908		Q3908	GLY			LEU	R3570	ILE	A3369	A3369	◆
L4116	GLY	R3909		R3909	GLY			VAL	Q3572	ALA	V3373	V3373	◆
L4117	GLY	T3910		T3910	GLY			ALA	Q3572	ALA	A3374	A3374	◆
L4118	GLY	N3914		N3914	GLY			VAL		ARG	M3437	E3375	◆
L4119	GLY	I3915		I3915	GLY			ALA			M3437	E3375	◆
L4120	GLY				GLY			ALA			M3437	E3375	◆
L4121	GLY				GLY			ALA			M3437	E3375	◆
L4122	GLY				GLY			ALA			M3437	E3375	◆
L4123	GLY				GLY			ALA			M3437	E3375	◆
L4124	GLY				GLY			ALA			M3437	E3375	◆
L4125	GLY				GLY			ALA			M3437	E3375	◆
L4126	GLY				GLY			ALA			M3437	E3375	◆
L4127	GLY				GLY			ALA			M3437	E3375	◆
L4128	GLY				GLY			ALA			M3437	E3375	◆
L4129	GLY				GLY			ALA			M3437	E3375	◆
L4130	GLY				GLY			ALA			M3437	E3375	◆

- Molecule 1: Ryanodine receptor 1

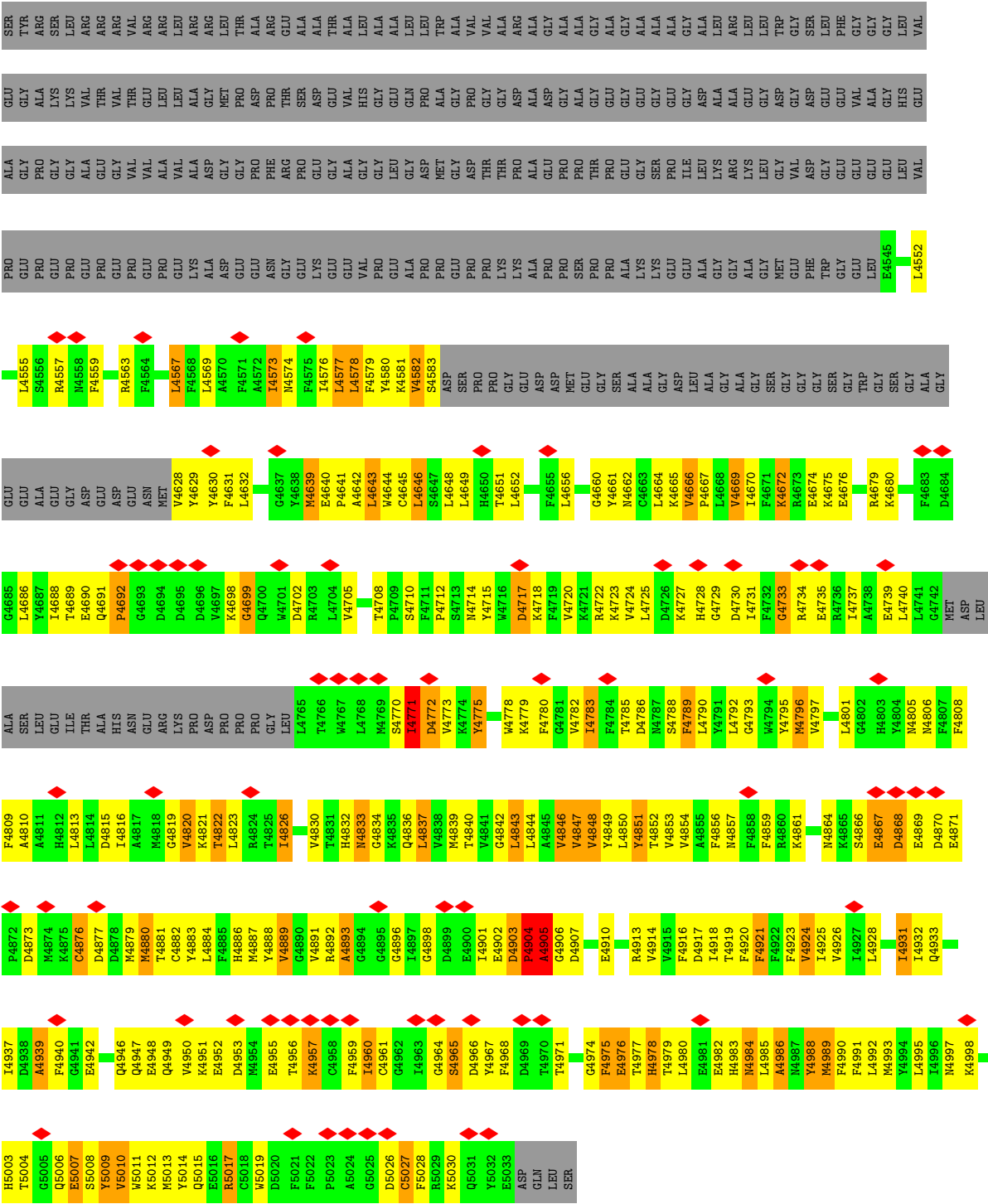










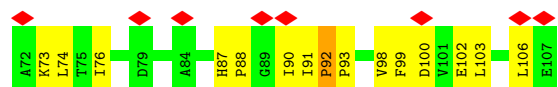
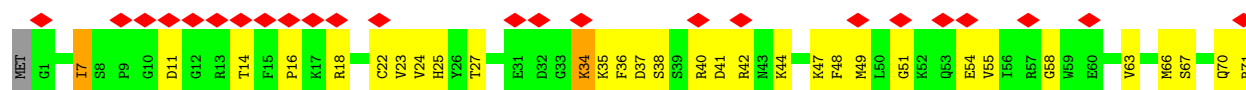


• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A

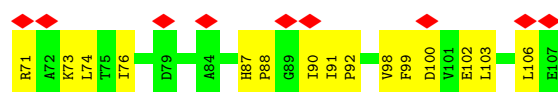
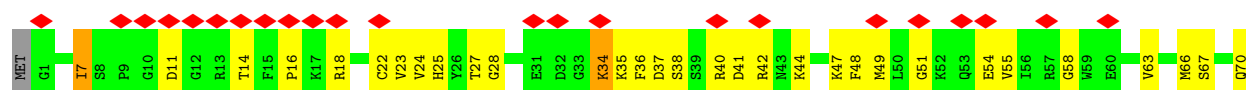




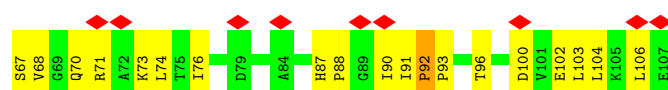
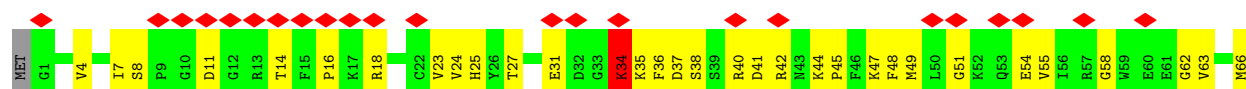
- Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A



- Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A



- Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	30000	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.243	Depositor
Minimum map value	-0.085	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.075	Depositor
Map size ($\text{\AA}$)	482.40002, 482.40002, 482.40002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.34, 1.34, 1.34	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	1.67	381/27312 (1.4%)	1.36	188/37004 (0.5%)
1	C	1.67	375/27312 (1.4%)	1.36	190/37004 (0.5%)
1	E	1.67	373/27312 (1.4%)	1.36	192/37004 (0.5%)
1	G	1.67	370/27312 (1.4%)	1.35	177/37004 (0.5%)
2	B	1.16	0/851	1.17	2/1146 (0.2%)
2	D	1.16	0/851	1.17	1/1146 (0.1%)
2	F	1.16	0/851	1.17	1/1146 (0.1%)
2	H	1.18	1/851 (0.1%)	1.15	1/1146 (0.1%)
All	All	1.66	1500/112652 (1.3%)	1.35	752/152600 (0.5%)

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	36
1	C	0	35
1	E	0	36
1	G	0	34
All	All	0	141

The worst 5 of 1500 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2926	LEU	CA-C	-18.30	1.30	1.53
1	G	1976	ARG	NE-CZ	11.56	1.45	1.33
1	G	1976	ARG	CD-NE	11.19	1.61	1.46
1	G	454	PRO	CA-C	-10.47	1.46	1.51
1	A	1976	ARG	CD-NE	9.57	1.59	1.46

The worst 5 of 752 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1224	GLU	CA-C-N	12.90	132.88	119.85
1	A	1224	GLU	C-N-CA	12.90	132.88	119.85
1	C	1224	GLU	CA-C-N	12.85	132.83	119.85
1	C	1224	GLU	C-N-CA	12.85	132.83	119.85
1	G	1224	GLU	CA-C-N	12.41	132.39	119.85

There are no chirality outliers.

5 of 141 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	31	GLU	Mainchain,Peptide
1	A	329	ARG	Mainchain,Peptide
1	A	734	GLY	Peptide
1	A	841	GLY	Mainchain,Peptide
1	A	894	GLY	Mainchain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	26843	0	24428	1227	0
1	C	26843	0	24428	1231	0
1	E	26843	0	24428	1235	0
1	G	26843	0	24427	1248	0
2	B	832	0	831	60	0
2	D	832	0	831	57	0
2	F	832	0	831	60	0
2	H	832	0	831	60	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
3	E	1	0	0	0	0
3	G	1	0	0	0	0
All	All	110704	0	101035	4875	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 23.

