



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 09:06 AM UTC

PDB ID : 5GKZ / pdb_00005gkz
EMDB ID : EMD-9519
Title : Structure of RyR1 in a closed state (C3 conformer)
Authors : Bai, X.C.; Yan, Z.; Wu, J.P.; Yan, N.
Deposited on : 2016-07-07
Resolution : 4.00 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:

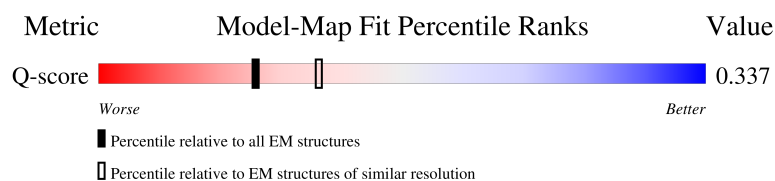
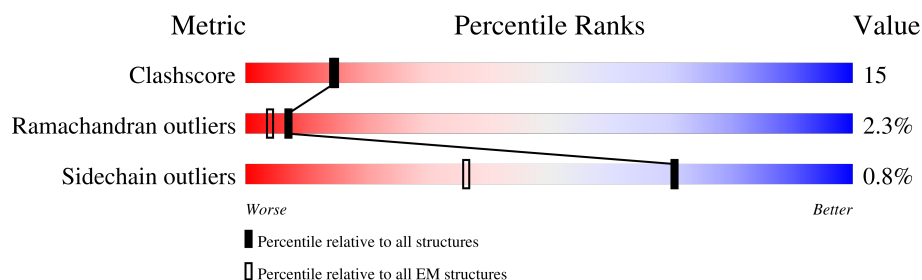
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.00 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	7587 (3.50 - 4.50)

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	 14% 47% 23% • 27%
1	C	5037	 14% 48% 23% • 27%
1	E	5037	 14% 47% 23% • 27%
1	G	5037	 14% 48% 23% • 27%

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Mol	Chain	Length	Quality of chain
2	B	108	 19% 67% 31% ..
2	D	108	 19% 65% 33% ..
2	F	108	 19% 68% 31% ..
2	H	108	 19% 69% 29% ..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 111000 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	3660	Total	C	N	O	S	0	0
			26917	17107	4682	4971	157		
1	C	3660	Total	C	N	O	S	0	0
			26917	17107	4682	4971	157		
1	E	3660	Total	C	N	O	S	0	0
			26917	17107	4682	4971	157		
1	G	3660	Total	C	N	O	S	0	0
			26917	17107	4682	4971	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		

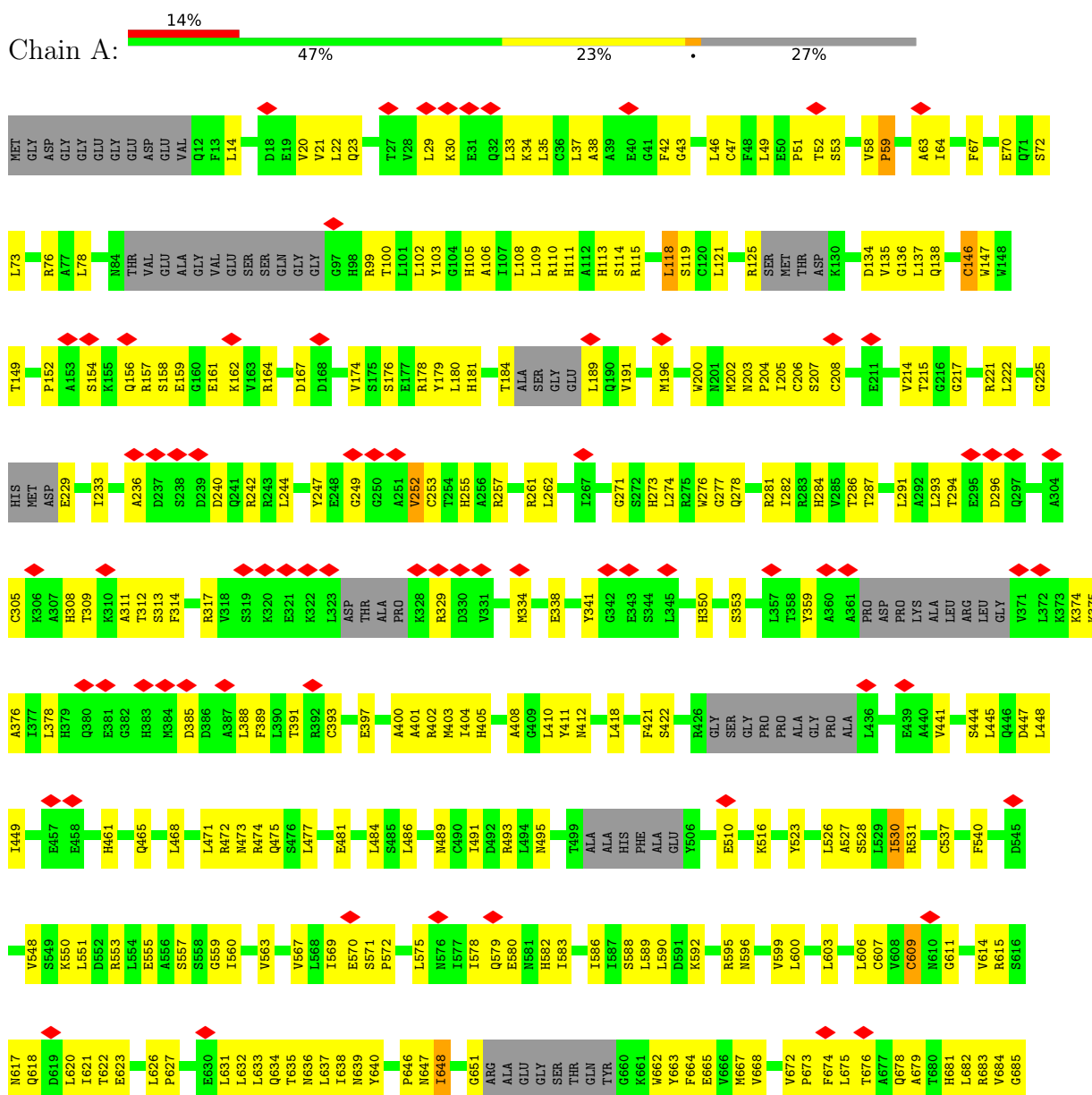
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

