



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:02 PM UTC

PDB ID : 5TB0 / pdb_00005tb0
EMDB ID : EMD-8391
Title : Structure of rabbit RyR1 (EGTA-only dataset, all particles)
Authors : Clarke, O.B.; des Georges, A.; Zalk, R.; Marks, A.R.; Hendrickson, W.A.;
Frank, J.
Deposited on : 2016-09-10
Resolution : 4.40 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:

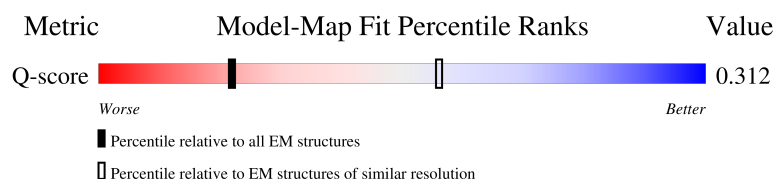
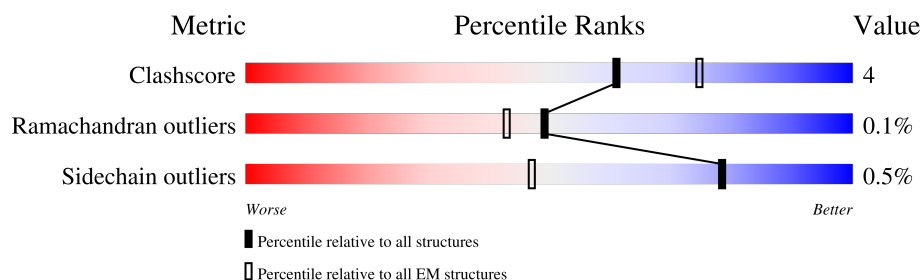
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.40 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	3132 (3.91 - 4.90)

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	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	B	4416	52% 85% 10% 5%
2	E	4416	52% 85% 10% 5%
2	G	4416	51% 84% 10% 5%
2	I	4416	52% 84% 10% 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	G	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		

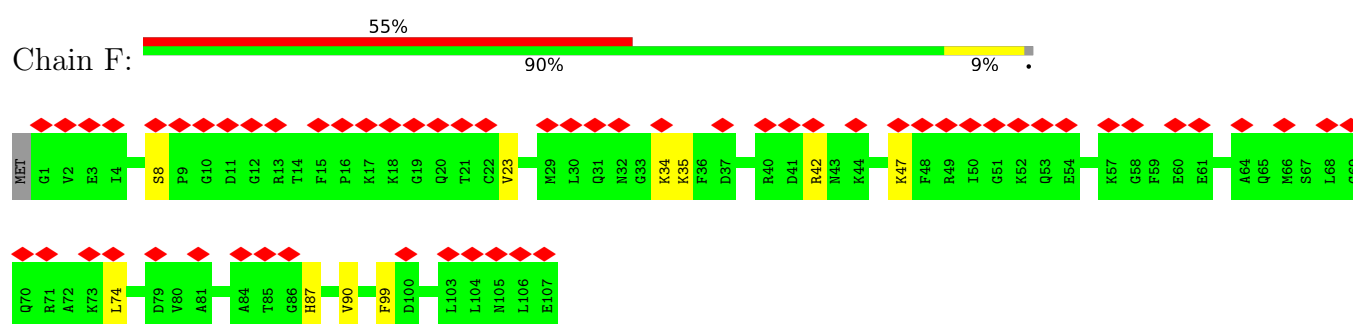
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

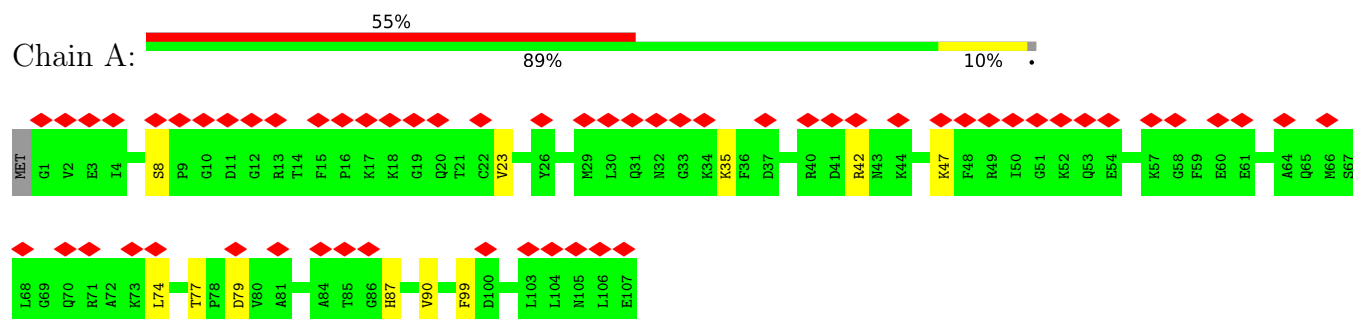
3 Residue-property plots [i](#)

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.

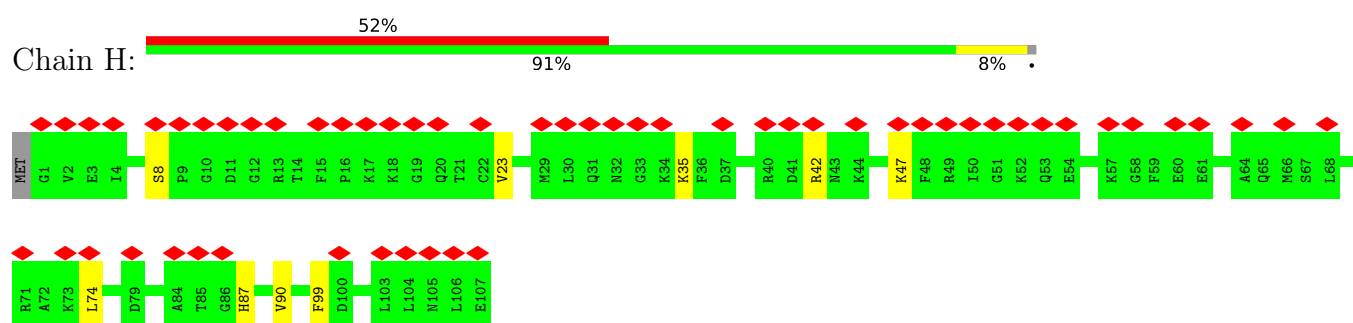
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



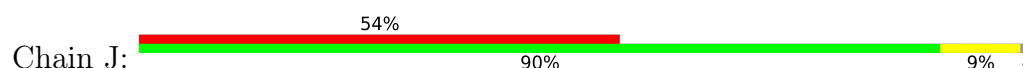
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

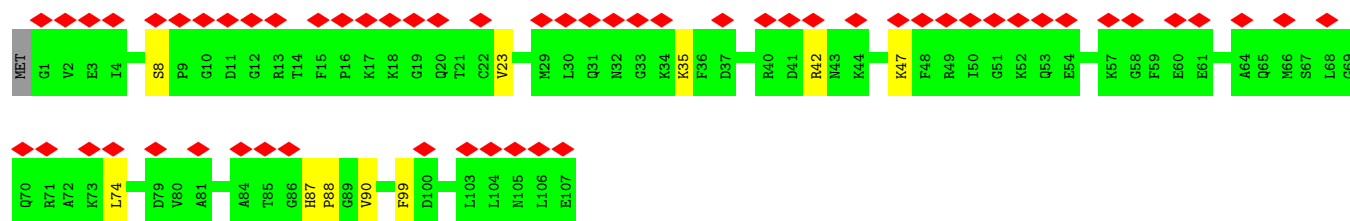


- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



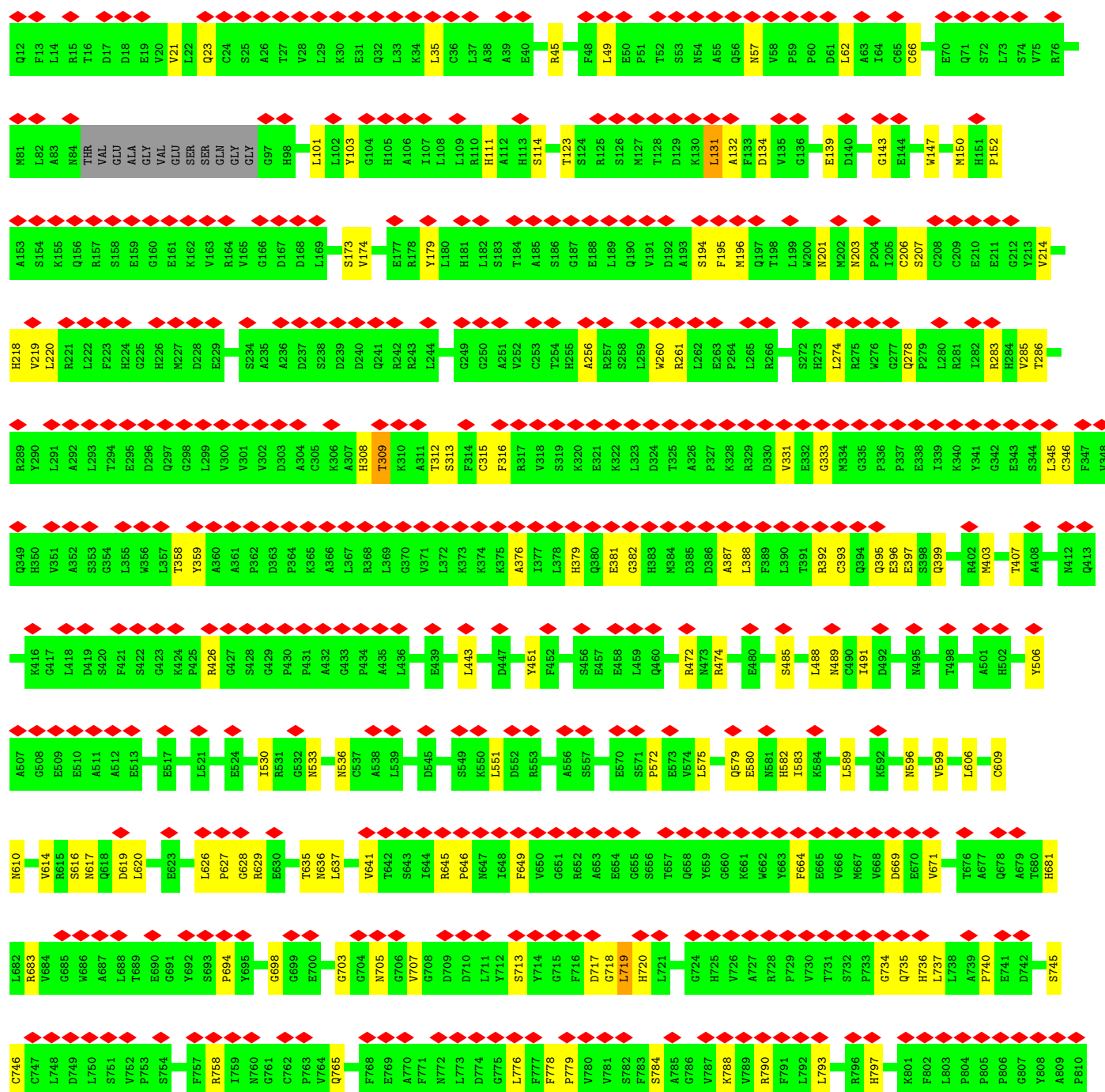
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B





