



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 12:33 PM UTC

PDB ID : 5GL0 / pdb_00005gl0
EMDB ID : EMD-9520
Title : Structure of RyR1 in a closed state (C4 conformer)
Authors : Bai, X.C.; Yan, Z.; Wu, J.P.; Yan, N.
Deposited on : 2016-07-07
Resolution : 4.20 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:

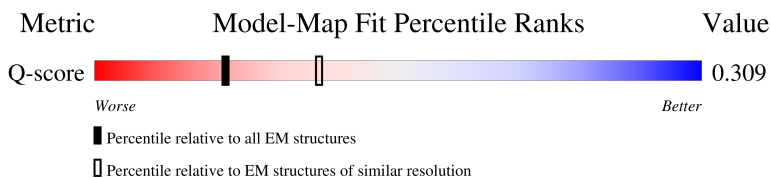
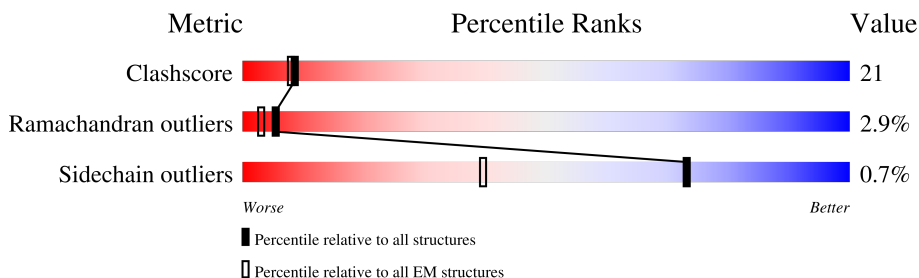
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.20 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.



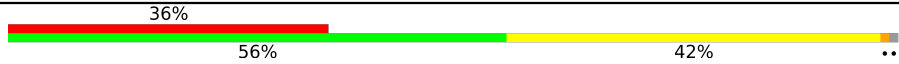

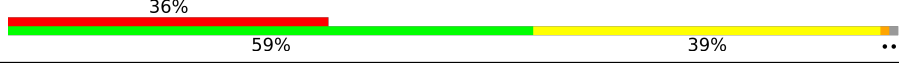
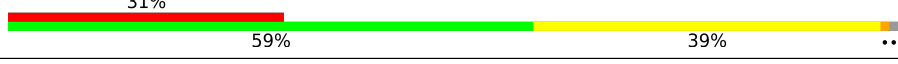
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	5410 (3.70 - 4.70)

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	<p>24% (Poor fit), 42% (0 outliers), 27% (1 outlier), 27% (2 outliers), 27% (3+ outliers)</p>
1	C	5037	<p>24% (Poor fit), 42% (0 outliers), 27% (1 outlier), 27% (2 outliers), 27% (3+ outliers)</p>
1	E	5037	<p>24% (Poor fit), 42% (0 outliers), 27% (1 outlier), 27% (2 outliers), 27% (3+ outliers)</p>
1	G	5037	<p>24% (Poor fit), 42% (0 outliers), 27% (1 outlier), 27% (2 outliers), 27% (3+ outliers)</p>

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Mol	Chain	Length	Quality of chain
2	B	108	
2	D	108	
2	F	108	
2	H	108	

2 Entry composition [i](#)

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
			Total	C	N	O	S		
1	A	3660	26917	17107	4682	4971	157	0	0
1	C	3660	26917	17107	4682	4971	157	0	0
1	E	3660	26917	17107	4682	4971	157	0	0
1	G	3660	26917	17107	4682	4971	157	0	0

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

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

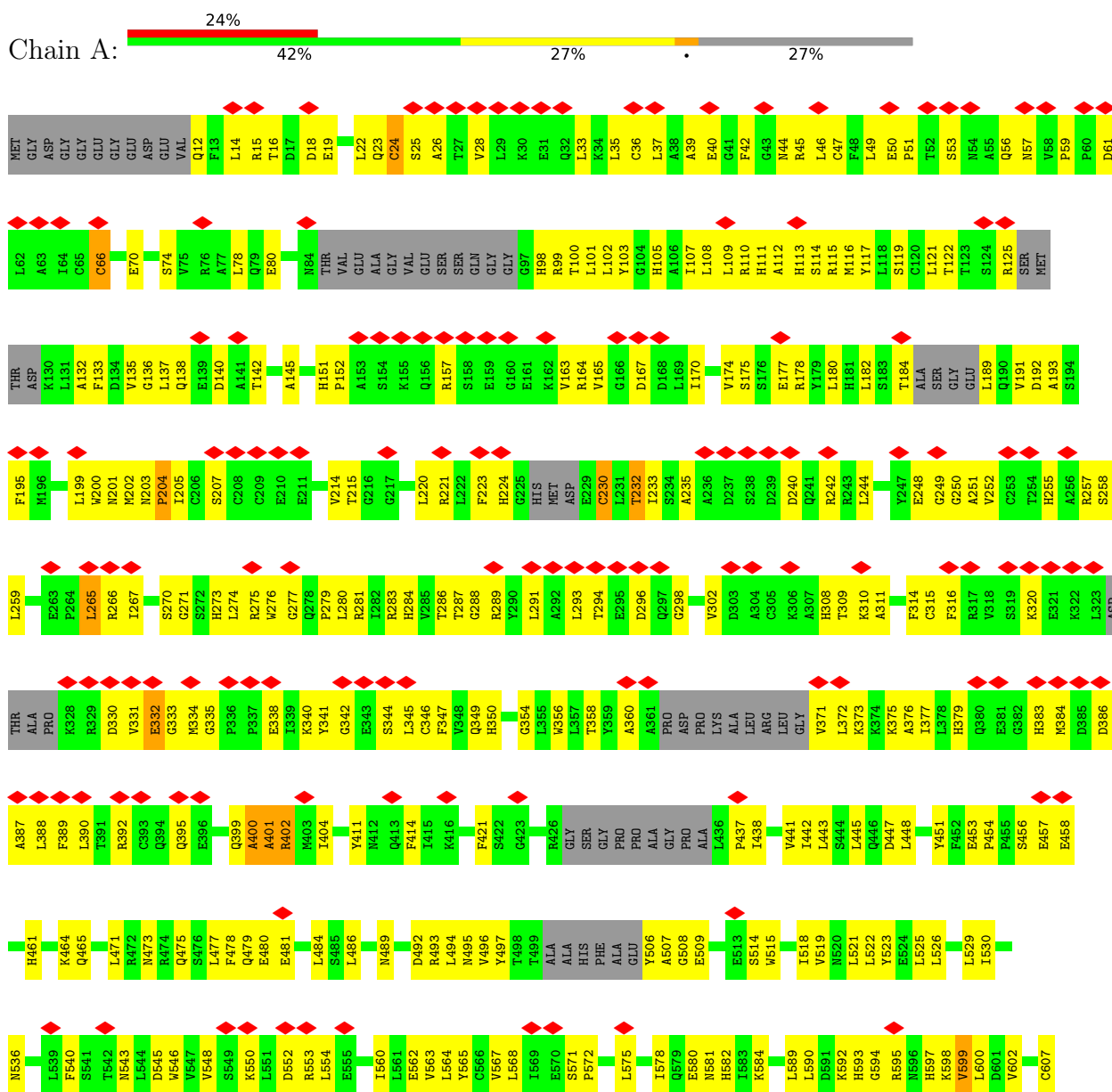
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

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	

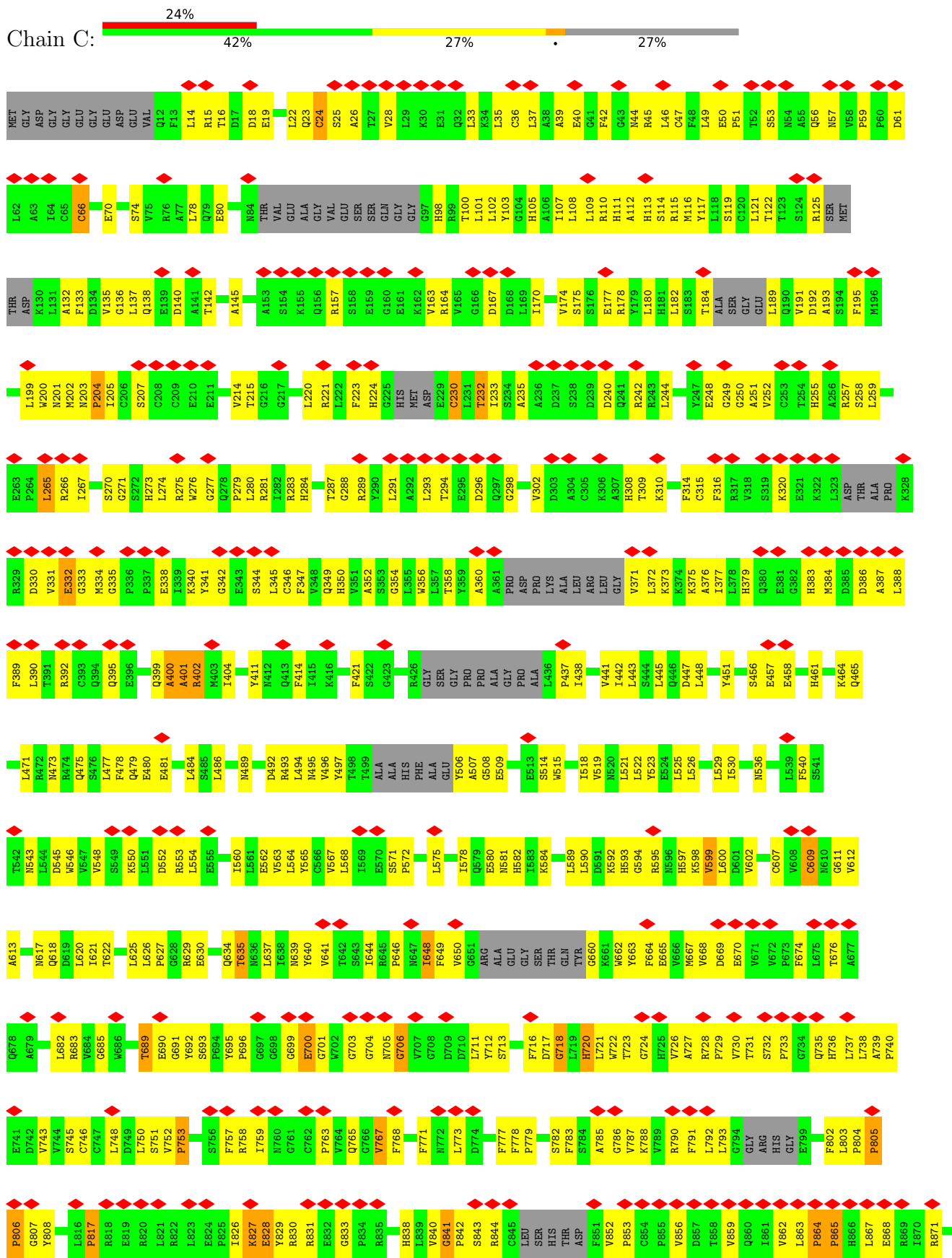
3 Residue-property plots

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.

