



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 02:39 PM UTC

PDB ID : 5TB1 / pdb_00005tb1
EMDB ID : EMD-8392
Title : Structure of rabbit RyR1 (EGTA-only dataset, class 1)
Authors : Clarke, O.B.; des Georges, A.; Zalk, R.; Marks, A.R.; Hendrickson, W.A.; Frank, J.
Deposited on : 2016-09-10
Resolution : 4.60 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:

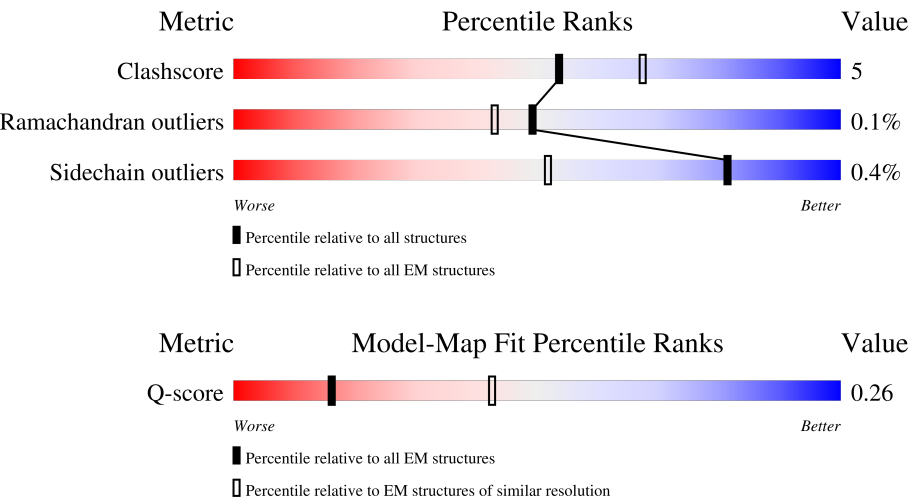
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.60 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	2407 (4.10 - 5.10)

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	82% 73%26%
1	F	108	83% 70%29%
1	H	108	81% 73%26%
1	J	108	82% 74%25%

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Mol	Chain	Length	Quality of chain
2	B	4416	70% 83% 11% 5%
2	E	4416	71% 83% 12% 5%
2	G	4416	70% 83% 11% 5%
2	I	4416	70% 83% 11% 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	I	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	G	4194	Total	C	N	O	S	0	0
			29499	18686	5228	5428	157		

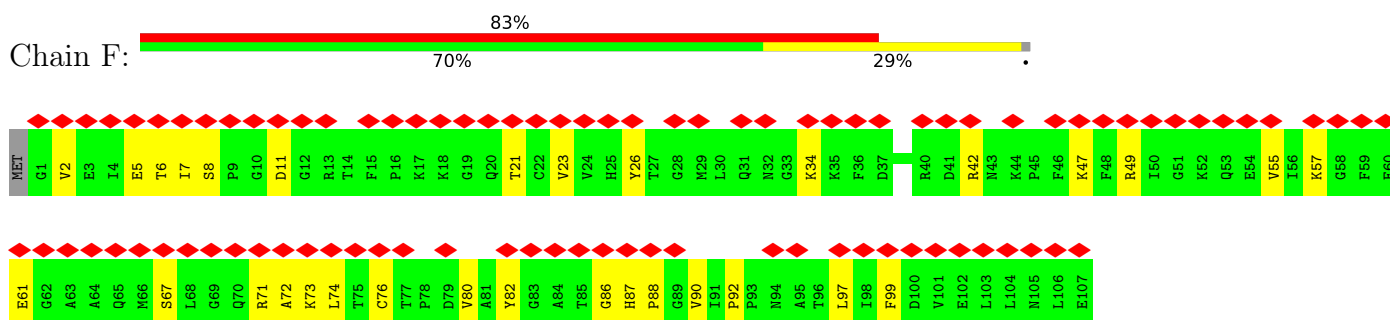
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

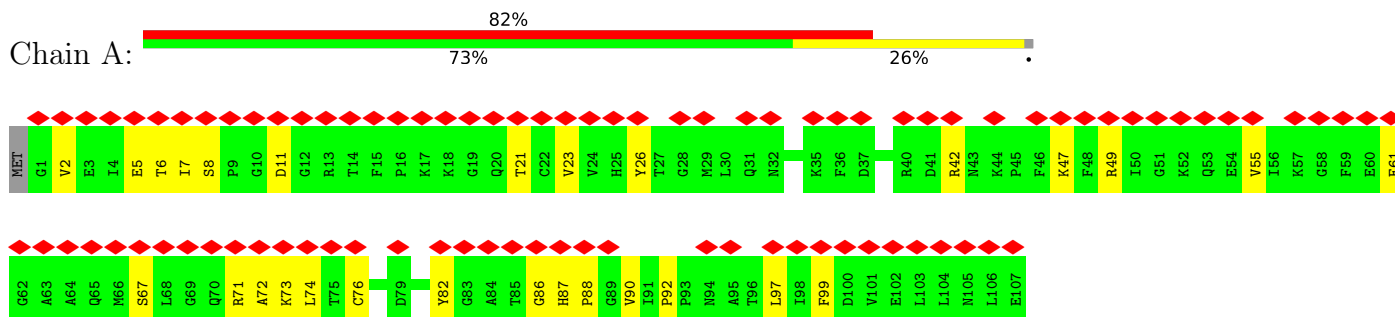
3 Residue-property plots [i](#)

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.

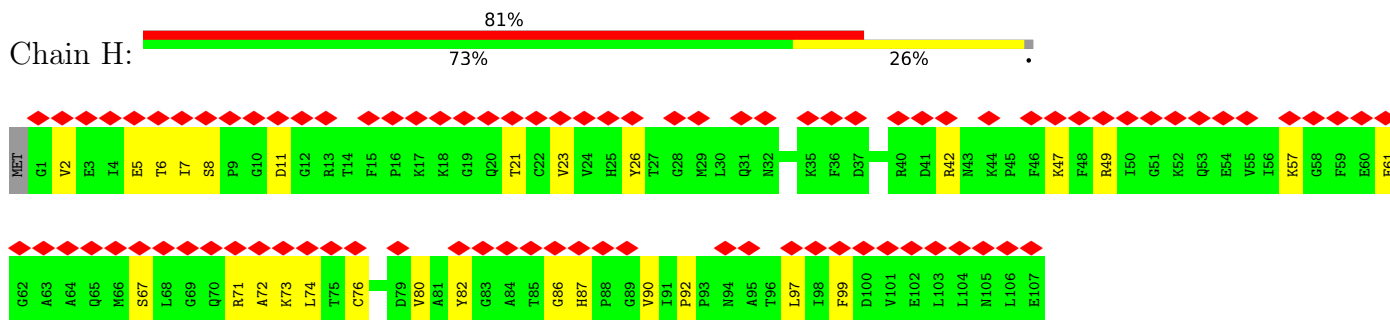
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



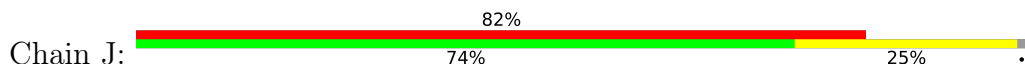
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

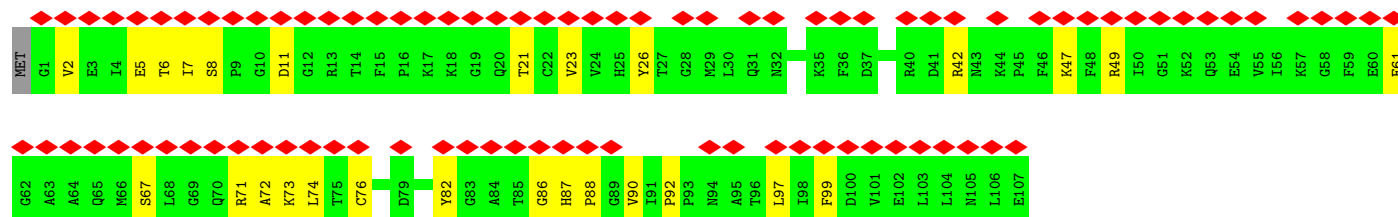


- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

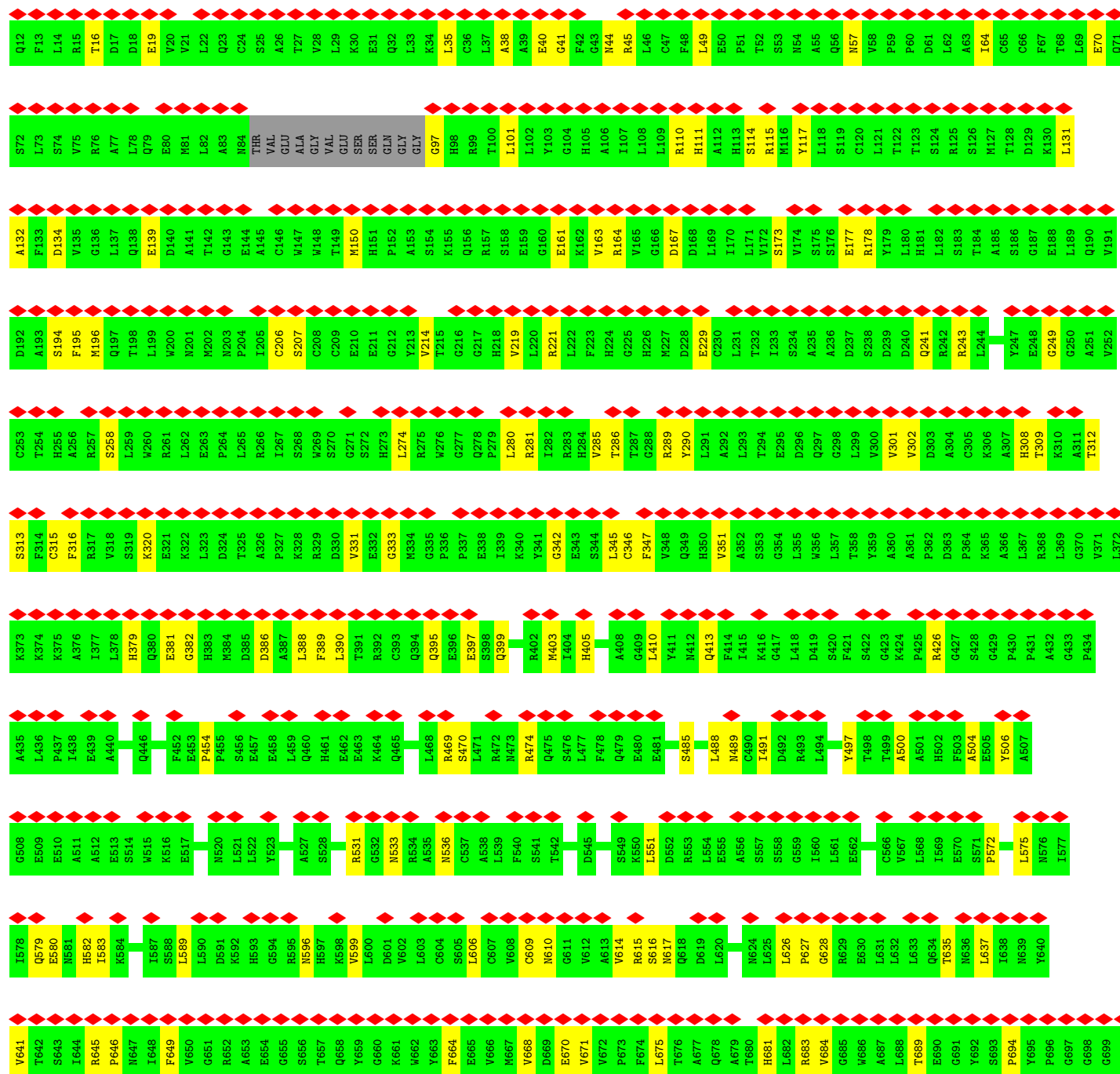
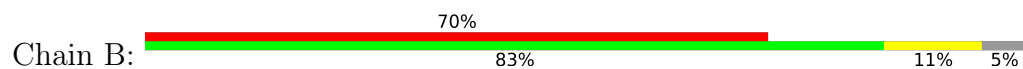


- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B





• Molecule 2: Ryanodine receptor 1

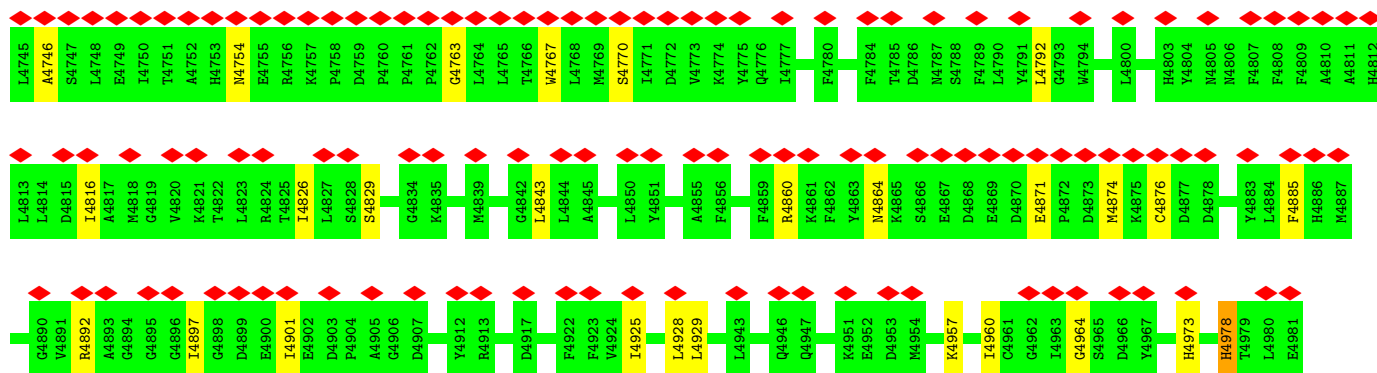


G701	G702	G703	G704	N705	G706	G707	G708	G709	D710	L711	L712	S713	Y714	G715	F716	D717	G718	L719	H720	L721	F722	T723	G724	H725	F726	A727	R728	F729	V730	T731	S732	P733	G734	Q735	H736	L737	L738	A739	P740	E741	D742	P743	V744	S745	C746	C747	L748	D749	L750	S751	V752	P753	S754	I755	S756	F757	R758	I759	L760
G761	C762	P763		G766	V767	F768	E769	A770	F771	N772	L773	D774	G775	L776	F777	F778	P779	V780	Y781	S782	F783	S784	A785	G786	H787	K788	V789	R790	F791	L792	L793	G794	G795	V796	H797	G798	E799	F800	R801	F802	L803	P804	P805	P806	G807	Y808	A809	H812	E813	A814	V815	L816	P817	R818	E819	R820	L821	R822	
L823	E824	P825	I826	K827	E828	Y829	R830	R831	E832	G833	P834	R835	G836	P837	H838	L839	V840	G841	P842	S843	R844	C845	L846	S847	H848	T849	D850	F851	V852	P853	C854	P855	V856	D857	THR	GLN	I861	V862	L863	P864	P865	H866	L867	E868	R869	I870	R871	E872	K873	A874	L875	E876	N877	I878	H879	E880	L881	W882	
A883	L884	T885	R886	I887	E888	Q889	G890	W891	T892	Y893	G894	P895	V896	R897	D898	D899	N900	K901	R902	L903	H904	C945	L946	S947	H948	T949	D950	F951	V952	P953	C954	P955	V956	E917	R918	N919	Y920	N921	L922	Q923	M924	S925	G926	E927	T928	L929	K930	T931	L932	L933	A934	L935	G936	C937	H938	V939	G940	M941	A942
D943	E944	K945	A946	E947	D948	N949	L950	K951	K952	T953	K954	L955	P956	K957	T958	Y959	M960	M961	S962	N963	G964	Y965	K966	P967	A968	P969	L970	D971	L972	S973	H974	Y975	R976	L977	T978	P979	A980	Q981	T982	T983	L984	V985	D986	A987	L988	A989	E990	N991	A997	R998	D999	R1000	V1001	A1002	Q1003	G1004	W1005	S1006	
Y1007	S1008	A1009	VAL	GLN	ASP	ILE	PRO	ALA	ARG	ASN	PRO	R1020	L1021	V1022	P1023	Y1024	R1025	L1026	L1027	D1028	E1029	T1031	K1032	R1033	S1034	M1035	R1036	D1037	S1038	L1039	C1040	Q1041	A1042	V1043	R1044	T1045	L1046	L1047	G1048	Y1049	G1050	Y1051	M1052	I1053	E1054	PRO	ASP	GLN	PRO	ASP	GLU	PRO	SER	GLN	VAL	GLU	ASN	GLN	
SER	ARG	TRP	D1070	R1071	V1072	R1073	I1074	F1075	R1076	A1077	E1078	K1079	S1080	Y1081	Q1084	S1085	G1086	R1087	W1088	F1089	F1090	E1091	F1092	E1093	A1094	V1095	T1096	T1097	G1098	E1099	M1100	R1101	V1102	G1103	W1104	A1105	P1107	E1108	R1109	R1110	P1111	D1112	V1113	E1114	L1115	G1116	A1117	D1118	E1119	L1120	A1121	Y1122	V1123	F1124	N1125	G1126	H1127		
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P1190	V1191	C1192	S1193	L1194	G1195	P1196	G1197	Q1198	V1199	G1200	H1201	L1202	N1203	L1204	G1205	Q1206	D1207	V1208	S1209	S1210	L1211	F1212	F1213	F1214	A1215	I1216	C1217	G1218	L1219	Q1220	E1221	G1222	F1223	F1226	A1227	Q1231	R1232	P1233	V1234	T1235	T1236	W1237	F1238	S1239	K1240	P1243	Q1244	F1245	P1247	P1250	E1251	H1252	P1253	H1254					
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X1515	X1516	X1519	X1520	X1521	X1522	X1523	X1524	X1525	X1526	X1527	X1528	X1529	X1530	X1531	X1532	X1533	X1534	X1535	X1536	X1537	X1538	X1539	X1540	X1541	X1542	X1543	X1544	X1545	X1546	X1547	X1548	X1549	X1550	X1551	X1552	X1553	X1554	X1555	X1556	X1557	X1558	M1573	P1574	S1575	A1577	M1579	F1580	E1583	R1584	K1585	M1586	P1587	A1588	P1589					
Q1590	C1591	P1592	L1595	E1596	V1597	Q1598	M1599	L1600	V1603	S1604	W1605	P1606	R1607	M1608	F1612	L1613	Q1614	V1615	GLU	THR	ARG	ARG	ALA	GLY	E1622	R1623	L1624	G1625	W1626	A1627	V1628	Q1629	C1630	Q1631	D1632	P1633	L1634	T1635	M1636	M1637	A1638	L1639	H1640	E1643	E1644	N1645	R1646	C1647	M1648	D1649	I1650	L1653	S1654	E1655					

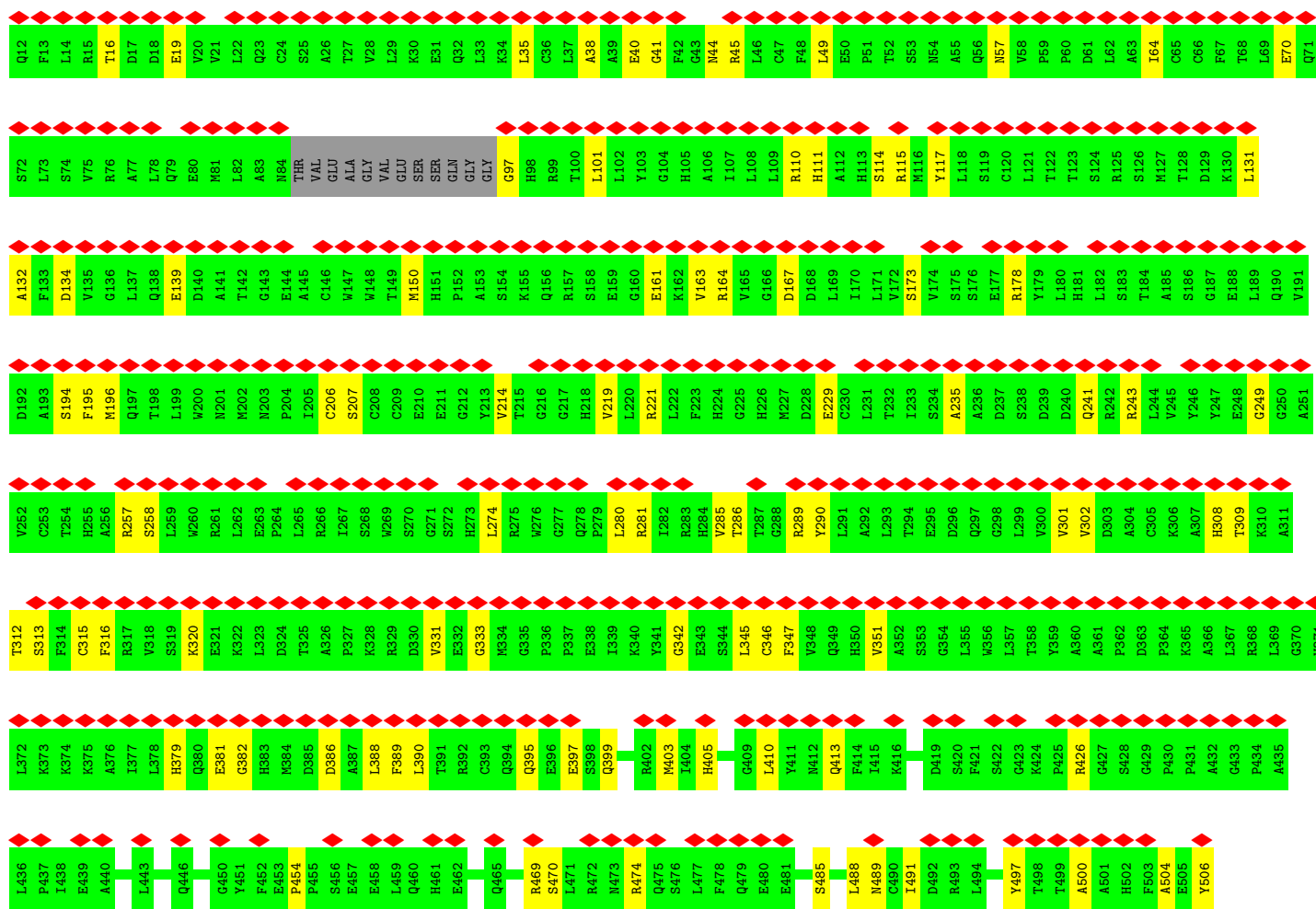
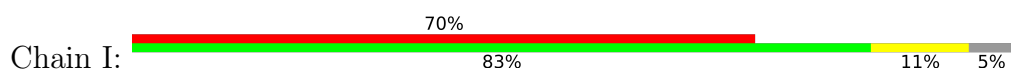


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X3353	X3354	X3355	X3356	X3357	X3358	X3359	X3360	X3361	X3362	X3363	X3364	X3365	X3366	X3367	X3368	X3369	X3370	X3371	X3372	X3373	X3374	X3375	X3376	X3377	X3378	X3379	X3380	X3381	X3382	X3383	X3384	X3385	X3386	X3387	X3388	X3389	X3390	X3391	X3392	X3393	X3394	X3395	X3396	X3397	X3398	X3399	X3400	X3401	X3402	X3403	X3404	X3405	X3406	X3407	X3408	X3409	X3410	X3411	X3412																																																																																																																																		
X3293	X3294	X3295	X3296	X3297	X3298	X3299	X3300	X3301	X3302	X3303	X3304	X3305	X3306	X3307	X3308	X3309	X3310	X3311	X3312	X3313	X3314	X3315	X3316	X3317	X3318	X3319	X3320	X3321	X3322	X3323	X3324	X3325	X3326	X3327	X3328	X3329	X3330	X3331	X3332	X3333	X3334	X3335	X3336	X3337	X3338	X3339	X3340	X3341	X3342	X3343	X3344	X3345	X3346	X3347	X3348	X3349	X3350	X3351	X3352																																																																																																																																		
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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	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	X3060	X3061	X3062	X3063	X3064	X3065	X3066	X3067	X3068	X3069	X3070	X3071	X3072	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	X3100	X3101	X3102	X3103	X3104	X3105	X3106	X3107	X3108	X3109	X3110	X3111	X3112	X3113	X3114	X3115	X3116	X3117	X3118	X3119	X3120	X3121	X3122	X3123	X3124	X3125	X3126	X3127	X3128	X3129	X3130	X3131	X3132	X3133	X3134	X3135	X3136	X3137	X3138	X3139	X3140	X3141	X3142	X3143	X3144	X3145	X3146	X3147	X3148	X3149	X3150	X3151	X3152	X3153	X3154	X3155	X3156
G2887	R2888	X2889	X2890	X2891	X2892	X2893	L2894	E2895	A2896	X2897	G2898	X2899	X2900	T2901	H2902	P2903	L2904	L2905	V2906	P2907	X2908	D2909	T2910	L2911	T2912	A2913	X2914	E2915	X2916	A2917	X2918	D2919	R2920	E2921	X2922	A2923	Q2924	E2925	L2926	L2927	X2928	P2929	X2930	L2931	Q2932	X2933	Q2934	X2935	A2936	V2937	T2938	X2939	X2940	X2941	X2942	X2943	X2944	X2945	X2946	X2947	X2948																																																																																																																																
R2827	E2828	E2829	E2830	GLU	GLU	ARG	THR	GLU	LYS	LYS	THR	ARG	LYS	ILE	SER	GLN	THR	ALA	GLN	THR	TYR	ASP	PRO	ARG	GLU	GLY	Y2855	N2856	P2857	Q2858	P2859	P2860	D2861	L2862	S2863	G2864	V2865	T2866	L2867	S2868	R2869	E2870	L2871	Q2872	A2873	M2874	A2875	E2876	Q2877	L2878	A2879	E2880	N2881	Y2882	H2883	N2884	T2885	W2886																																																																																																																																			
A2767	F2768	D2769	K2770	I2771	Q2772	N2773	N2774	W2775	S2776	Y2777	G2778	E2779	N2780	E2781	V2782	D2783	E2784	L2785	K2786	T2787	H2788	P2789	N2790	L2791	R2792	P2793	Y2794	K2795	T2796	F2797	S2798	E2799	K2800	D2801	K2802	E2803	L2804	Y2805	R2806	W2807	P2808	I2809	K2810	E2811	S2812	L2813	K2814	A2815	M2816	I2817	A2818	W2819	E2820	W2821	T2822	I2823	E2824	K2825	A2826																																																																																																																																		
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	P2735	D2736	P2737	R2738	P2739	V2740	E2741	T2742	L2743	N2744	W2745	W2746	X2747	P2748	E2749	K2750	L2751	D2752	X2753	P2754	I2755	N2756	K2757	P2758	A2759	E2760	E2761	X2762	T2763	E2764	K2765	W2766																																																																																																																																		
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	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																																																																																																																																		
X2553	X2554	X2555	X2556	X2557	X2558	X2561	X2562	X2563	X2564	X2565	X2566	X2567	X2568	X2569	X2570	X2574	X2575	X2576	X2577	X2580	X2581	X2582	X2583	X2584	X2585	X2586	X2587	X2588	X2589	X2590	X2591	X2592	X2593	X2594	X2595	X2596	X2597	X2598	X2599	X2600	X2601	X2602	X2603	X2604	X2605	X2606	X2607	X2608	X2609	X2610	X2611	X2612	X2613	X2614	X2615	X2616																																																																																																																																					