• Molecule 2: Ryanodine receptor 1

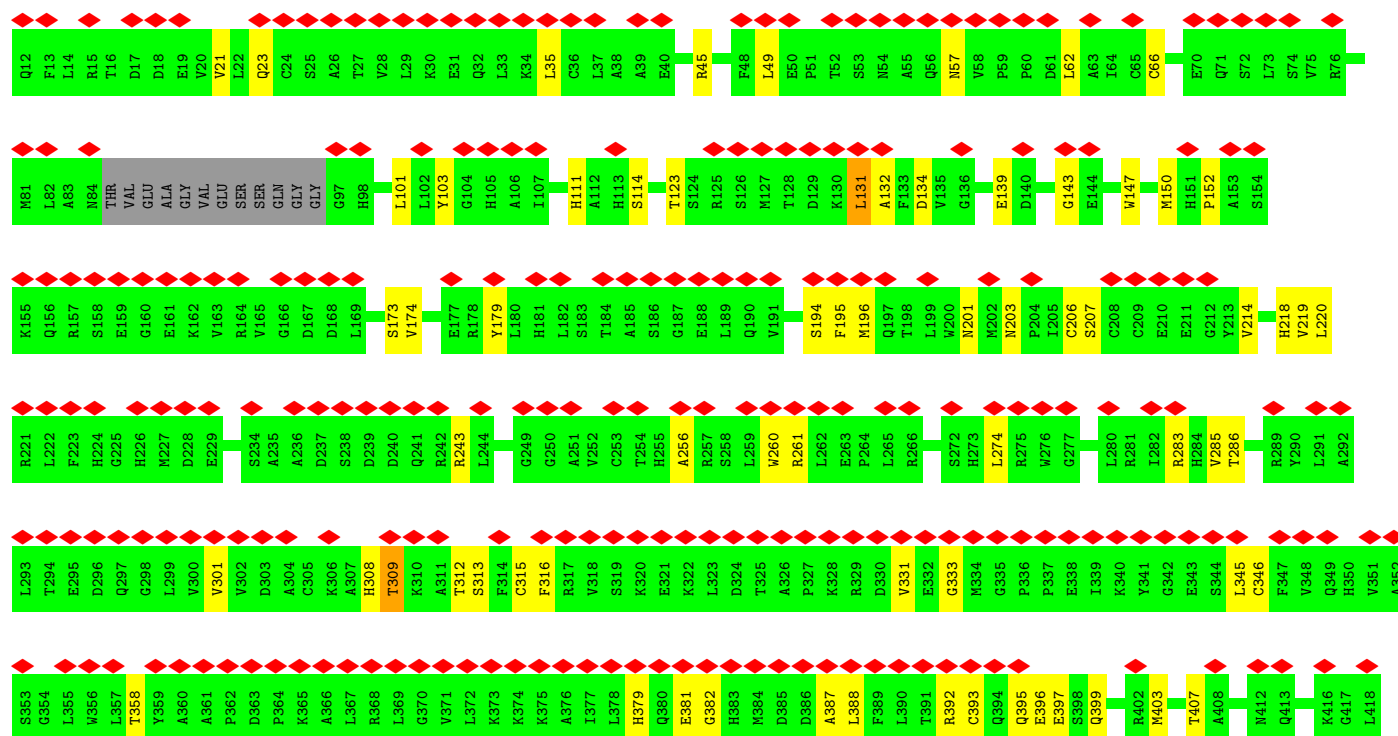
Chain B: 52% 85% 10% 5%





L2911	T2912	A2913	K2914	E2915	K2916	A2917	Q2858	P2857	Q2858	P2859	D2860	D2861	L2862	S2863	G2864	V2865	T2866	L2867	R2868	R2869	E2870	L2871	E2811	S2812	L2813	K2814	A2815	E2816	L2817	A2818	W2819	E2820	Y2821	H2822	N2884	T2885	W2886	G2887	R2888	K2889	K2890	K2891	G2892	E2893	L2894	E2895	A2896	K2897	G2898	G2899	G2900	T2901	H2902	P2903	L2904	L2905	K2967	K2968	K2969	D2908	D2909	K2971	K2972
L2791	R2792	P2793	Y2794	T2796	F2797	S2798	E2799	K2800	D2801	K2802	E2803	L2804	T2805	R2806	W2807	P2808	L2809	K2810	E2811	S2812	L2813	K2814	A2815	E2816	L2817	A2818	W2819	E2820	Y2821	T2822	L2823	K2824	K2825	A2826	R2827	E2828	G2829	E2830	GLU	GLU	ARG	THR	GLU	LYS	LYS	LYS	THR	ARG	LYS	ILE	SER	GLN	THR	ALA	GLN	THR	THR	TVR	ASP				
PRO	ARG	GLU	GLY	Y2855	N2856	P2857	Q2858	P2859	D2860	D2861	L2862	S2863	G2864	V2865	T2866	L2867	R2868	R2869	E2870	L2871	E2811	S2812	L2813	K2814	A2815	E2816	L2817	A2818	W2819	E2820	Y2821	T2822	L2823	K2824	K2825	A2826	R2827	E2828	G2829	E2830	GLU	GLU	ARG	THR	GLU	LYS	LYS	LYS	THR	ARG	LYS	ILE	SER	GLN	THR	ALA	GLN	THR	THR	TVR	ASP		
L2159	T2162	L2166	L2167	Q2173	L2177	N2187	N2188	K2189	Q2193	D2194	L2195	R2199	M2208	E2209	N2213	G2216	Q2217	G2218	E2219	T2220	K2221	E2222	L2223	P2226	V2229	R2234	F2235	L2236	N2246	F2251	D2252	H2253	Y2256	E2259	G2262	T2263	G2264	G2266	M2267	Q2268	G2269	S2270																					
GLU	GLU	PRO	GLU	GLU	GLU	THR	SER	LEU	SER	SER	ARG	LEU	ARG	SER	LEU	LEU	THR	VAL	ARG	LEU	VAL	LYS	LYS	GLU	LYS	PRO	GLU	GLU	LEU	PRO	ALA	GLU	GLU	K2089	K2090	Q2095	E2096	V2102	V2103	R2104	L2124	Q2127	L2131	T2143	S2147	E2150																	
T1985	M1986	S1987	A1988	A1989	E1990	T1991	A1992	R1993	R1994	T1995	R1996	E1997	F1998	R1999	S2000	P2001	F2002	Q2003	E2004	Q2005	T2006	N2007	L2010	H2011	F2012	K2013	D2014	E2015	A2016	D2017	E2018	E2019	D2020	C2021	F2022	L2023	F2024	E2025	D2026	I2027	R2028	Q2029	D2030	L2031	Q2032	D2033	A2040	H2041	C2042	G2043	T2044	Q2045	L2046	E2047	G2048	GLU	GLU						





X1443	X1444	X1445	X1446	X1447	X1448	X1449	X1450	X1455	X1456	X1457	X1458	X1459	X1460	X1468	X1475	X1476	X1477	X1478	X1479	X1480	X1481	X1482	X1483	X1487	X1490	X1491	X1495	X1496	X1497	X1502	X1505	X1510	X1513	X1514	X1515	X1516	X1517	X1518	X1519	X1520	X1521	X1522	X1523	X1524	X1525	X1526	X1527	X1528	X1529									
Q1220	E1221	A1227	I1228	N1229	M1230	Q1231	W1237	Q1244	E1251	H1252	P1253	H1254	Y1255	E1256	R1259	M1260	D1261	G1262	T1263	V1264	D1265	T1266	P1267	P1268	C1269	L1270	R1271	L1272	A1273	X1276	X1277	X1278	X1279	X1280	X1283	X1284	X1285	X1292	X1430	X1431	X1434	X1437	X1438	X1439	X1440	X1441	X1442											
S1136	E1137	S1145	G1146	D1147	G1150	C1151	M1152	L1155	T1156	E1157	I1161	F1162	T1163	E1167	M1170	S1171	D1172	S1173	G1174	S1175	E1176	T1177	A1178	F1179	R1180	E1181	I1182	E1183	D1186	L1194	G1195	Q1198	V1199	G1200	H1201	L1202	M1203	L1204	G1205	Q1206	D1207	S1210	L1211	R1212	F1213	F1214	A1215	I1216	C1217									
VAL	GLU	ASN	GLN	SER	ARG	TRP	D1070	R1071	V1072	R1073	R1076	A1077	E1078	K1079	S1085	G1086	R1087	W1088	Y1089	E1093	A1094	V1095	T1096	T1097	A1098	E1099	M1100	R1101	V1102	G1103	P1107	E1108	L1109	D1112	L1115	G1116	A1117	D1118	E1119	L1120	V1123	F1124	N1125	G1126	H1127	R1128	G1129	Q1130	R1131	L1134	G1135							
Q1003	G1004	W1005	S1006	Y1007	A1008	A1009	VAL	GLN	ASP	ILE	PRO	ALA	ARG	ASN	PRO	R1020	L1021	V1022	P1023	Y1024	R1025	L1026	L1027	D1028	E1029	A1030	T1031	K1032	R1033	S1034	M1035	R1036	D1037	S1038	L1039	C1040	Q1041	A1042	V1043	R1044	T1045	L1046	L1047	G1048	Y1049	G1050	Y1051	N1052	I1053	E1054	PRO	PRO	ASP	GLN	GLU	PRO	SER	GLN
G940	W941	A942	D943	E944	K945	A946	E947	D948	N949	L950	K951	K952	K954	L955	P956	K957	T958	Y959	M960	N961	S962	N963	G964	Y965	K966	P967	A968	P969	L970	D971	L972	S973	H974	V975	R976	L977	T978	P979	A980	Q981	T982	T983	L984	V985	D986	R987	L988	A989	E990	N991	G992	A997	R998	D999	V1001	A1002		
E880	L881	W882	A883	L884	T885	R886	T887	E888	Q889	G890	W891	T892	W893	G894	P895	W896	R897	D898	D899	N900	K901	R902	L903	H904	P905	C906	L907	V908	N909	F910	H911	S912	C854	P855	V856	D857	THR	VAL	GLN	L861	V862	L863	P864	P865	H866	L867	R868	T870	R871	E872	K873	L874	A875	E876	N877	T878	H879	
L748	D749	L750	S751	V752	P753	S754	F757	R758	I759	N760	G761	G762	F763	V764	Q765	F768	E769	A770	F771	G773	D774	G775	L776	F777	F778	P779	W780	W781	S784	A785	G786	W787	K788	W789	R790	F791	L792	L793	R796	K801	F802	L803	P804	P805	T806	R807	Q808	E741	D742	S745	C746	E813						
V684	G685	W686	A687	L688	T689	E690	G691	Y692	S693	P694	Y695	G698	G699	E700	G703	G704	N705	G706	V707	D708	D710	L711	W712	S713	Y714	G715	F716	D717	G718	L719	H720	L721	G724	W725	V726	K661	W662	Y663	F664	E665	V666	M667	V668	D669	E670	V671	T676	A677	Q678	A679	T680	H681	L682	R683				
D419	S420	F421	S422	G423	K424	P425	R426	G427	S428	G429	P430	P431	A432	G433	P434	A435	L436	E439	L443	D447	Y451	F452	S456	E457	E458	L459	Q460	S470	L471	R472	M473	R474	E480	S485	L488	M489	C490	L491	D492	H495	T498	A501	H502	Y506	A507	G508												



X3548	X3439	X3377	X3186	X3050	X2972	T2910	ASP	M2790	X2700	X2640
X3549	X3440	X3378	X3187	X3051	X2973	L2911	PRO	L2791	X2701	X2641
X3550	X3441	X3379	X3188	X3052	X2974	T2912	ARG	R2792	X2702	X2642
X3551	X3442	X3380	X3189	X3053	X2975	A2913	GLU	P2793	X2703	X2643
X3552	X3443	X3381	X3190	X3054	X2976	A2914	GLY	Y2794	X2704	X2644
X3553	X3446	X3382	X3191	X3055	X2976	E2915		K2795	X2705	X2645
X3554	X3447	X3383	X3192	X3056	X2976	E2916		T2796	F2796	X2646
X3555	X3448	X3384	X3193	X3057	X2976	A2917		P2797	D2796	X2647
X3556	X3449	X3385	X3194	X3058	X2976	E2918		P2798	P2737	X2648
X3557	X3450	X3386	X3195	X3059	X2976	D2919		P2799	P2738	X2649
X3558		X3387	X3196	X3060	X3000	R2920		R2800	P2739	X2650
X3559		X3388	X3197	X3061	X3001	E2921		D2801	V2740	X2651
X3560	X3453	X3389	X3198	X3062	X3002	R2922		L2862	E2741	X2652
X3561	X3454	X3390	X3199	X3063	X3003	A2923		S2863	T2742	X2653
X3562	X3455	X3391	X3200	X3063	X3003	A2923		E2803	L2743	X2654
X3563	X3456	X3392	X3201	X3134	X3004	Q2924		L2804	N2744	X2655
X3564	X3457	X3393	X3202	X3135	X3005	E2925		R2805	V2745	X2656
X3565		X3394	X3203	X3136	X3006	L2926		L2867	L2746	X2657
X3566	X3463	X3395	X3204	X3137	X3007	L2927		S2868	I2747	X2658
X3567	X3464	X3396	X3205	X3138	X3008	K2928		R2869	P2748	X2659
X3568	X3465	X3397	X3206	X3139	X3009	F2929		E2870	E2749	X2660
X3569	X3466	X3398	X3207	X3140	X3010	L2930		K2810	K2750	X2661
X3570	X3467	X3399	X3208	X3141	X3011	Q2931		E2811	L2751	X2662
X3571	X3468	X3400	X3209	X3142	X3012	M2932		S2812	D2752	X2663
X3572	X3511	X3401	X3210	X3143	X3013	R2933		L2813	S2753	X2664
X3573	X3512	X3402	X3211	X3144	X3014	G2934		K2814	F2754	X2665
X3574	X3513	X3403	X3212	X3145	X3015	Y2935		A2815	L2755	X2666
X3575	X3514	X3404	X3213	X3146	X3016	A2936		M2816	N2756	X2667
X3576	X3515	X3405	X3214	X3147	X3017	V2937		L2817	K2757	X2668
X3577	X3516	X3406	X3215	X3148	X3018	T2938		A2818	F2758	X2669
X3578	X3517	X3407	X3216	X3149	X3019	R2939		W2819	A2759	X2670
X3579	X3518	X3408	X3217	X3150	X3020	X2942		E2820	E2760	X2671
X3580	X3519	X3409	X3218	X3151	X3021	X2943		W2821	Y2761	X2672
X3581	X3520	X3410	X3219	X3152	X3022	X2944		T2822	T2762	X2673
X3582	X3521	X3411	X3220	X3153	X3023	X2945		L2823	H2763	X2674
X3583	X3522	X3412	X3221	X3154	X3024	X2946		E2824	E2764	X2675
X3584	X3523	X3413	X3222	X3155	X3025	X2947		K2825	K2765	X2676
X3585	X3524	X3414	X3223	X3156	X3026	X2948		A2826	Y2766	X2677
X3586	X3525	X3415	X3224	X3157	X3027	X2949		R2827	A2767	X2678
X3587	X3526	X3416	X3225	X3158	X3028	X2950		E2828	F2768	X2679
X3588	X3527	X3417	X3226	X3159	X3029	X2951		Q2829	T2769	X2680
X3589	X3528	X3418	X3227	X3160	X3030	X2952		E2830	K2770	X2681
X3590	X3529	X3419	X3228	X3161	X3031	X2953		GLU	I2771	X2682
X3591	X3530	X3420	X3229	X3162	X3032	X2954		ARG	Q2772	X2683
X3592	X3531	X3421	X3230	X3163	X3033	X2955		THR	N2773	X2684
X3593	X3532	X3422	X3231	X3170	X3034	X2956		GLU	N2774	X2685
X3594	X3533	X3423	X3232	X3171	X3035	X2957		LYS	W2775	X2686
X3595	X3534	X3424	X3233	X3172	X3036	X2958		LYS	S2776	X2687
X3596	X3535	X3425	X3234	X3173	X3037	X2959		THR	Y2777	X2688
X3597	X3536	X3426	X3235	X3174	X3038	X2960		ARG	G2778	X2689
X3598	X3537	X3427	X3236	X3175	X3039	X2961		LYS	E2779	X2690
X3599	X3538	X3428	X3237	X3176	X3040	X2962		ILE	N2780	X2691
X3600	X3539	X3429	X3238	X3177	X3041	X2963		GLN	V2781	X2692
X3601	X3540	X3430	X3239	X3178	X3042	X2964		THR	D2782	X2693
X3602	X3541	X3431	X3240	X3179	X3043	X2965		ALA	E2783	X2694
X3603	X3542	X3432	X3241	X3180	X3044	X2966		GLN	E2784	X2695
X3604	X3543	X3433	X3242	X3181	X3045	X2967		THR	L2785	X2696
X3605	X3544	X3434	X3243	X3182	X3046	X2968		LYS	K2786	X2697
X3606	X3545	X3435	X3244	X3183	X3047	X2969		THR	T2787	X2698
X3607	X3546	X3436	X3245	X3184	X3048	X2970		TYR	H2788	X2699
X3608	X3547	X3437	X3246	X3185	X3049	X2971				X2699



