



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 03:29 PM UTC

PDB ID : 5TB4 / pdb_00005tb4
EMDB ID : EMD-8395
Title : Structure of rabbit RyR1 (EGTA-only dataset, class 4)
Authors : Clarke, O.B.; des Georges, A.; Zalk, R.; Marks, A.R.; Hendrickson, W.A.; Frank, J.
Deposited on : 2016-09-11
Resolution : 4.50 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:

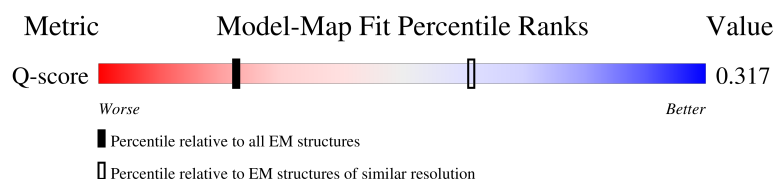
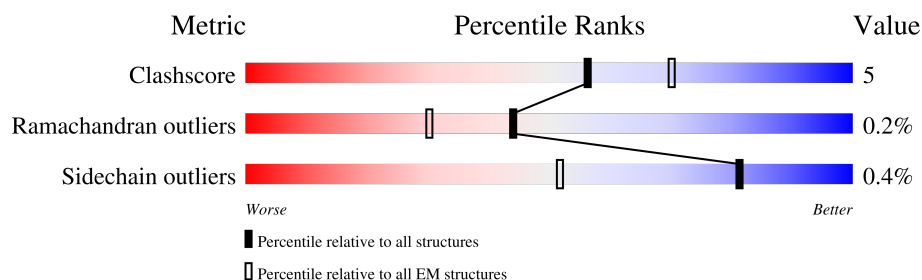
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.50 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	2937 (4.00 - 5.00)

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	108	
1	F	108	
1	H	108	
1	J	108	

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Mol	Chain	Length	Quality of chain			
2	B	4416	39%			
2	E	4416	84%			
2	G	4416	11%			
2	I	4416	5%			

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 121272 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

- Molecule 2 is a protein called Ryanodine receptor 1.

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

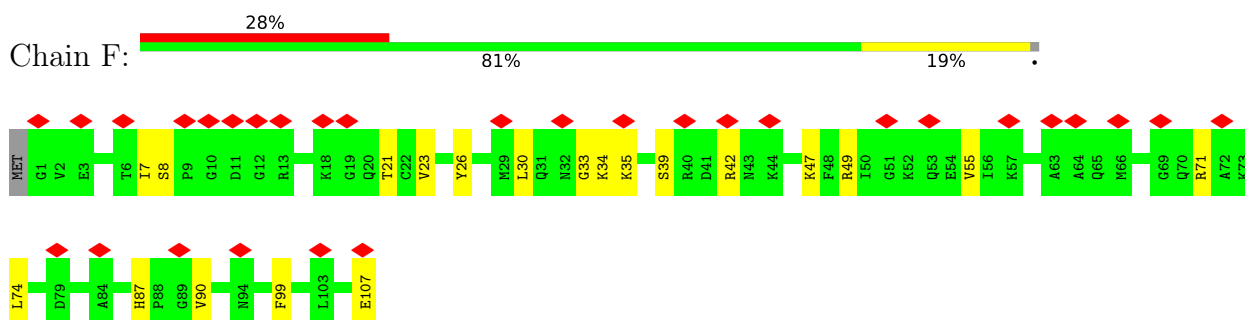
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

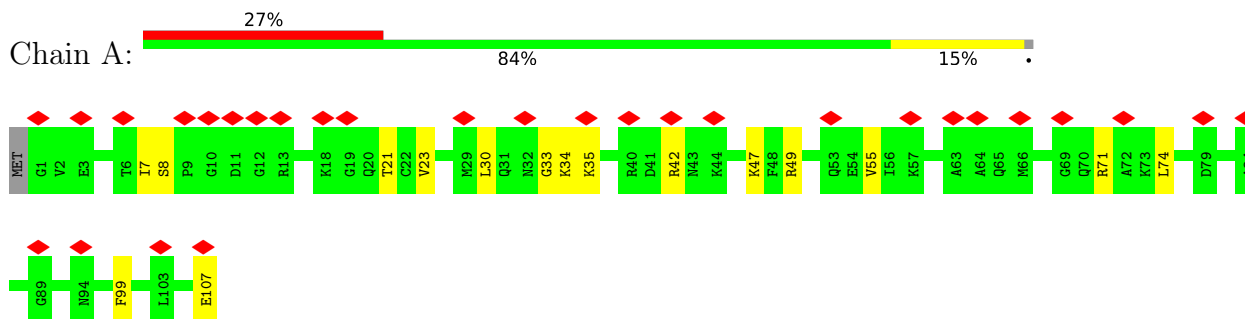
3 Residue-property plots [i](#)

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

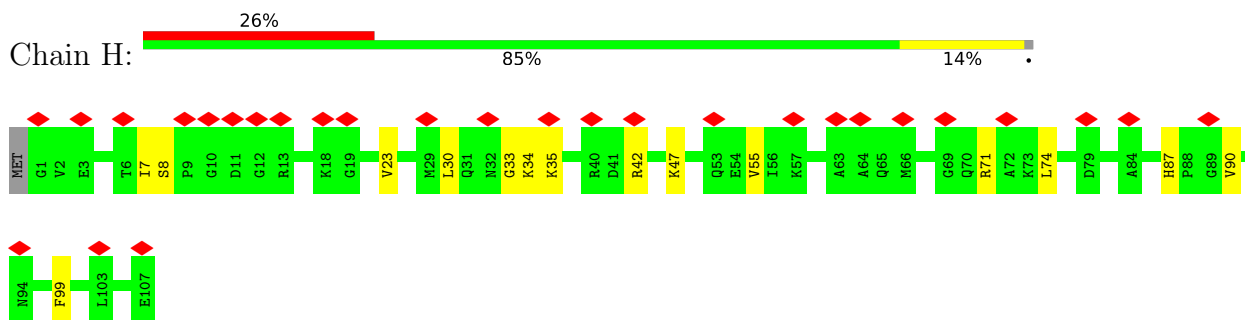
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



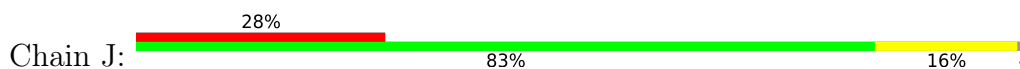
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

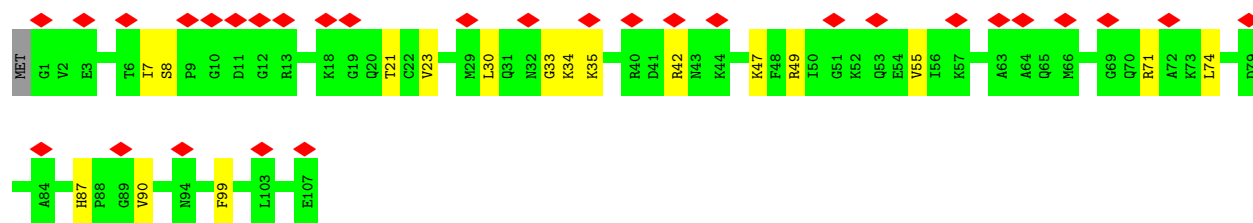


- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

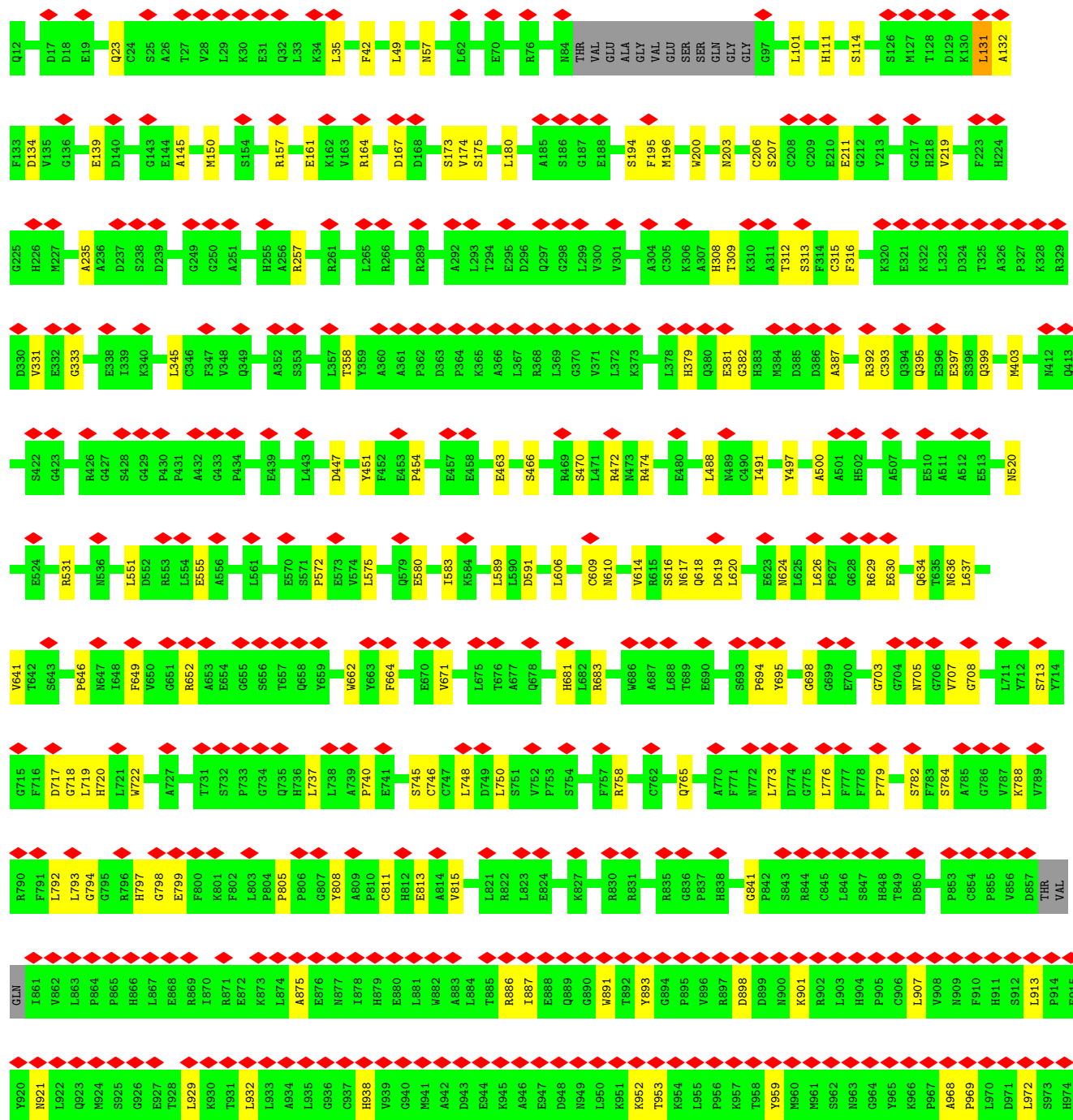
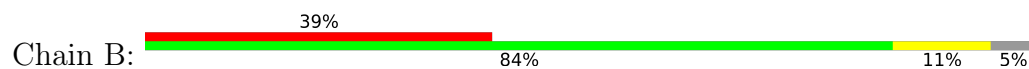


- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B





• Molecule 2: Ryanodine receptor 1



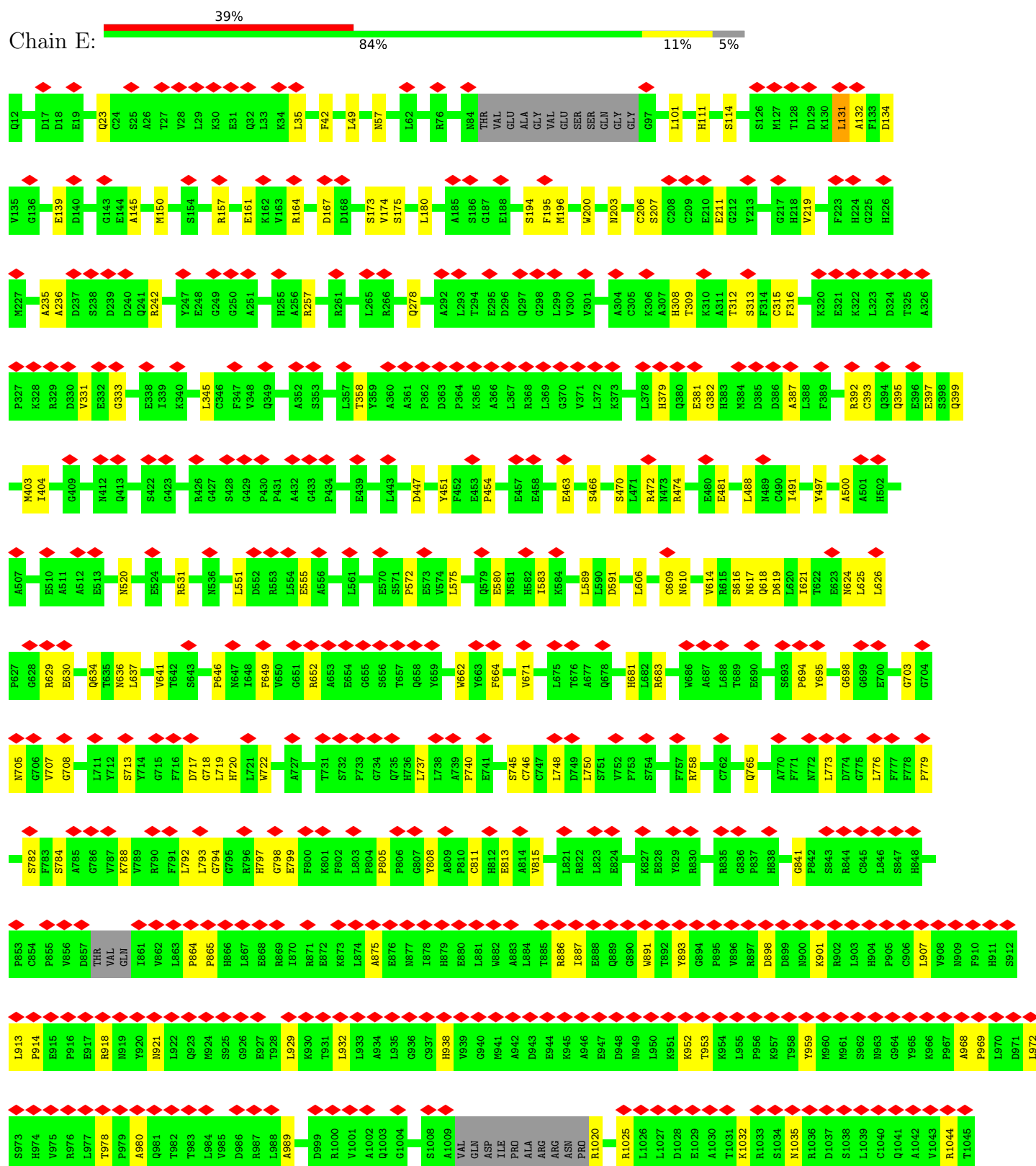






• Molecule 2: Ryanodine receptor 1

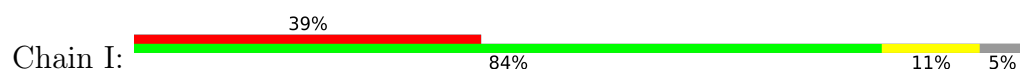
Chain E:

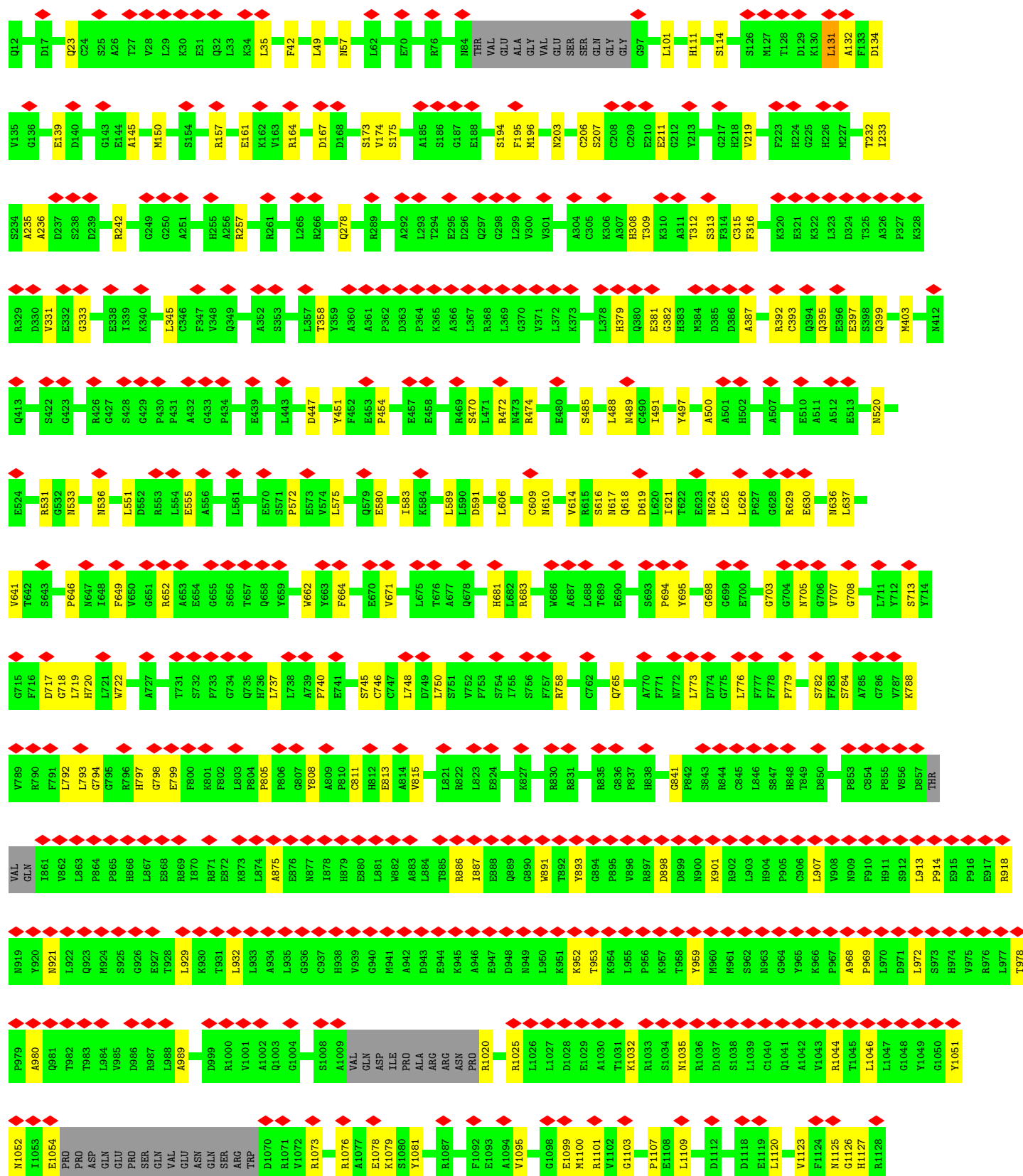






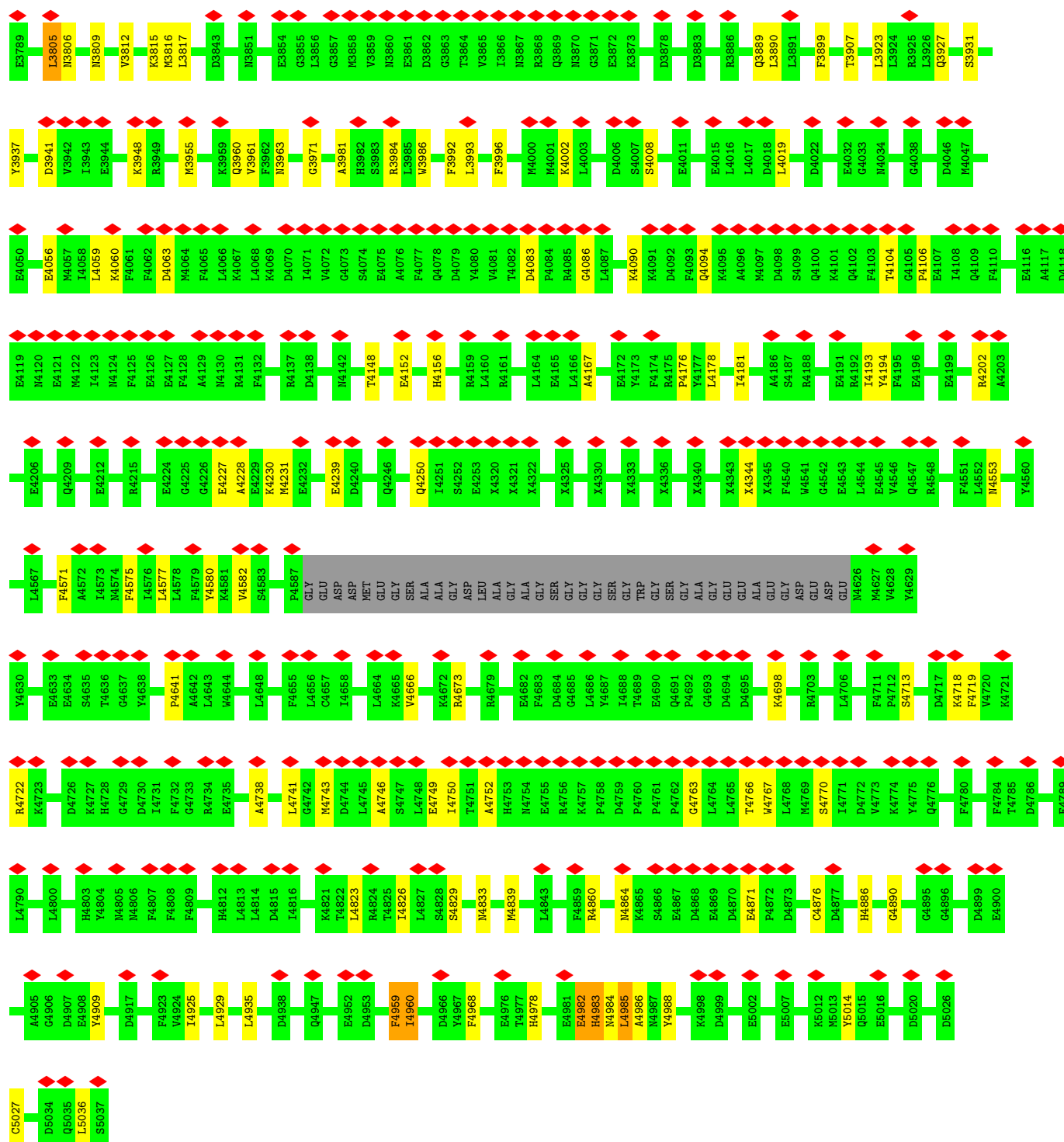
- Molecule 2: Ryanodine receptor 1





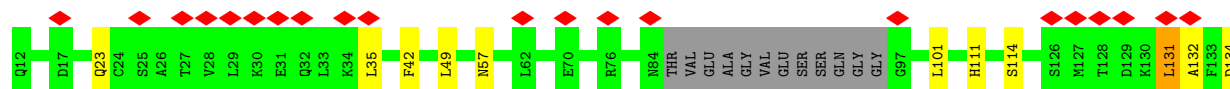


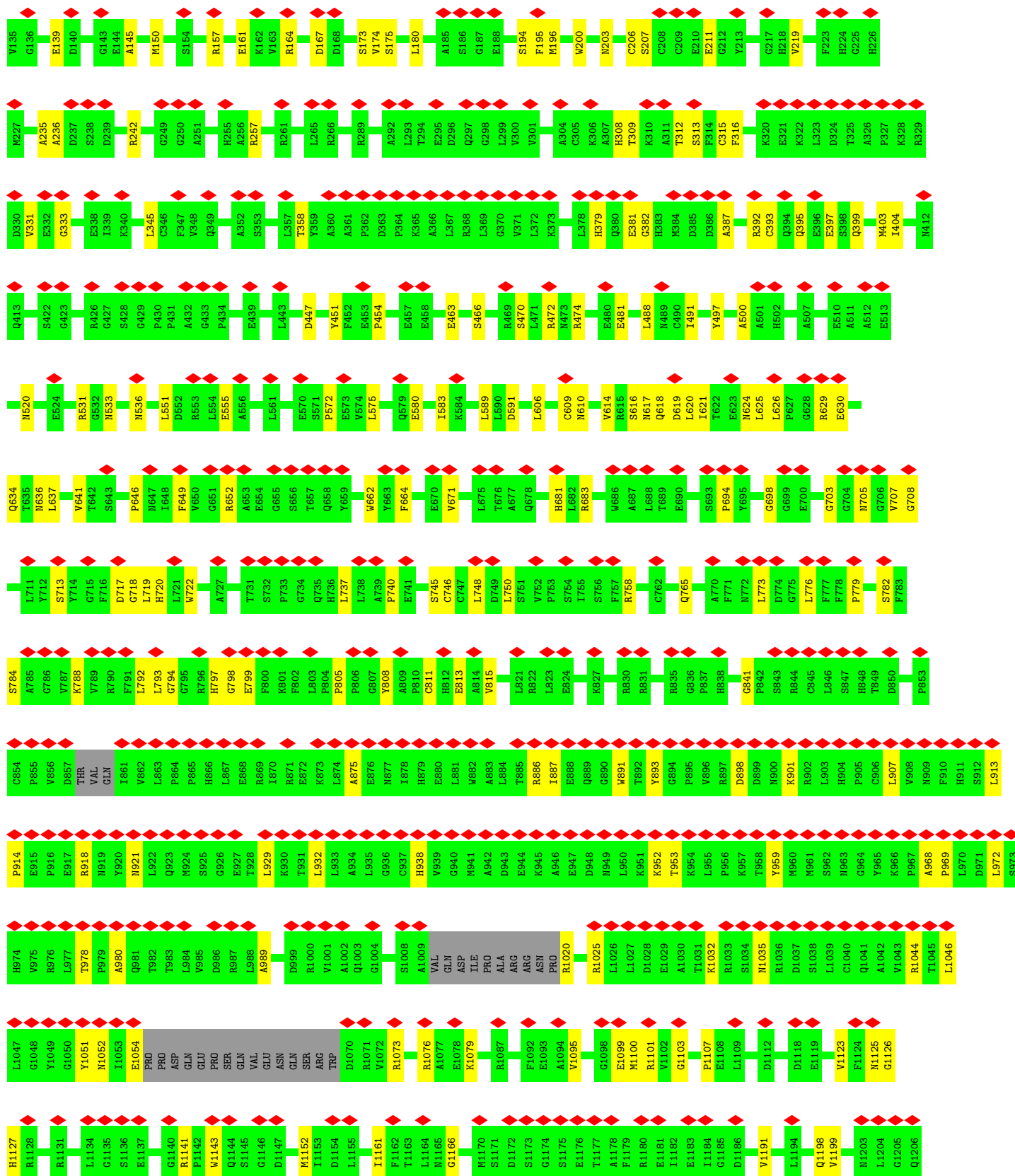
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R3707	L3710	T3711	E3712	K3713	D3717	Y3720	A3726	D3727	L3728	N3729	S3732	C3733	H3734	L3735	E3736	E3737	G3738	G3739	E3740	N3741	GLY	GLU	ALA	GLU	GLU	E3747	E3748	V3749	E3750	V3751	S3752	F3753	E3754	E3755	K3756	E3757	N3758	E3759	K3760	Q3761	R3762	Q3766	S3768	K3769	L3770	H3771	E3772	R3773	L3780																														
X3518	X3519	X3520	X3526	X3529	X3530	X3531	X3532	X3533	X3534	X3535	X3536	X3539	X3540	X3541	X3542	X3543	X3544	X3545	X3546	X3547	X3548	X3549	X3550	X3551	X3552	X3553	X3554	X3555	X3556	X3557	X3558	X3559	X3560	X3561	X3562	X3563	X3564	X3565	X3566	X3567	X3568	X3569	X3575	X3579	X3580	X3581	X3582	X3583	X3584	X3585	X3586	X3587	X3588	X3589	X3590																								
X3396	X3397	X3398	X3399	X3400	X3401	X3402	X3403	X3404	X3405	X3406	X3407	X3408	X3409	X3410	X3411	X3412	X3413	X3414	X3415	X3416	X3417	X3421	X3422	X3433	X3434	X3435	X3436	X3439	X3440	X3441	X3442	X3443	X3450	X3451	X3452	X3453	X3454	X3455	X3456	X3457	X3458	X3459	X3463	X3464	X3465	X3466	X3467	X3468	X3511	X3512	X3513	X3516	X3517																										
X3261	X3262	X3263	X3264	X3265	X3266	X3267	X3268	X3269	X3270	X3271	X3272	X3273	X3274	X3275	X3276	X3277	X3278	X3279	X3280	X3281	X3282	X3283	X3284	X3285	X3286	X3287	X3288	X3289	X3290	X3291	X3292	X3293	X3294	X3295	X3296	X3297	X3298	X3299	X3302	X3303	X3304	X3309	X3312	X3313	X3314	X3318	X3323	X3324	X3325	X3326	X3327	X3328	X3332																										
X3042	X3043	X3044	X3045	X3046	X3047	X3048	X3051	X3052	X3053	X3057	X3060	X3061	X3062	X3063	X3064	X3065	X3066	X3067	X3068	X3069	X3070	X3073	X3074	X3075	X3076	X3077	X3078	X3079	X3080	X3081	X3082	X3083	X3084	X3085	X3086	X3087	X3088	X3089	X3090	X3091	X3092	X3093	X3094	X3095	X3096	X3097	X3098	X3099	X3102	X3103	X3104	X3109	X3112	X3113	X3114	X3118	X3123	X3124	X3125	X3126	X3127	X3128	X3132																
X2948	X2949	X2950	X2951	X2952	X2953	X2954	X2955	X2956	X2957	X2958	X2959	X2960	X2961	X2962	X2963	X2964	X2968	X2969	X2970	X2973	X2974	X2975	X2976	X2977	X2978	X2979	X2980	X2981	X2982	X2983	X2984	X2985	X2986	X2987	X2988	X2989	X2990	X2991	X2992	X2993	X2994	X2995	X2996	X2997	X2998	X2999	X3000	X3001	X3002	X3014	X3015	X3016	X3019	X3020	X3021	X3022	X3023	X3027	X3028	X3029	X3030	X3031	X3032	X3033	X3034	X3035	X3036	X3037	X3038	X3039	X3040	X3041							
V2866	G2867	R2868	K2869	L2870	L2871	L2872	L2873	L2874	L2875	L2876	L2877	L2878	L2879	L2880	L2881	L2882	L2883	L2884	L2885	L2886	L2887	L2888	L2889	L2890	L2891	L2892	L2893	L2894	L2895	L2896	L2897	L2898	L2899	L2900	L2901	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	L2938	R2939	X2942	X2943	X2944	X2945	X2946	X2947
X2948	X2949	X2950	X2951	X2952	X2953	X2954	X2955	X2956	X2957	X2958	X2959	X2960	X2961	X2962	X2963	X2964	X2968	X2969	X2970	X2973	X2974	X2975	X2976	X2977	X2978	X2979	X2980	X2981	X2982	X2983	X2984	X2985	X2986	X2987	X2988	X2989	X2990	X2991	X2992	X2993	X2994	X2995	X2996	X2997	X2998	X2999	X3000	X3001	X3002	X3014	X3015	X3016	X3019	X3020	X3021	X3022	X3023	X3027	X3028	X3029	X3030	X3031	X3032	X3033	X3034	X3035	X3036	X3037	X3038	X3039	X3040	X3041							
X3186	X3191	X3192	X3193	X3194	X3195	X3196	X3197	X3198	X3199	X3200	X3203	X3204	X3205	X3206	X3207	X3208	X3209	X3210	X3211	X3212	X3213	X3214	X3215	X3216	X3217	X3218	X3219	X3220	X3221	X3222	X3223	X3226	X3227	X3228	X3229	X3230	X3231	X3232	X3233	X3234	X3235	X3236	X3241	X3242	X3243	X3244	X3245	X3246	X3247	X3248	X3249	X3250	X3251	X3252	X3253	X3254																							
X3261	X3262	X3263	X3264	X3265	X3266	X3267	X3268	X3269	X3270	X3271	X3272	X3273	X3274	X3275	X3276	X3277	X3278	X3279	X3280	X3281	X3282	X3283	X3284	X3285	X3286	X3287	X3288	X3289	X3290	X3291	X3292	X3293	X3294	X3295	X3296	X3297	X3298	X3299	X3302	X3303	X3304	X3309	X3312	X3313	X3314	X3318	X3323	X3324	X3325	X3326	X3327	X3328	X3332																										
X3333	X3334	X3335	X3336	X3337	X3338	X3339	X3340	X3341	X3342	X3343	X3344	X3345	X3346	X3347	X3348	X3349	X3350	X3351	X3352	X3353	X3354	X3355	X3356	X3357	X3358	X3359	X3360	X3363	X3364	X3365	X3366	X3367	X3368	X3369	X3373	X3374	X3375	X3376	X3377	X3378	X3379	X3380	X3381	X3382	X3383	X3384	X3385	X3386	X3387	X3388	X3389	X3390	X3391	X3392	X3393	X3394	X3395																						
X3396	X3397	X3398	X3399	X3400	X3401	X3402	X3403	X3404	X3405	X3406	X3407	X3408	X3409	X3410	X3411	X3412	X3413	X3414	X3415	X3416	X3417	X3421	X3422	X3433	X3434	X3435	X3436	X3439	X3440	X3441	X3442	X3443	X3450	X3451	X3452	X3453	X3454	X3455	X3456	X3457	X3458	X3459	X3463	X3464	X3465	X3466	X3467	X3468	X3511	X3512	X3513	X3516	X3517																										
X3518	X3519	X3520	X3526	X3529	X3530	X3531	X3532	X3533	X3534	X3535	X3536	X3539	X3540	X3541	X3542	X3543	X3544	X3545	X3546	X3547	X3548	X3549	X3550	X3551	X3552	X3553	X3554	X3555	X3556	X3557	X3558	X3559	X3560	X3561	X3562	X3563	X3564	X3565	X3566	X3567	X3568	X3569	X3575	X3579	X3580	X3581	X3582	X3583	X3584	X3585	X3586	X3587	X3588	X3589	X3590																								
X3591	X3592	X3596	X3600	X3606	X3607	X3608	X3609	X3610	X3611	X3612	X3613	L3641	X3642	N3643	L3644	H3647	R3648	A3649	K3658	A3659	A3660	A3661	I3662	L3663	T3664	E3665	D3666	H3667	S3668	F3669	D3670	D3671	R3672	M3673	L3674	D3675	D3676	K3679	A3680	G3681	E3682	Q3683	E3684	E3685	E3686	E3687	E3688	E3689	V3690	E3691	E3692	K3693																											