The worst 5 of 4875 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4880:MET:HA	1:G:4578:LEU:HD11	1.26	1.17
1:A:4578:LEU:HD11	1:C:4880:MET:HA	1.18	1.17
1:E:4578:LEU:HD11	1:G:4880:MET:HA	1.25	1.16
1:C:4578:LEU:HD11	1:E:4880:MET:HA	1.17	1.10
1:A:702:TRP:CD1	2:B:34:LYS:HZ1	1.71	1.08

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	3483/5037 (69%)	3132 (90%)	258 (7%)	93 (3%)	4	25
1	C	3483/5037 (69%)	3133 (90%)	254 (7%)	96 (3%)	4	24
1	E	3483/5037 (69%)	3134 (90%)	255 (7%)	94 (3%)	4	25
1	G	3483/5037 (69%)	3137 (90%)	252 (7%)	94 (3%)	4	25
2	B	105/108 (97%)	95 (90%)	9 (9%)	1 (1%)	12	48
2	D	105/108 (97%)	95 (90%)	9 (9%)	1 (1%)	12	48
2	F	105/108 (97%)	96 (91%)	8 (8%)	1 (1%)	12	48
2	H	105/108 (97%)	97 (92%)	8 (8%)	0	100	100
All	All	14352/20580 (70%)	12919 (90%)	1053 (7%)	380 (3%)	6	25

5 of 380 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	806	PRO
1	A	900	ASN
1	A	914	PRO

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Mol	Chain	Res	Type
1	A	916	PRO
1	A	971	ASP

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	2502/4276 (58%)	2471 (99%)	31 (1%)	63	74
1	C	2504/4276 (59%)	2474 (99%)	30 (1%)	63	74
1	E	2501/4276 (58%)	2470 (99%)	31 (1%)	63	74
1	G	2501/4276 (58%)	2472 (99%)	29 (1%)	63	74
2	B	89/90 (99%)	88 (99%)	1 (1%)	65	75
2	D	89/90 (99%)	88 (99%)	1 (1%)	65	75
2	F	89/90 (99%)	88 (99%)	1 (1%)	65	75
2	H	89/90 (99%)	88 (99%)	1 (1%)	65	75
All	All	10364/17464 (59%)	10239 (99%)	125 (1%)	61	74

5 of 125 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	4207	MET
1	G	1459	GLN
1	E	939	VAL
1	G	1458	HIS
1	G	4082	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 200 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	1459	GLN
1	E	4547	GLN
2	H	87	HIS

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Mol	Chain	Res	Type
1	E	1719	HIS
1	E	3700	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 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

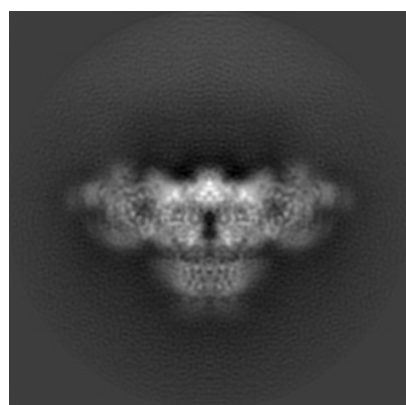
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9521. These allow visual inspection of the internal detail of the map and identification of artifacts.

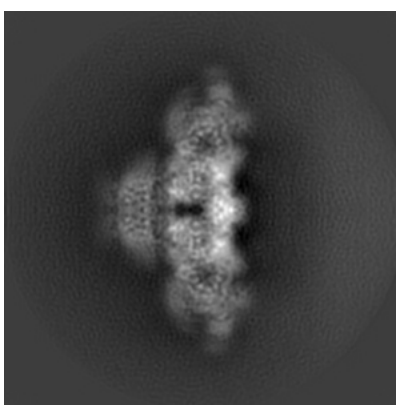
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

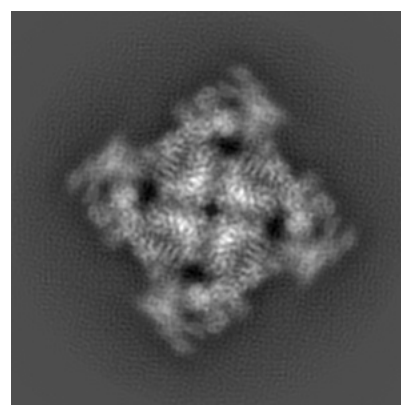
6.1.1 Primary map



X



Y

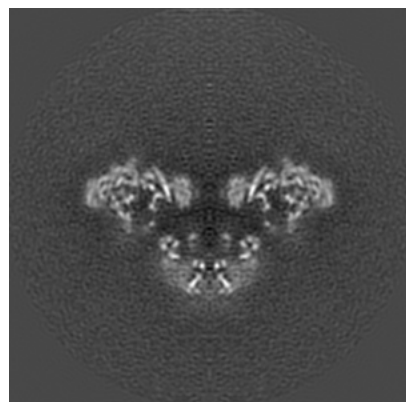


Z

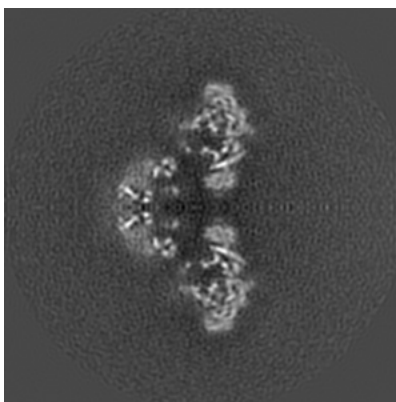
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