• Molecule 2: Ryanodine receptor 1

Chain E: 52% 85% 10% 5%

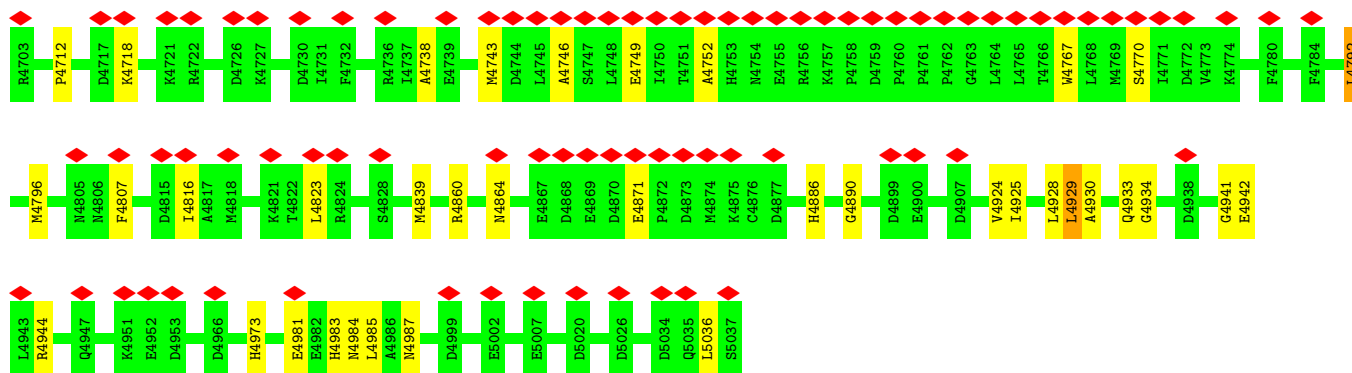




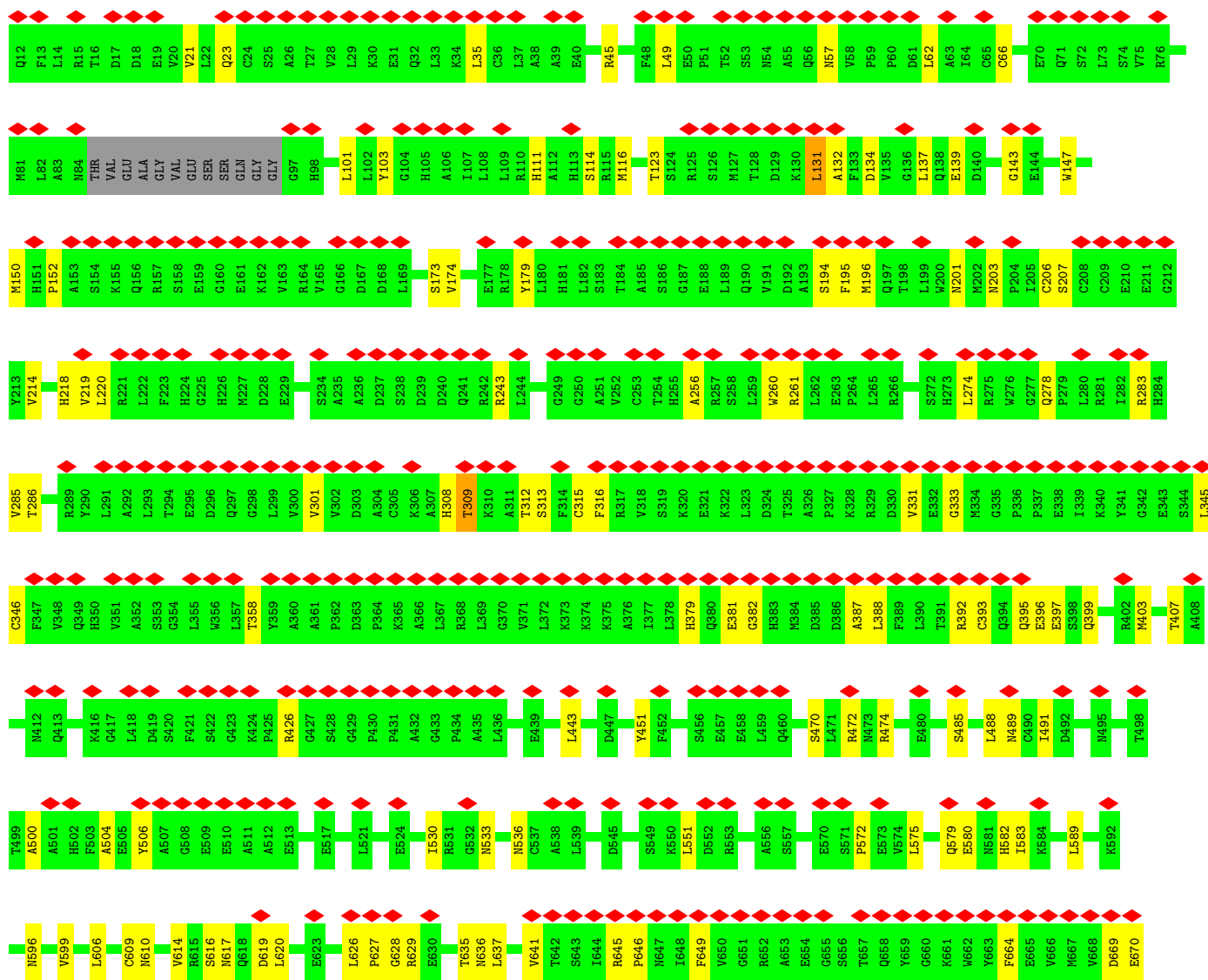
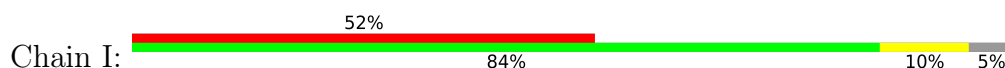


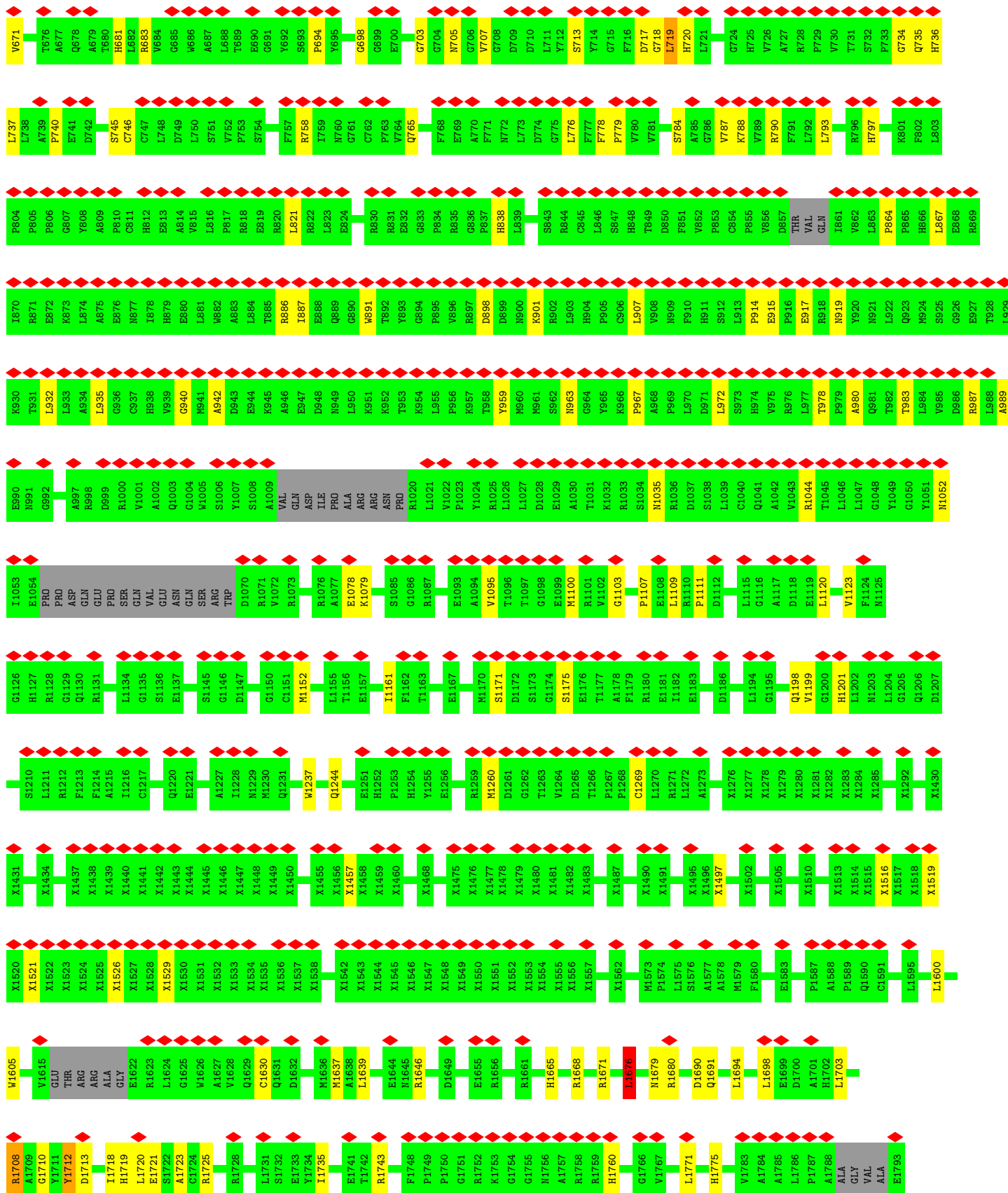
X3195	X3196	X3197	X3198	X3199	X3200	X3201	X3202	X3203	X3204	X3205	X3206	X3207	X3208	X3209	X3210	X3211	X3212	X3213	X3214	X3215	X3216	X3217	X3218	X3219	X3220	X3221	X3222	X3223	X3224	X3225	X3226	X3227	X3228	X3229	X3230	X3231	X3232	X3233	X3234	X3235	X3236	X3237	X3238	X3239	X3240	X3241	X3242	X3243	X3244	X3245	X3246	X3247	X3248	X3249	X3250	X3251	X3252	X3253	X3254	X3255	X3256	X3257	X3258	X3259	X3260	X3261	X3262	X3263
X2999	X3000	X3001	X3002	X3003	X3004	X3005	X3006	X3007	X3008	X3009	X3010	X3011	X3012	X3013	X3014	X3015	X3016	X3017	X3018	X3019	X3020	X3021	X3022	X3023	X3024	X3025	X3026	X3027	X3028	X3029	X3030	X3031	X3032	X3033	X3034	X3035	X3036	X3037	X3038	X3039	X3040	X3041	X3042	X3043	X3044	X3045	X3046	X3047	X3048	X3049	X3050	X3051	X3052	X3053	X3054	X3055	X3056	X3057	X3058	X3059								
D2919	R2920	E2921	K2922	A2923	Q2924	E2925	L2926	L2927	K2928	F2929	L2930	Q2931	M2932	N2933	Q2934	Y2935	A2936	V2937	T2938	R2939	X2942	X2943	X2944	X2945	X2946	X2947	X2948	X2949	X2950	X2951	X2952	X2953	X2954	X2955	X2956	X2957	X2958	X2959	X2960	X2961	X2962	X2963	X2964	X2965	X2966	X2967	X2968	X2969	X2970	X2971	X2972	X2973	X2974	X2975	X2976	X2995	X2996	X2997	X2998									
P2859	P2860	D2861	L2862	S2863	G2864	T2865	T2866	L2867	S2868	R2869	E2870	L2871	Q2872	A2873	M2874	A2875	E2876	Q2877	L2878	A2879	E2880	N2881	Y2882	H2883	N2884	T2885	W2886	G2887	R2888	K2889	K2890	K2891	Q2892	E2893	L2894	E2895	A2896	K2897	G2898	G2899	G2900	T2901	H2902	P2903	L2904	L2905	V2906	P2907	L2908	P2909	T2910	L2911	T2912	A2913	K2914	E2915	T2916	A2917	R2918									
E2799	K2800	D2801	K2802	E2803	L2804	Y2805	R2806	W2807	P2808	L2809	K2810	E2811	S2812	L2813	K2814	A2815	M2816	L2817	A2818	W2819	E2820	W2821	T2822	L2823	E2824	K2825	A2826	R2827	E2828	E2829	E2830	GLU	GLU	ARG	THR	GLU	LYS	LYS	LYS	THR	ARG	LYS	ILE	SER	GLN	THR	ALA	GLN	THR	TYR	ASP	PRO	ARG	GLU	GLY	Y2855	N2856	P2857	Q2858									
P2739	V2740	E2741	T2742	L2743	N2744	V2745	L2746	L2747	P2748	E2749	K2750	L2751	D2752	S2753	F2754	L2755	N2756	K2757	F2758	A2759	E2760	Y2761	T2762	H2763	E2764	K2765	N2766	A2767	F2768	D2769	K2770	I2771	Q2772	N2773	N2774	W2775	S2776	Y2777	G2778	E2779	N2780	V2781	D2782	E2783	E2784	L2785	K2786	T2787	H2788	P2789	M2790	L2791	R2792	P2793	Y2794	K2795	T2796	F2797	S2798									
X2649	X2650	X2651	X2652	X2653	X2654	X2655	X2656	X2657	X2658	X2659	X2660	X2661	X2662	X2663	X2664	X2665	X2666	X2667	X2668	X2669	X2670	X2671	X2672	X2673	X2674	X2675	X2676	X2677	X2678	X2679	X2680	X2681	X2682	X2683	X2684	X2685	X2686	X2687	X2688	X2689	X2690	X2691	X2692	X2693	X2694	X2695	X2696	X2697	X2698	X2699	X2700	X2701	X2702	X2703	N2734	F2735	D2736	P2737	R2738									
X2580	X2581	X2582	X2583	X2584	X2585	X2586	X2589	X2595	X2596	X2597	X2598	X2599	X2600	X2601	X2602	X2605	X2606	X2607	X2612	X2613	X2614	X2615	X2616	X2617	X2618	X2619	X2620	X2621	X2622	X2623	X2624	X2625	X2626	X2627	X2628	X2629	X2630	X2631	X2632	X2633	X2634	X2635	X2636	X2637	X2638	X2639	X2640	X2641	X2642	X2643	X2644	X2645	X2646	X2647	X2648													
X2497	X2498	X2499	X2500	X2513	X2514	X2515	X2516	X2517	X2518	X2519	X2520	X2521	X2522	X2523	X2524	X2525	X2526	X2527	X2528	X2529	X2530	X2531	X2532	X2533	X2534	X2535	X2536	X2537	X2538	X2539	X2540	X2541	X2542	X2546	X2557	X2558	X2561	X2562	X2563	X2564	X2565	X2566	X2567	X2568	X2569	X2570	X2571	X2572	X2573	X2574	X2575	X2576	X2577															
V2416	H2417	L2418	G2419	H2420	A2421	L2422	M2423	S2424	F2425	Y2426	A2427	A2428	L2429	I2430	D2431	L2432	L2433	G2434	C2435	A2437	H2441	K2447	L2451	A2455	I2456	L2457	R2458	S2459	L2460	V2461	P2462	L2463	D2464	D2465	L2466	I2469	I2470	S2471	L2472	P2473	L2474	Q2475	I2476	P2477	T2478	L2479	X2487	X2488	X2489	X2490	X2493	X2494																
R2355	L2356	L2357	I2358	R2359	K2360	P2361	E2362	G2365	P2366	A2367	L2368	R2369	G2370	E2371	G2372	G2373	S2374	G2375	C2310	L2377	A2378	A2379	I2380	E2381	E2382	A2383	L2384	R2385	L2386	S2387	E2388	D2389	P2390	A2391	R2392	D2393	G2394	P2395	GLY	VAL	ARG	ARG	ASP	ARG	ARG	GLU	HIS	PHE	GLY	GLU	GLU	PRO	PRO	GLU	GLU	N2414	R2415											
E2285	L2288	Q2291	E2292	Q2293	D2294	L2295	E2296	K2297	S2300	Y2301	G2304	C2305	G2306	L2307	Q2308	S2309	C2310	L2377	A2378	A2379	I2380	E2381	E2382	A2383	L2384	R2385	L2386	S2387	E2388	D2389	P2390	A2391	R2392	D2393	G2394	P2395	GLY	VAL	ARG	ARG	ASP	ARG	ARG	GLU	HIS	PHE	GLY	GLU	GLU	PRO	PRO	GLU	GLU	N2414	R2415													

