wwPDB EM Validation Summary Report (i)

Nov 11, 2026 – 03:09 PM EST

PDB ID	:	9Z9M / pdb_00009z9m
EMDB ID	:	EMD-73951
Title	:	Closed-state T4825I mouse/rabbit RyR1 under non-activating condition (5 mM EGTA)
Authors	:	Chen, Y.S.; Van Petegem, F.
Deposited on	:	2025-11-18
Resolution	:	2.67 Å(reported)
Based on initial model	:	7TZC

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 (i) 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 (i)) were used in the production of this report:

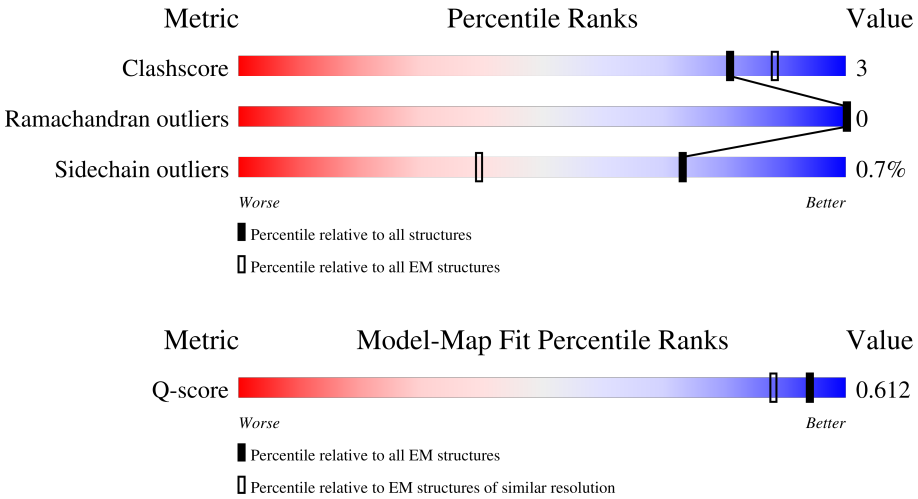
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

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 2.67 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.



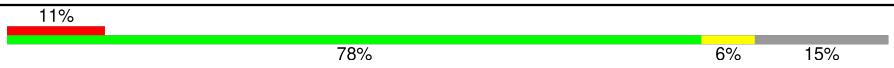
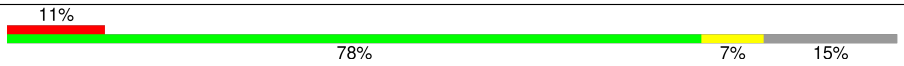
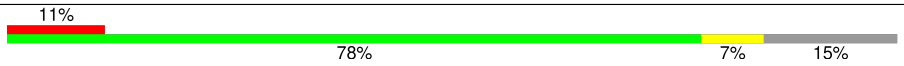
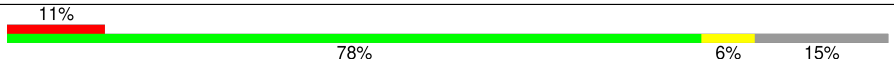
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	9182 (2.17 - 3.17)

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 <=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	110	87% 11%
1	C	110	87% 11%
1	E	110	87% 11%
1	G	110	87% 11%

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Mol	Chain	Length	Quality of chain
2	B	5037	
2	D	5037	
2	F	5037	
2	H	5037	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 136616 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	A	108	Total	C	N	O	S	0	0
			819	516	144	155	4		
1	C	108	Total	C	N	O	S	0	0
			819	516	144	155	4		
1	E	108	Total	C	N	O	S	0	0
			819	516	144	155	4		
1	G	108	Total	C	N	O	S	0	0
			819	516	144	155	4		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	SER	-	expression tag	UNP P68106
A	0	ASN	-	expression tag	UNP P68106
A	1	ALA	-	expression tag	UNP P68106
C	-1	SER	-	expression tag	UNP P68106
C	0	ASN	-	expression tag	UNP P68106
C	1	ALA	-	expression tag	UNP P68106
E	-1	SER	-	expression tag	UNP P68106
E	0	ASN	-	expression tag	UNP P68106
E	1	ALA	-	expression tag	UNP P68106
G	-1	SER	-	expression tag	UNP P68106
G	0	ASN	-	expression tag	UNP P68106
G	1	ALA	-	expression tag	UNP P68106

- Molecule 2 is a protein called Ryanodine receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	4262	Total	C	N	O	S	3	0
			33334	21288	5762	6060	224		
2	D	4262	Total	C	N	O	S	3	0
			33334	21288	5762	6060	224		
2	F	4262	Total	C	N	O	S	3	0
			33334	21288	5762	6060	224		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	4262	Total	C	N	O	S	3	0
			33334	21288	5762	6060	224		

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	5	GLY	-	insertion	UNP P11716
B	68	ILE	THR	conflict	UNP P11716
B	208	GLY	CYS	conflict	UNP P11716
B	213	PHE	TYR	conflict	UNP P11716
B	235	PRO	ALA	conflict	UNP P11716
B	236	SER	ALA	conflict	UNP P11716
B	251	PRO	ALA	conflict	UNP P11716
B	4825	ILE	THR	engineered mutation	UNP P11716
D	5	GLY	-	insertion	UNP P11716
D	68	ILE	THR	conflict	UNP P11716
D	208	GLY	CYS	conflict	UNP P11716
D	213	PHE	TYR	conflict	UNP P11716
D	235	PRO	ALA	conflict	UNP P11716
D	236	SER	ALA	conflict	UNP P11716
D	251	PRO	ALA	conflict	UNP P11716
D	4825	ILE	THR	engineered mutation	UNP P11716
F	5	GLY	-	insertion	UNP P11716
F	68	ILE	THR	conflict	UNP P11716
F	208	GLY	CYS	conflict	UNP P11716
F	213	PHE	TYR	conflict	UNP P11716
F	235	PRO	ALA	conflict	UNP P11716
F	236	SER	ALA	conflict	UNP P11716
F	251	PRO	ALA	conflict	UNP P11716
F	4825	ILE	THR	engineered mutation	UNP P11716
H	5	GLY	-	insertion	UNP P11716
H	68	ILE	THR	conflict	UNP P11716
H	208	GLY	CYS	conflict	UNP P11716
H	213	PHE	TYR	conflict	UNP P11716
H	235	PRO	ALA	conflict	UNP P11716
H	236	SER	ALA	conflict	UNP P11716
H	251	PRO	ALA	conflict	UNP P11716
H	4825	ILE	THR	engineered mutation	UNP P11716

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

Mol	Chain	Residues	Atoms	AltConf
3	B	1	Total Zn 1 1	0
3	D	1	Total Zn 1 1	0
3	F	1	Total Zn 1 1	0
3	H	1	Total Zn 1 1	0

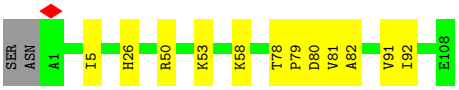
3 Residue-property plots (i)

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

Chain A:

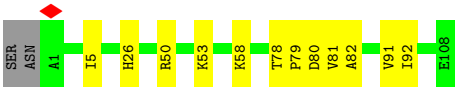




• Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

Chain C:

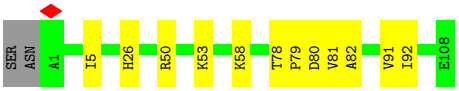




• Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

Chain E:

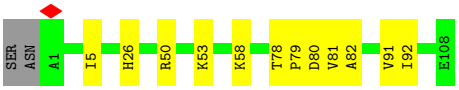




• Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

Chain G:

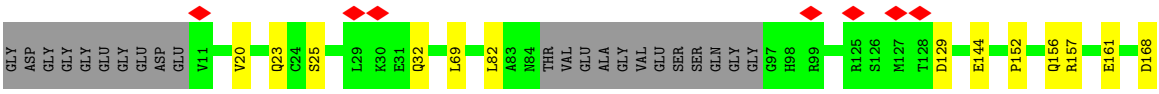


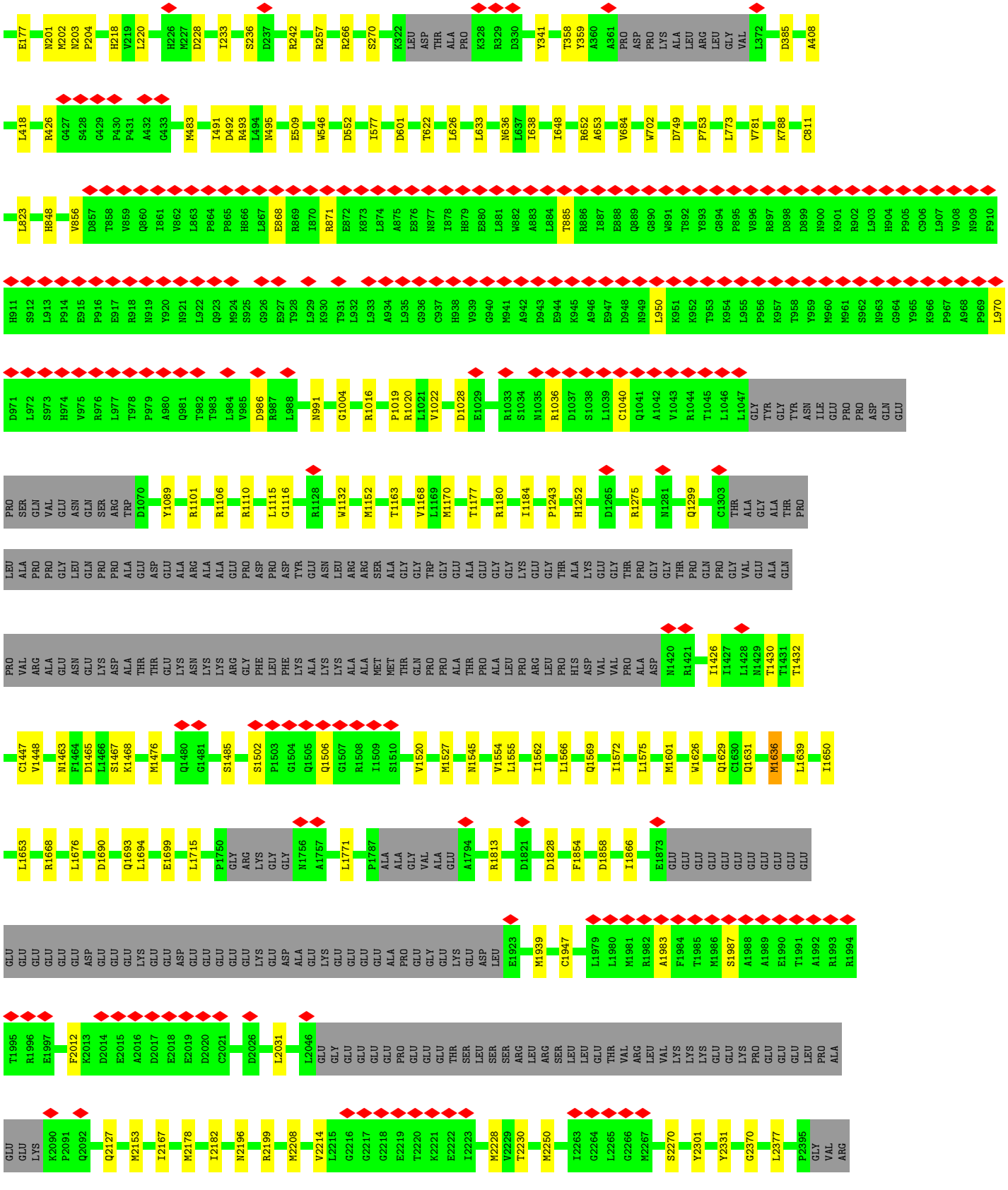


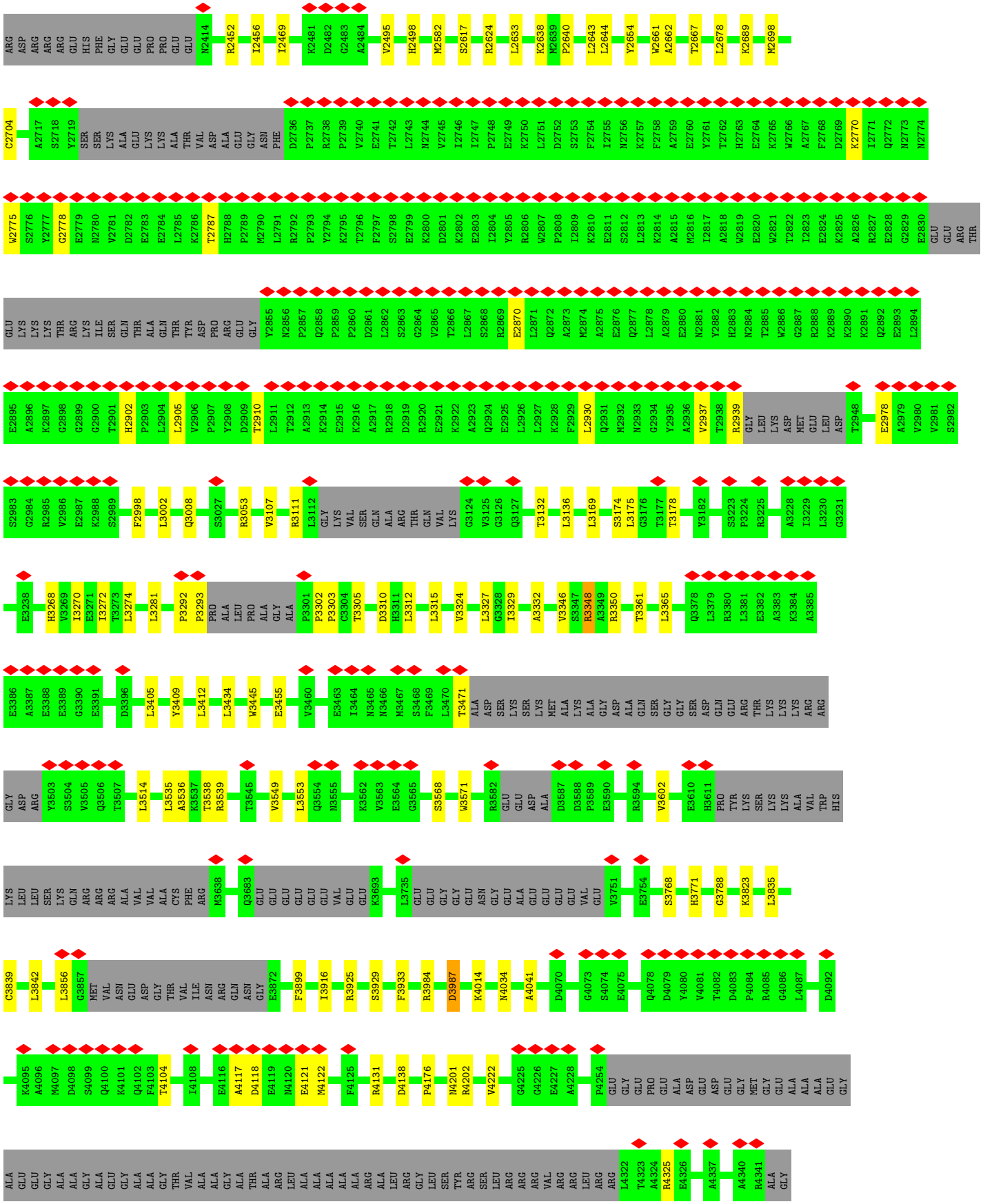
• Molecule 2: Ryanodine receptor 1

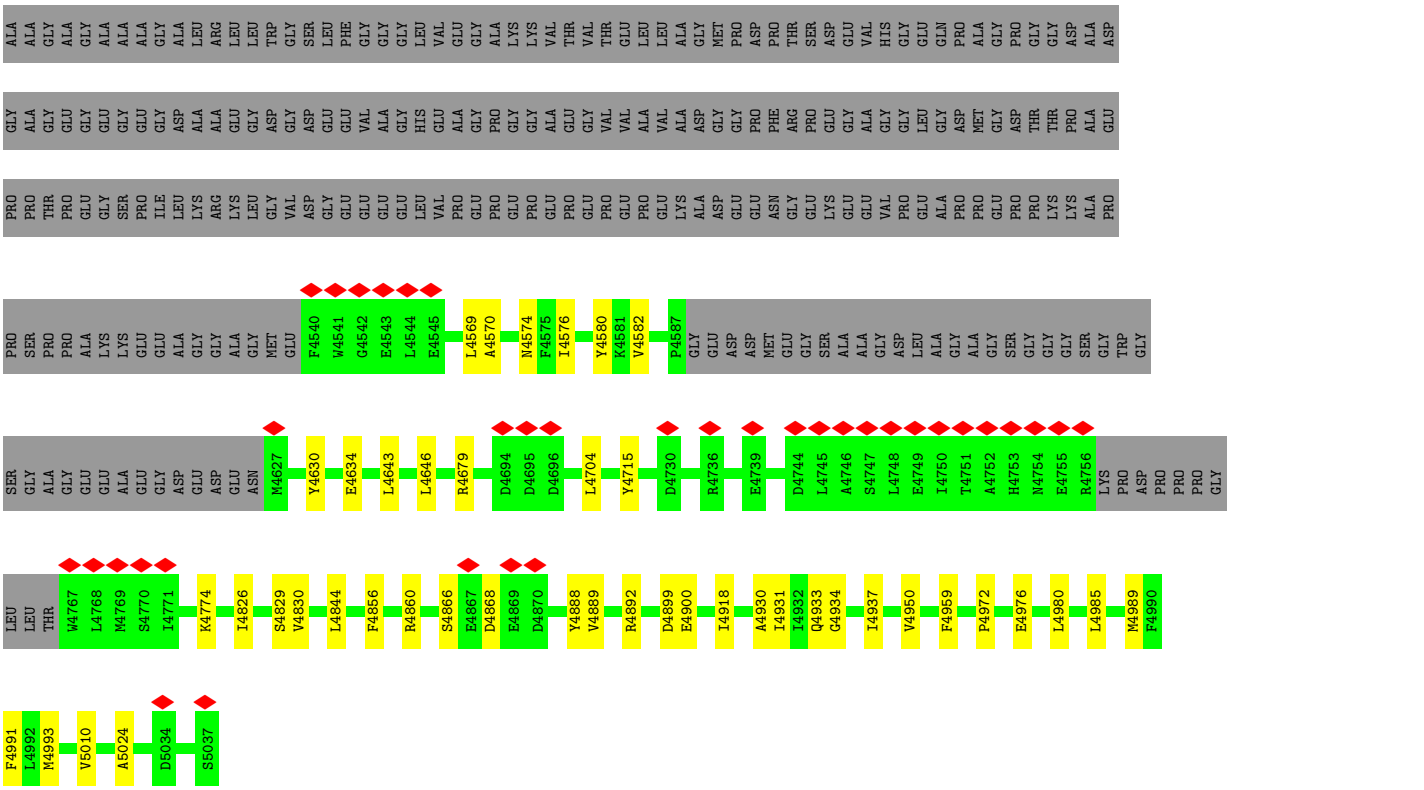
Chain B:






E177 N201 M202 N203 P204 H218 V219 L220 H226 M227 D228 I233 S236 D237 R242 R257 R266 S270 K322 LEU ASP THR ALA PRO K328 R329 D330 Y341 T358 Y359 A360 A361 PRO ASP PRO LYS ALA LEU ARG LEU GLY VAL L372 D385 A408
L418 R426 G427 S428 G429 P430 P431 A432 G433 M483 I491 D492 R493 L494 N495 E509 W546 D552 I577 D601 T622 L626 L633 N636 L637 I638 I648 R652 A653 V684 W702 D749 P753 L773 V781 K788 C811
L823 H848 V856 D857 T858 V859 Q860 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 R886 I887 E888 Q889 G890 W891 T892 Y893 G894 P895 V896 R897 D898 D899 N900 K901 R902 L903 H904 P905 C906 L907 V908 N909 F910
H911 S912 L913 P914 E915 P916 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 V975 R976 L977 T978 P979 A980 Q981 T982 T983 L984 V985 D986 R987 L988 N991 G1004 R1016 P1019 R1020 L1021 V1022 D1028 E1029 R1033 S1034 N1035 R1036 D1037 S1038 L1039 C1040 Q1041 A1042 V1043 R1044 T1045 L1046 L1047 GLY TYR GLY TYR ASN ILE GLU PRO PRO ASP GLN GLU
PRO SER GLN VAL GLU ASN GLN SER ARG TRP D1070 Y1089 R1101 R1106 R1110 L1115 G1116 R1128 W1132 M1152 T1163 V1168 L1169 M1170 T1177 R1180 I1184 P1243 H1252 D1265 R1275 N1281 Q1299 C1303 THR ALA GLY ALA THR PRO
LEU ALA PRO PRO GLY LEU GLN PRO PRO ALA GLU GLU ASP GLU ALA ARG ALA ALA GLU PRO ASP PRO ASP TYR GLU ASN LEU ARG ARG SER ALA GLY GLY TRP GLY GLU ALA GLU GLY GLY LYS GLU GLY THR ALA LYS GLU GLY THR PRO GLY GLY THR PRO GLN PRO GLY VAL GLU ALA GLN
PRO VAL ARG ALA GLU ASN GLU LYS ASP ALA THR THR GLU LYS ASN LYS LYS ARG GLY PHE LEU PHE LYS ALA LYS LYS ALA ALA MET MET THR GLN PRO PRO ALA THR PRO ALA LEU PRO ARG LEU PRO HIS ASP VAL VAL PRO ALA ASP N1420 R1421 I1426 T1427 L1428 N1429 T1430 T1431 T1432
C1447 V1448 N1463 F1464 D1465 L1466 S1467 K1468 M1476 Q1480 G1481 S1485 S1502 P1503 G1504 Q1505 Q1506 G1507 R1508 I1509 S1510 V1520 M1527 N1545 V1554 L1555 I1562 L1566 Q1569 I1572 L1575 M1601 W1626 Q1629 C1630 Q1631 M1636 L1639 I1650
L1653 R1668 L1676 D1690 Q1693 L1694 E1699 L1715 P1750 GLY ARG LYS GLY GLY N1756 A1757 L1771 P1787 ALA ALA GLY VAL ALA GLU A1794 R1813 D1821 D1828 F1854 D1858 I1866 E1873 GLU GLU GLU GLU GLU GLU GLU GLU GLU GLU
GLU GLU GLU GLU GLU ASP GLU GLU GLU LYS GLU GLU ASP GLU GLU GLU GLU GLU LYS GLU ASP ALA GLU LYS GLU GLU GLU GLU ALA PRO GLU GLY GLU LYS GLU ASP LEU E1923 M1939 C1947 L1979 L1980 M1981 R1982 A1983 F1984 T1985 M1986 S1987 A1988 A1989 E1990 T1991 A1992 R1993 R1994
T1995 R1996 E1997 F2012 K2013 D2014 E2015 A2016 D2017 E2018 E2019 D2020 C2021 D2026 L2031 L2046 GLU GLY GLU GLU GLU GLU PRO GLU GLU GLU THR SER LEU SER SER ARG LEU ARG SER LEU LEU GLU THR VAL ARG LEU VAL LYS LYS LYS GLU GLU LYS PRO GLU GLU GLU LEU PRO ALA
GLU GLU LYS K2090 P2091 Q2092 Q2127 M2153 I2167 M2178 I2182 N2196 R2199 M2208 V2214 L2215 G2216 G2217 G2218 E2219 T2220 K2221 E2222 I2223 M2228 V2229 T2230 M2250 I2263 G2264 L2265 G2266 M2267 S2270 Y2301 Y2331 G2370 L2377 P2395 GLY VAL ARG

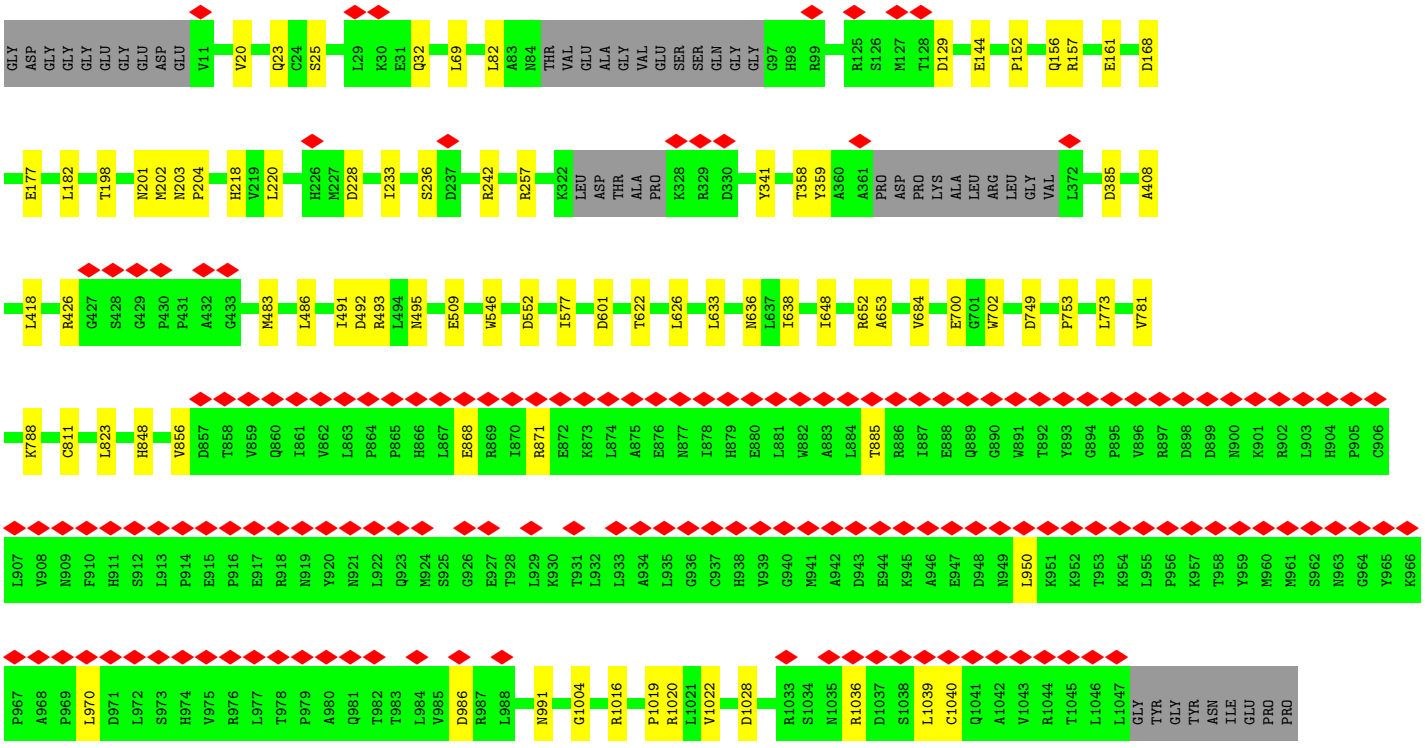

ARG ASP ARG ARG ARG GLU HIS PHE GLY GLU GLU PRO PRO GLU GLU N2414 R2452 I2456 I2469 K2481 D2482 G2483 A2484 V2495 H2498 M2582 S2617 R2624 L2633 K2638 M2639 P2640 L2643 L2644 Y2654 W2661 A2662 T2667 L2678 K2689 M2698
C2704 A2717 S2718 Y2719 SER SER LYS ALA GLU LYS LYS ALA THR VAL ASP ALA GLU GLY ASN PHE D2736 P2737 R2738 P2739 V2740 E2741 T2742 L2743 N2744 V2745 I2746 I2747 P2748 E2749 K2750 L2751 D2752 S2753 F2754 I2755 N2756 K2757 F2758 A2759 E2760 Y2761 T2762 H2763 E2764 K2765 W2766 A2767 F2768 D2769 K2770 I2771 Q2772 N2773 N2774
W2775 S2776 Y2777 G2778 E2779 N2780 V2781 D2782 E2783 E2784 L2785 K2786 T2787 H2788 P2789 M2790 L2791 R2792 P2793 Y2794 K2795 T2796 F2797 S2798 E2799 K2800 D2801 K2802 E2803 I2804 Y2805 R2806 W2807 P2808 I2809 K2810 E2811 S2812 L2813 K2814 A2815 M2816 I2817 A2818 W2819 E2820 W2821 T2822 I2823 E2824 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 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 G2887 R2888 K2889 K2890 K2891 Q2892 E2893 L2894
E2895 A2896 K2897 G2898 G2899 G2900 T2901 H2902 P2903 L2904 L2905 V2906 P2907 Y2908 D2909 T2910 L2911 T2912 A2913 K2914 E2915 K2916 A2917 R2918 D2919 R2920 E2921 K2922 A2923 Q2924 E2925 L2926 L2927 K2928 F2929 L2930 Q2931 M2932 N2933 G2934 Y2935 A2936 V2937 T2938 R2939 GLY LEU LYS ASP MET GLU LEU ASP T2948 E2978 A2979 V2980 V2981 S2982
S2983 G2984 R2985 V2986 E2987 K2988 S2989 F2998 L3002 Q3008 S3027 R3053 V3107 R3111 L3112 GLY LYS VAL SER GLN ALA ARG THR GLN VAL LYS G3124 V3125 G3126 Q3127 T3132 L3136 L3169 S3174 L3175 G3176 T3177 T3178 Y3182 S3223 P3224 R3225 A3228 I3229 L3230 G3231
E3238 H3268 V3269 I3270 E3271 I3272 T3273 L3274 L3281 P3292 P3293 PRO ALA LEU PRO ALA GLY ALA P3301 P3302 P3303 C3304 T3305 D3310 H3311 L3312 L3315 V3324 L3327 G3328 I3329 A3332 V3346 S3347 R3348 A3349 R3350 T3361 L3365 Q3378 L3379 R3380 L3381 E3382 A3383 K3384 A3385
E3386 A3387 E3388 E3389 G3390 E3391 D3396 L3405 Y3409 L3412 L3434 W3445 E3455 V3460 E3463 I3464 N3465 N3466 M3467 S3468 F3469 L3470 T3471 ALA ASP SER LYS SER LYS MET ALA LYS ALA GLY ASP ALA GLN SER GLY GLY SER ASP GLN GLU ARG THR LYS LYS LYS ARG ARG
GLY ASP ARG Y3503 S3504 V3505 Q3506 T3507 L3514 L3535 A3536 K3537 T3538 R3539 T3545 V3549 L3553 Q3554 N3555 K3562 Y3563 E3564 G3565 S3568 W3571 R3582 GLU GLU ASP ALA D3587 D3588 P3589 E3590 R3594 V3602 E3610 H3611 PRO TYR LYS SER LYS LYS ALA VAL TRP HIS
LYS LEU LEU SER LYS GLN ARG ARG ALA VAL VAL ALA CYS PHE ARG M3638 Q3683 GLU GLU GLU GLU GLU VAL GLU GLU K3693 L3735 GLU GLU GLY GLY GLU ASN GLY GLU ALA GLU GLU GLU GLU VAL GLU V3751 E3754 S3768 H3771 G3788 K3823 L3835
C3839 L3842 L3856 G3857 MET VAL ASN GLU ASP GLY THR VAL ILE ASN ARG GLN ASN GLY E3872 F3899 I3916 R3925 S3929 F3933 R3984 D3987 K4014 N4034 A4041 D4070 G4073 S4074 E4075 Q4078 D4079 Y4080 V4081 T4082 D4083 P4084 R4085 G4086 L4087 D4092
K4095 A4096 M4097 D4098 S4099 Q4100 K4101 Q4102 F4103 T4104 I4108 E4116 A4117 D4118 E4119 N4120 E4121 M4122 F4125 R4131 D4138 P4176 N4201 R4202 V4222 G4225 G4226 E4227 A4228 P4254 GLU GLY GLU PRO GLU ALA ASP GLU ASP GLU GLY MET GLY GLU ALA ALA ALA GLU GLY
ALA GLU GLU GLY ALA ALA GLY GLY ALA GLU GLY ALA ALA ALA GLY THR VAL ALA ALA GLY ALA THR ALA ARG LEU ALA ALA ALA ALA ARG ALA ARG LEU SER TYR ARG SER LEU ARG ARG ARG VAL ARG ARG LEU ARG L4322 T4323 A4324 R4325 E4326 A4337 A4340 R4341 ALA GLY