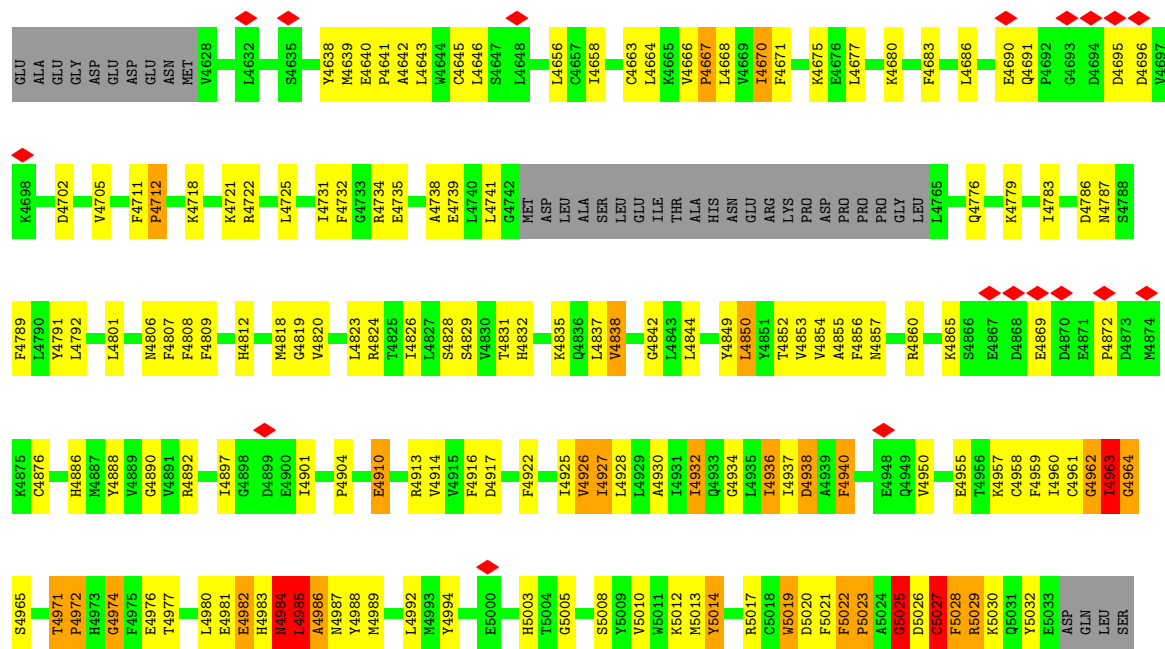




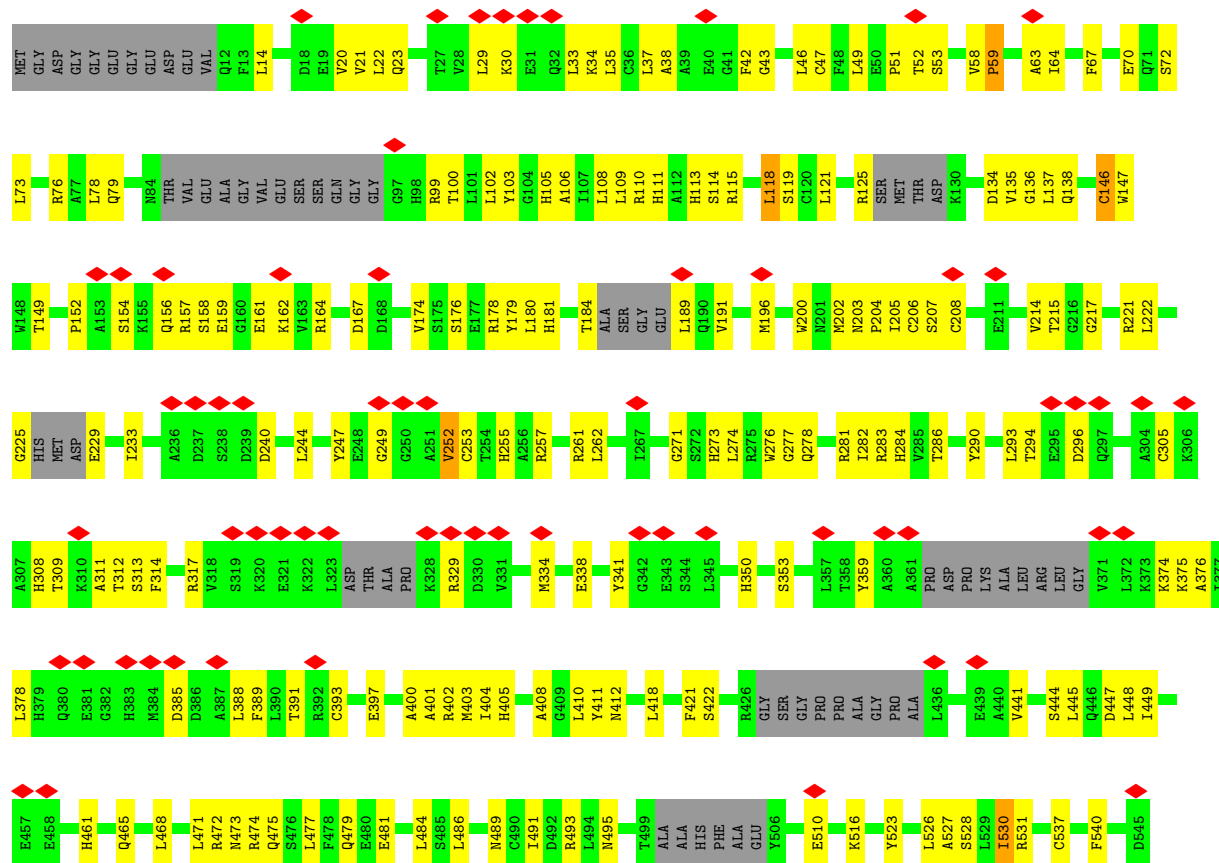


P2616	P2631	P2634	GLU	PHE	ALA	K2638	M2639	P2640	L2657	P2658	T2659	G2660	TRP	ALA	ASN	PHE	GLY	VAL	T2667	L2679	T2682	L2686	ALA	HIS	LYS	LYS	Y2691	P2701	L2706	A2707	G2708	A2709	L2710	P2711	P2712	ASP	TYR	VAL	ASP	ALA	ALA	SER	TYR	SER	SER	LYS	LYS	ALA	GLU	LYS	ALA	ALA	THR									
VAL	ASP	ALA	GLU	GLY	N2734	F2735	D2736	P2737	R2738	P2739	V2740	E2741	T2742	L2743	N2744	V2745	I2746	I2747	P2748	E2749	K2750	L2751	D2752	S2753	F2754	I2755	N2756	K2757	F2758	A2759	E2760	Y2761	T2762	H2763	E2764	K2765	W2766	A2767	F2768	D2769	K2770	I2771	Q2772	N2773	N2774	W2775	S2776	Y2777	G2778	E2779	LYS	N2780	I2781	SER	GLN	D2782	E2783	E2784	L2785	K2786	T2787	H2788
P2789	M2790	L2791	R2792	P2793	Y2794	T2795	T2796	T2797	S2798	E2799	K2800	D2801	K2802	E2803	L2804	V2805	R2806	W2807	P2808	L2809	K2810	E2811	S2812	L2813	K2814	A2815	M2816	L2817	A2818	W2819	E2820	Y2821	T2822	L2823	E2824	K2825	A2826	R2827	E2828	G2829	E2830	GLU	GLU	ARG	ALA	THR	GLU	LYS	LYS	LYS	THR	ARG	LYS	ILE	SER	GLN	THR	THR	ALA	GLN	THR	
Y2849	D2850	P2851	R2852	E2853	G2854	T2855	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	Y2881	H2883	N2884	V2885	W2886	G2887	R2888	K2889	L2890	K2891	Q2892	E2893	L2894	E2895	A2896	K2897	G2898	G2899	G2900	T2901	H2902	P2903	L2904	L2905	V2906	P2907	Y2908				
D2909	T2910	L2911	T2912	A2913	K2914	E2915	K2916	A2917	R2918	D2919	R2920	E2921	K2922	A2923	Q2924	E2925	L2926	L2927	K2928	F2929	Q2931	M2932	N2933	G2934	Y2935	A2936	V2937	T2938	R2939	LEU	LYS	ASP	MET	GLU	LEU	ASP	THR	SER	SER	ILE	GLU	LYS	ARG	PHE	ALA	PHE	PHE	LEU	GLN	GLN	LEU	ARG	TRP	MET	ASP							
ILE	SER	GLN	PHE	ILE	ALA	HIS	LEU	ALA	VAL	VAL	SER	SER	GLY	ARG	VAL	GLU	LYS	PRO	HIS	GLN	GLU	ILE	PHE	PHE	ALA	LYS	ILE	LEU	PRO	THR	PHE	ASN	HIS	CYS	LEU	Y3016	F3017	L3018	S3019	T3020	P3021	A3022	K3023	V3024	S3027	S3032																
N3033	K3036	I3039	THR	THR	SER	LEU	F3043	P3062	ALA	VAL	VAL	ASN	CYS	L3068	H3069	I3070	L3071	S3074	P3085	E3086	I3087	A3090	GLY	LEU	GLY	SER	F3095	F3096	E3097	S3098	E3104	K3105	M3106	V3107	E3108	R3111	L3112	G3113	K3114	V3115	S3116	GLN	ALA	ARG	THR	GLN	VAL	LYS	GLY	VAL	GLY	GLN										
ASN	LEU	TYR	T3132	L3137	P3138	Q3151	F3152	GLY	ASP	ASP	VAL	ILE	L3158	D3159	V3163	S3164	C3165	F3166	R3167	S3171	I3172	L3175	T3178	LYS	ASN	THR	TYR	V3183	E3184	K3185	L3186	R3187	P3188	A3189	L3190	A3195	R3196	A3199	A3200	MET	PRO	VAL	A3204	F3205	P3208	E3212	Y3213	N3214														
S3217	VAL	THR	THR	THR	LYS	SER	PRO	ARG	ARG	ALA	ILE	GLY	PRO	ASN	SER	VAL	GLU	MET	CYS	PRO	ASP	ILE	VAL	LEU	ARG	LEU	MET	ALA	ASP	ILE	GLY	ALA	ARG	TYR	THR	GLU	MET	PRO	PRO	HIS	VAL	ILE	T3273	L3274	P3275																	
M3276	L3277	C3278	S3279	Y3280	L3281	P3282	R3283	R3287	P3288	E3290	ALA	PRO	PRO	P3294	A3295	L3296	P3297	A3298	P3301	P3302	P3303	C3304	N3313	SER	LEU	LEU	G3317	M3318	I3319	L3320	R3321	D3330	E3331	A3339	VAL	PHE	ALA	GLN	PRO	ILE	V3346	P3351	L3354	H3355	S3356	H3357	F3358	P3360	T3361	I3362												
G3363	ARG	LEU	K3367	K3371	Q3378	E3386	G3390	E3391	L3392	L3393	V3394	R3395	D3396	E3397	PHE	SER	VAL	VAL	LEU	C3402	R3403	L3404	L3405	Y3406	P3410	L3411	L3412	L3413	N3418	R3419	R3420	A3421	H3422	Y3423	L3424	THR	GLU	P3427	N3428	A3431	E3432	F3435	ARG	M3437	V3438	E3445	GLN	N3457	V3460													
N3465	S3468	F3469	L3470	THR	ALA	ALA	ASP	SER	SER	LYS	M3478	G3482	S3486	S3489	D3490	Q3491	GLU	ARG	T3494	K3495	K3496	K3497	S3504	VAL	GLN	THR	SER	LEU	ILE	VAL	ALA	Y3513	K3516	M3517	L3518	P3519	M3524	C3525	A3526	P3527	THR	ASP	GLN	ASP	LEU	ILE	MET	LEU	ALA	K3537	T3538											
A3541	L3542	K3543	D3544	THR	ASP	GLU	GLU	V3549	R3550	D3554	H3558	P3567	S3568	L3569	R3570	W3571	D3572	MET	ALA	LEU	TYR	ARG	GLY	PRO	GLY	ARG	GLU	GLU	ASP	ALA	LYS	ILE	VAL	ARG	ARG	VAL	VAL	GLN	GLU	VAL	SER	ALA	LEU	GLU	GLN	THR	GLU															