GLU	N4626	X4340	R4137	G4073	R3984	L3856	E3736	N3643	X3554	X3449	X3866	X3325	X3265
GLY	N4627	X4341	N4142	S4074	L3993	G3857	E3737	L3644	X3555	X3450	X3887	X3326	X3266
ASP	N4628	X4342	F3996	E4075	F3996	M3858	G3738	R3648	X3556	X3451	X3888	X3327	X3267
GLU	N4629	X4343	N4145	A4076	F3996	V3859	G3739	N3651	X3557	X3452	X3889	X3328	X3268
N4630	N4630	X4344	N4152	A4077	M4000	N3860	E3740	X3654	X3558	X3453	X3890	X3329	X3269
N4631	N4631	X4345	H4153	Q4078	M4001	E3861	N3741	L3654	X3559	X3454	X3891	X3330	X3270
N4632	N4632	F4540	N4154	Y4080	K4002	D3862	GLU	X3658	X3560	X3455	X3892	X3331	X3271
N4633	N4633	N4541	N4155	Y4081	L4003	G3863	ALA	X3659	X3561	X3456	X3893	X3332	X3272
N4634	N4634	E4542	N4156	T4082	A4004	V3864	GLU	X3660	X3562	X3457	X3894	X3333	X3273
N4635	N4635	E4543	N4156	Q4083	Q4005	T3866	GLU	X3661	X3563	X3458	X3895	X3334	X3274
N4636	N4636	N4544	N4156	P4084	Q4006	N3867	E3747	X3662	X3564	X3459	X3896	X3335	X3275
N4637	N4637	E4545	S4007	R4085	S4007	N3867	E3748	X3663	X3565	X3460	X3897	X3336	X3276
N4638	N4638	N4546	N4161	Q4086	N4011	N3868	V3749	X3664	X3566	X3461	X3898	X3337	X3277
N4639	N4639	N4547	L4164	L4012	E4011	N3868	E3750	X3665	X3567	X3462	X3899	X3338	X3278
N4640	N4640	N4572	L4166	L4013	N4012	N3870	V3751	X3666	X3568	X3463	X3900	X3339	X3279
N4641	N4641	N4572	E4168	F4093	L4013	N3871	S3752	X3667	X3569	X3464	X3901	X3340	X3280
N4642	N4642	N4572	E4172	Q4094	D4018	E3872	F3753	X3668	X3570	X3465	X3902	X3341	X3281
N4643	N4643	N4572	E4172	K4095	Q4020	N3882	E3754	X3669	X3571	X3466	X3903	X3342	X3282
N4644	N4644	N4572	E4172	A4096	K4021	N3883	E3755	X3670	X3572	X3467	X3904	X3343	X3283
N4645	N4645	N4572	E4172	D4098	D4022	D3878	E3756	X3671	X3573	X3468	X3905	X3344	X3284
N4646	N4646	N4572	E4172	N4098	N4034	N3877	E3757	X3672	X3574	X3469	X3906	X3345	X3285
N4647	N4647	N4572	E4172	N4099	N4034	N3878	E3758	X3673	X3575	X3470	X3907	X3346	X3286
N4648	N4648	N4572	E4172	Q4100	N4034	N3879	E3759	X3674	X3576	X3471	X3908	X3347	X3287
N4649	N4649	N4572	E4172	Q4101	N4034	N3880	E3760	X3675	X3577	X3472	X3909	X3348	X3288
N4650	N4650	N4572	E4172	Q4102	N4034	N3881	E3761	X3676	X3578	X3473	X3910	X3349	X3289
N4651	N4651	N4572	E4172	F4103	N4034	N3882	E3762	X3677	X3579	X3474	X3911	X3350	X3290
N4652	N4652	N4572	E4172	T4104	N4034	N3883	E3763	X3678	X3580	X3475	X3912	X3351	X3291
N4653	N4653	N4572	E4172	N4105	N4034	N3884	E3764	X3679	X3581	X3476	X3913	X3352	X3292
N4654	N4654	N4572	E4172	N4106	N4034	N3885	E3765	X3680	X3582	X3477	X3914	X3353	X3293
N4655	N4655	N4572	E4172	N4107	N4034	N3886	E3766	X3681	X3583	X3478	X3915	X3354	X3294
N4656	N4656	N4572	E4172	N4108	N4034	N3887	E3767	X3682	X3584	X3479	X3916	X3355	X3295
N4657	N4657	N4572	E4172	N4109	N4034	N3888	E3768	X3683	X3585	X3480	X3917	X3356	X3296
N4658	N4658	N4572	E4172	N4110	N4034	N3889	E3769	X3684	X3586	X3481	X3918	X3357	X3297
N4659	N4659	N4572	E4172	N4111	N4034	N3890	E3770	X3685	X3587	X3482	X3919	X3358	X3298
N4660	N4660	N4572	E4172	N4112	N4034	N3891	E3771	X3686	X3588	X3483	X3920	X3359	X3299
N4661	N4661	N4572	E4172	N4113	N4034	N3892	E3772	X3687	X3589	X3484	X3921	X3360	X3300
N4662	N4662	N4572	E4172	N4114	N4034	N3893	E3773	X3688	X3590	X3485	X3922	X3361	X3301
N4663	N4663	N4572	E4172	N4115	N4034	N3894	E3774	X3689	X3591	X3486	X3923	X3362	X3302
N4664	N4664	N4572	E4172	N4116	N4034	N3895	E3775	X3690	X3592	X3487	X3924	X3363	X3303
N4665	N4665	N4572	E4172	N4117	N4034	N3896	E3776	X3691	X3593	X3488	X3925	X3364	X3304
N4666	N4666	N4572	E4172	N4118	N4034	N3897	E3777	X3692	X3594	X3489	X3926	X3365	X3305
N4667	N4667	N4572	E4172	N4119	N4034	N3898	E3778	X3693	X3595	X3490	X3927	X3366	X3306
N4668	N4668	N4572	E4172	N4120	N4034	N3899	E3779	X3694	X3596	X3491	X3928	X3367	X3307
N4669	N4669	N4572	E4172	N4121	N4034	N3900	E3780	X3695	X3597	X3492	X3929	X3368	X3308
N4670	N4670	N4572	E4172	N4122	N4034	N3901	E3781	X3696	X3598	X3493	X3930	X3369	X3309
N4671	N4671	N4572	E4172	N4123	N4034	N3902	E3782	X3697	X3599	X3494	X3931	X3370	X3310
N4672	N4672	N4572	E4172	N4124	N4034	N3903	E3783	X3698	X3600	X3495	X3932	X3371	X3311
N4673	N4673	N4572	E4172	N4125	N4034	N3904	E3784	X3699	X3601	X3496	X3933	X3372	X3312
N4674	N4674	N4572	E4172	N4126	N4034	N3905	E3785	X3700	X3602	X3497	X3934	X3373	X3313
N4675	N4675	N4572	E4172	N4127	N4034	N3906	E3786	X3701	X3603	X3498	X3935	X3374	X3314
N4676	N4676	N4572	E4172	N4128	N4034	N3907	E3787	X3702	X3604	X3499	X3936	X3375	X3315
N4677	N4677	N4572	E4172	N4129	N4034	N3908	E3788	X3703	X3605	X3500	X3937	X3376	X3316
N4678	N4678	N4572	E4172	N4130	N4034	N3909	E3789	X3704	X3606	X3501	X3938	X3377	X3317
N4679	N4679	N4572	E4172	N4131	N4034	N3910	E3790	X3705	X3607	X3502	X3939	X3378	X3318
N4680	N4680	N4572	E4172	N4132	N4034	N3911	E3791	X3706	X3608	X3503	X3940	X3379	X3319
N4681	N4681	N4572	E4172	N4133	N4034	N3912	E3792	X3707	X3609	X3504	X3941	X3380	X3320
N4682	N4682	N4572	E4172	N4134	N4034	N3913	E3793	X3708	X3610	X3505	X3942	X3381	X3321
N4683	N4683	N4572	E4172	N4135	N4034	N3914	E3794	X3709	X3611	X3506	X3943	X3382	X3322
N4684	N4684	N4572	E4172	N4136	N4034	N3915	E3795	X3710	X3612	X3507	X3944	X3383	X3323
N4685	N4685	N4572	E4172	N4137	N4034	N3916	E3796	X3711	X3613	X3508	X3945	X3384	X3324
N4686	N4686	N4572	E4172	N4138	N4034	N3917	E3797	X3712	X3614	X3509	X3946	X3385	X3325
N4687	N4687	N4572	E4172	N4139	N4034	N3918	E3798	X3713	X3615	X3510	X3947	X3386	X3326
N4688	N4688	N4572	E4172	N4140	N4034	N3919	E3799	X3714	X3616	X3511	X3948	X3387	X3327
N4689	N4689	N4572	E4172	N4141	N4034	N3920	E3800	X3715	X3617	X3512	X3949	X3388	X3328
N4690	N4690	N4572	E4172	N4142	N4034	N3921	E3801	X3716	X3618	X3513	X3950	X3389	X3329
N4691	N4691	N4572	E4172	N4143	N4034	N3922	E3802	X3717	X3619	X3514	X3951	X3390	X3330
N4692	N4692	N4572	E4172	N4144	N4034	N3923	E3803	X3718	X3620	X3515	X3952	X3391	X3331
N4693	N4693	N4572	E4172	N4145	N4034	N3924	E3804	X3719	X3621	X3516	X3953	X3392	X3332
N4694	N4694	N4572	E4172	N4146	N4034	N3925	E3805	X3720	X3622	X3517	X3954	X3393	X3333
N4695	N4695	N4572	E4172	N4147	N4034	N3926	E3806	X3721	X3623	X3518	X3955	X3394	X3334
N4696	N4696	N4572	E4172	N4148	N4034	N3927	E3807	X3722	X3624	X3519	X3956	X3395	X3335
N4697	N4697	N4572	E4172	N4149	N4034	N3928	E3808	X3723	X3625	X3520	X3957	X3396	X3336
N4698	N4698	N4572	E4172	N4150	N4034	N3929	E3809	X3724	X3626	X3521	X3958	X3397	X3337
N4699	N4699	N4572	E4172	N4151	N4034	N3930	E3810	X3725	X3627	X3522	X3959	X3398	X3338
N4700	N4700	N4572	E4172	N4152	N4034	N3931	E3811	X3726	X3628	X3523	X3960	X3399	X3339
N4701	N4701	N4572	E4172	N4153	N4034	N3932	E3812	X3727	X3629	X3524	X3961	X3400	X3340
N4702	N4702	N4572	E4172	N4154	N4034	N3933	E3813	X3728	X3630	X3525	X3962	X3401	X3341
N4703	N4703	N4572	E4172	N4155	N4034	N3934	E3814	X3729	X3631	X3526	X3963	X3402	X3342
N4704	N4704	N4572	E4172	N4156	N4034	N3935	E3815	X3730	X3632	X3527	X3964	X3403	X3343
N4705	N4705	N4572	E4172	N4157	N4034	N3936	E3816	X3731	X3633	X3528	X3965	X3404	X3344
N4706	N4706	N4572	E4172	N4158	N4034	N3937	E3817	X3732	X3634	X3529	X3966	X3405	X3345
N4707	N4707	N4572	E4172	N4159	N4034	N3938	E3818	X3733	X3635	X3530	X3967	X3406	X3346
N4708	N4708	N4572	E4172	N4160	N4034	N3939	E3819	X3734	X3636	X3531	X3968	X3407	X3347
N4709	N4709	N4572	E4172	N4161	N4034	N3940	E3820	X3735	X3637	X3532	X3969	X3408	X3348
N4710	N4710	N4572	E4172	N4162	N4034	N3941	E3821	X3736	X3638	X3533	X3970	X3409	X3349
N4711	N4711	N4572	E4172	N4163	N4034	N3942	E3822	X3737	X3639	X3534	X3971	X3410	X3350
N4712	N4712	N4572	E4172	N4164	N4034	N3943	E3823	X3738	X3640	X3535	X3972	X3411	X3351
N4713	N4713	N4572	E4172	N4165	N4034	N3944	E3824	X3739	X3641	X3536	X3973	X3412	X3352
N4714	N4714	N4572	E4172	N4166	N4034	N3945	E3825	X3740	X3642	X3537	X3974	X3413	X3353
N4715	N4715	N4572	E4172	N4167	N4034	N3946	E3826	X3741	X3643	X3538	X3975	X3414	X3354
N4716	N4716	N4572	E4172	N4168	N4034	N3947	E3827	X3742	X3644	X3539	X3976	X3415	X3355
N4717	N4717	N4572	E4172	N4169	N4034	N3948	E3828	X3743	X3645	X3540	X3977	X3416	X3356
N4718	N4718	N4572	E4172	N4170	N4034	N3949	E3829	X3744	X3646	X3541	X3978	X3417	X3357
N4719	N4719	N4572	E4172	N4171	N4034	N3950	E3830	X3745	X3647	X3542	X3979	X3418	X3358
N4720	N4720	N4572	E4172										