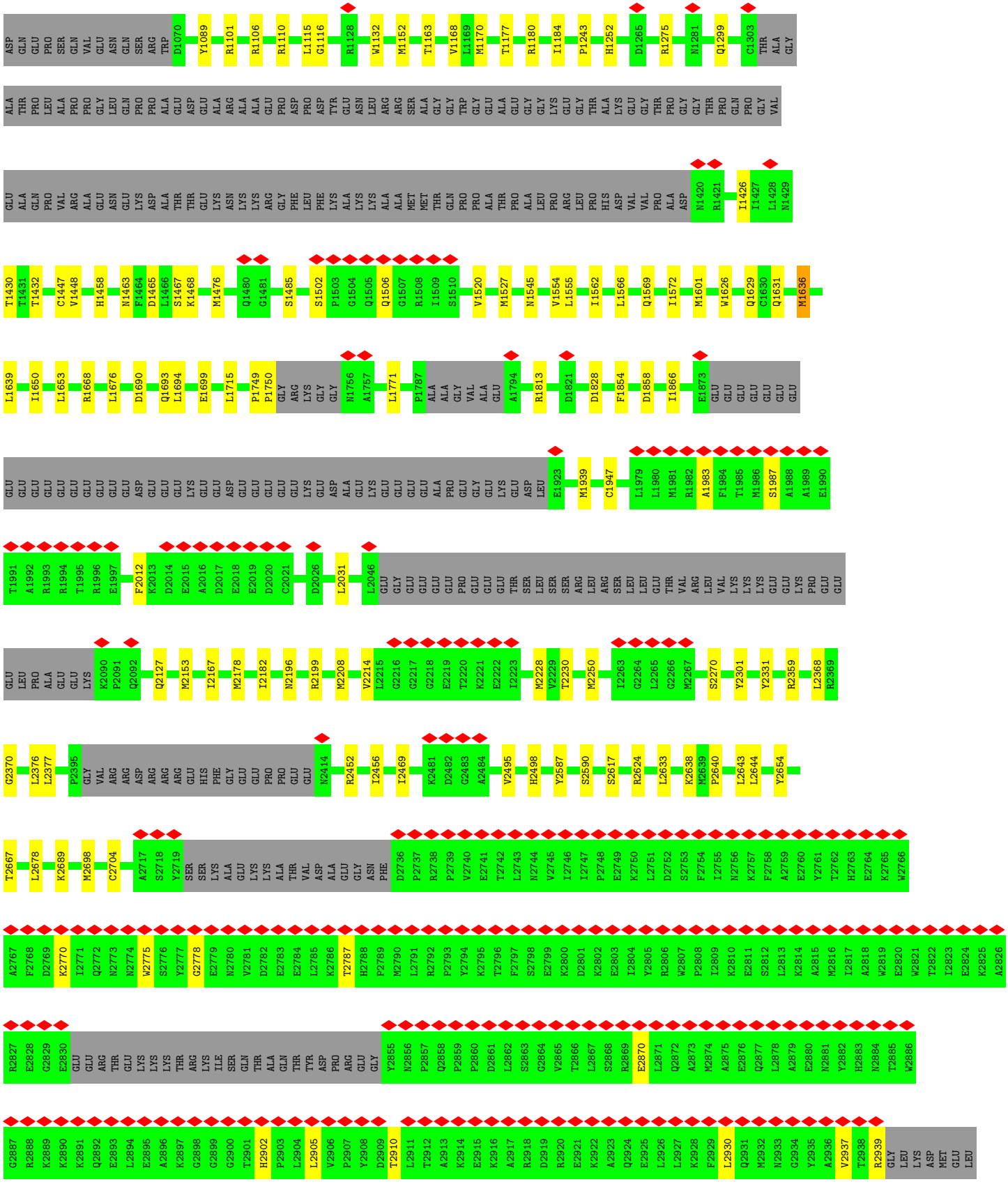


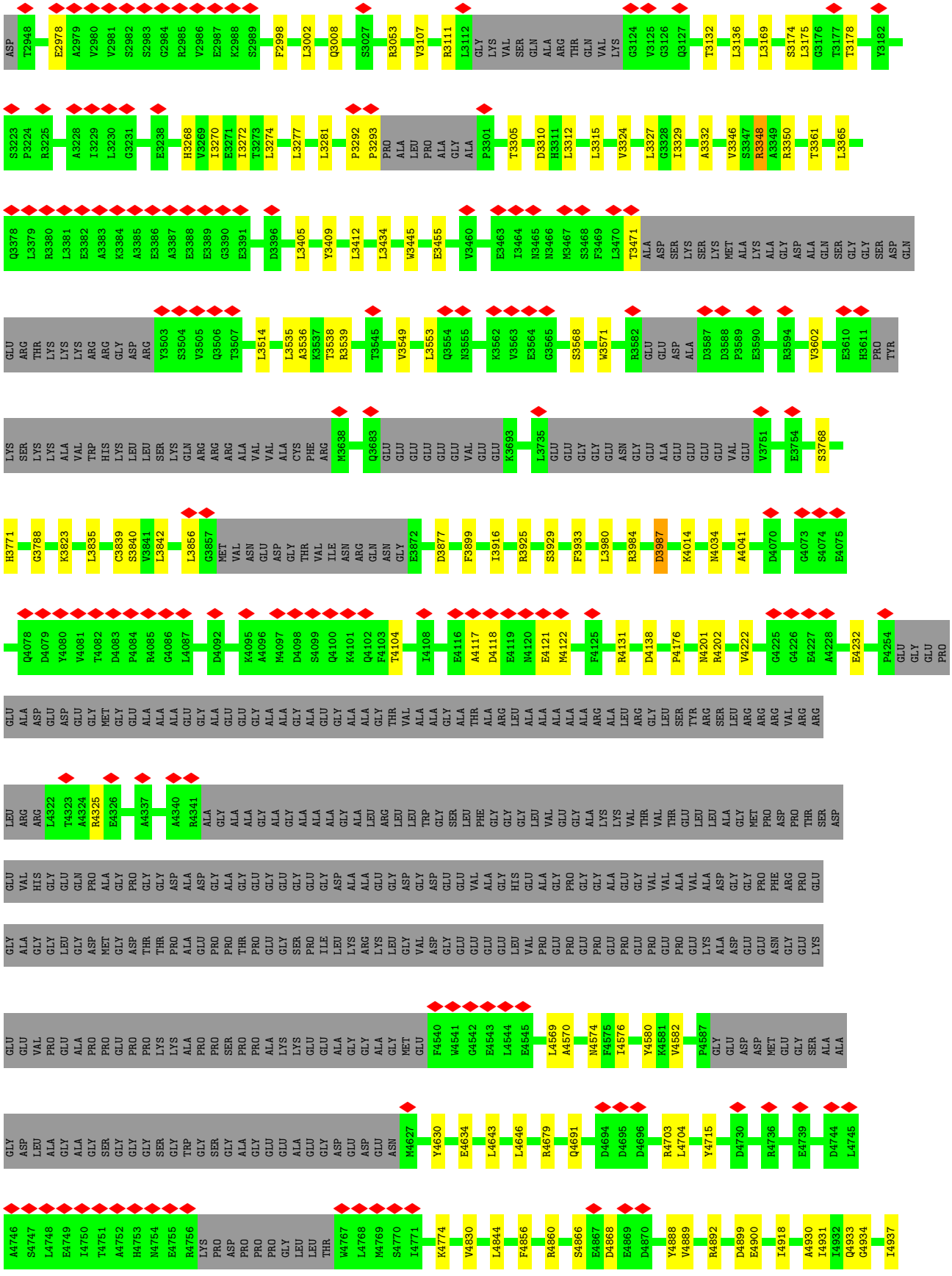
• Molecule 2: Ryanodine receptor 1

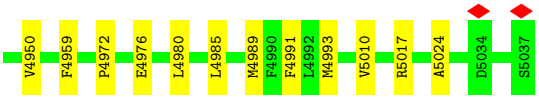
Chain D:






ASP GLN GLU PRO SER GLN VAL GLU ASN GLN SER ARG TRP D1070 Y1089 R1101 R1106 R1110 L1115 G1116 R1128 W1132 M1152 T1163 V1168 L1169 M1170 T1177 R1180 I1184 P1243 H1252 D1265 R1275 N1281 Q1299 C1303 THR ALA GLY
ALA THR PRO LEU ALA PRO PRO GLY LEU GLN PRO PRO ALA GLU ASP GLU ALA ARG ALA ALA GLU PRO ASP PRO ASP TYR GLU ASN LEU ARG ARG SER ALA GLY GLY TRP GLY GLU ALA GLU GLY GLY LYS GLU GLY GLY THR PRO GLY GLY THR PRO GLN PRO GLY VAL
GLU ALA GLN PRO VAL ARG ALA GLU ASN GLU LYS ASP ALA THR THR GLU LYS ASN LYS LYS ARG GLY PHE LEU PHE LYS ALA LYS LYS ALA ALA MET MET THR GLN PRO PRO ALA THR PRO ALA LEU PRO ARG LEU PRO HIS ASP VAL VAL PRO ALA ASP N1420 R1421 I1426 I1427 L1428 N1429
T1430 T1431 T1432 C1447 V1448 H1458 N1463 F1464 D1465 L1466 S1467 K1468 M1476 Q1480 G1481 S1485 S1502 P1503 G1504 Q1505 Q1506 G1507 R1508 I1509 S1510 V1520 M1527 N1545 V1554 L1555 I1562 L1566 Q1569 I1572 M1601 W1626 Q1629 C1630 Q1631 M1636
L1639 I1650 L1653 R1668 L1676 D1690 Q1693 L1694 E1699 L1715 P1749 P1750 GLY ARG LYS GLY GLY N1756 A1757 L1771 P1787 ALA ALA GLY VAL ALA GLU A1794 R1813 D1821 D1828 F1854 D1858 I1866 E1873 GLU GLU GLU GLU GLU GLU
GLU GLU GLU GLU GLU GLU GLU GLU GLU ASP GLU GLU GLU LYS GLU GLU ASP GLU GLU GLU GLU GLU GLU LYS GLU ASP ALA GLU LYS GLU GLU GLU GLU ALA PRO GLU GLY GLU GLU GLU LYS GLU ASP LEU E1923 M1939 C1947 L1979 L1980 M1981 R1982 A1983 F1984 T1985 M1986 S1987 A1988 A1989 E1990
T1991 A1992 R1993 R1994 T1995 R1996 E1997 F2012 K2013 D2014 E2015 A2016 D2017 E2018 E2019 D2020 C2021 D2026 L2031 L2046 GLU GLY GLU GLU GLU GLU PRO GLU GLU GLU THR SER LEU SER SER ARG LEU ARG SER LEU LEU GLU THR VAL ARG LEU VAL LYS LYS LYS GLU GLU LYS PRO GLU GLU
GLU LEU PRO ALA GLU GLU LYS K2090 P2091 Q2092 Q2127 M2153 I2167 M2178 I2182 N2196 R2199 M2208 V2214 L2215 G2216 G2217 G2218 E2219 T2220 K2221 E2222 I2223 M2228 V2229 T2230 M2250 I2263 G2264 L2265 G2266 M2267 S2270 Y2301 Y2331 R2359 L2368 R2369
G2370 L2376 L2377 P2395 GLY VAL ARG ARG ASP ARG ARG ARG GLU HIS PHE GLY GLU GLU PRO PRO GLU GLU N2414 R2452 I2456 I2469 K2481 D2482 G2483 A2484 V2495 H2498 Y2587 S2590 S2617 R2624 L2633 K2638 M2639 P2640 L2643 L2644 Y2654
T2667 L2678 K2689 M2698 C2704 A2717 S2718 Y2719 SER SER LYS ALA GLU LYS LYS ALA THR VAL ASP ALA GLU GLY ASN PHE D2736 P2737 R2738 R2739 V2740 E2741 T2742 L2743 N2744 V2745 I2746 I2747 P2748 E2749 K2750 L2751 D2752 S2753 F2754 I2755 N2756 K2757 F2758 A2759 E2760 Y2761 T2762 H2763 E2764 K2765 W2766
A2767 F2768 D2769 K2770 I2771 Q2772 N2773 N2774 W2775 S2776 Y2777 G2778 E2779 N2780 V2781 D2782 E2783 E2784 L2785 K2786 T2787 H2788 P2789 M2790 L2791 R2792 P2793 Y2794 K2795 T2796 F2797 S2798 E2799 K2800 D2801 K2802 E2803 I2804 Y2805 R2806 W2807 P2808 I2809 K2810 E2811 S2812 L2813 K2814 A2815 M2816 I2817 A2818 W2819 E2820 W2821 T2822 I2823 E2824 K2825 A2826
R2827 E2828 G2829 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 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
G2887 R2888 K2889 K2890 K2891 Q2892 E2893 L2894 E2895 A2896 K2897 G2898 G2899 G2900 T2901 H2902 P2903 L2904 L2905 V2906 P2907 Y2908 D2909 T2910 L2911 T2912 A2913 K2914 E2915 K2916 A2917 R2918 D2919 R2920 E2921 K2922 A2923 Q2924 E2925 L2926 L2927 K2928 F2929 L2930 Q2931 M2932 N2933 G2934 Y2935 A2936 V2937 T2938 R2939 GLY LEU LYS ASP MET GLU LEU

