Uniprot Accession: A0A0G2JW01 Uncharacterized protein 2 -1 -Regulation: log2 Fold Change **S110 S142** SV-cycling-dependent **S36** S106 S115 T117 **S236 S289** T35 **S157** not-affected I C Domains and Regions: T113 S134 S139 S355 S235 T55 **S119** S318 S326 DOMAIN: HP S136 **S51 REGION: Disordered** -1 **-**-2 **-**

300

400

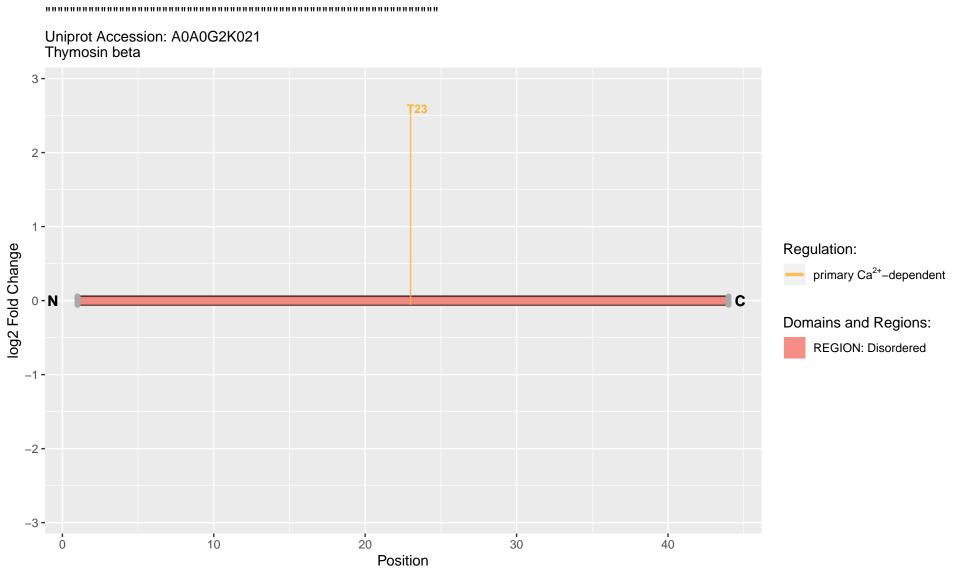
200

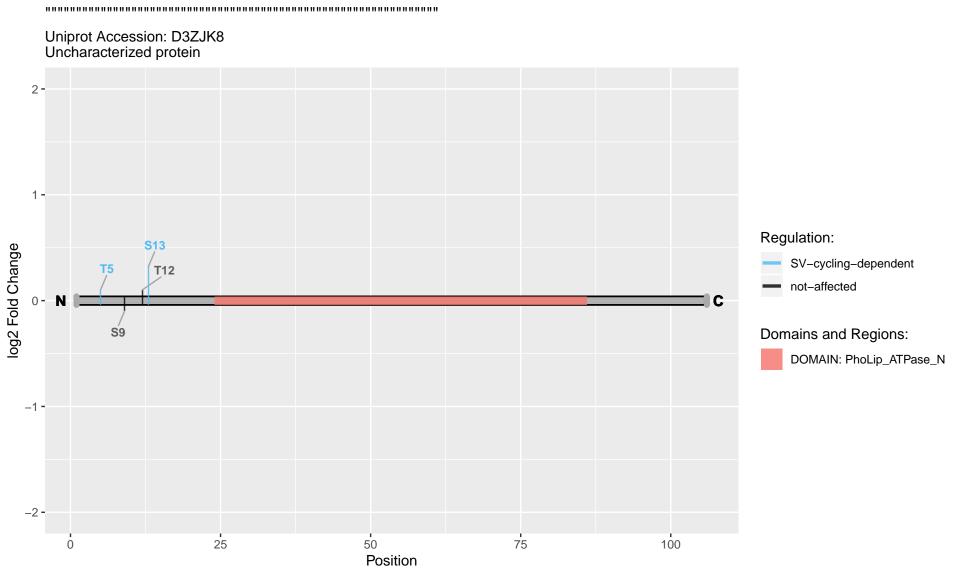
Position

100

Uniprot Accession: A0A0G2JW65 Uncharacterized protein 2 -**S745** Regulation: S783 primary Ca²⁺-dependent log2 Fold Change not-affected S725 Domains and Regions: DOMAIN: DH **S773 S777** DOMAIN: N-terminal Ras-GEF S717 DOMAIN: PH **REGION: Disordered** -1 **-**-2 **-**200 400 600 800 Position

Uniprot Accession: A0A0G2JZ27 Uncharacterized protein 2 -Regulation: primary Ca²⁺-dependent log2 Fold Change S388 S636 S727 SV-cycling-dependent \$380 \$384 \$420 \$424 S621 not-affected S416 Domains and Regions: **S16** S500 S496 DOMAIN: FH2 T477 S483 **REGION: Disordered** -1 **-**-2 **-**500 750 250 1000 1250 Position



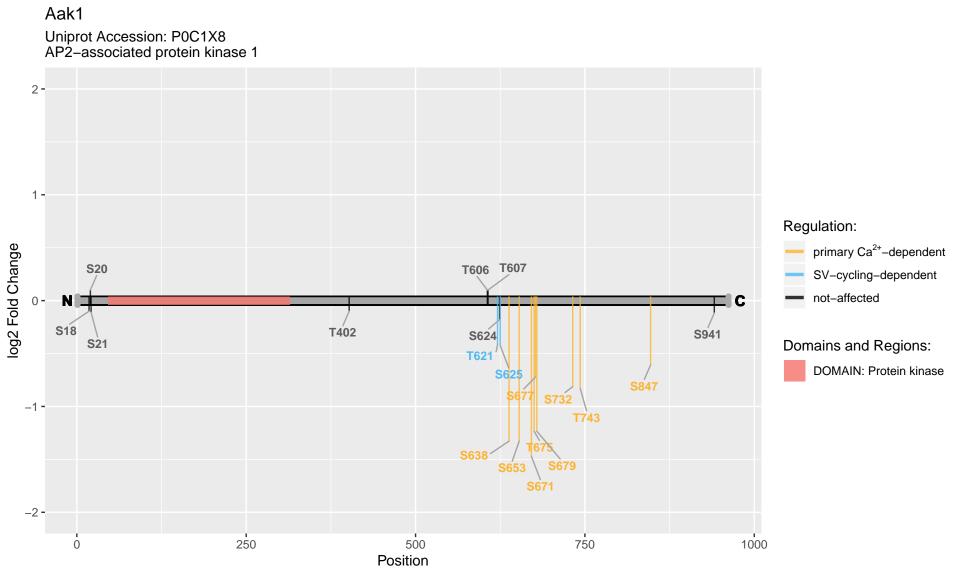


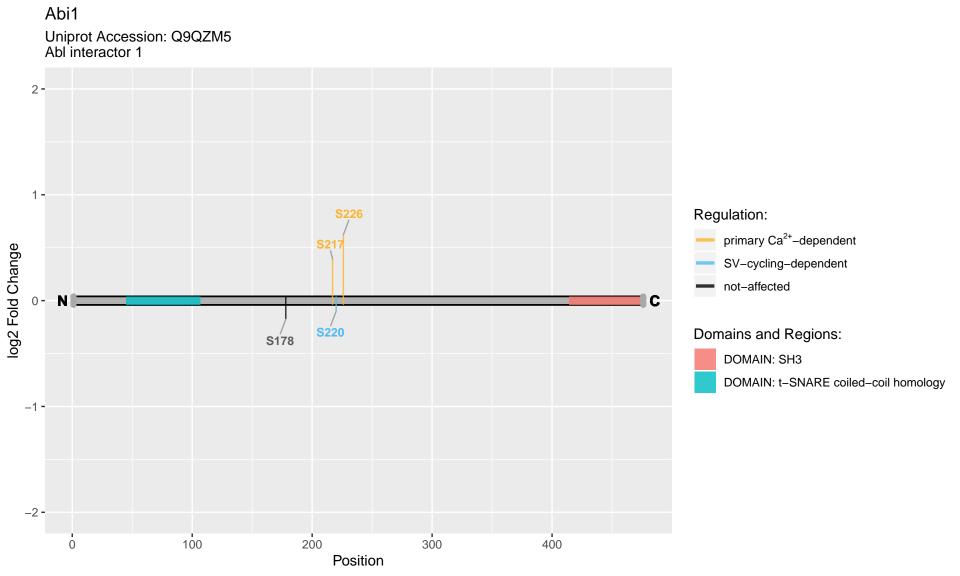
Uniprot Accession: M0R970 Uncharacterized protein 2 -Regulation: log2 Fold Change primary Ca²⁺-dependent Domains and Regions: REGION: Disordered **S71** -1 **-**-2 **-**75 25 100 Position

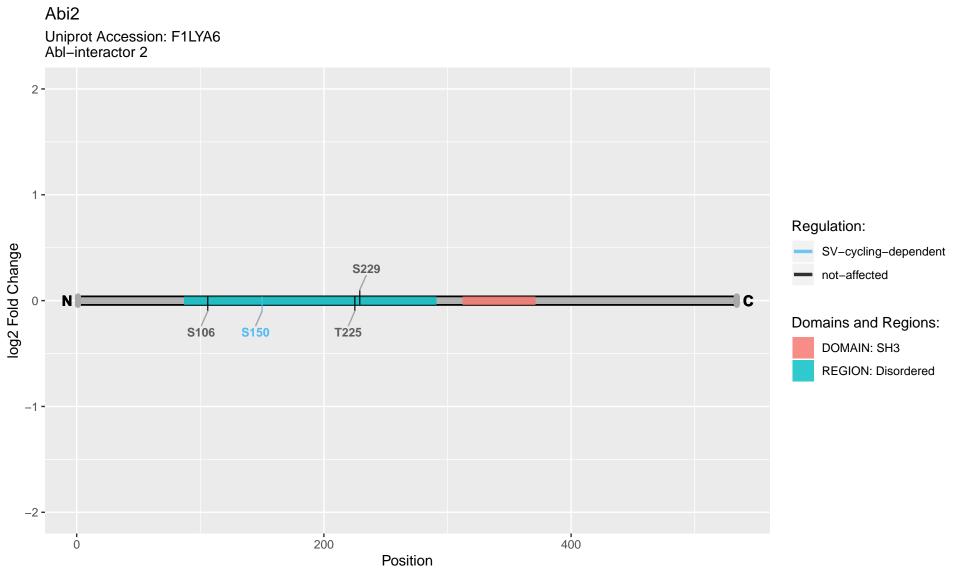
Uniprot Accession: O08654 UPF0183 protein C16orf70 homolog 2 log2 Fold Change Regulation: SV-cycling-dependent not-affected **S270** -1 **-**-2 **-**200 300 400 100 Position

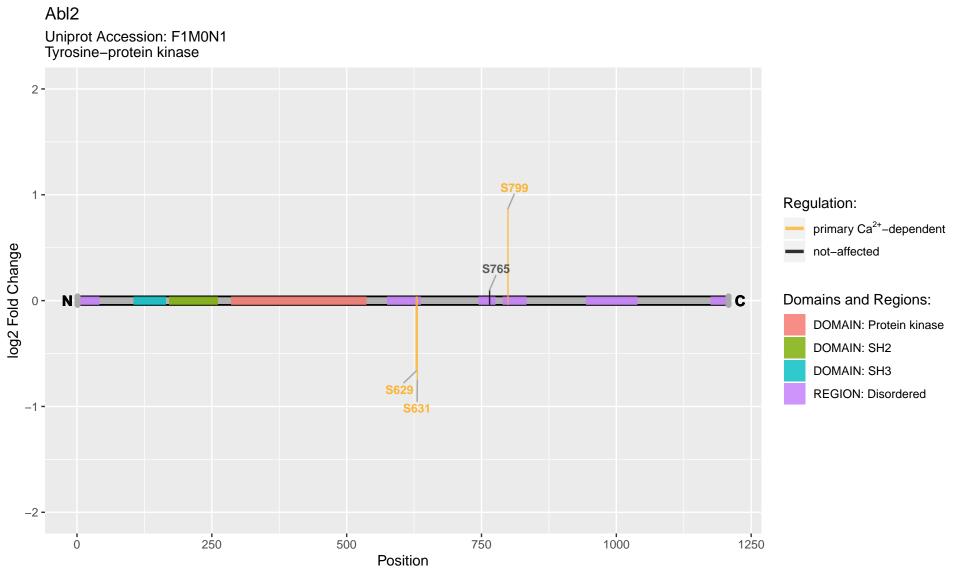
Uniprot Accession: P0CD96 Overexpressed in colon carcinoma 1 protein homolog 2 -**S28** log2 Fold Change T30 Regulation: primary Ca²⁺-dependent not-affected -1 **-**-2 **-**20 40 60 Position

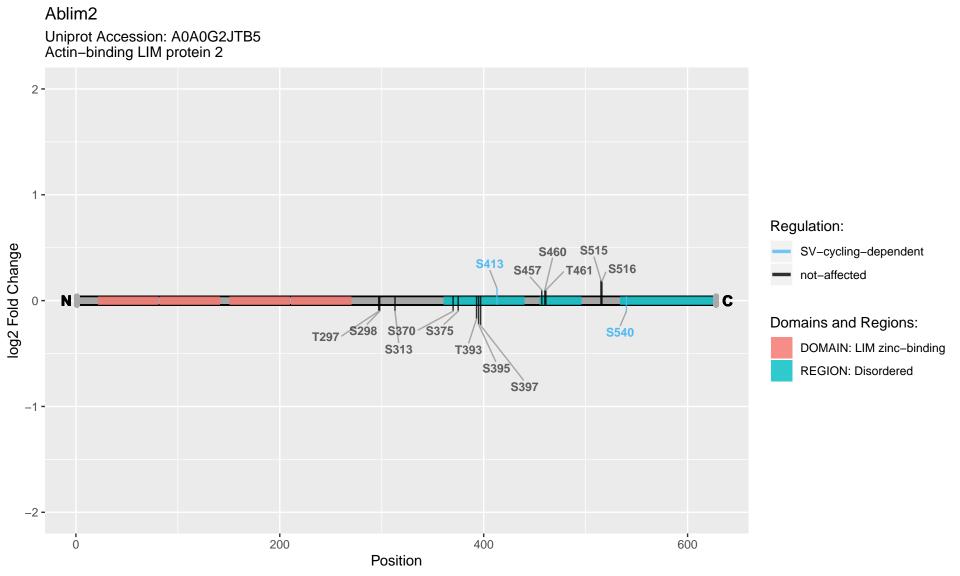
Uniprot Accession: Q63003 5E5 antigen 2 -**S404** S611 log2 Fold Change S690 S695 **S251** Regulation: SV-cycling-dependent C not-affected -1 **-**-2 **-**200 600 400 800 Position