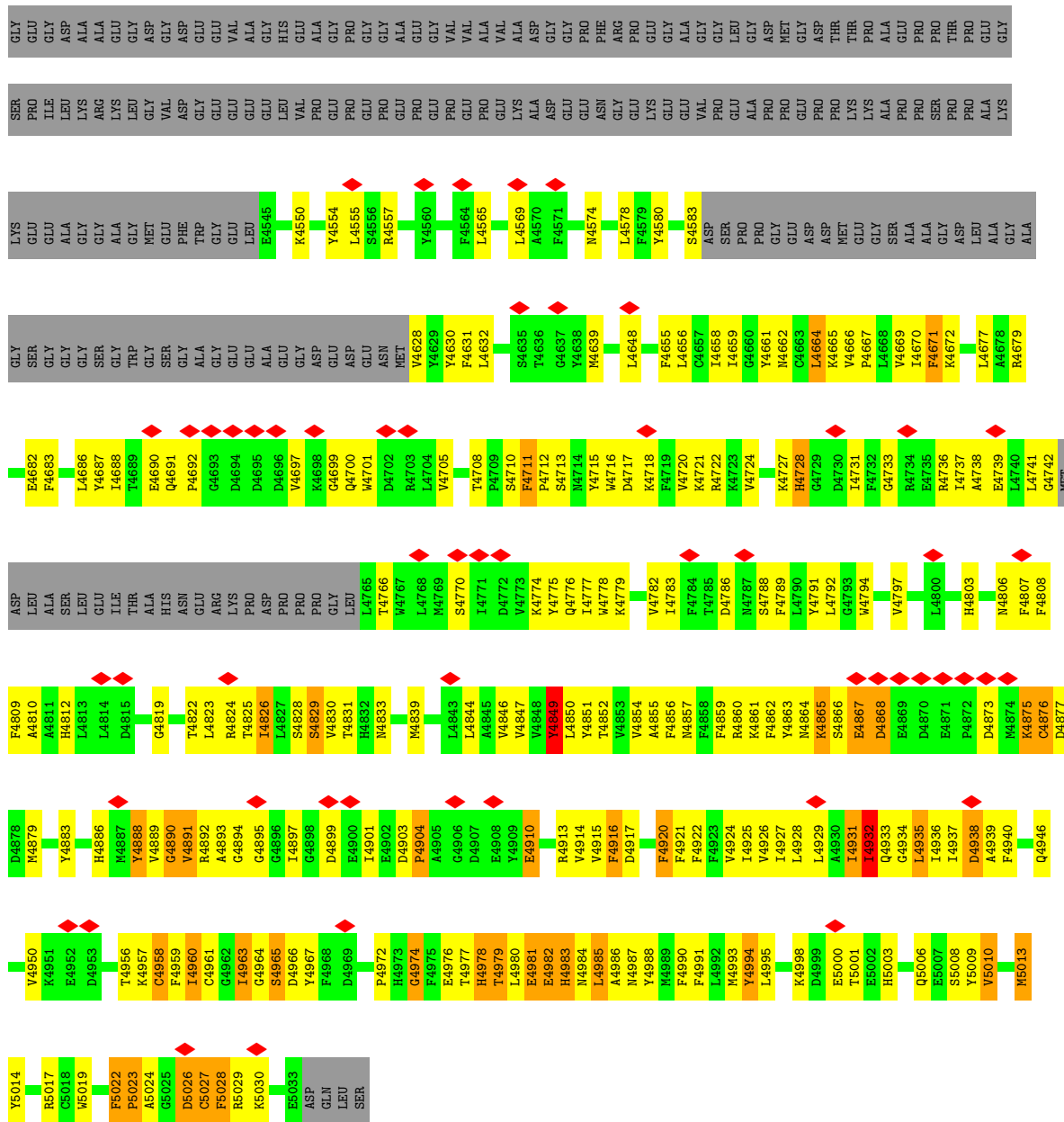
• Molecule 1: Ryanodine receptor 1



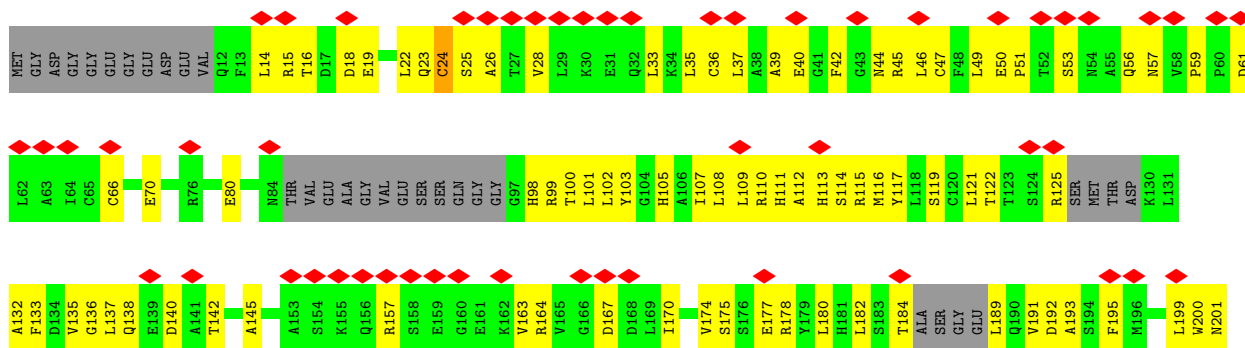
F3206	L3206	E3207	P3208	Q3209	L3210	N3211	E3212	Y3213	N3214	A3215	C3216	S3217	VAL	TYR	THR	THR	THR	LYS	SER	PRO	ARG	ARG	GLU	ARG	ALA	HIS	ILE	LEU	GLY	LEU	PRO	ASN	SER	VAL	VAL	I3172	I3173	S3174	L3175	G3176	T3177	T3178	LYS	ASN	THR	TYR	V3183	E3184	L3186	R3187	P3188	A3189	L3190	L3194	A3195	R3196	L3197	A3198	A3199	A3200	PRO	VAL	A3204
V3080	M3081	K3082	G3083	S3084	P3085	E3086	I3087	V3088	K3089	T3090	P3021	A3022	K3023	V3024	L3025	F3096	E3097	S3098	A3099	S3100	E3101	D3102	L3103	G3165	F3166	R3167	L3168	L3169	E3108	N3109	L3110	R3111	L3112	G3113	K3114	V3115	S3116	GLN	ALA	ARG	THR	V3183	E3184	L3186	R3187	P3188	A3189	L3190	L3194	A3195	R3196	L3197	A3198	A3199	A3200	PRO	VAL	A3204					
THR	HIS	CYS	LEU	Y3016	F3017	I3087	S3019	T3020	P3021	A3022	K3023	V3024	L3025	H3030	A3031	S3032	H3033	K3036	E3037	M3038	I3039	THR	SER	SER	F3043	C3044	K3045	L3046	V3050	A3051	H3052	S3055	D3060	A3061	ALA	VAL	VAL	ASN	ALA	VAL	VAL	ASN	CYS	L3068	H3069	I3070	L3071	A3072	R3073	S3074	L3075	D3076	A3077	R3078	T3079								
SER	ILE	GLU	LYS	ARG	THR	GLU	LYS	LYS	THR	ARG	THR	GLN	ALA	THR	GLN	THR	Y2849	D2850	P2851	R2852	E2853	G2854	Y2855	N2856	P2857	Q2858	P2860	D2861	L2862	S2863	G2864	V2865	T2866	L2867	K2868	Q2872	A2873	M2874	E2875	E2876	Q2877	L2878	A2879	E2880	N2881	Y2882	H2883	N2884	T2885	W2886	A2887	R2888	K2889										
K2890	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	L2930	Q2931	M2932	N2933	G2934	Y2935	A2936	V2937	T2938	R2939	G2940	LEU	LYS	ASP	MET	GLU	ASP	SER						
K2770	I2771	Q2772	N2773	N2774	N2775	S2776	Y2777	E2778	G2779	N2780	V2781	E2782	E2783	E2784	L2785	K2786	T2787	H2788	P2789	N2790	L2791	R2792	P2793	Y2794	K2795	T2796	F2797	S2798	E2799	K2800	D2801	K2802	E2803	L2804	Y2805	R2806	W2807	F2808	I2809	E2810	E2811	S2812	L2813	K2814	N2816	L2817	A2818	W2819	E2820	W2821	T2822	L2823	E2824	K2825	A2826	E2828	G2829						
L2710	P2711	P2712	ASP	TYR	VAL	ASP	ALA	THR	SER	SER	LYS	ALA	GLN	LYS	LYS	ASP	THR	N2734	F2735	D2736	P2737	R2738	P2739	V2740	T2741	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										
L2474	Q2475	I2476	THR	THR	LEU	GLY	ASP	GLY	ALA	LEU	VAL	GLN	P80	LYS	MET	SER	ALA	SER	F2494	Y2495	P2496	D2497	H2498	K2499	A2500	S2501	L2506	D2507	R2508	Y2509	Y2510	GLY	ILE	GLU	N9514	F2517	L2518	L2519	H2520	V2521	L2522	ASP	V2524	L2527	A2532	L2536	ASP	THR	ALA	THR	PHE	SER	THR										
T2544	E2545	M2546	A2549	L2550	N2551	R2552	Y2553	L2554	C2555	L2556	A2557	U2558	L2559	T2560	L2561	T2562	THR	LYS	CYS	ALA	P2567	L2568	F2569	A2570	G2571	T2572	R2575	Y2586	TYR	ARG	LEU	SER	R2591	Q2599	R2600	D2601	M2608	A2609	LEU	CYS	ARG	TYR	ILE	R2615	P2616	S2617	M2618	L2619	Q2620	L2623	R2624	R2625	L2626										
V2627	F2628	D2629	P2630	P2631	M2634	GLU	PHE	ALA	K2638	M2639	P2640	L2641	Y2648	T2654	Y2655	C2656	L2657	P2658	T2659	G2660	TRP	ALA	ASN	PHE	GLY	VAL	T2667	S2668	E2669	F2679	L2682	F2683	S2684	S2685	L2686	ALA	HIS	LYS	LYS	D2691	D2692	Q2693	R2697	P2701	C2702	L2703	C2704	A2705	L2706	A2707	G2708	A2709											
K2770	I2771	Q2772	N2773	N2774	N2775	S2776	Y2777	E2778	G2779	N2780	V2781	E2782	E2783	E2784	L2785	K2786	T2787	H2788	P2789	N2790	L2791	R2792	P2793	Y2794	K2795	T2796	F2797	S2798	E2799	K2800	D2801	K2802	E2803	L2804	Y2805	R2806	W2807	F2808	I2809	E2810	E2811	S2812	L2813	K2814	N2816	L2817	A2818	W2819	E2820	W2821	T2822	L2823	E2824	K2825	A2826	E2828	G2829						
E2830	GLU	HIS	ARG	THR	GLU	LYS	LYS	THR	ARG	LYS	ILE	SER	GLN	THR	GLN	THR	Y2849	D2850	P2851	R2852	E2853	G2854	Y2855	N2856	P2857	Q2858	P2860	D2861	L2862	S2863	G2864	V2865	T2866	L2867	K2868	Q2872	A2873	M2874	E2875	E2876	Q2877	L2878	A2879	E2880	N2881	Y2882	H2883	N2884	T2885	W2886	A2887	R2888	K2889										
K2890	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	L2930	Q2931	M2932	N2933	G2934	Y2935	A2936	V2937	T2938	R2939	G2940	LEU	LYS	ASP	MET	GLU	ASP	SER						
SER	ILE	GLU	LYS	ARG	THR	GLU	LYS	LYS	THR	ARG	LYS	ILE	SER	GLN	THR	GLN	THR	Y2849	D2850	P2851	R2852	E2853	G2854	Y2855	N2856	P2857	Q2858	P2860	D2861	L2862	S2863	G2864	V2865	T2866	L2867	K2868	Q2872	A2873	M2874	E2875	E2876	Q2877	L2878	A2879	E2880	N2881	Y2882	H2883	N2884	T2885	W2886	A2887	R2888	K2889									
PHE	THR	HIS	CYS	LEU	Y3016	F3017	I3087	S3019	T3020	P3021	A3022	K3023	V3024	L3025	H3030	A3031	S3032	H3033	K3036	E3037	M3038	I3039	THR	SER	SER	F3043	C3044	K3045	L3046	V3050	A3051	H3052	S3055	D3060	A3061	ALA	VAL	VAL	ASN	ALA	VAL	VAL	ASN	CYS	L3068	H3069	I3070	L3071	A3072	R3073	S3074	L3075	D3076	A3077	R3078	T3079							
V3080	M3081	K3082	G3083	S3084	P3085	E3086	I3087	V3088	K3089	T3090	P3021	A3022	K3023	V3024	L3025	F3096	E3097	S3098	A3099	S3100	E3101	D3102	L3103	G3165	F3166	R3167	L3168	L3169	E3108	N3109	L3110	R3111	L3112	G3113	K3114	V3115	S3116	GLN	ALA	ARG	THR	V3183	E3184	L3186	R3187	P3188	A3189	L3190	L3194	A3195	R3196	L3197	A3198	A3199	A3200	PRO	VAL	A3204					