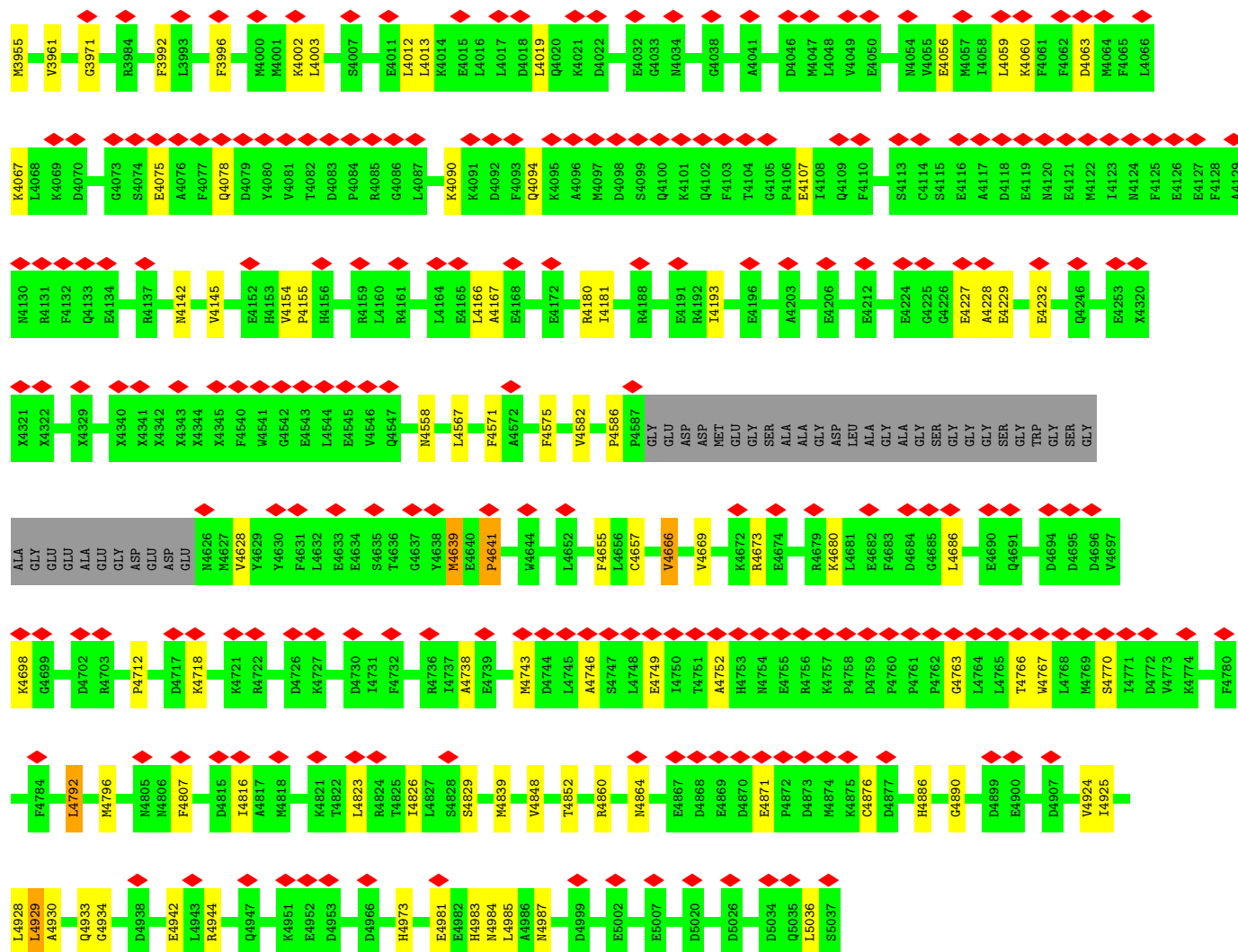
• Molecule 2: Ryanodine receptor 1











4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	55564	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.081	Depositor
Minimum map value	-0.049	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	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	0.21	0/834	0.48	0/1123
1	F	0.21	0/834	0.48	0/1123
1	H	0.21	0/834	0.47	0/1123
1	J	0.21	0/834	0.47	0/1123
2	B	0.25	0/25428	0.55	3/34534 (0.0%)
2	E	0.25	0/25428	0.55	3/34534 (0.0%)
2	G	0.25	0/25428	0.55	3/34534 (0.0%)
2	I	0.25	0/25428	0.55	3/34534 (0.0%)
All	All	0.25	0/105048	0.55	12/142628 (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	18
2	E	0	18
2	G	0	18
2	I	0	18
All	All	0	76

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	131	LEU	CA-CB-CG	5.46	135.39	116.30
2	B	131	LEU	CA-CB-CG	5.45	135.38	116.30
2	E	131	LEU	CA-CB-CG	5.45	135.36	116.30
2	I	131	LEU	CA-CB-CG	5.45	135.36	116.30
2	G	4639	MET	CA-C-N	5.16	134.38	121.80

There are no chirality outliers.

5 of 76 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	6	0
1	F	818	0	824	6	0
1	H	818	0	824	5	0
1	J	818	0	824	6	0
2	B	29499	0	24749	243	0
2	E	29499	0	24750	240	0
2	G	29499	0	24749	252	0
2	I	29499	0	24749	252	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	102293	975	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 975 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:I:2291:GLN:HB3	2:I:2294:ASP:H	1.55	0.72
2:B:2291:GLN:HB3	2:B:2294:ASP:H	1.55	0.71
2:G:2291:GLN:HB3	2:G:2294:ASP:H	1.55	0.71
2:E:2291:GLN:HB3	2:E:2294:ASP:H	1.55	0.71
2:B:1260:MET:HB2	2:B:1269:CYS:H	1.62	0.65

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	105/108 (97%)	95 (90%)	10 (10%)	0	100	100
1	F	105/108 (97%)	95 (90%)	10 (10%)	0	100	100
1	H	105/108 (97%)	95 (90%)	10 (10%)	0	100	100
1	J	105/108 (97%)	95 (90%)	10 (10%)	0	100	100
2	B	3235/4416 (73%)	2874 (89%)	357 (11%)	4 (0%)	48	83
2	E	3235/4416 (73%)	2873 (89%)	358 (11%)	4 (0%)	48	83
2	G	3235/4416 (73%)	2875 (89%)	356 (11%)	4 (0%)	48	83
2	I	3235/4416 (73%)	2873 (89%)	358 (11%)	4 (0%)	48	83
All	All	13360/18096 (74%)	11875 (89%)	1469 (11%)	16 (0%)	49	83

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	1708	ARG
2	G	1708	ARG
2	E	1708	ARG
2	I	1708	ARG
2	B	1932	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	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%)	2480 (100%)	13 (0%)	81	81
2	E	2493/3022 (82%)	2480 (100%)	13 (0%)	81	81
2	G	2493/3022 (82%)	2480 (100%)	13 (0%)	81	81
2	I	2493/3022 (82%)	2480 (100%)	13 (0%)	81	81
All	All	10324/12444 (83%)	10272 (100%)	52 (0%)	78	81

5 of 52 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	719	LEU
2	E	4792	LEU
2	I	4929	LEU
2	E	1600	LEU
2	E	2339	VAL

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

Mol	Chain	Res	Type
2	E	395	GLN
2	E	3814	GLN
2	I	3998	HIS
2	E	582	HIS
2	E	1693	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	G	14
2	E	14
2	I	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	73.03
1	G	4345:UNK	C	4540:PHE	N	73.03
1	E	4345:UNK	C	4540:PHE	N	73.03
1	I	4345:UNK	C	4540:PHE	N	73.03

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	3613:UNK	C	3639:THR	N	46.34

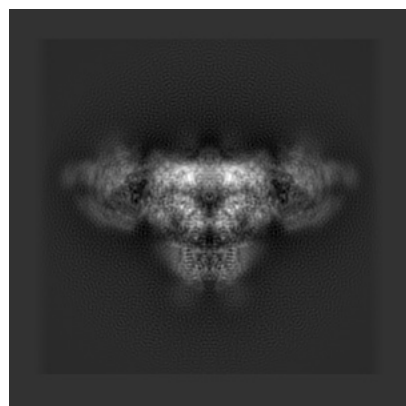
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8391. These allow visual inspection of the internal detail of the map and identification of artifacts.