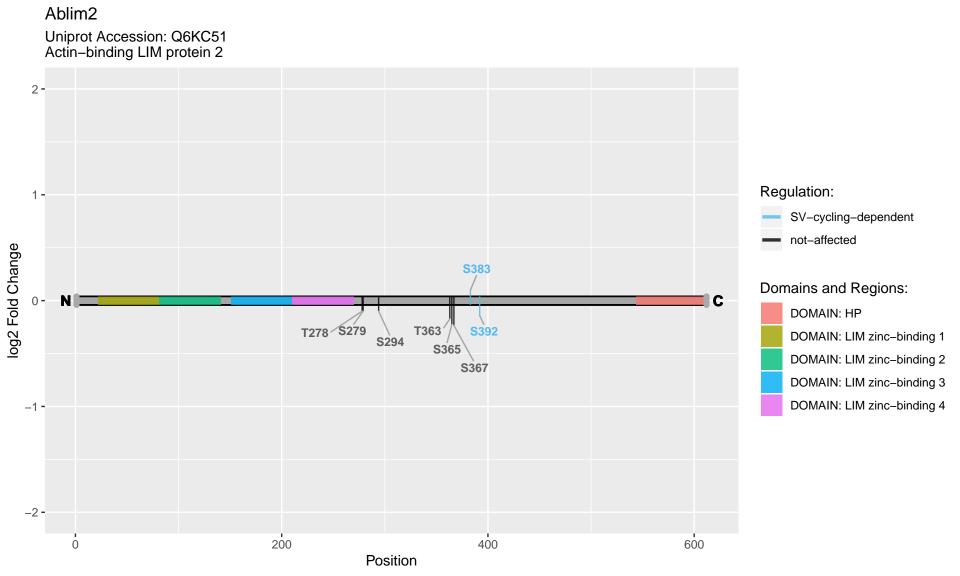


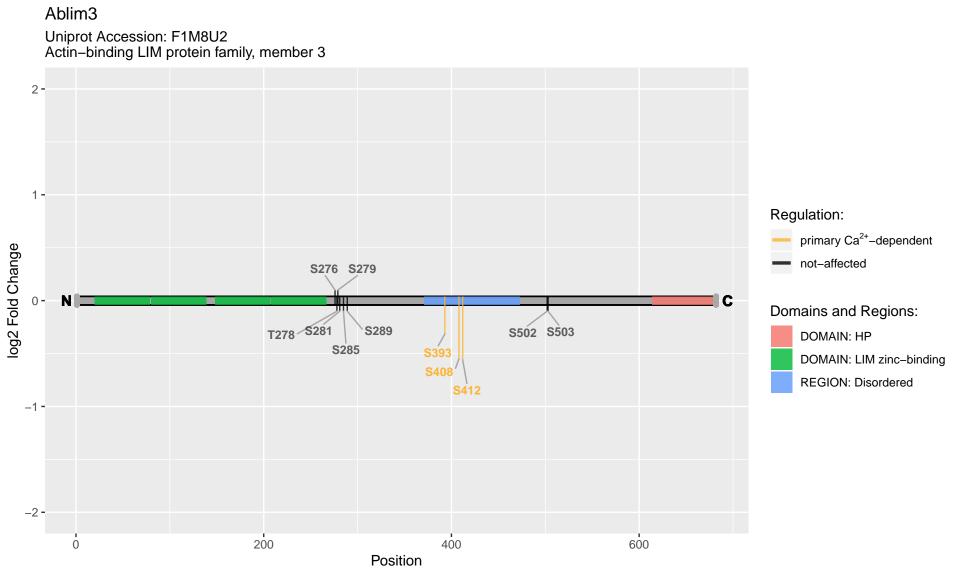


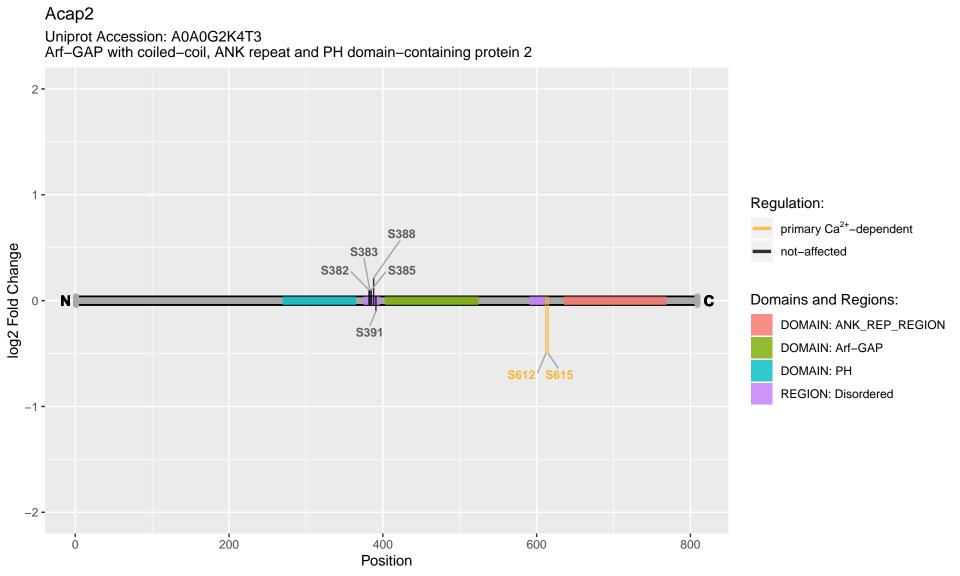


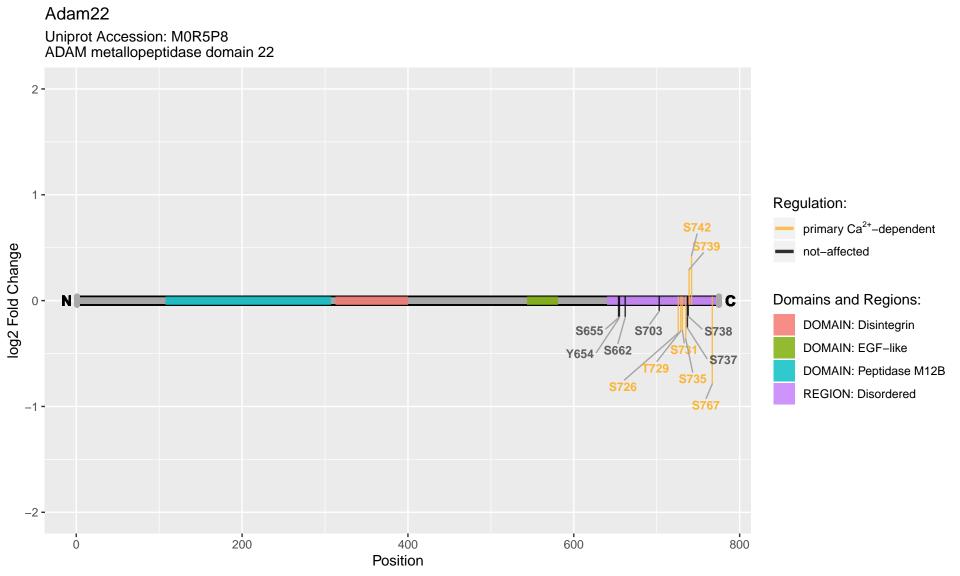


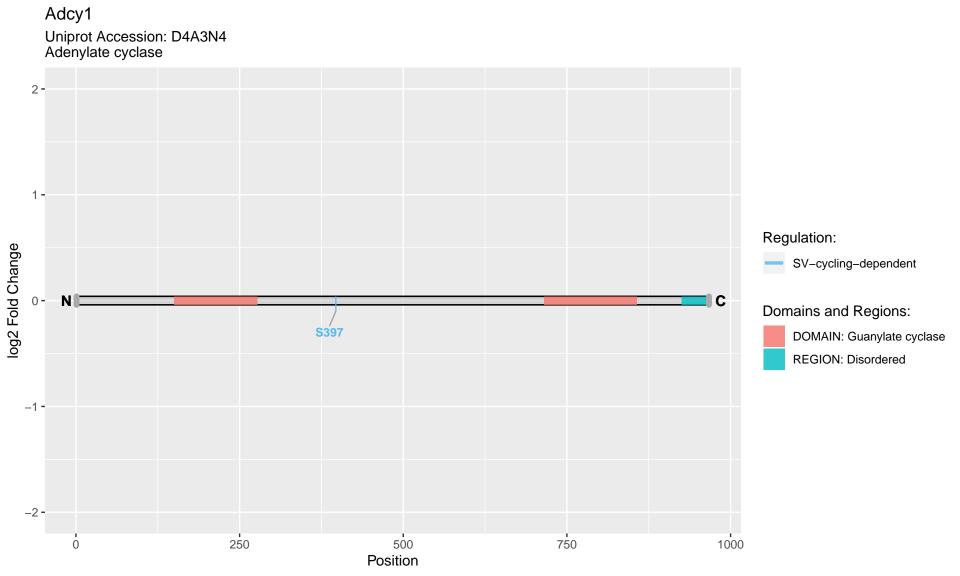


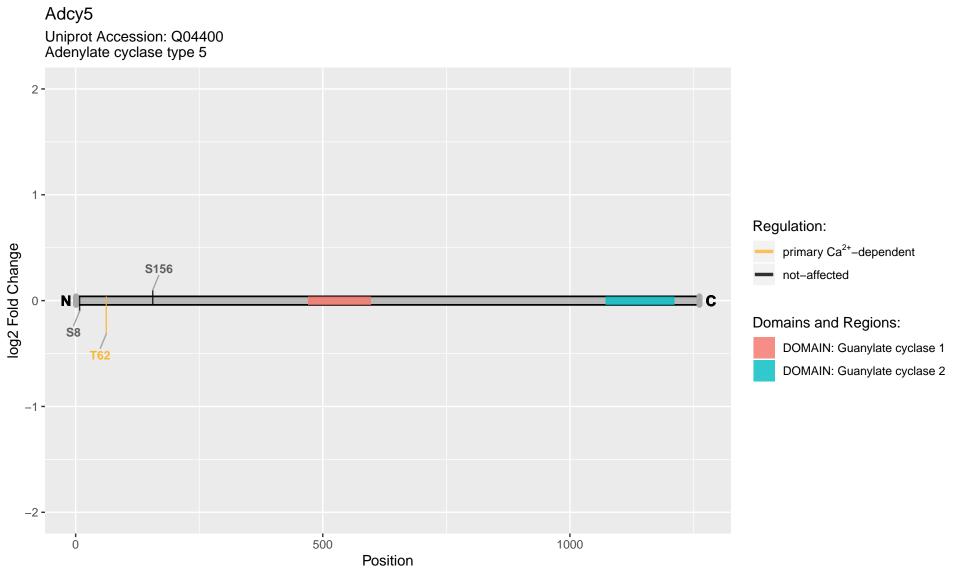


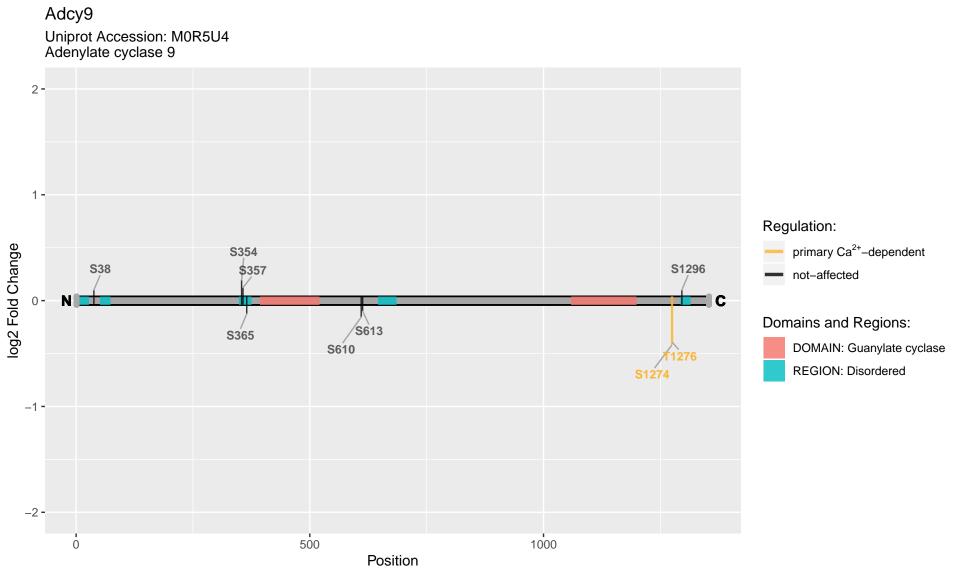


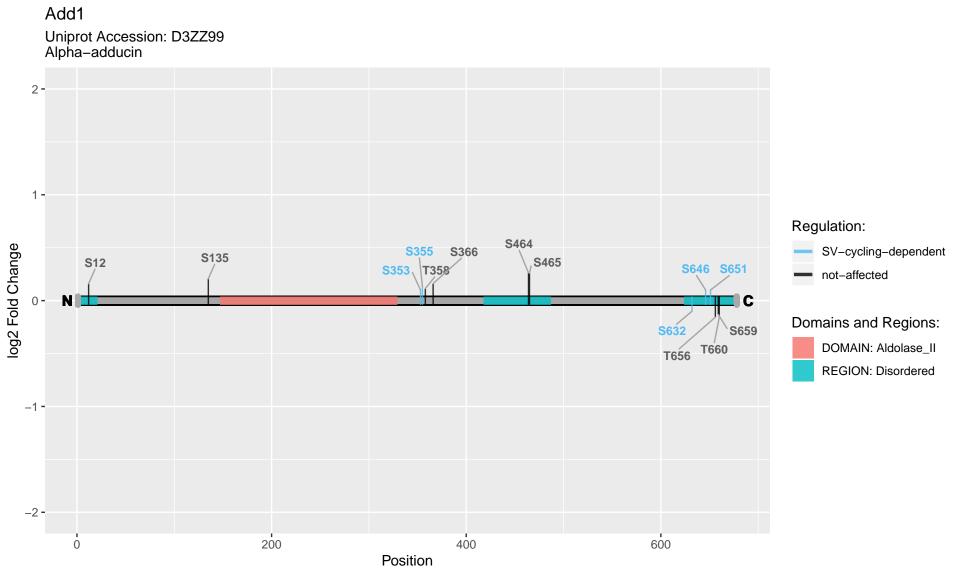


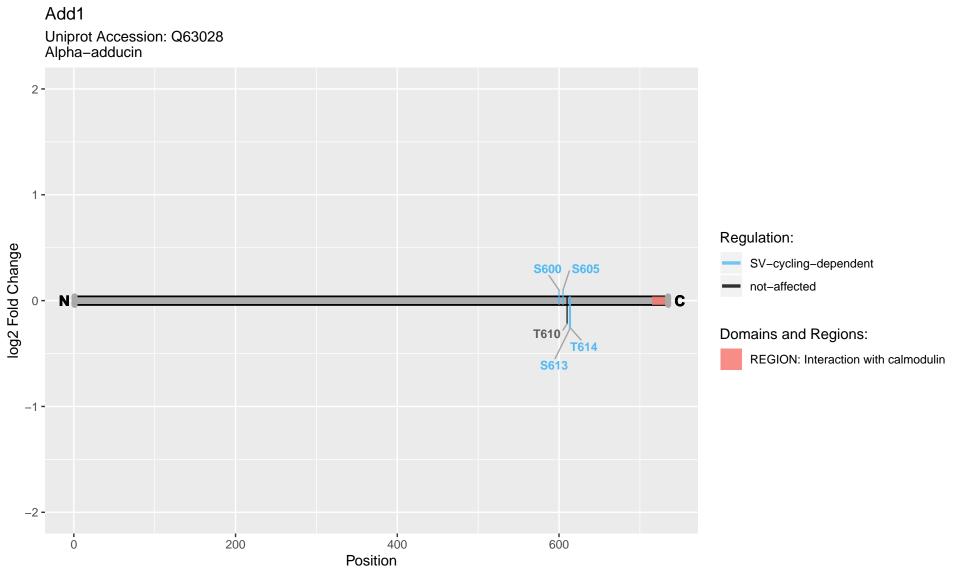


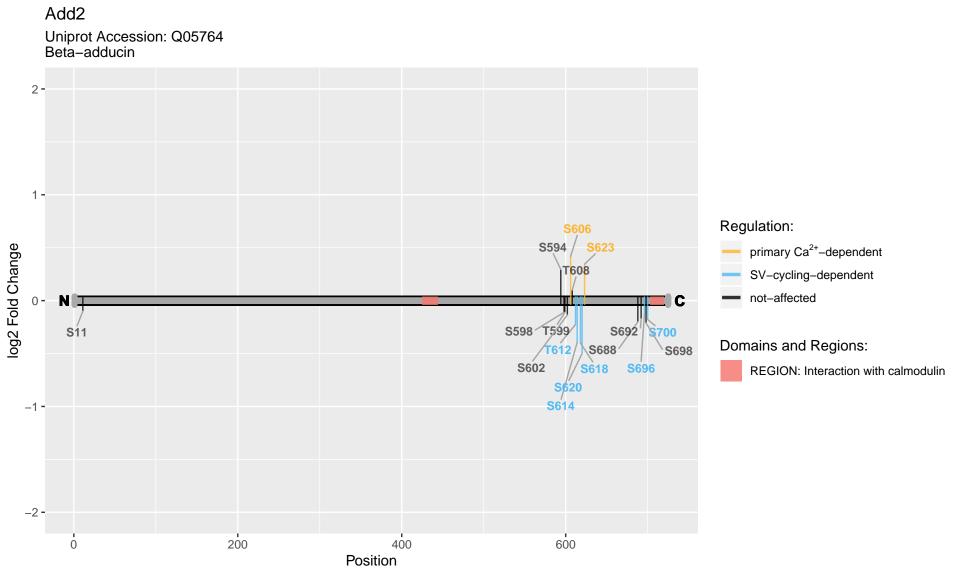


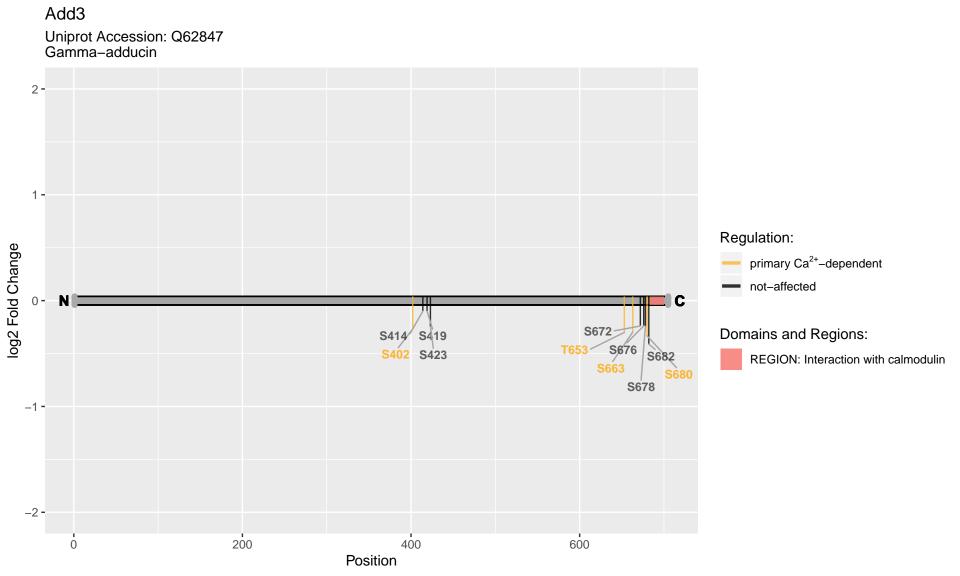


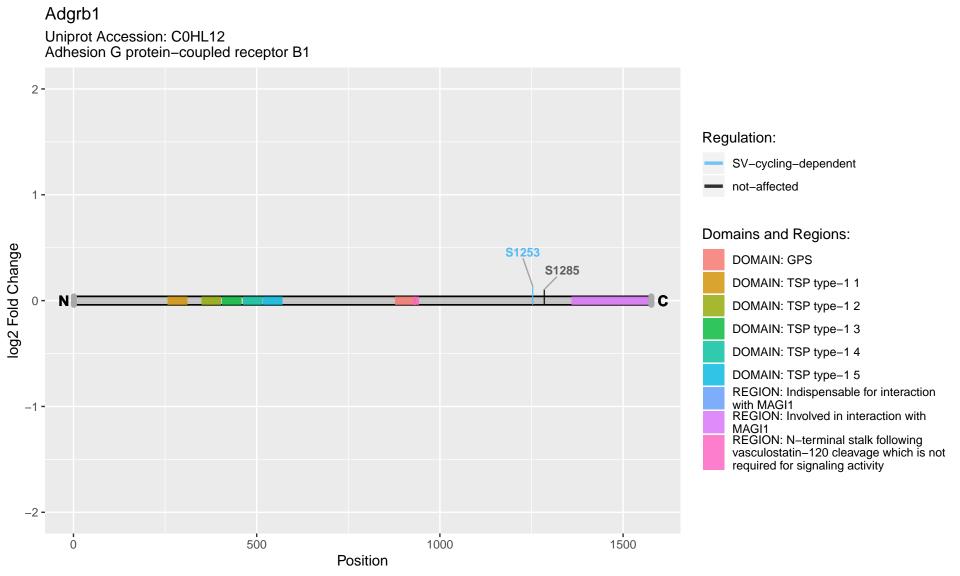


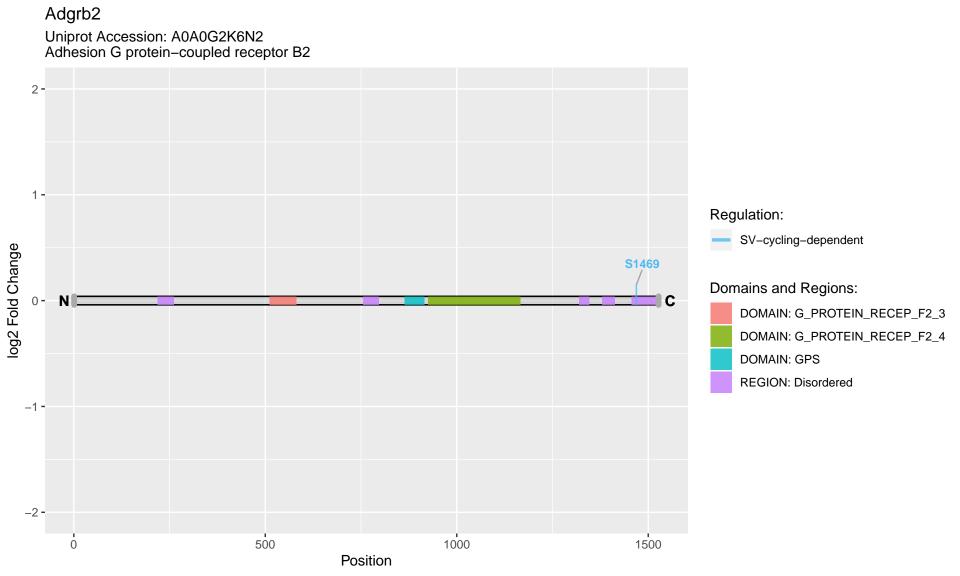


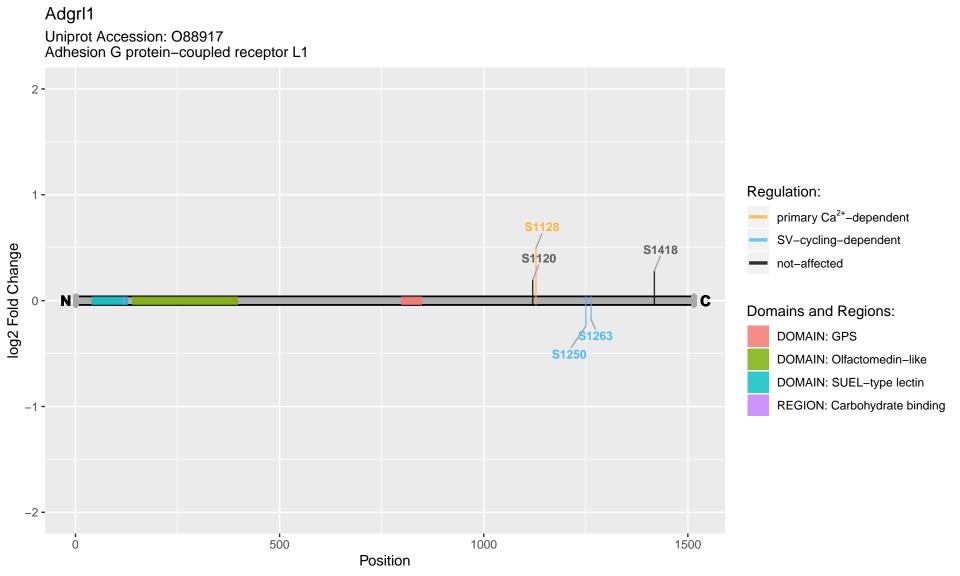


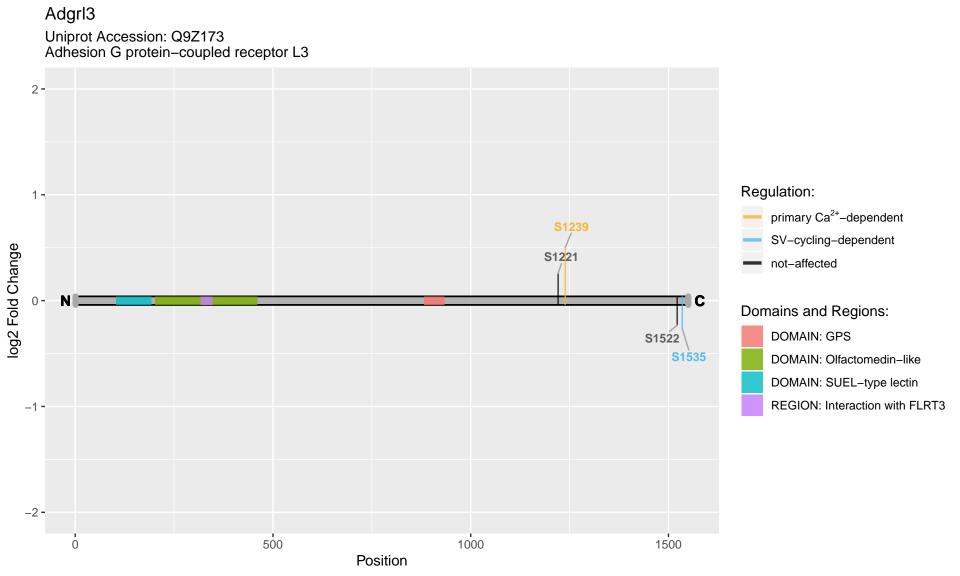


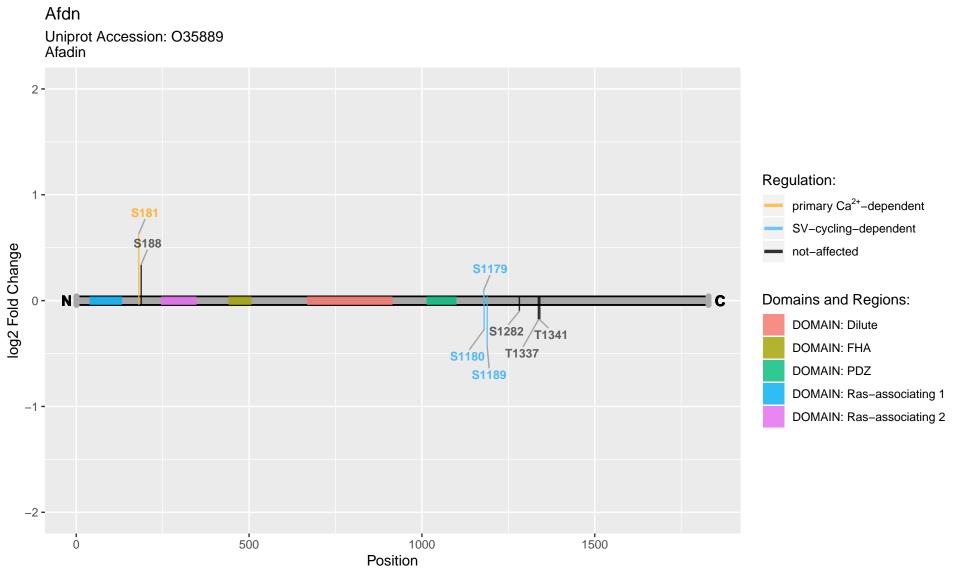


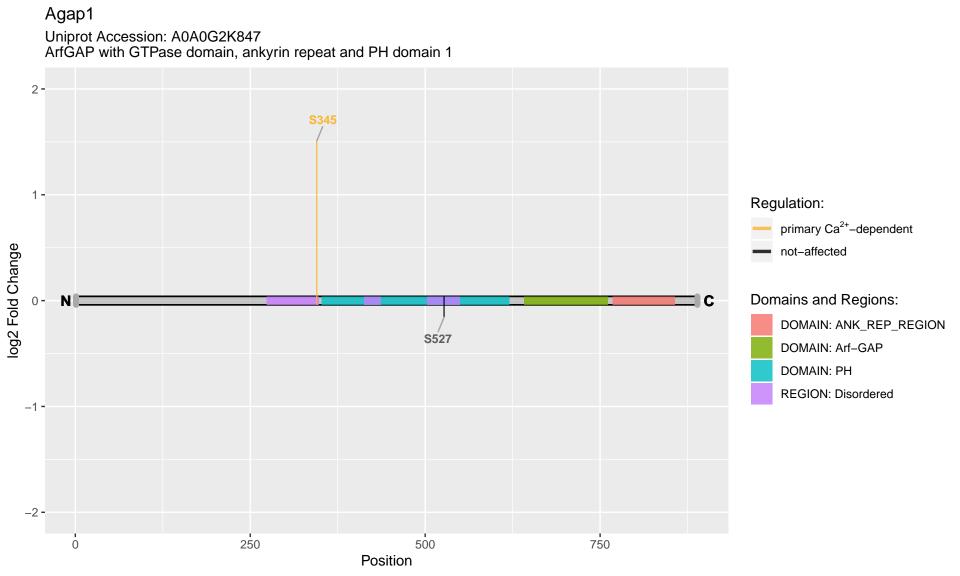


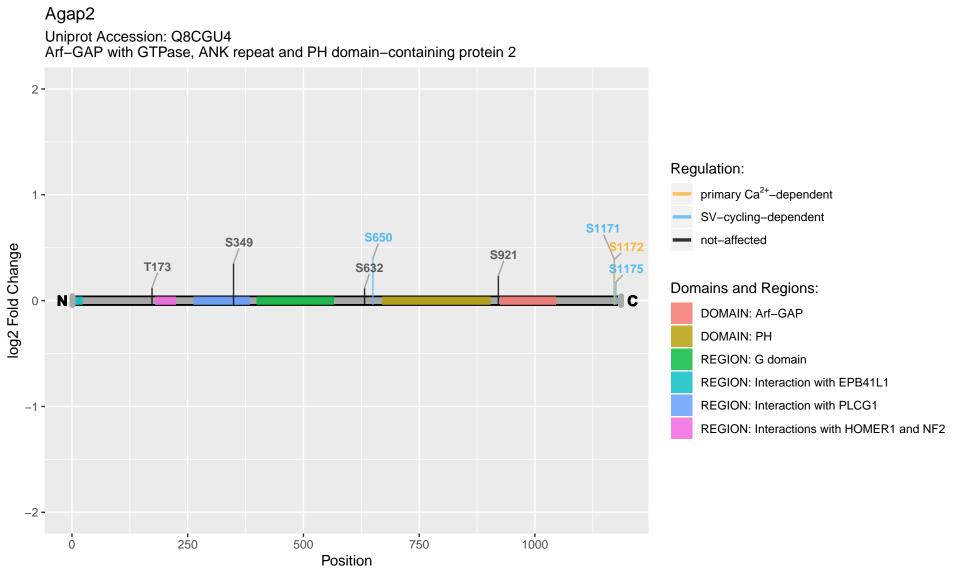


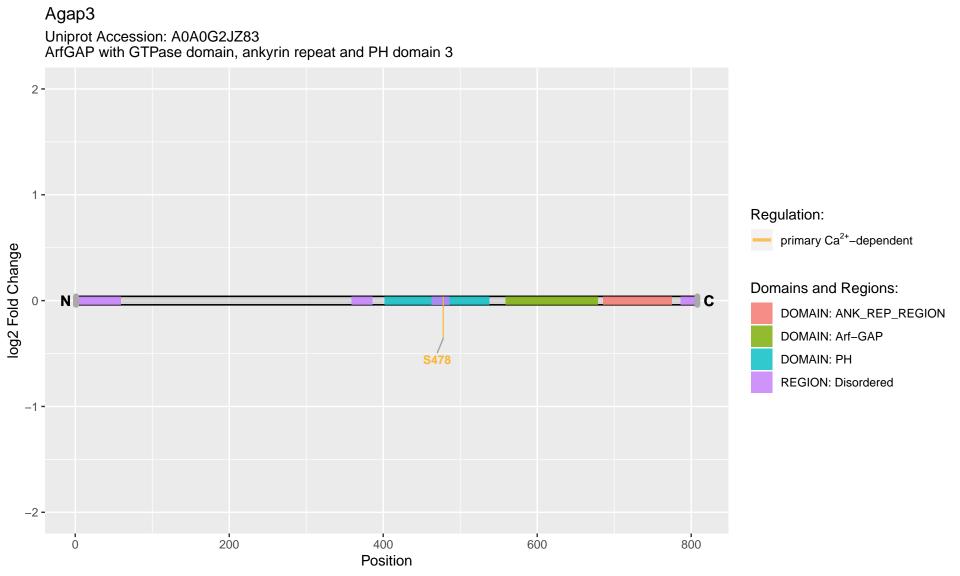


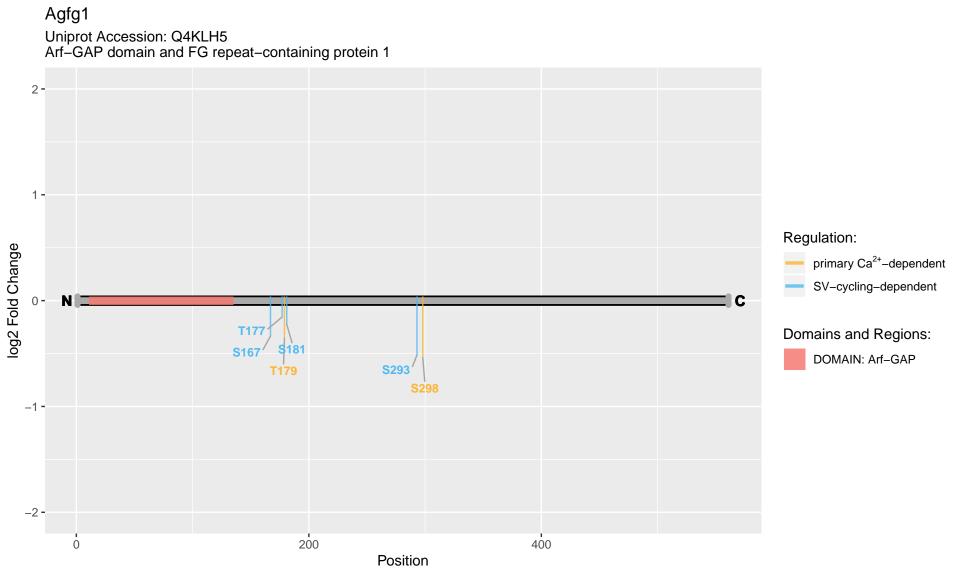


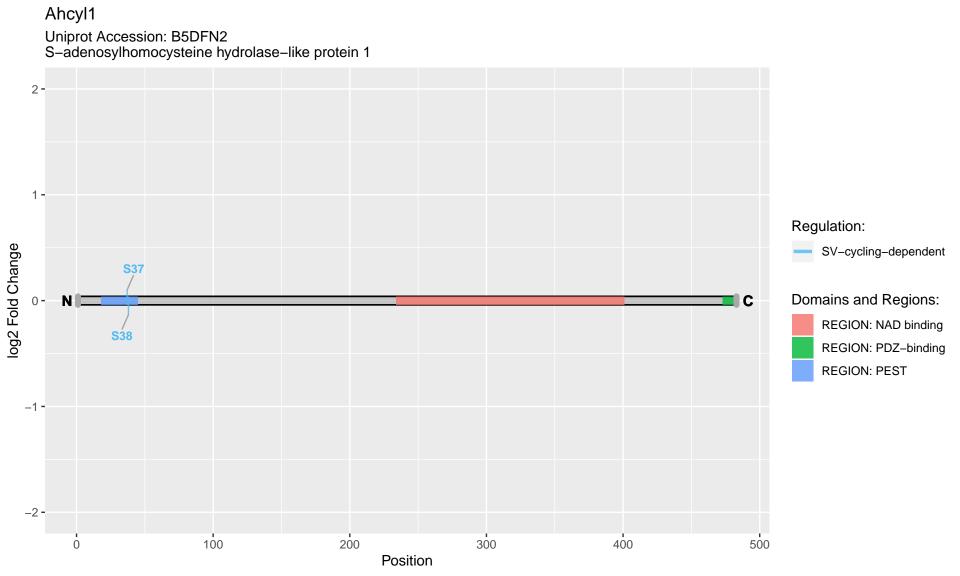


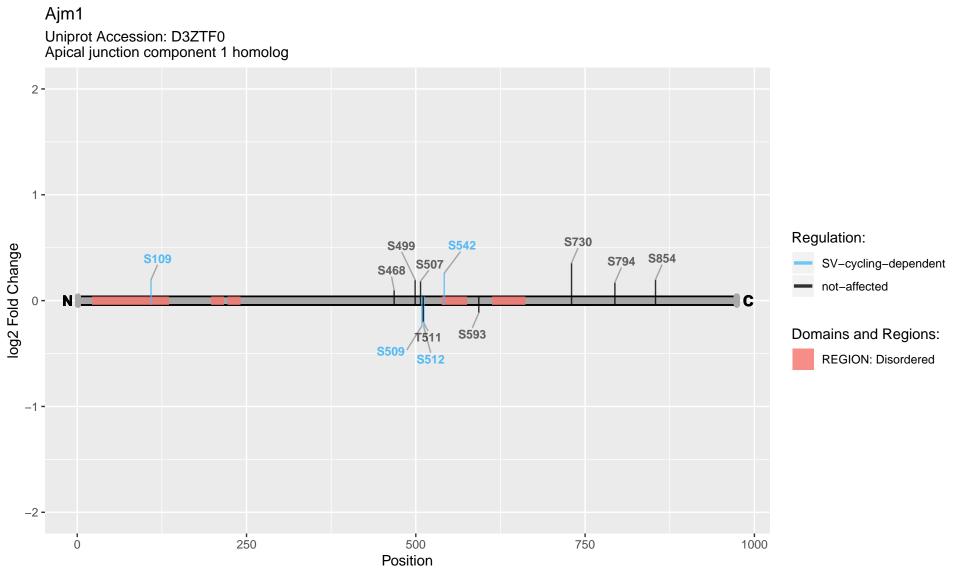


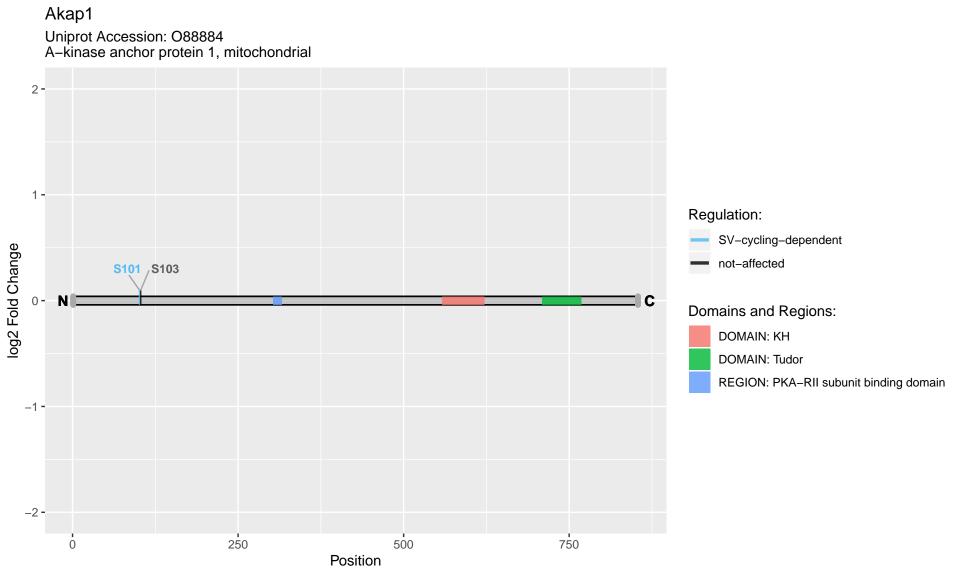


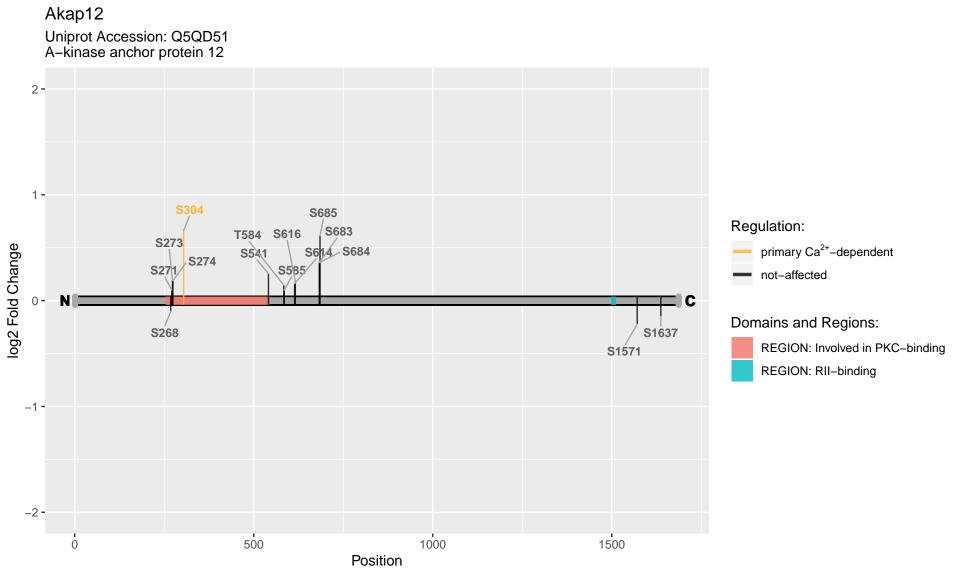


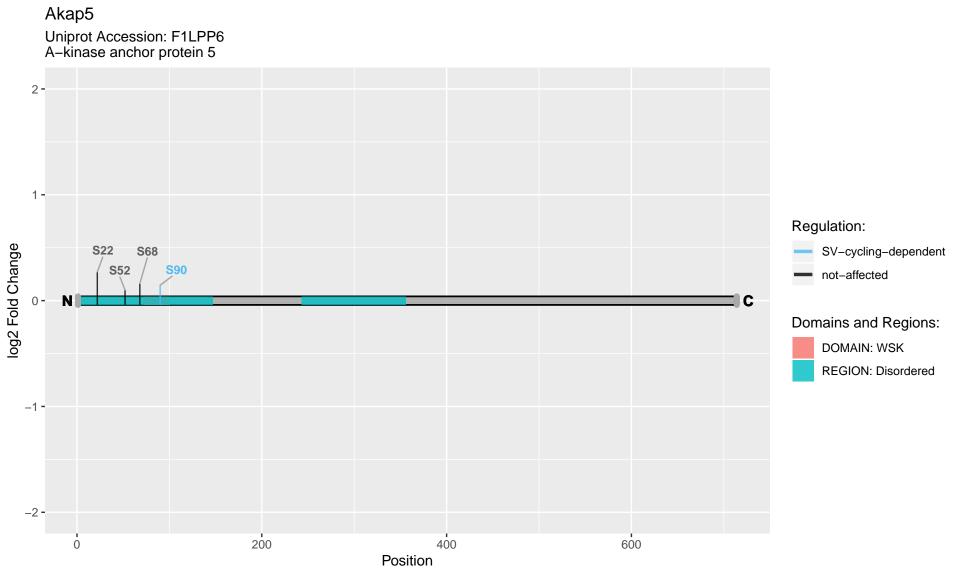


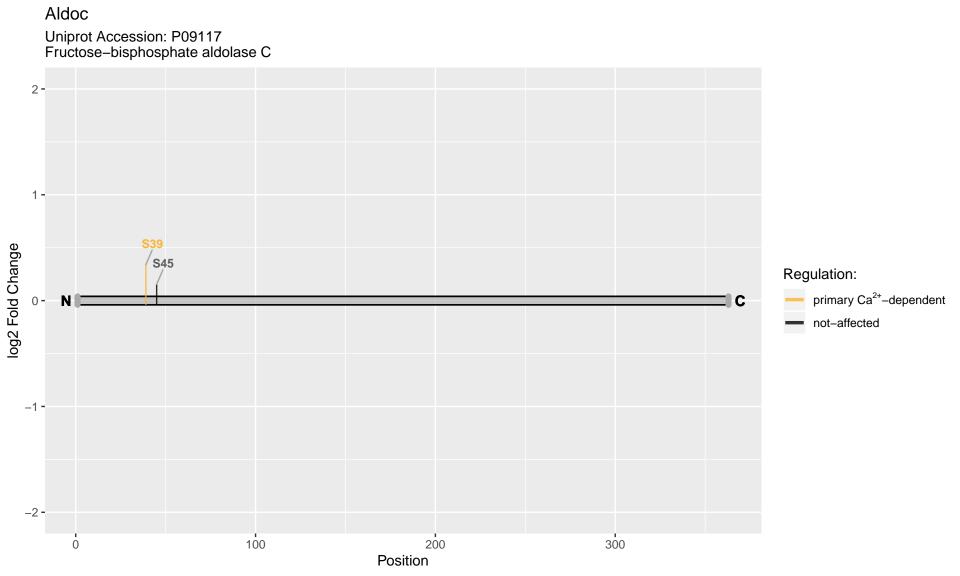


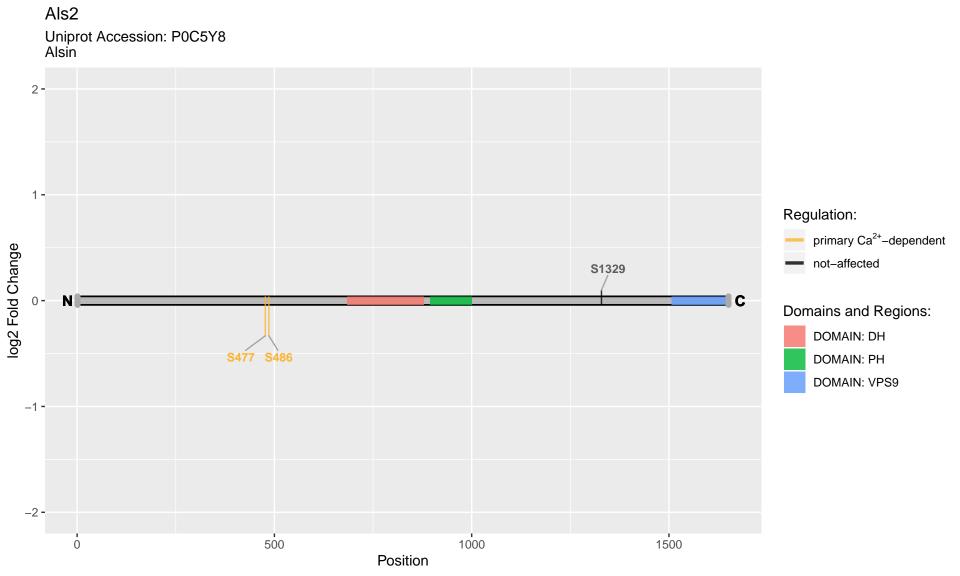


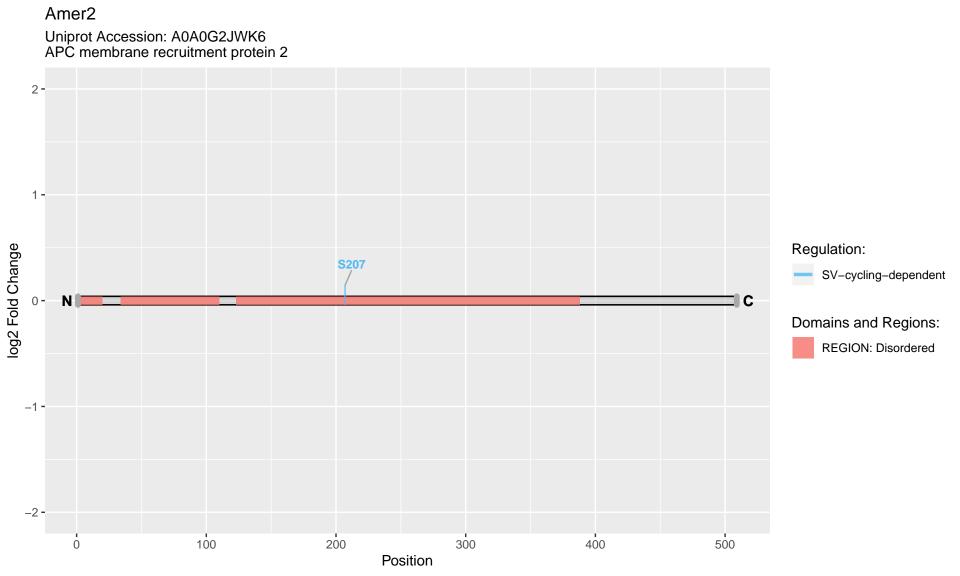


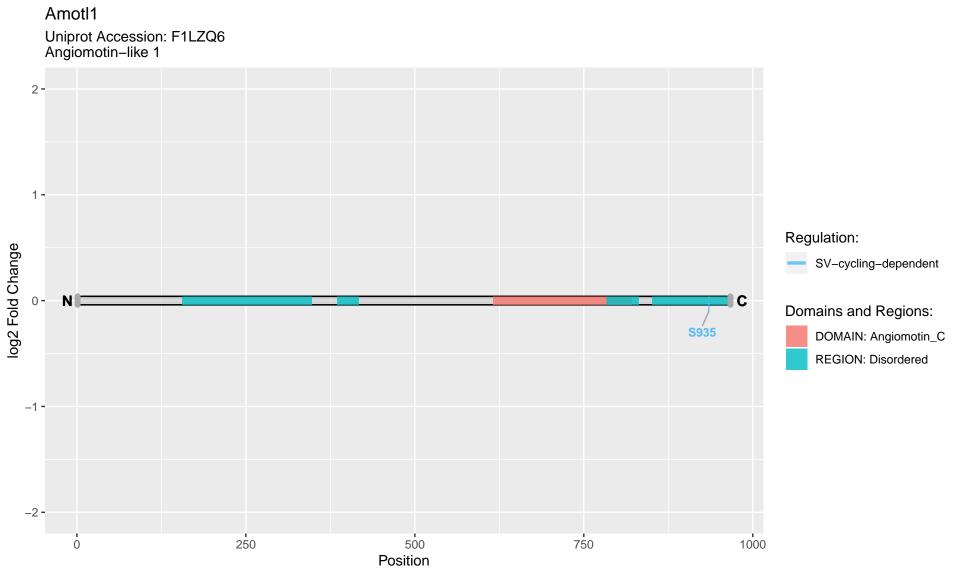


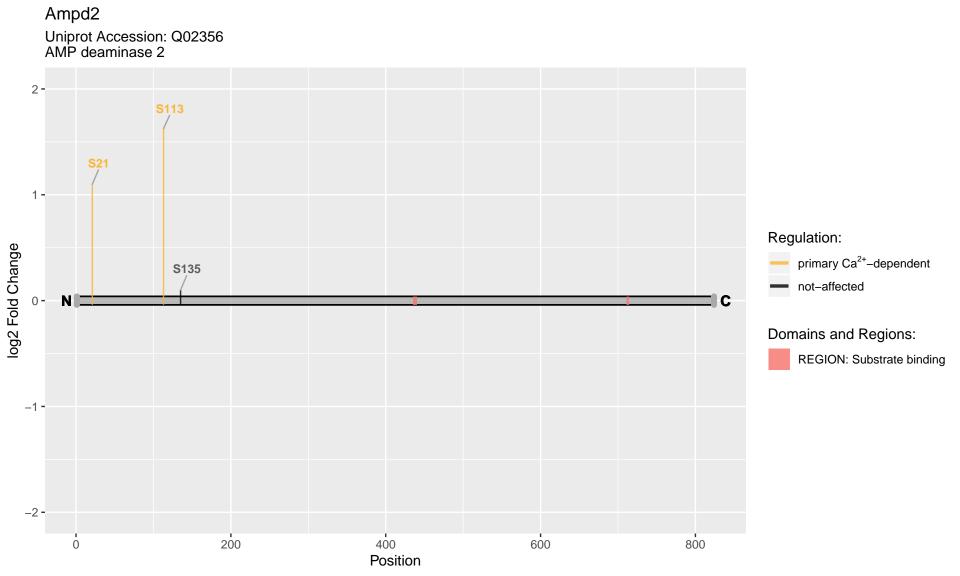


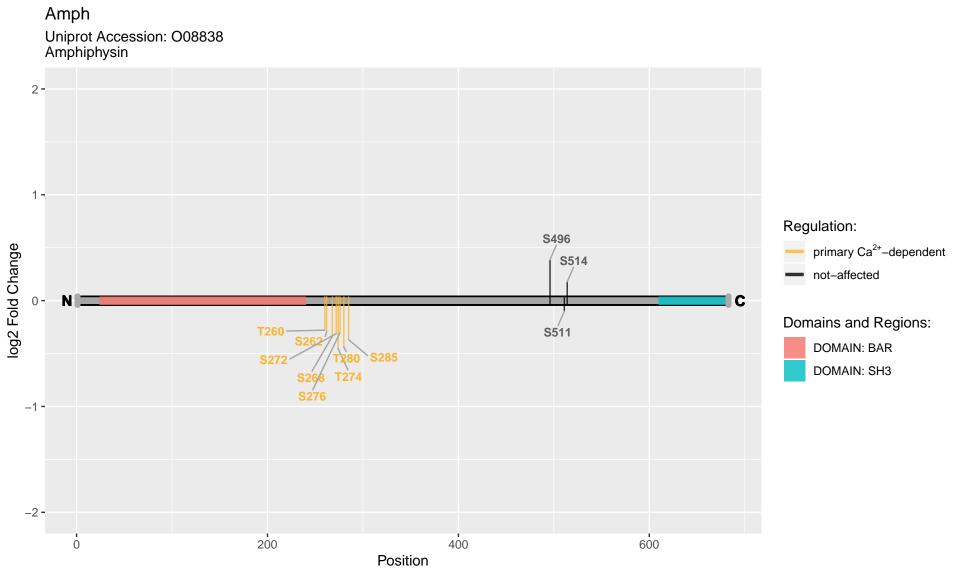


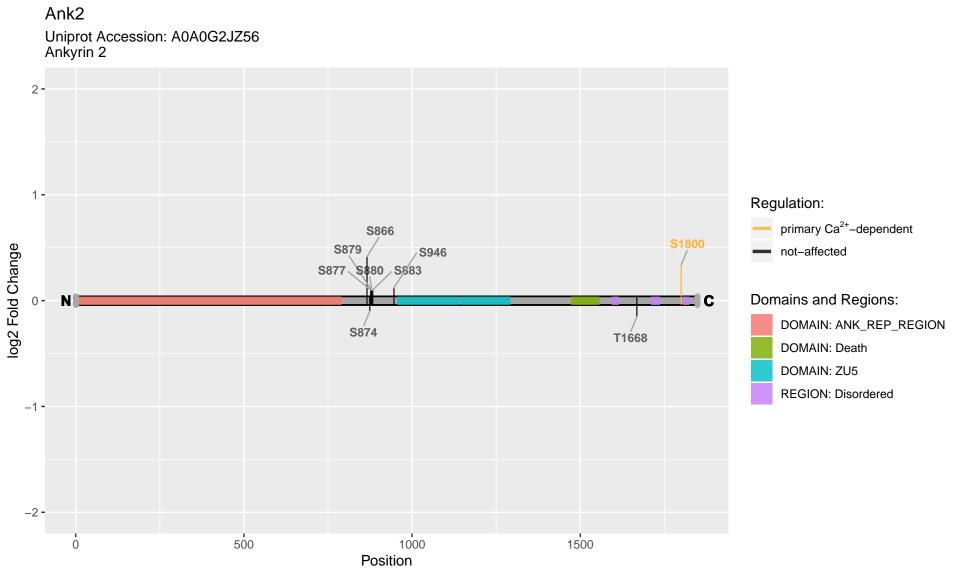


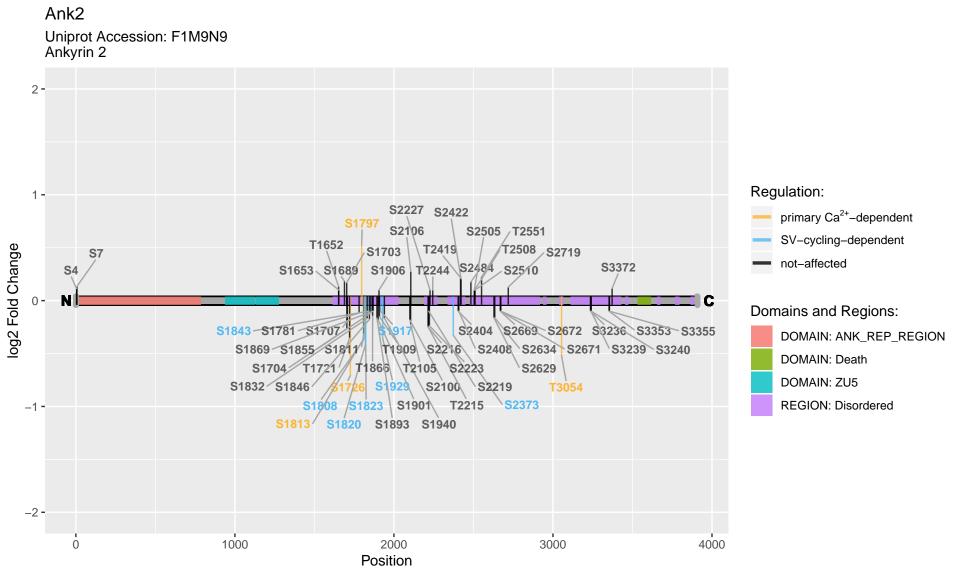


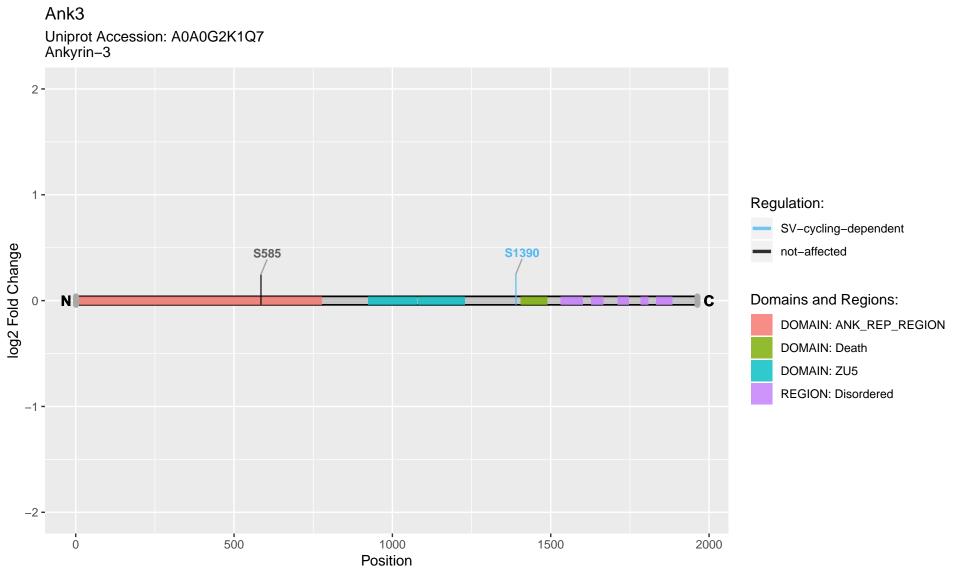


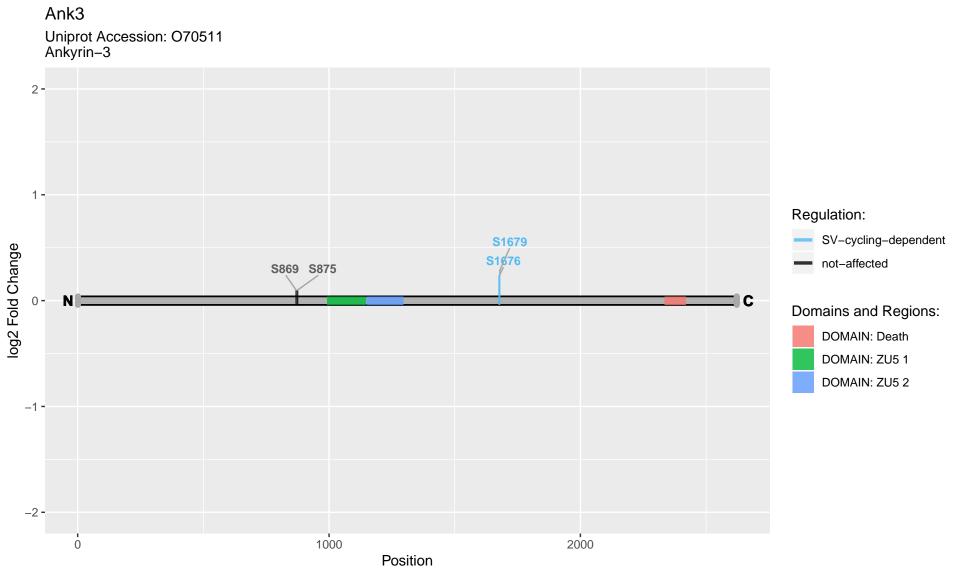


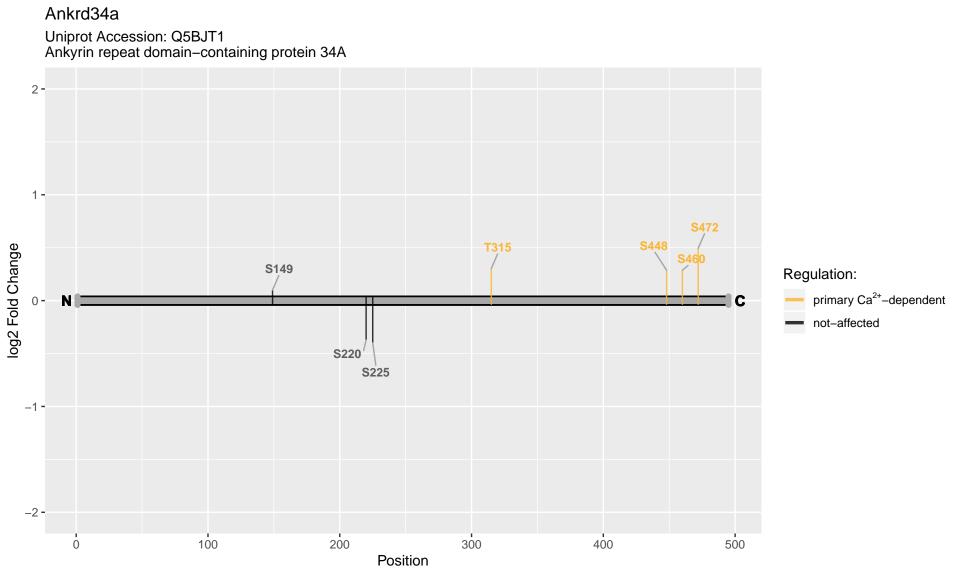


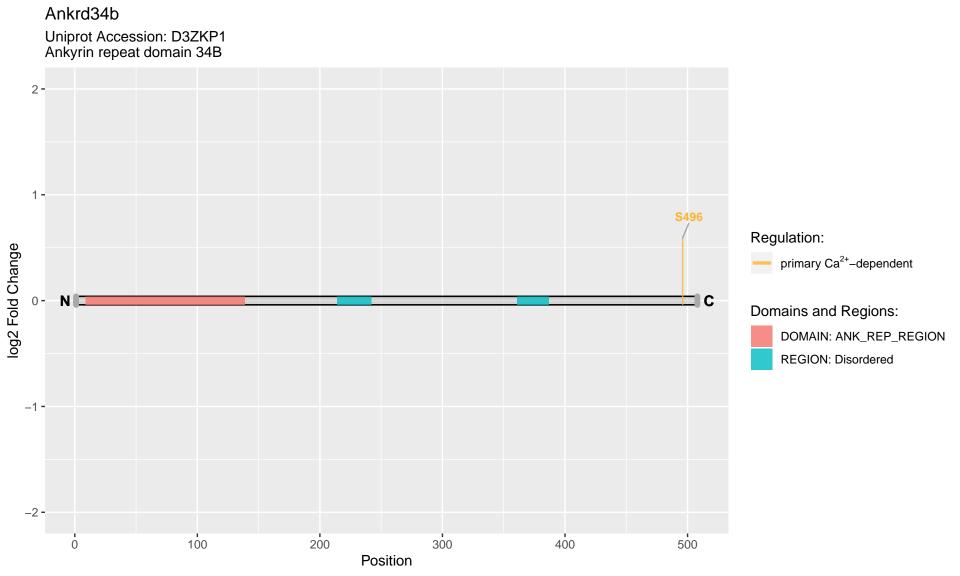


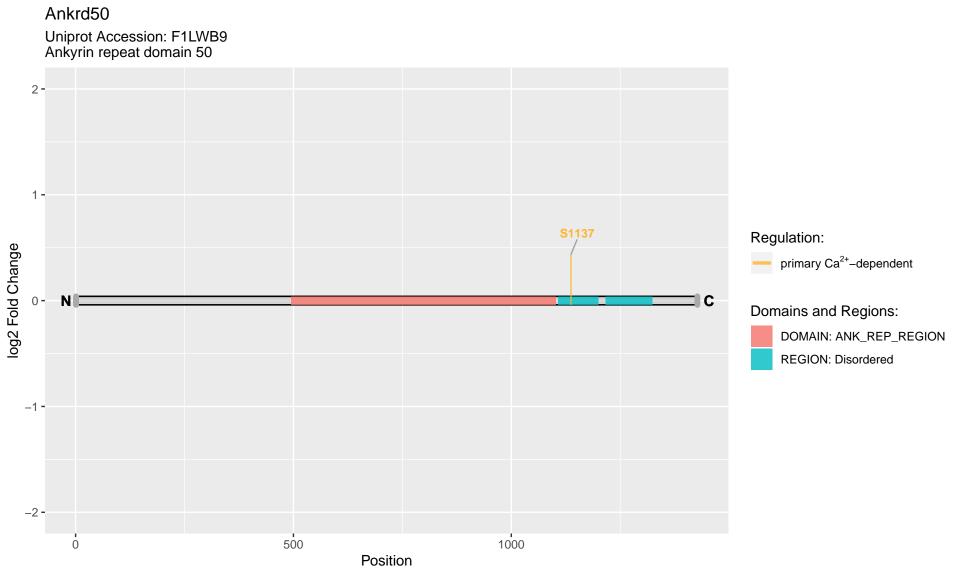


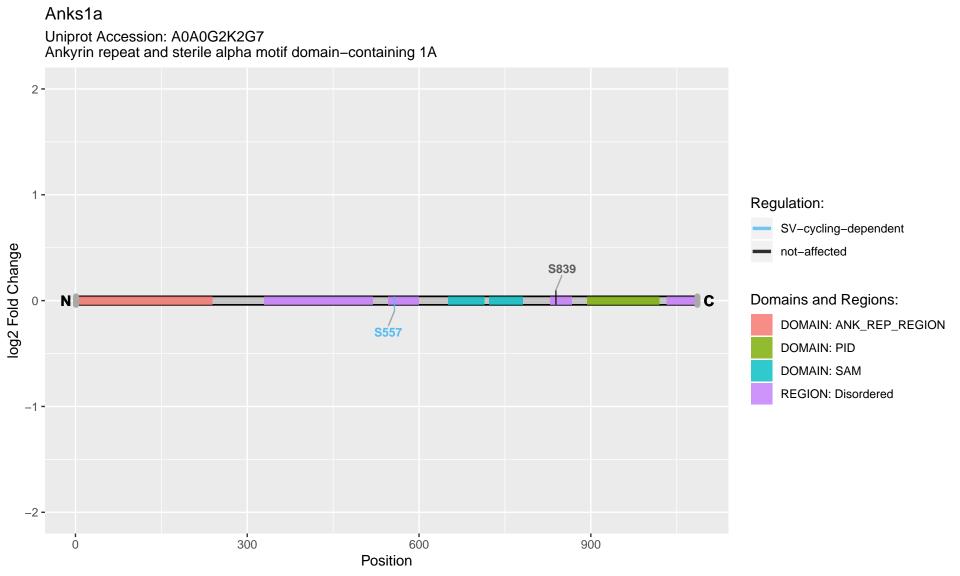


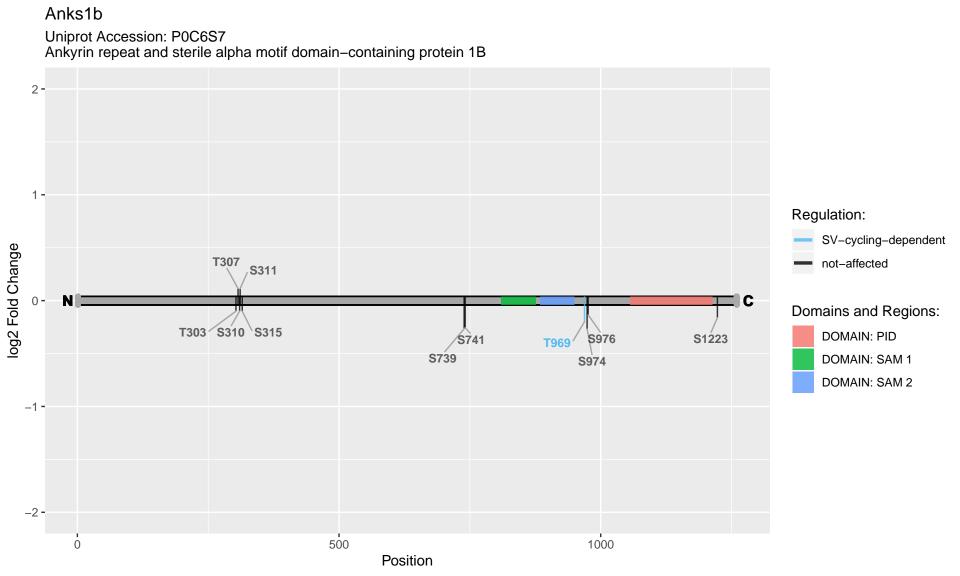


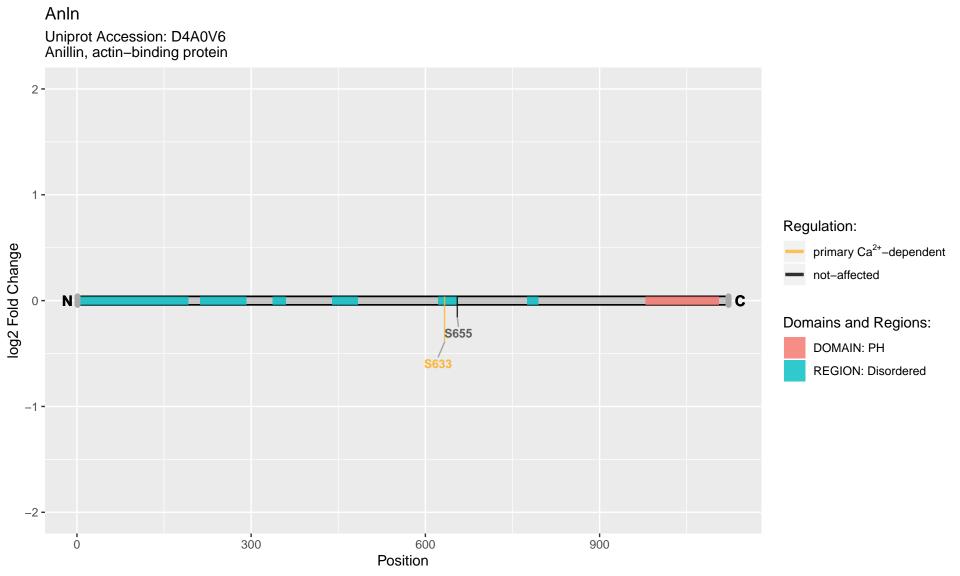


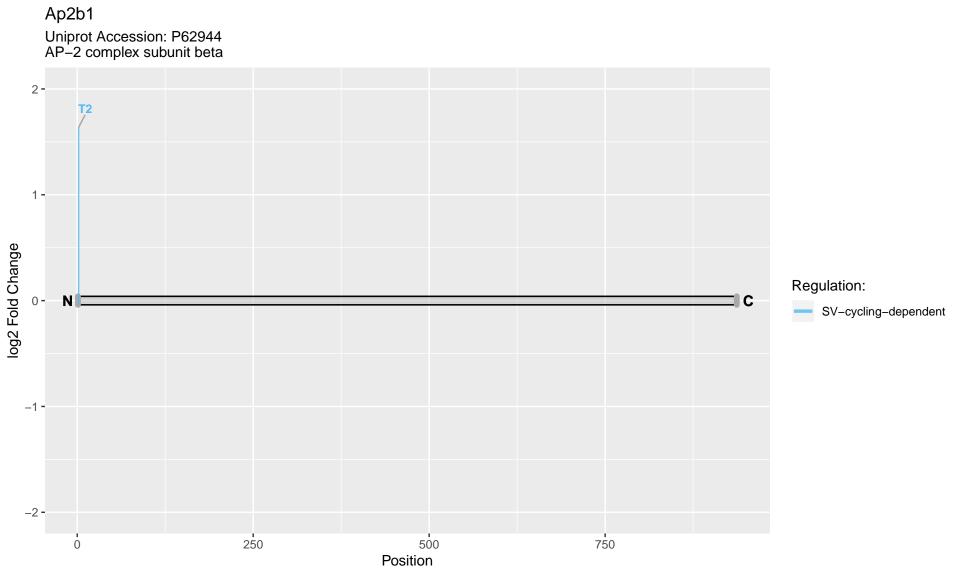


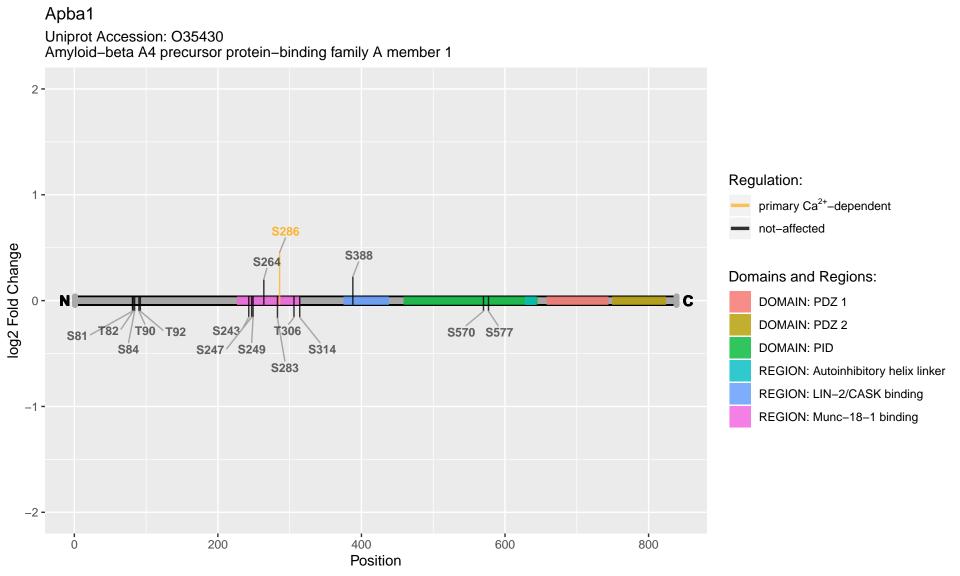


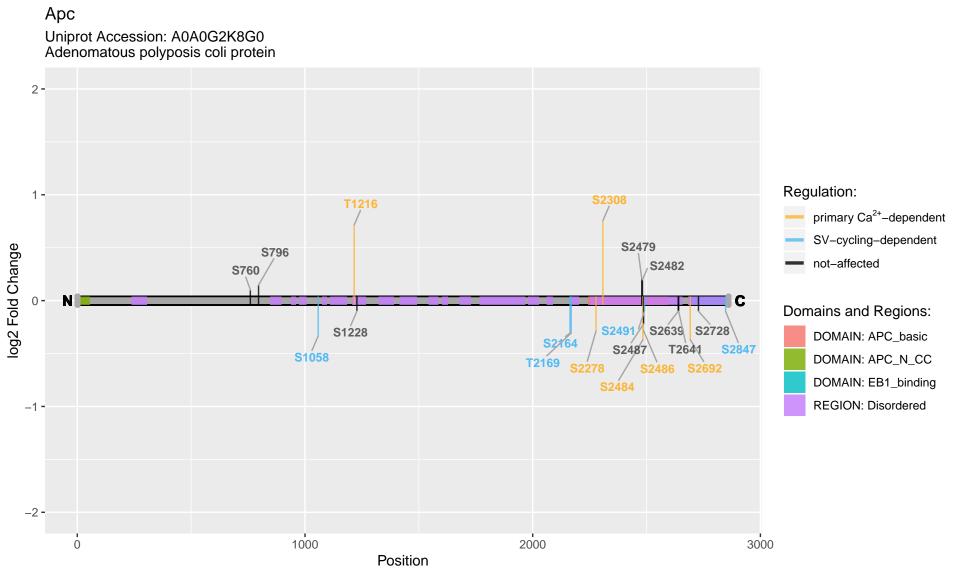


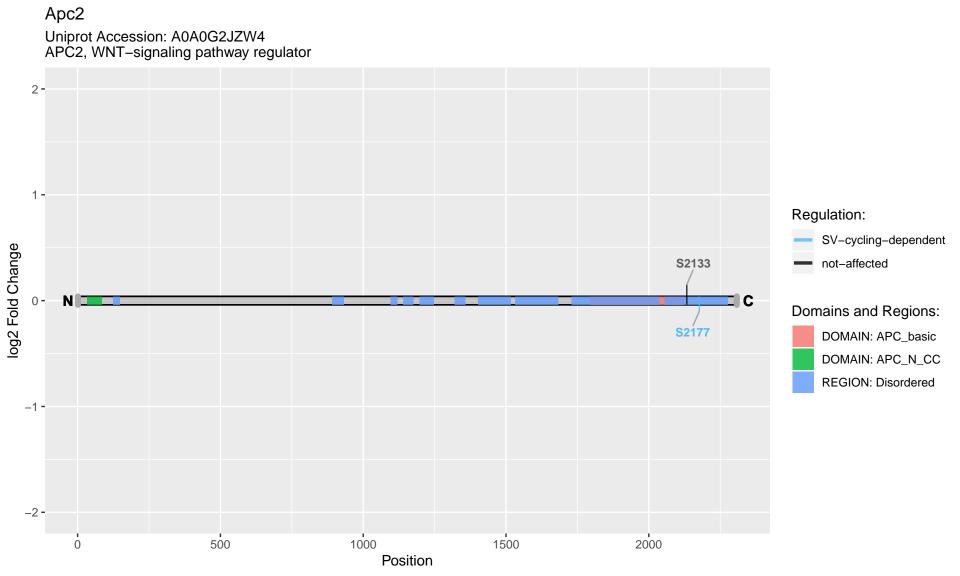


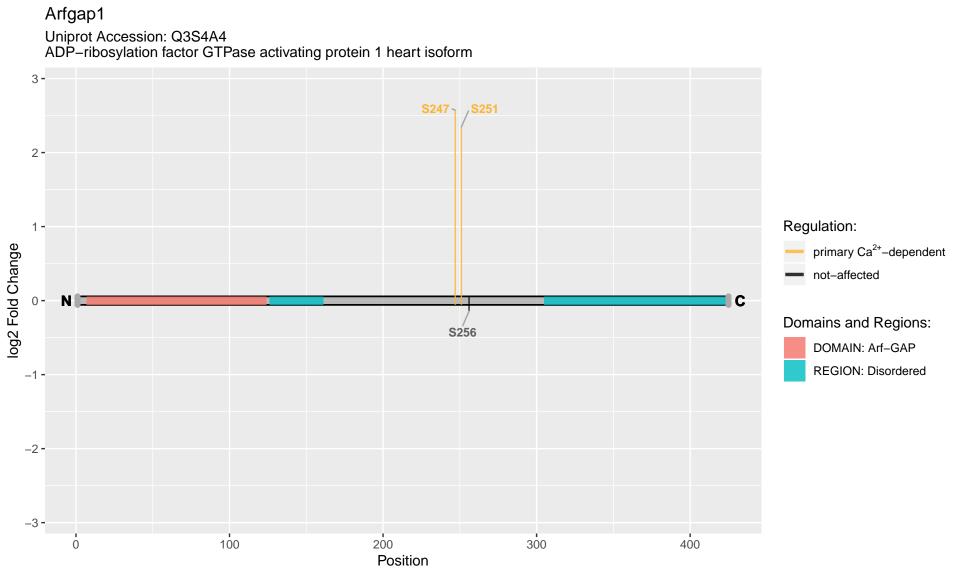


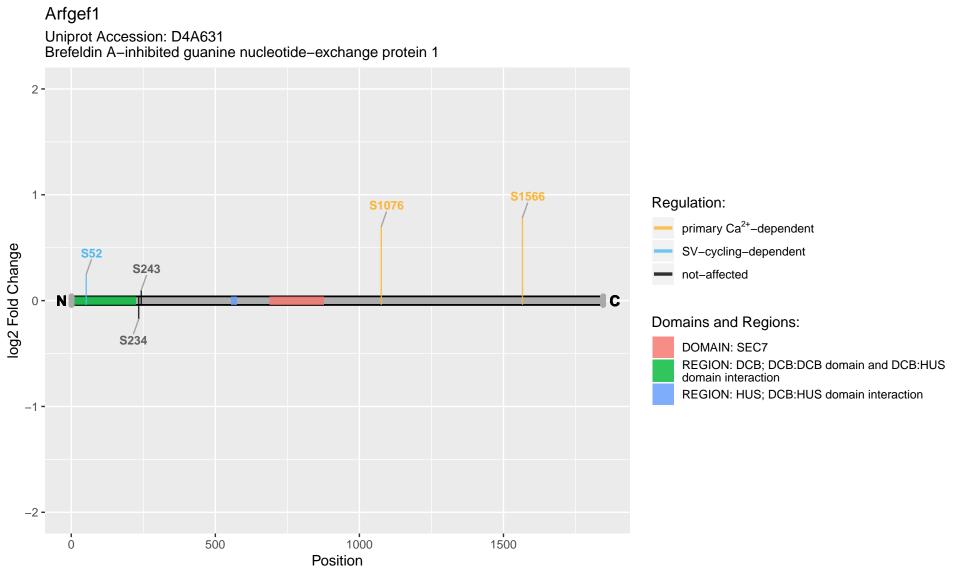


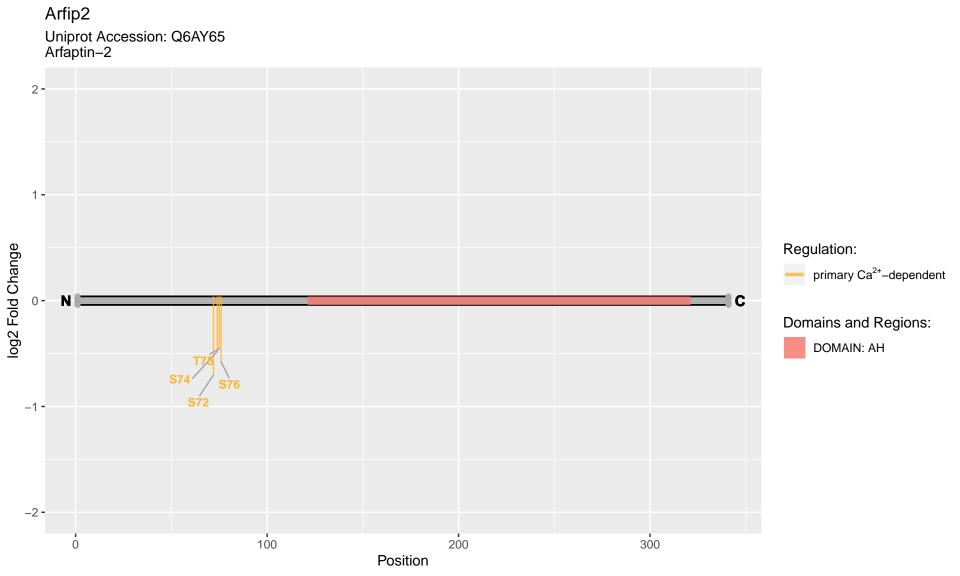


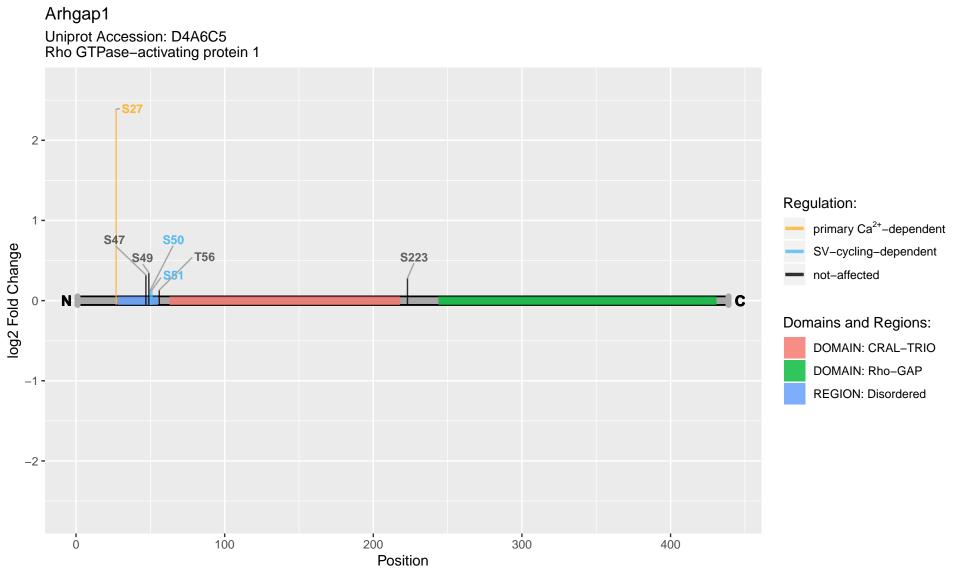


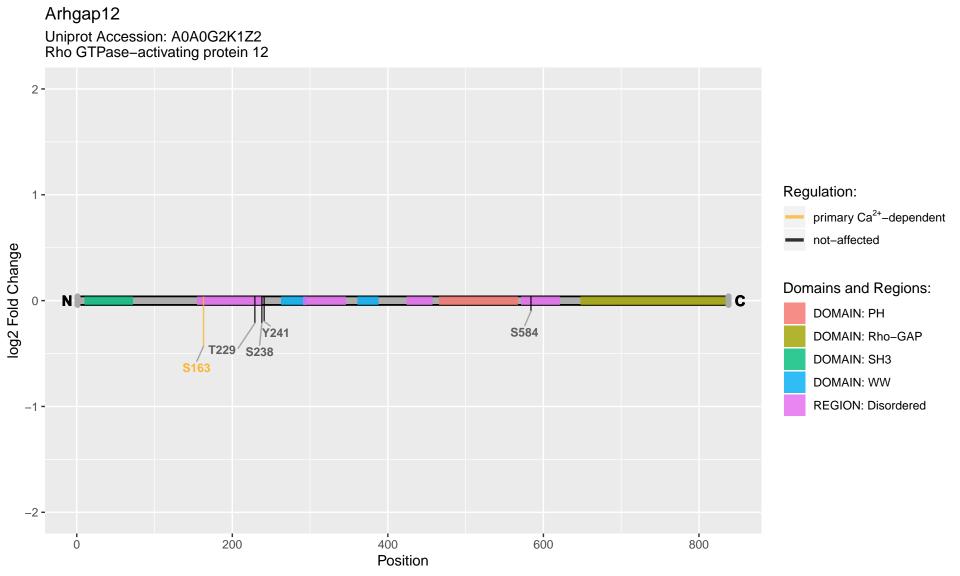


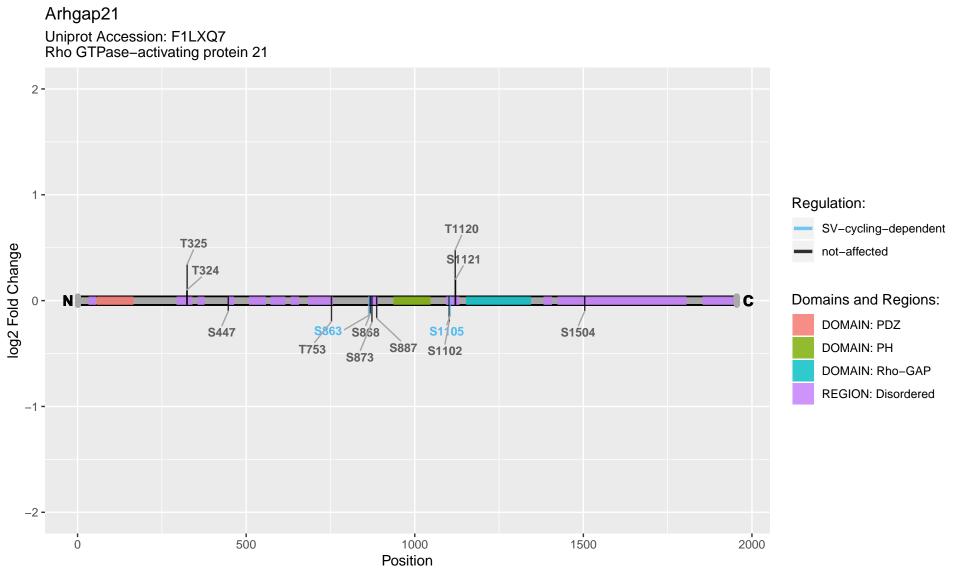


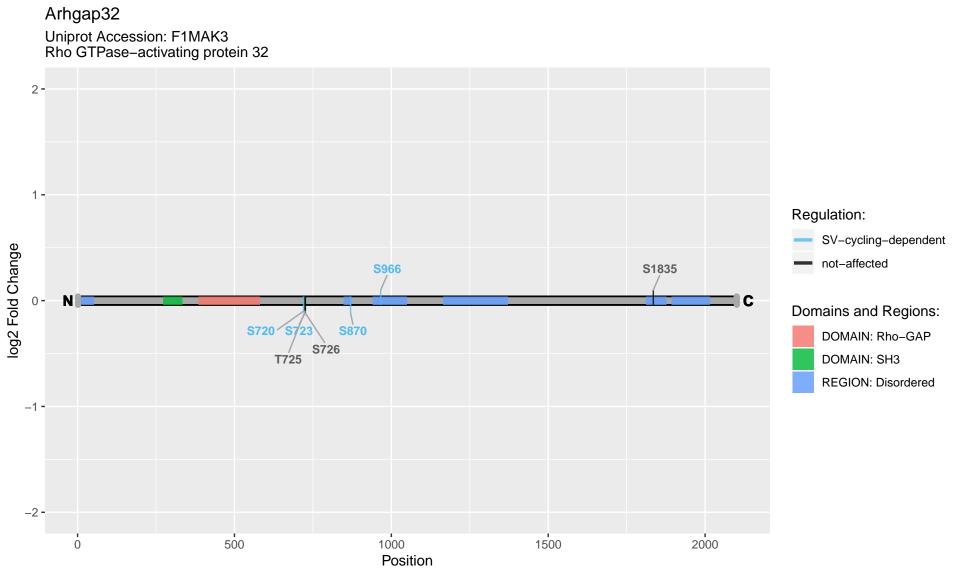


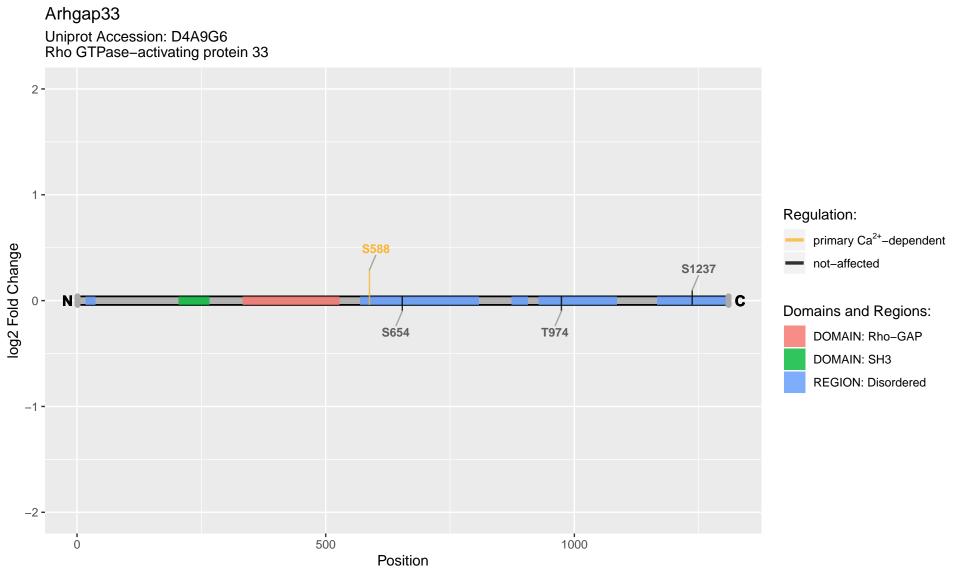


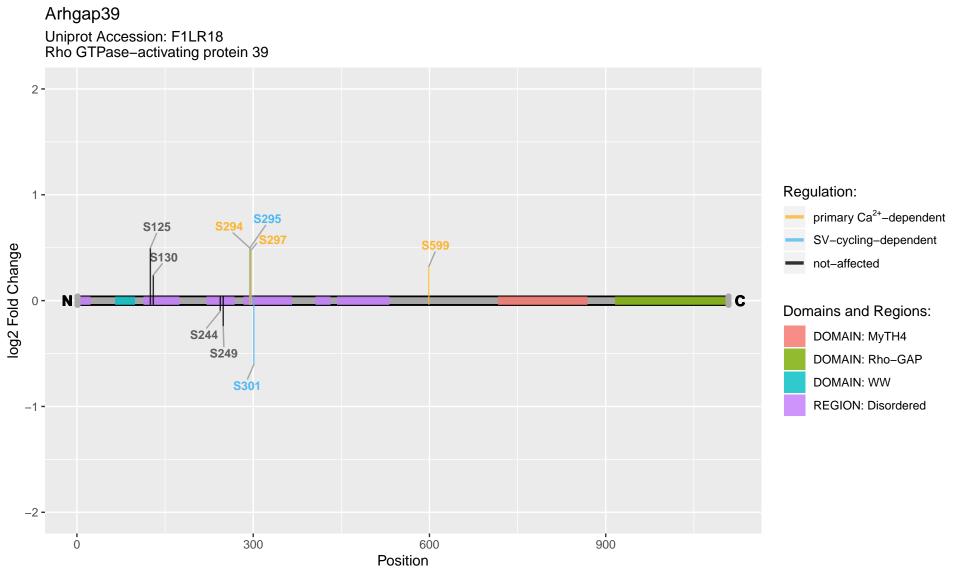


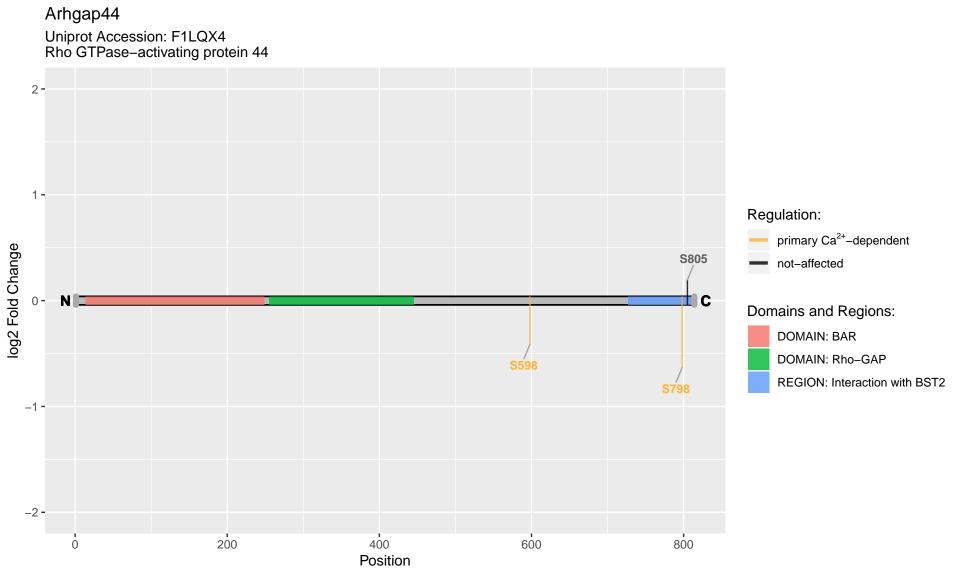


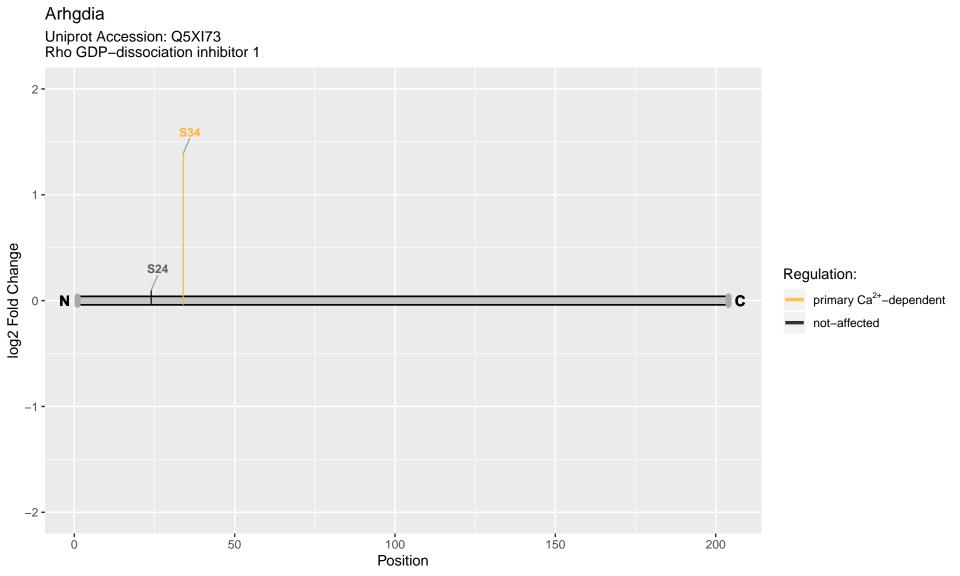


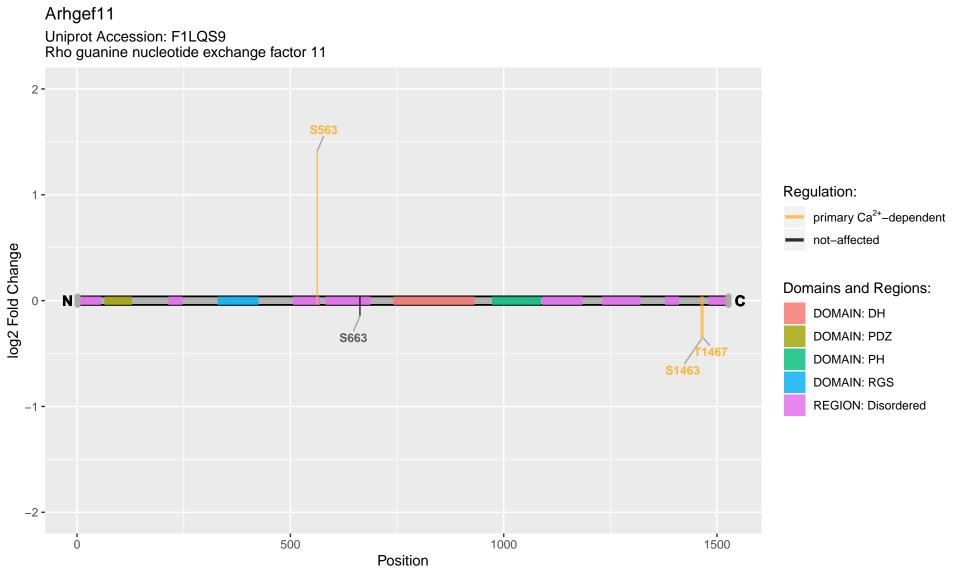


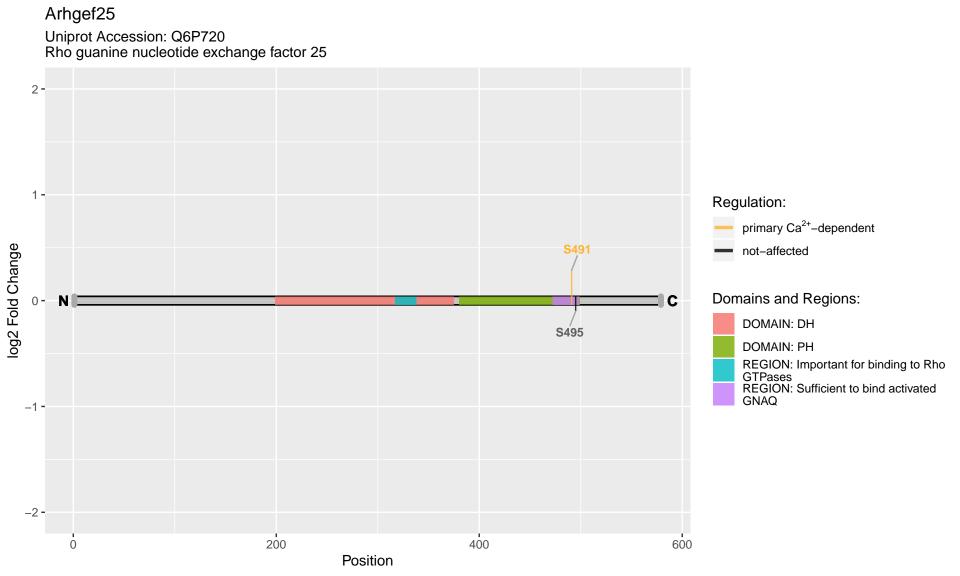


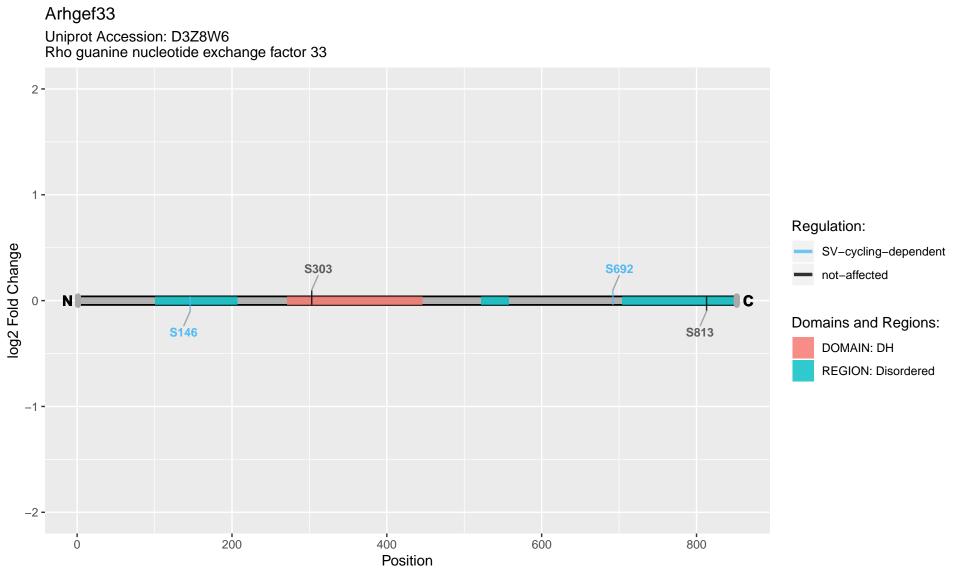


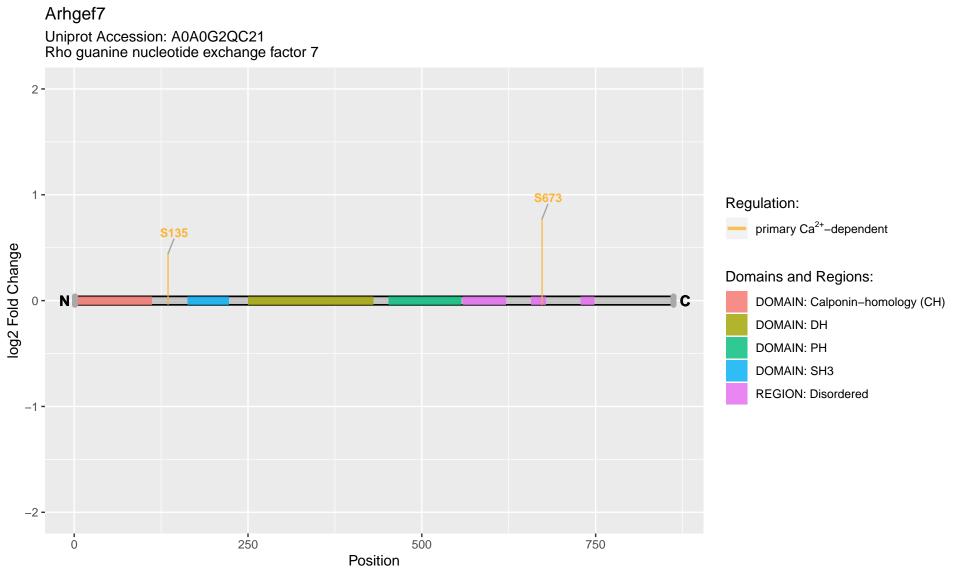


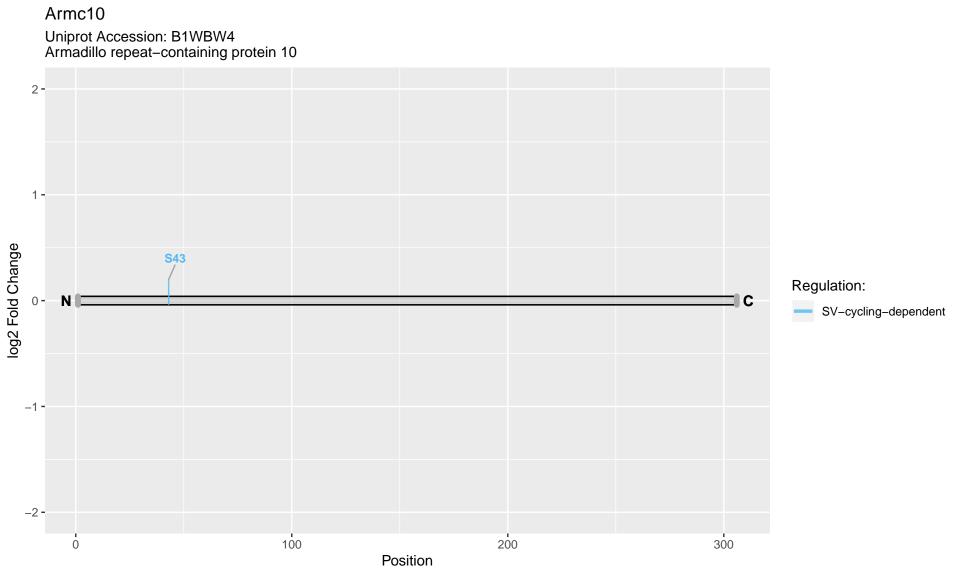


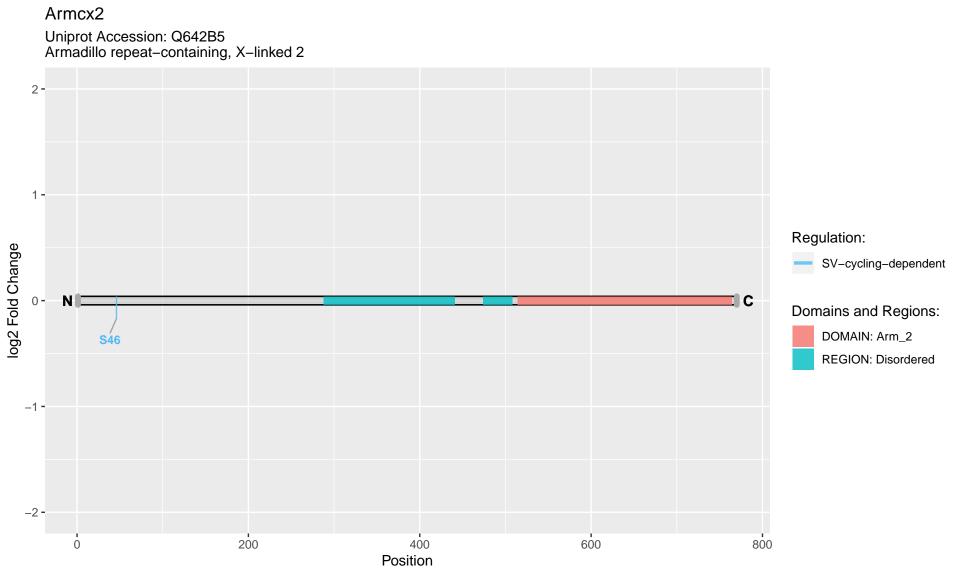


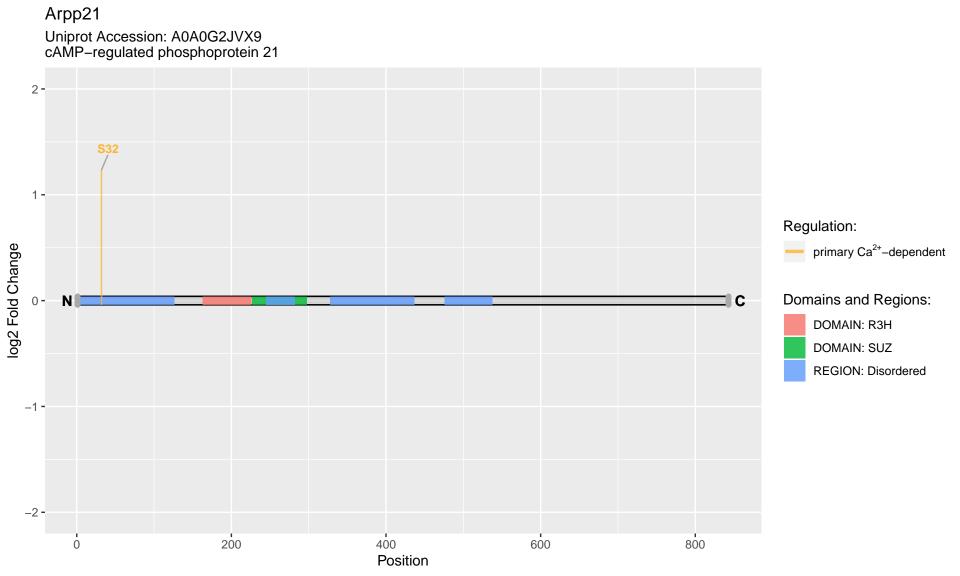


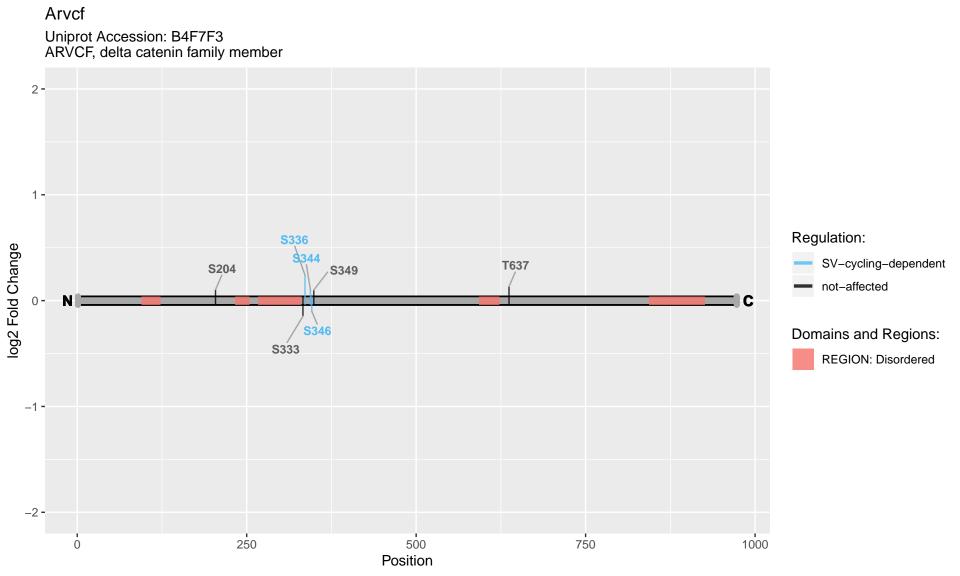


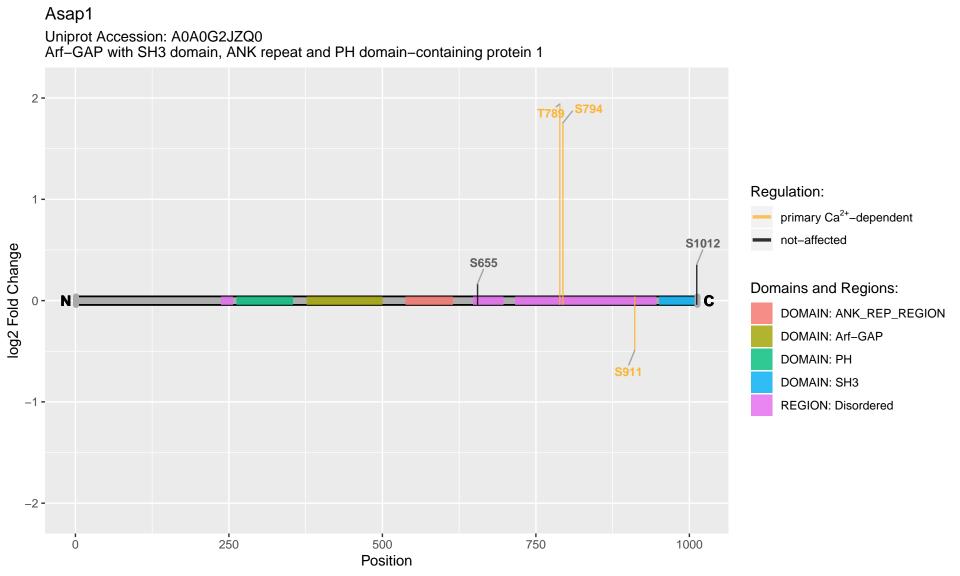


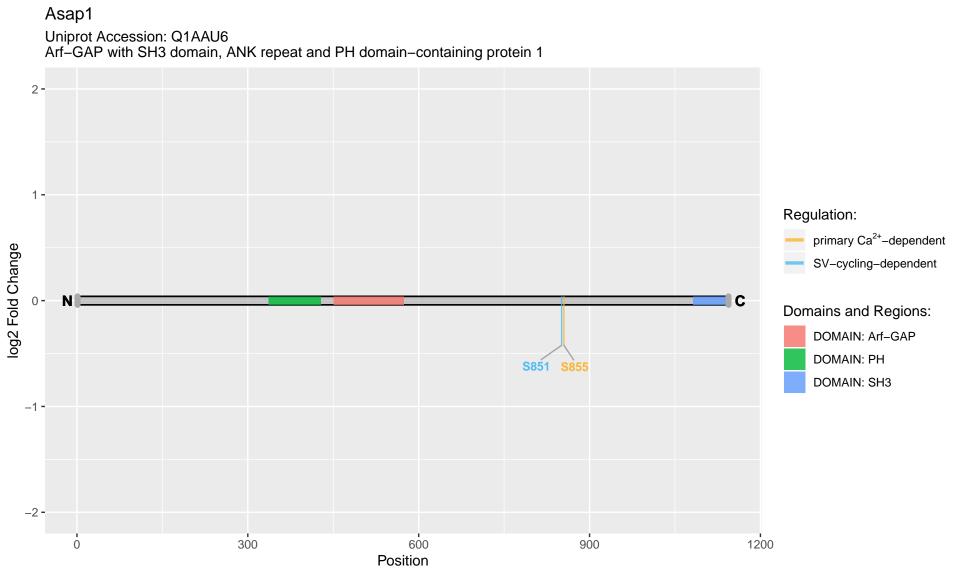


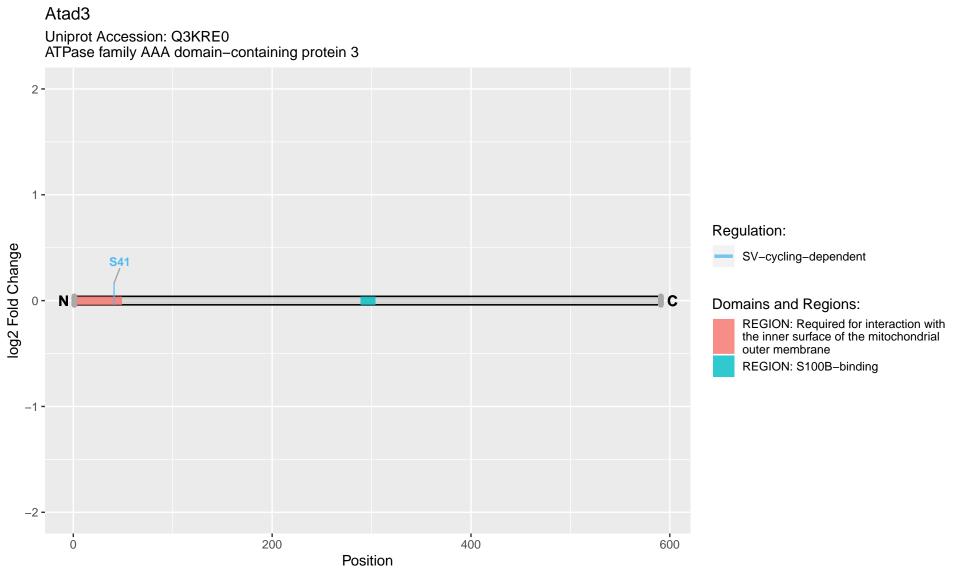


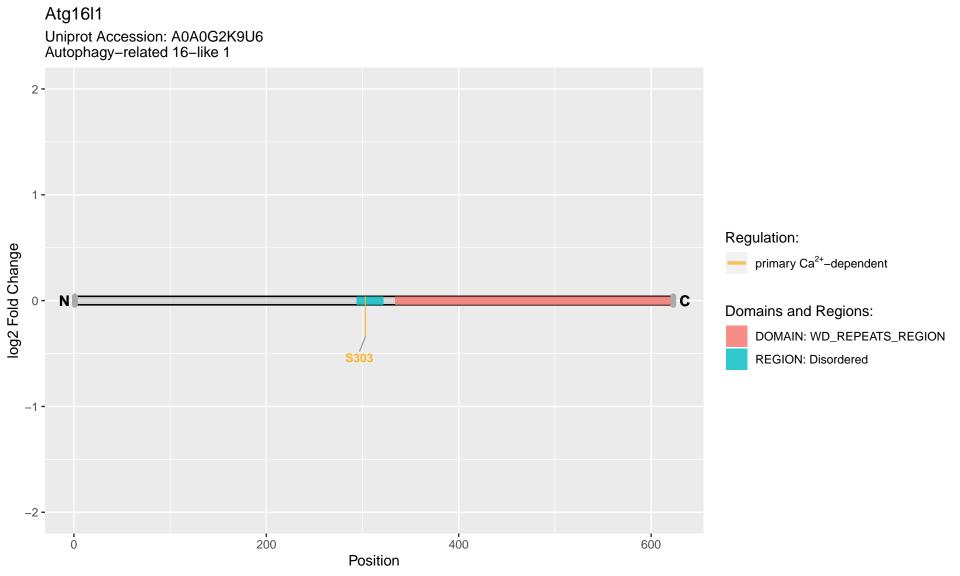


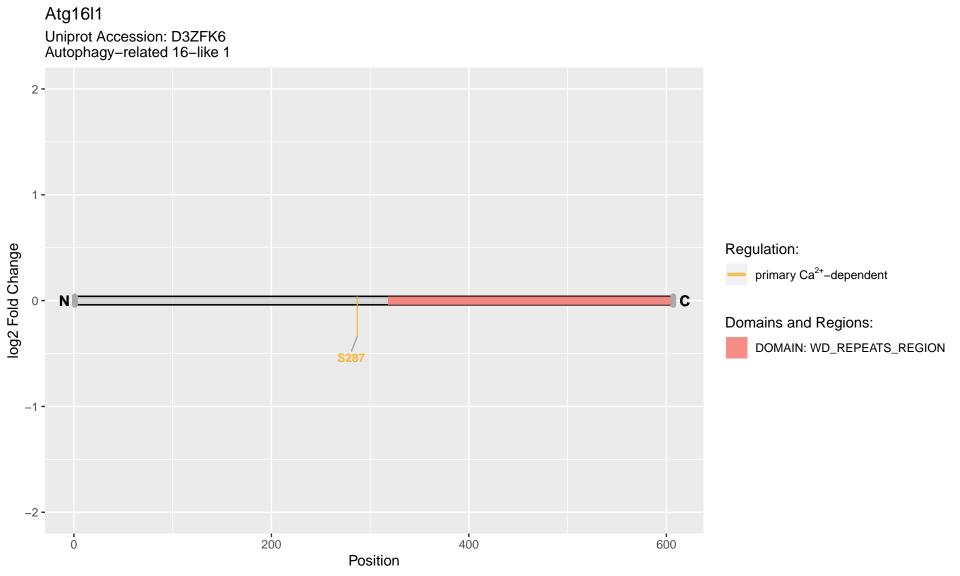


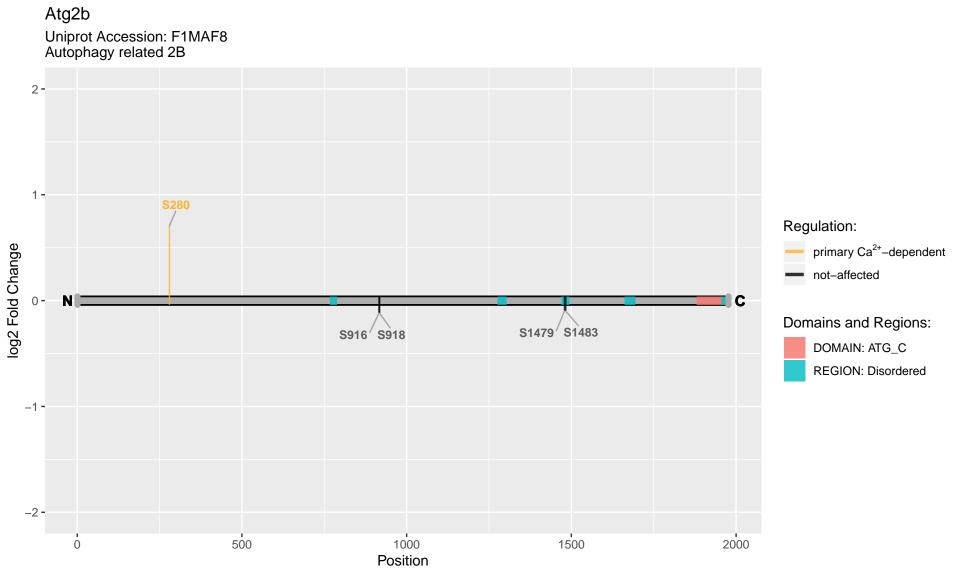


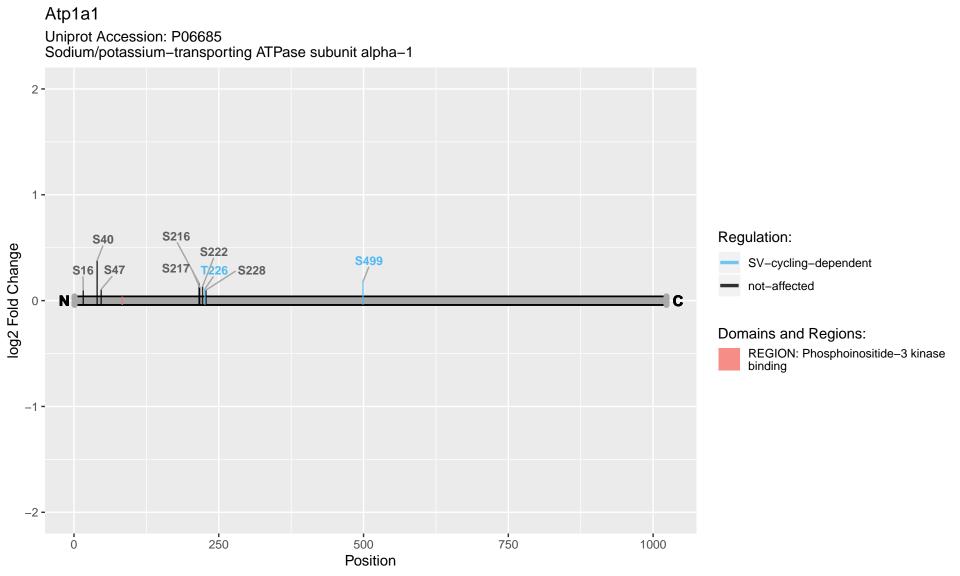


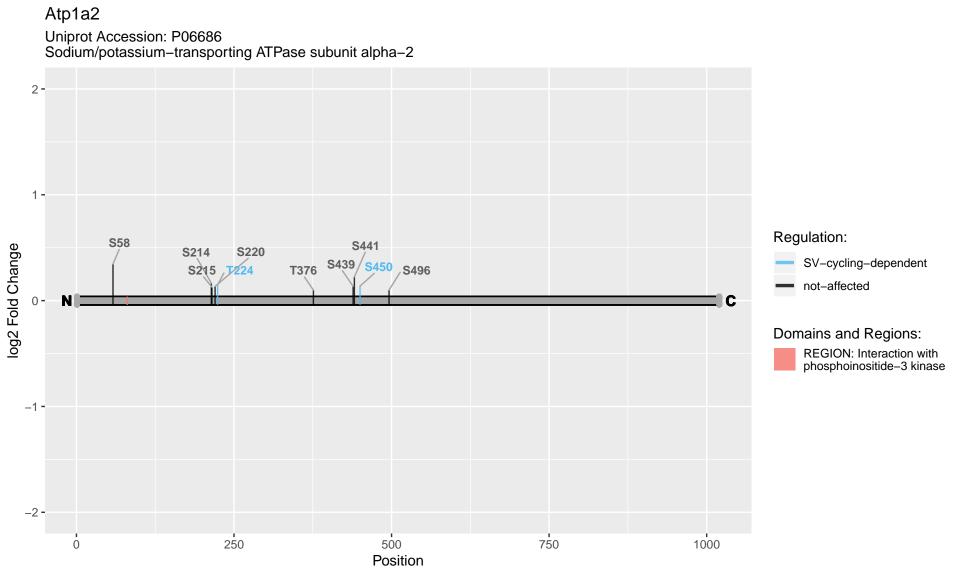


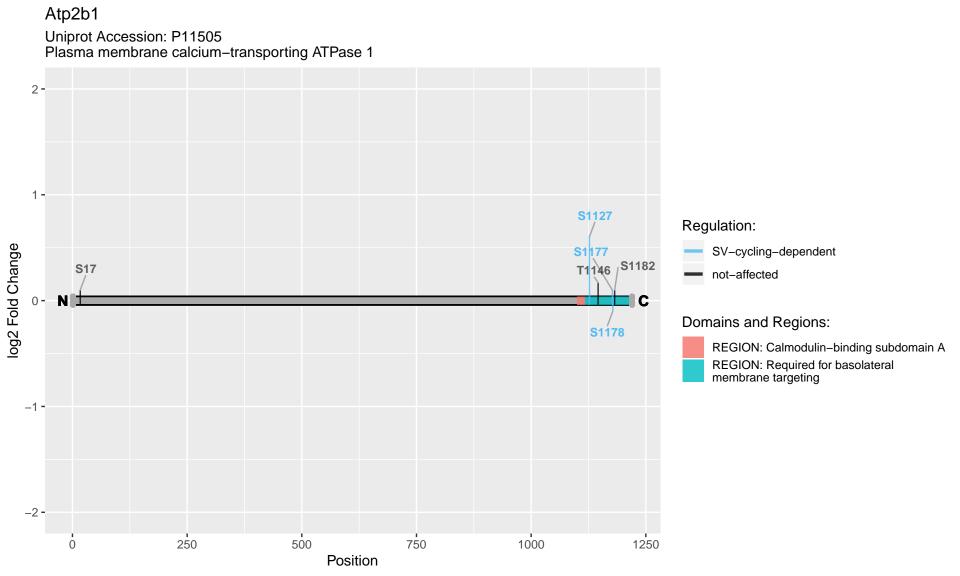


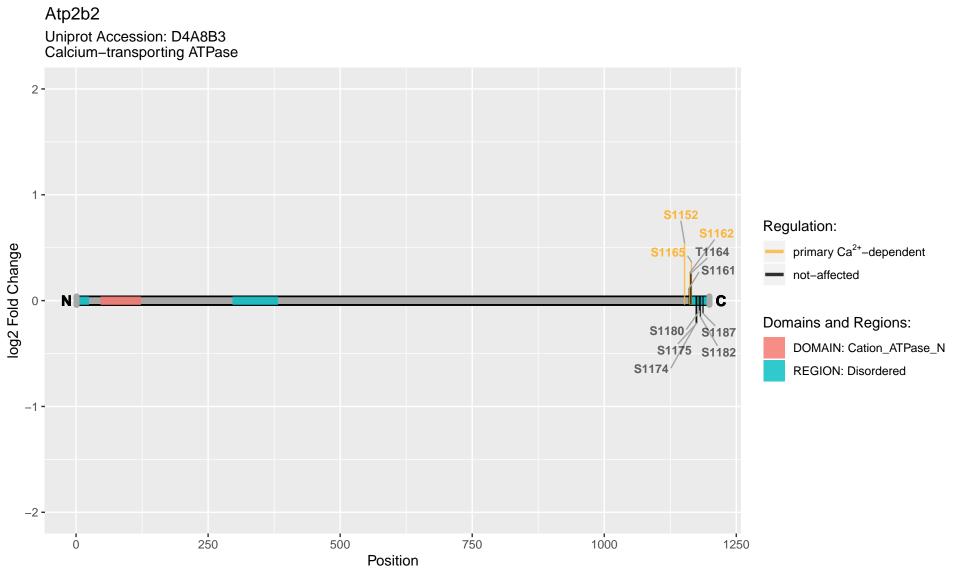


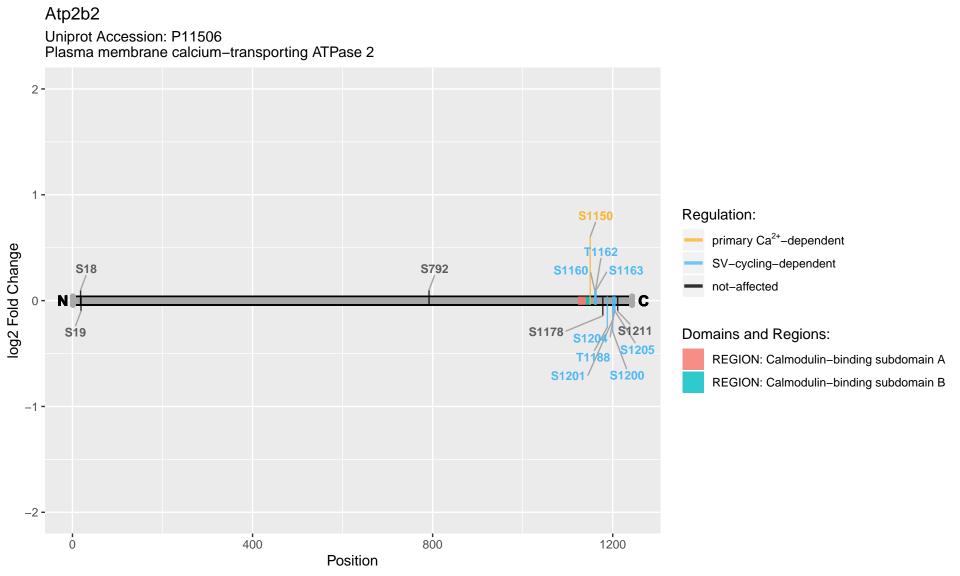


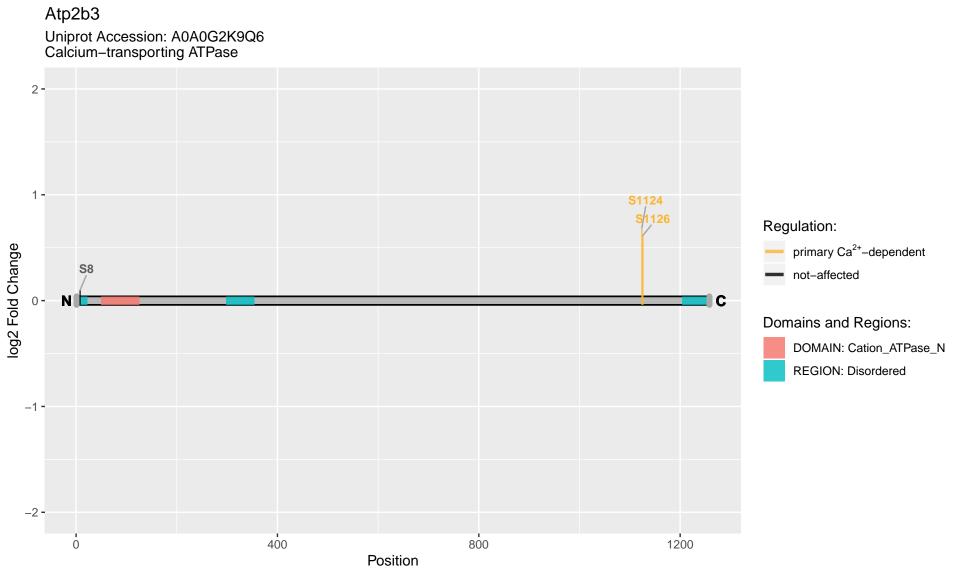


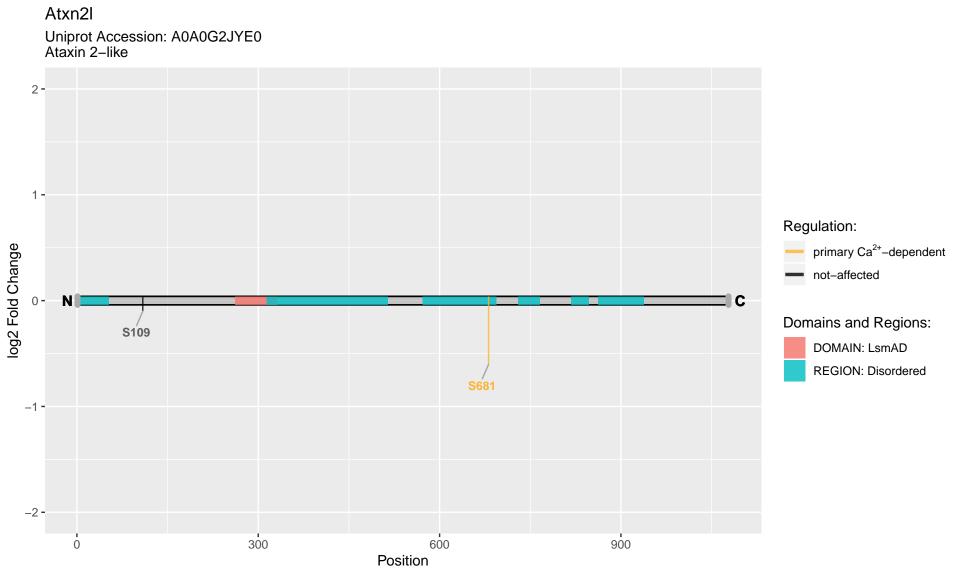


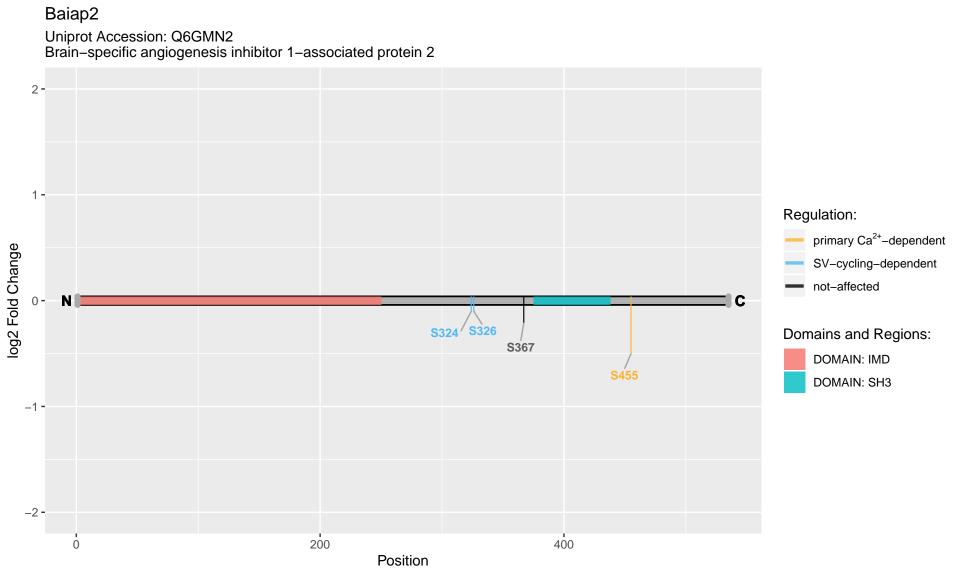


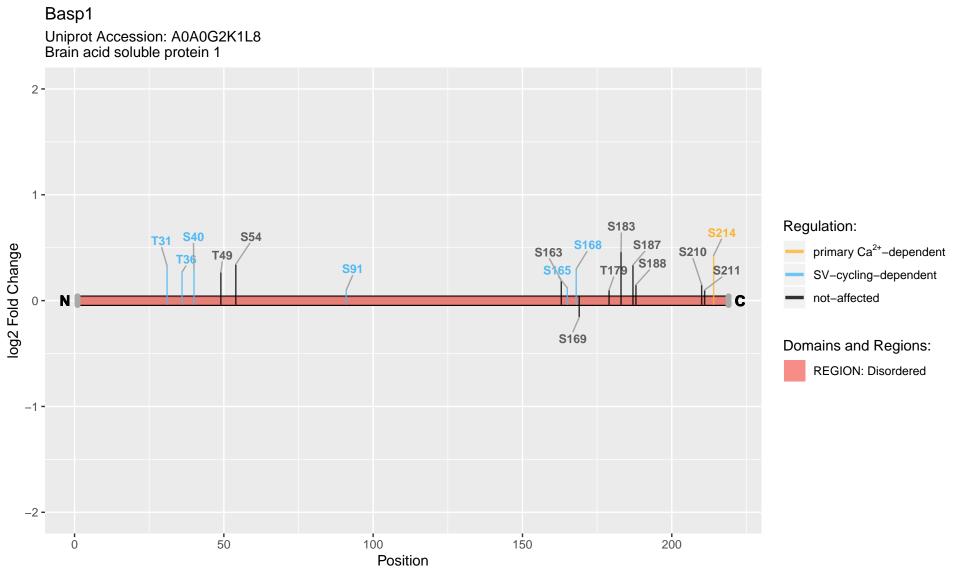


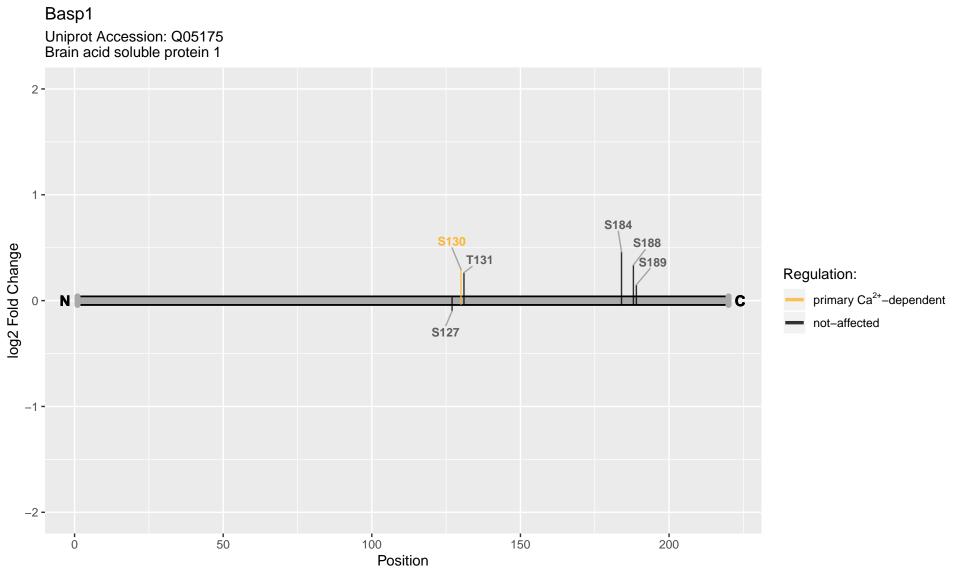


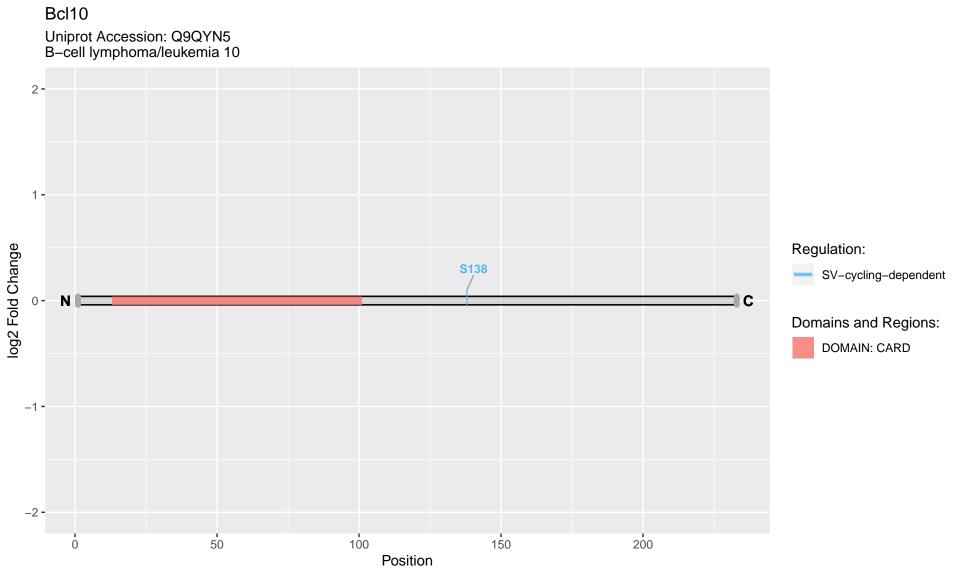


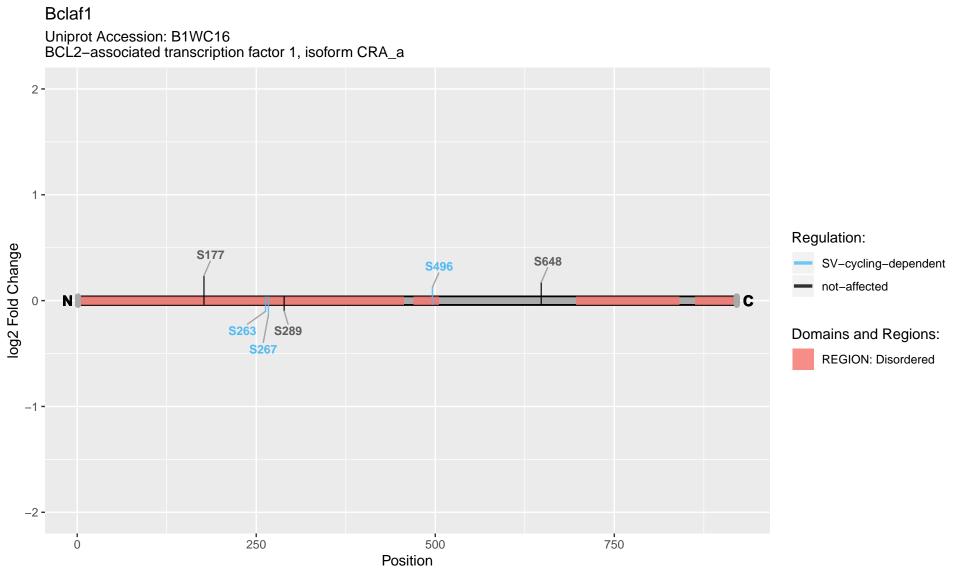


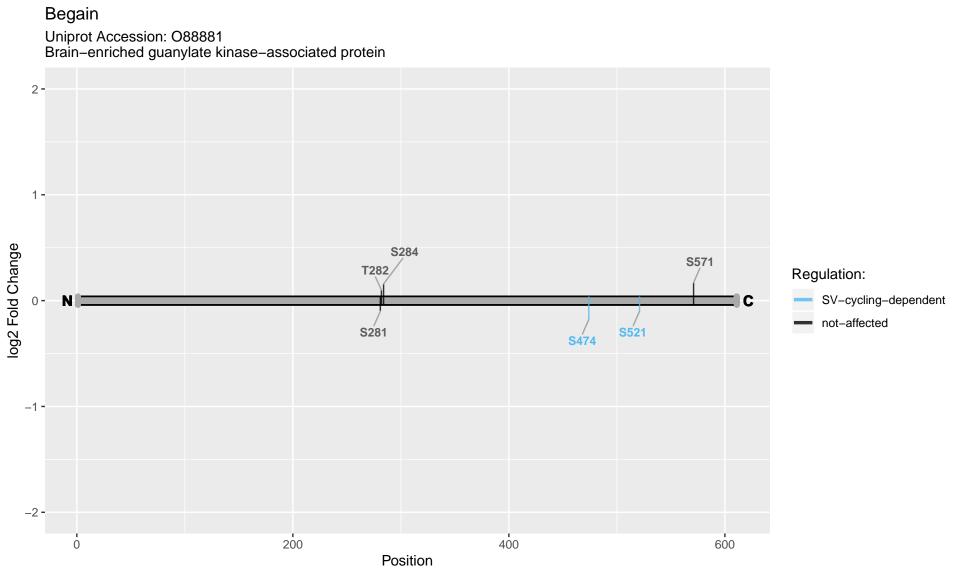


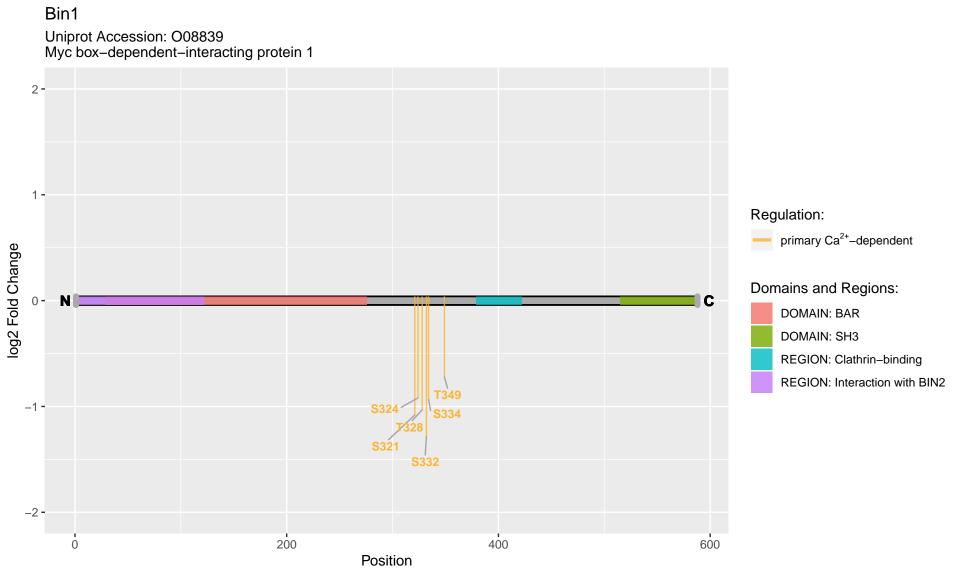


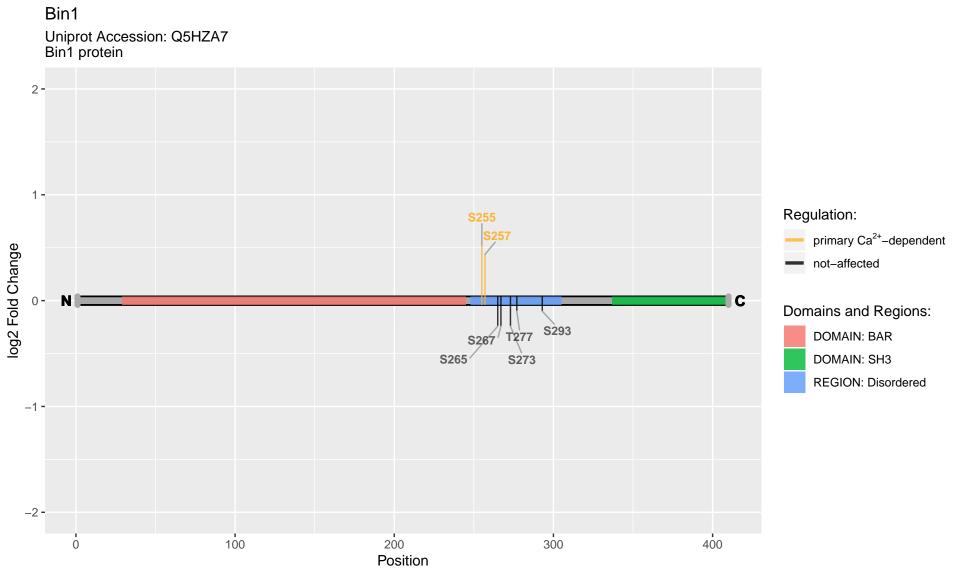


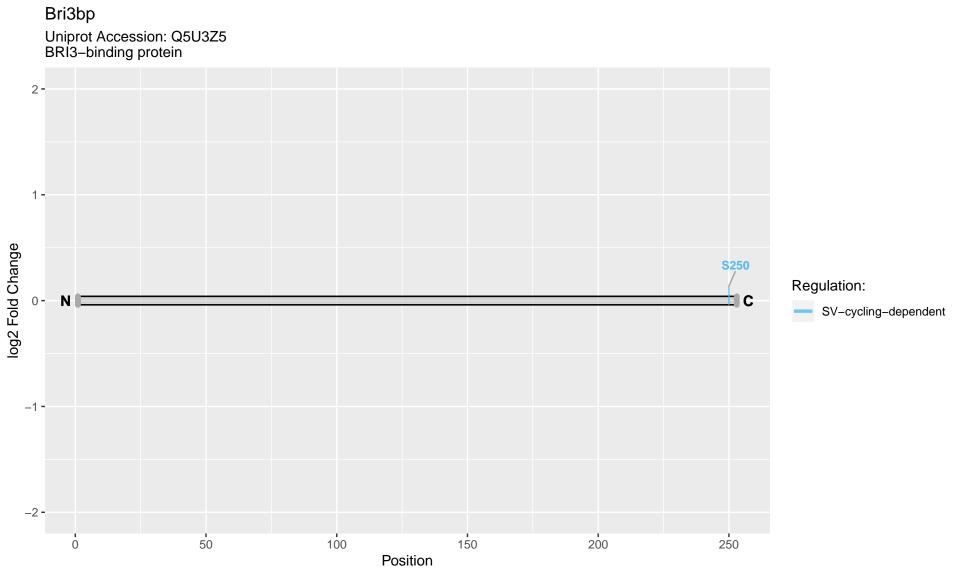


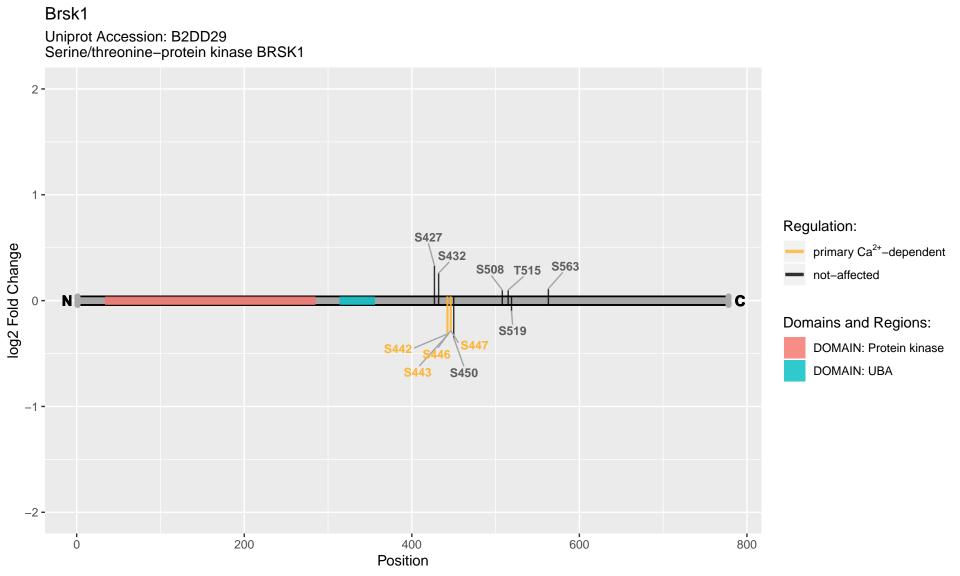


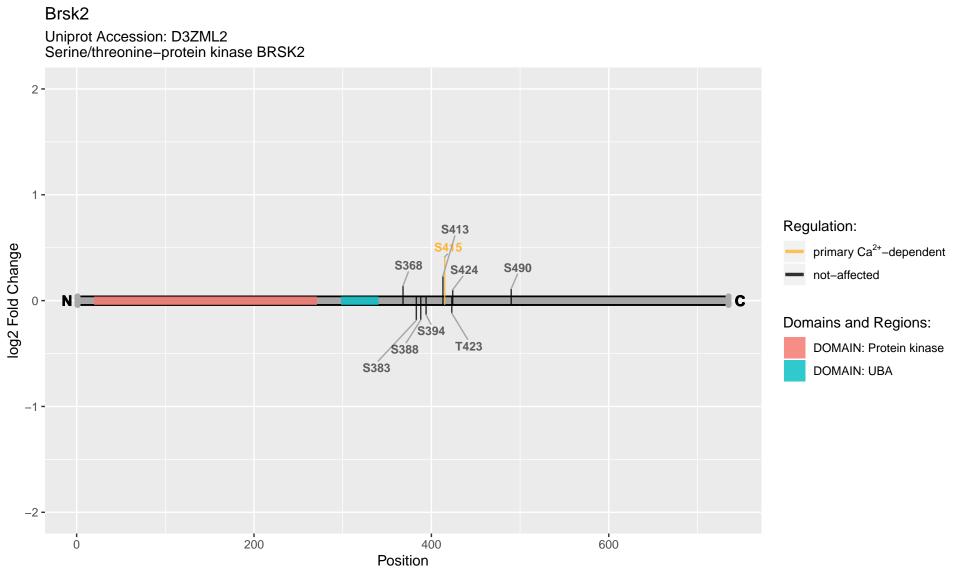


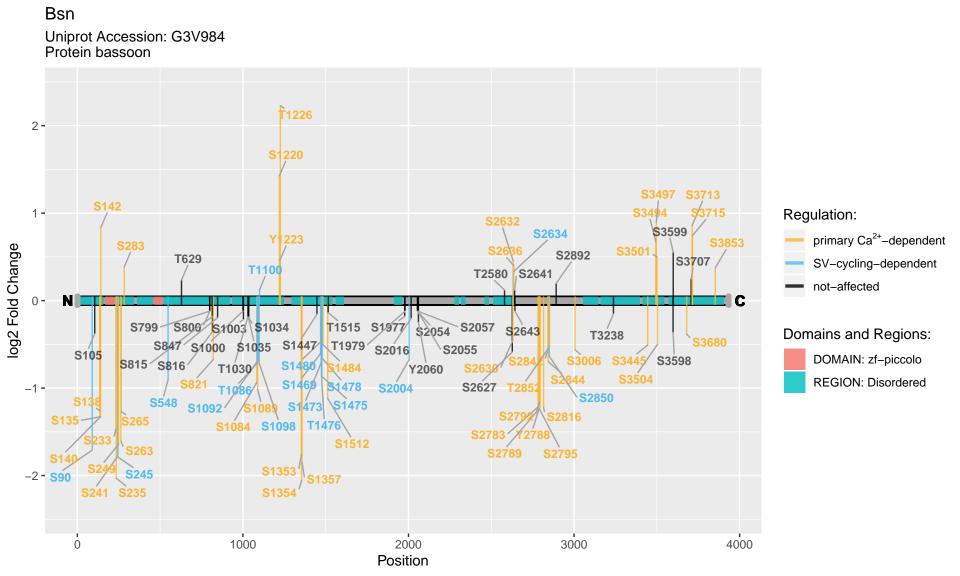


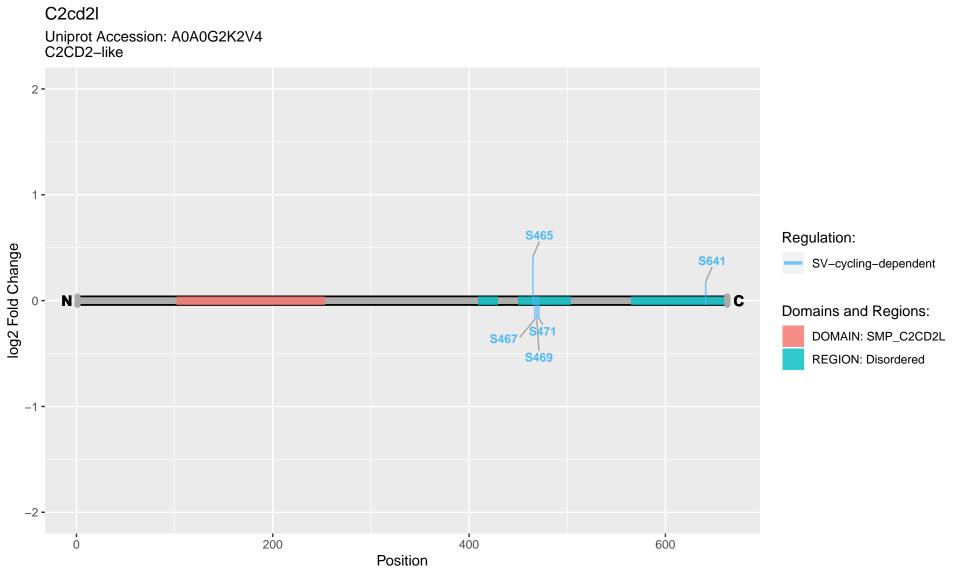


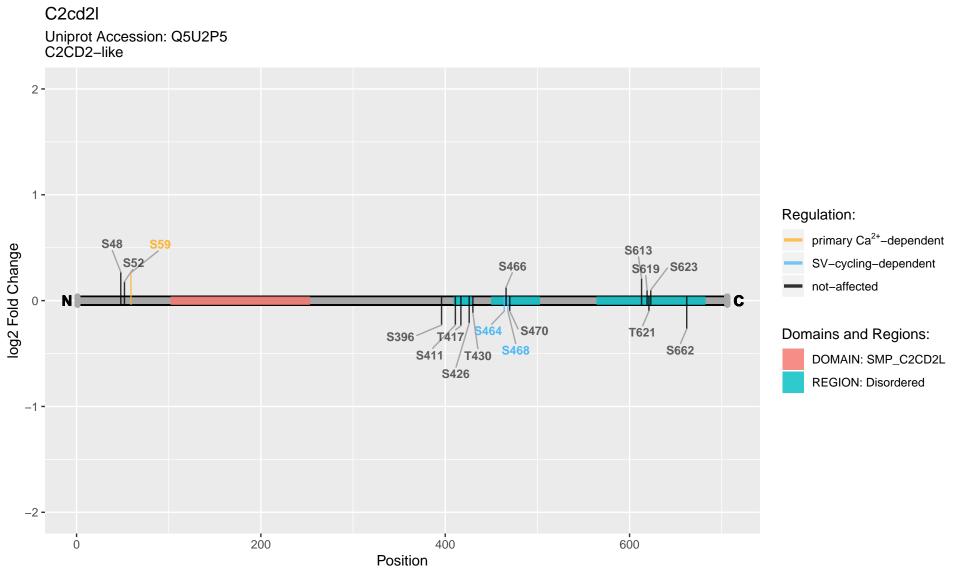


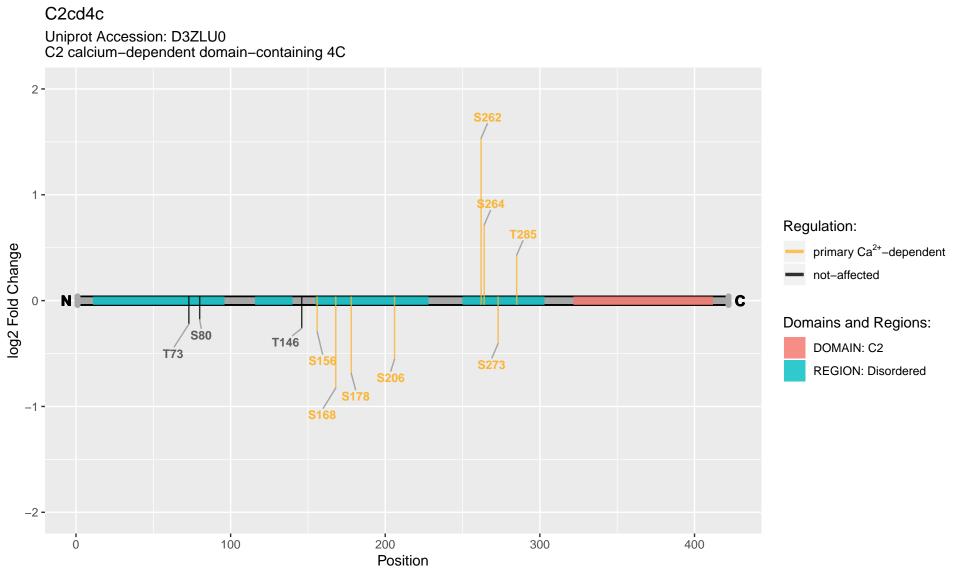


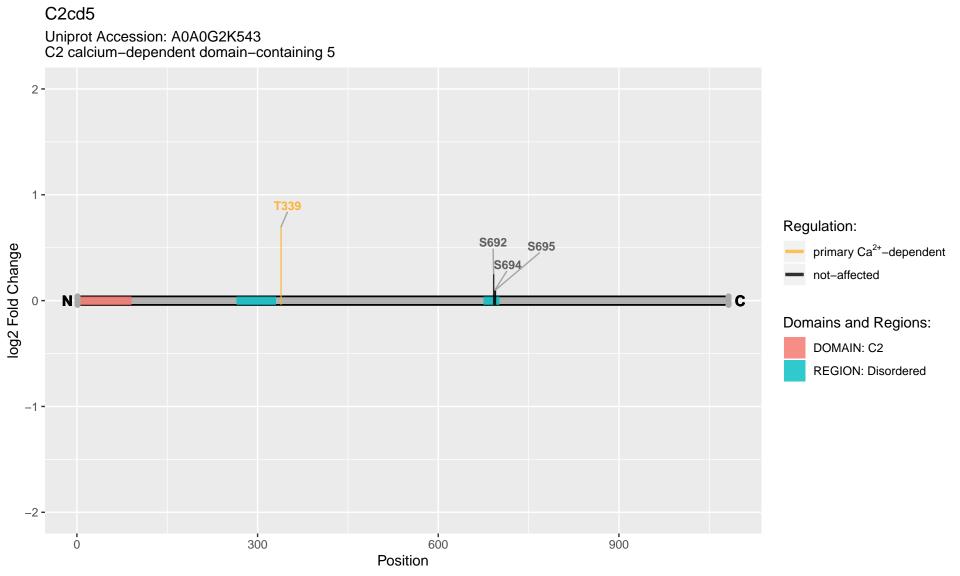


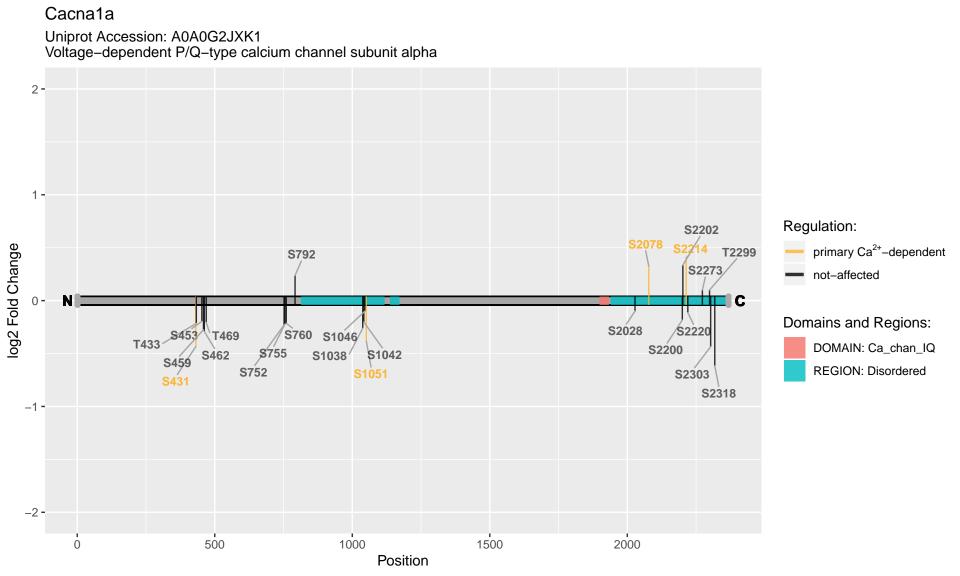


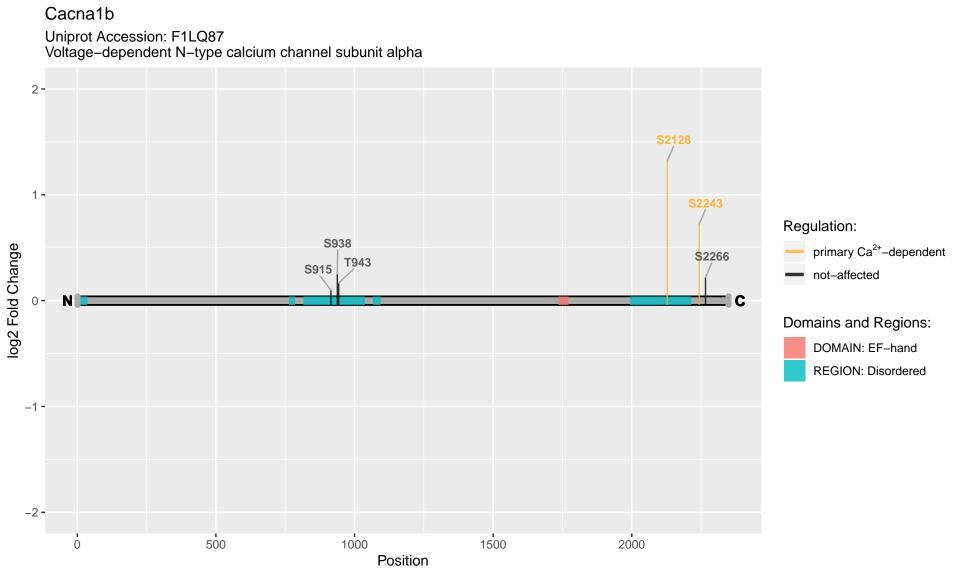


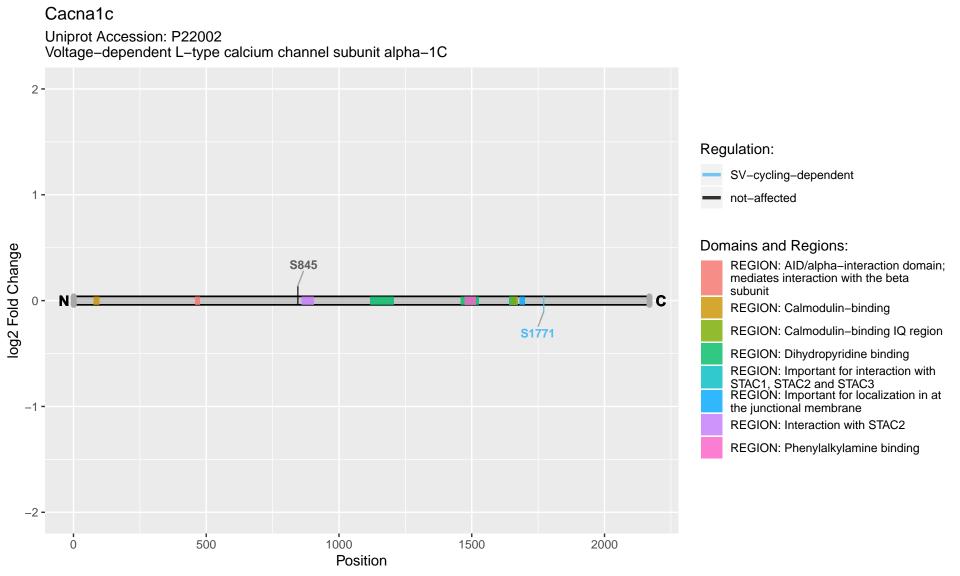


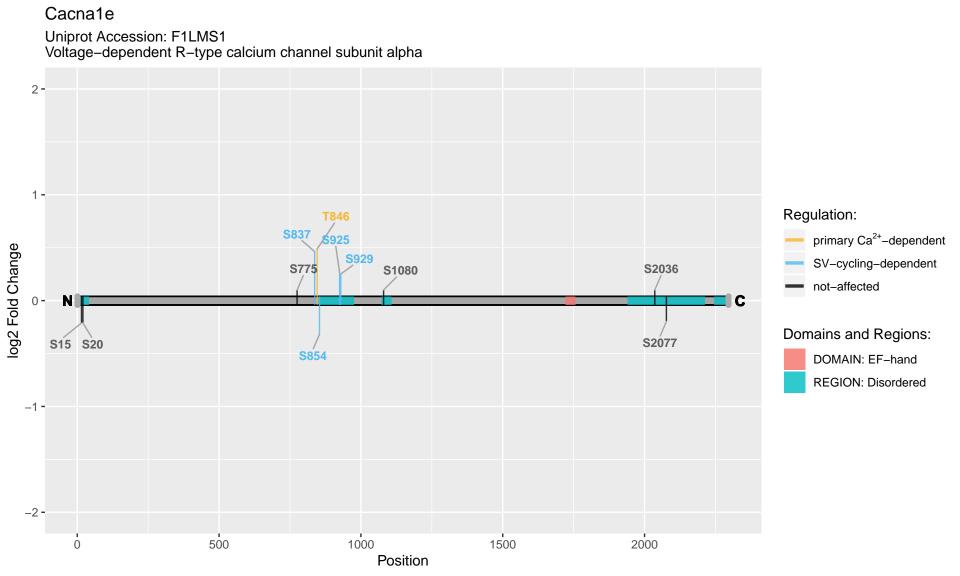


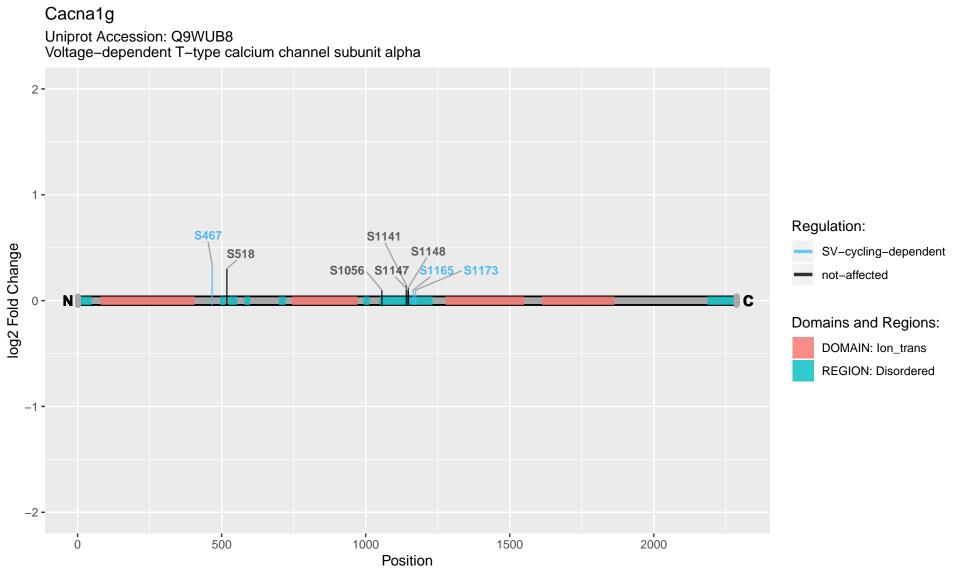


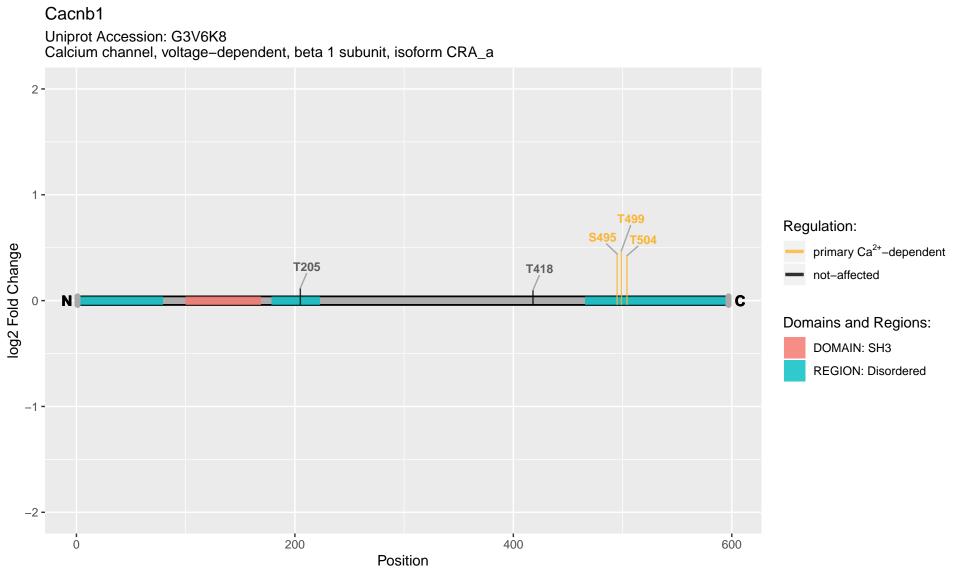


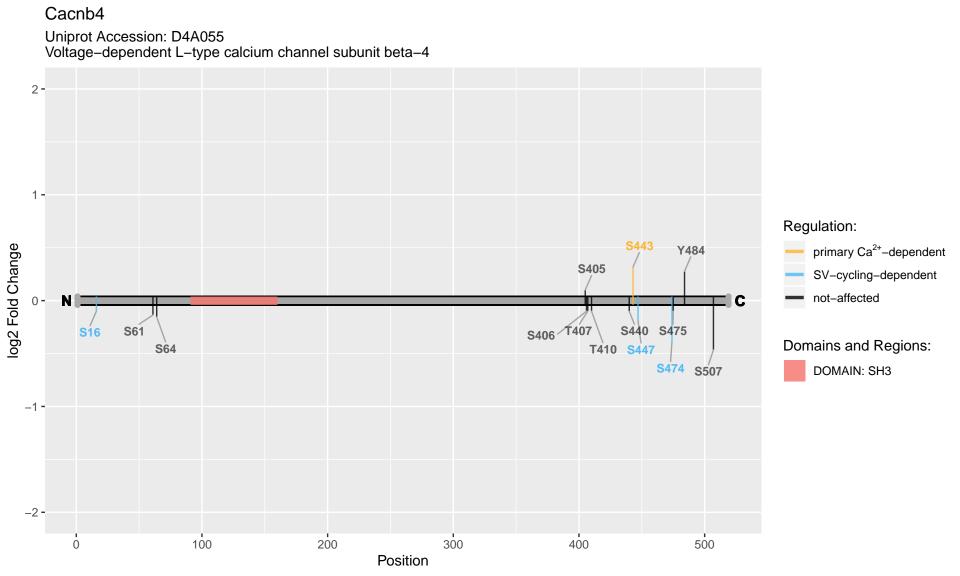


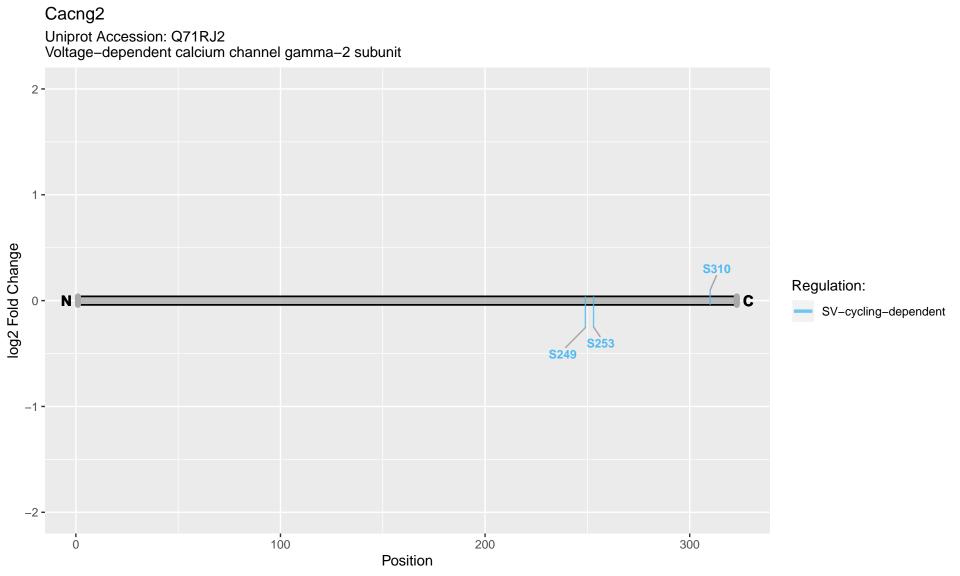


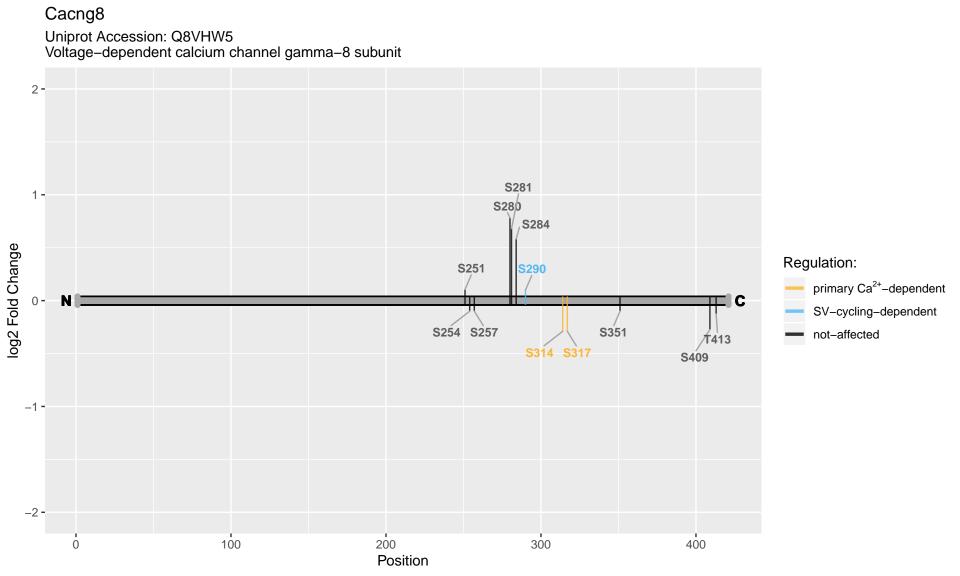


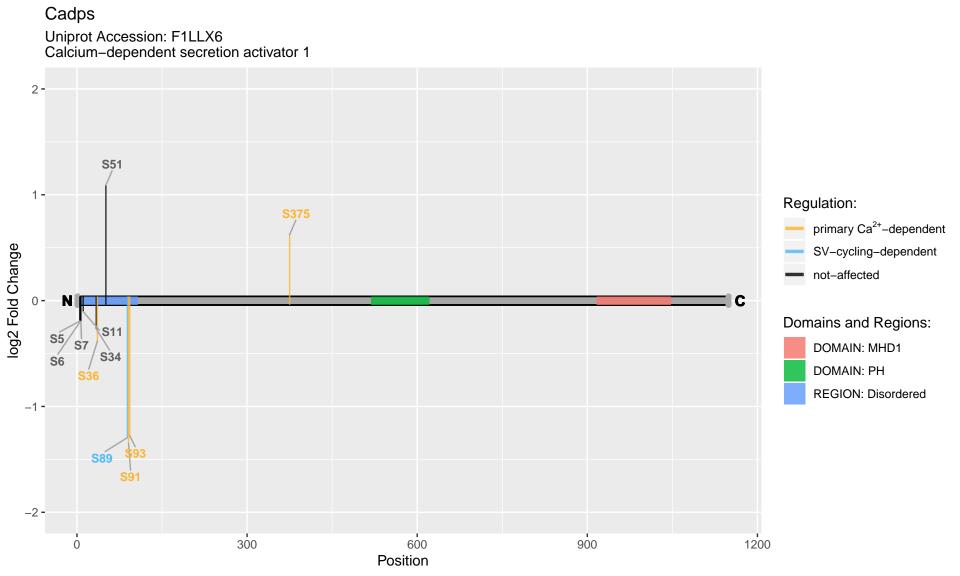


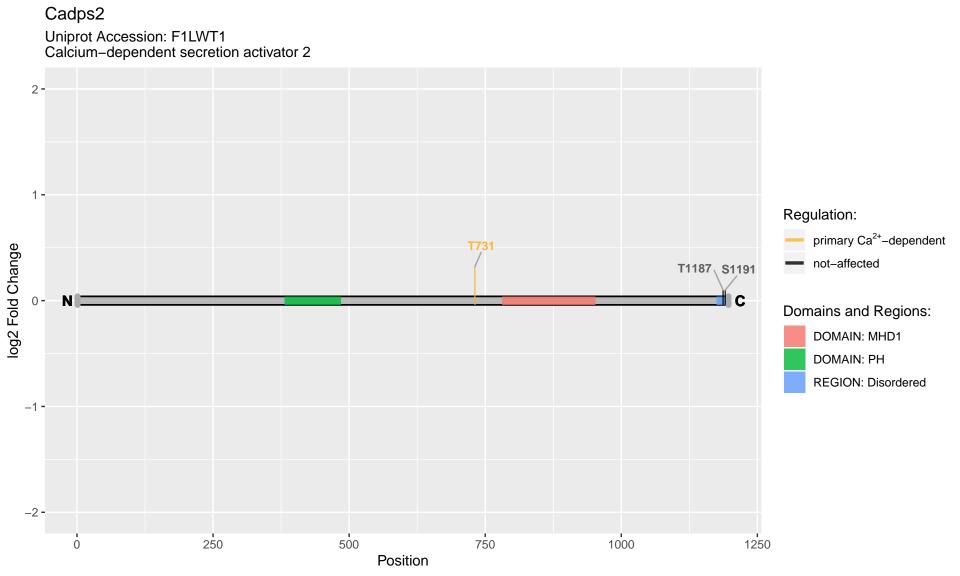


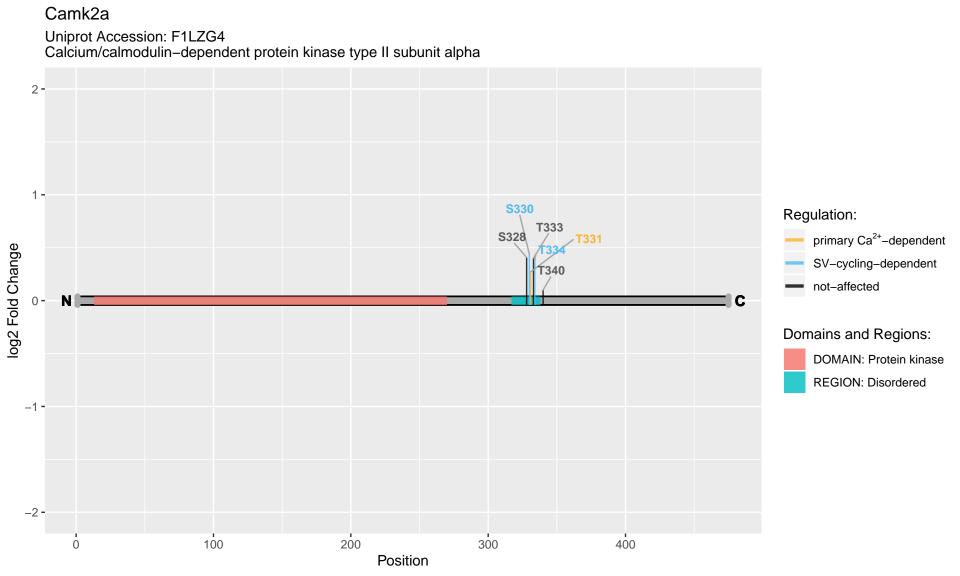


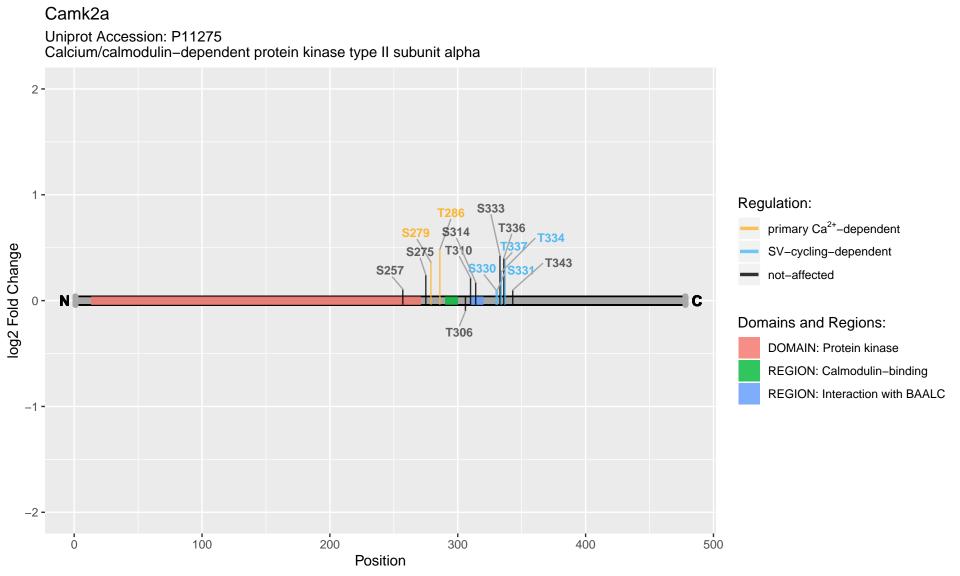


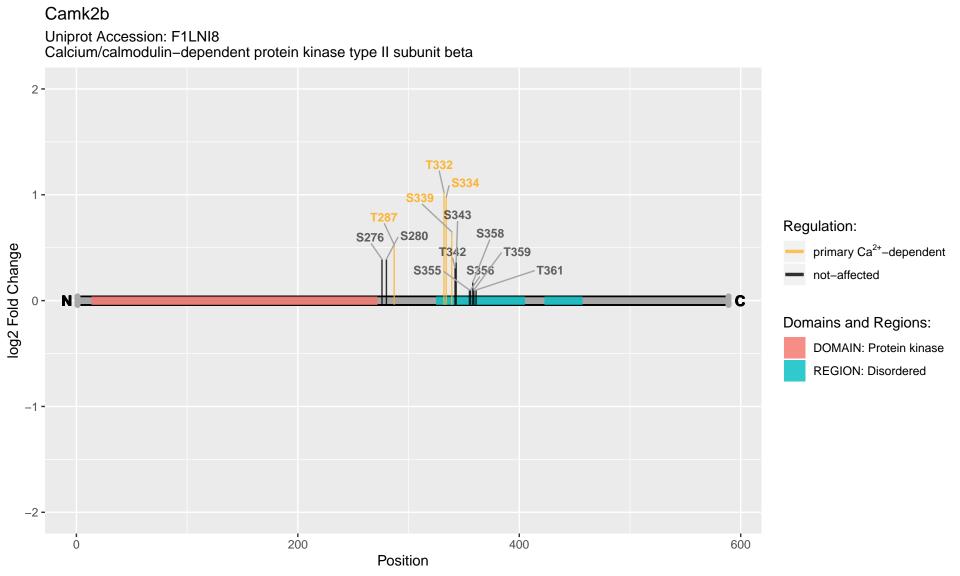


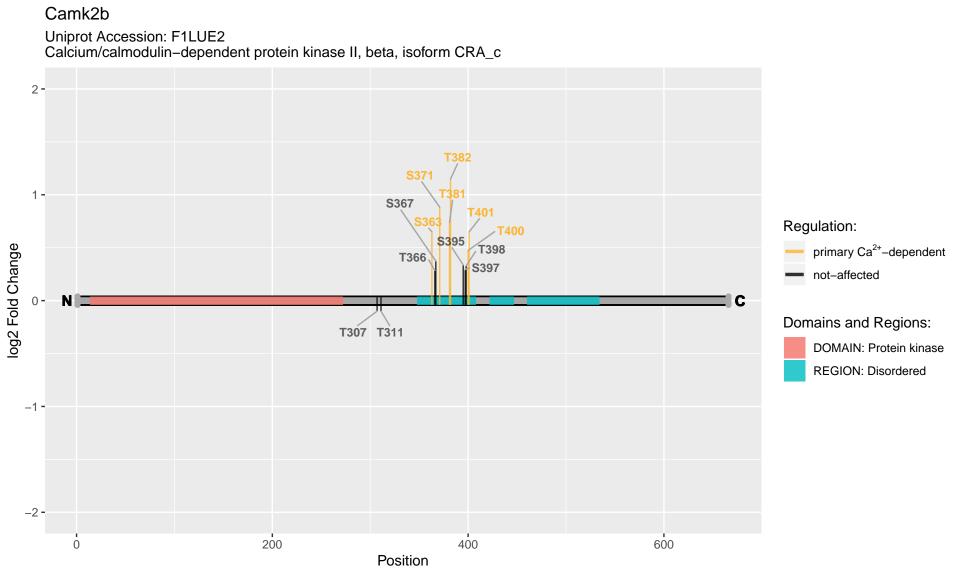


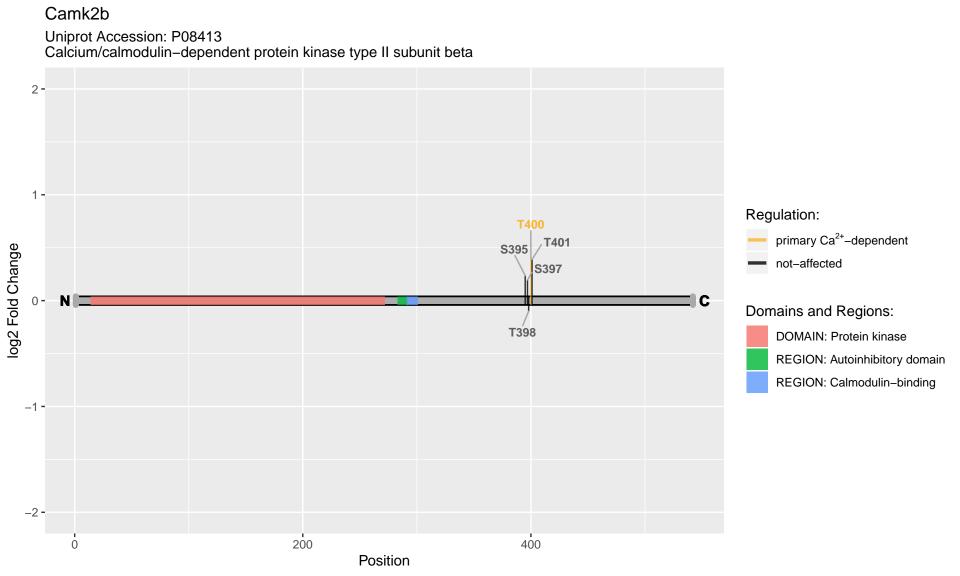


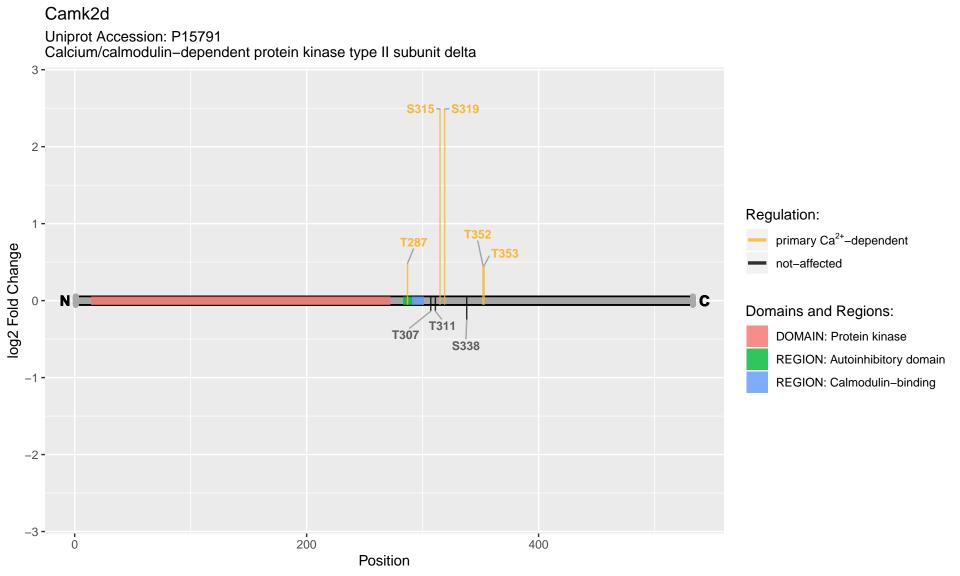


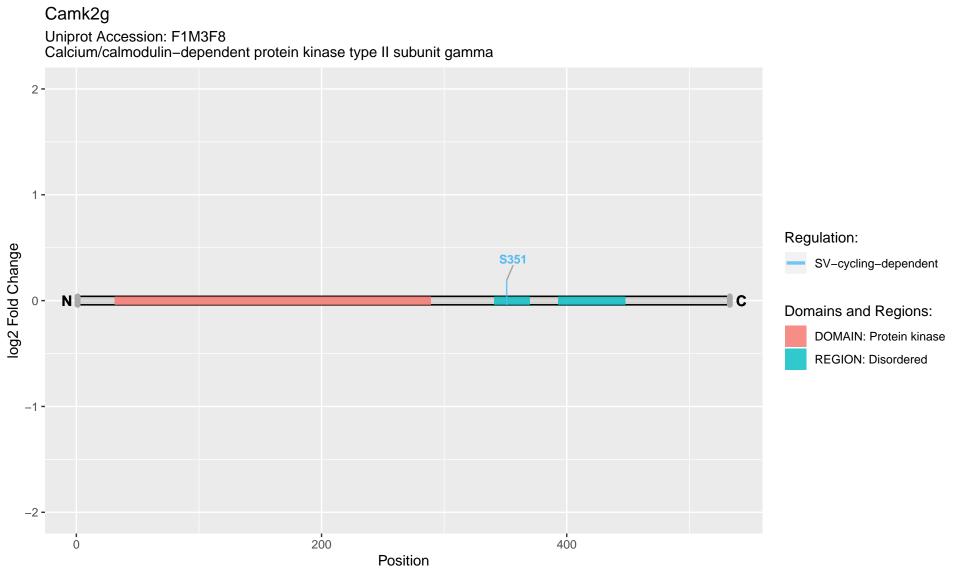


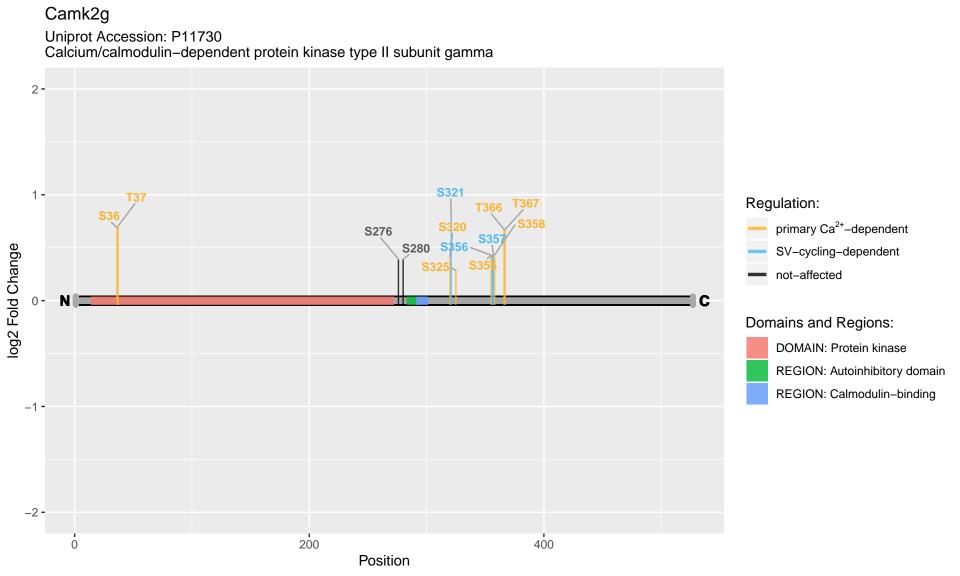


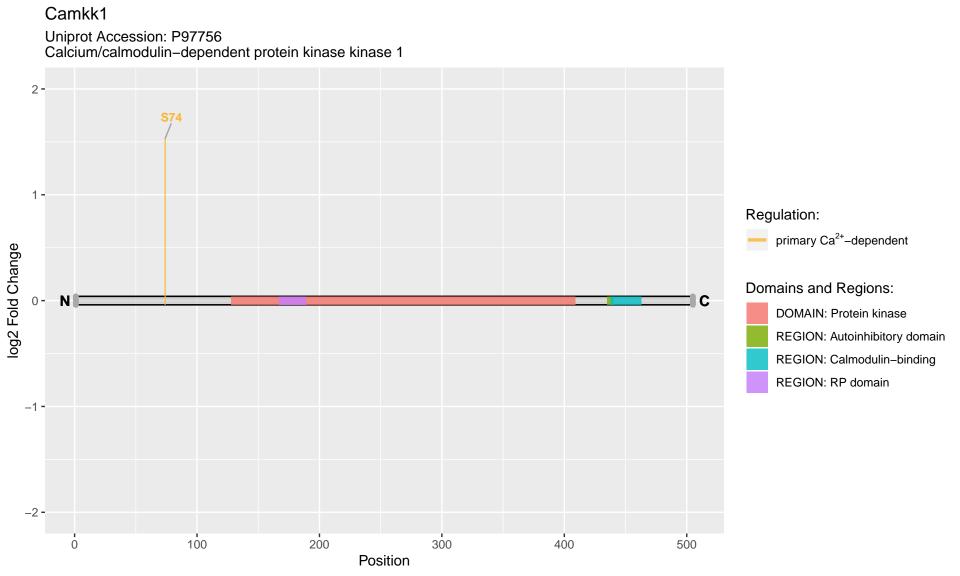


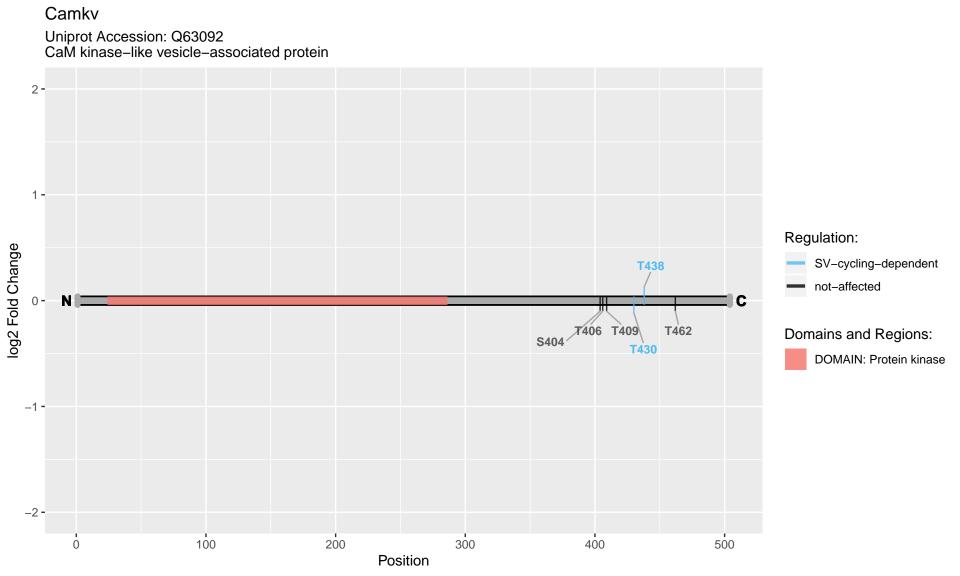


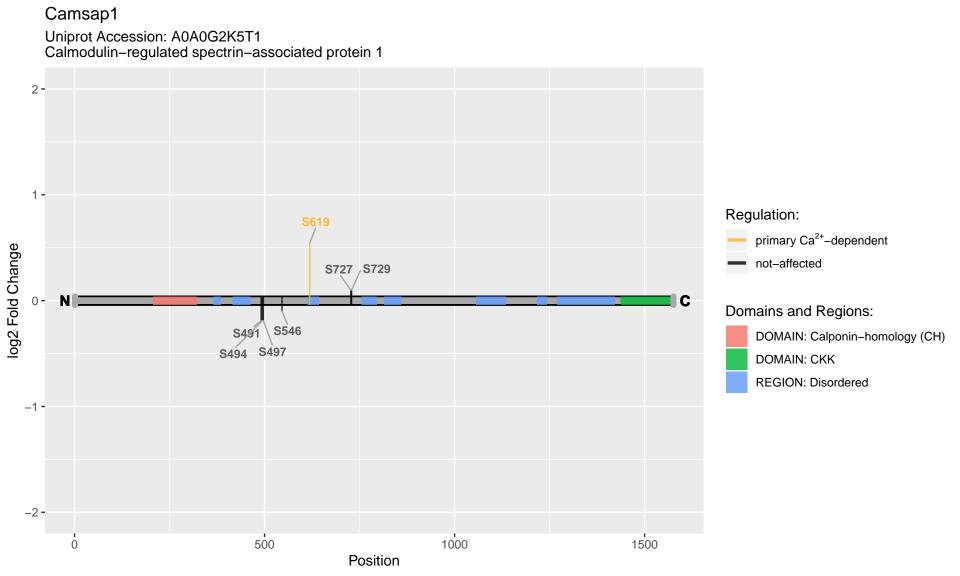


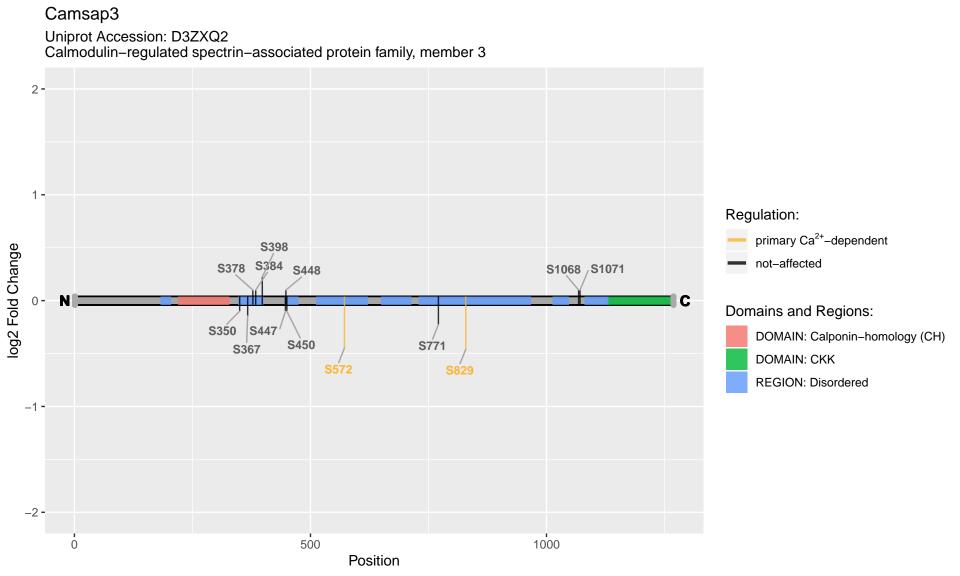


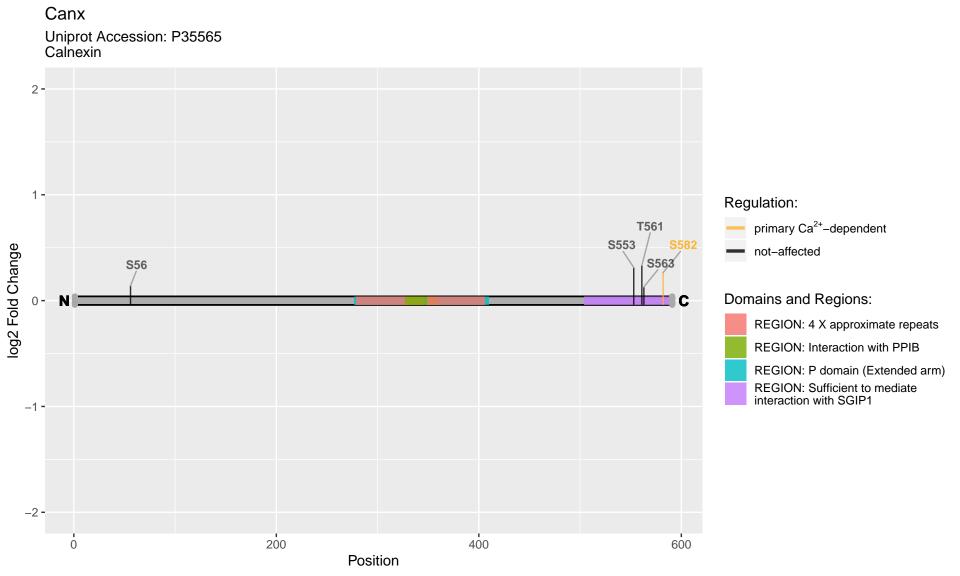


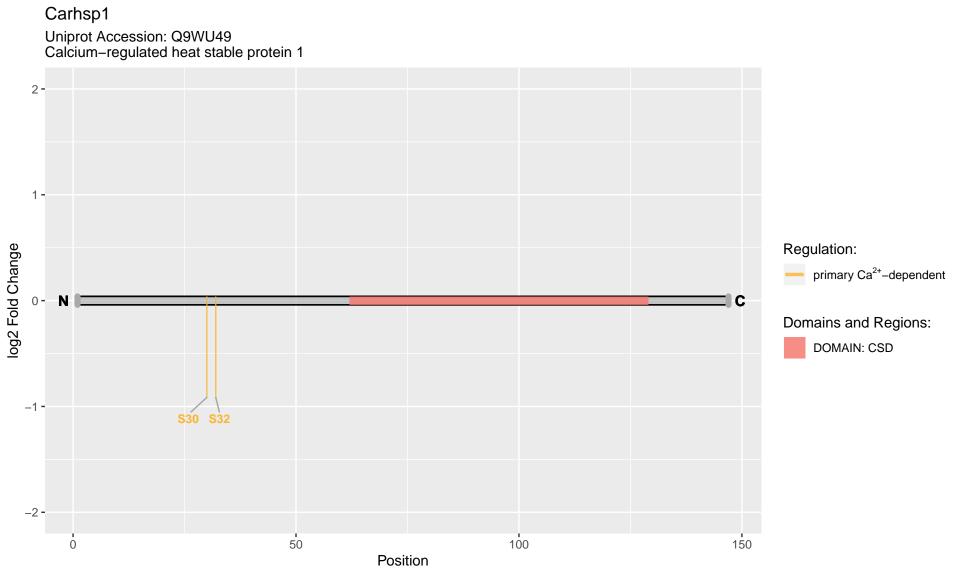


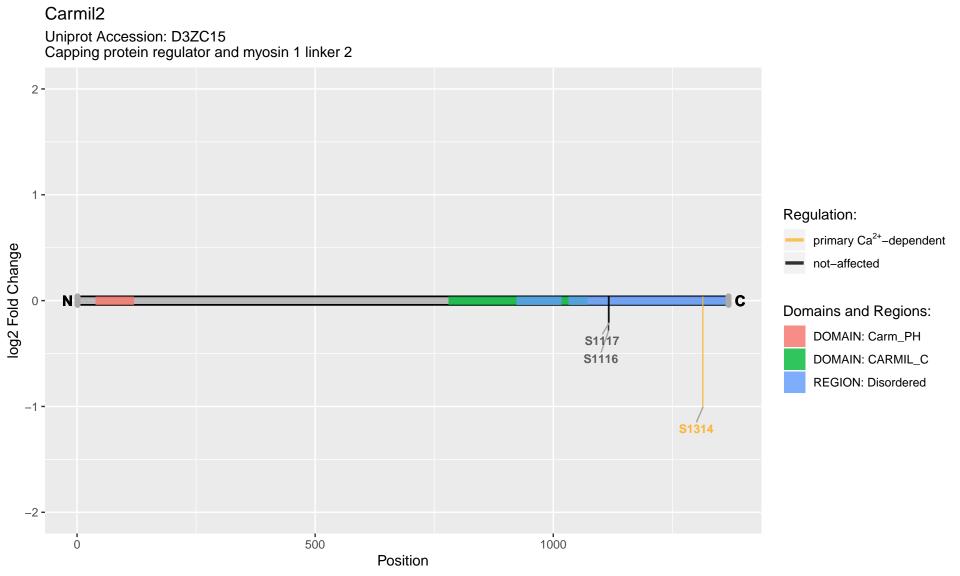


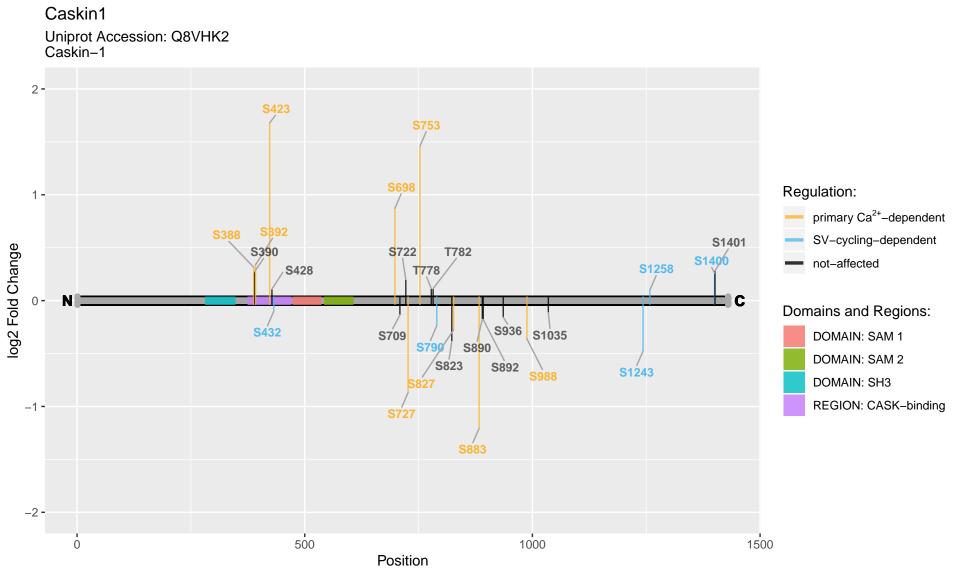


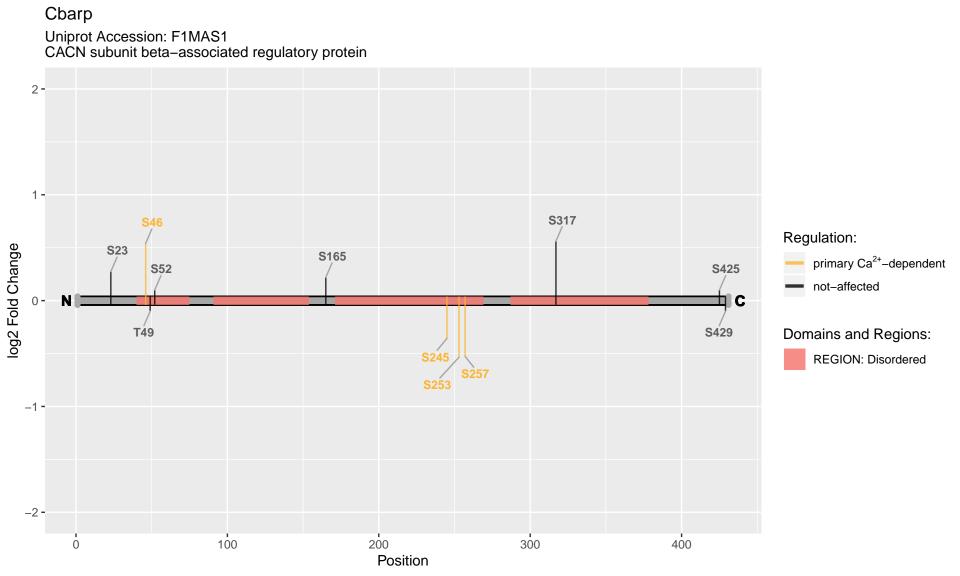


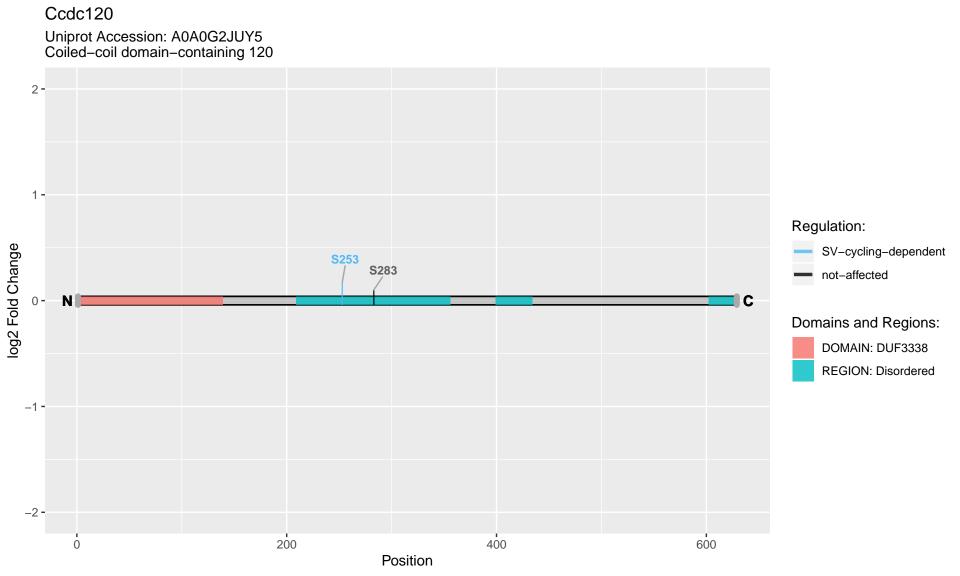


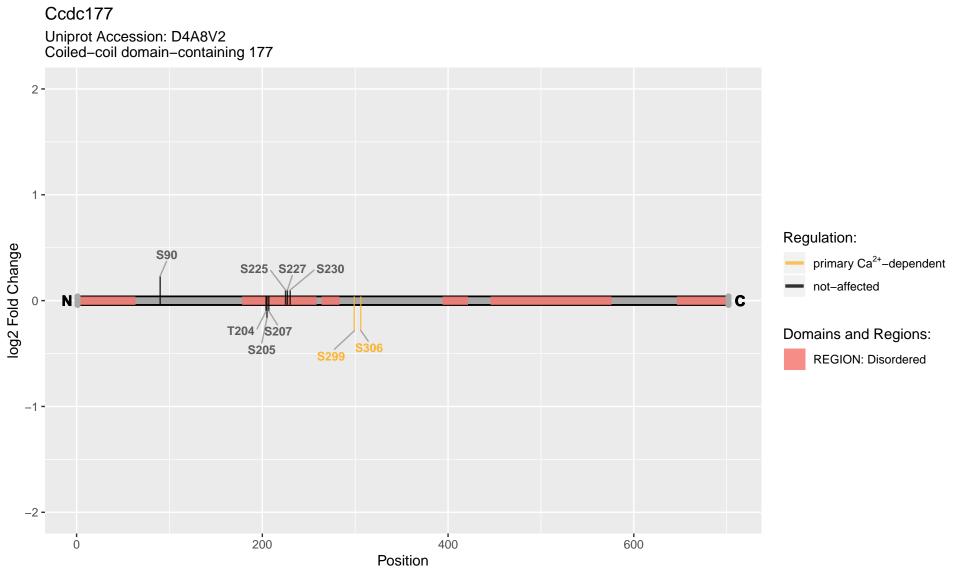


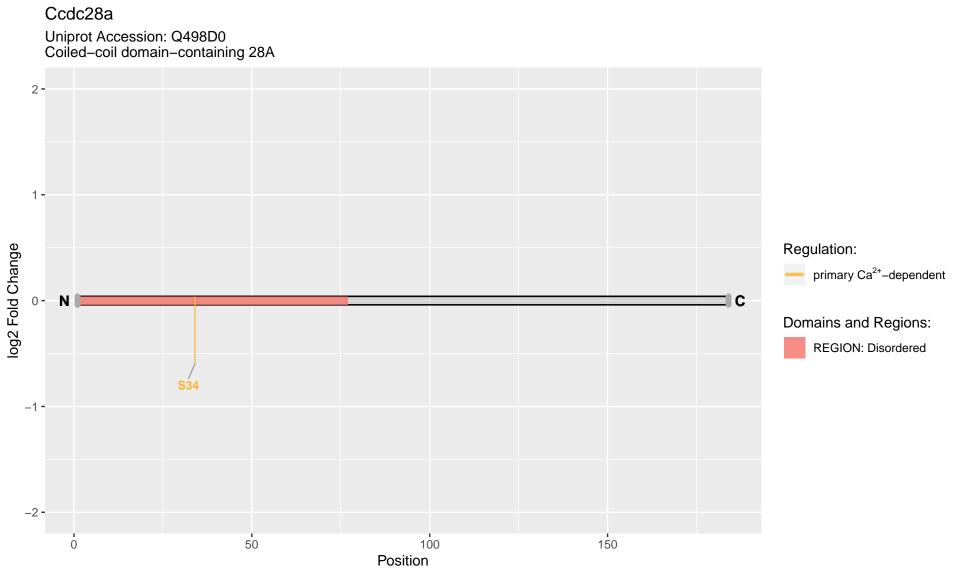


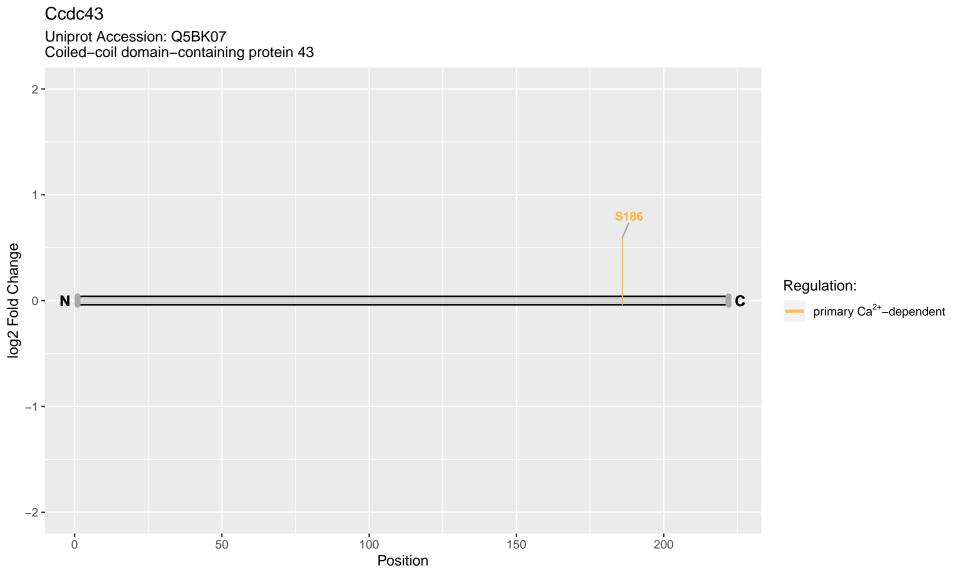


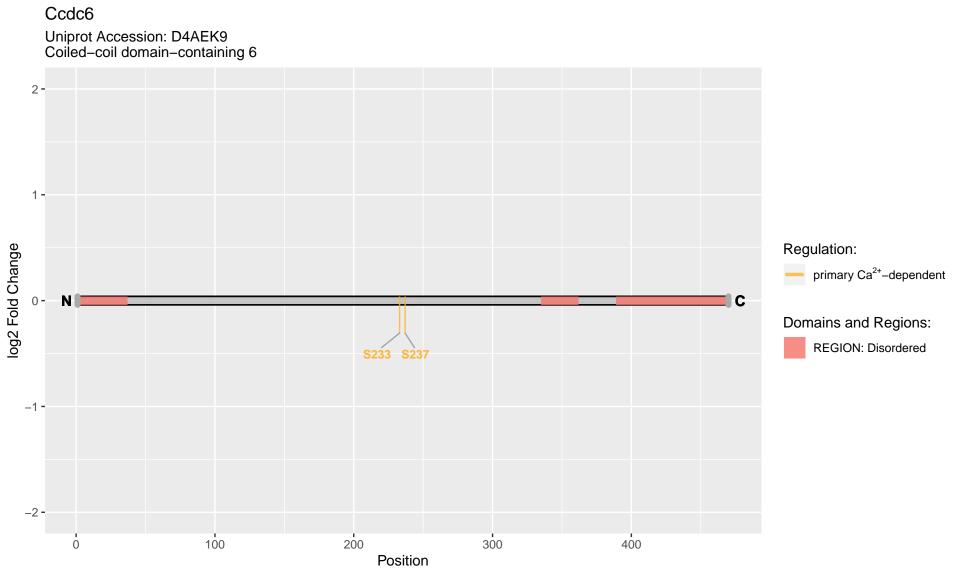


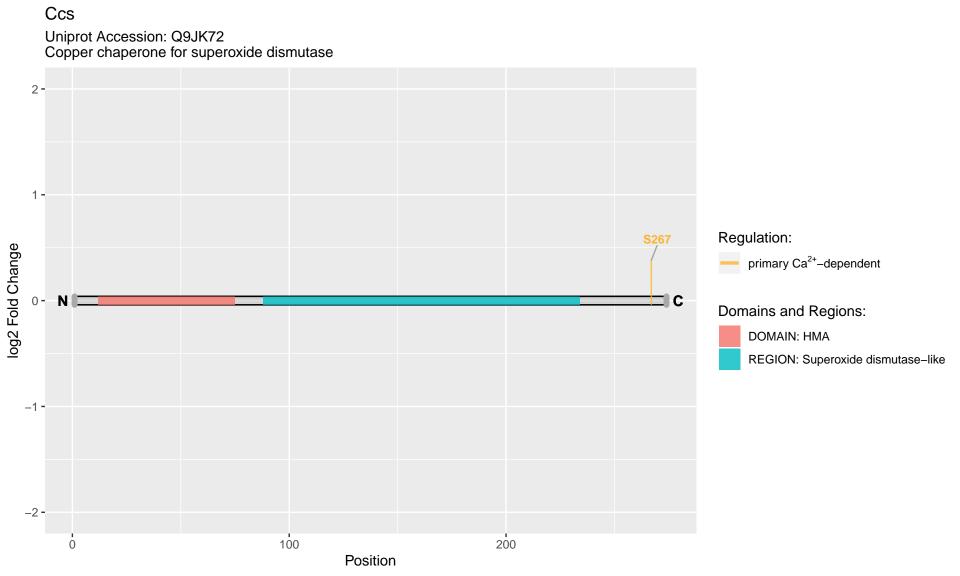


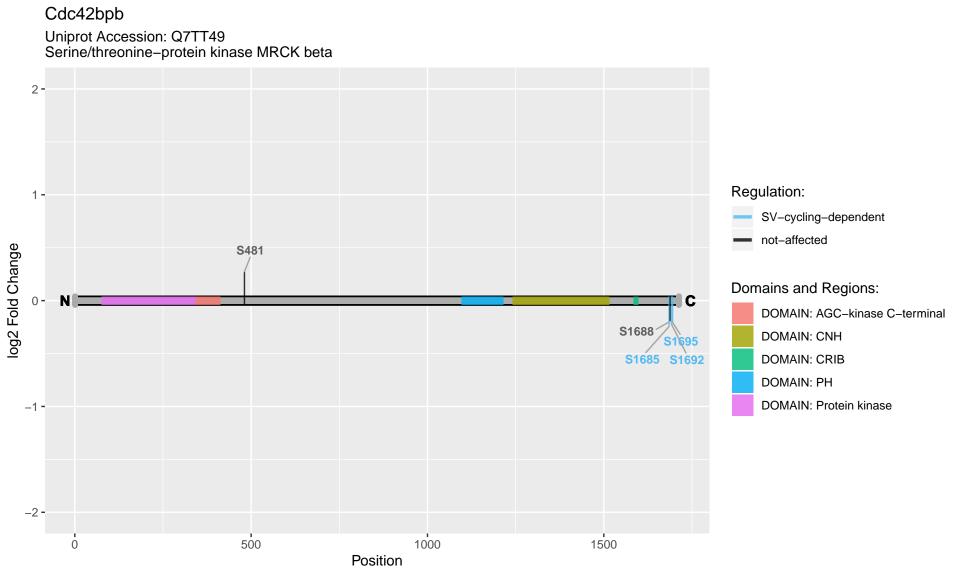


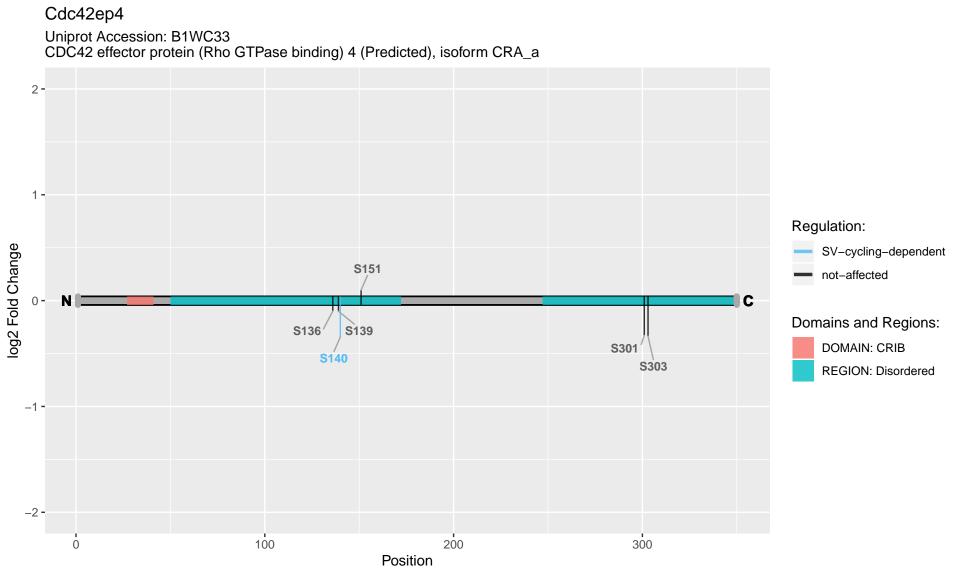