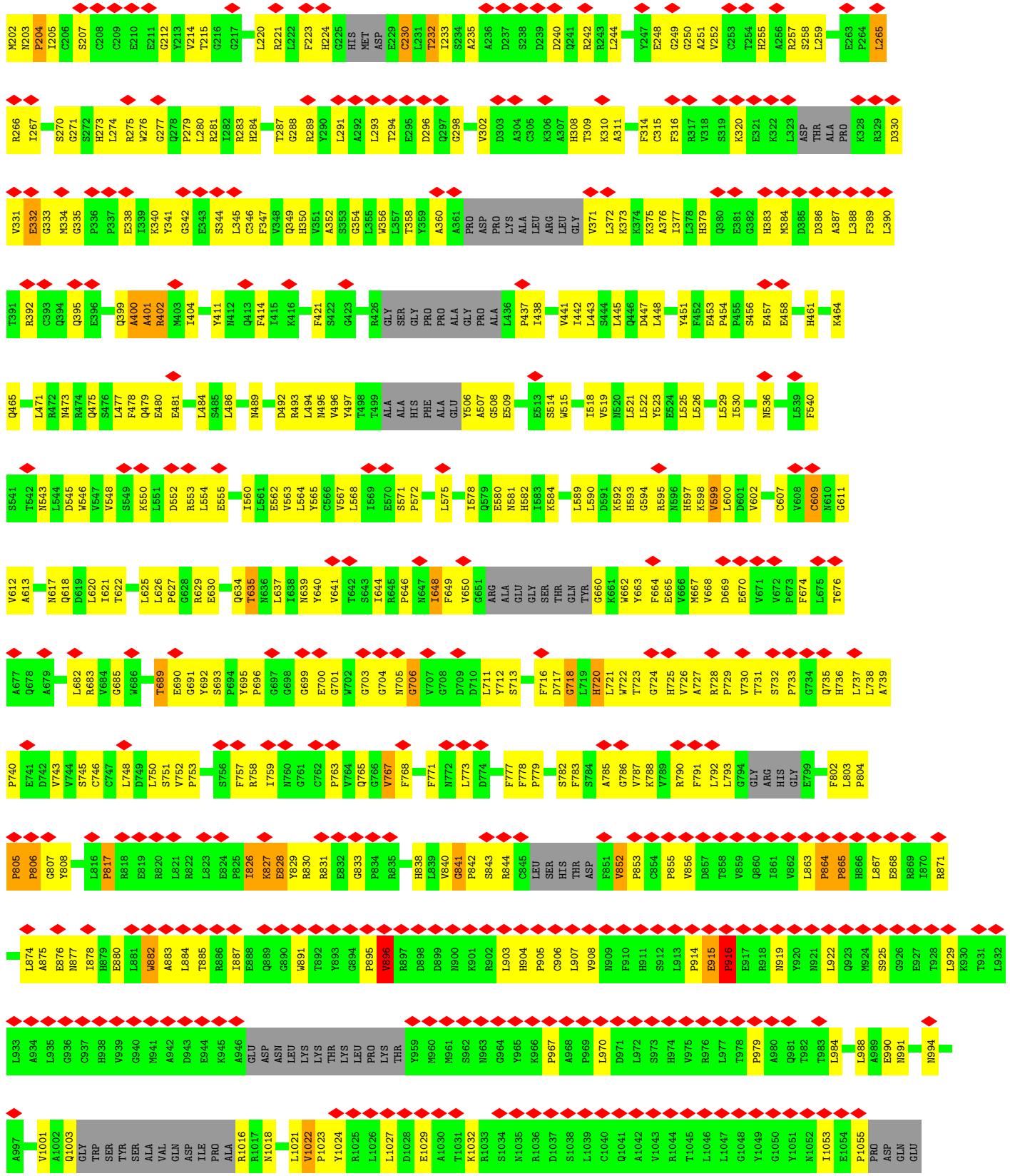


ALA	R2638	R2639	P2640	L2641	Y2648	Y2654	Y2655	C2656	L2657	P2658	G2660	TRP	ALA	ASN	PHE	GLY	VAL	T2667	S2668	E2669	F2679	L2682	F2683	D2684	S2685	L2686	ALA	HIS	LYS	LYS	Y2691	D2692	Q2693	R2697	P2701	C2702	L2703	C2704	A2705	I2706	A2707	G2708	A2709	L2710	P2711	P2712	ASP	TYR	VAL	ASP	ALA	SER										
TYR	E2779	N2780	V2781	D2782	E2783	E2784	L2785	K2786	D2850	H2787	H2788	P2789	M2790	L2791	R2792	P2793	Y2794	K2795	P2796	T2797	F2797	S2798	E2741	T2742	L2743	N2744	V2745	I2746	I2747	P2748	E2749	K2750	L2751	D2752	S2753	F2754	D2692	Q2693	K2757	F2758	A2759	E2760	Y2761	T2762	H2763	E2764	K2765	W2766	A2767	F2768	D2769	K2770	I2771	Q2772	N2773	N2774	W2775	S2776	Y2777	G2778		
THR	ARG	LYS	ILE	SER	GLN	THR	ALA	GLN	THR	Y2849	D2850	P2851	R2852	E2853	G2854	Y2855	M2856	P2857	Q2858	P2859	P2860	D2861	L2862	S2863	G2864	Y2865	T2866	L2867	S2868	R2869	E2870	L2871	Q2872	A2873	M2874	A2875	E2876	Q2877	L2878	A2879	E2880	M2881	Y2882	H2883	M2884	T2885	W2886	I2887	E2888	A2826	R2827	K2828	E2829	E2830	GLU	GLU	ARG	THR	GLU	LYS	LYS	LYS
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	L2930	Q2931	M2932	N2933	G2934	Y2935	A2936	V2937	T2938	R2939	LEU	LEU	ASP	MET	GLU	LEU	THR	SER	SER	ILE	GLU	LYS	ARG	PHE	ALA	PHE	GLY					
PHE	LEU	GLN	LEU	LEU	LEU	ARG	TRP	MET	ASP	ILE	ALA	HIS	LEU	GLU	GLU	VAL	VAL	SER	SER	GLY	ARG	VAL	LYS	LYS	PRO	HIS	GLN	GLU	ILE	LYS	PHE	ALA	LYS	ILE	LEU	LEU	PRO	LEU	ILE	ASN	ASN	CYS	LEU	Y3016	F3017	L3018																
S3019	T3020	P3021	K3022	K3023	V3024	L3025	H3030	A3031	S3032	M3033	K3036	E3037	M3038	I3039	THR	SER	LEU	F3043	K3044	K3045	L3046	V3050	R3051	H3052	S3055	D3060	A3061	P3062	VAL	VAL	ASN	ASN	CYS	L3068	H3069	I3070	L3071	A3072	R3073	S3074	K3075	D3076	A3077	R3078	T3079	V3080	M3081	K3082	S3083	G3084	P3085	E3086	I3087	V3088								
K3089	A3090	GLY	LEU	ARG	SER	F3095	F3096	E3097	S3098	A3099	S3100	E3101	D3102	I3103	E3104	K3105	E3108	M3109	L3110	R3111	L3112	G3113	K3114	V3115	S3116	GLN	ALA	ALA	THR	THR	VAL	THR	THR	V3183	E3184	K3185	L3186	R3187	P3188	A3189	L3190	L3194	A3195	R3196	L3197	A3198	A3199	A3200	MET	PRO	VAL	A3204	F3205	L3206	E3207	P3208	Q3209	L3210	N3211	L3212	E3213	Y3213
Q3151	F3152	GLY	ASP	VAL	ILE	L3158	D3159	D3160	V3161	Q3162	V3163	S3164	C3165	Y3166	R3167	T3168	L3169	I3172	Y3173	S3174	L3175	G3176	T3177	S3178	ASN	LEU	THR	TYR	V3183	E3184	K3185	L3186	R3187	P3188	A3189	L3190	L3194	A3195	R3196	L3197	A3198	A3199	A3200	MET	PRO	VAL	A3204	F3205	L3206	E3207	P3208	Q3209	L3210	N3211	L3212	E3213	Y3213					
M3214	A3215	C3216	S3217	VAL	TYR	THR	THR	LYS	PRO	ARG	ARG	ALA	ILE	LEU	GLY	LEU	PRO	ASN	SER	VAL	GLU	GLU	MET	CYS	PRO	ASP	ILE	PRO	VAL	ASP	ARG	ARG	LEU	MET	ALA	ASP	ILE	ILE	GLY	GLY	ALA	ALA	TYR	THR	GLU	MET	PRO	HIS	VAL	VAL	GLU	ILE	T3273									
L3274	P3275	M3276	L3277	C3278	S3279	Y3280	L3281	P3282	R3283	W3284	W3285	E3286	R3287	G3288	P3289	ALA	PRO	P3294	A3295	L3296	P3297	A3298	G3299	A3300	P3301	P3302	P3303	C3304	T3305	A3306	D3310	H3311	L3312	N3313	SER	LEU	G3317	N3318	L3319	L3320	R3321	I3322	L3323	V3324	N3325	N3326	L3327	G3328	E3331	A3332	T3333	W3334	M3335	K3336								
R3337	L3338	A3339	PHE	VAL	ALA	GLN	PRO	ILE	V3346	S3347	R3348	A3349	R3350	P3351	E3352	L3353	L3354	H3355	S3356	H3357	F3358	I3359	P3360	T3361	I3362	G3363	ARG	LEU	LEU	ARG	K3367	R3368	A3369	G3370	K3371	V3372	V3373	A3374	E3375	E3376	E3377	Q3378	L3379	R3380	L3381	E3382	A3383	K3384	E3385	E3386	A3387	E3388	E3389	K3390	E3391	L3392	L3393	V3394	R3395	D3396		
E3397	PHE	SER	VAL	LEU	C3402	R3403	D3404	L3405	Y3406	A3407	L3408	Y3409	P3410	L3411	L3412	L3413	R3414	Y3415	Y3416	D3417	N3418	N3419	R3420	H3421	H3422	W3423	L3424	THR	GLU	P3427	N3430	A3431	E3432	E3433	L3434	F3435	ARG	R3437	V3438	G3439	E3440	I3441	F3442	I3443	Y3444	W3445	K3446	K3447	S3448	H3449	N3450	F3451	K3452	R3453	E3454	E3455	GLN	R3457				