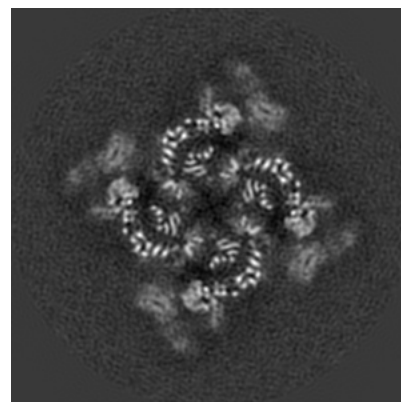
6.2.1 Primary map



X Index: 180



Y Index: 180

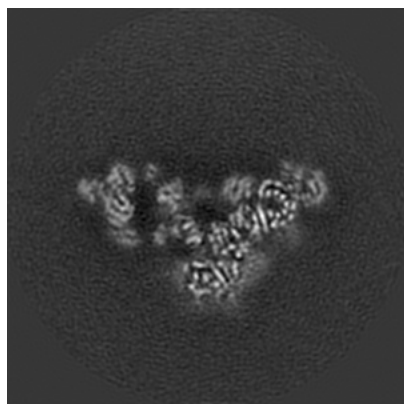


Z Index: 180

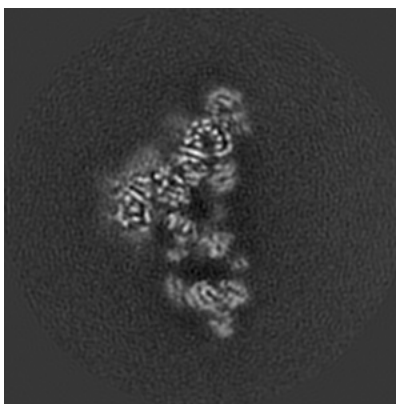
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

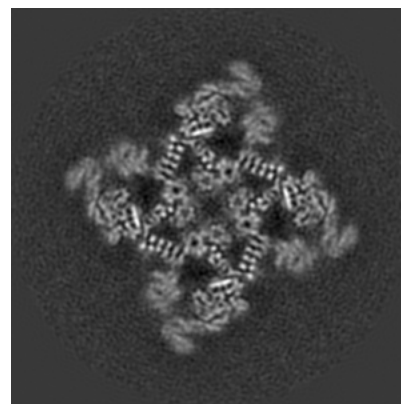
6.3.1 Primary map



X Index: 169



Y Index: 191

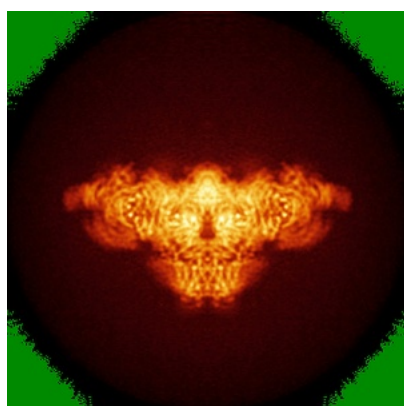


Z Index: 190

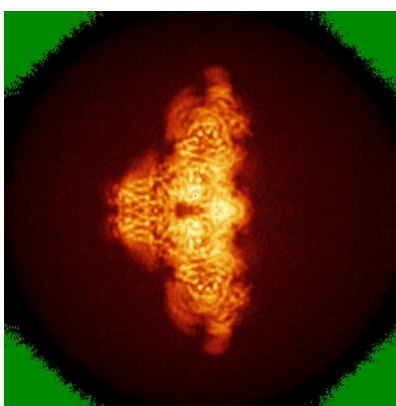
The images above show the largest variance slices of the map in three orthogonal directions.