• Molecule 2: Ryanodine receptor 1

Chain G: 39% 84% 11% 5%





X2673	X2674	X2675	X2676	X2686	X2687	X2688	X2689	X2690	X2691	X2692	X2693	X2694	X2695	X2696	X2697	X2698	X2699	X2700	X2701	X2702	X2703	N2734	X2735	X2736	X2737	X2738	X2739	E2741	X2742	X2743	N2744	X2745	X2746	X2747	X2748	E2749	X2750	X2751	X2752	S2753	X2754	X2755	X2756	X2757	X2758	A2759	E2760	X2761	X2762	H2763	E2764	X2765	X2766	A2767	X2768	X2770
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R2336	F2337	A2338	V2339	F2340	V2341	N2342	G2343	V2346	E2347	E2348	N2349	A2350	N2351	R2355	F2364	G2365	F2366	A2367	L2368	R2369	G2370	E2371	G2372	G2373	S2374	G2375	L2376	L2377	A2378	E2381	I2384	R2385	E2388	D2389	P2390	D2393	G2394	P2395	GLY	VAL	ARG	ARG	ASP	ARG	ARG	ARG	GLU	HIS	PHE	GLY	GLU					
GLU	PRO	PRO	GLU	N2414	R2415	V2416	M2423	L2432	R2435	C2436	A2437	P2438	E2439	N2440	H2441	L2442	G2448	R2454	A2455	L2463	D2464	D2465	L2466	I2469	L2472	P2473	L2474	Q2475	L2476	P2477	T2478	L2479	X2487	X2488	X2489	X2490	X2494	X2523	X2524	X2529	X2532	X2536	X2537	X2538												
G2218	E2219	T2220	K2221	E2222	L2223	R2224	R2234	N2246	Q2247	D2252	H2253	L2257	G2262	I2263	G2264	L2265	G2266	M2267	Q2268	G2269	S2270	T2271	P2272	L2273	A2276	A2277	E2285	Q2291	E2292	Q2293	D2294	L2295	E2296	Y2301	G2304	S2309	L2314	A2315	K2316	G2317	D2320	C2326	G2327	R2330												
ARG	LEU	VAL	LYS	LYS	LYS	GLU	GLU	LYS	PRO	GLU	GLU	ALA	GLU	K2089	K2090	R2104	R2126	Q2127	Y2128	L2131	R2140	S2147	T2167	V2168	Q2169	M2170	L2177	Q2180	N2187	N2188	K2189	V2190	P2195	N2196	R2199	M2208	E2209	L2314	A2315	K2316	G2317	D2320	C2326	G2327	R2330											
Q2005	M2008	L2009	H2011	F2012	K2013	D2014	E2015	A2016	D2017	E2018	E2019	D2020	C2021	P2022	L2023	E2025	D2026	I2027	R2028	Q2029	D2030	L2031	Q2032	D2033	A2040	H2041	C2042	G2043	Q2045	L2046	E2047	G2048	GLU	GLU	GLU	PRO	GLU	GLU	THR	SER	LEU	SER	SER	SER	ARG	LEU	SER	LEU	THR	VAL						
ALA	PRO	GLU	GLY	LYS	LYS	ASP	L1922	E1923	E1924	G1925	Q1928	P1932	E1944	D1948	Q1949	E1950	L1958	A1959	A1960	R1964	Q1973	R1974	S1975	R1976	Y1977	A1978	L1979	L1980	M1981	R1982	A1983	F1984	T1985	M1986	S1987	A1988	A1989	E1990	T1991	A1992	R1993	R1994	T1995	F1998	R1999	S2000	P2001	P2002	Q2003	E2004						
P1829	V1830	G1831	G1832	F1838	V1839	P1840	L1848	I1853	D1856	E1857	D1858	V1859	K1860	E1873	E1874	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU						
L1731	S1732	E1733	L1738	T1739	P1740	T1742	R1743	A1744	I1745	F1748	P1749	P1750	G1751	R1752	K1753	G1754	G1755	N1756	A1757	R1758	R1759	G1764	V1765	G1766	V1767	R1772	H1775	A1784	A1785	L1786	P1787	A1788	ALA	GLY	VAL	E1793	A1794	P1795	A1796	R1797	I1802	A1806	G1816	H1825	A1826	R1827	D1828									
X1523	X1524	X1525	X1526	X1527	X1528	X1529	X1530	X1531	X1532	X1533	X1534	X1535	X1536	X1537	X1543	X1544	X1545	X1546	X1547	X1548	X1549	X1550	X1551	X1555	X1563	E1583	R1584	K1585	R1594	L1595	L1600	V1603	M1608	V1615	GLU	THR	ARG	ARG	ALA	GLY	E1622	R1623	A1627	V1628	Q1629	Q1631	D1632									
D1207	S1210	L1211	R1212	F1213	I1216	L1219	Q1220	E1221	G1222	F1223	M1229	T1236	M1237	P1250	E1251	R1259	G1262	T1263	V1264	D1265	R1271	X1276	X1277	X1282	X1441	X1442	X1445	X1446	X1447	X1448	X1449	X1475	X1476	X1477	X1480	X1495	X1516	X1519	X1520	X1521	X1522															

V3812	L3710	X3600	X3401	X3338	X3266	X3194	X3047	X2953	K2891	GLU	Q2771
X3815	T3711	X3606	X3402	X3339	X3267	X3195	X3048	X2954	Q2892	GLU	Q2772
X3816	E3712	X3607	X3403	X3340	X3268	X3196	X3049	X2955	E2893	ARG	Q2773
L3817	X3713	X3608	X3404	X3341	X3269	X3197	X3051	X2956	L2894	THR	Q2774
		X3609	X3405	X3342	X3270	X3198	X3052	X2957	E2895	GLU	Q2775
		X3610	X3406	X3343	X3271	X3199	X3053	X2958	L2896	LVS	Q2776
D3843	D3717	X3611	X3407	X3344	X3272	X3200	X3057	X2959	A2897	LVS	Q2777
	Y3720	X3612	X3408	X3345	X3273			X2960	K2897	THR	Q2778
		X3613	X3409	X3346	X3274			X2961	Q2898	ARG	
	A3726		X3410	X3347	X3275	X3203		X2962	Q2899	LVS	E2779
D3727	D3727		X3411	X3348	X3276	X3204	X3060	X2963	Q2900	ILE	E2780
	S3732		X3412	X3349	X3277	X3205	X3061	X2964	T2901	SER	
C3733	C3733		X3413	X3350	X3278	X3206	X3062		H2902	GLN	V2781
H3734	H3734	L3641	X3414	X3351	X3279	X3207	X3063	X2968	P2903	THR	D2782
C3857	C3857	L3642	X3415	X3352	X3280	X3208	X3134	X2969	L2904	ALA	E2783
C3858	C3858	L3644	X3416	X3353	X3281	X3209	X3135	X2970	L2905	GLN	E2784
V3859	V3736		X3417	X3354	X3282	X3210	X3136		V2906	TVR	L2785
N3860	E3737	H3647		X3355	X3283	X3211	X3137	X2973	Q2907	ASP	K2786
E3861	E3738	R3648	X3421	X3356	X3284	X3212	X3138	X2974	P2908	PRD	T2787
E3862	G3739	A3649	X3422	X3357	X3285	X3213	X3139	X2975	D2909	ARG	H2788
C3863	E3740		X3433	X3358	X3286	X3214	X3140	X2976	T2910	GLU	P2789
T3864	X3741		X3434	X3359	X3287	X3215	X3141	X2995	L2911	THR	L2791
V3865	GLY	K3658	X3435	X3360	X3288	X3216	X3142	X2996	T2912	TVR	R2792
V3866	GLU	A3659	X3436	X3361	X3289	X3217	X3143	X2997	A2913	ASP	P2793
L3866	ALA	A3660		X3362	X3290	X3218	X3144	X2998	K2914	THR	V2794
N3867	T3662	V3661	X3439	X3363	X3291	X3219	X3145	X2999	E2915	GLY	P2855
N3868	L3663	L3663	X3440	X3364	X3292	X3220		X3000	K2916		P2857
			X3441	X3365	X3293	X3221		X3001	A2917		Q2858
Q3869	E3747	X3556	X3442	X3366	X3294	X3222	X3148	X3002	R2918		P2859
L3870	E3748	X3557	X3443	X3367	X3295	X3223	X3149		D2919		P2860
C3871	V3749	X3558		X3368	X3296		X3150		K2920		D2861
E3872	E3750	X3559		X3369	X3297	X3226	X3151	X3014	E2921		L2862
K3873	V3751	X3560			X3298	X3227	X3156	X3015	K2922		S2863
	S3752		X3450	X3373	X3299	X3228	X3157	X3016	L2923		G2864
	F3753		X3451	X3374	X3300	X3229	X3158		Q2924		V2865
	E3754		X3452	X3375	X3301	X3230	X3159		E2925		T2866
	E3755		X3453	X3376	X3302	X3231	X3160		L2926		L2867
	K3756		X3454	X3377	X3303	X3232	X3161		Q2872		S2868
	E3757	D3675	X3455	X3378	X3304	X3233	X3162		R2869		T2804
	M3758	D3676	X3456	X3379		X3234	X3163		Q2870		E2803
	E3759		X3457	X3380		X3235	X3164		L2871		V2805
	K3760		X3458	X3381		X3236	X3165		X2872		R2806
	Q3761		X3459	X3382		X3237	X3166		A2873		Q2807
	R3762			X3383		X3238	X3167		M2874		P2808
			X3463	X3384		X3239	X3168		A2875		L2809
	Q3766		X3464	X3385		X3240	X3169		E2876		K2810
	Q3767		X3465	X3386		X3241	X3170		Q2877		E2811
	S3768		X3466	X3387		X3242	X3171		M2878		S2812
	R3769		X3467	X3388		X3243	X3172		L2879		L2813
	L3770		X3468	X3389		X3244	X3173		Q2880		K2814
	L3771		X3469	X3390		X3245	X3174		N2881		E2815
	H3771		X3470	X3391		X3246	X3175		Y2882		M2816
	T3772		X3471	X3392		X3247	X3176		Y2883		L2817
	R3773		X3472	X3393		X3248	X3177		H2884		A2818
			X3473	X3394		X3249	X3178		Y2885		Q2819
	Q3779		X3474	X3395		X3250	X3179		W2886		W2821
	L3780		X3475	X3396		X3251	X3180		G2887		T2822
			X3476	X3397		X3252	X3181		K2888		E2823
	L3805		X3477	X3398		X3253	X3182		K2889		E2824
	N3806		X3478	X3399		X3254	X3183		K2890		K2825
			X3479	X3400		X3255	X3184				A2826
			X3480			X3256	X3185				E2827
			X3481			X3257	X3186				E2828
			X3482			X3258	X3187				Q2829
			X3483			X3259	X3188				E2830
			X3484			X3260	X3189				
			X3485			X3261	X3190				
			X3486			X3262	X3191				
			X3487			X3263	X3192				
			X3488			X3264	X3193				
			X3489			X3265					
			X3490								
			X3491								
			X3492								
			X3493								
			X3494								



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	55564	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.076	Depositor
Minimum map value	-0.043	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.025	Depositor
Map size (Å)	502.0, 502.0, 502.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.255, 1.255, 1.255	Depositor

5 Model quality

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	0.20	0/834	0.46	0/1123
1	F	0.20	0/834	0.46	0/1123
1	H	0.20	0/834	0.46	0/1123
1	J	0.21	0/834	0.46	0/1123
2	B	0.23	0/25428	0.53	7/34534 (0.0%)
2	E	0.23	0/25428	0.53	7/34534 (0.0%)
2	G	0.23	0/25428	0.53	7/34534 (0.0%)
2	I	0.23	0/25428	0.54	8/34534 (0.0%)
All	All	0.23	0/105048	0.53	29/142628 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	F	0	1
1	H	0	1
1	J	0	1
2	B	0	14
2	E	0	14
2	G	0	14
2	I	0	14
All	All	0	60

There are no bond length outliers.