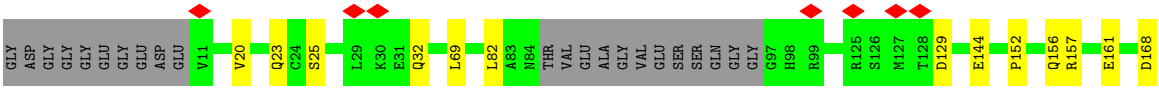

ASP T2948 E2978 A2979 V2980 V2981 S2982 S2983 G2984 R2985 V2986 E2987 K2988 S2989 F2998 L3002 Q3008 S3027 R3053 V3107 R3111 L3112 GLY LYS VAL SER GLN ALA ARG THR GLN VAL LYS G3124 V3125 G3126 Q3127 T3132 L3136 L3169 S3174 L3175 G3176 T3177 T3178 Y3182
S3223 P3224 R3225 A3228 I3229 L3230 G3231 E3238 H3268 V3269 I3270 E3271 I3272 T3273 L3274 L3277 L3281 P3292 P3293 PRO ALA LEU PRO ALA GLY ALA P3301 T3305 D3310 H3311 L3312 L3315 V3324 L3327 G3328 I3329 A3332 V3346 S3347 R3348 A3349 R3350 T3361 L3365
Q3378 L3379 R3380 L3381 E3382 A3383 K3384 A3385 E3386 A3387 E3388 E3389 G3390 E3391 D3396 L3405 Y3409 L3412 L3434 W3445 E3455 V3460 E3463 I3464 N3465 N3466 M3467 S3468 F3469 L3470 T3471 ALA ASP SER LYS SER LYS MET ALA LYS ALA GLY ASP ALA GLN SER GLY GLY SER ASP GLN
GLU ARG THR LYS LYS LYS ARG ARG GLY ASP ARG Y3503 S3504 V3505 Q3506 T3507 L3514 L3535 A3536 K3537 T3538 R3539 T3545 V3549 L3553 Q3554 N3555 K3562 V3563 E3564 G3565 S3568 W3571 R3582 GLU GLU ASP ALA D3587 D3588 P3589 E3590 R3594 V3602 E3610 H3611 PRO TYR
LYS SER LYS LYS ALA VAL TRP HIS LYS LEU LEU SER LYS GLN ARG ARG ARG ALA VAL VAL ALA CYS PHE ARG M3638 Q3683 GLU GLU GLU GLU GLU GLU VAL GLU GLU K3693 L3735 GLU GLU GLY GLY GLU ASN GLY GLU ALA GLU GLU GLU VAL GLU V3751 E3754 S3768
H3771 G3788 K3823 L3835 C3839 S3840 V3841 L3842 L3856 G3857 MET VAL ASN GLU ASP GLY THR VAL ILE ASN ARG GLN ASN GLY E3872 D3877 F3899 I3916 R3925 S3929 F3933 L3980 R3984 D3987 K4014 N4034 A4041 D4070 G4073 S4074 E4075
Q4078 D4079 Y4080 V4081 T4082 D4083 P4084 R4085 G4086 L4087 D4092 K4095 A4096 M4097 D4098 S4099 Q4100 K4101 Q4102 F4103 T4104 I4108 E4116 A4117 D4118 E4119 N4120 E4121 M4122 F4125 R4131 D4138 P4176 N4201 R4202 V4222 G4225 G4226 E4227 A4228 E4232 P4254 GLU GLY GLU PRO
GLU ALA ASP GLU ASP GLU GLY MET GLY GLU ALA ALA ALA GLU GLY ALA GLY ALA GLU GLU GLY GLY ALA ALA GLY ALA GLY ALA GLU GLY ALA ALA GLY THR VAL ALA ALA GLY ALA THR ALA ARG LEU ALA ALA ALA ALA ALA ARG ALA LEU ARG GLY LEU SER TYR ARG SER LEU ARG ARG ARG VAL ARG ARG
LEU ARG ARG L4322 T4323 A4324 R4325 E4326 A4337 A4340 R4341 ALA GLY ALA ALA GLY ALA GLY ALA ALA GLY ALA LEU ARG LEU LEU TRP GLY SER LEU PHE GLY GLY GLY LEU LEU VAL GLU GLY ALA LYS VAL THR VAL THR GLU LEU LEU ALA ALA GLY MET PRO ASP PRO THR SER ASP
GLU VAL HIS GLY GLU GLN PRO ALA GLY PRO GLY GLY GLY ASP ALA ASP GLY ALA GLY GLU GLY GLU GLY GLY ALA ALA GLY ASP GLY ASP GLU GLU VAL ALA GLY HIS GLU ALA GLY PRO GLY GLY ALA GLU GLY VAL VAL ALA ALA VAL ALA ASP GLY GLY PRO PHE ARG PRO GLU
GLY ALA GLY GLY LEU GLY ASP MET GLY ASP THR THR PRO ALA ALA GLU PRO ALA PRO THR PRO GLU GLY SER PRO ILE LEU LYS ARG LYS LEU GLY VAL ASP GLY GLU GLU GLU GLU GLU VAL LEU PRO GLU PRO GLU PRO GLU PRO GLU PRO GLU GLU PRO GLU GLU LYS ALA ASP GLU GLU GLU ASN GLY GLU GLU LYS
GLU GLU VAL PRO GLU ALA PRO PRO GLU PRO PRO LYS LYS ALA PRO PRO SER PRO PRO ALA LYS LYS GLU GLU ALA GLY GLY ALA LEU GLY MET GLU F4540 W4541 G4542 E4543 L4544 E4545 L4569 A4570 N4574 F4575 I4576 Y4580 K4581 V4582 P4587 GLY GLU ASP ASP MET GLU GLY SER ALA ALA
GLY ASP LEU ALA GLY ALA GLY GLY SER GLY GLY SER GLY GLY TRP GLY GLY ALA GLU GLY ASP GLY GLU ASP ASN M4627 Y4630 E4634 L4643 L4646 R4679 Q4691 D4694 D4695 D4696 R4703 L4704 Y4715 D4730 R4736 E4739 D4744 L4745
A4746 S4747 L4748 E4749 I4750 T4751 A4752 H4753 N4754 E4755 R4756 LYS PRO ASP PRO PRO PRO GLY LEU LEU THR W4767 L4768 M4769 S4770 I4771 K4774 V4830 L4844 F4856 R4860 S4866 E4867 D4868 E4869 D4870 Y4888 V4889 R4892 D4899 E4900 I4918 A4930 I4931 I4932 Q4933 G4934 I4937

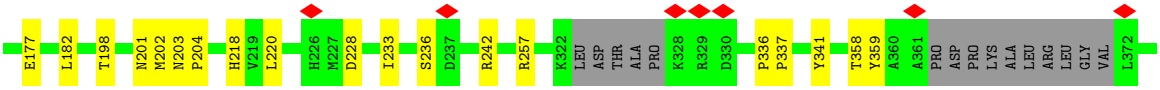


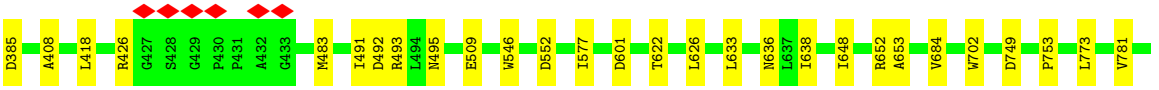
• Molecule 2: Ryanodine receptor 1

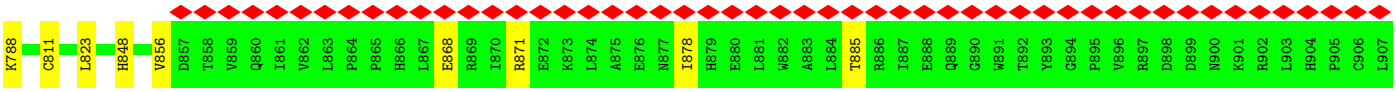
Chain F:

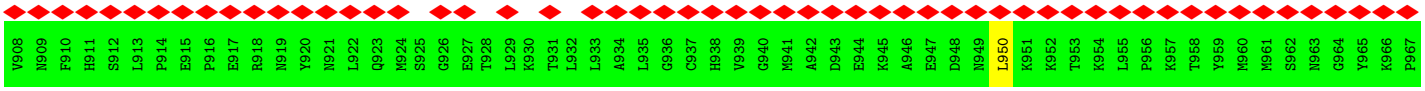


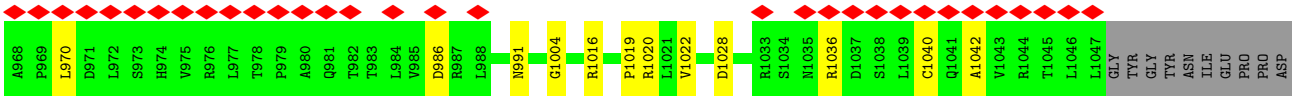


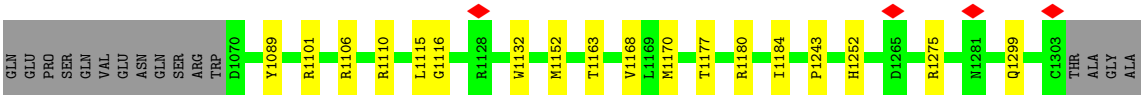




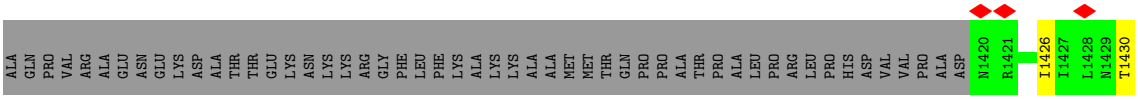


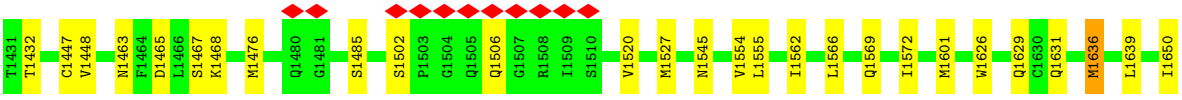


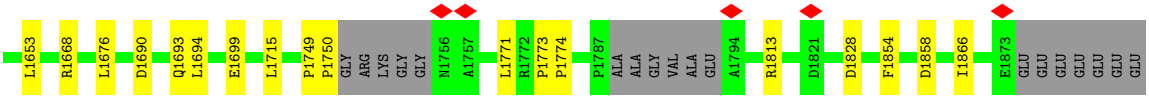


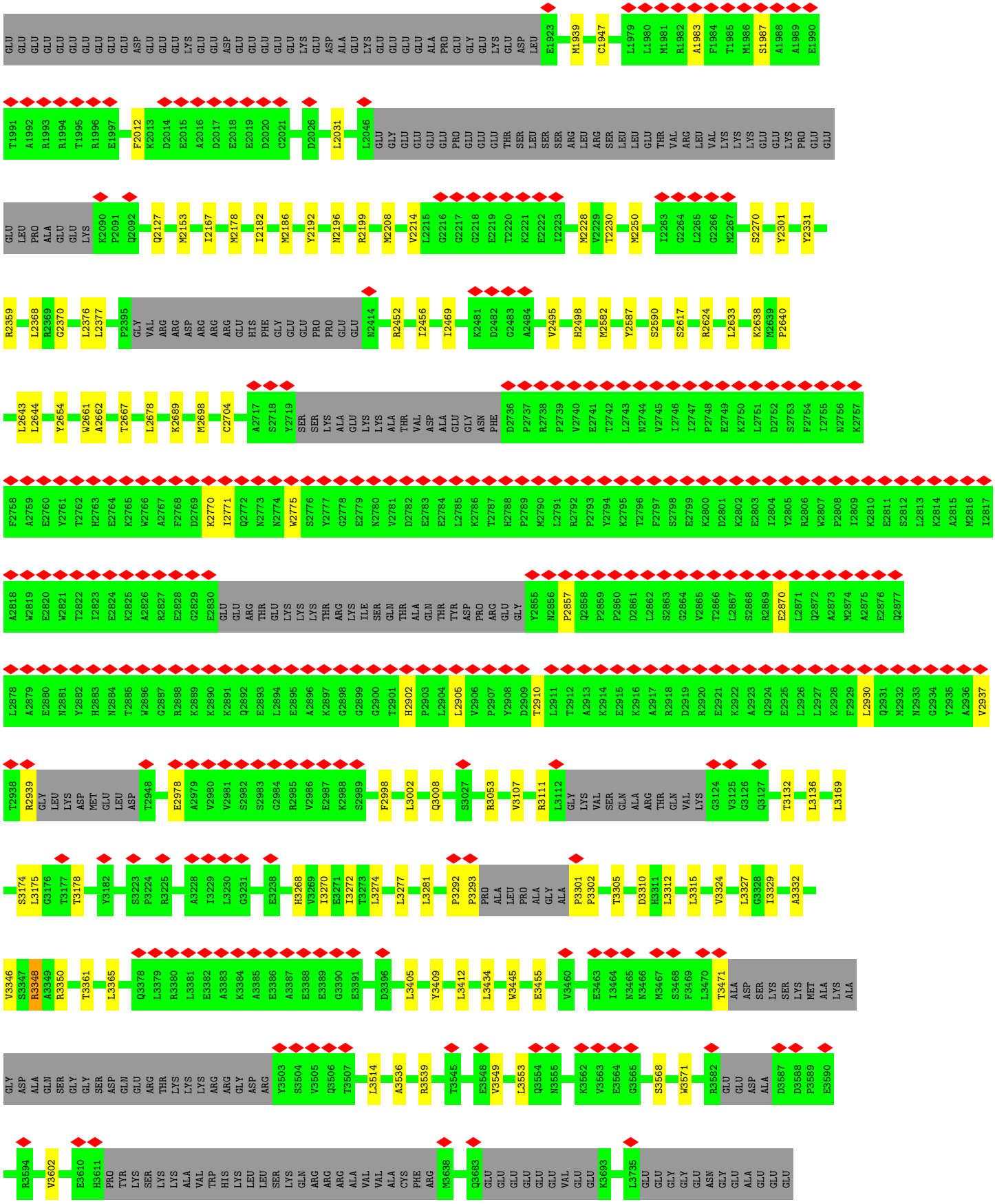


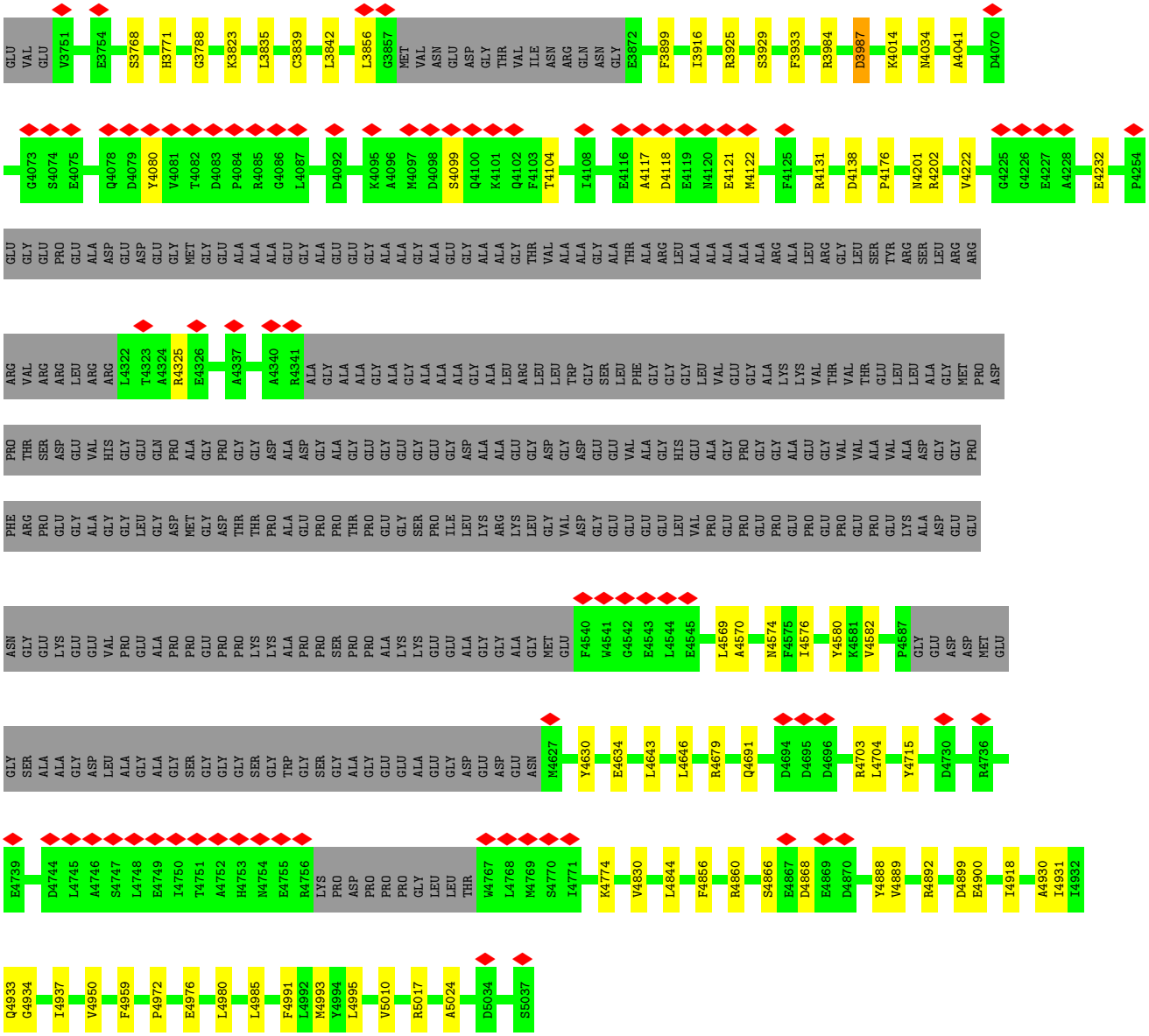








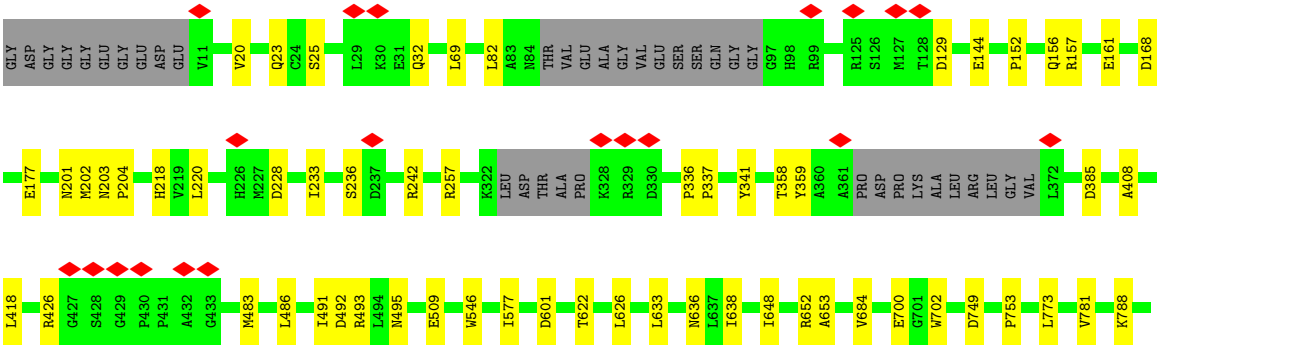

GLU GLU GLU GLU GLU GLU GLU GLU GLU ASP GLU GLU GLU LYS GLU GLU ASP GLU GLU GLU GLU GLU LYS GLU ASP ALA GLU LYS GLU GLU GLU GLU ALA PRO GLU GLY GLU LYS GLU ASP LEU
E1923 M1939 C1947
L1979 L1980 M1981 R1982 A1983 F1984 T1985 M1986 S1987 A1988 A1989 E1990
T1991 A1992 R1993 R1994 T1995 R1996 E1997
F2012 K2013 D2014 E2015 A2016 D2017 E2018 E2019 D2020 C2021 D2026 L2031 L2046
GLU GLY GLU GLU GLU GLU PRO GLU GLU GLU THR SER LEU SER SER ARG LEU ARG SER LEU LEU GLU THR VAL ARG LEU VAL LYS LYS LYS GLU GLU LYS PRO GLU GLU
GLU LEU PRO ALA GLU GLU LYS
K2090 P2091 Q2092 Q2127 M2153 I2167 M2178 I2182 M2186 Y2192 N2196 R2199 M2208 V2214 L2215 G2216 G2217 G2218 E2219 T2220 K2221 E2222 I2223 M2228 V2229 T2230 M2250 I2263 G2264 L2265 G2266 M2267 S2270 Y2301 Y2331
R2359 L2368 R2369 G2370 L2376 L2377 P2395 GLY VAL ARG ARG ASP ARG ARG ARG GLU HIS PHE GLY GLU GLU PRO PRO GLU GLU N2414 R2452 I2456 I2469 K2481 D2482 G2483 A2484 V2495 H2498 M2582 Y2587 S2590 S2617 R2624 L2633 K2638 M2639 P2640
L2643 L2644 Y2654 W2661 A2662 T2667 L2678 K2689 M2698 C2704 A2717 S2718 Y2719 SER SER LYS ALA GLU LYS LYS ALA THR VAL ASP ALA GLU GLY ASN PHE D2736 P2737 R2738 P2739 V2740 E2741 T2742 L2743 N2744 V2745 I2746 I2747 P2748 E2749 K2750 L2751 D2752 S2753 F2754 I2755 N2756 K2757
F2758 A2759 E2760 Y2761 T2762 H2763 E2764 K2765 W2766 A2767 F2768 D2769 K2770 I2771 Q2772 N2773 N2774 W2775 S2776 Y2777 G2778 E2779 N2780 V2781 D2782 E2783 E2784 L2785 K2786 T2787 H2788 P2789 M2790 L2791 R2792 P2793 Y2794 K2795 T2796 P2797 S2798 E2799 K2800 D2801 K2802 E2803 I2804 Y2805 R2806 W2807 P2808 I2809 K2810 E2811 S2812 L2813 K2814 A2815 M2816 I2817
A2818 W2819 E2820 W2821 T2822 I2823 E2824 K2825 A2826 R2827 E2828 G2829 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 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 G2887 R2888 K2889 K2890 K2891 Q2892 E2893 L2894 E2895 A2896 K2897 G2898 G2899 G2900 T2901 H2902 P2903 L2904 L2905 V2906 P2907 Y2908 D2909 T2910 L2911 T2912 A2913 K2914 E2915 K2916 A2917 R2918 D2919 R2920 E2921 K2922 A2923 Q2924 E2925 L2926 L2927 K2928 F2929 L2930 Q2931 M2932 N2933 G2934 Y2935 A2936 V2937
T2938 R2939 GLY LEU LYS ASP MET GLU LEU ASP T2948 E2978 A2979 V2980 V2981 S2982 S2983 G2984 R2985 V2986 E2987 K2988 S2989 F2998 L3002 Q3008 S3027 R3053 V3107 R3111 L3112 GLY LYS VAL SER GLN ALA ARG THR GLN VAL LYS G3124 V3125 G3126 Q3127 T3132 L3136 L3169
S3174 L3175 G3176 T3177 T3178 Y3182 S3223 P3224 R3225 A3228 I3229 L3230 G3231 E3238 H3268 V3269 I3270 E3271 I3272 T3273 L3274 L3277 L3281 P3292 P3293 PRO ALA LEU PRO ALA GLY ALA P3301 P3302 T3305 D3310 H3311 L3312 L3315 V3324 L3327 G3328 I3329 A3332
V3346 S3347 R3348 A3349 R3350 T3361 L3365 Q3378 L3379 R3380 L3381 E3382 A3383 K3384 A3385 E3386 A3387 E3388 E3389 G3390 E3391 D3396 L3405 Y3409 L3412 L3434 W3445 E3455 V3460 E3463 I3464 N3465 N3466 M3467 S3468 F3469 L3470 T3471 ALA ASP SER LYS SER LYS MET ALA LYS ALA
GLY ASP ALA GLN SER GLY GLY SER ASP GLN GLU ARG THR LYS LYS LYS ARG ARG GLY ASP ARG Y3503 S3504 V3505 Q3506 T3507 L3514 A3536 R3539 T3545 E3548 V3549 L3553 Q3554 M3555 K3562 V3563 E3564 G3565 S3568 W3571 R3582 GLU GLU ASP ALA D3587 D3588 P3589 E3590
R3594 V3602 E3610 H3611 PRO TYR LYS SER LYS LYS ALA VAL TRP HIS LYS LEU LEU SER LYS GLN ARG ARG ARG ALA VAL VAL ALA CYS PHE ARG M3638 Q3683 GLU GLU GLU GLU GLU VAL GLU GLU K3693 L3735 GLU GLU GLY GLY GLU ASN GLY GLU ALA GLU GLU GLU