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

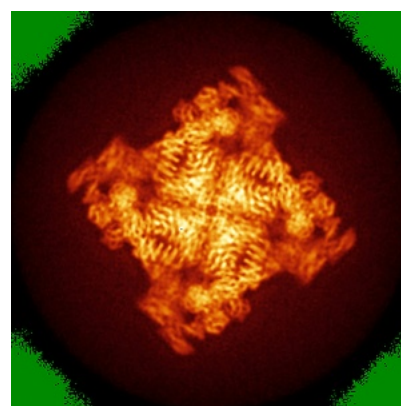
6.4.1 Primary map



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

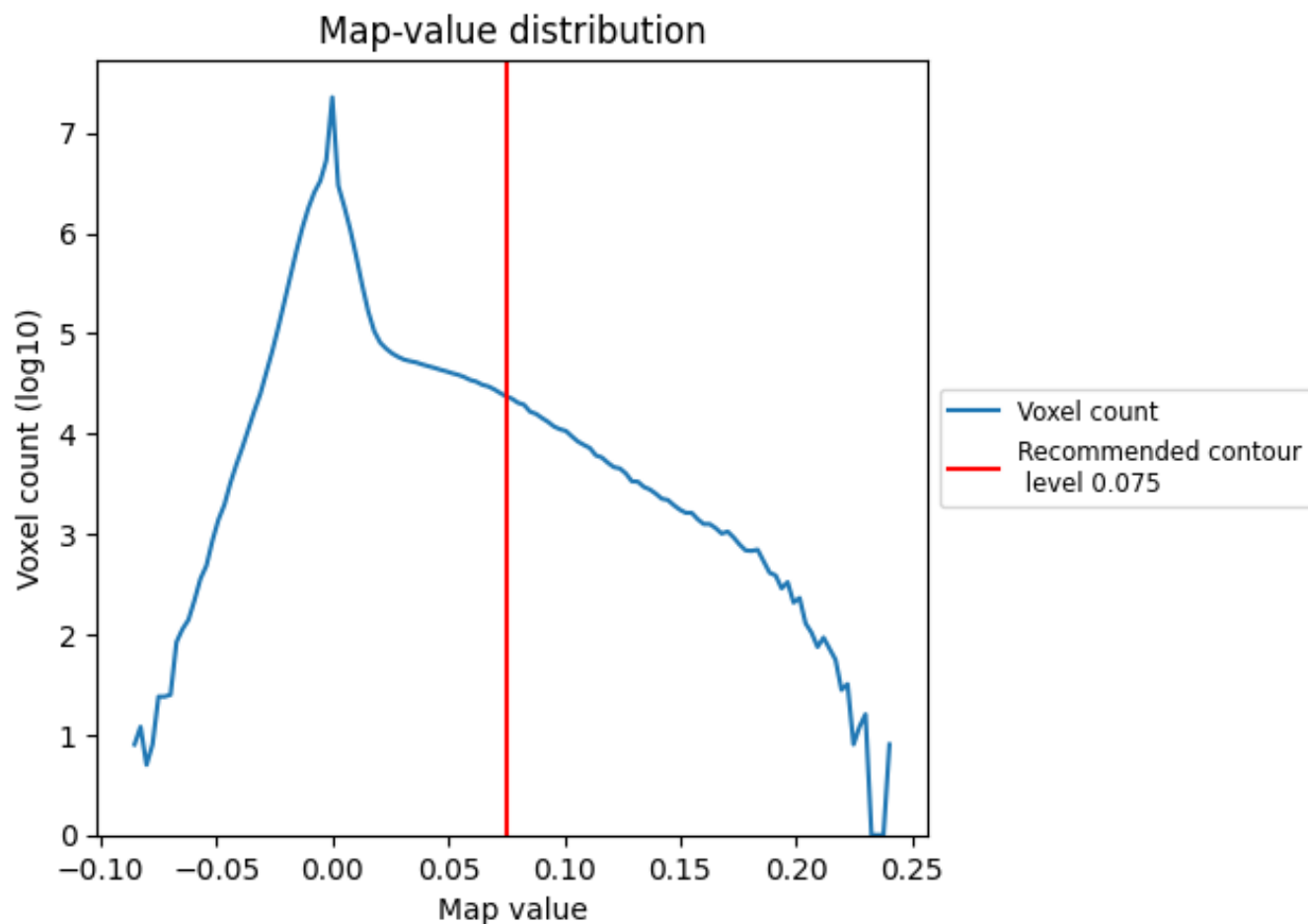
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

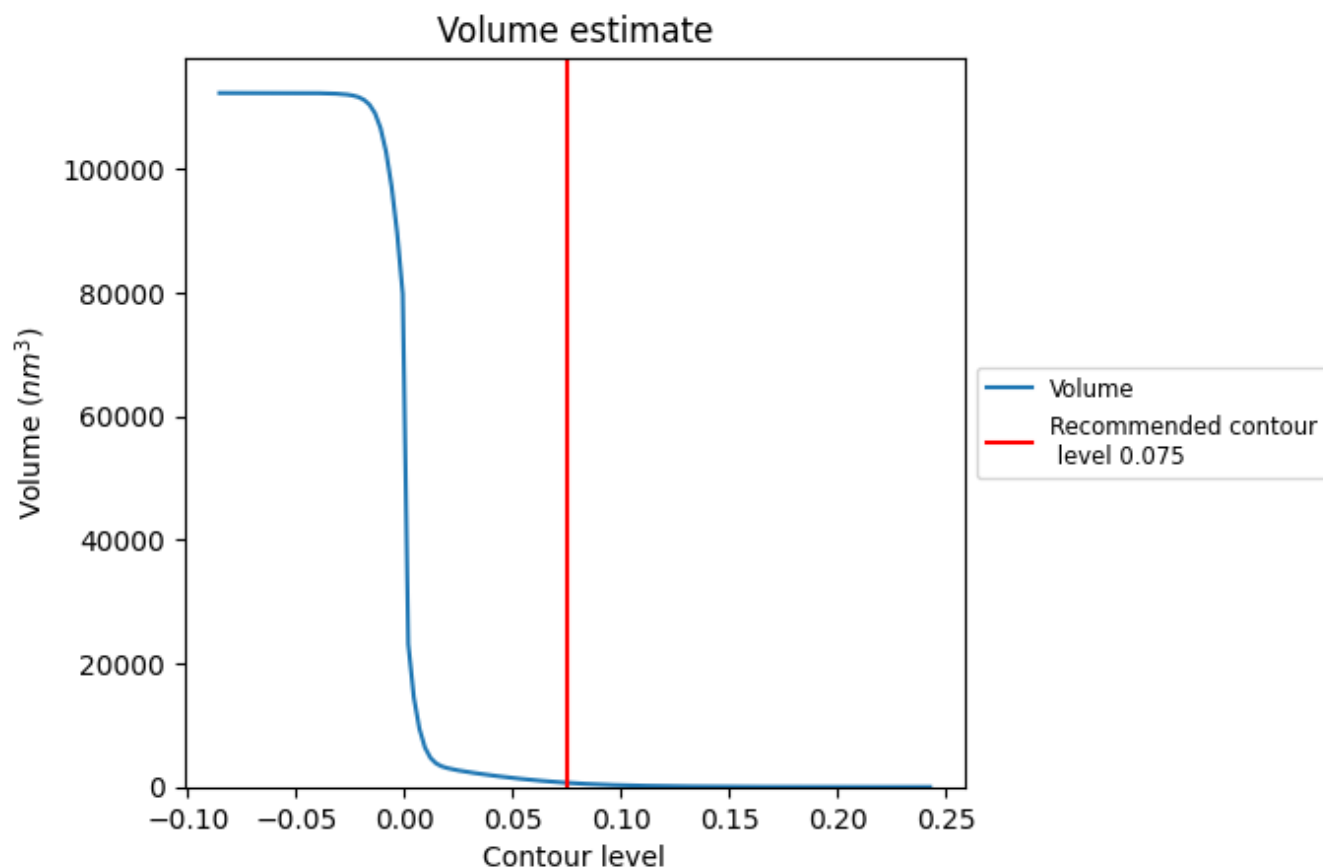
This section contains the results of statistical analysis of the map.