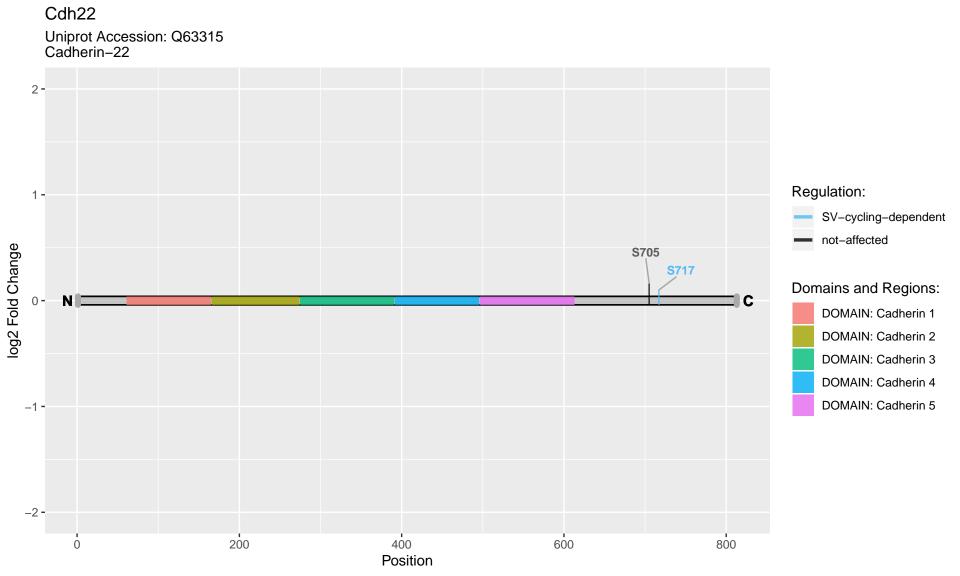


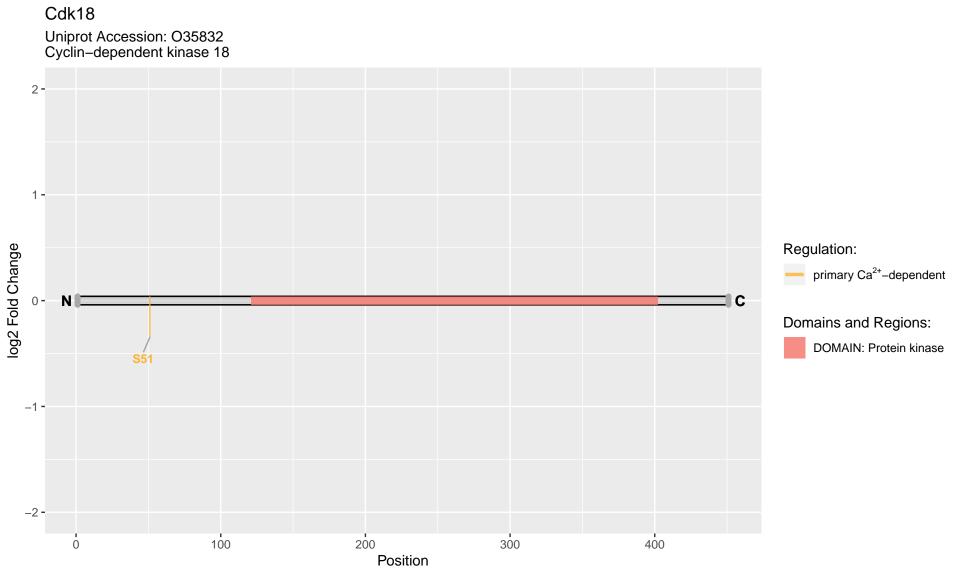


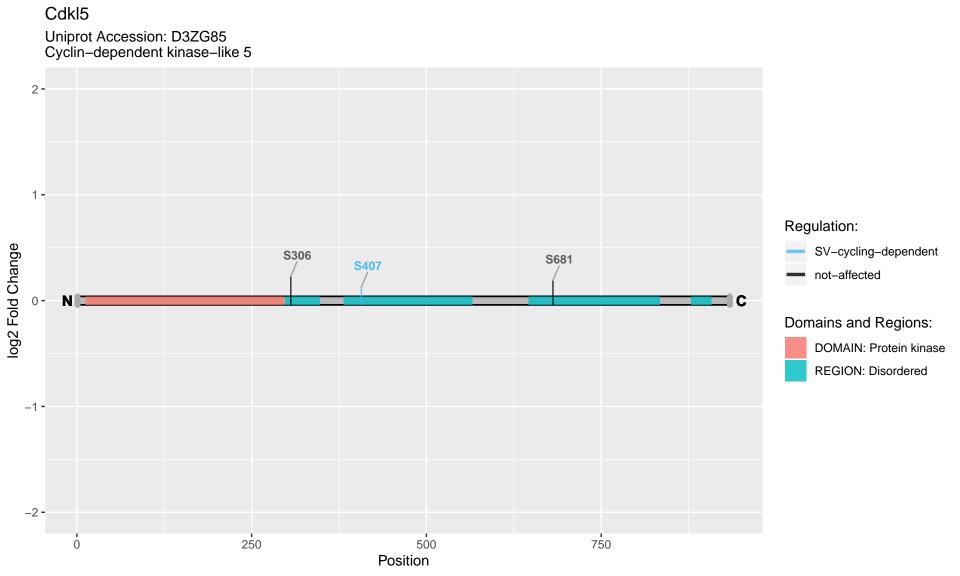


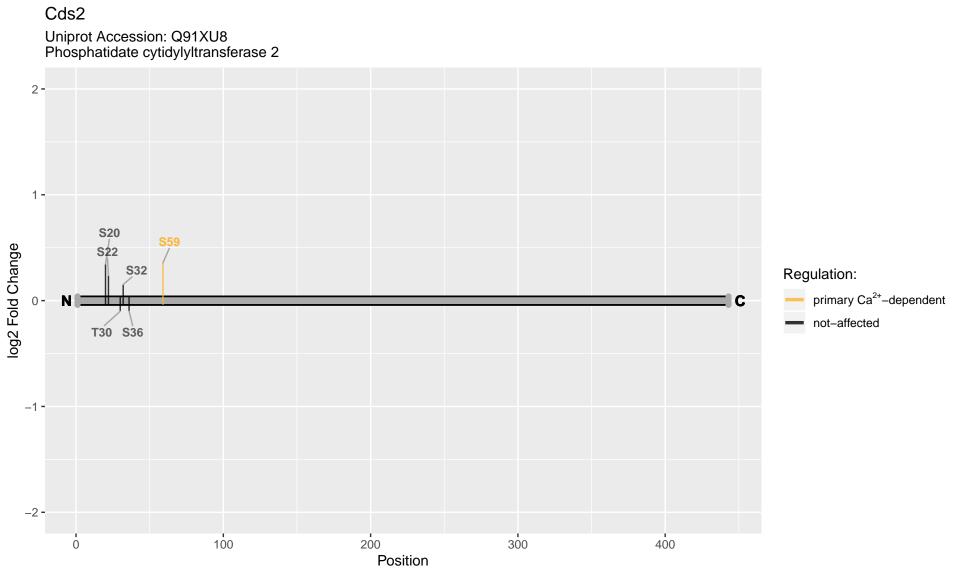


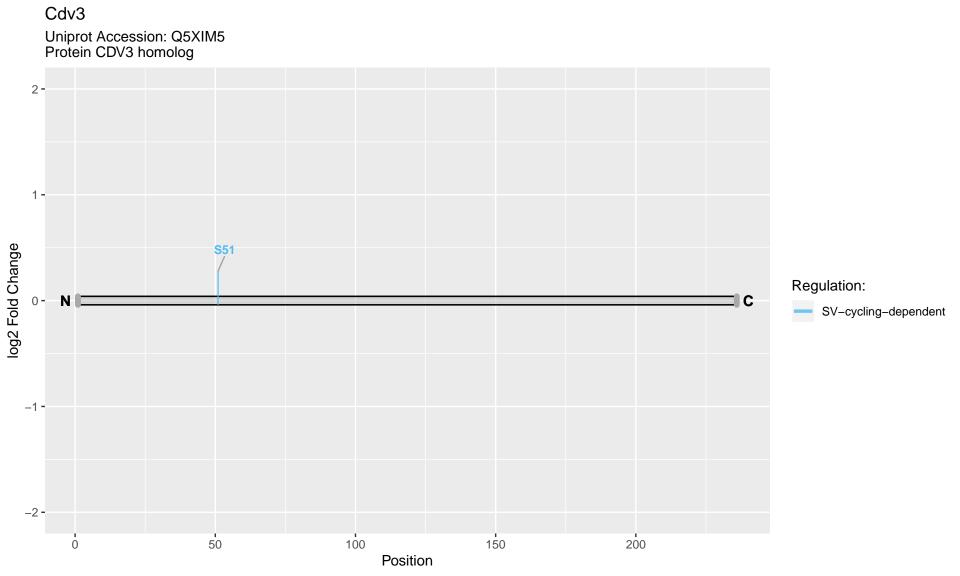


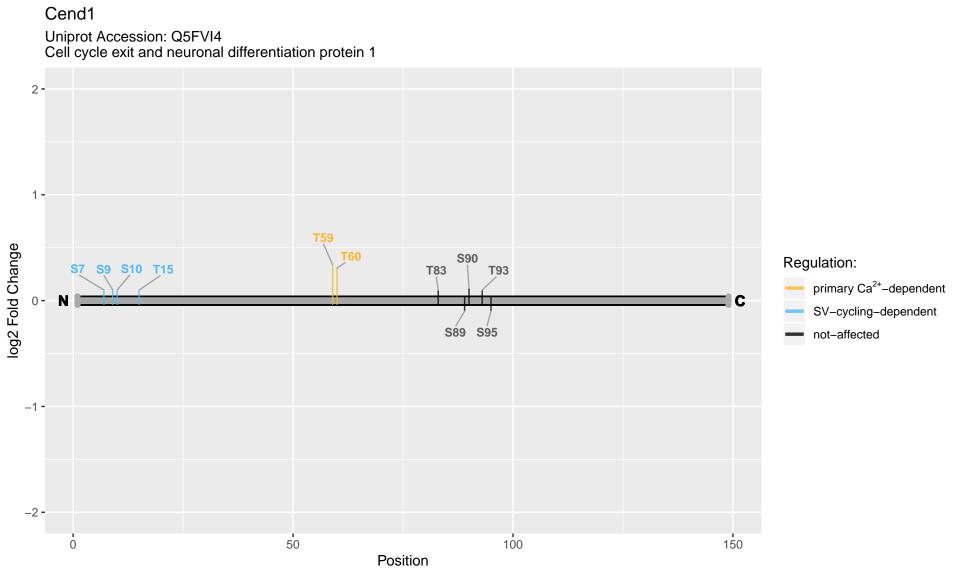


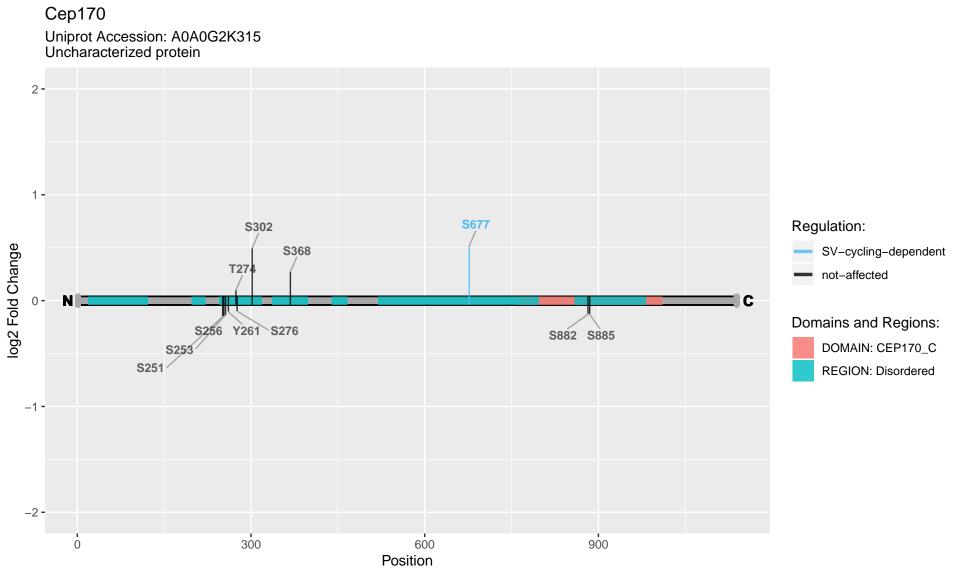


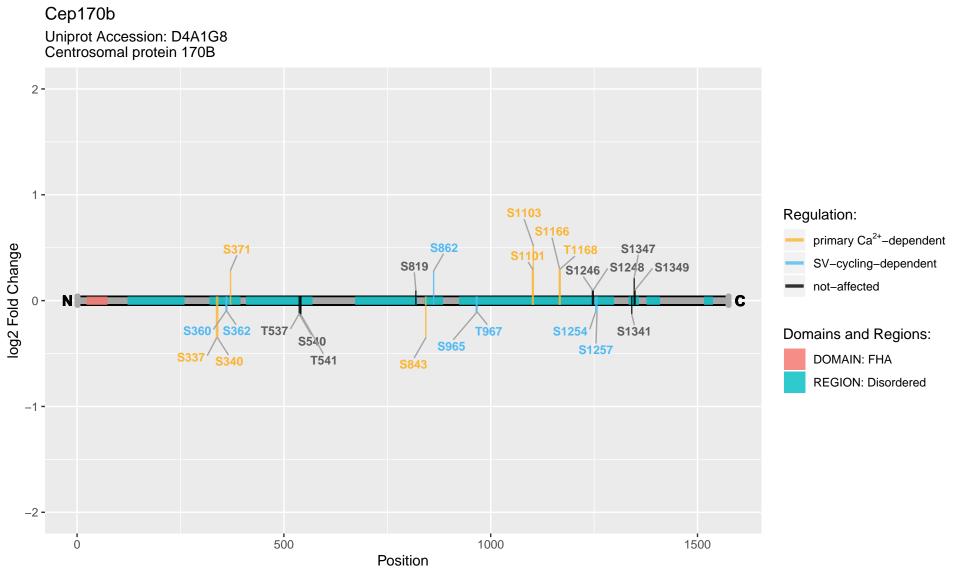


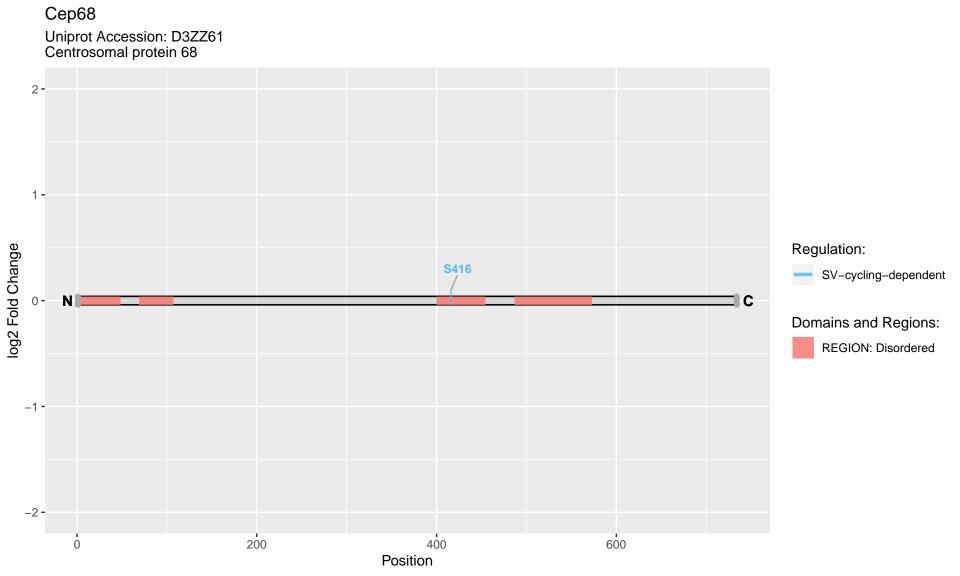


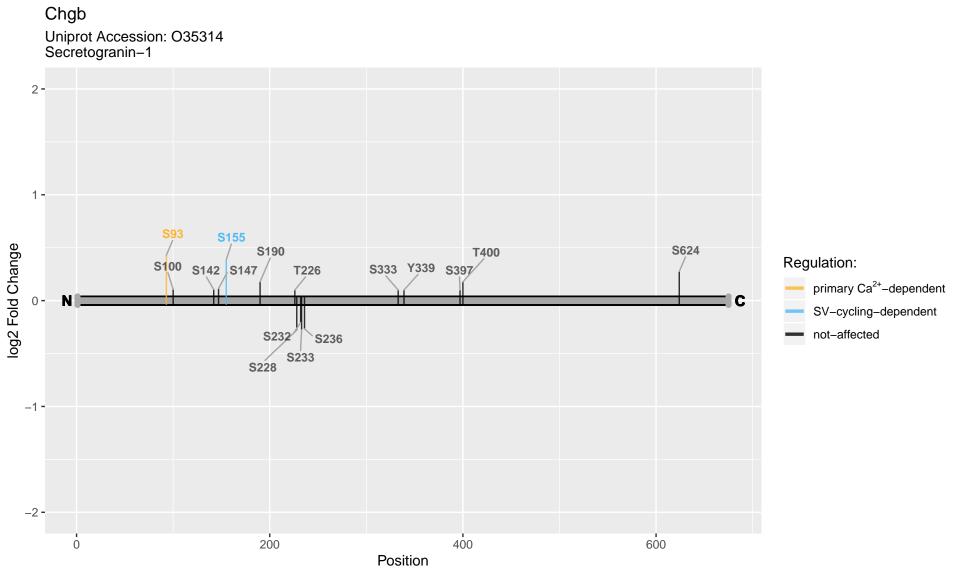


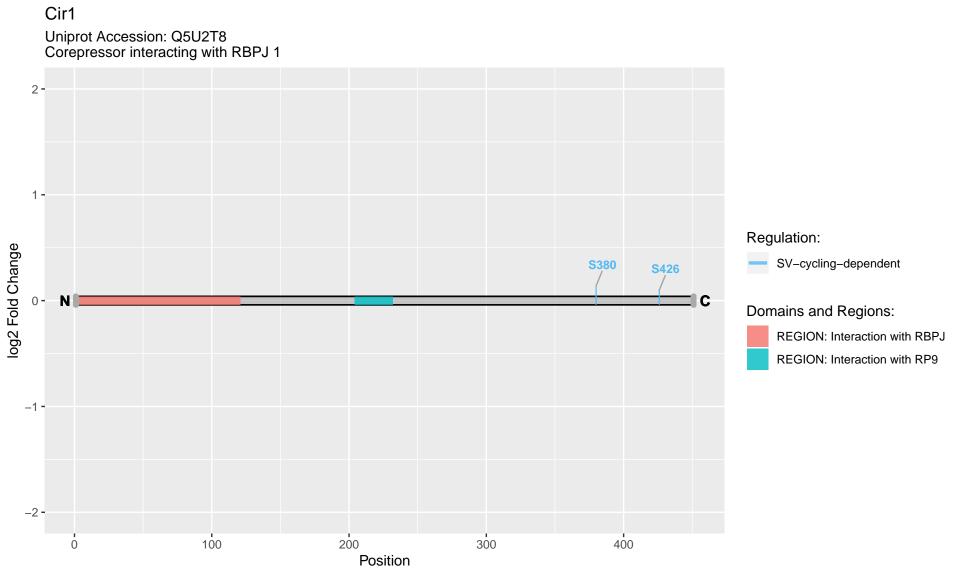


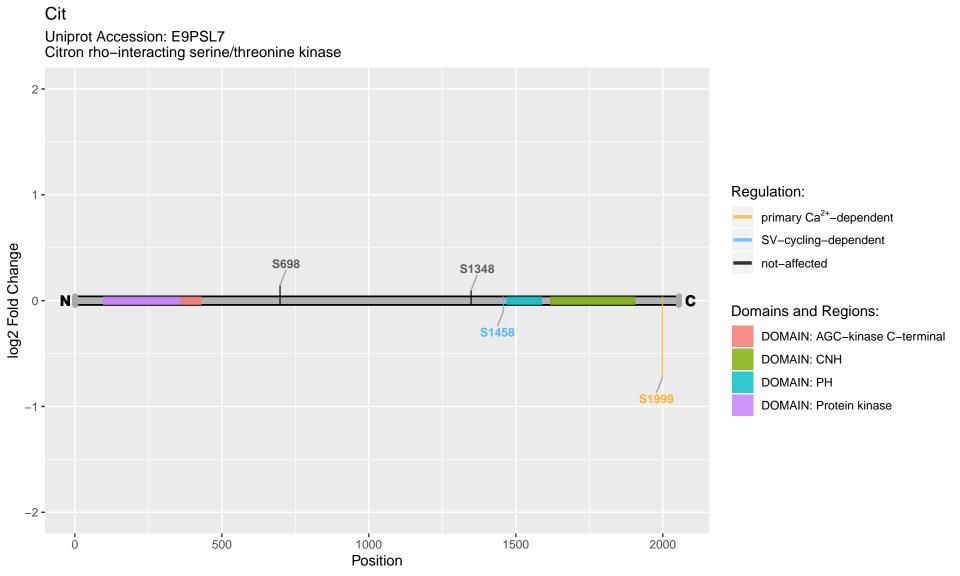


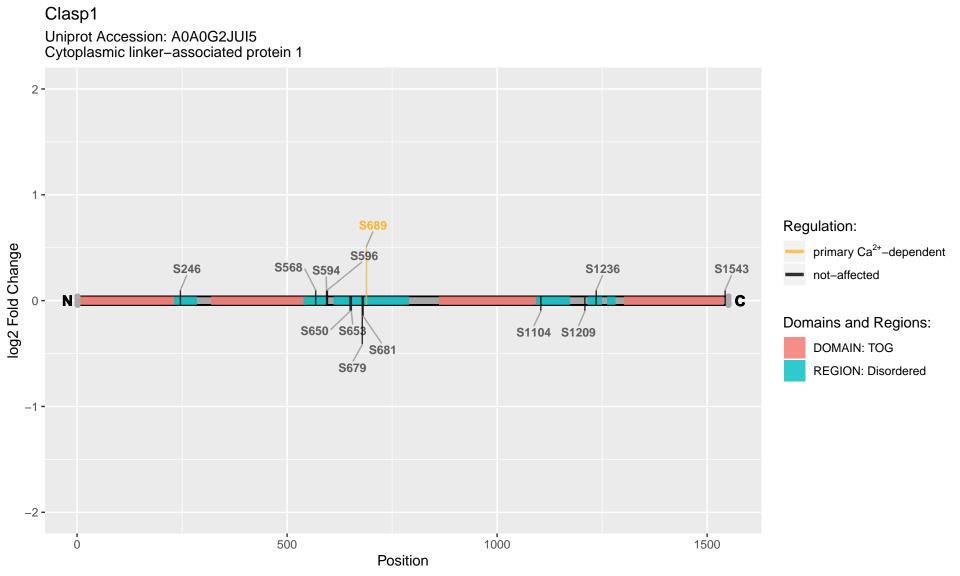


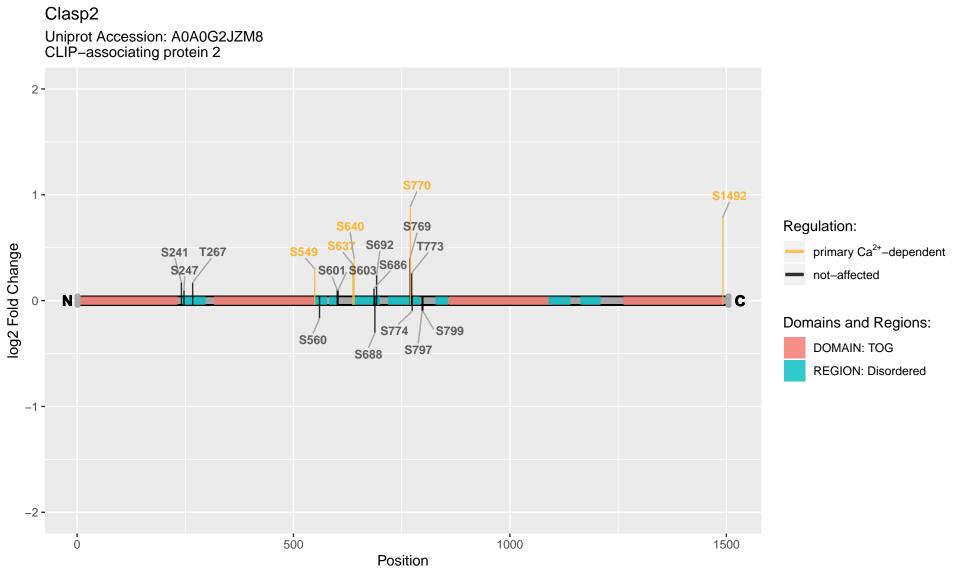


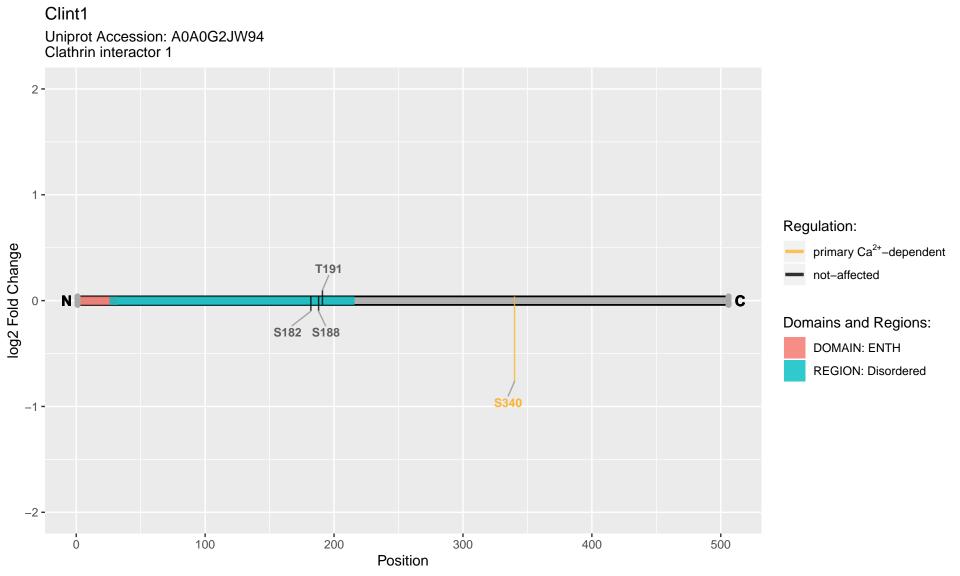


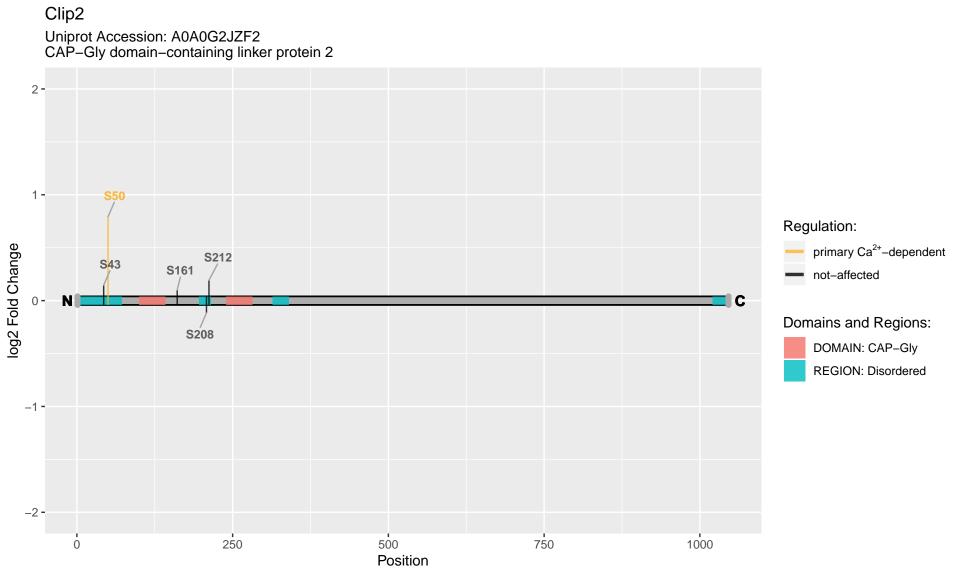


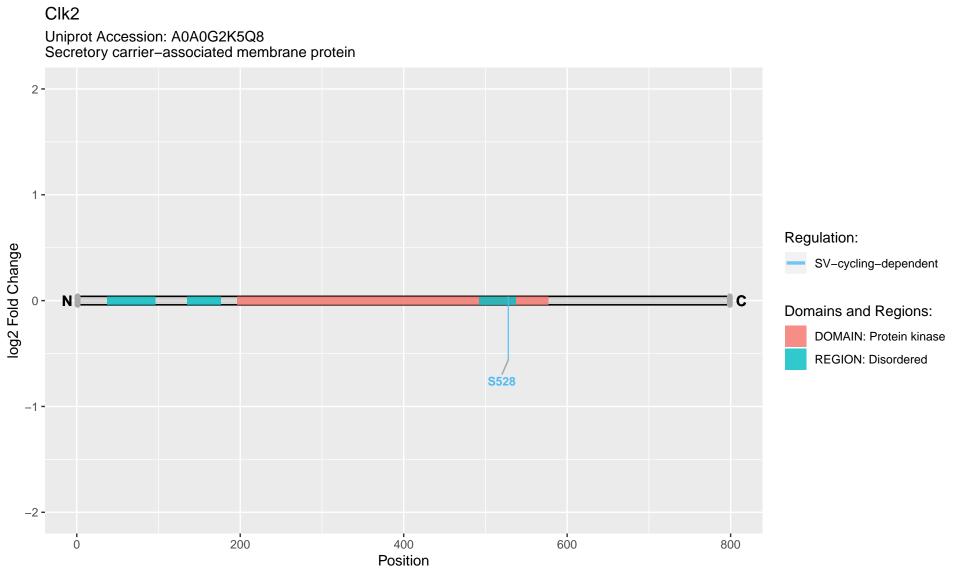


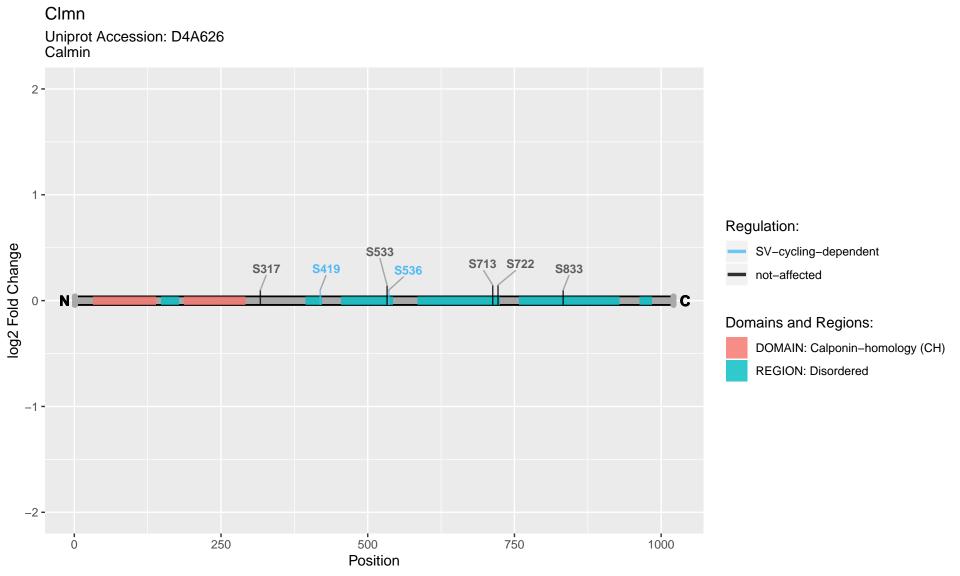


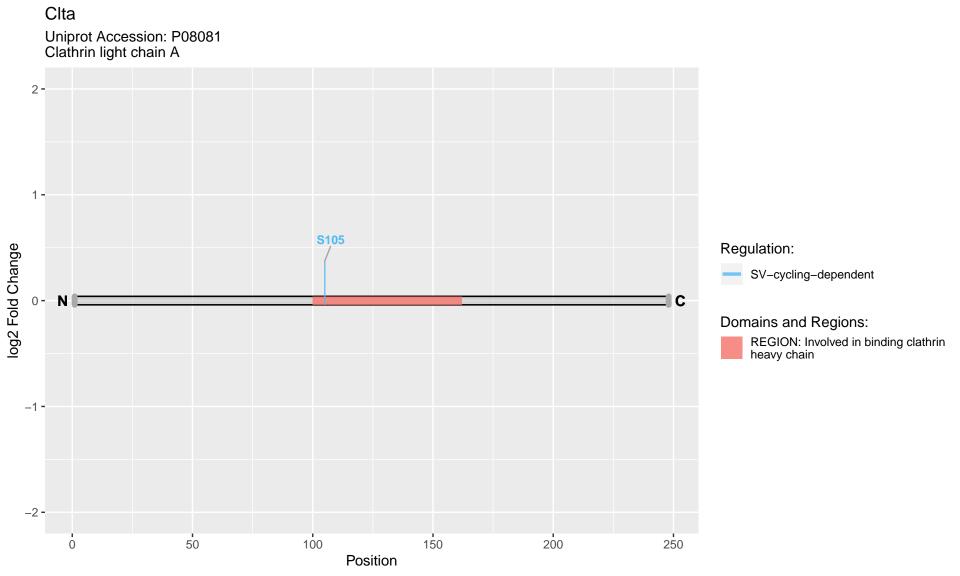


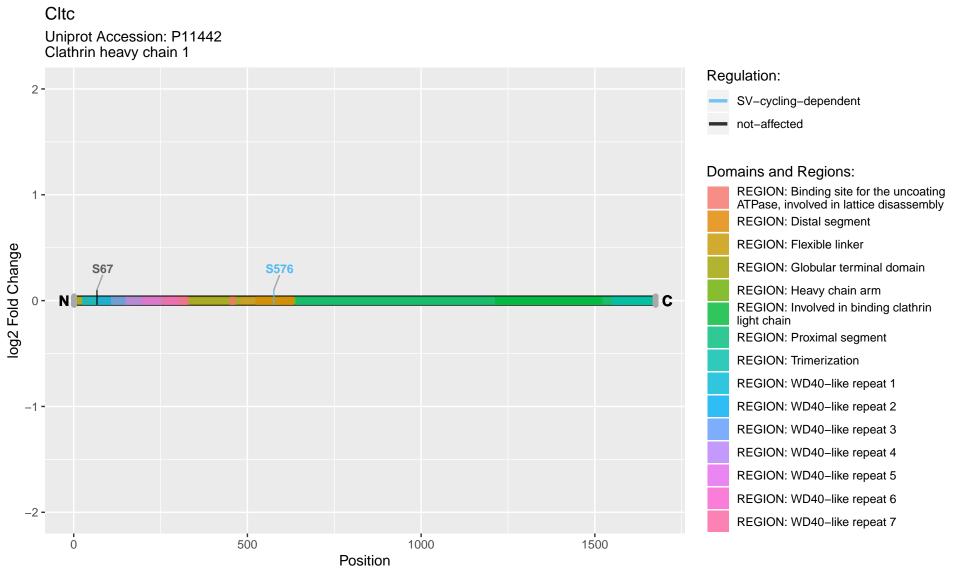


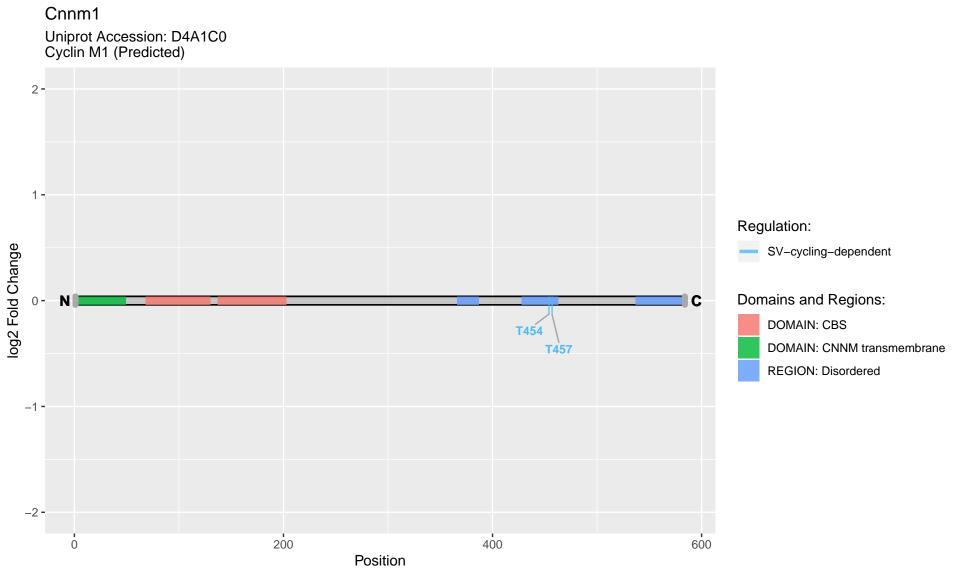


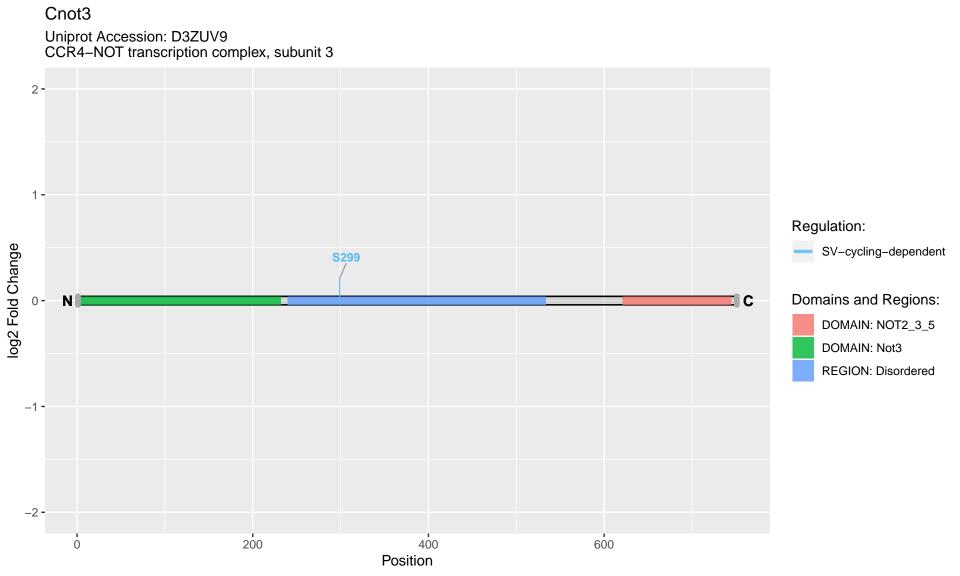


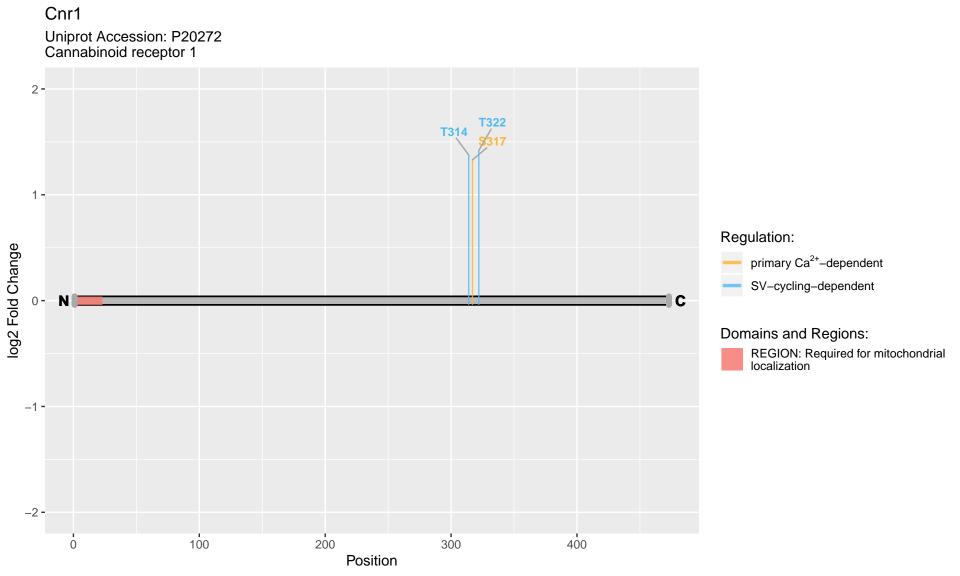


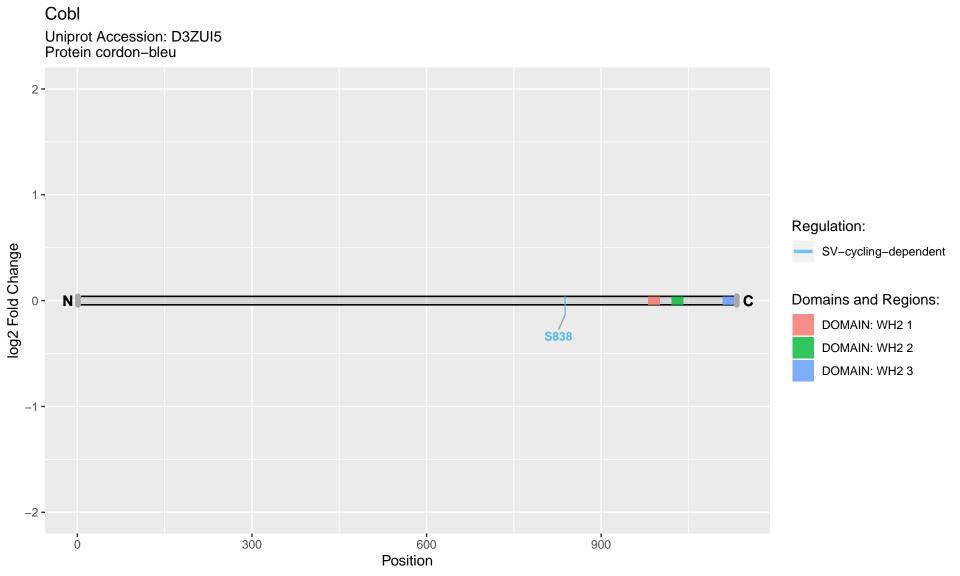


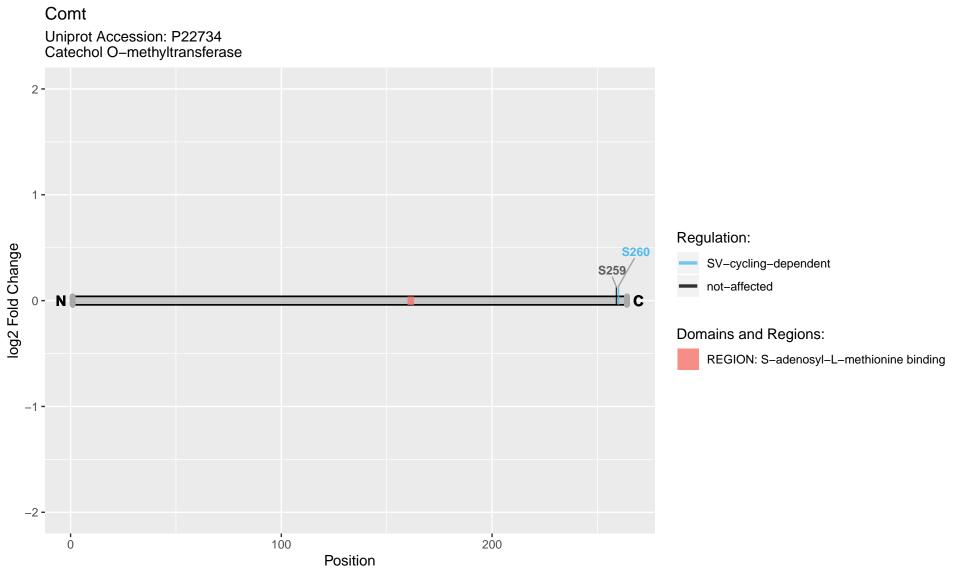


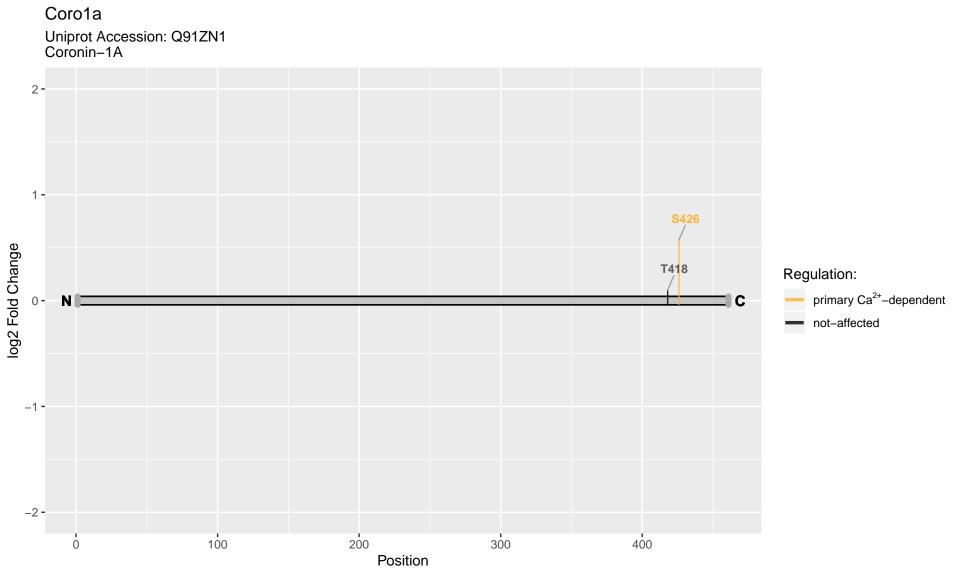


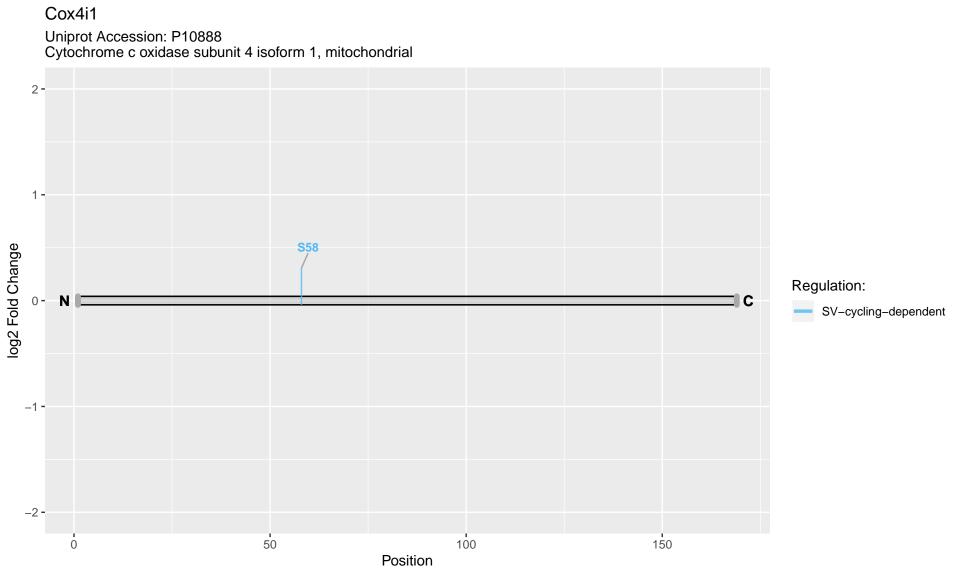


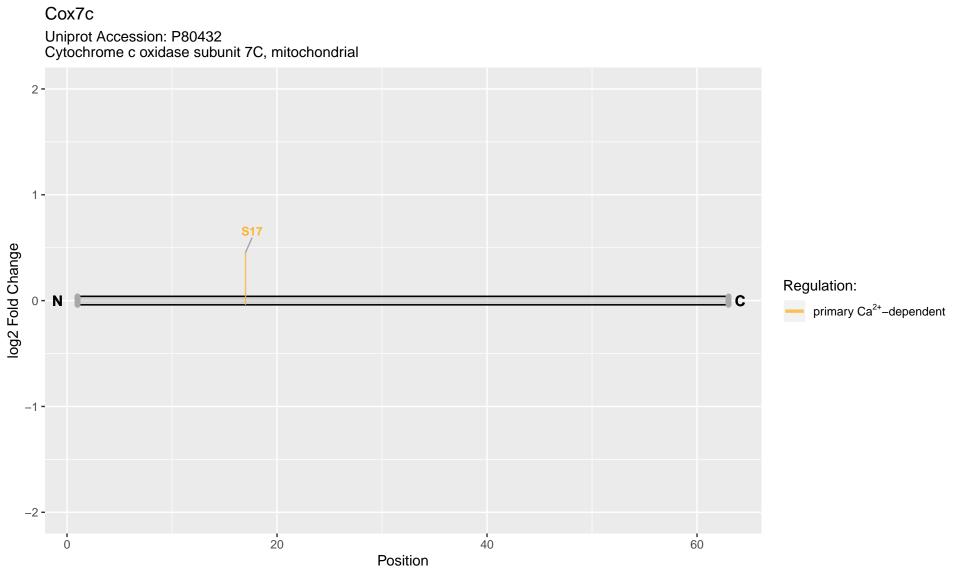


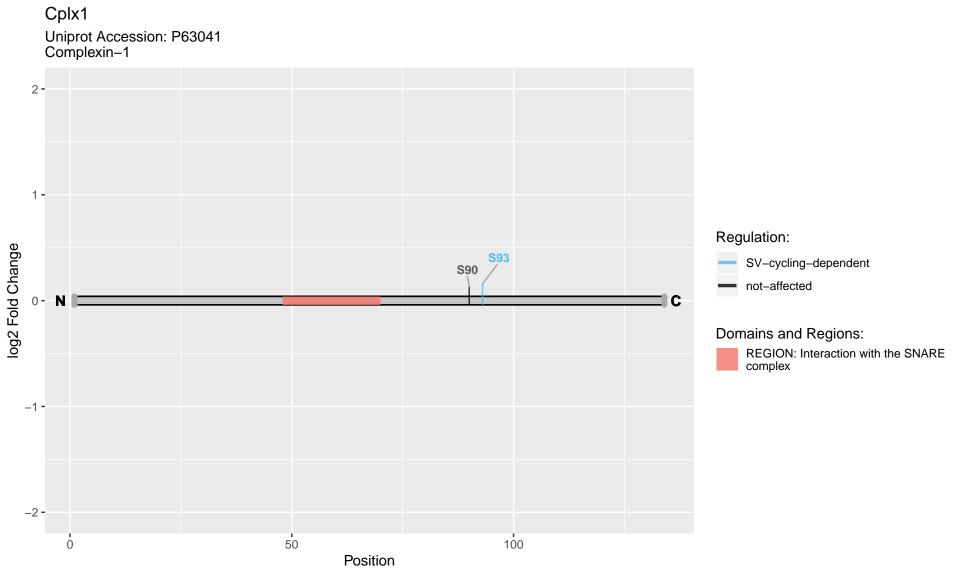


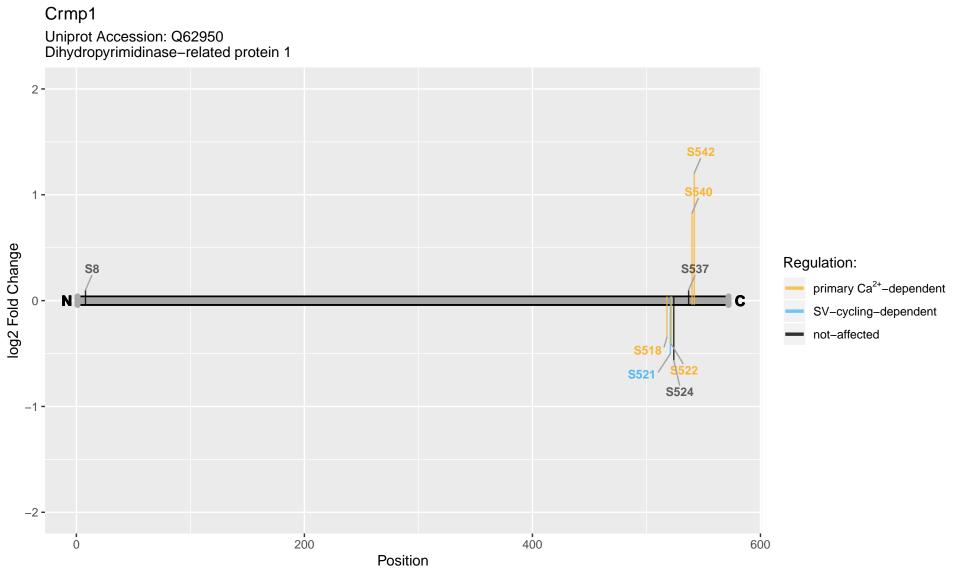


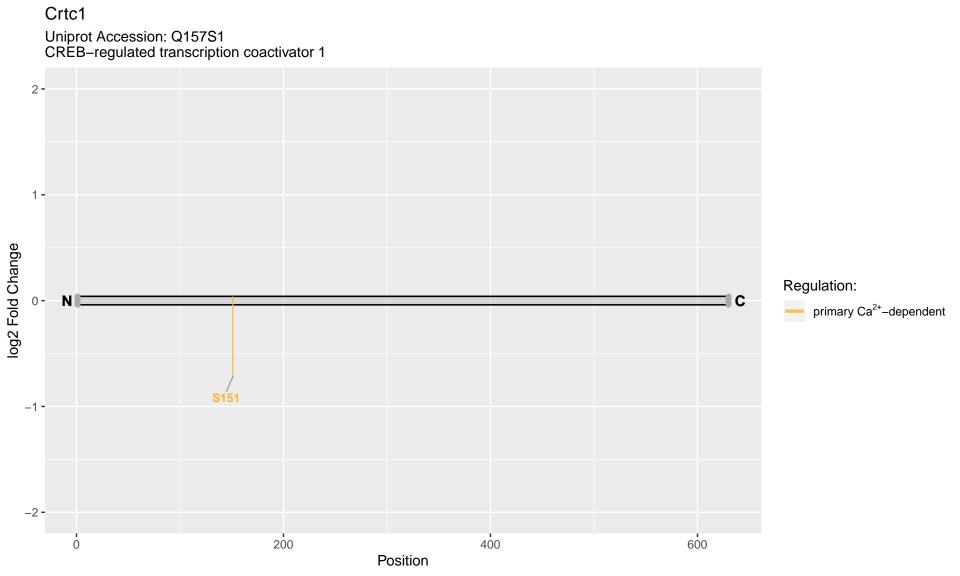


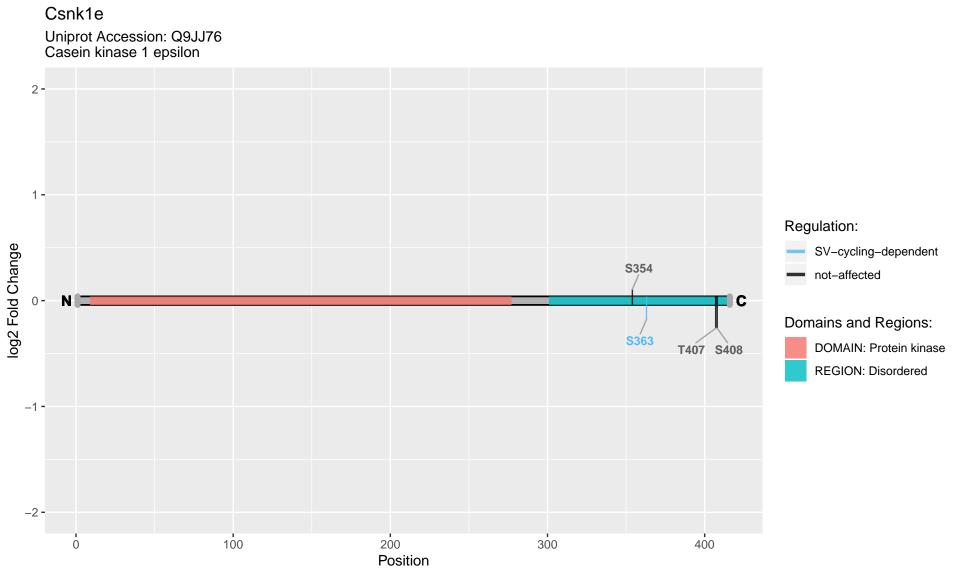


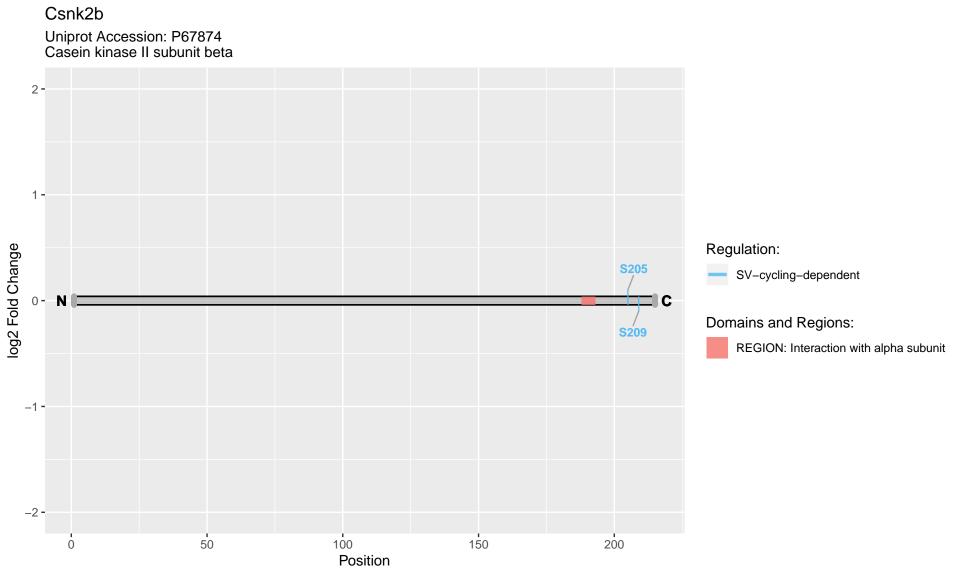


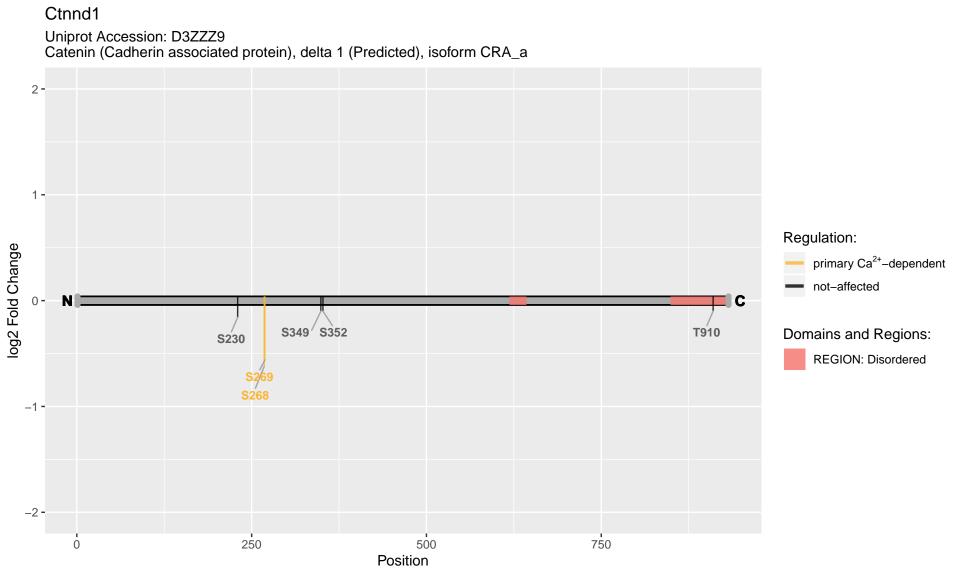


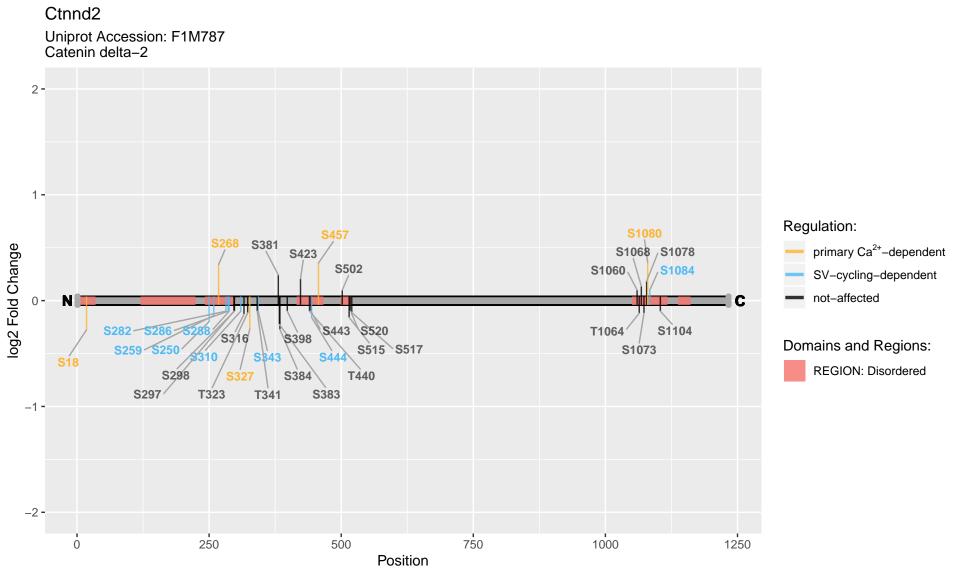


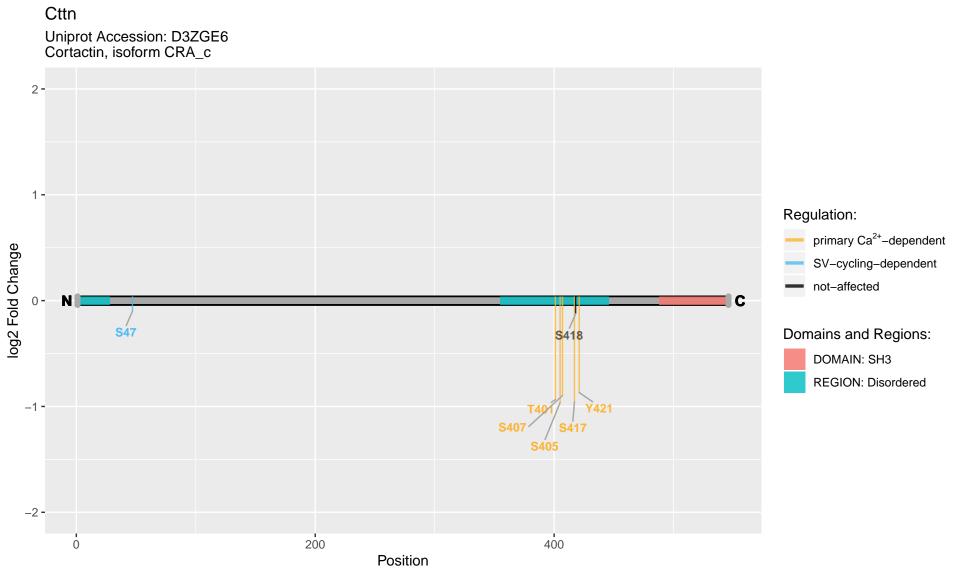


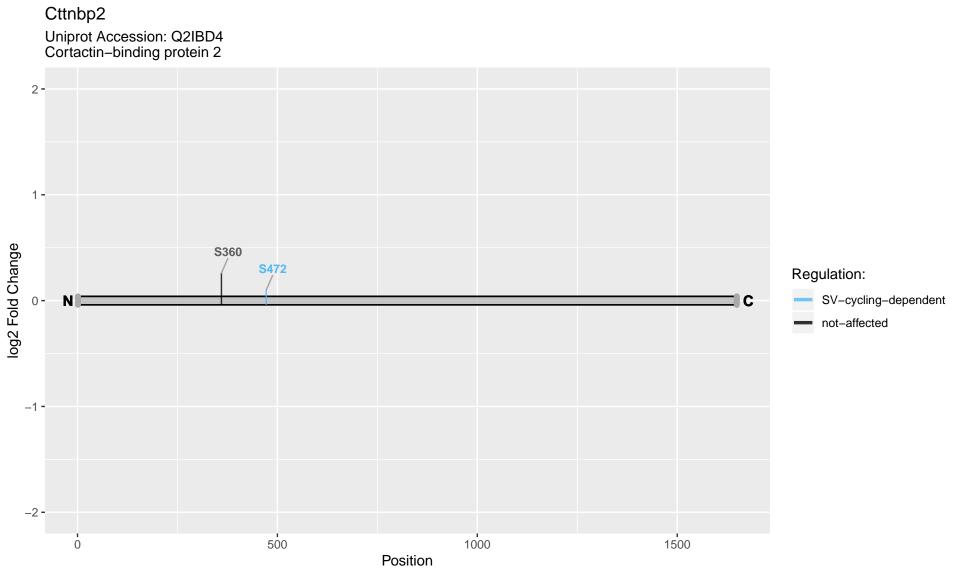


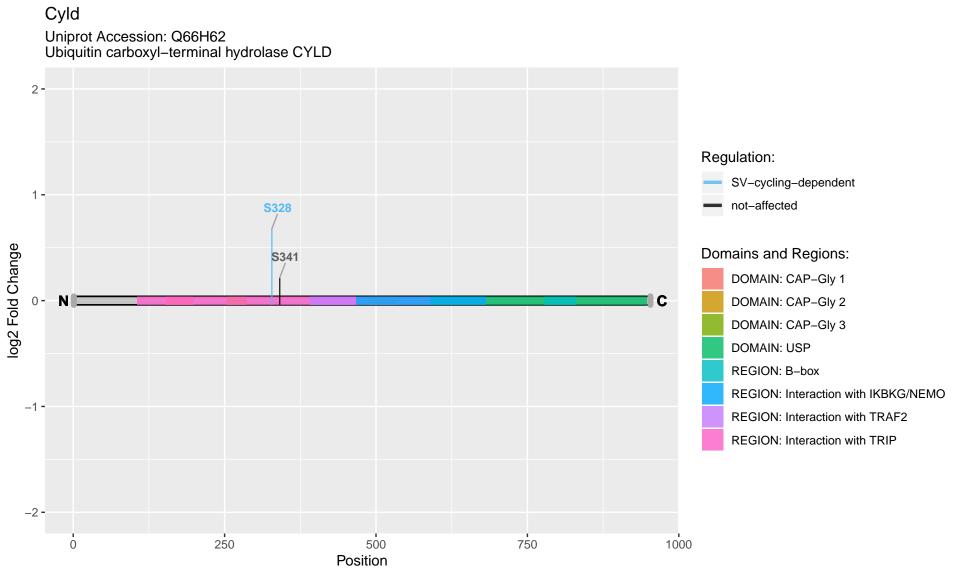


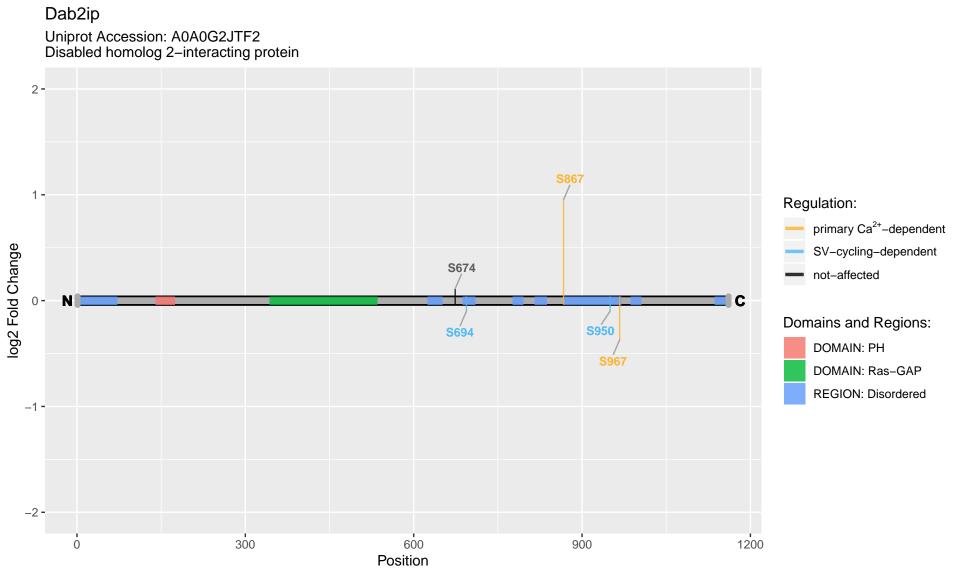


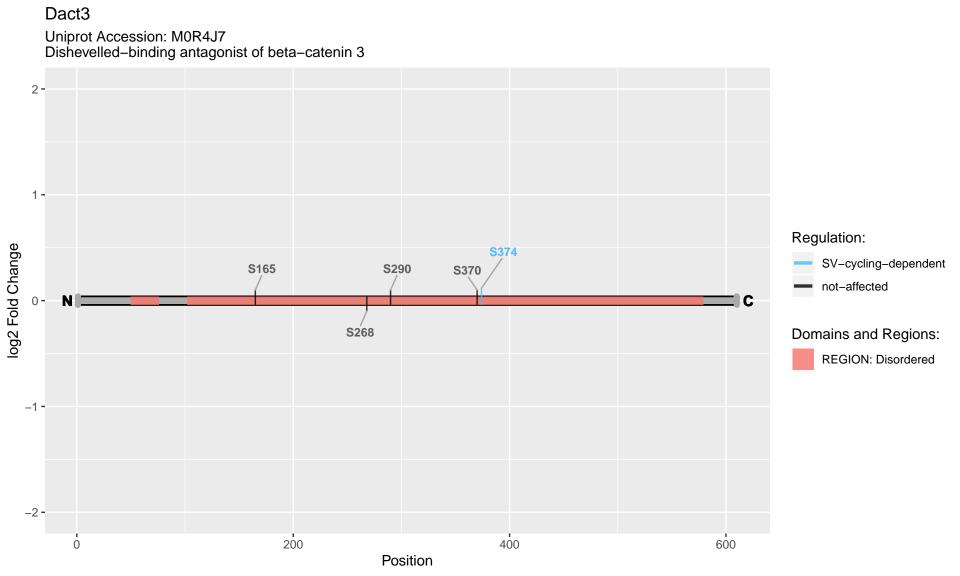


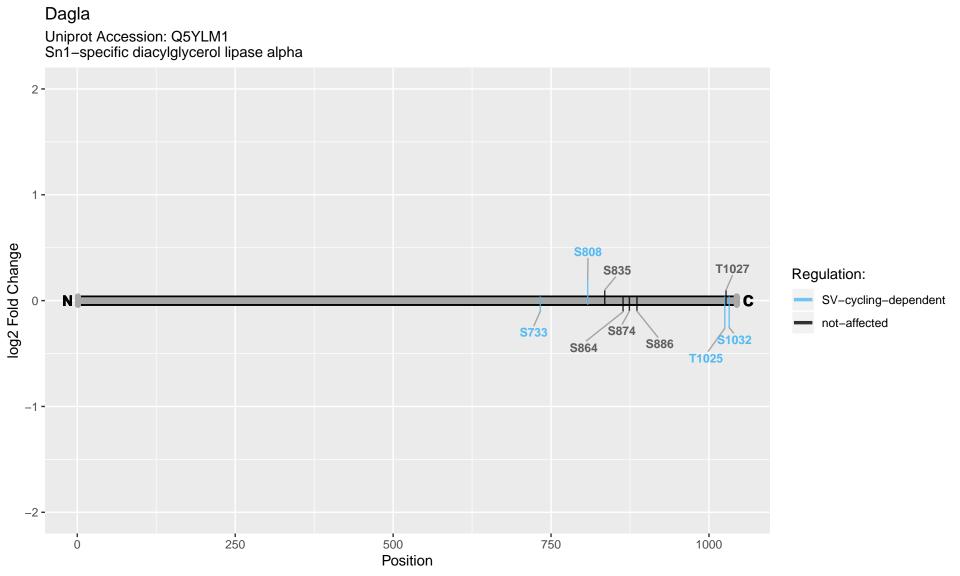


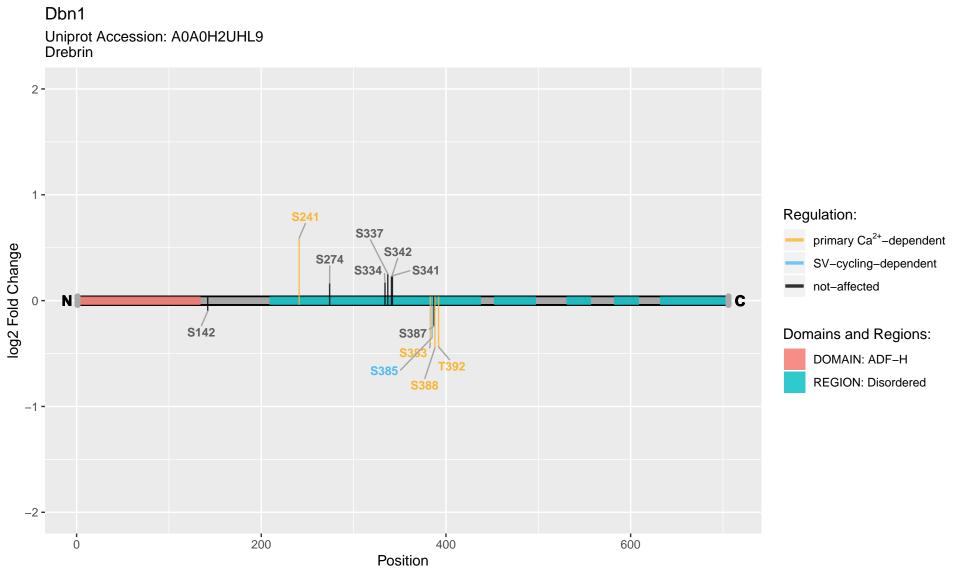


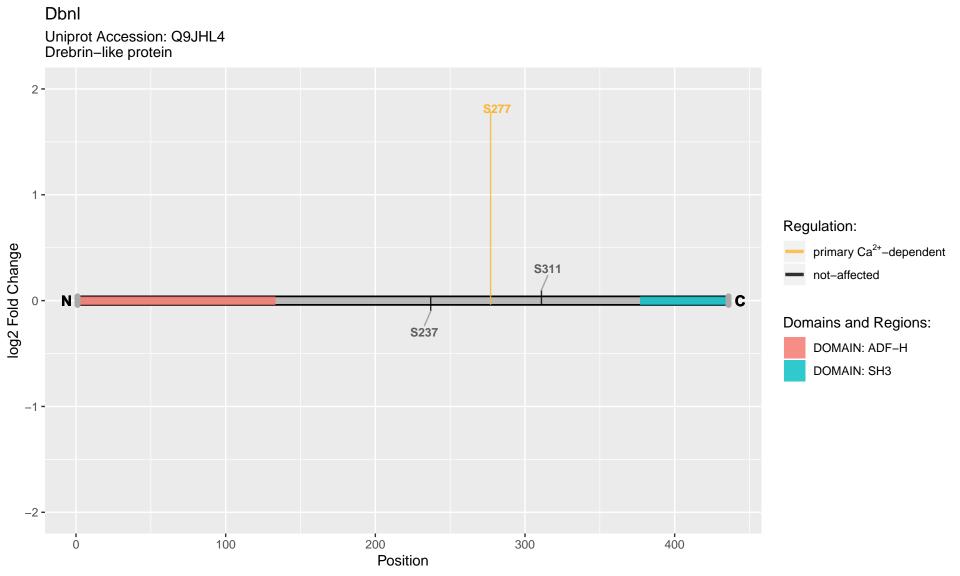


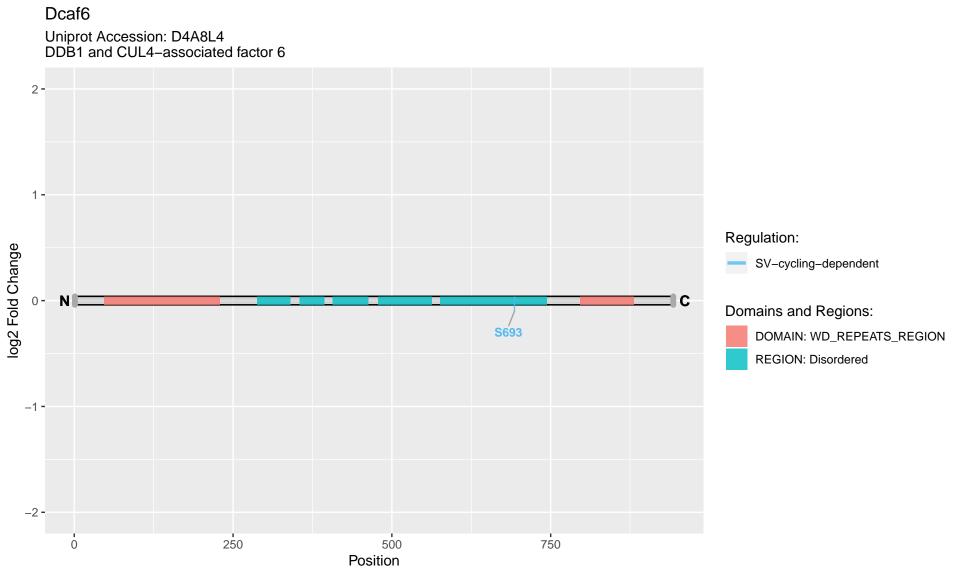


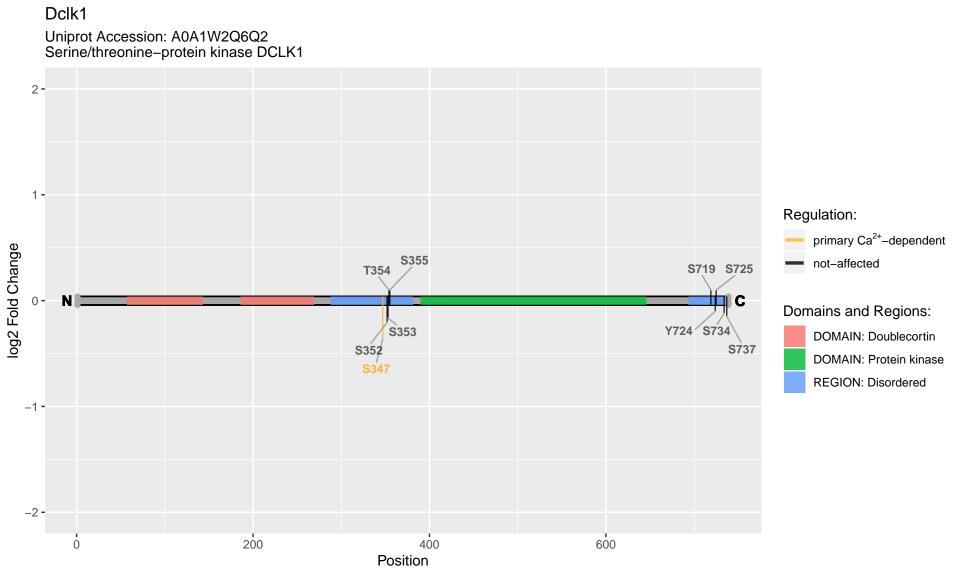


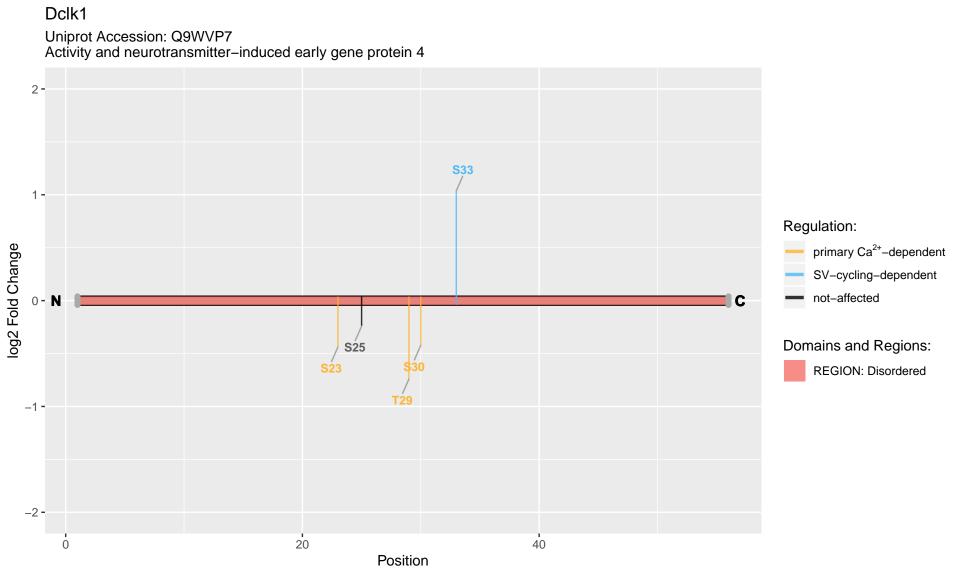


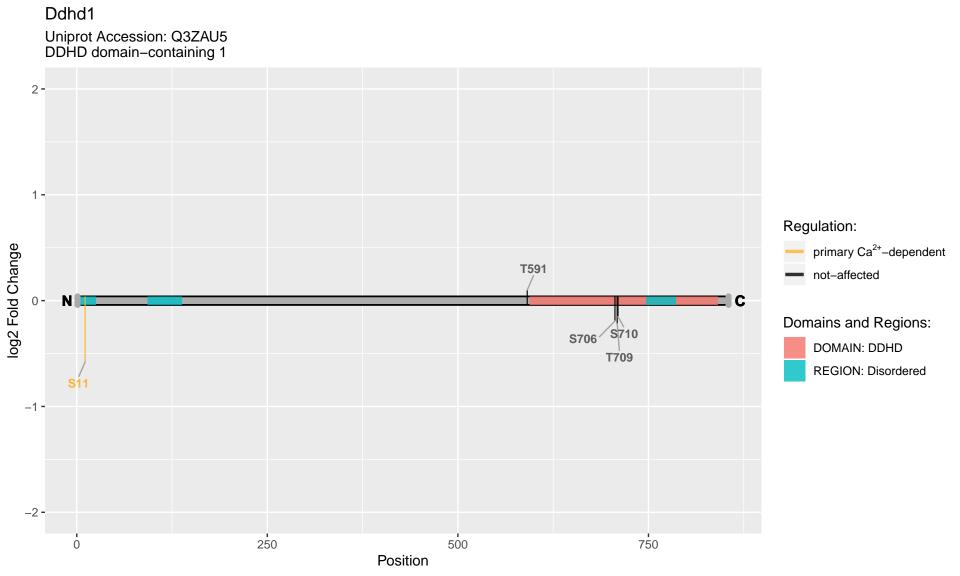


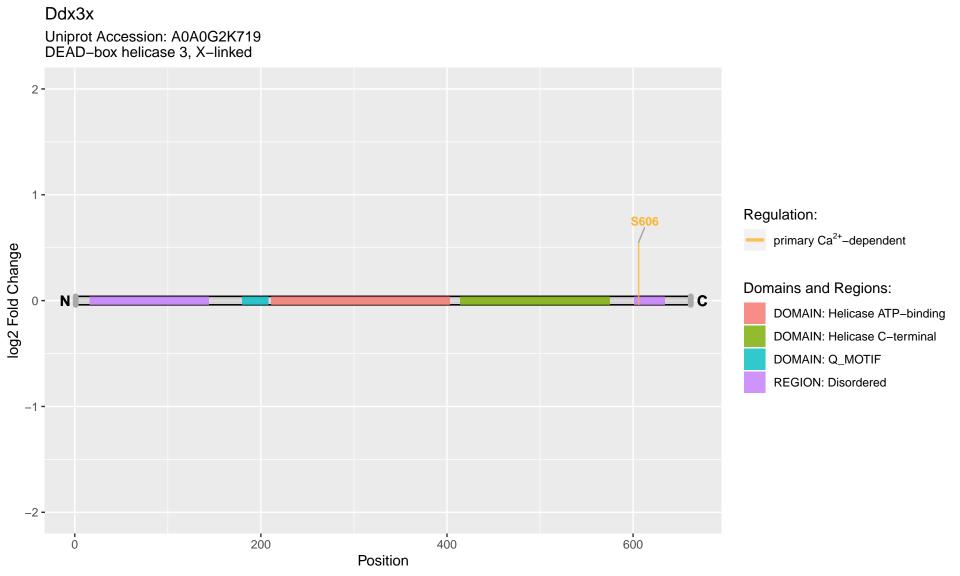


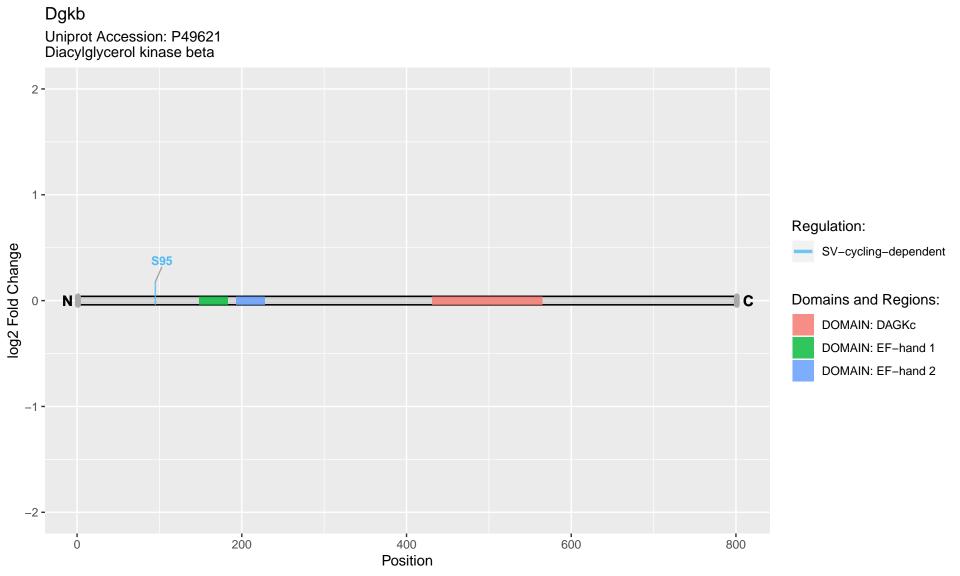


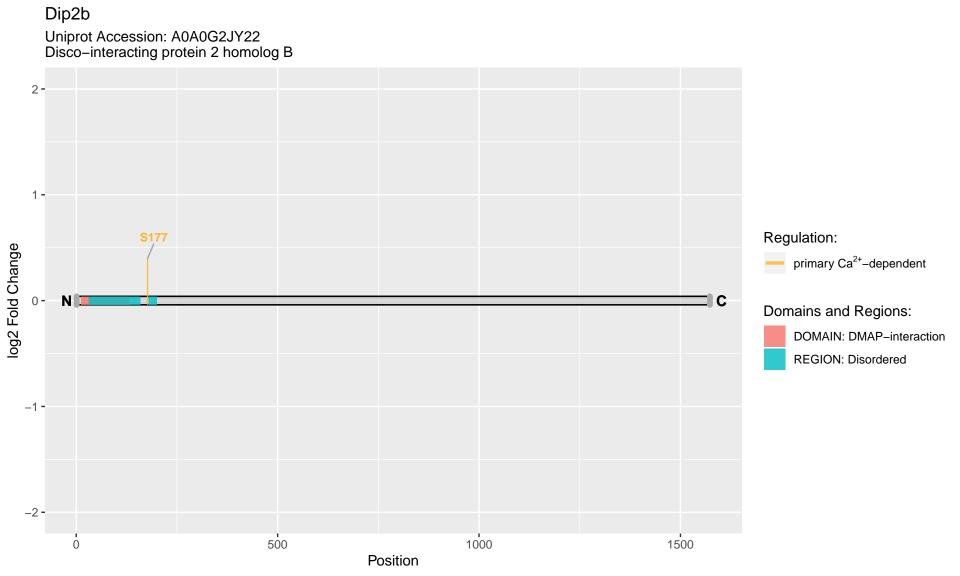


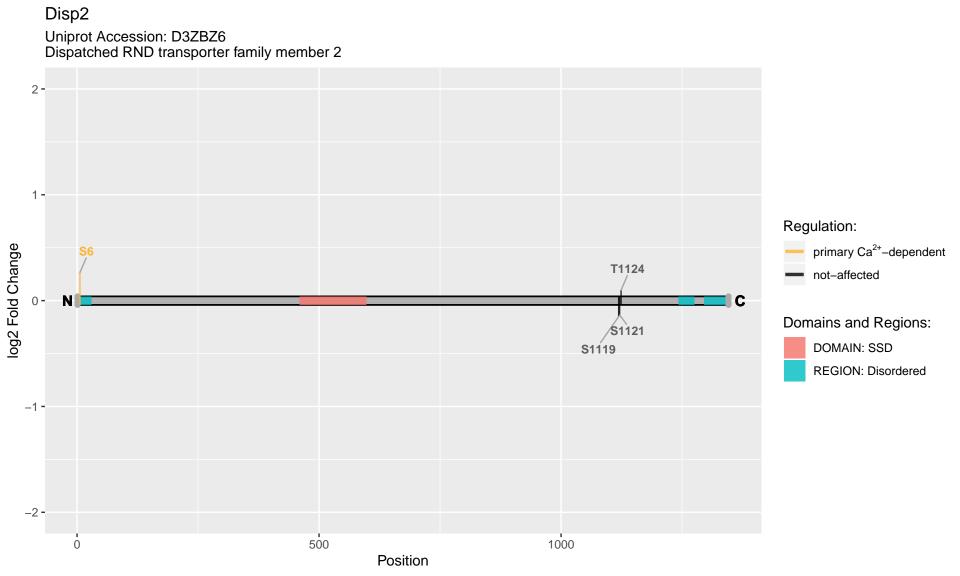


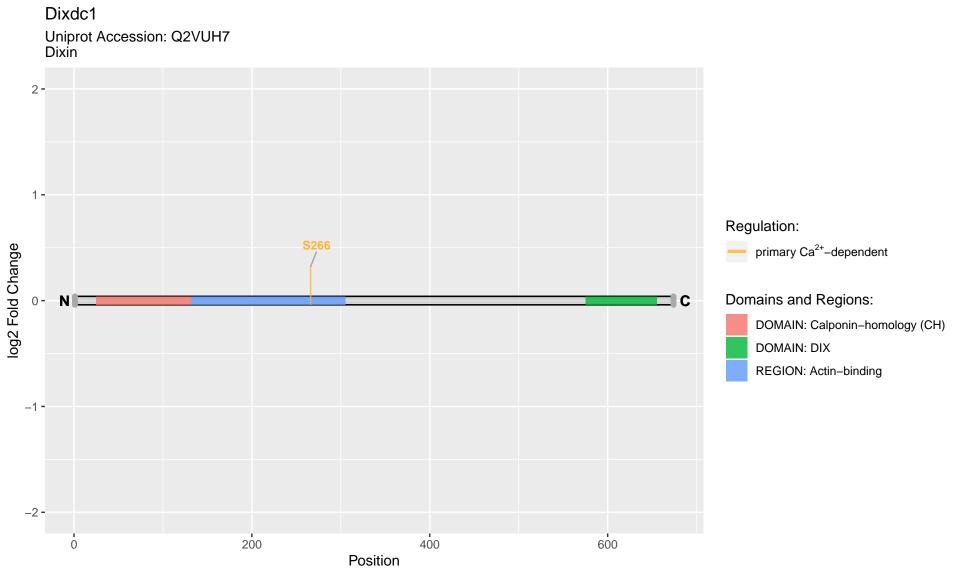


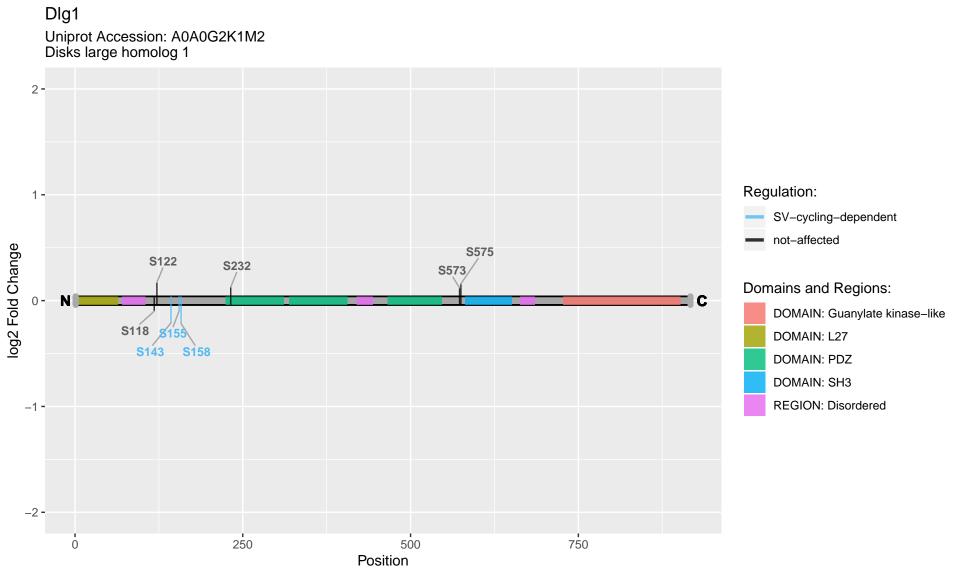


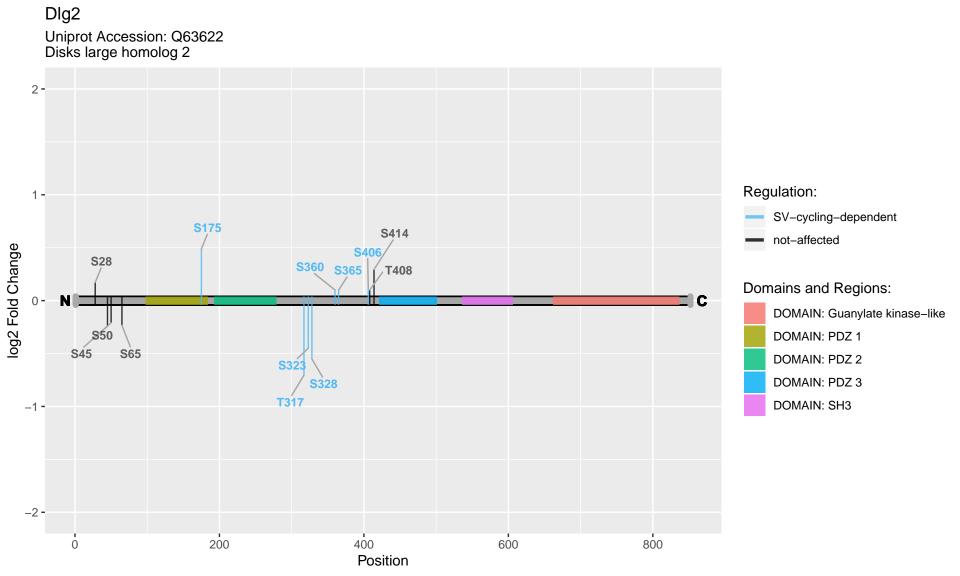


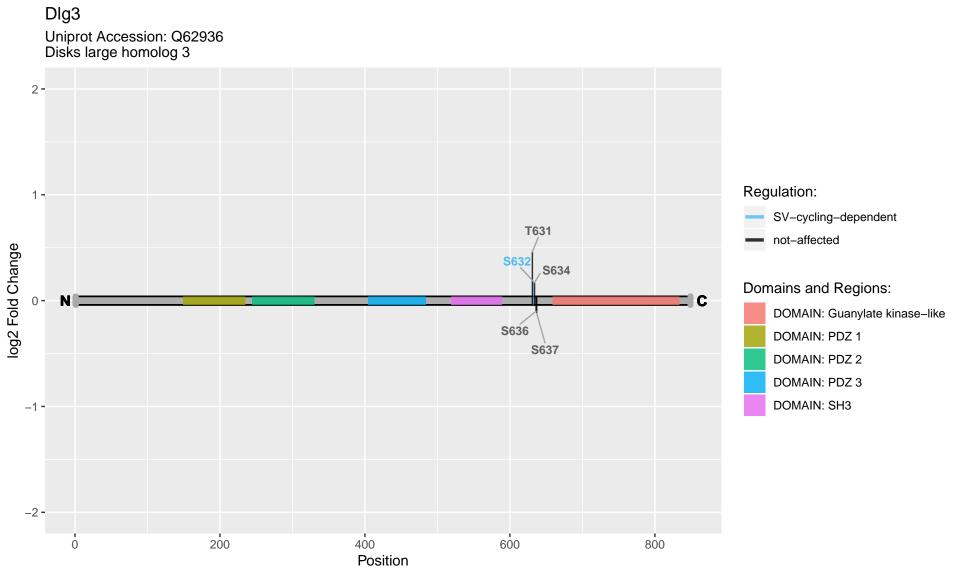


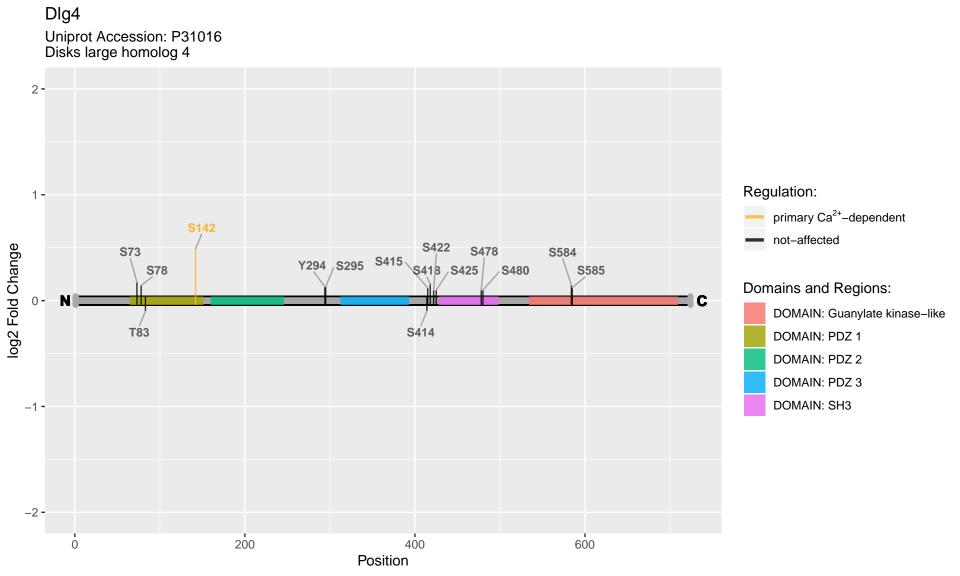


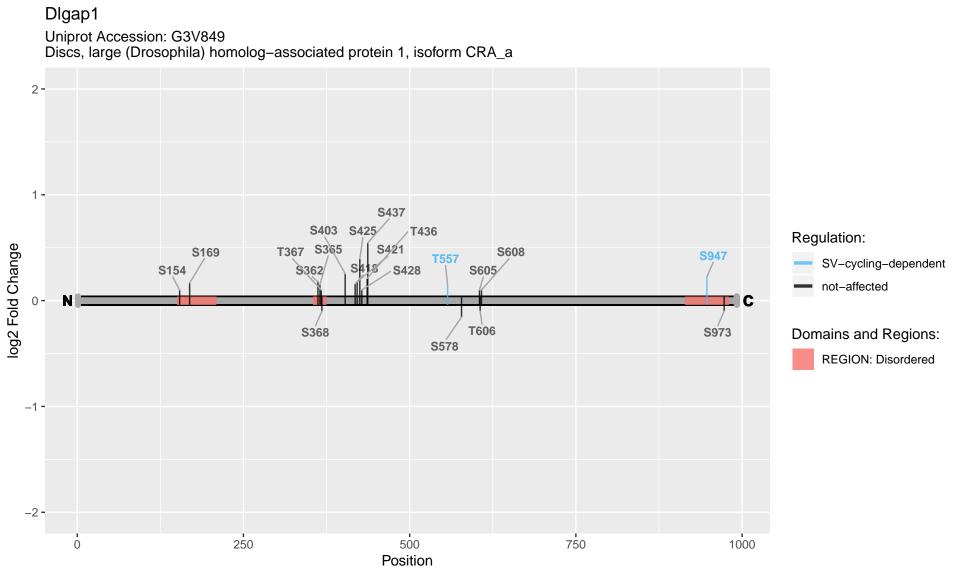


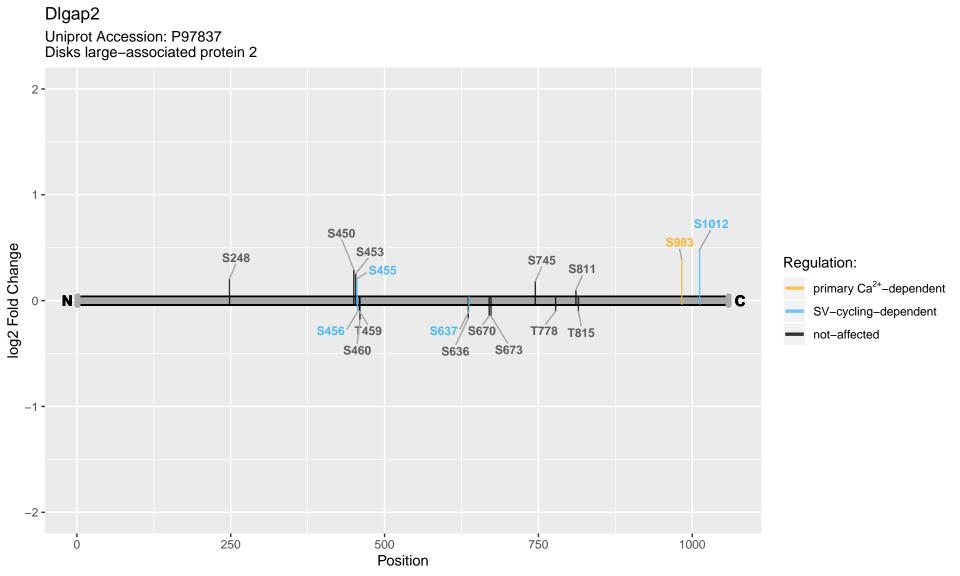


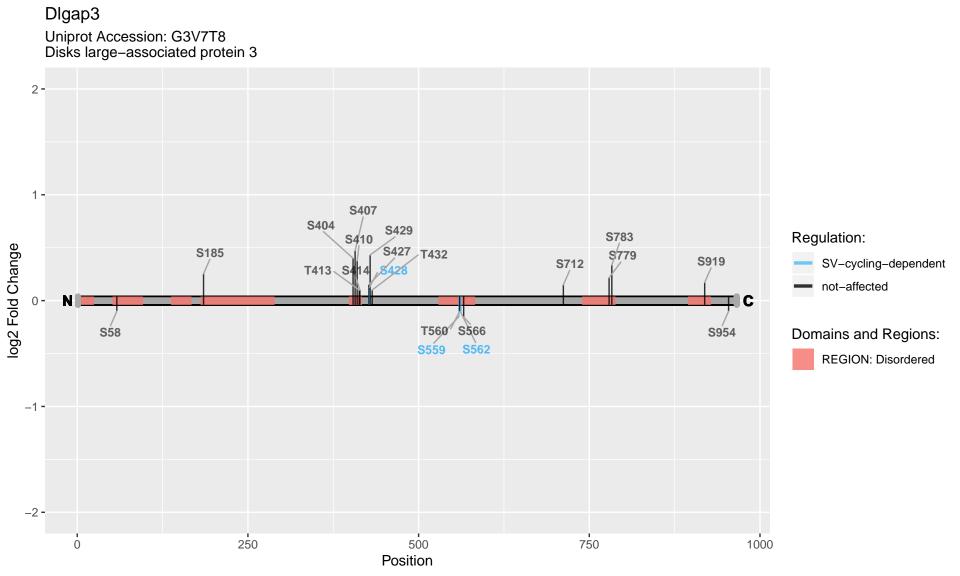


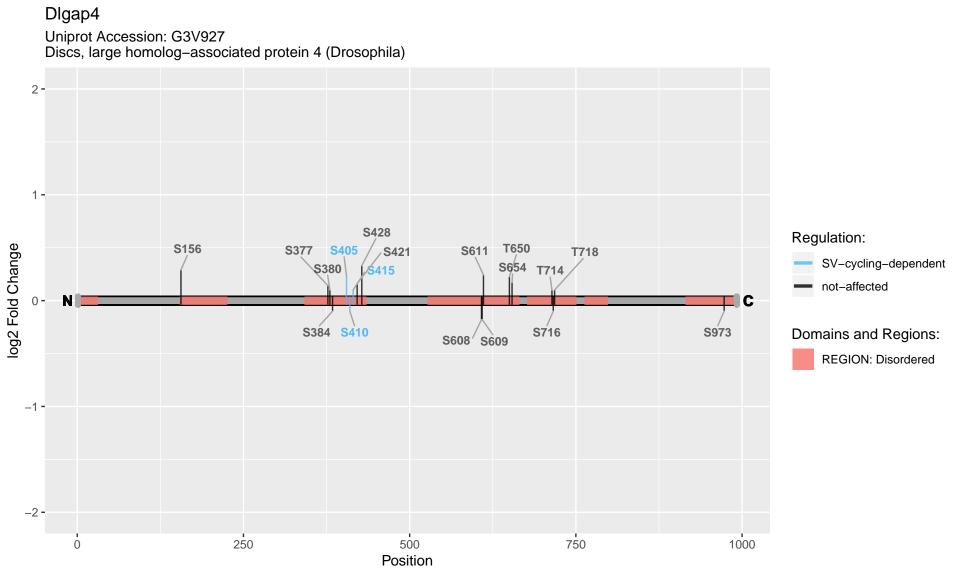


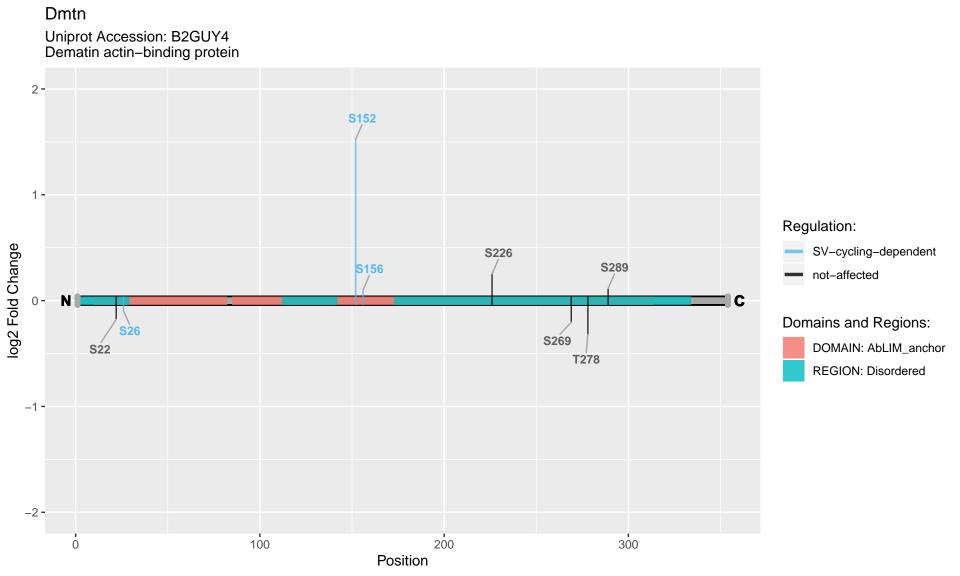


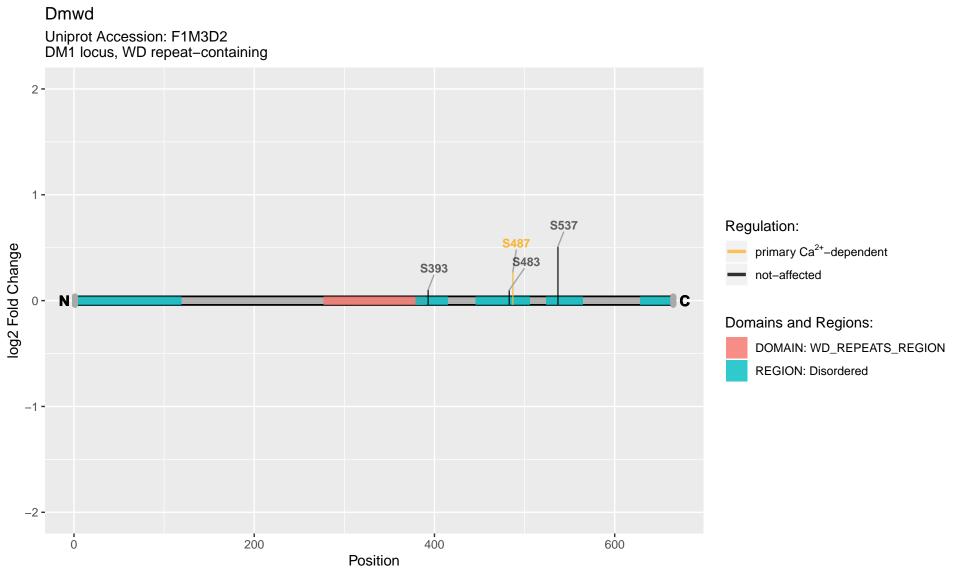


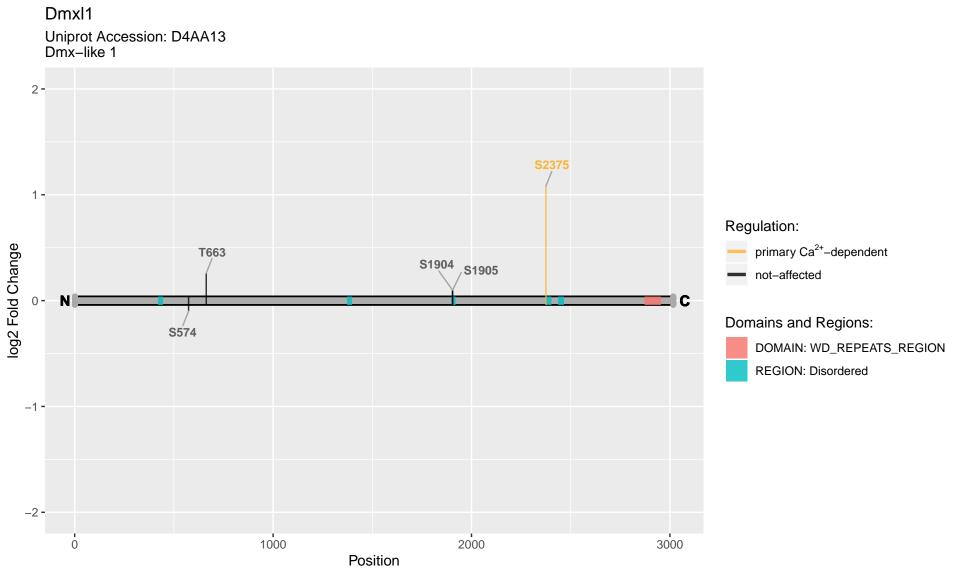


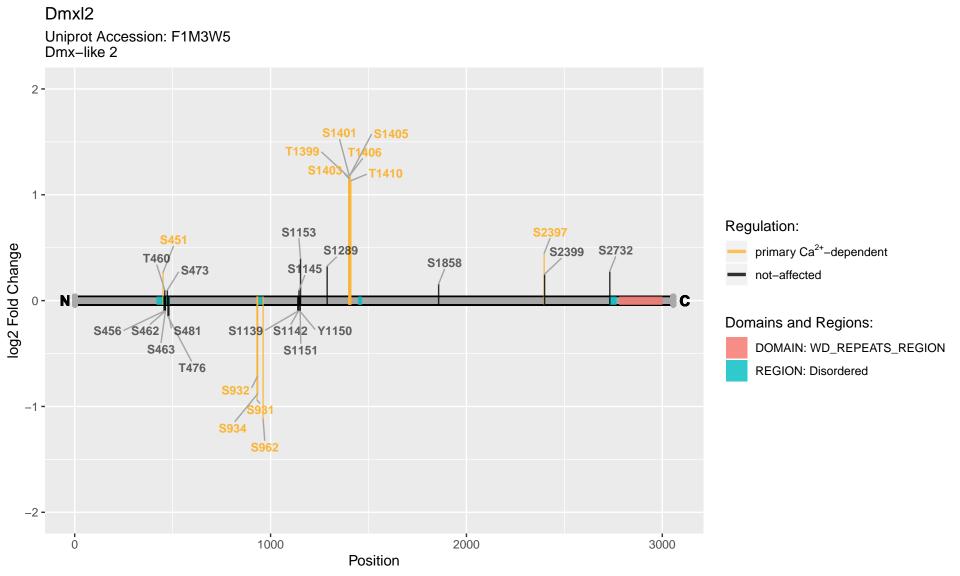


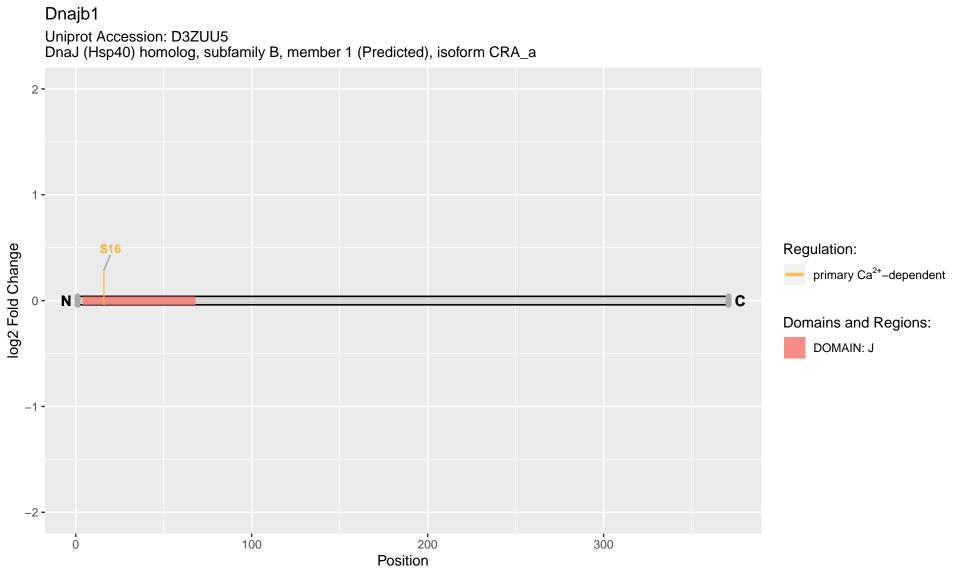


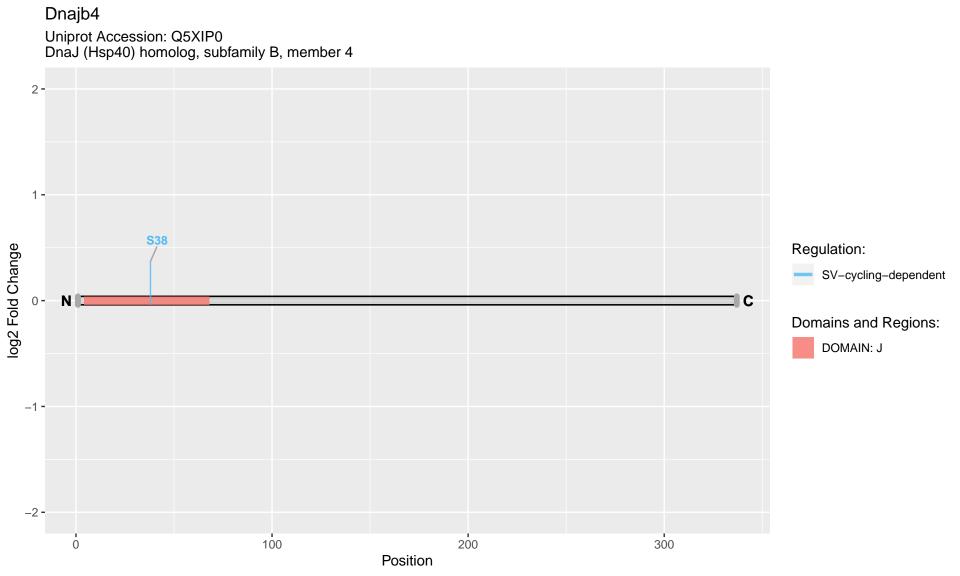


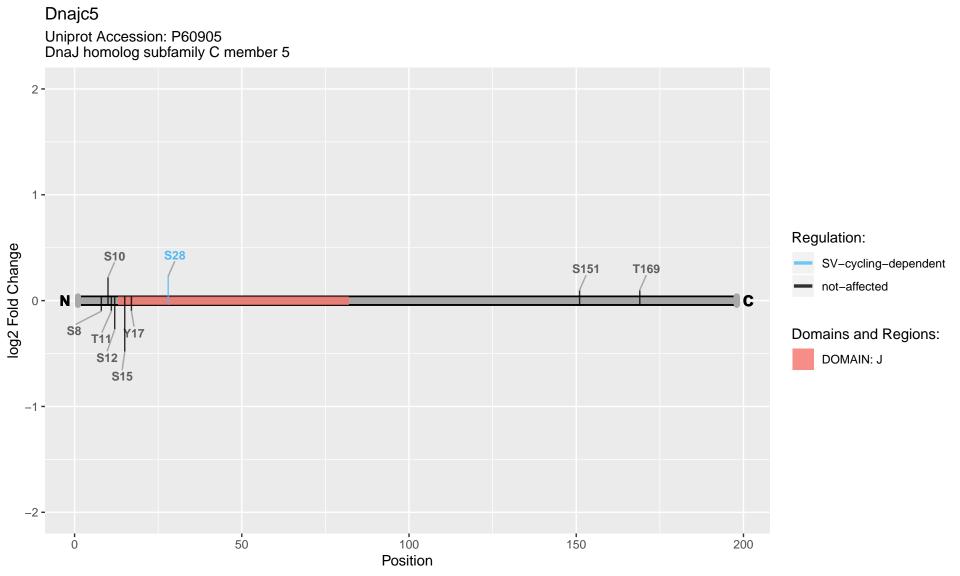


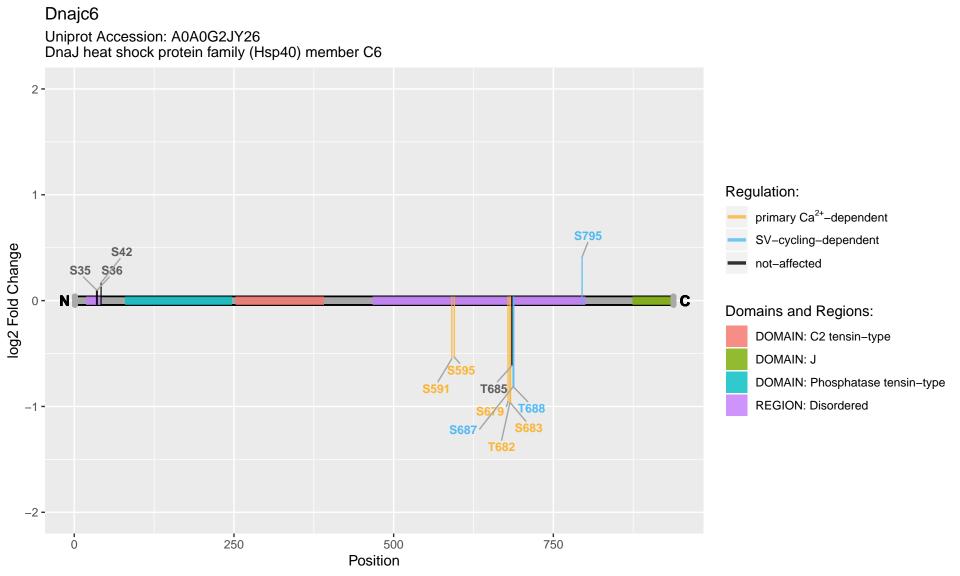


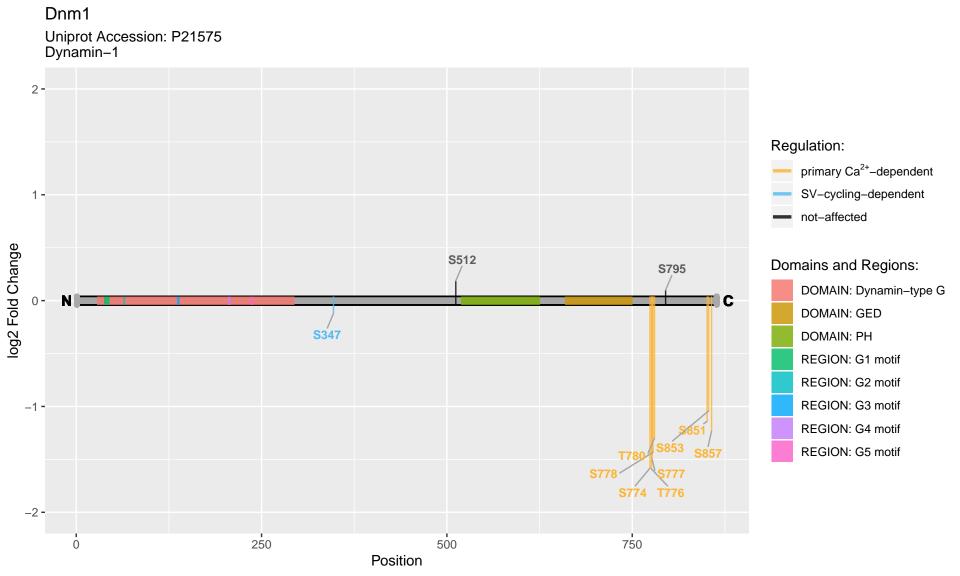


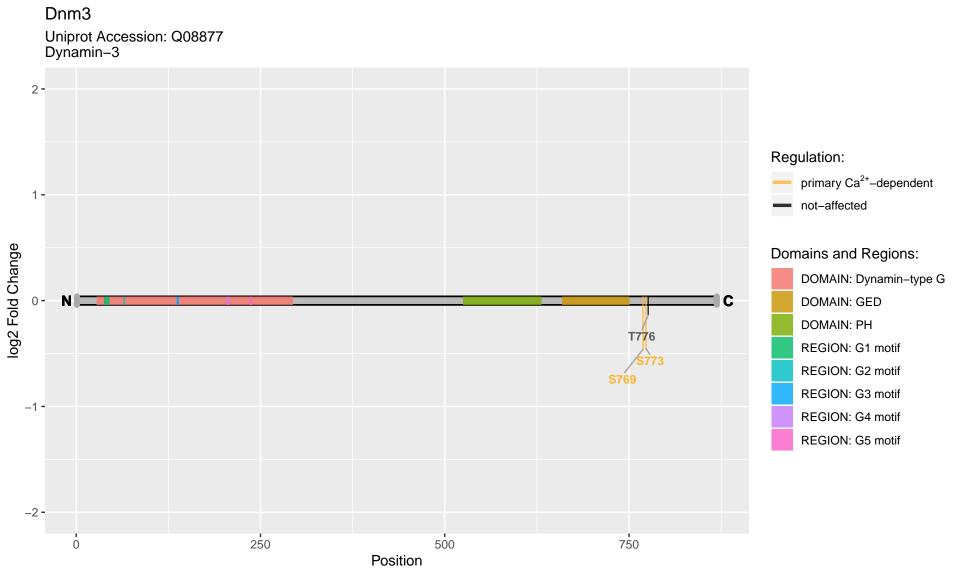


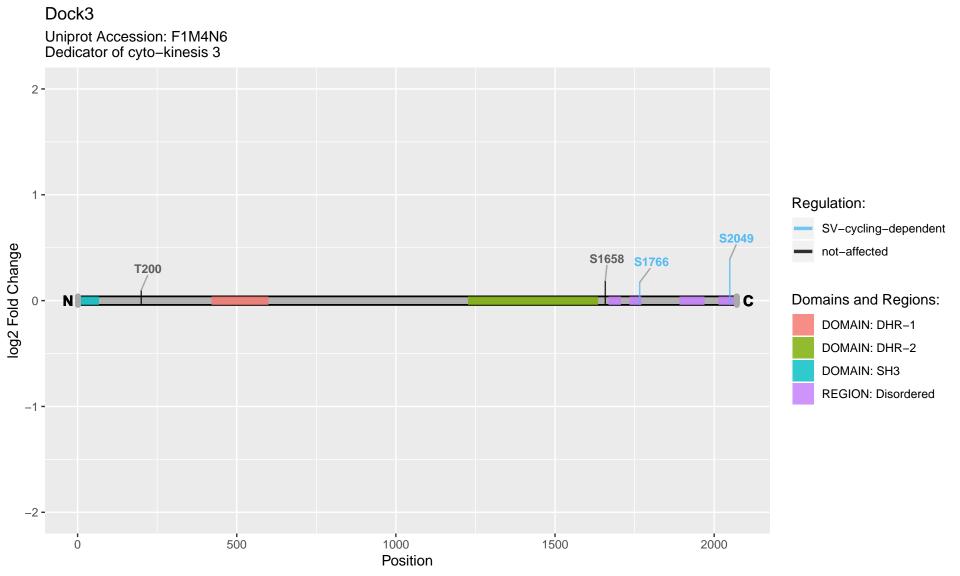


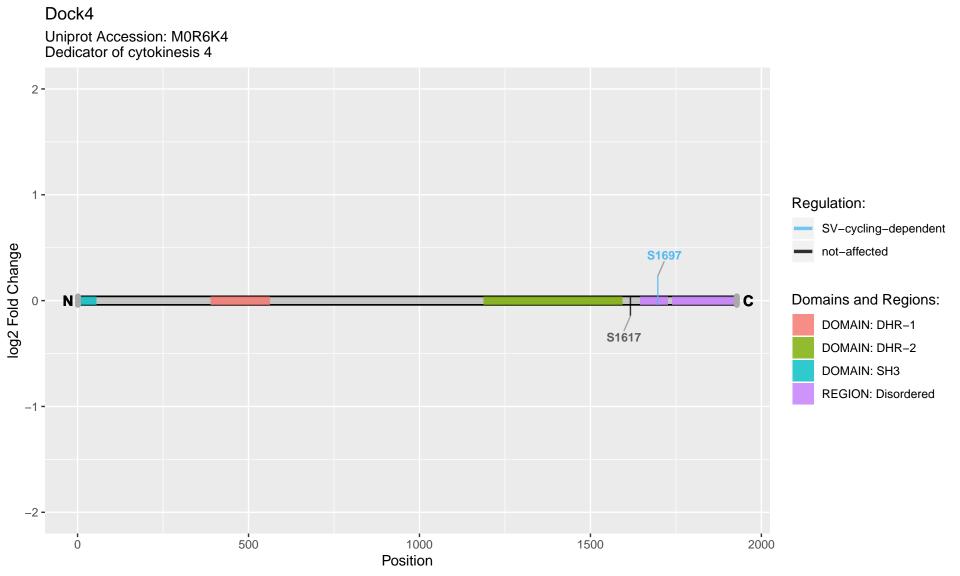


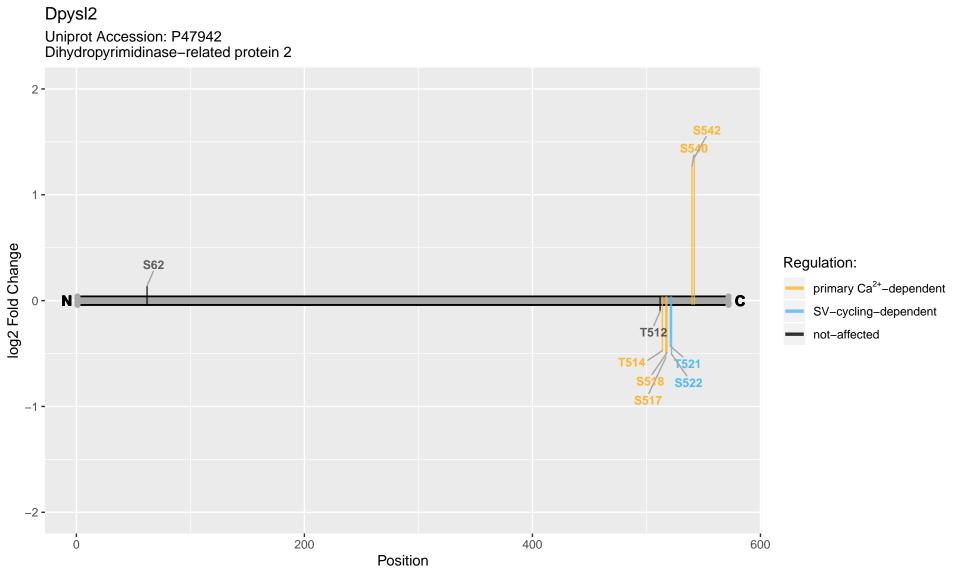


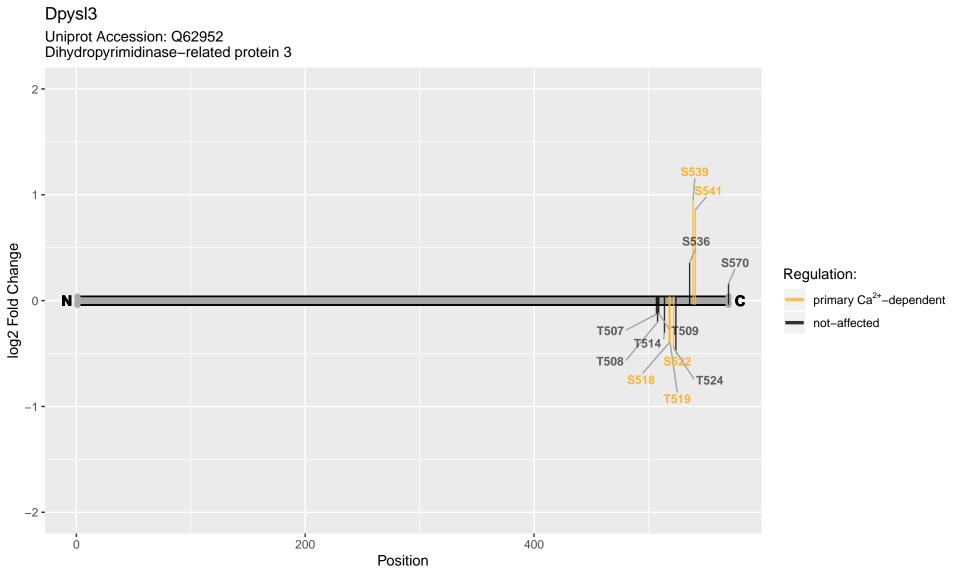


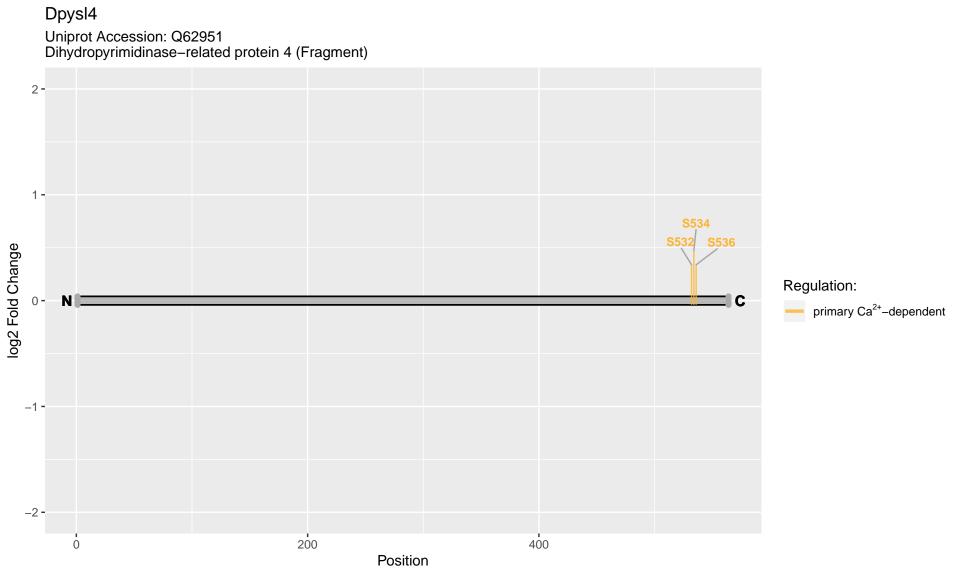


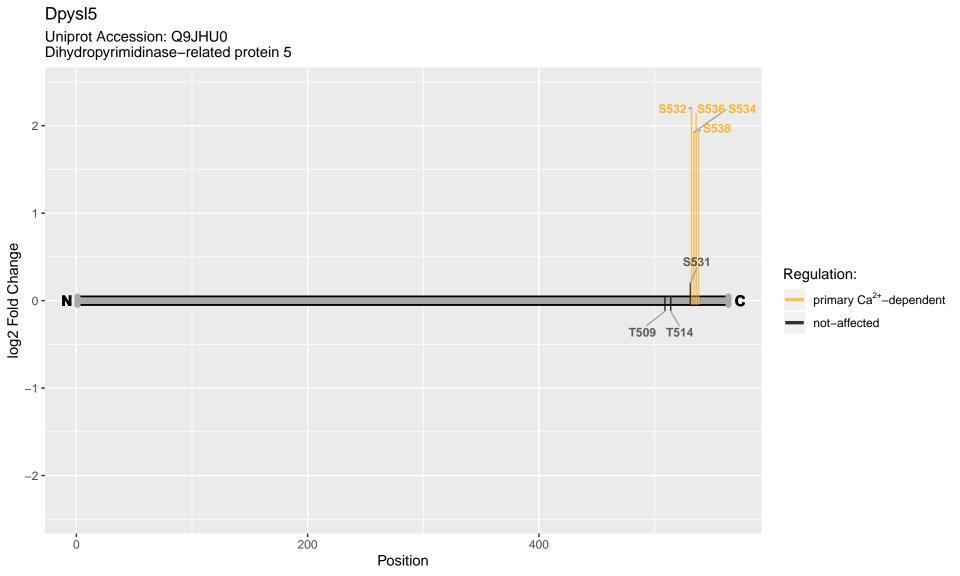


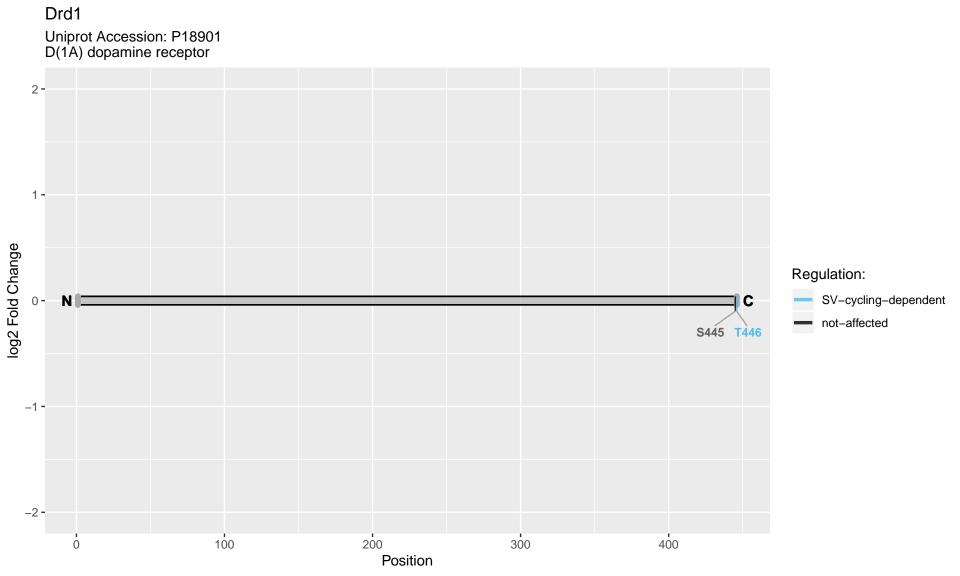


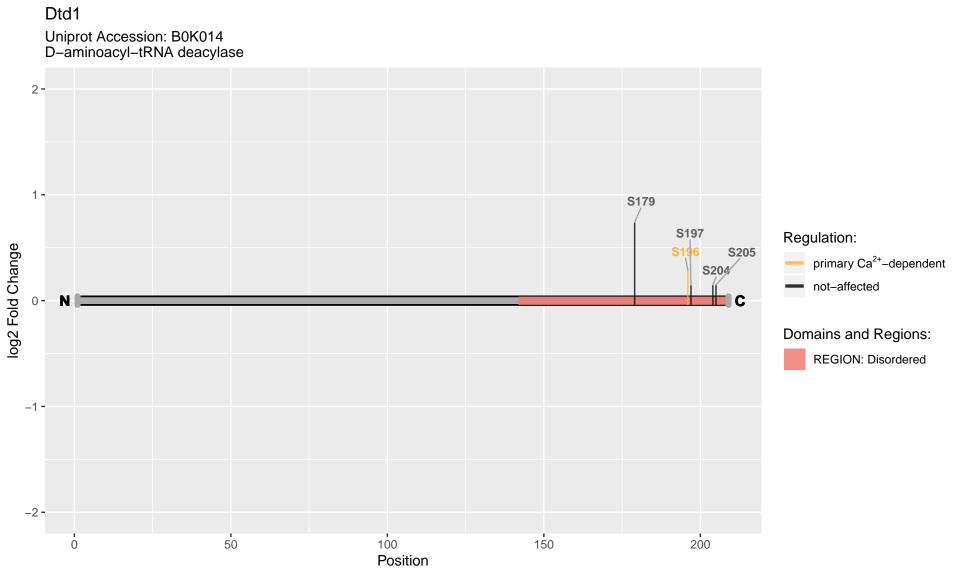


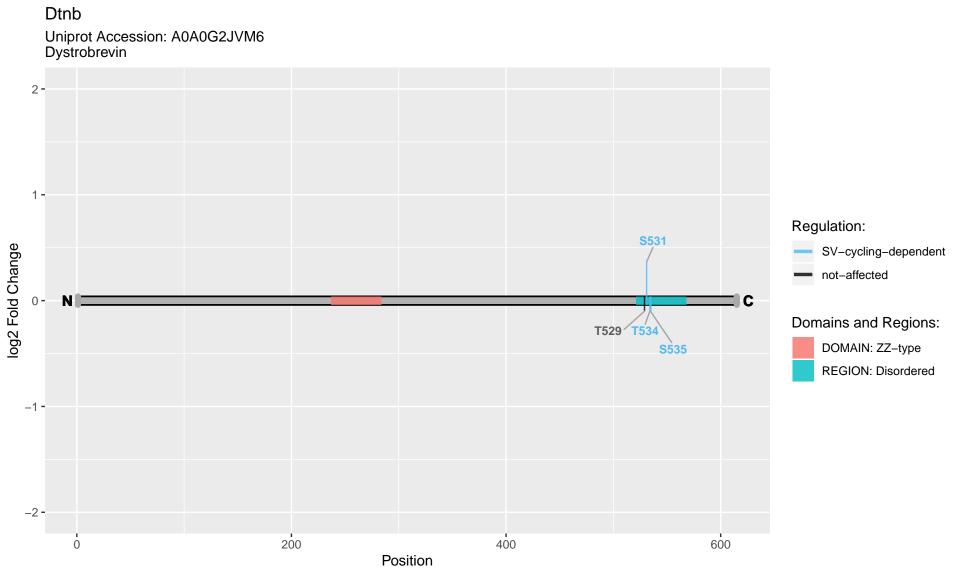


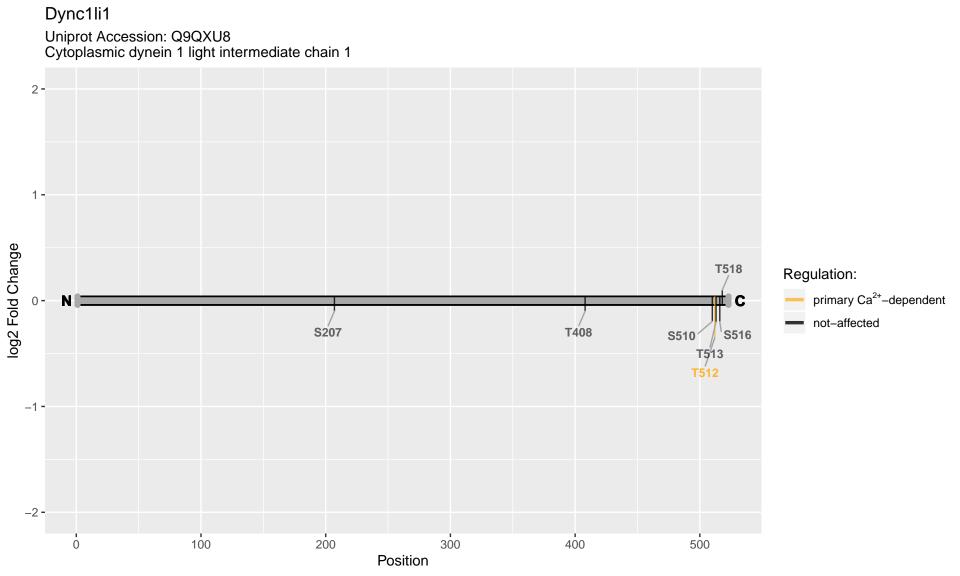


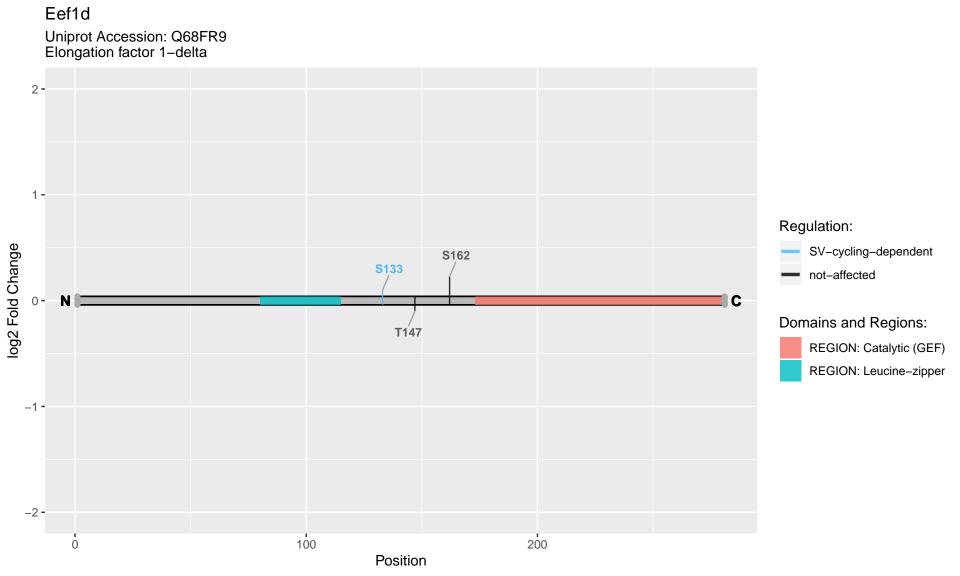


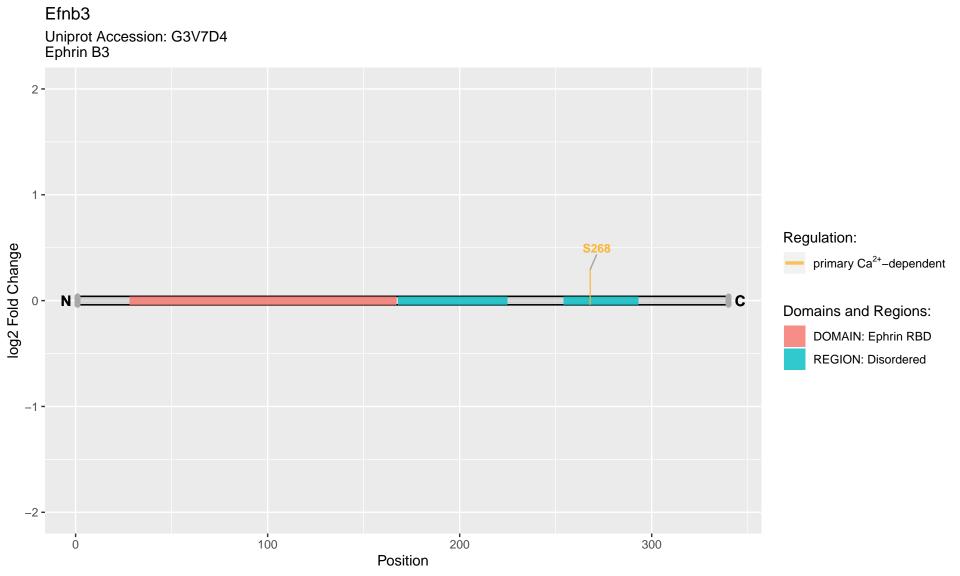


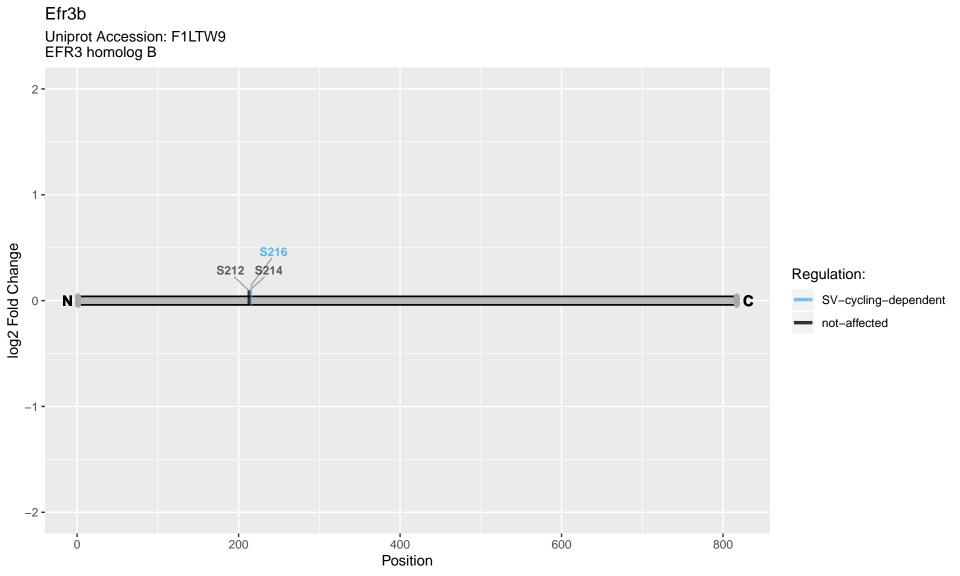


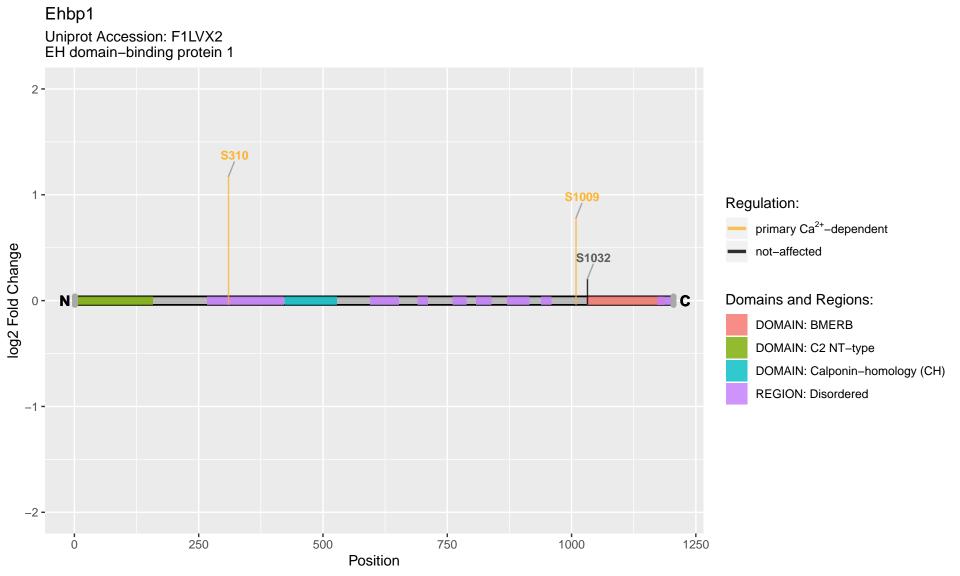


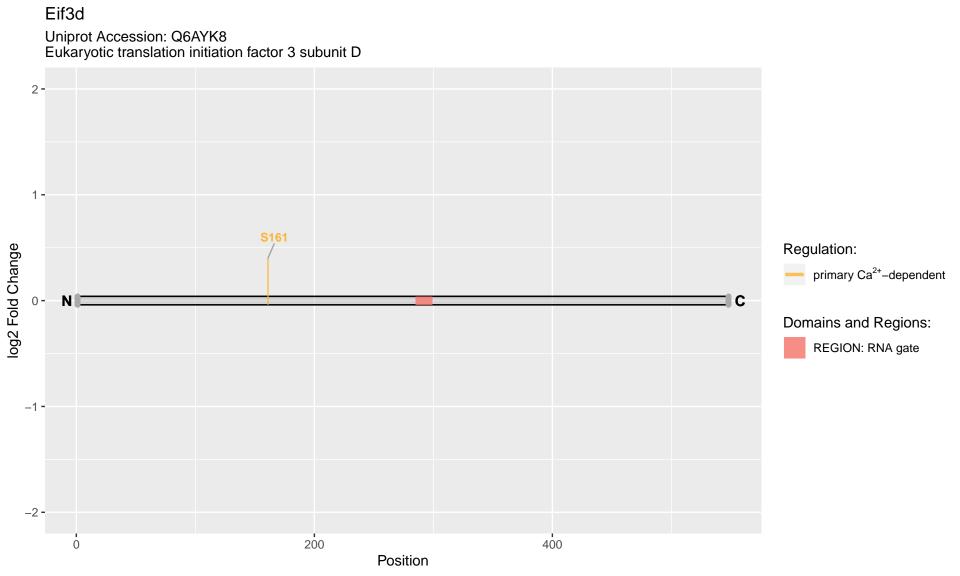






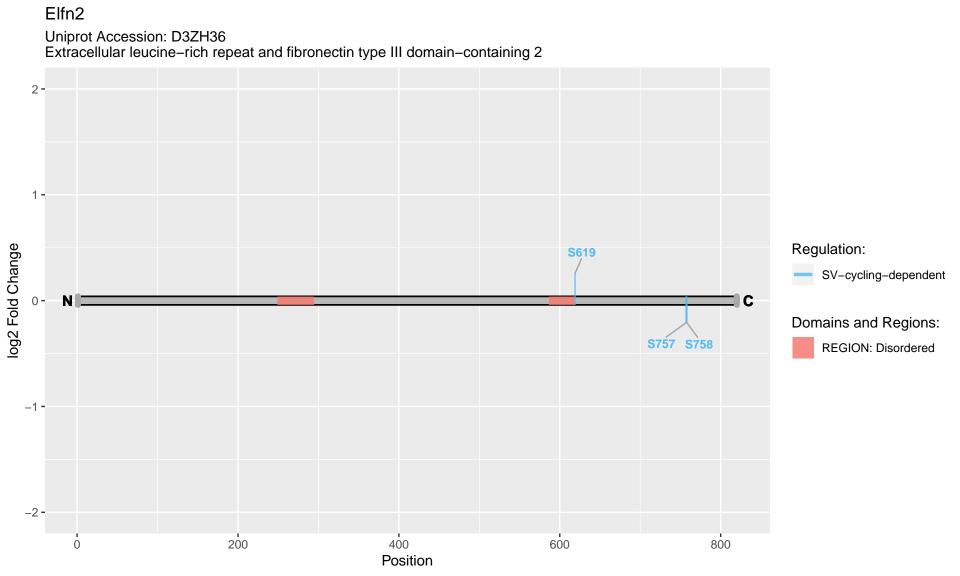


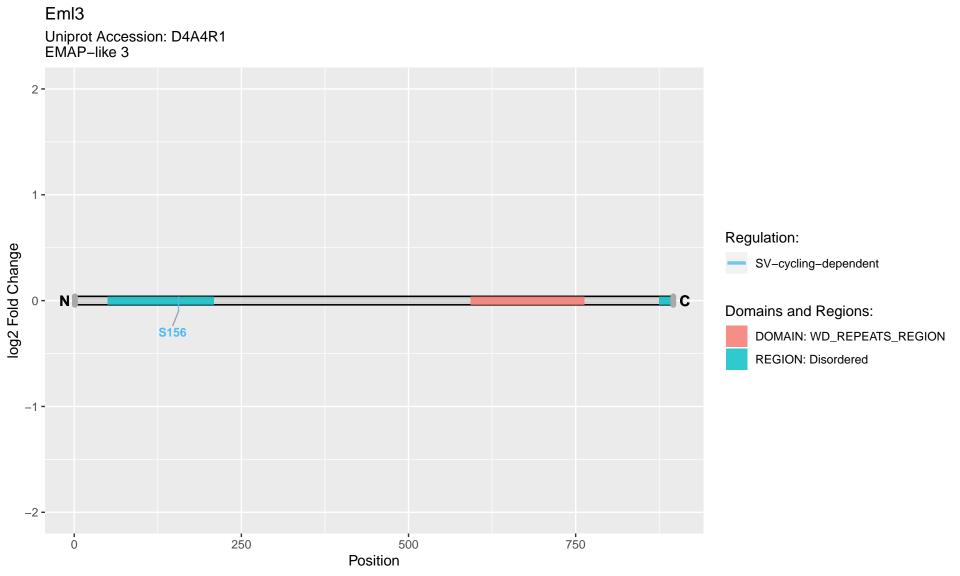


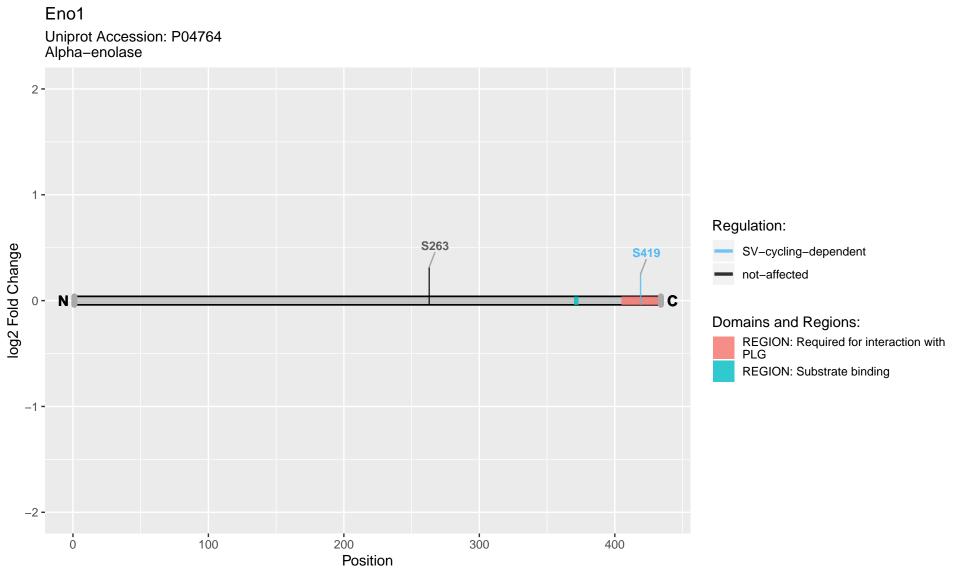


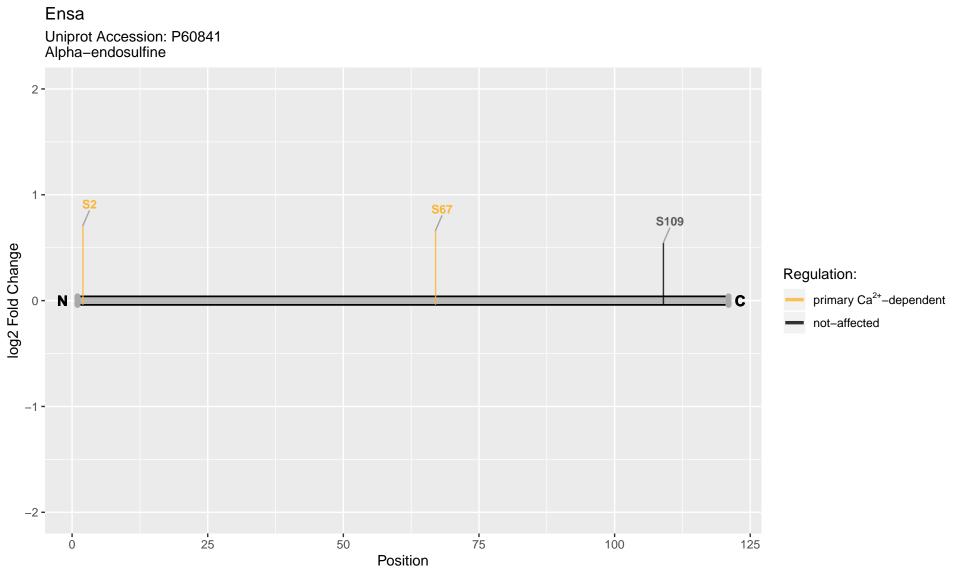
Eif4b Uniprot Accession: Q5RKG9 Eukaryotic translation initiation factor 4B **S340** 2 -1 -**S495** Regulation: log2 Fold Change primary Ca²⁺-dependent S498 S131 **S544** S49₇ not-affected C Domains and Regions: S489 S425 T420 DOMAIN: RRM **T427 REGION: Disordered** S488 S418 **S504 -1-**-2 **-**200 600 400 Position

Eif4g3 Uniprot Accession: A0A0G2JY73 Eukaryotic translation initiation factor 4 gamma, 3 2 -S1186 Regulation: primary Ca²⁺-dependent log2 Fold Change SV-cycling-dependent **S526** Domains and Regions: DOMAIN: MI DOMAIN: W2 **REGION: Disordered** -1 **-**-2 **-**500 1000 1500 Position

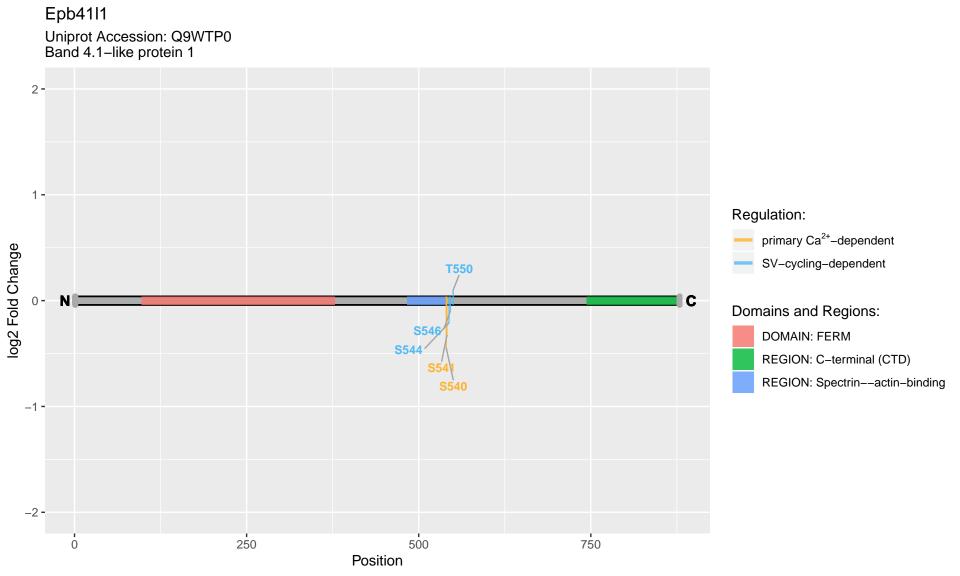


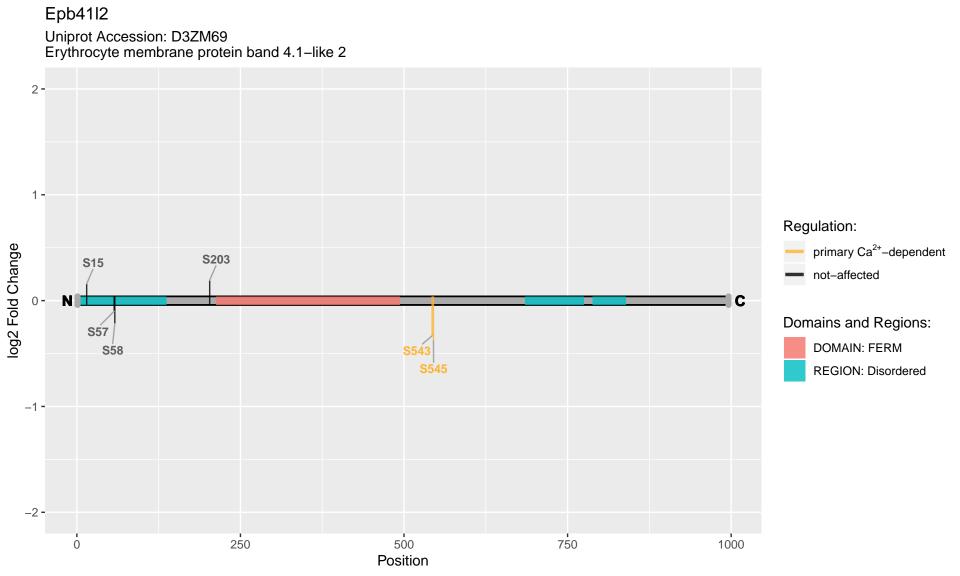




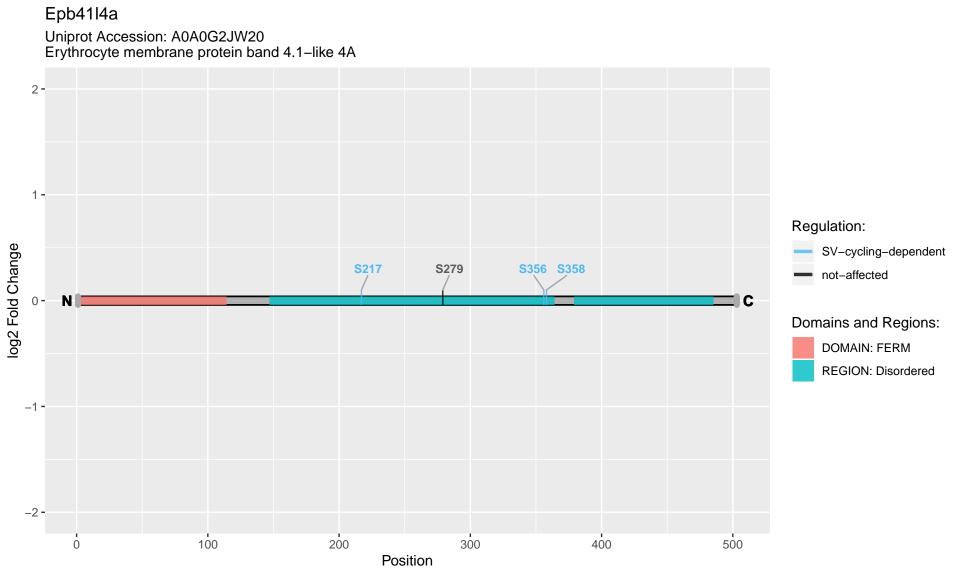


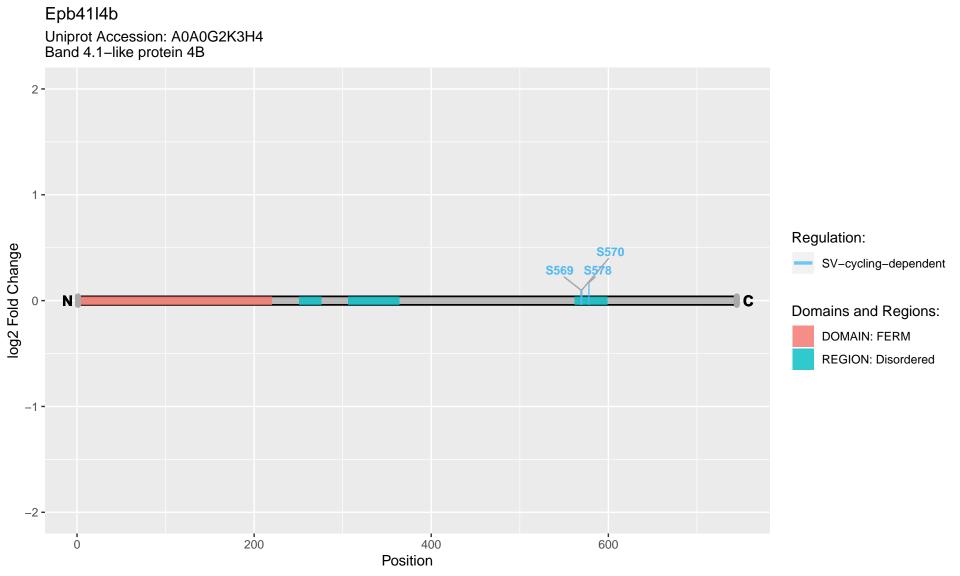
Epb41I1 Uniprot Accession: A0A0G2K0F3 Band 4.1–like protein 1–like 2 -1 -Regulation: S461 T475 T1252 primary Ca²⁺-dependent S1236 S430 log2 Fold Change T489 S1393 S1540 SV-cycling-dependent S1250 S1349 T488 / T550 not–affected NI **S443** S510 Domains and Regions: S1337 S1338 T30 S1322 S1343 T1324 DOMAIN: FERM T33 S441 S1320 **REGION: Disordered S540 S1311** -1 **-**-2 **-**500 1000 1500 Position

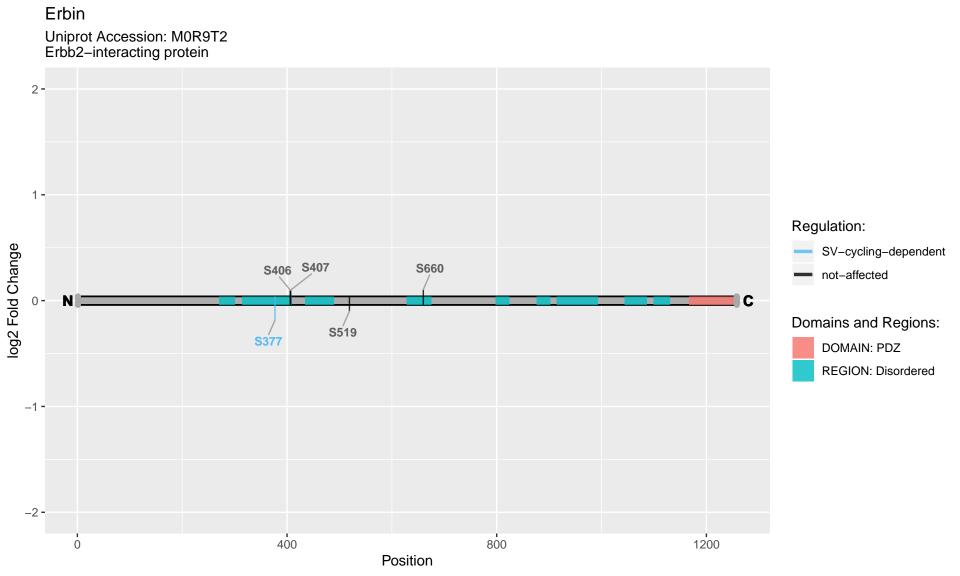


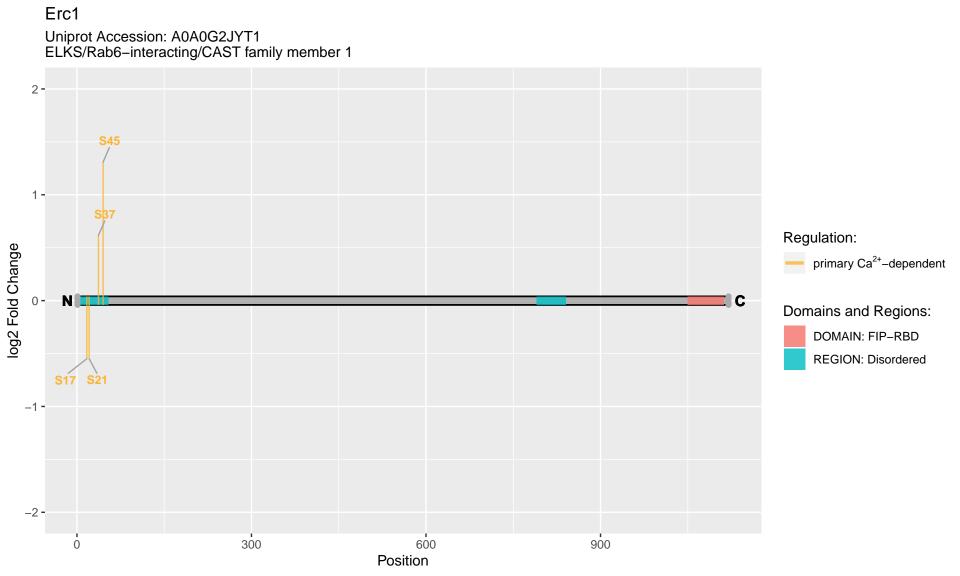


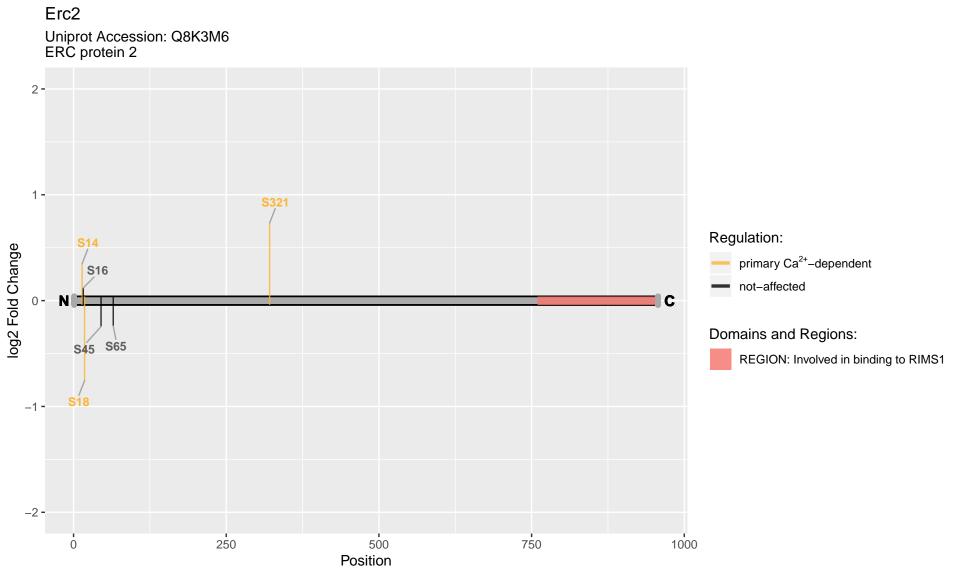
Epb41I3 Uniprot Accession: G3V874 Erythrocyte membrane protein band 4.1-like 3 2 -1 -Regulation: **S524 S774** primary Ca²⁺-dependent S801 log2 Fold Change T522 **S446 S743** S766 SV-cycling-dependent T495 **S578** S808 not-affected S66 S95 **S520** Domains and Regions: T472 DOMAIN: FERM **S96 S**91 **S463 REGION: Disordered** -1 **-**-2 **-**250 750 500 1000 Position