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	2190	VAL	N-CA-C	-8.75	104.21	112.96
2	I	2190	VAL	N-CA-C	-8.75	104.21	112.96
2	G	2190	VAL	N-CA-C	-8.75	104.21	112.96
2	B	2190	VAL	N-CA-C	-8.72	104.24	112.96
2	I	2242	ILE	N-CA-C	6.02	112.66	106.21

There are no chirality outliers.

5 of 60 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	8	SER	Peptide
2	B	139	GLU	Peptide
1	F	8	SER	Peptide
1	H	8	SER	Peptide
1	J	8	SER	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	818	0	824	11	0
1	F	818	0	824	12	0
1	H	818	0	824	9	0
1	J	818	0	824	11	0
2	B	29499	0	24757	276	0
2	E	29499	0	24757	274	0
2	G	29499	0	24757	265	0
2	I	29499	0	24757	270	0
3	B	1	0	0	0	0
3	E	1	0	0	0	0
3	G	1	0	0	0	0
3	I	1	0	0	0	0
All	All	121272	0	102324	1096	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 5.

The worst 5 of 1096 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:2291:GLN:HB3	2:G:2294:ASP:H	1.51	0.76
2:E:2291:GLN:HB3	2:E:2294:ASP:H	1.51	0.76
2:B:2291:GLN:HB3	2:B:2294:ASP:H	1.51	0.75
2:I:2291:GLN:HB3	2:I:2294:ASP:H	1.51	0.74
2:G:4673:ARG:HH22	2:G:4698:LYS:HB2	1.57	0.70

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	105/108 (97%)	97 (92%)	8 (8%)	0	100	100
1	F	105/108 (97%)	97 (92%)	8 (8%)	0	100	100
1	H	105/108 (97%)	97 (92%)	8 (8%)	0	100	100
1	J	105/108 (97%)	97 (92%)	8 (8%)	0	100	100
2	B	3235/4416 (73%)	2891 (89%)	337 (10%)	7 (0%)	43	77
2	E	3235/4416 (73%)	2893 (89%)	335 (10%)	7 (0%)	43	77
2	G	3235/4416 (73%)	2891 (89%)	337 (10%)	7 (0%)	43	77
2	I	3235/4416 (73%)	2893 (89%)	335 (10%)	7 (0%)	43	77
All	All	13360/18096 (74%)	11956 (90%)	1376 (10%)	28 (0%)	44	77

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	1708	ARG
2	B	1932	PRO
2	E	1708	ARG
2	E	1932	PRO
2	I	1708	ARG

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	88/89 (99%)	88 (100%)	0	100	100
1	F	88/89 (99%)	88 (100%)	0	100	100
1	H	88/89 (99%)	88 (100%)	0	100	100
1	J	88/89 (99%)	88 (100%)	0	100	100
2	B	2493/3022 (82%)	2483 (100%)	10 (0%)	84	82
2	E	2493/3022 (82%)	2483 (100%)	10 (0%)	84	82
2	G	2493/3022 (82%)	2483 (100%)	10 (0%)	84	82
2	I	2493/3022 (82%)	2483 (100%)	10 (0%)	84	82
All	All	10324/12444 (83%)	10284 (100%)	40 (0%)	81	82

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	I	4983	HIS
2	G	3663	LEU
2	I	4985	LEU
2	G	1600	LEU
2	G	4959	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 180 such sidechains are listed below:

Mol	Chain	Res	Type
2	I	2127	GLN
2	G	379	HIS
2	I	3704	HIS
2	I	4102	GLN
2	G	1598	GLN

5.3.3 RNA ⓘ

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](#)

The following chains have linkage breaks:

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

The worst 5 of 56 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	4345:UNK	C	4540:PHE	N	74.04
1	E	4345:UNK	C	4540:PHE	N	74.04
1	I	4345:UNK	C	4540:PHE	N	74.04
1	G	4345:UNK	C	4540:PHE	N	74.04

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	3613:UNK	C	3639:THR	N	46.14

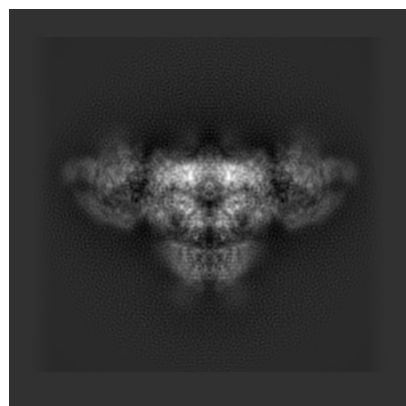
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8395. These allow visual inspection of the internal detail of the map and identification of artifacts.

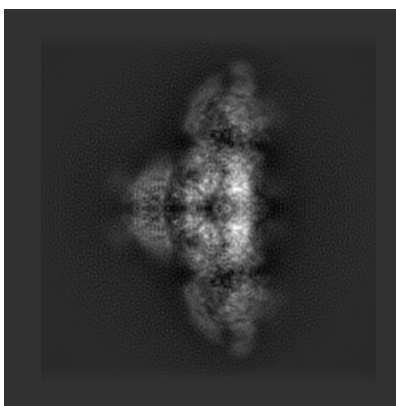
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

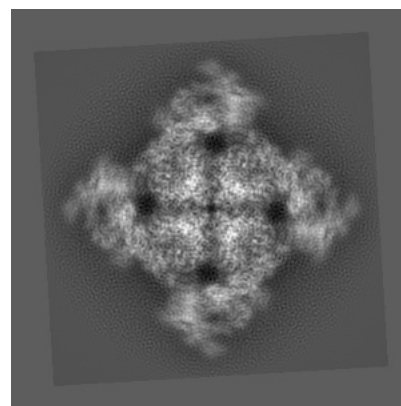
6.1.1 Primary map



X

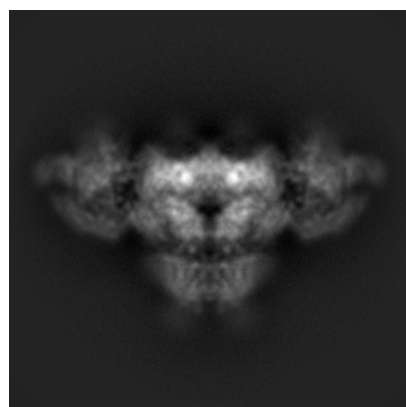


Y

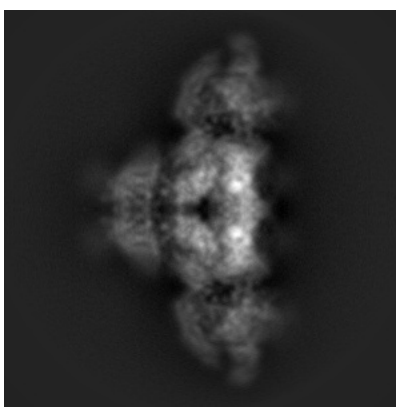


Z

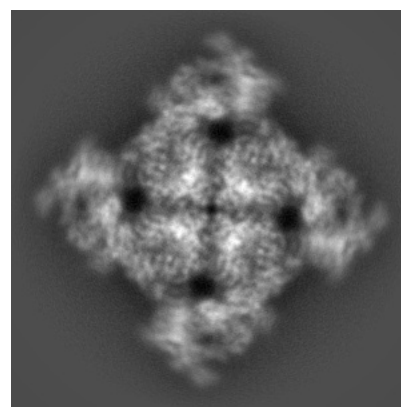
6.1.2 Raw map



X



Y

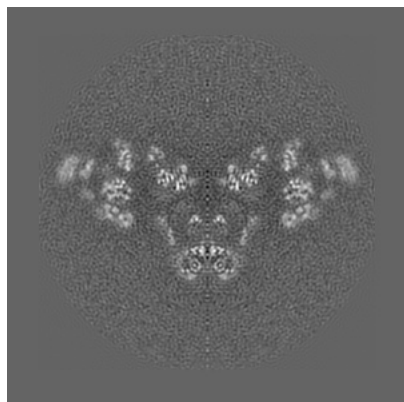


Z

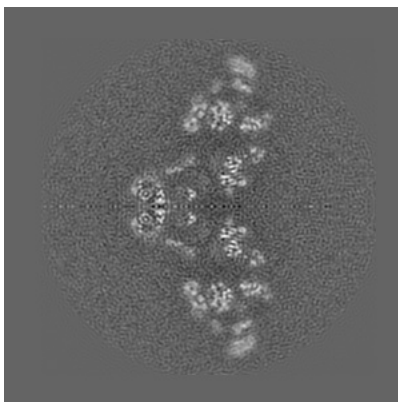
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

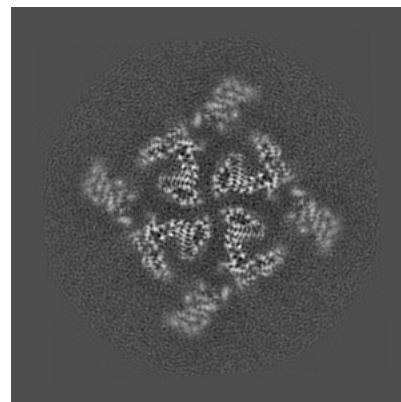
6.2.1 Primary map



X Index: 200

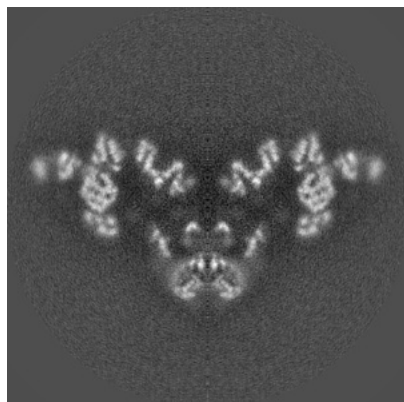


Y Index: 200

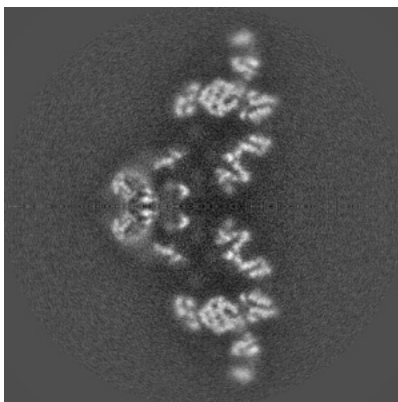


Z Index: 200

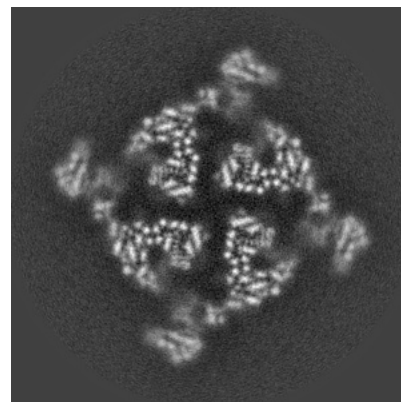
6.2.2 Raw map



X Index: 168



Y Index: 168

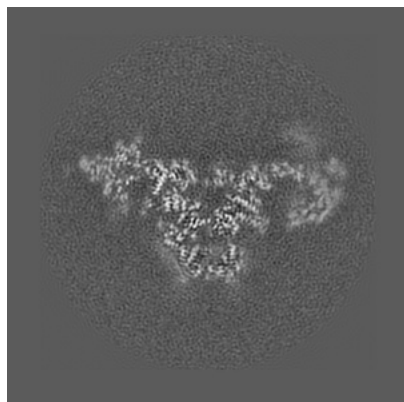


Z Index: 168

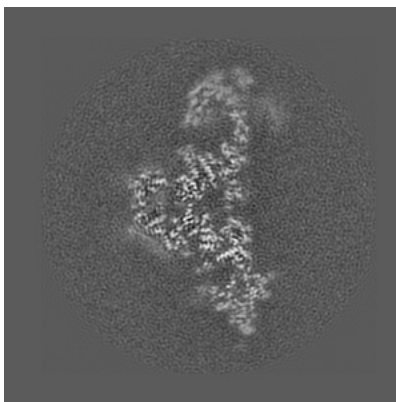
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