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.

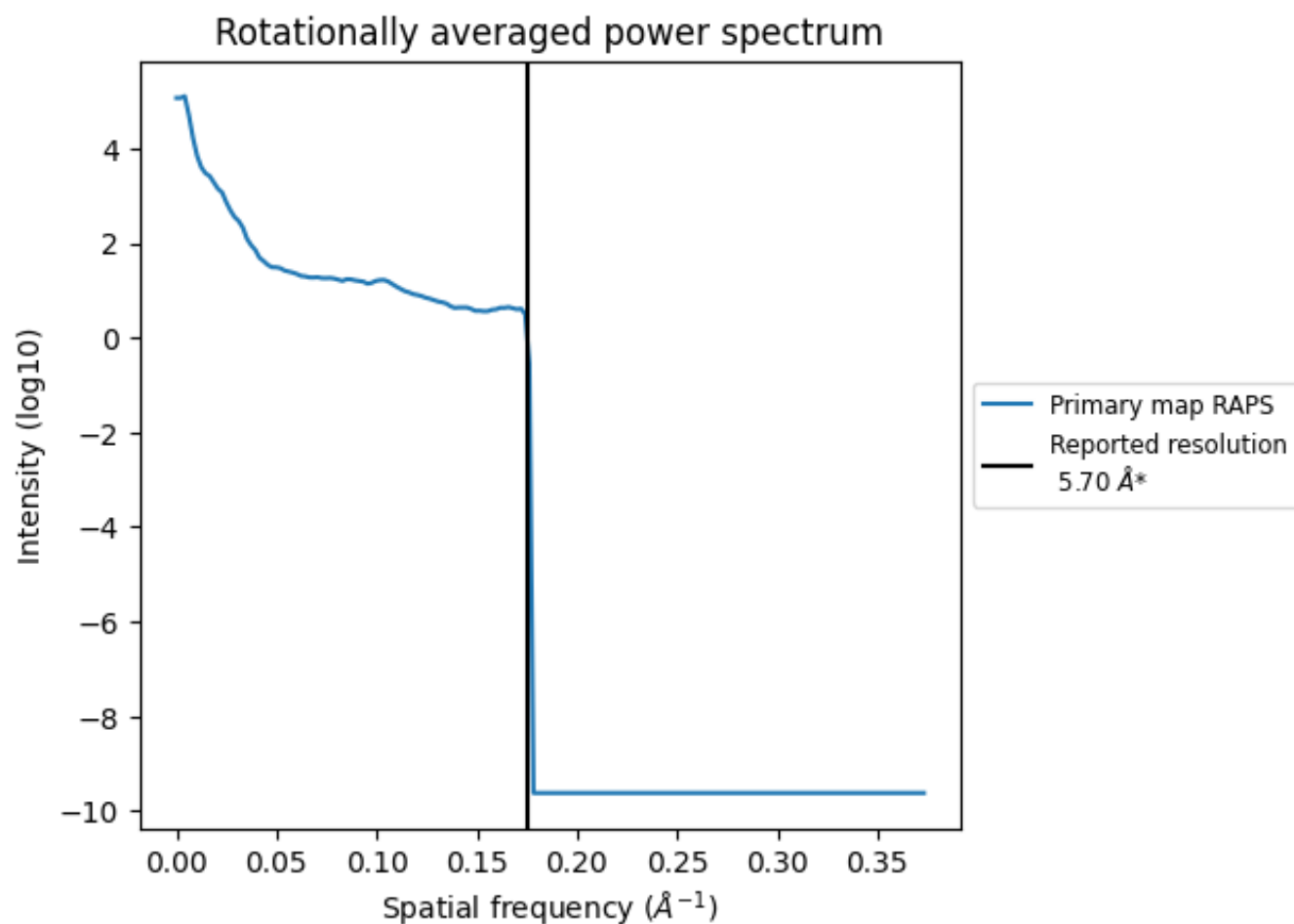
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 679 nm^3 ; this corresponds to an approximate mass of 613 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 0.175 Å⁻¹