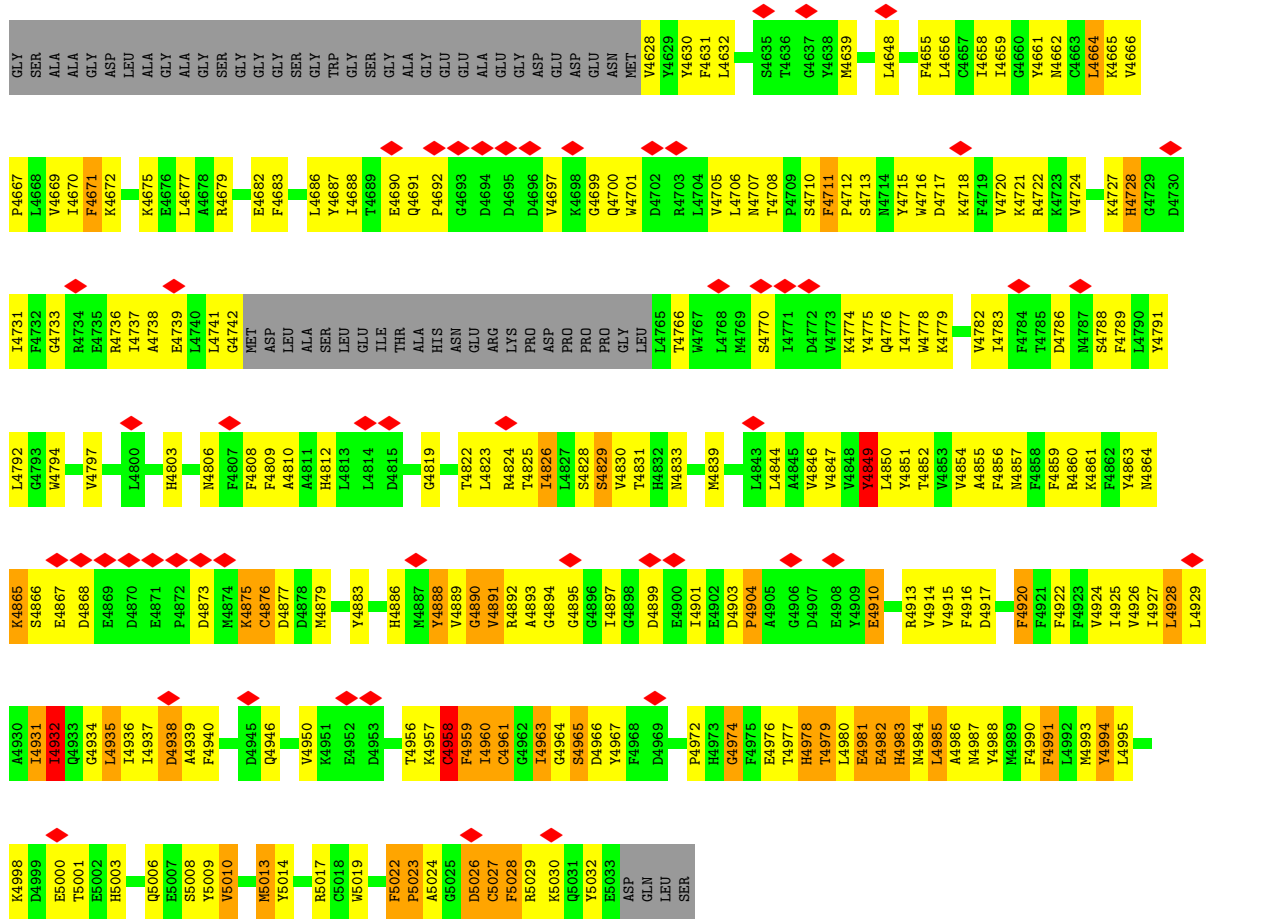


• Molecule 1: Ryanodine receptor 1

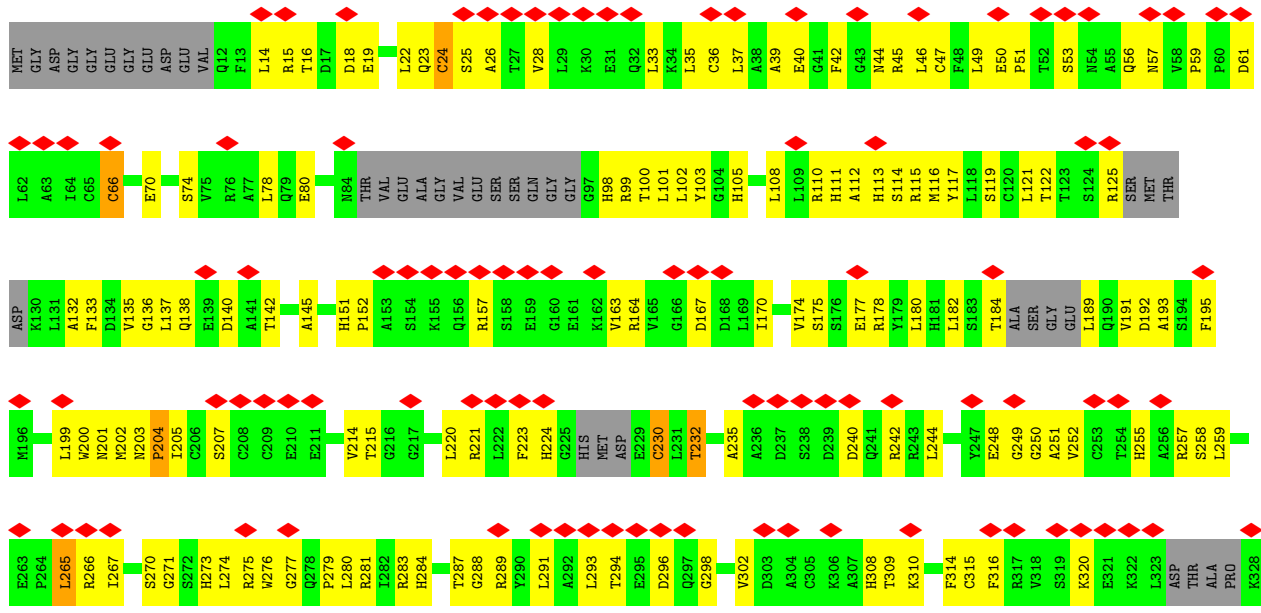




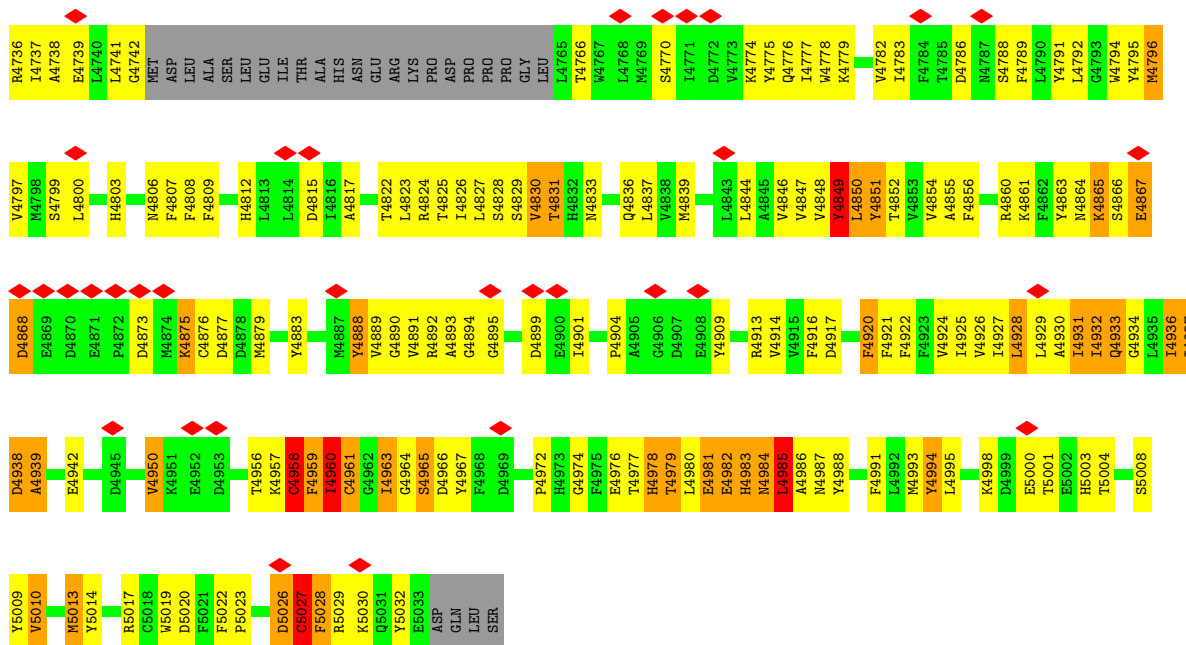
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E2896	A2896	K2897	G2898	G2899	G2900	T2901	H2902	P2903	L2904	L2905	V2906	P2907	Y2908	D2909	T2910	L2911	T2912	A2913	K2914	E2915	P2916	A2917	R2918	D2919	R2920	E2921	P2922	A2923	Q2924	E2925	L2926	L2927	K2928	F2929	L2930	Q2931	M2932	N2933	G2934	Y2935	A2936	V2937	T2938	R2939	G2940	LEU	LYS	ASP	MET	GLU	ASP	LYS	THR	SER	ILE	GLU	LYS	ARG				
PHE	ALA	PHE	GLY	PHE	LEU	GLN	LEU	ARG	TRP	MET	ASP	ILE	SER	GLN	GLU	PHE	ILE	ALA	HIS	LEU	GLU	ALA	VAL	VAL	SER	SER	GLY	GLY	ARG	VAL	LYS	SER	PRO	HIS	GLU	GLN	GLU	LYS	ILE	LYS	PHE	PHE	ALA	ALA	ILE	ASN	GLN	TYR	PHE	THR	ASN	HIS	CYS									
LEU	Y3016	F3017	H3018	S3019	T3020	P3021	A3022	K3023	V3024	L3025	H3030	A3031	S3032	N3033	K3036	E3037	M3038	I3039	THR	SER	LEU	F3043	C3044	K3045	L3046	V3050	R3051	H3052	S3055	D3060	A3061	P3062	ALA	VAL	VAL	ASN	ASN	PRO	L3068	H3069	I3070	L3071	A3072	R3073	S3074	L3075	D3076	A3077	R3078	T3079	V3080	M3081	K3082	S3083	G3084							
P3085	E3086	I3087	H3088	K3089	A3090	GLY	LEU	SER	ARG	F3095	F3096	E3097	S3098	A3099	S3100	E3101	D3102	I3103	E3104	K3105	E3108	M3109	L3110	R3111	L3112	G3113	K3114	V3115	S3116	ALA	ARG	THR	THR	VAL	LYS	ASN	THR	THR	V3183	E3184	K3185	L3186	R3187	P3188	A3189	L3190	L3194	A3195	R3196	L3197	A3198	A3199	A3200	MET	PRO	VAL	A3204	F3205	L3206	F3144	Q3145	H3146
I3147	A3148	Q3149	H3150	Q3151	F3152	GLY	ASP	ASP	VAL	L3158	D3159	D3160	V3161	Q3162	V3163	S3164	C3165	Y3166	R3167	T3168	L3169	I3172	Y3173	S3174	L3175	G3176	T3177	T3178	LYS	ASN	THR	THR	V3183	E3184	K3185	L3186	R3187	P3188	A3189	L3190	L3194	A3195	R3196	L3197	A3198	A3199	A3200	MET	PRO	VAL	A3204	F3205	L3206	F3144	Q3145	H3146						
L3210	N3211	E3212	Y3213	N3214	A3215	C3216	S3217	VAL	THR	THR	LYS	SER	PRO	ARG	GLU	ARG	ALA	ILE	LEU	GLY	PRO	ASN	SER	VAL	GLU	MET	CYS	PRO	ASP	ILE	PRO	VAL	LEU	ASP	ARG	LEU	ALA	ASP	ILE	GLY	GLY	LEU	ALA	SER	GLY	ALA	TYR	THR	GLU	MET	HIS	PRO	VAL									
I3273	L3274	M3275	N3276	L3277	C3278	S3279	V3280	L3281	P3282	K3283	M3284	R3285	E3286	K3287	G3288	F3289	E3290	ALA	PRO	PRO	P3294	A3295	L3296	F3297	A3298	G3299	A3300	P3301	P3302	P3303	C3304	T3305	A3306	D3310	H3311	L3312	N3313	SER	LEU	G3317	N3318	L3319	L3320	R3321	I3322	V3324	N3325	N3326	L3327	E3331	A3332	T3333										
M3334	M3335	K3336	R3337	L3338	A3339	VAL	PHE	ALA	GLN	PRO	V3346	S3347	R3348	A3349	M3351	E3352	L3353	L3354	H3355	S3356	H3357	F3358	I3359	P3360	T3361	I3362	G3363	ARG	LEU	ARG	K3367	R3368	A3369	G3370	K3371	V3372	V3373	A3374	E3375	E3376	E3377	Q3378	L3379	R3380	L3381	E3382	A3383	K3384	E3386	A3387	E3388	E3389	G3390	E3391	L3392	L3393						
V3394	R3395	D3396	E3397	PHE	SER	VAL	C3402	R3403	D3404	L3405	Y3406	A3407	L3408	Y3409	F3410	L3411	L3412	T3413	R3414	F3415	V3416	D3417	N3418	N3419	R3420	A3421	H3422	V3423	L3424	THR	GLU	P3427	M3430	A3431	E3432	E3433	L3434	F3435	ARG	M3437	V3438	G3439	E3440	I3441	F3442	V3444	Y3444	W3445	S3446	K3447	S3448	H3449	N3450	F3451	K3452	R3453	E3454					
E3455	GLN	N3457	F3458	V3459	V3460	Q3461	N3462	E3463	L3464	N3465	N3466	M3467	S3468	F3469	L3470	THR	ALA	ASP	SER	LYS	M3478	A3479	K3480	A3481	G3482	D3483	A3484	Q3485	S3486	G3487	G3488	S3489	D3490	Q3491	GLU	ARG	T3494	K3495	K3496	K3497	R3498	R3499	G3500	Y3503	S3504	VAL	GLN	THR	SER	ILE	LEU	VAL	ALA	ALA	TYR	N3513	L3514					
L3518	P3519	I3520	G3521	L3522	N3523	M3524	C3525	A3526	P3527	THR	ASP	GLN	ARG	VAL	GLN	GLU	ILE	MET	VAL	SER	ALA	K3537	T3538	R3539	Y3540	A3541	L3542	K3543	A3544	THR	ASP	GLU	GLU	V3549	R3550	E3551	F3552	L3553	Q3554	L3557	H3558	L3559	Q3560	G3561	K3562	V3563	E3564	P3567	S3568	L3569	R3570	W3571	Q3572	MET	ALA	LEU	VAL	TYR	ARG	GLY	LEU	