HIS	GLU	L3844	L3923	F3992	M4064	H4153	K4230	ALA	SER	ASP	ASP
PRO	GLU	Q3850	L3924	L3993	PHE	H4156	K4231	ALA	LEU	GLU	GLY
TYR	GLU	N3851	R3925	F5994	LEU	H4157	F4234	ARG	PHE	GLU	GLY
LYS	GLU	K3852	L3926	V3995	LEU	H4158	V4235	ALA	GLY	VAL	GLY
LYS	GLU	R3768	Q3927	F3996	LEU	F4159	V4236	LEU	GLY	ALA	GLY
VAL	VAL	R3769	E3928	A3987	ASP	R4159	C4238	ARG	LEU	HIS	GLY
ALA	GLU	L3770	S3929	R3998	I4071	M4162	E4239	GLY	VAL	GLU	VAL
TRP	GLU	H3771	F3930	M3999	A4076	F4163	I4247	LEU	SER	ALA	ALA
LYS	GLU	T3772	S3931	K3998	F4077	E4164	I4251	ARG	GLY	PRO	PRO
HIS	GLU	G3774	D3932	M4001	Q4078	E4165	SER	ALA	GLY	GLY	GLY
LYS	GLU	A3775	F3933	L4002	L4003	E4166	I4251	LEU	VAL	ALA	ALA
LEU	GLU	M3778	Y3935	A4004	D4079	A4167	GLU	ARG	THR	GLY	GLY
LEU	GLU	V3779	Y3937	Q4005	D4083	I4170	PRO	ARG	THR	GLY	GLY
SER	GLY	L3780	ASP	L4012	P4084	F4174	GLU	VAL	THR	GLY	GLY
GLN	GLY	Q3781	THR	L4013	R4085	R4175	GLY	ARG	GLU	VAL	VAL
ARG	THR	M3782	THR	L4016	G4086	F4176	PRO	ARG	LEU	ALA	ALA
ARG	ILE	I3783	ASN	L4019	L4087	Y4177	GLU	LEU	LEU	VAL	VAL
ARG	ASN	S3784	ASN	L4019	I4088	L4178	ALA	ARG	LEU	ALA	ALA
ALA	GLN	A3785	ARG	Q4020	S4089	C4179	ASP	ARG	LEU	ASP	ASP
VAL	ASN	C3786	ASN	Q4021	K4090	G4178	GLU	LEU	ASP	GLY	GLY
VAL	GLY	D3717	GLY	D4022	Q4100	R4180	ASP	ALA	PRO	GLY	GLY
ALA	GLY	E3718	LYS	M4023	Q4102	E4181	GLY	ALA	ASP	ALA	ALA
CYS	GLY	M3793	LYS	V4024	Q4105	E4182	GLY	ALA	THR	GLY	GLY
PHE	GLY	V3794	LYS	M4026	G4106	M4184	GLY	ALA	GLY	ALA	ALA
ARG	GLY	T3797	VAL	L4027	I4108	E4186	ALA	ALA	VAL	ALA	ALA
ARG	GLY	L3798	VAL	L4028	S4113	S4187	ALA	ALA	GLY	GLY	GLY
MET	GLY	K3799	ALA	V3957	E4113	I4190	GLY	ALA	GLY	GLY	GLY
THR	GLY	M3723	ALA	A3958	C4114	E4191	GLY	ALA	GLY	GLY	GLY
LEU	GLY	Y3725	ALA	K3959	S4115	R4192	ALA	ALA	GLY	GLY	GLY
TYR	GLY	A3726	ALA	F3962	E4116	F4193	GLY	ALA	PRO	PRO	PRO
ASN	GLY	D3727	ALA	N3963	A4117	E4194	GLY	ALA	ALA	ASP	ASP
LEU	GLY	I3728	ALA	S3964	D4118	F4195	ALA	ALA	GLY	GLY	GLY
LEU	GLY	M3729	ALA	L3965	E4119	S4198	ALA	ALA	VAL	VAL	VAL
ASN	GLY	K3731	ALA	E3967	M4120	M4201	ALA	ALA	GLY	GLY	GLY
F3645	GLY	C3732	ALA	L3966	E4121	R4202	ALA	ALA	GLY	GLY	GLY
H3646	GLY	S3733	ALA	T3967	M4122	E4205	ALA	ALA	GLY	GLY	GLY
H3647	GLY	HIS	ALA	Q3970	I4123	F4206	ALA	ALA	GLY	GLY	GLY
E3655	GLY	LEU	ALA	C3971	E4127	F4207	ALA	ALA	GLY	GLY	GLY
S3656	GLY	LEU	ALA	P3972	R4131	H4208	ALA	ALA	GLY	GLY	GLY
Y3657	GLY	GLU	ALA	C3973	PHE	K4214	ALA	ALA	GLY	GLY	GLY
K3658	GLY	GLU	ALA	Q3977	GLN	F4217	ALA	ALA	GLY	GLY	GLY
I3662	GLY	GLY	ALA	L3978	GLY	V4222	ALA	ALA	GLY	GLY	GLY
L3663	GLY	GLY	ALA	S3979	GLY	G4225	ALA	ALA	GLY	GLY	GLY
T3664	GLY	GLY	ALA	L3980	GLY	G4226	ALA	ALA	GLY	GLY	GLY
H3667	GLY	GLY	ALA	A3981	GLY	E4227	ALA	ALA	GLY	GLY	GLY
S3668	GLY	GLY	ALA	L3985	GLY	A4228	ALA	ALA	GLY	GLY	GLY
T3674	GLY	GLY	ALA	W3986	GLY	E4229	ALA	ALA	GLY	GLY	GLY
D3675	GLY	GLY	ALA	V3986	GLY		ALA	ALA	GLY	GLY	GLY
L3677	GLY	GLY	ALA	F3987	GLY		ALA	ALA	GLY	GLY	GLY
S3678	GLY	GLY	ALA	L3988	GLY		ALA	ALA	GLY	GLY	GLY
K3679	GLY	GLY	ALA	A3988	GLY		ALA	ALA	GLY	GLY	GLY
A3680	GLY	GLY	ALA	V3989	GLY		ALA	ALA	GLY	GLY	GLY
F3753	GLY	GLY	ALA	G3991	GLY		ALA	ALA	GLY	GLY	GLY
E3754	GLY	GLY	ALA		GLY		ALA	ALA	GLY	GLY	GLY
E3755	GLY	GLY	ALA		GLY		ALA	ALA	GLY	GLY	GLY