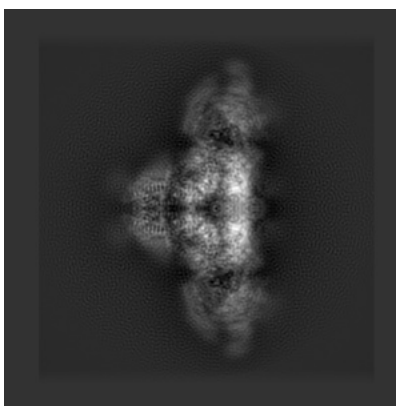
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

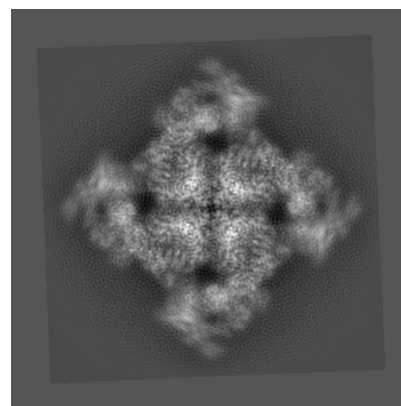
6.1.1 Primary map



X

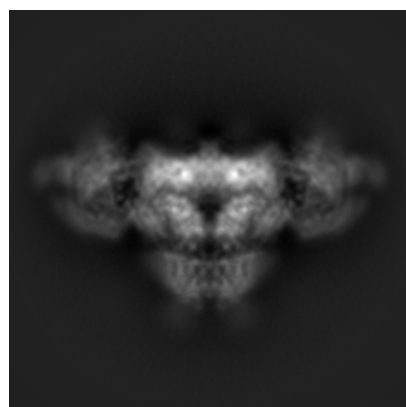


Y

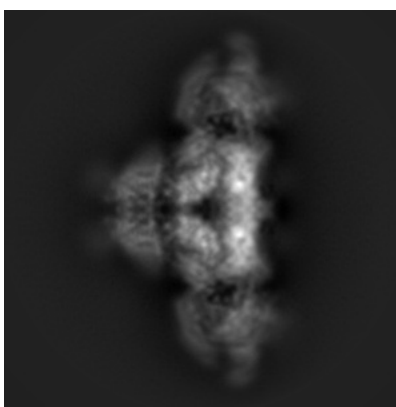


Z

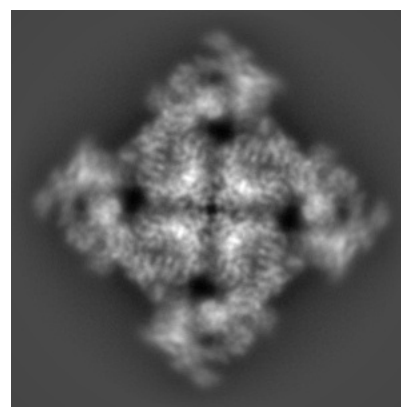
6.1.2 Raw map



X



Y



Z

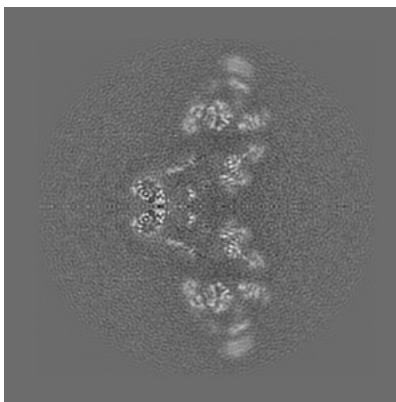
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

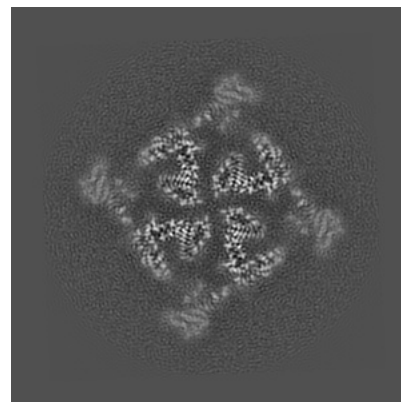
6.2.1 Primary map



X Index: 200

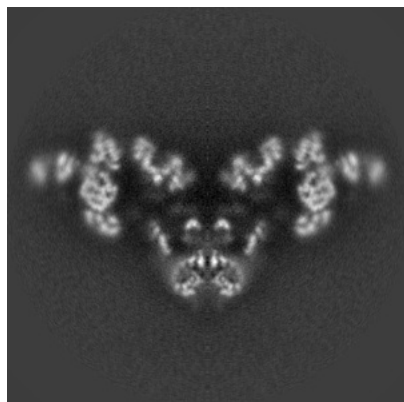


Y Index: 200

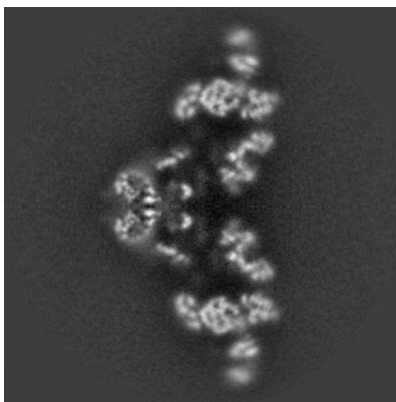


Z Index: 200

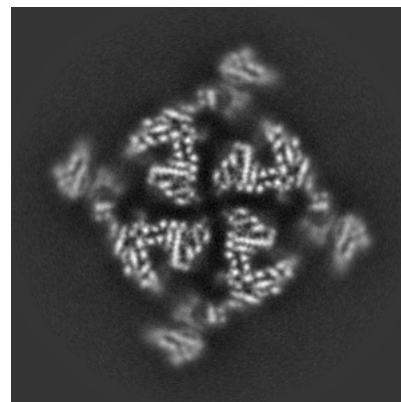
6.2.2 Raw map



X Index: 168



Y Index: 168

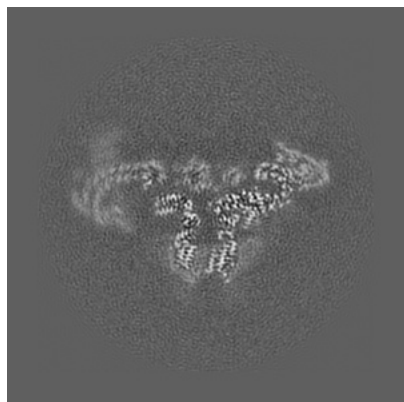


Z Index: 168

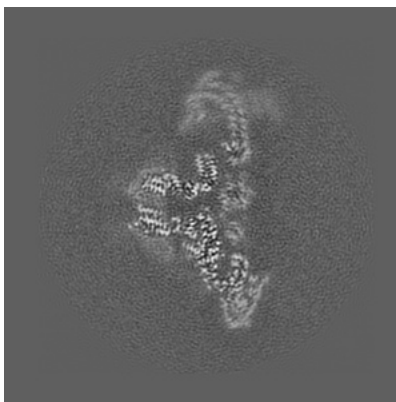
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

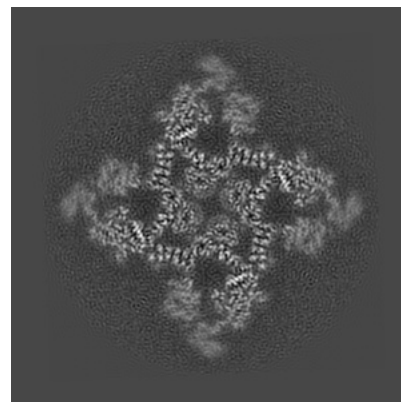
6.3.1 Primary map



X Index: 176

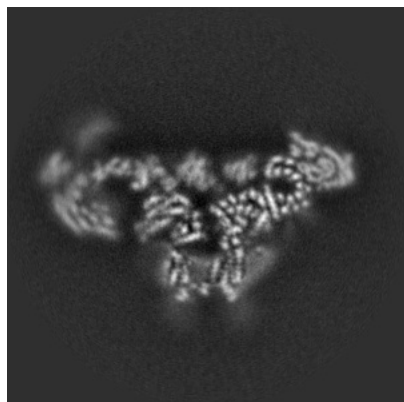


Y Index: 176

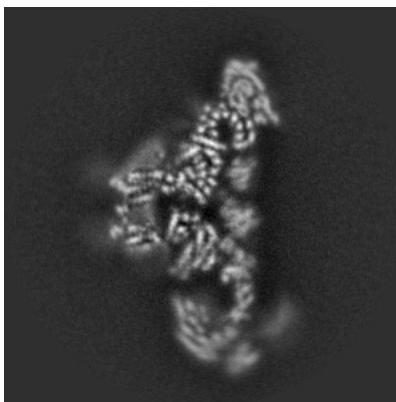


Z Index: 228

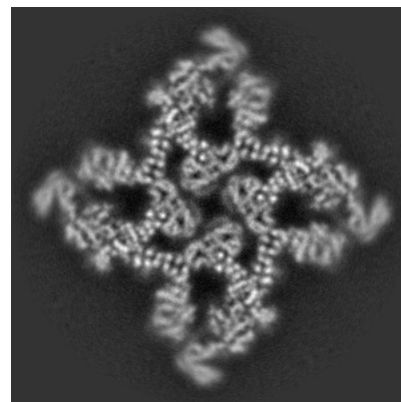
6.3.2 Raw map



X Index: 147



Y Index: 189

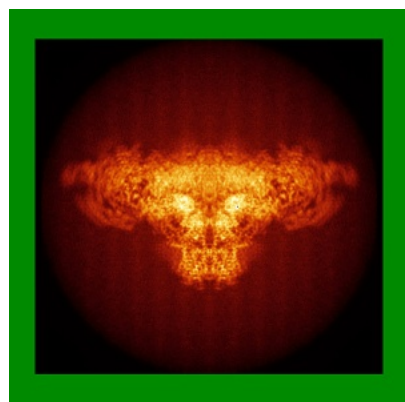


Z Index: 196

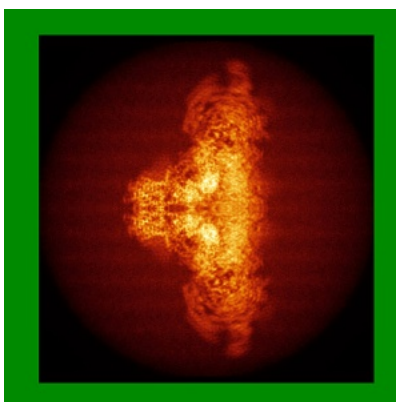
The images above show the largest variance slices of the map in three orthogonal directions.

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

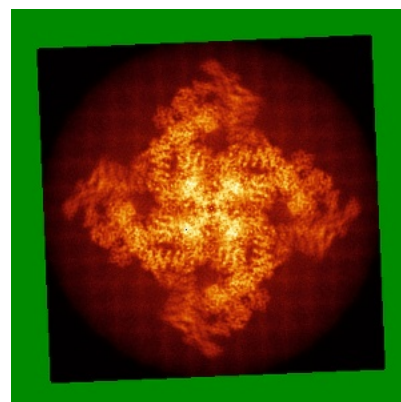
6.4.1 Primary map



X

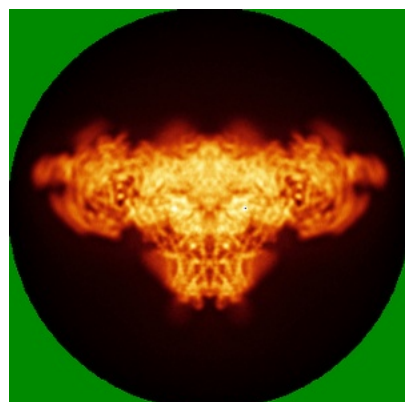


Y

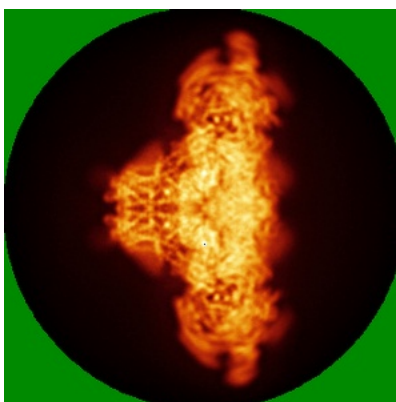


Z

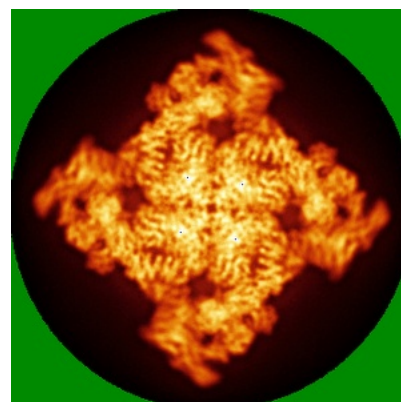
6.4.2 Raw map



X



Y

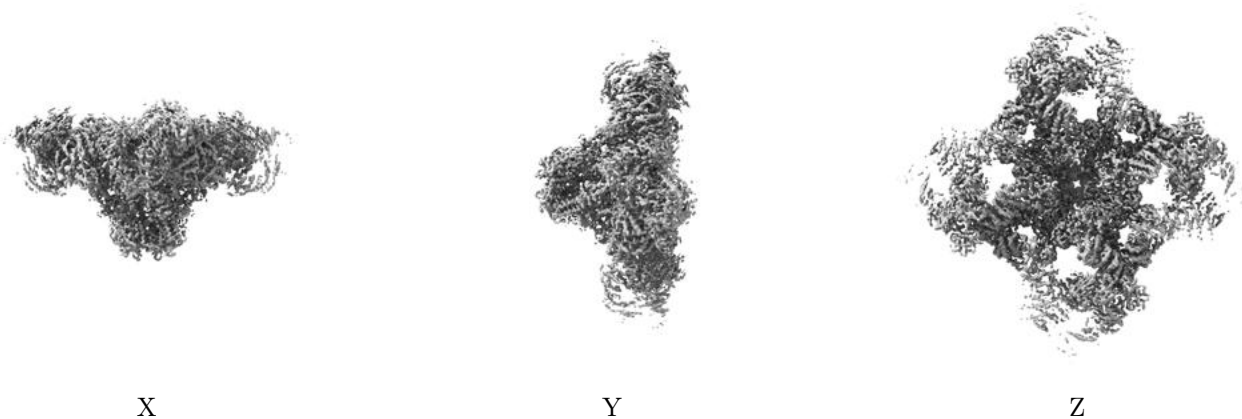


Z

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.