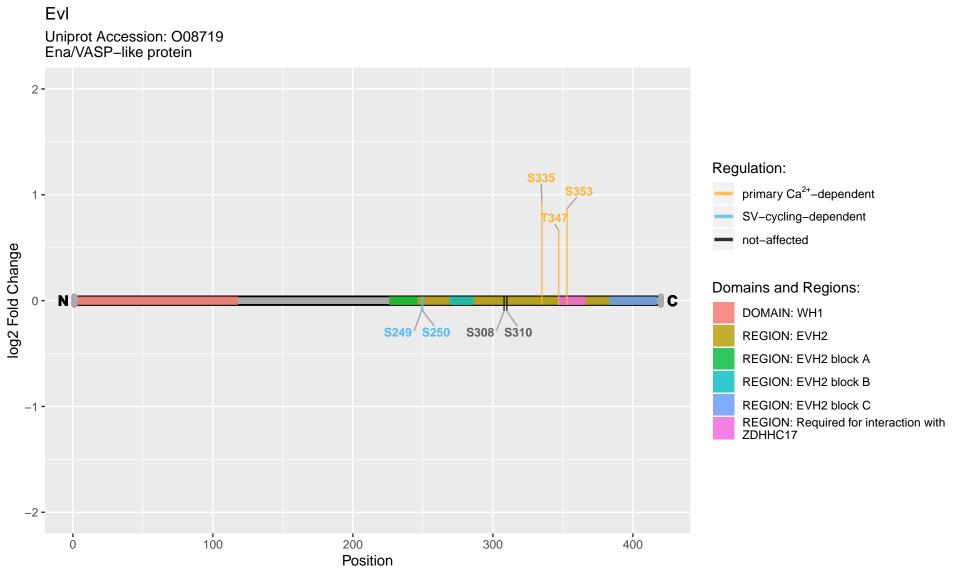


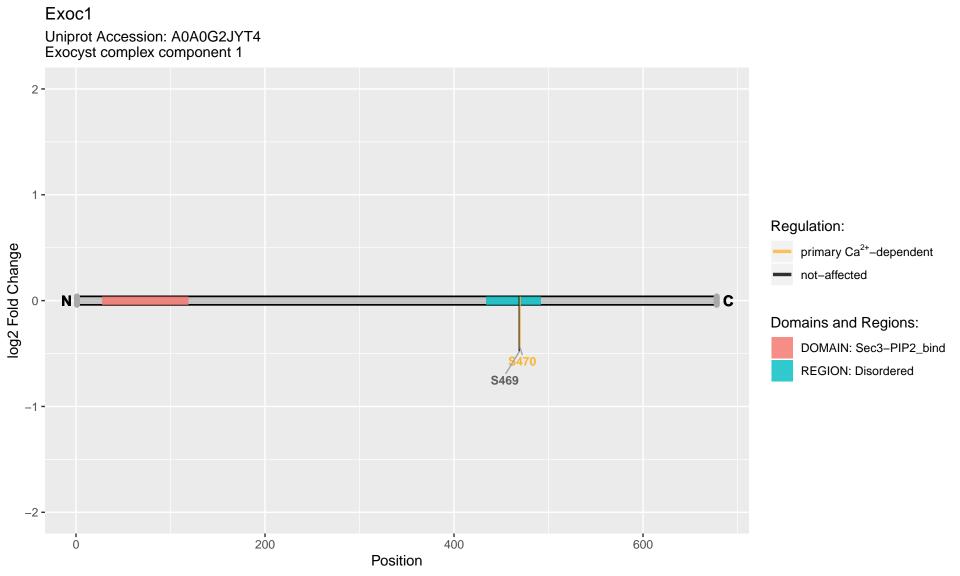


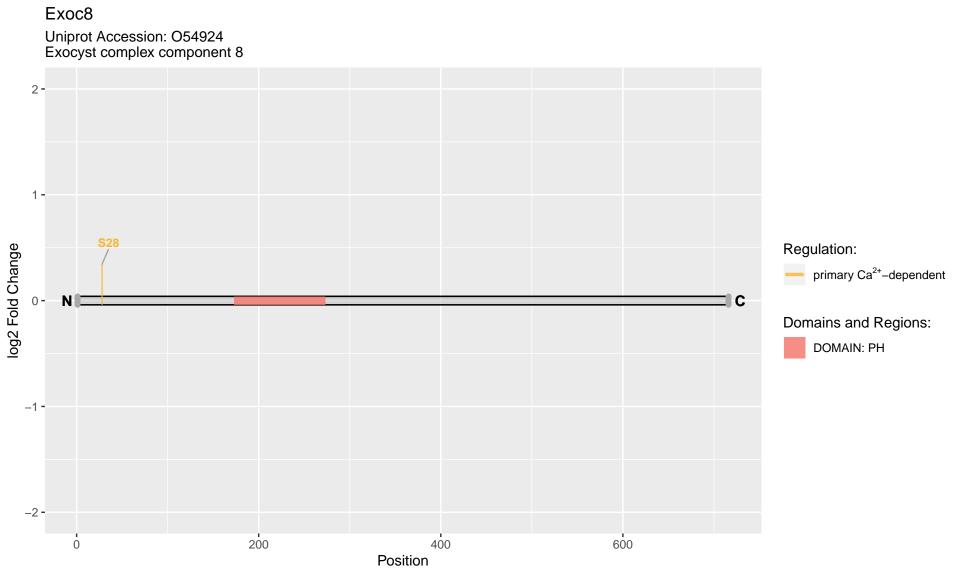


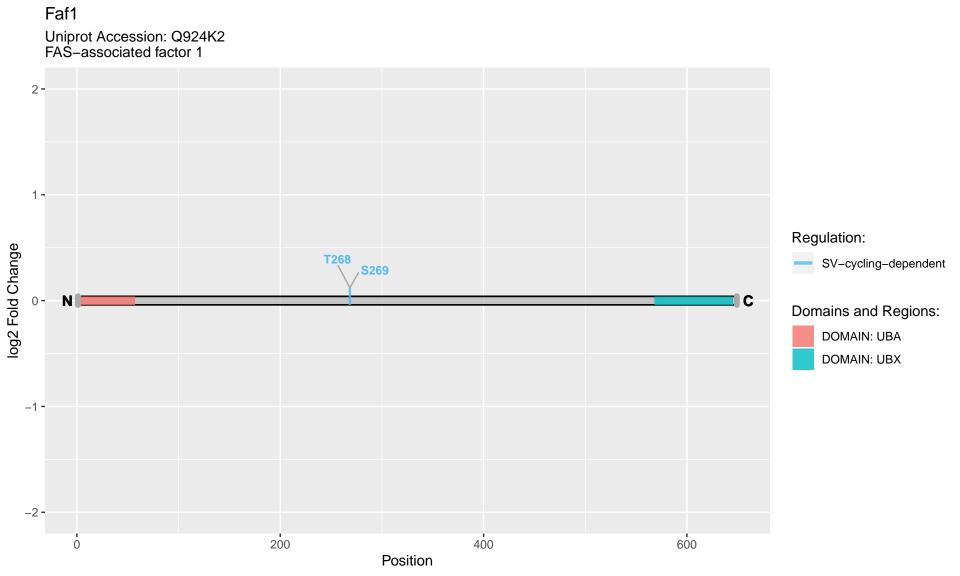


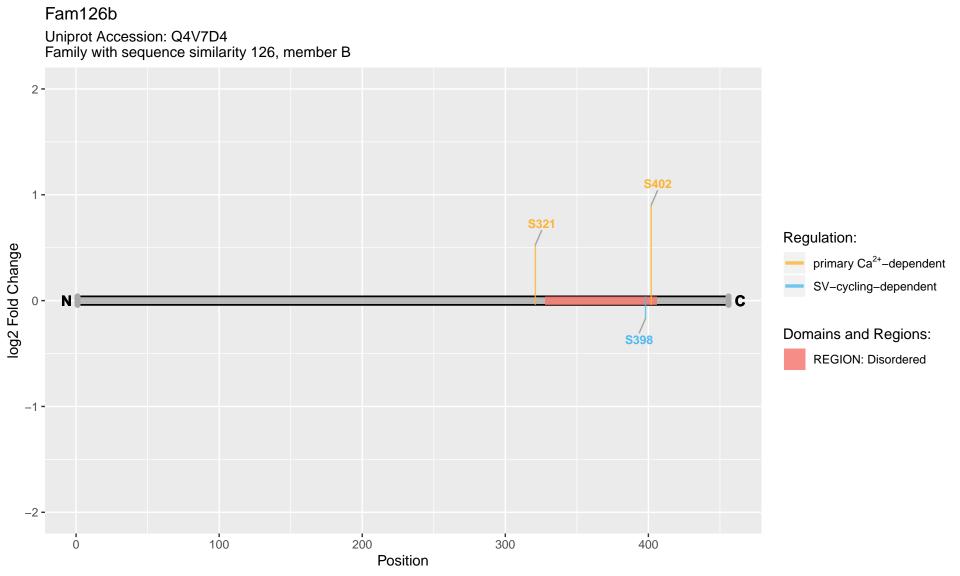
Etl4 Uniprot Accession: M0R5H1 Enhancer trap locus 4 2 -\$1775 1 -Regulation: **S1088 T59 S528** primary Ca²⁺-dependent log2 Fold Change T488 S1051 SV-cycling-dependent S1054 not–affected S331 S486 S1065 Domains and Regions: **S887** S492 S344 S1881 S1914 S1917 DOMAIN: AIP3 S479 S1910 **REGION: Disordered** -1 **-**-2 **-**500 1500 1000 2000 Position

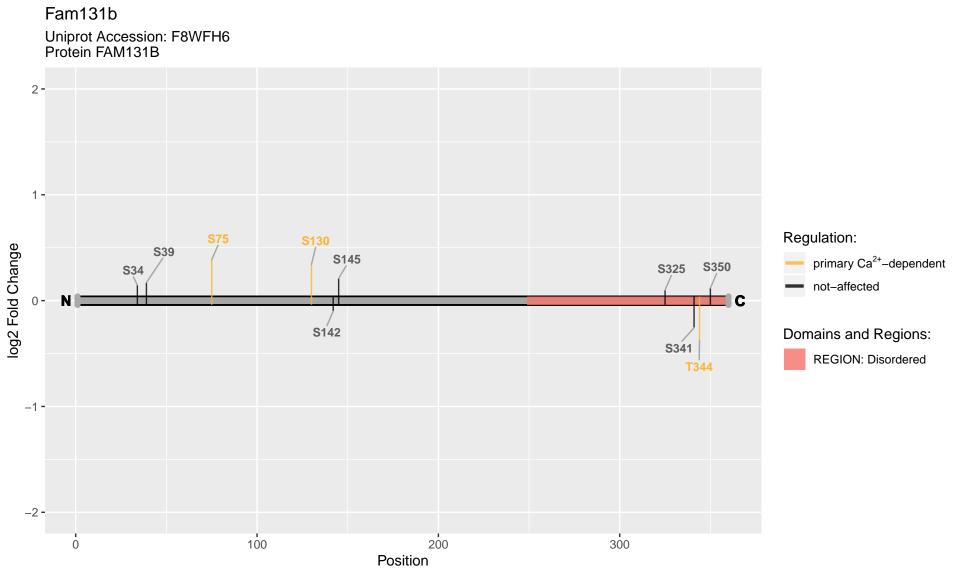


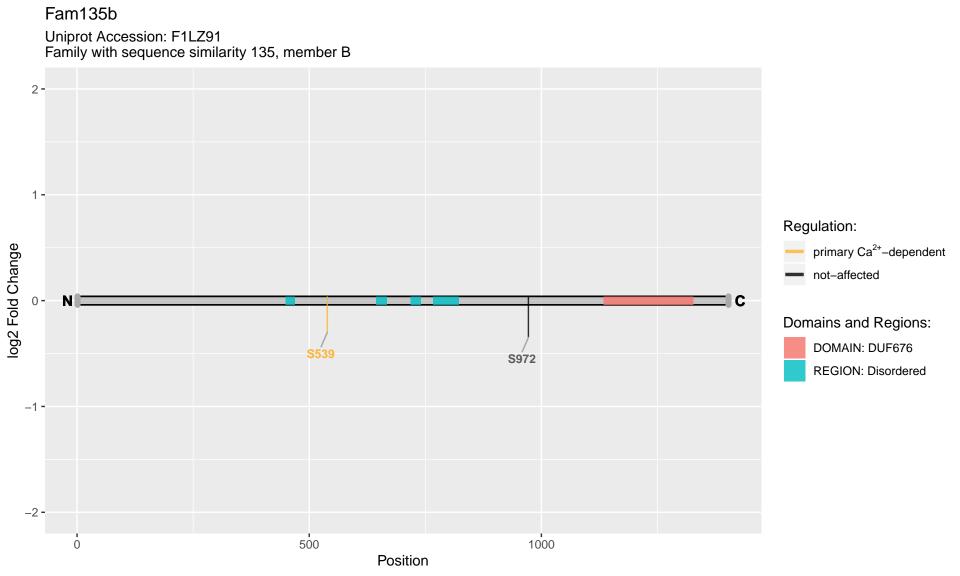


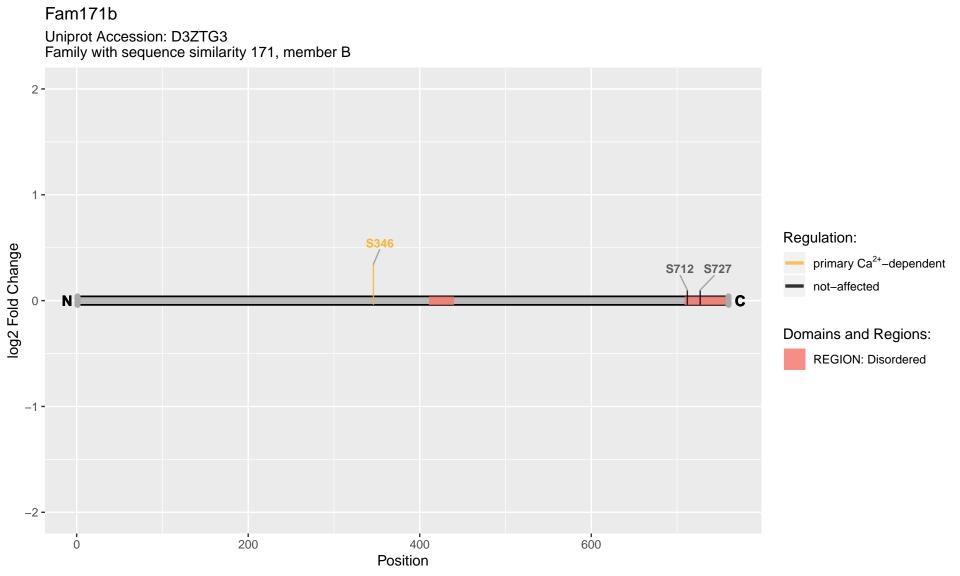


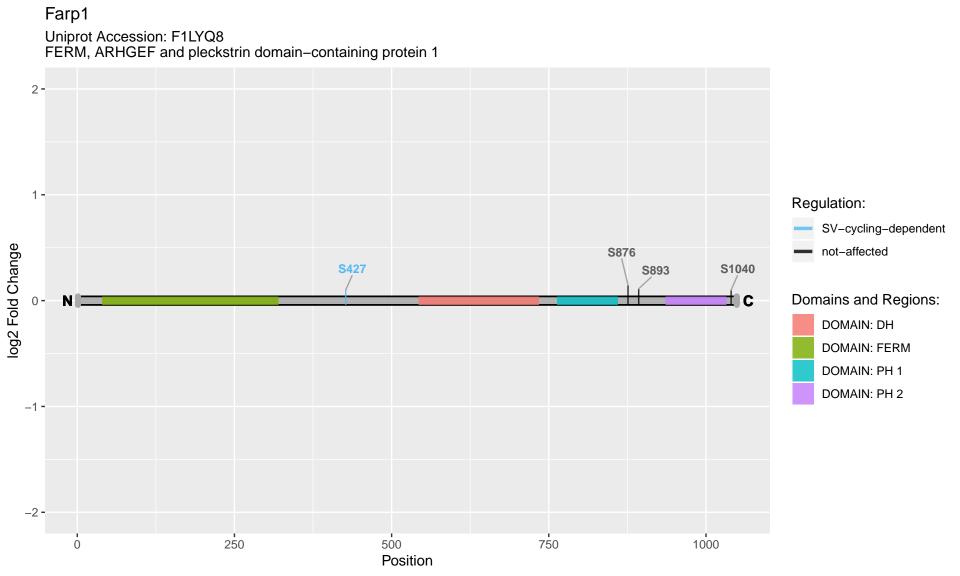


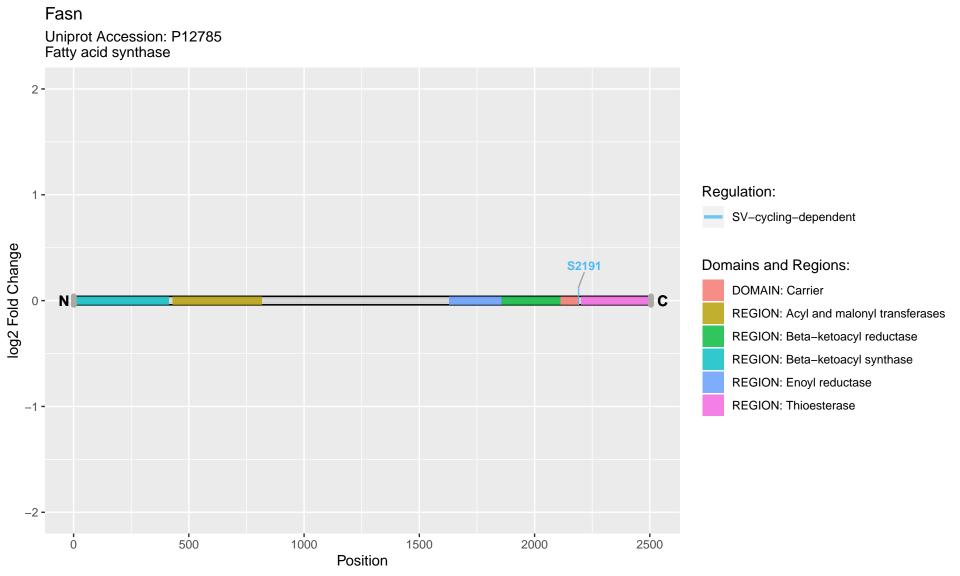


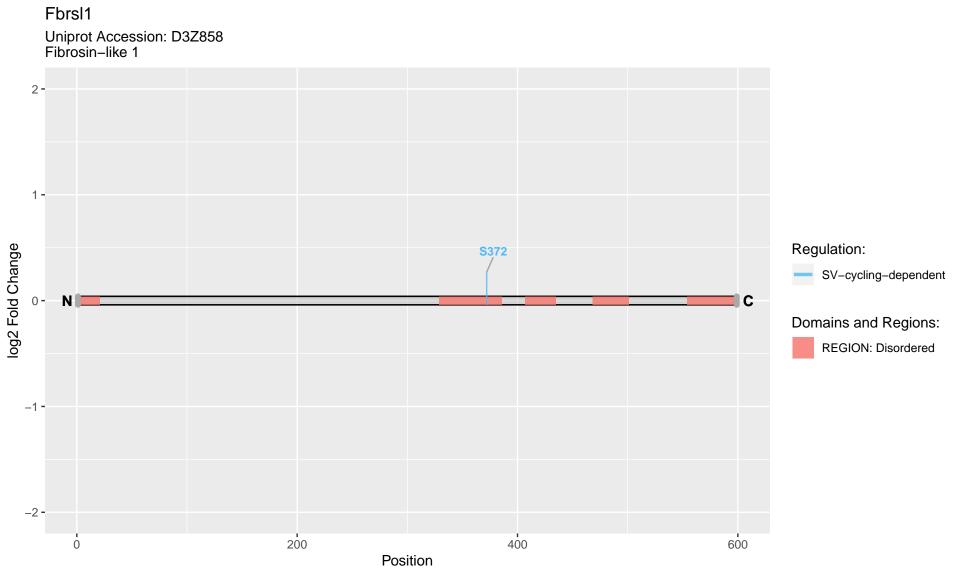


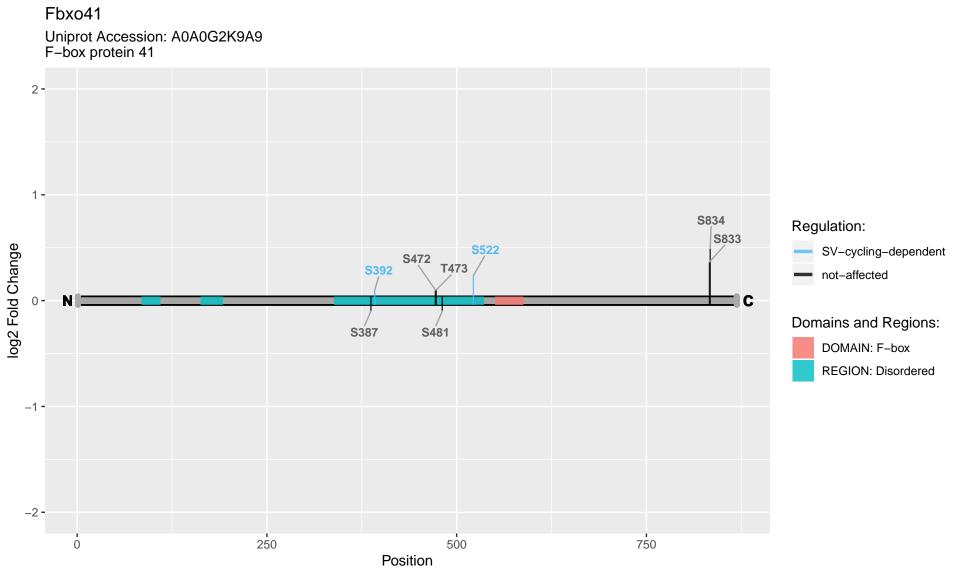


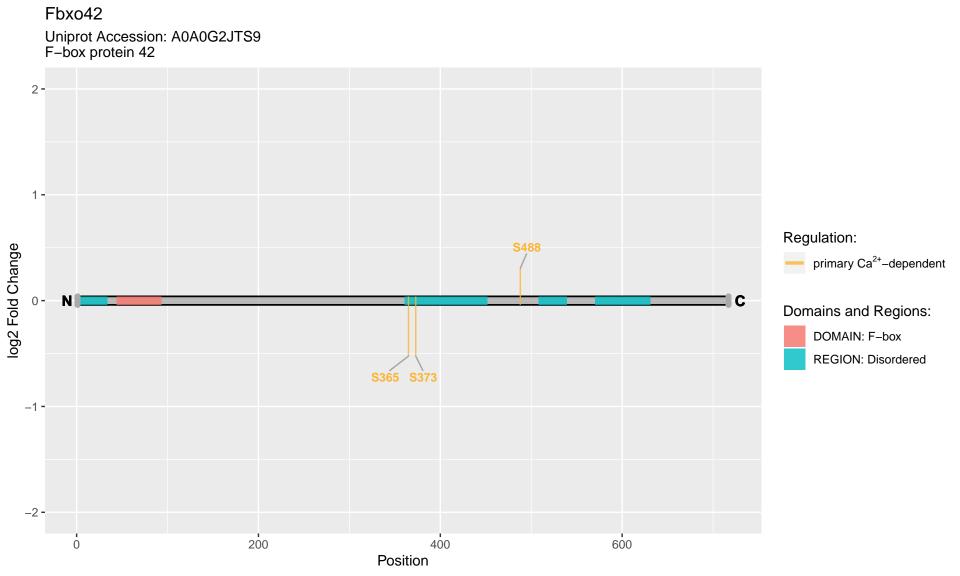


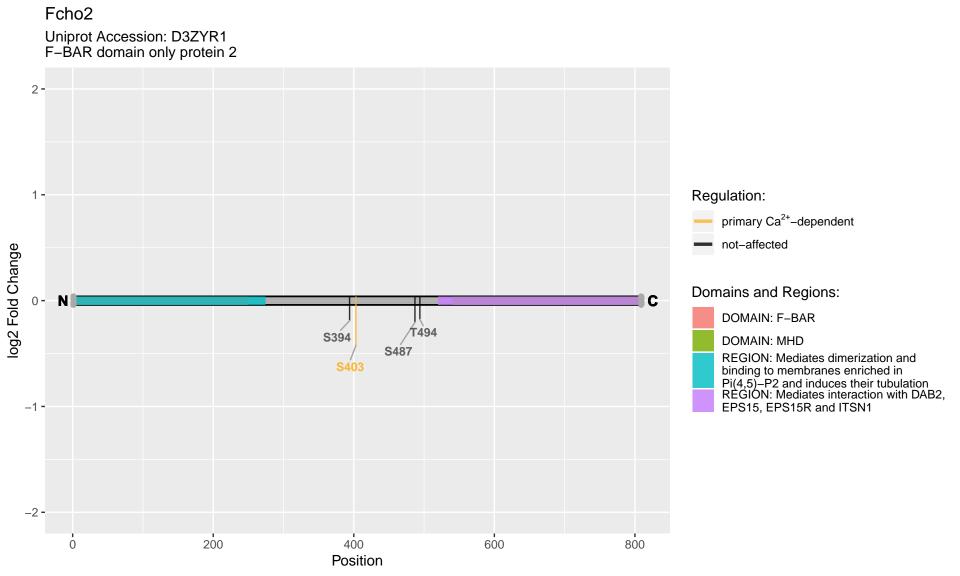




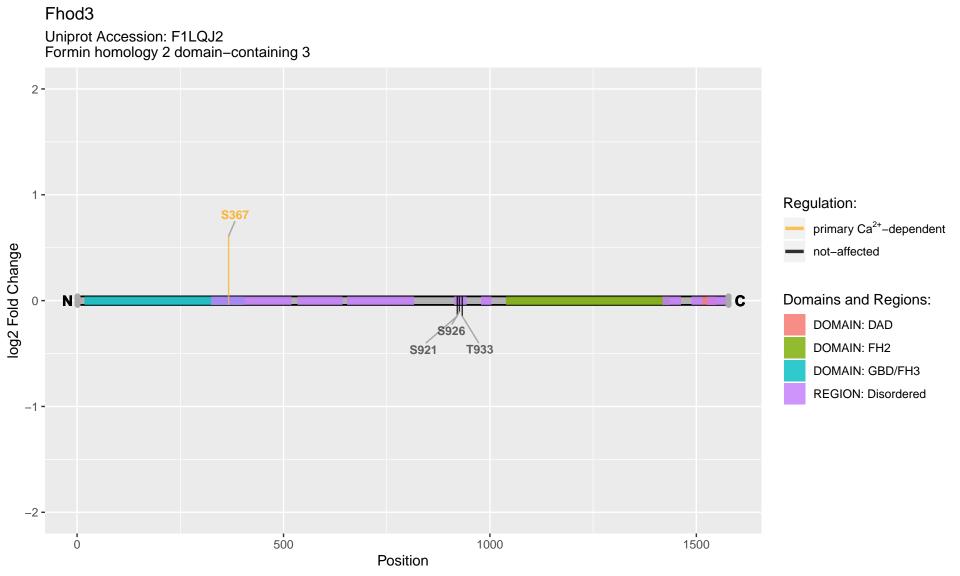


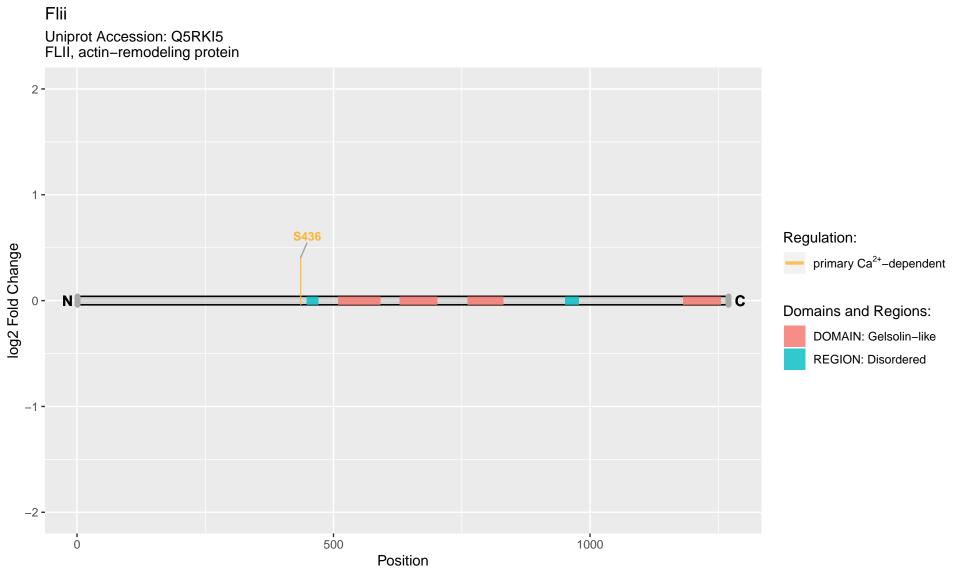




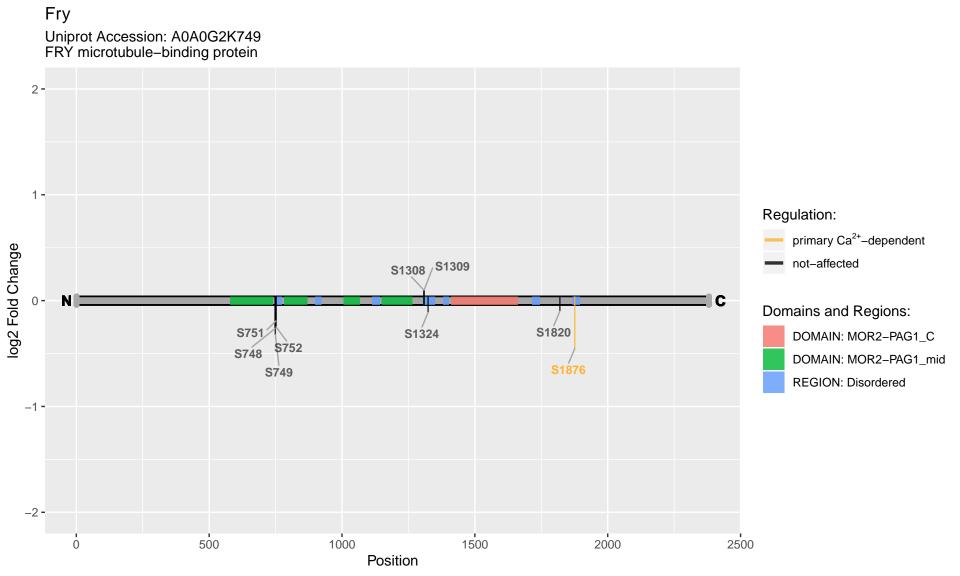


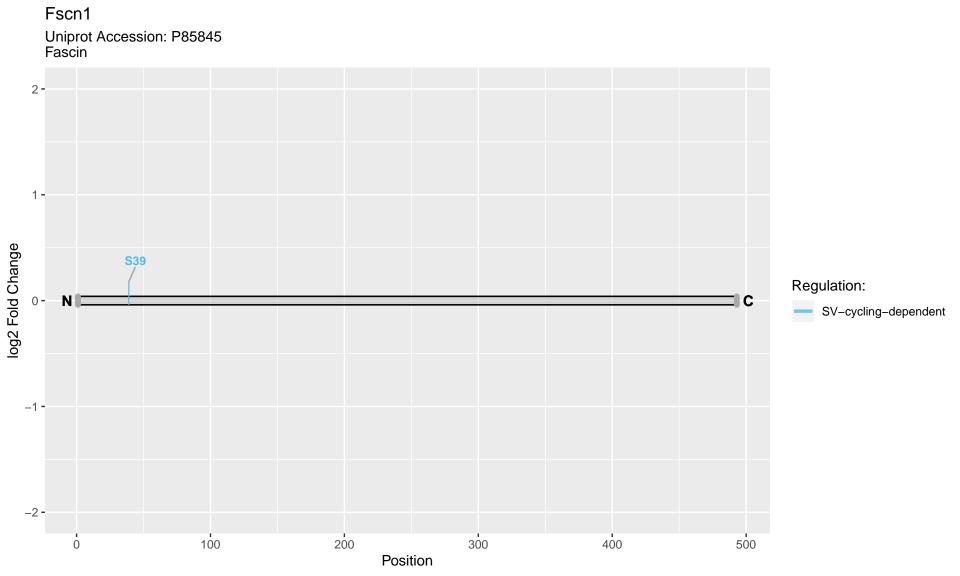
Fgf14 Uniprot Accession: Q8R5L7 Fibroblast growth factor 14 2 log2 Fold Change **S210** Regulation: SV-cycling-dependent -1 **-**-2 **-**50 150 200 100 250 Position

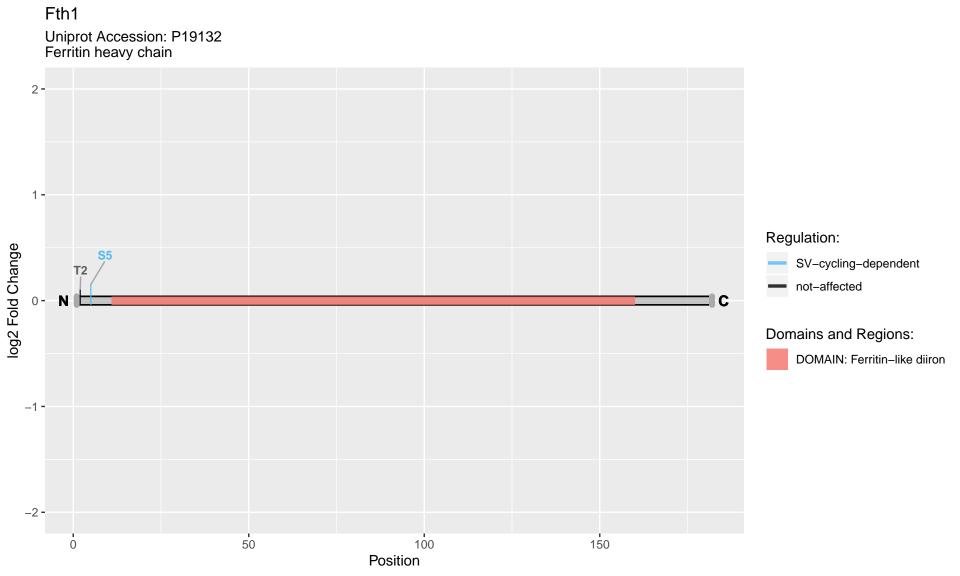


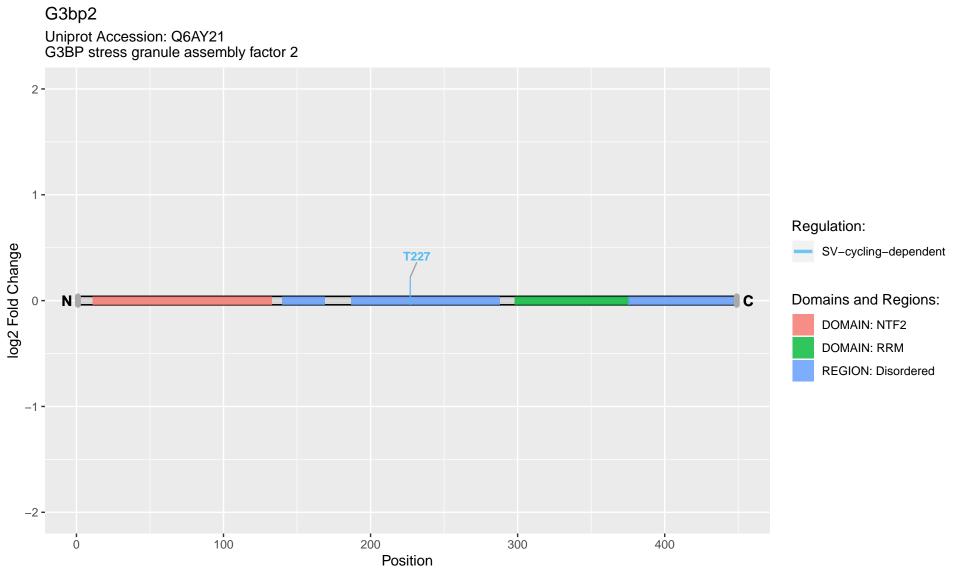


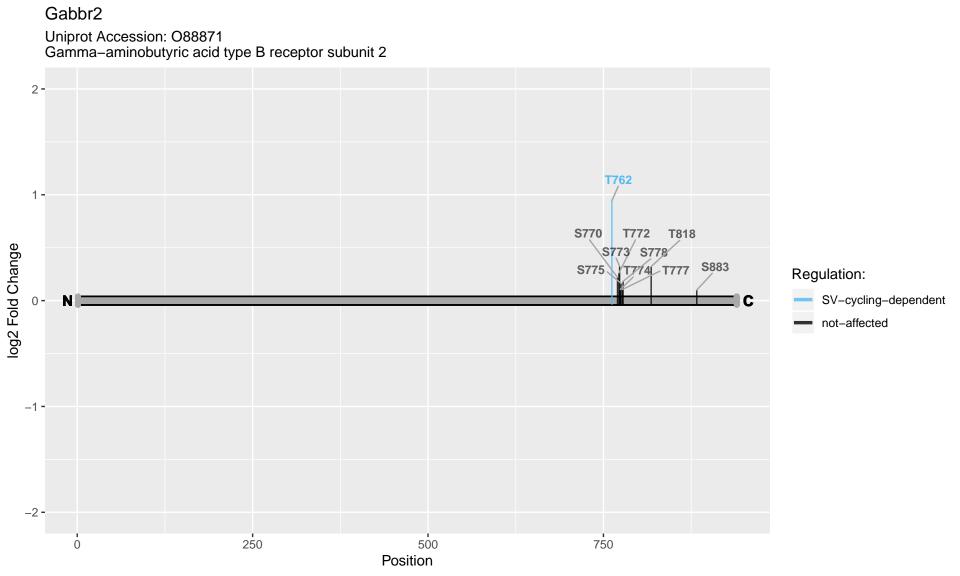
Frs2 Uniprot Accession: A0A0G2JZZ5 Fibroblast growth factor receptor substrate 2 2 -Regulation: log2 Fold Change SV-cycling-dependent **S437** not-affected Domains and Regions: **S374** DOMAIN: IRS-type PTB **REGION: Disordered** -1 **-**-2 **-**100 200 300 400 500 Position