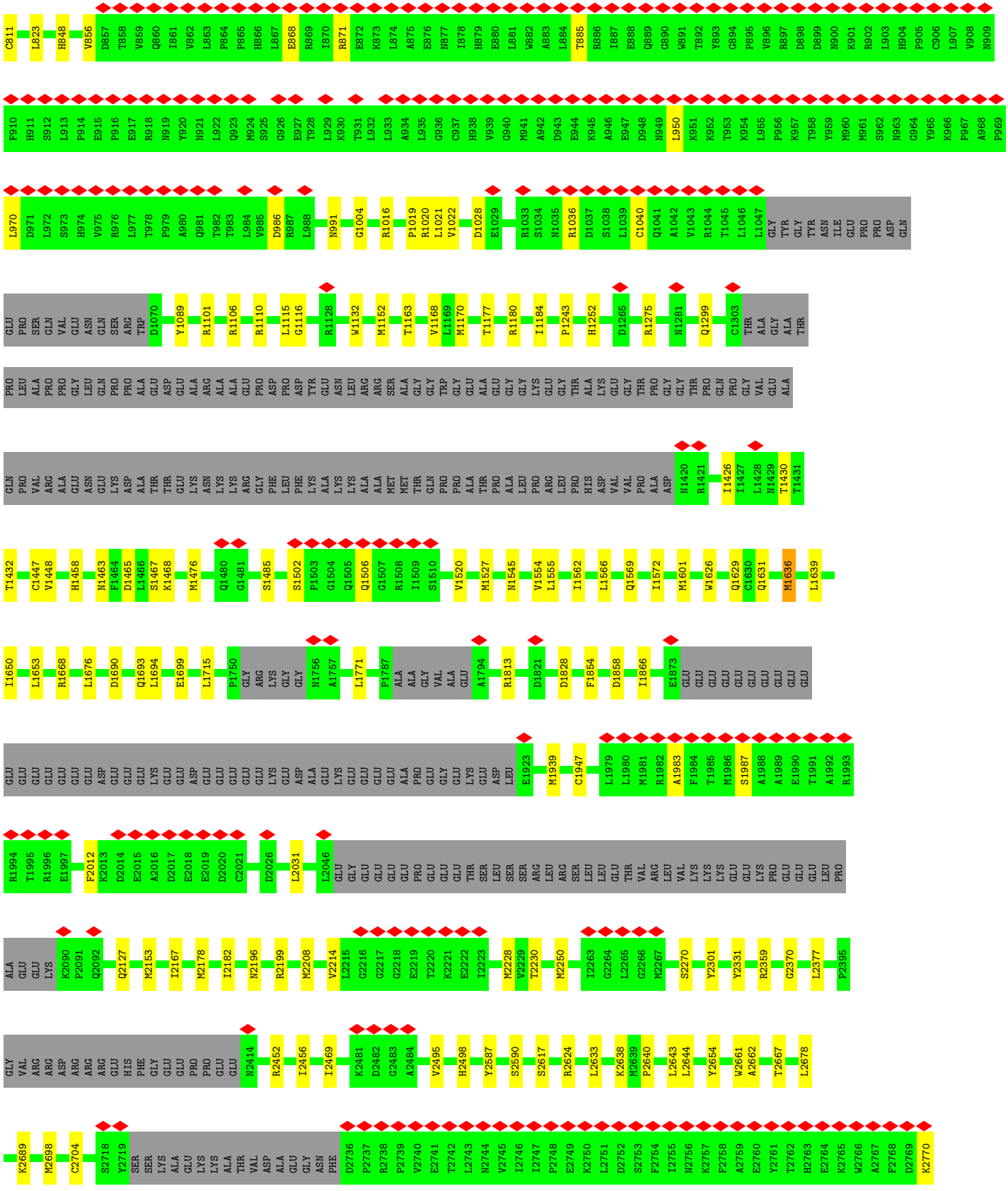


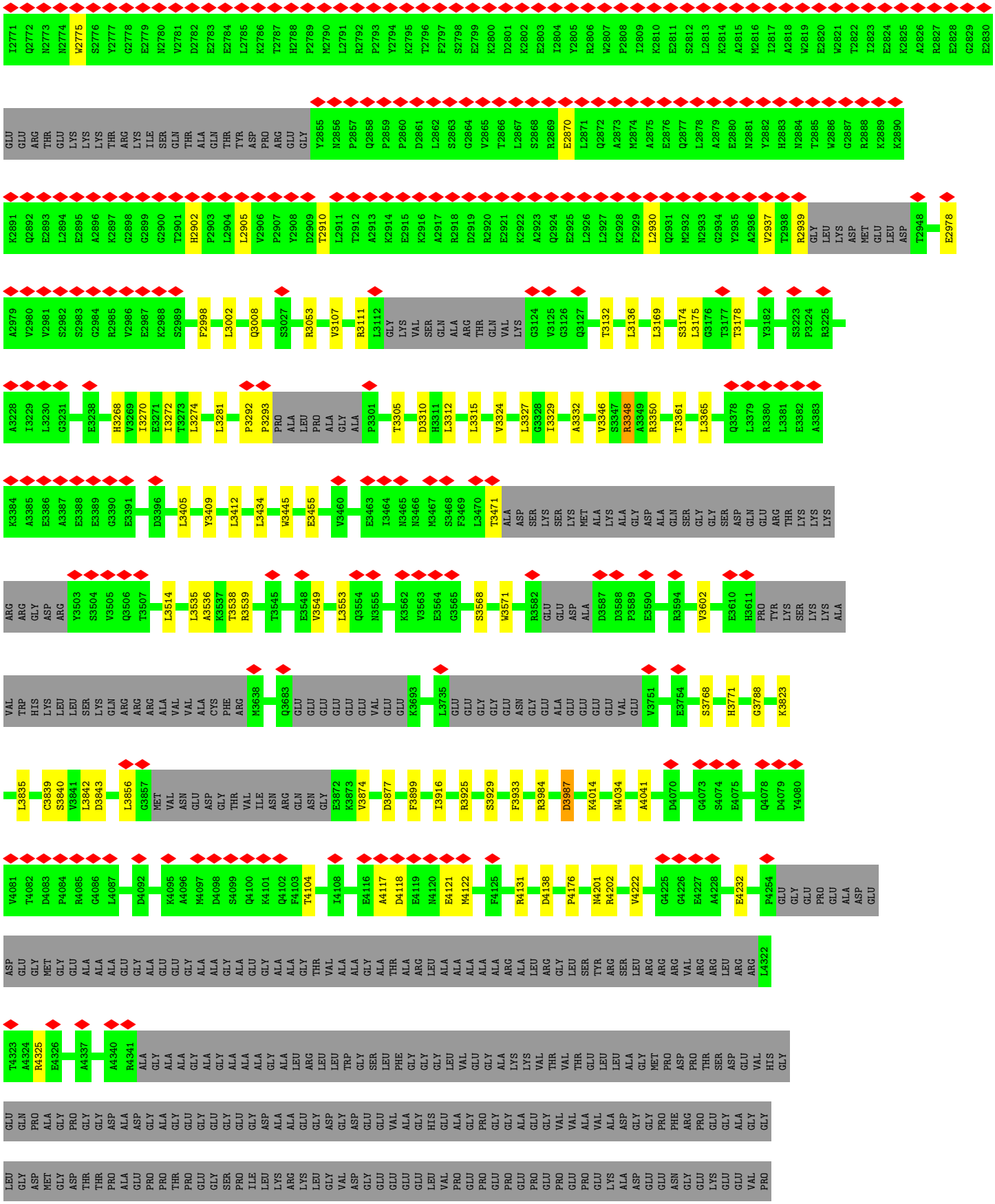
• Molecule 2: Ryanodine receptor 1

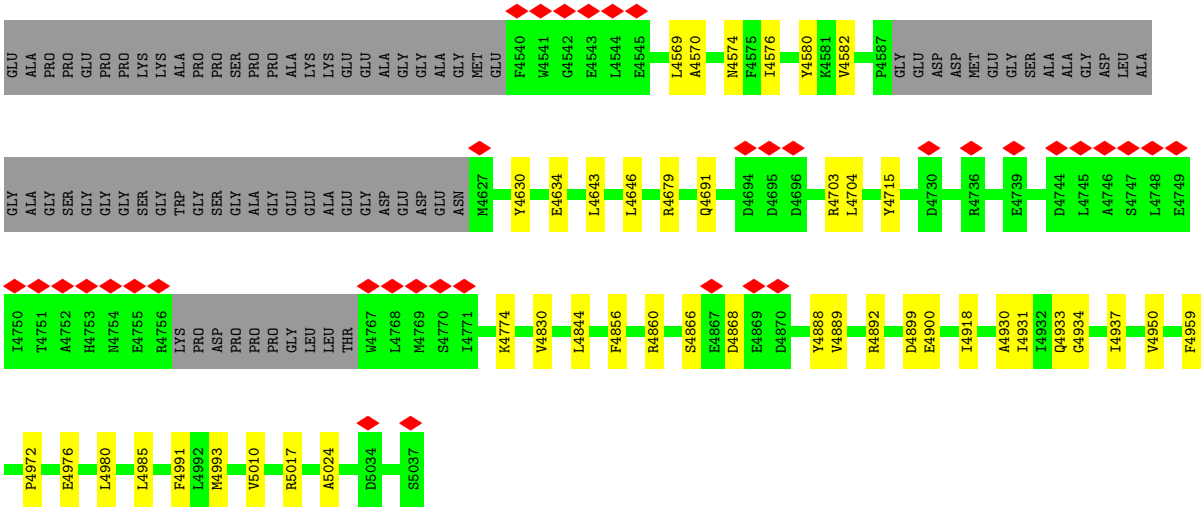
Chain H:






C811 L823 H848 V856 D857 T858 V859 Q860 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 R886 I887 E888 Q889 G890 W891 T892 Y893 G894 P895 V896 R897 D898 D899 N900 K901 R902 L903 H904 P905 C906 L907 V908 N909
P910 H911 S912 L913 P914 E915 P916 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 V975 R976 L977 T978 P979 A980 Q981 T982 T983 L984 V985 D986 R987 L988 N991 G1004 R1016 P1019 R1020 L1021 V1022 D1028 E1029 R1033 S1034 N1035 R1036 D1037 S1038 L1039 C1040 Q1041 A1042 V1043 R1044 T1045 L1046 L1047 GLY TYR GLY TYR ASN ILE GLU PRO PRO ASP GLN
GLU PRO SER GLN VAL GLU ASN GLN SER ARG TRP D1070 Y1089 R1101 R1106 R1110 L1115 G1116 R1128 W1132 M1152 T1163 V1168 L1169 M1170 T1177 R1180 I1184 P1243 H1252 D1265 R1275 N1281 Q1299 C1303 THR ALA GLY ALA THR
PRO LEU ALA PRO PRO GLY LEU GLN PRO PRO ALA GLU ASP GLU ALA ARG ALA ALA ALA GLU PRO ASP PRO ASP TYR GLU ASN LEU ARG ARG SER ALA GLY GLY TRP GLY GLU ALA GLU GLY GLY LYS GLU GLY THR ALA LYS GLU GLY THR PRO GLY GLY THR PRO GLN PRO GLY VAL GLU ALA
GLN PRO VAL ARG ALA GLU ASN GLU LYS ASP ALA THR THR GLU LYS ASN LYS LYS ARG GLY PHE LEU PHE LYS ALA LYS LYS ALA ALA MET MET THR GLN PRO PRO ALA THR PRO ALA LEU PRO ARG LEU PRO HIS ASP VAL VAL PRO ALA ASP N1420 R1421 I1426 I1427 L1428 N1429 T1430 T1431
T1432 C1447 V1448 H1458 N1463 F1464 D1465 L1466 S1467 K1468 M1476 Q1480 G1481 S1485 S1502 P1503 G1504 Q1505 Q1506 G1507 R1508 I1509 S1510 V1520 M1527 N1545 V1554 L1555 I1562 L1566 Q1569 I1572 M1601 W1626 Q1629 C1630 Q1631 M1636 L1639
I1650 L1653 R1668 L1676 D1690 Q1693 L1694 E1699 L1715 P1750 GLY ARG LYS GLY GLY N1756 A1757 L1771 P1787 ALA ALA GLY VAL ALA GLU A1794 R1813 D1821 D1828 F1854 D1858 I1866 E1873 GLU GLU GLU GLU GLU GLU GLU GLU
GLU GLU GLU GLU GLU GLU ASP GLU GLU GLU LYS GLU GLU ASP GLU GLU GLU GLU GLU LYS GLU ASP ALA GLU LYS GLU GLU GLU GLU ALA PRO GLU GLY GLU LYS GLU ASP LEU E1923 M1939 C1947 L1979 L1980 M1981 R1982 A1983 F1984 T1985 M1986 S1987 A1988 A1989 E1990 T1991 A1992 R1993
R1994 T1995 R1996 E1997 F2012 K2013 D2014 E2015 A2016 D2017 E2018 E2019 D2020 C2021 D2026 L2031 L2046 GLU GLY GLU GLU GLU GLU PRO GLU GLU GLU THR SER LEU SER SER ARG LEU ARG SER LEU LEU GLU THR VAL ARG LEU VAL LYS LYS LYS GLU GLU LYS PRO GLU GLU GLU LEU PRO
ALA GLU GLU LYS K2090 P2091 Q2092 Q2127 M2153 I2167 M2178 I2182 N2196 R2199 M2208 V2214 L2215 G2216 G2217 G2218 E2219 T2220 K2221 E2222 I2223 M2228 V2229 T2230 M2250 I2263 G2264 L2265 G2266 M2267 S2270 Y2301 Y2331 R2359 G2370 L2377 P2395
GLY VAL ARG ARG ASP ARG ARG ARG GLU HIS PHE GLY GLU GLU PRO PRO GLU GLU N2414 R2452 I2456 I2469 K2481 D2482 G2483 A2484 V2495 H2498 Y2587 S2590 S2617 R2624 L2633 K2638 M2639 P2640 L2643 L2644 Y2654 W2661 A2662 T2667 L2678
K2689 M2698 C2704 S2718 Y2719 SER SER LYS ALA GLU LYS LYS ALA THR VAL ASP ALA GLU GLY ASN PHE D2736 P2737 R2738 P2739 V2740 E2741 T2742 L2743 N2744 V2745 I2746 I2747 P2748 E2749 K2750 L2751 D2752 S2753 F2754 I2755 N2756 K2757 F2758 A2759 E2760 Y2761 T2762 H2763 E2764 K2765 W2766 A2767 F2768 D2769 K2770


I2771 Q2772 N2773 N2774 W2775 S2776 Y2777 G2778 E2779 N2780 V2781 D2782 E2783 E2784 L2785 K2786 T2787 H2788 P2789 M2790 L2791 R2792 P2793 Y2794 K2795 T2796 F2797 S2798 E2799 K2800 D2801 K2802 E2803 I2804 Y2805 R2806 W2807 P2808 I2809 K2810 E2811 S2812 L2813 K2814 A2815 M2816 I2817 A2818 W2819 E2820 W2821 T2822 I2823 E2824 K2825 A2826 R2827 E2828 G2829 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 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 G2887 R2888 K2889 K2890
K2891 Q2892 E2893 L2894 E2895 A2896 K2897 G2898 G2899 G2900 T2901 H2902 P2903 L2904 L2905 V2906 P2907 Y2908 D2909 T2910 L2911 T2912 A2913 K2914 E2915 K2916 A2917 R2918 D2919 R2920 E2921 K2922 A2923 Q2924 E2925 L2926 L2927 K2928 F2929 L2930 Q2931 M2932 N2933 G2934 Y2935 A2936 V2937 T2938 R2939 GLY LEU LYS ASP MET GLU LEU ASP T2948 E2978
A2979 V2980 V2981 S2982 S2983 G2984 R2985 V2986 E2987 K2988 S2989 F2998 L3002 Q3008 S3027 R3053 V3107 R3111 L3112 GLY LYS VAL SER GLN ALA ARG THR GLN VAL LYS G3124 V3125 G3126 Q3127 T3132 L3136 L3169 S3174 L3175 G3176 T3177 T3178 Y3182 S3223 P3224 R3225
A3228 I3229 L3230 G3231 E3238 H3268 V3269 I3270 E3271 I3272 T3273 L3274 L3281 P3292 P3293 PRO ALA LEU PRO ALA GLY ALA P3301 T3305 D3310 H3311 L3312 L3315 V3324 L3327 G3328 I3329 A3332 V3346 S3347 R3348 A3349 R3350 T3361 L3365 Q3378 L3379 R3380 L3381 E3382 A3383
K3384 A3385 E3386 A3387 E3388 E3389 G3390 E3391 D3396 L3405 Y3409 L3412 L3434 W3445 E3455 V3460 E3463 I3464 N3465 N3466 M3467 S3468 F3469 L3470 T3471 ALA ASP SER LYS SER LYS MET ALA LYS ALA GLY ASP ALA GLN SER GLY GLY SER ASP GLN GLU ARG THR LYS LYS LYS
ARG ARG GLY ASP ARG Y3503 S3504 V3505 Q3506 T3507 L3514 L3535 A3536 K3537 T3538 R3539 T3545 E3548 V3549 L3553 Q3554 N3555 K3562 V3563 E3564 G3565 S3568 W3571 R3582 GLU GLU ASP ALA D3587 D3588 P3589 E3590 R3594 V3602 E3610 H3611 PRO TYR LYS SER LYS LYS ALA
VAL TRP HIS LYS LEU LEU SER LYS GLN ARG ARG ARG ALA VAL VAL ALA CYS PHE ARG M3638 Q3683 GLU GLU GLU GLU GLU GLU VAL GLU GLU K3693 L3735 GLU GLU GLY GLY GLU ASN GLY GLU ALA GLU GLU GLU GLU VAL GLU V3751 E3754 S3768 H3771 G3788 K3823
L3835 C3839 S3840 V3841 L3842 D3843 L3856 G3857 MET VAL ASN GLU ASP GLY THR VAL ILE ASN ARG GLN ASN GLY E3872 K3873 V3874 D3877 F3899 I3916 R3925 S3929 F3933 R3984 D3987 K4014 N4034 A4041 D4070 G4073 S4074 E4075 Q4078 D4079 Y4080
V4081 T4082 D4083 P4084 R4085 G4086 L4087 D4092 K4095 A4096 M4097 D4098 S4099 Q4100 K4101 Q4102 F4103 T4104 I4108 E4116 A4117 D4118 E4119 N4120 E4121 M4122 F4125 R4131 D4138 P4176 N4201 R4202 V4222 G4225 G4226 E4227 A4228 E4232 P4254 GLU GLY GLU PRO GLU ALA ASP GLU
ASP GLU GLY MET GLY GLU ALA ALA ALA GLU GLY ALA GLU GLU GLY ALA ALA ALA GLY ALA GLU GLU GLY ALA ALA ALA GLY THR VAL ALA ALA GLY ALA THR ARG LEU ALA ALA ALA ALA ALA ARG ALA LEU ARG GLY LEU SER TYR ARG SER LEU ARG ARG ARG VAL ARG ARG LEU ARG ARG L4322
T4323 A4324 R4325 E4326 A4337 A4340 R4341 ALA GLY ALA ALA GLY GLY ALA GLY GLY ALA ALA ALA GLY ALA GLY LEU ARG LEU LEU TRP GLY SER LEU PHE GLY GLY GLY LEU VAL GLU GLY ALA LYS LYS VAL THR VAL THR GLU LEU LEU ALA GLY MET PRO ASP PRO THR SER ASP GLU VAL HIS GLY
GLU GLN PRO ALA GLY PRO GLY GLY ASP ALA ASP GLY ALA GLY GLU GLY GLY GLU GLY ALA GLY GLU GLY ASP GLY VAL VAL ALA GLU GLY ALA GLY HIS GLU ALA GLY PRO GLY GLY ALA GLU GLY VAL VAL ALA ASP GLY GLY PRO PHE ARG PRO GLU GLY ALA GLY GLY
LEU GLY ASP MET GLY ASP THR THR PRO ALA GLU PRO PRO THR PRO GLU GLY SER PRO ILE LEU LYS ARG LYS LEU GLY VAL ASP GLY GLU GLU GLU GLU LEU VAL PRO GLU PRO PRO GLU PRO GLU PRO GLU GLU LYS ALA ASP GLU ASN GLY GLU LYS GLU GLU VAL PRO


GLU ALA PRO PRO GLU PRO PRO LYS LYS ALA PRO PRO SER PRO PRO ALA LYS LYS GLU GLU ALA GLY GLY ALA GLY MET GLU
F4540 W4541 G4542 E4543 L4544 E4545
L4569 A4570
N4574 F4575 I4576
Y4580 K4581 V4582
P4587
GLY GLU ASP ASP MET GLU GLY SER ALA ALA GLY ASP LEU ALA
GLY ALA GLY SER GLY GLY GLY SER GLY TRP GLY SER GLY ALA GLY GLU GLU ALA GLU GLY ASP GLU ASP GLU ASN
M4627
Y4630
E4634
L4643
L4646
R4679
Q4691
D4694 D4695 D4696
R4703 L4704
Y4715
D4730
R4736
E4739
D4744 L4745 A4746 S4747 L4748 E4749
I4750 T4751 A4752 H4753 N4754 E4755 R4756
LYS PRO ASP PRO PRO PRO GLY LEU LEU THR
W4767 L4768 M4769 S4770 I4771
K4774
V4830
L4844
F4856
R4860
S4866
E4867
D4868
E4869 D4870
Y4888 V4889
R4892
D4899 E4900
I4918
A4930 I4931 I4932 Q4933 G4934
I4937
V4950
F4959
P4972
E4976
L4980
L4985
F4991 L4992 M4993
V5010
R5017
A5024
D5034
S5037

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	131257	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.753	Depositor
Minimum map value	0.000	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.086	Depositor
Map size (Å)	477.696, 477.696, 477.696	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.933, 0.933, 0.933	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	0.14	0/835	0.37	0/1126
1	C	0.14	0/835	0.37	0/1126
1	E	0.14	0/835	0.37	0/1126
1	G	0.14	0/835	0.37	0/1126
2	B	0.15	0/34093	0.35	0/46246
2	D	0.15	0/34093	0.35	0/46246
2	F	0.15	0/34093	0.35	0/46246
2	H	0.15	0/34093	0.35	0/46246
All	All	0.15	0/139712	0.36	0/189488

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	819	0	818	5	0
1	C	819	0	818	5	0
1	E	819	0	818	5	0
1	G	819	0	818	5	0
2	B	33334	0	32599	194	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	33334	0	32599	200	0
2	F	33334	0	32599	201	0
2	H	33334	0	32599	195	0
3	B	1	0	0	0	0
3	D	1	0	0	0	0
3	F	1	0	0	0	0
3	H	1	0	0	0	0
All	All	136616	0	133668	713	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 3.