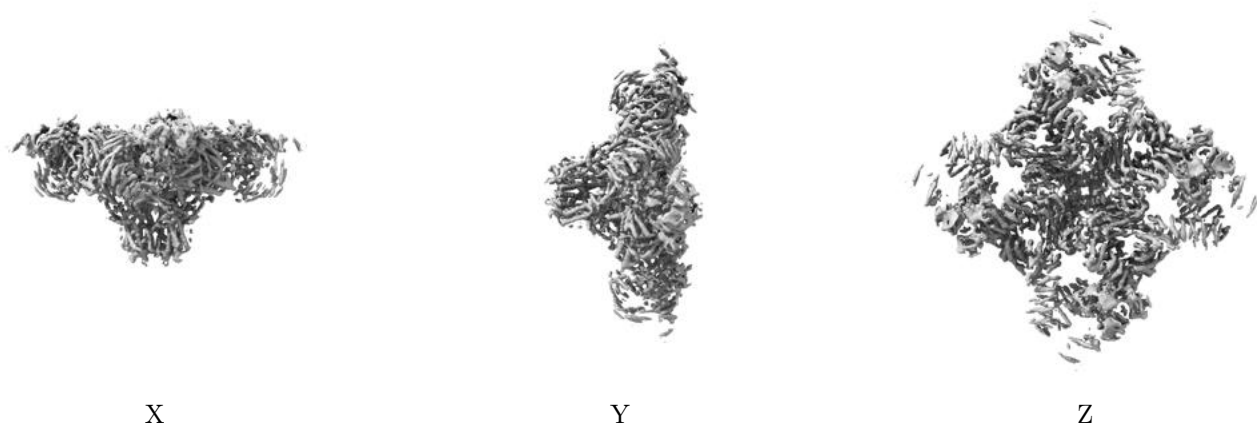
6.5 Orthogonal surface views [i](#)

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.

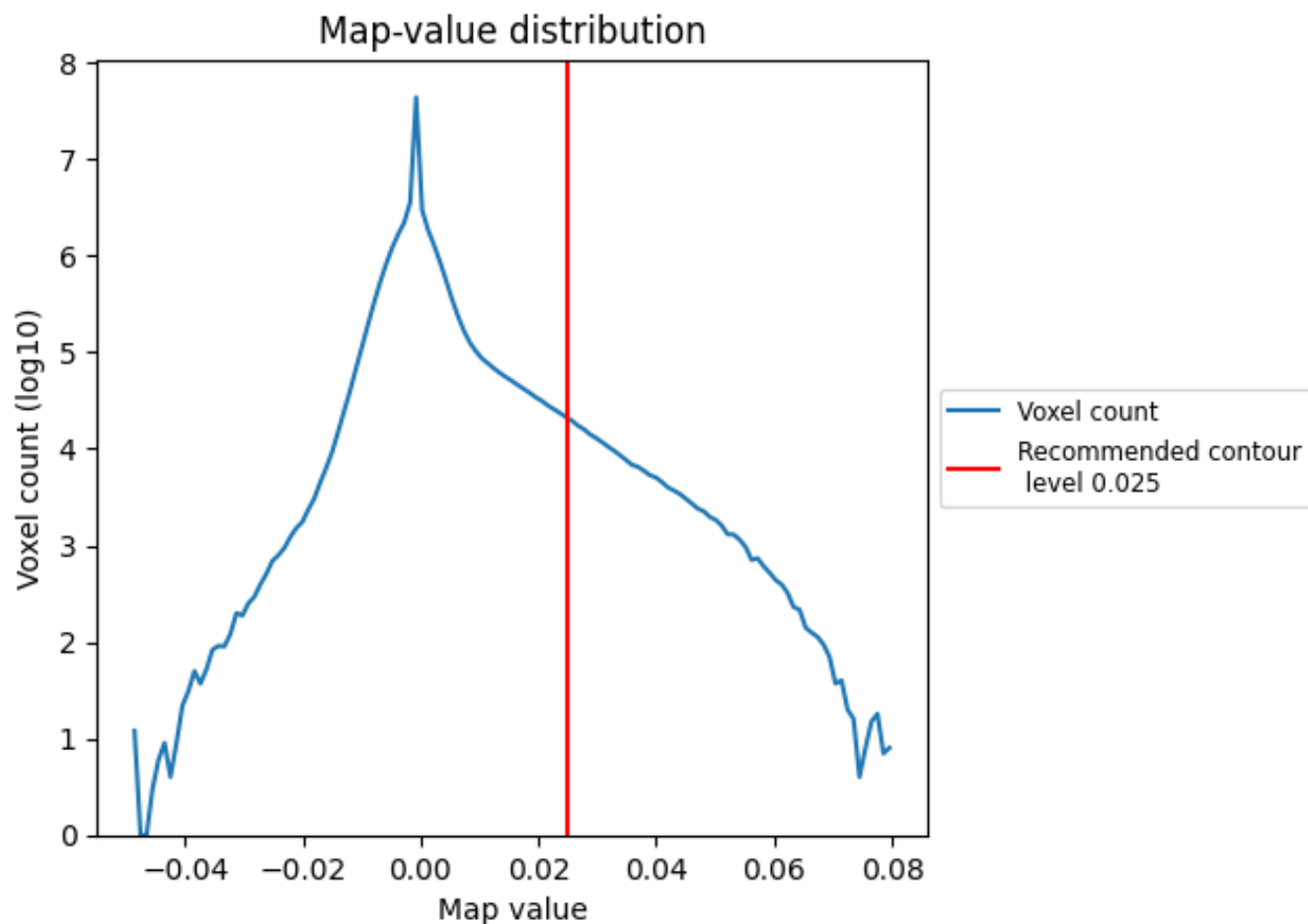
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

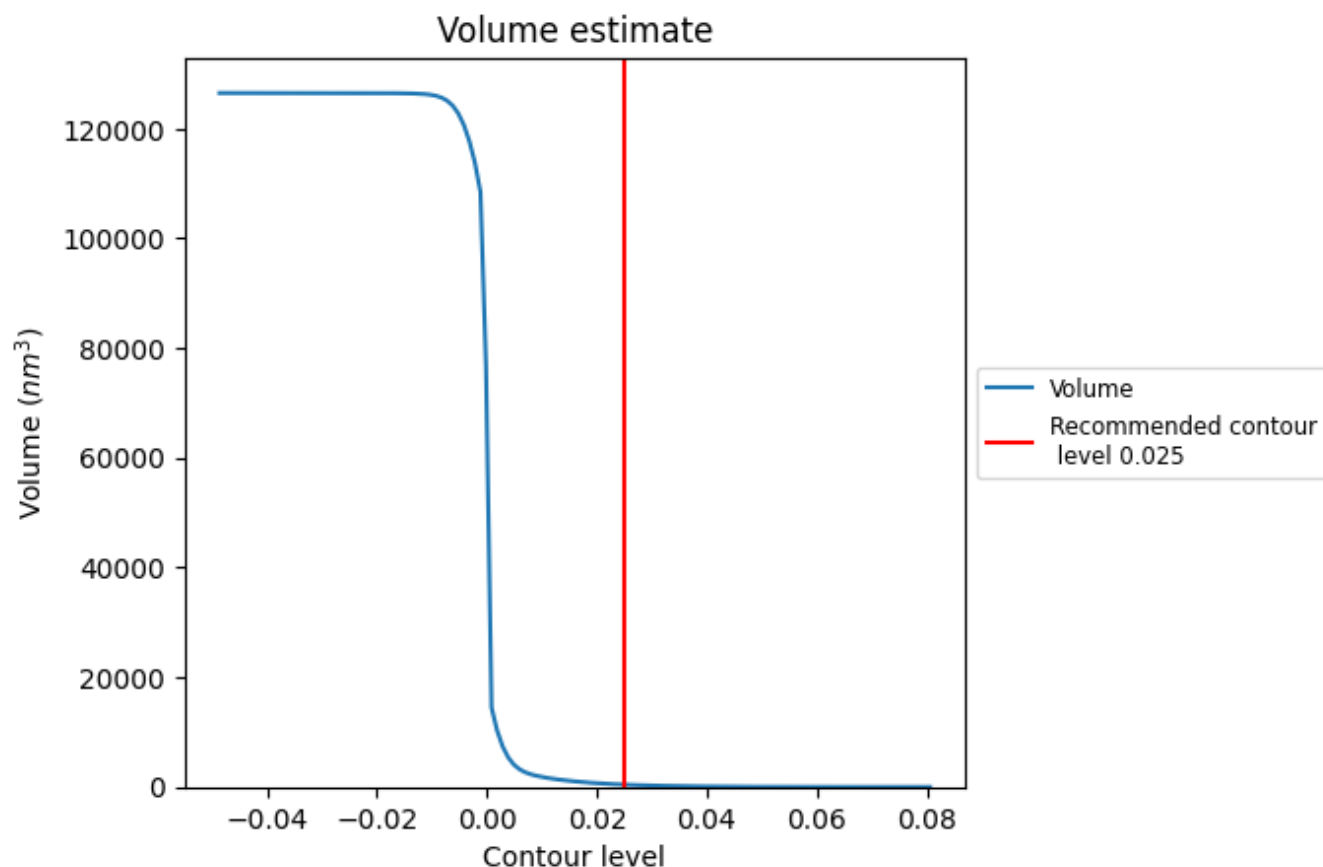
This section contains the results of statistical analysis of the map.

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.

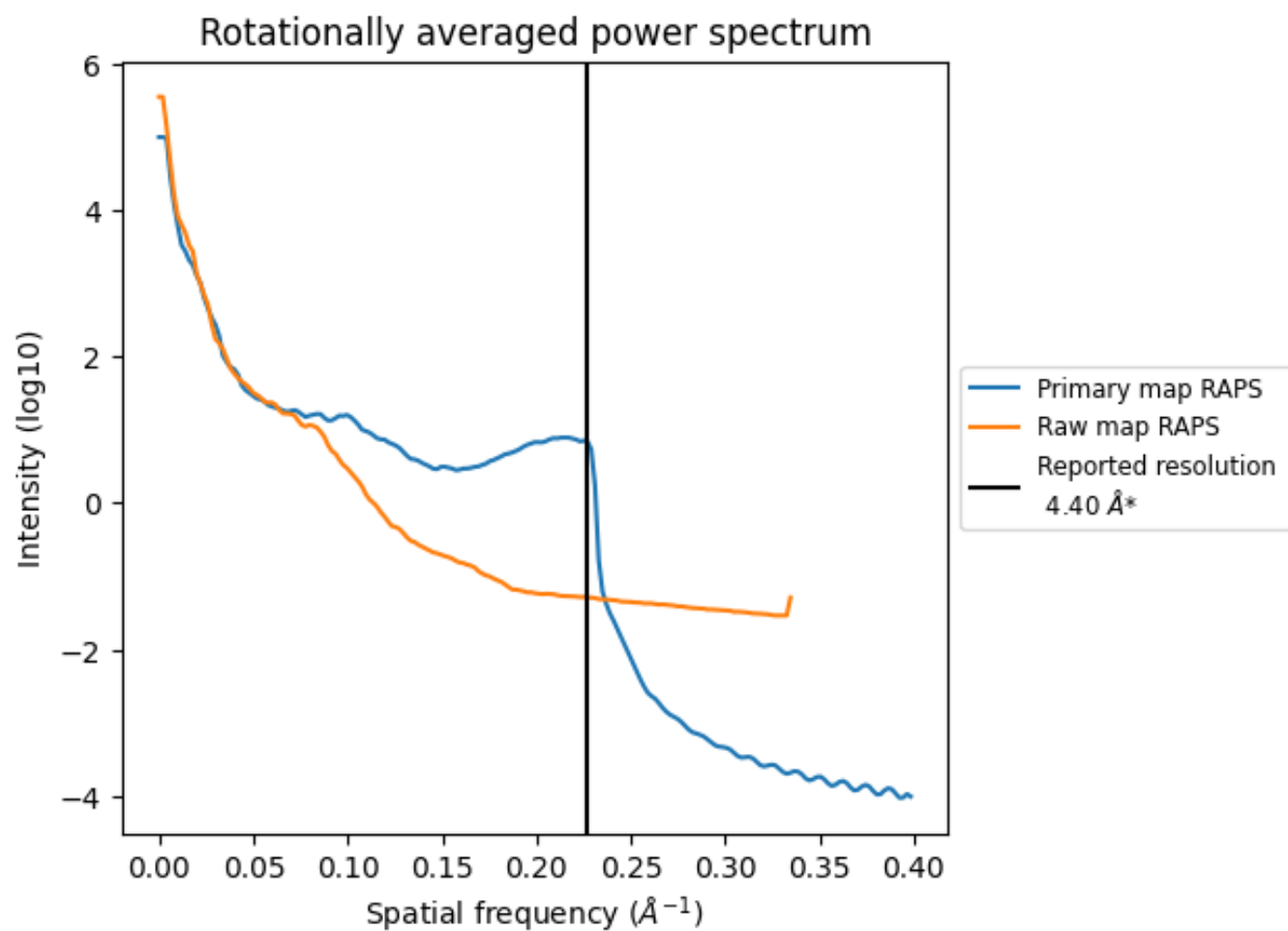
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 422 nm³; this corresponds to an approximate mass of 381 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 ⓘ