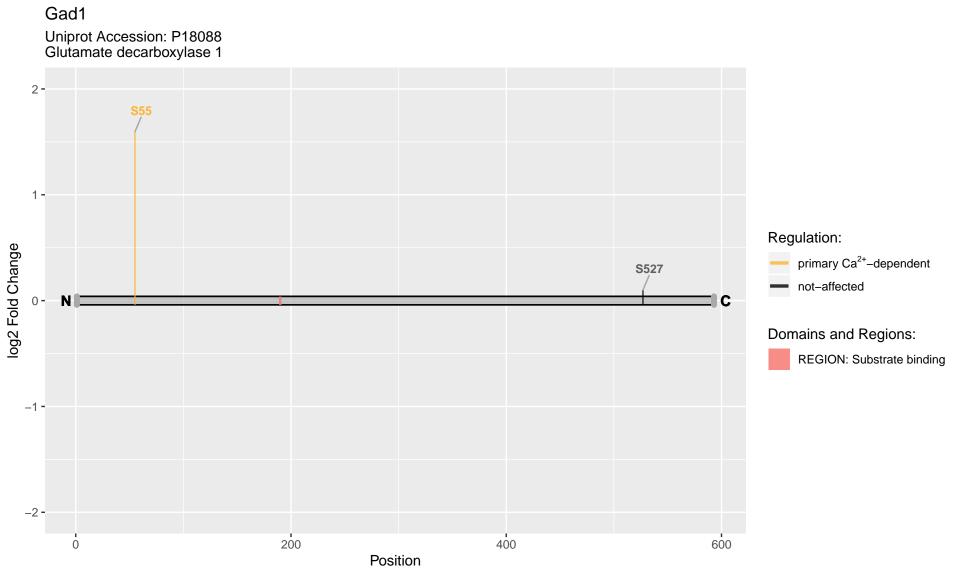


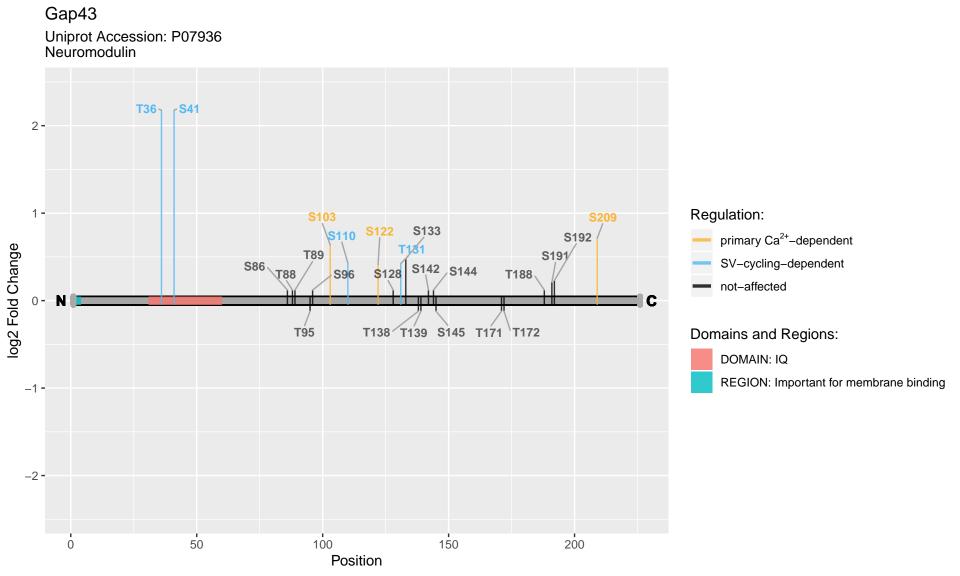


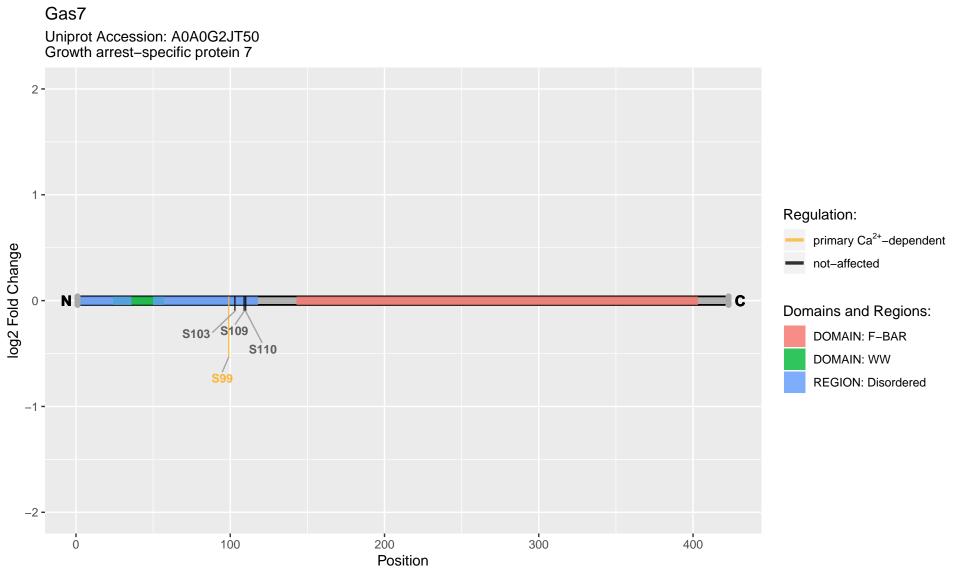


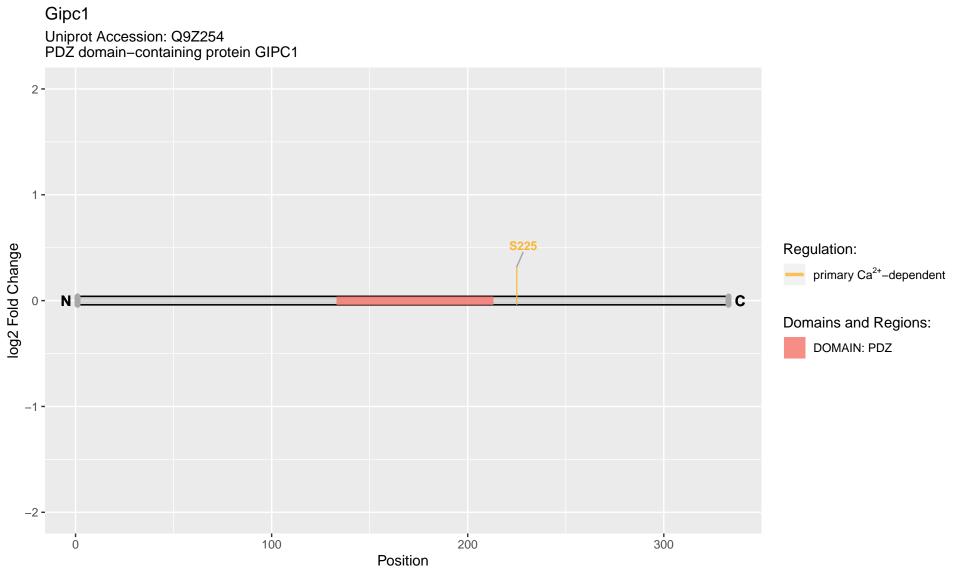


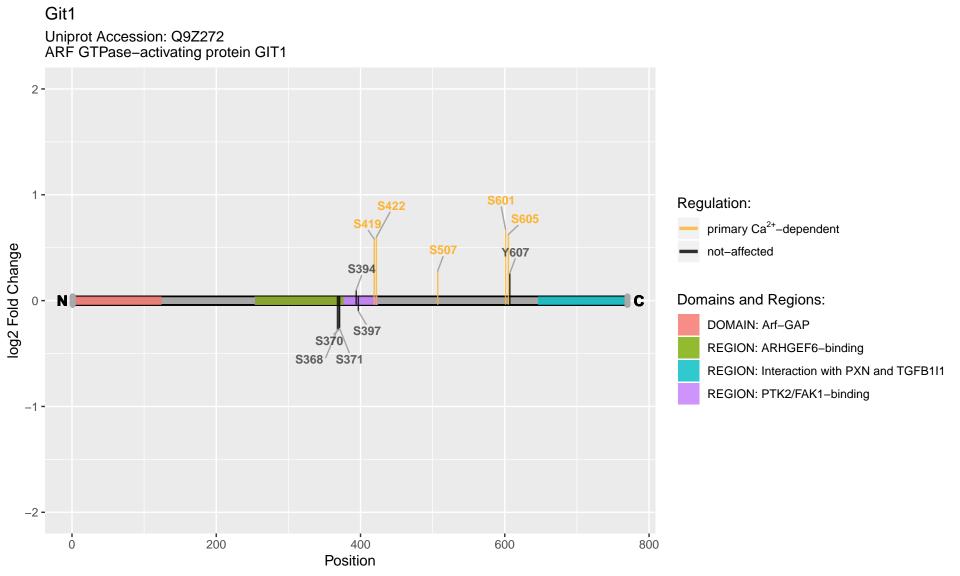


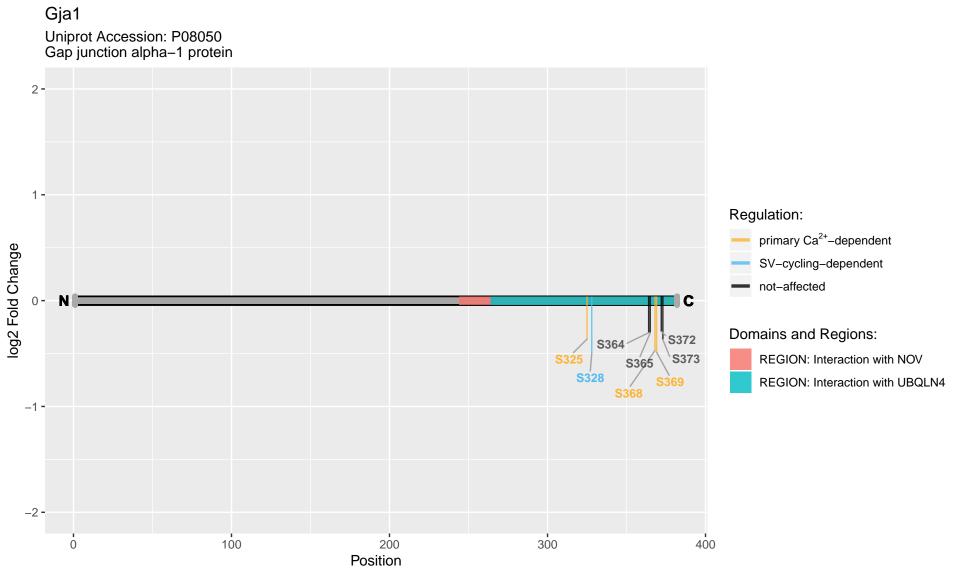


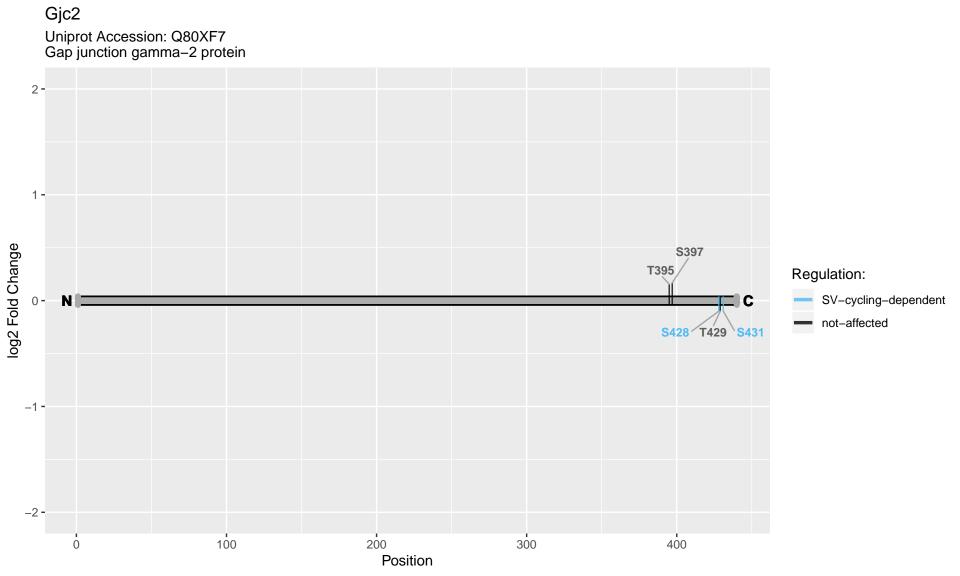


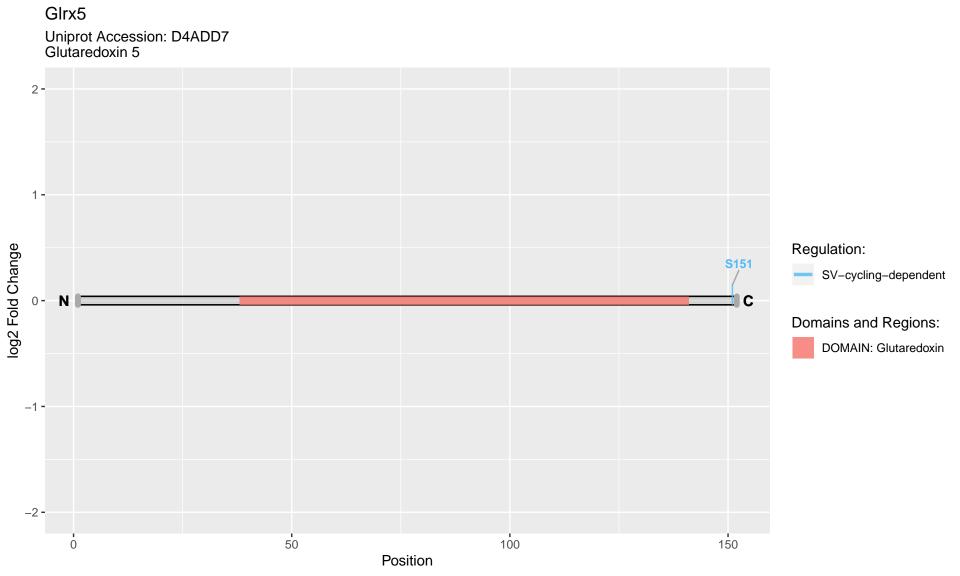


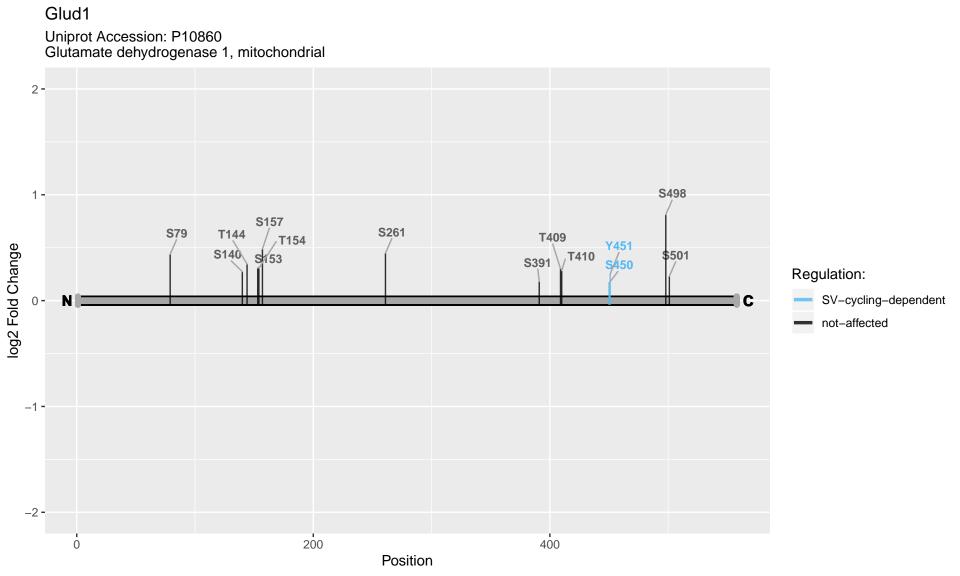


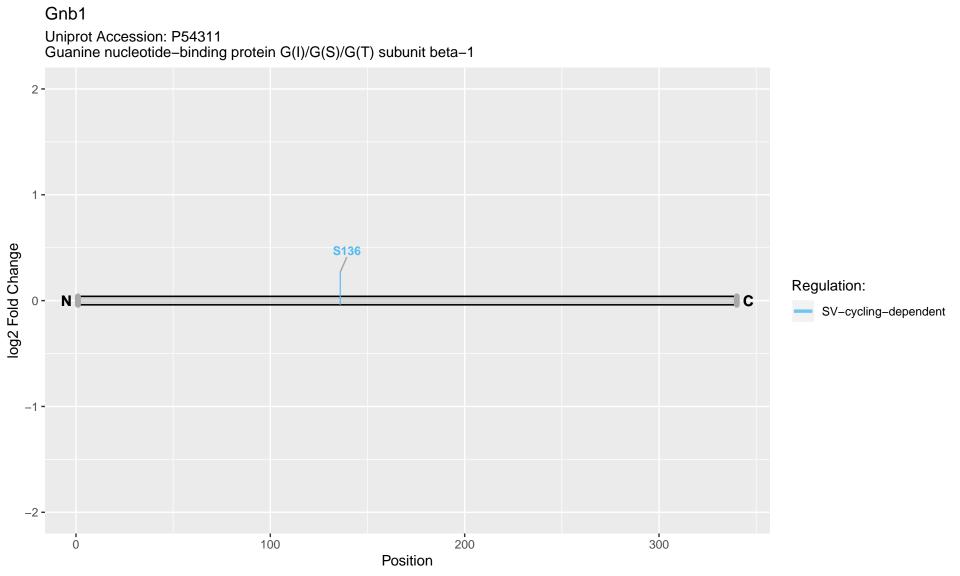


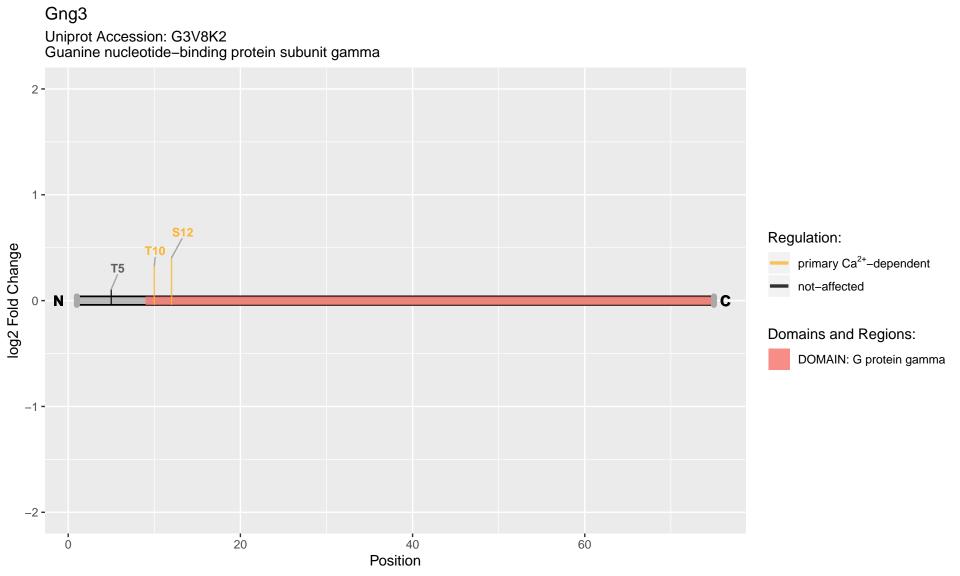


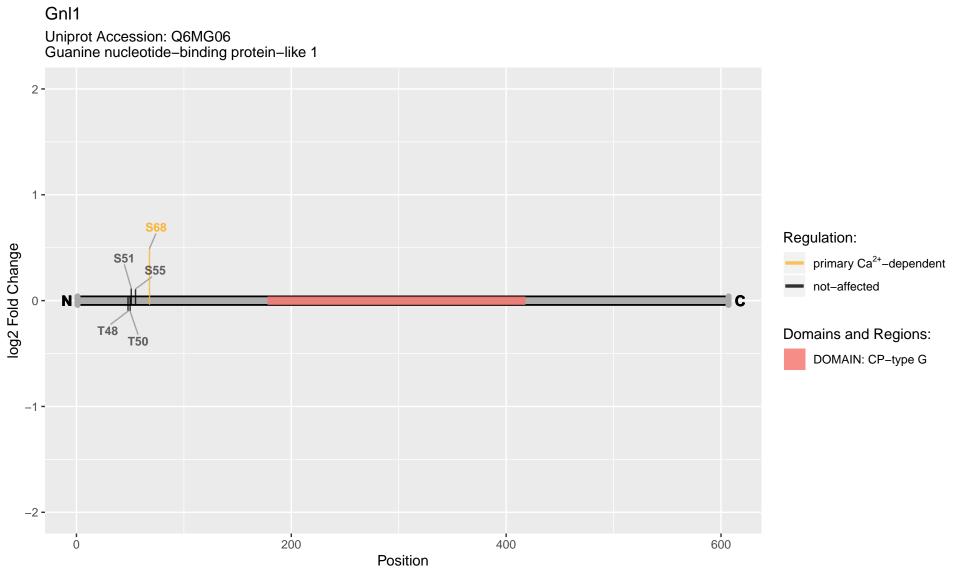


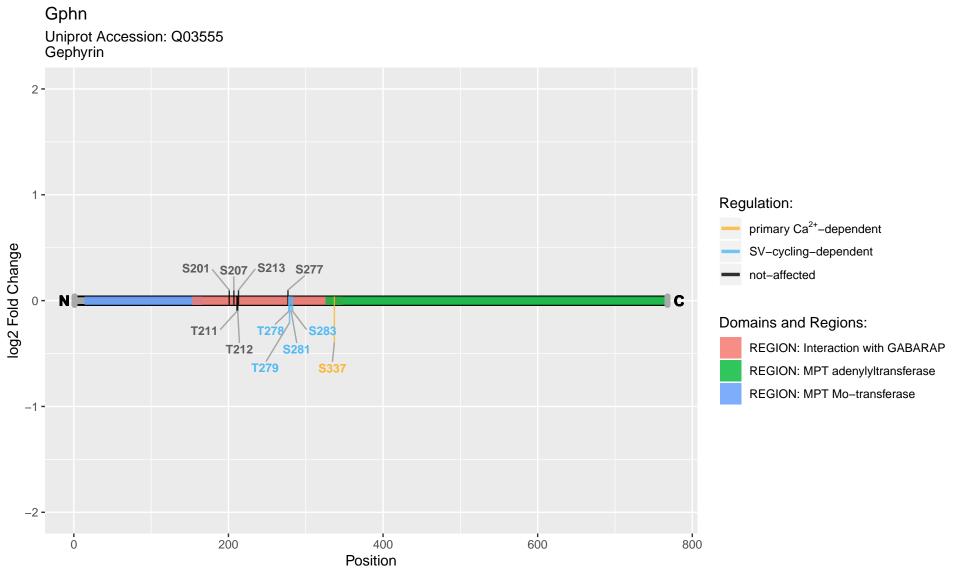


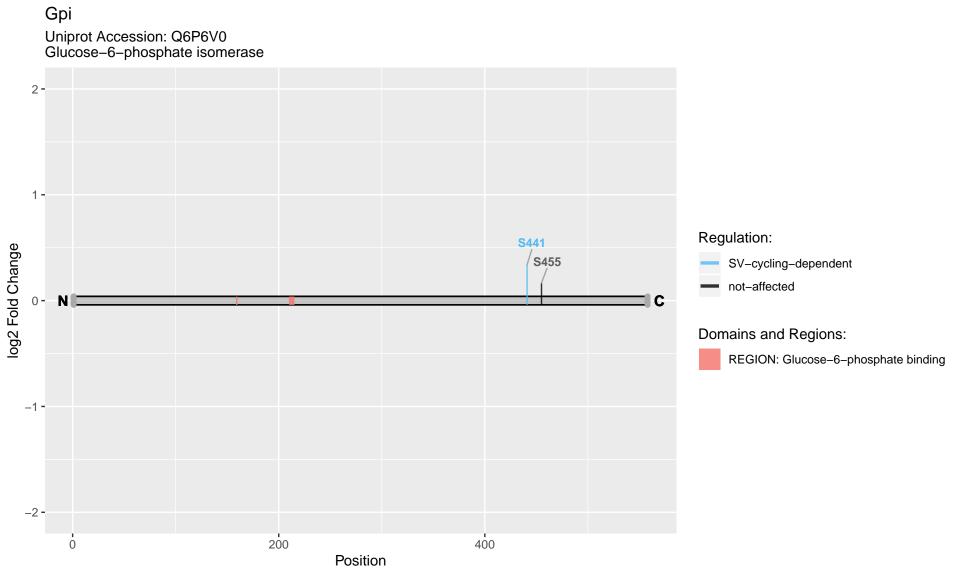


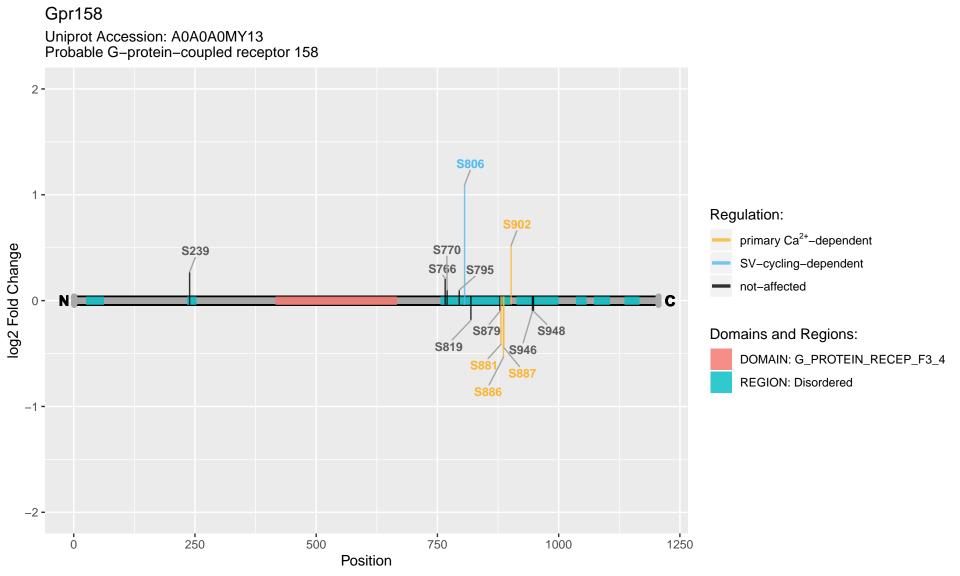


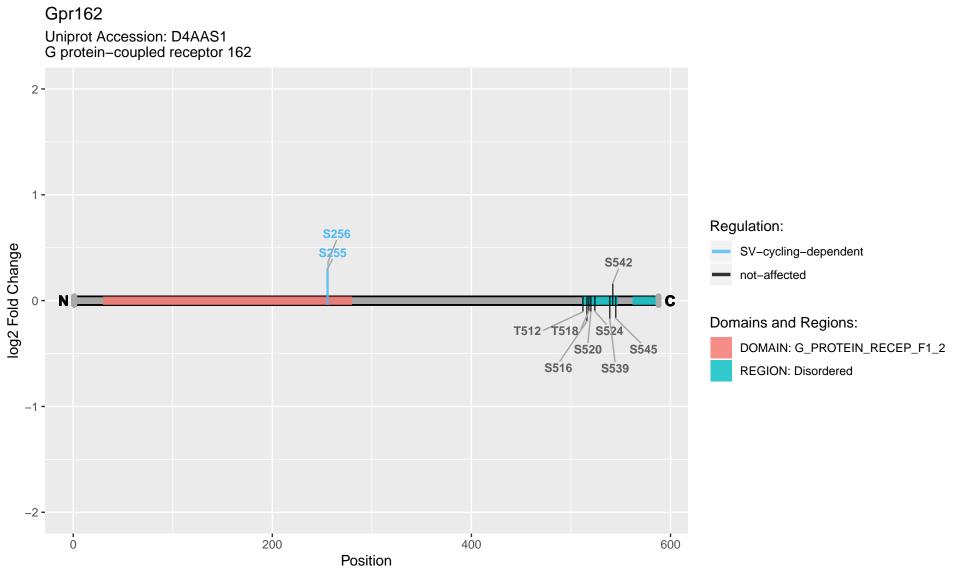


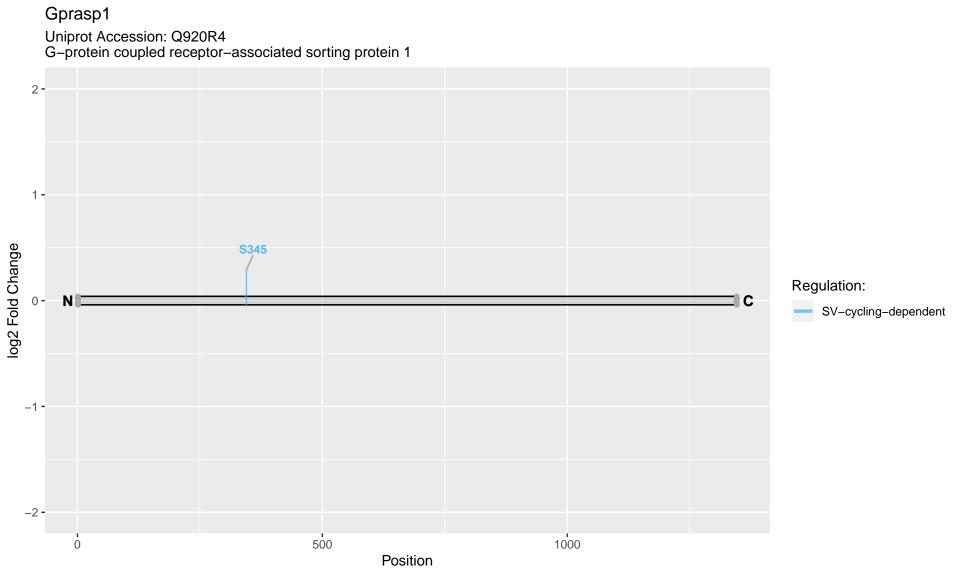


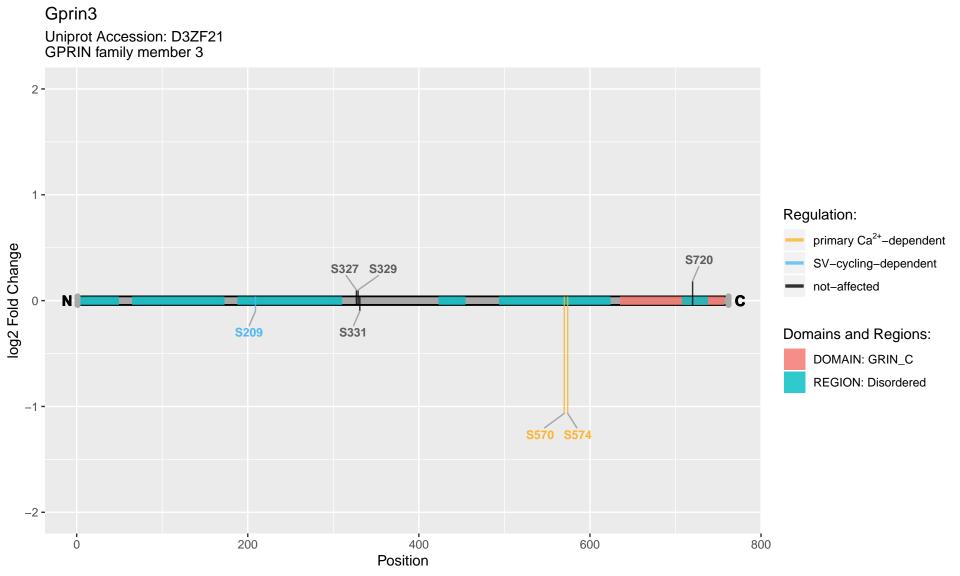


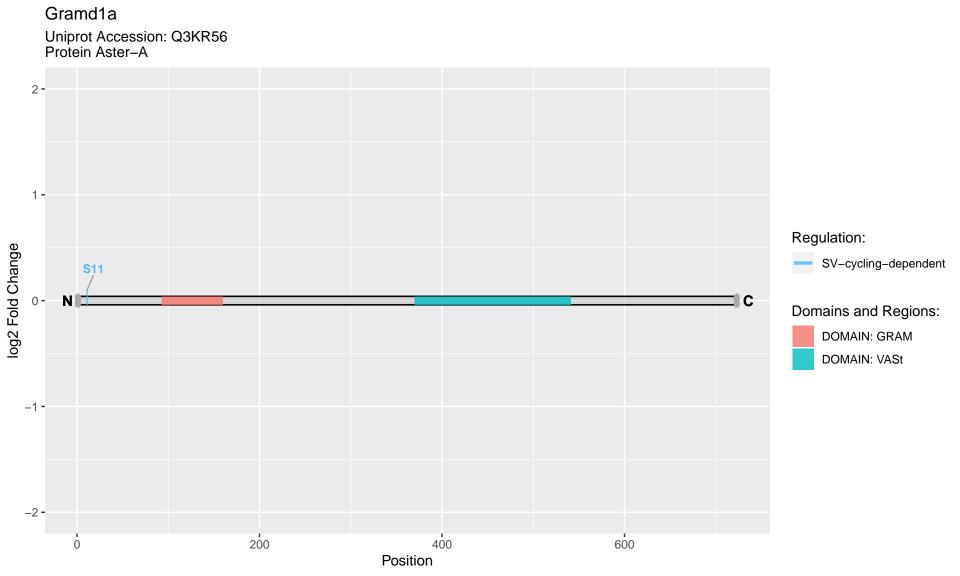


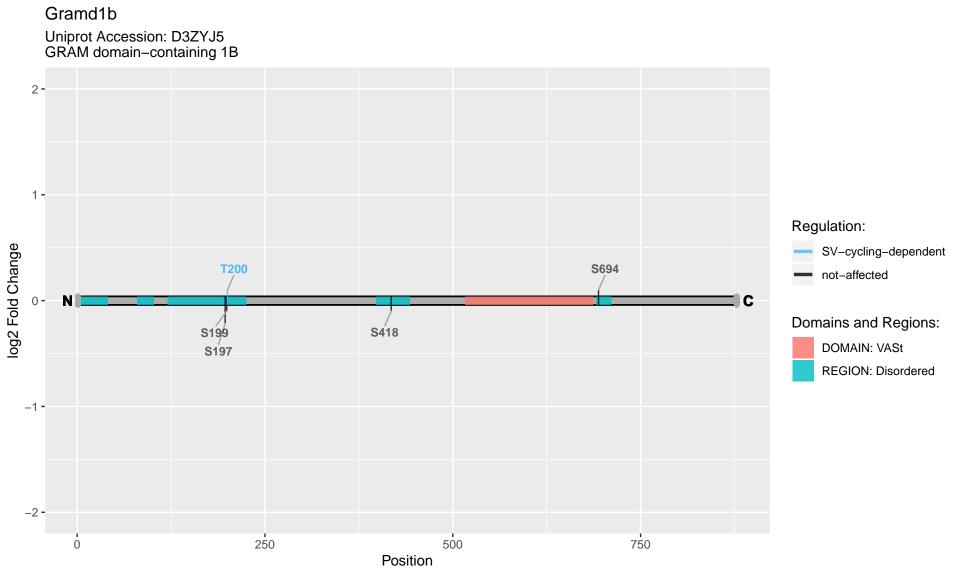


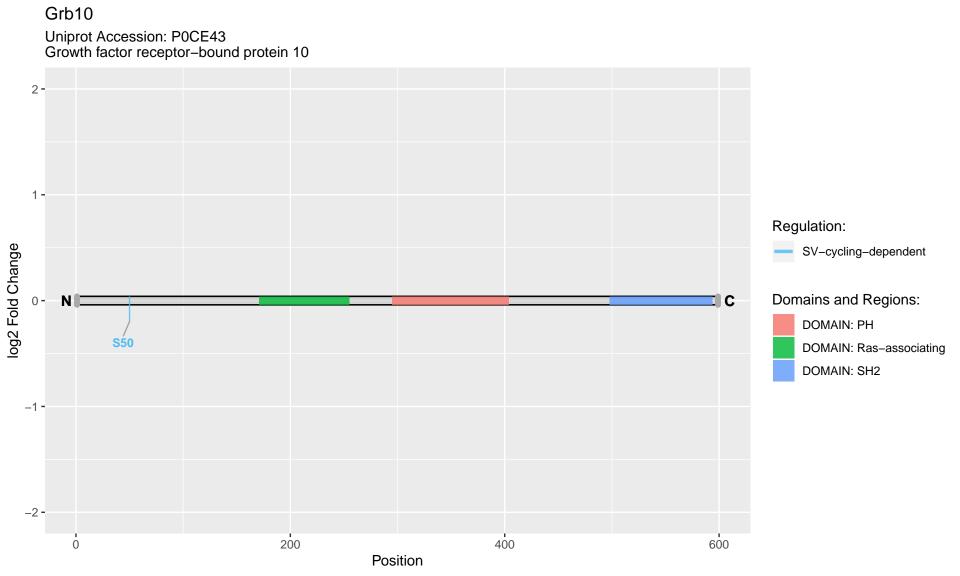


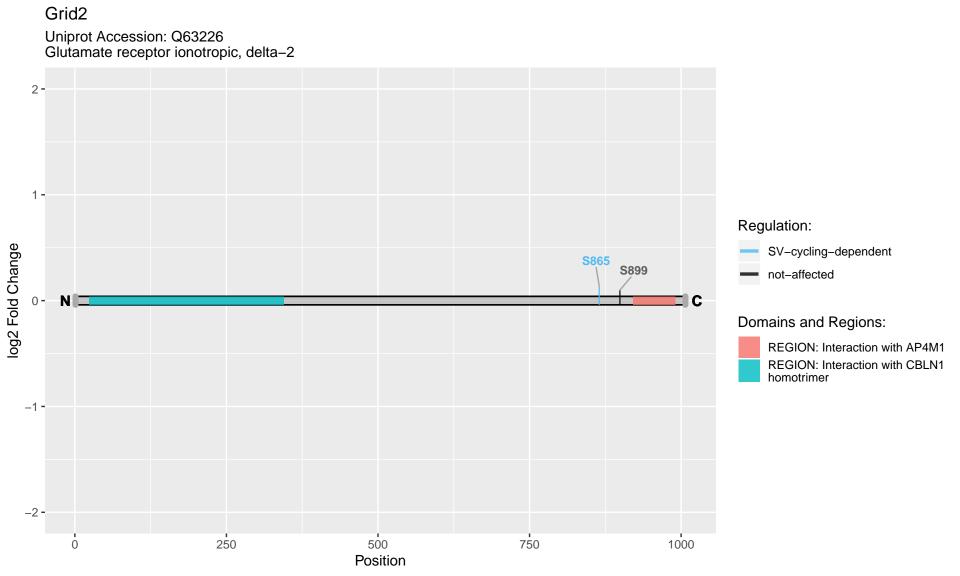


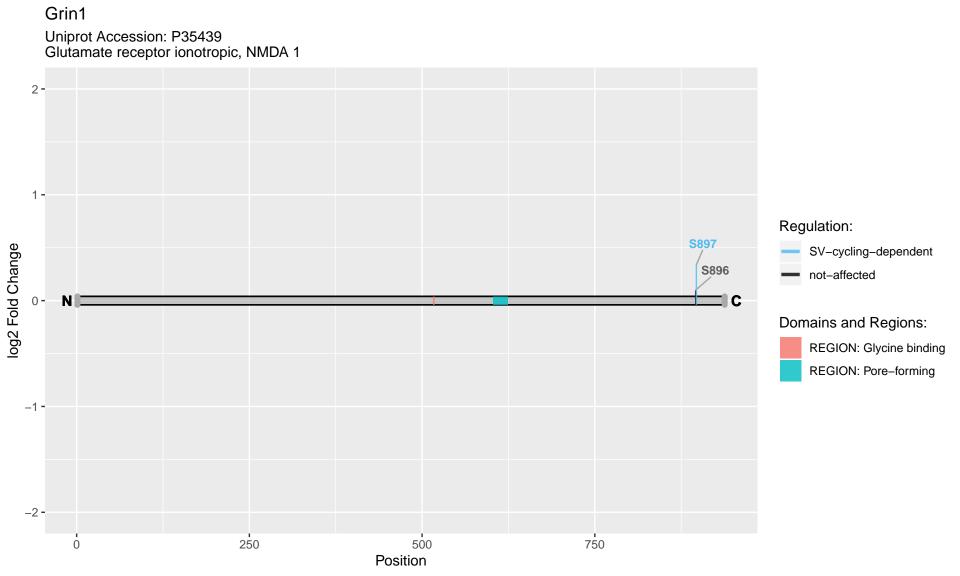


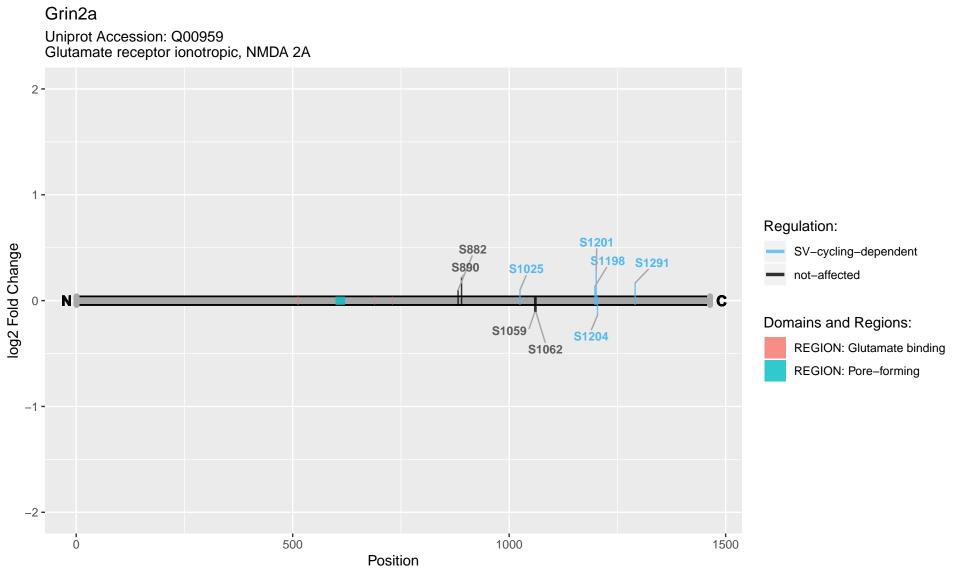


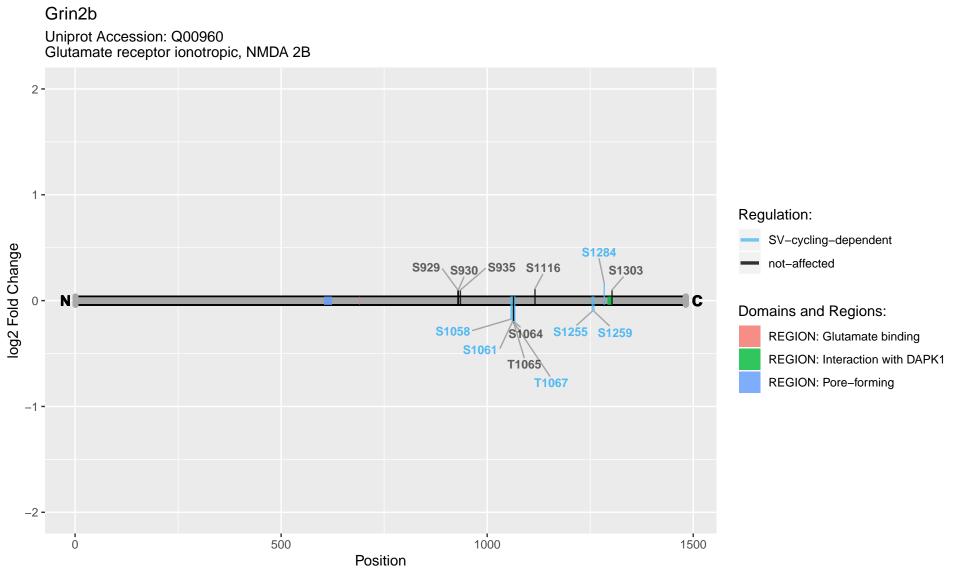


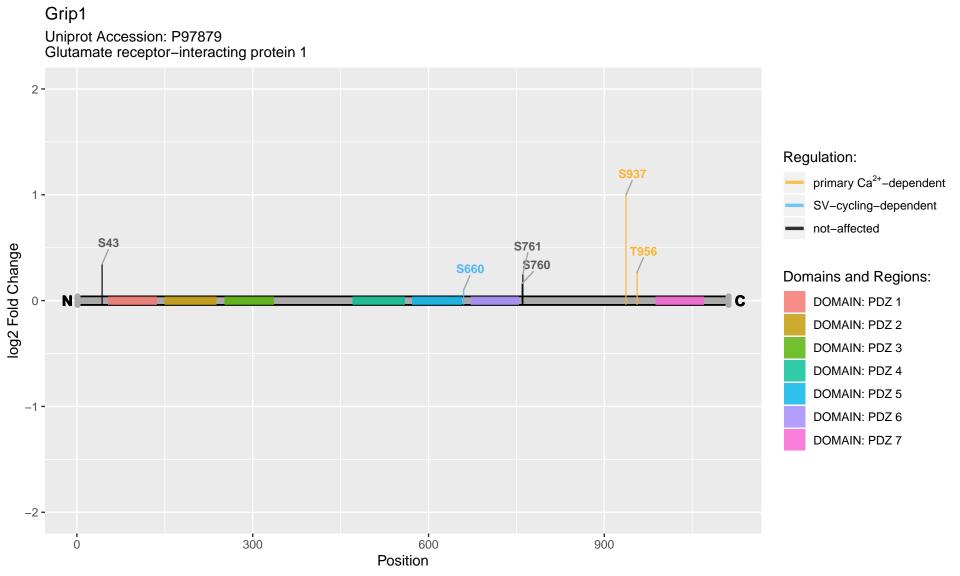


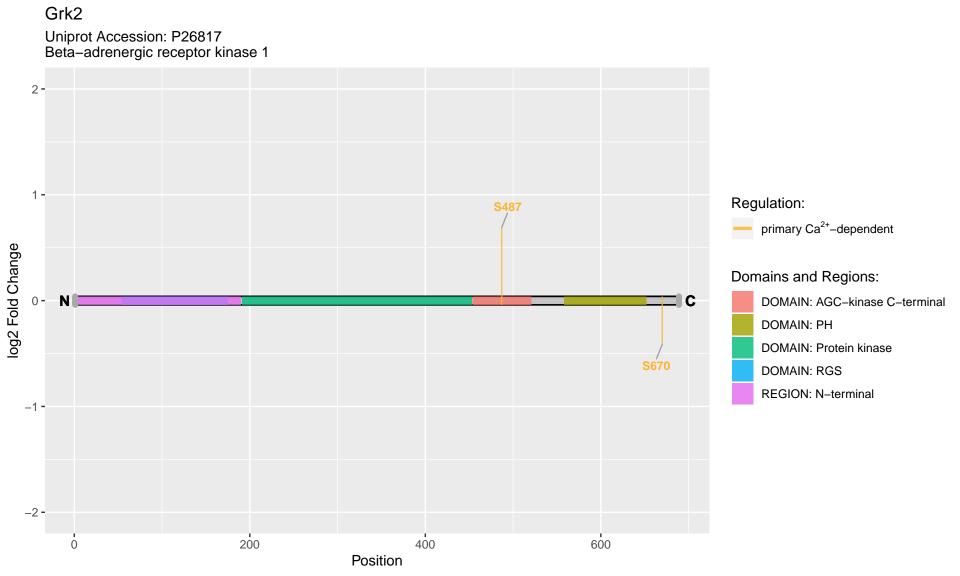


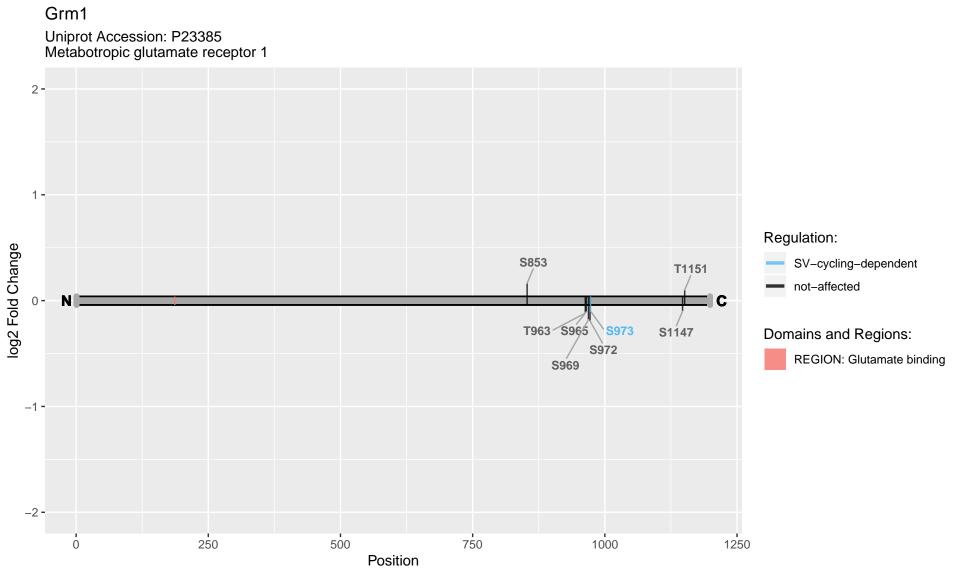


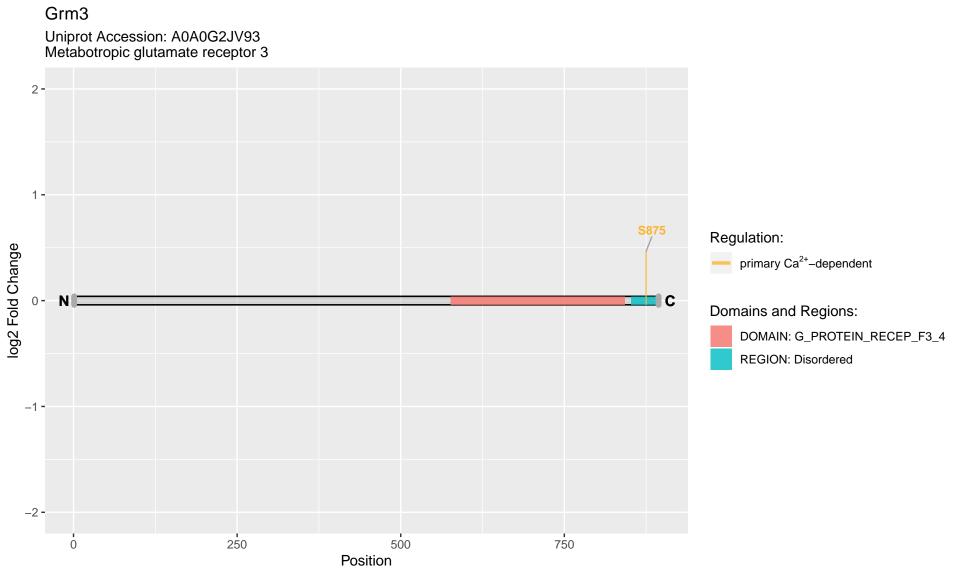


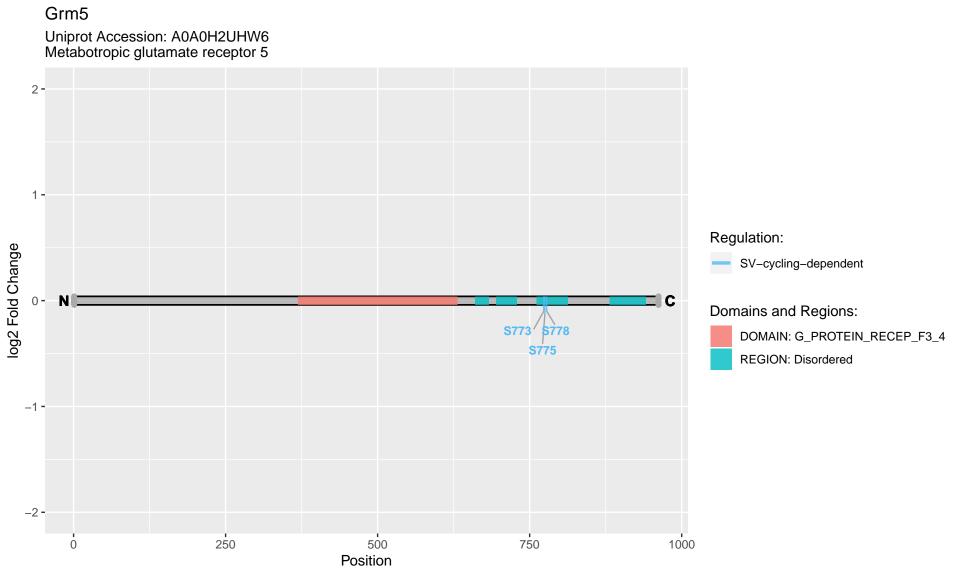


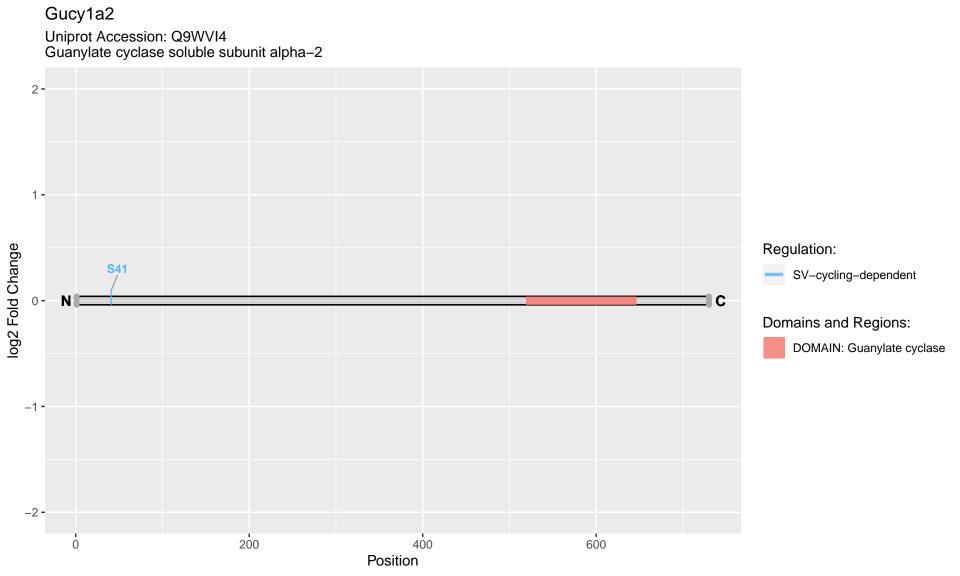


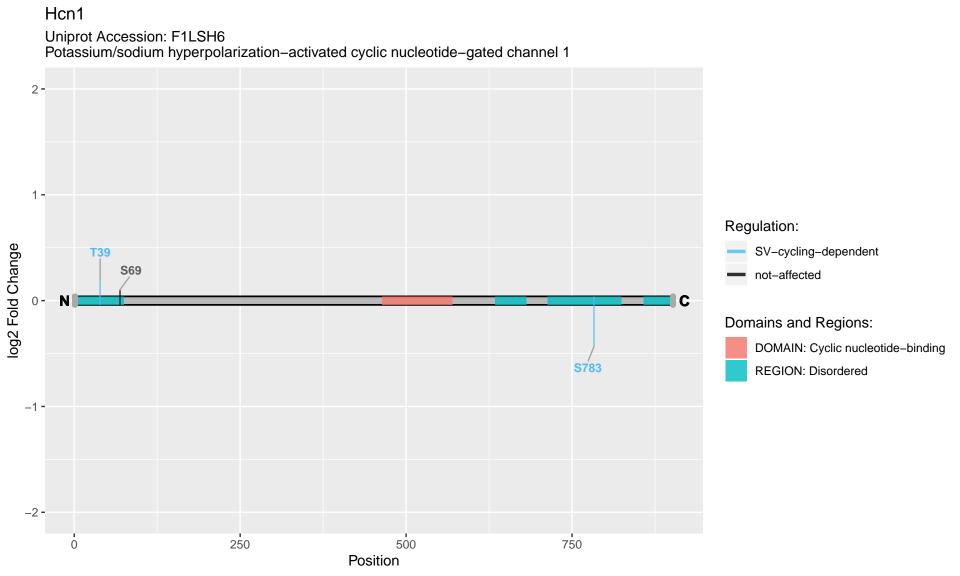


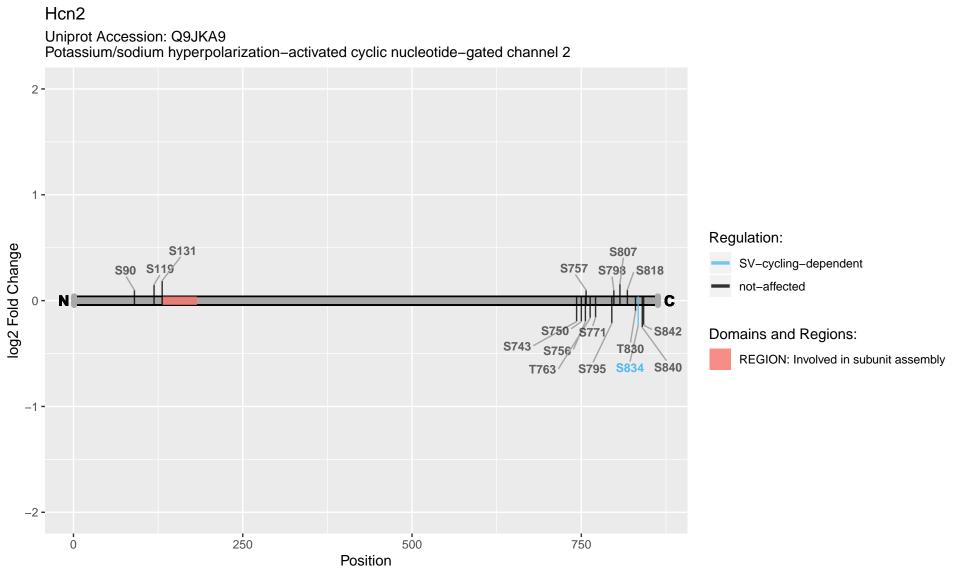


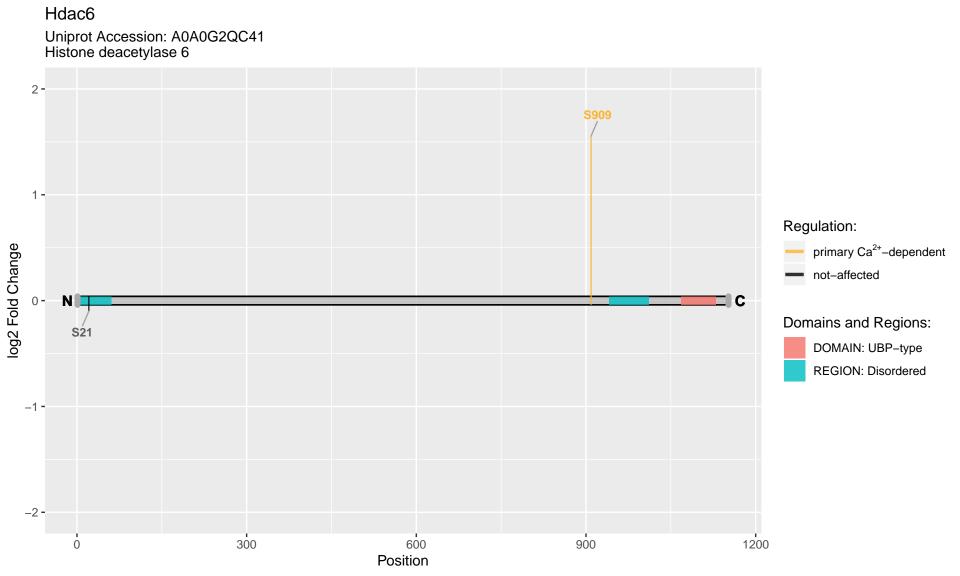


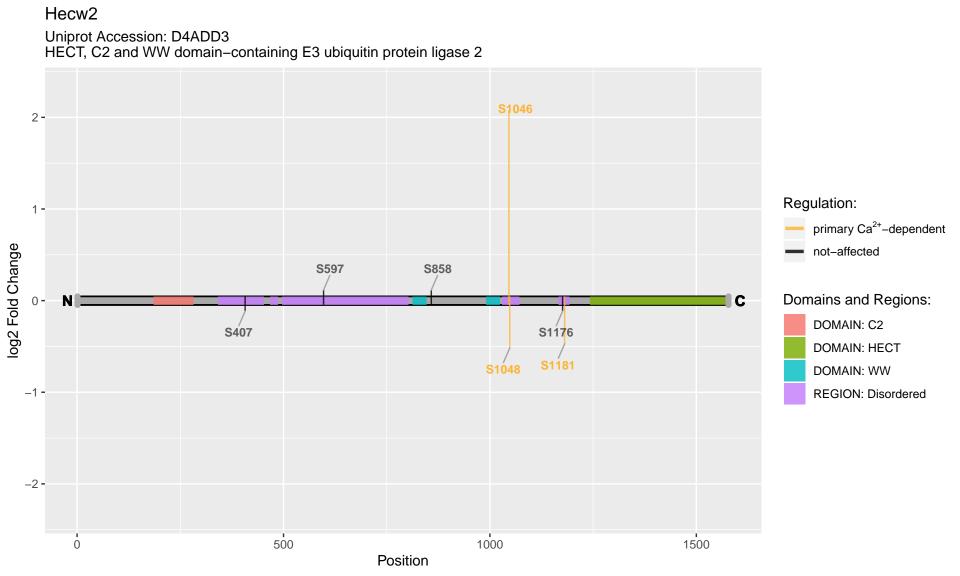


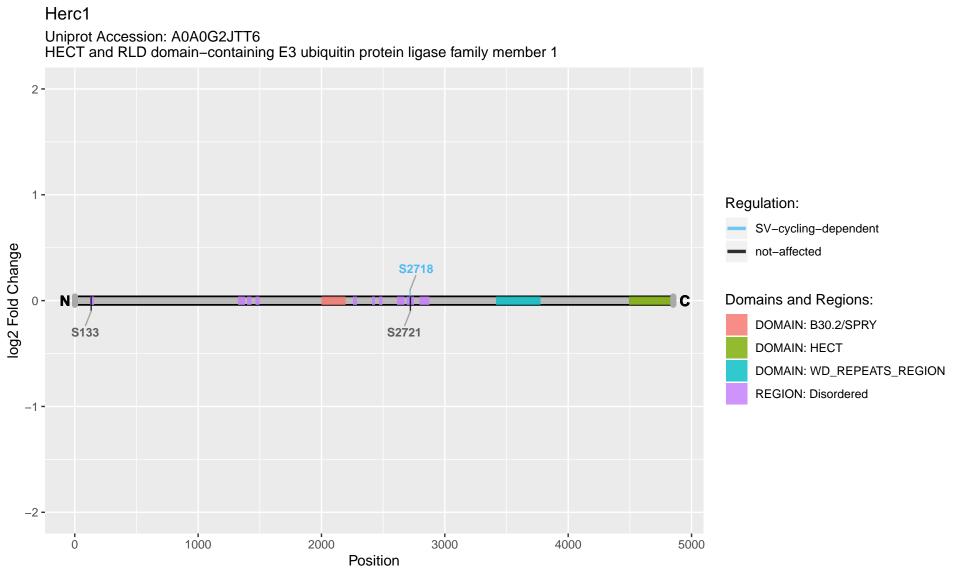


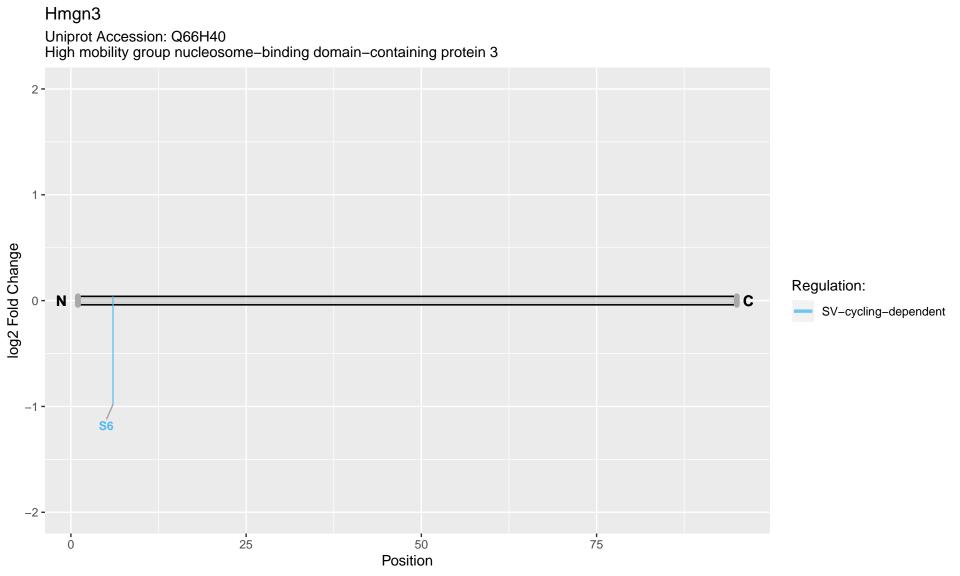


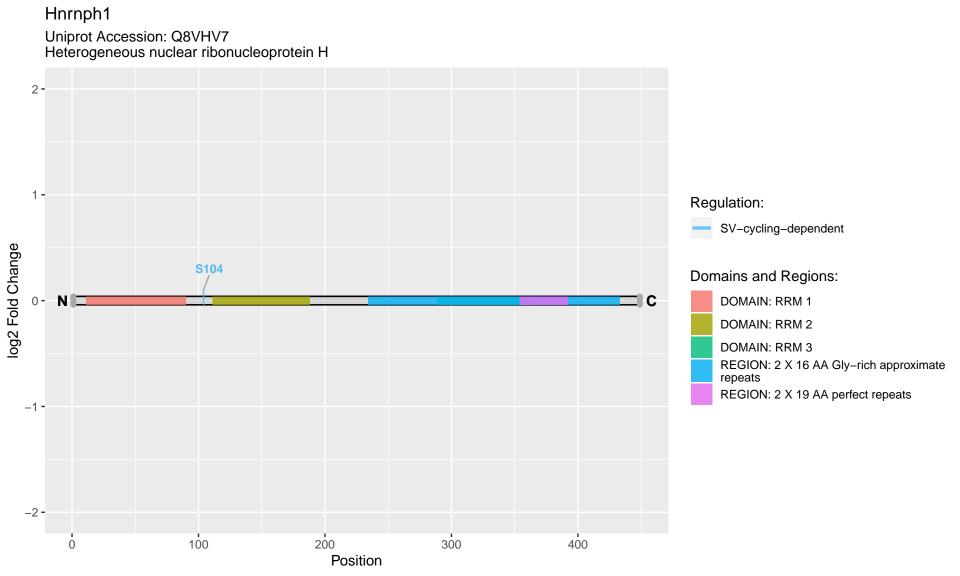


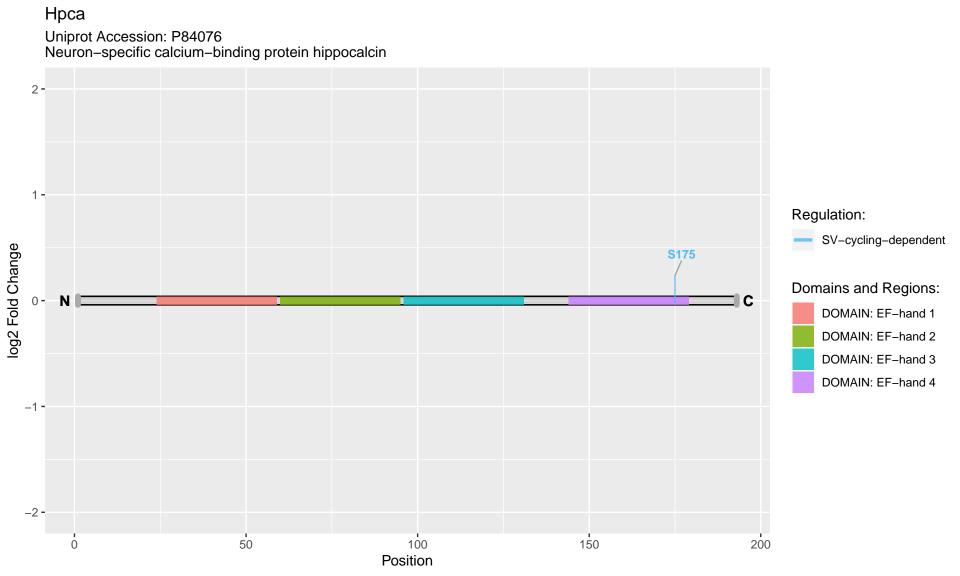


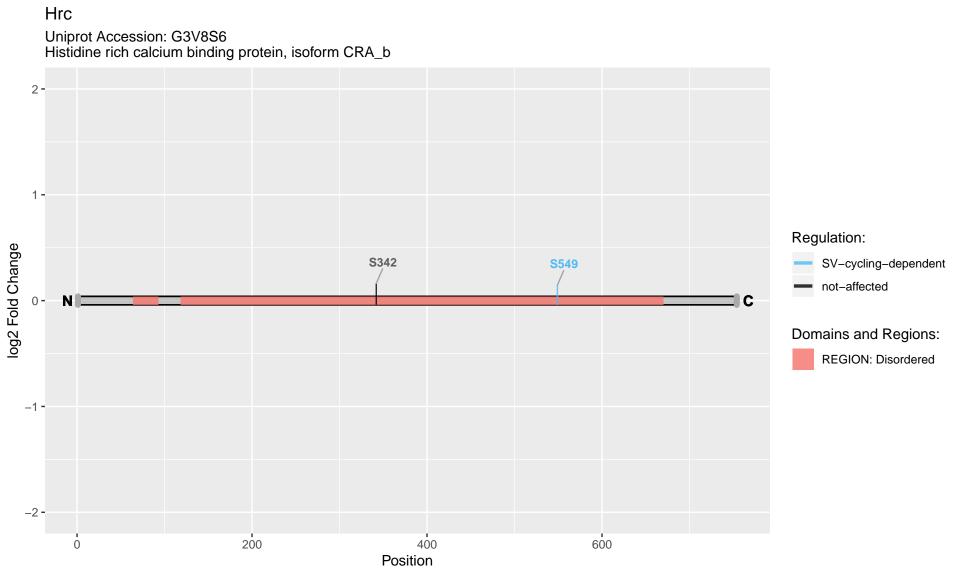


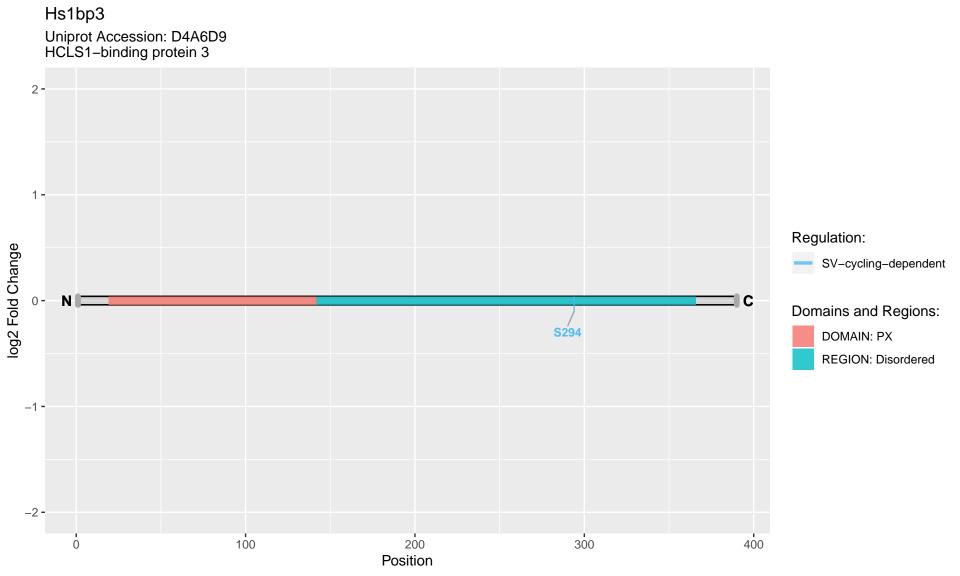


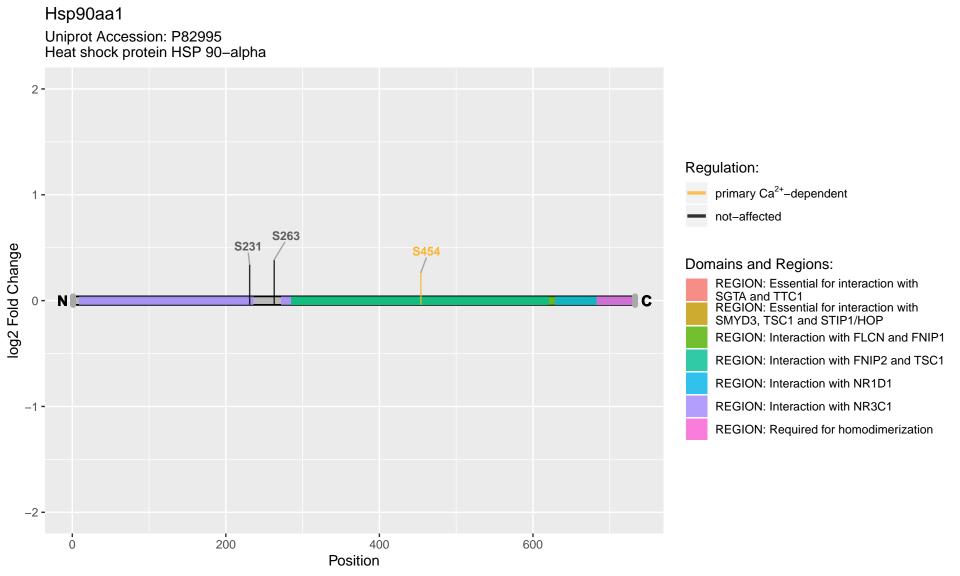


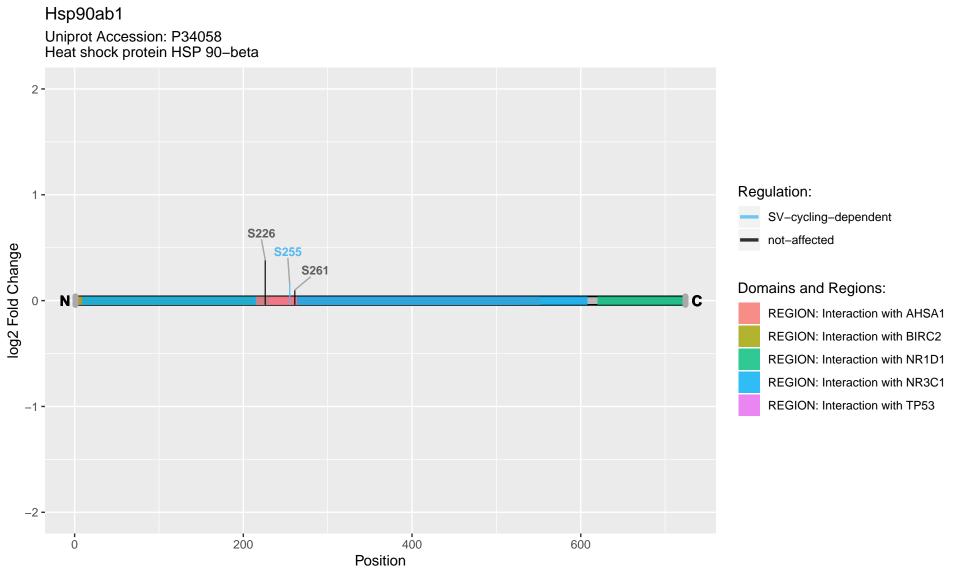


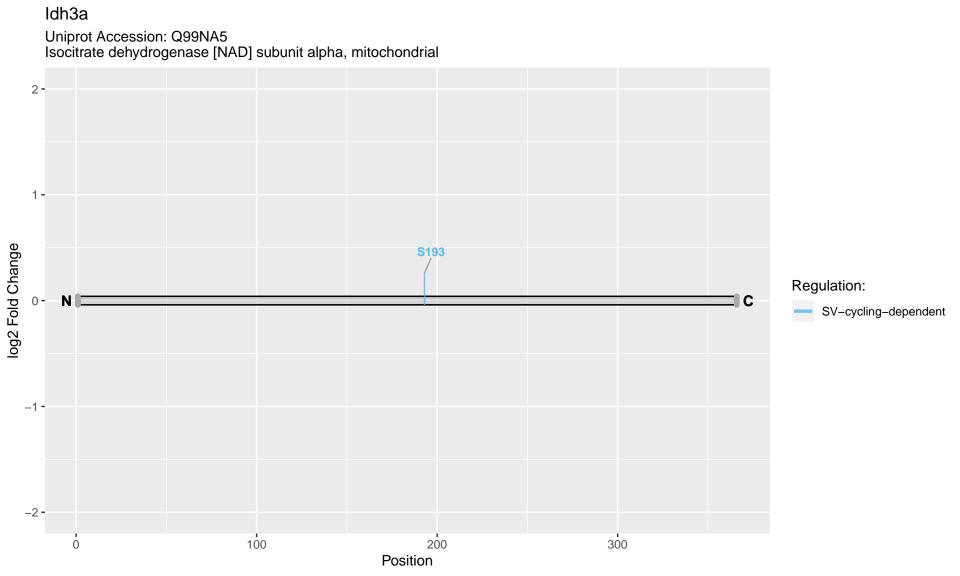


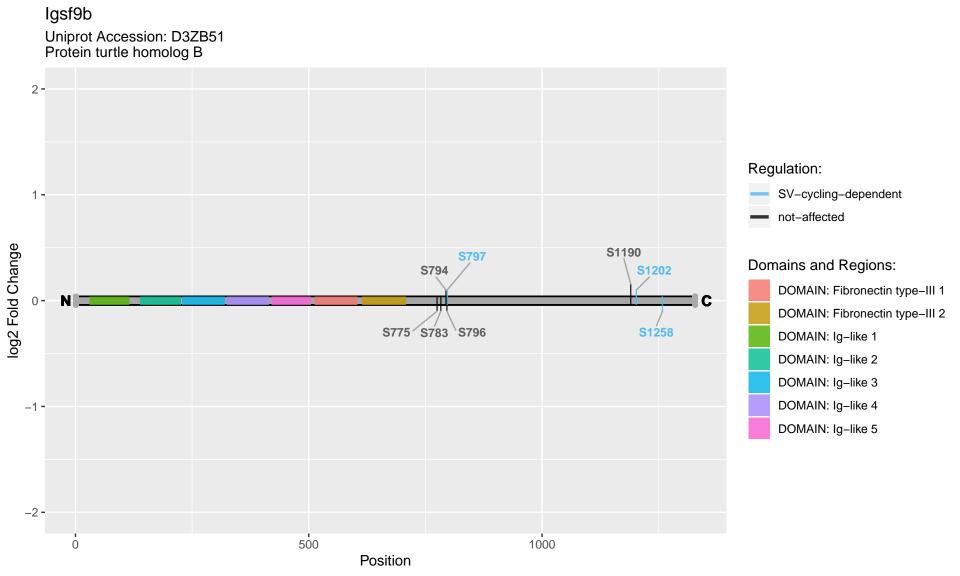


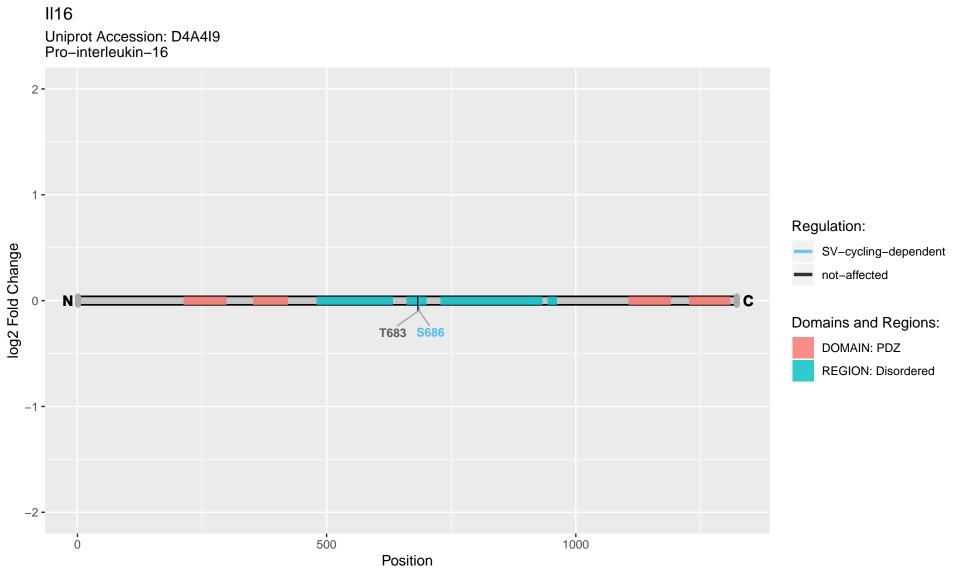


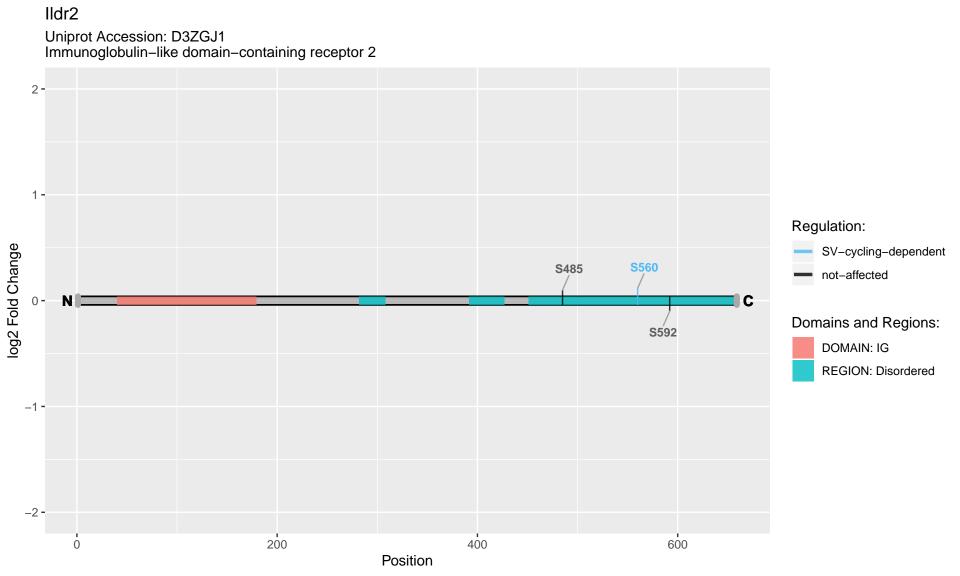


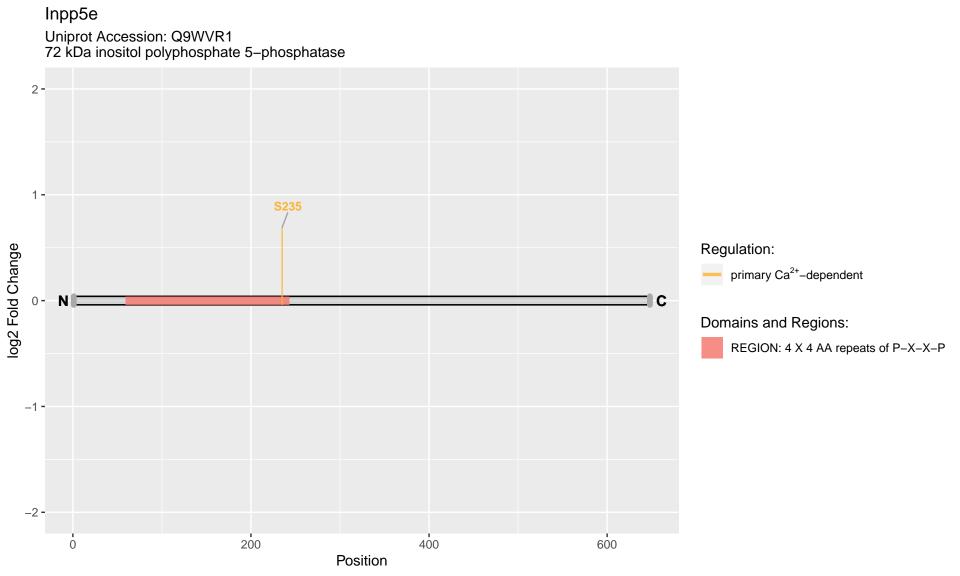


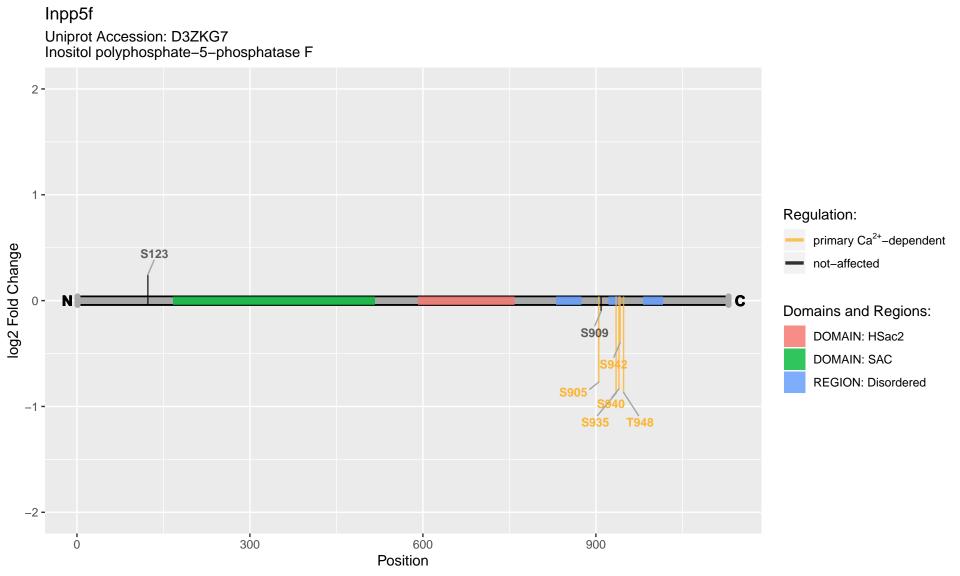


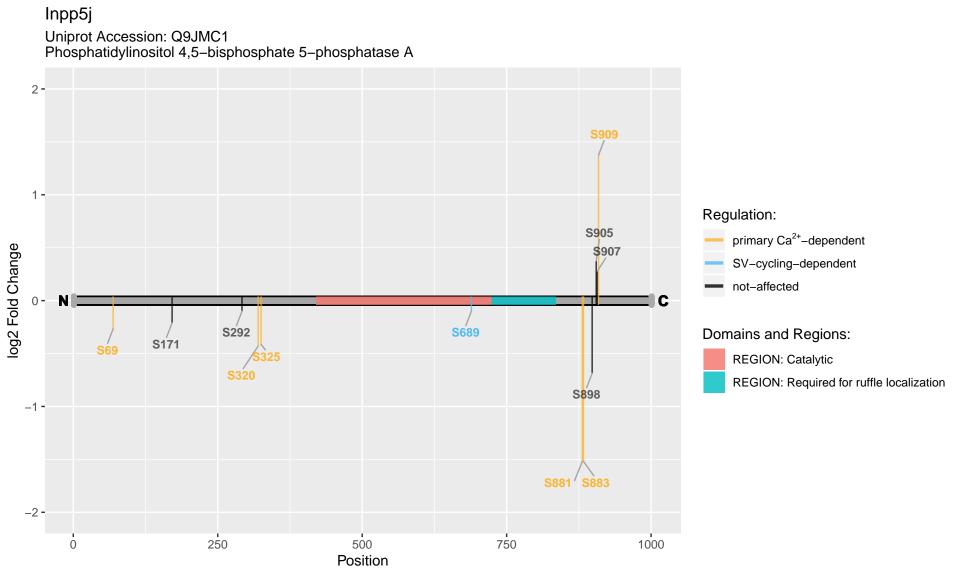


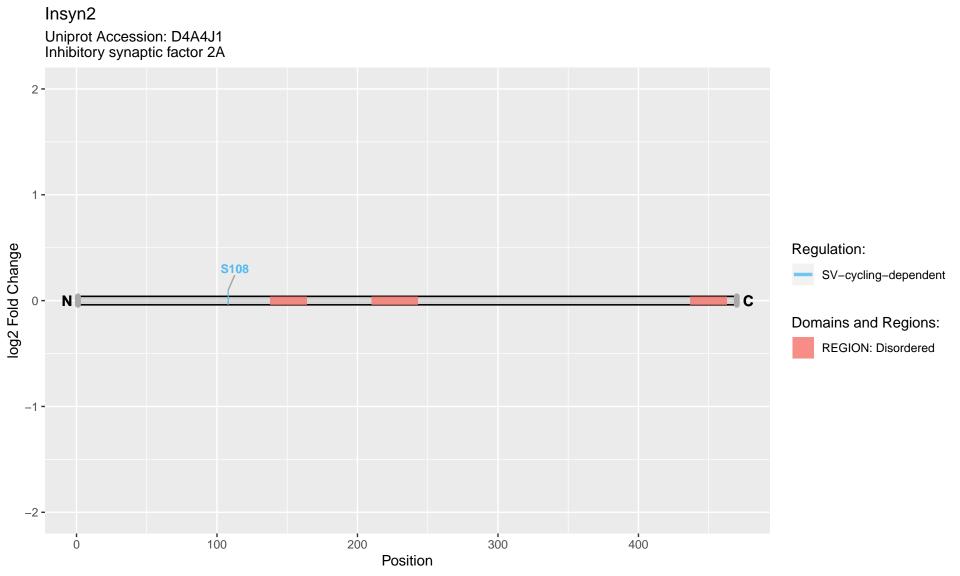


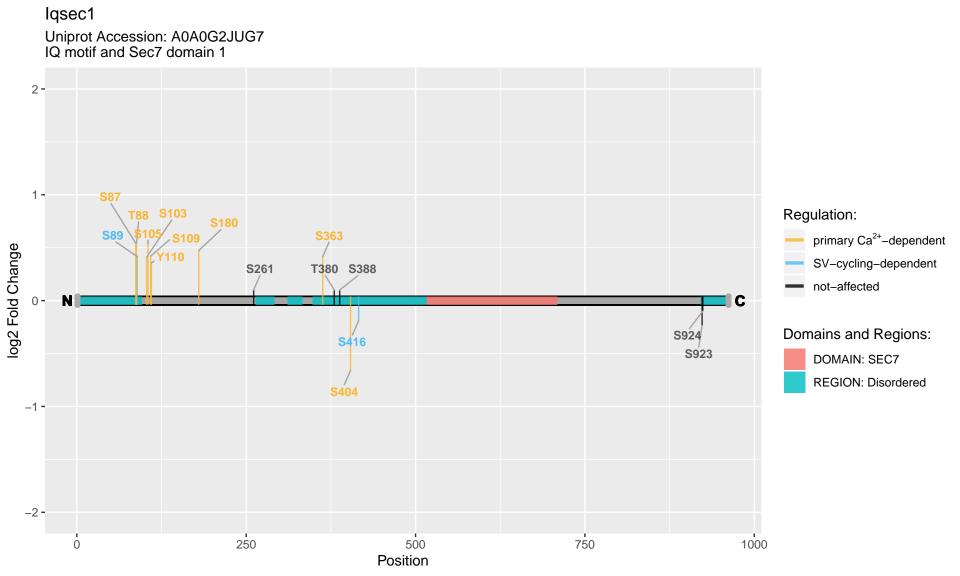


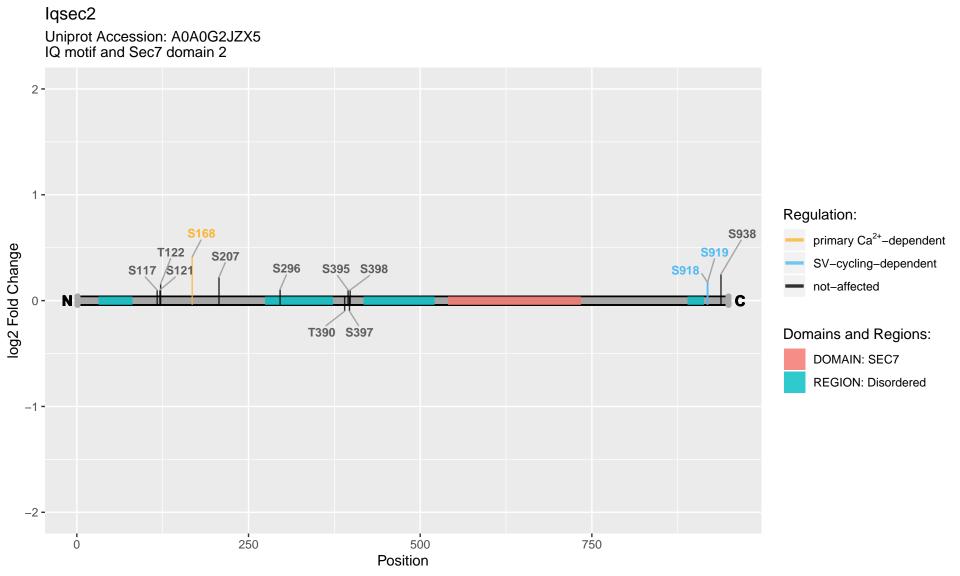


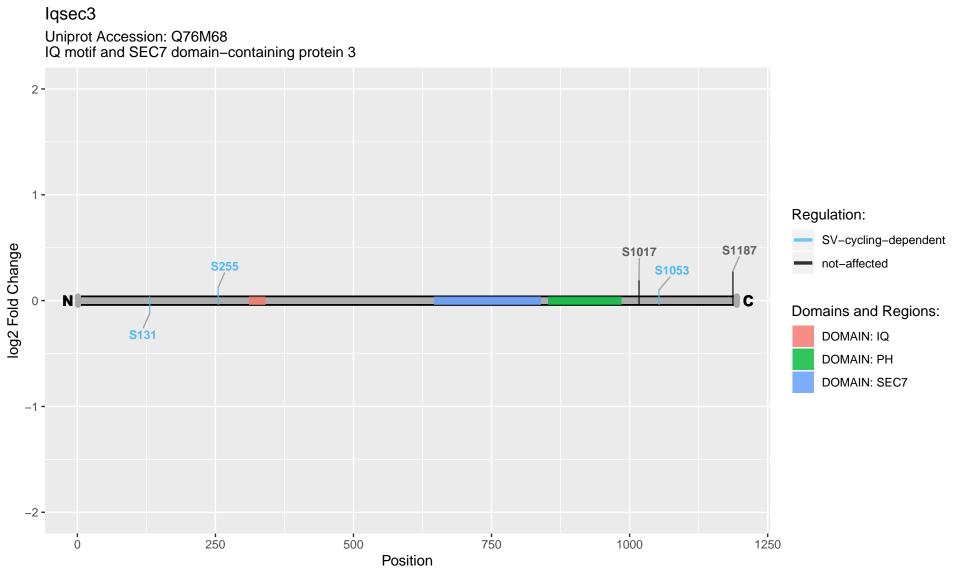


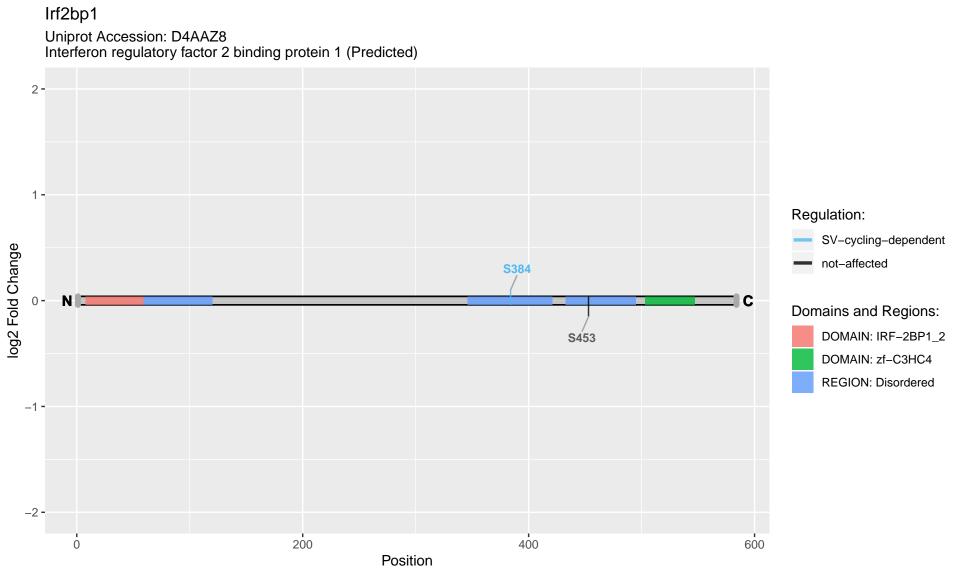


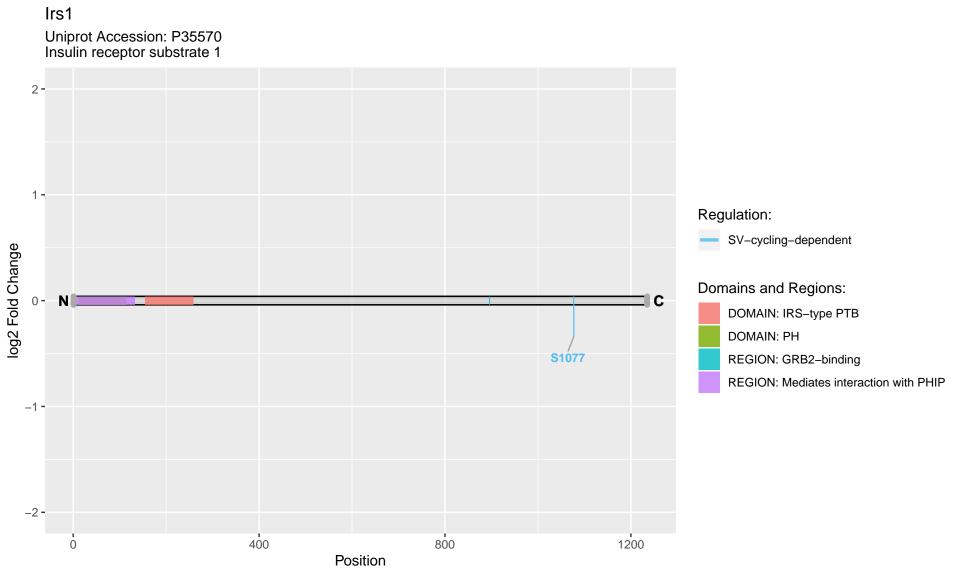


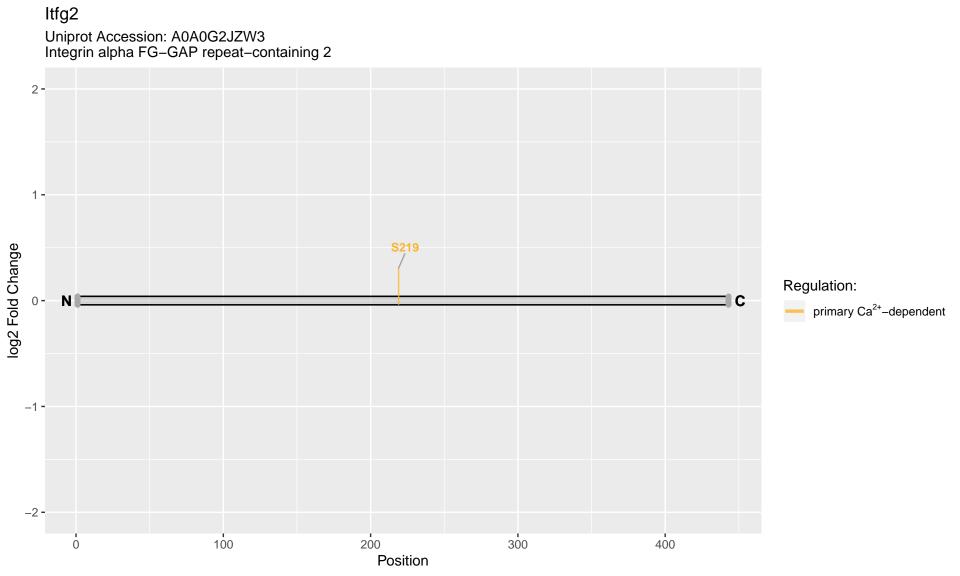


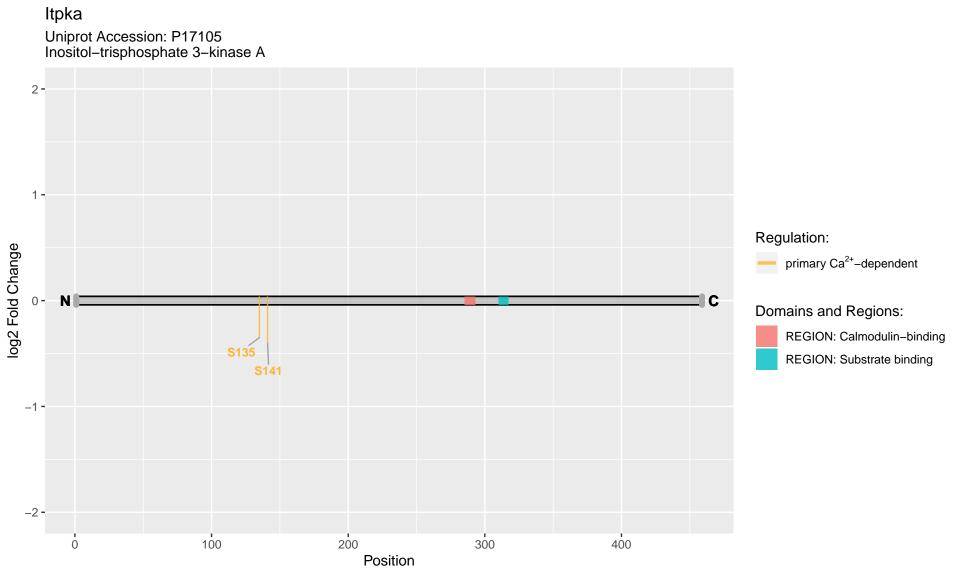


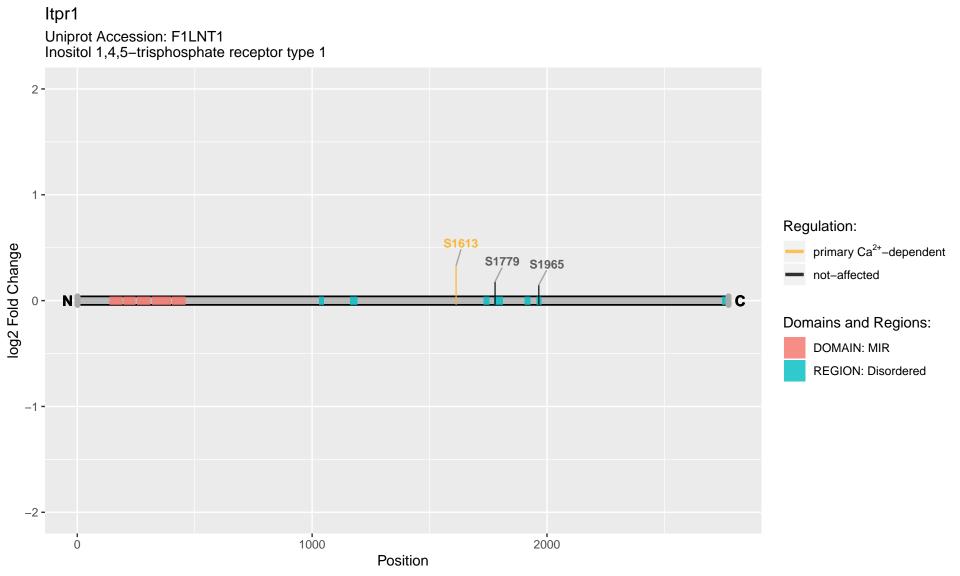


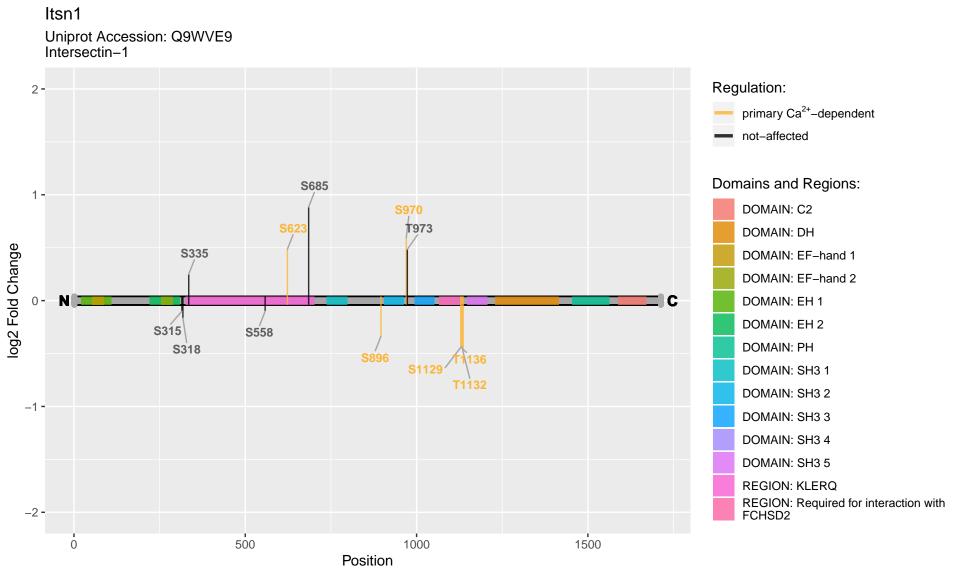


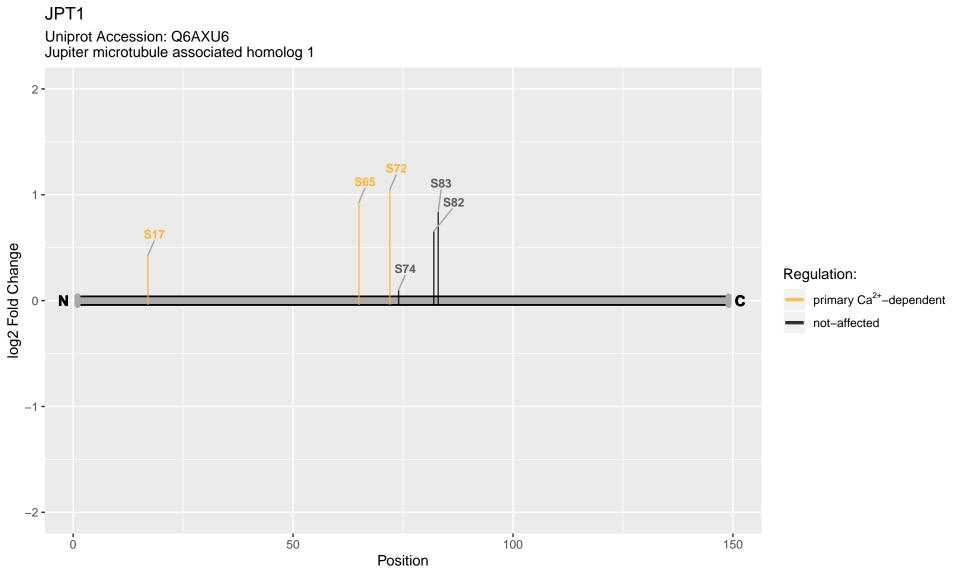


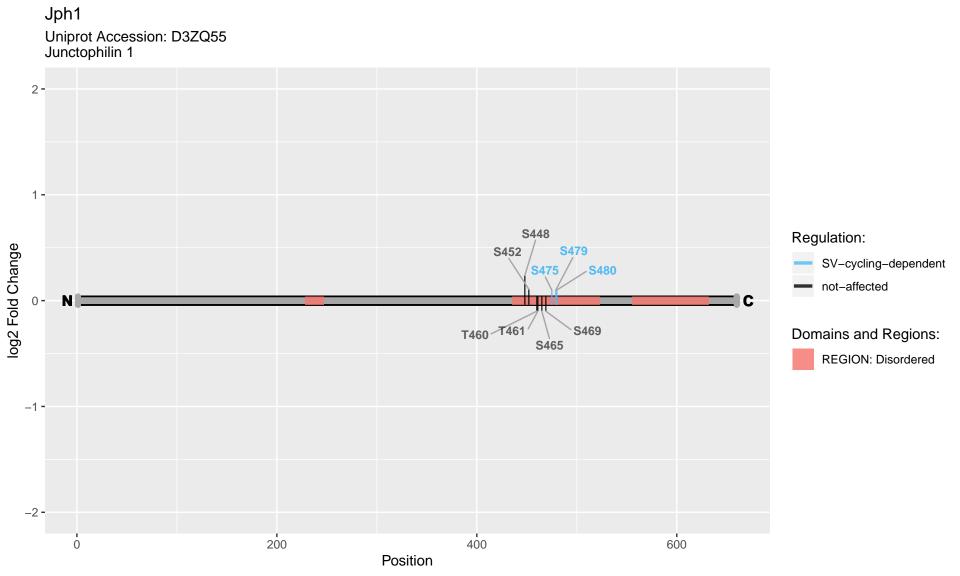


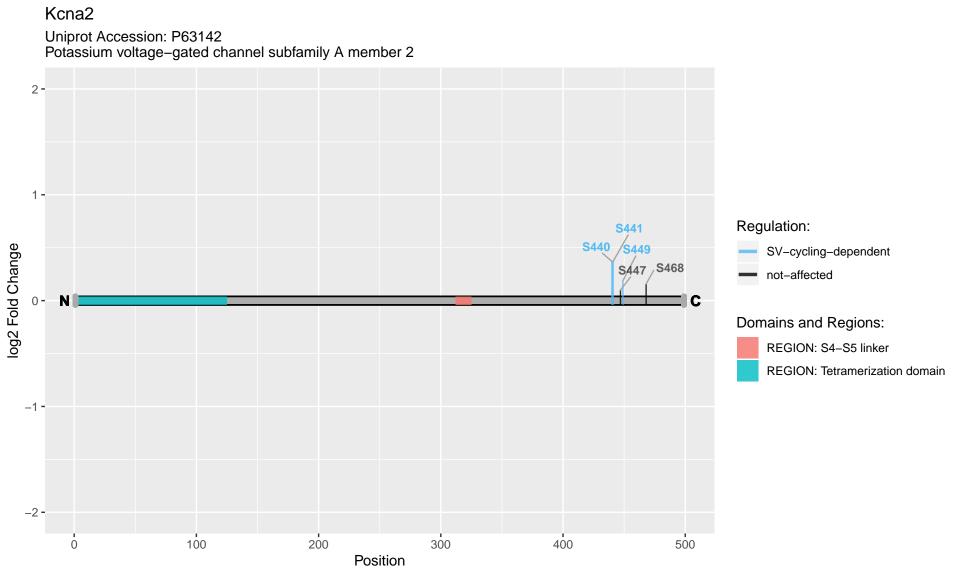


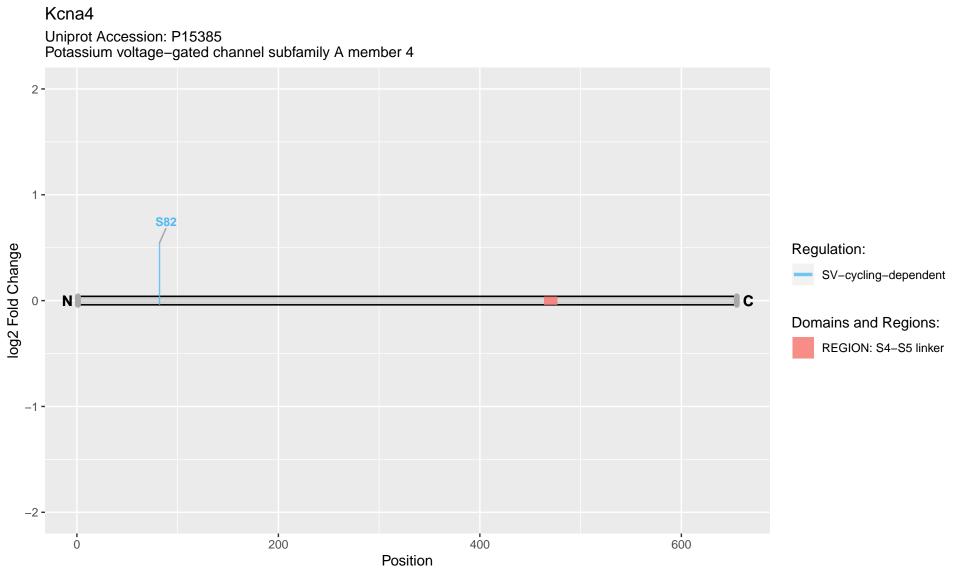


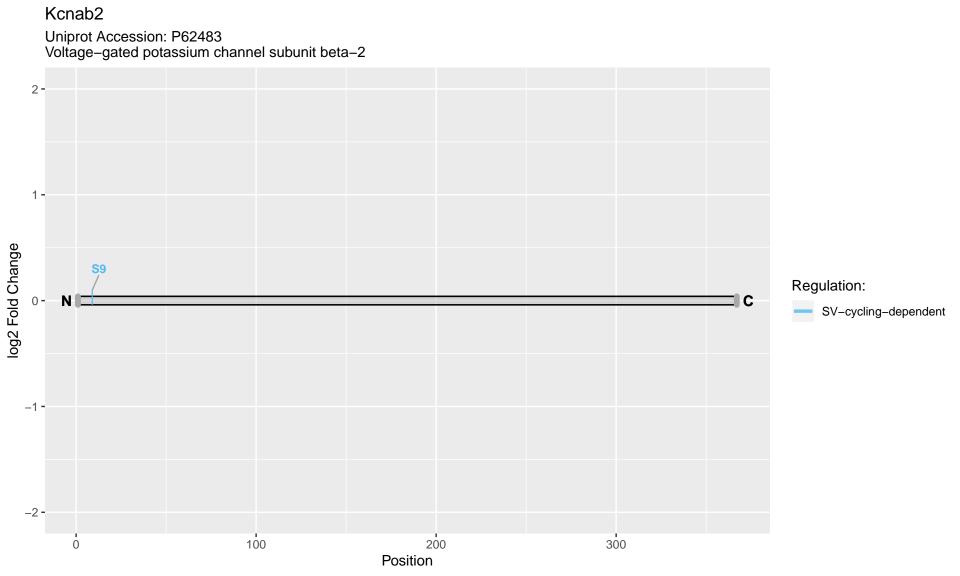


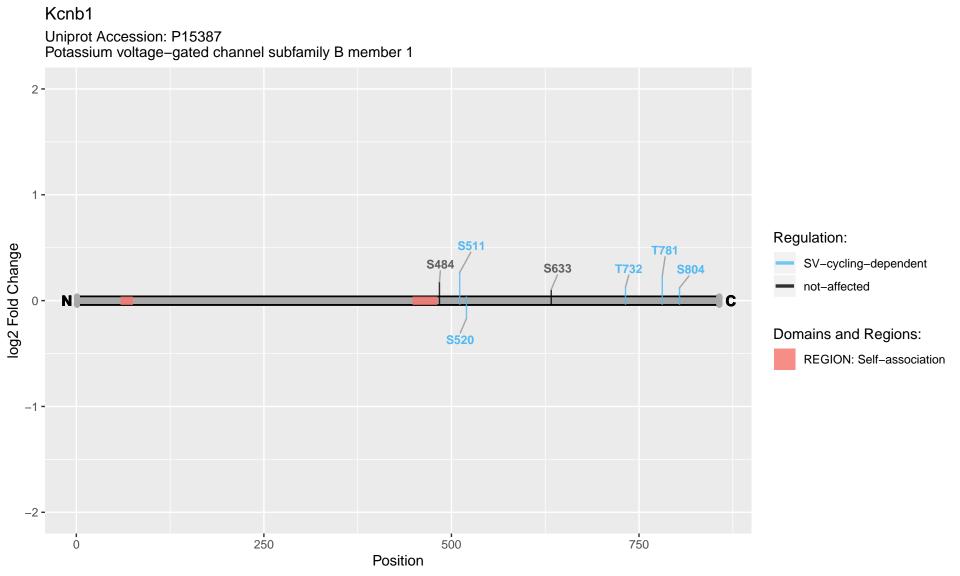


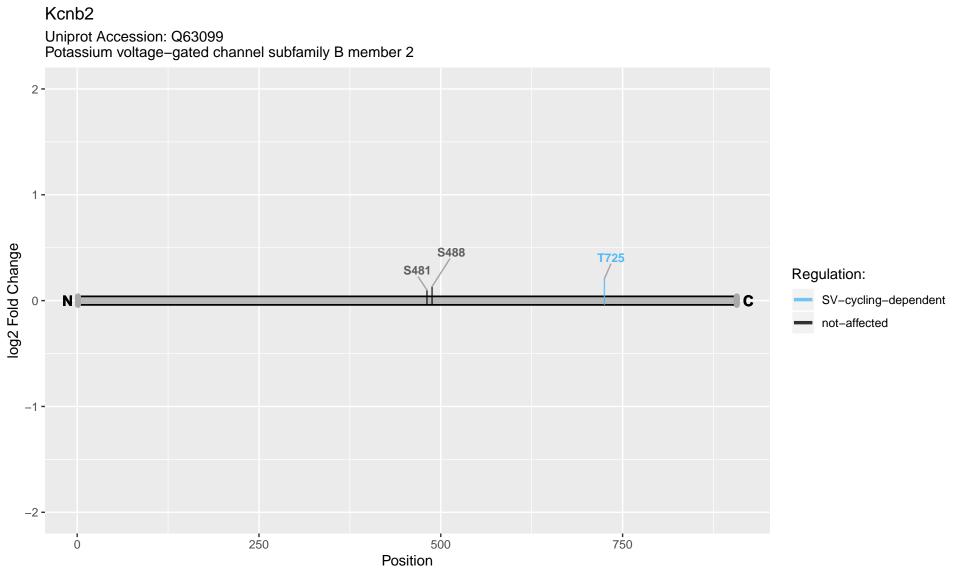


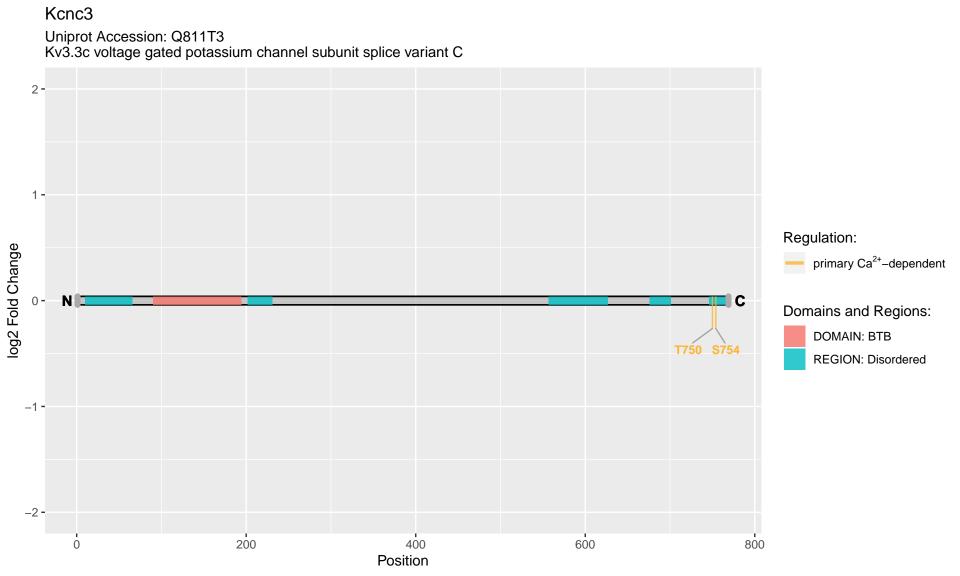


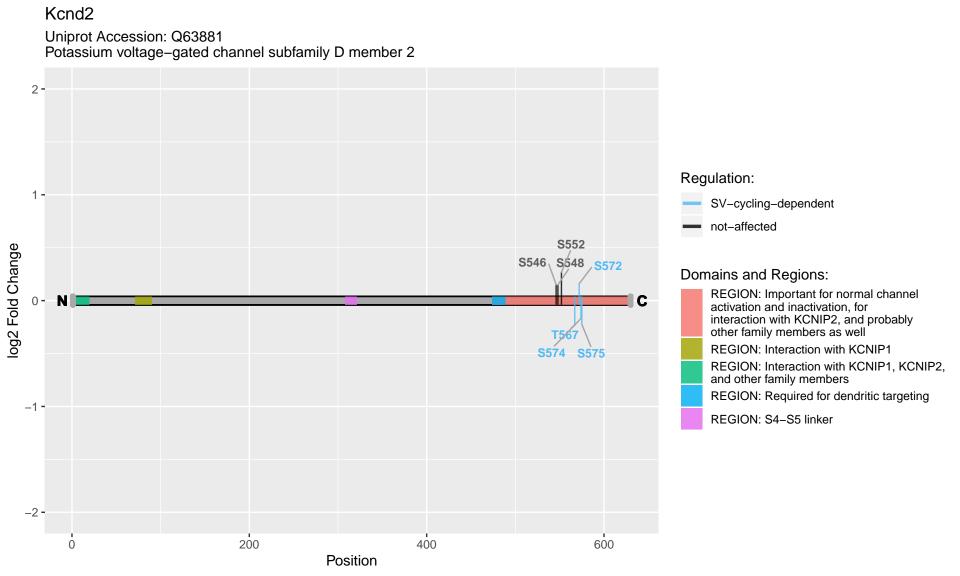


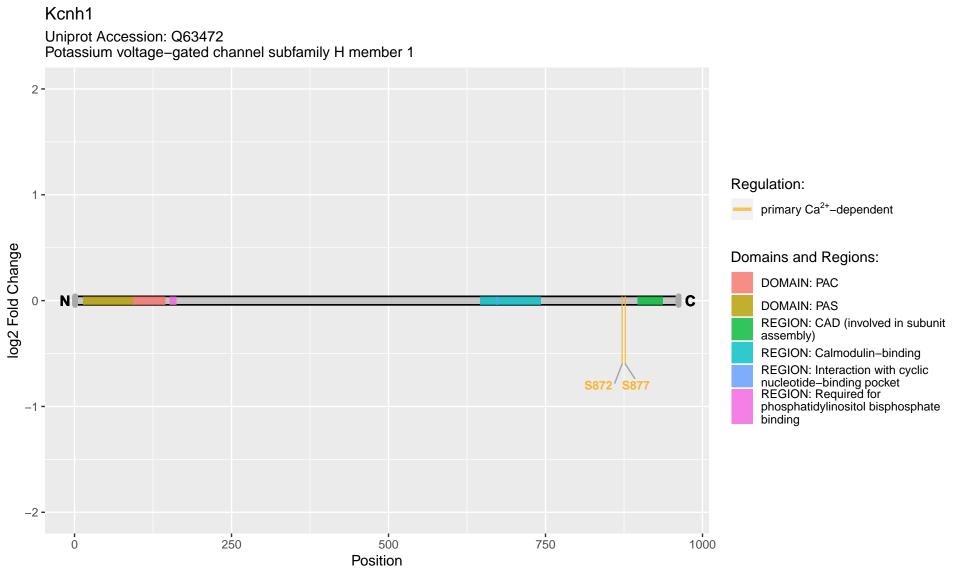


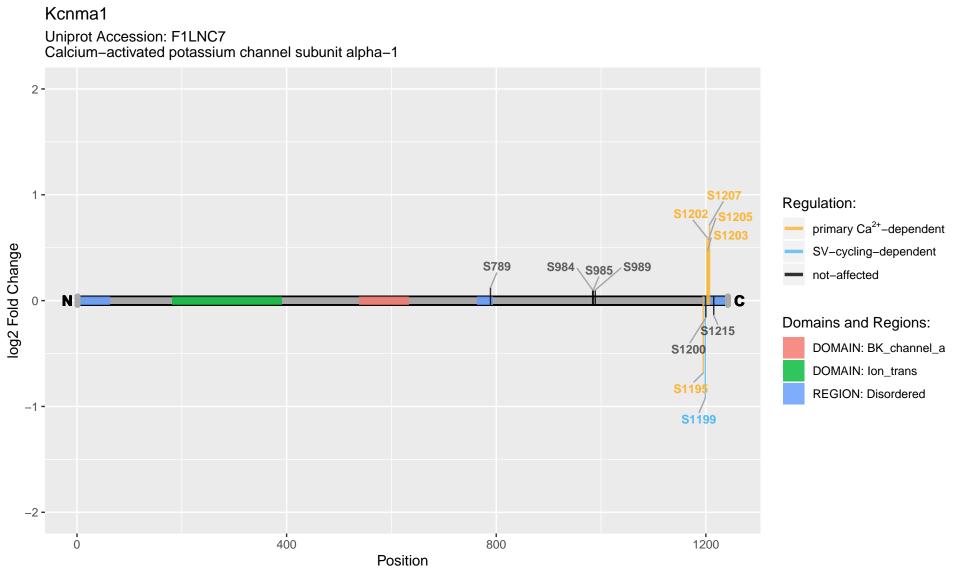


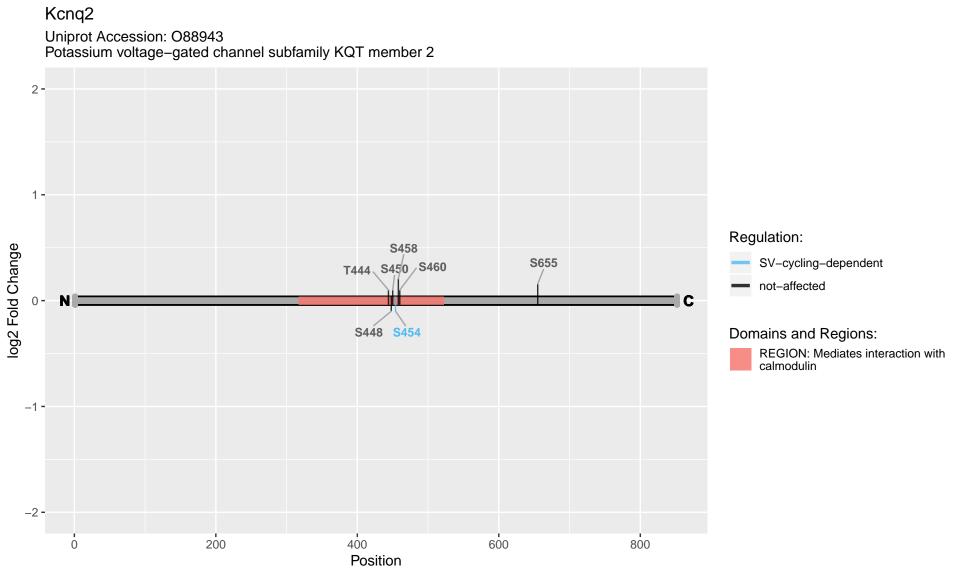


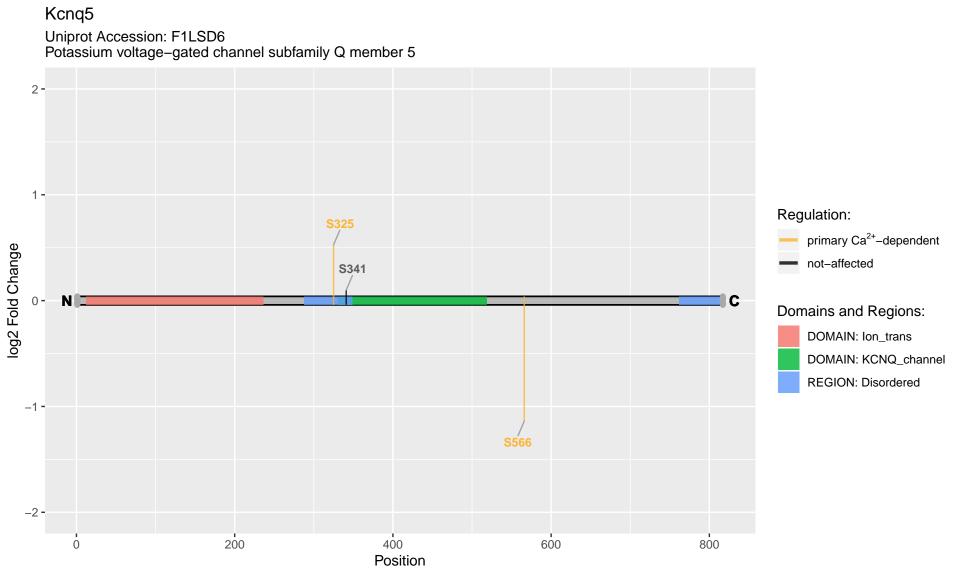


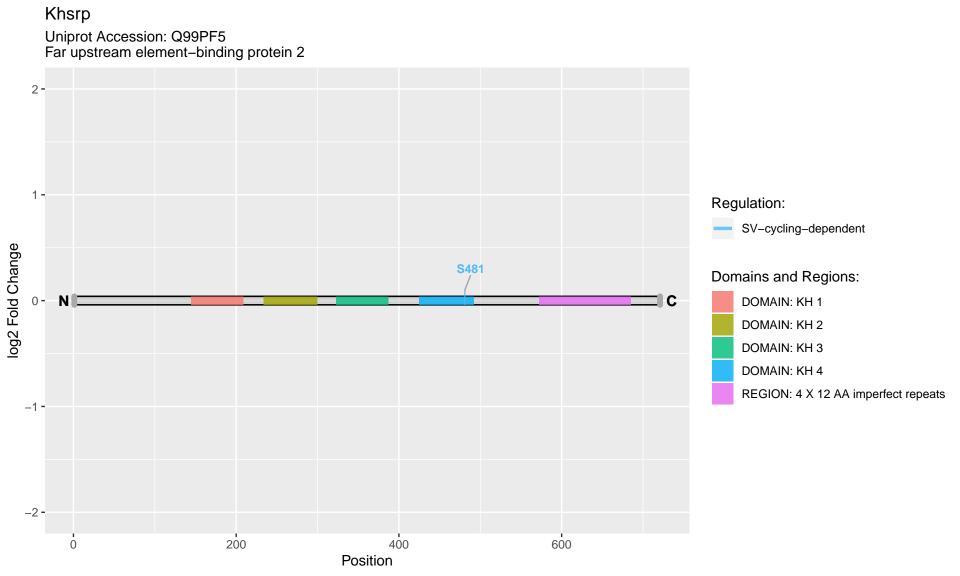


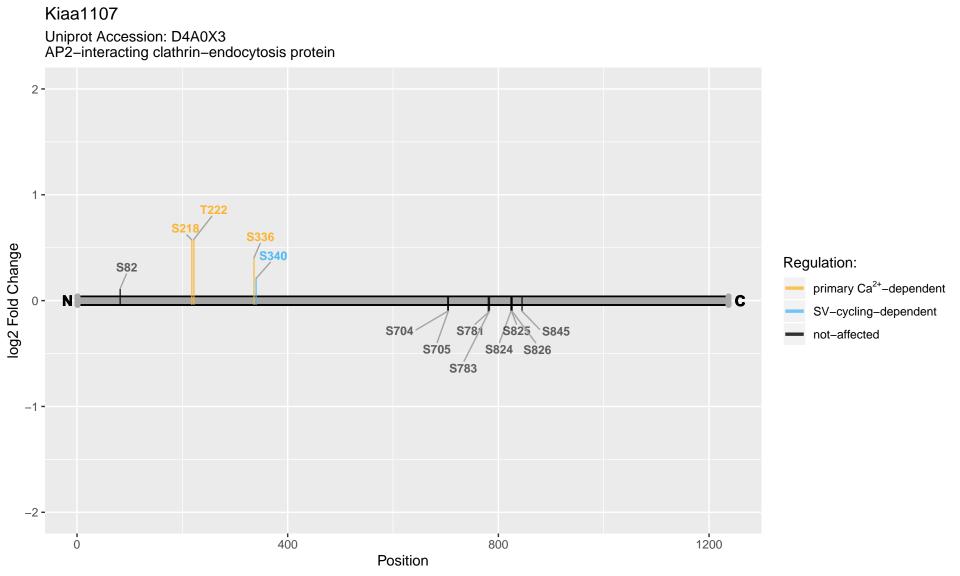


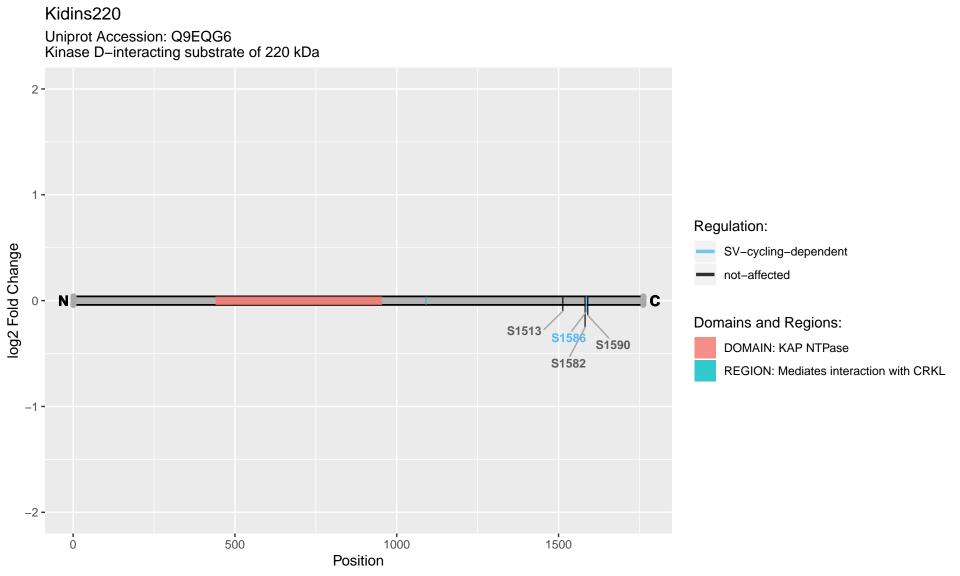


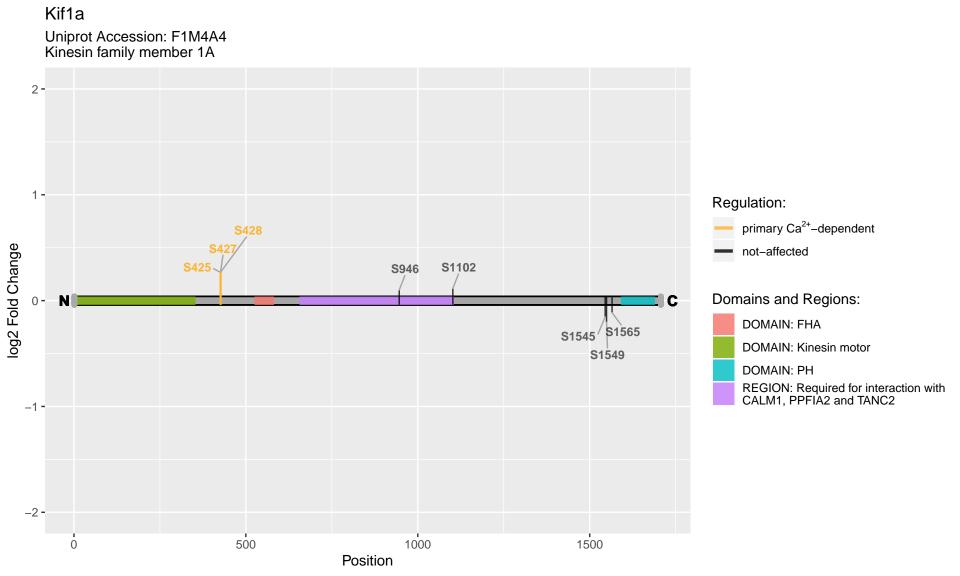


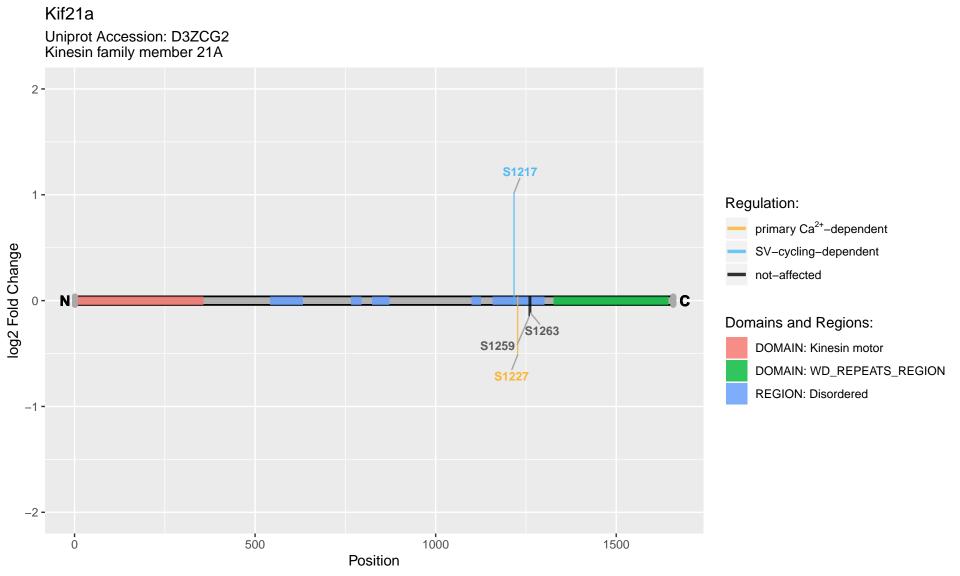


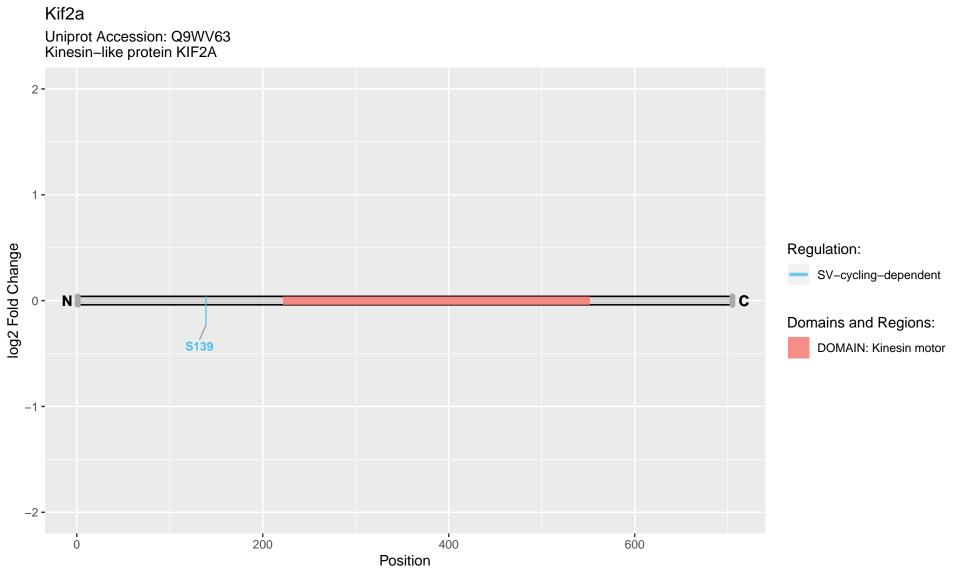


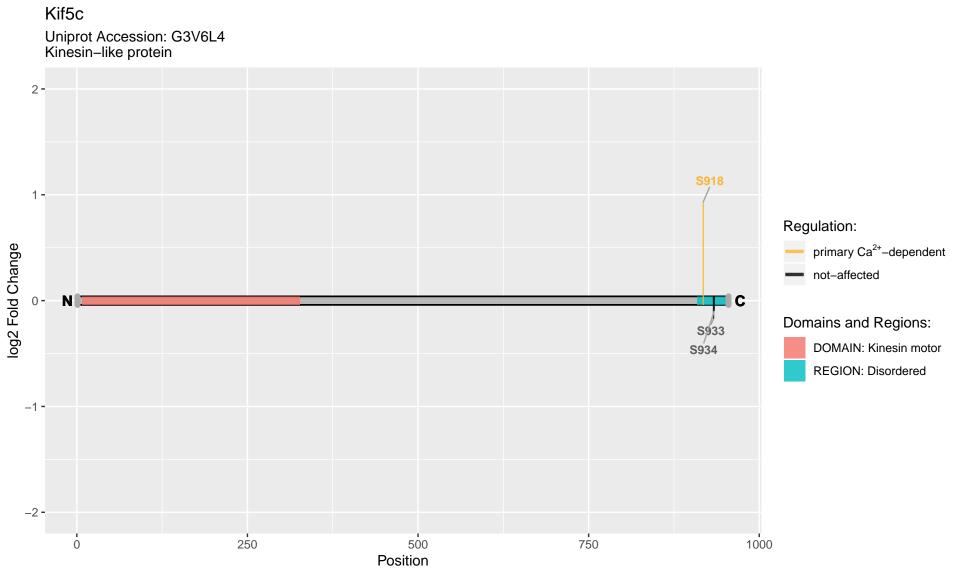


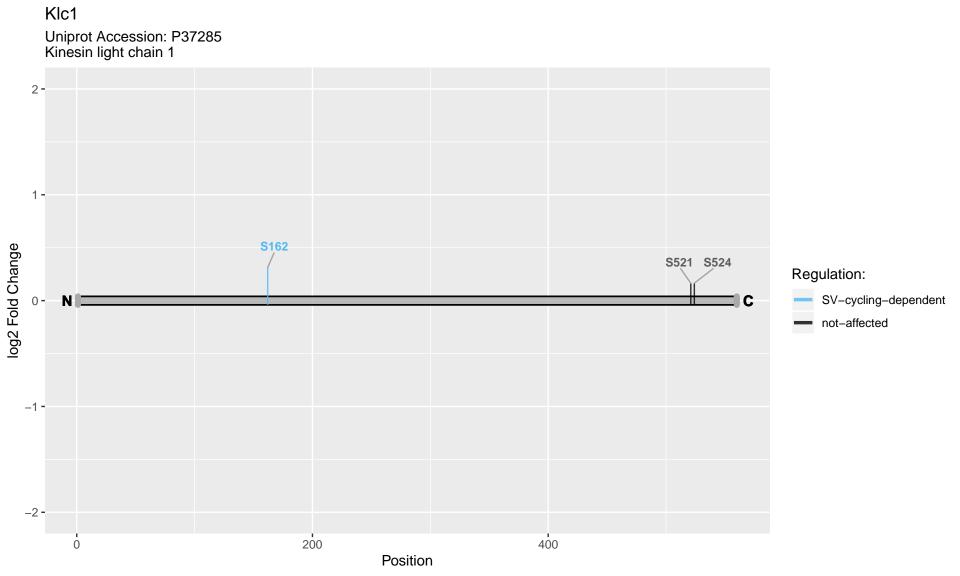


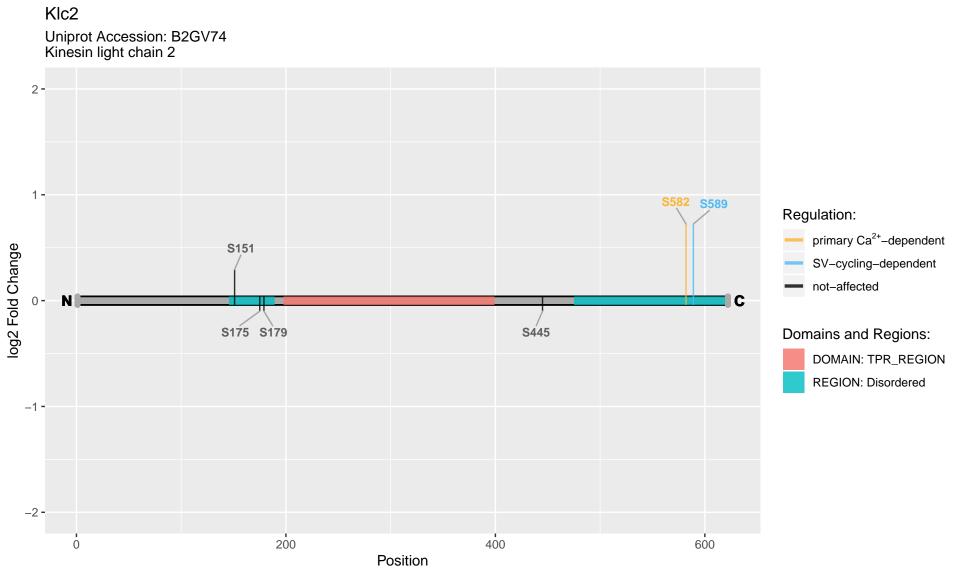


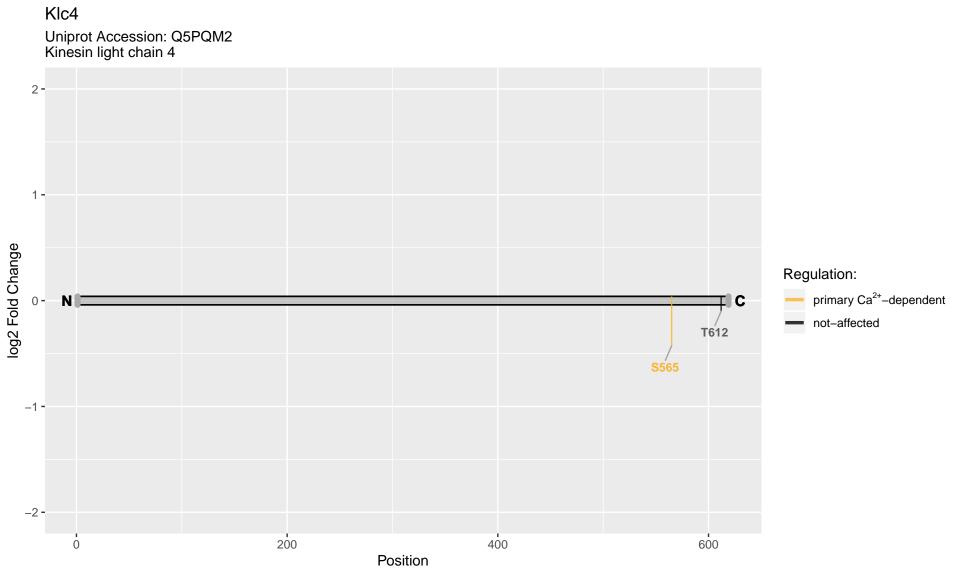


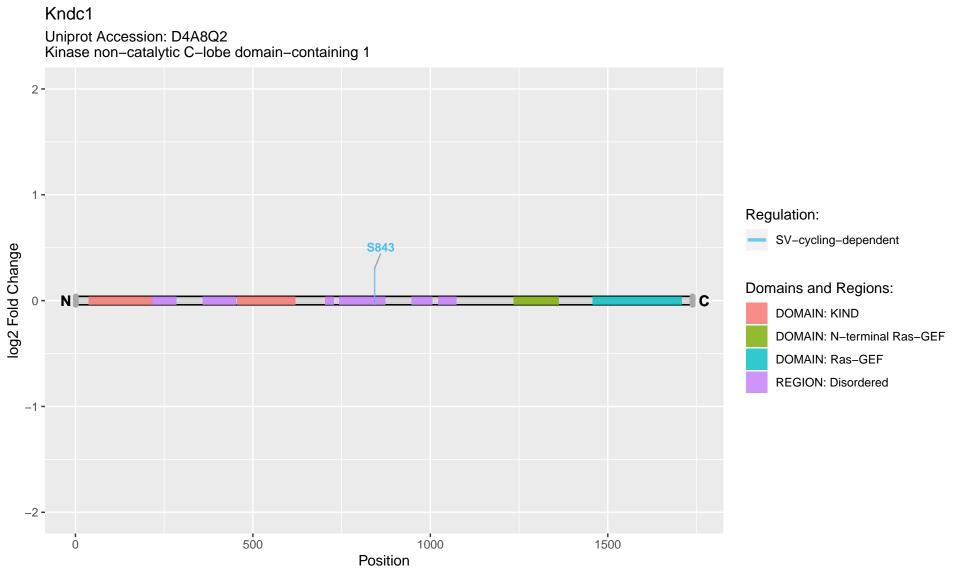


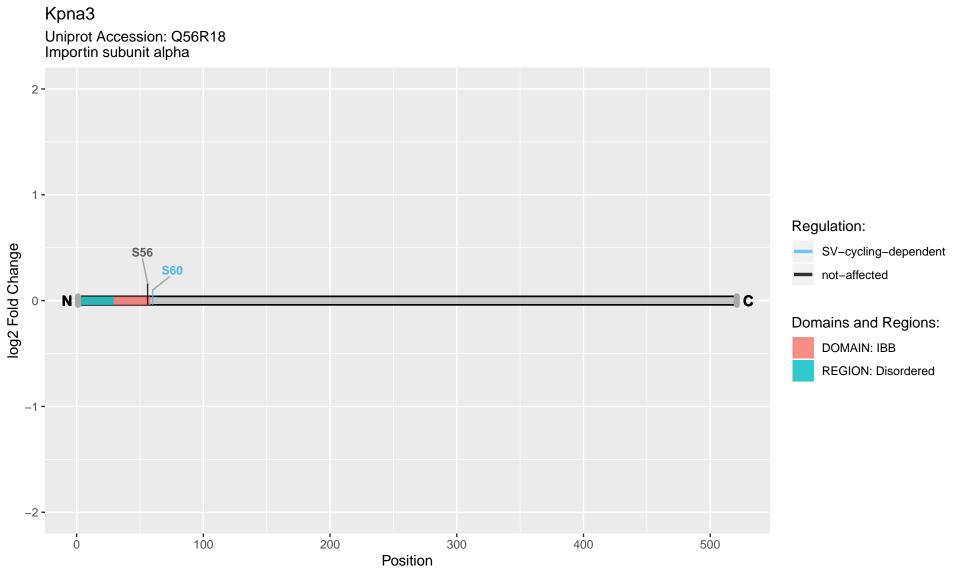


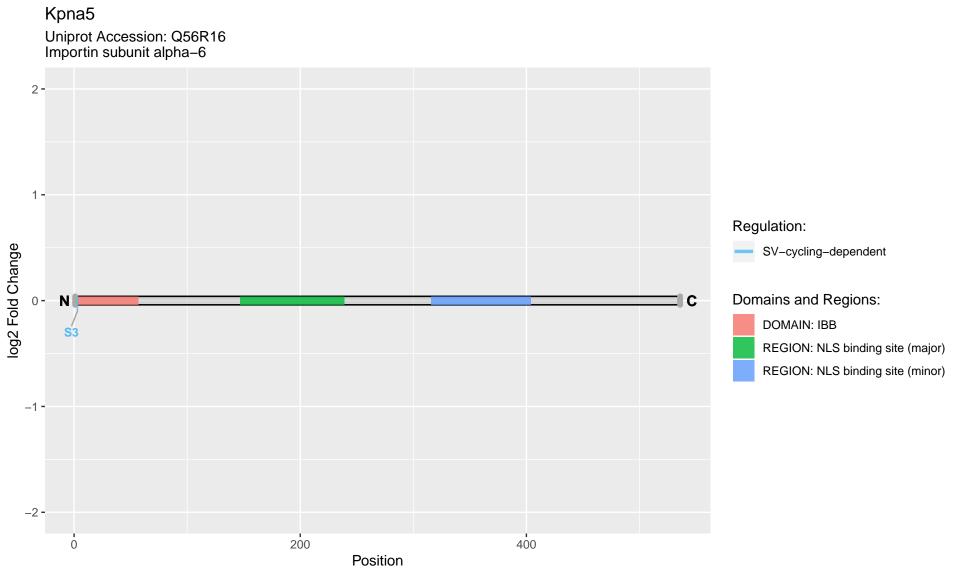


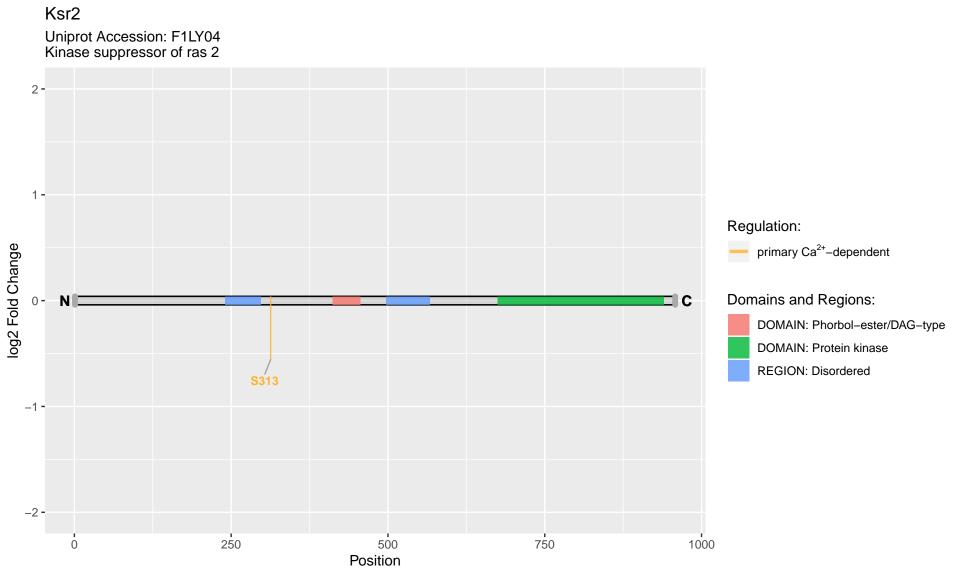


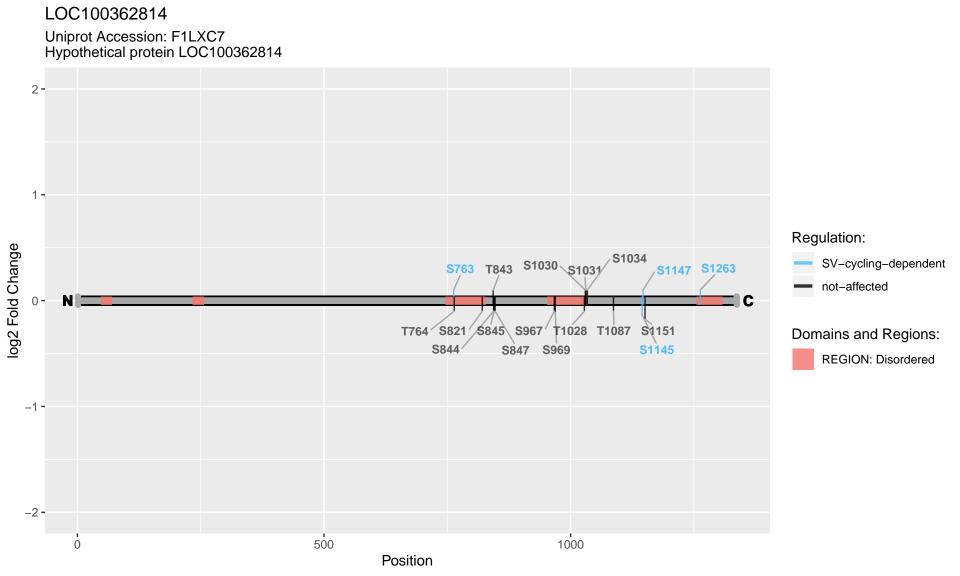


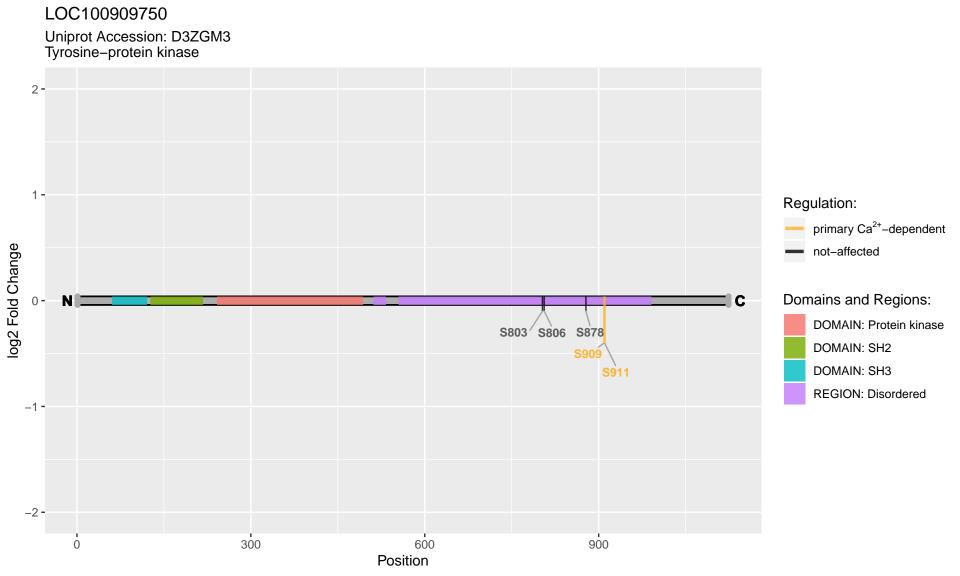


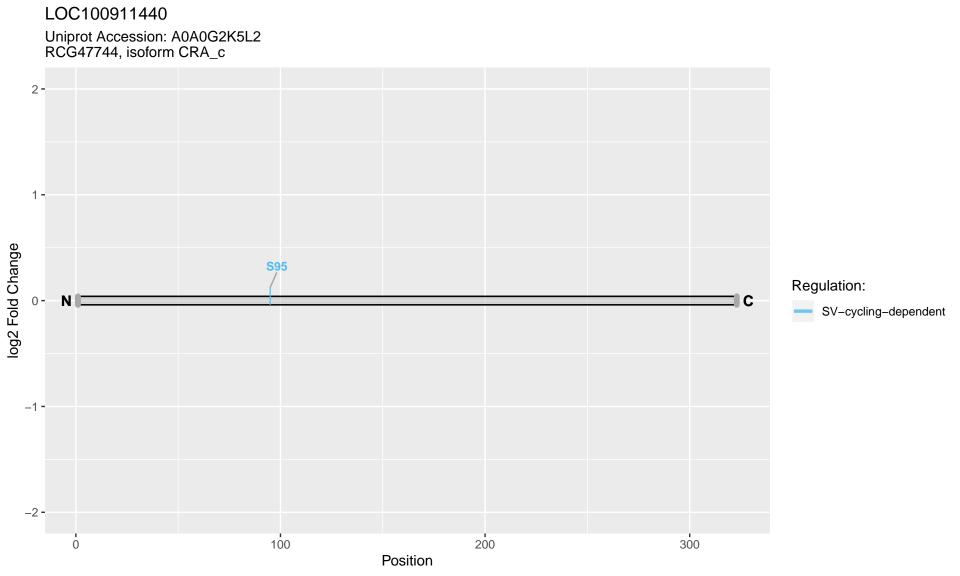


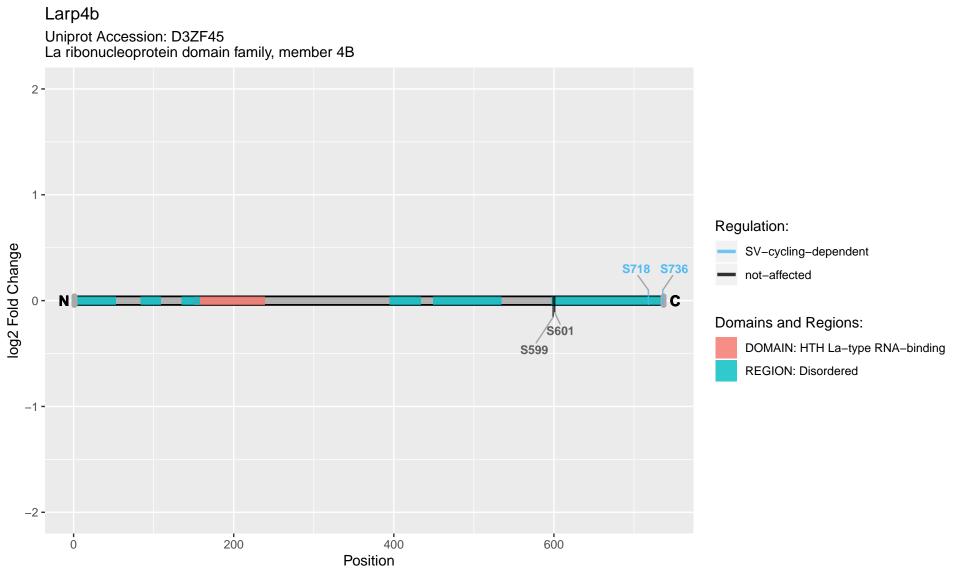


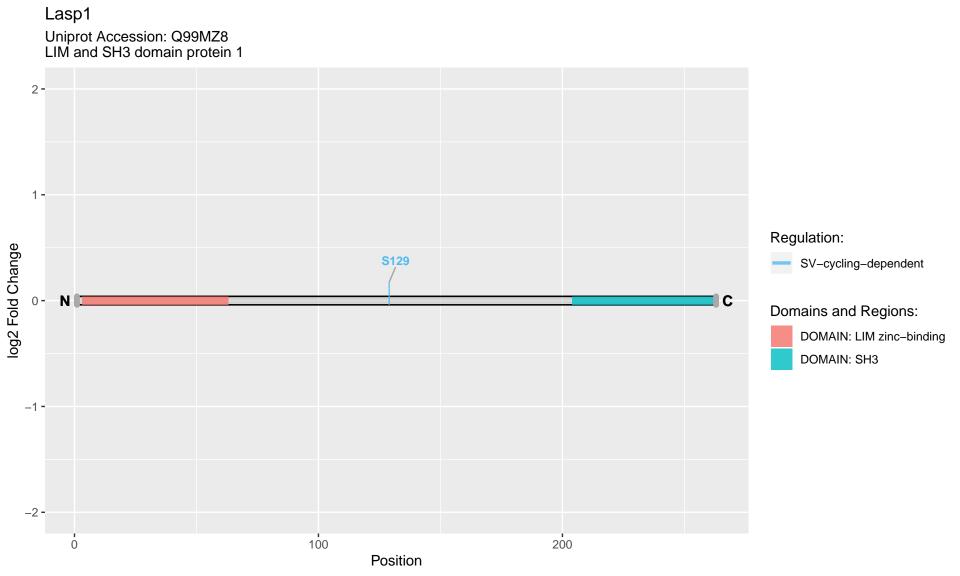


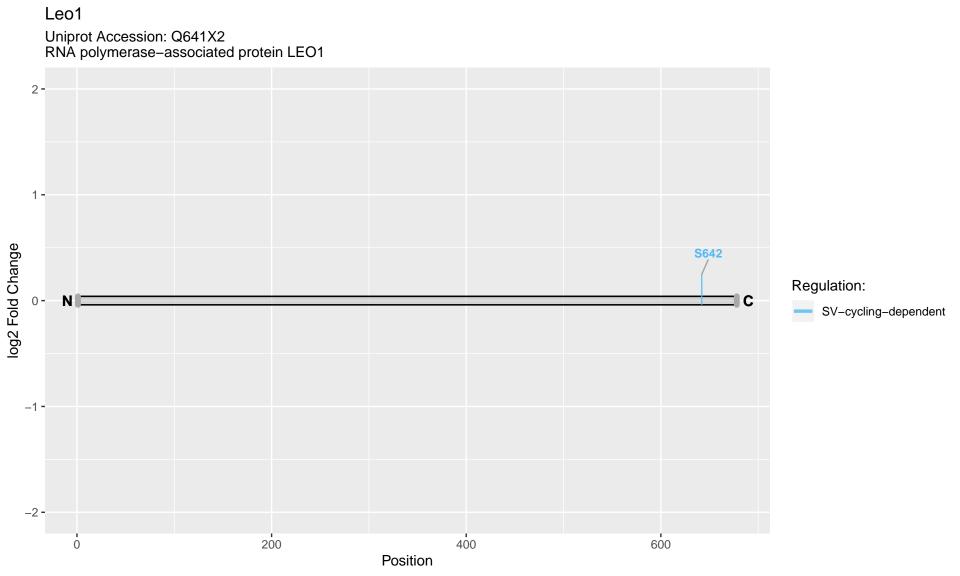


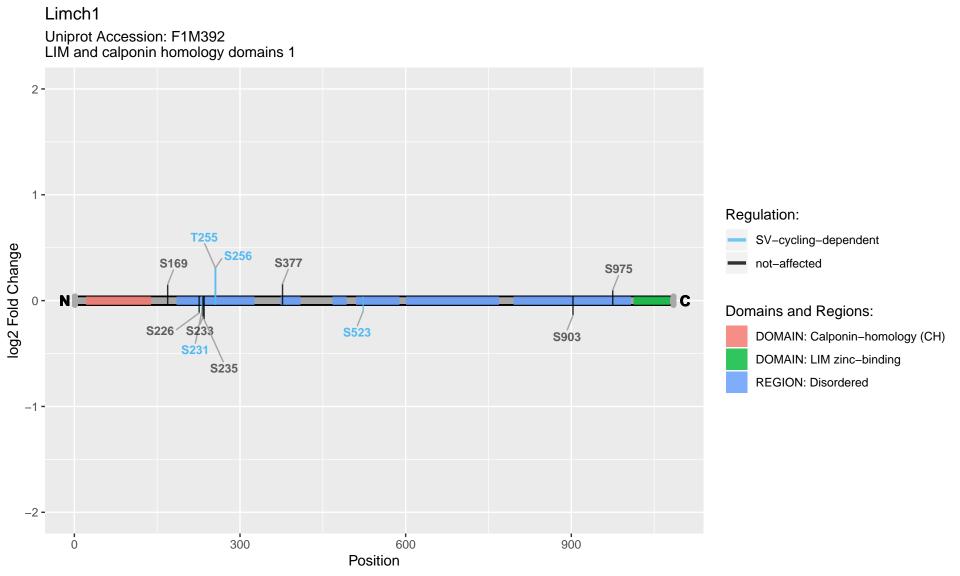


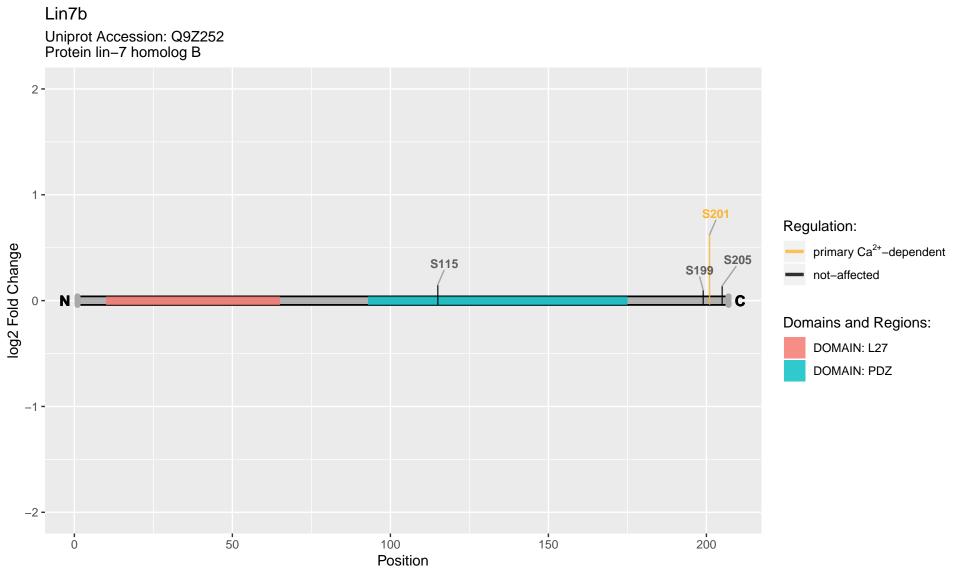


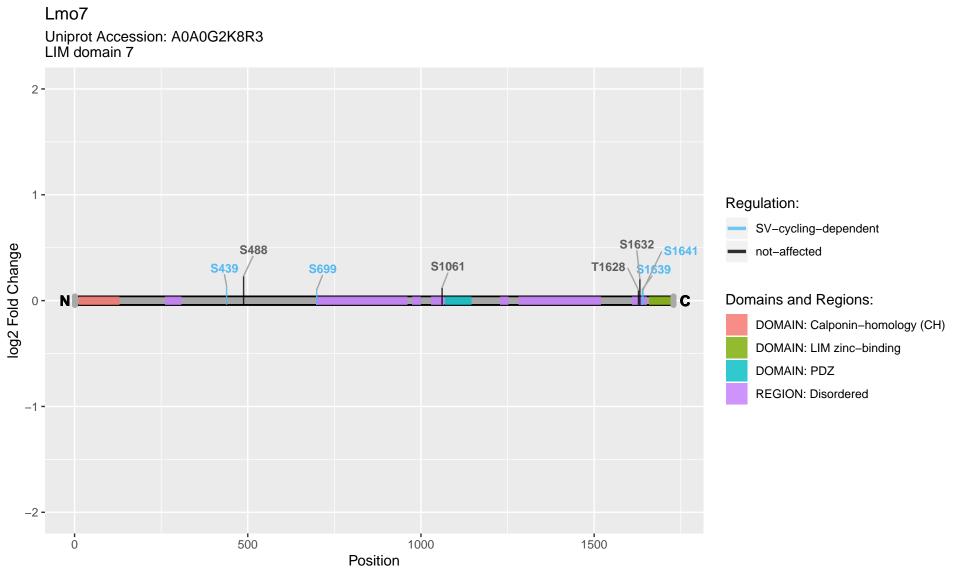


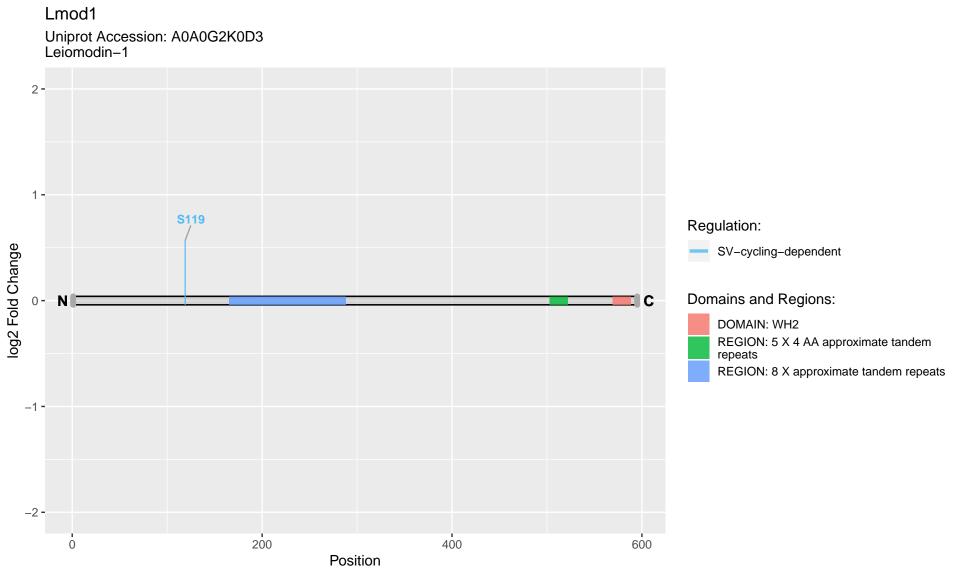


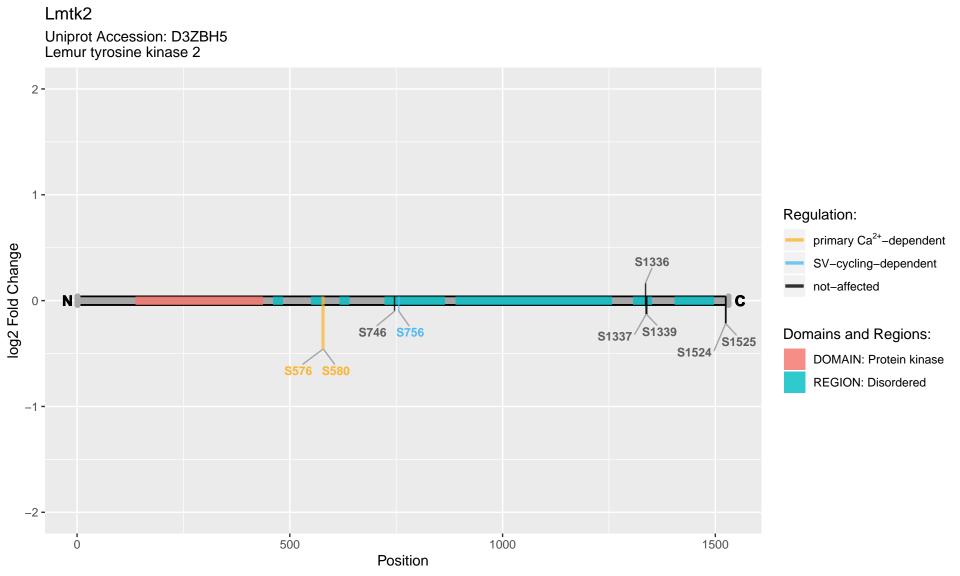


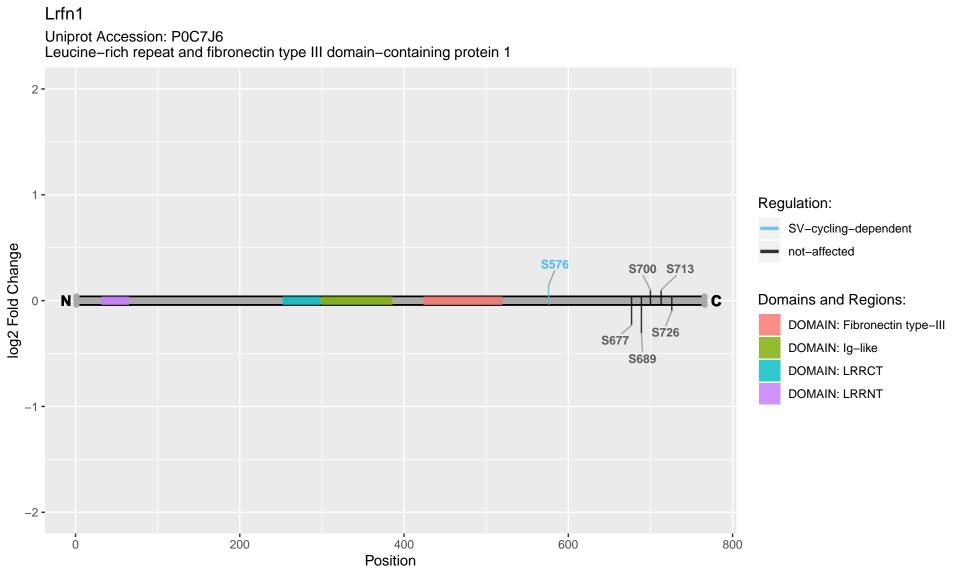


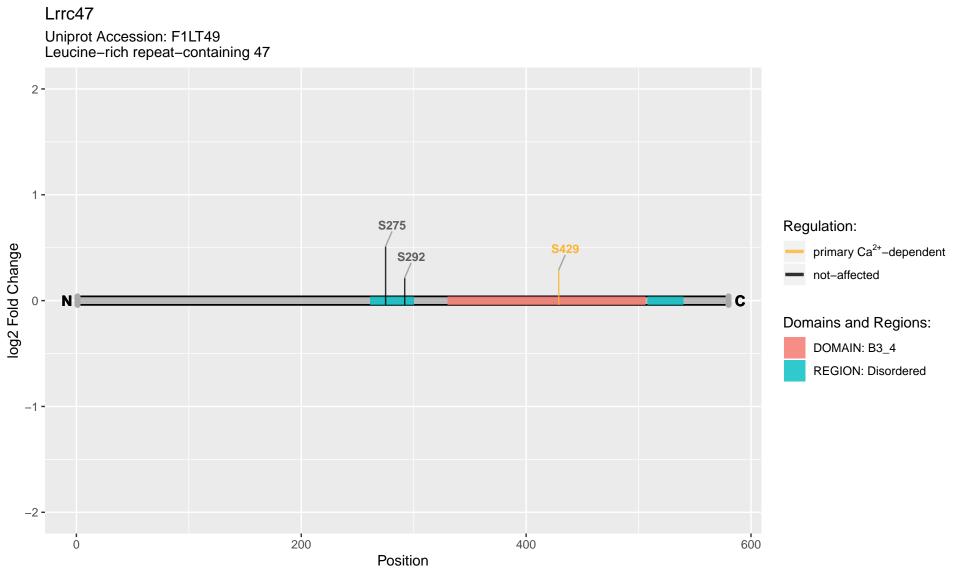


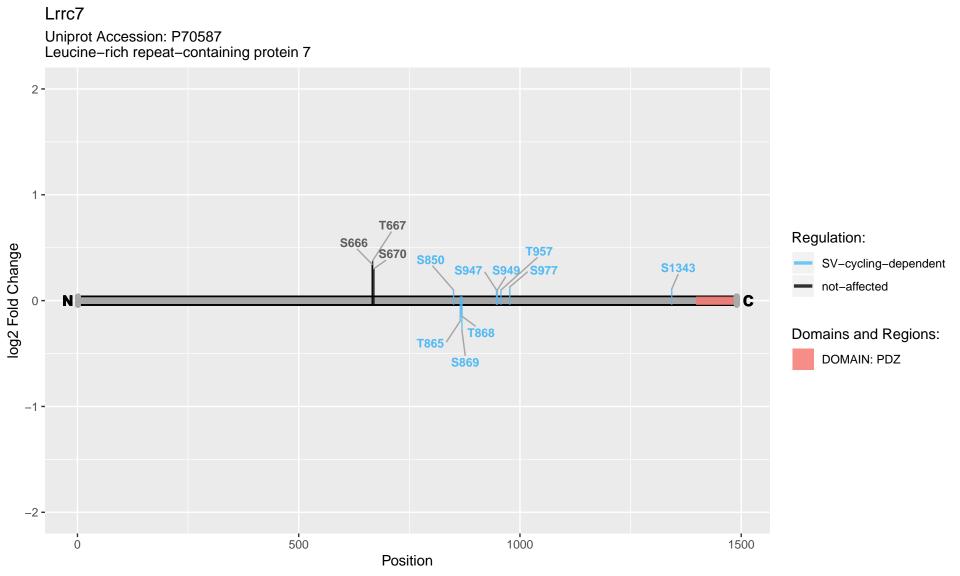


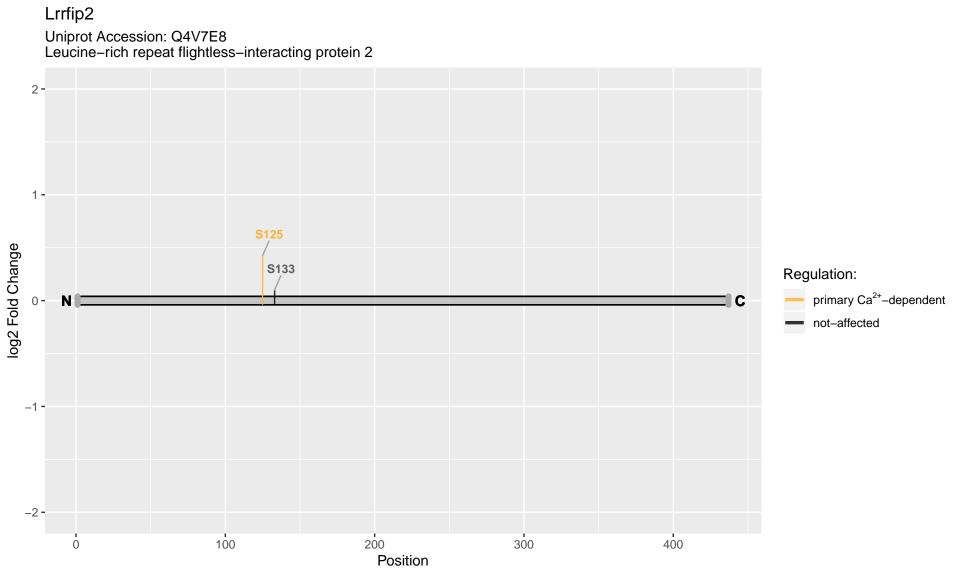


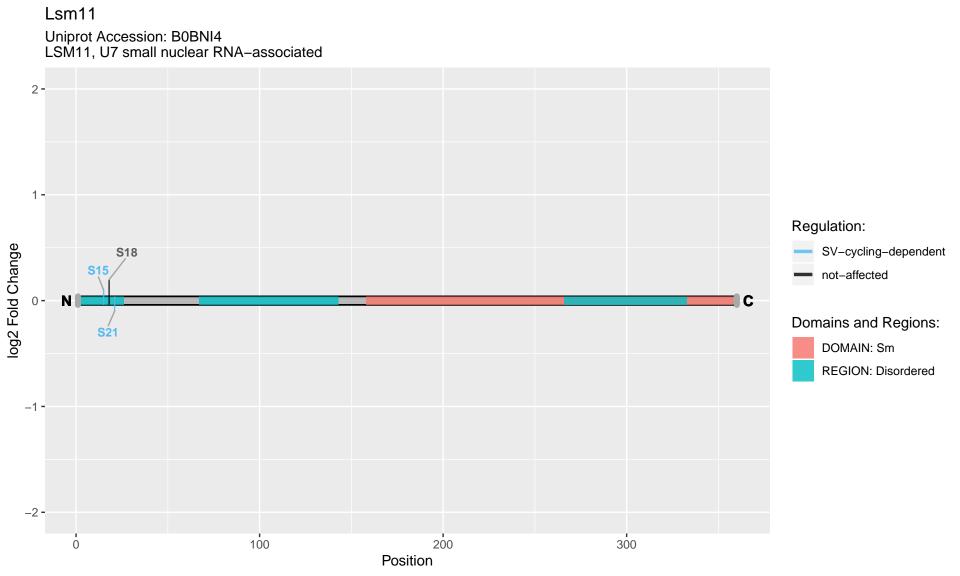