• Molecule 2: Ryanodine receptor 1

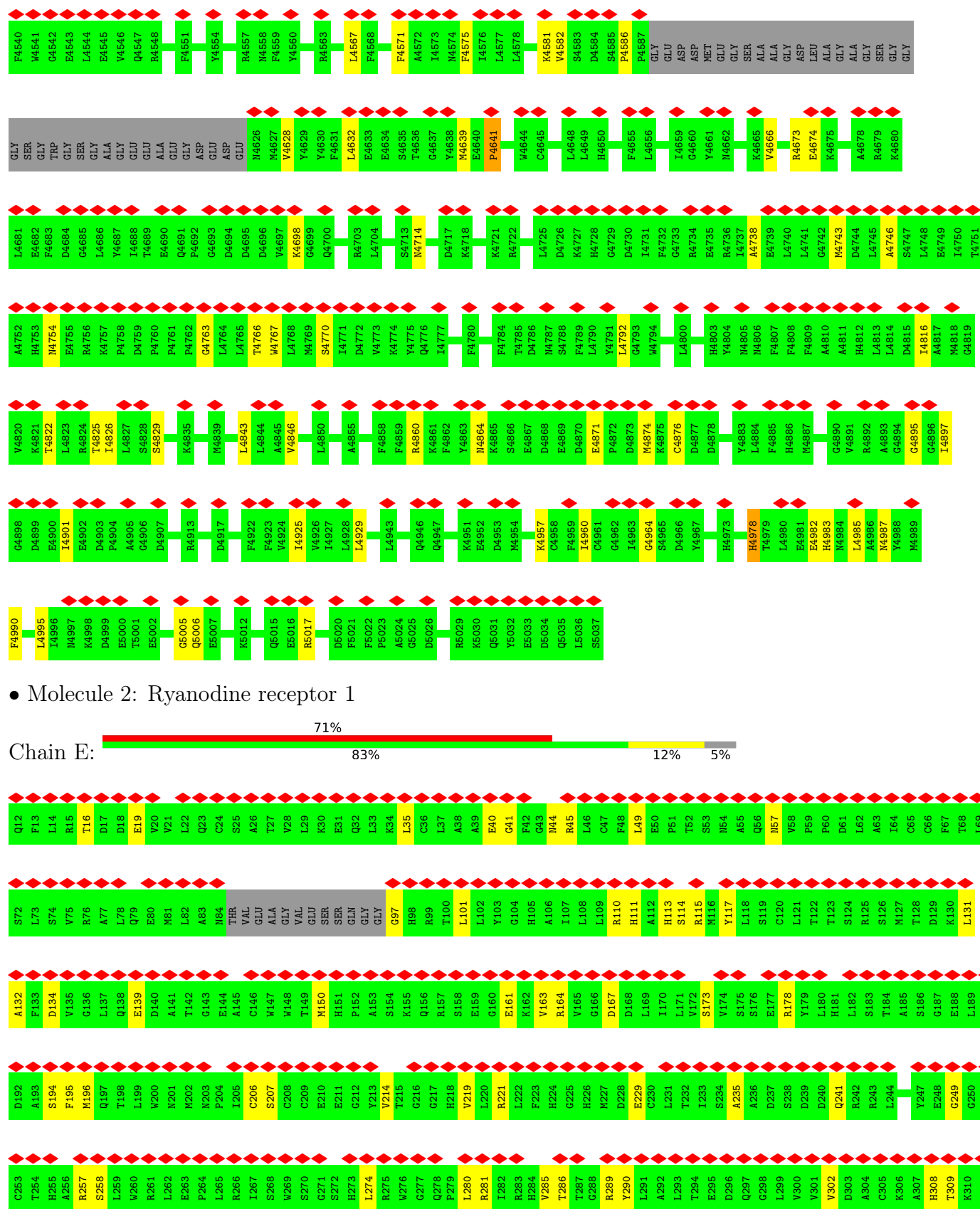


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VAL	GLN	ASP	ILE	PRO	ALA	ARG	ARG	ASN	PRO	R1020	L1021	L1021	V1022	P1023	Y1024	R1025	L1026	L1027	M960	M961	S962	N963	G964	Y965	K966	P967	A968	P969	L970	D971	S972	H974	V975	R976	L977	T978	P979	A980	Q981	T982	T983	L984	V985	D986	R987	L988	T928	L929	K930	T931	L932	L933	A934	L935	G936	C937	H938	V939	G940	N941	A942	D943	E944	K945
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G766	V767	F768	E769	A770	F771	N772	L773	D774	G775	L776	F777	F778	P779	W780	P842	S843	R844	C845	L846	S847	H848	T849	D850	F851	W852	P853	C854	P855	R856	D857	THR	VAL	GLN	I861	V862	L863	P864	P865	H866	L867	E868	R869	I870	R871	E872	K873	L874	A875	E876	N877	I878	H879	E880	L881	W882	A883	L884	T885						
G704	N705	G706	V707	G708	D709	D710	L711	Y712	S713	Y714	G715	F716	D717	G718	L719	H720	L721	W722	T723	G724	H725	V726	A727	R728	F729	V730	T731	S732	P733	G734	Q735	H736	L737	L738	A739	P740	E741	D742	V743	W744	S745	C746	C747	L748	D749	L750	L688	T689	E690	G691	Y692	N693	S693	P694	Y695	P696	G697	G698	E700	G703				
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I578	Q579	E580	N581	H582	I583	I586	I587	S588	L589	L590	H593	G594	R595	N596	H597	K598	V599	L600	D601	C604	S605	L606	C607	V608	C609	N610	G611	V612	A613	V614	R615	S616	N617	Q618	D619	L620	N624	L625	L626	P627	G628	R629	E630	L631	L632	L633	Q634	T635	N636	L637	I638	N639	Y640	V641	T642									
A507	G508	E509	E510	A511	A512	E513	S514	V515	K516	E517	N520	L521	L522	Y523	E524	A527	S528	R531	G532	N533	R534	A535	N536	C537	A538	L539	F540	S541	T542	S549	K550	L551	D552	R553	L554	E555	A556	S557	S558	G559	I560	L561	E562	C566	V567	L568	I569	E570	S571	P572	L575	N576	I577											

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K2221	E2222	I2223	R2224	F2225	P2226	K2227	M2228	V2229	R2234	F2235	Y2236	F2239	I2242	S2243	R2244	R2248	F2251	D2252	H2253	Y2256	L2257	N2260	S2261	G2262	L2263	G2264	L2265	G2266	M2267	Q2268	G2269	P2272	L2273	D2274	V2275	A2276	A2277	A2278	S2279	N2283	N2284	E2285	L2286	A2287	L2288	A2289	L2290	Q2291	E2292	Q2293																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
A2137	R2140	A2141	Y2142	T2143	I2144	S2147	E2150	M2153	S2154	L2155	L2156	R2163	L2166	I2167	V2168	Q2169	M2170	G2171	P2172	Q2173	I2179	N2184	T2185	L2186	N2187	N2188	K2189	Y2192	Q2193	N2196	R2199	A2200	H2204	M2208	E2209	V2210	M2211	V2212	N2213	V2214	L2215	G2216	G2217	G2218	E2219	T2220																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
SER	ARG	LEU	ARG	SER	LEU	LEU	THR	VAL	ARG	LEU	VAL	LEU	LYS	LYS	GLU	LYS	PRO	GLU	GLU	LEU	PRO	ALA	GLU	K2089	K2090	E1963	E2025	D2026	I2027	R2028	Q2029	D2030	L2031	F2034	H2035	Q2036	D2037	L2038	L2039	A2040	H2041	C2042	G2043	I2044	Q2045	L2046	E2047	G2048	GLU	GLU	GLU	GLU	PRO	GLU	GLU	GLU	THR	SER	LEU	SER																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
L1927	Q1928	M1929	K1930	L1931	P1932	Y1935	N1941	L1942	L1943	E1944	Y1945	F1946	C1947	D1948	H1953	R1954	A1959	A1960	F1961	A1962	E1963	R1964	Y1965	K1968	L1969	Q1970	A1971	N1972	Q1973	R1974	S1975	R1976	Y1977	A1978	L1979	L1980	M1981	R1982	A1983	F1984	T1985	M1986	Q1987	A1988	L1989	E1990	T1991	A1992	R1993	R1994	T1995	R1996	E1997	F1998																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
M1865	E1869	V1870	F1871	L1872	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	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	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	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	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	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	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	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	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	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	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	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	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	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	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	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	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	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	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	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	GLU	GLU	GLU

X3231	X3171	X3035	X2957	X2895	GLU	W2775	X2685	X2625	X2563	X2493	G2419	R2369
X3232	X3172	X3036	X2958	A2896	LYS	S2776	X2686	X2626	X2564	X2494	I2422	R2360
X3233	X3173	X3037	X2959	G2897	LYS	Y2777	X2687	X2627	X2565	X2497	M2423	E2362
X3234	X3174	X3038	X2960	G2898	THR	G2778	X2688	X2628	X2566	X2498	S2424	C2363
X3235	X3175	X3039	X2961	G2899	ARG	E2779	X2689	X2629	X2567	X2499	F2425	F2364
X3236	X3176	X3040	X2962	G2900	LYS	N2780	X2690	X2630	X2568	X2500	Y2426	Q2365
X3241	X3177	X3041	X2963	T2901	SER	X2781	X2691	X2631	X2569	X2501	A2427	P2366
X3242	X3178	X3042	X2964	T2902	GLN	D2782	X2692	X2632	X2570	X2502	L2428	A2367
X3243	X3179	X3043	X2965	P2903	THR	E2783	X2693	X2633	X2571	X2506	A2428	L2368
X3244	X3180	X3044	X2966	L2904	ALA	E2784	X2694	X2634	X2574	X2507	I2430	R2369
X3245	X3181	X3045	X2967	L2905	GLN	L2785	X2695	X2635	X2575	X2508	D2431	G2370
X3246	X3182	X3046	X2968	V2906	THR	K2786	X2696	X2636	X2576	X2511	L2432	E2371
X3247	X3183	X3047	X2969	P2907	ASP	T2787	X2697	X2637	X2577	X2512	L2433	G2372
X3248	X3184	X3048	X2970	Y2908	PRO	H2788	X2698	X2638	X2578	X2513	G2434	G2373
X3249	X3185	X3049	X2971	D2909	GLU	P2789	X2699	X2639	X2579	X2514	R2435	G2374
X3250	X3186	X3050	X2972	T2910	ARG	M2790	X2700	X2640	X2580	X2515	C2436	S2375
X3251	X3187	X3051	X2973	T2911	GLY	L2791	X2701	X2641	X2581	X2516	A2437	G2376
X3252	X3188	X3052	X2974	T2912		R2792	X2702	X2642	X2582	X2517	P2438	L2377
X3253	X3189	X3053	X2975	G2913	Y2855	P2793	X2703	X2643	X2583	X2518	H2441	L2378
X3254	X3190	X3054	X2976	K2914	P2856	Y2794	X2704	X2644	X2584	X2519	L2442	A2378
X3261	X3191	X3055	X2977	K2915	Q2858	D2795	N2754	X2645	X2585	X2520	G2446	T2380
X3262	X3192	X3056	X2978	K2916	P2859	T2796	F2735	X2646	X2586	X2521	K2447	E2381
X3263	X3193	X3057	X2979	D2861	P2860	F2797	D2756	X2647	X2587	X2522	G2448	E2382
X3264	X3194	X3058	X2980	L2862	D2861	S2798	R2738	X2648	X2588	X2523	E2449	A2383
X3265	X3195	X3059	X2981	S2863	G2864	E2799	P2739	X2649	X2589	X2524	F2450	T2384
X3266	X3196	X3060	X3000	G2864	V2865	K2800	V2740	X2650	X2590	X2525	A2451	R2385
X3267	X3197	X3061	X3001	V2865	D2801	D2801	E2741	X2651	X2591	X2526	L2452	L2386
X3268	X3198	X3062	X3002	T2867	T2866	K2802	T2742	X2652	X2592	X2527	R2453	S2387
X3269	X3199	X3063	X3003	S2867	S2868	E2803	L2743	X2653	X2593	X2528	R2454	E2388
X3270	X3200	X3134	X3004	Q2924	R2869	L2804	L2744	X2654	X2594	X2529	A2455	D2389
X3271	X3201	X3135	X3005	Q2925	R2869	Y2805	V2745	X2655	X2595	X2530	I2456	P2390
X3272	X3202	X3136	X3006	E2925	E2870	R2806	V2746	X2656	X2596	X2531	L2457	R2391
X3273	X3203	X3137	X3007	L2927	L2871	W2807	L2747	X2657	X2597	X2532	R2458	A2392
X3274	X3204	X3138	X3008	K2928	Q2872	P2808	I2747	X2658	X2598	X2533	S2459	D2393
X3275	X3205	X3139	X3009	F2929	A2873	L2809	P2748	X2659	X2599	X2534	L2460	G2394
X3276	X3206	X3140	X3010	L2930	M2874	K2810	K2750	X2660	X2600	X2535	L2460	P2395
X3277	X3207	X3141	X3011	Q2931	E2875	E2811	L2751	X2661	X2602	X2536	L2463	GLY
X3278	X3208	X3142	X3012	M2932	A2876	S2812	D2752	X2662	X2603	X2537	D2464	VAL
X3279	X3209	X3143	X3013	Q2933	Q2877	L2813	D2753	X2663	X2604	X2538	D2465	ARG
X3280	X3210	X3144	X3014	G2934	L2878	K2814	F2754	X2664	X2605	X2539	L2466	ARG
X3281	X3211	X3145	X3015	Y2935	A2879	A2815	L2755	X2665	X2606	X2540	V2467	ASP
X3282	X3212	X3146	X3016	A2936	E2880	M2816	I2756	X2666	X2607	X2541	G2468	ARG
X3283	X3213	X3147	X3017	T2937	N2881	L2817	K2757	X2667	X2608	X2542	I2470	ARG
X3284	X3214	X3148	X3018	Y2938	Y2882	A2818	F2758	X2668	X2609	X2543	S2471	GLU
X3285	X3215	X3149	X3019	R2939	H2883	W2819	A2759	X2669	X2610	X2544	L2472	HIS
X3286	X3216	X3150	X3020	X2942	N2884	E2820	E2760	X2670	X2611	X2550	P2473	PHE
X3287	X3217	X3151	X3021	L2943	T2885	W2821	T2761	X2671	X2612	X2551	L2474	GLY
X3288	X3218	X3152	X3022	X2944	W2886	T2822	Y2762	X2672	X2613	X2552	Q2475	GLU
X3289	X3219	X3153	X3023	L2945	G2887	R2822	T2762	X2673	X2614	X2555	I2476	PRO
X3290	X3220	X3154	X3024	X2946	R2888	L2823	H2763	X2674	X2615	X2556	L2476	GLU
X3291	X3221	X3155	X3025	X2947	E2824	E2824	E2764	X2675	X2616	X2557	P2477	GLU
X3292	X3222	X3156	X3026	X2948	K2825	K2825	K2765	X2676	X2617	X2558	L2478	N2414
X3293	X3223	X3157	X3027	L2949	A2826	A2826	W2766	X2677	X2618	X2559	L2479	R2415
X3294	X3224	X3158	X3028	X2950	R2827	R2827	A2767	X2678	X2619	X2560	X2487	V2416
X3295	X3225	X3159	X3029	X2951	E2828	E2828	F2768	X2679	X2620	X2561	X2488	H2417
X3296	X3226	X3160	X3030	X2952	E2830	G2829	D2769	X2680	X2621	X2562	X2489	L2418
X3297	X3227	X3161	X3031	X2953	E2831	E2830	K2770	X2681	X2622	X2562	X2490	
X3298	X3228	X3162	X3032	X2954	GLU	GLU	I2771	X2682	X2623			
X3299	X3229	X3163	X3033	X2955	ARG	THR	Q2772	X2683	X2624			
X3300	X3230	X3170	X3034	X2956			N2774	X2684	X2625			