PRO	GLY	ARG	GLU	GLU	ASP	ALA	ASP	PRO	GLU	ILE	VAL	ARG	ARG	VAL	GLN	GLU	VAL	VAL	SER	ALA	ALA	K3537	T3538	R3539	Y3540	A3541	L3542	K3543	A3544	THR	ASP	GLU	GLU	V3549	R3550	E3551	F3552	L3553	Q3554	L3557	H3558	L3559	Q3560	G3561	K3562	V3563	E3564	P3567	S3568	L3569	R3570	W3571	Q3572	MET	ALA	LEU	VAL	TYR	ARG	GLY	LEU	



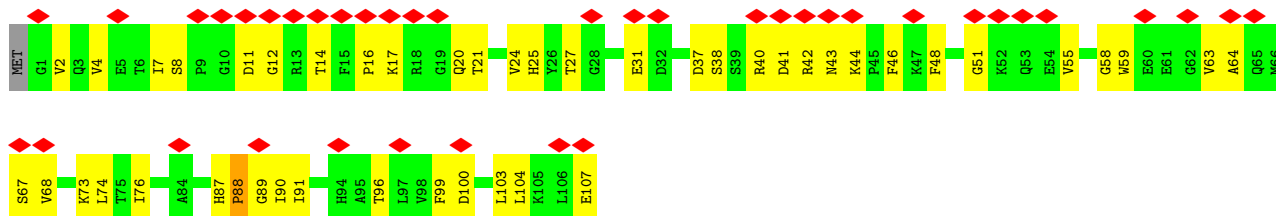
• Molecule 1: Ryanodine receptor 1



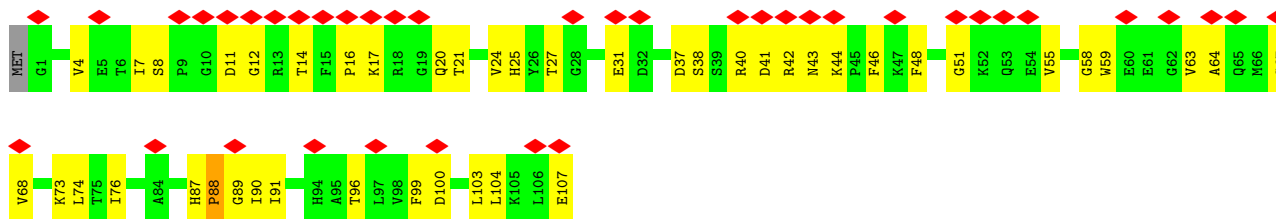
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F389	L390	T391	R392	C393	Q394	Q395	E396	Q399	A400	A401	R402	M403	I404	Y411	M412	Q413	S414	F415	I416	R417	M418	F421	S422	G423	R426	GLY	SER	GLY	PRO	PRO	ALA	ALA	PRO	ASP	PRO	ALA	LYS	ALA	P437	I438	V441	I442	L443	S444	L445	Q446	D447	L448	Y451	F452	E453	L454	P455	S456	E457	E458	H461		
K464	Q465	S466	R469	S470	L471	R472	M473	R474	Q475	W476	L477	F478	Q479	E480	E481	L484	Q485	L486	M489	D492	R493	L494	M495	V496	L497	T498	L499	ALA	ALA	HIS	PHE	ALA	GLU	Y506	A507	G508	E509	E513	S514	W515	I518	V519	N520	L521	L522	Y523	E524	R525	N526	L529	I530								
N536	L539	F540	S541	T542	N543	L544	D545	M546	V547	V548	S549	K550	L551	D552	R553	L554	E555	I560	L561	V562	V563	L564	Y565	G566	V567	L568	I569	E570	S571	P572	L575	I578	Q579	E580	N581	H582	I583	K584	L589	L590	D591	K592	H593	G594	R595	N596	H597	K598	V599	L600	V602								
C607	V608	C609	M610	G611	V612	A613	N617	Q618	D619	L620	I621	T622	L625	L626	P627	G628	R629	E630	Q634	T635	N636	L637	M638	N639	Y640	V641	T642	L643	I644	R645	P646	N647	I648	F649	V650	G651	ARG	ALA	GLU	GLY	SER	THR	TYR	G660	V661	W662	Y663	F664	E665	V666	M667	A727	R728	P729	V730	T731	S732	P733	G734
V672	P673	F674	L675	T676	A677	Q678	A679	L682	R683	L684	V685	G686	T689	E690	G691	Y692	S693	P694	V695	P696	G697	G698	M699	G699	T700	G701	W702	G703	G704	N705	G706	V707	G708	D709	D710	L711	Y712	S713	F716	D717	G718	L719	H720	L721	W722	T723	G724	H725	V726	A727	R728	P729	V730	T731	S732	P733	G734		
H736	L737	L738	R739	P740	F741	Q742	V743	W744	S745	C746	C747	L748	D749	L750	S751	P753	S756	F757	R758	I759	M760	G761	C762	P763	W764	Q765	G766	V767	F768	F771	N772	L773	D774	F777	F778	P779	V780	V781	S782	F783	S784	A785	G786	W787	K788	V789	R790	F791	L792	L793	G794	GLY	ARG	HIS					
GLY	E799	F802	L803	P804	P805	P806	G807	E808	L816	P817	R818	E819	R820	L821	R822	L823	E824	P825	I826	K827	E828	Y829	R830	R831	E832	G833	P834	R835	H838	L839	Y840	G841	P842	S843	R844	LEU	SER	HIS	THR	ASP	F851	Y852	P853	C854	P855	V856	D857	T858	Y859	Q860	I861	V862	L863	P864	P865				
H866	L867	E868	R869	L870	R871	L874	A875	E876	M877	L878	E880	L881	W882	A883	L884	T885	R886	I887	E888	Q889	E890	G890	H891	T892	Y893	G894	P895	V896	R897	D898	D899	N900	K901	R902	R903	H904	P905	C906	L907	Y908	N909	F910	H911	L913	P914	E915	P916	E917	R918	N919	N921	Q923	R924	S925	G926				
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A989	E990	N991	N994	A997	Q1003	GLY	TRP	SER	SER	TRP	ALA	VAL	GLN	ASP	ILE	ALA	R1016	R1017	N1018	L1021	V1022	P1023	Y1024	R1025	L1026	L1027	D1028	E1029	M1000	T1031	K1032	R1033	S1034	N1035	R1036	D1037	S1038	L1039	P1040	Q1041	A1042	V1043	R1044	T1045	S973	L1046	H974	G1048	Y1049	L1050	Y1051	N1052	I1053	E1054	P1055				
PRO	ASP	GLN	PRO	GLN	VAL	ASN	GLN	ARG	TRP	ASP	R1071	V1072	R1073	A1077	E1078	K1079	S1085	G1086	R1087	W1088	Y1089	F1090	E1091	F1092	E1093	A1094	V1095	T1096	M1100	R1101	A1105	R1106	P1107	E1108	L1109	R1110	P1111	D1112	V1113	E1114	L1115	D1118	E1119	L1120	N1125	G1126	H1127	R1128											
G1129	Q1130	R1131	W1132	H1133	L1134	G1136	S1136	E1137	L1138	F1139	G1140	H1141	F1142	W1143	Q1144	D1147	V1148	M1152	I1153	D1154	L1155	T1156	I1160	I1161	F1162	E1167	V1168	L1169	MET	SER	ASP	SER	GLY	SER	GLU	THR	A1178	F1179	I1182	E1183	I1184	G1185	D1186	G1187	F1188	L1189	P1190	V1191	C1192	S1193	L1194	G1195	P1196	G1197					