• Molecule 1: Ryanodine receptor 1

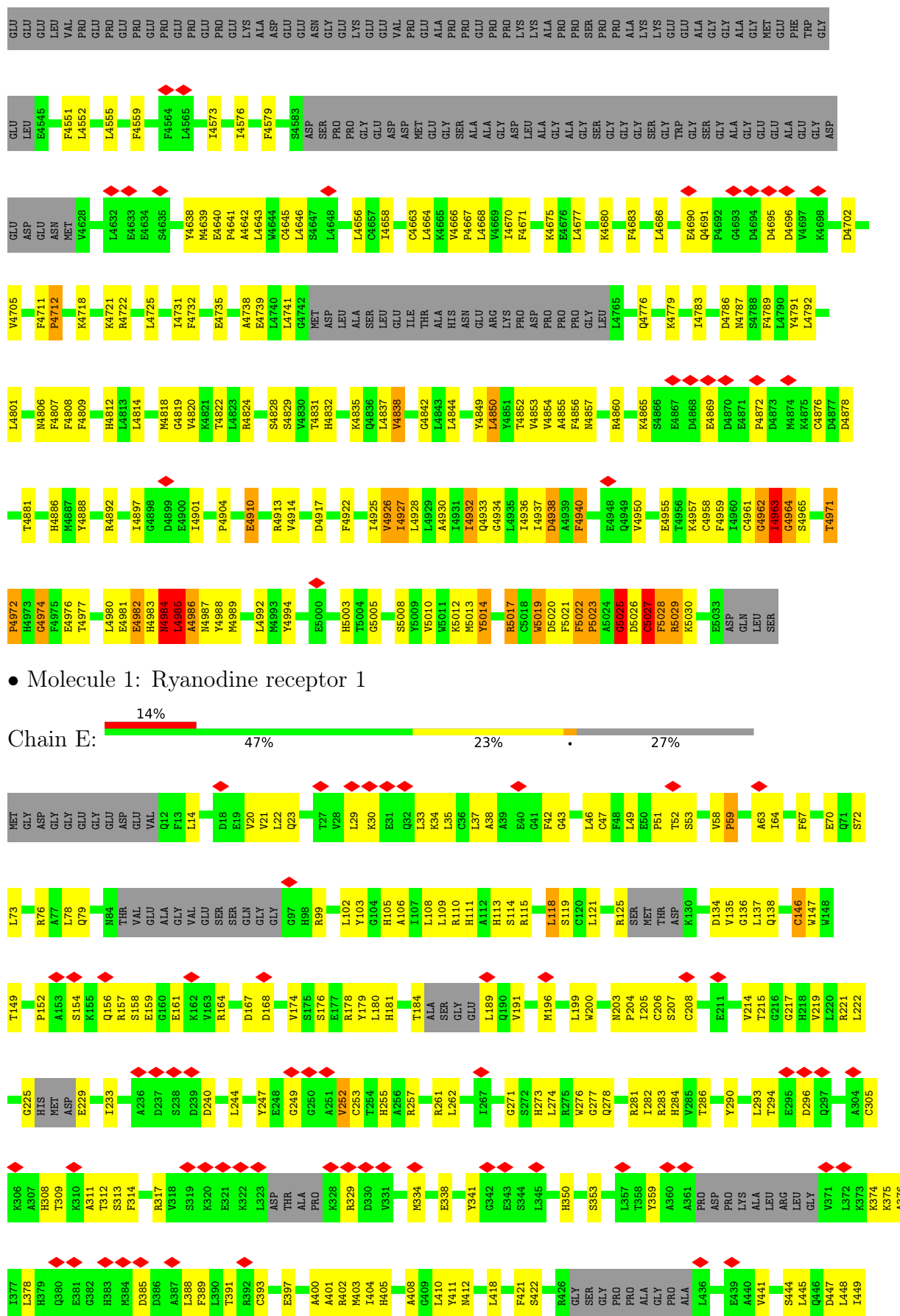
















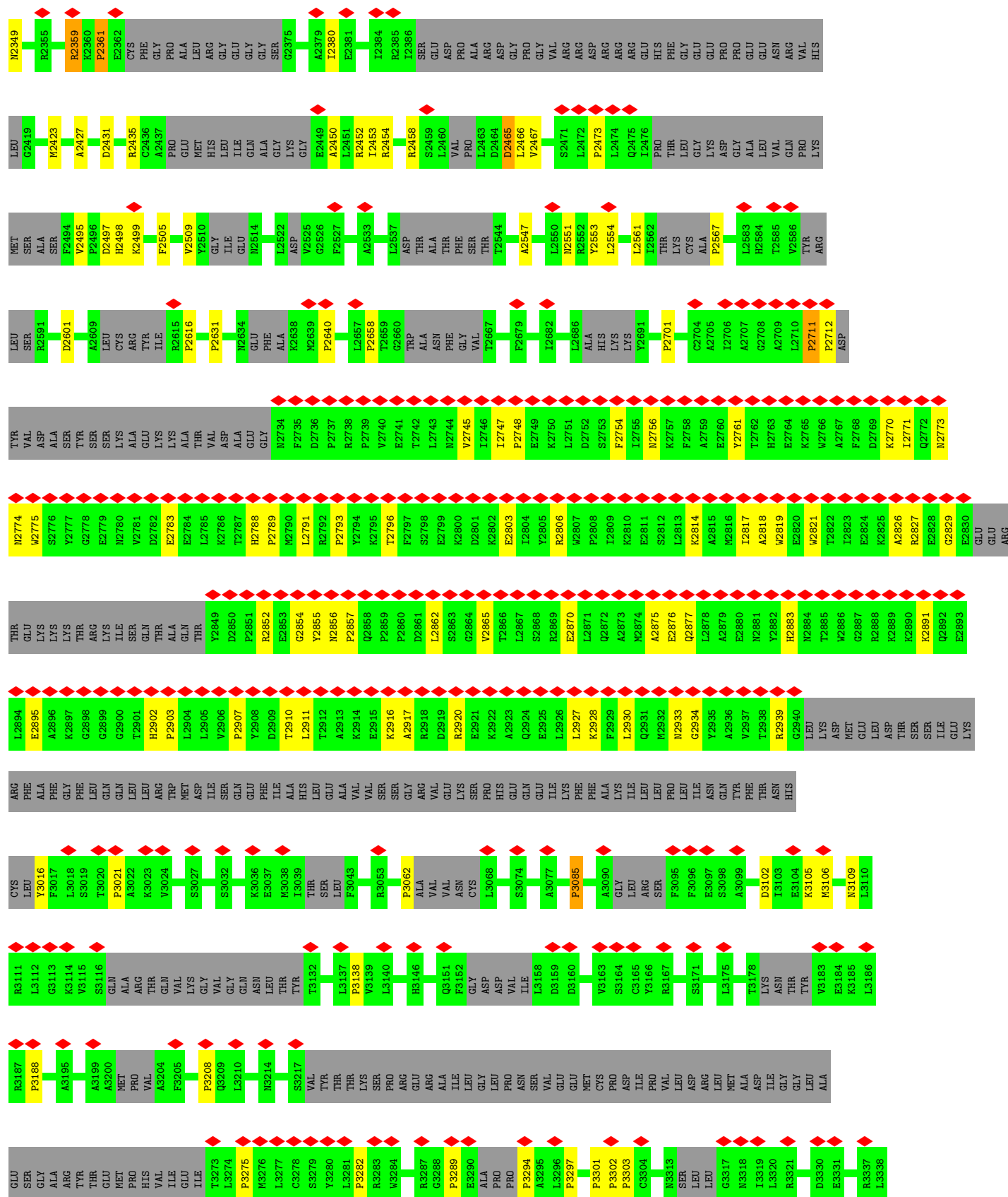




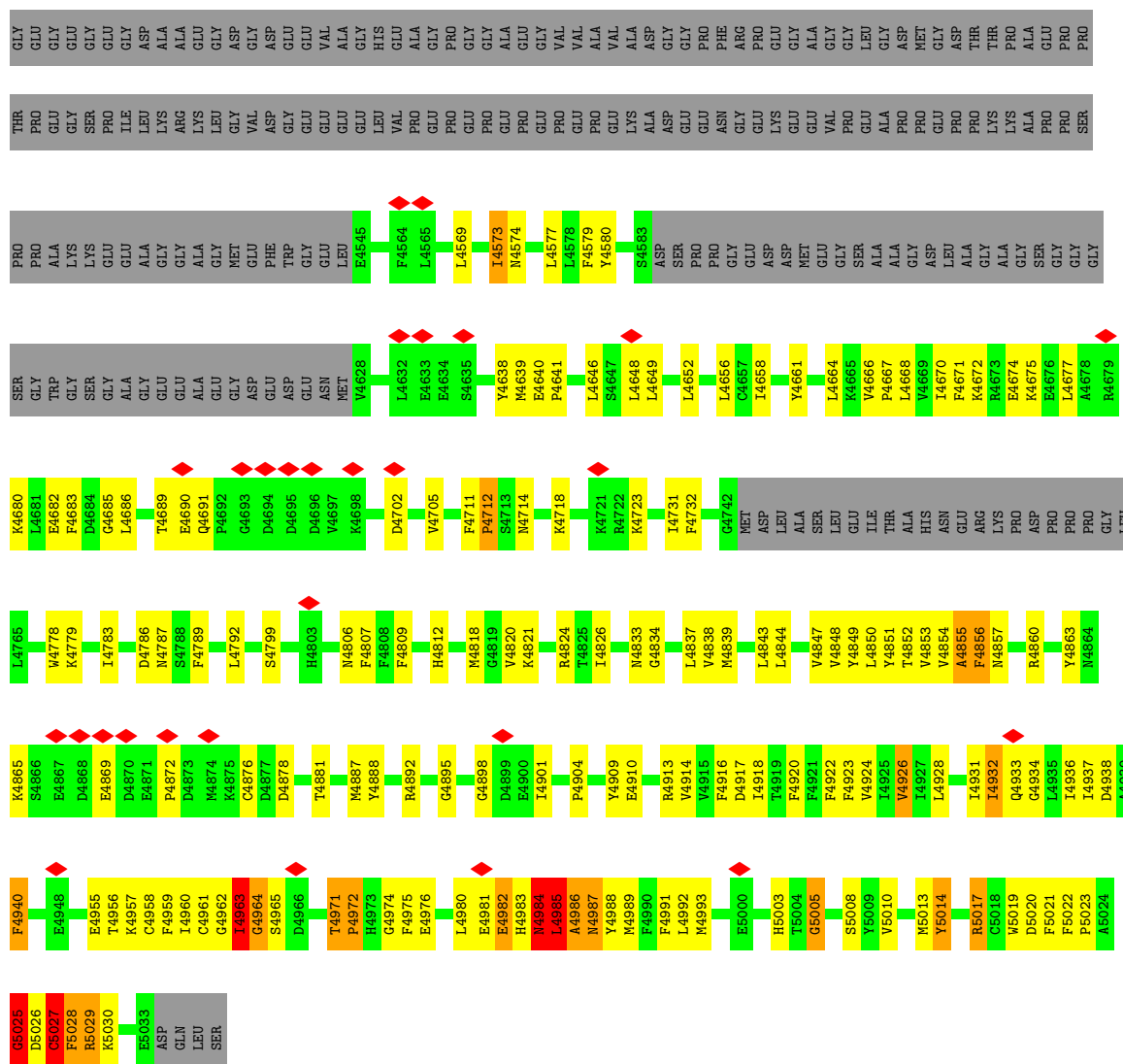










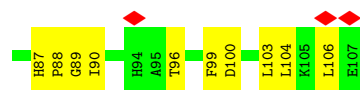


• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A

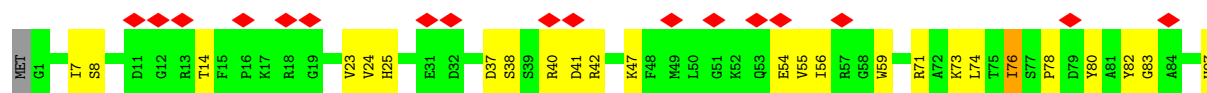


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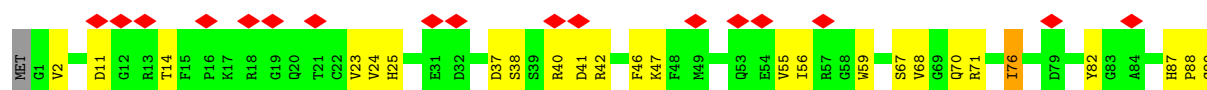




- Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A



- 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	64000	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	0.428	Depositor
Minimum map value	-0.192	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.085	Depositor
Map size (Å)	482.40002, 482.40002, 482.40002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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	1.22	177/27385 (0.6%)	1.09	113/37104 (0.3%)
1	C	1.22	170/27385 (0.6%)	1.09	113/37104 (0.3%)
1	E	1.22	174/27385 (0.6%)	1.09	109/37104 (0.3%)
1	G	1.23	175/27385 (0.6%)	1.08	111/37104 (0.3%)
2	B	0.81	1/851 (0.1%)	0.92	2/1146 (0.2%)
2	D	0.81	1/851 (0.1%)	0.92	2/1146 (0.2%)
2	F	0.81	1/851 (0.1%)	0.92	2/1146 (0.2%)
2	H	0.85	1/851 (0.1%)	0.90	0/1146
All	All	1.21	700/112944 (0.6%)	1.08	452/153000 (0.3%)

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	20
1	C	0	20
1	E	0	20
1	G	0	20
All	All	0	80

The worst 5 of 700 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	4180	ARG	CA-C	-13.31	1.38	1.52
1	A	4180	ARG	CA-C	-12.89	1.38	1.52
1	G	4988	TYR	CG-CD2	-12.82	1.12	1.39
1	E	4180	ARG	CA-C	-12.79	1.38	1.52
1	E	4190	ILE	C-O	-12.23	1.12	1.23

The worst 5 of 452 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	4083	ASP	CA-C-N	18.33	142.75	119.84
1	G	4083	ASP	C-N-CA	18.33	142.75	119.84
1	E	915	GLU	CA-C-N	18.30	142.71	119.84
1	E	915	GLU	C-N-CA	18.30	142.71	119.84
1	G	915	GLU	CA-C-N	18.28	142.69	119.84

There are no chirality outliers.

5 of 80 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1464	PHE	Mainchain,Peptide
1	A	1465	ASP	Peptide
1	A	697	GLY	Mainchain,Peptide
1	A	807	GLY	Mainchain,Peptide
1	A	841	GLY	Mainchain,Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	26917	0	24461	826	0
1	C	26917	0	24461	810	0
1	E	26917	0	24461	812	0