A4186	S4187	R4188	R4189	I4190	E4191	R4192	R4193	Y4194	F4195	E4196	E4199	R4202	A4203	Q4204	W4205	E4206	M4207	R4215	Q4216	F4219	D4220	N4223	E4224	Q4225	G4226	E4227	A4228	E4229	K4230	M4231	E4232	E4239	D4240	L4247	I4251	S4252	E4253	X4320	X4321	X4322	X4330	X4336	X4337	X4338	X4339	X4340	X4341	X4342	X4343	X4344	X4345	X4346	X4347	X4348	X4349	X4350	X4351	X4352	X4353	X4354	X4355	X4356	X4357	X4358	X4359	X4360
E4116	A4117	D4118	E4119	M4120	E4121	M4122	I4123	M4124	F4125	E4126	E4127	F4128	A4129	M4130	R4131	F4132	Q4133	E4134	P4135	A4136	R4137	D4138	I4139	F4140	M4141	N4142	L4147	E4152	H4156	R4159	L4160	M4161	M4162	F4163	L4164	E4165	L4166	A4167	E4168	S4169	I4170	L4171	E4172	Y4173	F4174	R4175	P4176	Y4177	R4180	I4181	E4182	X4343	M4184	G4185												
V4055	E4056	L4059	K4060	F4061	D4062	D4063	M4064	F4065	L4066	K4067	L4068	K4069	D4070	I4071	V4072	G4073	S4074	E4075	A4076	F4077	Q4078	D4079	Y4080	V4081	T4082	D4083	P4084	R4085	G4086	L4087	I4088	S4089	K4090	K4091	D4092	F4093	Q4094	K4095	A4096	M4097	D4098	S4099	Q4100	L4101	Q4102	F4103	T4104	G4105	P4106	I4107	L4108	Q4109	F4110	L4111	L4112	S4113	C4114	S4115								
H3982	S3983	R3984	L3985	W3986	F3992	L3993	H3994	V3995	F3996	A3997	H3998	M3999	M4000	K4002	L4003	A4004	Q4005	D4006	S4007	S4008	Q4009	I4010	E4011	L4012	L4013	K4014	E4015	L4016	D4018	L4019	Q4020	K4021	D4022	L4027	L4030	L4031	E4032	Q4033	M4034	V4035	V4036	M4037	G4038	M4039	I4040	A4041	R4042	M4047	L4048	Y4049	E4050	M4054														
V3902	L3903	R3904	T3907	Q3908	S3909	T3910	T3911	Y3922	L3923	L3924	R3925	E3928	S3929	I3930	S3931	F3932	Y3934	W3935	Y3936	Y3937	S3938	G3939	K3940	D3941	V3942	I3943	E3944	E3945	Q3946	G3947	K3948	R3949	N3950	A3954	R3955	Q3959	Q3960	F3961	F3962	N3963	E3967	Q3970	G3971	P3972	C3973	N3976	Q3977	A3981																		
K3821	D3822	K3823	K3824	E3825	F3828	F3829	Q3830	Q3833	M3836	L3842	D3843	F3847	E3848	R3849	Q3850	N3851	F3852	A3853	E3854	G3855	G3856	G3857	M3858	S3859	N3860	E3861	N3862	G3863	T3864	V3865	L3866	N3867	R3868	Q3869	N3870	G3871	E3872	Q3873	F3874	N3875	A3876	D3877	E3878	F3880	D3883	L3888	Q3889	N3897	F3899																	
E3747	E3748	V3749	E3750	V3751	S3752	F3753	E3754	E3755	K3756	E3757	M3758	E3759	K3760	Q3761	L3762	L3763	L3764	Y3765	Q3766	Q3767	R3768	R3769	L3770	H3771	T3772	R3773	S3706	R3707	L3710	T3711	E3712	K3713	T3639	P3640	L3641	N3642	N3643	L3644	H3647	R3648	A3649	C3650	N3651	N3652	F3653	S3656	Y3657	K3658	A3659	A3660	W3661	L3662	L3663	T3664	E3665	D3666	H3667	S3668	F3669							
E3670	D3671	I3674	D3675	D3676	K3679	A3680	G3681	E3682	Q3683	E3684	E3685	E3686	E3687	E3688	E3689	V3690	E3691	E3692	K3693	K3694	F3705	S3706	R3707	L3710	T3711	E3712	K3713	S3714	K3715	L3716	D3717	E3718	D3719	Y3720	L3721	V3722	K3723	A3724	Y3725	A3726	C3733	H3734	L3735	E3736	E3737	Q3738	G3739	E3740	N3741	GLU	GLU	ALA	GLU													
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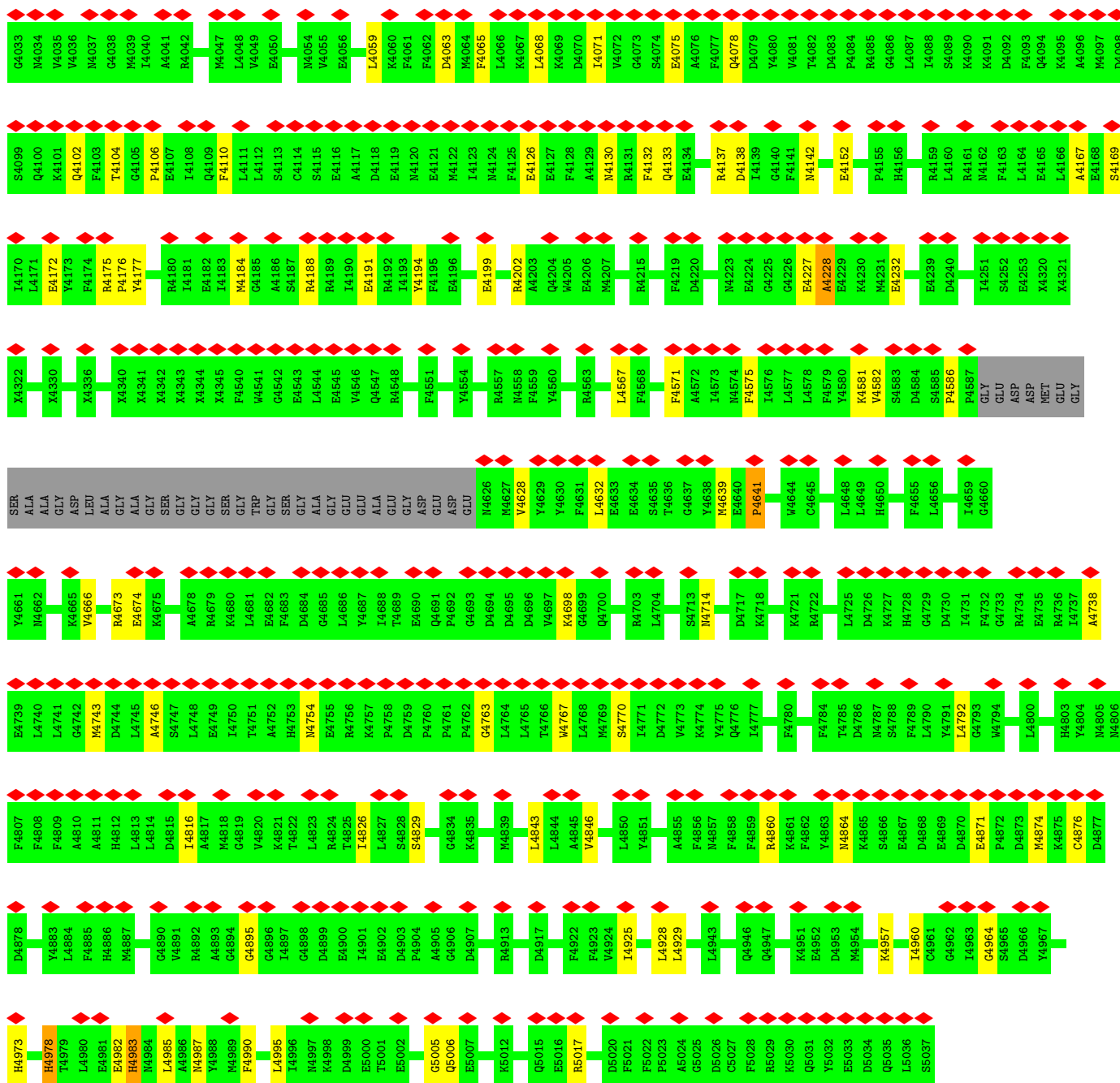


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			M961	K901	G841	V781	H720	G660	V599			C393	G333
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			R1036	P969	F851	W790	P729	V668	C509	T542		H405	E343
			D1037	D971	W852	F791	W730	D669	G611	D545		A408	L345
			L972	L972	L913	L793	S732	V671	V612			L410	F347
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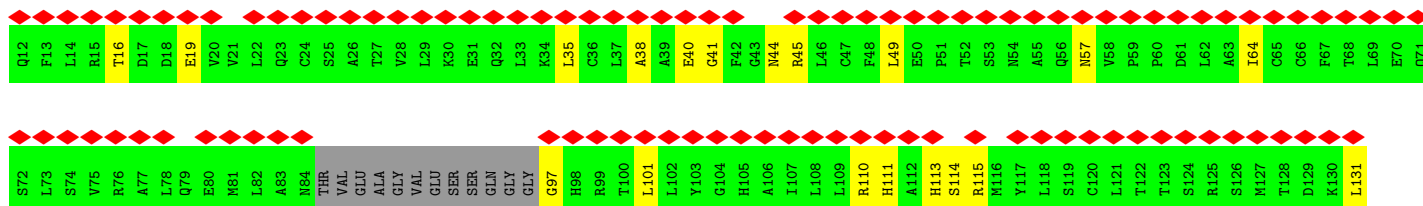
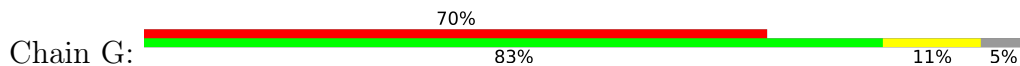


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X3290	X3291	X3292	X3293	X3294	X3295	X3296	X3297	X3298	X3299	X3300	X3301	X3302	X3303	X3304	X3305	X3306	X3307	X3308	X3309	X3310	X3311	X3312	X3313	X3314	X3315	X3316	X3317	X3318	X3319	X3320	X3321	X3322	X3323	X3324	X3325	X3326	X3327	X3328	X3329	X3330	X3331	X3332	X3333	X3334	X3335	X3336	X3337	X3338	X3339	X3340	X3341	X3342	X3343	X3344	X3345	X3346	X3347	X3348	X3349												
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X3410	X3411	X3412	X3413	X3414	X3415	X3416	X3417	X3418	X3419	X3420	X3421	X3422	X3423	X3424	X3425	X3426	X3427	X3428	X3429	X3430	X3431	X3432	X3433	X3434	X3435	X3436	X3437	X3438	X3439	X3440	X3441	X3442	X3443	X3444	X3445	X3446	X3447	X3448	X3449	X3450	X3451	X3452	X3453	X3454	X3455	X3456	X3457	X3458	X3459	X3460	X3461	X3462	X3463	X3464	X3465	X3466	X3467	X3468	X3511												
X3512	X3513	X3514	X3515	X3516	X3517	X3518	X3519	X3520	X3521	X3522	X3523	X3524	X3525	X3526	X3527	X3528	X3529	X3530	X3531	X3532	X3533	X3534	X3537	X3538	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	X3570	X3571	X3572													
X3573	X3574	X3575	X3576	X3577	X3578	X3579	X3580	X3581	X3582	X3583	X3584	X3585	X3586	X3587	X3588	X3589	X3590	X3591	X3592	X3593	X3594	X3595	X3596	X3597	X3598	X3599	X3600	X3601	X3602	X3603	X3604	X3605	X3606	X3607	X3608	X3609	X3610	X3611	X3612	X3613	T3614	T3615	P3616	L3641	Y3642	N3643	L3644	H3647	R3648	A3649	C3650	N3651	M3652	F3653	S3656	Y3657	K3658	A3659													
A3660	W3661	I3662	L3663	T3664	E3665	D3666	H3667	S3668	F3669	I3674	D3675	D3676	K3679	G3680	G3681	G3682	Q3683	Q3684	E3685	E3686	E3687	E3688	E3689	V3690	E3691	E3692	K3693	K3694	H3704	F3705	S3706	R3707	L3710	T3711	E3712	K3713	S3714	L3715	L3716	D3717	E3718	D3719	Y3720	L3721	Y3722	K3723	A3724	A3725	K3731	H3734	L3735	E3736																			
E3737	Q3738	G3739	E3740	N3741	L3742	Q3743	Q3744	Q3745	Q3746	Q3747	Q3748	Q3749	Q3750	Q3751	Q3752	Q3753	Q3754	Q3755	Q3756	Q3757	Q3758	Q3759	Q3760	Q3761	Q3762	Q3763	Q3764	Q3765	Q3766	Q3767	Q3768	Q3769	Q3770	Q3771	Q3772	Q3773	Q3774	Q3775	Q3776	Q3777	Q3778	Q3779	Q3780	Q3781	Q3782	Q3783	Q3784	Q3785	Q3786	Q3787	Q3788	Q3789	Q3790	Q3791	Q3792	Q3793	Q3794	Q3795	Q3796	Q3797	Q3798	Q3799	Q3800	Q3801	Q3802	Q3803	Q3804	Q3805	Q3806	Q3807	Q3808
N3809	A3810	K3815	N3816	L3817	Y3818	Y3819	L3820	K3821	D3822	K3823	K3824	E3825	F3828	F3829	Q3830	Q3833	M3836	L3842	D3843	F3847	E3848	R3849	Q3850	N3851	K3852	A3853	E3854	G3855	L3856	G3857	N3858	V3859	E3861	D3862	G3863	T3864	V3865	I3866	N3867	R3868	Q3869	N3870	G3871	E3872	K3873	V3874	N3875	A3876	D3877	D3878	E3879	F3880																			
L3883	L3884	F3885	R3886	F3887	L3888	Q3889	E3893	N3897	D3898	F3899	Y3902	L3903	R3904	L3905	Q3906	T3907	G3908	N3909	T3910	T3911	T3912	I3913	Y3922	L3923	L3924	R3925	E3928	S3929	L3930	S3931	D3932	F3933	V3934	Y3935	Y3936	Y3937	S3938	G3939	K3940	D3941	V3942	I3943	E3944	E3945	Q3946	G3947	K3948	R3949	N3950	A3954	M3955	E4032																			
X3204	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	X3060	X3061	X3062	X3063	X3134	X3135	X3136	X3137	X3138	X3139	X3140	X3141	X3142	X3143	X3144	X3145	X3146	X3147	X3148	X3149	X3150	X3151	X3152	X3153												
X3154	X3155	X3156	X3157	X3158	X3159	X3160	X3161	X3162	X3163	X3170	X3171	X3172	X3173	X3174	X3175	X3176	X3177	X3178	X3179	X3180	X3181	X3182	X3183	X3184	X3185	X3186	X3187	X3188	X3189	X3190	X3191	X3192	X3193	X3194	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	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	X3300	X3301	X3302	X3303	X3304	X3305	X3306	X3307	X3308	X3309	X3310	X3311	X3312	X3313	X3314	X3315	X3316	X3317	X3318	X3319	X3320	X3321	X3322	X3323	X3324	X3325	X3326	X3327	X3328	X3329	X3330	X3331	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	X3361	X3362	X3363	X3364	X3365	X3366	X3367	X3368	X3369	X3370	X3371	X3372	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	X3418	X3419	X3420	X3421	X3422	X3423	X3424	X3425	X3426	X3427	X3428	X3429	X3430	X3431	X3432	X3433	X3434	X3435	X3436	X3437	X3438	X3439	X3440	X3441	X3442	X3443	X3444	X3445	X3446	X3447	X3448	X3449	X3450	X3451	X3452	X3453	X3454	X3455	X3456	X3457	X3458	X3459	X3460	X3461	X3462	X3463	X3464	X3465	X3466	X3467	X3468	X3511												
X3512	X3513	X3514	X3515	X3516	X3517	X3518	X3519	X3520	X3521	X3522	X3523	X3524																																																											