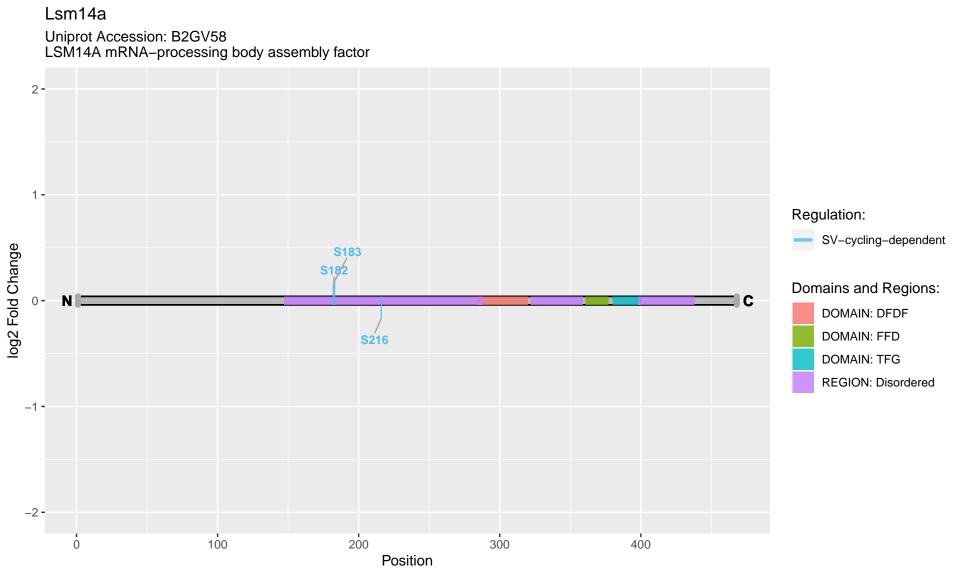


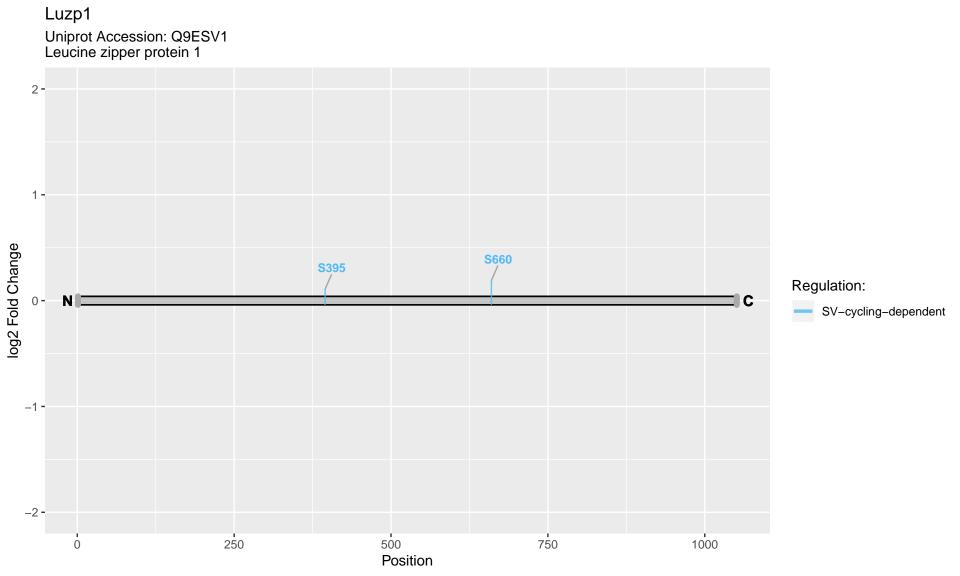


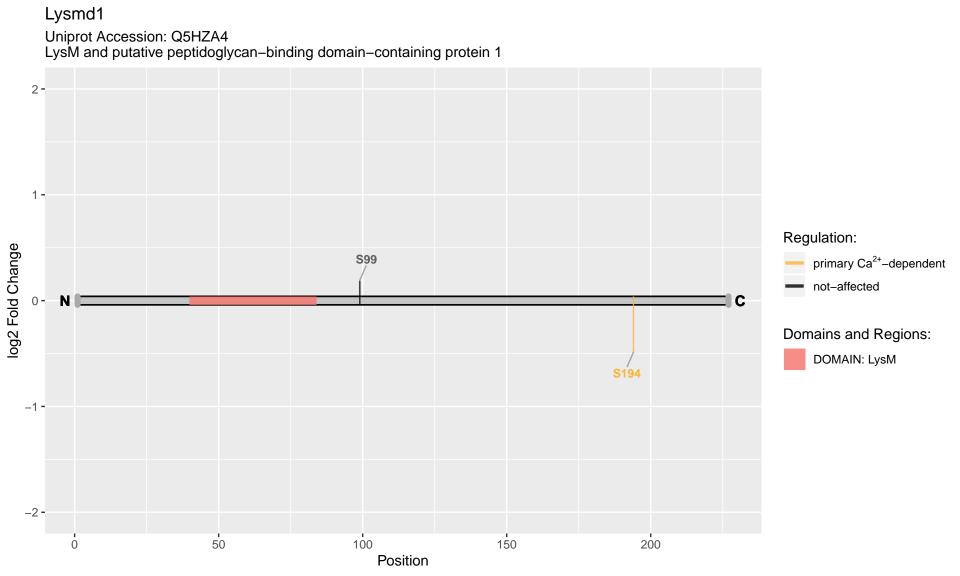


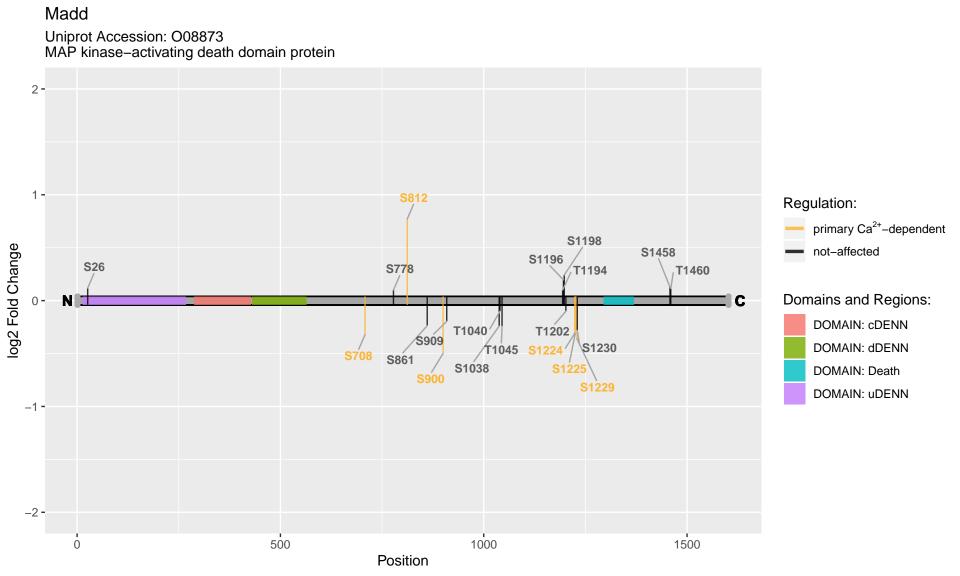


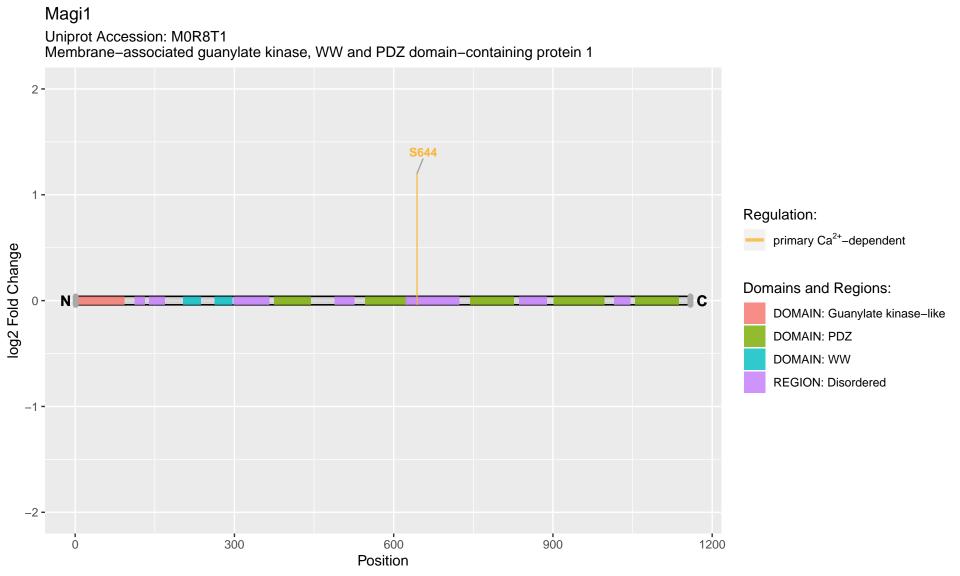


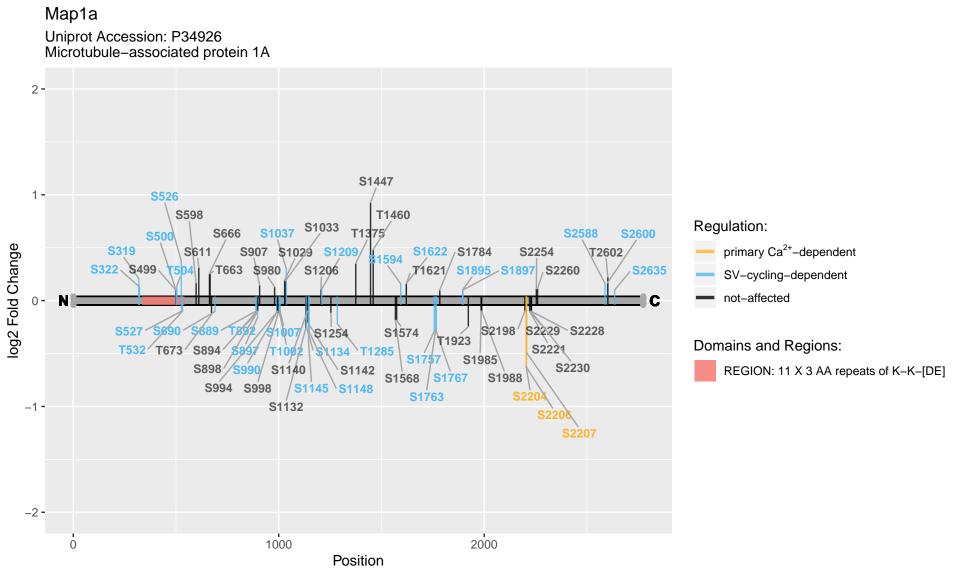


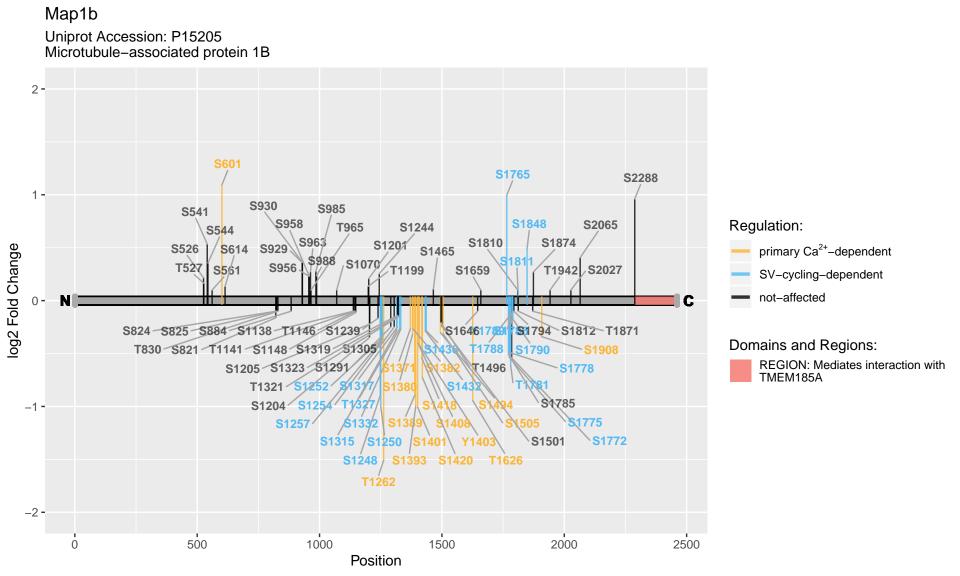


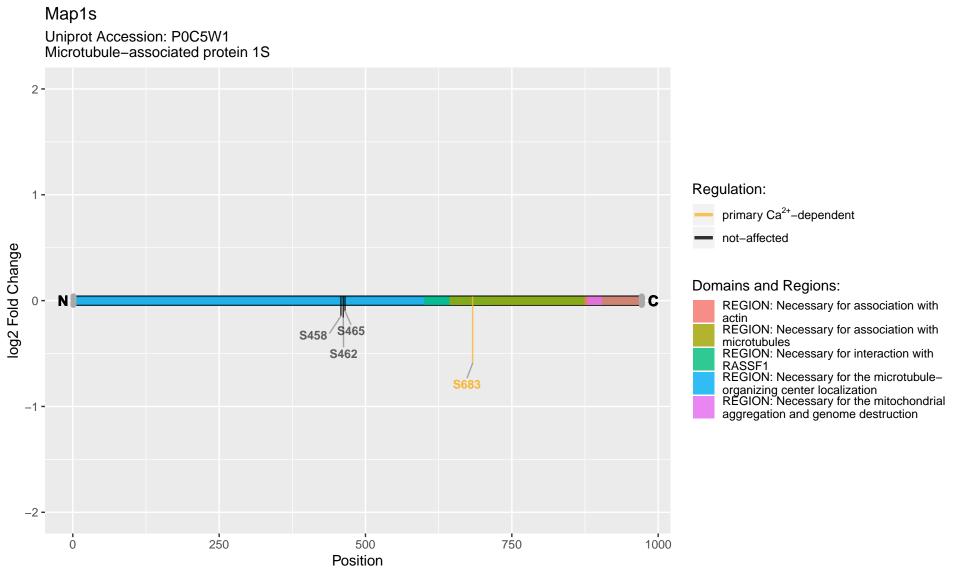


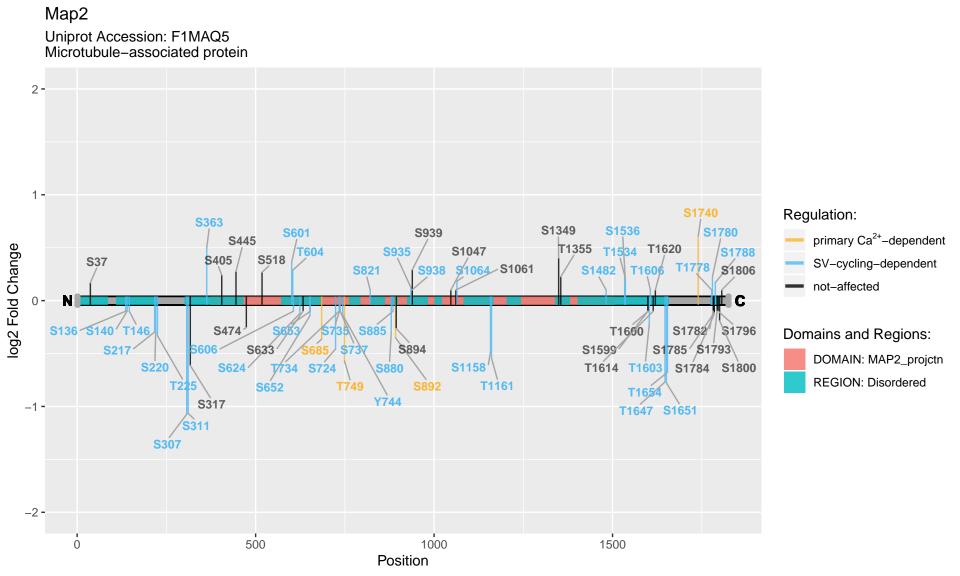


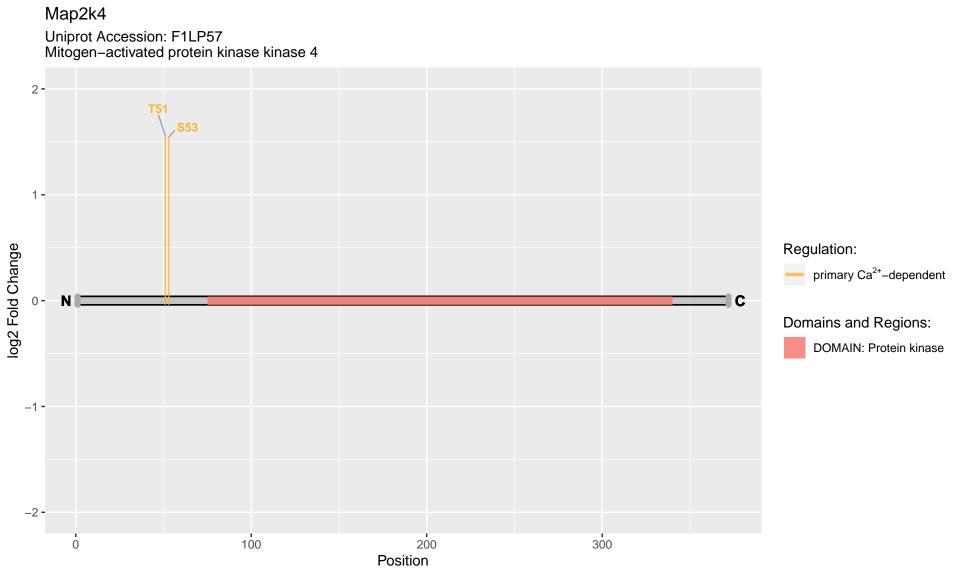


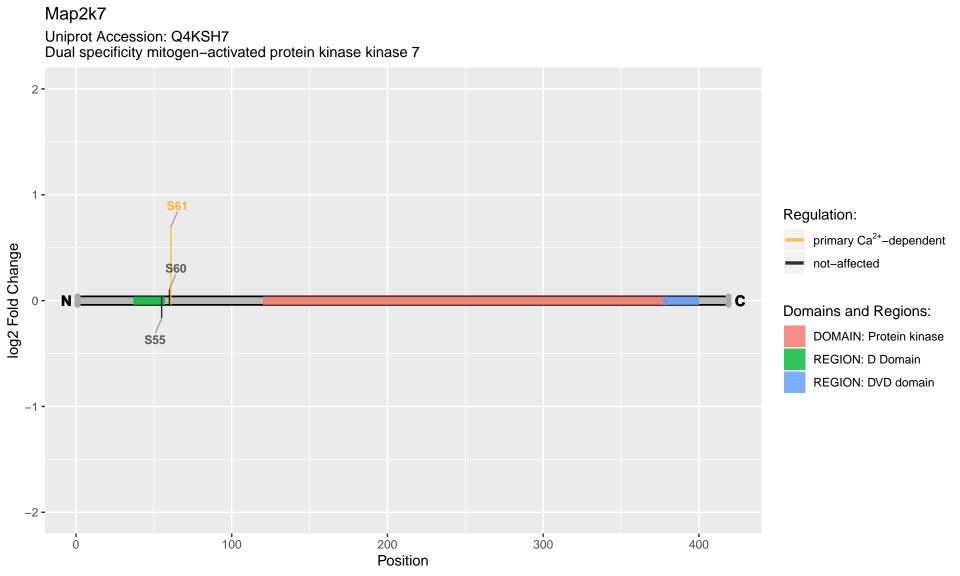


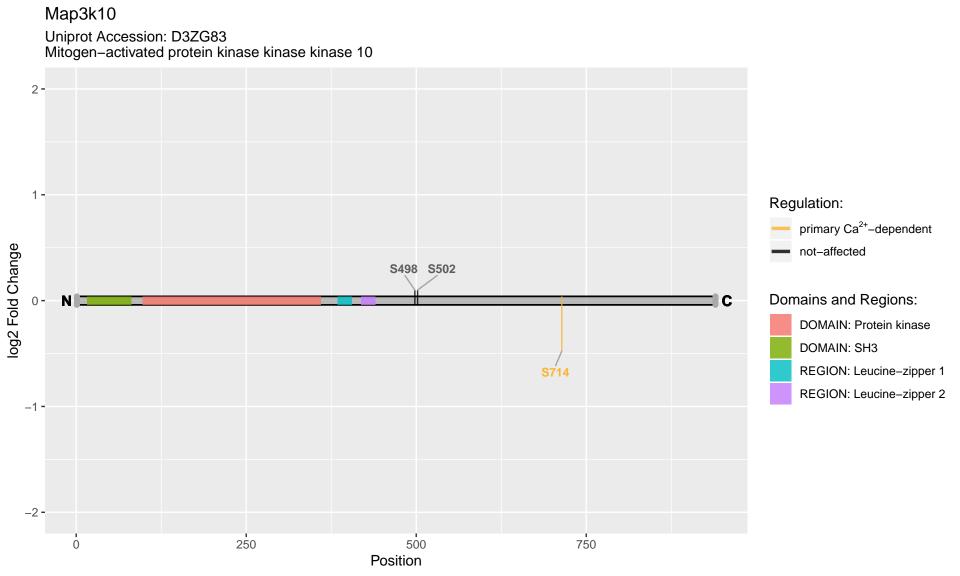


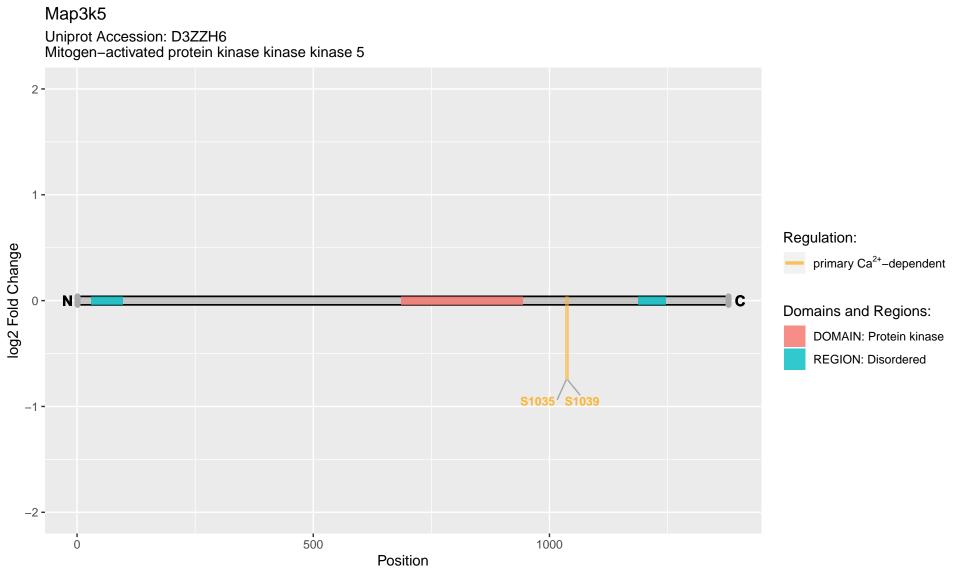


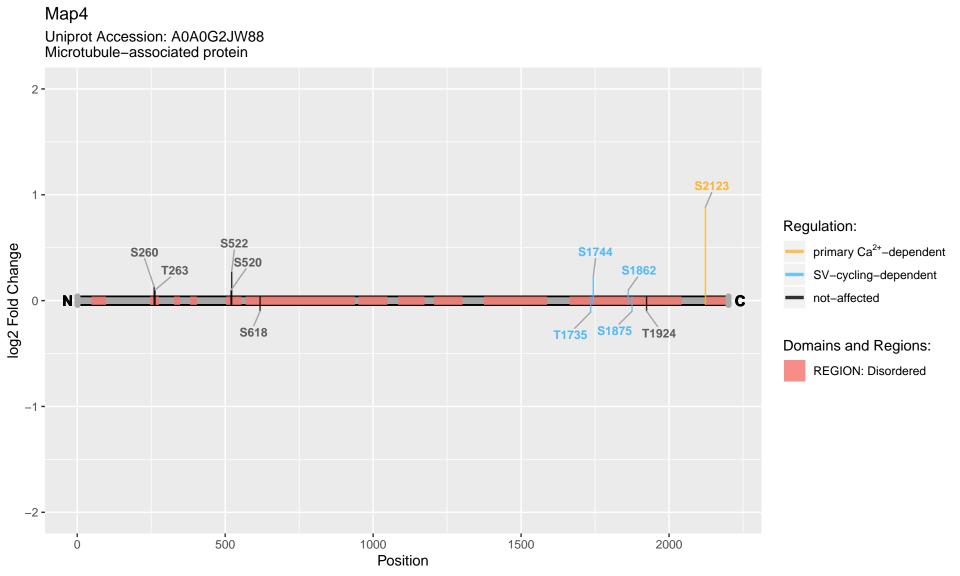


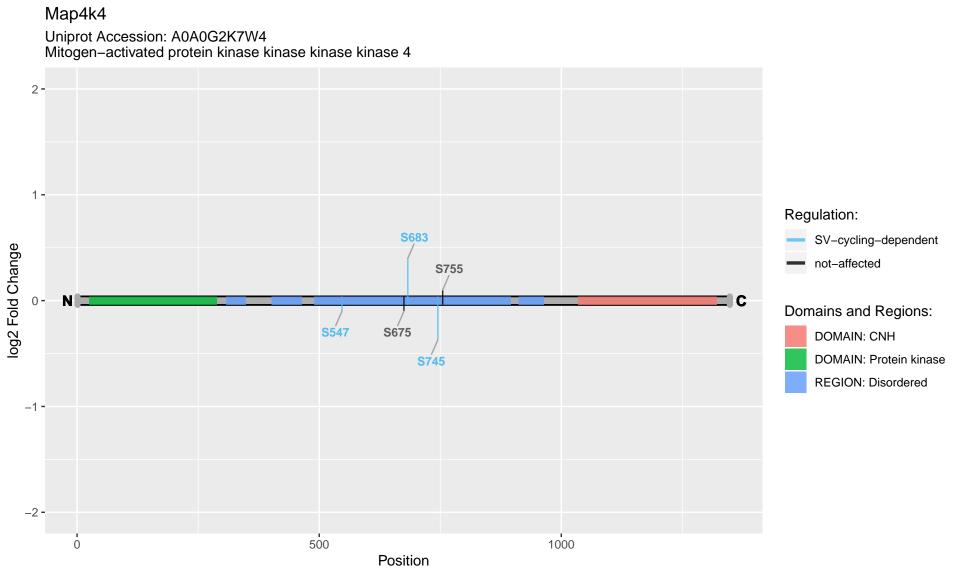


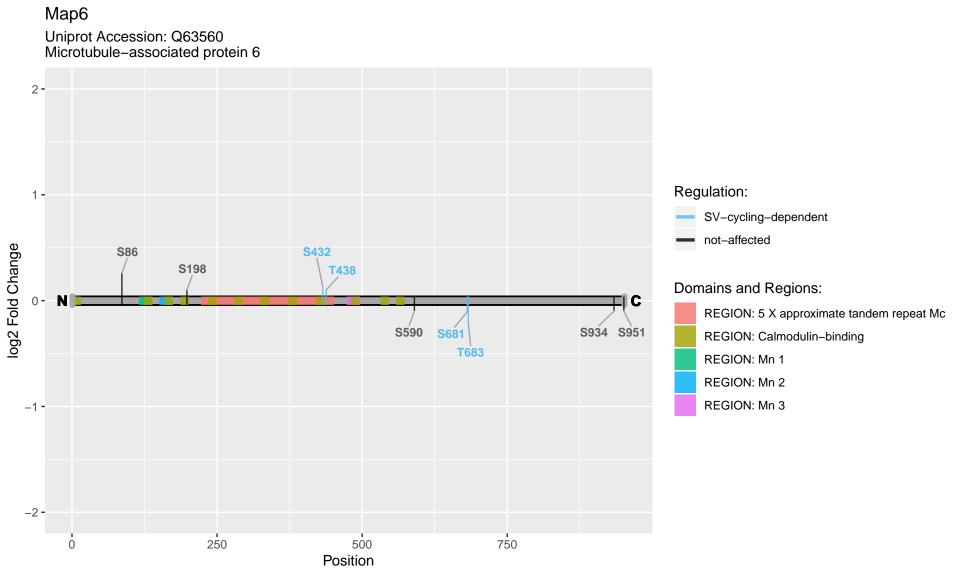


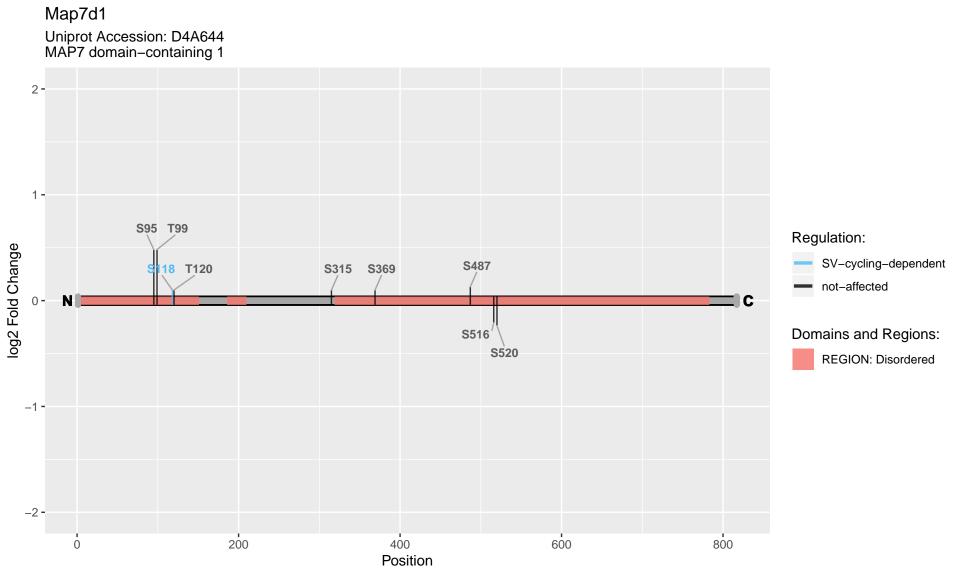


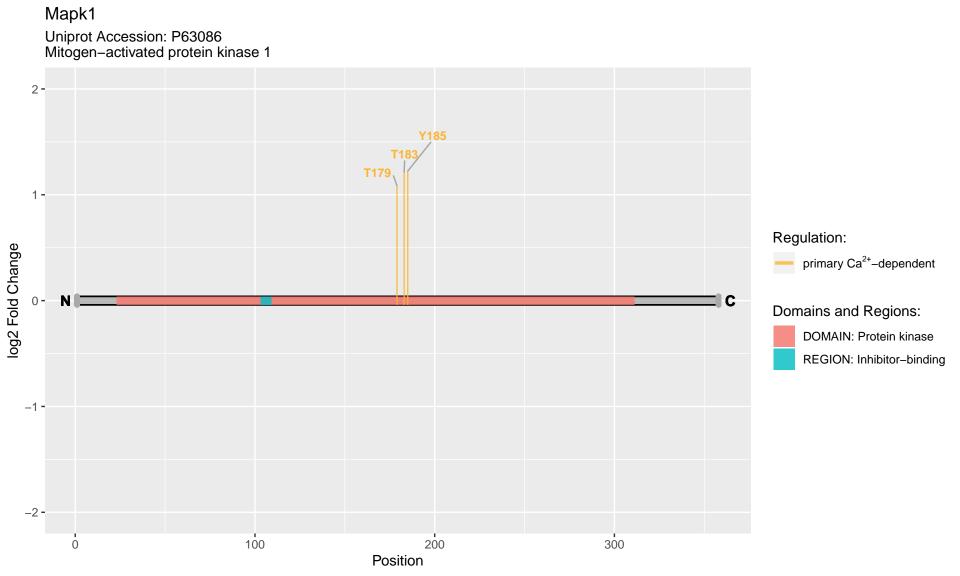


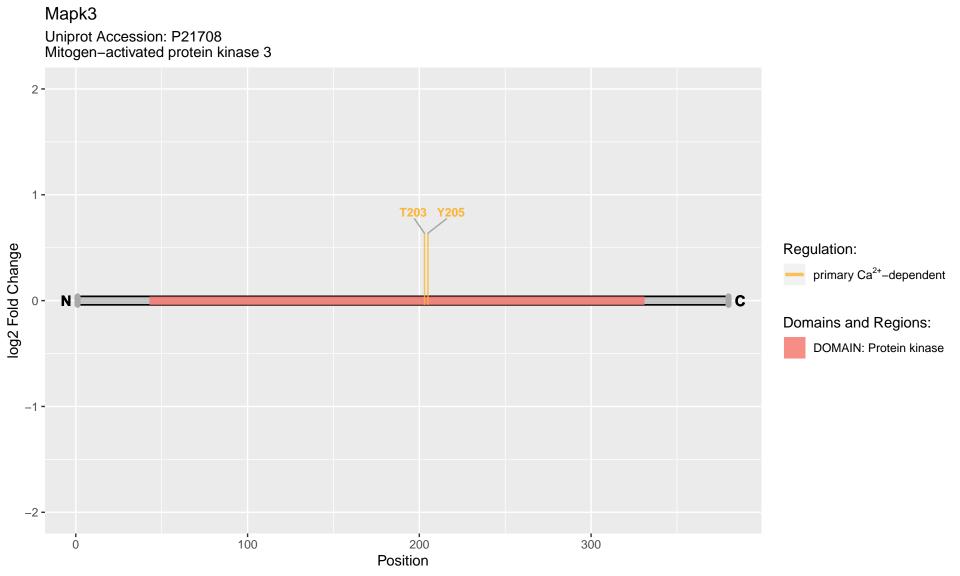


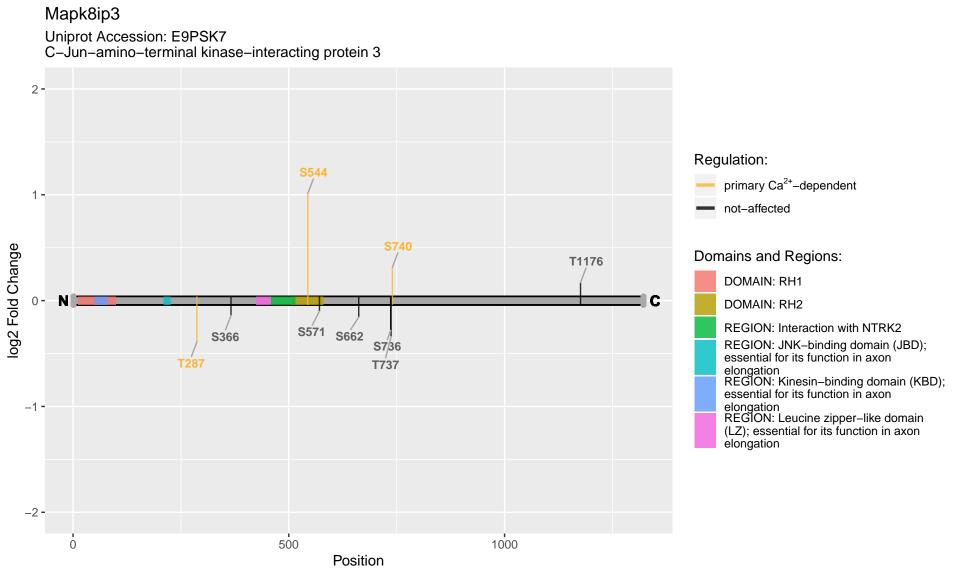


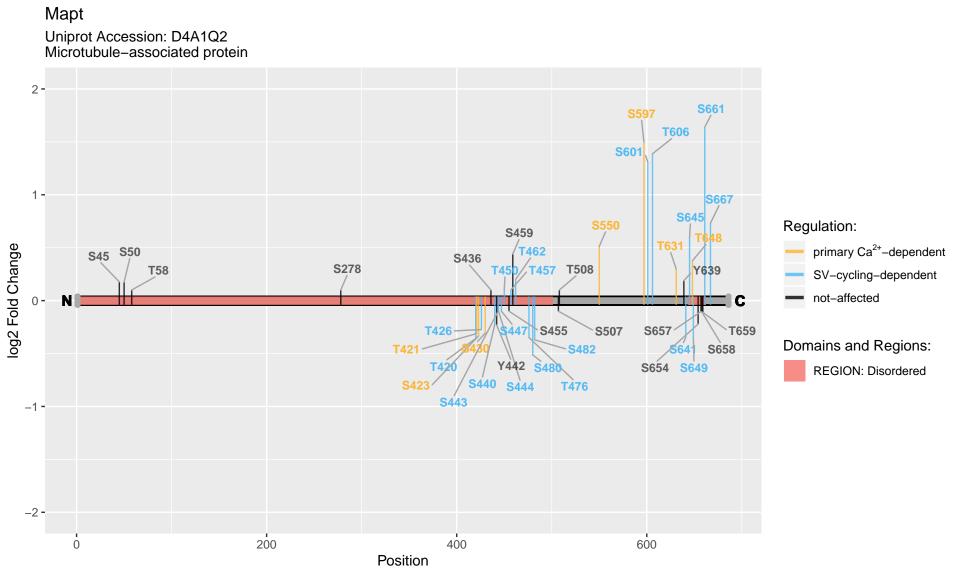


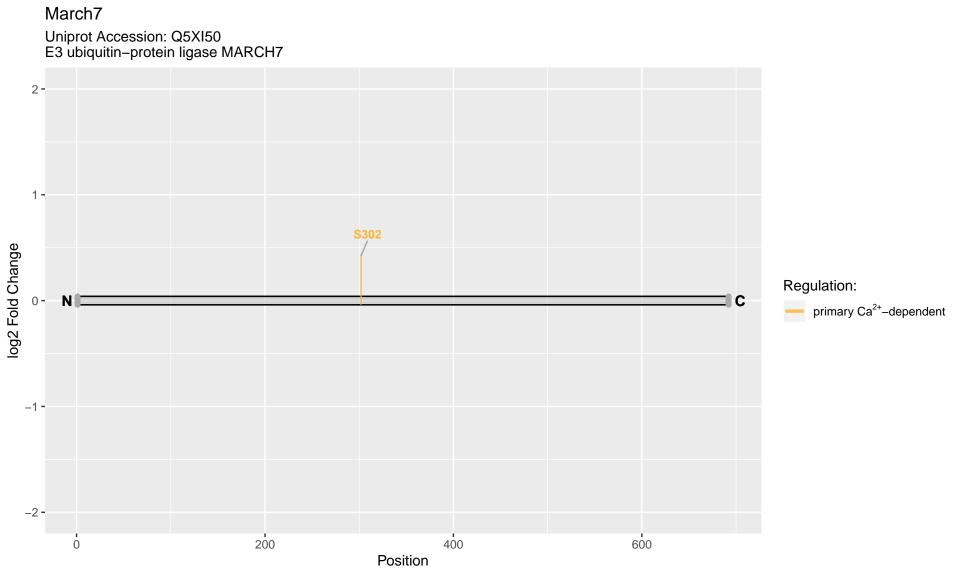


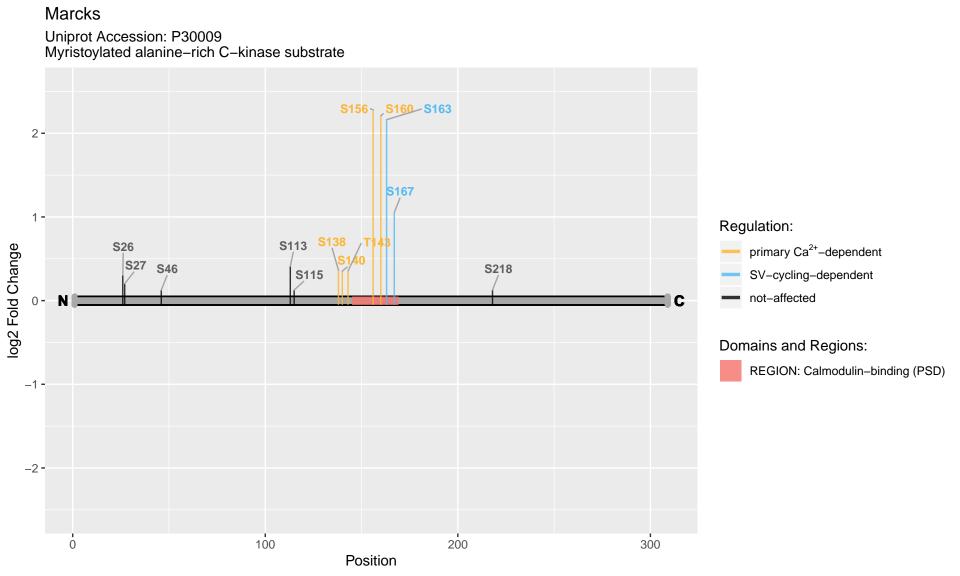


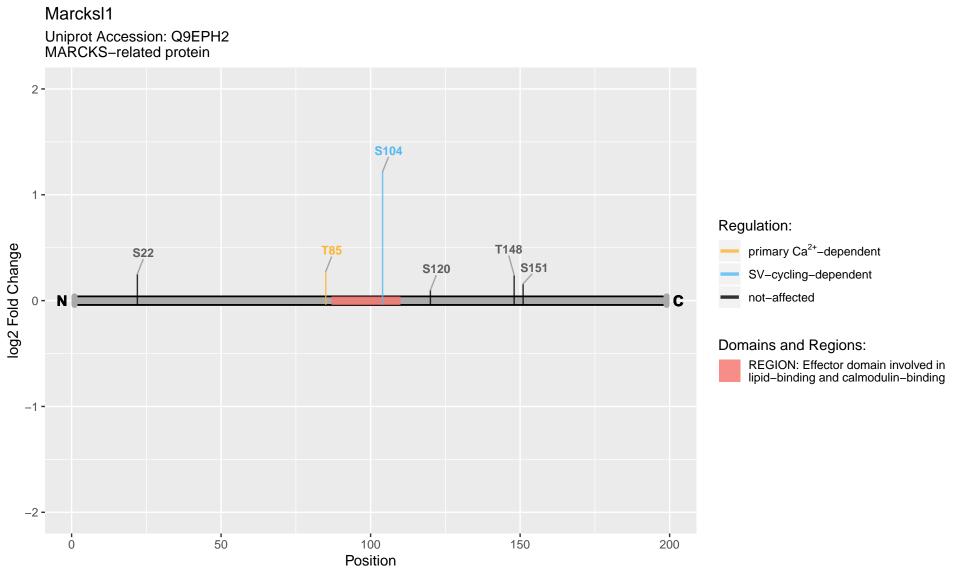


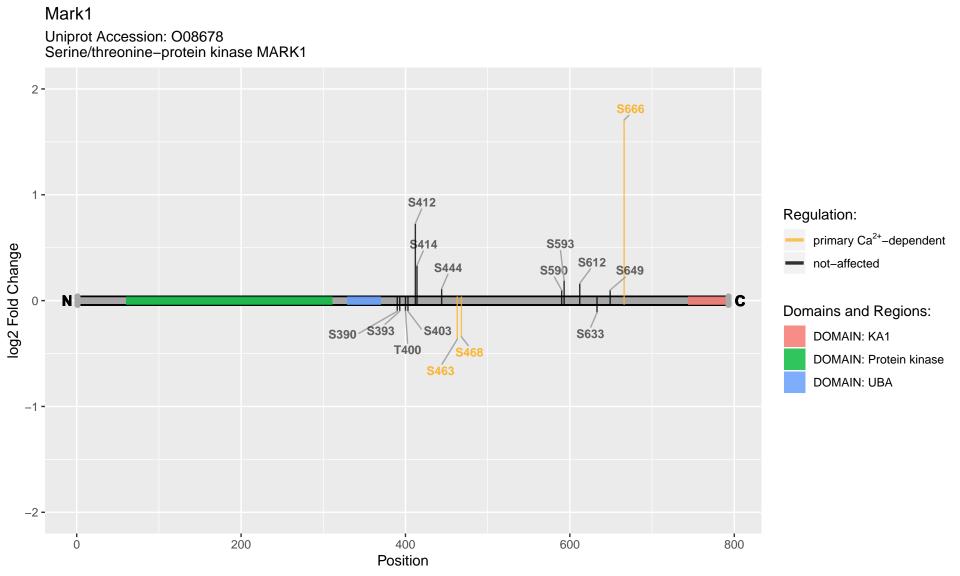


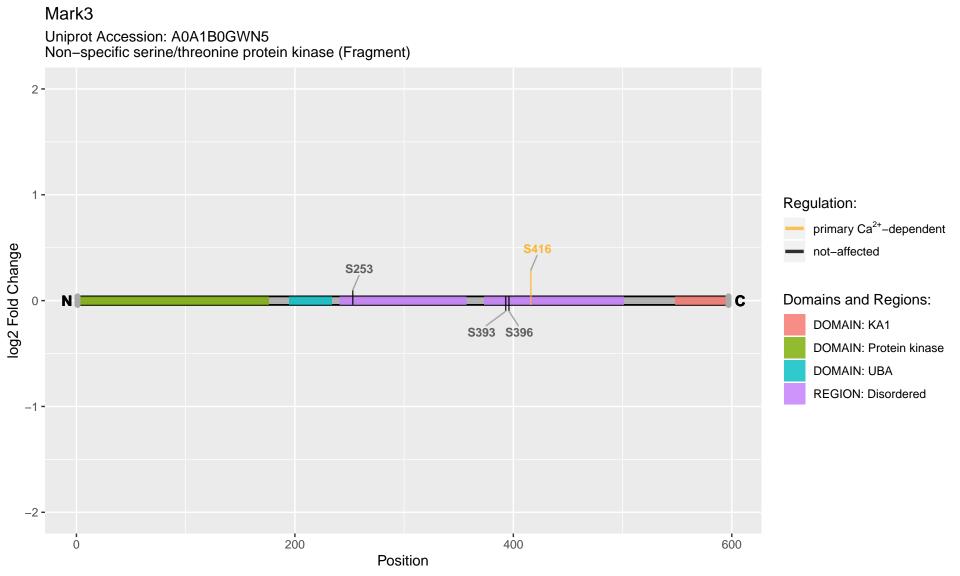


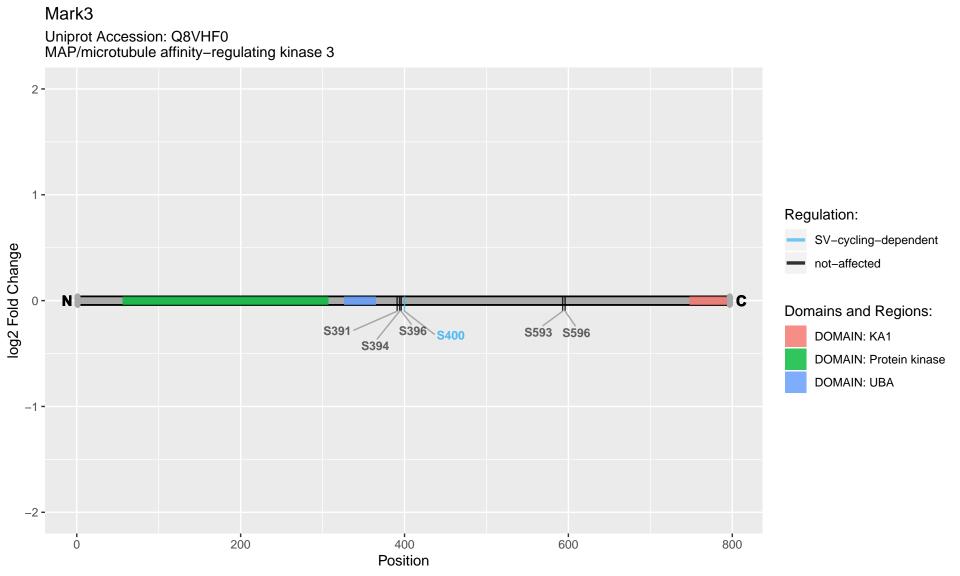


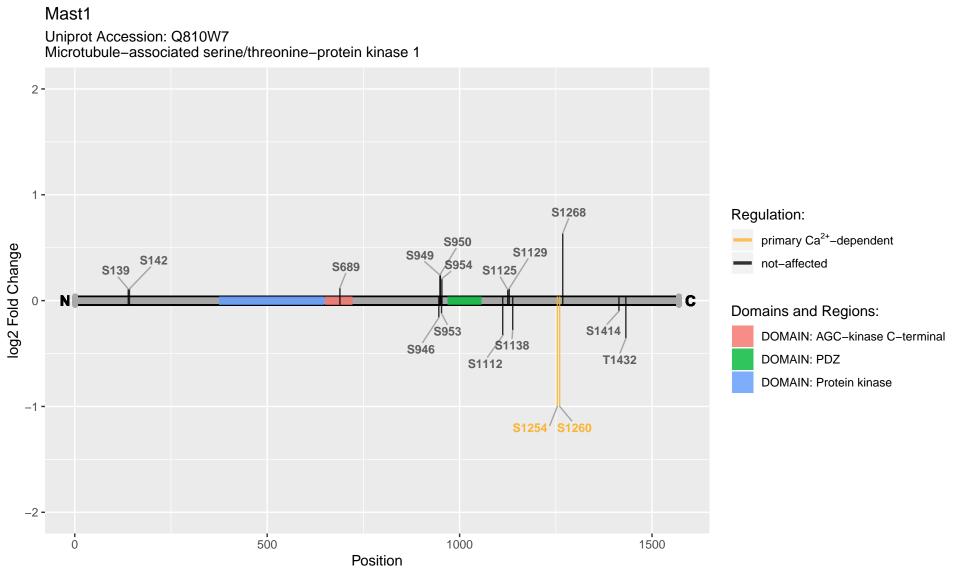


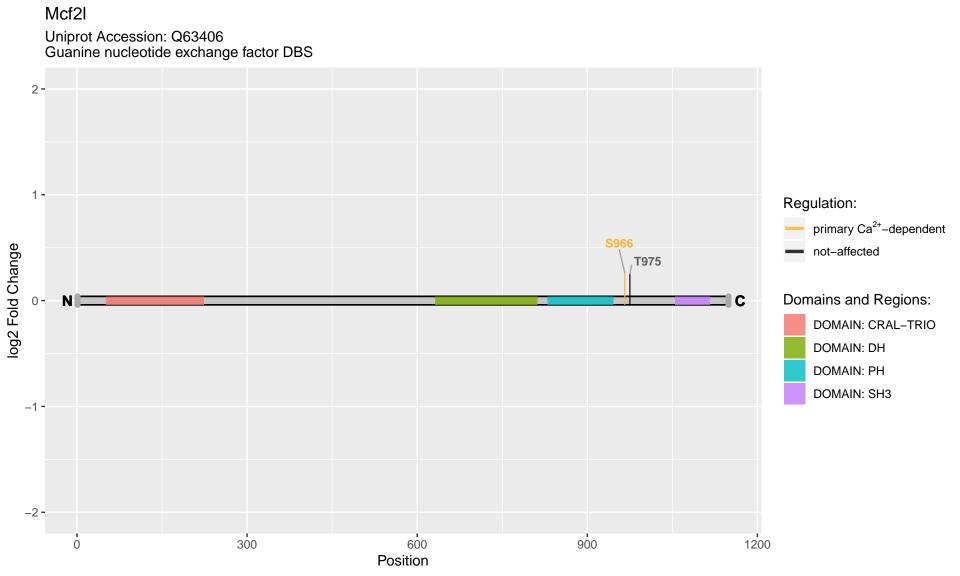


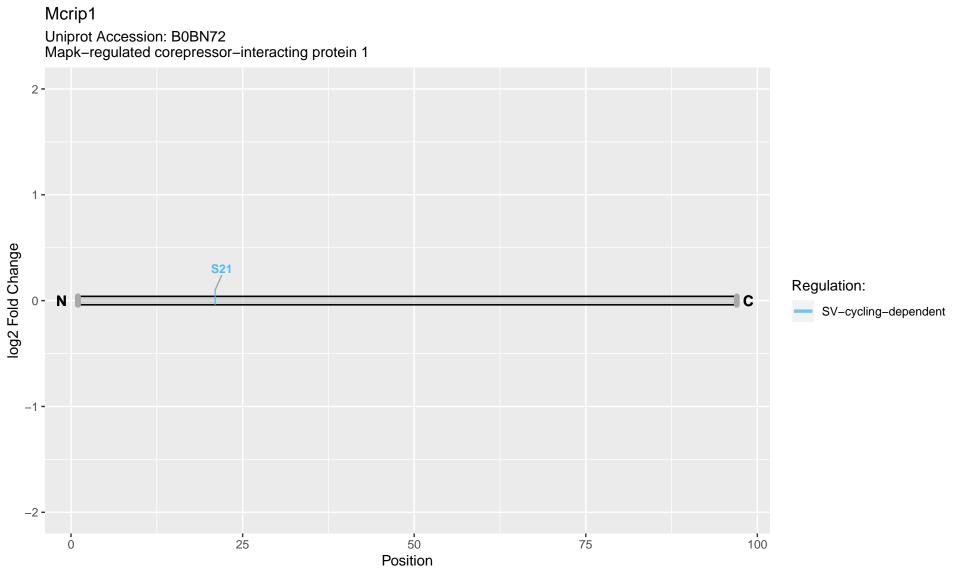


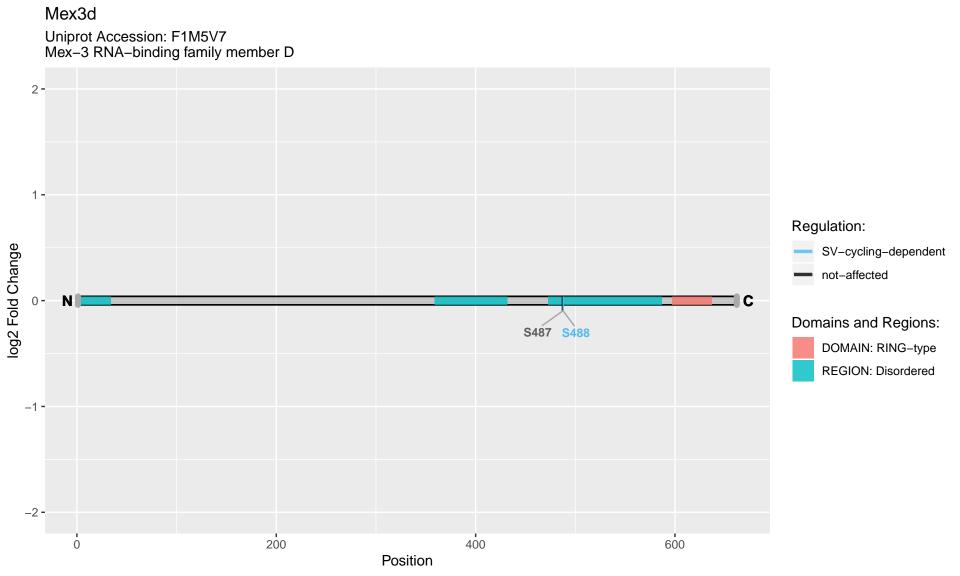


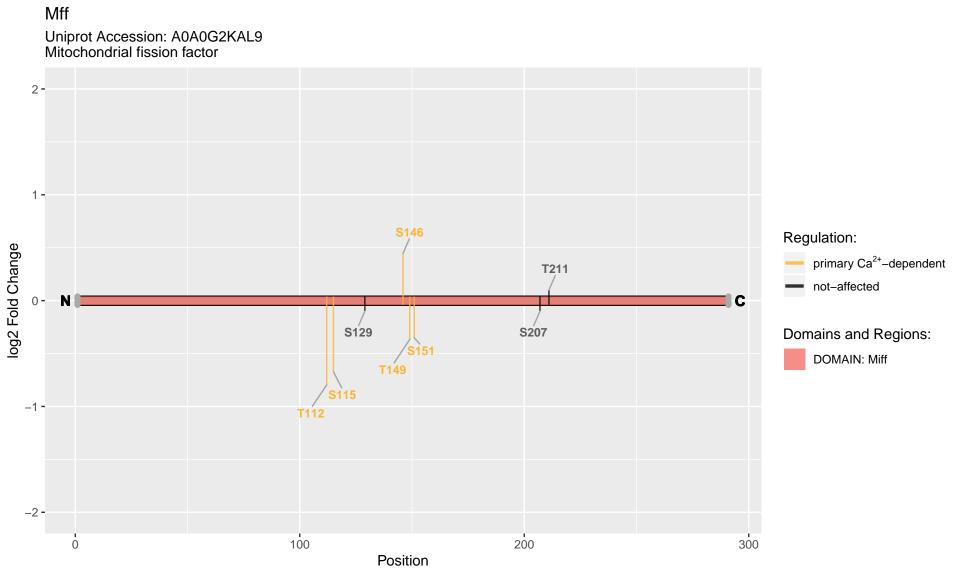


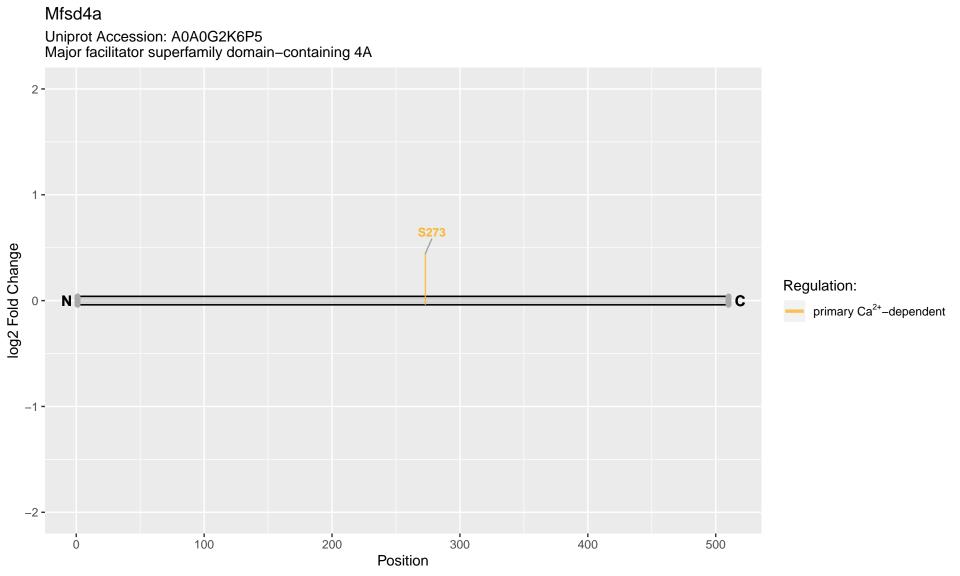


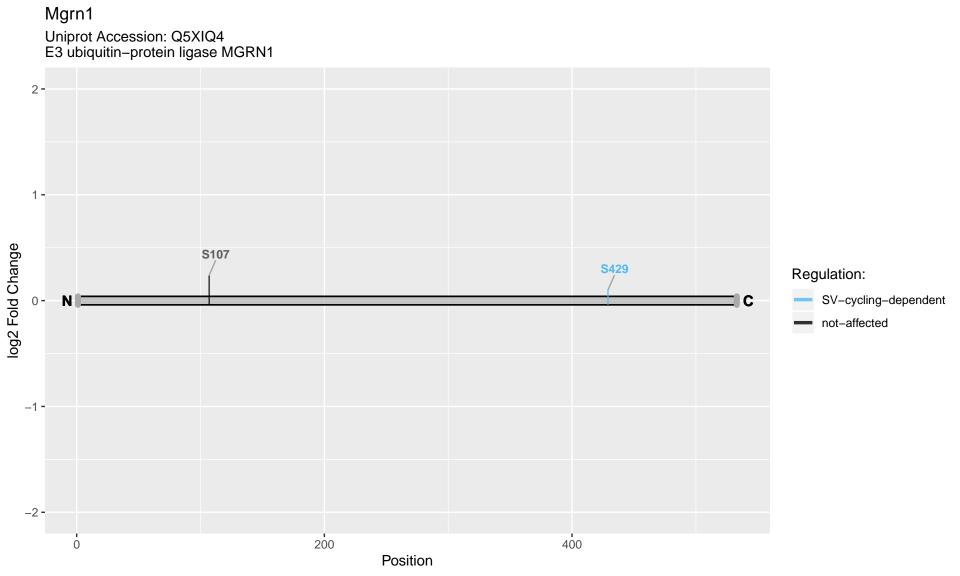


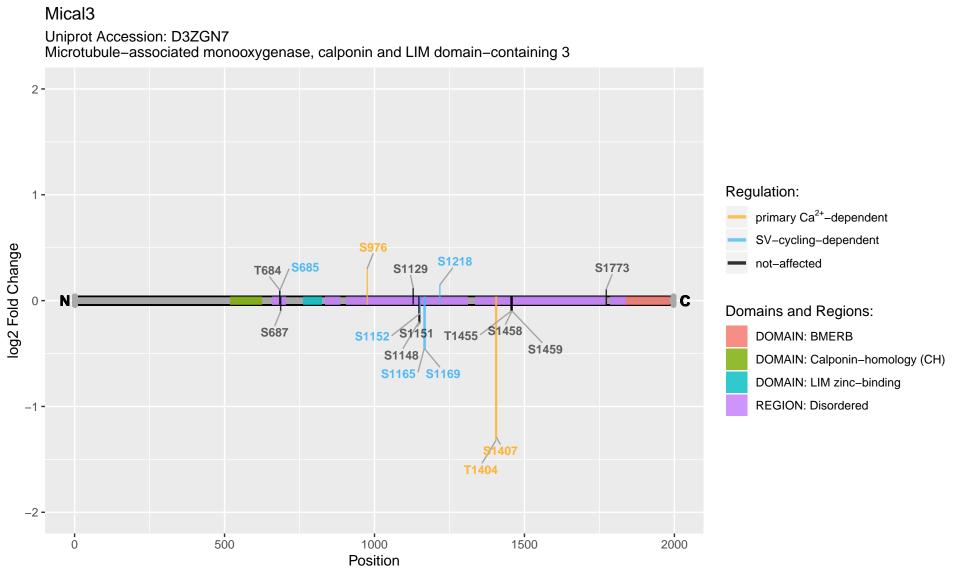


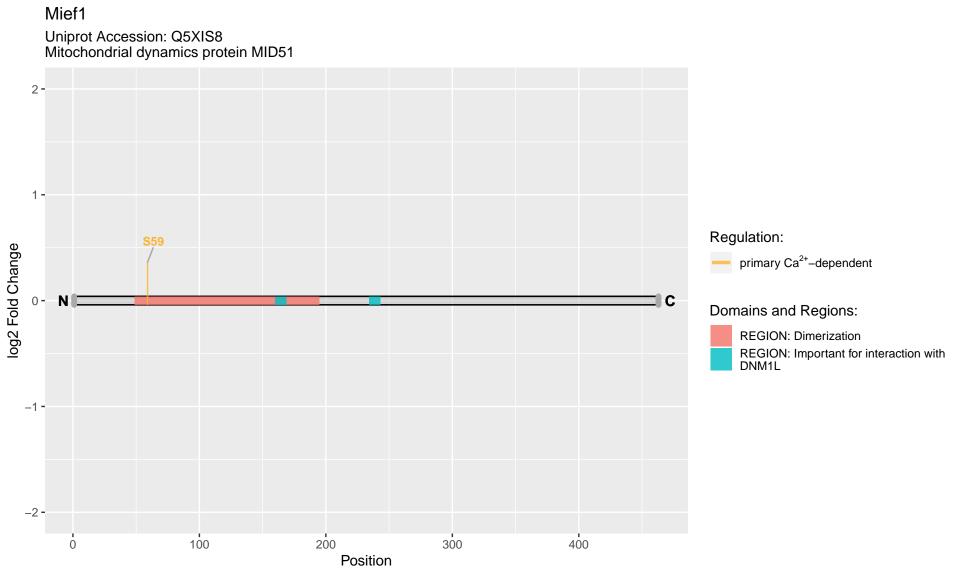


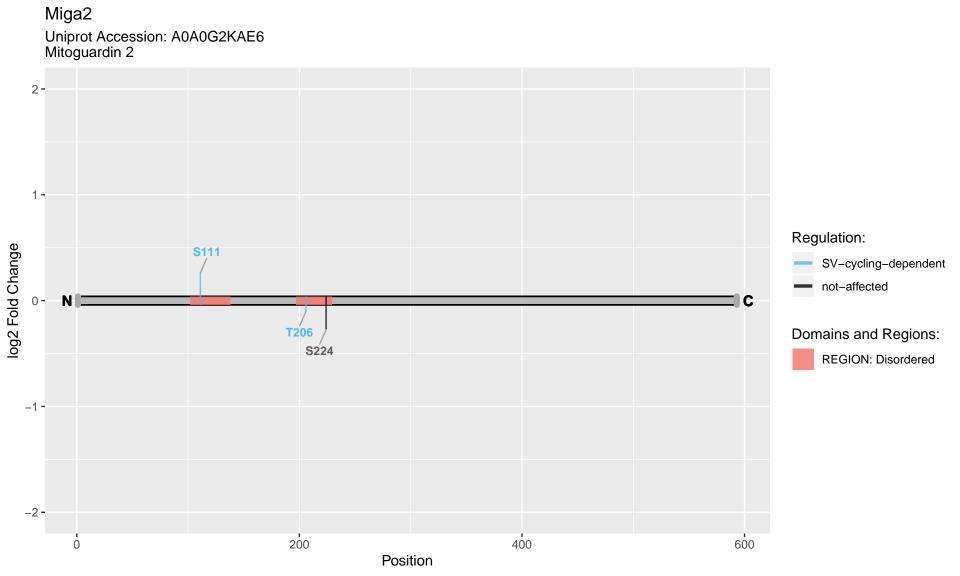


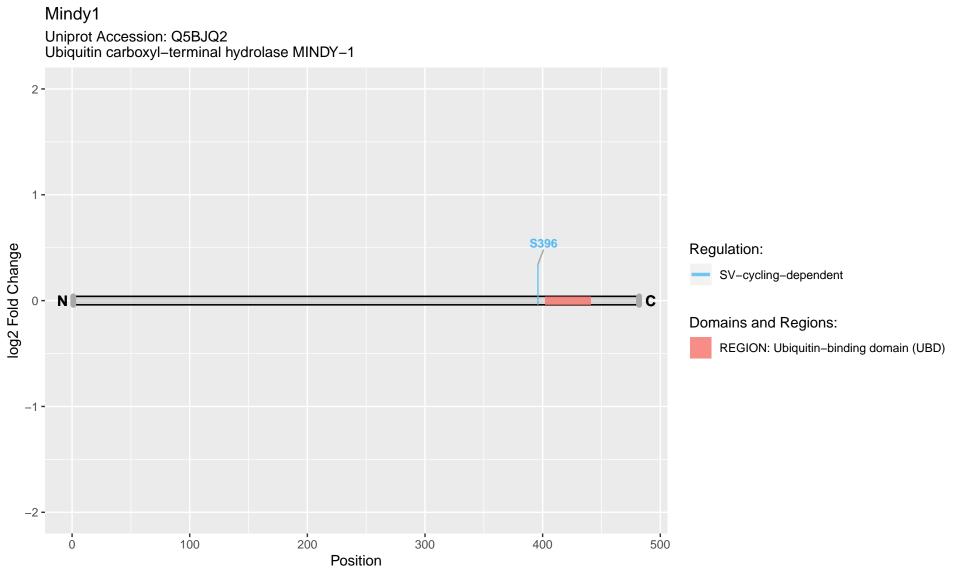


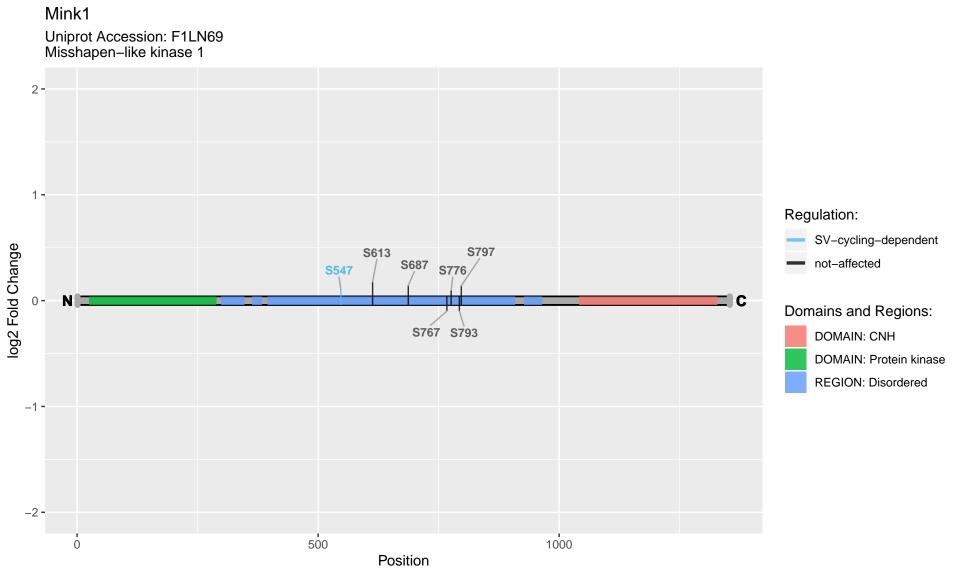


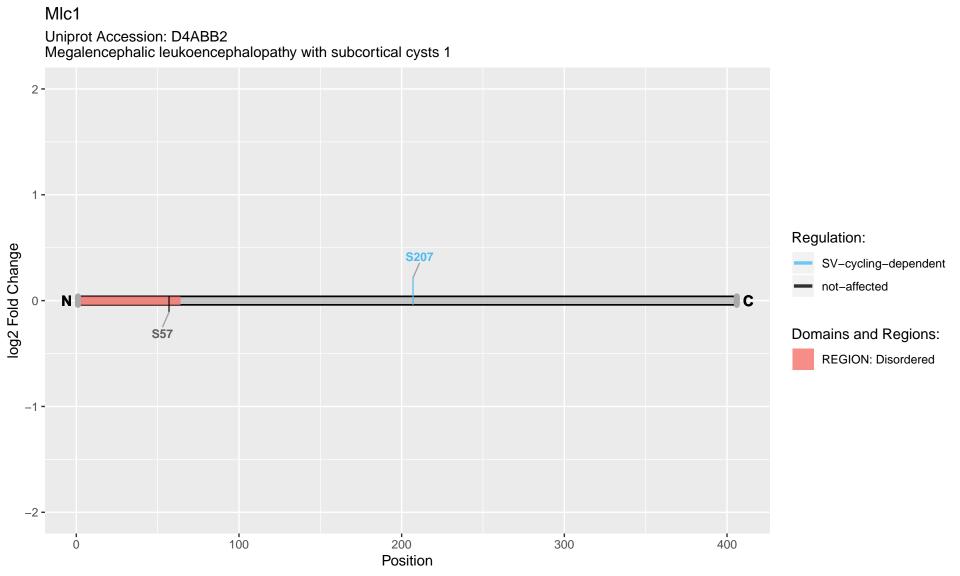


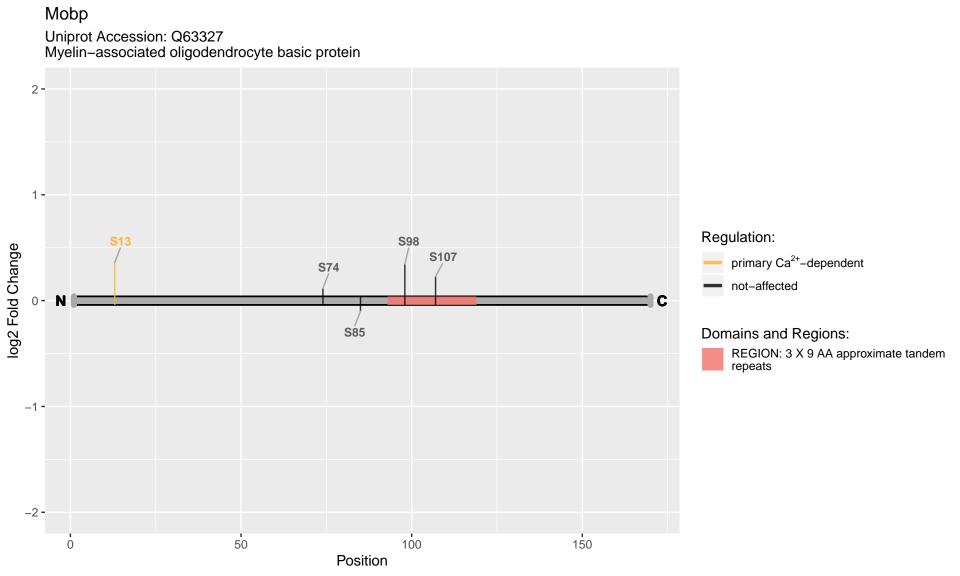


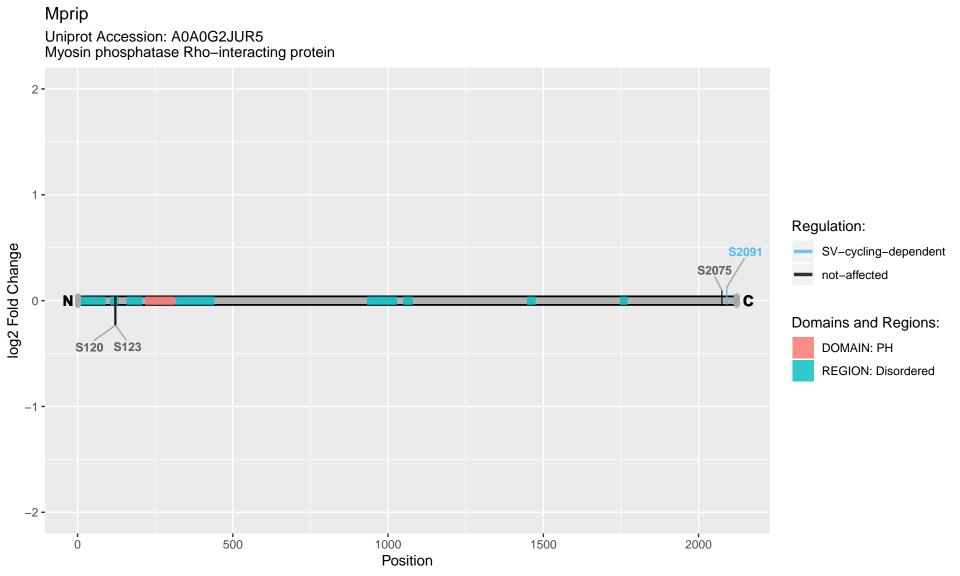


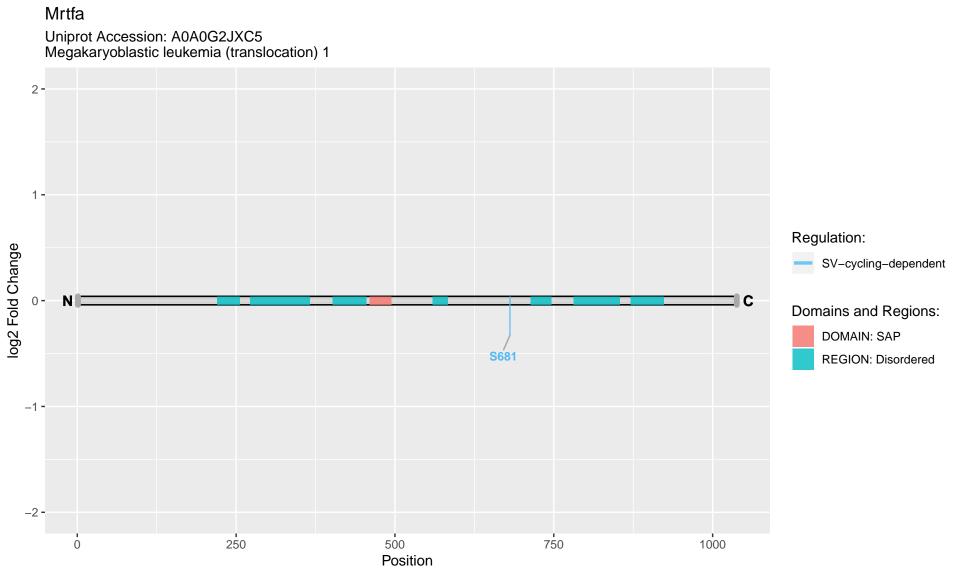


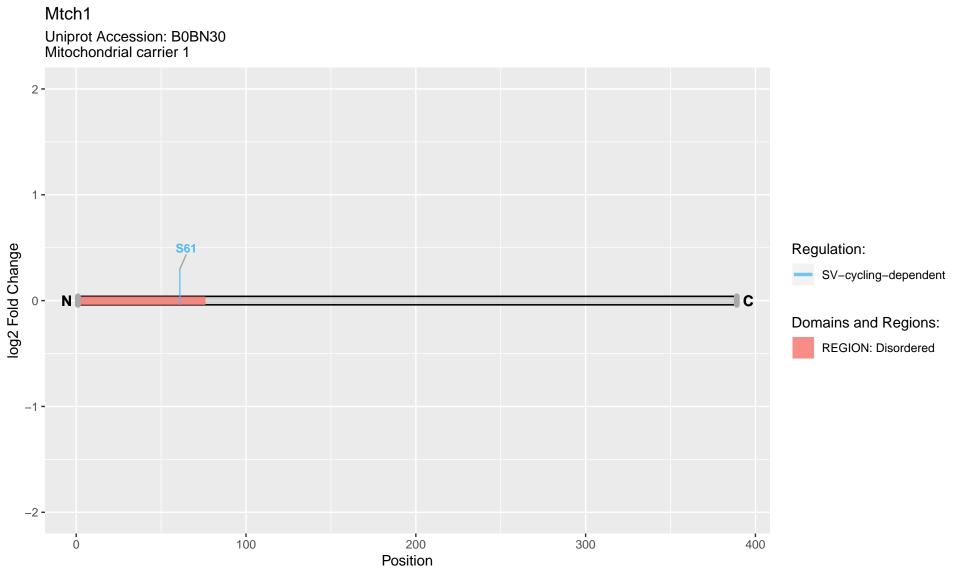


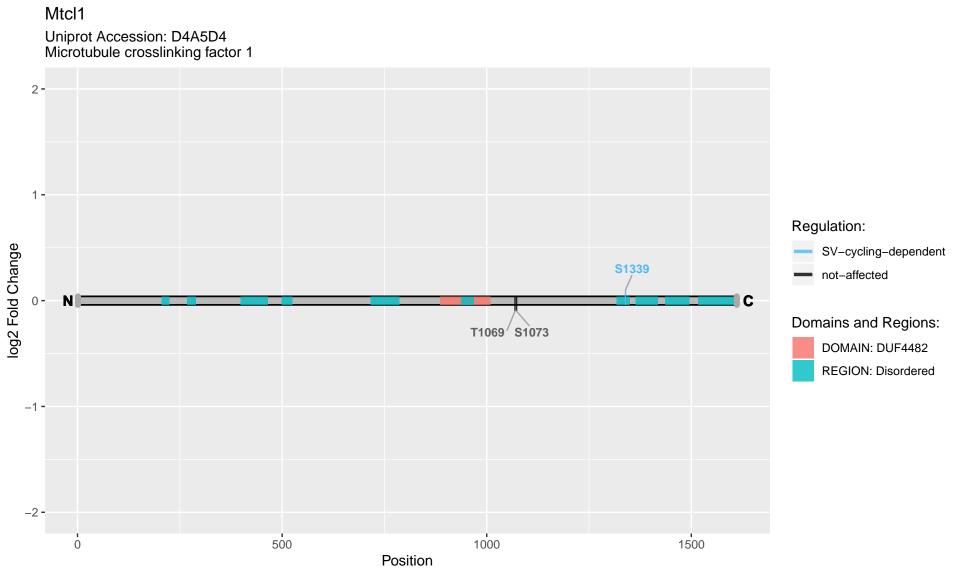


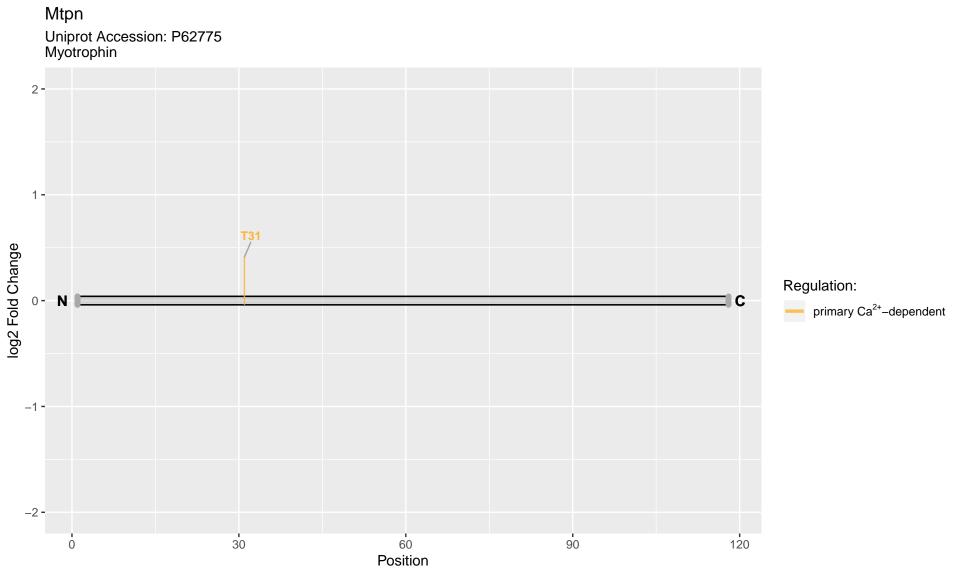


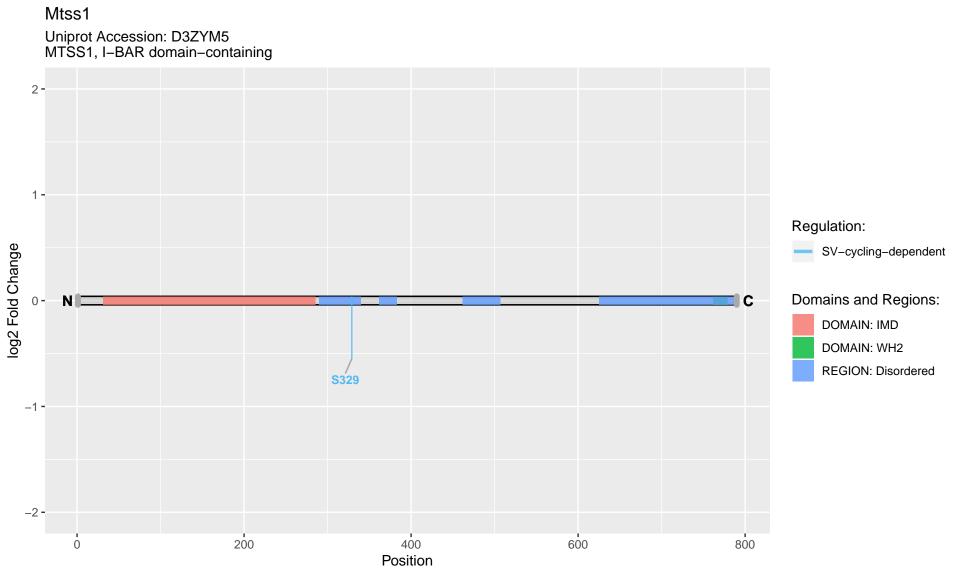


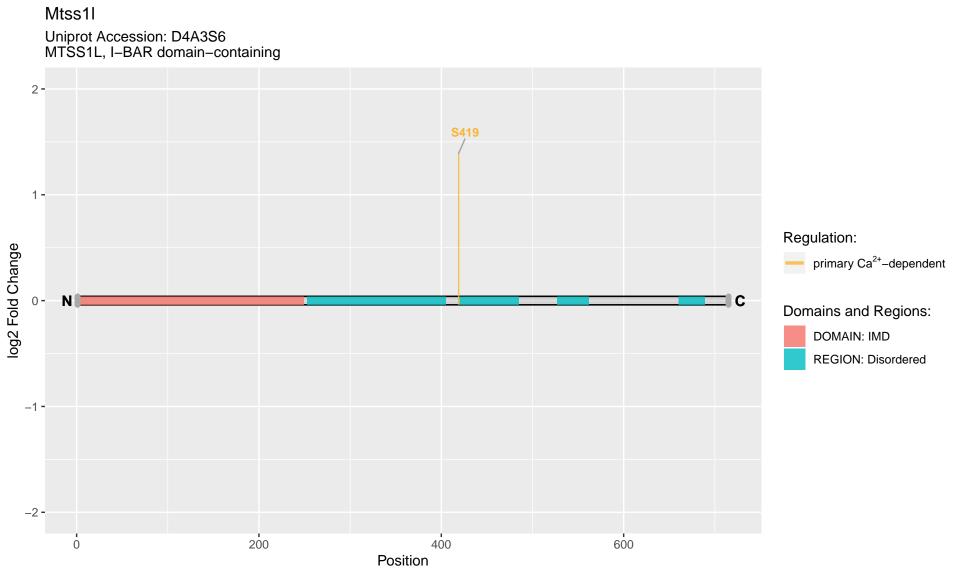


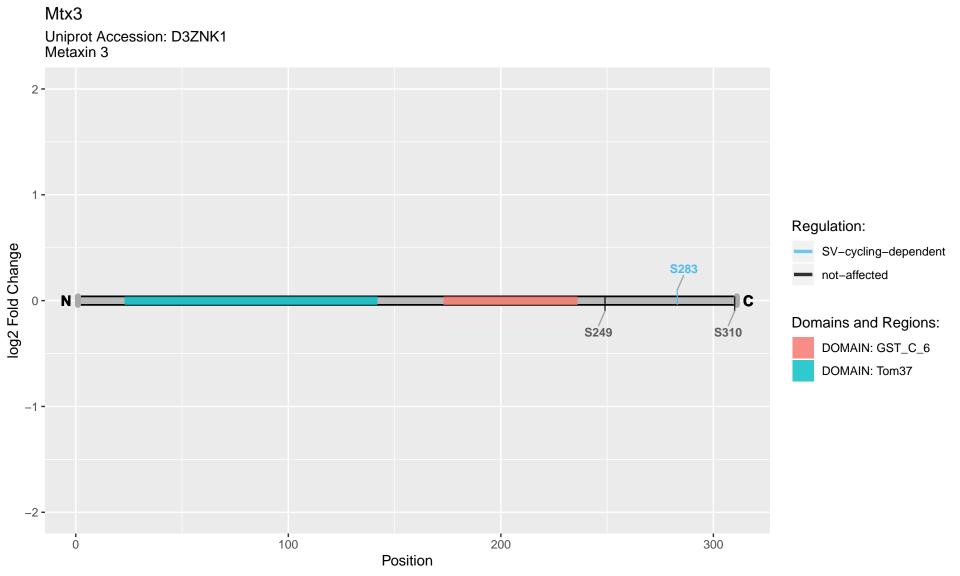


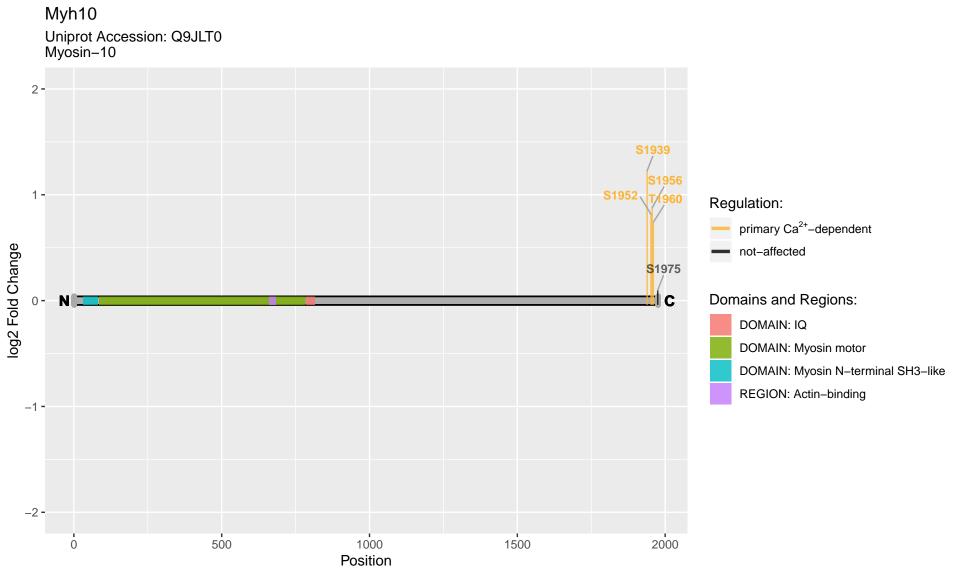


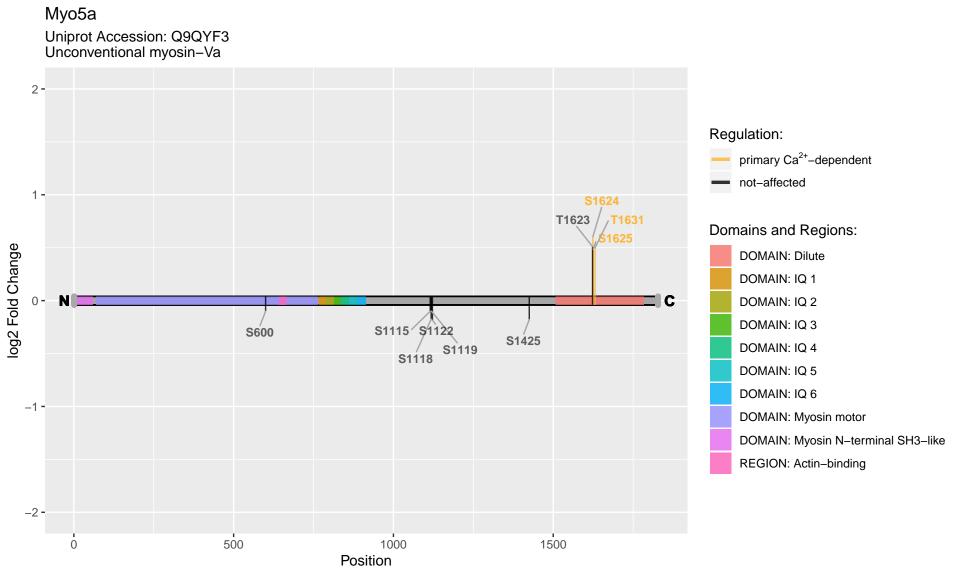


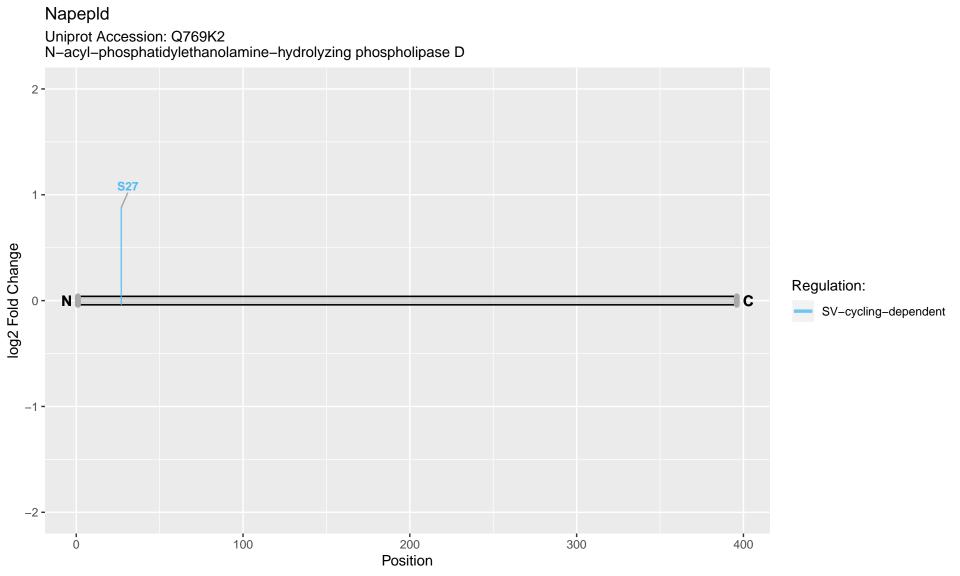


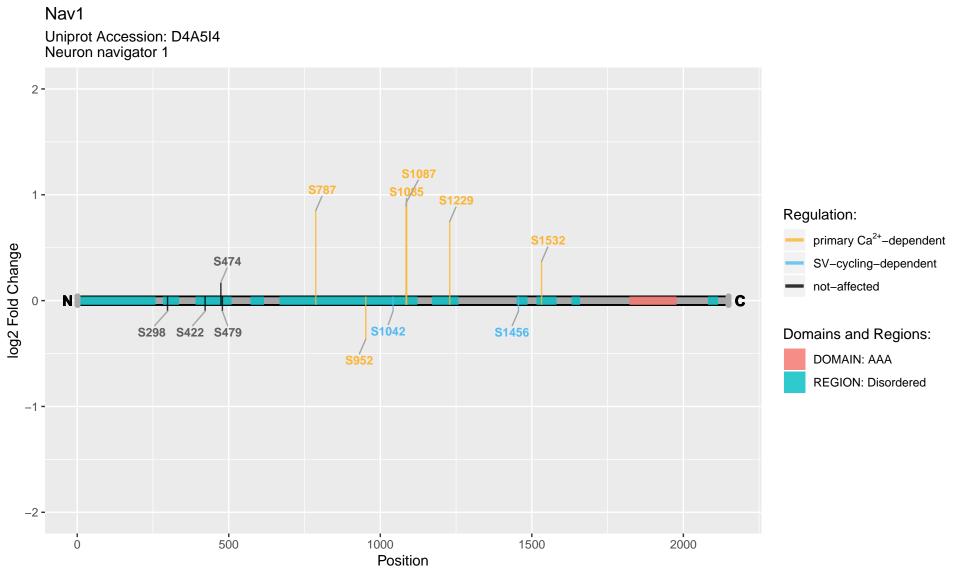


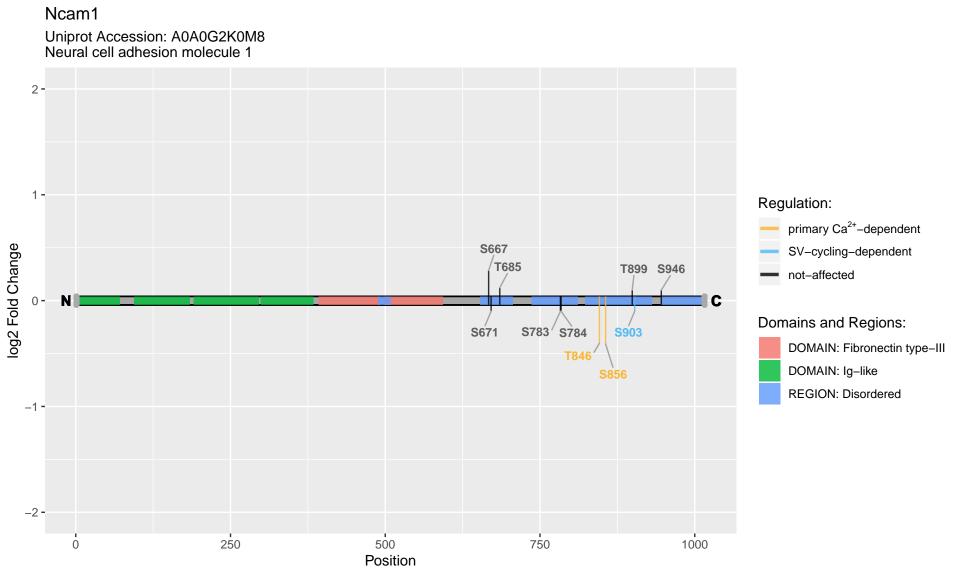


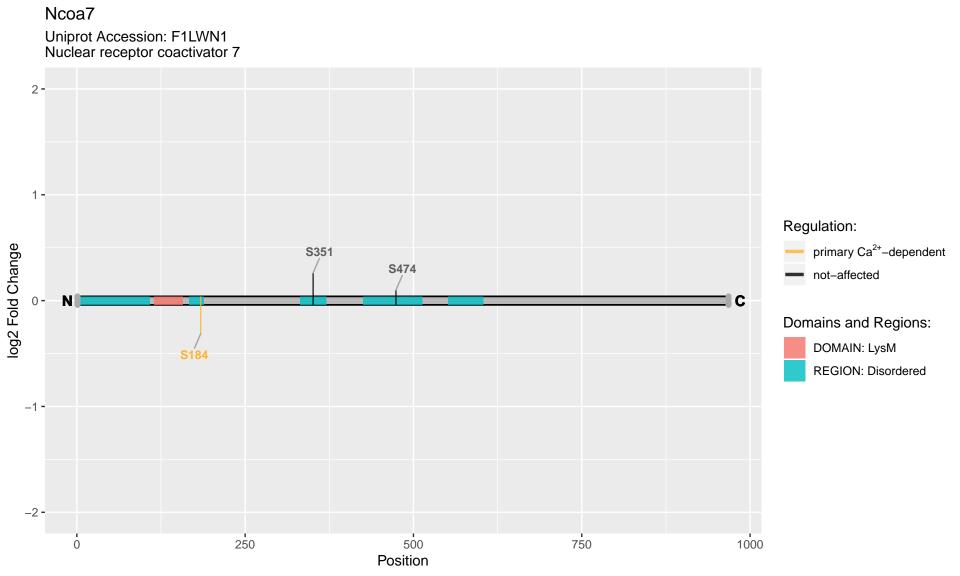


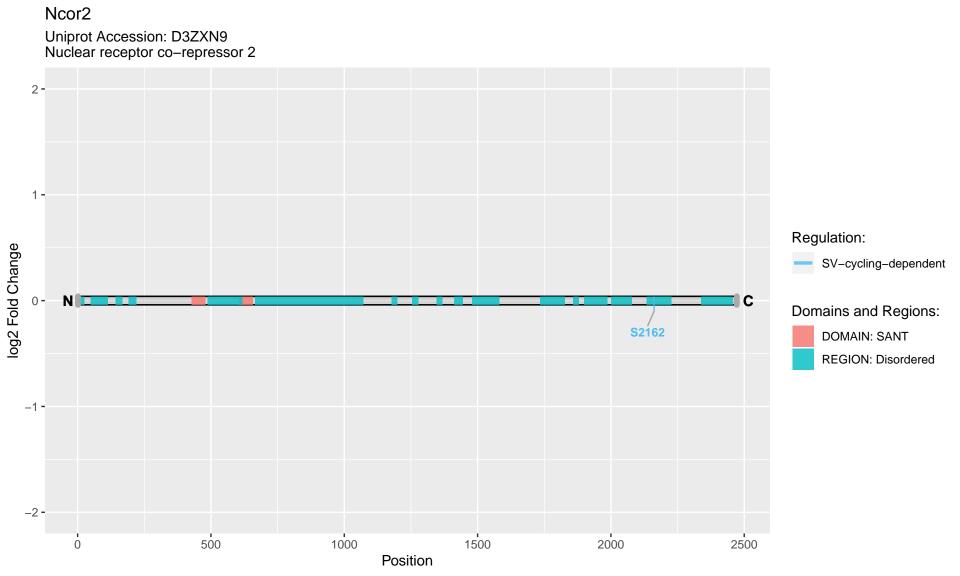


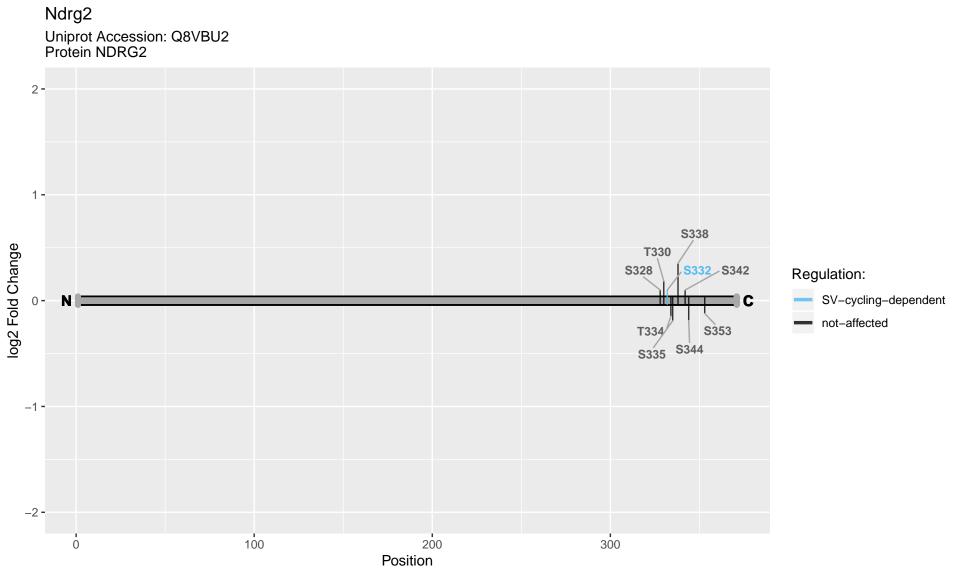


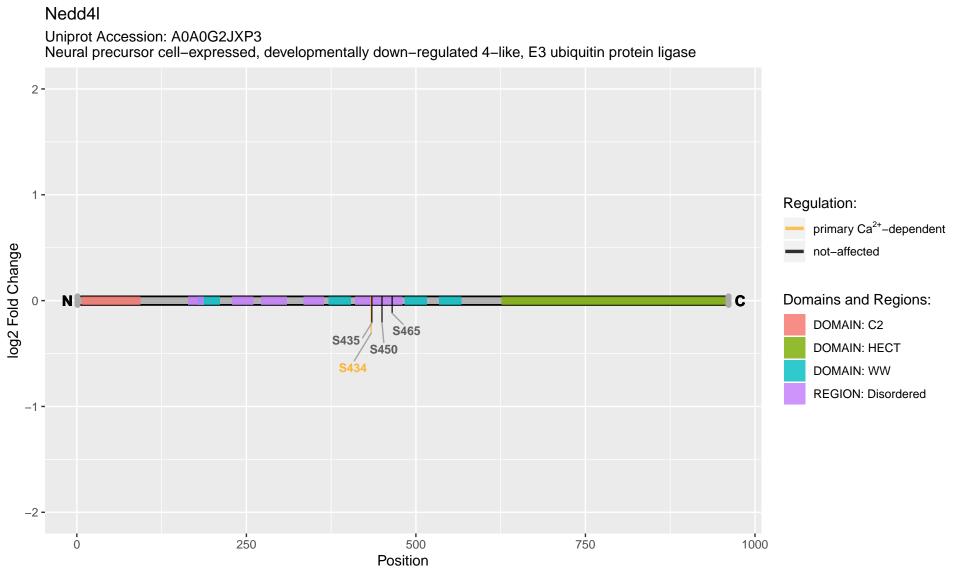


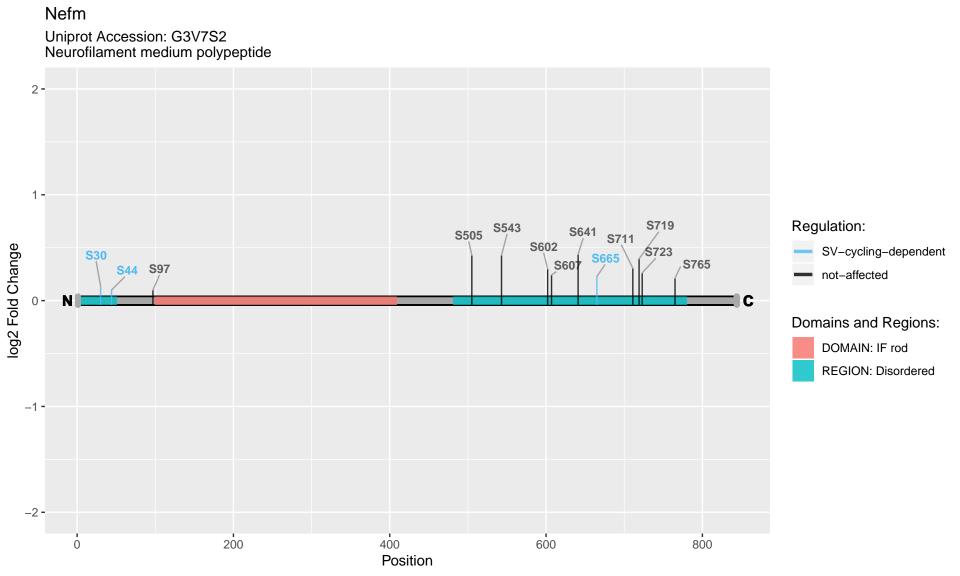


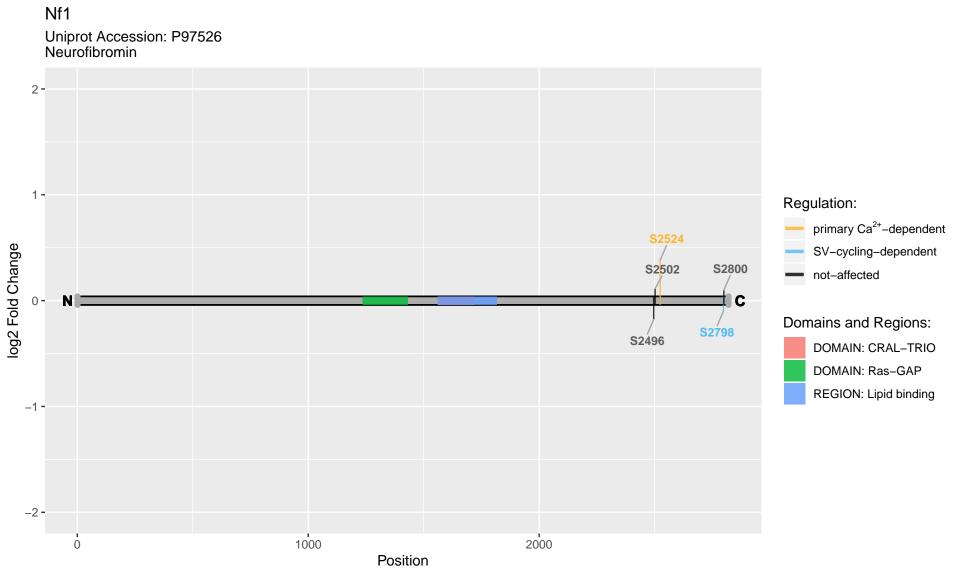


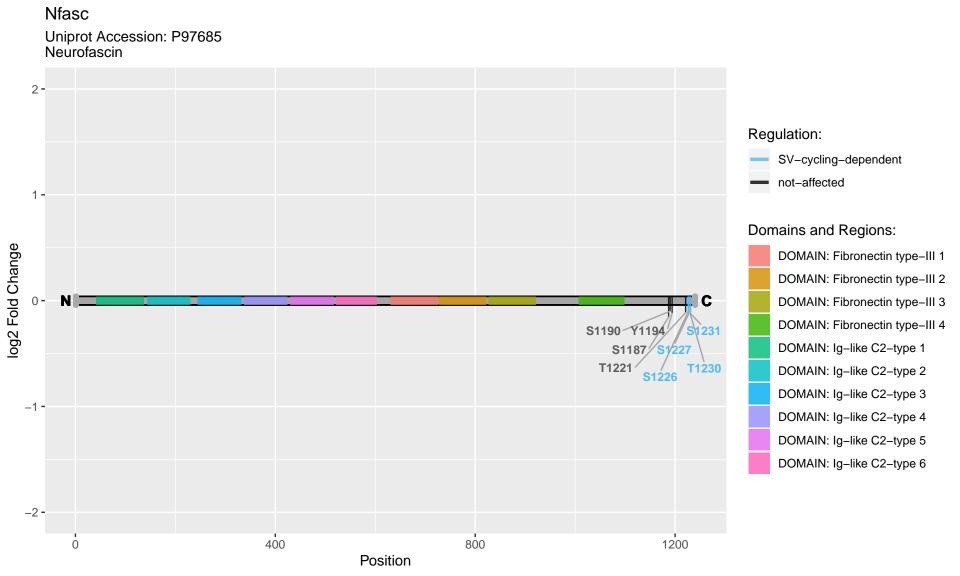


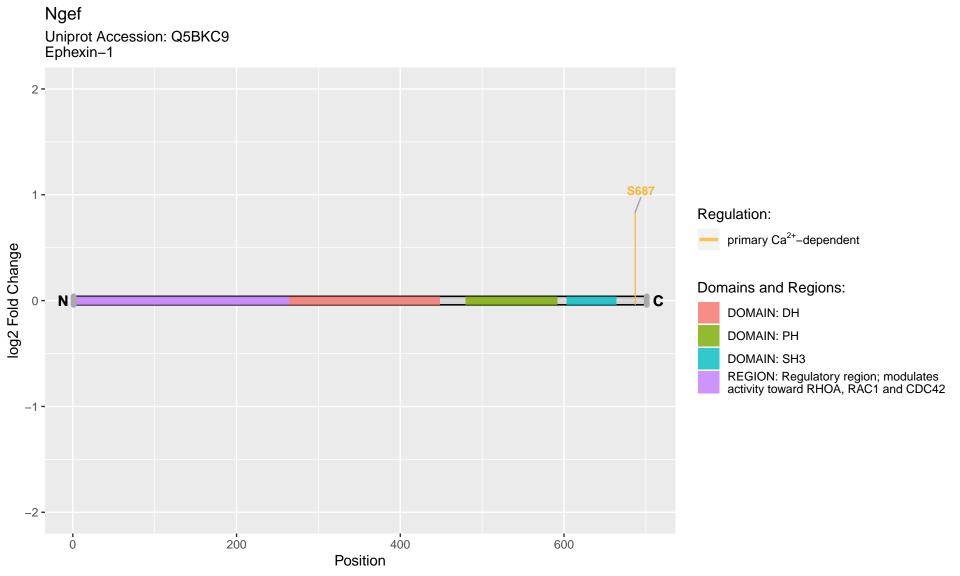


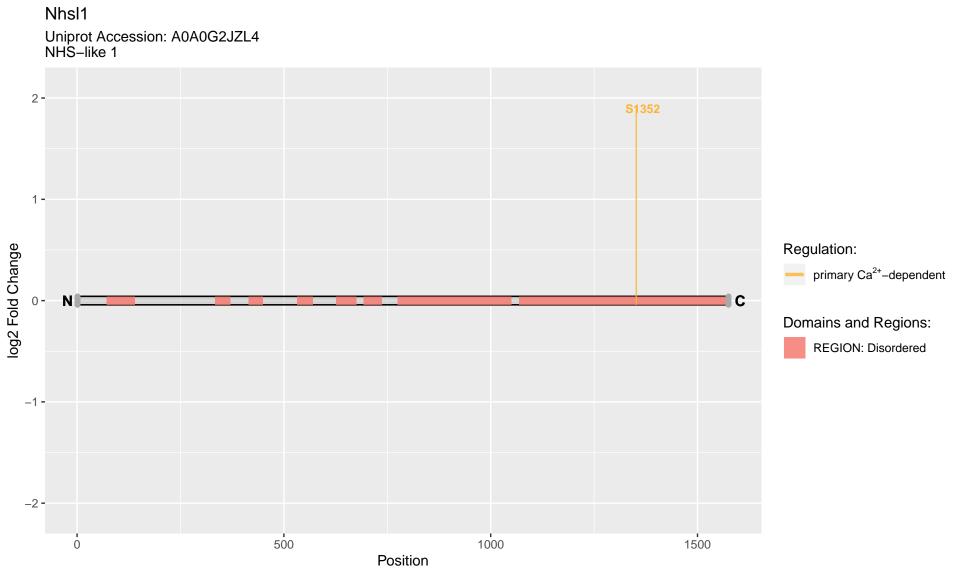


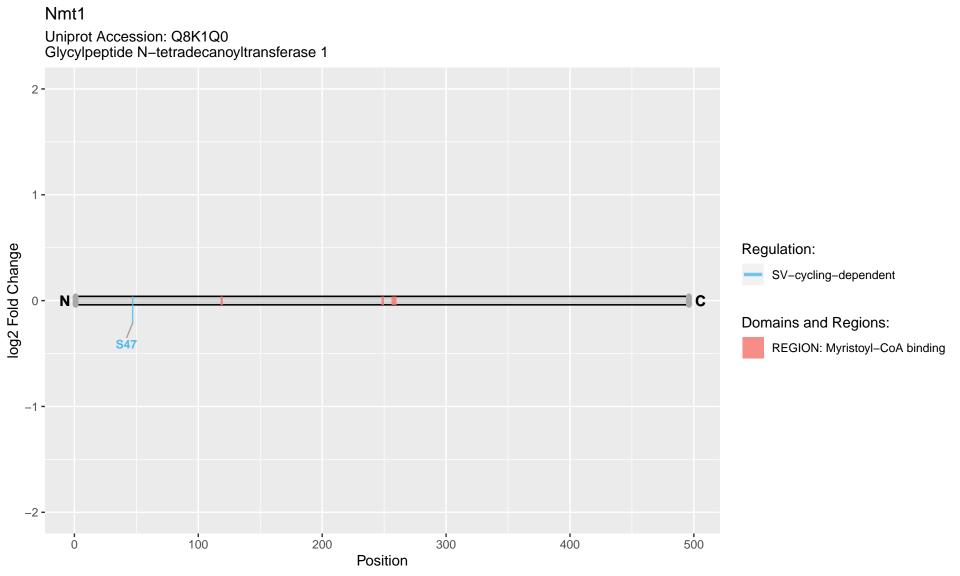


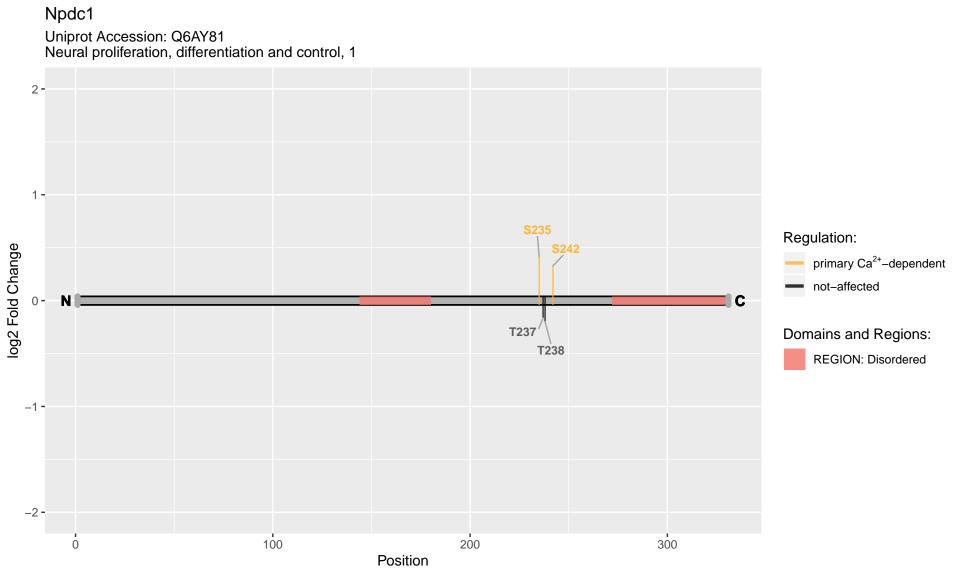


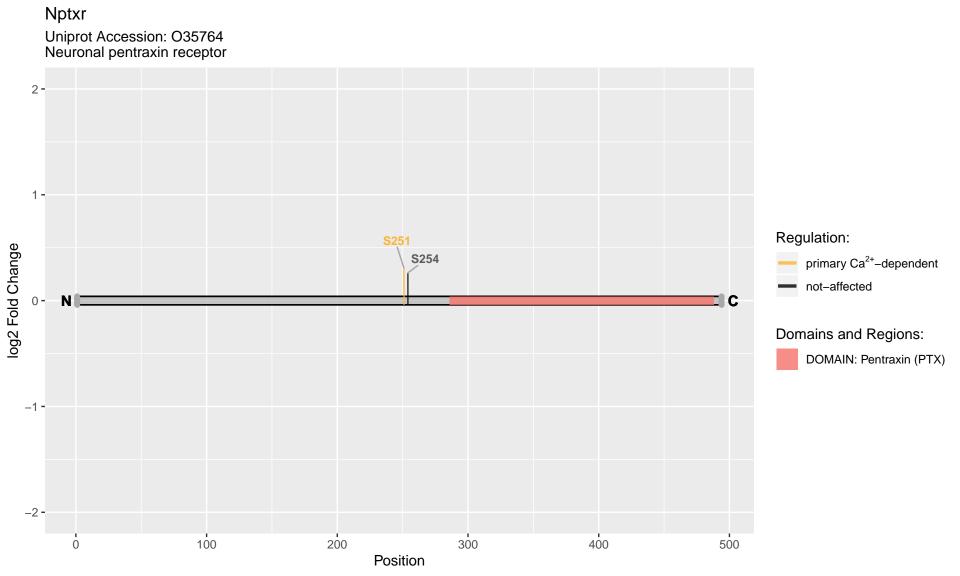


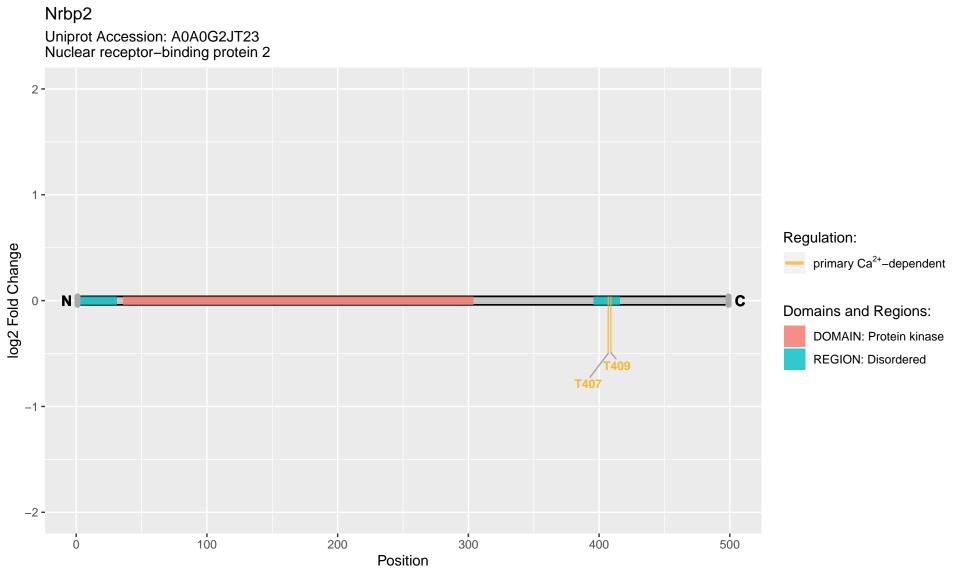


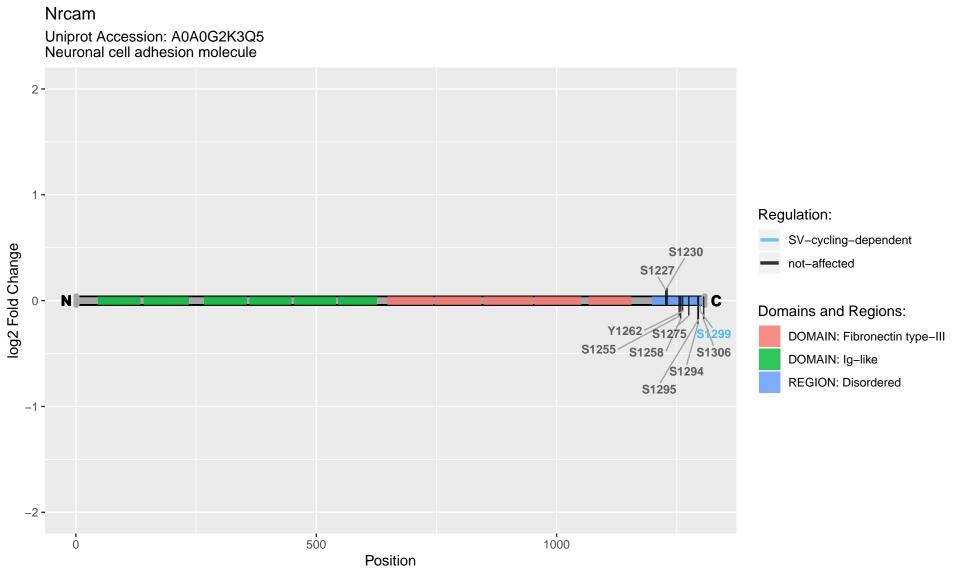


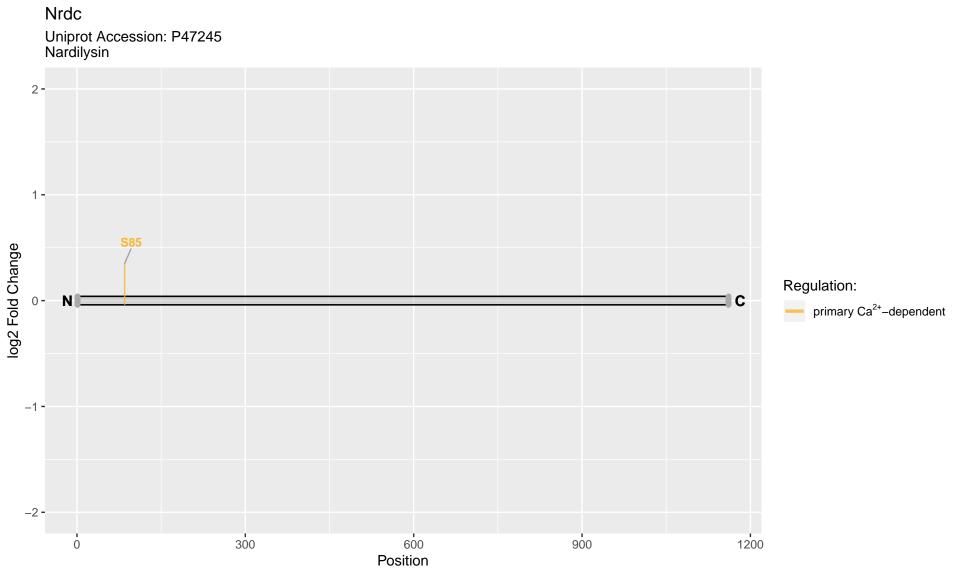


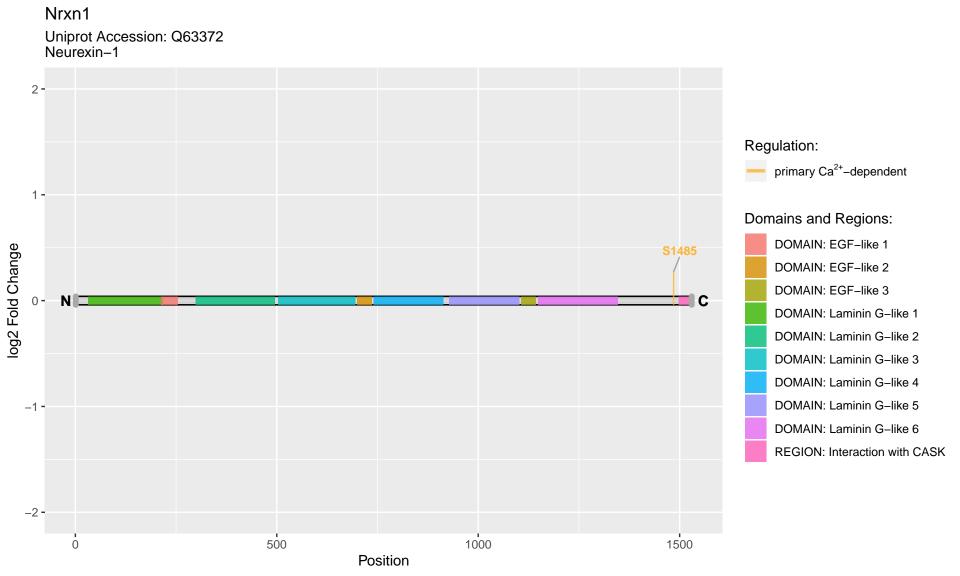


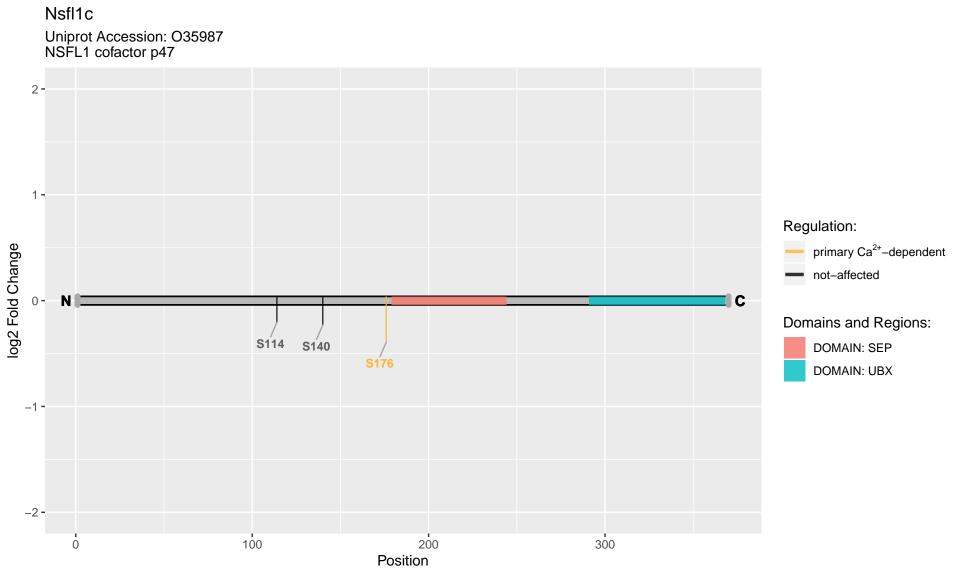


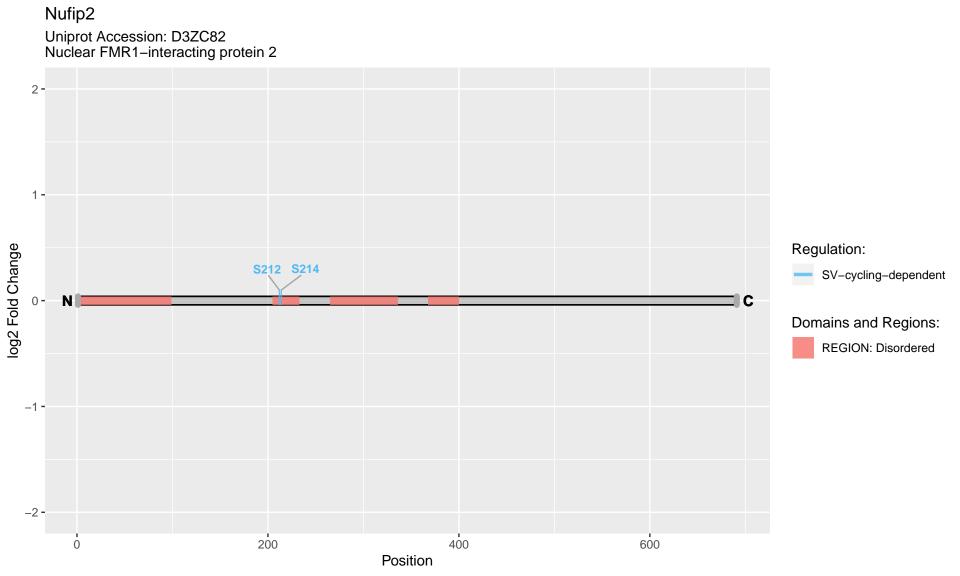


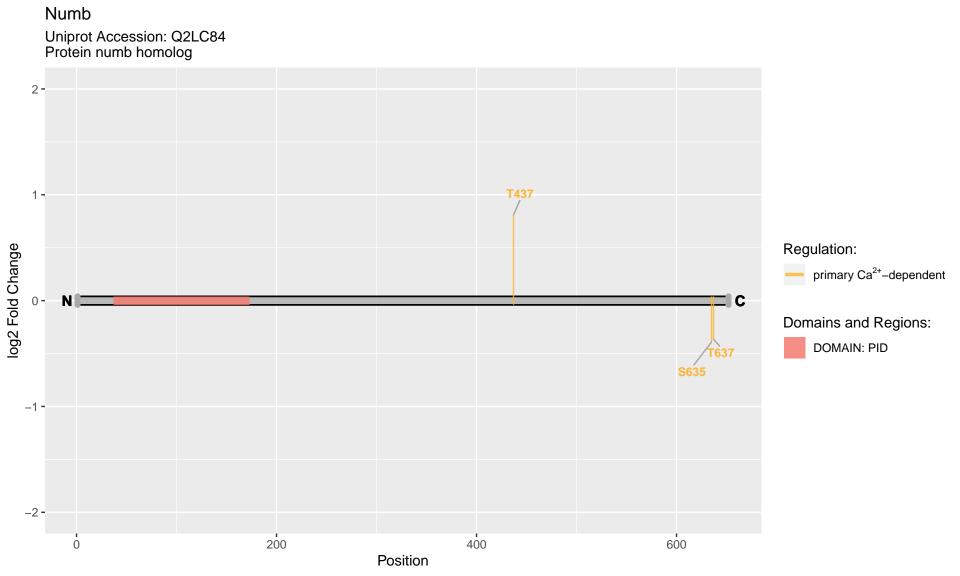


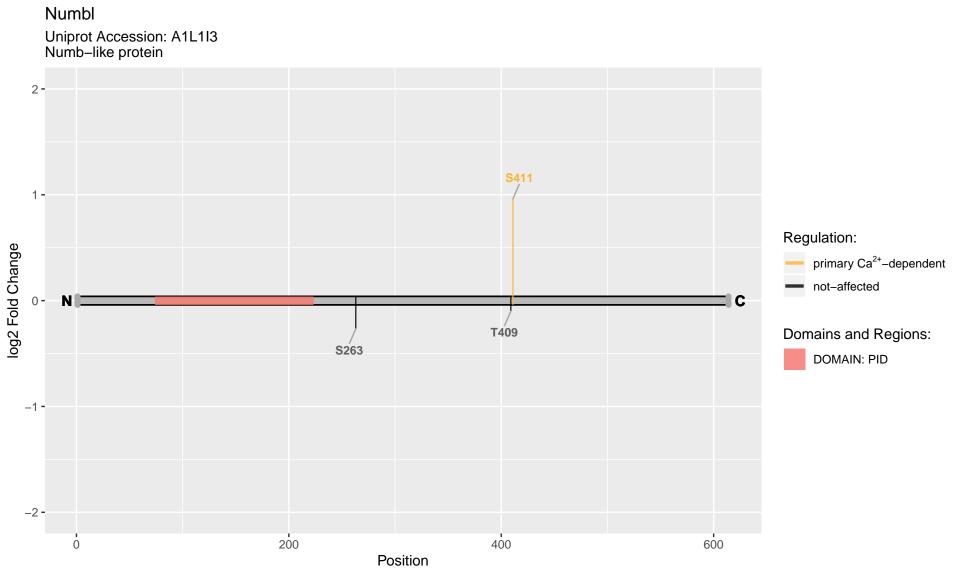


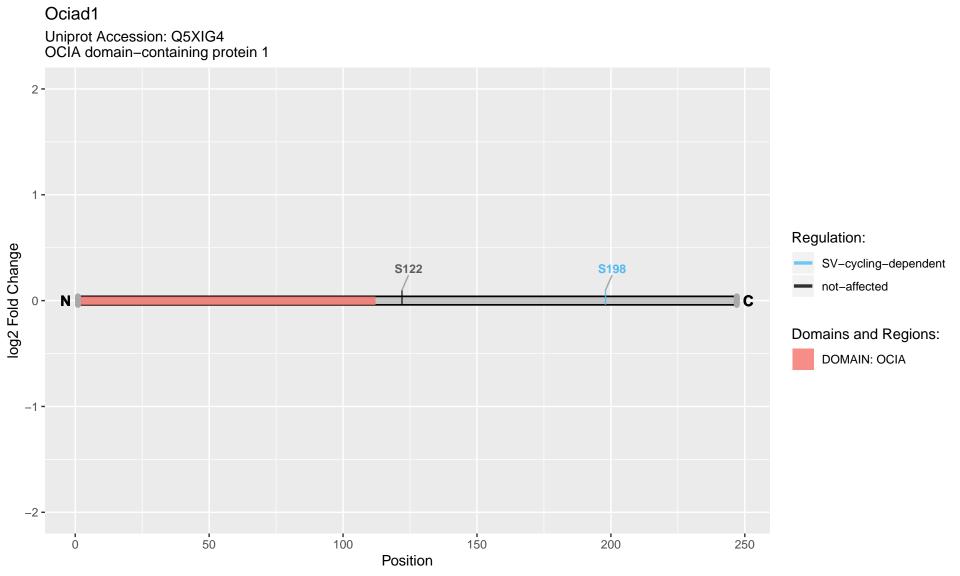


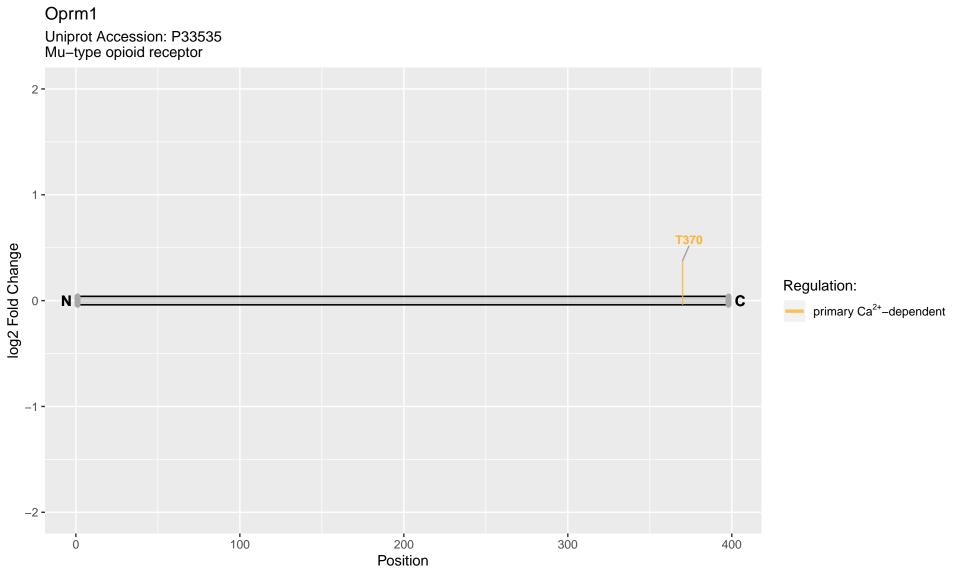


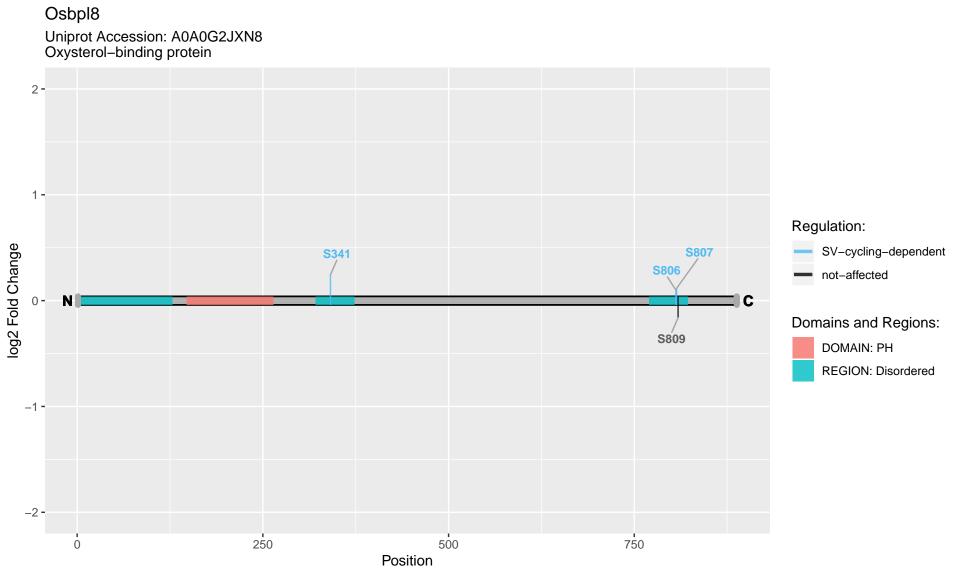


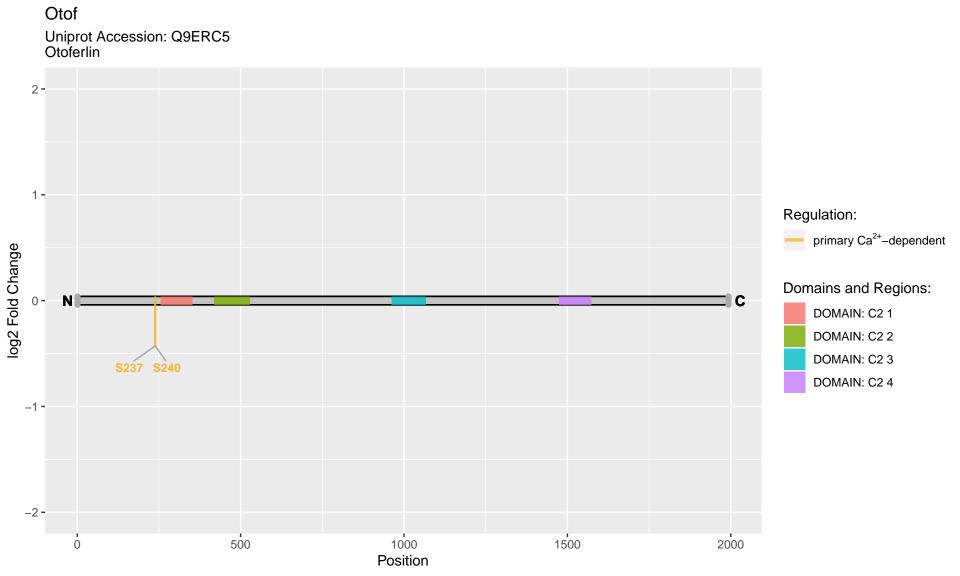


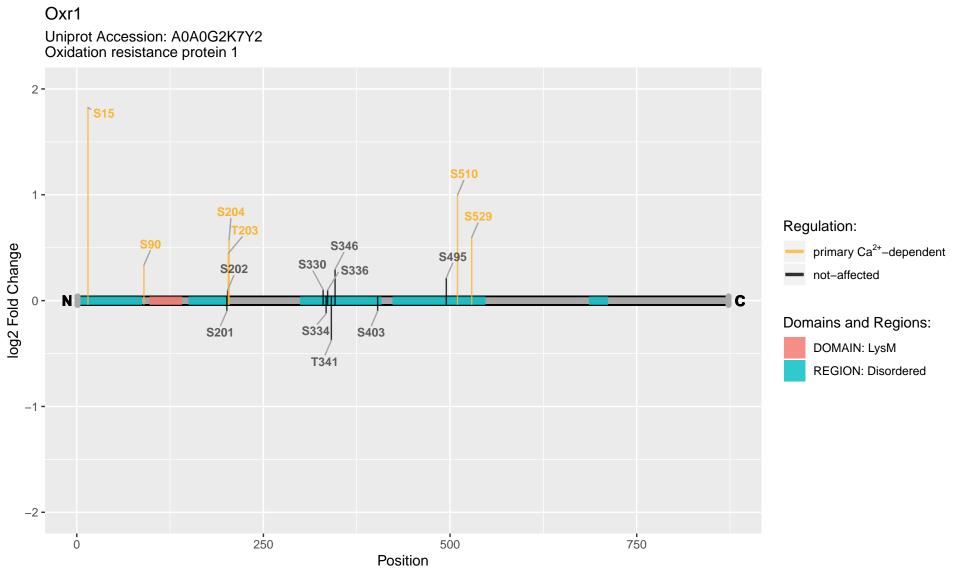


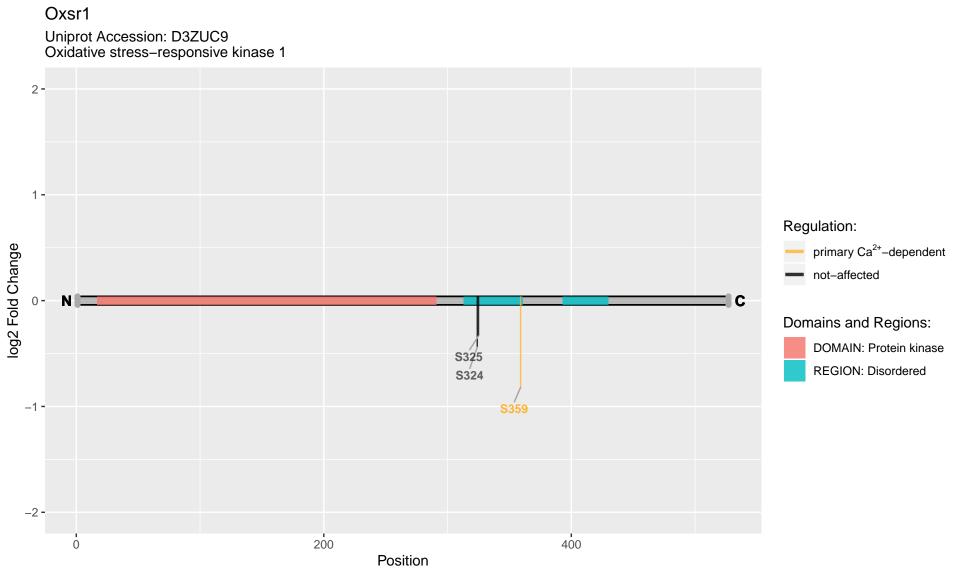


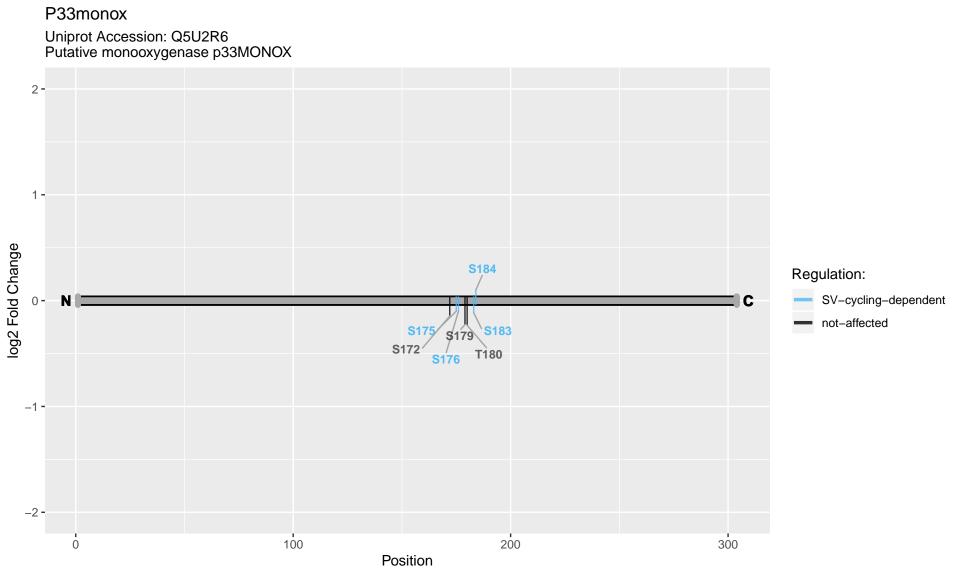


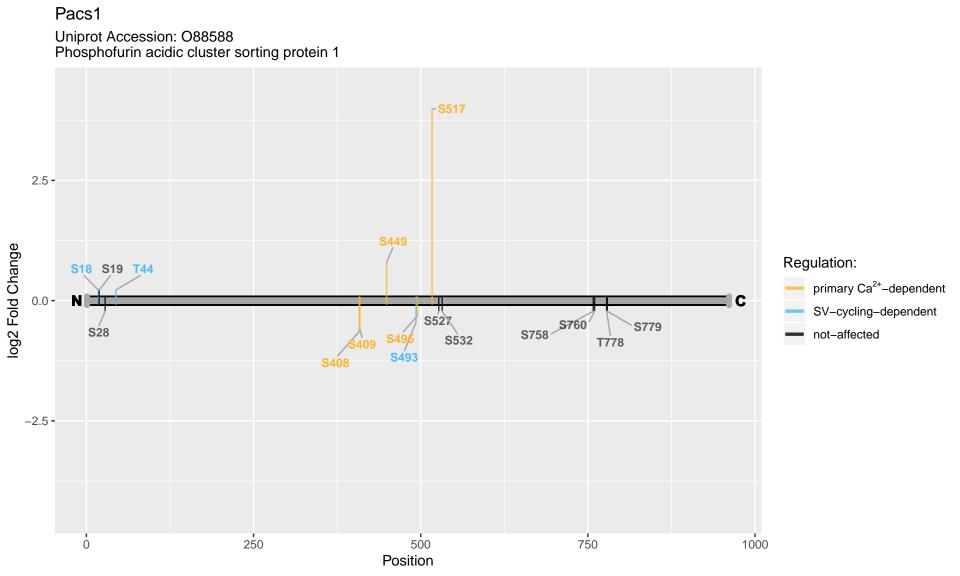


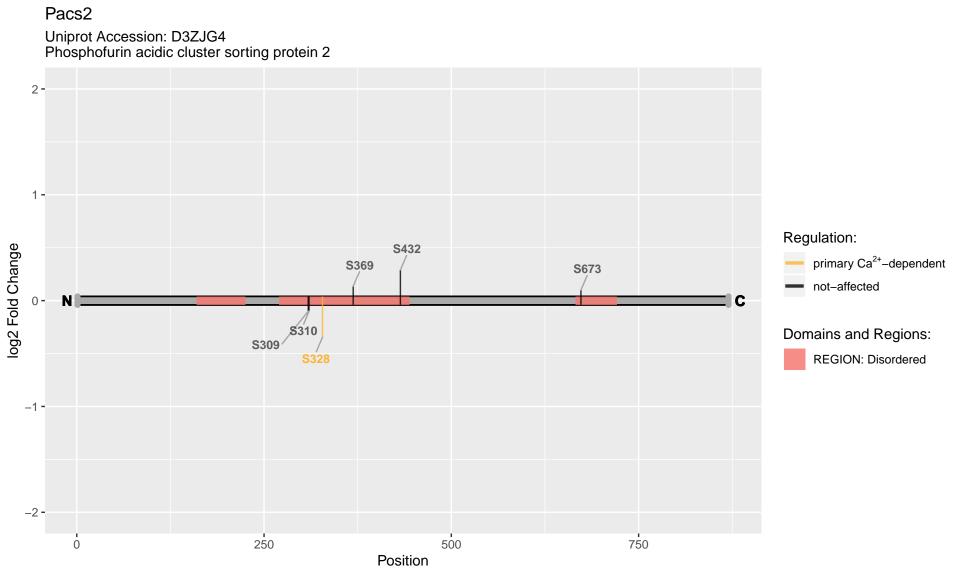


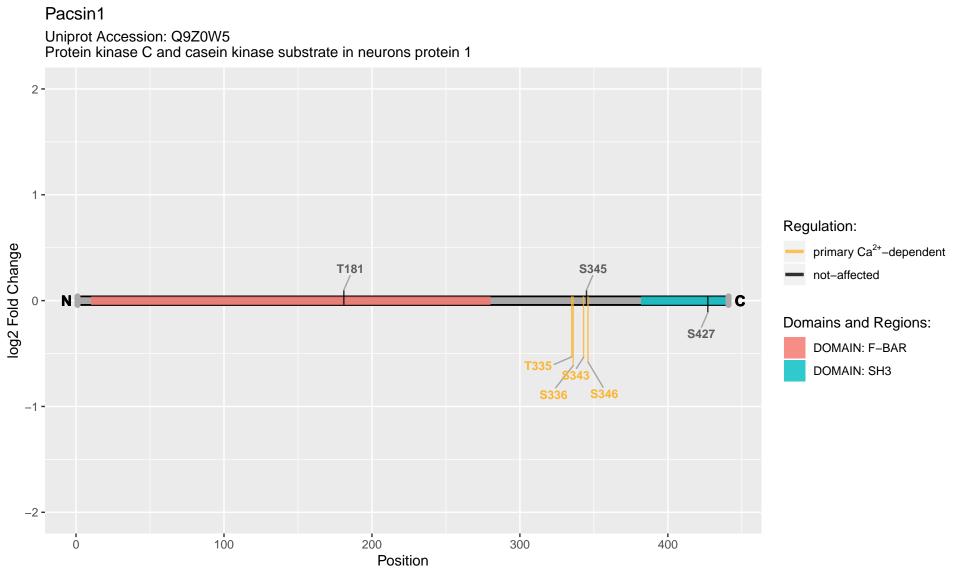


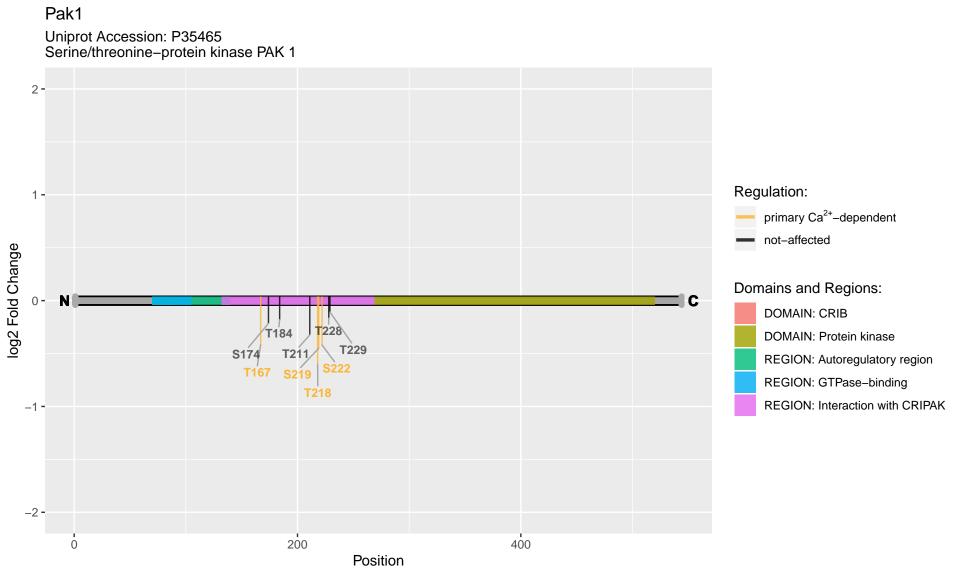


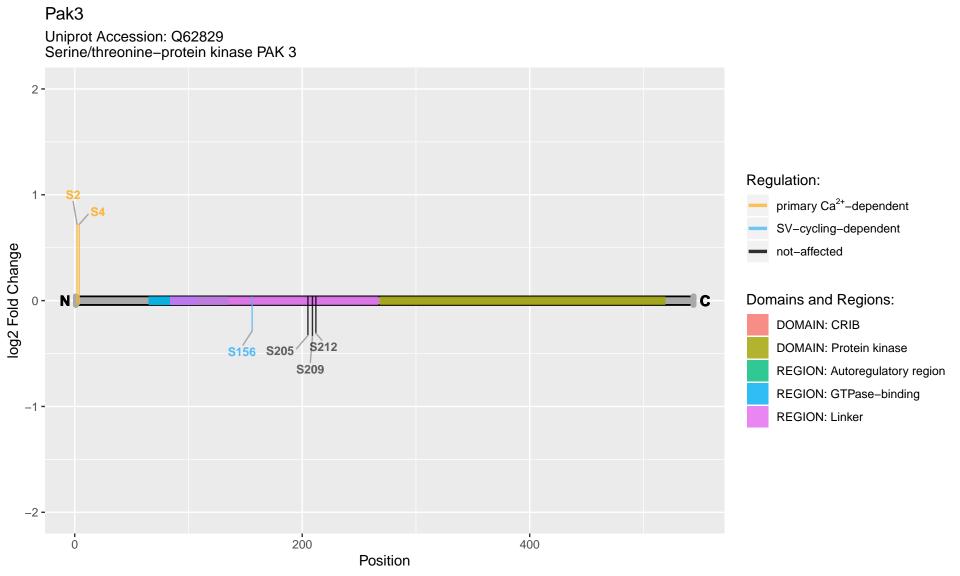


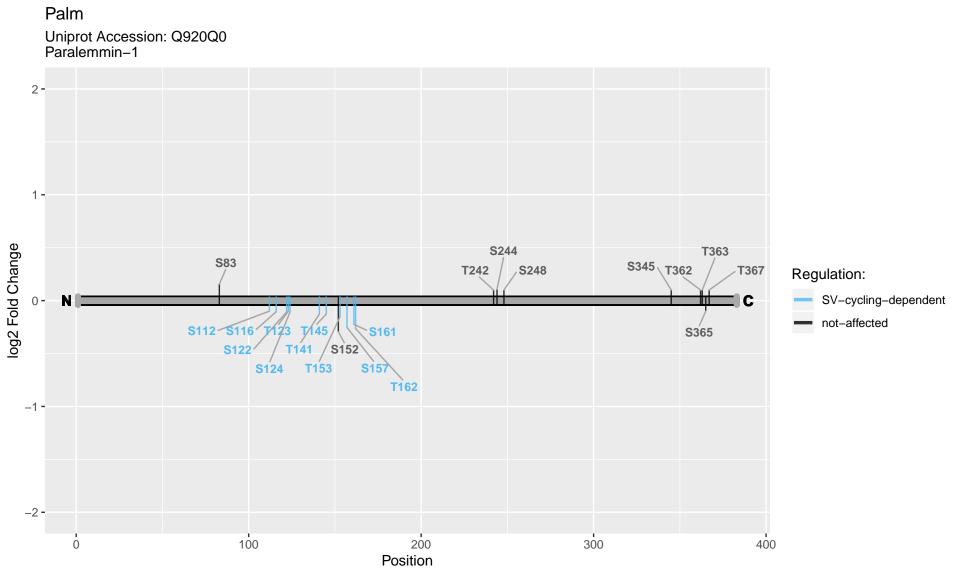


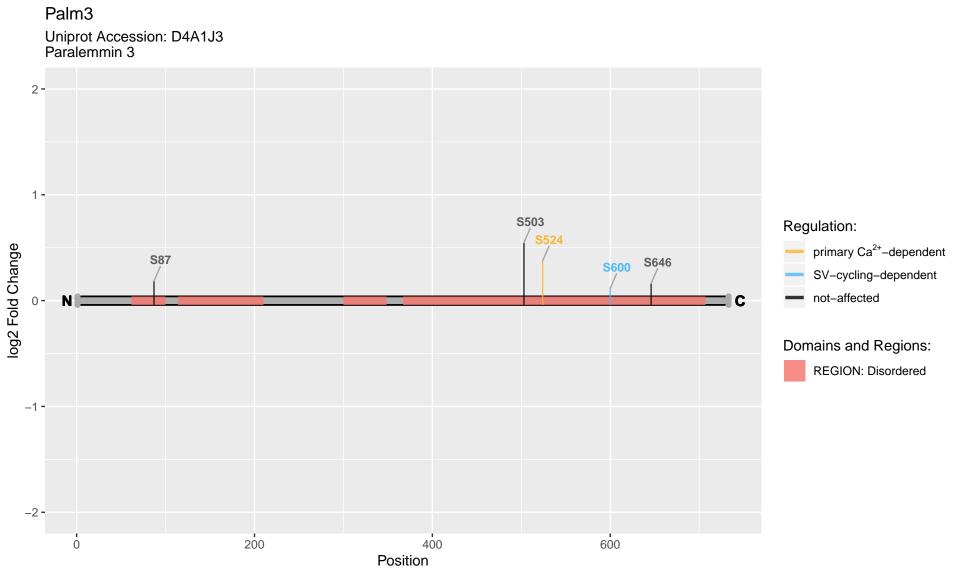


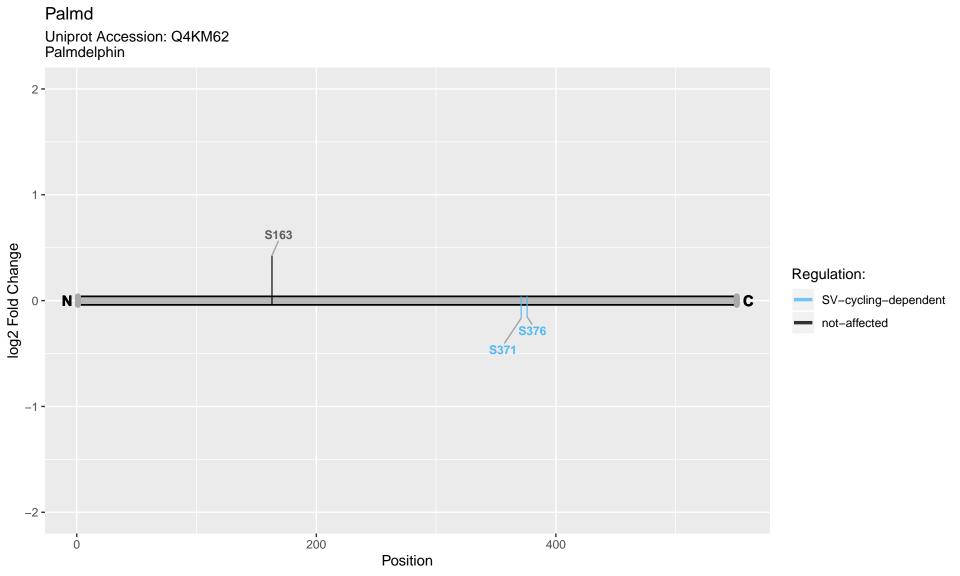


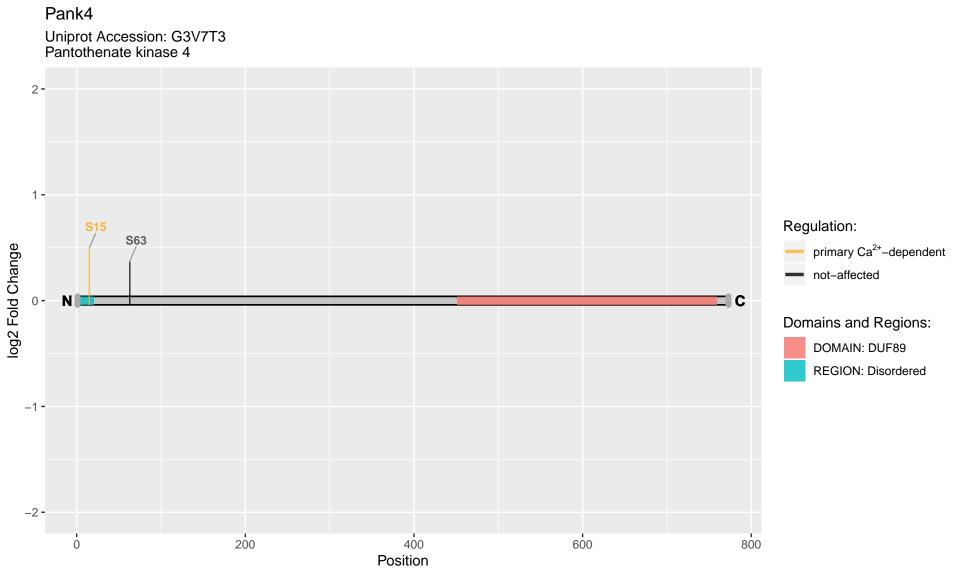


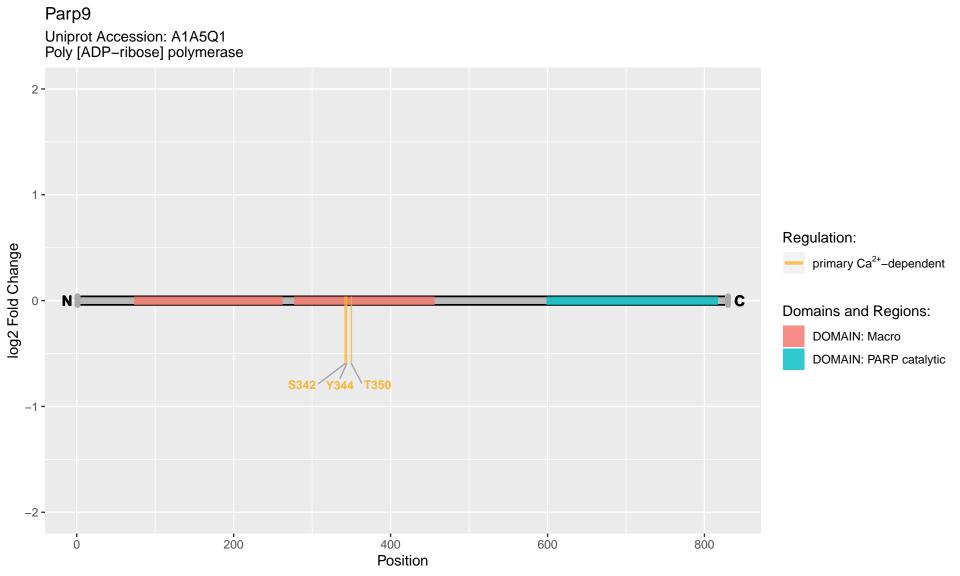


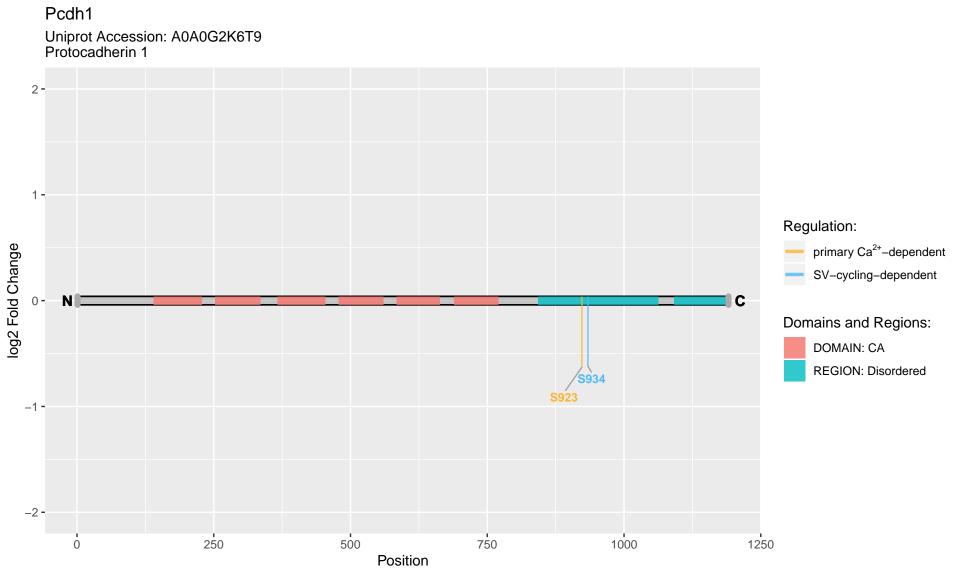


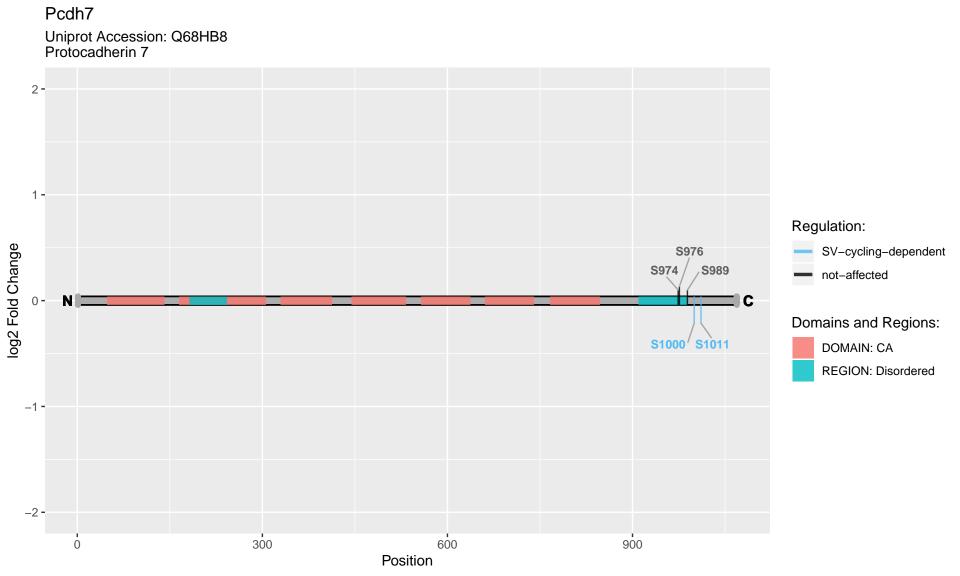


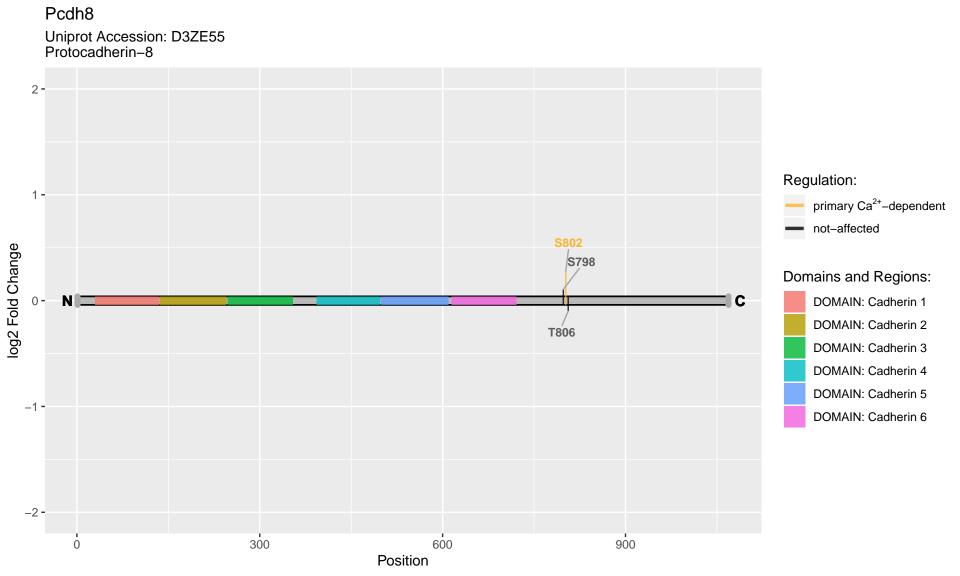


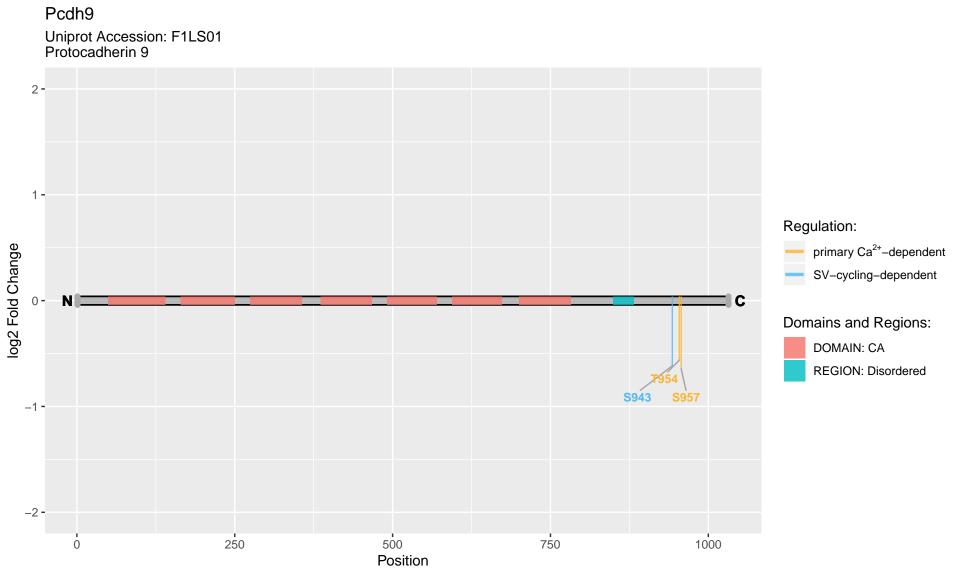


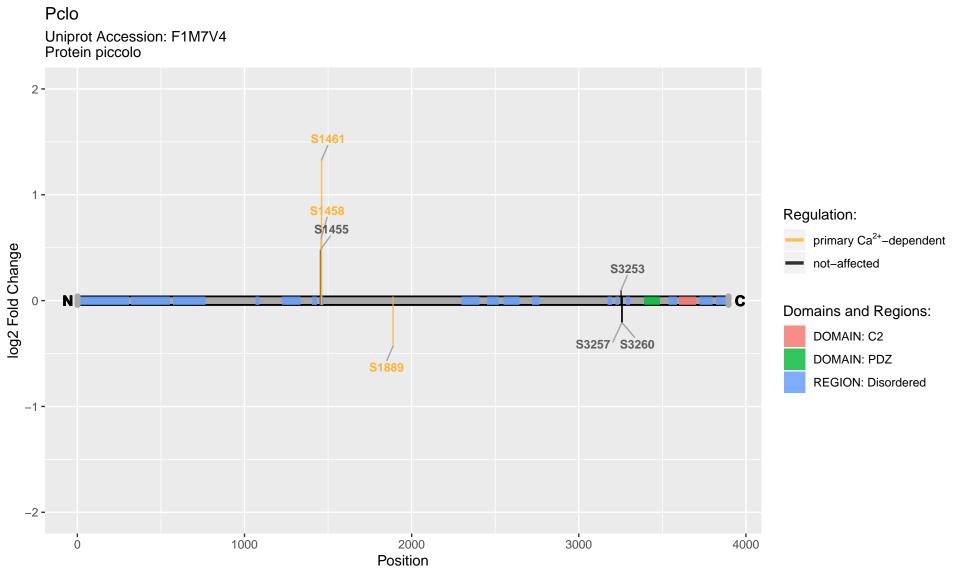


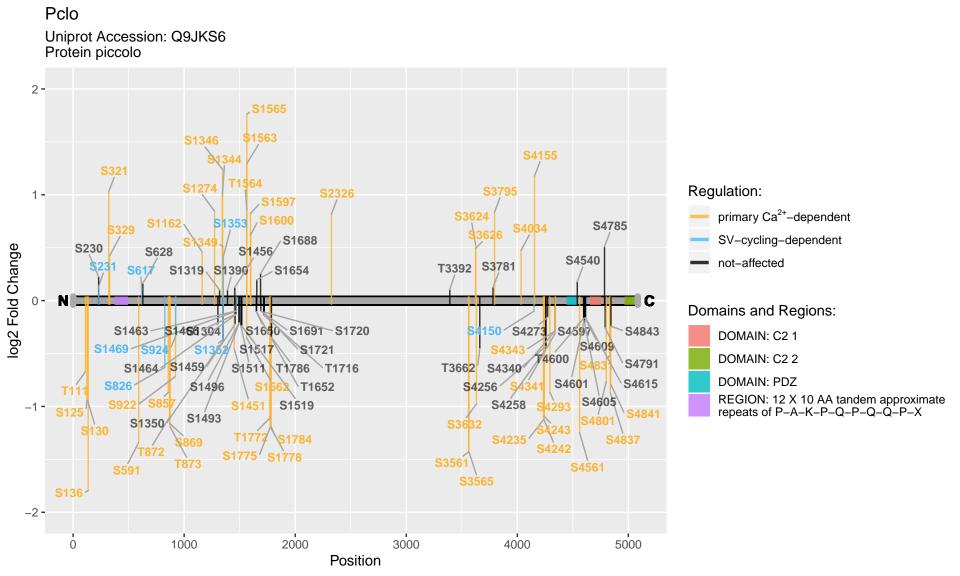


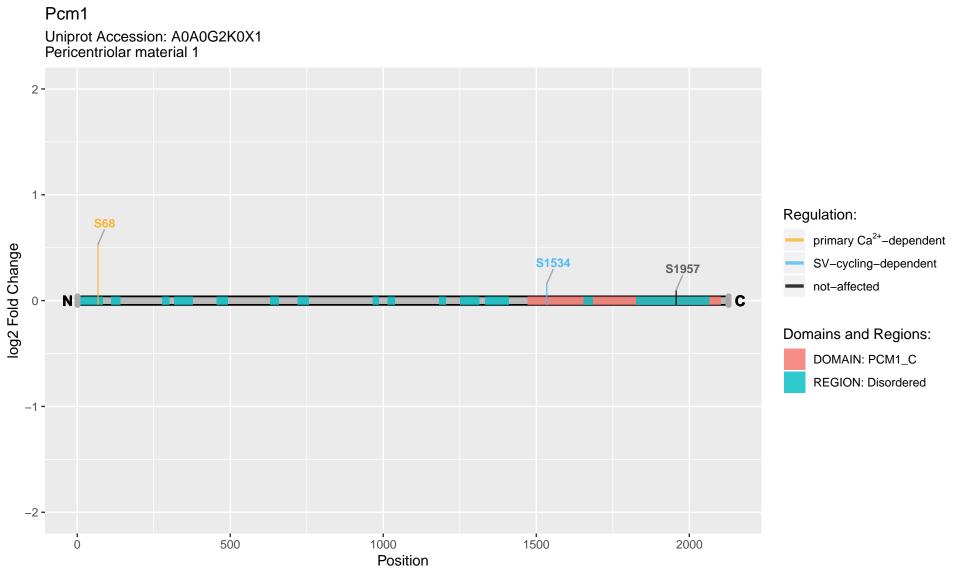


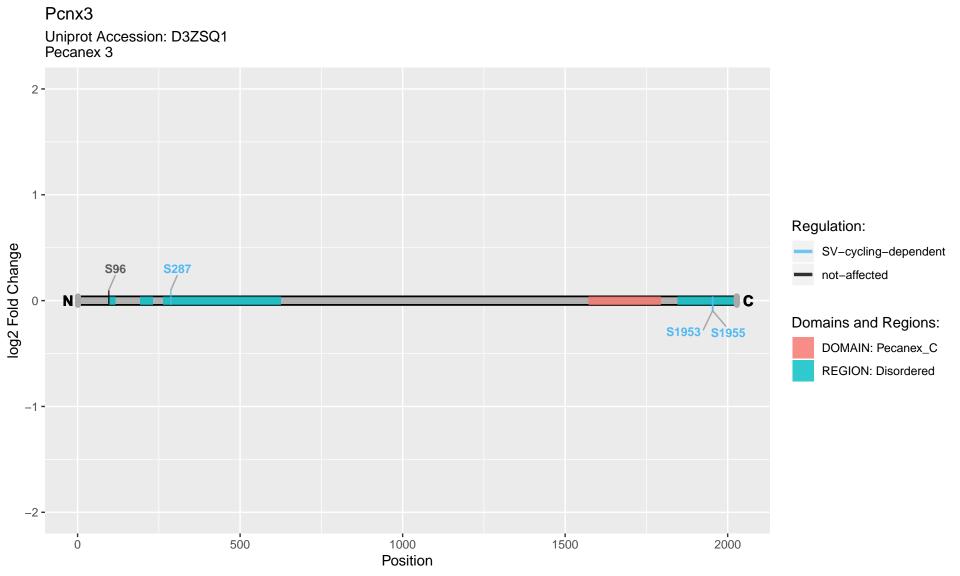


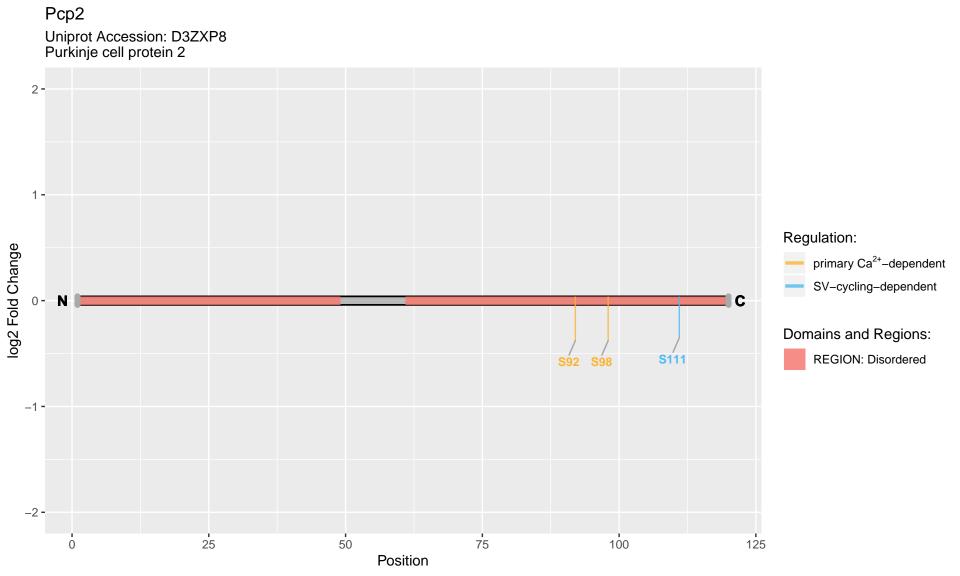


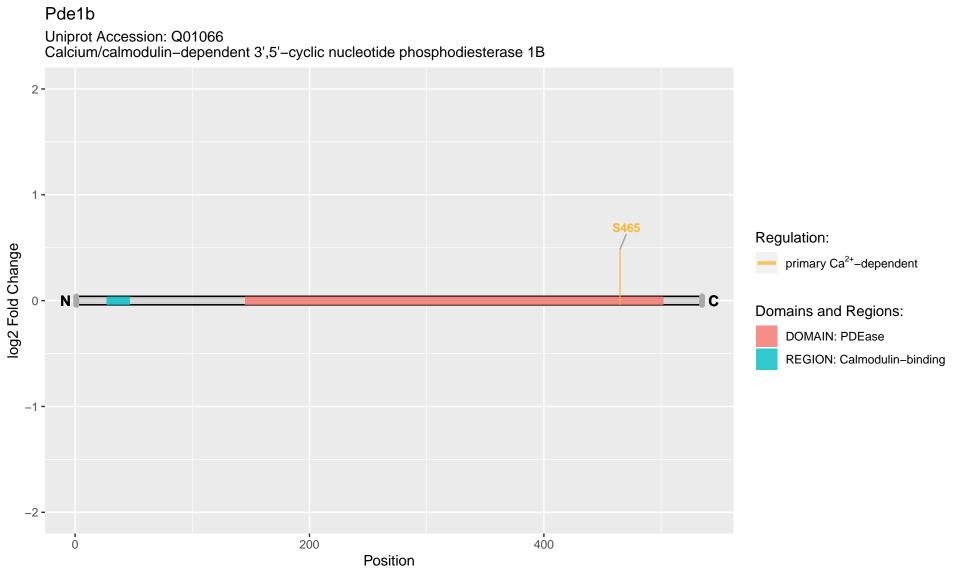


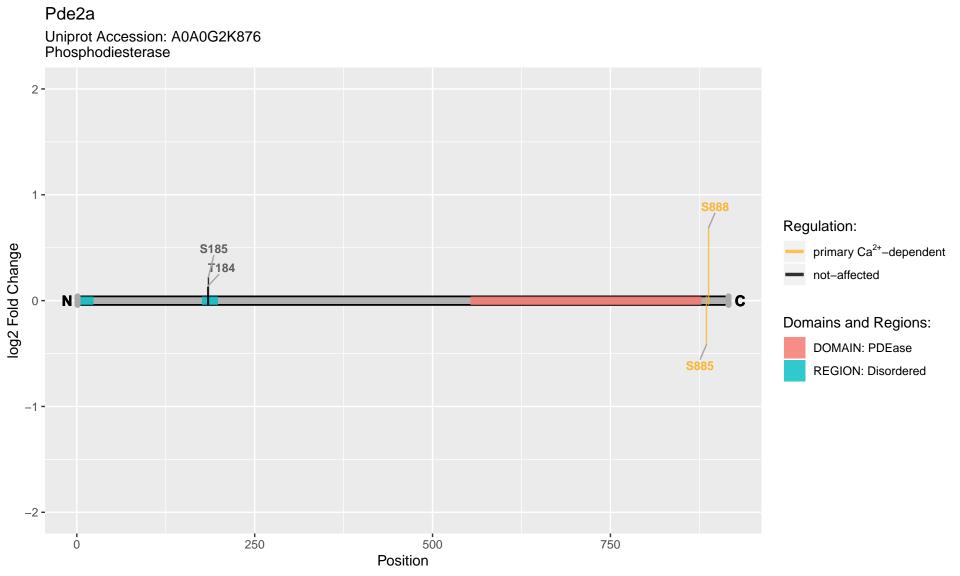


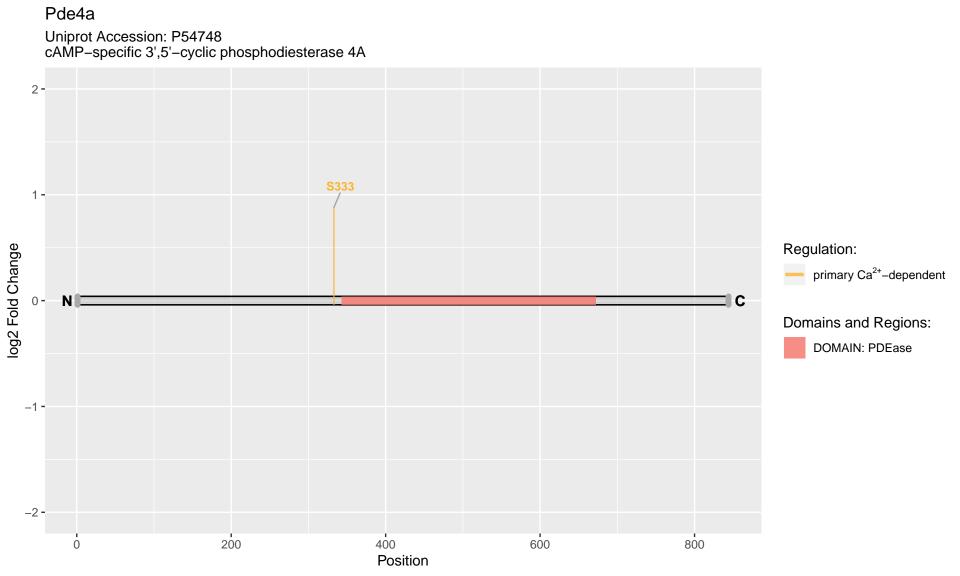