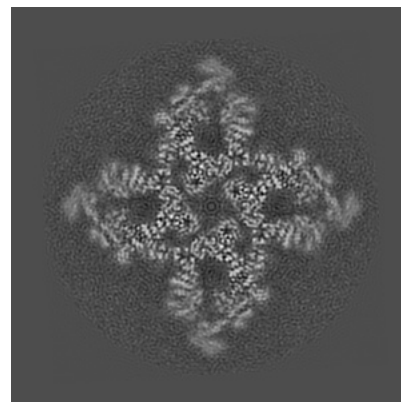
6.3.1 Primary map



X Index: 217

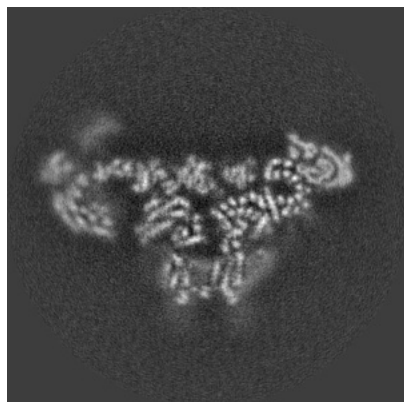


Y Index: 183

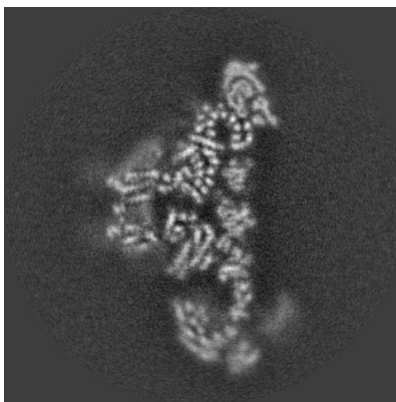


Z Index: 232

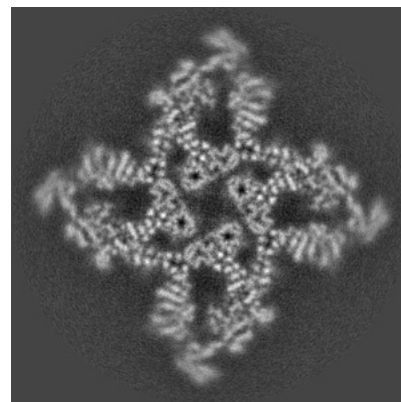
6.3.2 Raw map



X Index: 147



Y Index: 189

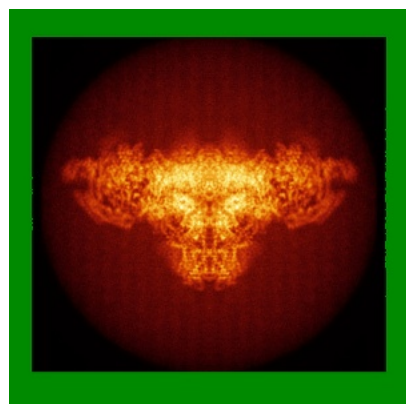


Z Index: 195

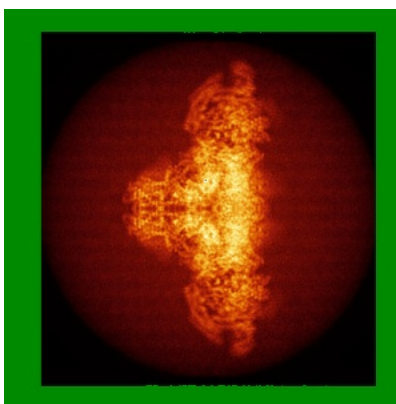
The images above show the largest variance slices of the map in three orthogonal directions.

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

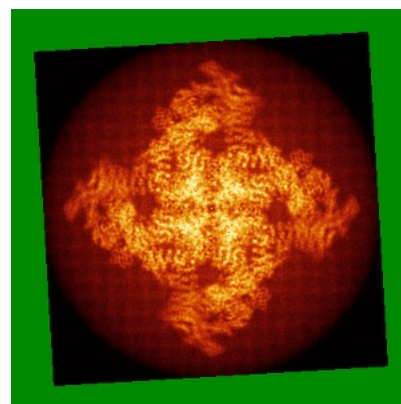
6.4.1 Primary map



X

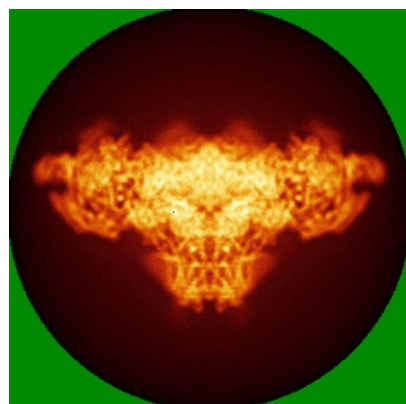


Y

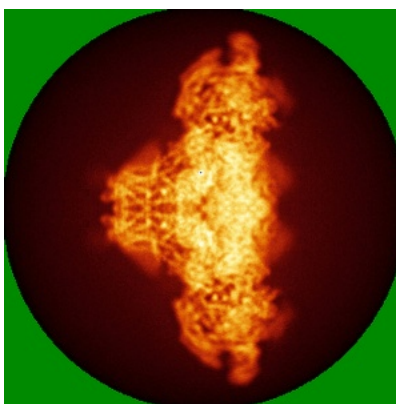


Z

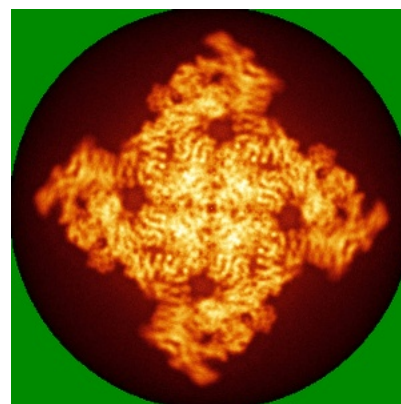
6.4.2 Raw map



X



Y

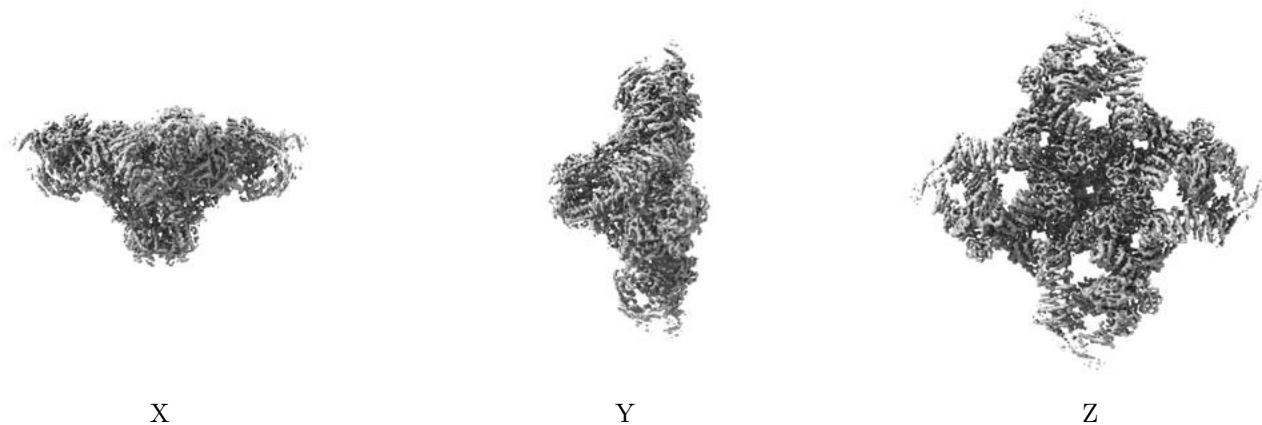


Z

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

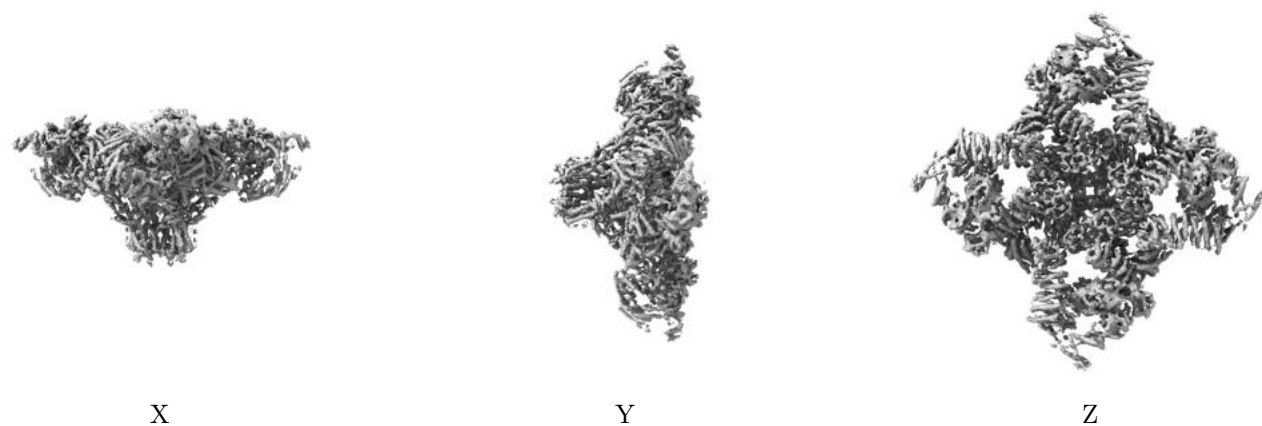
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