• Molecule 2: Ryanodine receptor 1



K945	A946	E947	D948	N949	L950	K951	K952	T953	K954	L955	P956	K957	T958	Y959	M960	M961	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	A988	A989	N990	A997	R998	D999	R1000	V1001	A1002	Q1003	G1004	V1005	S1006	Y1007	S1008				
P825	T826	R827	P828	Y829	R830	R831	E832	T833	G834	P835	G836	P837	H838	L839	G841	P842	S843	R844	G845	L846	S847	H848	T849	D850	P851	W852	P853	C854	P855	W856	D857	THR	VAL	G798	R800	P802	L803	P804	R805	H806	L807	E808	R809	R871	E872	R873	L874	A875	E876	N877	L878	E880	L881	W882	A883	L884					
F763	G766	F767	F768	E769	A770	F771	N772	L773	D774	L776	F777	F778	F779	W780	Y781	S782	F783	S784	A785	G786	W787	K788	W789	R790	F791	L792	L793	G794	G795	R796	H797	G798	E799	F800	F802	L803	P804	P805	P806	G807	Y808	A809	H812	E813	A814	W815	L816	P817	R818	E819	R820	L821	R822	L823	E824						
G703	G704	N705	G706	V707	G708	D709	D710	L711	V712	S713	V714	G715	F716	D717	G718	L719	H720	L721	W722	T723	G724	H725	V726	A727	R728	F729	W730	T731	S732	P733	G734	Q735	H736	L737	L738	A739	E741	D742	V743	V744	S745	C746	C747	L748	D749	L750	S751	F752	F753	S754	T755	W756	F757	R758	L759	N760	G761	C762			
S643	T644	R645	P646	R647	T648	F649	V650	G651	R652	A653	G654	G655	S656	T657	Q658	Y659	G660	R661	W662	T663	F664	E665	V666	R667	W668	D669	E670	V671	V672	P673	F674	L675	T676	A677	C678	A679	T680	H681	L682	R683	V684	G685	W686	A687	L688	T689	E690	G691	S692	P693	P694	V695	P696	G697	G698	E699	E700	G701	W702		
Q579	E580	N581	H582	I583	K584	L587	S588	L589	H593	G594	R595	N596	H597	K598	V599	L600	D601	V602	L603	C604	S605	L606	C607	V608	C609	N610	G611	V612	A613	V614	R615	S616	N617	Q618	D619	L620	M624	L625	L626	P627	G628	R629	E630	L631	L632	L633	Q634	T635	N636	L637	L638	V639	Y640	V641	T642						
E510	A511	A512	E513	S514	W515	K516	E517	N520	L521	L522	Y523	A527	S528	R531	G532	N533	R534	A535	N536	C537	A538	L539	F540	S541	T542	D545	S549	K550	L551	D552	R553	L554	A555	S557	S558	D559	G559	T560	L561	E562	C566	V567	L568	L569	E570	S571	P572	E573	V574	L575	N576	L577	I578								
K373	K374	K375	A376	L377	L378	H379	Q380	E381	G382	H383	M384	D385	R386	A387	L388	F389	L390	T391	R392	C393	Q394	Q395	E396	E397	S398	Q399	R402	M403	I404	E405	A408	G409	L410	Y411	M412	Q413	F414	I415	K416	G417	L418	D419	S420	F421	S422	G423	R426	G427	S428	G429	P430	P431	A432	G433	P434	A435					
C253	T254	H255	A256	R257	S258	L259	W260	R261	L262	E263	P264	L265	R266	I267	S268	W269	T270	C271	S272	H273	L274	R275	W276	G277	Q278	P279	L280	R281	I282	R283	H284	V285	T286	T287	G288	R289	D288	E289	C290	L291	A292	L293	T294	I295	D296	Q297	G298	L299	V300	V301	Y302	D303	A304	C305	T306	A307	H308	T309	K310	A311	T312
D192	A193	S194	F195	M196	Q197	T198	L199	W200	N201	M202	N203	P204	E104	I205	C206	S207	W208	C208	C209	T149	M150	H151	E211	G212	Y213	V214	T215	G216	G217	H218	V219	L220	R221	L222	F223	H224	G225	H226	M227	D228	E229	C230	L231	T232	I233	S234	A235	A236	S238	D239	D240	Q241	R242	C243	L244	Y247	E248	C249	G250	A251	V252
S313	F314	C315	F316	R317	V318	S319	K320	E321	K322	L323	D324	T325	A326	P327	K328	R329	D330	V331	E332	G333	M334	G335	P336	P337	E338	I339	K340	Y341	G342	E343	H344	L345	C346	F347	V348	Q349	H350	S351	A352	S353	G354	L355	W356	L357	T358	Y359	V360	A361	P362	D363	A364	K365	A366	L367	R368	L369	G370	V371	L372		
K945	A946	E947	D948	N949	L950	K951	K952	T953	K954	L955	P956	K957	T958	Y959	M960	M961	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	A988	A989	N990	A997	R998	D999	R1000	V1001	A1002	Q1003	G1004	V1005	S1006	Y1007	S1008				



LYS	E1997	LEU	E2222	P2361	I2422	X2497	X2568	X2631	X2691	V2781	L2855
ILE	F1998	ARG	I2223	E2362	M2423	X2498	X2569	X2632	X2692	D2782	N2856
SER	R1999	SER	R2224	C2363	S2424	X2499	X2570	X2633	X2693	E2783	P2857
GLN	S2000	LEU	P2225	F2364	F2425	X2500	X2571	X2634	X2694	E2784	Q2858
ALA	P2001	LEU	P2226	G2365	Y2426	X2501	X2572	X2635	X2695	L2785	P2859
GLN	P2002	THR	K2227	P2366	A2427	X2502	X2573	X2636	X2696	K2786	T2859
THR	Q2003	VAL	K2228	A2367	A2428	X2506	X2574	X2637	X2697	T2787	Y2860
ASP	E2004	ARG	E2229	L2368	L2429	X2506	X2575	X2638	X2698	H2788	P2861
ARG	Q2005	LEU	V2230	R2369	I2430	X2511	X2576	X2639	X2699	M2789	Q2862
LEU	Q2006	VAL	R2234	G2370	G2434	X2512	X2577	X2640	X2700	M2790	GLY
LYS	L2006	LYS	F2235	E2371	R2435	X2513	X2578	X2641	X2701	L2791	N2855
LYS	N2007	LYS	Y2238	G2372	P2436	X2514	X2579	X2642	X2702	R2792	N2856
GLU	L2010	GLU	F2239	G2373	H2441	X2515	X2580	X2643	X2703	P2793	P2857
LYS	H2011	LYS	Y2240	S2374	L2442	X2516	X2581	X2644	X2704	T2794	P2858
LYS	P2012	PRO	I2242	G2375	H2442	X2517	X2582	X2645	X2705	K2795	Q2859
LYS	K2013	GLU	R2243	L2376	L2443	X2518	X2583	X2646	X2706	T2796	P2860
LYS	D2014	GLU	R2244	L2377	G2446	X2519	X2584	X2647	X2707	F2797	P2861
LYS	E2015	LEU	L2248	A2378	K2447	X2520	X2585	X2648	X2708	S2798	Q2862
LYS	A2016	LEU	R2249	A2379	E2448	X2521	X2586	X2649	X2709	E2799	L2862
ALA	D2017	ALA	F2251	T2380	E2449	X2522	X2587	X2650	X2710	K2800	S2863
GLU	E2018	GLU	D2252	E2381	E2450	X2523	X2588	X2651	X2711	D2801	Q2864
LYS	E2019	LEU	H2253	E2382	L2451	X2524	X2589	X2652	X2712	K2802	V2865
LYS	D2020	LEU	Y2256	L2383	R2452	X2525	X2590	X2653	X2713	E2803	T2866
LYS	C2021	LEU	L2257	L2384	R2453	X2526	X2591	X2654	X2714	L2743	L2867
LYS	P2022	LEU	L2258	R2385	L2454	X2527	X2592	X2655	X2715	N2744	Q2868
LYS	L2023	LEU	L2259	T2386	A2455	X2528	X2593	X2656	X2716	P2739	S2869
LYS	P2024	LEU	S2261	E2387	A2456	X2529	X2594	X2657	X2717	E2740	P2870
LYS	E2025	LEU	G2262	E2388	L2457	X2530	X2595	X2658	X2718	T2742	Q2871
LYS	D2026	LEU	L2263	D2328	R2458	X2531	X2596	X2659	X2719	L2743	L2872
LYS	I2027	LEU	L2264	C2329	S2459	X2532	X2597	X2660	X2720	N2744	Q2873
LYS	R2028	LEU	G2265	E2330	L2460	X2533	X2598	X2661	X2721	K2750	N2874
LYS	Q2029	LEU	L2266	D2331	L2461	X2534	X2599	X2662	X2722	L2751	L2875
LYS	P2034	LEU	L2267	L2332	L2462	X2535	X2600	X2663	X2723	D2752	A2876
LYS	H2035	LEU	Y2192	L2333	L2463	X2536	X2601	X2664	X2724	S2753	Q2877
LYS	Q2036	LEU	Q2193	D2334	L2464	X2537	X2602	X2665	X2725	F2754	L2878
LYS	A2040	LEU	N2196	F2337	L2465	X2538	X2603	X2666	X2726	L2755	L2879
LYS	H2041	LEU	P2113	A2338	G2466	X2539	X2604	X2667	X2727	N2756	A2880
LYS	C2042	LEU	E2115	E2339	I2467	X2540	X2605	X2668	X2728	K2757	N2881
LYS	G2043	LEU	R2118	F2340	L2470	X2541	X2606	X2669	X2729	F2758	L2882
LYS	L2044	LEU	H2204	V2341	S2471	X2542	X2607	X2670	X2730	A2759	H2883
LYS	Q2045	LEU	F2121	N2342	L2472	X2543	X2608	X2671	X2731	E2760	N2884
LYS	L2046	LEU	M2208	G2343	P2473	X2544	X2609	X2672	X2732	T2762	T2885
LYS	E2047	LEU	E2209	E2344	L2474	X2550	X2610	X2673	X2733	H2763	W2886
LYS	Q2048	LEU	V2210	S2345	Q2475	X2551	X2611	X2674	X2734	E2764	G2887
LYS	GLU	GLU	M2211	S2346	Q2476	X2552	X2612	X2675	X2735	L2675	L2888
LYS	GLU	GLU	V2212	E2347	L2477	X2553	X2613	X2676	X2736	K2766	K2889
LYS	PRO	PRO	N2213	E2348	T2478	X2554	X2614	X2677	X2737	L2677	L2890
LYS	GLU	GLU	L2214	N2349	L2479	X2555	X2615	X2678	X2738	A2767	K2891
LYS	GLU	GLU	L2215	A2350	X2488	X2556	X2616	X2679	X2739	F2768	E2892
LYS	GLU	GLU	G2216	A2351	X2489	X2557	X2617	X2680	X2740	D2769	Q2893
LYS	THR	THR	G2217	L2290	X2490	X2558	X2618	X2681	X2741	K2770	L2894
LYS	LEU	LEU	Q2218	Q2291	V2416	X2561	X2619	X2682	X2742	I2771	E2895
LYS	SER	SER	E2219	E2292	H2417	X2562	X2620	X2683	X2743	Q2772	A2896
LYS	SER	SER	T2220	Q2293	L2418	X2563	X2621	X2684	X2744	N2773	K2897
LYS	ARG	ARG	K2221	D2294	G2419	X2564	X2622	X2685	X2745	W2775	Q2898
LYS	ARG	ARG	L2295	L2295	X2496	X2565	X2623	X2686	X2746	S2776	G2899
LYS	ARG	ARG	L2295	L2295	X2496	X2566	X2624	X2687	X2747	Y2777	Q2900
LYS	ARG	ARG	L2295	L2295	X2496	X2567	X2625	X2688	X2748	E2778	
LYS	ARG	ARG	L2295	L2295	X2496	X2567	X2626	X2689	X2749	E2779	
LYS	ARG	ARG	L2295	L2295	X2496	X2567	X2627	X2690	X2750	N2780	

Q3833	K3766	Q3683	X3592	X3531	X3427	X3367	X3307	X3041	T2901
	E3757	E3684	X3593	X3532	X3428	X3368	X3308	X3042	H2902
	M3758	E3685	X3594	X3533	X3429	X3369	X3309	X2964	P2903
	E3769	E3686	X3595	X3534	X3430	X3370	X3310	X2965	L2904
	K3760	E3687	X3596	X3537	X3431	X3371	X3311	X2966	L2905
	Q3761	E3688	X3597	X3538	X3432	X3372	X3312	X2967	V2906
	R3762	E3689	X3598	X3539	X3433	X3373	X3313	X2968	P2907
	L3763	V3690	X3599	X3540	X3434	X3374	X3314	X2969	V2908
	E3765	E3691	X3600	X3541	X3435	X3375	X3315	X2970	D2909
	Q3766	E3692	X3601	X3542	X3436	X3376	X3316	X2971	T2910
	Q3767	K3693	X3602	X3543	X3437	X3377	X3317	X2972	L2911
	S3768	K3694	X3603	X3544			X3318	X2973	T2912
	R3769	X3604	X3604	X3545	X3440		X3319	X2974	A2913
	L3770	H3704	X3605	X3546	X3441		X3320	X2975	K2914
	H3711	F3705	X3606	X3547	X3442		X3321	X2976	E2915
	T3772	S3706	X3607	X3548	X3443		X3322	X2977	K2916
	R3773	R3707	X3608	X3549			X3323	X2978	A2917
	G3774		X3609	X3550	X3446		X3324	X2979	D2918
	E3777	L3710	X3610	X3551	X3447		X3325	X2999	D2919
	M3778	T3711	X3611	X3552	X3448		X3326	X3000	R2920
	V3779	E3712	X3612	X3553	X3449		X3327	X3001	E2921
	L3780	K3713	X3613	X3554	X3450		X3328	X3002	K2922
	Q3781	S3714	T3639	X3555	X3451		X3329	X3003	A2923
	M3782	K3715	P3640	X3556	X3452		X3330	X3004	Q2924
		L3716	X3655	X3557	X3453		X3331	X3005	E2925
	C3786	D3717	X3656	X3558	X3454		X3332	X3006	L2926
	K3787	E3718	X3657	X3559	X3455		X3333	X3007	L2927
	C3788	D3719	X3658	X3560	X3456		X3334	X3008	K2928
	E3789	X3720	X3659	X3561	X3457		X3335	X3009	F2929
	A3792	L3721	H3647	X3562	X3458		X3336	X3010	L2930
	M3723	Y3722	K3648	X3563	X3459		X3337	X3011	Q2931
	A3724	K3724	A3649	X3564	X3460		X3338	X3012	H2932
	Y3725	Y3725	C3650	X3565	X3461		X3339	X3013	K2933
	A3726	A3726	N3651	X3566	X3462		X3340	X3014	Q2934
	K3731	K3731	F3653	X3567	X3463		X3341	X3015	V2935
	H3734	H3734	S3656	X3568	X3464		X3342	X3016	A2936
	L3735	L3735	Y3657	X3569	X3465		X3343	X3017	V2937
	E3736	E3736	K3658	X3570	X3466		X3344	X3018	T2938
	E3737	E3737	A3659	X3571	X3467		X3345	X3019	R2939
	Q3738	Q3738	A3660	X3572	X3468		X3346	X3020	K2942
	K3815	K3738	W3661	X3573	X3511		X3347	X3021	K2943
	M3816	G3739	L3662	X3574	X3512		X3348	X3022	K2944
	L3817	E3740	L3663	X3575	X3513		X3349	X3023	K2945
	D3818	E3741	T3664	X3576	X3514		X3350	X3024	K2946
	Y3819	GLY	E3665	X3577	X3515		X3351	X3025	K2947
	L3820	GLU	D3666	X3578	X3516		X3352	X3026	K2948
	K3821	ALA	H3667	X3579	X3517		X3353	X3027	K2949
		GLU	S3668	X3580	X3518		X3354	X3028	K2950
	K3824	E3747	F3669	X3581	X3519		X3355	X3029	K2951
	E3825	E3748		X3582	X3520		X3356	X3030	K2952
	F3828	V3749	T3674	X3583	X3521		X3357	X3031	K2953
	F3829	E3750	D3675	X3584	X3522		X3358	X3032	K2954
	Q3830	V3751	D3676	X3585	X3523		X3359	X3033	K2955
		S3752	K3679	X3586	X3524		X3360	X3034	K2956
		F3753	A3680	X3587	X3525		X3361	X3035	K2957
		E3754	G3681	X3588	X3526		X3362	X3036	K2958
		E3755	E3682	X3589	X3527		X3363	X3037	K2959
				X3590	X3528		X3364	X3038	K2960
					X3529		X3365	X3039	K2961
					X3530		X3366	X3040	K2962