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

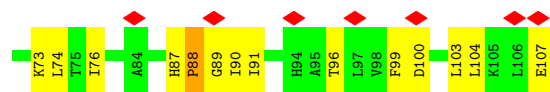


● Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A

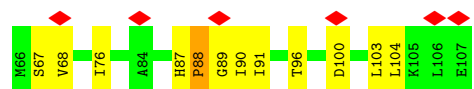
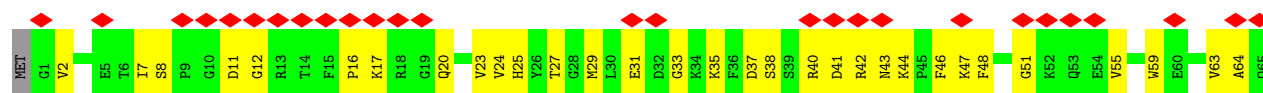


● Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A





- 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	47000	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	0.324	Depositor
Minimum map value	-0.144	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.09	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 [i](#)

5.1 Standard geometry [i](#)

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	1.20	141/27385 (0.5%)	1.11	132/37104 (0.4%)
1	C	1.20	149/27385 (0.5%)	1.11	135/37104 (0.4%)
1	E	1.20	146/27385 (0.5%)	1.11	133/37104 (0.4%)
1	G	1.19	149/27385 (0.5%)	1.10	120/37104 (0.3%)
2	B	0.74	0/851	0.97	1/1146 (0.1%)
2	D	0.74	0/851	0.97	1/1146 (0.1%)
2	F	0.74	0/851	0.97	1/1146 (0.1%)
2	H	0.76	0/851	0.96	1/1146 (0.1%)
All	All	1.19	585/112944 (0.5%)	1.10	524/153000 (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	19
1	C	0	19
1	E	0	19
1	G	0	19
All	All	0	76

The worst 5 of 585 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	4987	ASN	N-CA	-12.74	1.30	1.46
1	A	4987	ASN	N-CA	-12.65	1.31	1.46
1	E	4987	ASN	N-CA	-12.58	1.31	1.46
1	G	4181	ILE	CA-CB	-10.95	1.39	1.54
1	E	4181	ILE	CA-CB	-10.68	1.40	1.54

The worst 5 of 524 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	915	GLU	CA-C-N	19.17	143.81	119.84
1	A	915	GLU	C-N-CA	19.17	143.81	119.84
1	G	915	GLU	CA-C-N	19.15	143.77	119.84
1	G	915	GLU	C-N-CA	19.15	143.77	119.84
1	C	915	GLU	CA-C-N	19.08	143.69	119.84

There are no chirality outliers.

5 of 76 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1252	HIS	Peptide
1	A	1253	PRO	Peptide
1	A	1464	PHE	Mainchain
1	A	332	GLU	Mainchain,Peptide
1	A	841	GLY	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	26917	0	24461	1126	0
1	C	26917	0	24461	1131	0
1	E	26917	0	24461	1137	0
1	G	26917	0	24461	1133	0
2	B	832	0	831	40	0
2	D	832	0	831	39	0
2	F	832	0	831	38	0
2	H	832	0	831	37	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	4524	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 21.

The worst 5 of 4524 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:E:4826:ILE:CG2	1:G:4931:ILE:HD11	1.79	1.10
1:A:4879:MET:SD	1:G:4578:LEU:HA	1.92	1.10
1:A:4826:ILE:CG2	1:C:4931:ILE:HD11	1.86	1.05
1:E:4578:LEU:HA	1:G:4879:MET:SD	1.99	1.03
1:C:4826:ILE:CG2	1:E:4931:ILE:HD11	1.91	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%)	3173 (91%)	220 (6%)	103 (3%)	3	24
1	C	3496/5037 (69%)	3169 (91%)	223 (6%)	104 (3%)	3	23
1	E	3496/5037 (69%)	3169 (91%)	223 (6%)	104 (3%)	3	23
1	G	3496/5037 (69%)	3169 (91%)	226 (6%)	101 (3%)	3	24
2	B	105/108 (97%)	92 (88%)	12 (11%)	1 (1%)	12	47
2	D	105/108 (97%)	92 (88%)	12 (11%)	1 (1%)	12	47
2	F	105/108 (97%)	92 (88%)	12 (11%)	1 (1%)	12	47
2	H	105/108 (97%)	89 (85%)	15 (14%)	1 (1%)	12	47
All	All	14404/20580 (70%)	13045 (91%)	943 (6%)	416 (3%)	5	24

5 of 416 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	689	THR
1	A	720	HIS
1	A	806	PRO

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Mol	Chain	Res	Type
1	A	916	PRO
1	A	1253	PRO

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	2500/4276 (58%)	2483 (99%)	17 (1%)	76	78
1	C	2501/4276 (58%)	2484 (99%)	17 (1%)	76	78
1	E	2502/4276 (58%)	2483 (99%)	19 (1%)	73	77
1	G	2501/4276 (58%)	2477 (99%)	24 (1%)	68	75
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	10360/17464 (59%)	10283 (99%)	77 (1%)	73	78

5 of 77 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	862	VAL
1	G	4184	MET
1	G	885	THR
1	G	1096	THR
1	G	4932	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 207 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	465	GLN
1	E	2856	ASN
1	G	3704	HIS

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Mol	Chain	Res	Type
1	E	1127	HIS
1	E	1663	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.

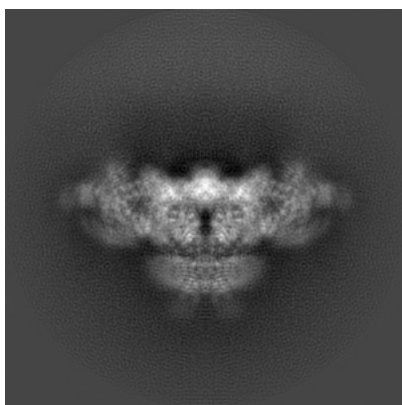
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9520. These allow visual inspection of the internal detail of the map and identification of artifacts.

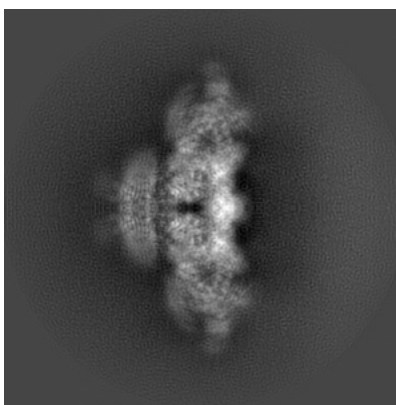
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

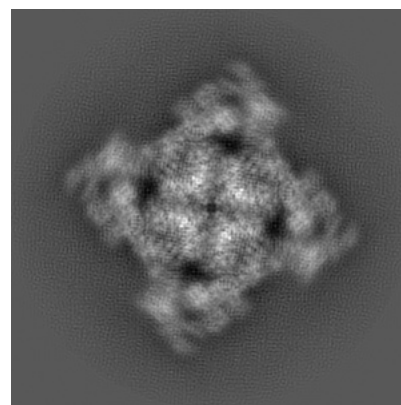
6.1.1 Primary map



X



Y

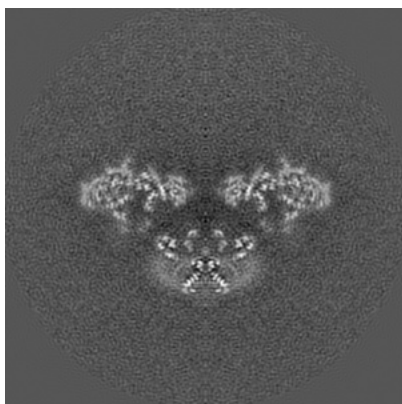


Z

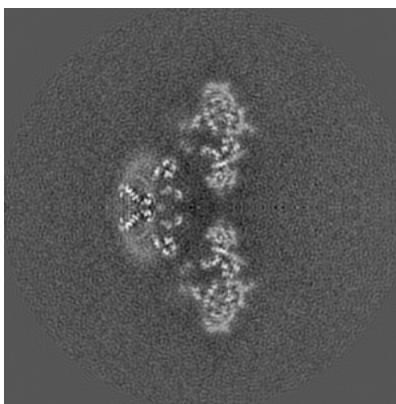
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

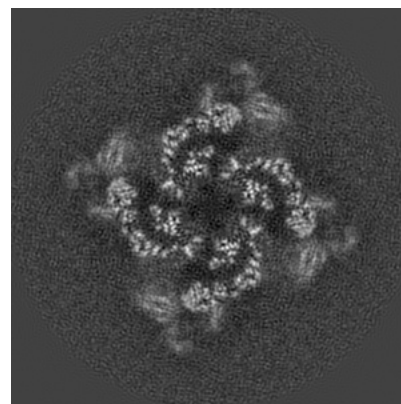
6.2.1 Primary map



X Index: 180



Y Index: 180

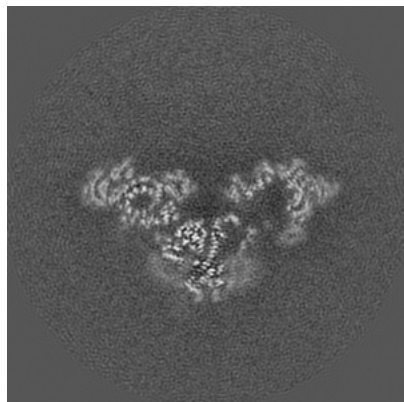


Z Index: 180

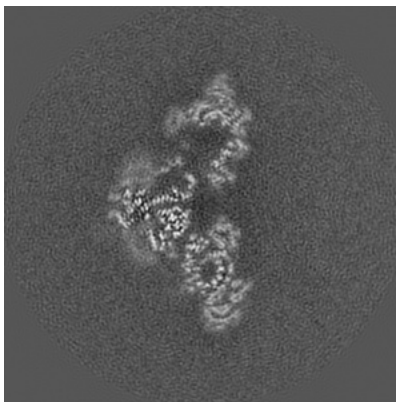
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

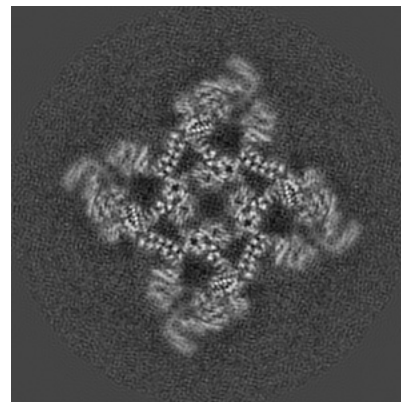
6.3.1 Primary map



X Index: 187



Y Index: 173

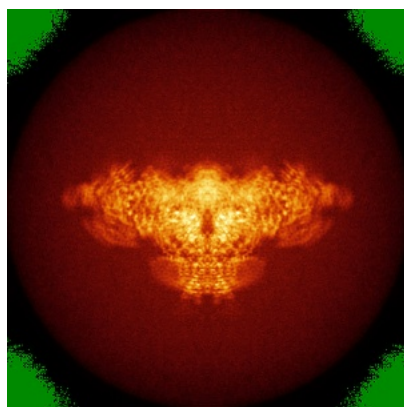


Z Index: 191

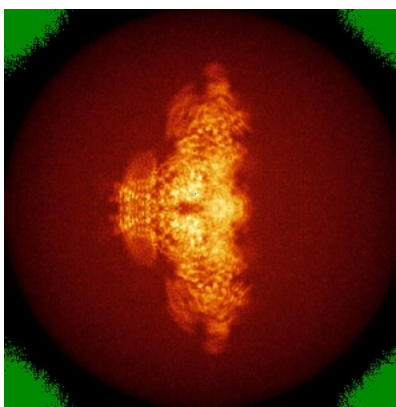
The images above show the largest variance slices of the map in three orthogonal directions.