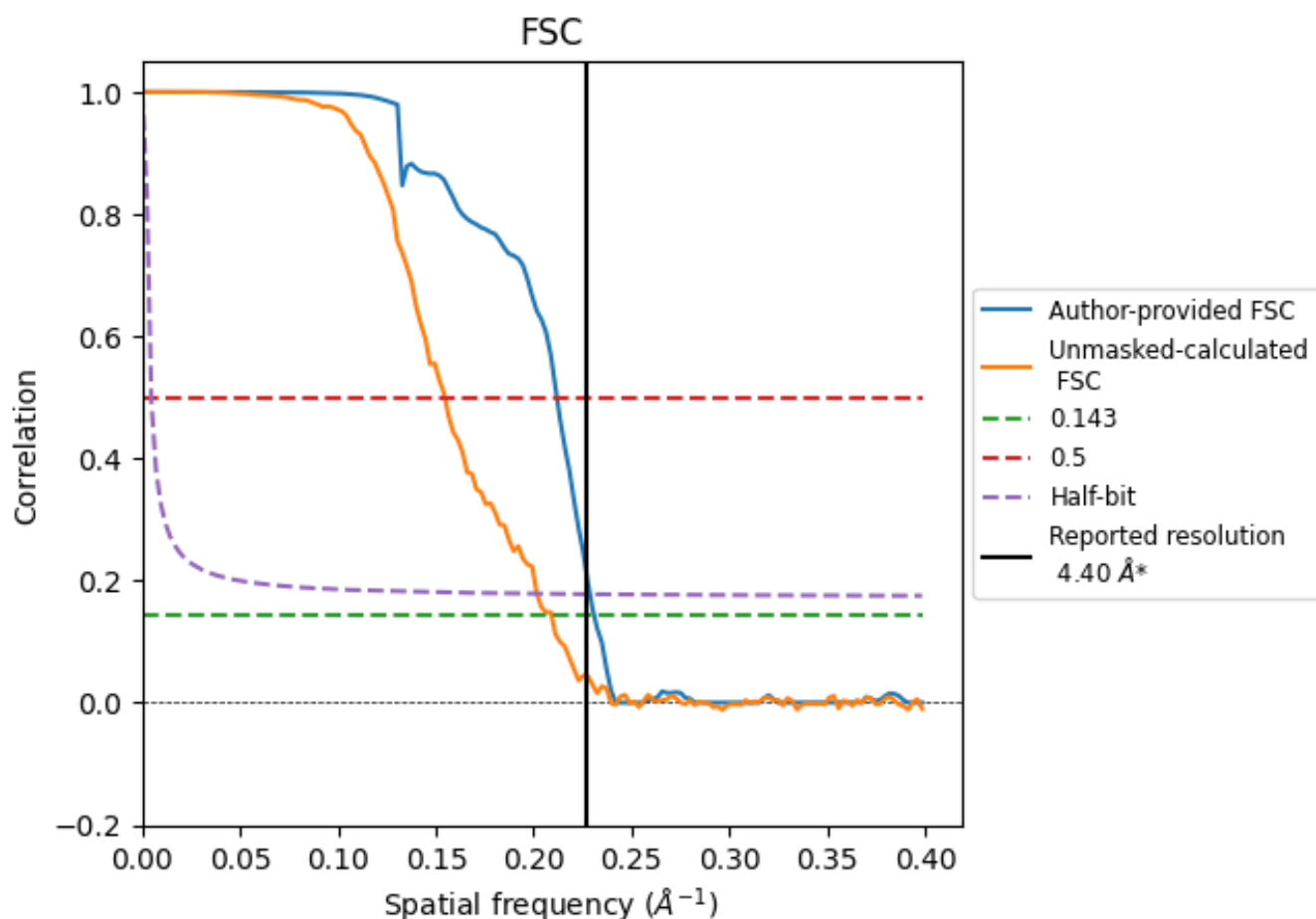


*Reported resolution corresponds to spatial frequency of 0.227 Å⁻¹

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 0.227 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

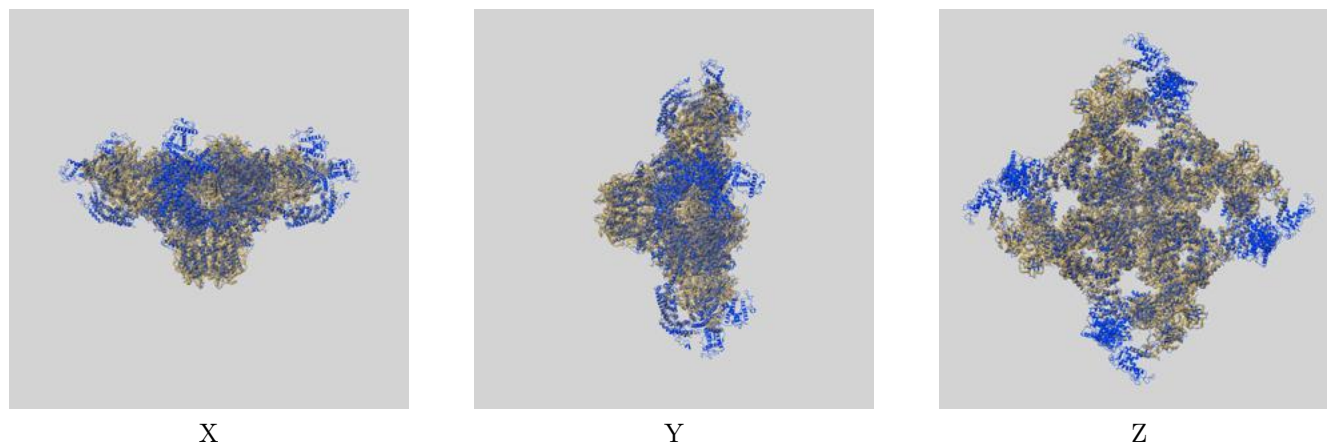
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.40	-	-
Author-provided FSC curve	4.33	4.72	4.37
Unmasked-calculated*	4.78	6.47	4.96

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

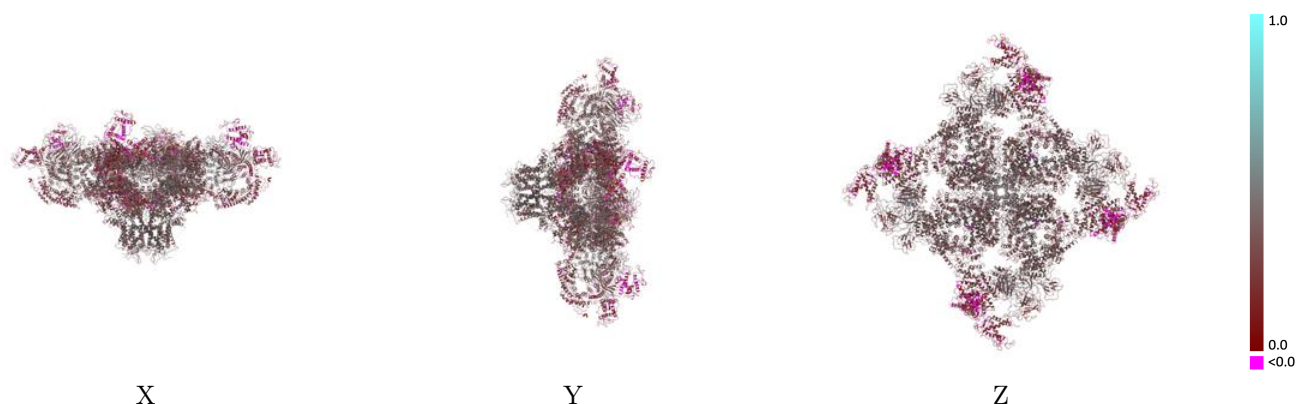
This section contains information regarding the fit between EMDB map EMD-8391 and PDB model 5TB0. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



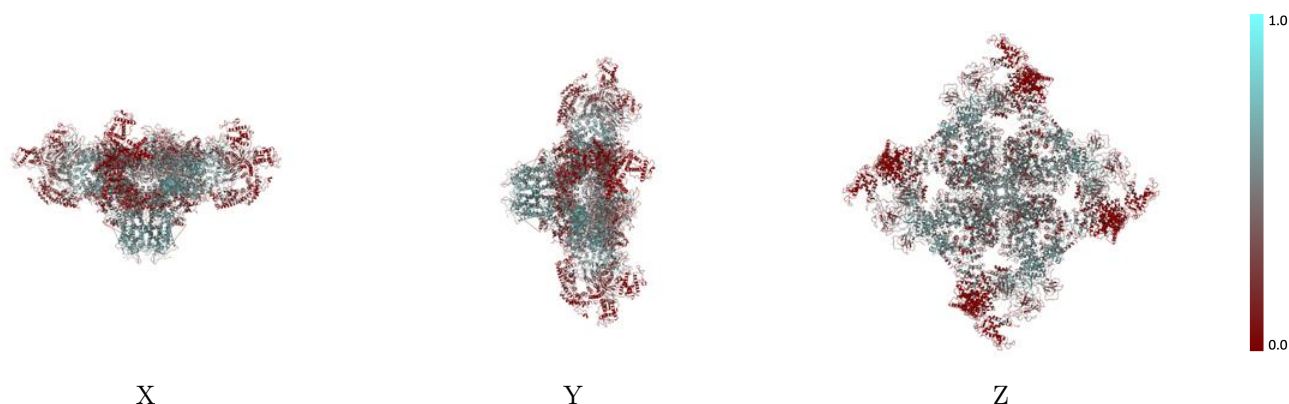
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



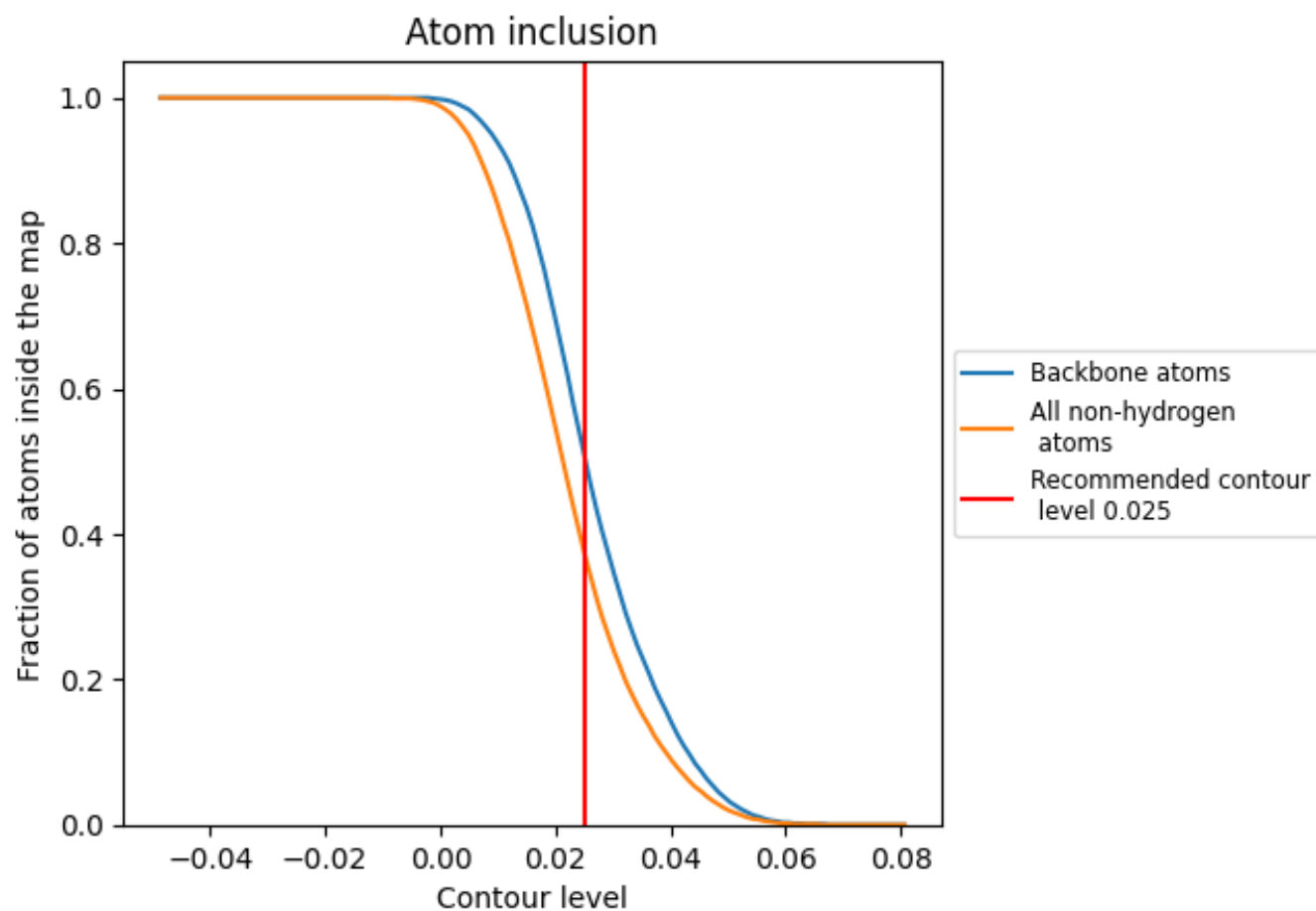
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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

9.4 Atom inclusion [i](#)



At the recommended contour level, 51% of all backbone atoms, 37% 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	0.3740	0.3120
A	0.3810	0.3450
B	0.3750	0.3110
E	0.3730	0.3110
F	0.3780	0.3490
G	0.3740	0.3110
H	0.3810	0.3480
I	0.3740	0.3110
J	0.3800	0.3450