1	G	26917	0	24461	788	0
2	B	832	0	831	34	0
2	D	832	0	831	35	0
2	F	832	0	831	33	0
2	H	832	0	831	28	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	111000	0	101168	3221	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 15.

The worst 5 of 3221 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:G:1782:PHE:O	2:H:82:TYR:OH	1.75	1.03
1:A:1782:PHE:O	2:B:82:TYR:OH	1.76	1.03
1:A:4888:TYR:CD1	1:G:4914:VAL:HG23	1.95	1.02
1:C:1782:PHE:O	2:D:82:TYR:OH	1.78	1.01
1:E:1782:PHE:O	2:F:82:TYR:OH	1.77	1.00

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	3496/5037 (69%)	3185 (91%)	227 (6%)	84 (2%)	4	30
1	C	3496/5037 (69%)	3185 (91%)	228 (6%)	83 (2%)	4	30
1	E	3496/5037 (69%)	3187 (91%)	226 (6%)	83 (2%)	4	30
1	G	3496/5037 (69%)	3192 (91%)	217 (6%)	87 (2%)	4	29
2	B	105/108 (97%)	96 (91%)	9 (9%)	0	100	100
2	D	105/108 (97%)	96 (91%)	9 (9%)	0	100	100
2	F	105/108 (97%)	96 (91%)	9 (9%)	0	100	100
2	H	105/108 (97%)	93 (89%)	12 (11%)	0	100	100
All	All	14404/20580 (70%)	13130 (91%)	937 (6%)	337 (2%)	7	31

5 of 337 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	701	GLY
1	A	915	GLU
1	A	916	PRO

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Mol	Chain	Res	Type
1	A	969	PRO
1	A	1589	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	2503/4276 (58%)	2483 (99%)	20 (1%)	73	77
1	C	2502/4276 (58%)	2483 (99%)	19 (1%)	73	77
1	E	2500/4276 (58%)	2481 (99%)	19 (1%)	73	77
1	G	2501/4276 (58%)	2481 (99%)	20 (1%)	73	77
2	B	89/90 (99%)	89 (100%)	0	100	100
2	D	89/90 (99%)	89 (100%)	0	100	100
2	F	89/90 (99%)	89 (100%)	0	100	100
2	H	89/90 (99%)	89 (100%)	0	100	100
All	All	10362/17464 (59%)	10284 (99%)	78 (1%)	70	77

5 of 78 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	5012	LYS
1	G	3758	MET
1	G	806	PRO
1	G	979	PRO
1	G	4850	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 264 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	1861	GLN
1	G	2420	HIS
1	G	5015	GLN

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Mol	Chain	Res	Type
1	C	1861	GLN
1	C	1665	HIS

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.

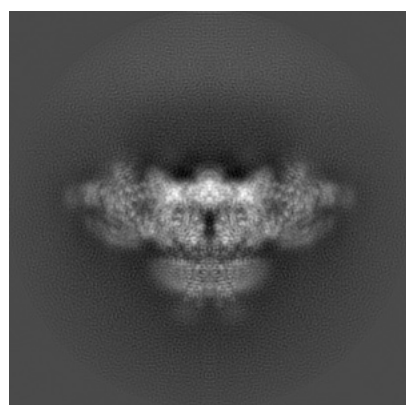
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9519. These allow visual inspection of the internal detail of the map and identification of artifacts.