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	0.058	Depositor
Minimum map value	-0.029	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	0.20	0/834	0.51	1/1123 (0.1%)
1	F	0.20	0/834	0.51	1/1123 (0.1%)
1	H	0.20	0/834	0.51	1/1123 (0.1%)
1	J	0.20	0/834	0.51	1/1123 (0.1%)
2	B	0.21	0/25428	0.52	3/34534 (0.0%)
2	E	0.21	0/25428	0.52	3/34534 (0.0%)
2	G	0.21	0/25428	0.52	3/34534 (0.0%)
2	I	0.21	0/25428	0.52	3/34534 (0.0%)
All	All	0.21	0/105048	0.52	16/142628 (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
2	B	0	16
2	E	0	16
2	G	0	16
2	I	0	16
All	All	0	64

There are no bond length outliers.

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	8	SER	N-CA-C	5.50	120.40	113.25
1	A	8	SER	N-CA-C	5.45	120.33	113.25
1	J	8	SER	N-CA-C	5.44	120.33	113.25
1	F	8	SER	N-CA-C	5.44	120.32	113.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	1829	PRO	N-CA-C	5.31	119.56	111.11

There are no chirality outliers.

5 of 64 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	139	GLU	Peptide
2	B	1676	LEU	Peptide
2	B	312	THR	Peptide
2	B	694	PRO	Peptide
2	B	808	TYR	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	16	0
1	F	818	0	824	19	0
1	H	818	0	824	16	0
1	J	818	0	824	15	0
2	B	29499	0	24746	281	0
2	E	29499	0	24746	286	0
2	G	29499	0	24746	275	0
2	I	29499	0	24746	273	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	102280	1154	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 1154 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:379:HIS:HD2	2:I:382:GLY:H	1.40	0.68
2:E:379:HIS:HD2	2:E:382:GLY:H	1.40	0.67
2:B:379:HIS:HD2	2:B:382:GLY:H	1.40	0.67
2:G:379:HIS:HD2	2:G:382:GLY:H	1.40	0.66
2:B:3773:ARG:HG3	2:B:3815:LYS:HZ3	1.61	0.65

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%)	92 (88%)	13 (12%)	0	100	100
1	F	105/108 (97%)	92 (88%)	13 (12%)	0	100	100
1	H	105/108 (97%)	92 (88%)	13 (12%)	0	100	100
1	J	105/108 (97%)	92 (88%)	13 (12%)	0	100	100
2	B	3235/4416 (73%)	2888 (89%)	343 (11%)	4 (0%)	48	83
2	E	3235/4416 (73%)	2888 (89%)	343 (11%)	4 (0%)	48	83
2	G	3235/4416 (73%)	2887 (89%)	344 (11%)	4 (0%)	48	83
2	I	3235/4416 (73%)	2888 (89%)	343 (11%)	4 (0%)	48	83
All	All	13360/18096 (74%)	11919 (89%)	1425 (11%)	16 (0%)	49	83

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	1708	ARG
2	I	1708	ARG
2	E	1708	ARG
2	G	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%)	2483 (100%)	10 (0%)	84	82
2	E	2493/3022 (82%)	2482 (100%)	11 (0%)	84	82
2	G	2493/3022 (82%)	2482 (100%)	11 (0%)	84	82
2	I	2493/3022 (82%)	2482 (100%)	11 (0%)	84	82
All	All	10324/12444 (83%)	10281 (100%)	43 (0%)	81	82

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	4792	LEU
2	G	1676	LEU
2	E	4978	HIS
2	G	131	LEU
2	G	3663	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 220 such sidechains are listed below:

Mol	Chain	Res	Type
2	I	4947	GLN
2	E	1972	ASN
2	G	4947	GLN
2	G	3700	GLN
2	E	201	ASN

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	I	14
2	E	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	73.36
1	I	4345:UNK	C	4540:PHE	N	73.36
1	E	4345:UNK	C	4540:PHE	N	73.36
1	G	4345:UNK	C	4540:PHE	N	73.36

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	3613:UNK	C	3639:THR	N	46.46

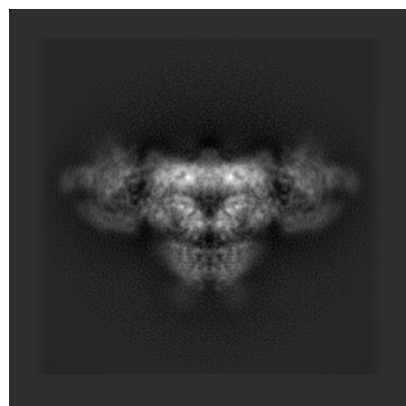
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8392. These allow visual inspection of the internal detail of the map and identification of artifacts.

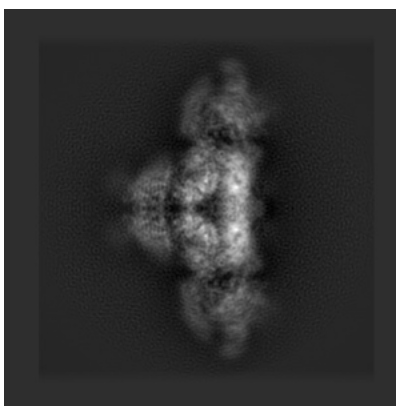
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

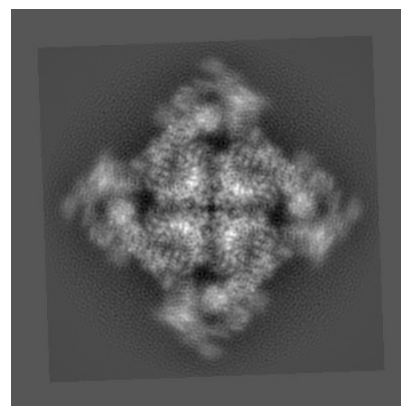
6.1.1 Primary map



X

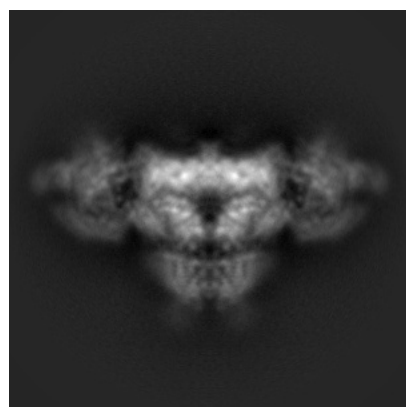


Y

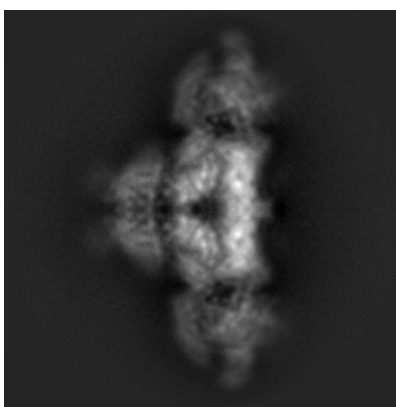


Z

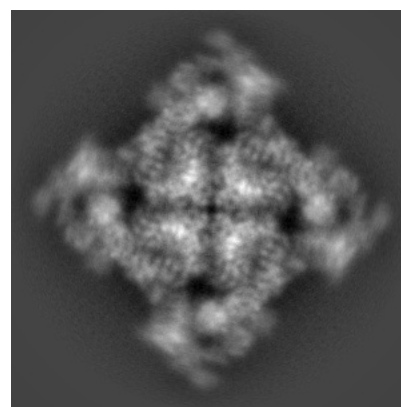
6.1.2 Raw map



X



Y

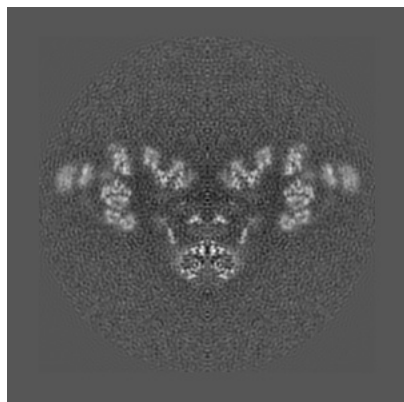


Z

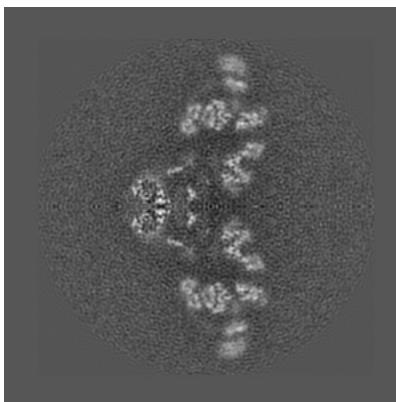
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

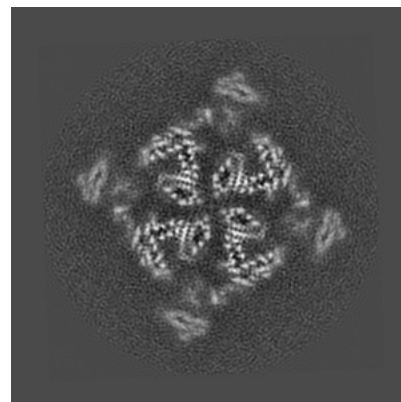
6.2.1 Primary map



X Index: 200

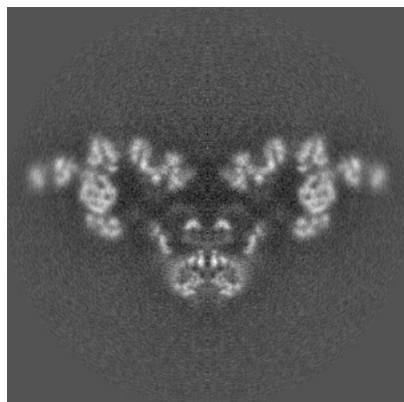


Y Index: 200

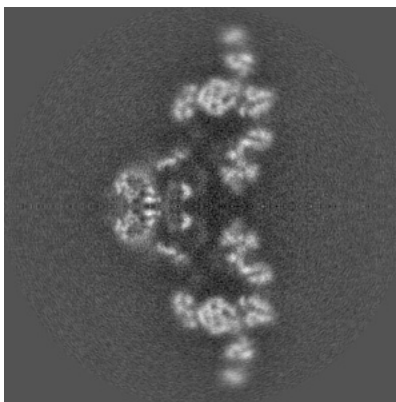


Z Index: 200

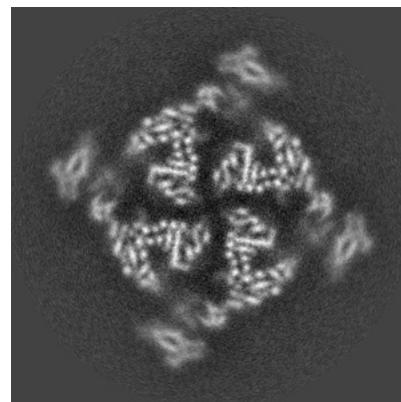
6.2.2 Raw map



X Index: 168



Y Index: 168

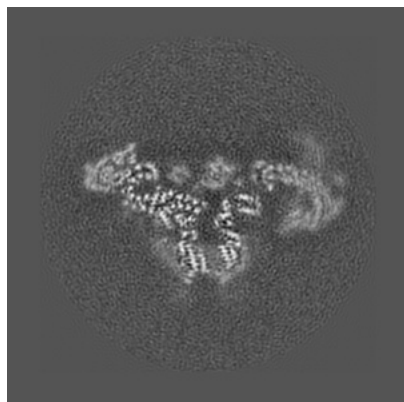


Z Index: 168

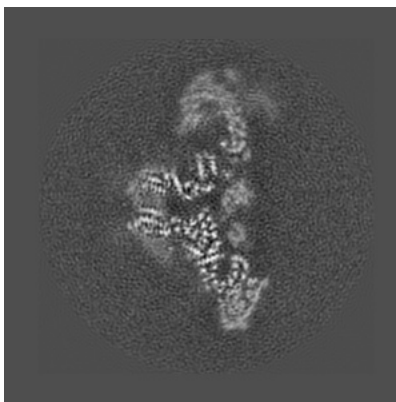
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