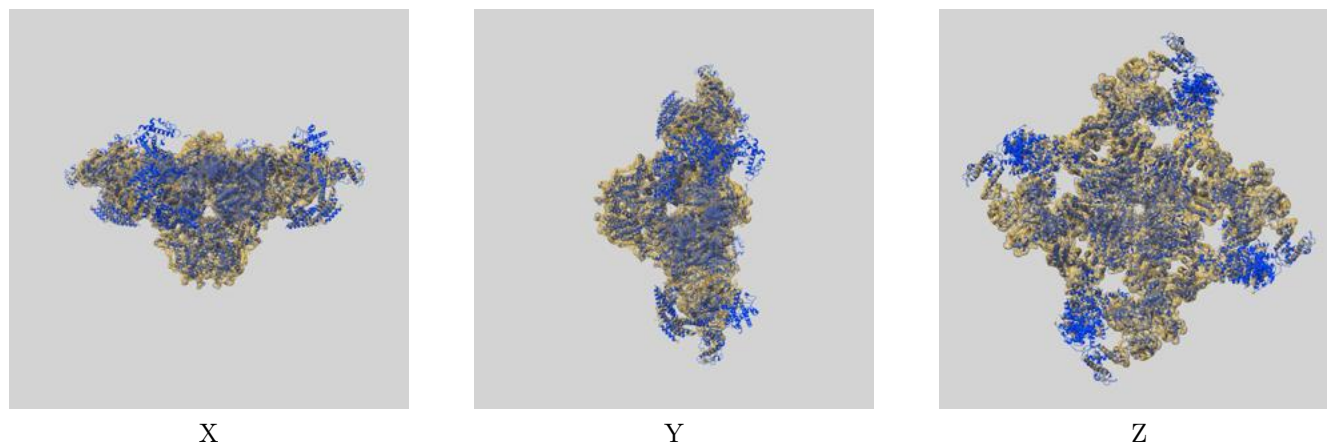
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

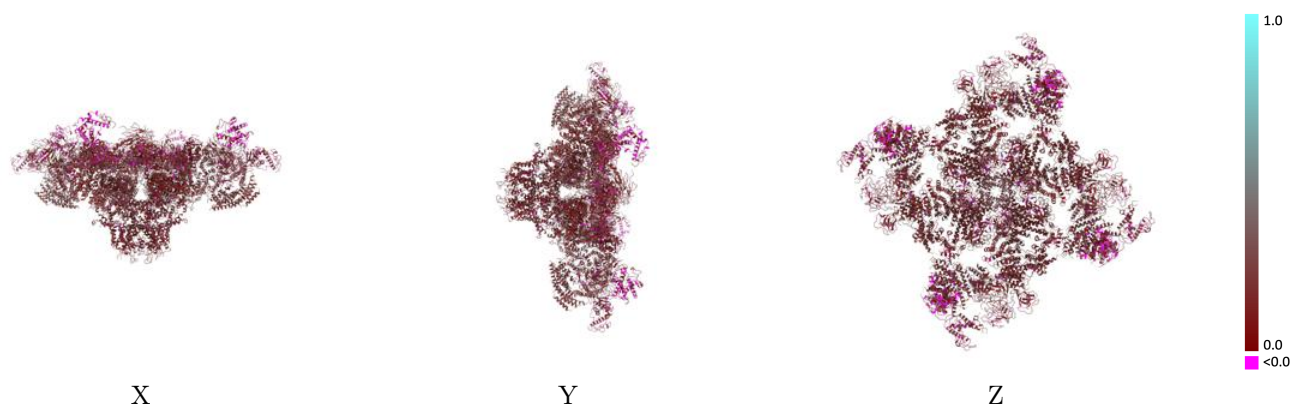
This section contains information regarding the fit between EMDB map EMD-9521 and PDB model 5GL1. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