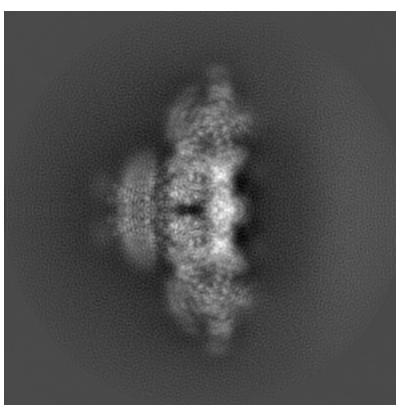
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

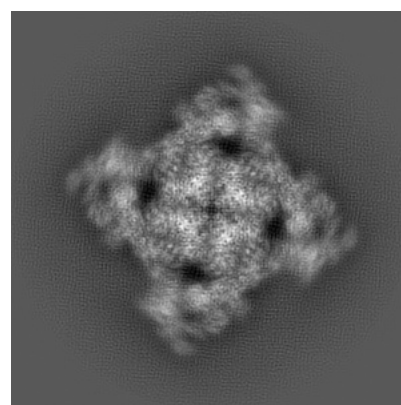
6.1.1 Primary map



X



Y

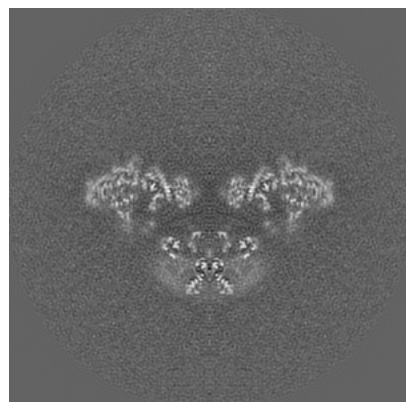


Z

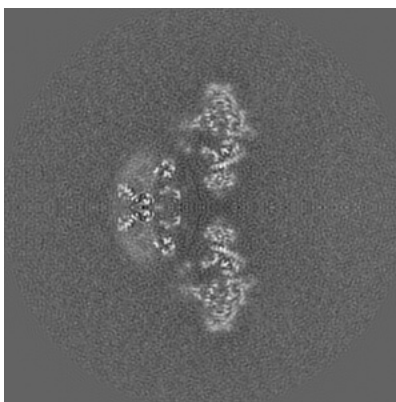
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

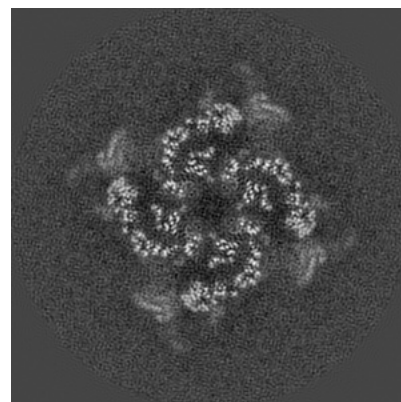
6.2.1 Primary map



X Index: 180



Y Index: 180

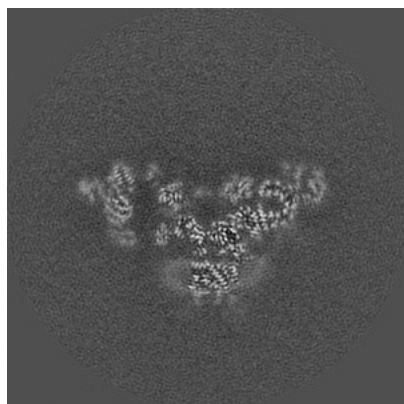


Z Index: 180

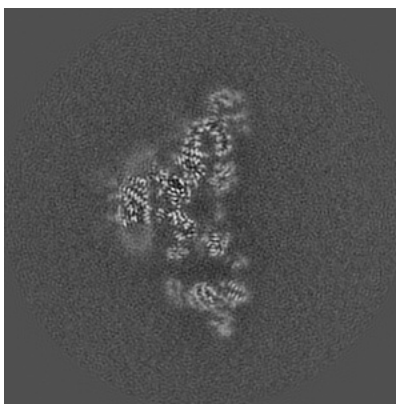
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

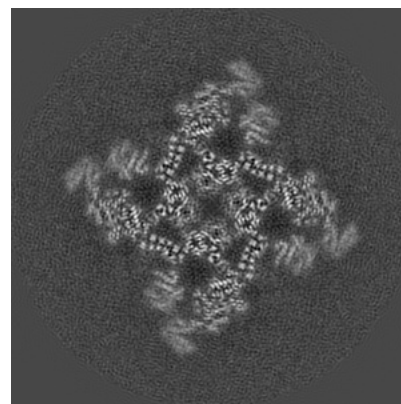
6.3.1 Primary map



X Index: 169



Y Index: 191

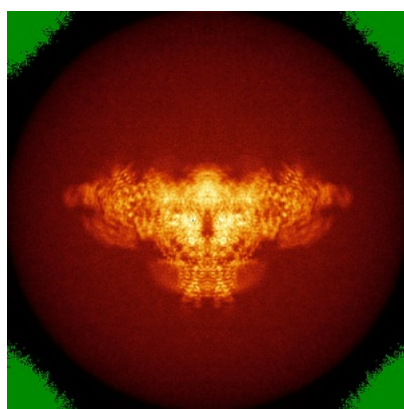


Z Index: 190

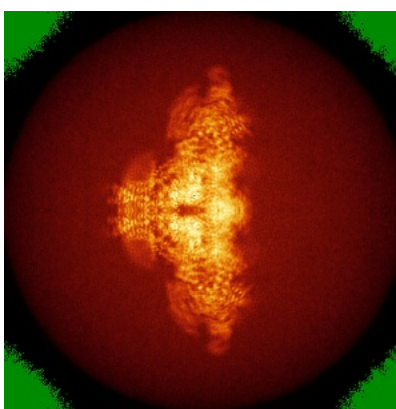
The images above show the largest variance slices of the map in three orthogonal directions.