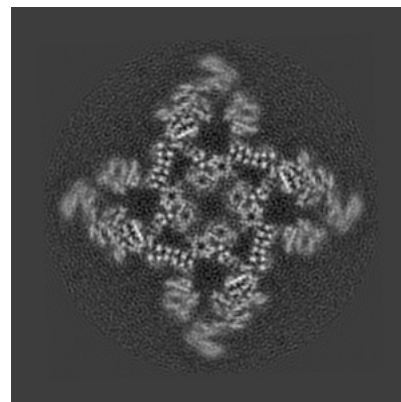
6.3.1 Primary map



X Index: 224

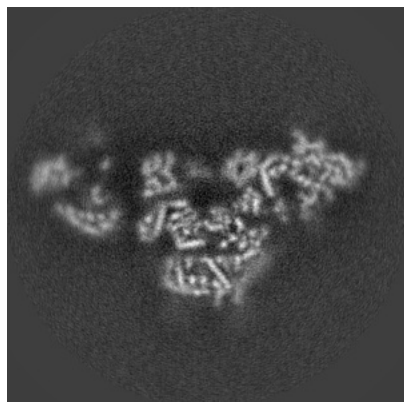


Y Index: 177

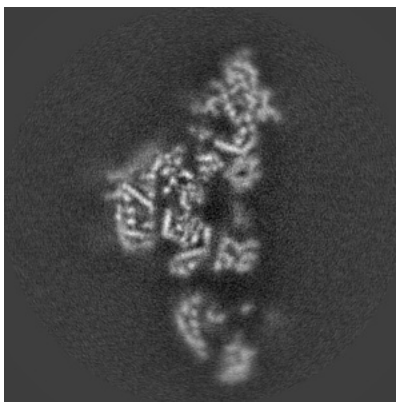


Z Index: 227

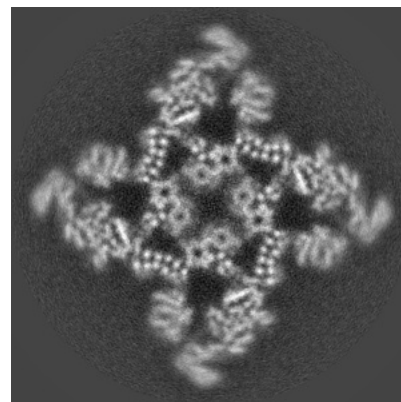
6.3.2 Raw map



X Index: 154



Y Index: 182

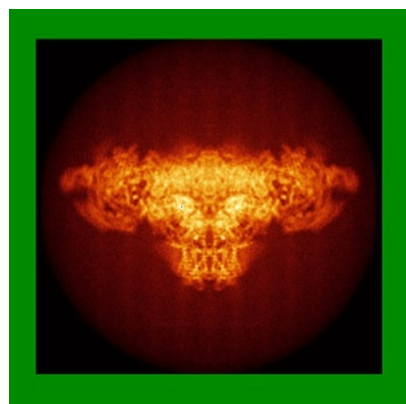


Z Index: 192

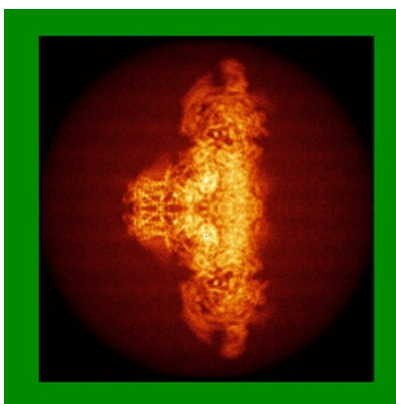
The images above show the largest variance slices of the map in three orthogonal directions.

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

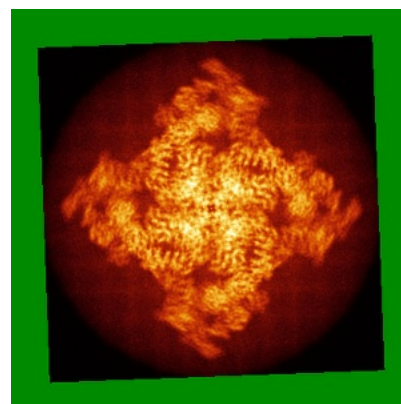
6.4.1 Primary map



X

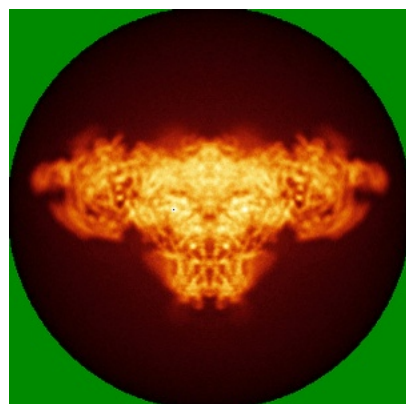


Y

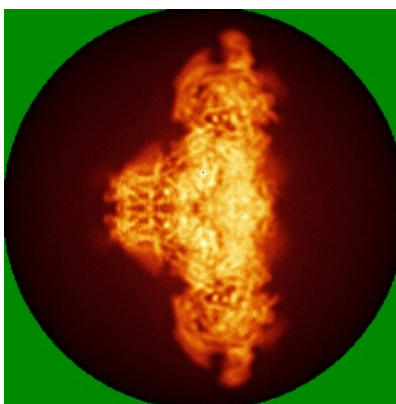


Z

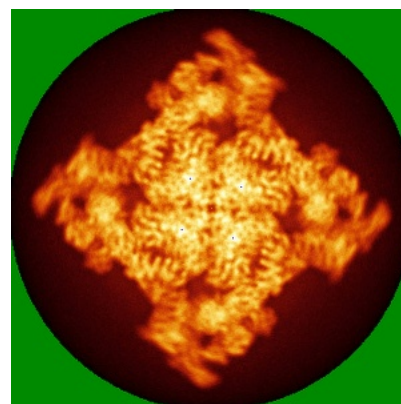
6.4.2 Raw map



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.

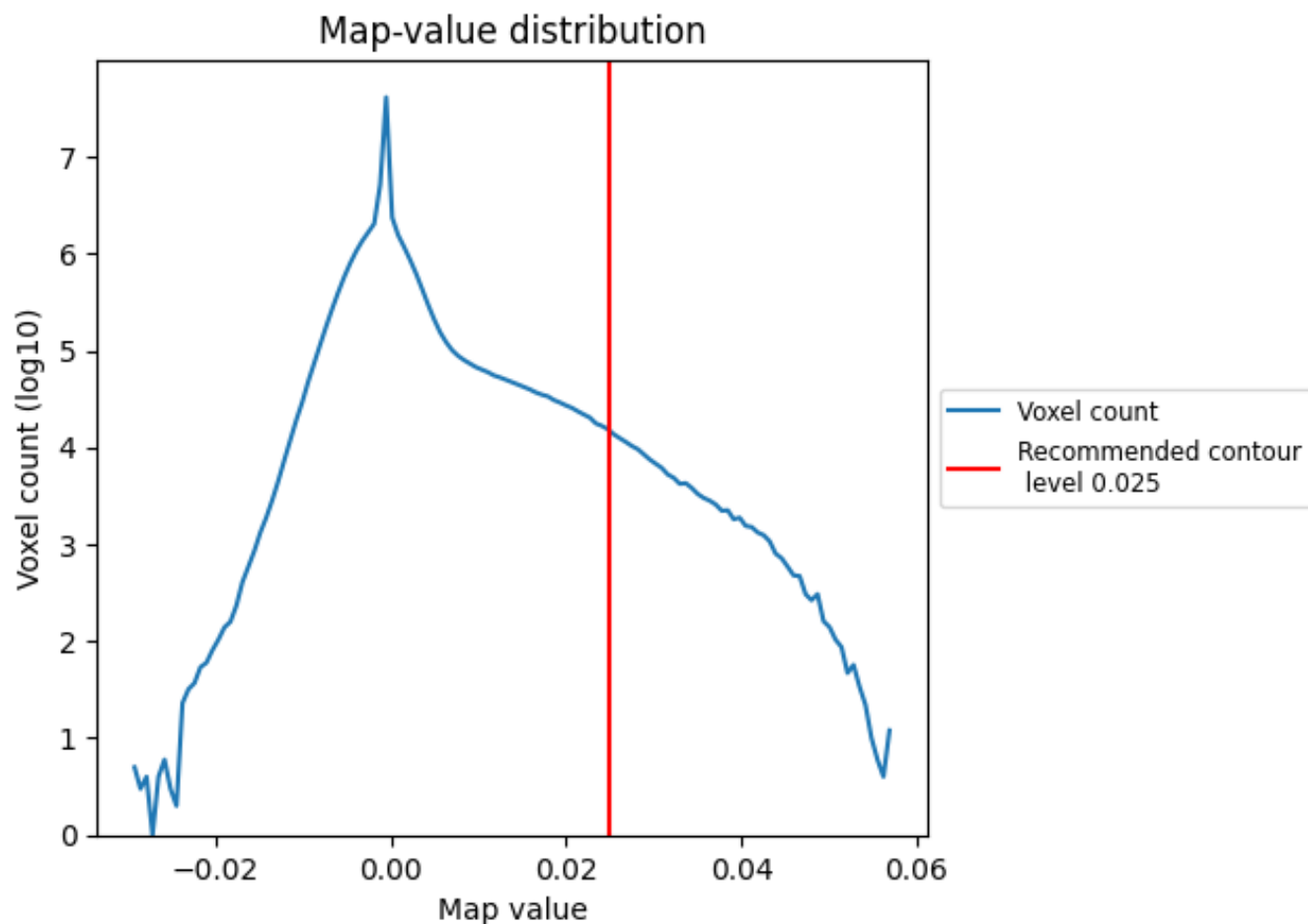
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

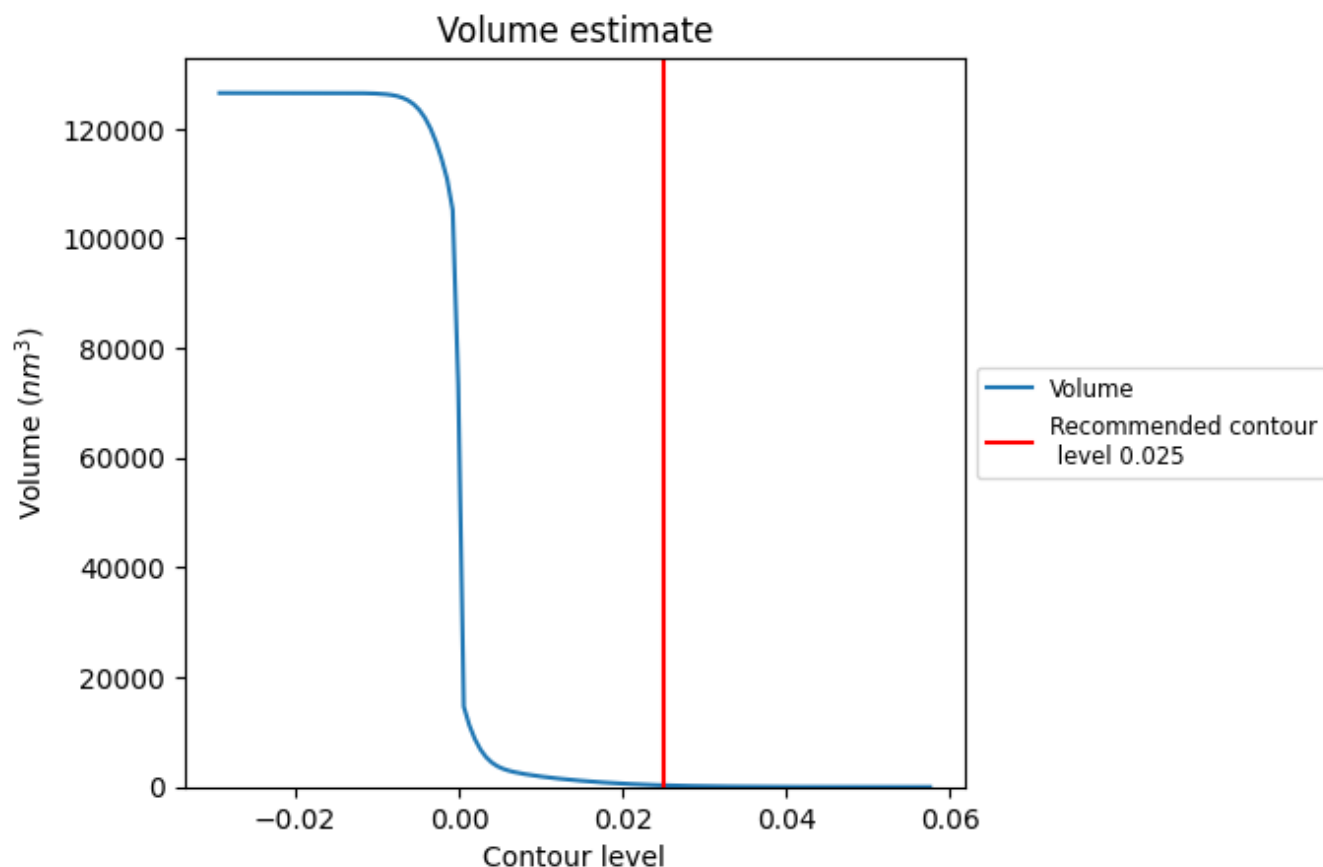
This section contains the results of statistical analysis of the map.

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.

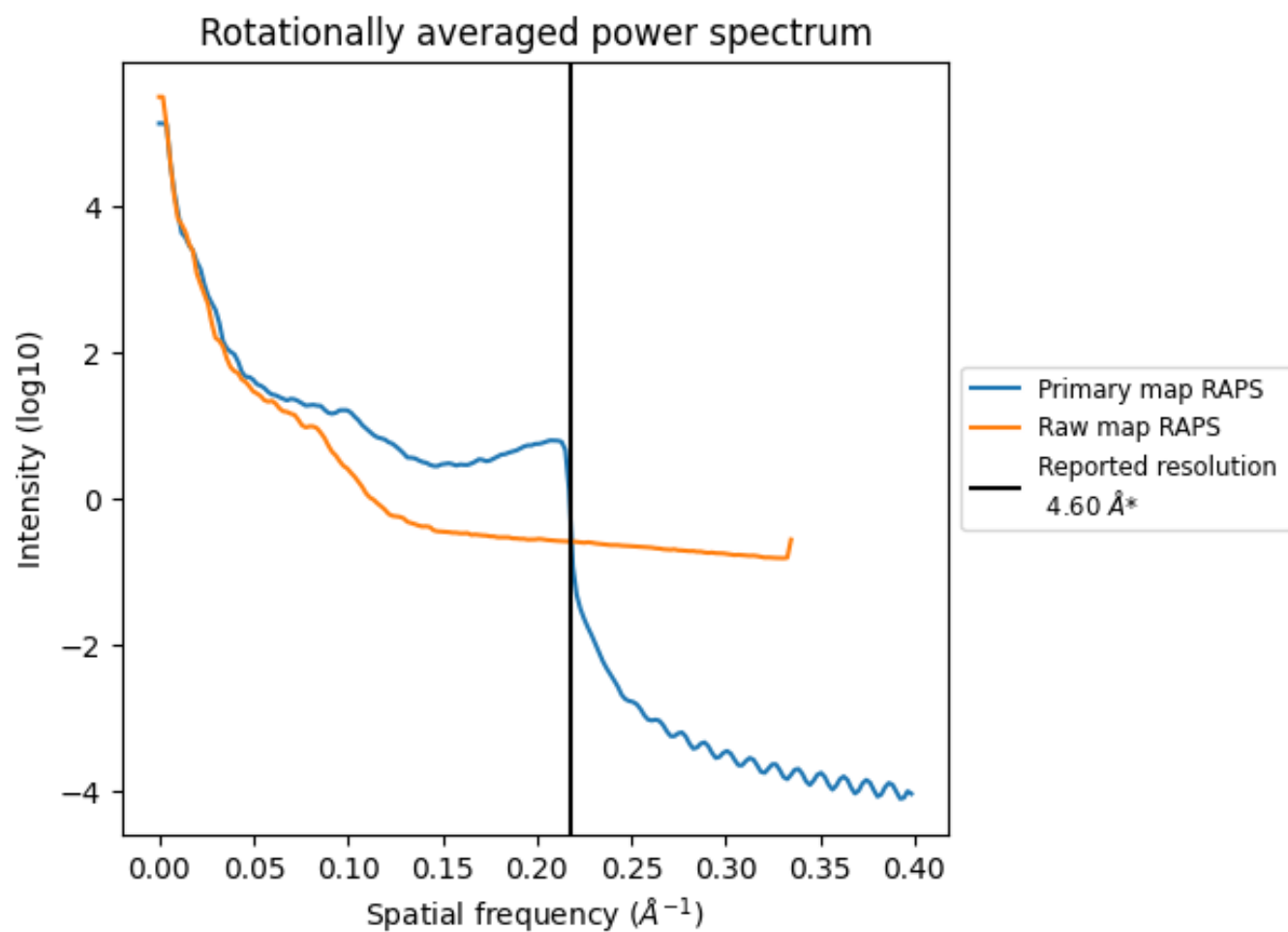
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 298 nm^3 ; this corresponds to an approximate mass of 269 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 ⓘ