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

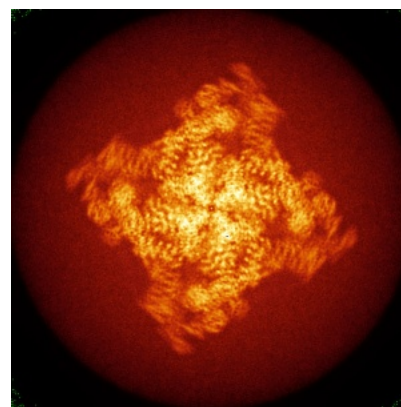
6.4.1 Primary map



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

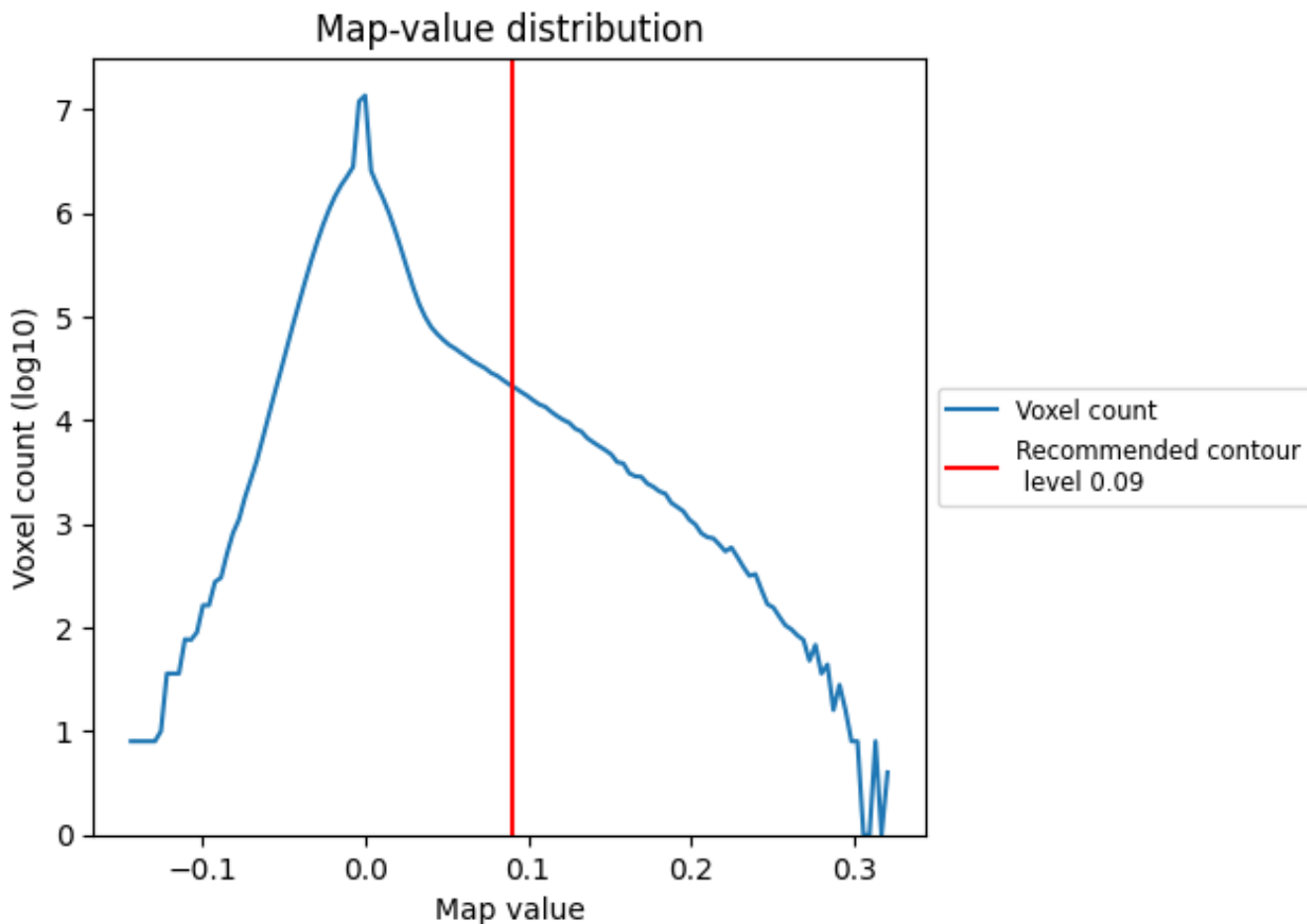
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

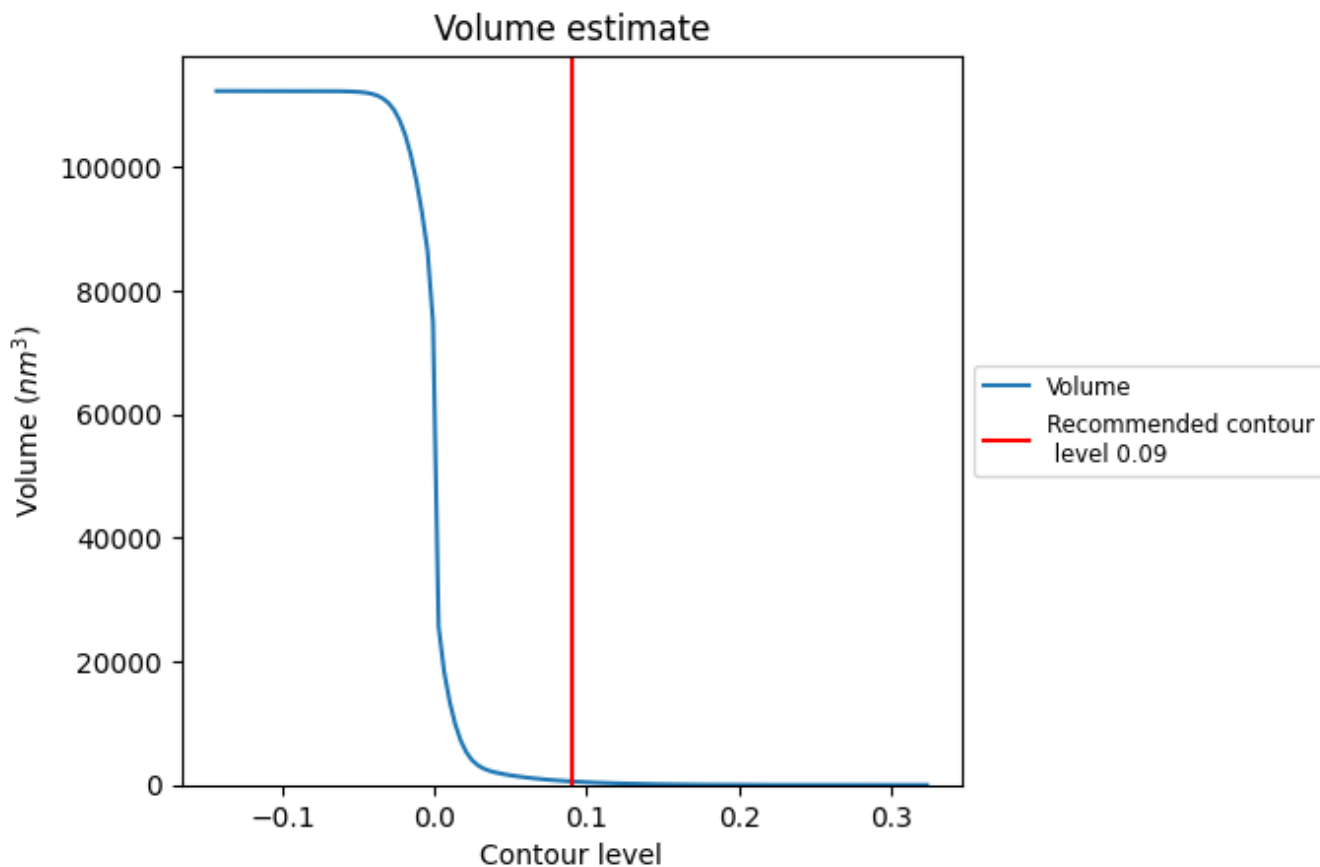
This section contains the results of statistical analysis of the map.

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.

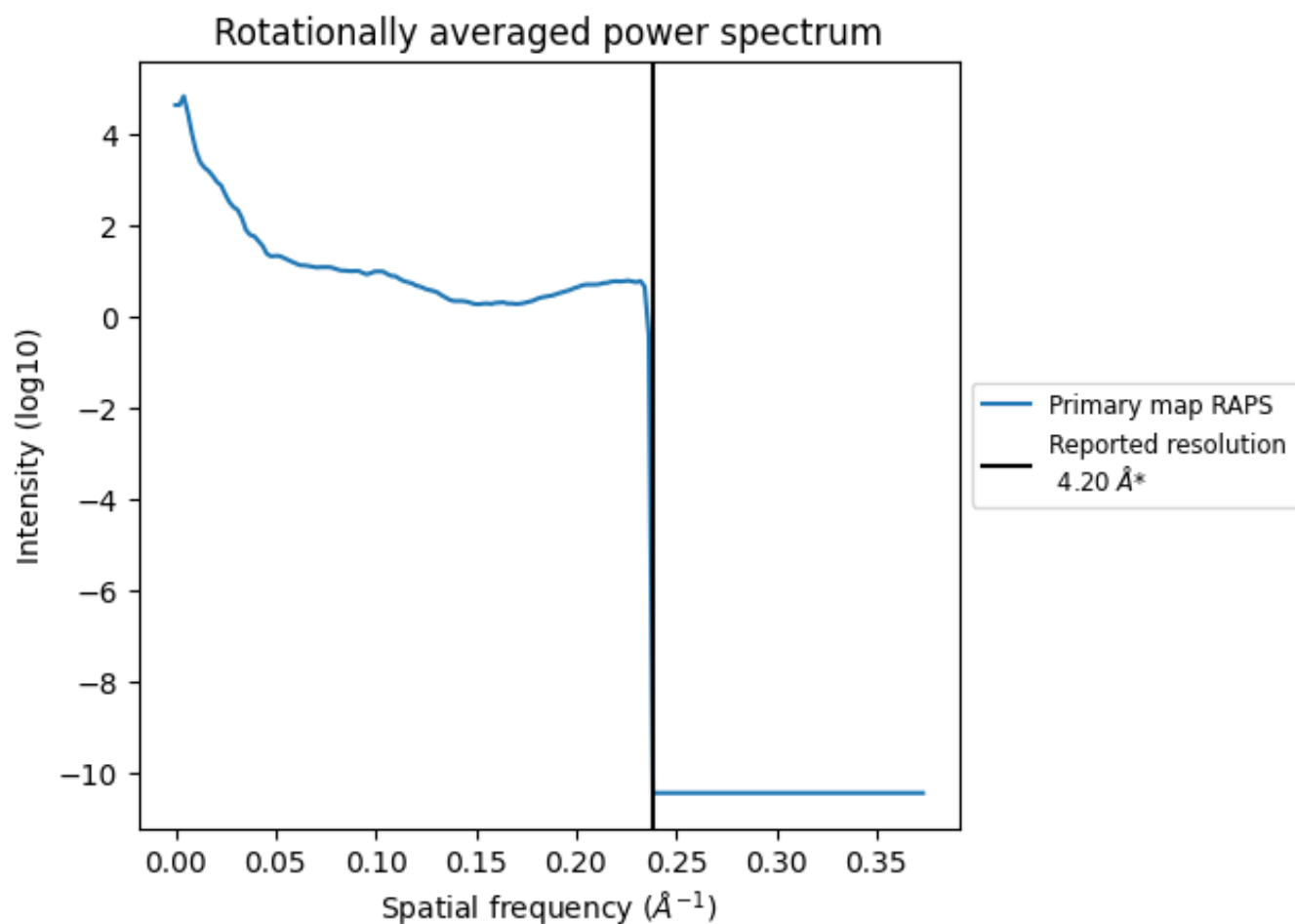
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 572 nm^3 ; this corresponds to an approximate mass of 517 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 0.238 Å⁻¹