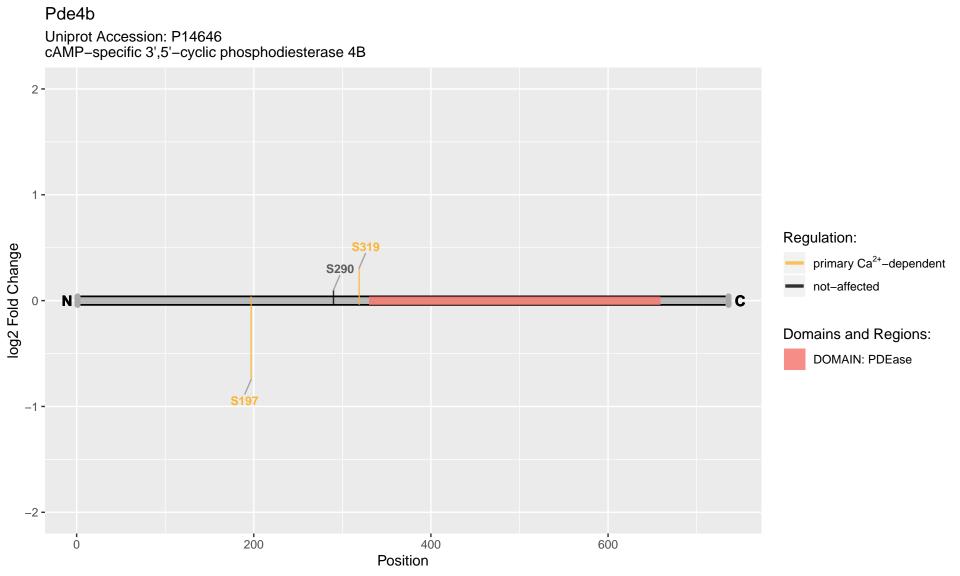


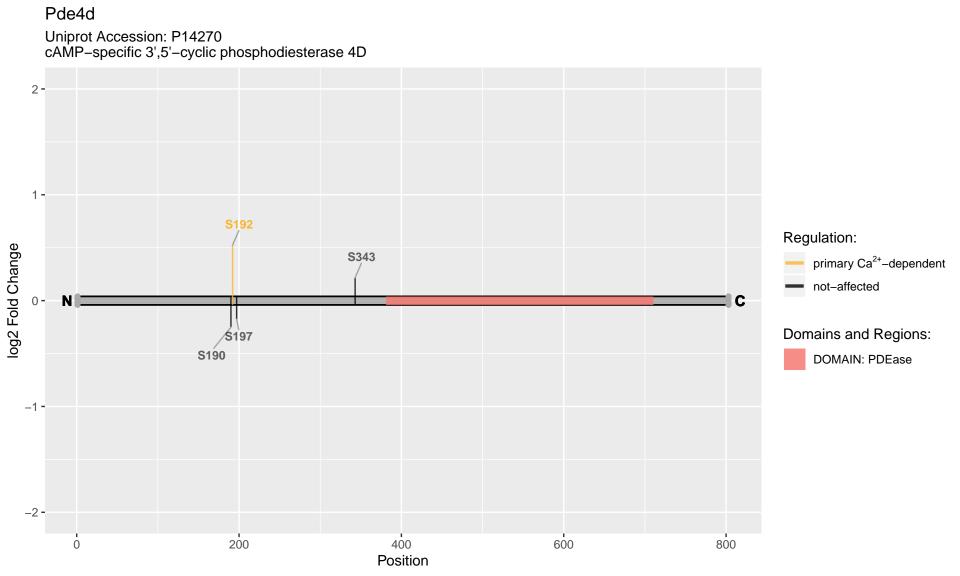


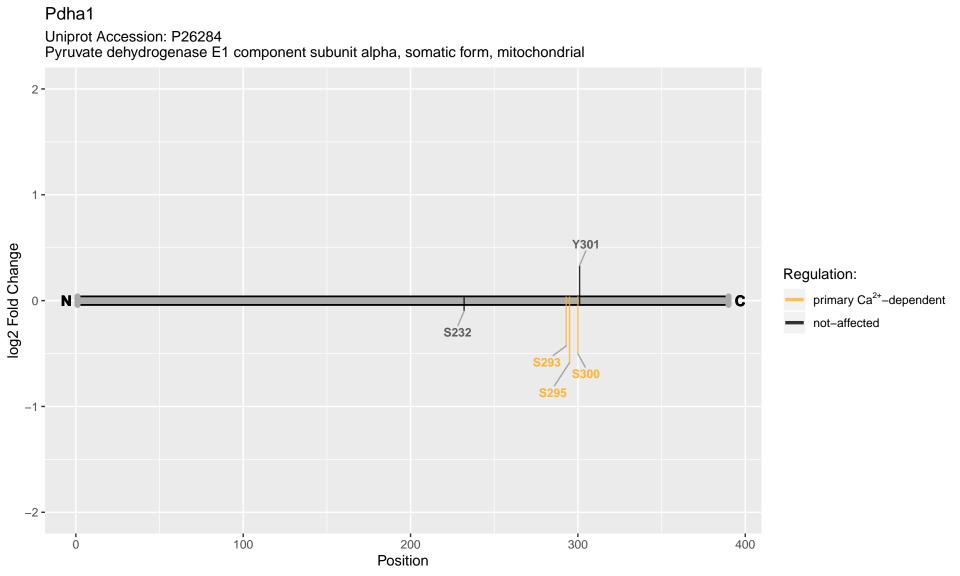


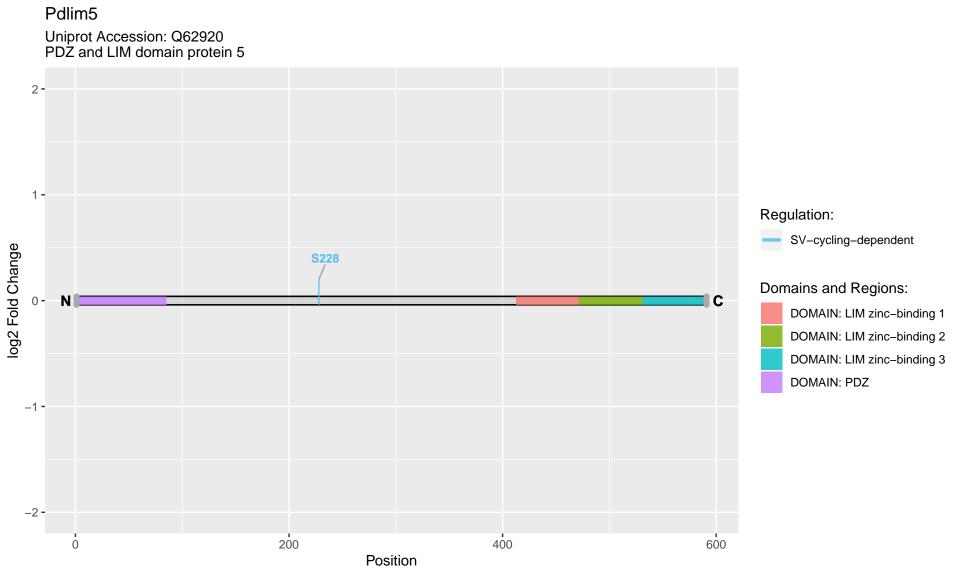


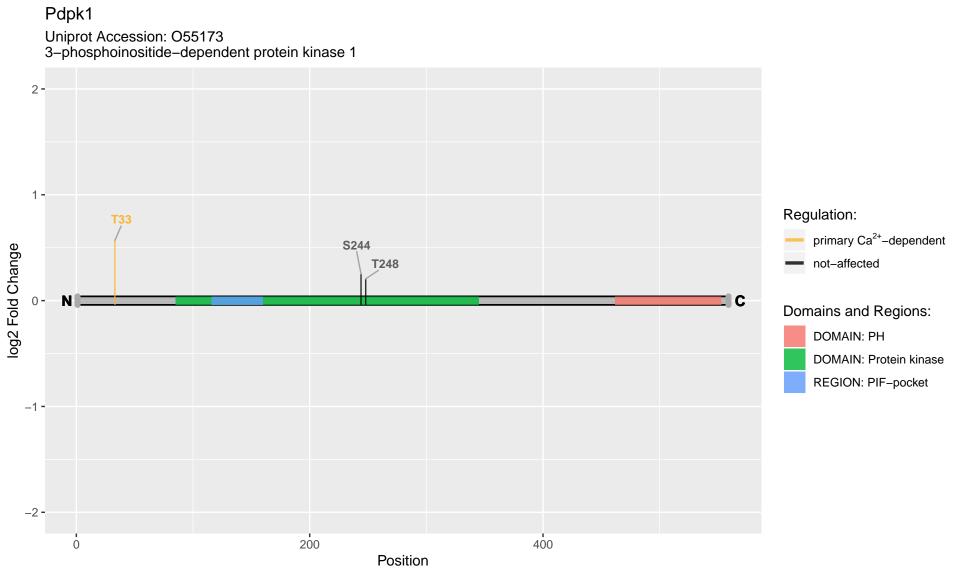


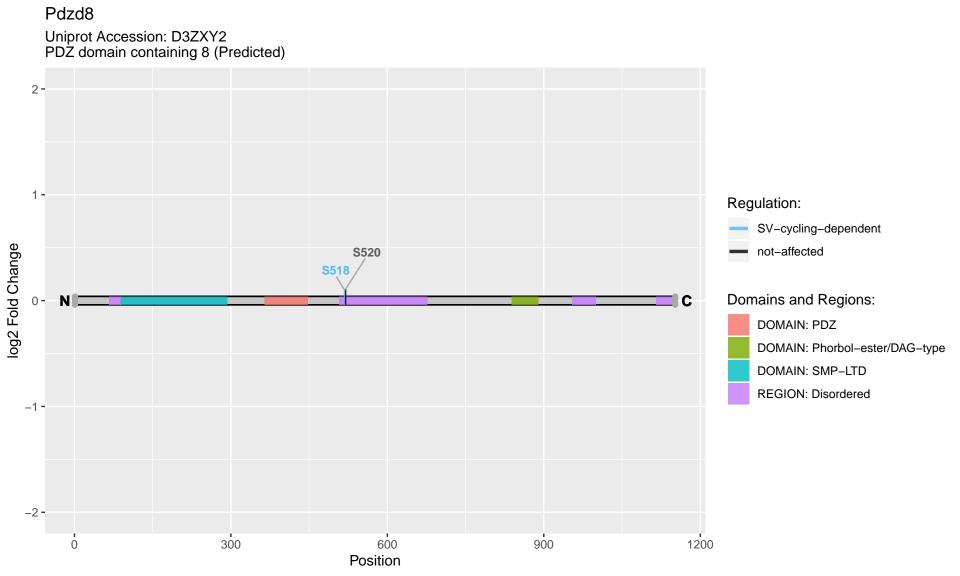


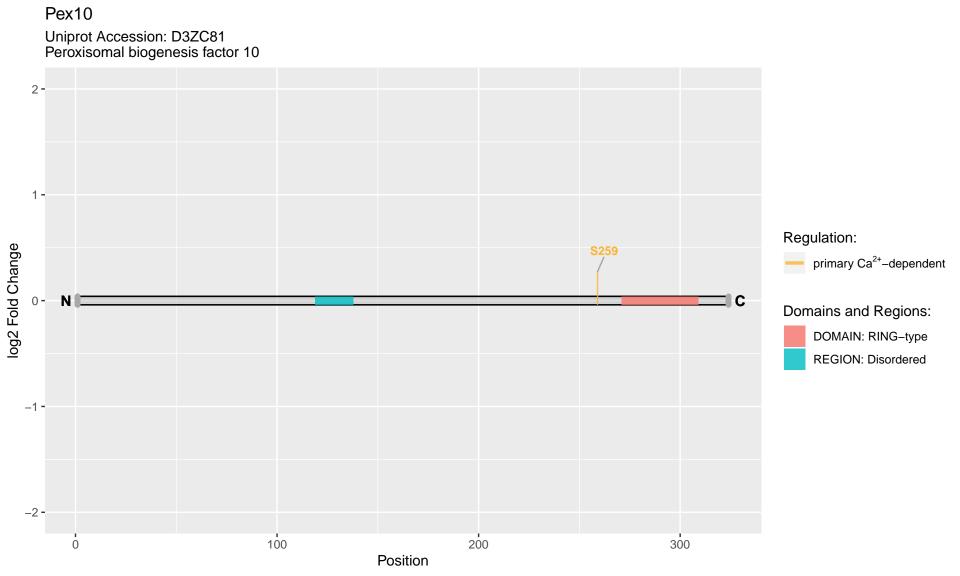


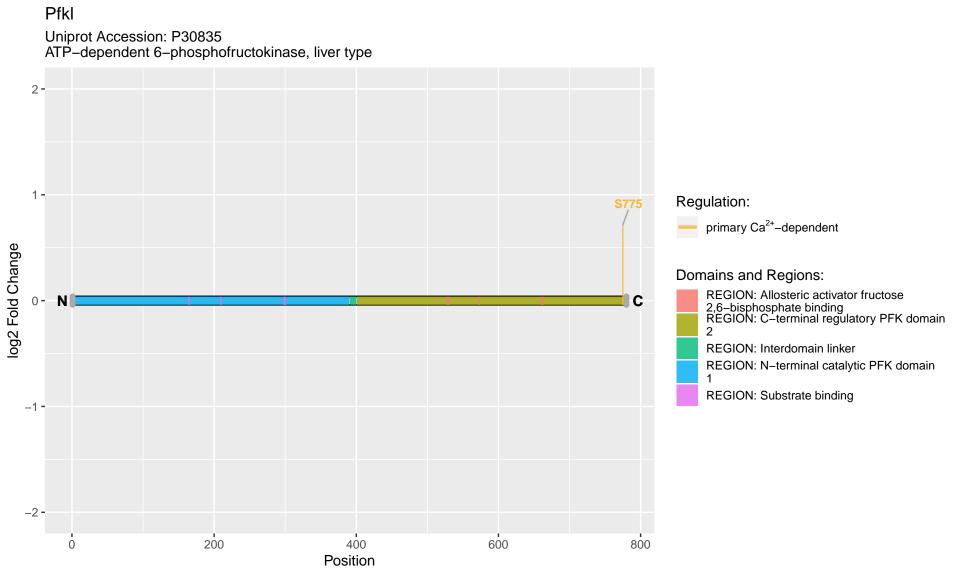


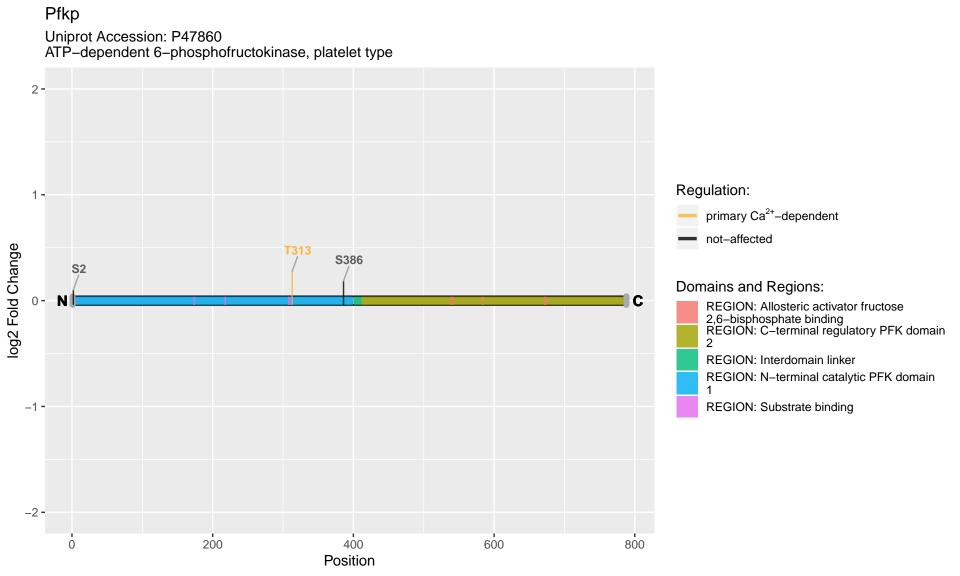


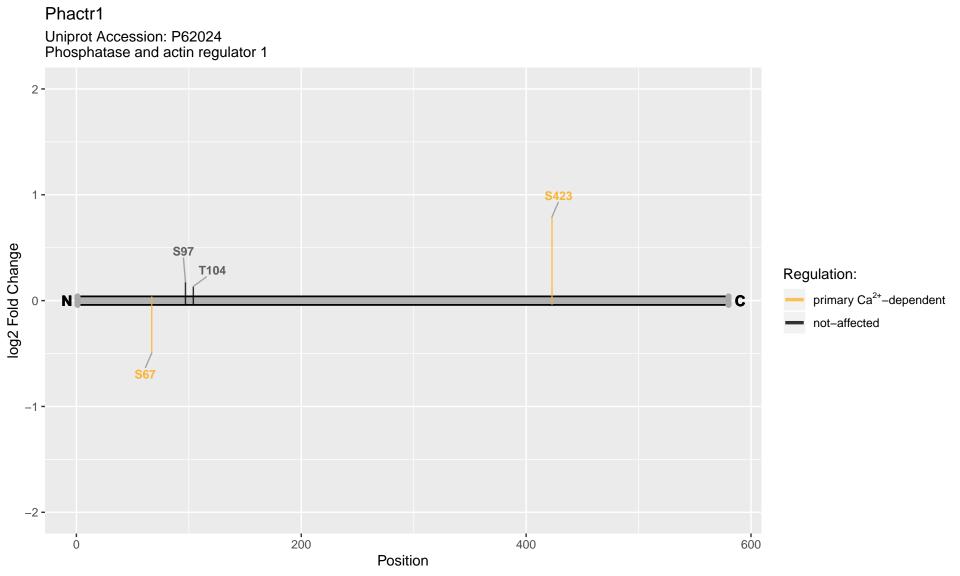


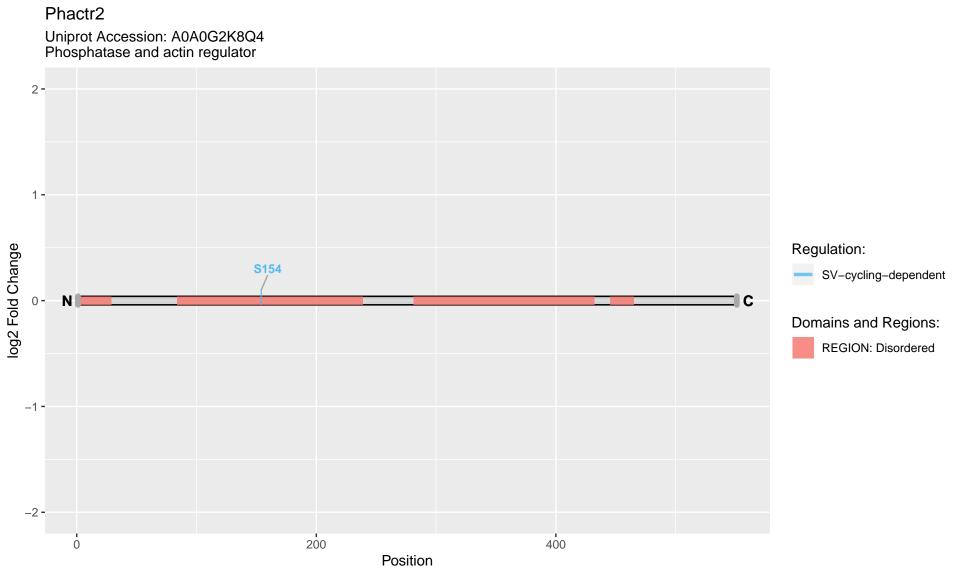


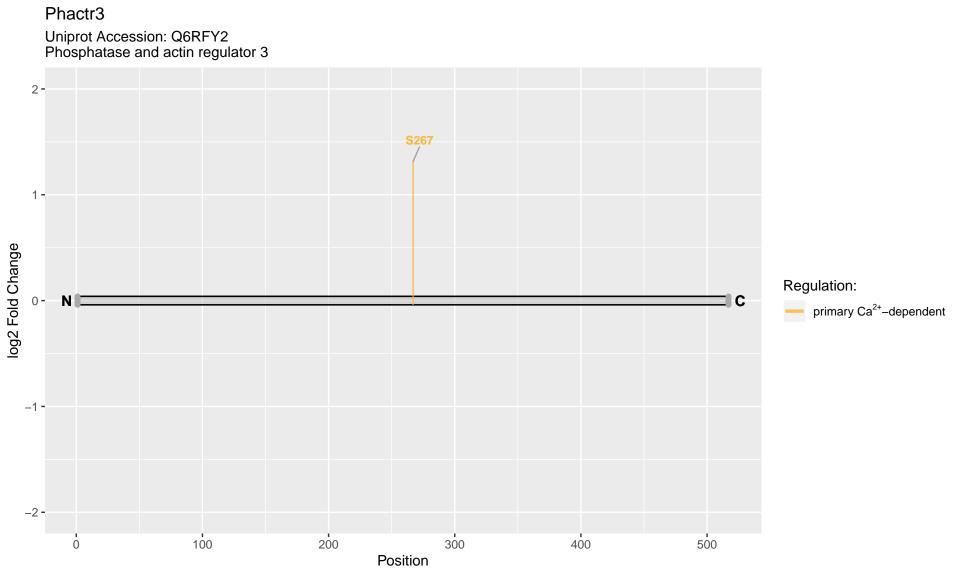


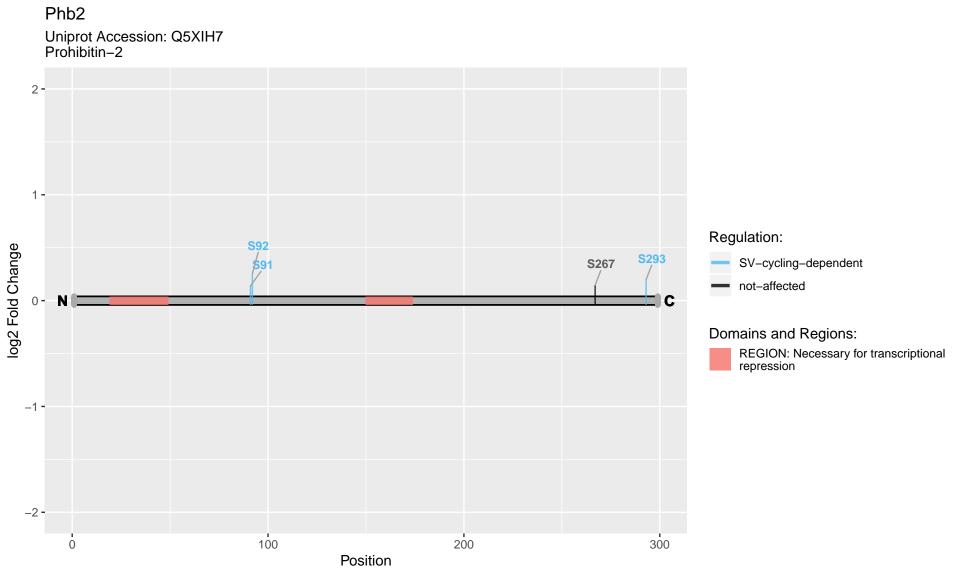


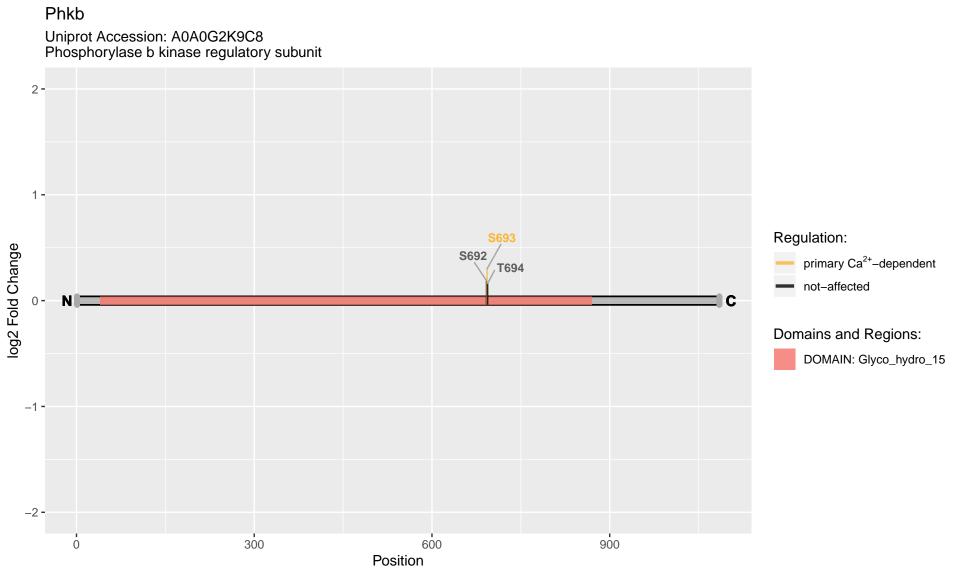


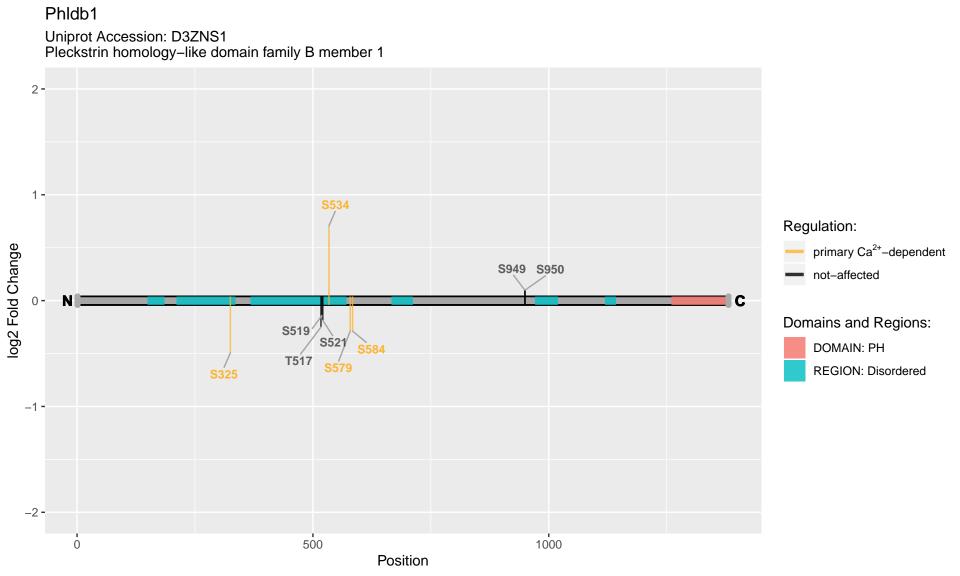


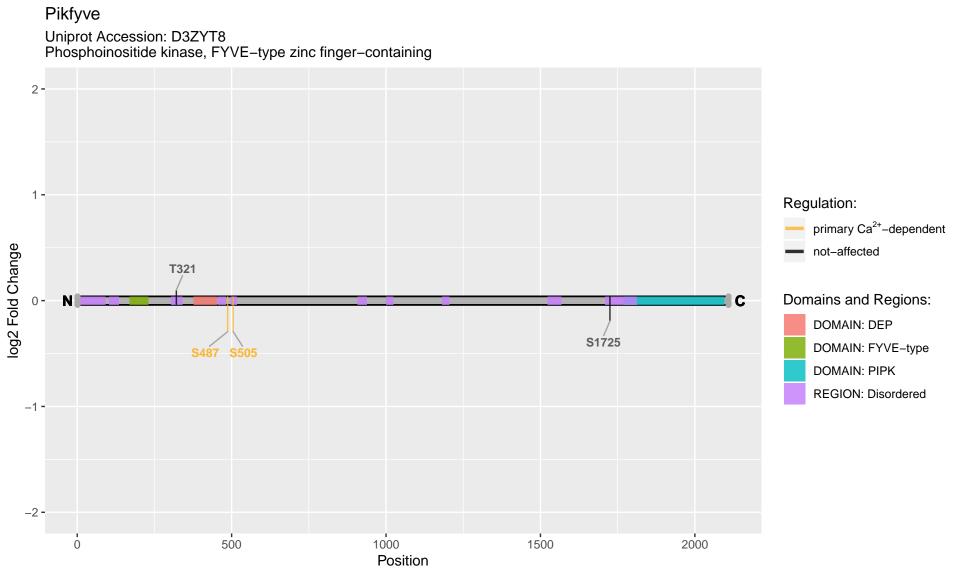


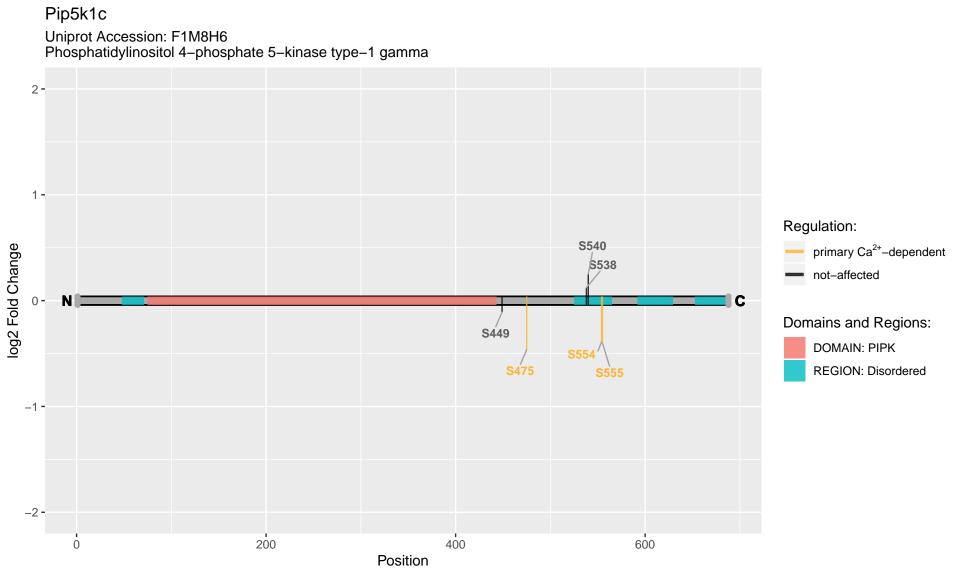


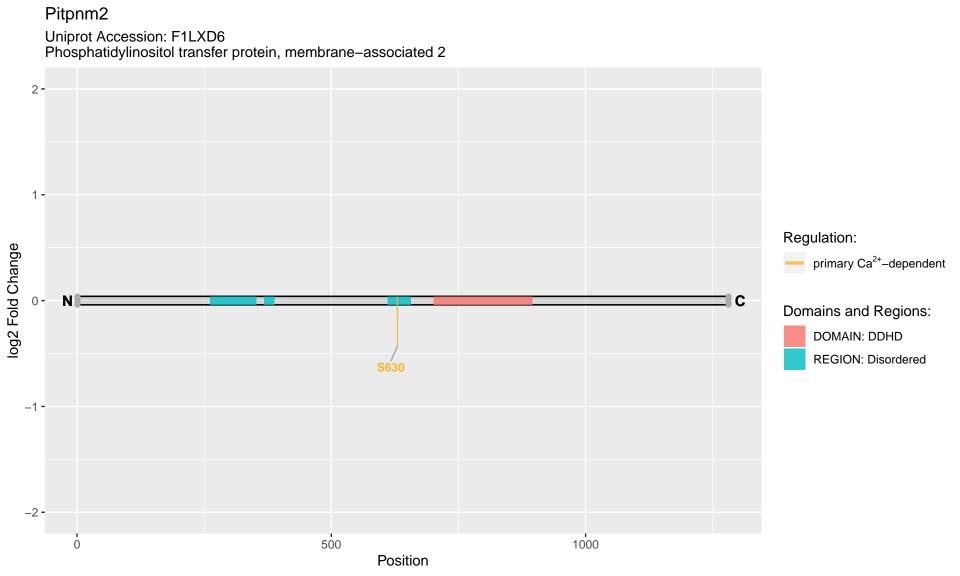


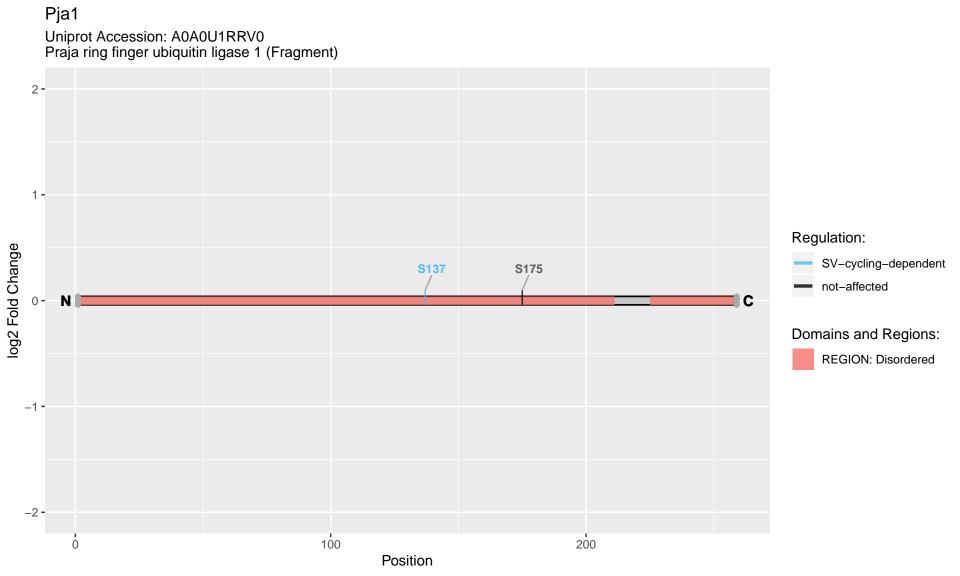


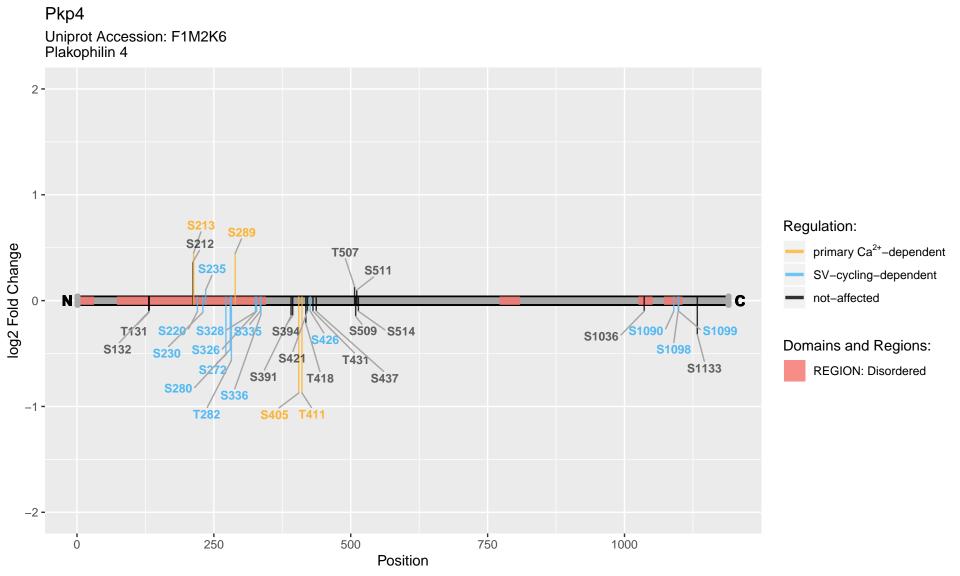


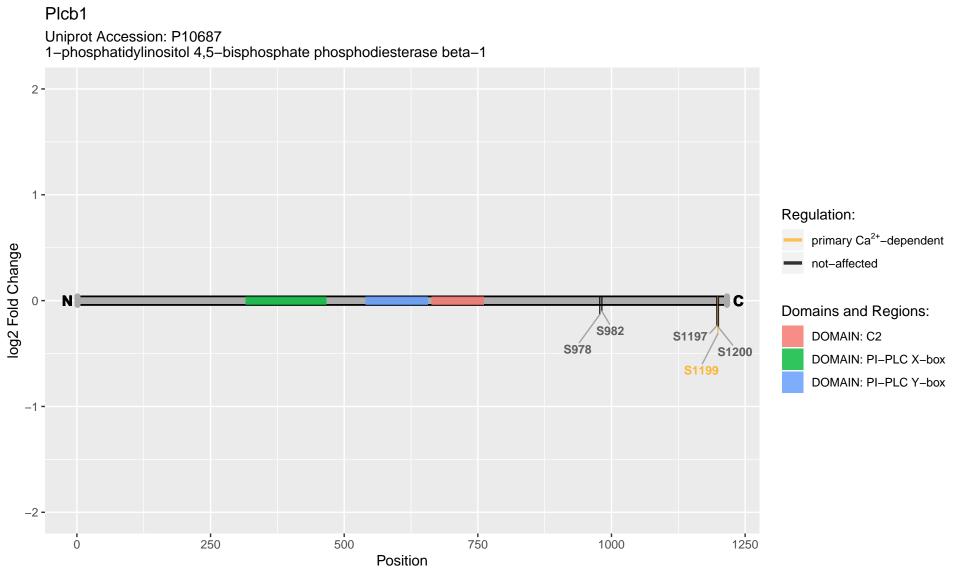


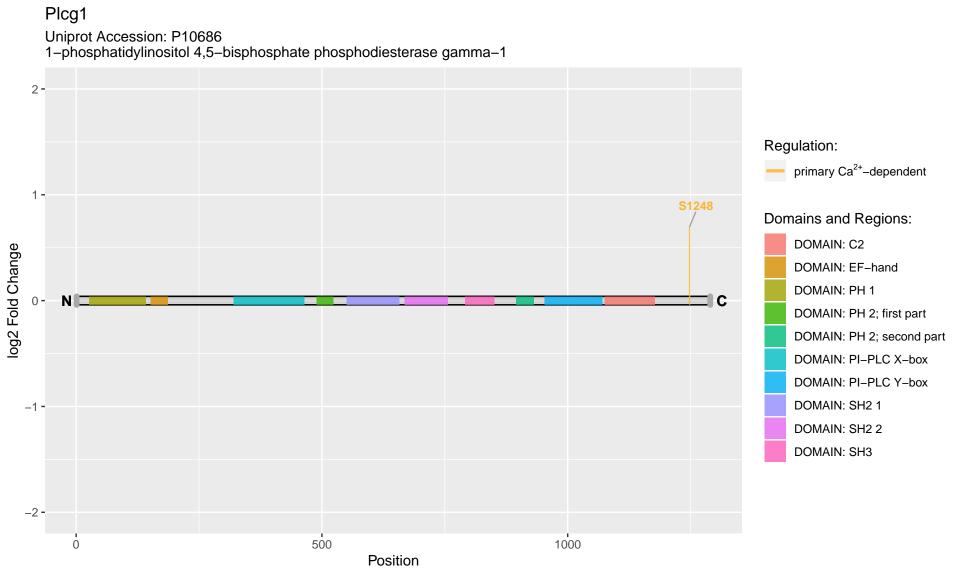


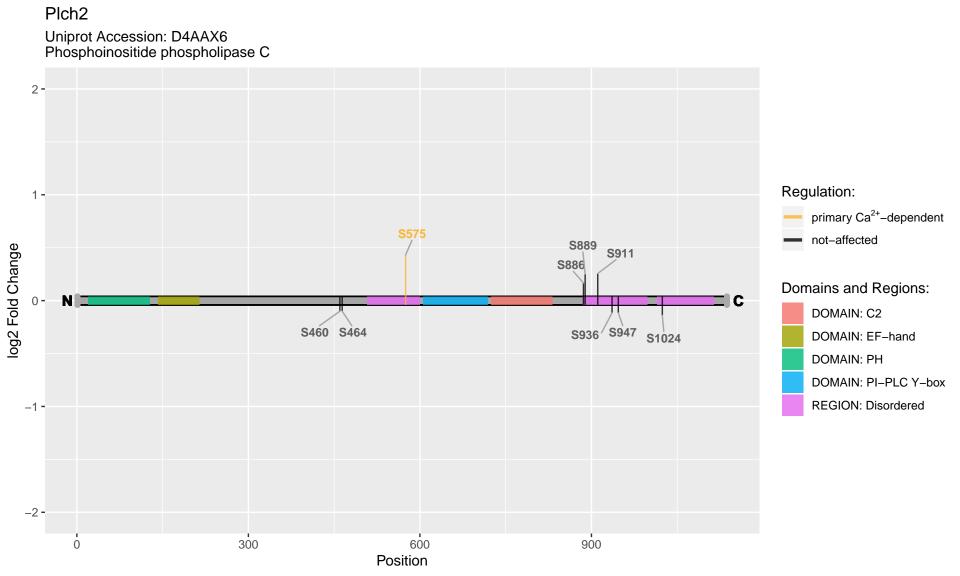


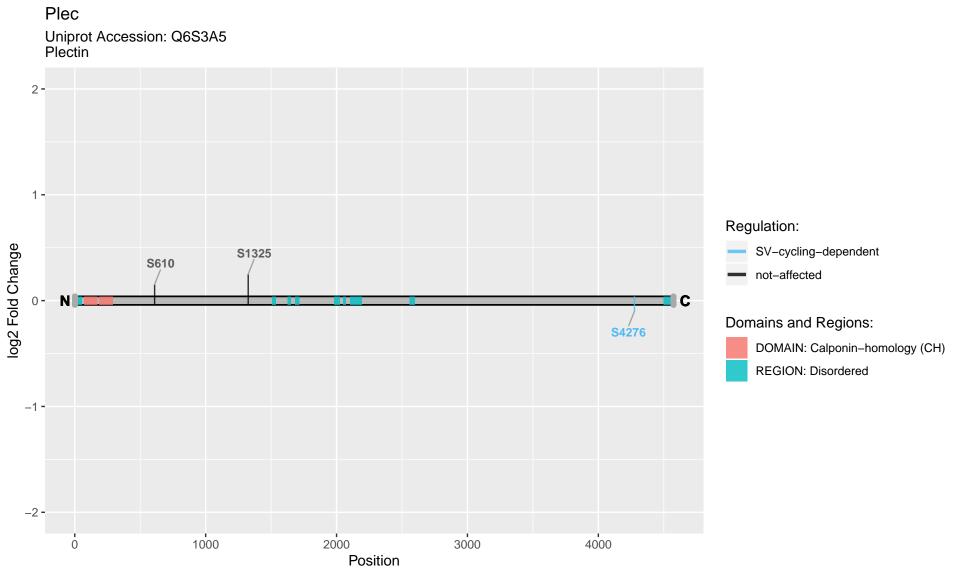


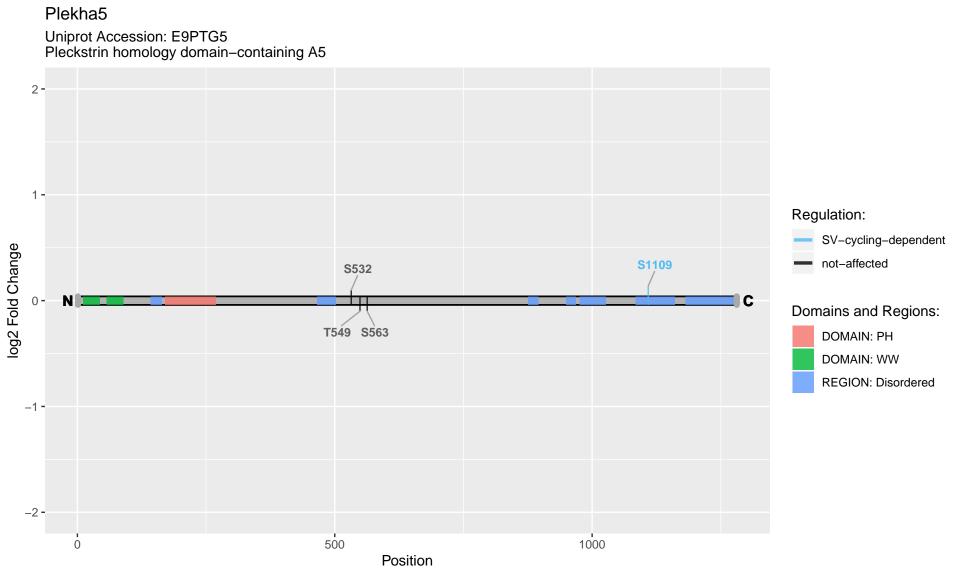


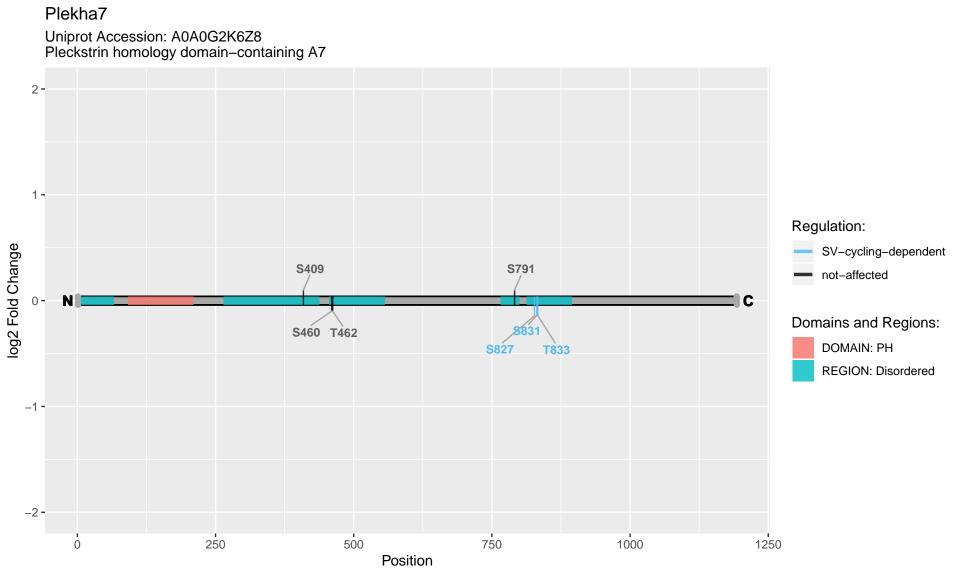


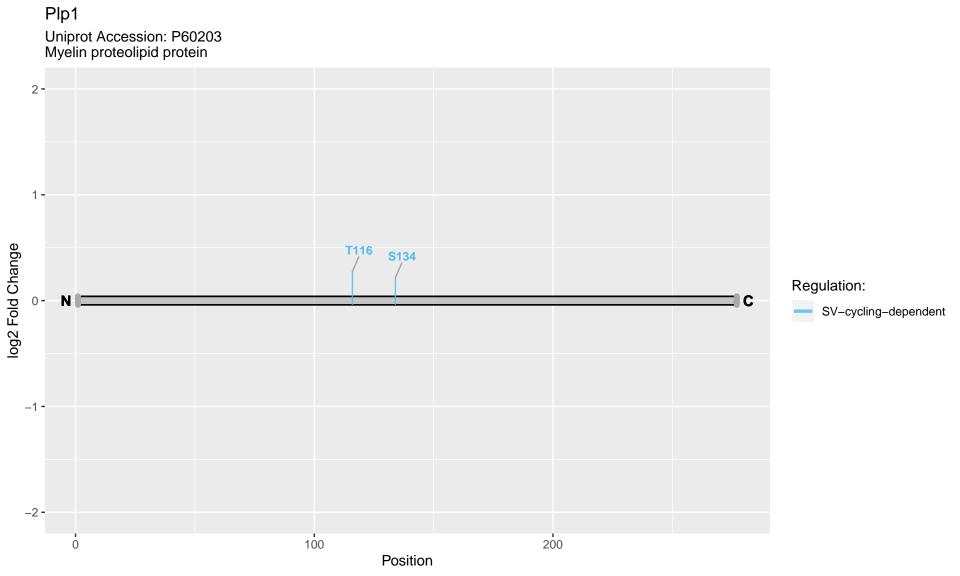


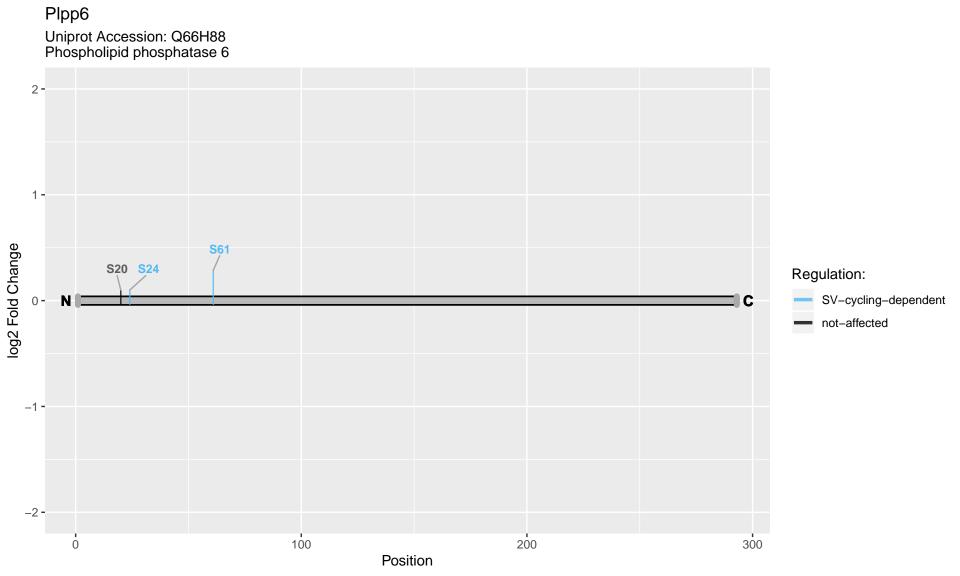


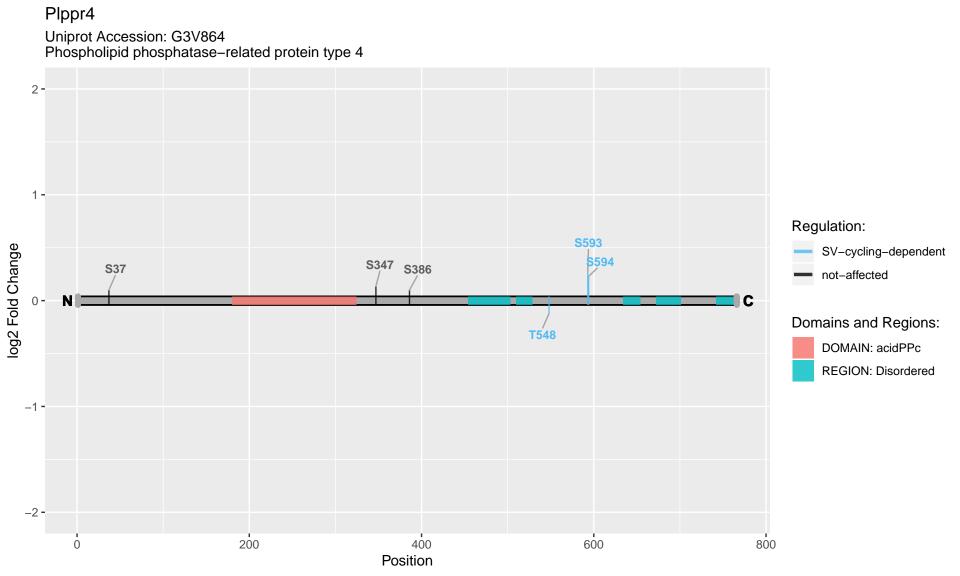


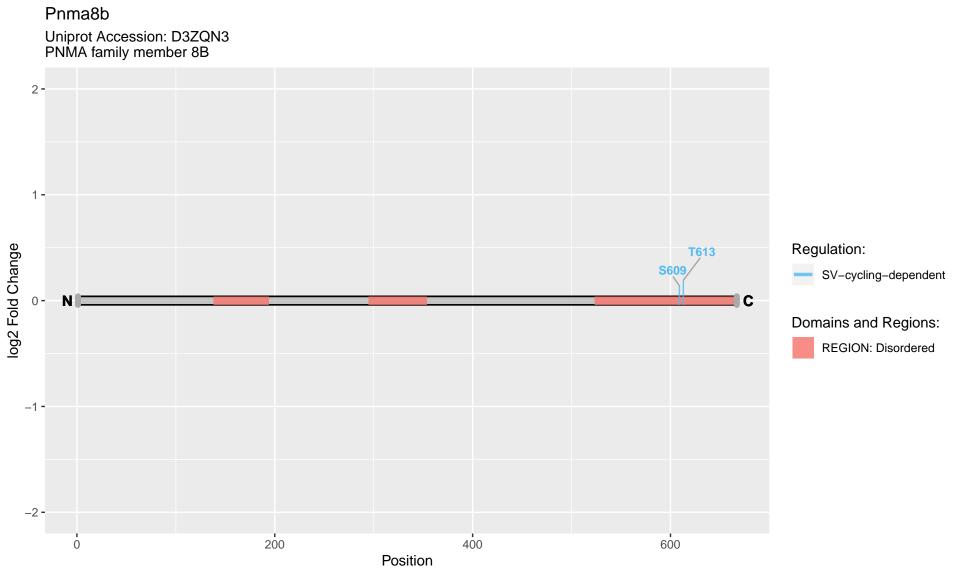


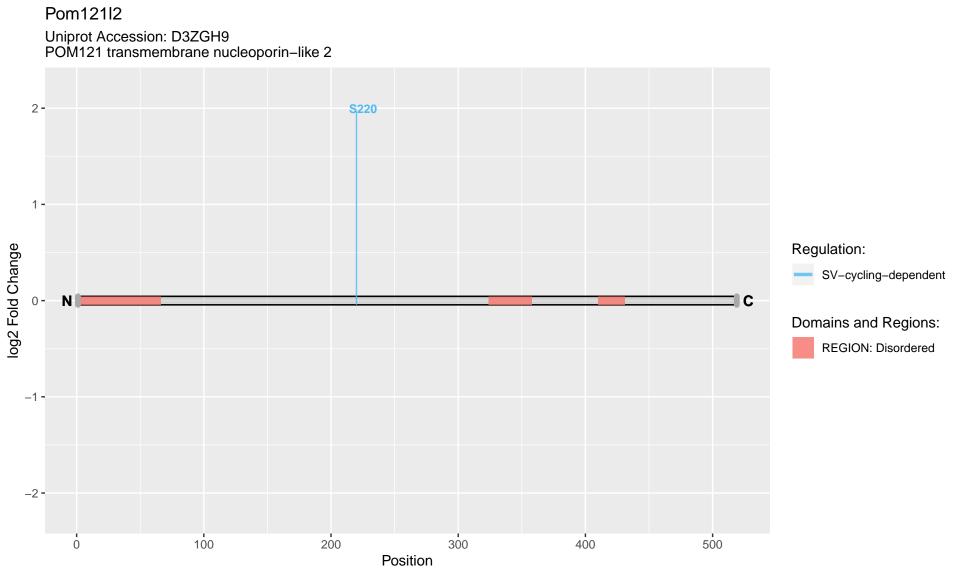


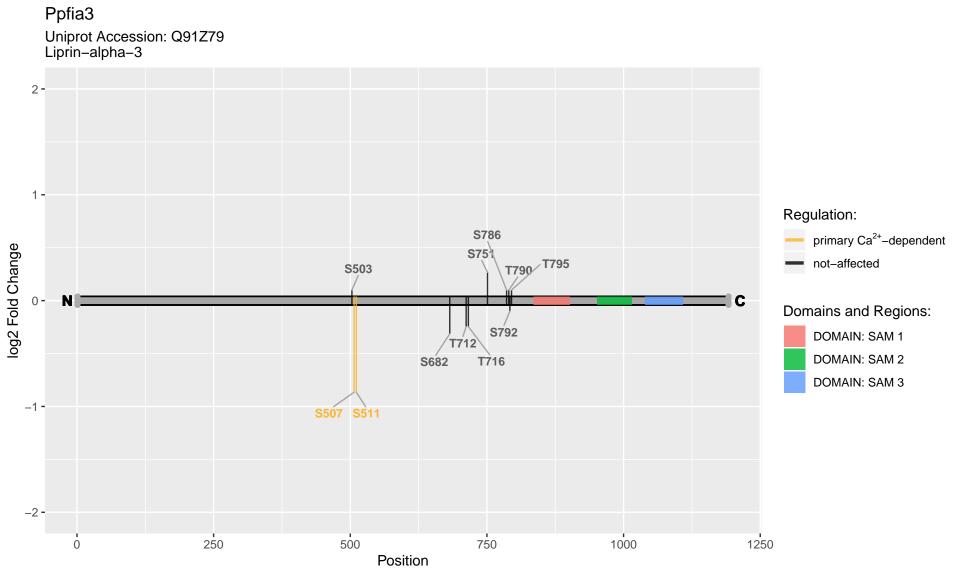


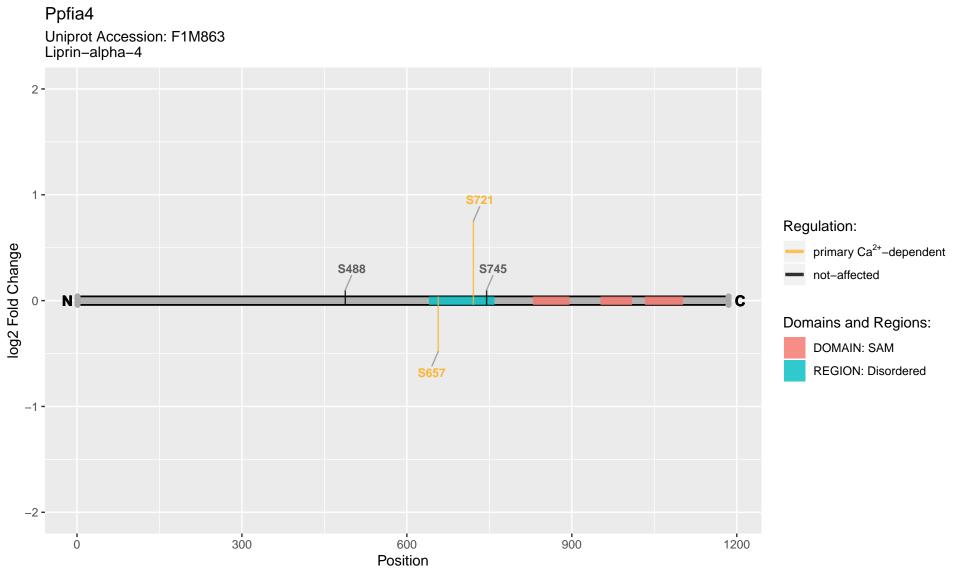


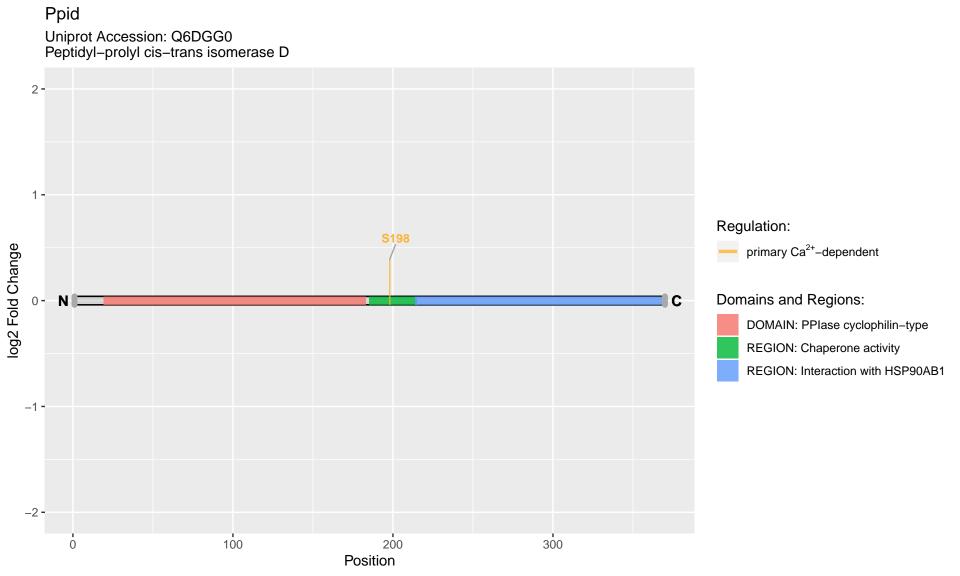


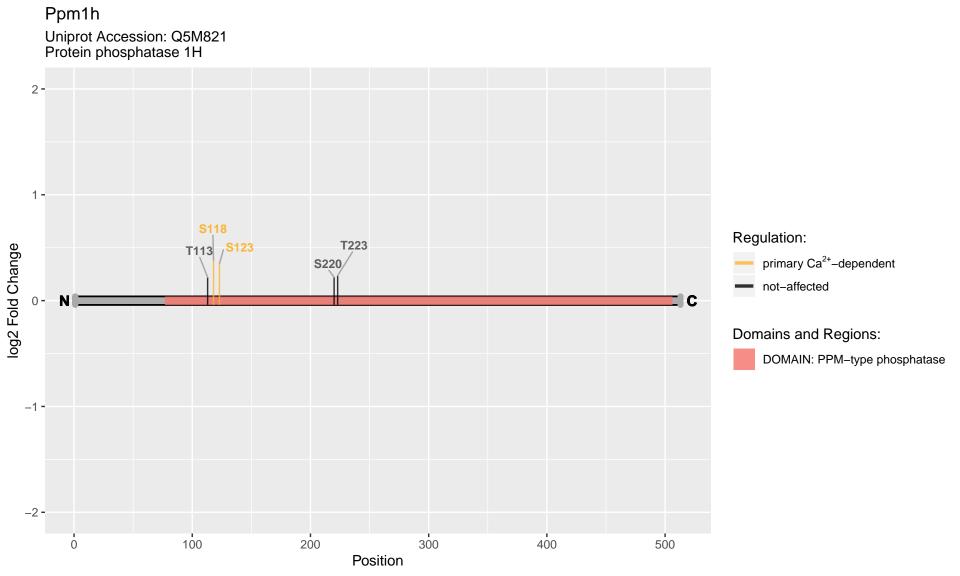


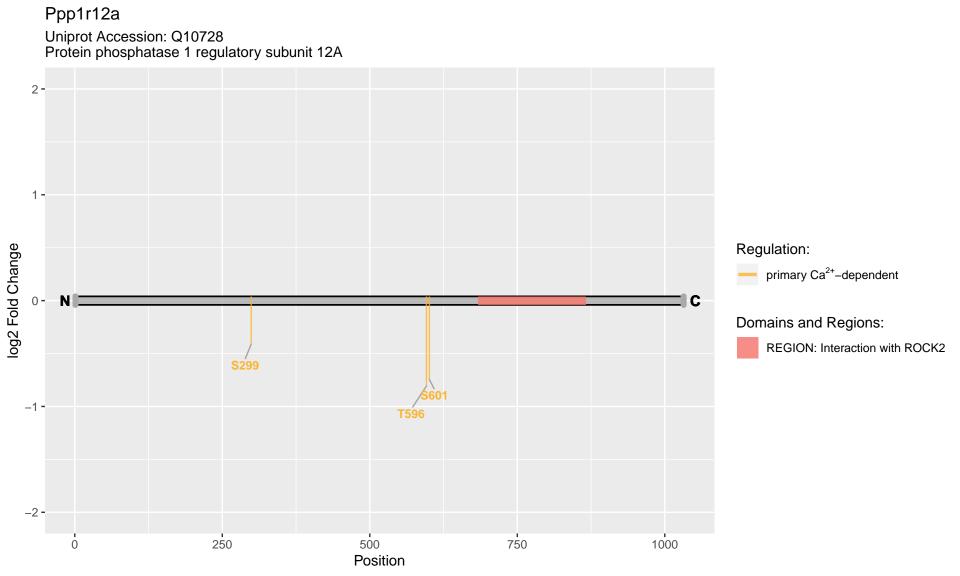


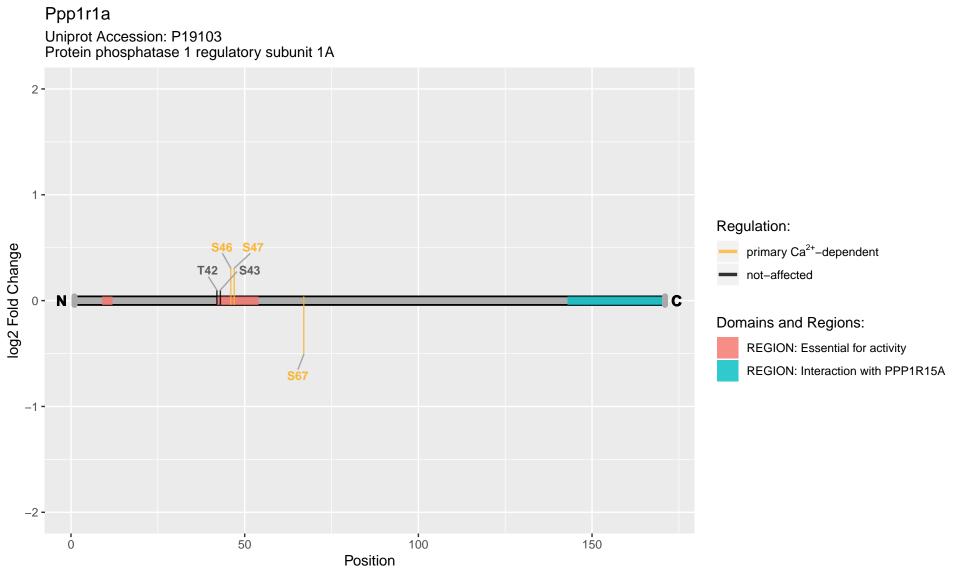


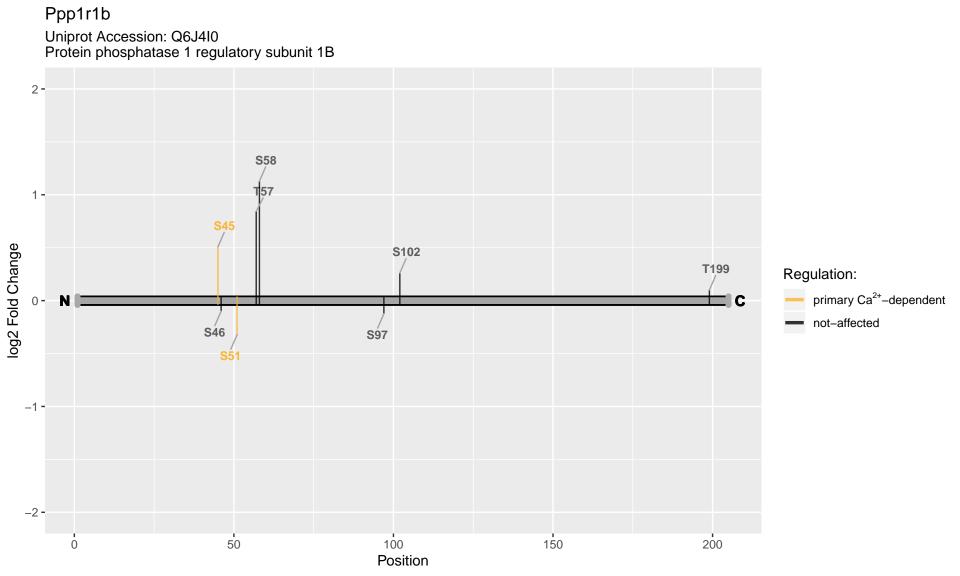


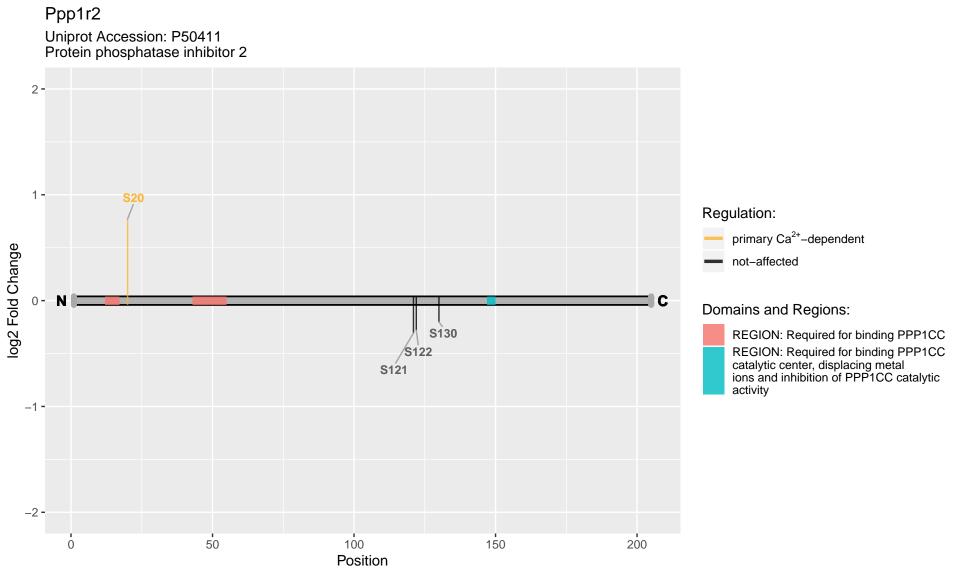


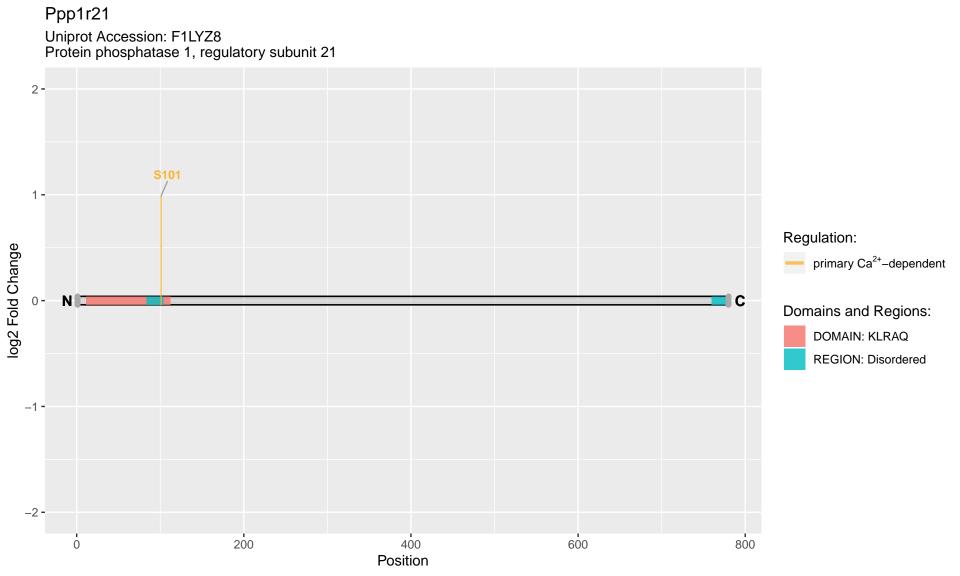


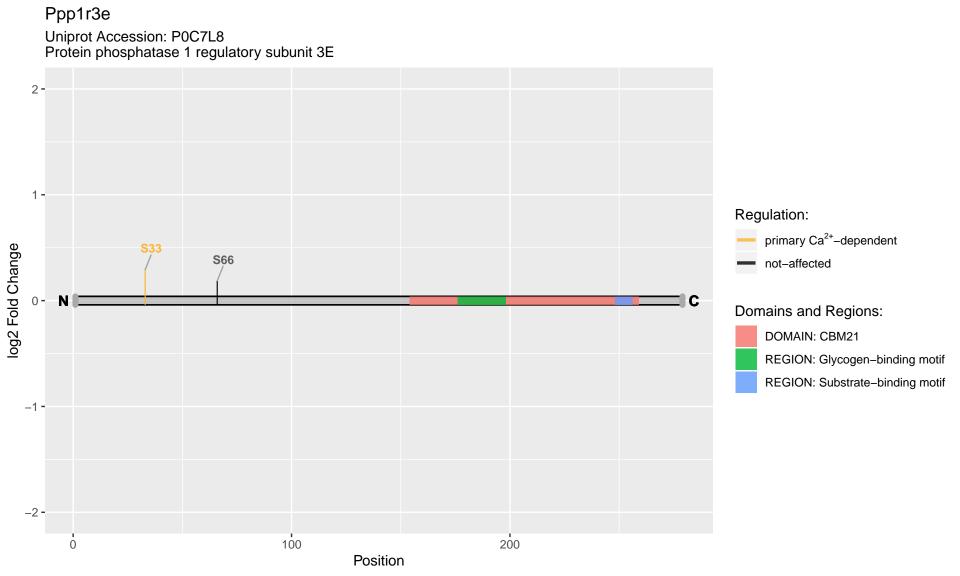


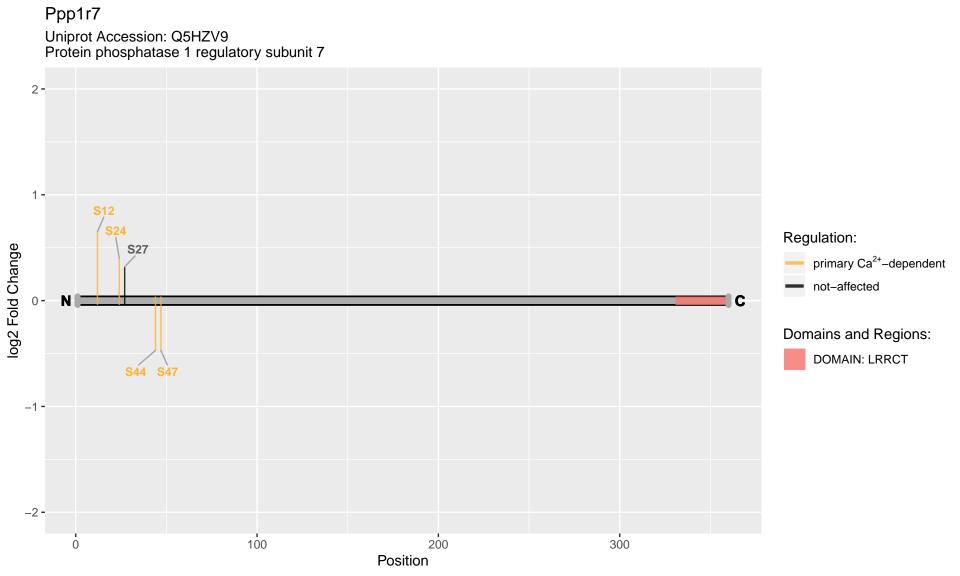


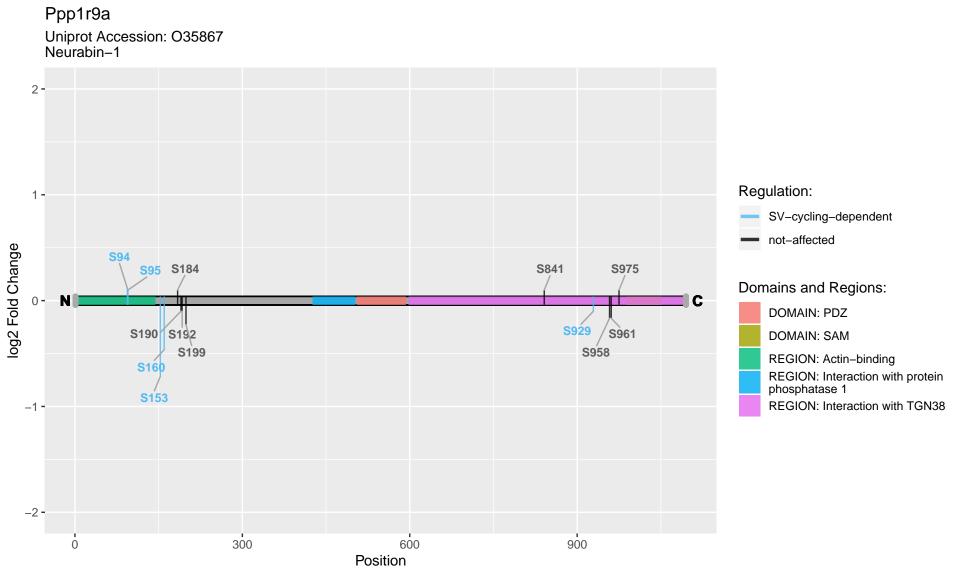


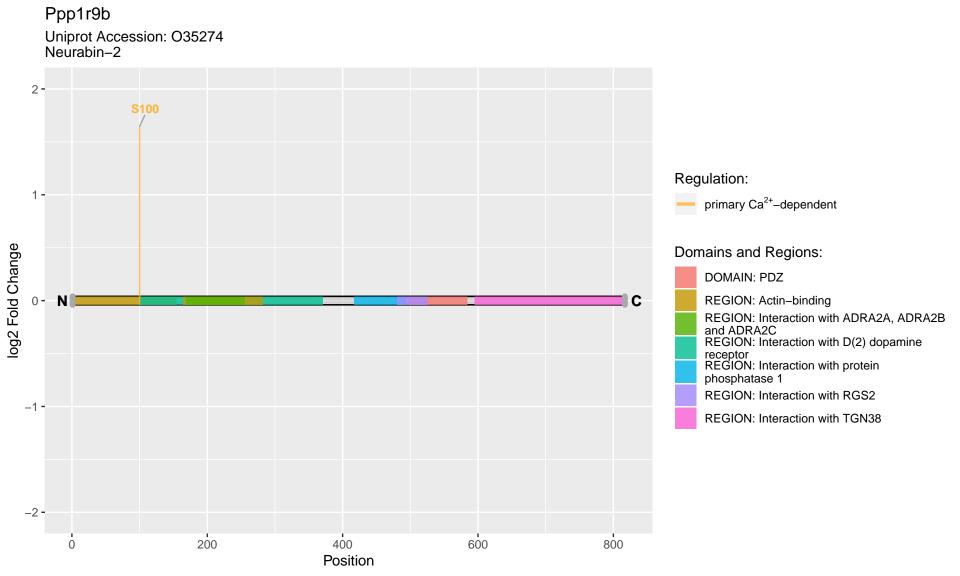


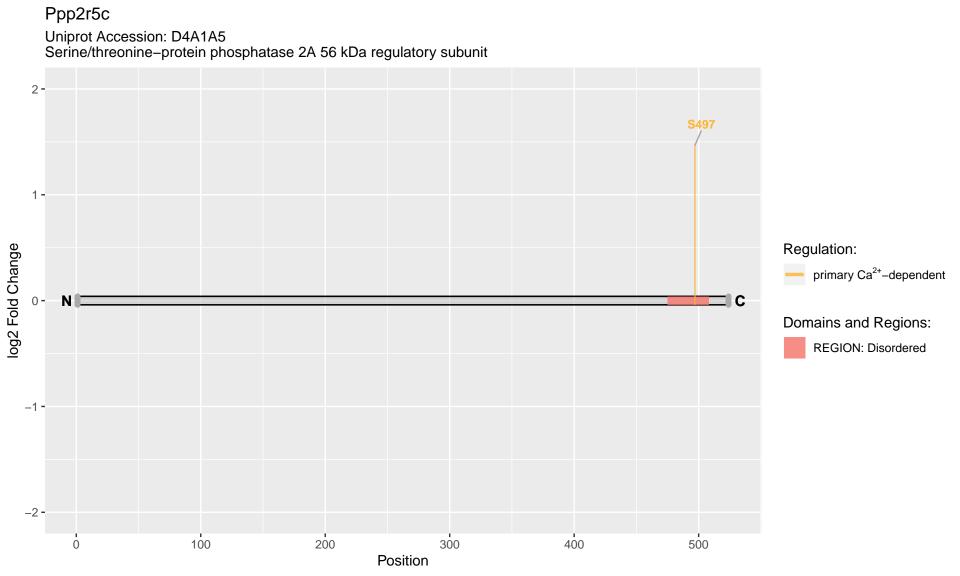


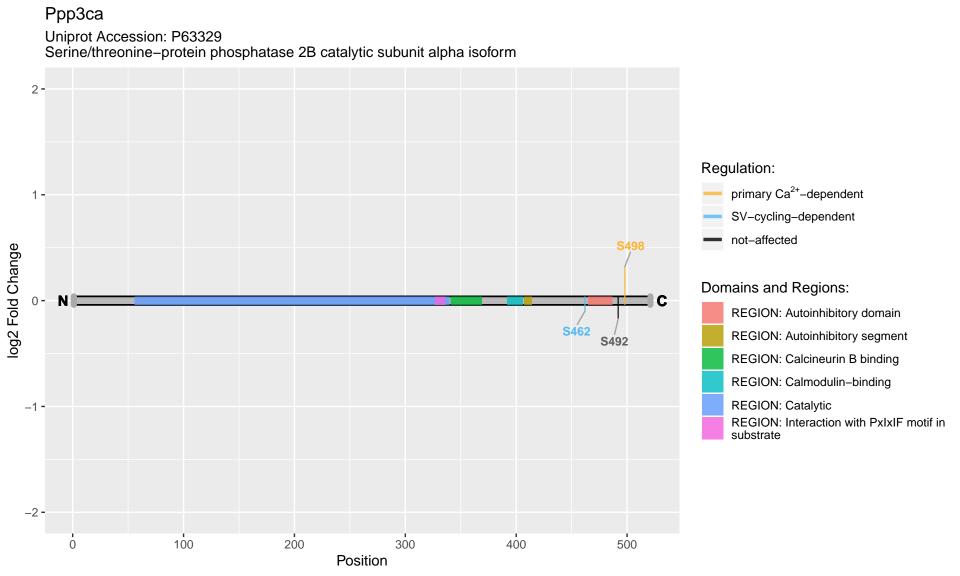


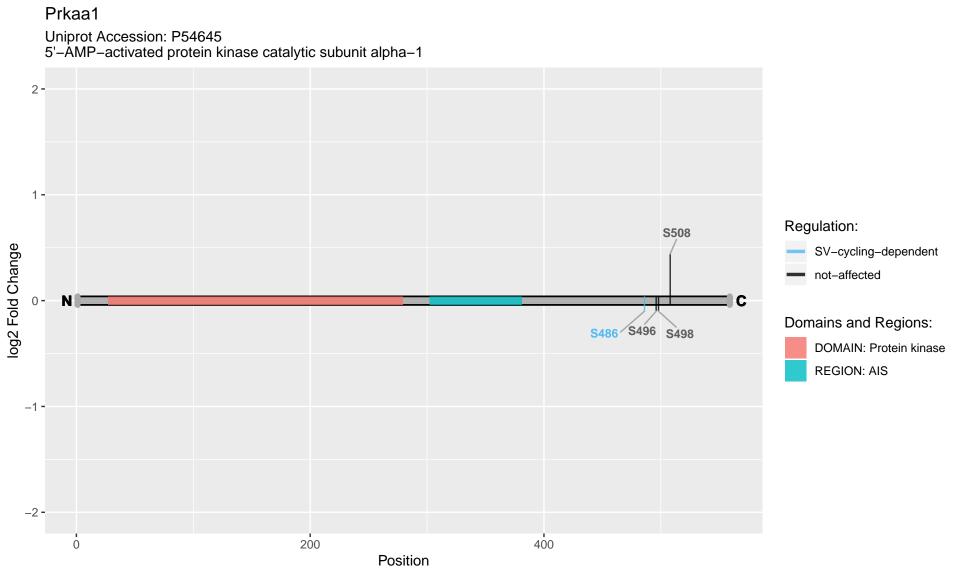


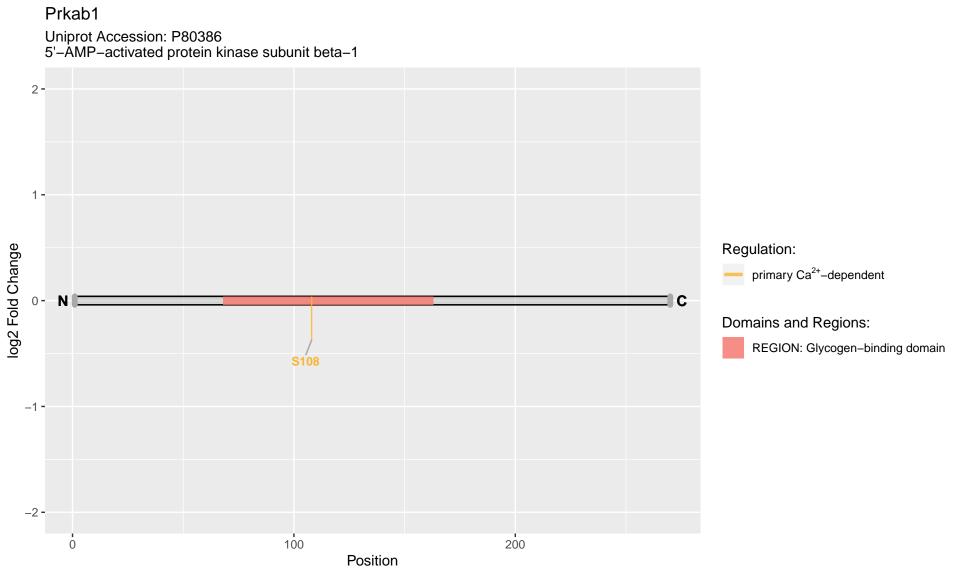


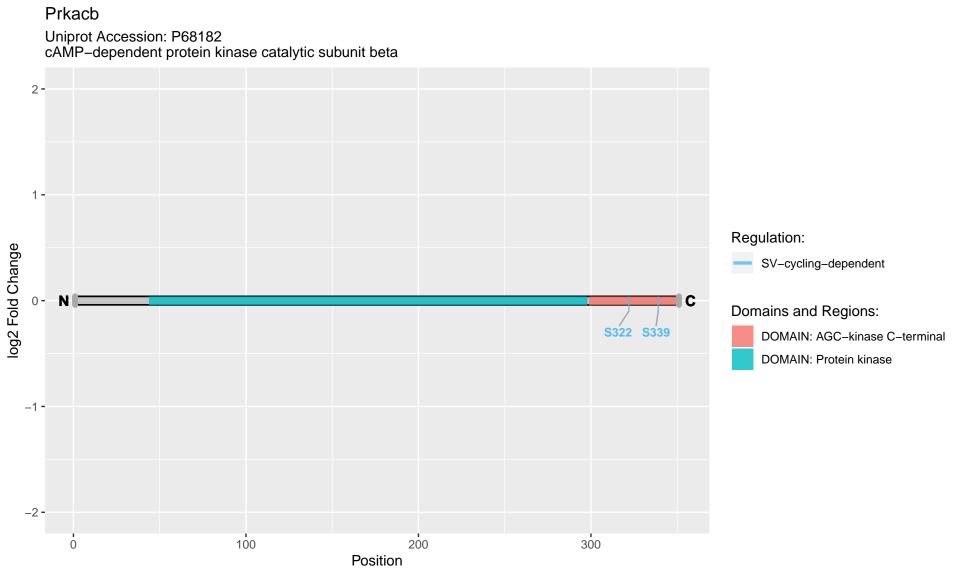


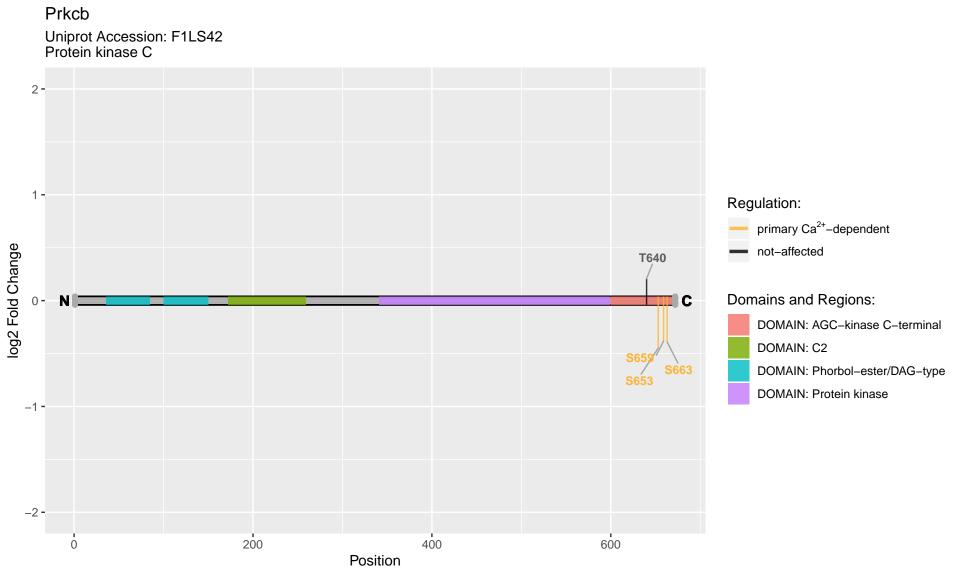


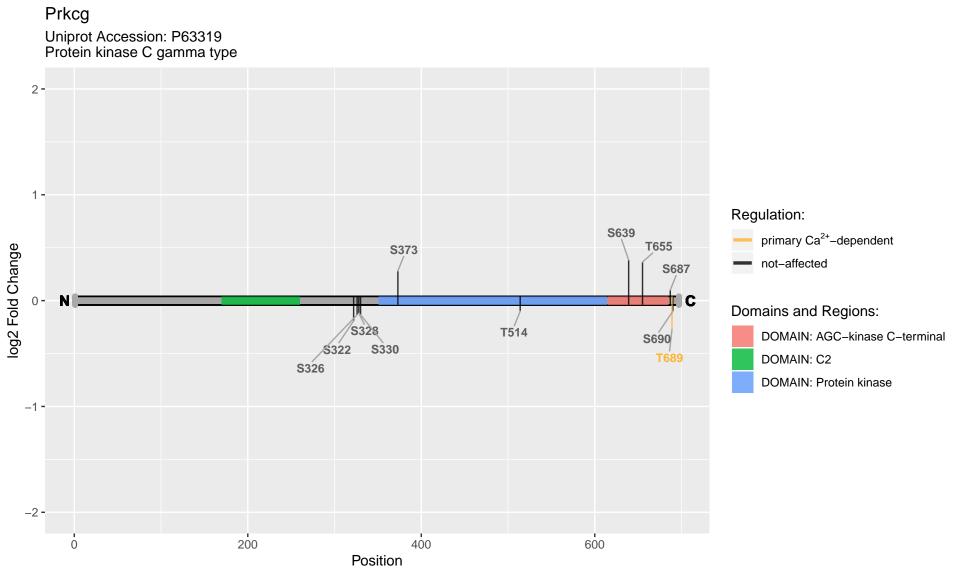


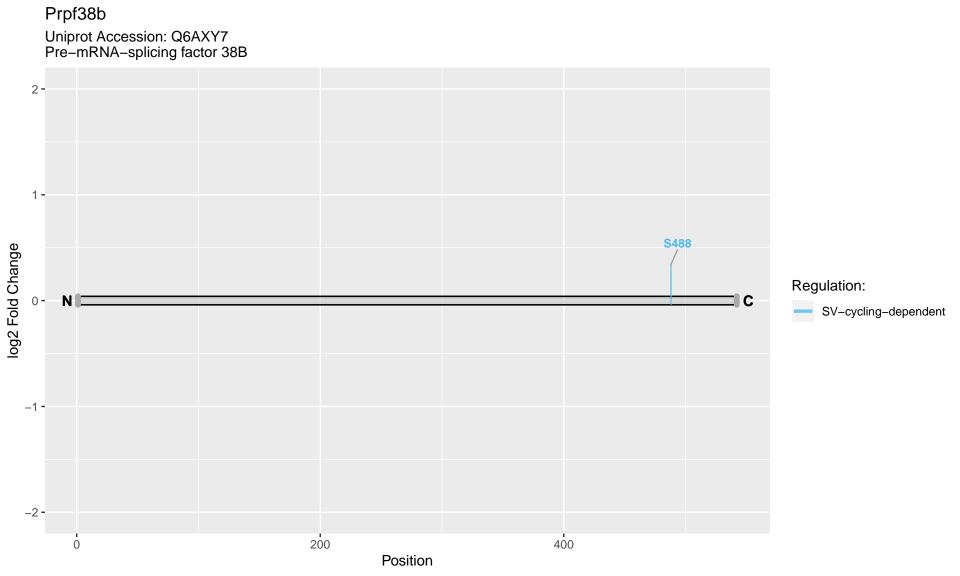


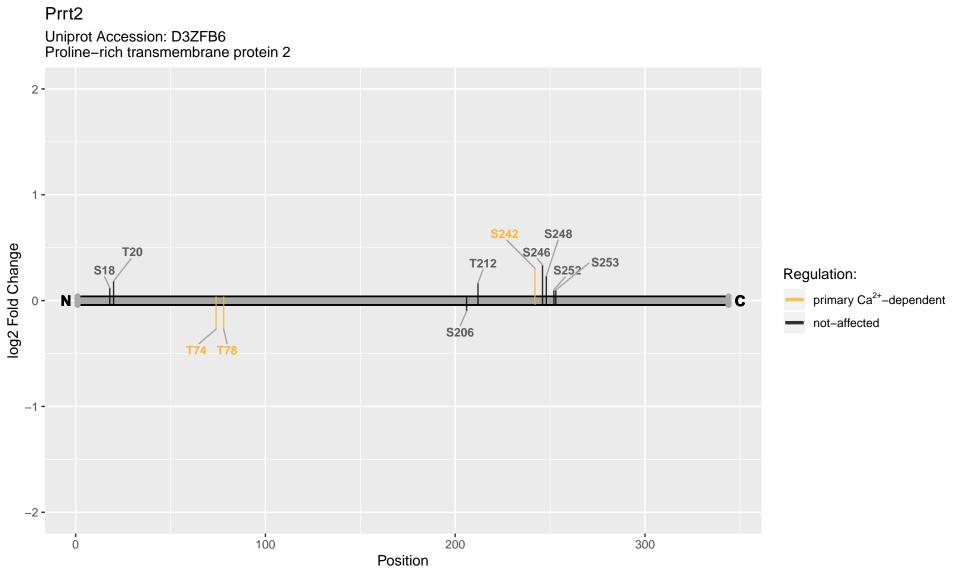


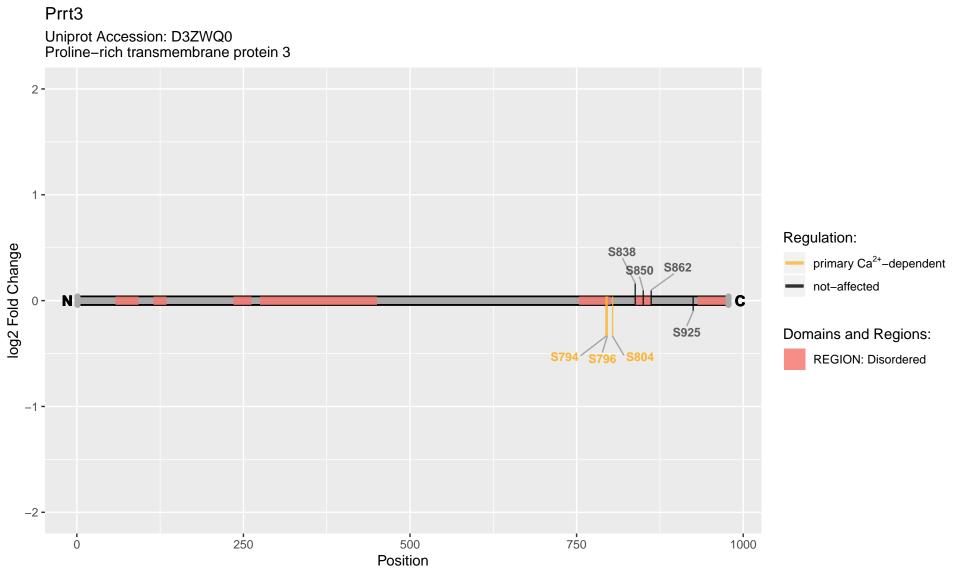


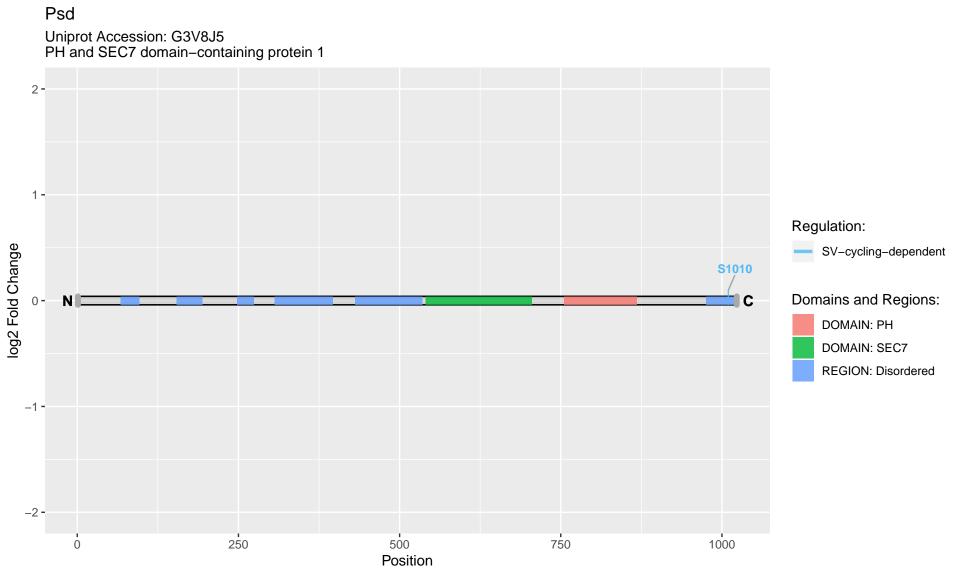


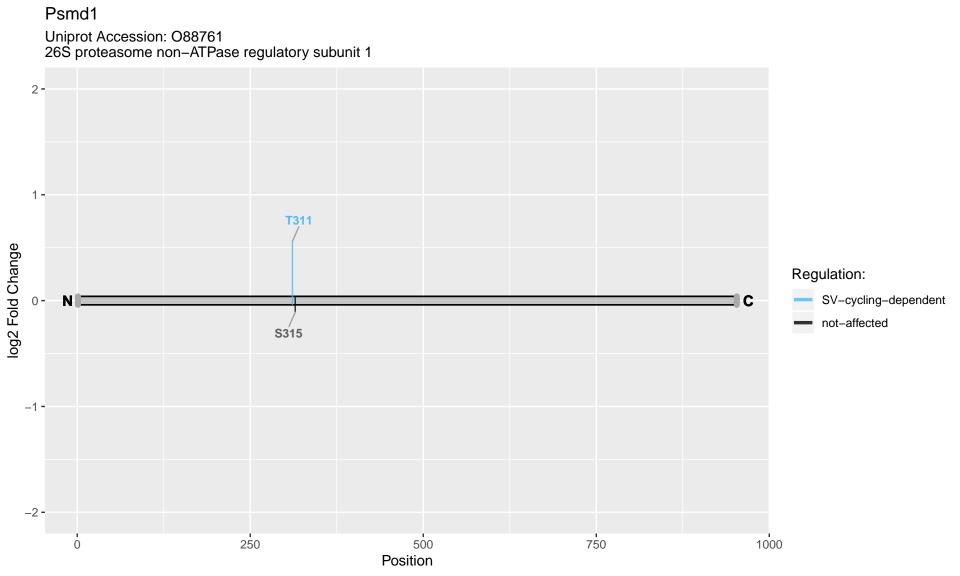


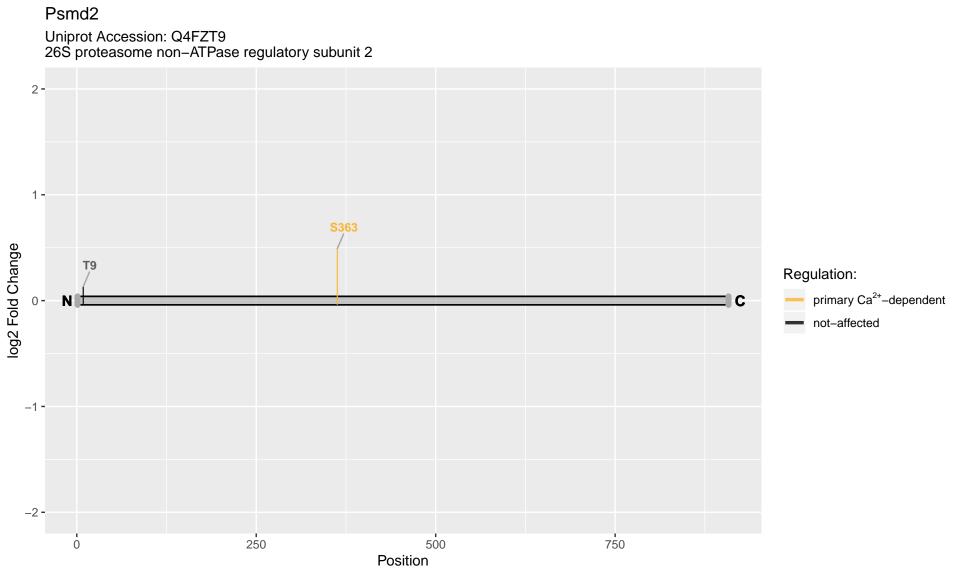


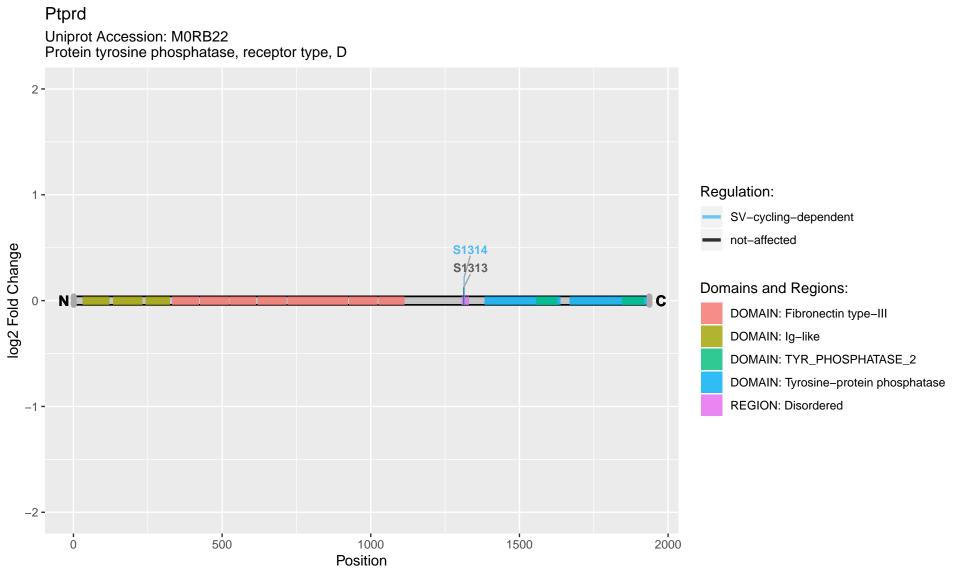


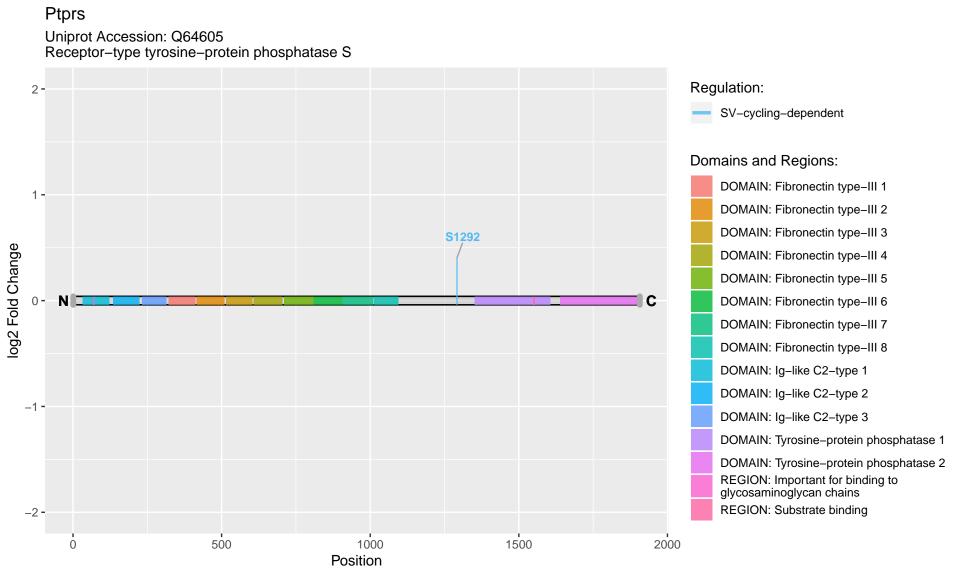


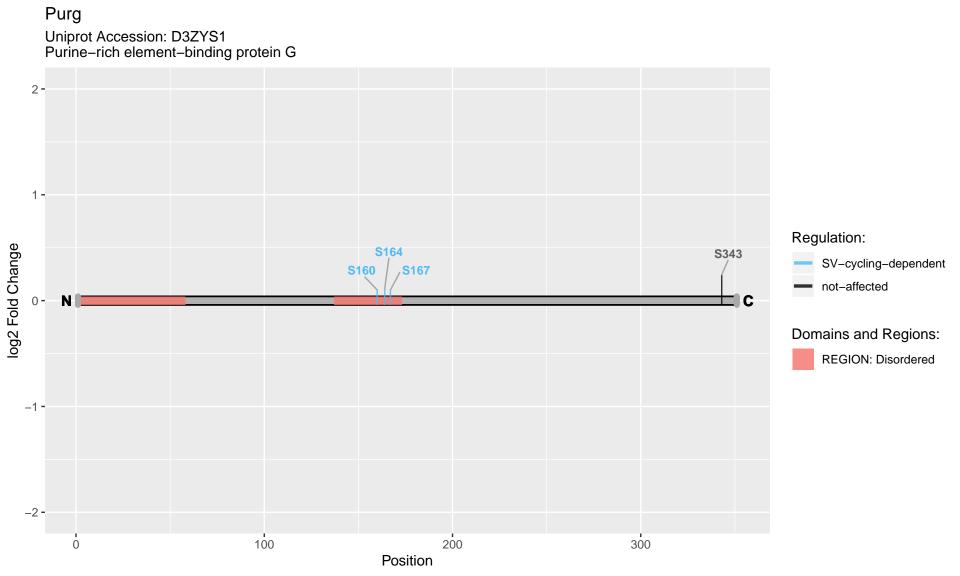


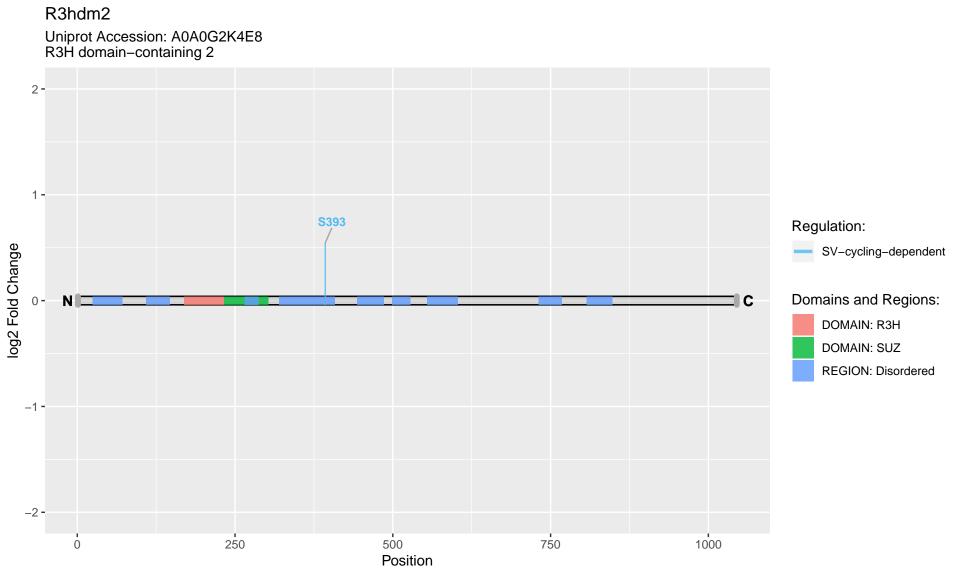


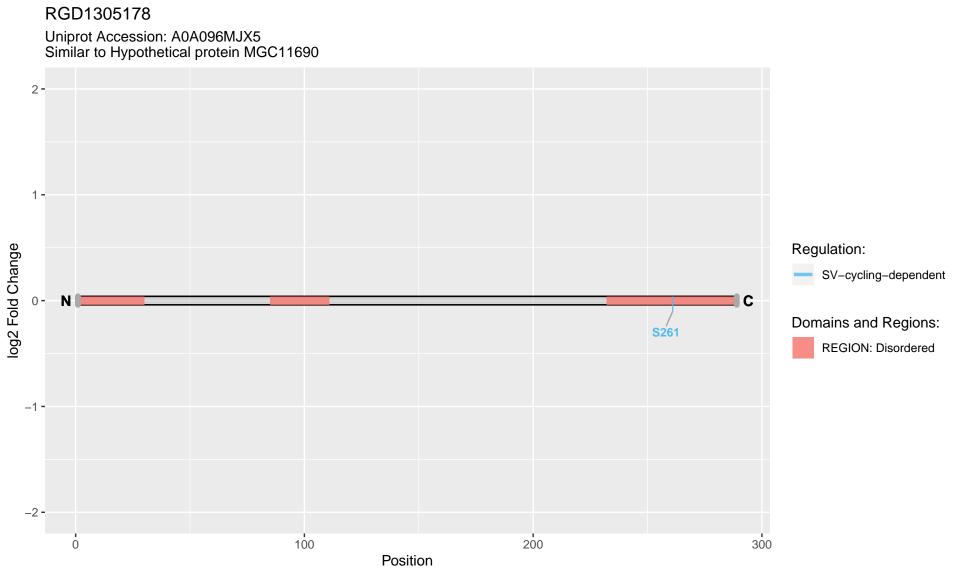


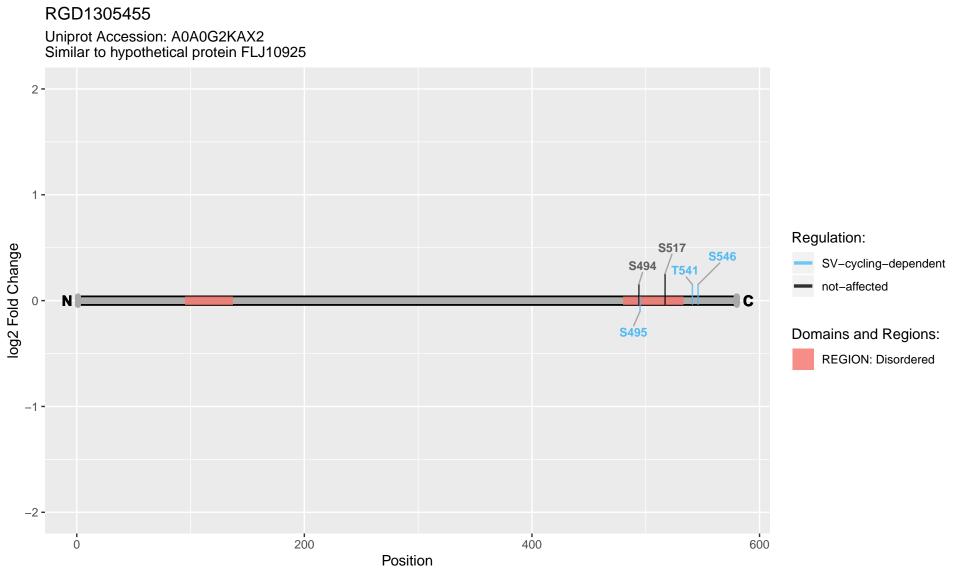


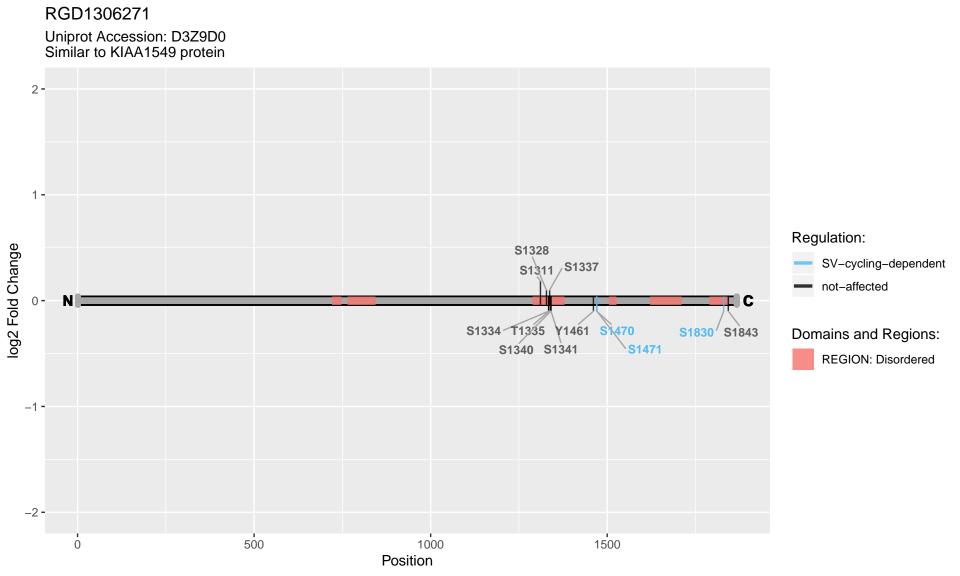


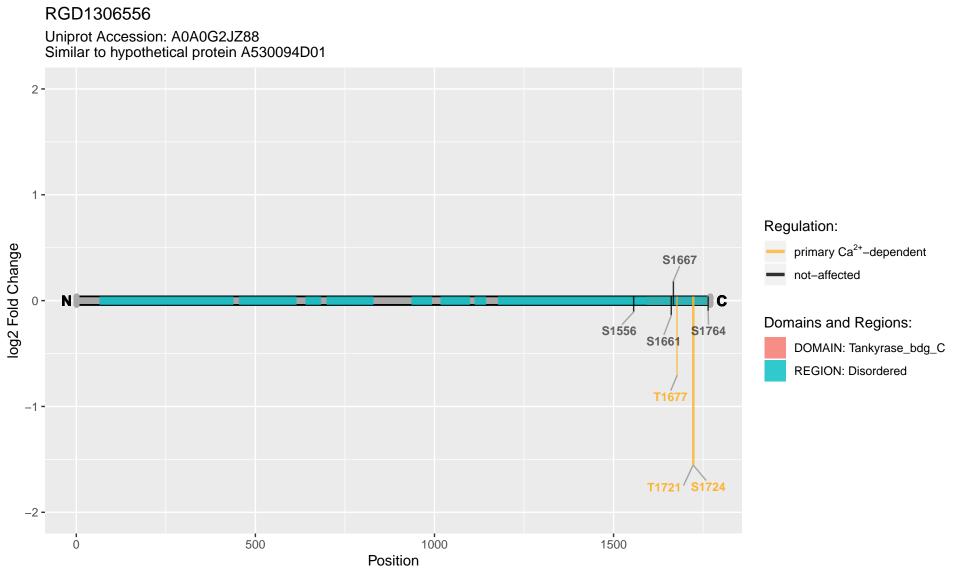


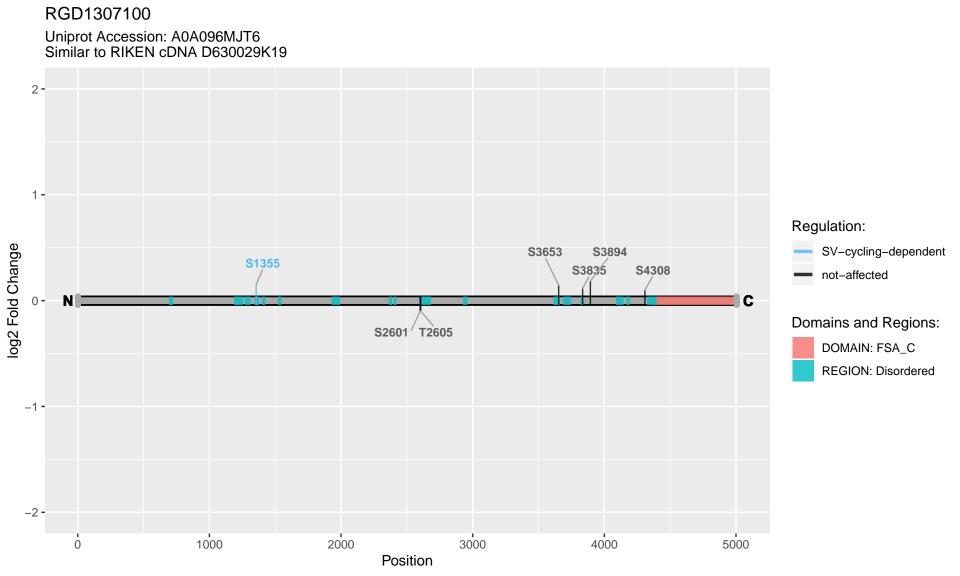


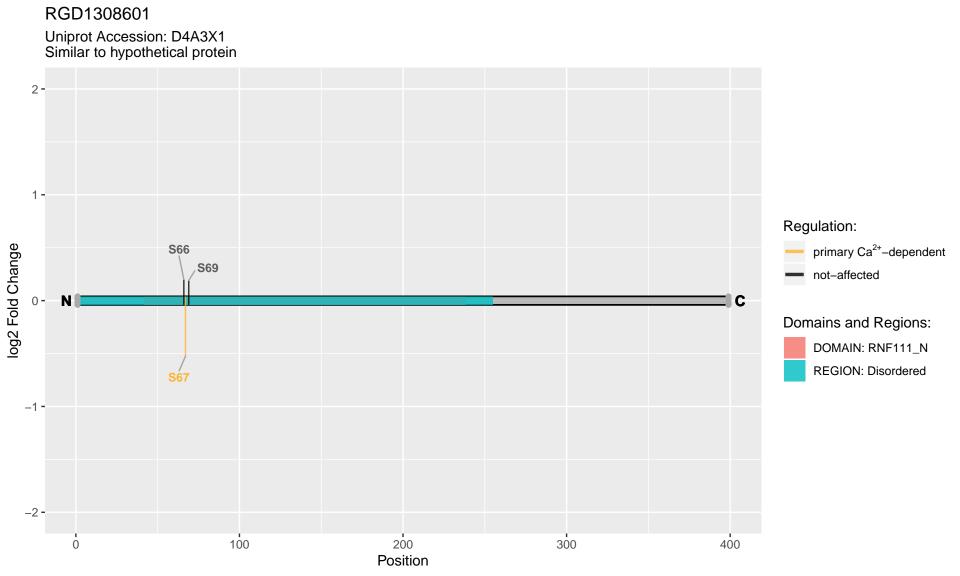


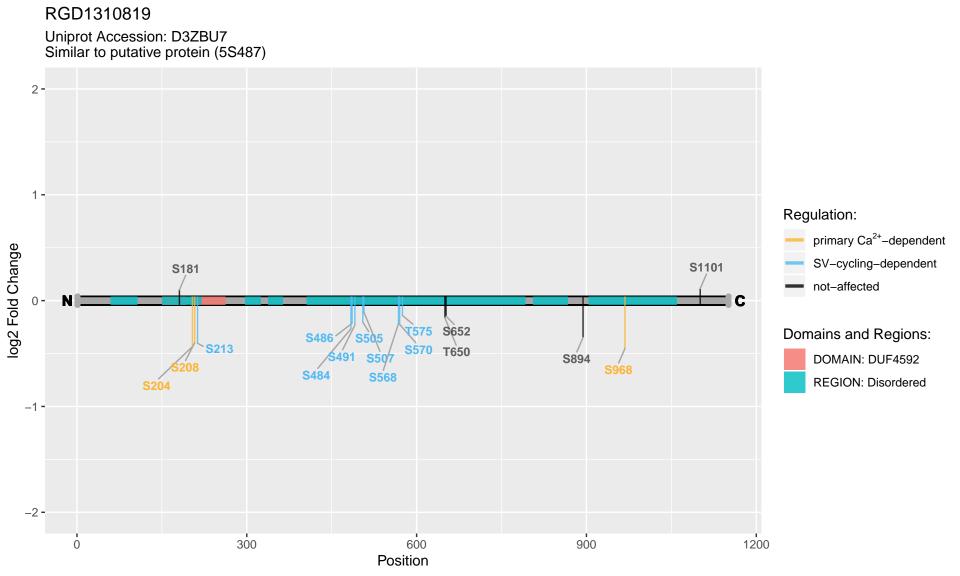


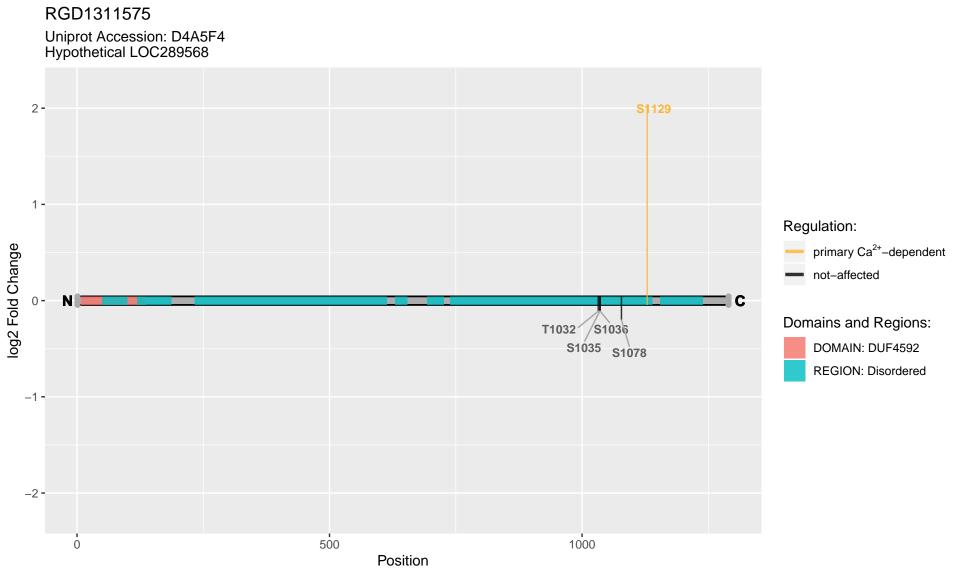


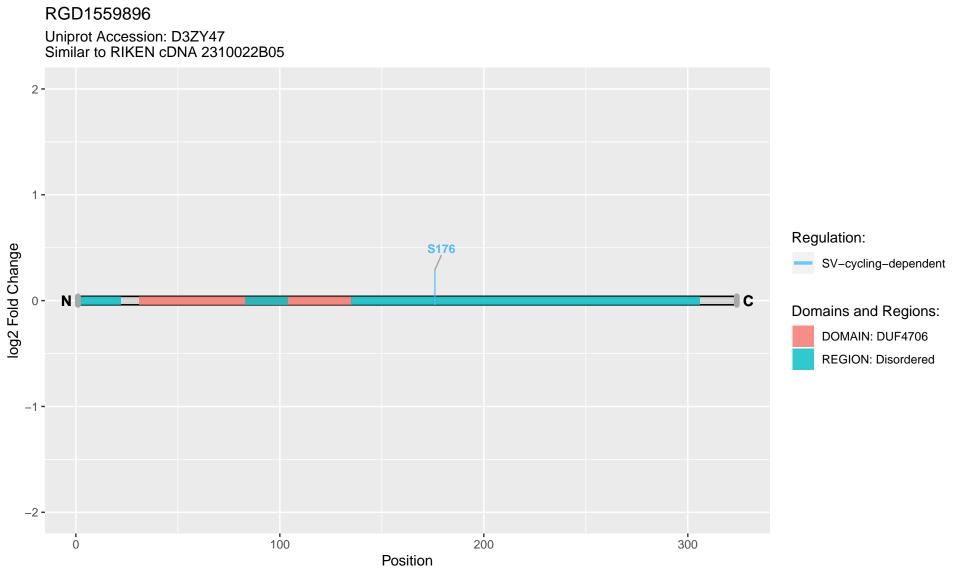


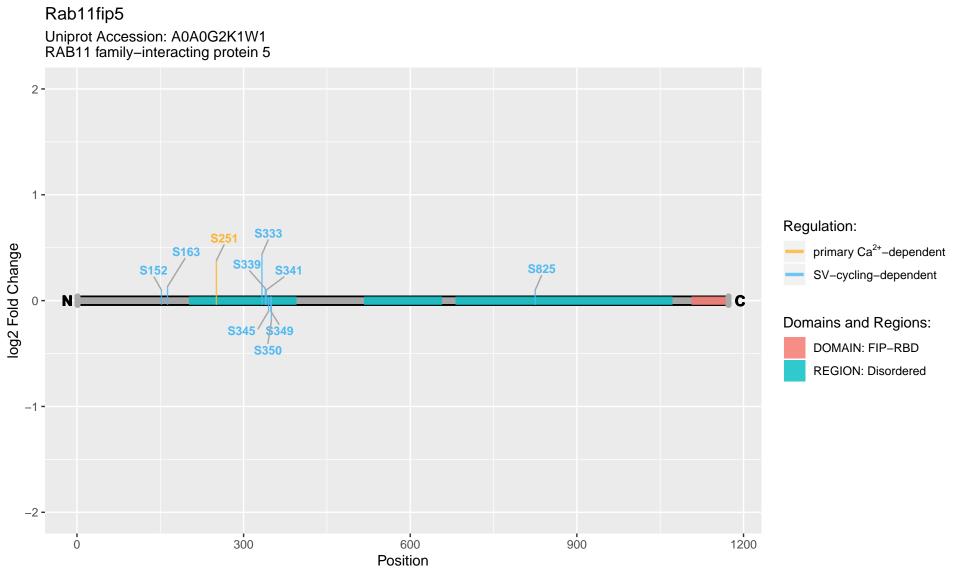


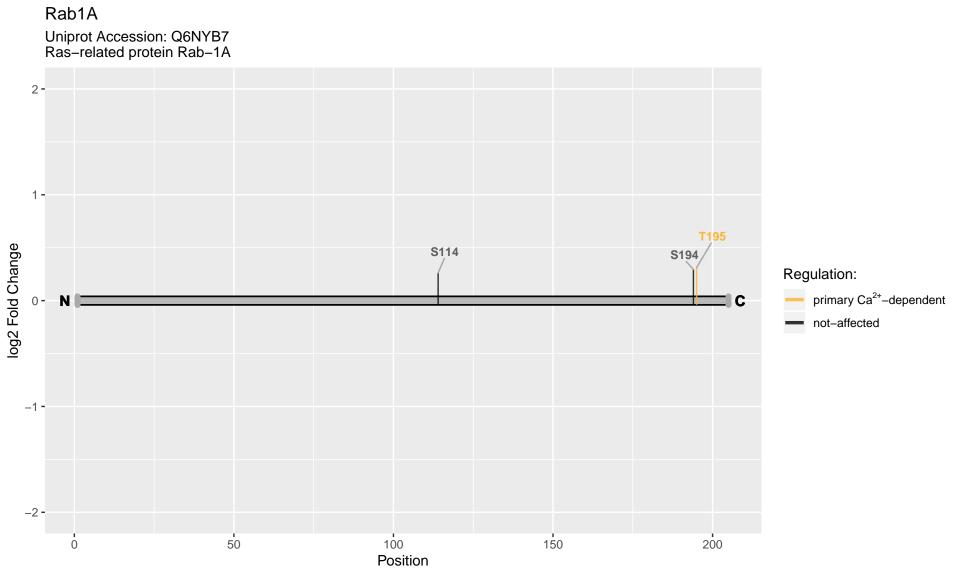


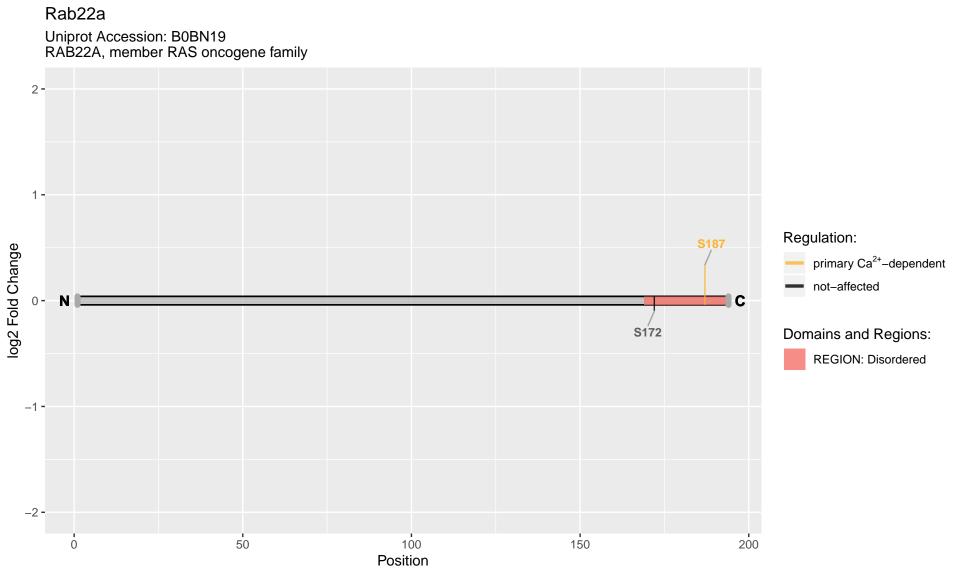


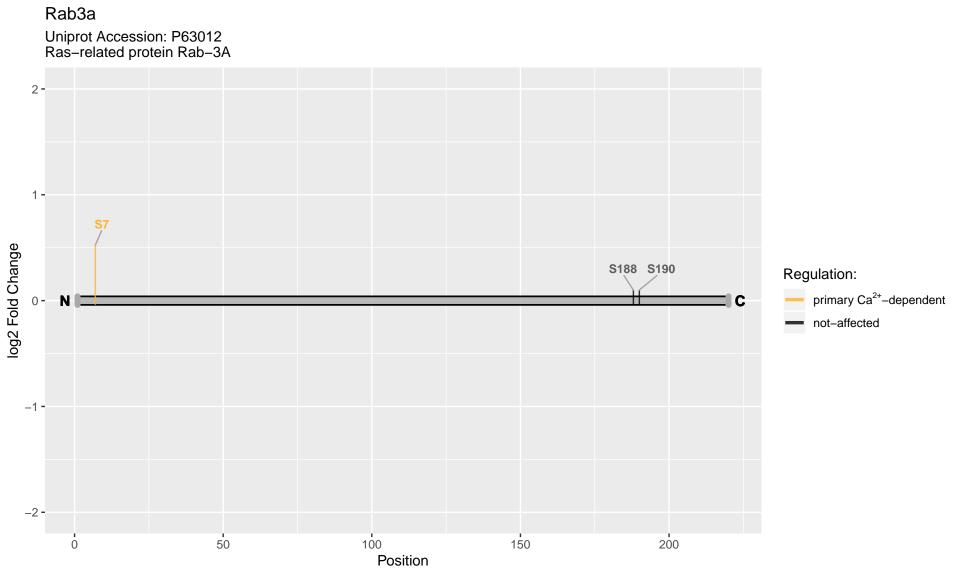


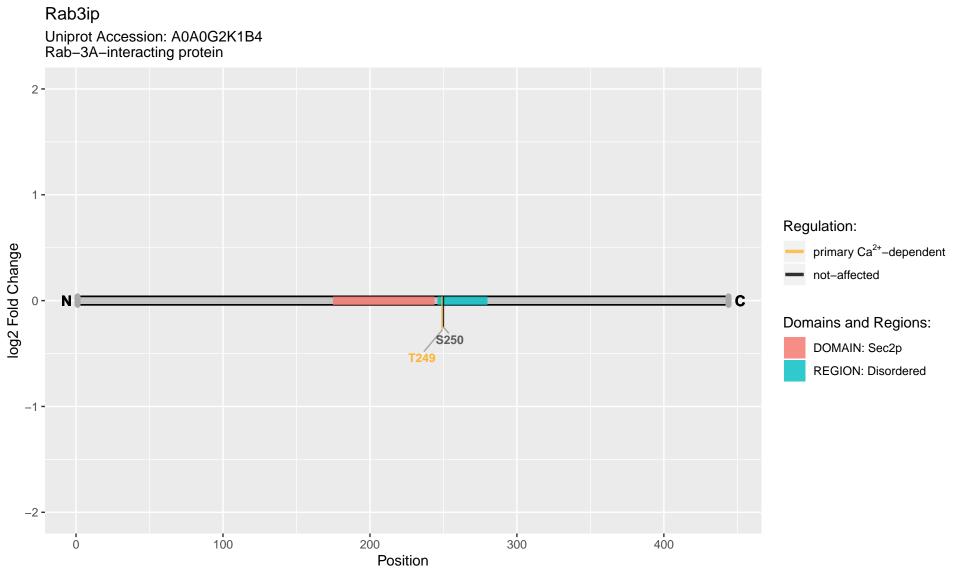


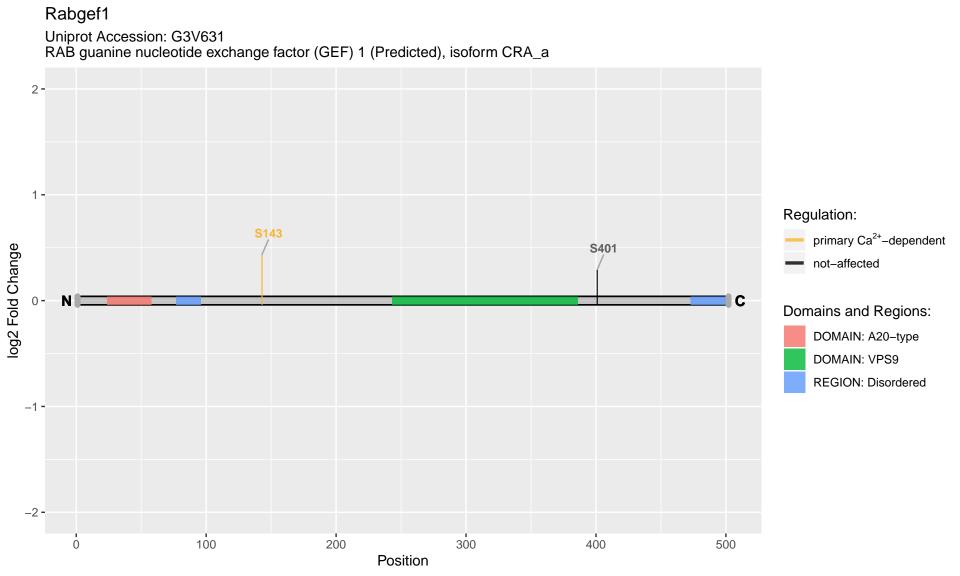


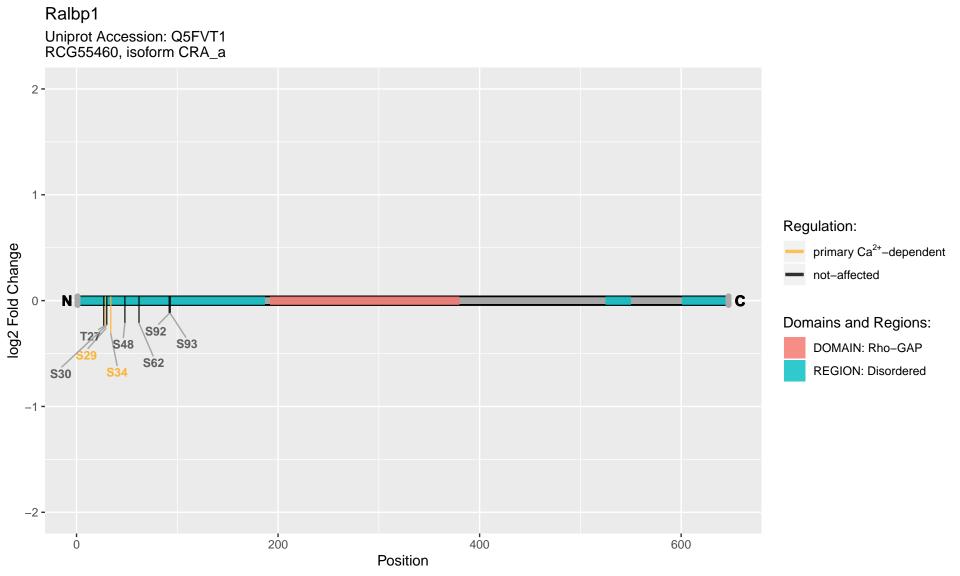


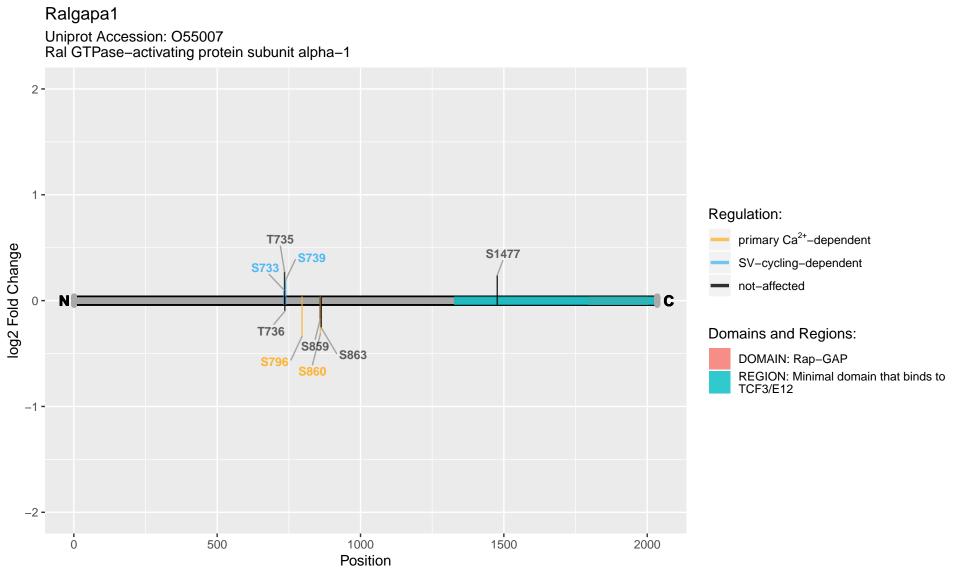


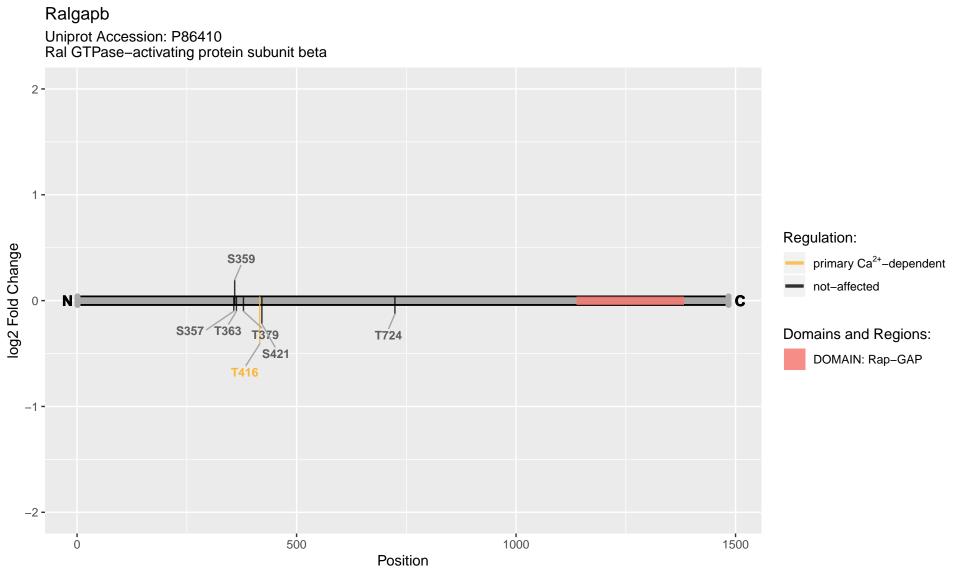


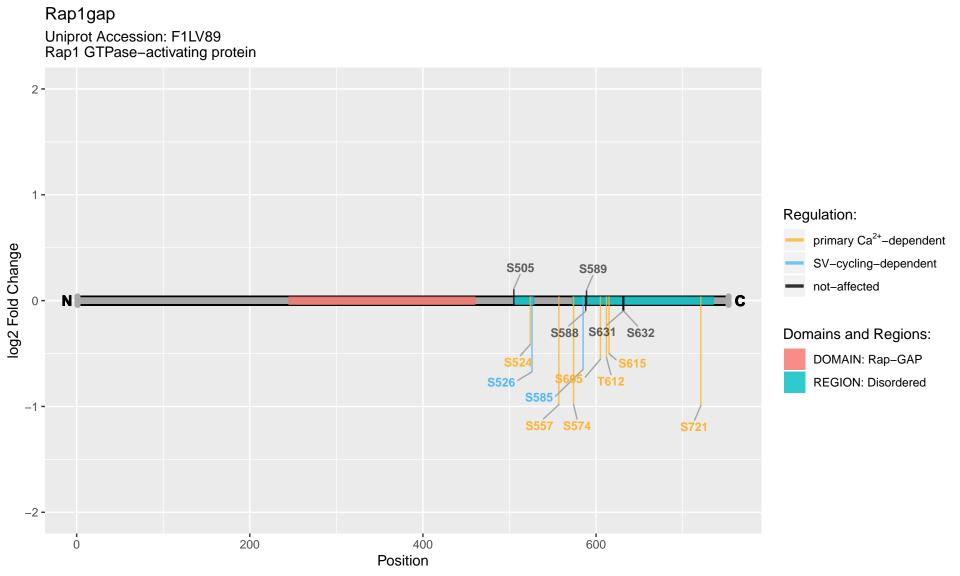


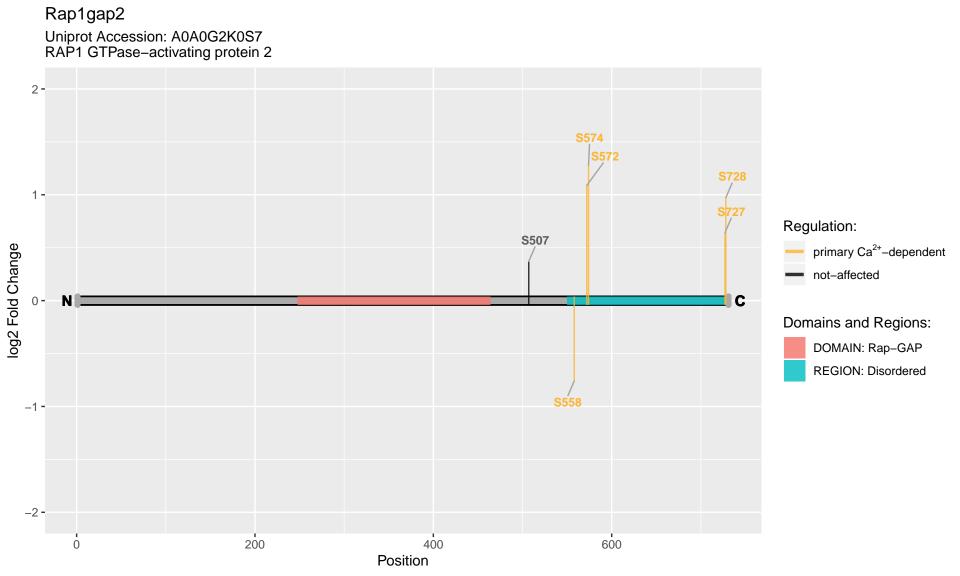


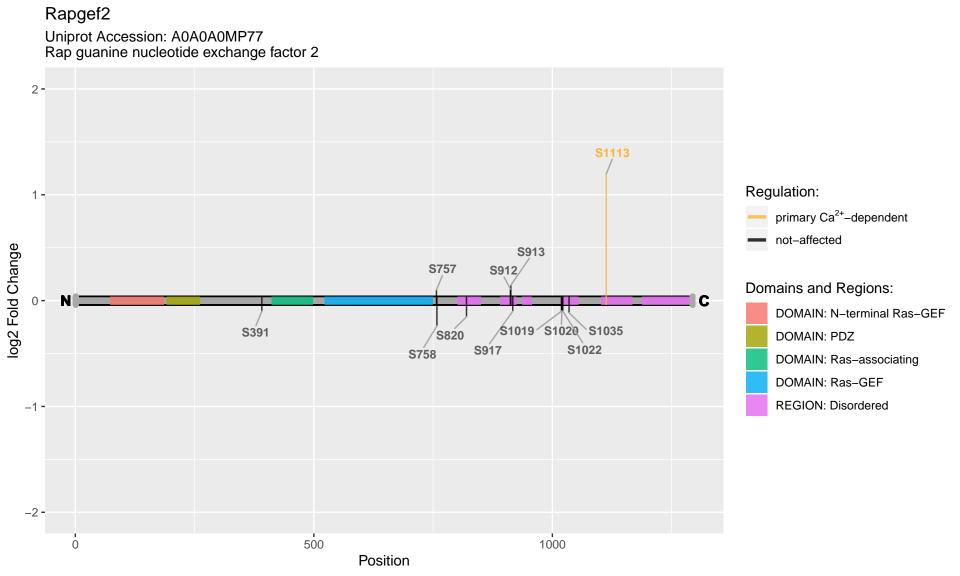


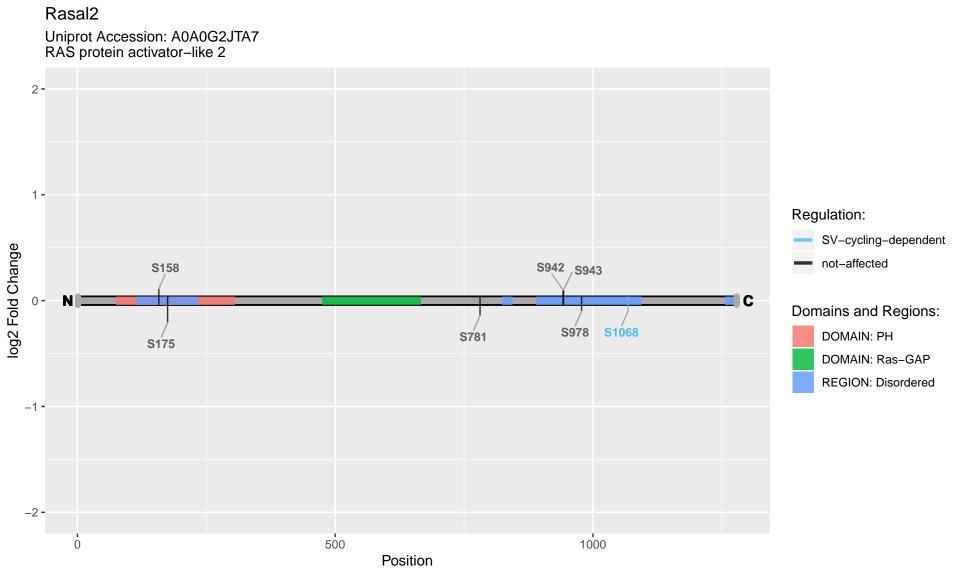


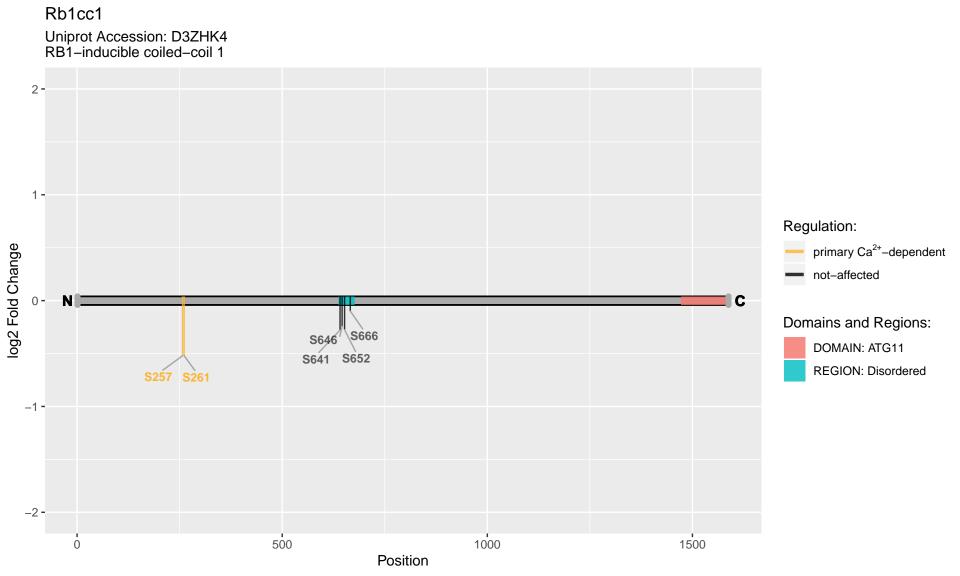


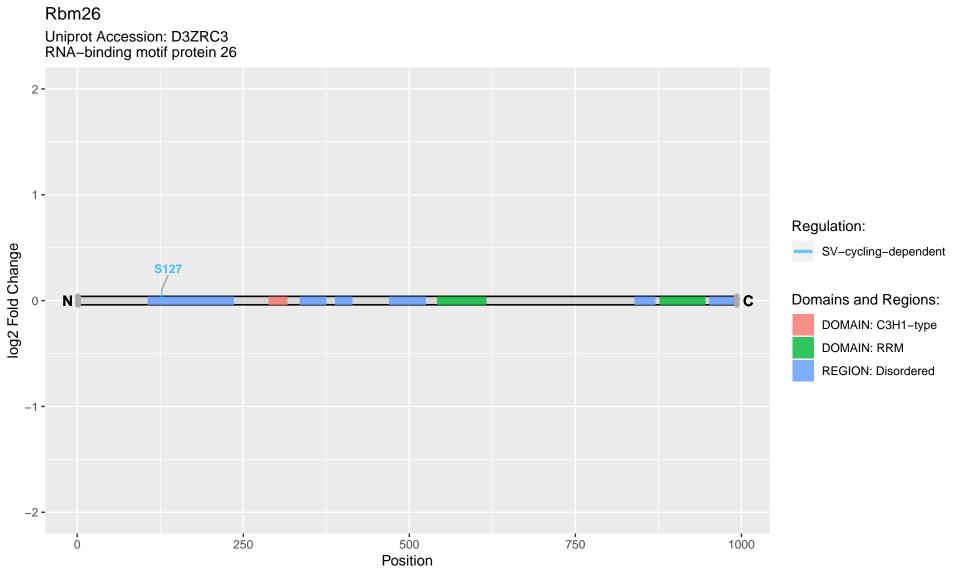


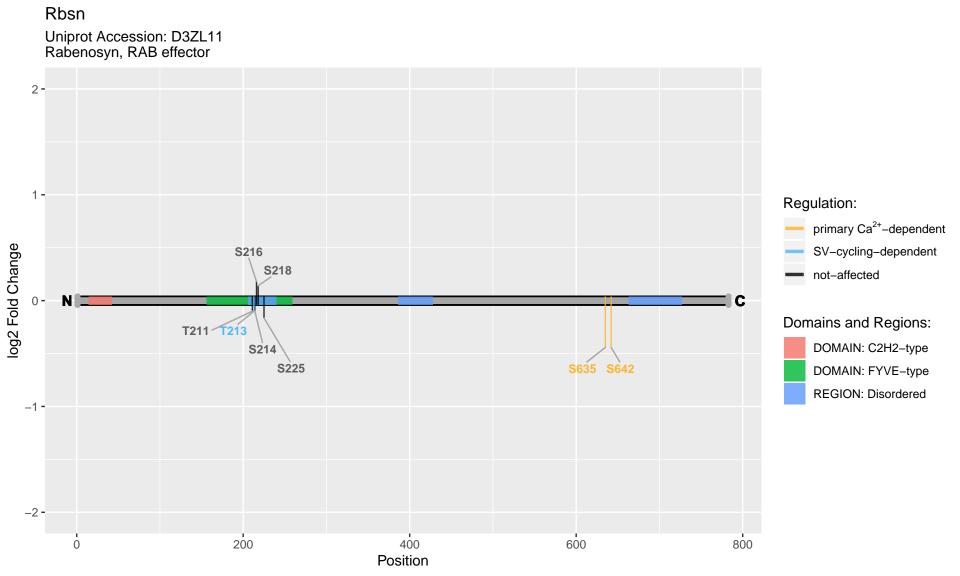


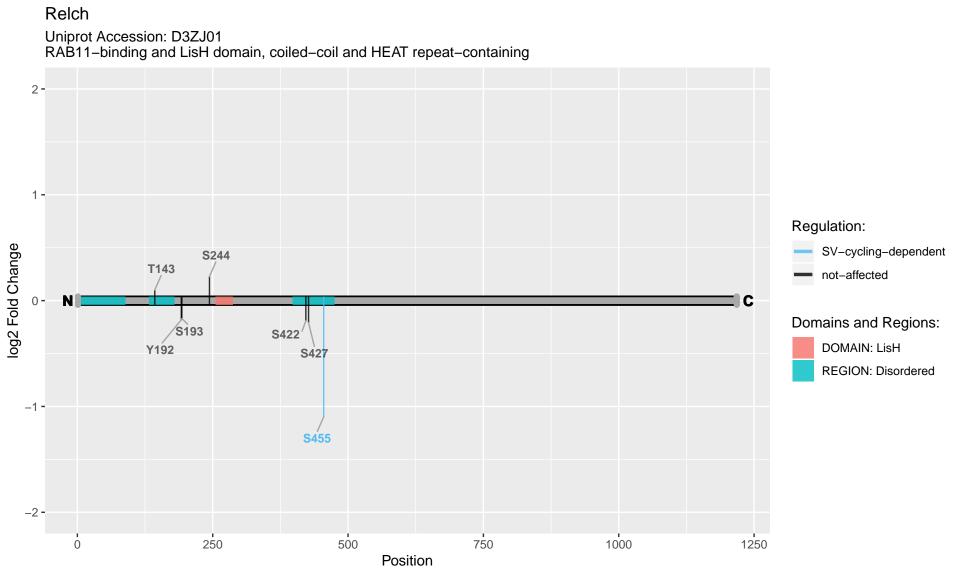


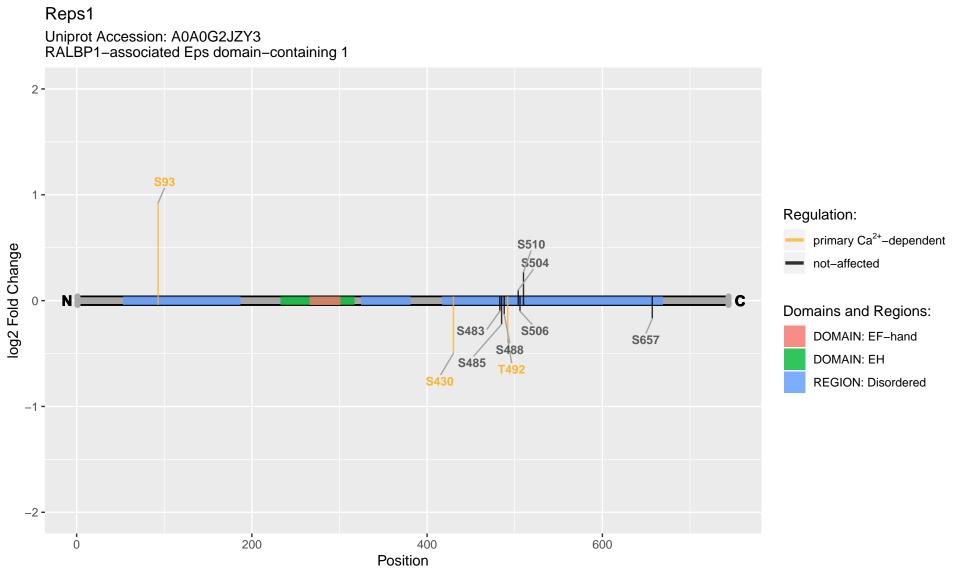


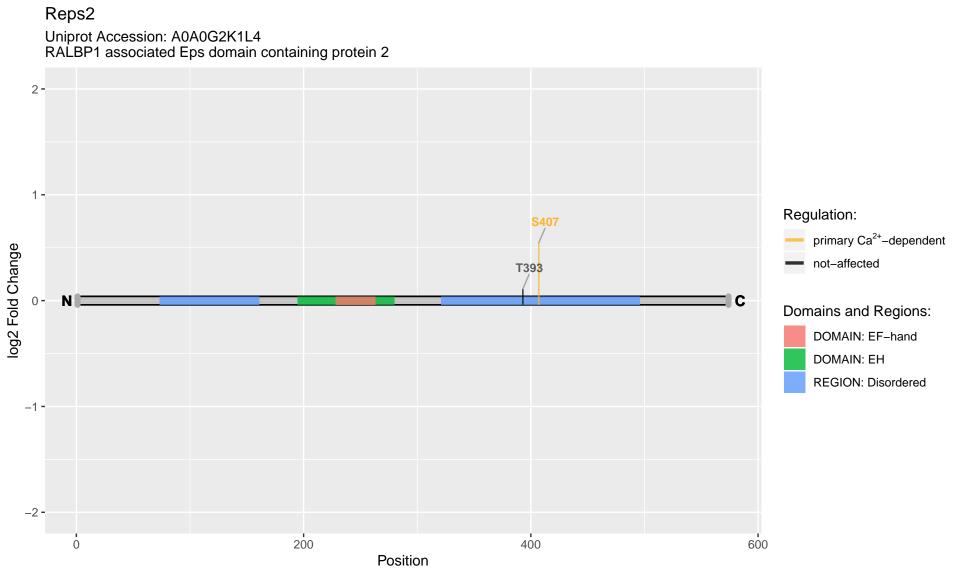


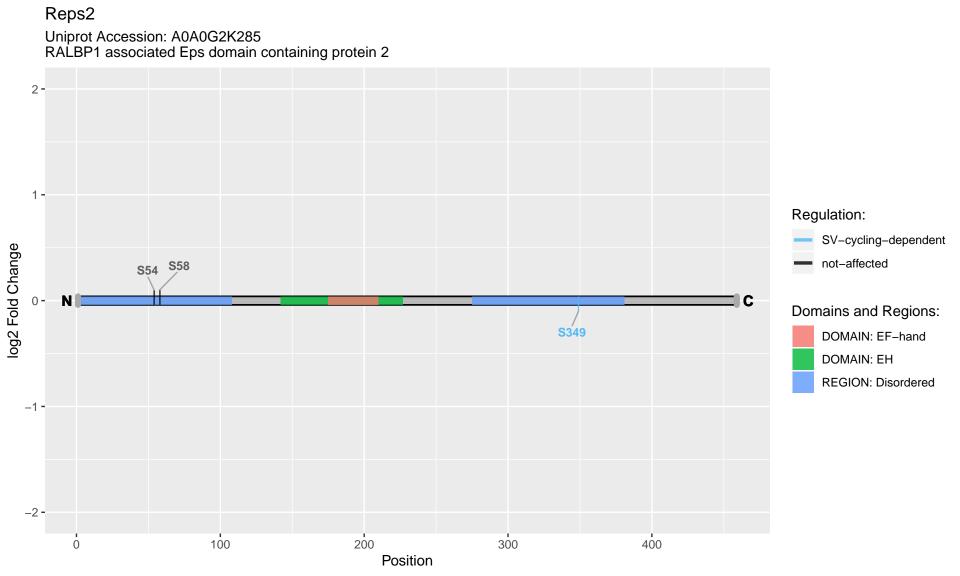


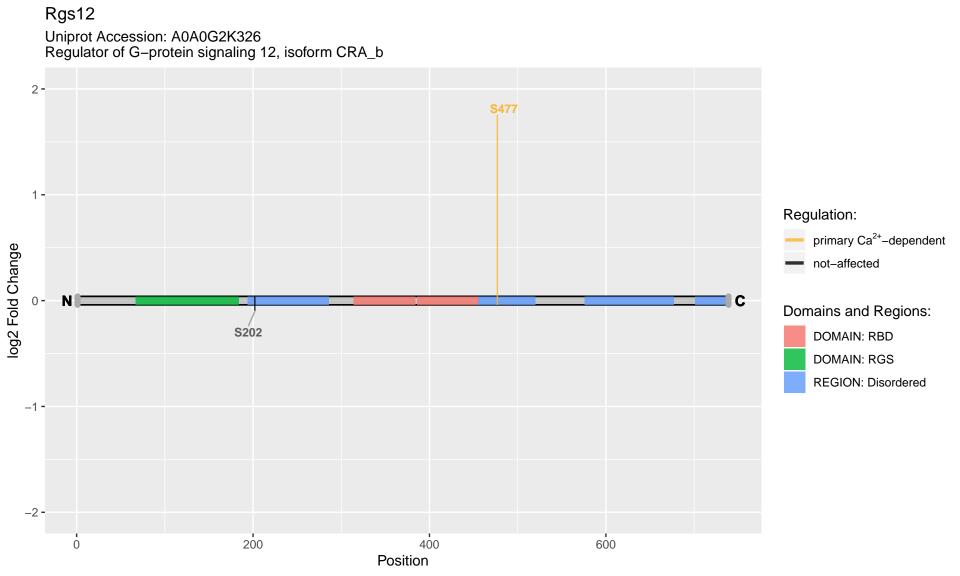


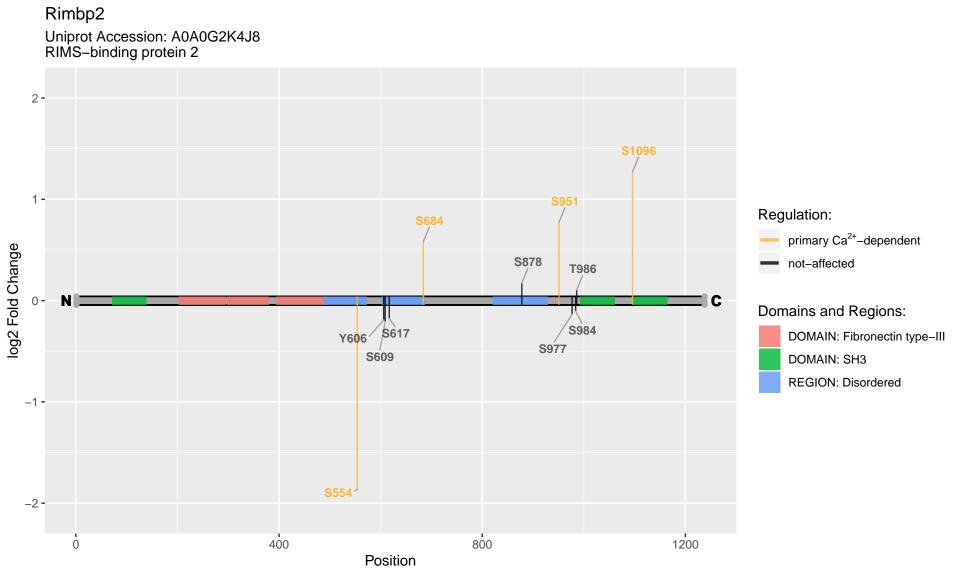




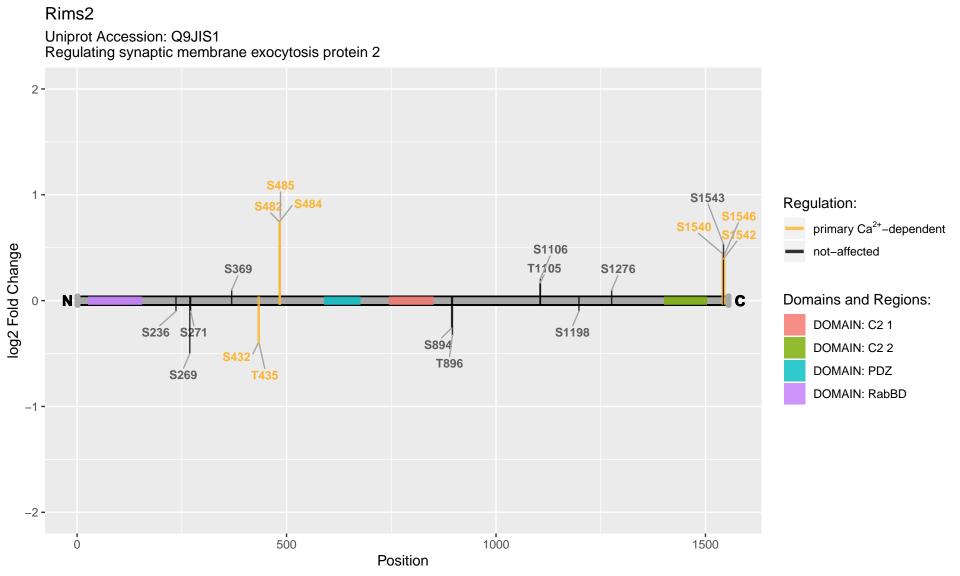


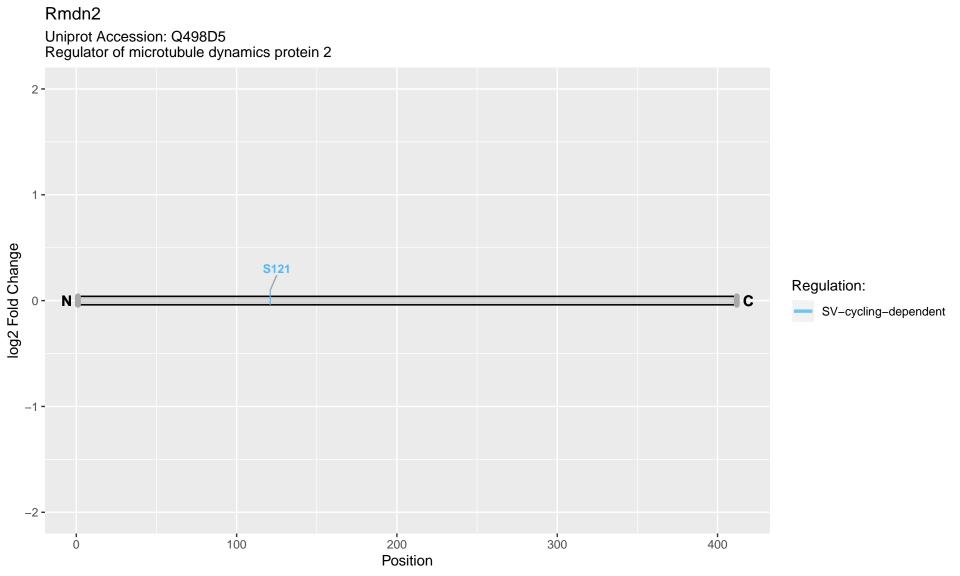


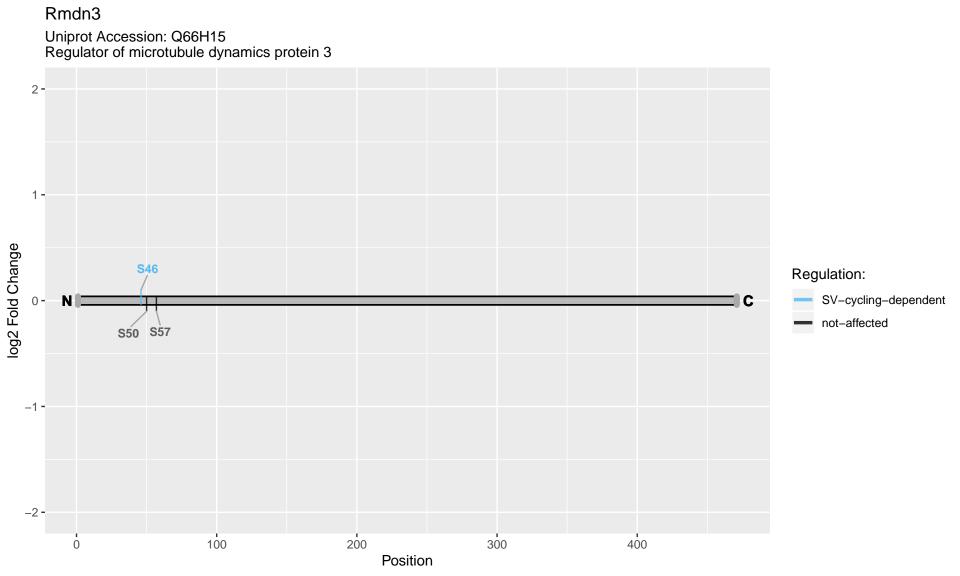


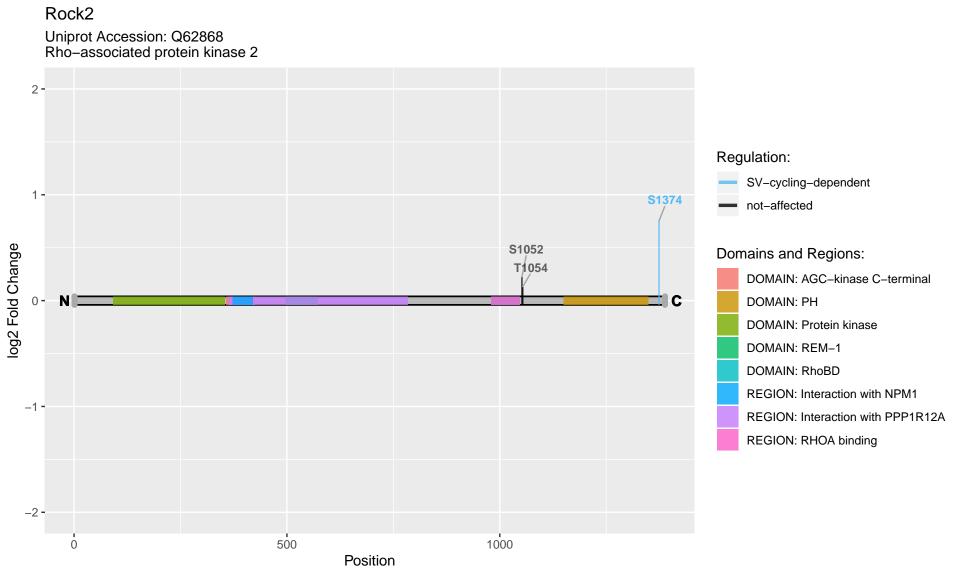


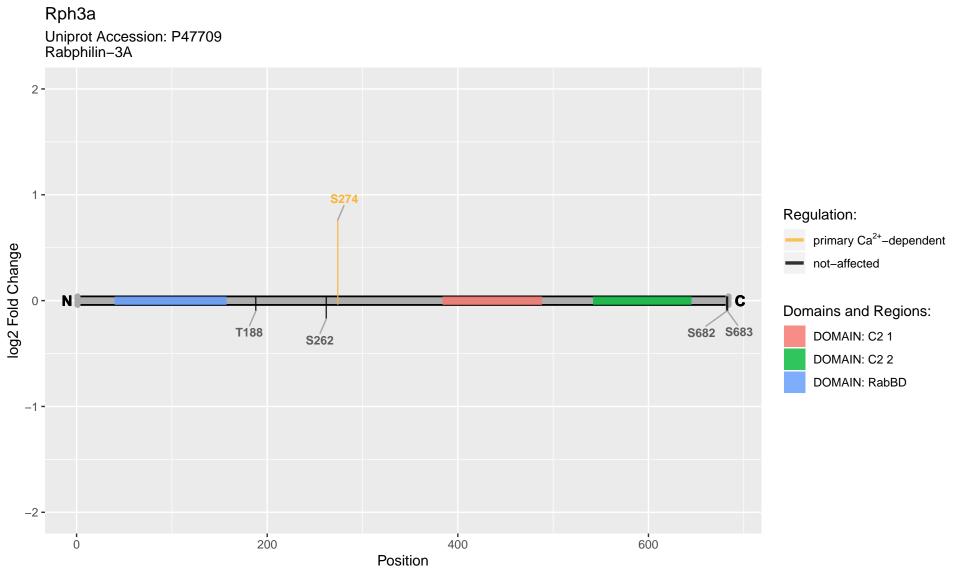