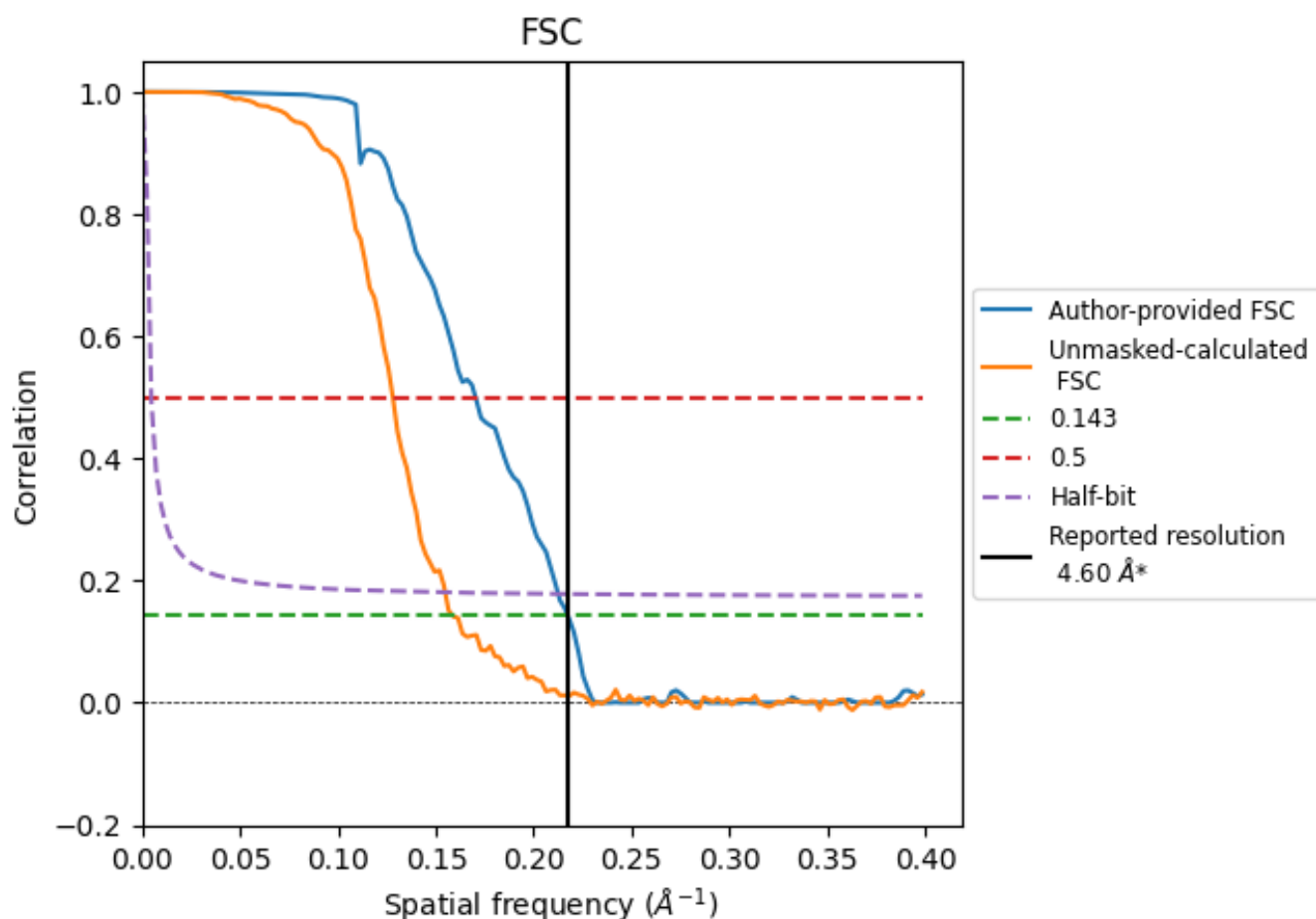


*Reported resolution corresponds to spatial frequency of 0.217 Å⁻¹

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 0.217 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

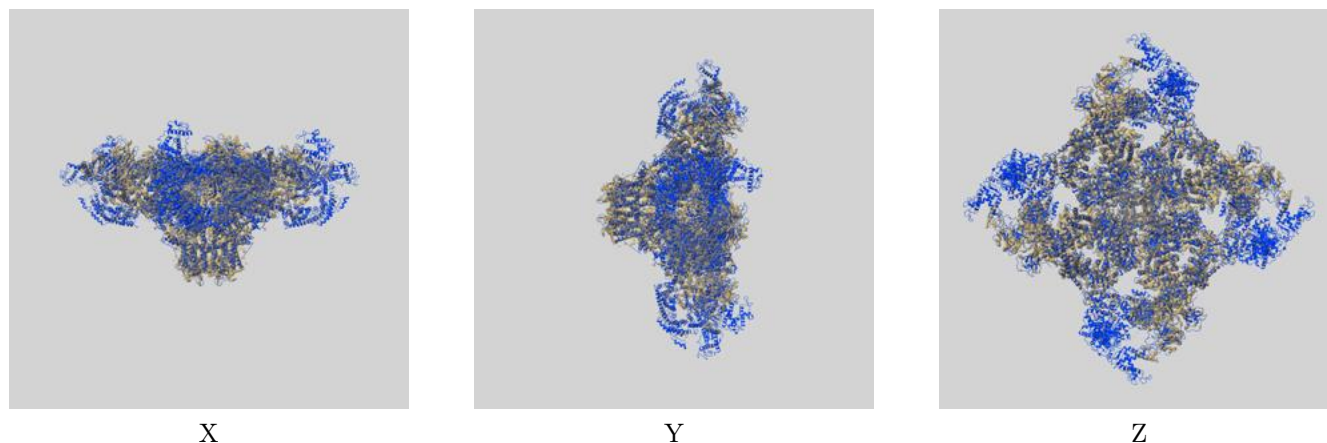
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.60	-	-
Author-provided FSC curve	4.60	5.87	4.71
Unmasked-calculated*	6.31	7.81	6.46

*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 6.31 differs from the reported value 4.6 by more than 10 %

9 Map-model fit [i](#)

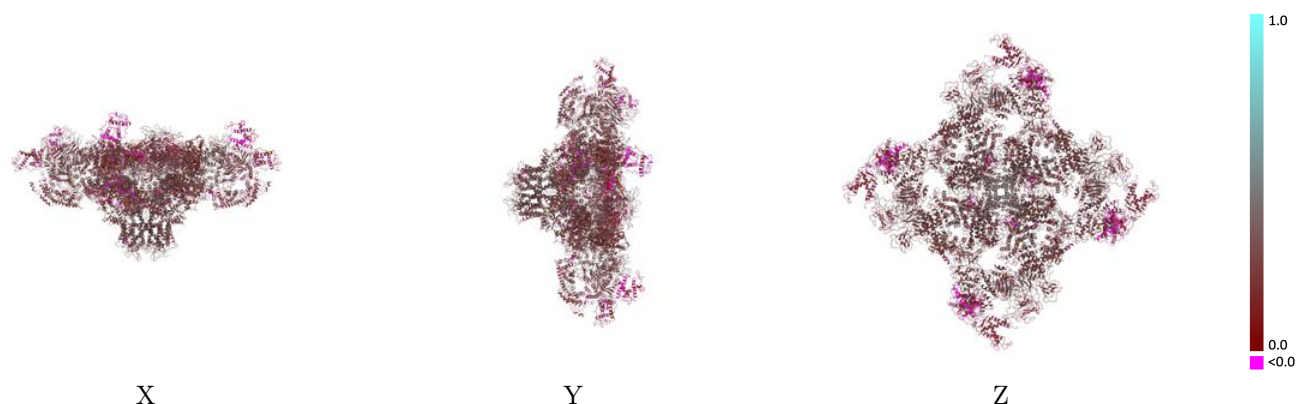
This section contains information regarding the fit between EMDB map EMD-8392 and PDB model 5TB1. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



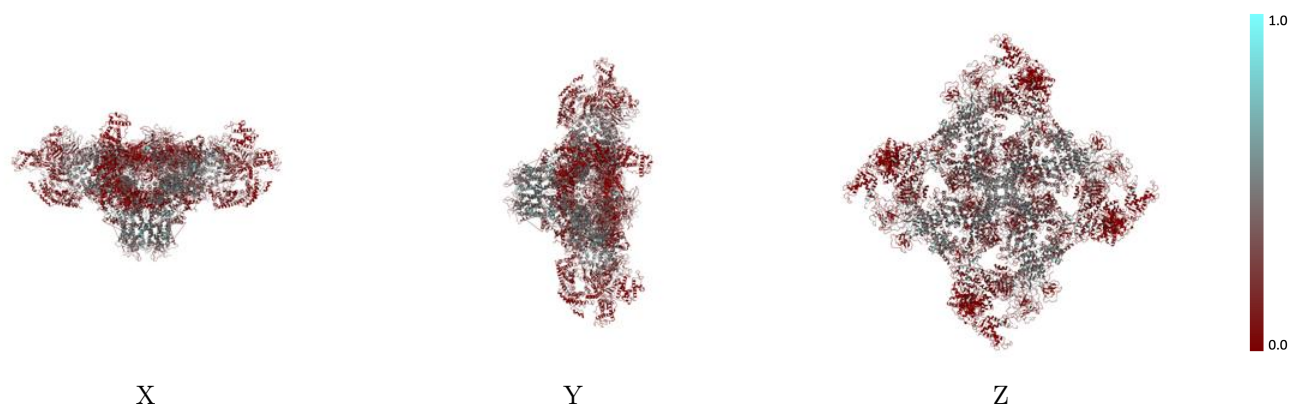
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



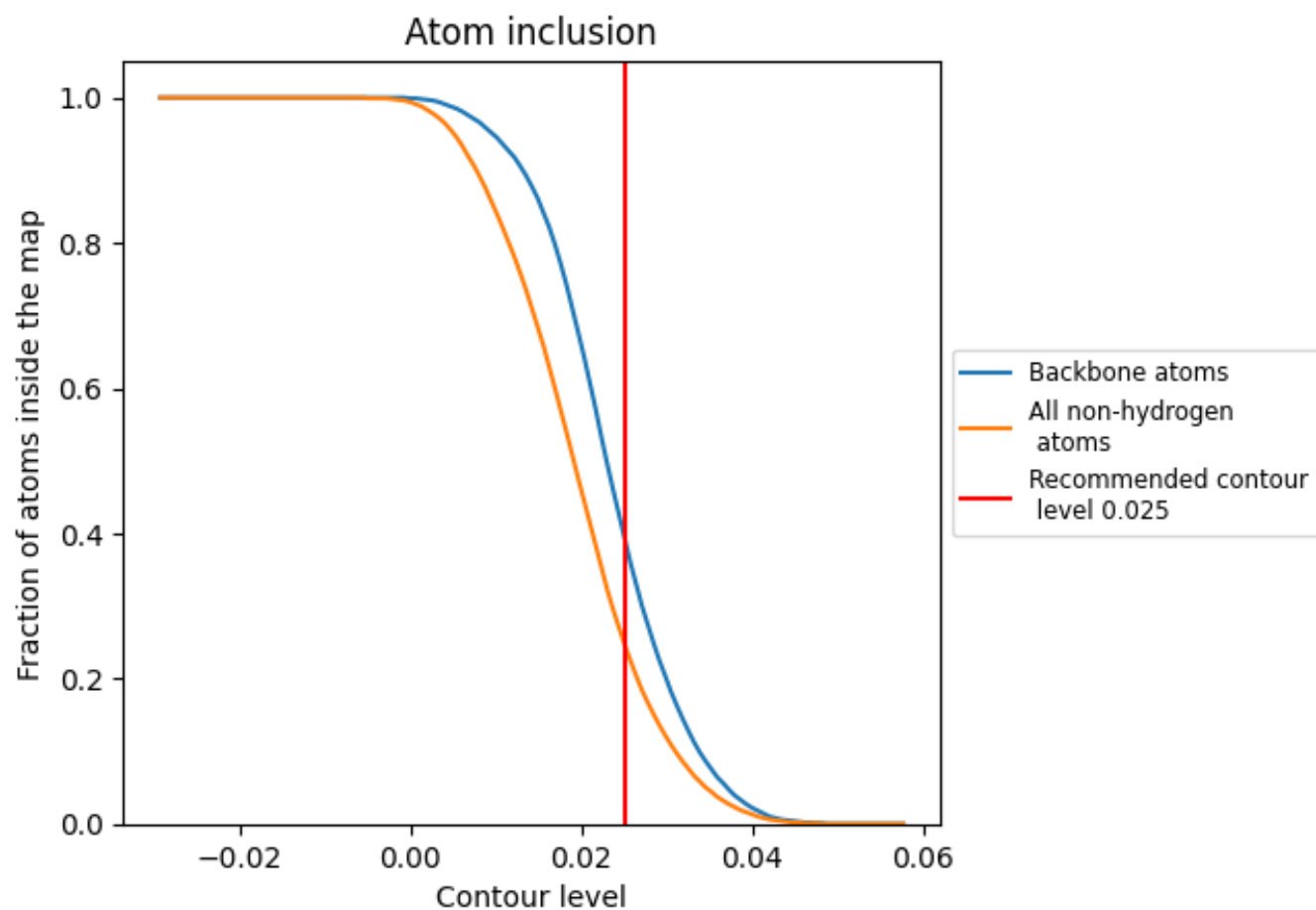
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



At the recommended contour level, 40% of all backbone atoms, 25% 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	0.2490	0.2600
A	0.1890	0.2650
B	0.2510	0.2600
E	0.2510	0.2600
F	0.1840	0.2700
G	0.2510	0.2600
H	0.1890	0.2670
I	0.2510	0.2590
J	0.1890	0.2640