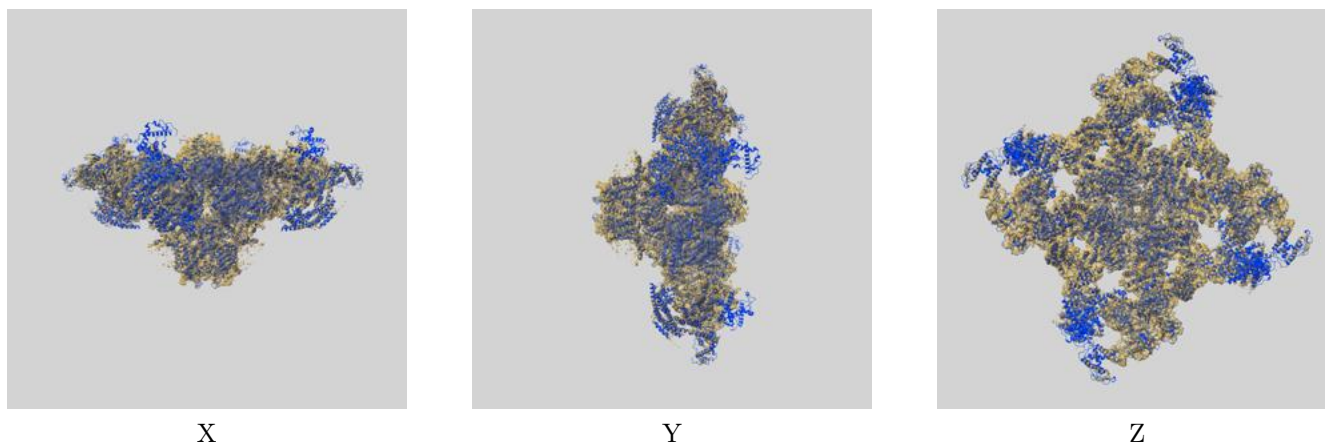
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

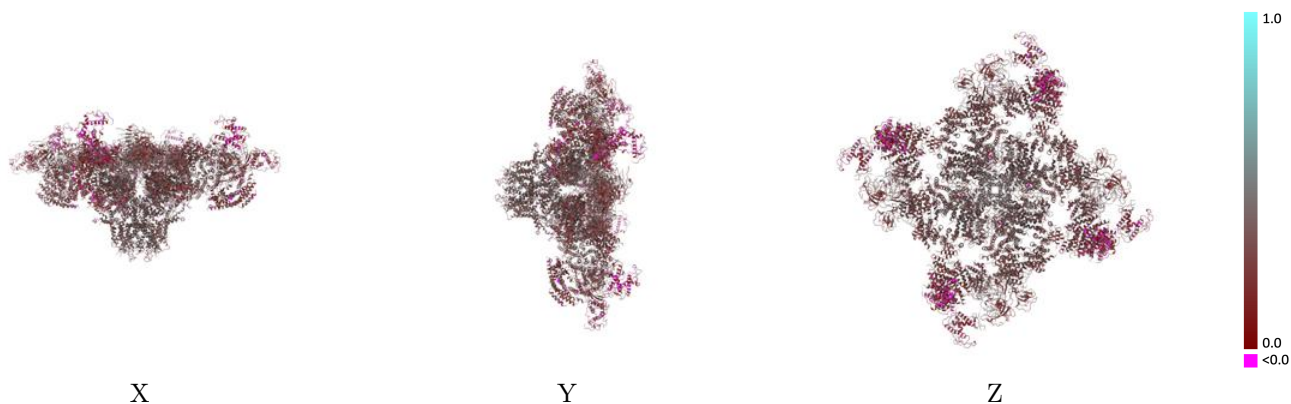
This section contains information regarding the fit between EMDB map EMD-9520 and PDB model 5GL0. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)



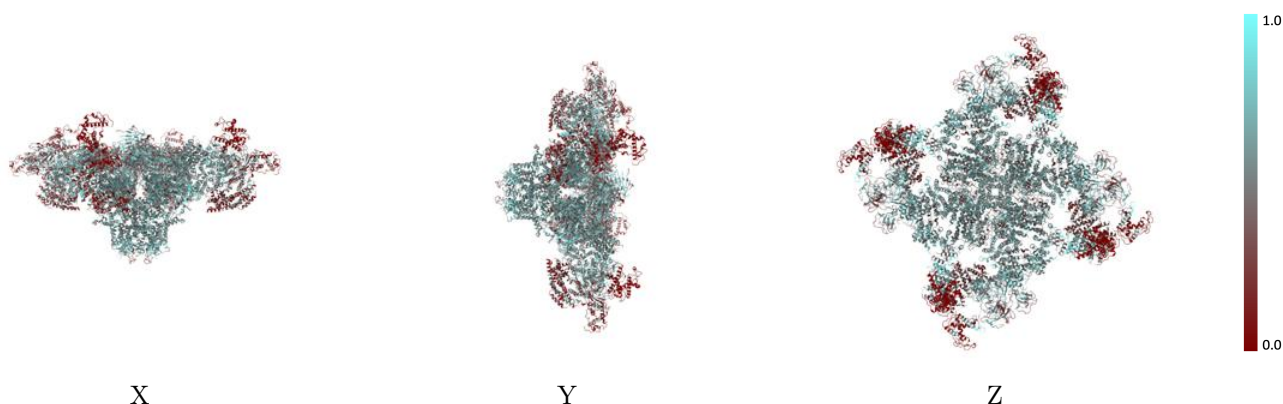
The images above show the 3D surface view of the map at the recommended contour level 0.09 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



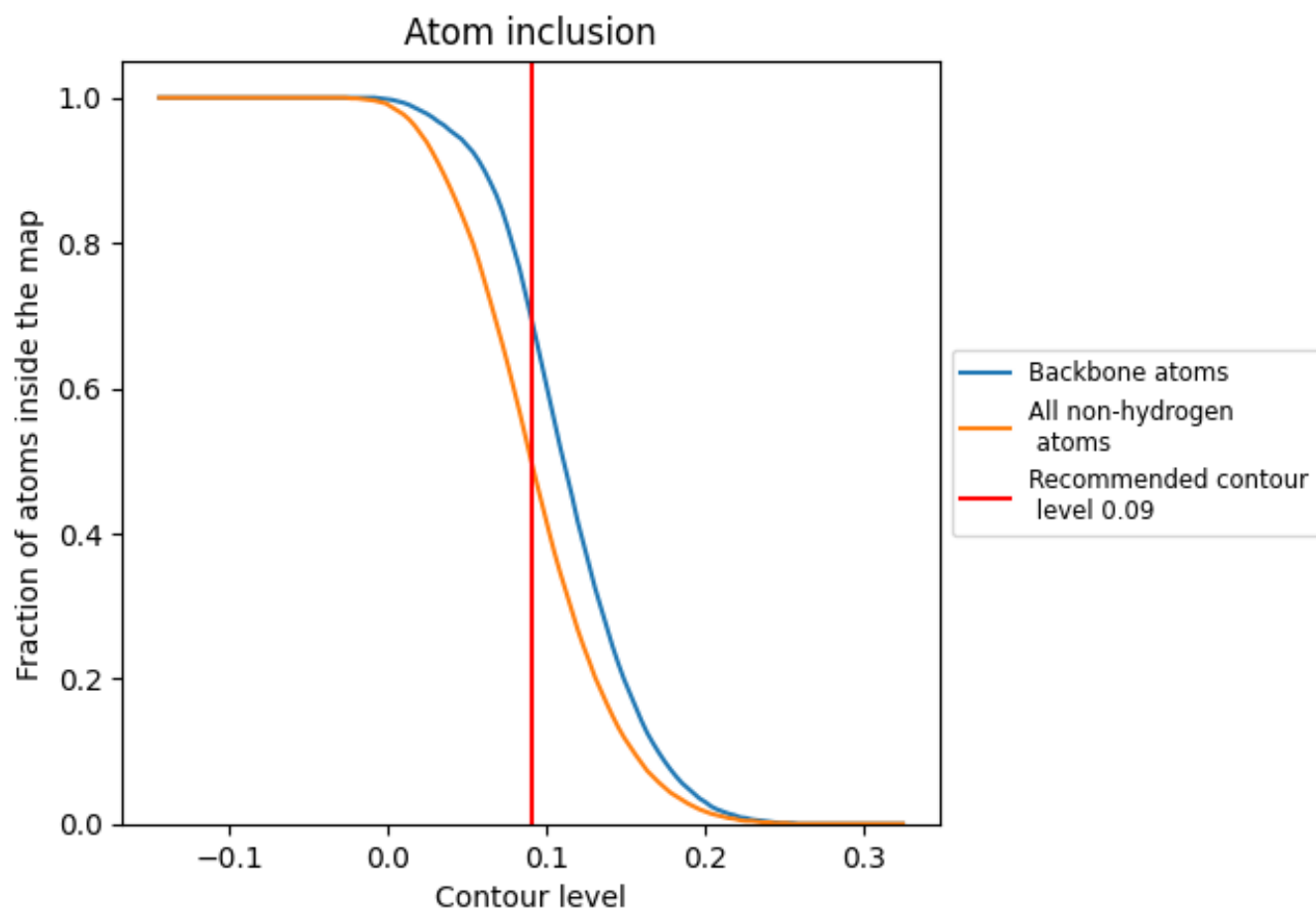
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.09).

9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 50% 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 (0.09) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5020	0.3090
A	0.5030	0.3090
B	0.4670	0.3060
C	0.5020	0.3090
D	0.4670	0.3070
E	0.5030	0.3090
F	0.4660	0.3010
G	0.5040	0.3100
H	0.4710	0.3070