The worst 5 of 713 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:B:4634:GLU:OE2	2:D:4325:ARG:NH1	2.20	0.75
2:F:4582:VAL:CG2	2:H:4856:PHE:CZ	2.70	0.75
2:F:4634:GLU:OE2	2:H:4325:ARG:NH1	2.20	0.74
2:B:4856:PHE:CZ	2:H:4582:VAL:CG2	2.70	0.74
2:D:4634:GLU:OE2	2:F:4325:ARG:NH1	2.20	0.74

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	106/110 (96%)	104 (98%)	2 (2%)	0	100	100
1	C	106/110 (96%)	104 (98%)	2 (2%)	0	100	100
1	E	106/110 (96%)	104 (98%)	2 (2%)	0	100	100
1	G	106/110 (96%)	104 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	4213/5037 (84%)	4166 (99%)	47 (1%)	0	100	100
2	D	4213/5037 (84%)	4166 (99%)	47 (1%)	0	100	100
2	F	4213/5037 (84%)	4166 (99%)	47 (1%)	0	100	100
2	H	4213/5037 (84%)	4166 (99%)	47 (1%)	0	100	100
All	All	17276/20588 (84%)	17080 (99%)	196 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	87/90 (97%)	85 (98%)	2 (2%)	44	71
1	C	87/90 (97%)	85 (98%)	2 (2%)	44	71
1	E	87/90 (97%)	85 (98%)	2 (2%)	44	71
1	G	87/90 (97%)	85 (98%)	2 (2%)	44	71
2	B	3529/4277 (82%)	3504 (99%)	25 (1%)	76	89
2	D	3529/4277 (82%)	3504 (99%)	25 (1%)	76	89
2	F	3529/4277 (82%)	3504 (99%)	25 (1%)	76	89
2	H	3529/4277 (82%)	3504 (99%)	25 (1%)	76	89
All	All	14464/17468 (83%)	14356 (99%)	108 (1%)	73	89

5 of 108 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	577	ILE
2	F	3409	TYR
2	H	3856	LEU
2	F	1022	VAL
2	F	2617	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 202 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	1482	ASN
2	F	4162	ASN
2	H	4707	ASN
2	F	1938	GLN
2	F	2772	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

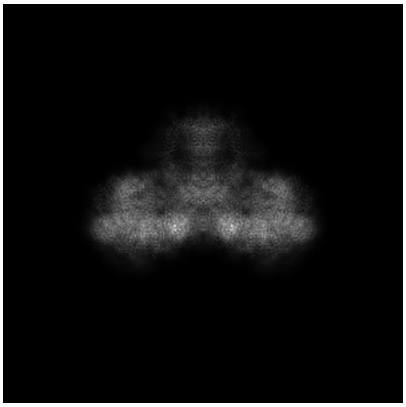
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-73951. These allow visual inspection of the internal detail of the map and identification of artifacts.

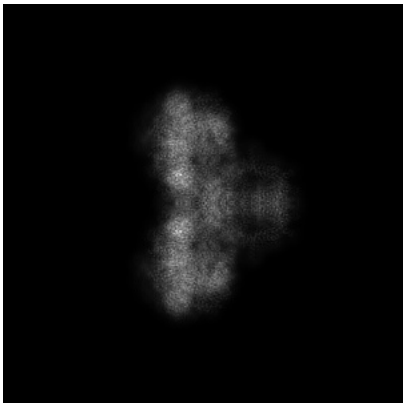
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

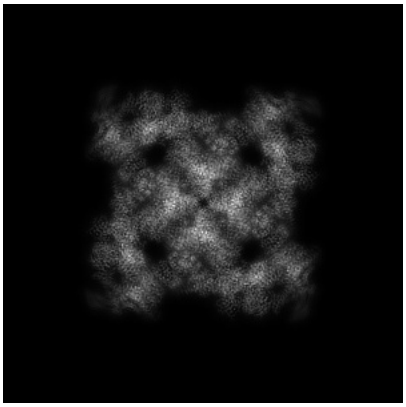
6.1.1 Primary map



X



Y

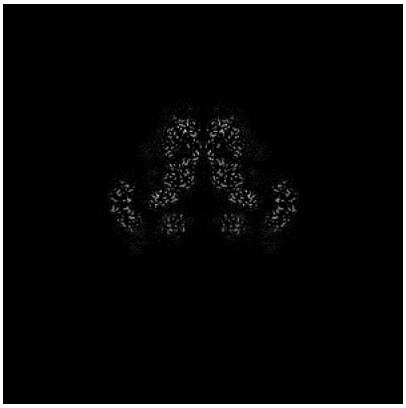


Z

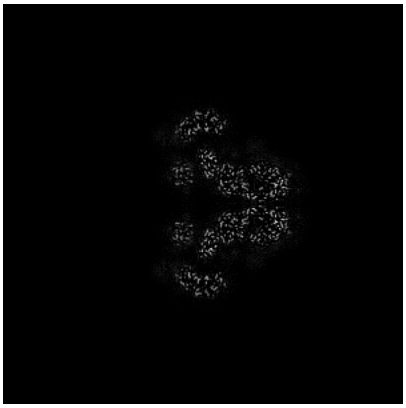
The images above show the map projected in three orthogonal directions.

6.2 Central slices

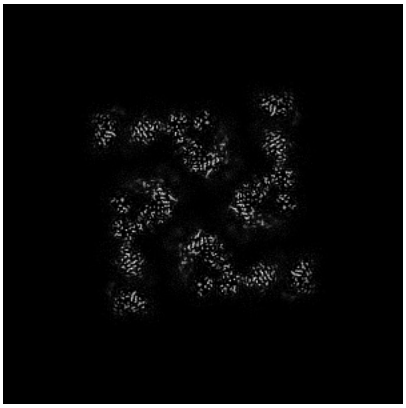
6.2.1 Primary map



X Index: 256



Y Index: 256

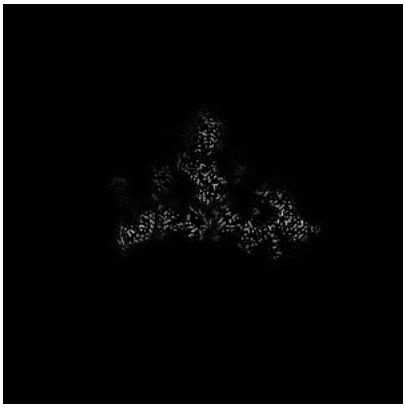


Z Index: 256

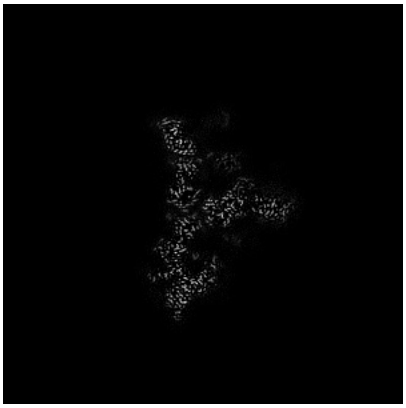
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

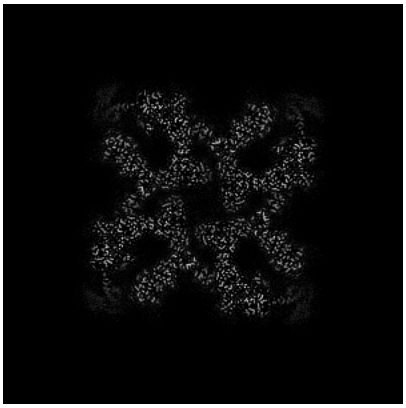
6.3.1 Primary map



X Index: 219



Y Index: 219

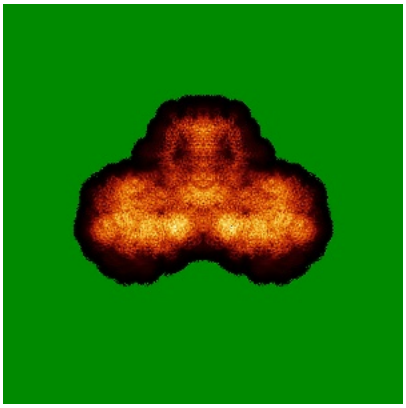


Z Index: 228

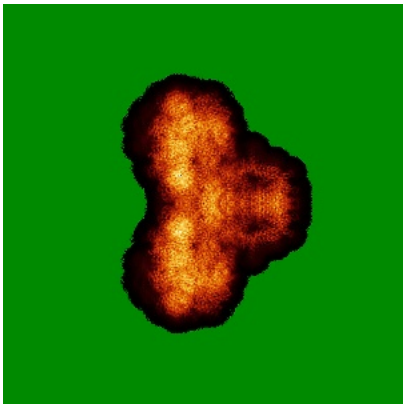
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

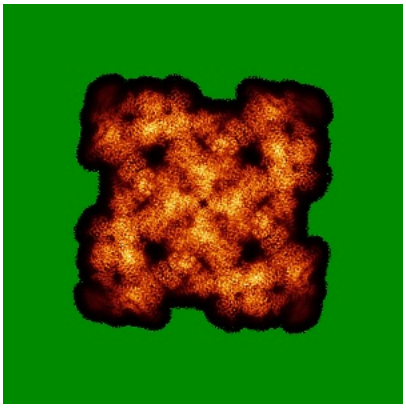
6.4.1 Primary map



X



Y

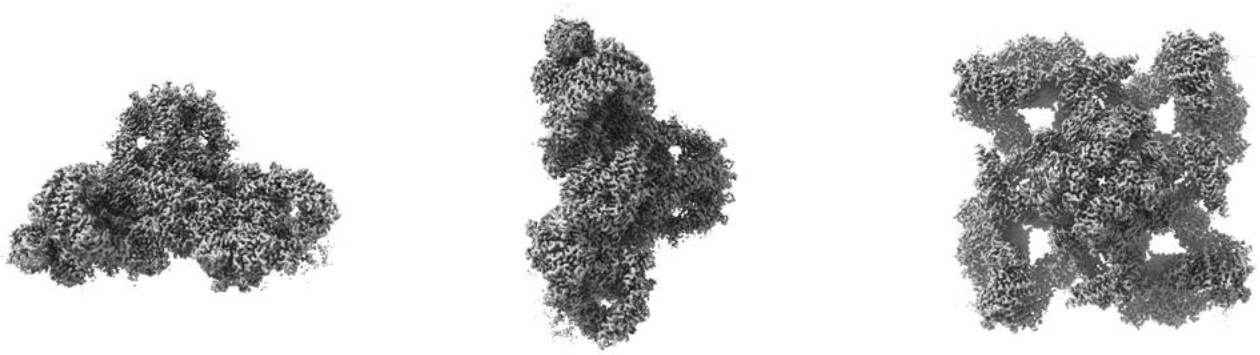


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.086. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

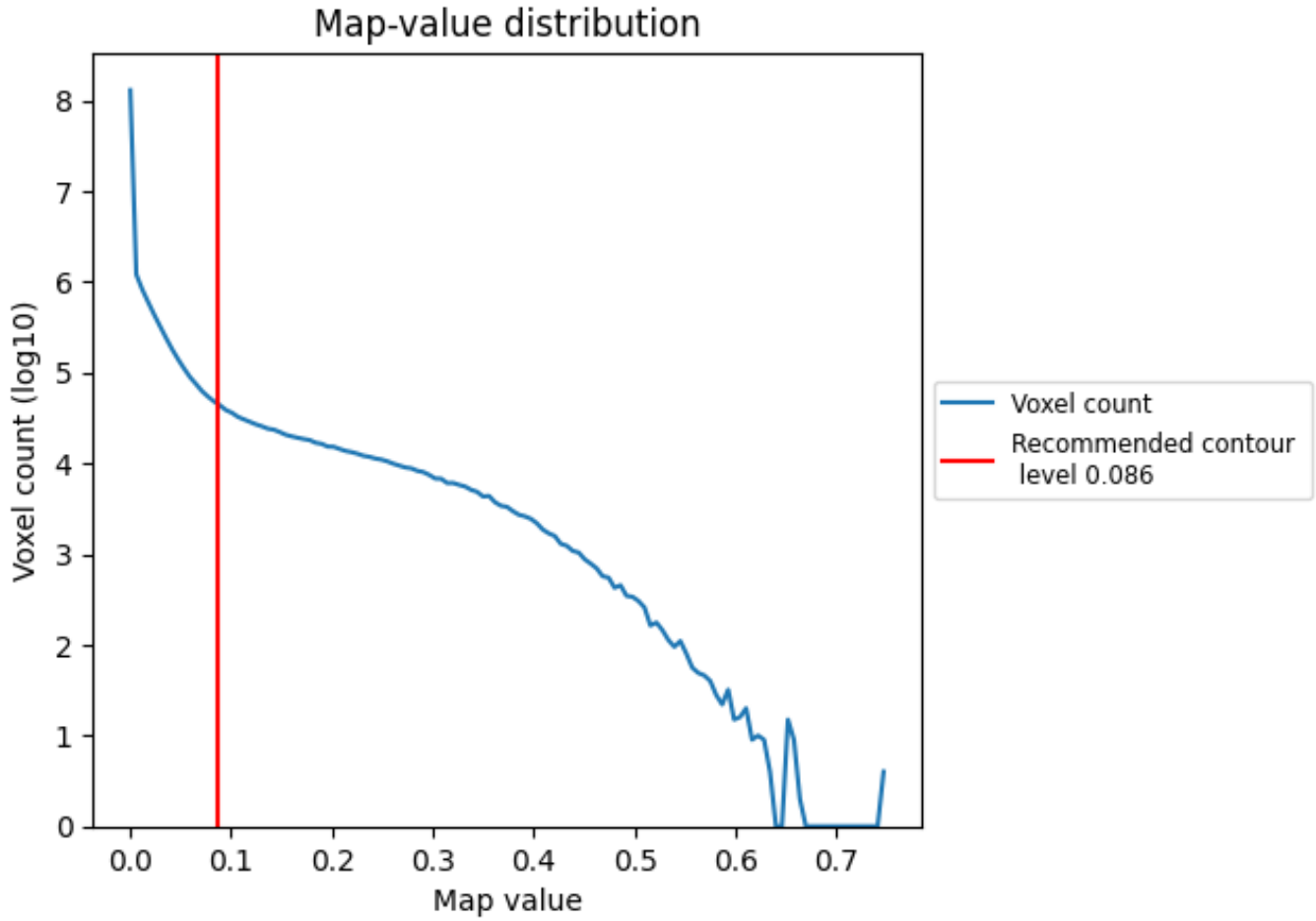
6.6 Mask visualisation (i)