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

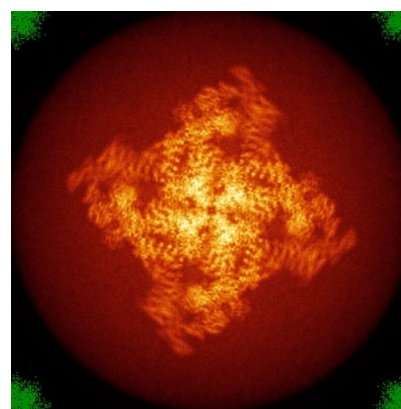
6.4.1 Primary map



X



Y

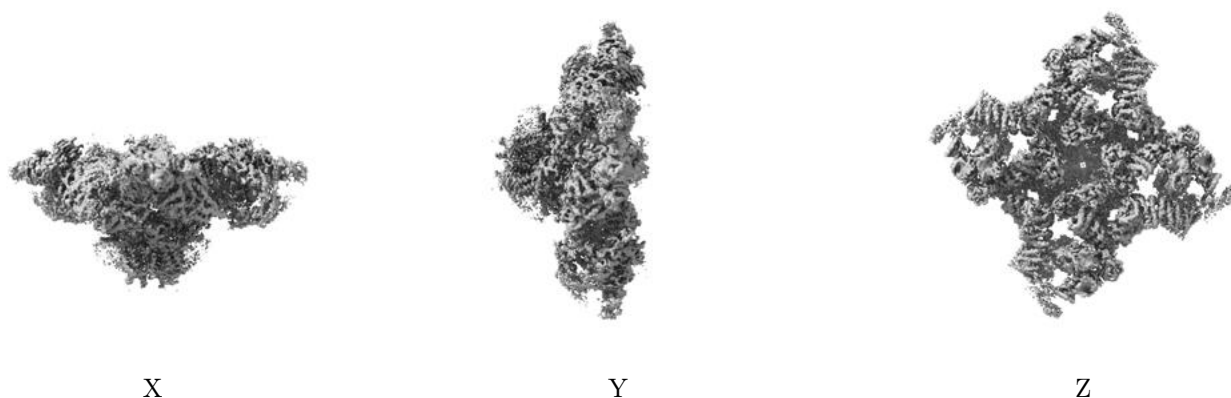


Z

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

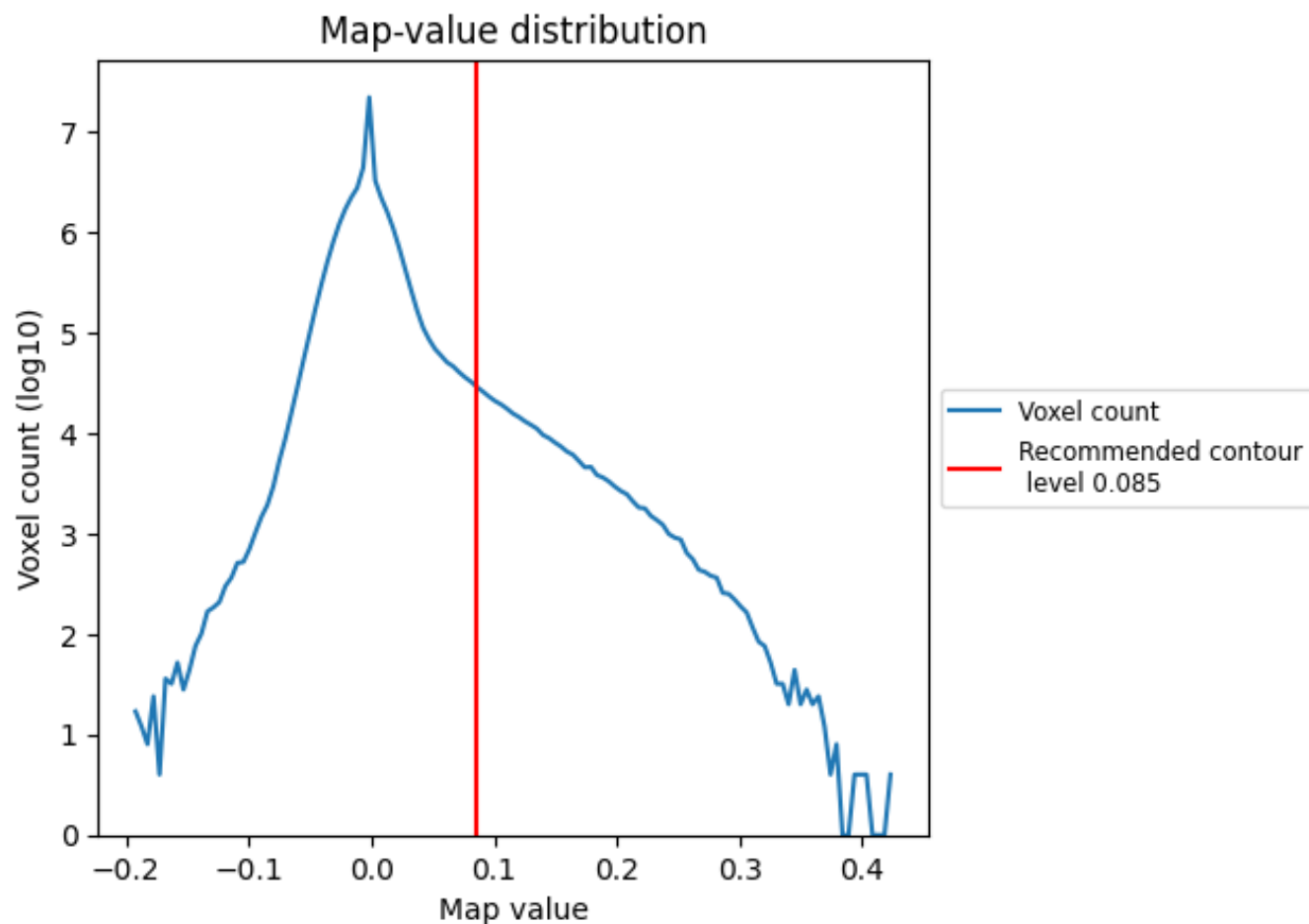
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

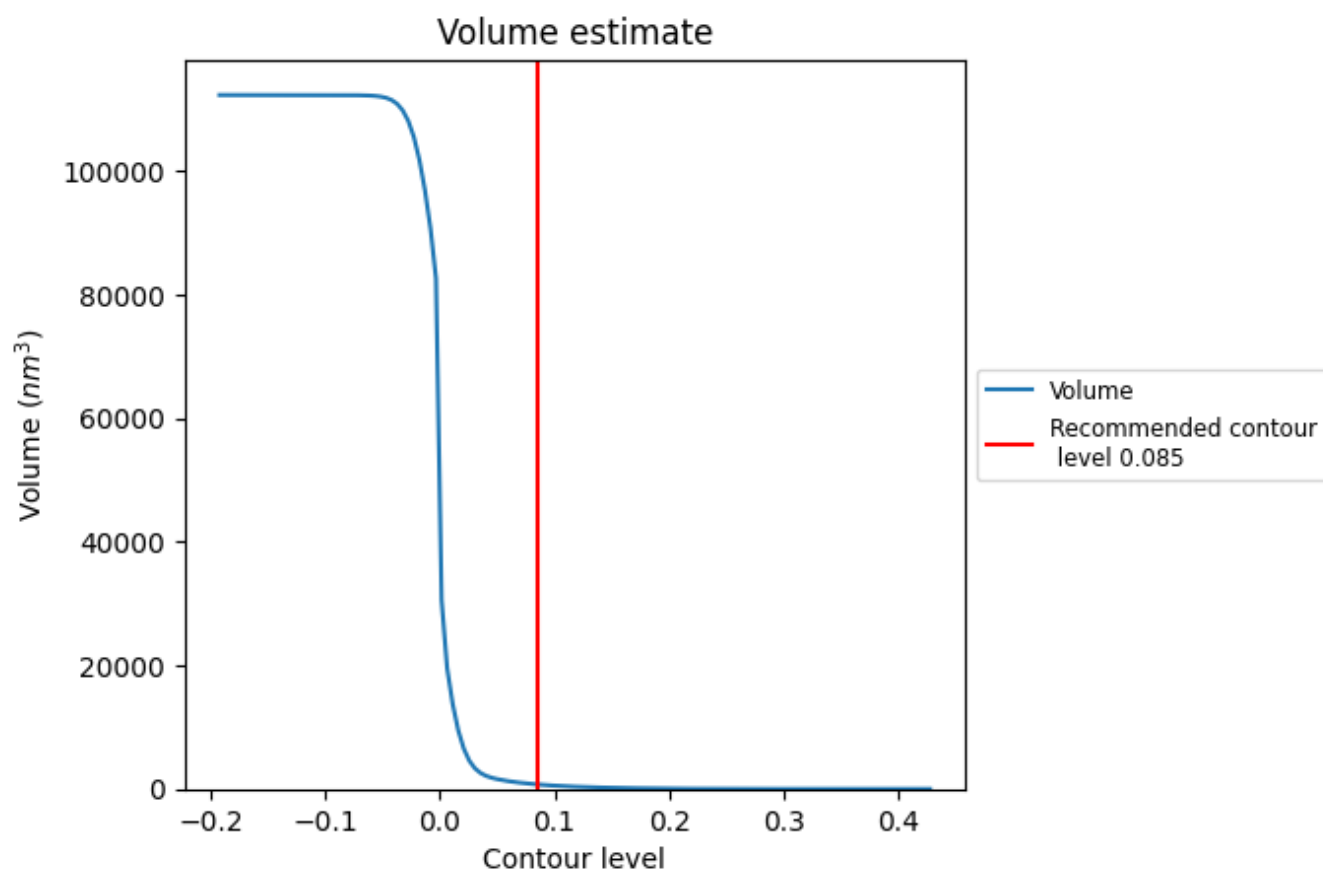
This section contains the results of statistical analysis of the map.

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.

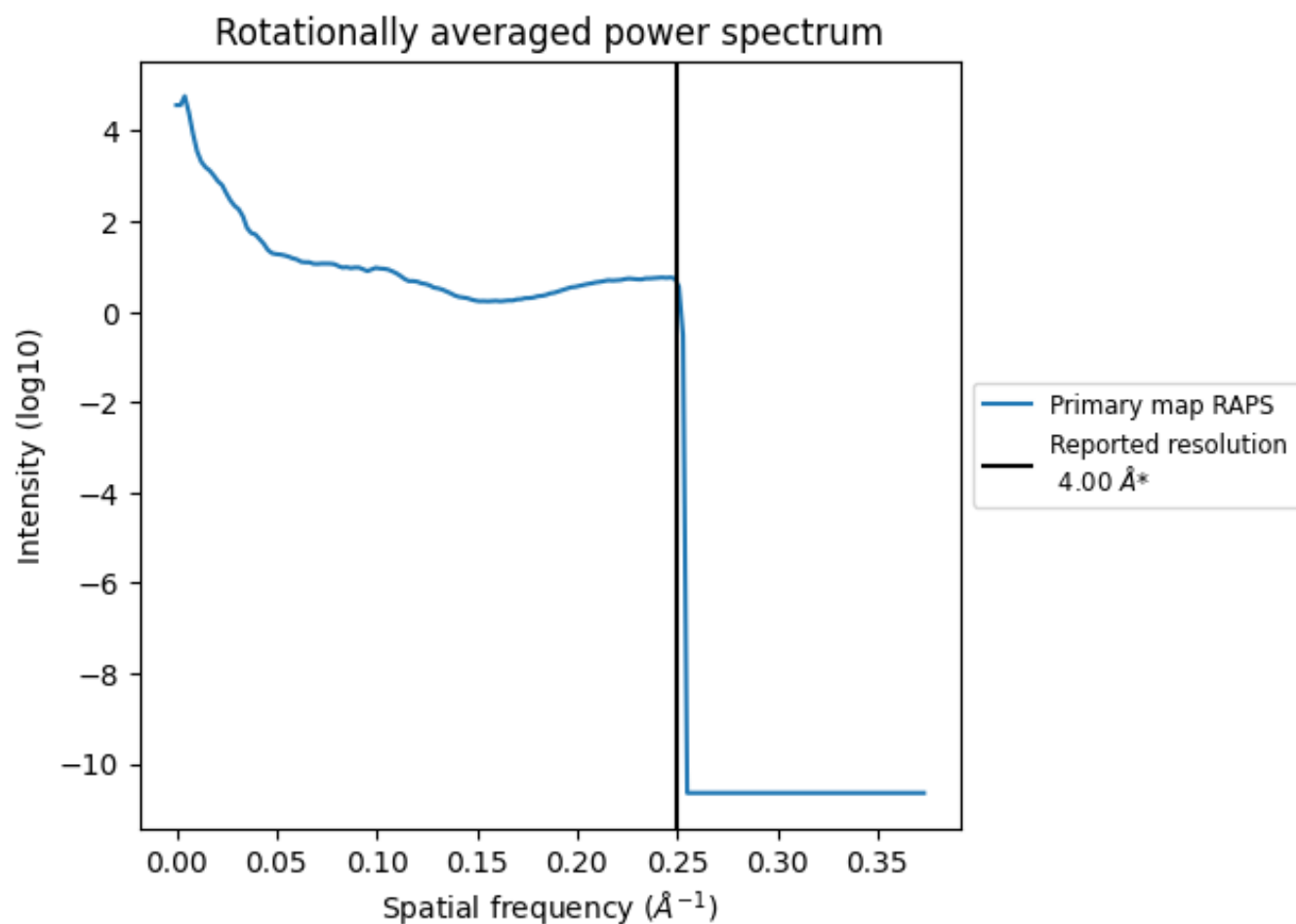
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 734 nm^3 ; this corresponds to an approximate mass of 663 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 0.250 $\text{\AA}^{-1}$