6.5.2 Raw map



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

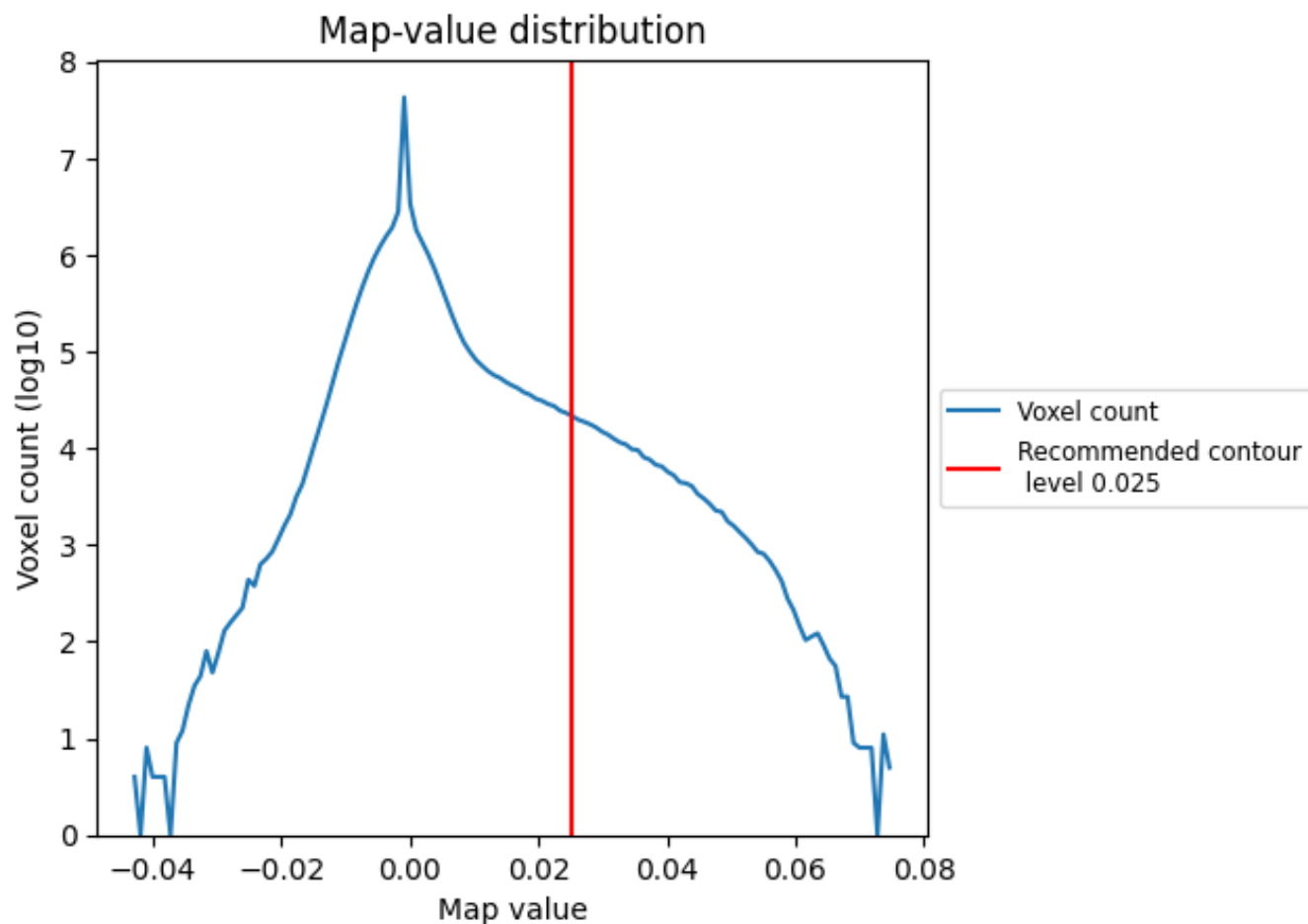
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

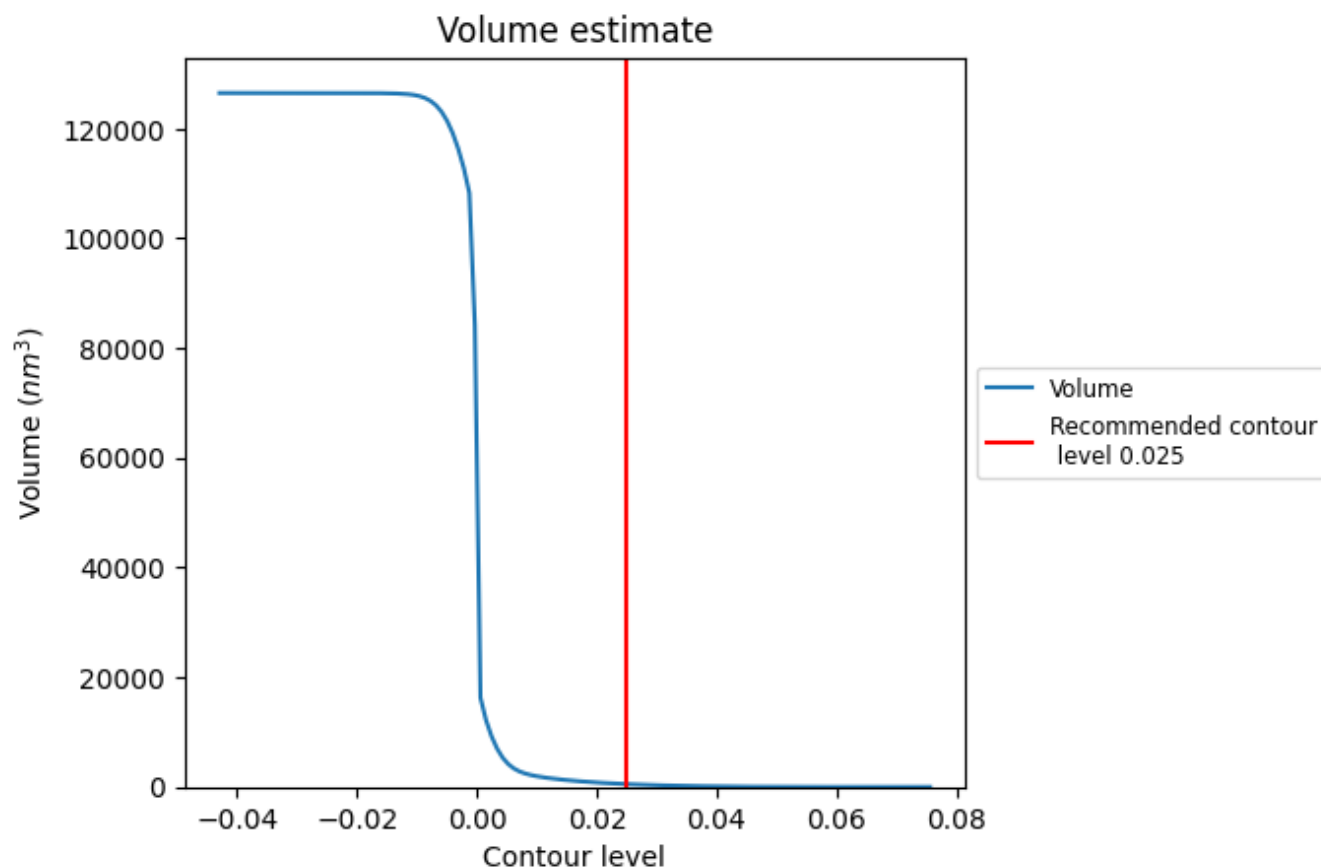
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

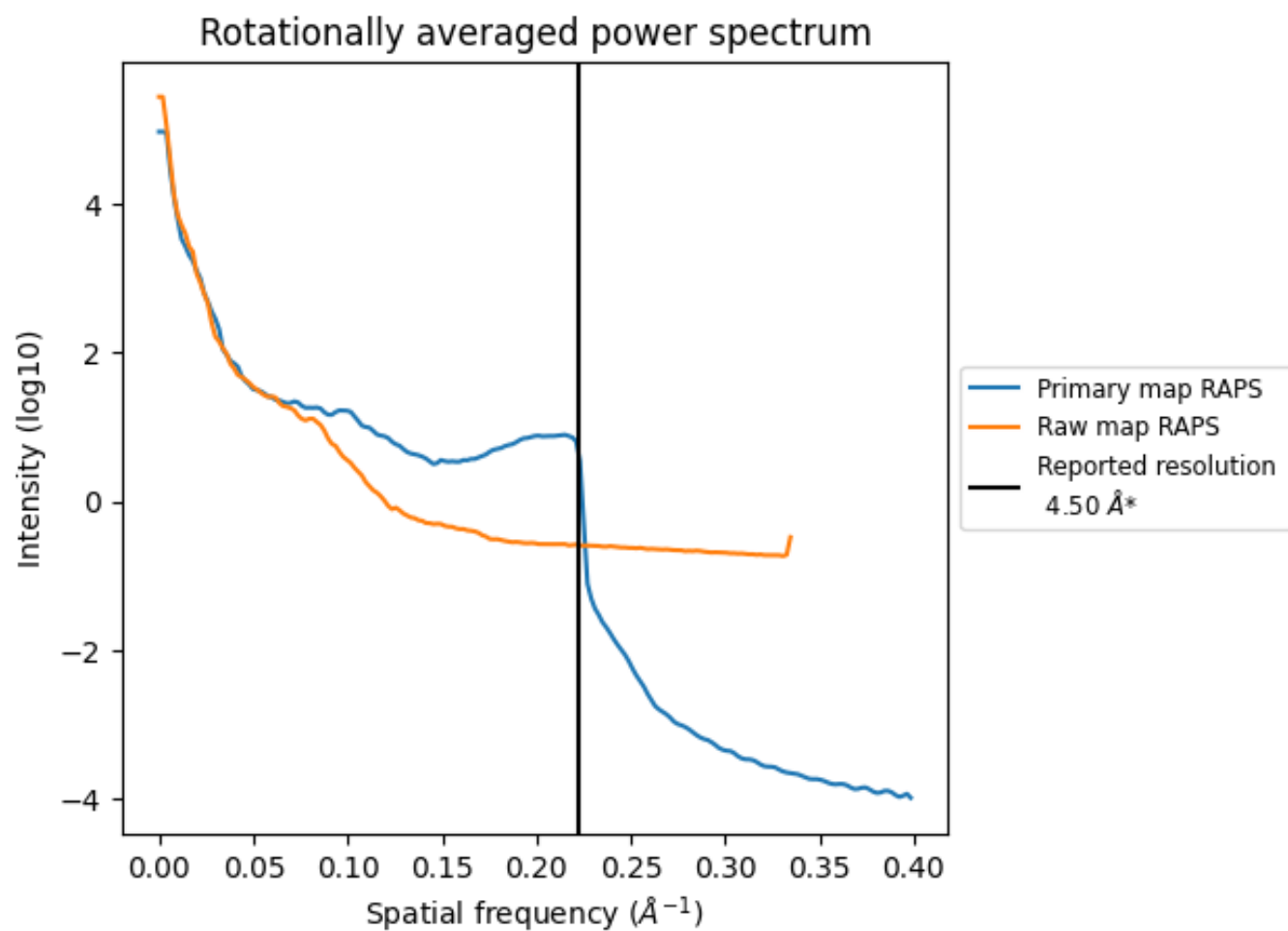
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 516 nm^3 ; this corresponds to an approximate mass of 466 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 ⓘ