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

7 Map analysis

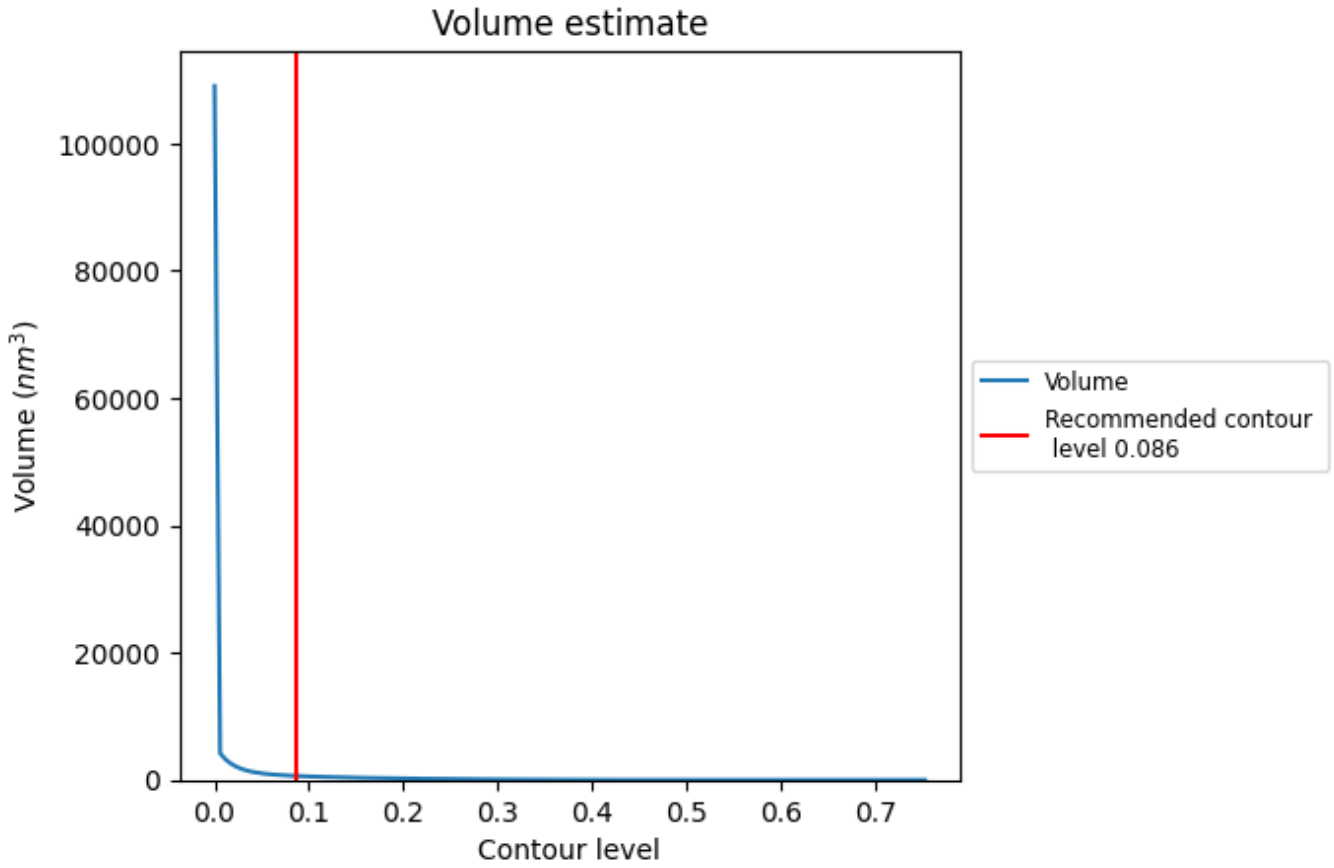
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

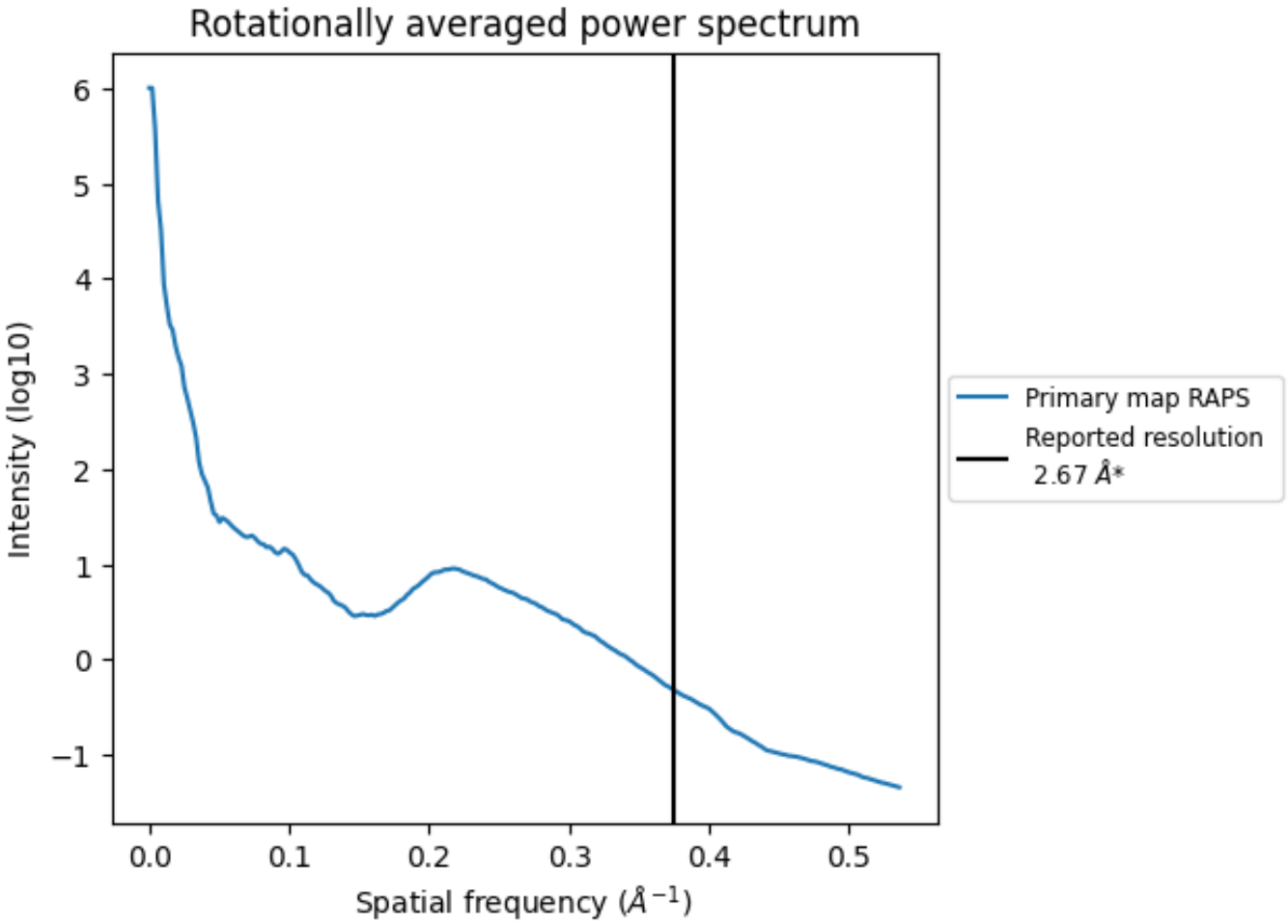
7.2 Volume estimate



The volume at the recommended contour level is 635 nm^3; this corresponds to an approximate mass of 574 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.375 $Å^{-1}$

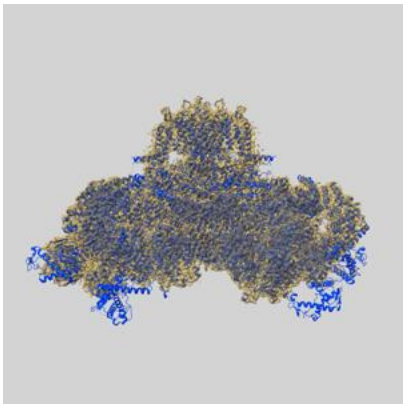
8 Fourier-Shell correlation

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

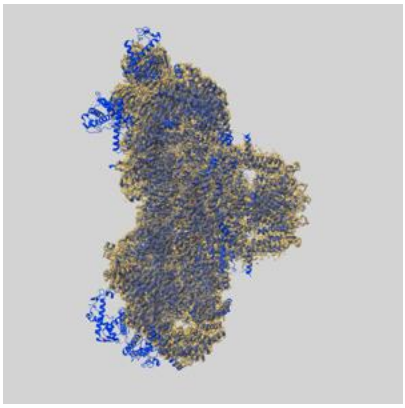
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-73951 and PDB model 9Z9M. Per-residue inclusion information can be found in section 3 on page 7.

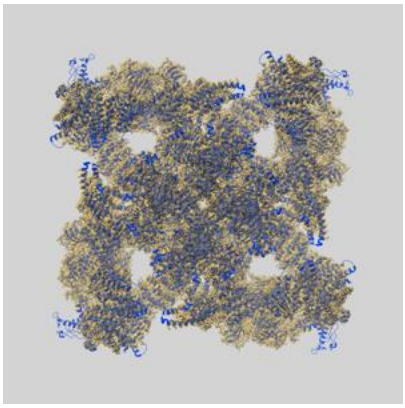
9.1 Map-model overlay



X



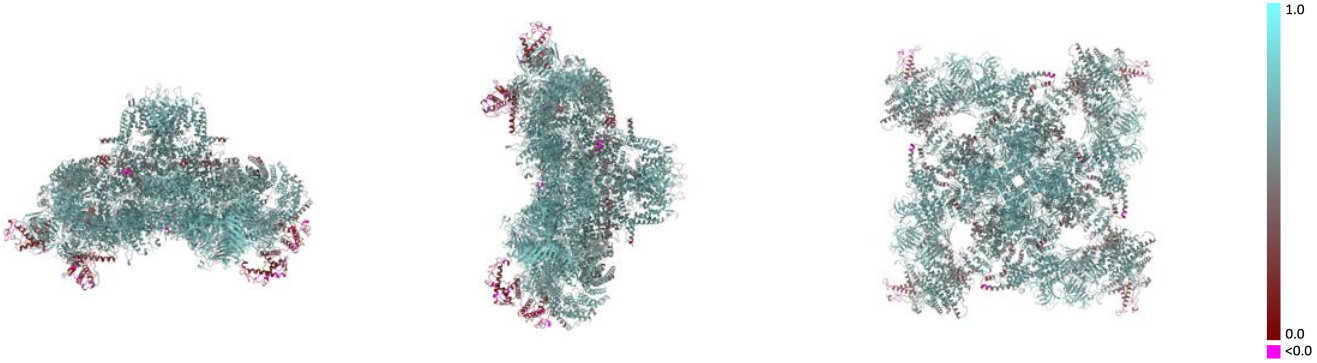
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.086 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.

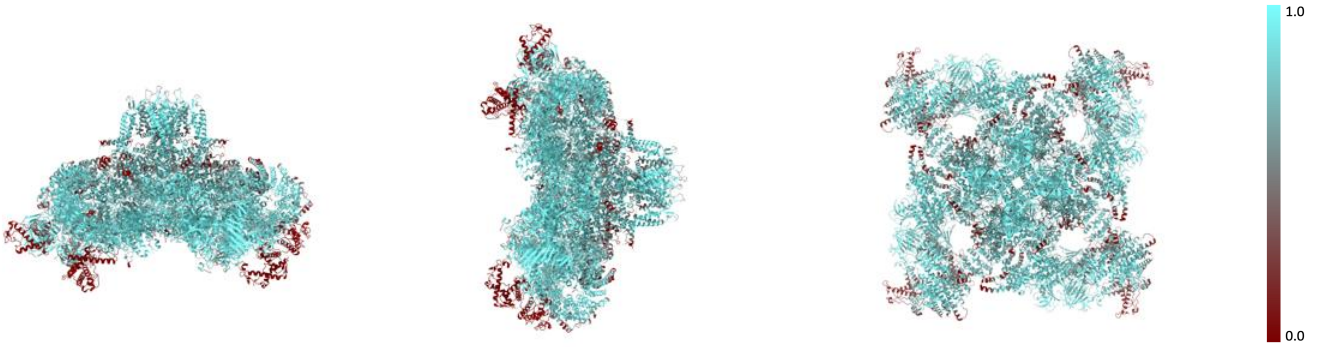
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

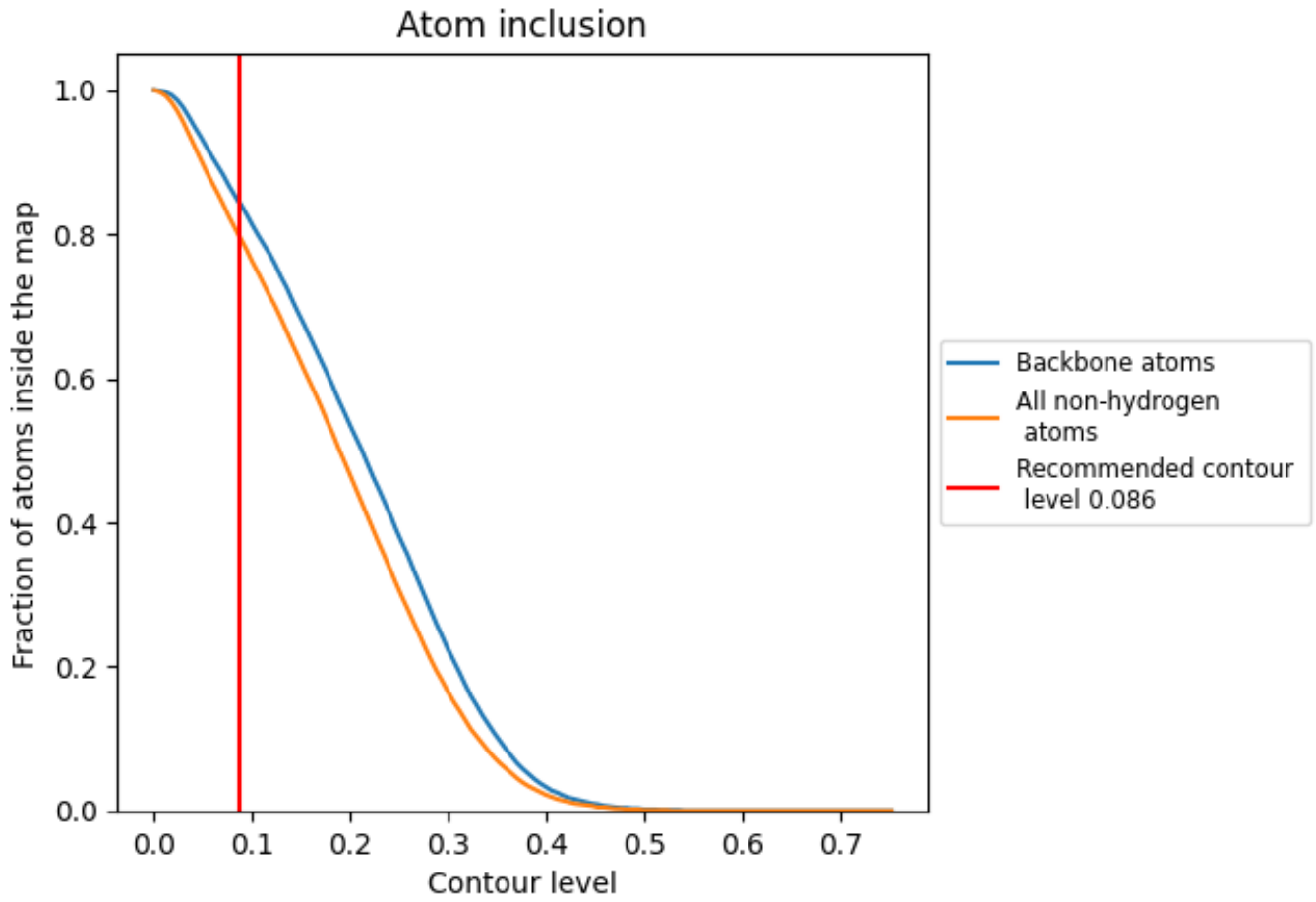
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.086).

9.4 Atom inclusion (i)



At the recommended contour level, 84% of all backbone atoms, 80% 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 (0.086) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7990	0.6120
A	0.9050	0.6770
B	0.7960	0.6110
C	0.9060	0.6770
D	0.7970	0.6110
E	0.9060	0.6750
F	0.7970	0.6100
G	0.9050	0.6770
H	0.7970	0.6110