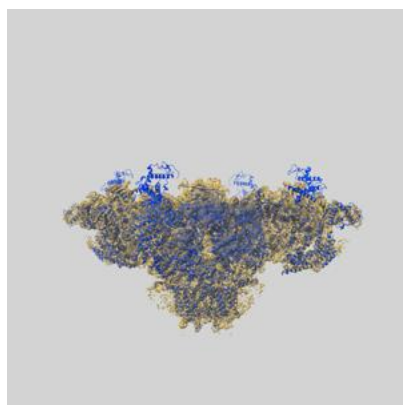
8 Fourier-Shell correlation

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

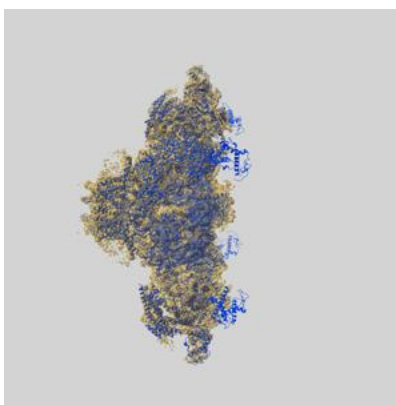
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-9519 and PDB model 5GKZ. Per-residue inclusion information can be found in section [3](#) on page [5](#).

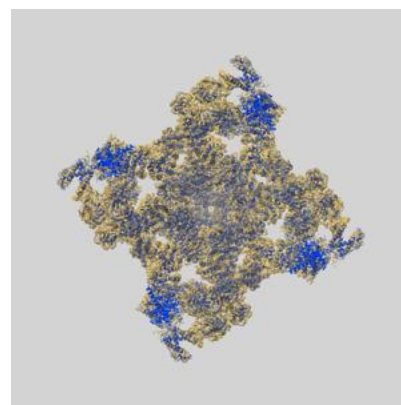
9.1 Map-model overlay [i](#)



X



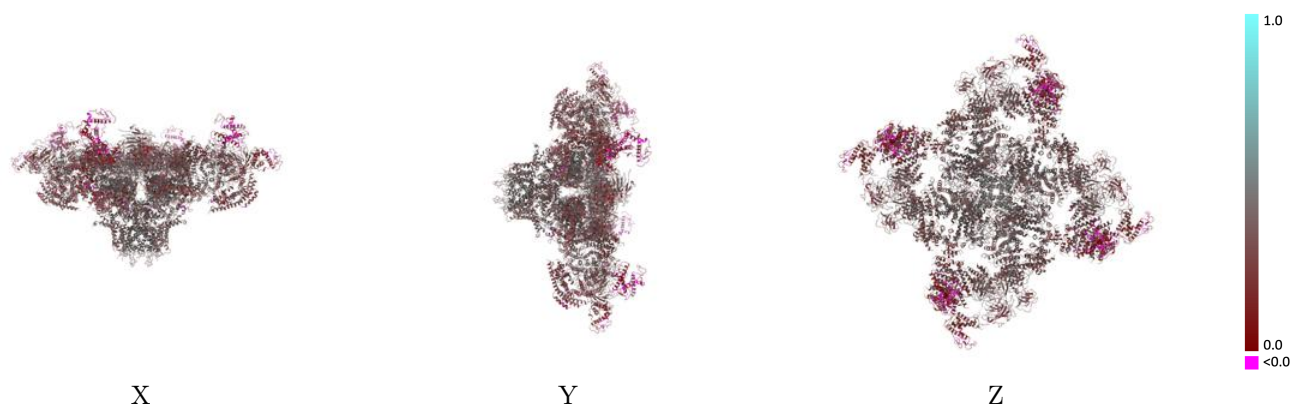
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.085 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](#)

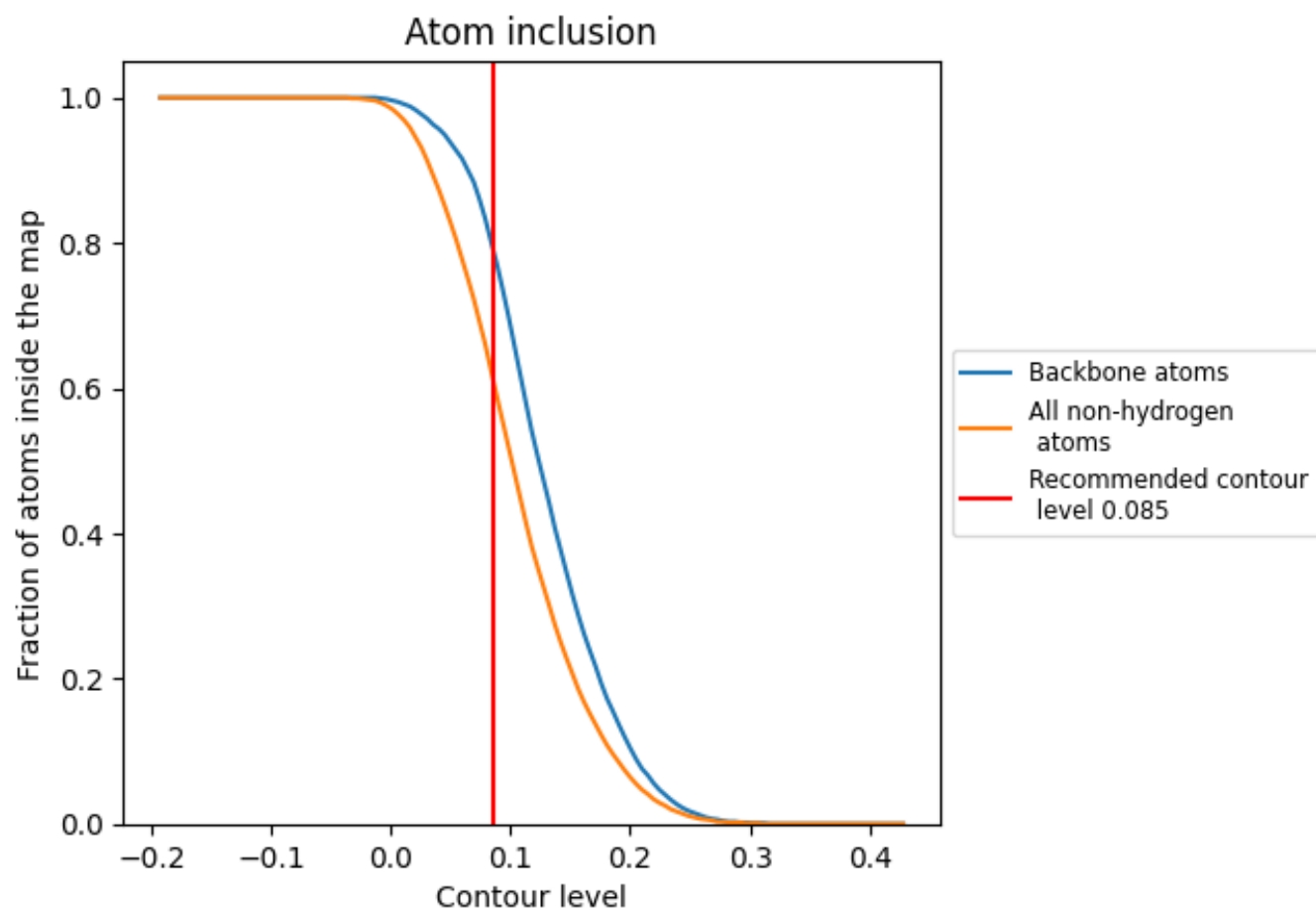


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 62% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.085) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6150	0.3370
A	0.6160	0.3370
B	0.5720	0.3390
C	0.6170	0.3360
D	0.5700	0.3370
E	0.6170	0.3360
F	0.5700	0.3360
G	0.6170	0.3400
H	0.5710	0.3380

1.0

0.0

<0.0