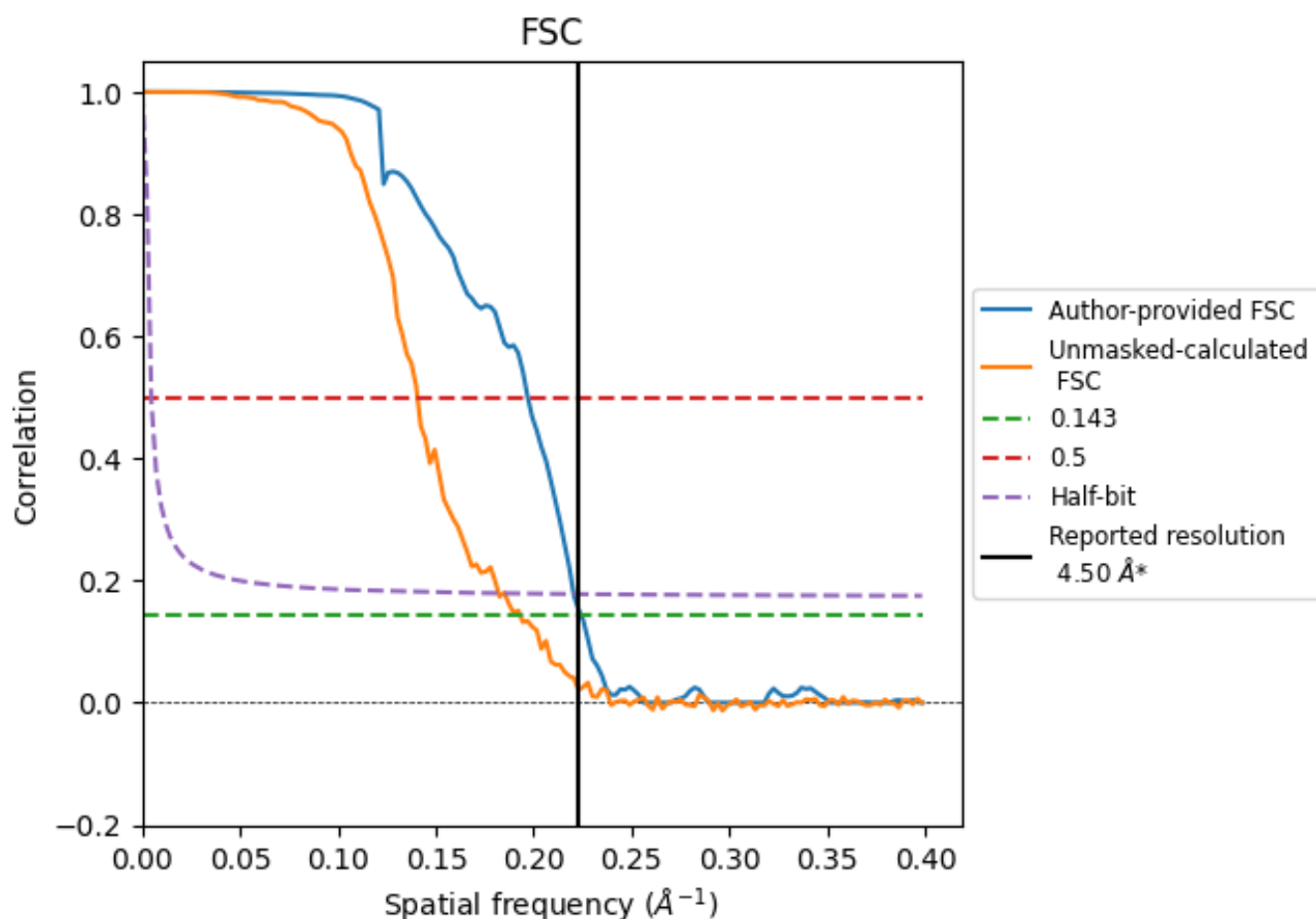


*Reported resolution corresponds to spatial frequency of 0.222 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.222 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

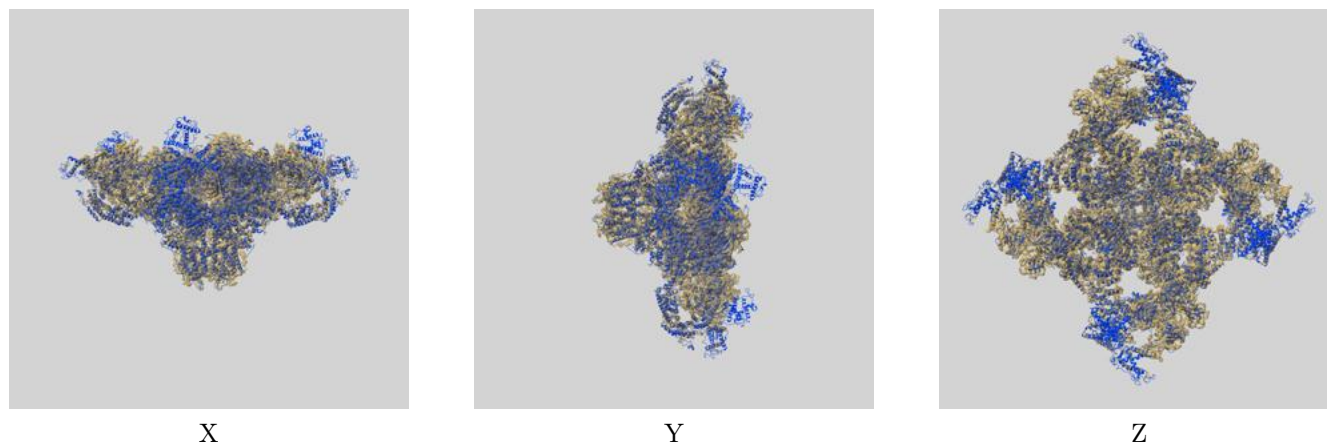
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.50	-	-
Author-provided FSC curve	4.46	5.08	4.54
Unmasked-calculated*	5.18	7.11	5.49

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.18 differs from the reported value 4.5 by more than 10 %

9 Map-model fit [i](#)

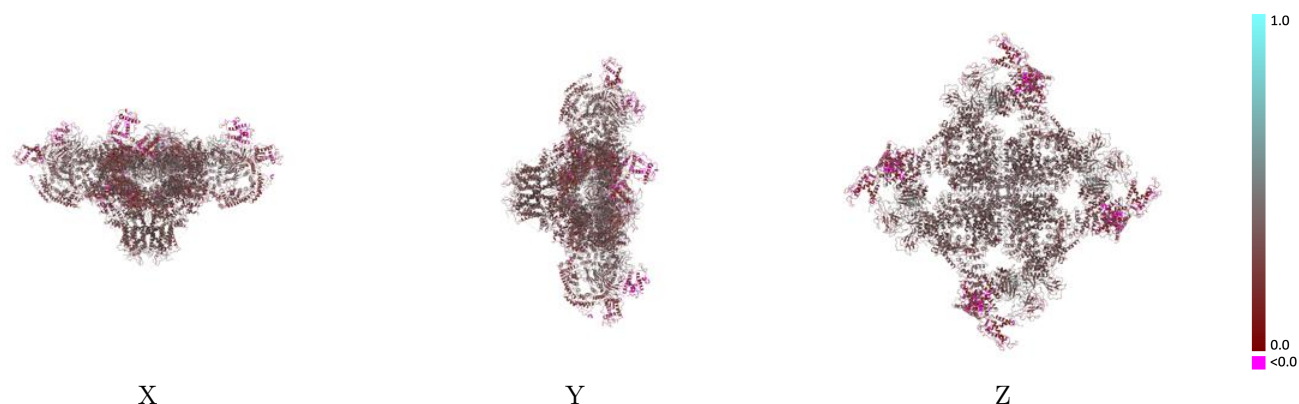
This section contains information regarding the fit between EMDB map EMD-8395 and PDB model 5TB4. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



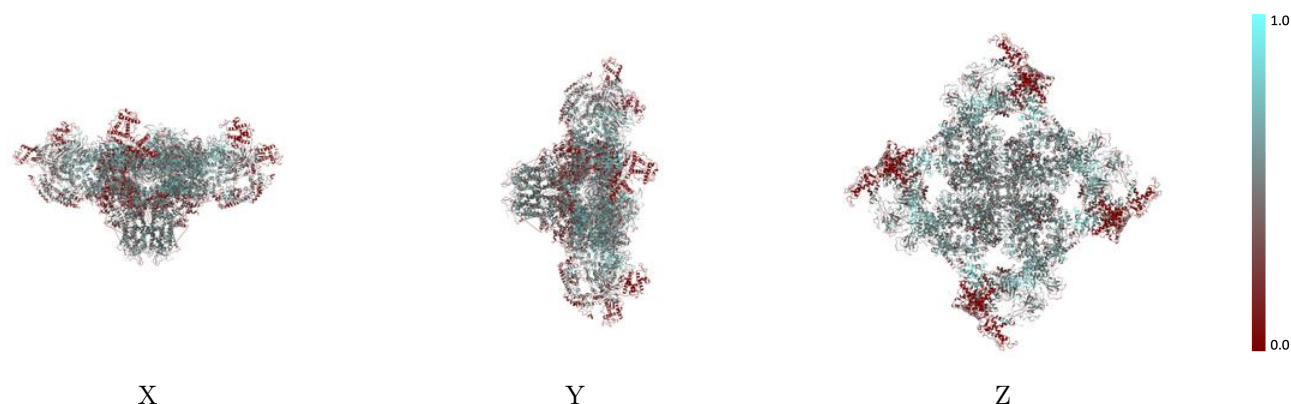
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



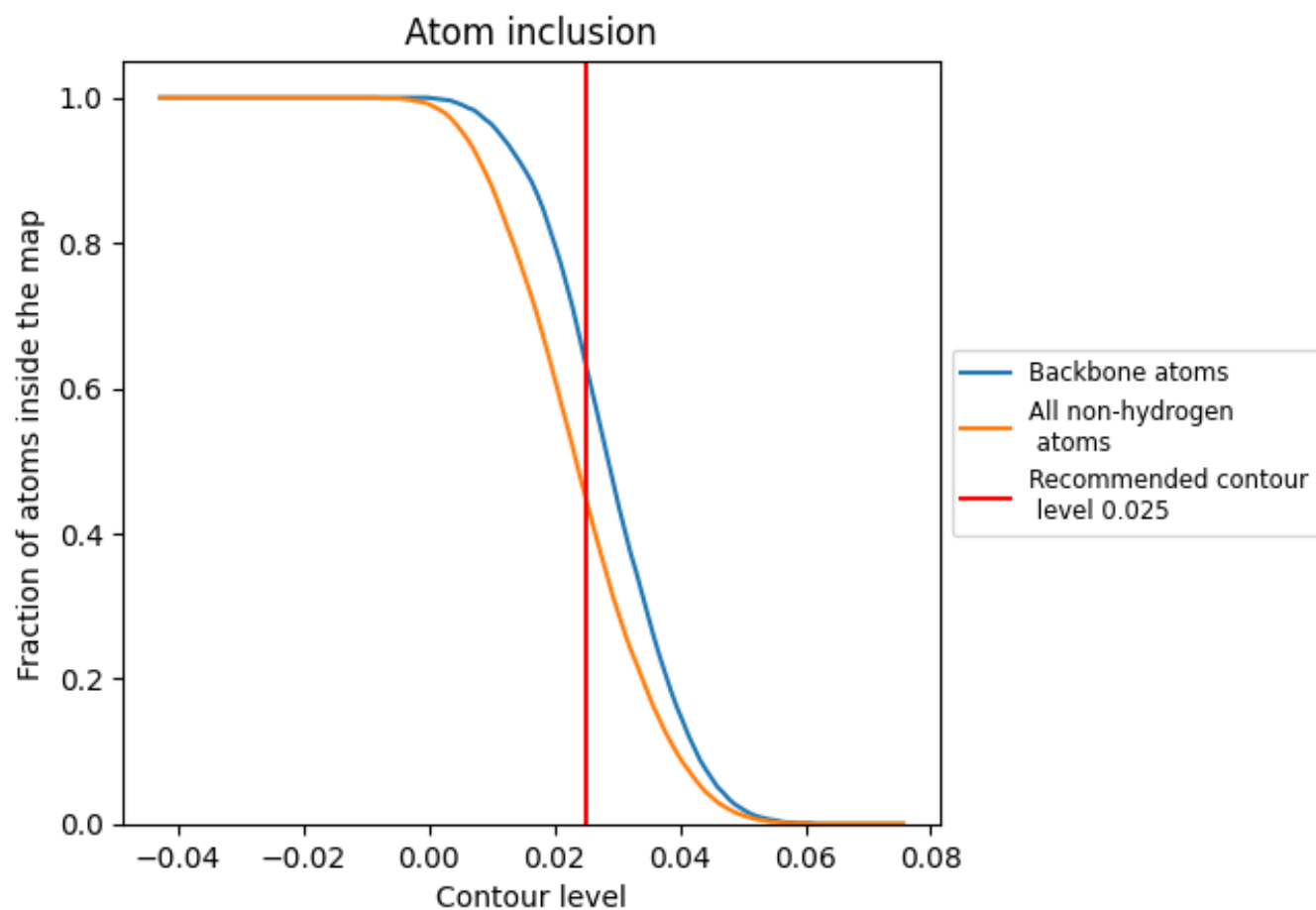
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.025).

9.4 Atom inclusion [i](#)



At the recommended contour level, 63% of all backbone atoms, 45% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4480	0.3170
A	0.4810	0.3380
B	0.4470	0.3160
E	0.4470	0.3160
F	0.4740	0.3420
G	0.4470	0.3160
H	0.4790	0.3410
I	0.4470	0.3160
J	0.4800	0.3400

1.0

0.0

<0.0