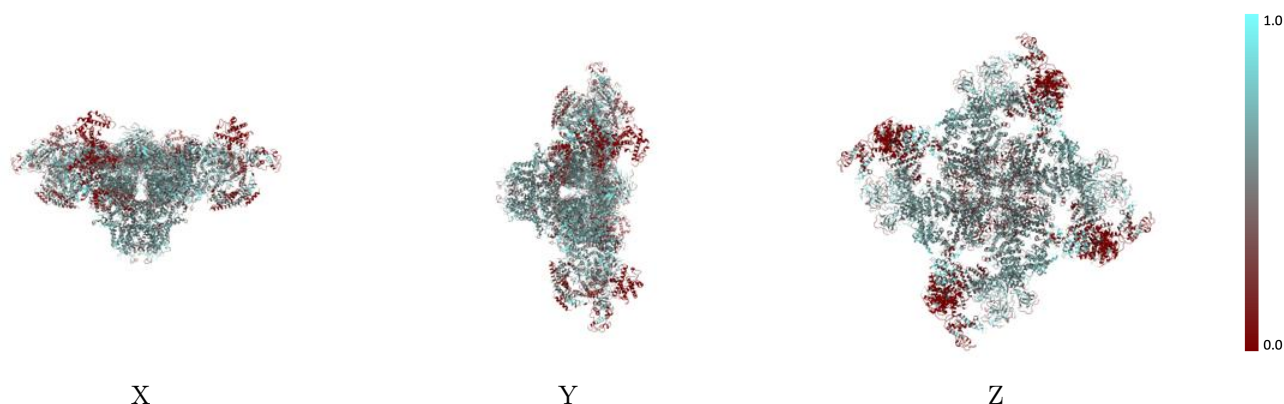
The images above show the 3D surface view of the map at the recommended contour level 0.075 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



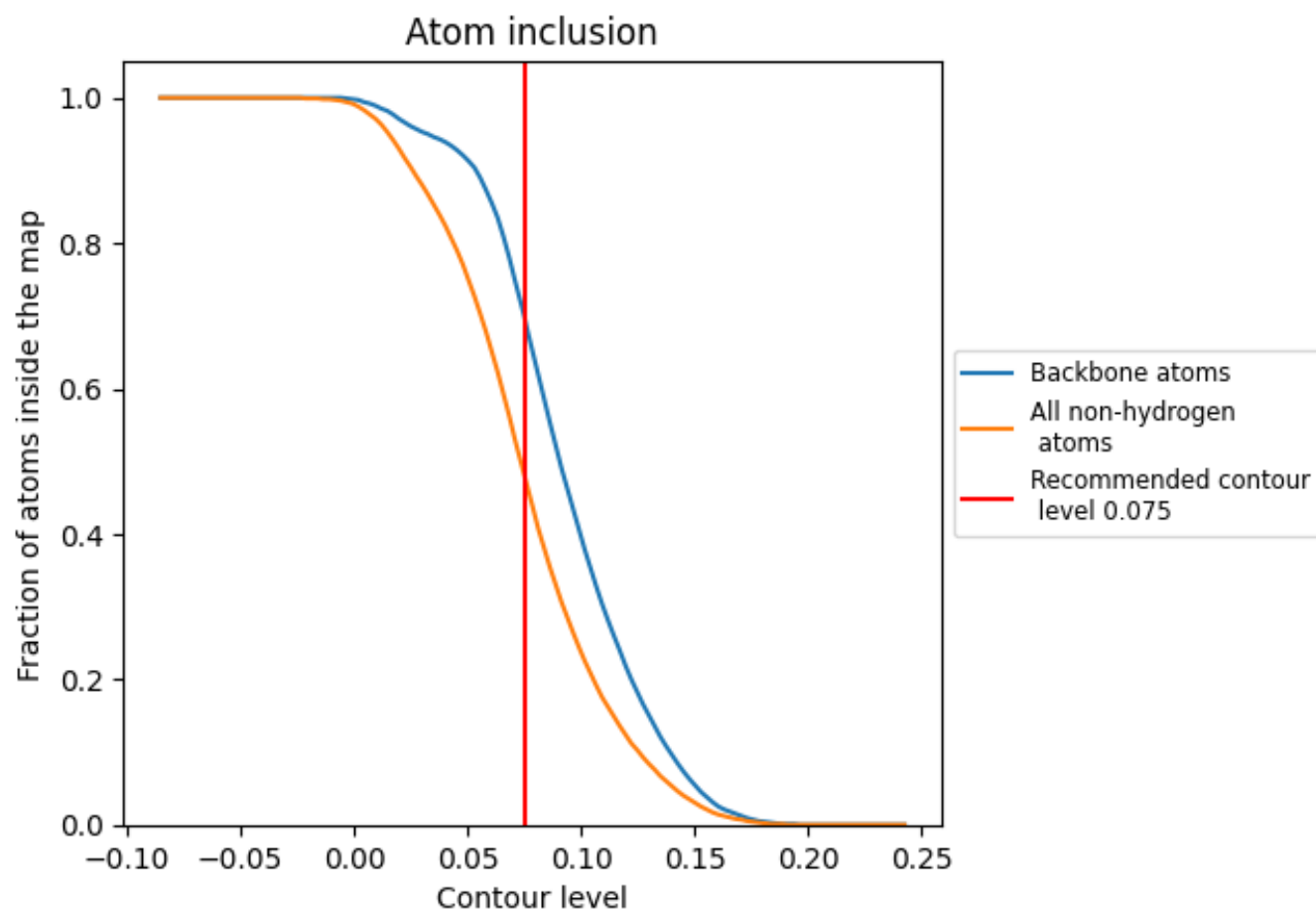
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.075).

9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 48% 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 (0.075) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4830	0.2010
A	0.4820	0.2020
B	0.4990	0.2060
C	0.4820	0.2010
D	0.4990	0.2080
E	0.4820	0.2010
F	0.5000	0.2050
G	0.4820	0.2010
H	0.4970	0.2040

1.0

0.0

<0.0