Rims1 Uniprot Accession: A0A0G2JT77 Regulating synaptic membrane exocytosis protein 1 2 -**S346 S95** Regulation: **S1233 S1408** primary Ca²⁺-dependent **S991 S723** S1202 SV-cycling-dependent S1355 **S413** S241 log2 Fold Change not-affected S1599 S1262 **S443** \$379 S1338/T1340 S1602 Domains and Regions: S908 S895 DOMAIN: C2 S1/174 `S1178 S447 S1370 T1176 DOMAIN: FYVE-type T744 DOMAIN: PDZ **S924 S745 S1078** DOMAIN: RabBD **S742** -1 **-S967 REGION: Disordered** S101 S1013 -2 **-**500 1000 1500 Position

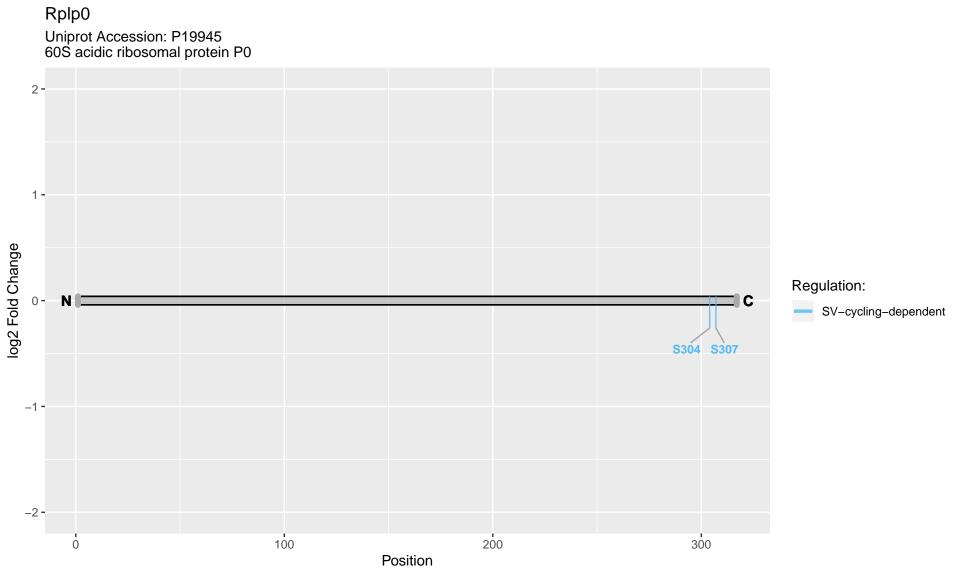


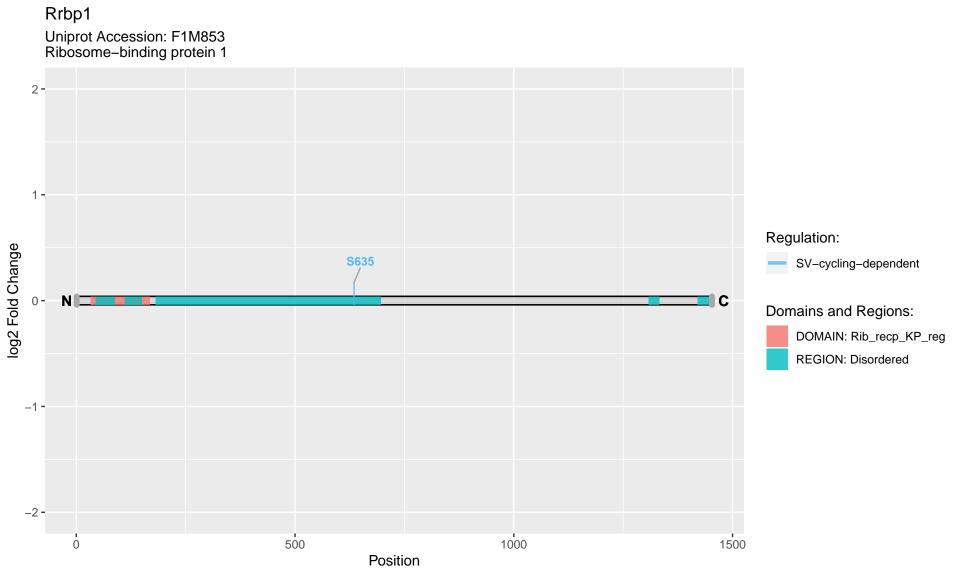


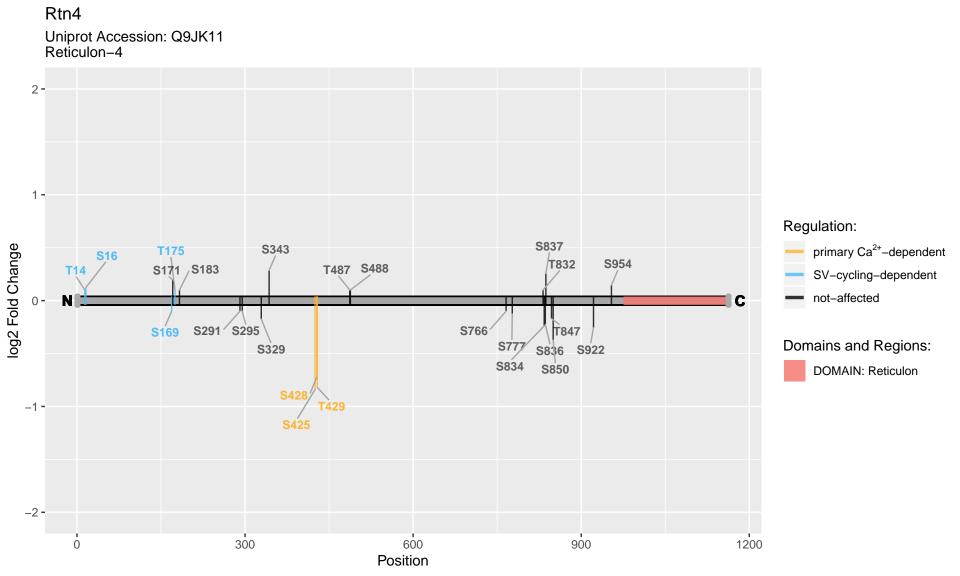


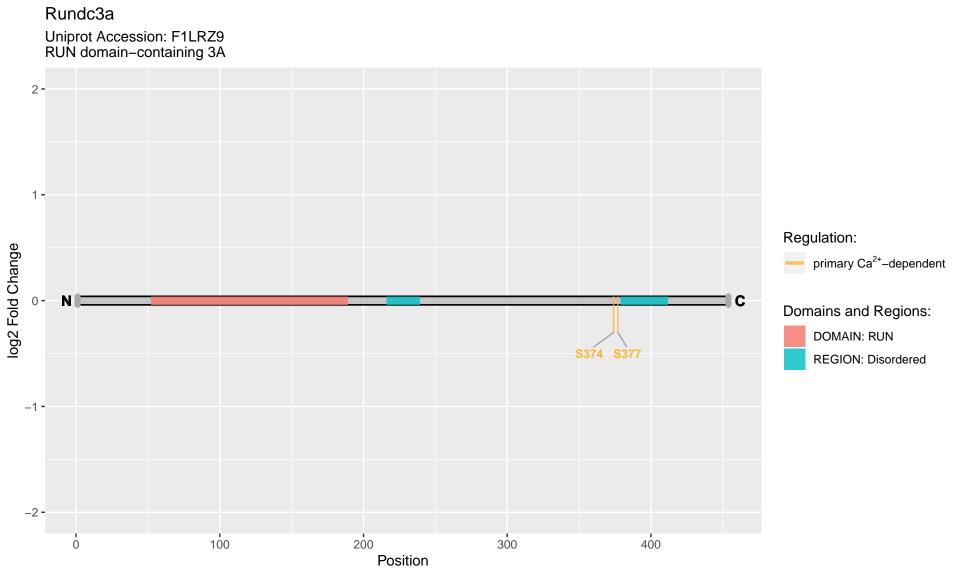


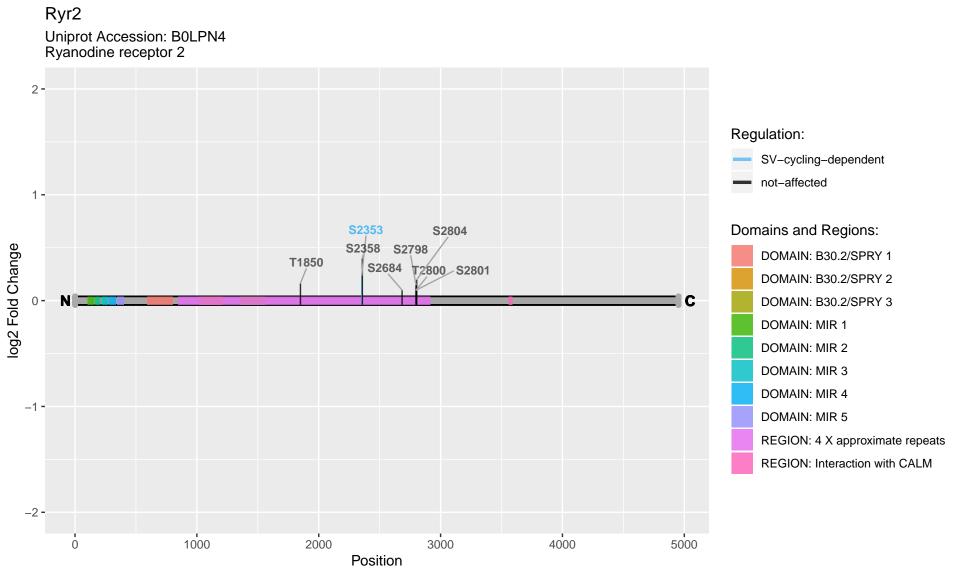


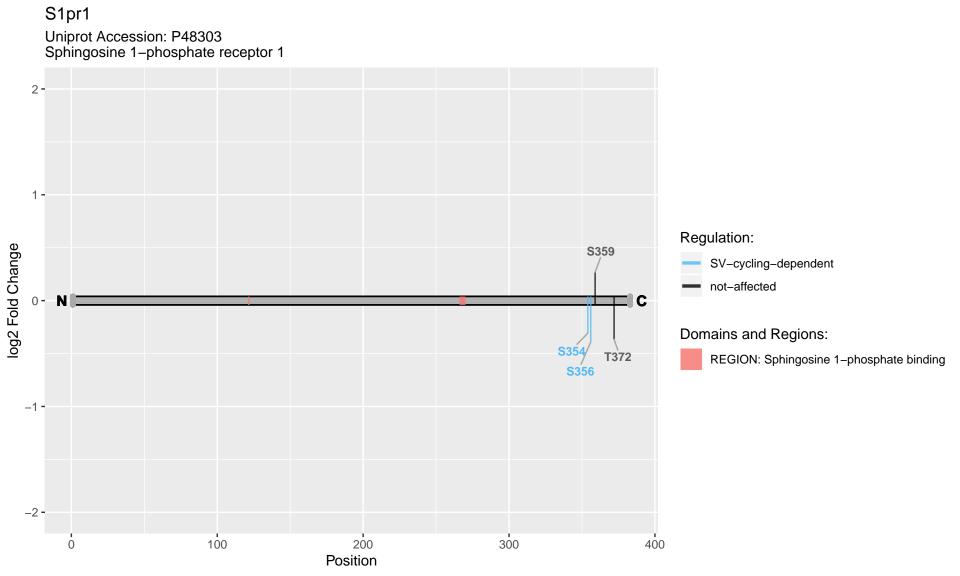


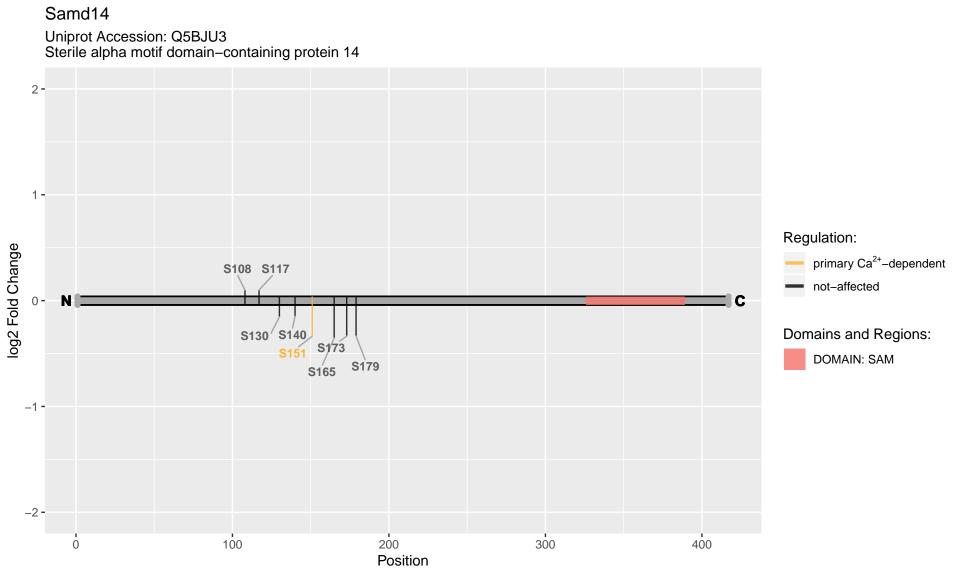


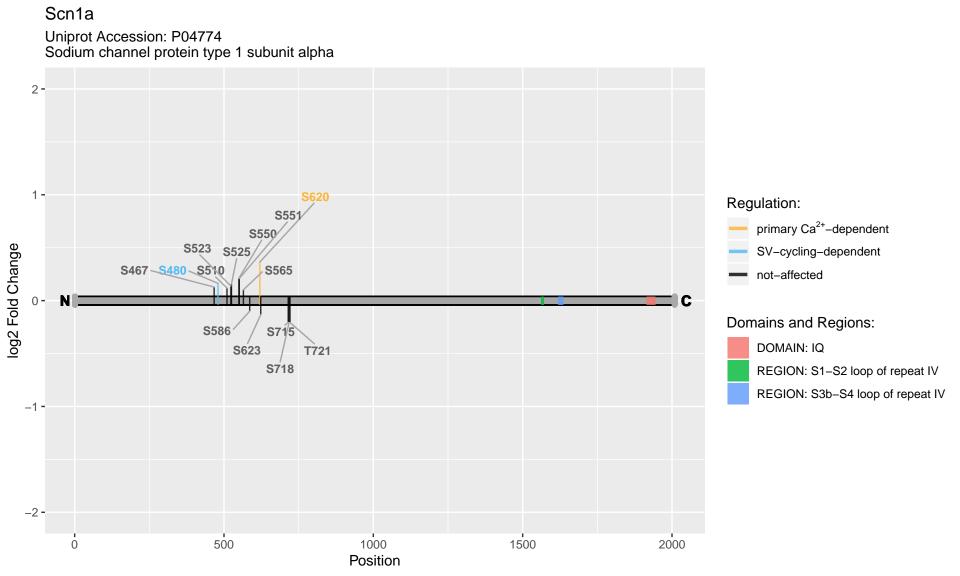


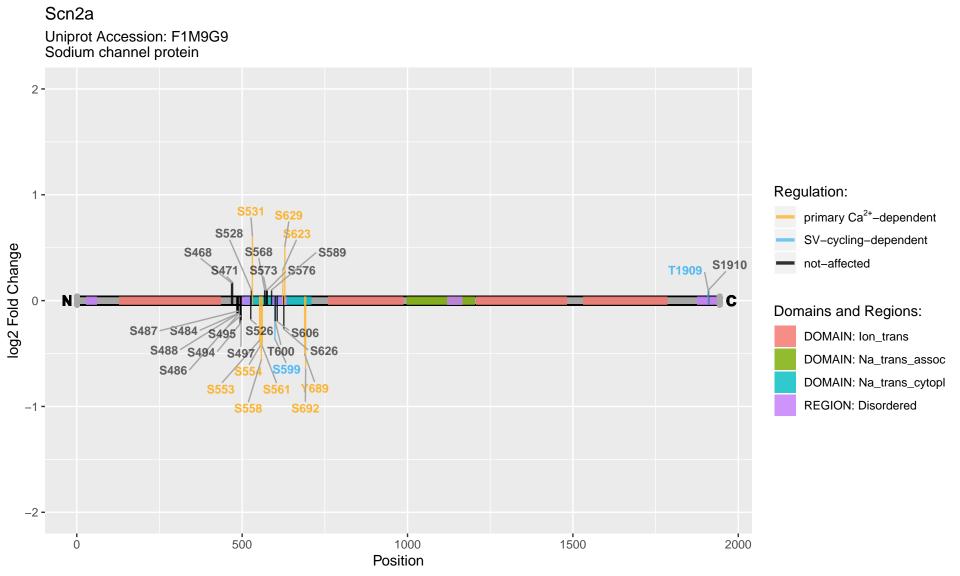


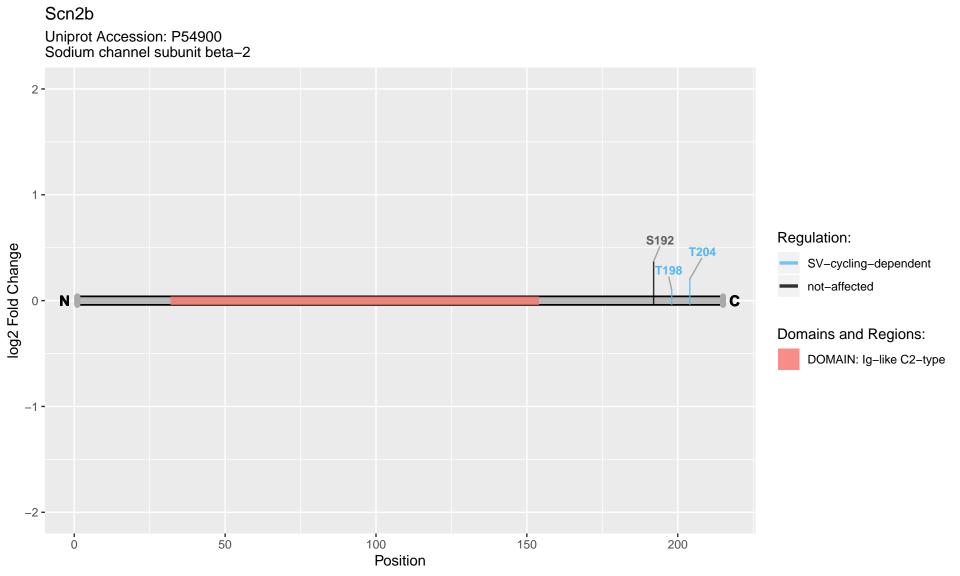


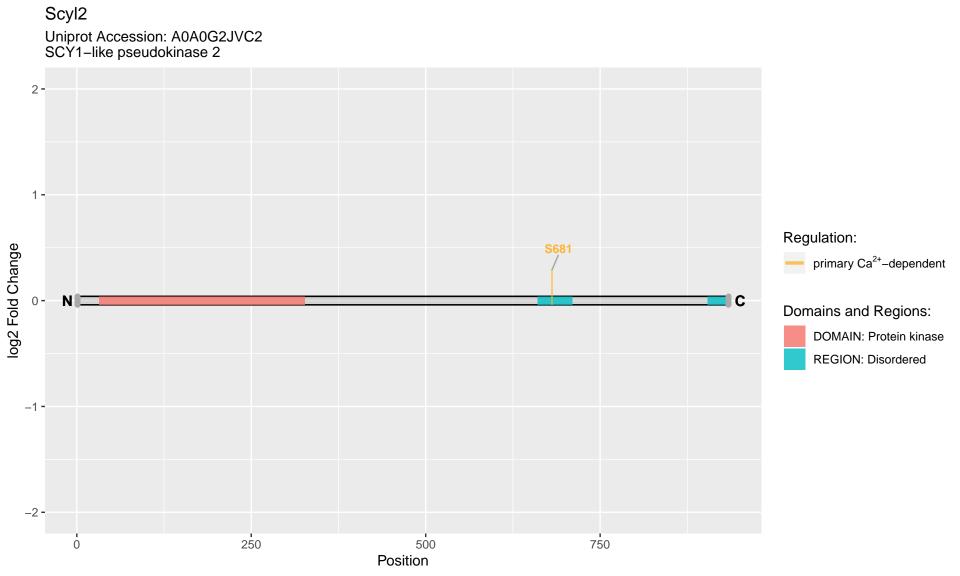


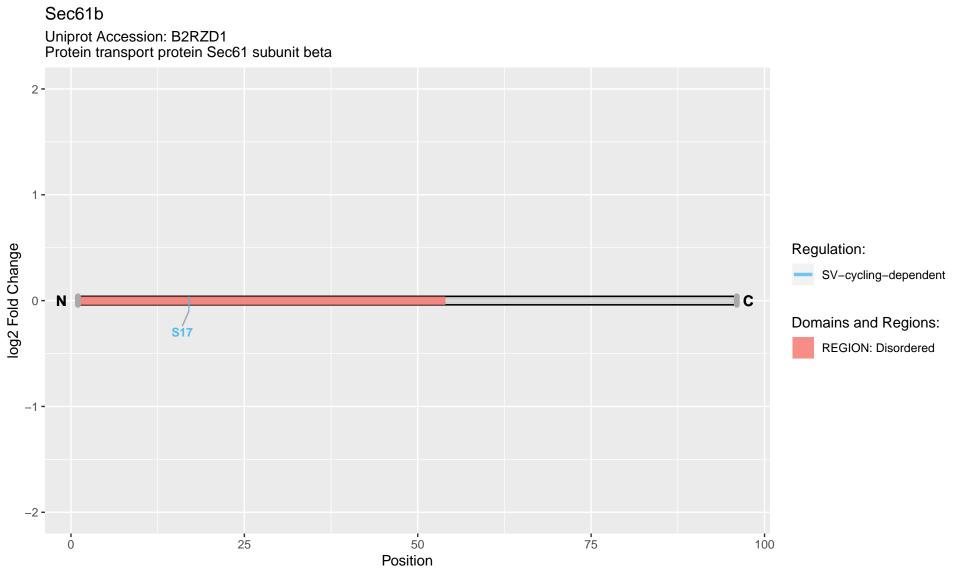


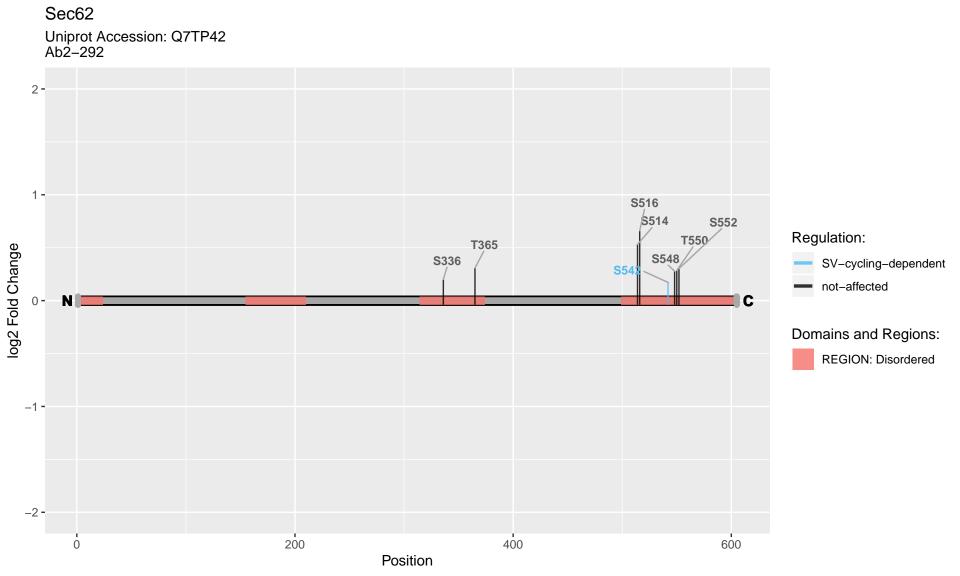


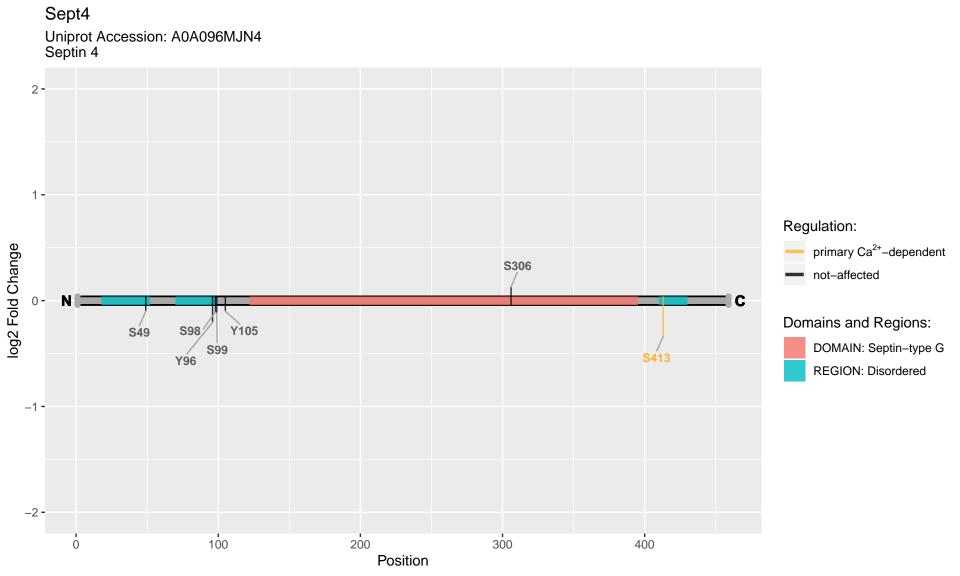


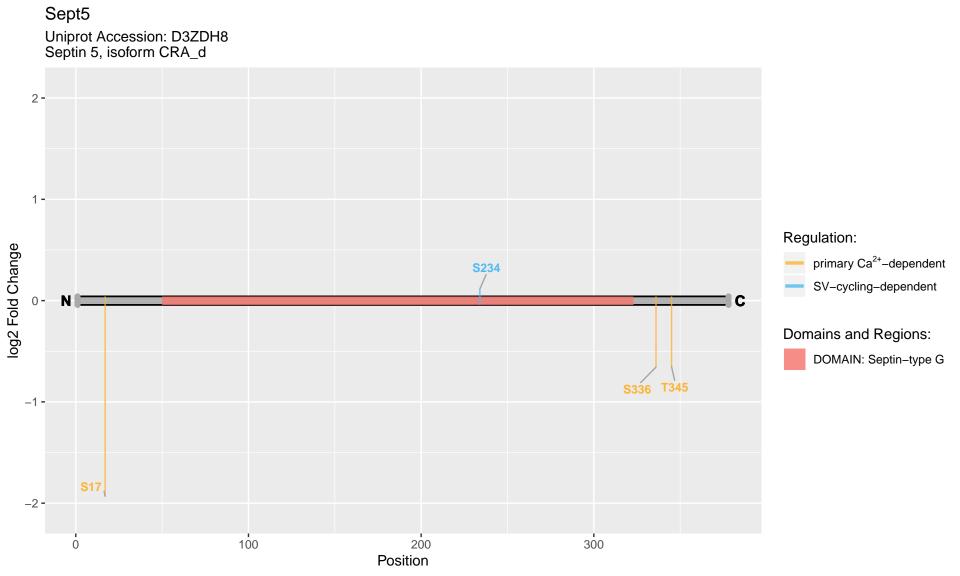


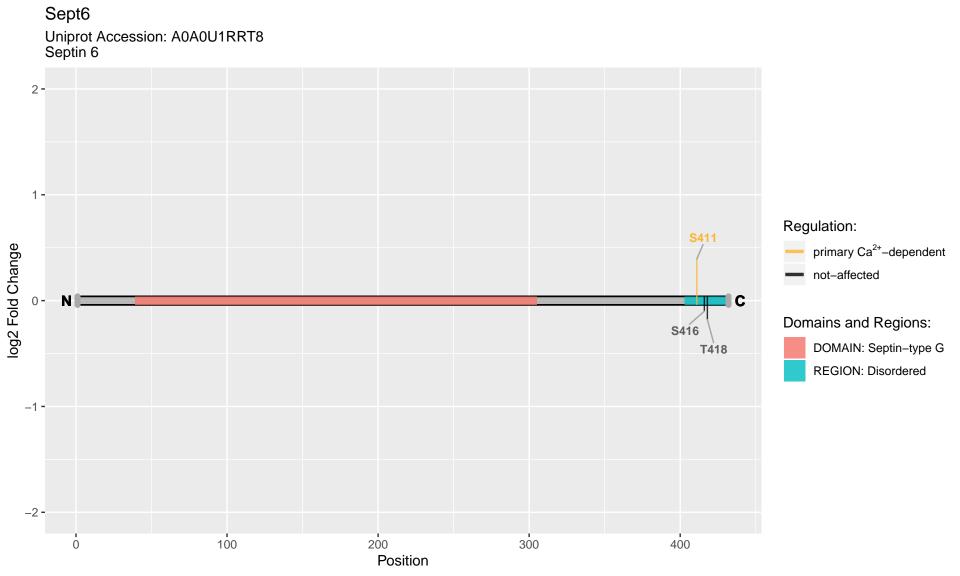


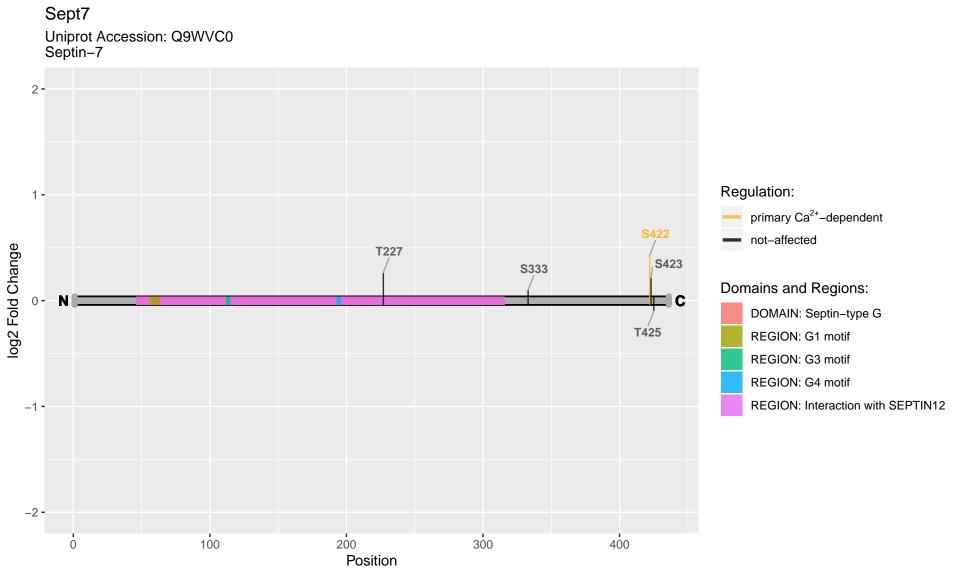


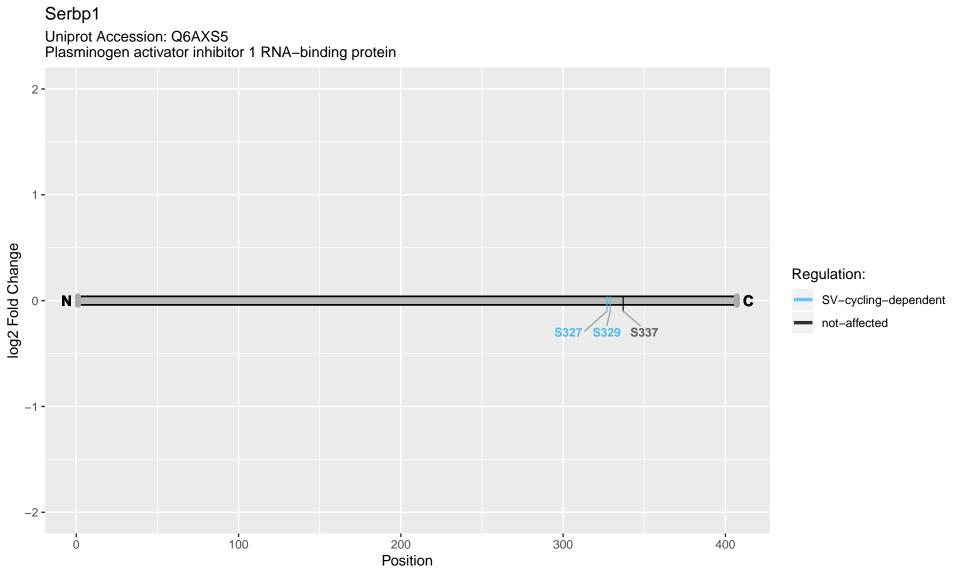


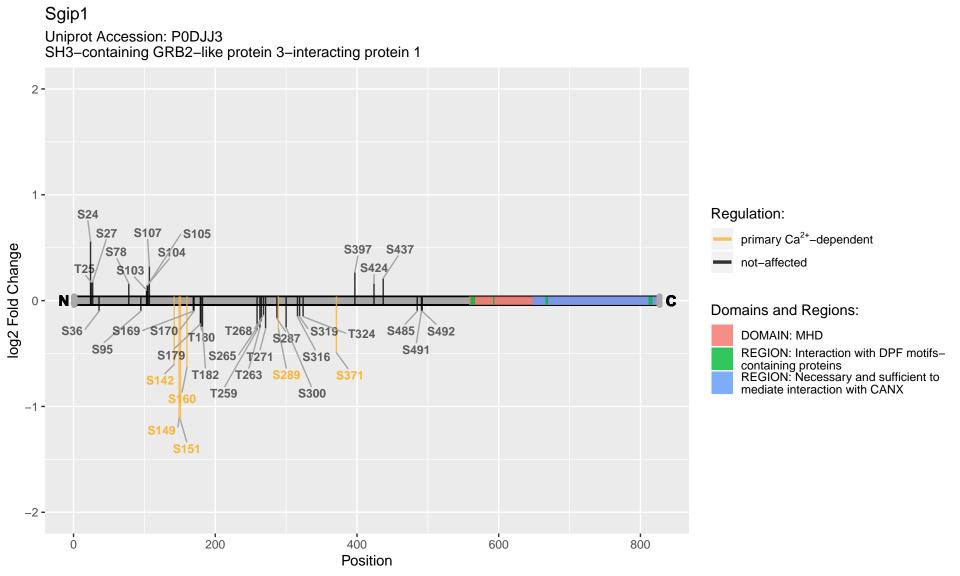


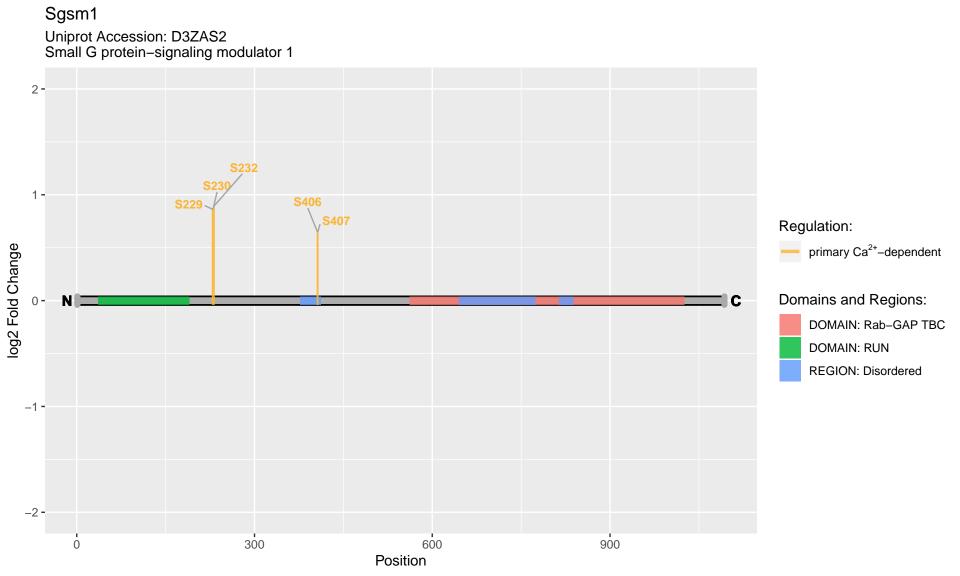


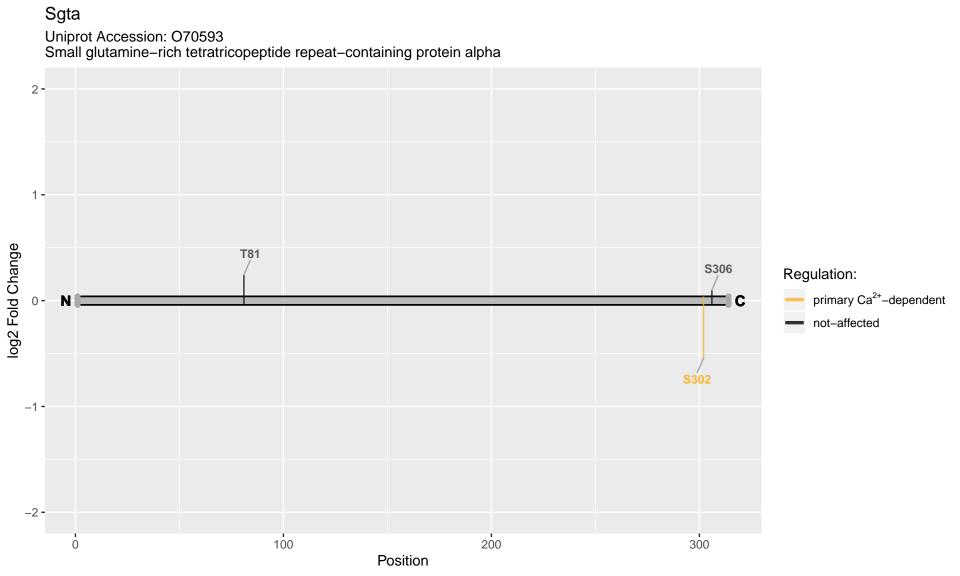


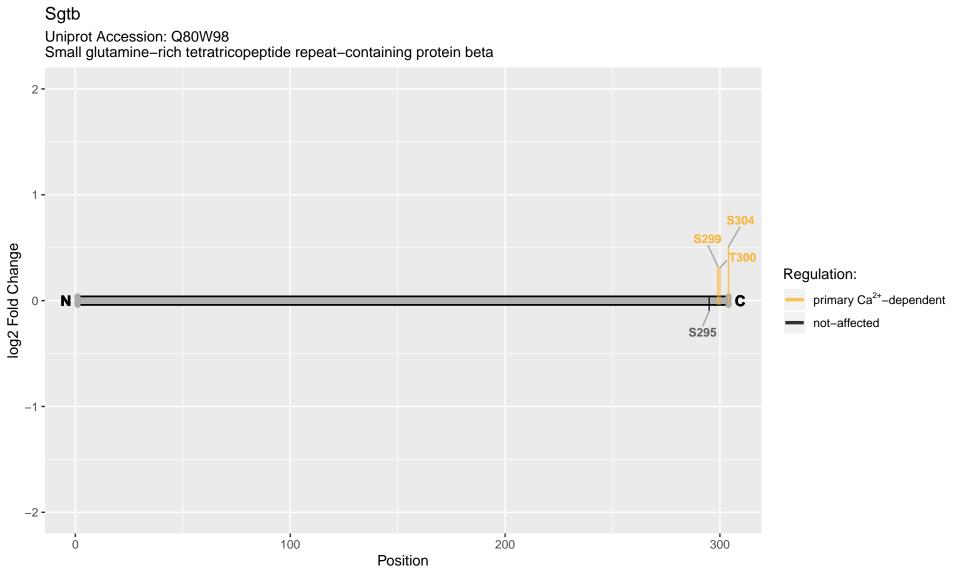


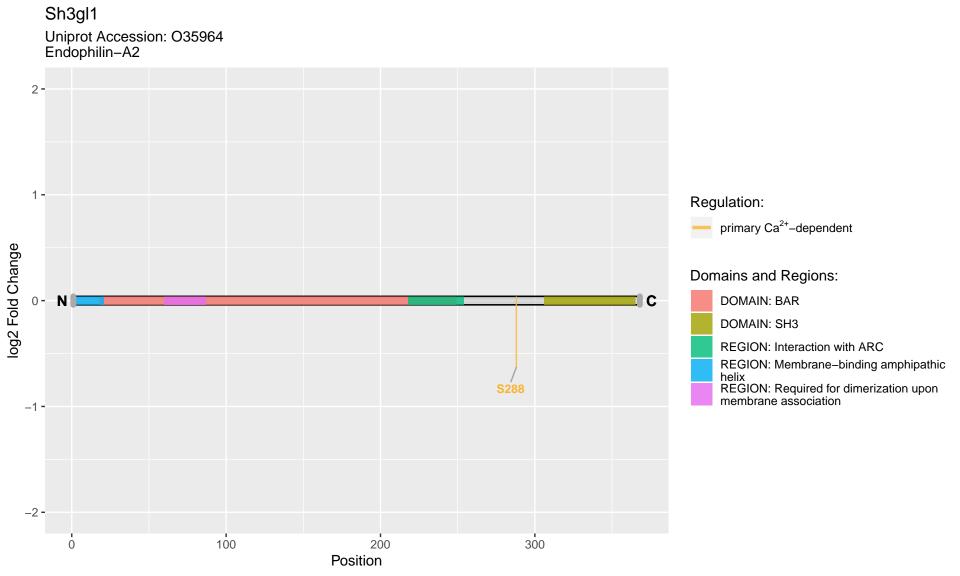


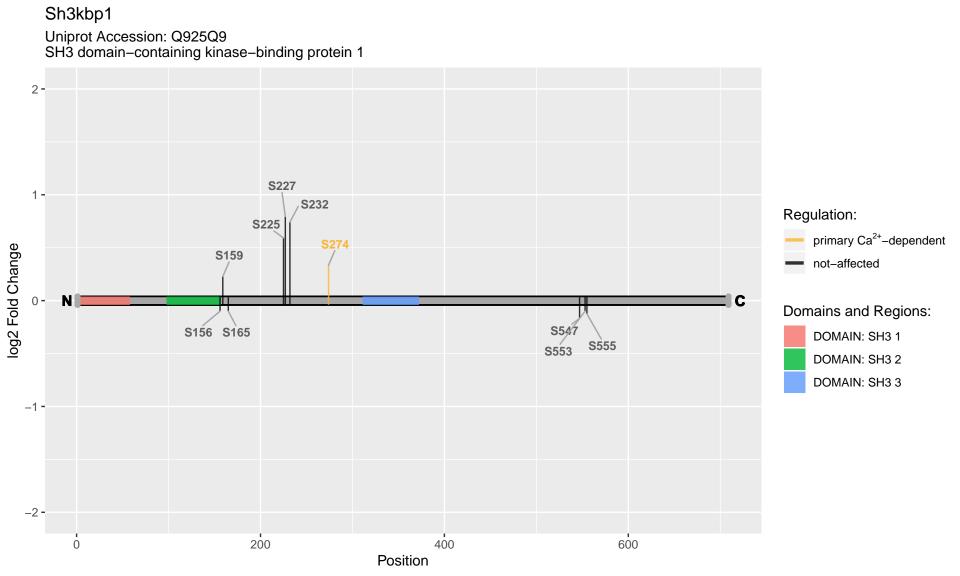


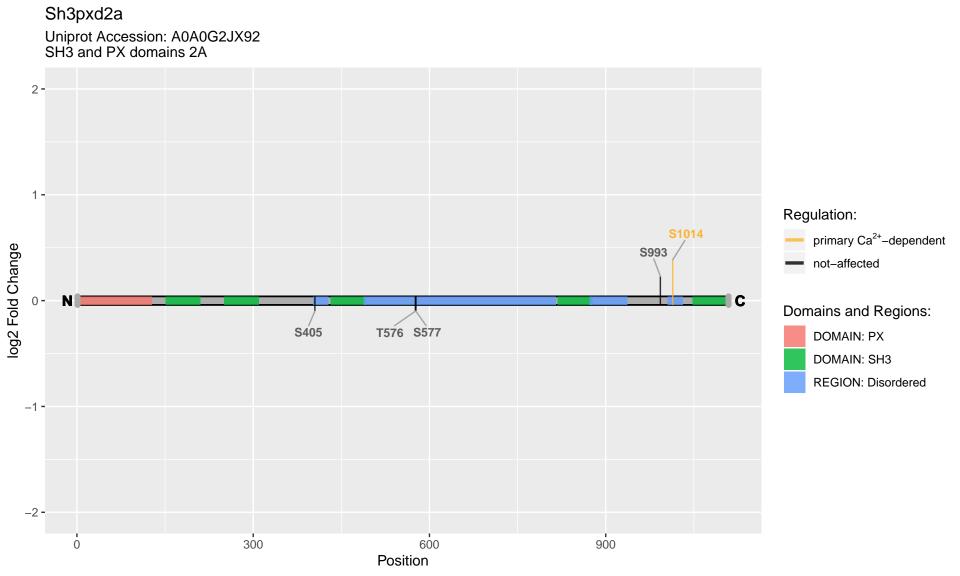


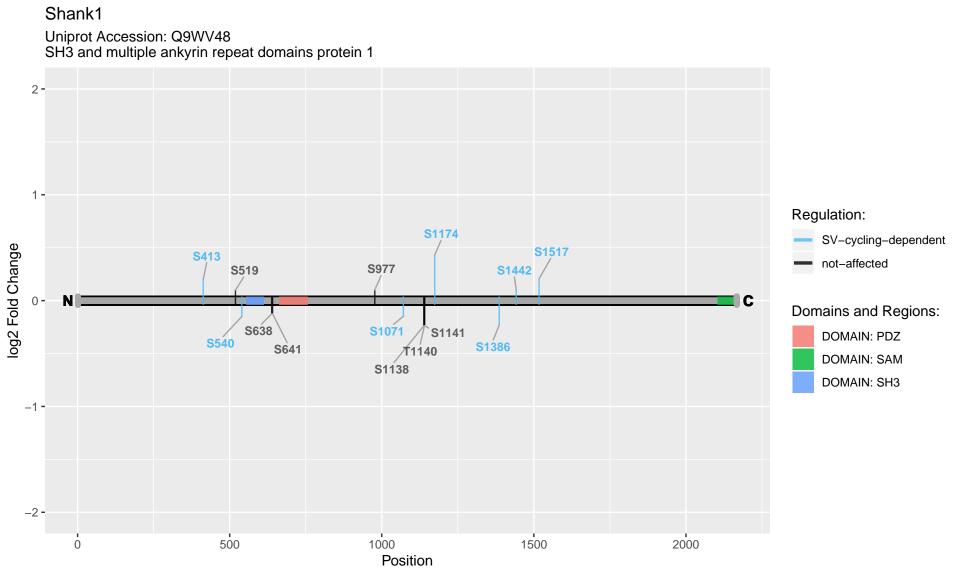


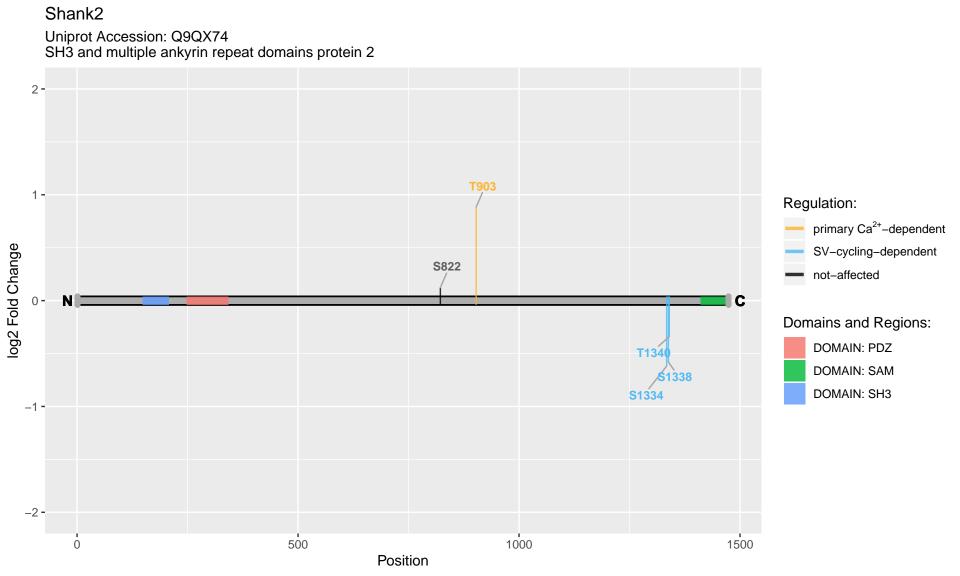


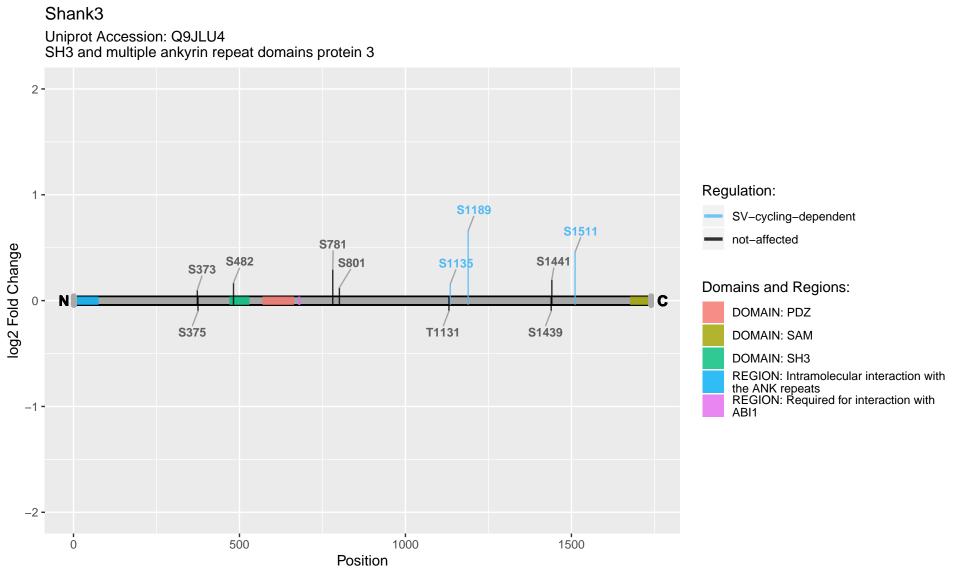


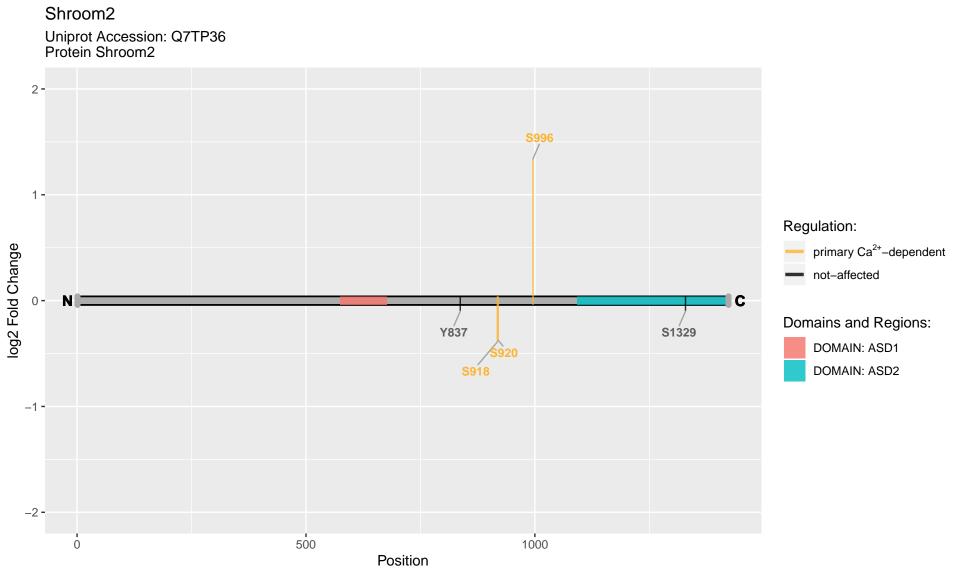


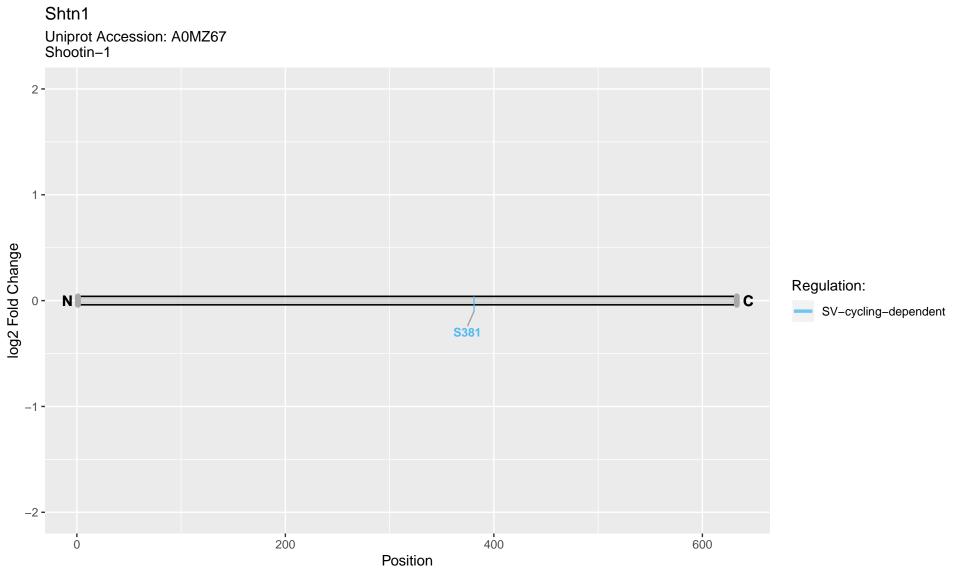






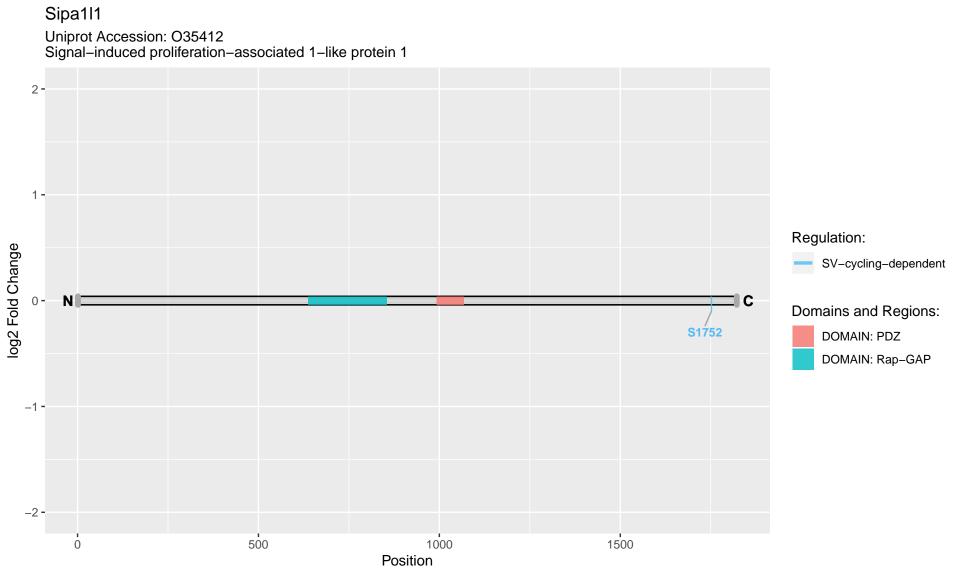


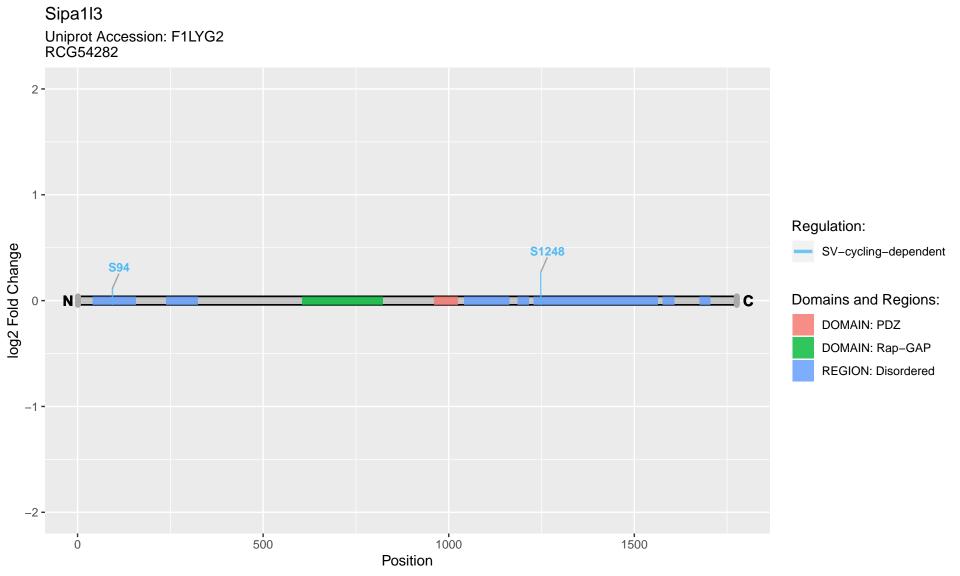


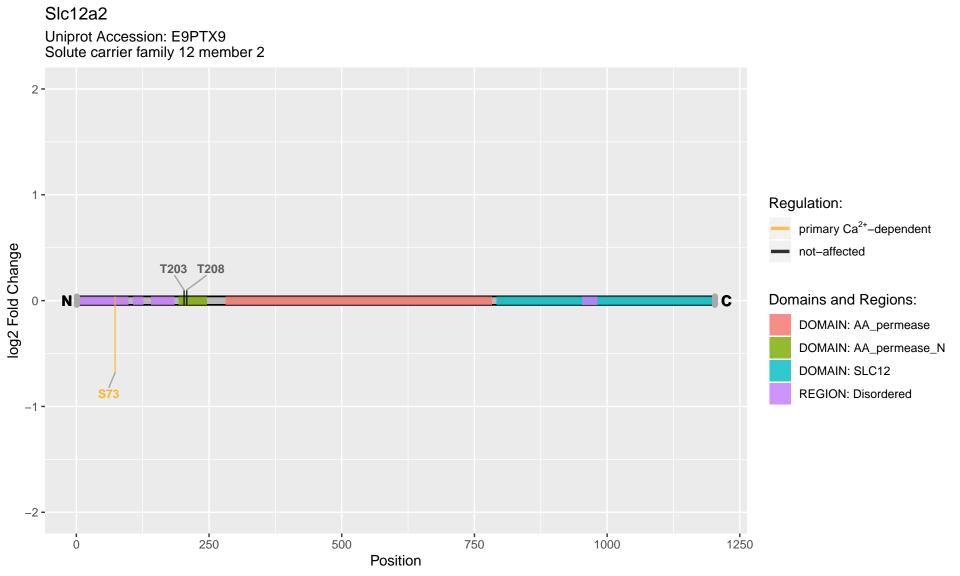


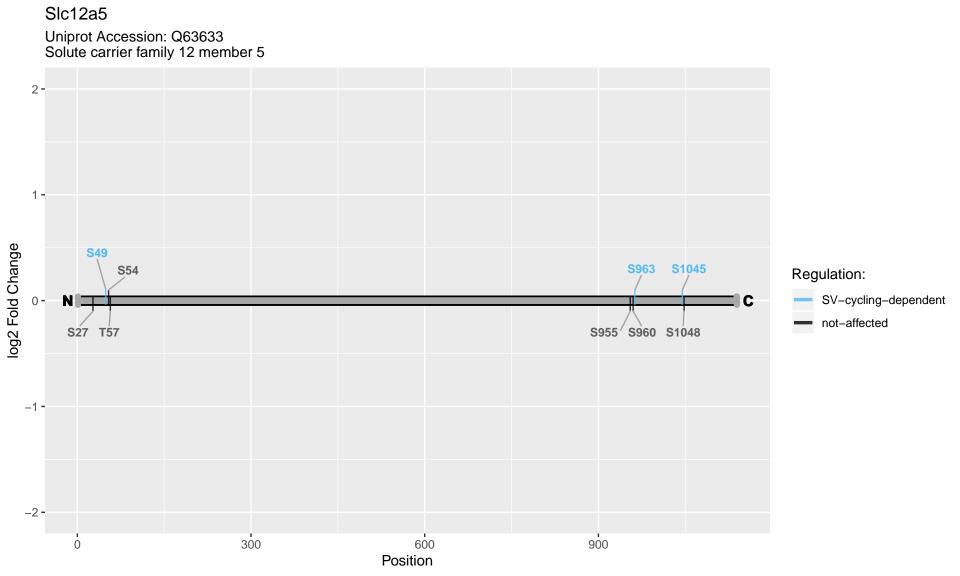
Sipa1I1 Uniprot Accession: A0A0G2KAW2 Signal-induced proliferation-associated 1 like 1, isoform CRA_b 2 -**S1192** 1 -Regulation: primary Ca²⁺-dependent **S288** log2 Fold Change SV-cycling-dependent S1564 **S1249** not-affected Domains and Regions: S1626 S1712 \$211 S208 DOMAIN: PDZ S210 DOMAIN: Rap-GAP **S1384 REGION: Disordered** -1 **-**-2 **-**500 1500 1000

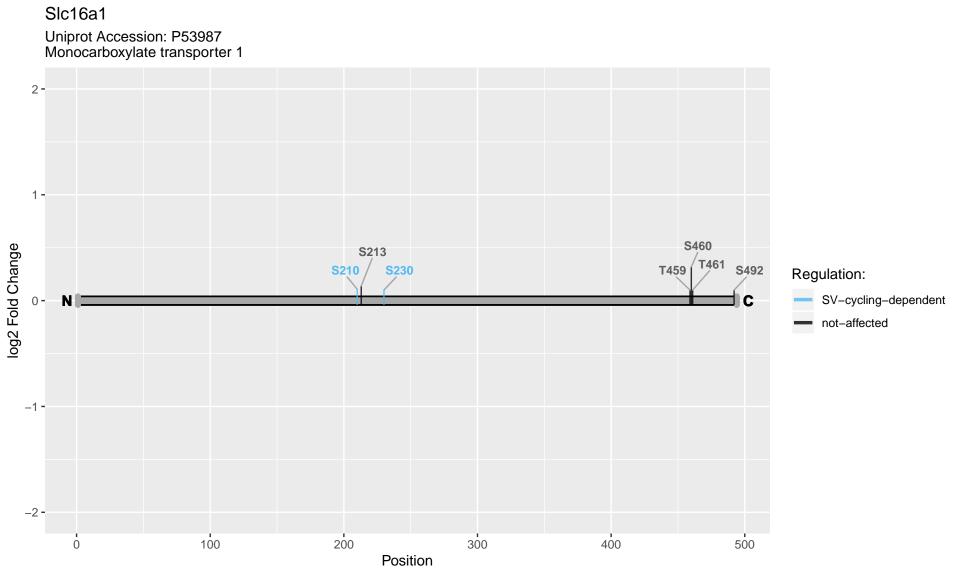
Position

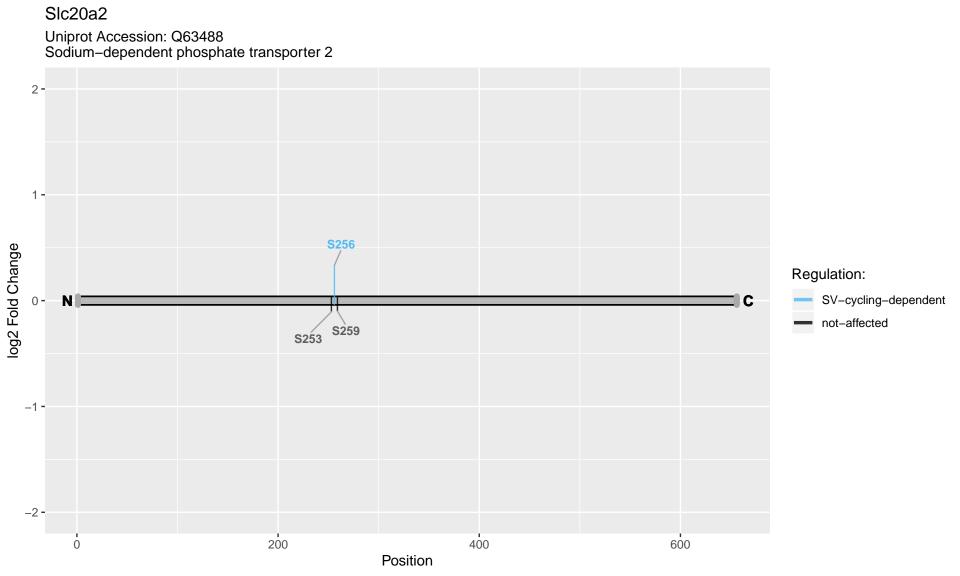


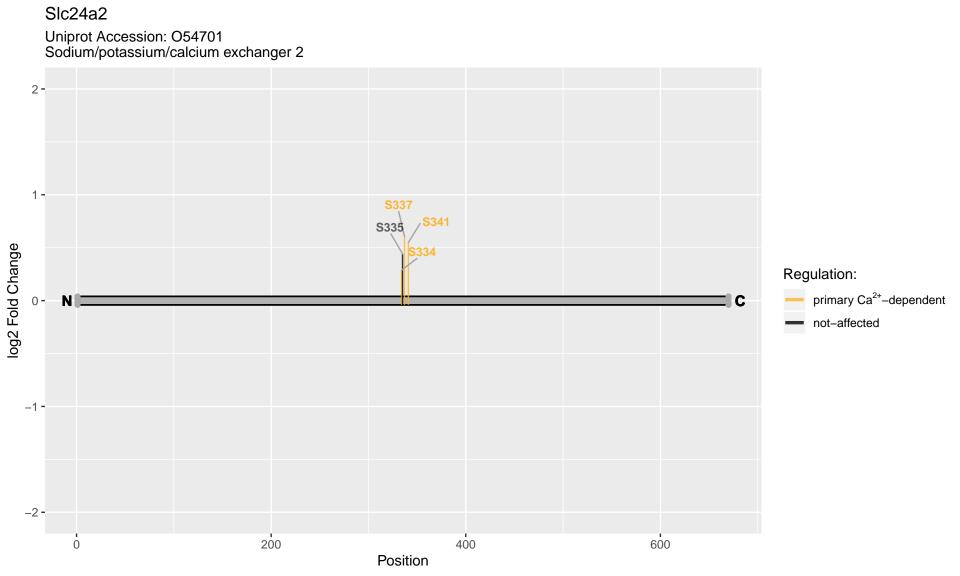


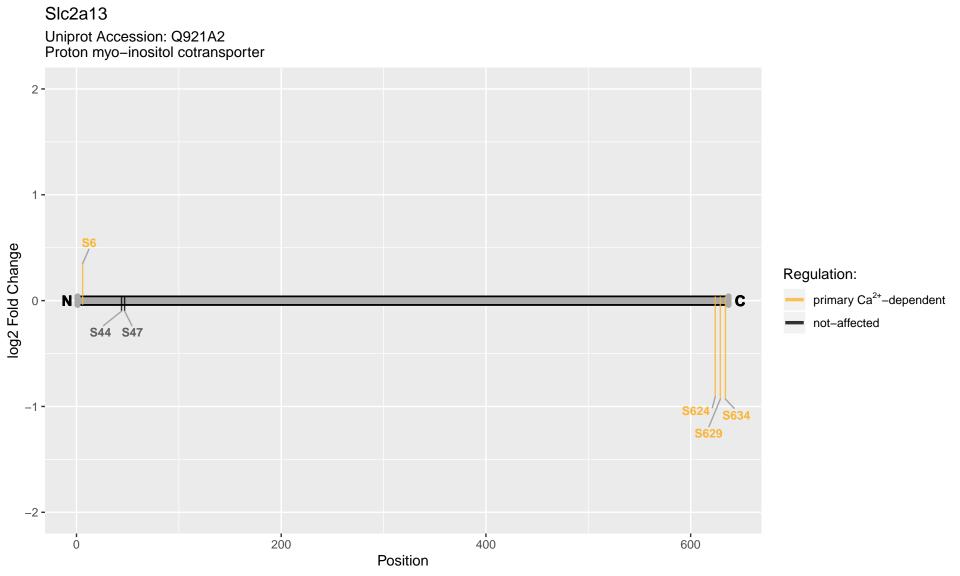


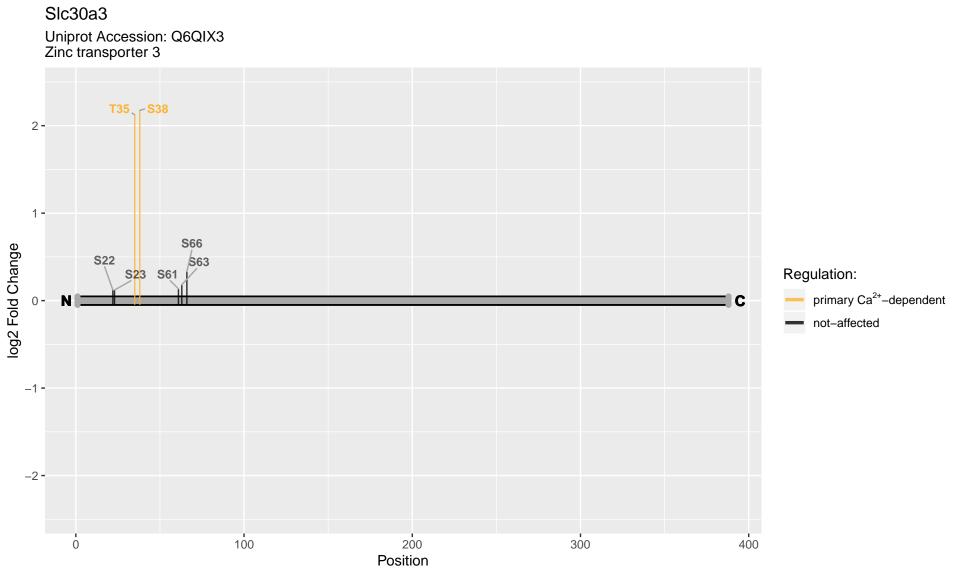


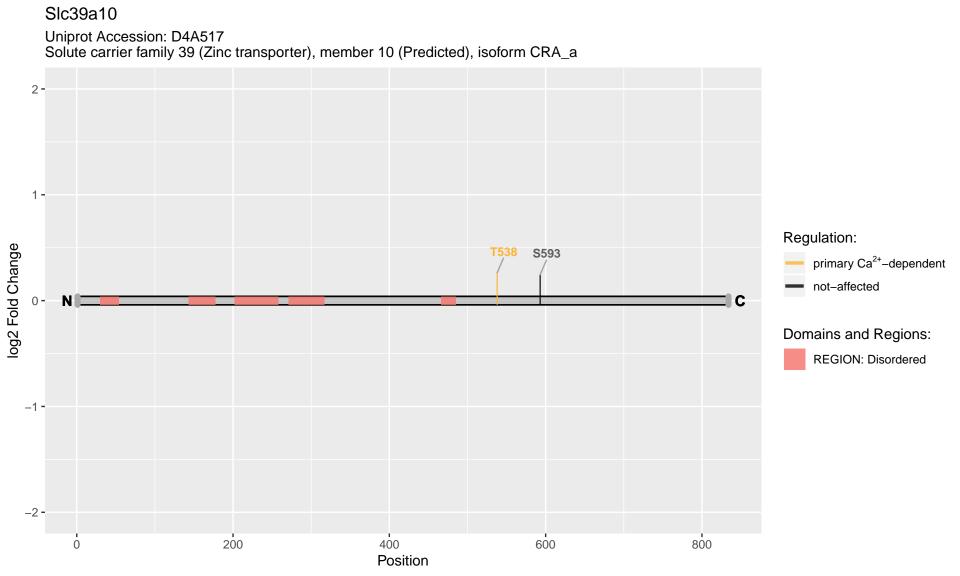


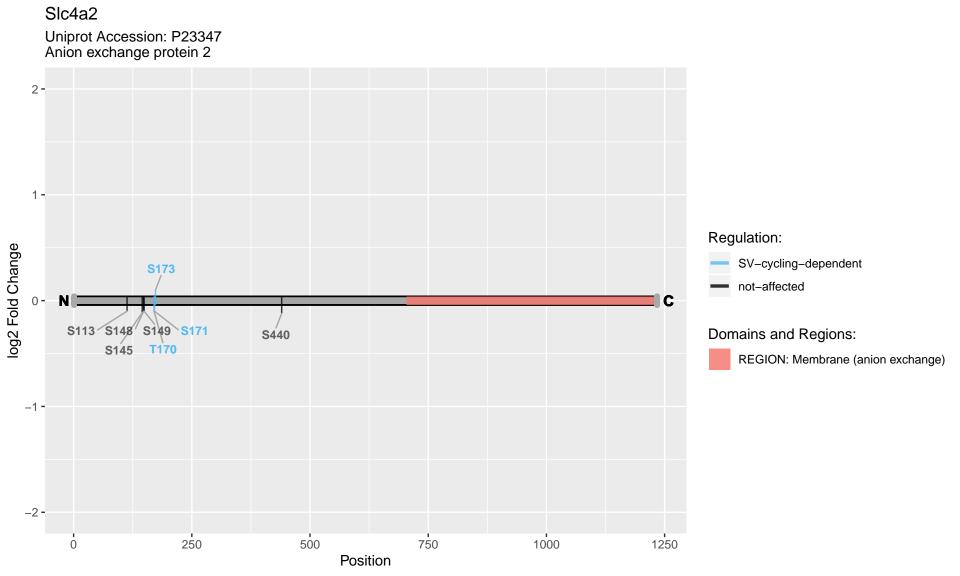




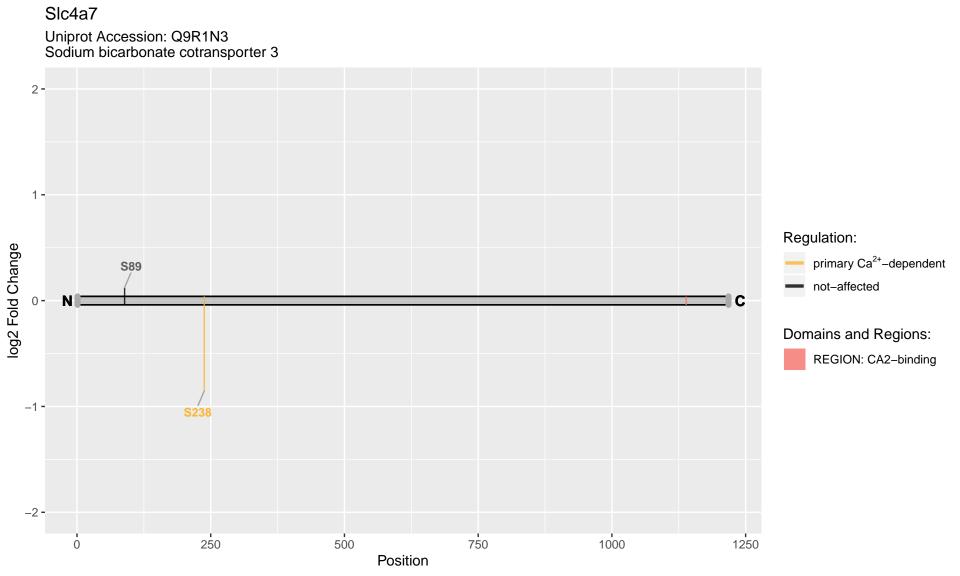


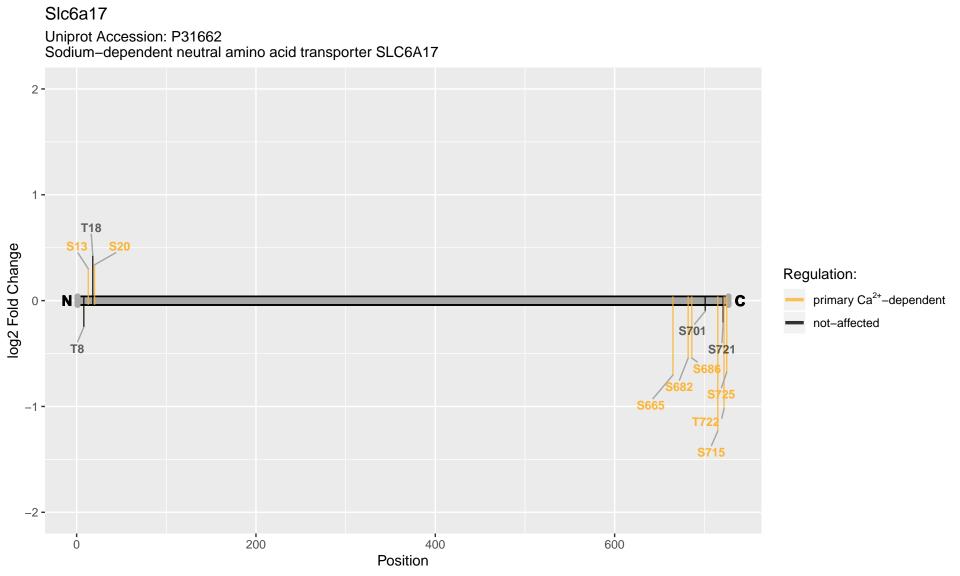


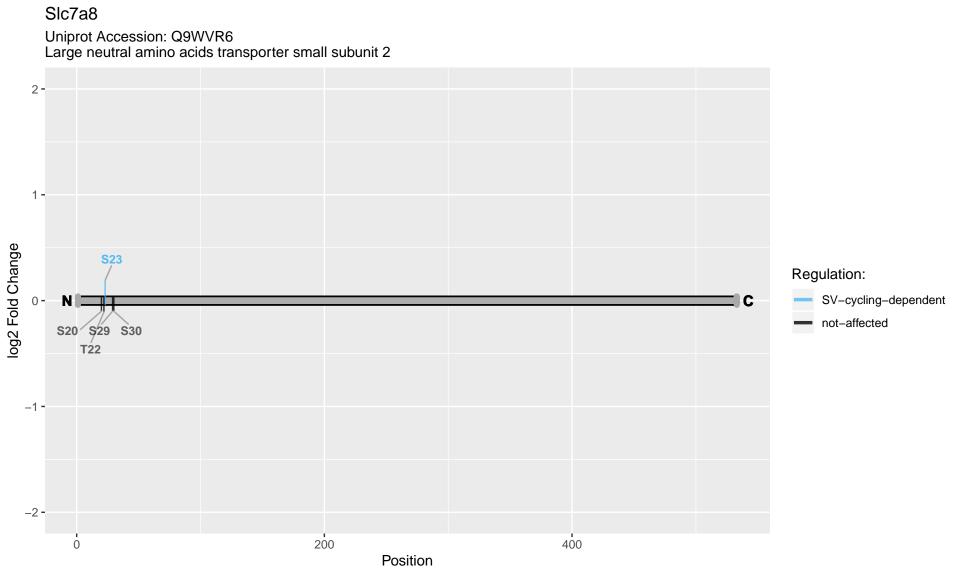


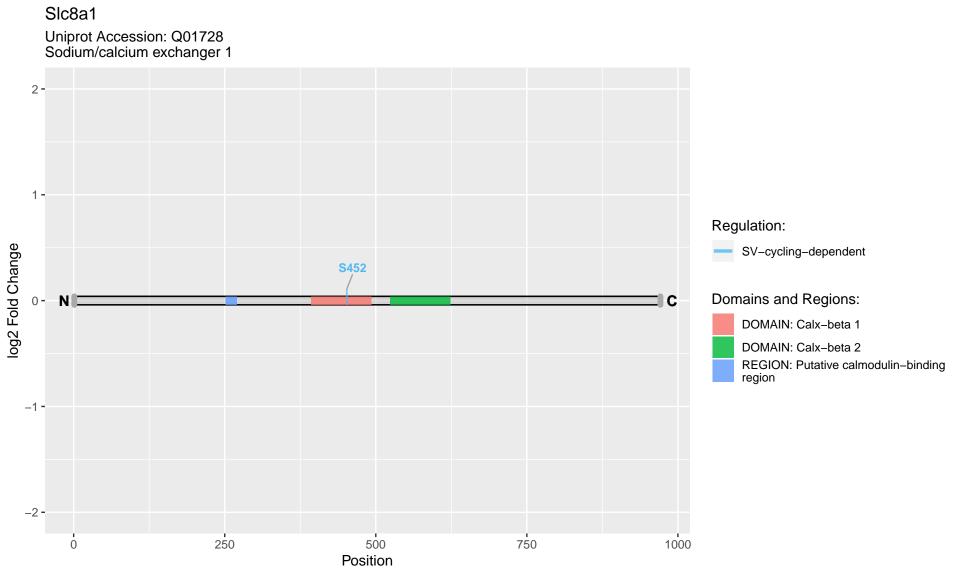


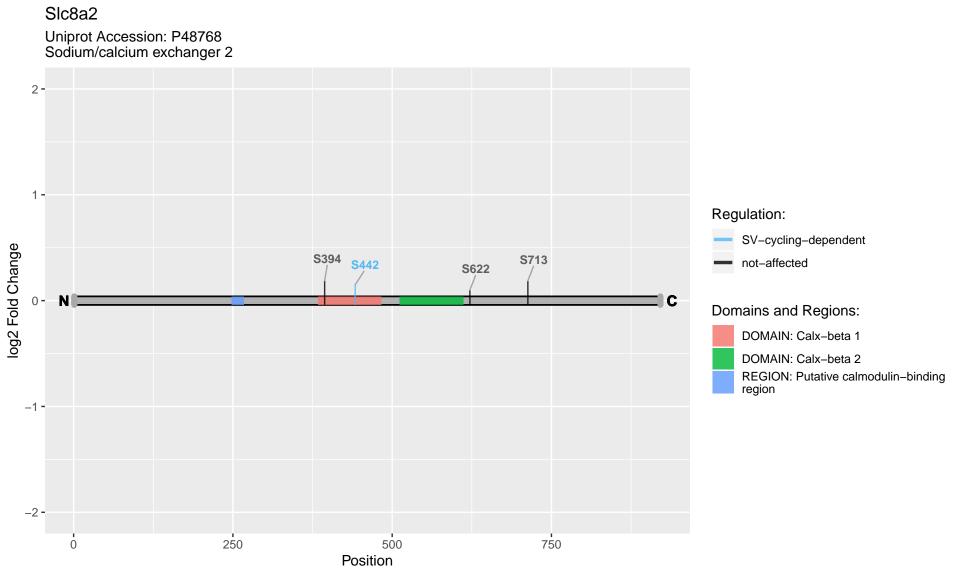
Slc4a4 Uniprot Accession: A0A0H2UHB7 Anion exchange protein 2 -1 -Regulation: primary Ca²⁺-dependent S1034 log2 Fold Change SV-cycling-dependent S1031 S1045 not-affected Domains and Regions: S1060 S1069 **S228** DOMAIN: Band_3_cyto S1065 **S237** DOMAIN: HCO3_cotransp **S260** T259 **REGION: Disordered** -1 **-S261** -2 **-**300 600 900 Position

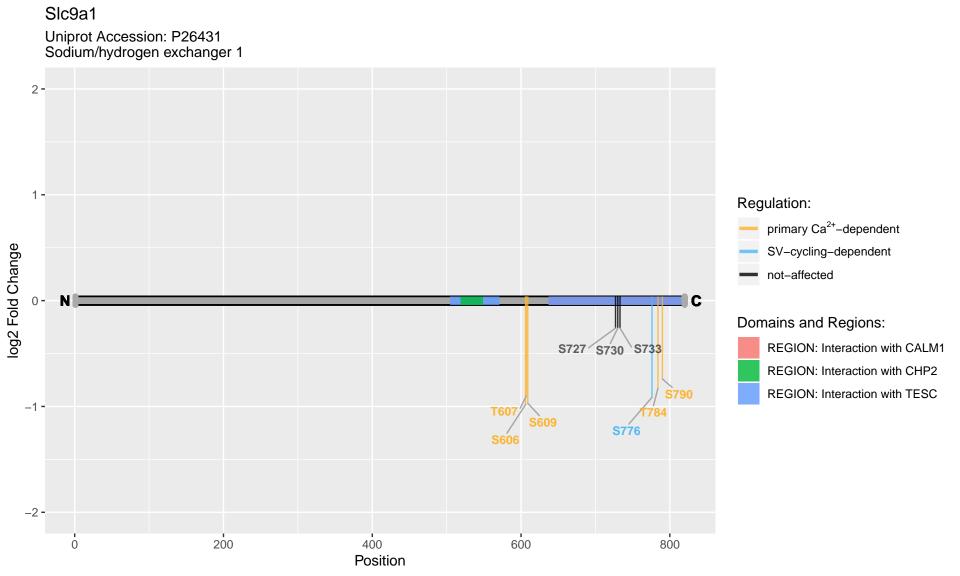


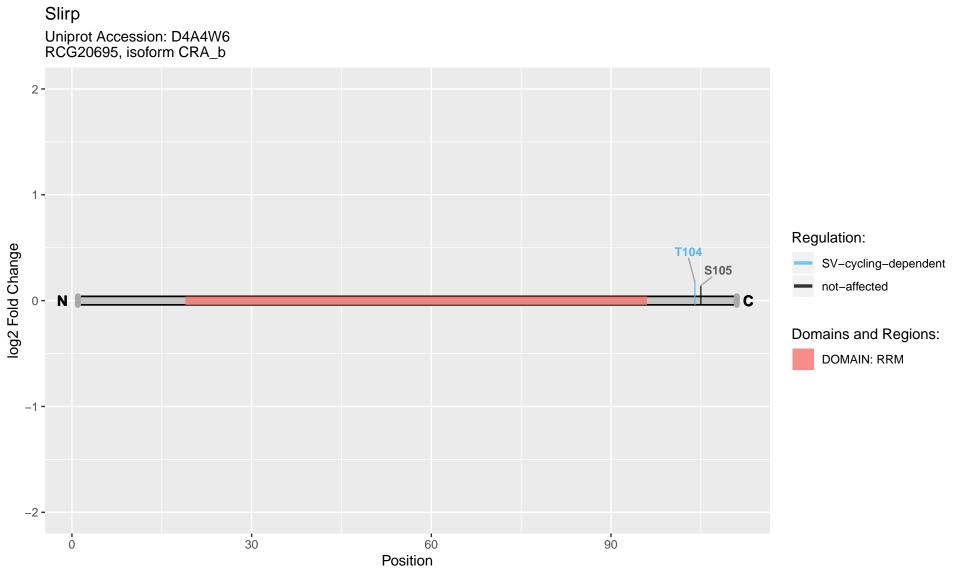


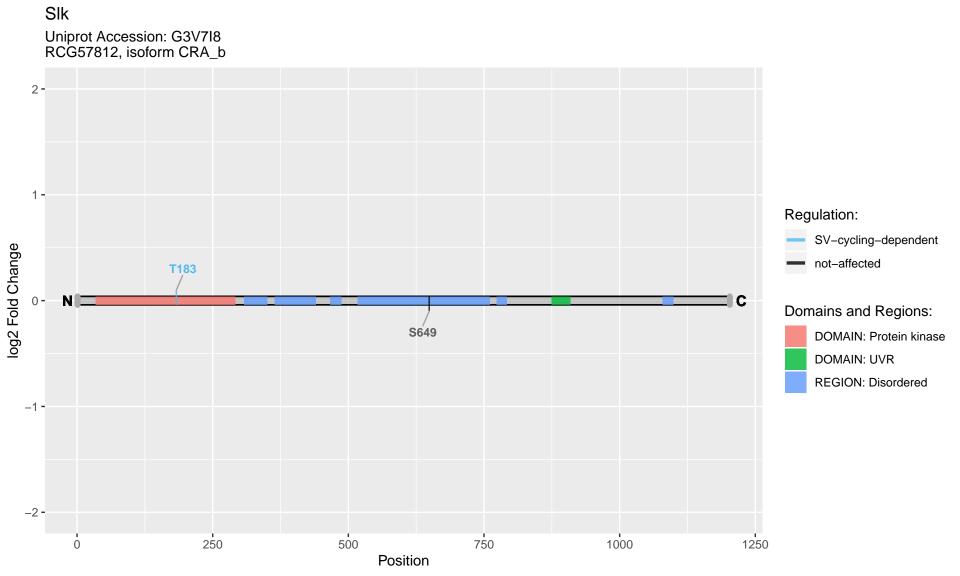


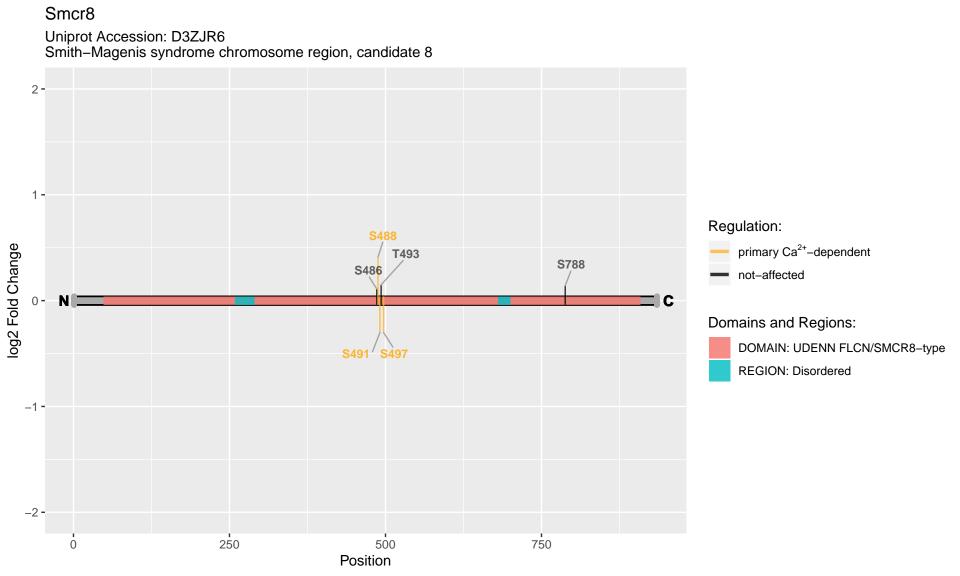


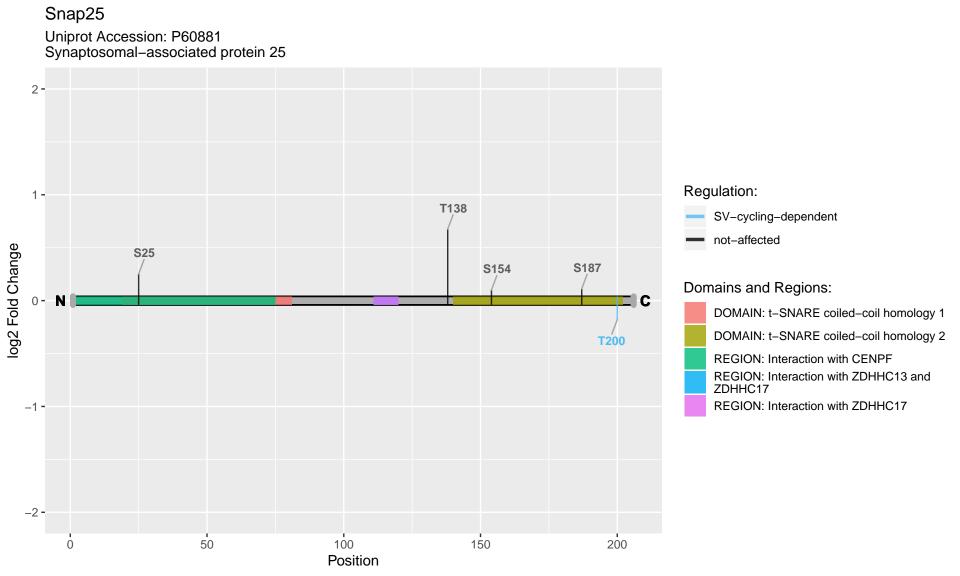




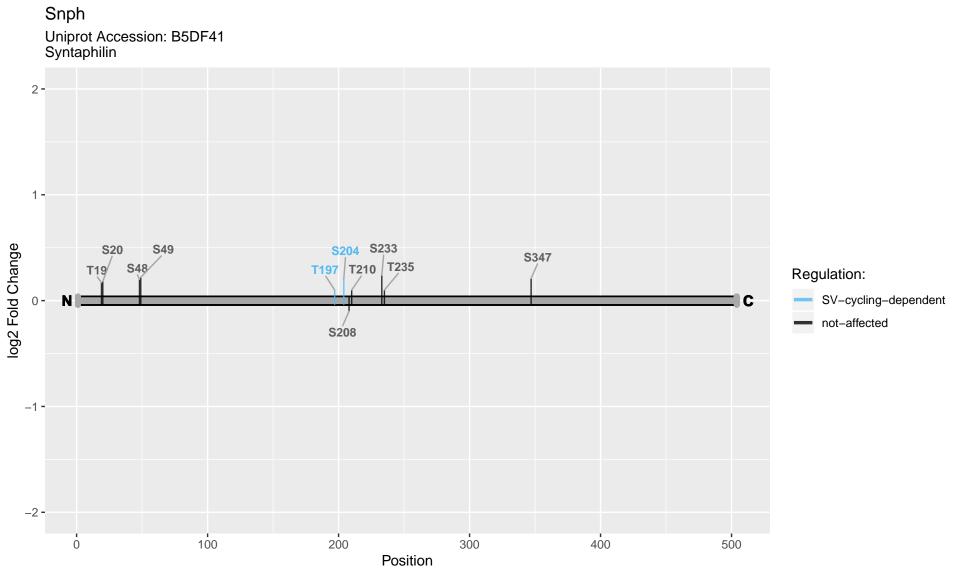


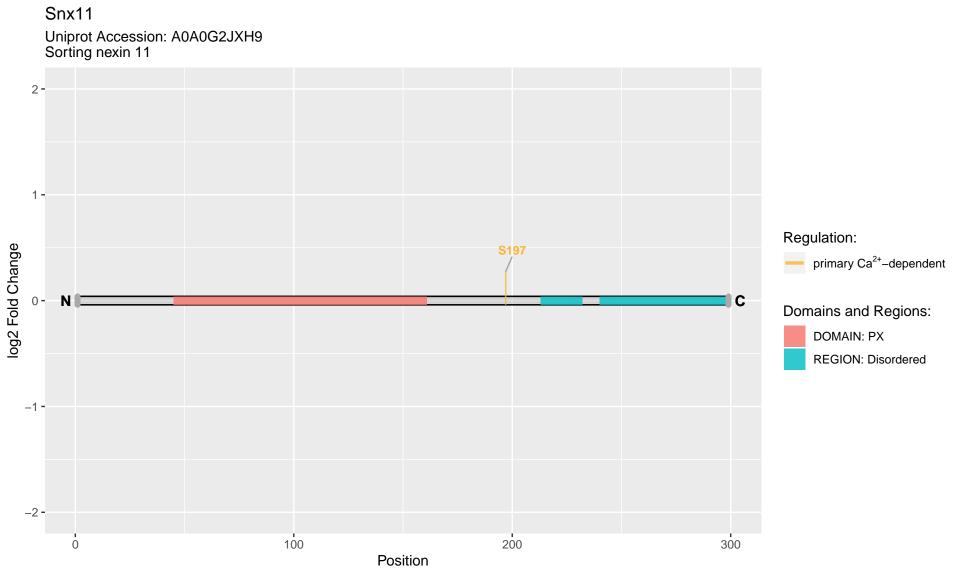


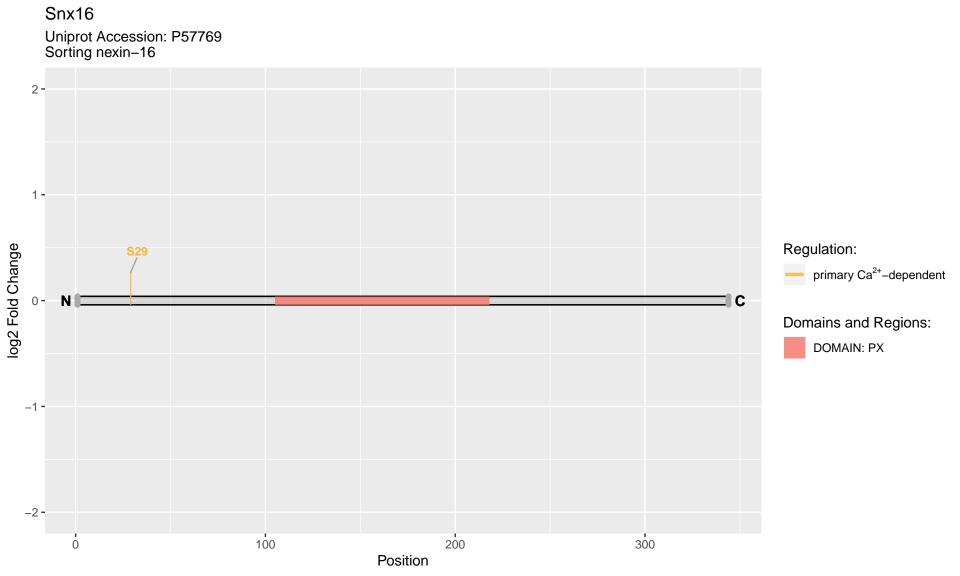


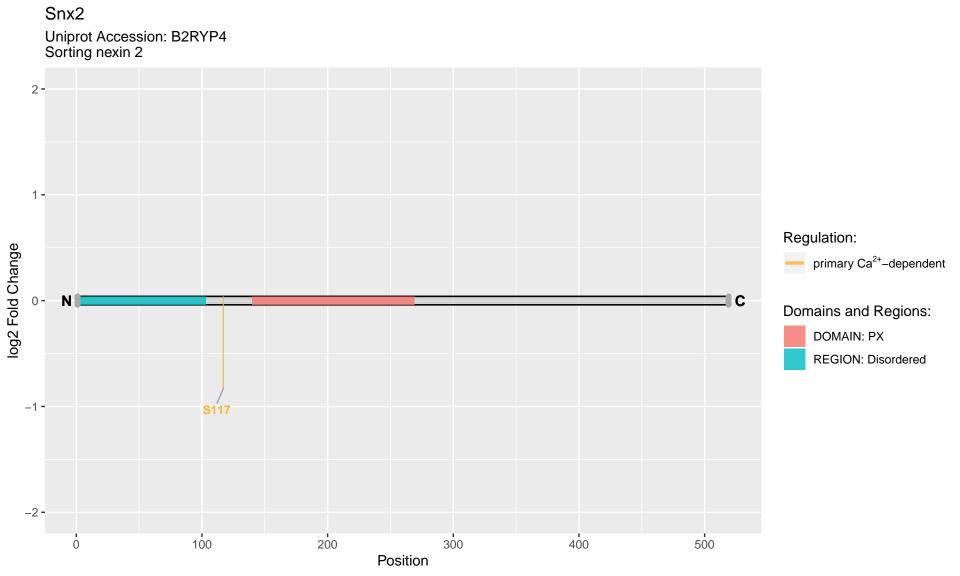


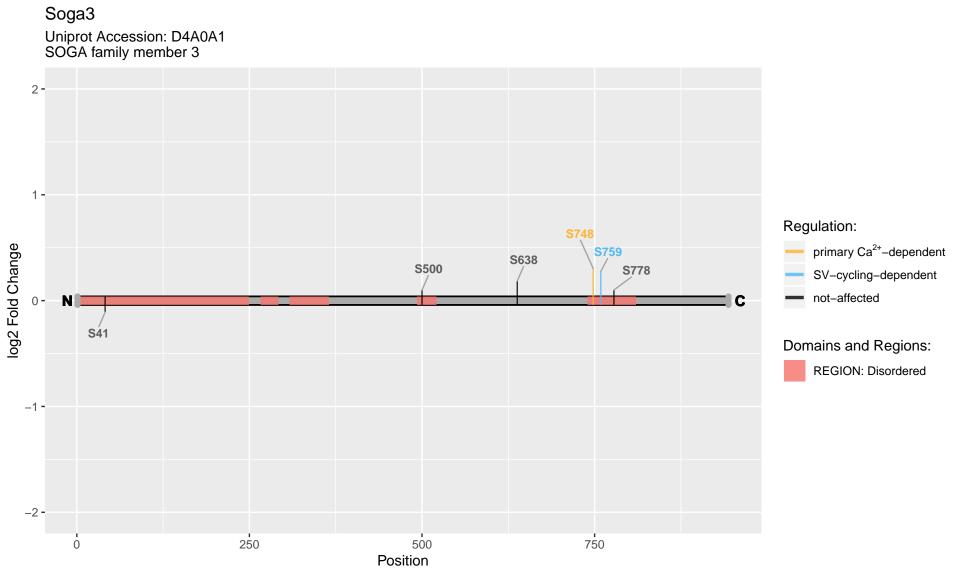
Snap91 Uniprot Accession: A0A0G2K0B6 Clathrin coat assembly protein AP180 2 -1 -Regulation: primary Ca²⁺-dependent **S323** log2 Fold Change **S595** SV-cycling-dependent S298 (S333 not-affected S294 S304 S303 T310 T315 S754 Domains and Regions: S314 S311 T308 DOMAIN: ENTH T307 **REGION: Disordered** -1 **-**-2 **-**250 750 500 Position



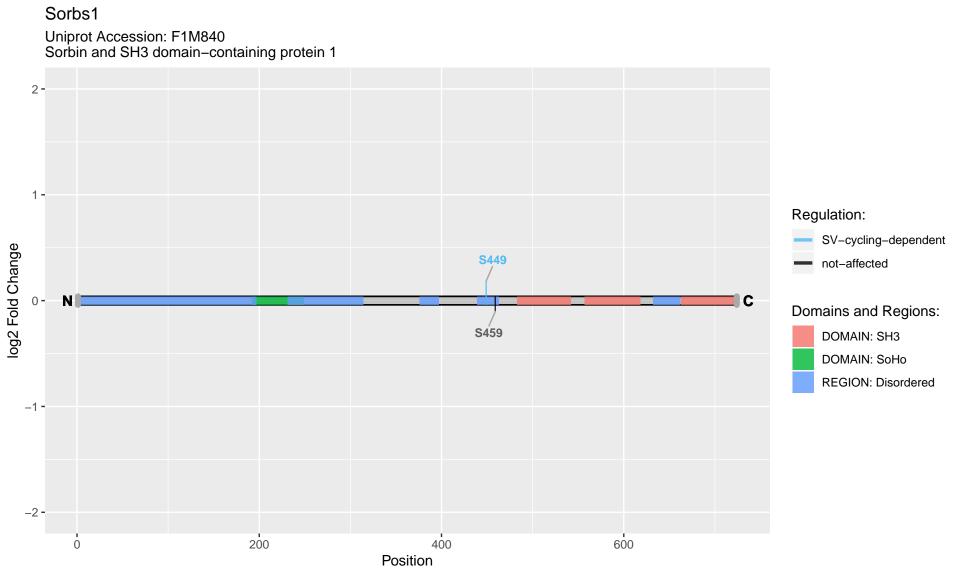


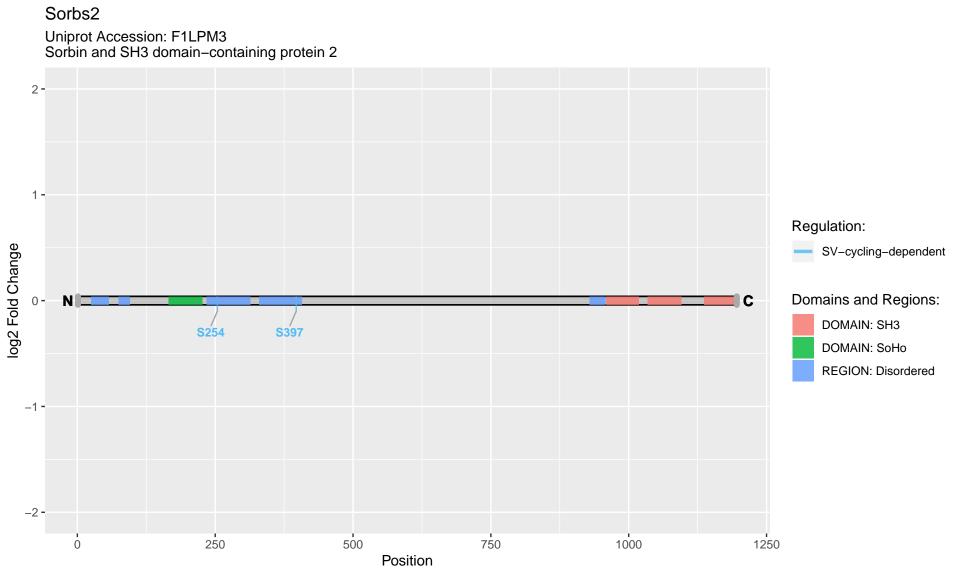


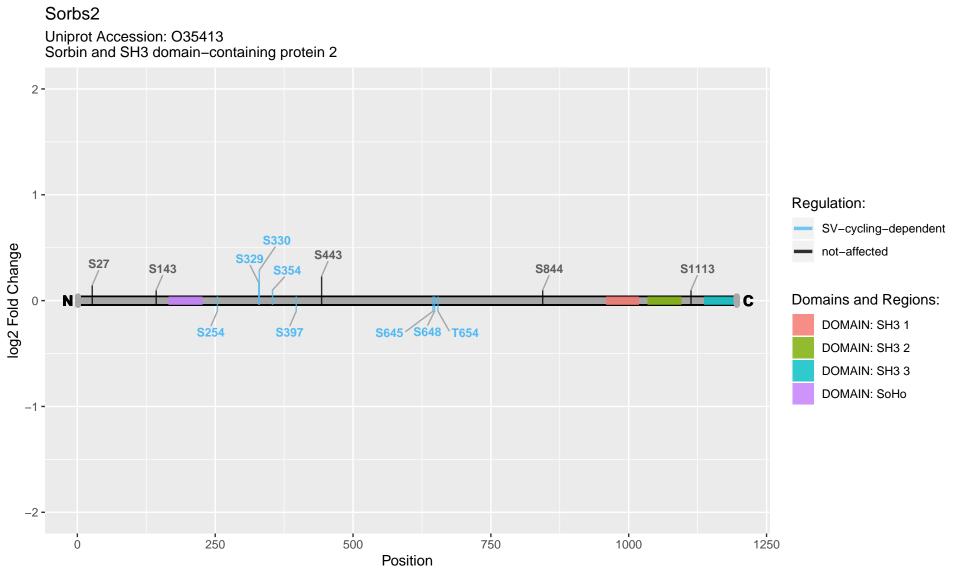


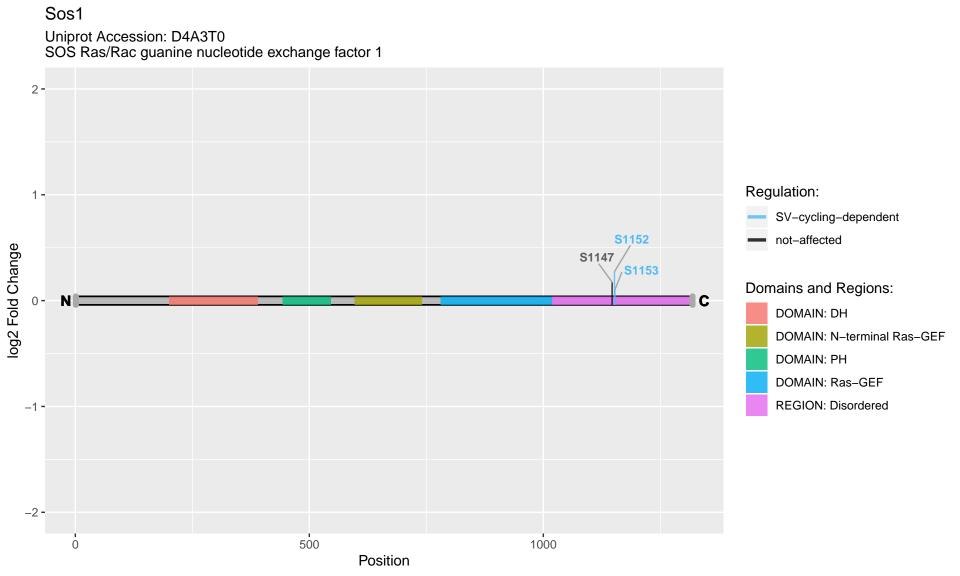


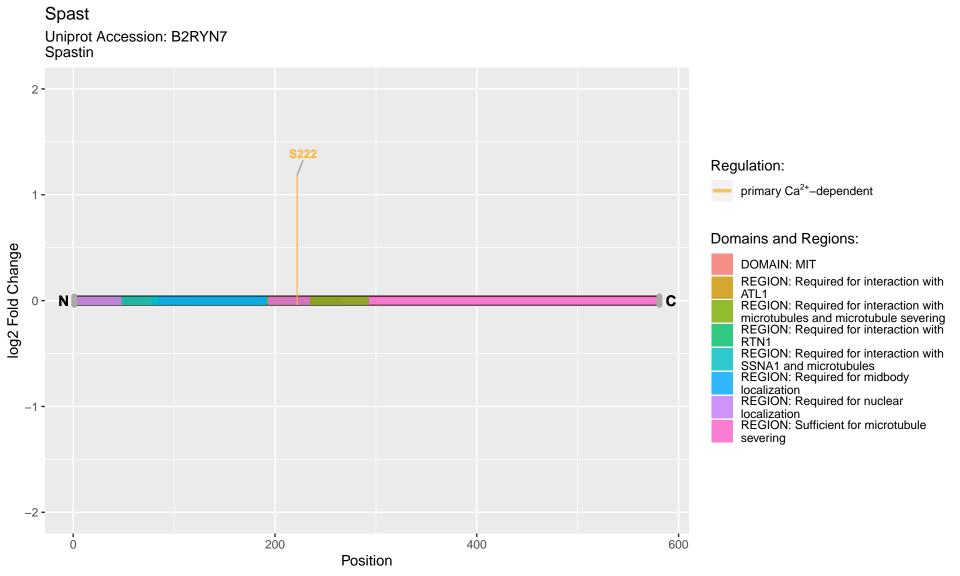
Sorbs1 Uniprot Accession: F1M820 Sorbin and SH3 domain—containing protein 1 2 -**S256** 1 -Regulation: primary Ca²⁺-dependent log2 Fold Change **S670** SV-cycling-dependent **S794 S470 S969 S791** not-affected C Domains and Regions: S967 DOMAIN: SH3 **S250 S62** DOMAIN: SoHo **S54 S1209 REGION: Disordered** -1 **-**-2 **-**500 1000 Position

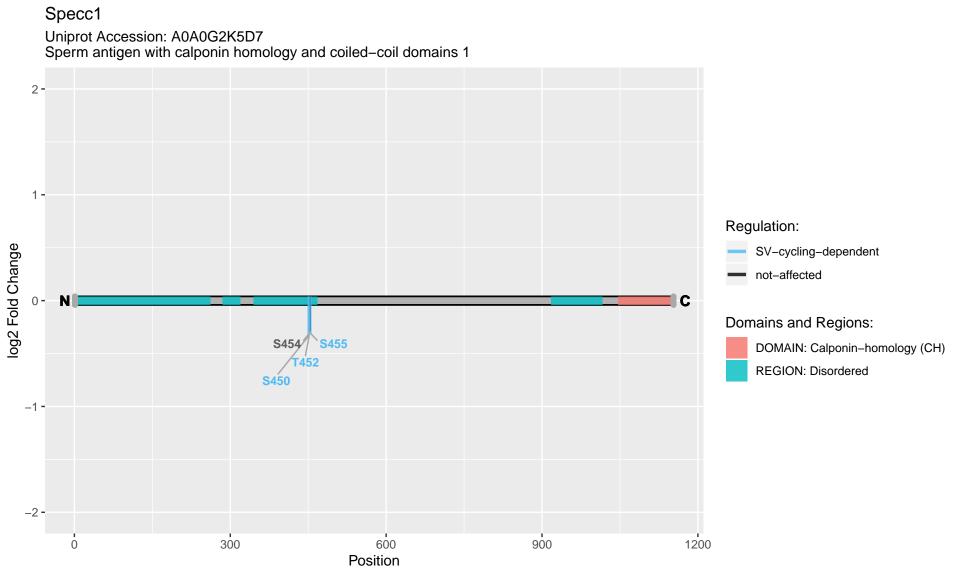


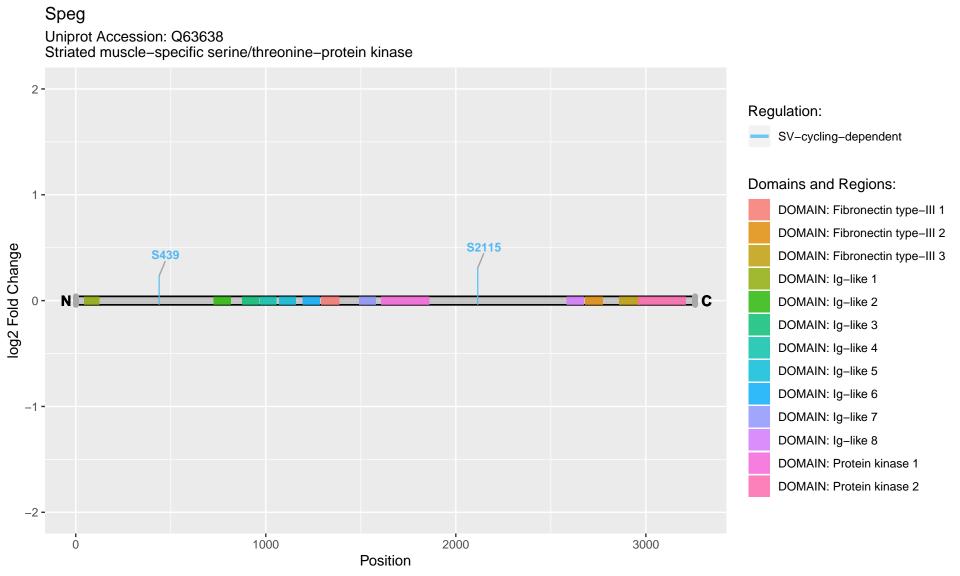


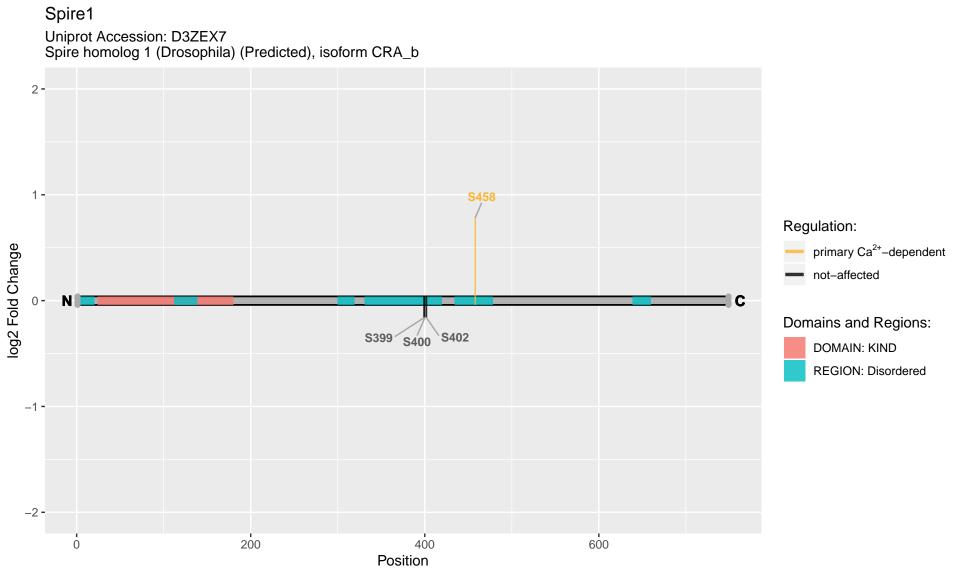


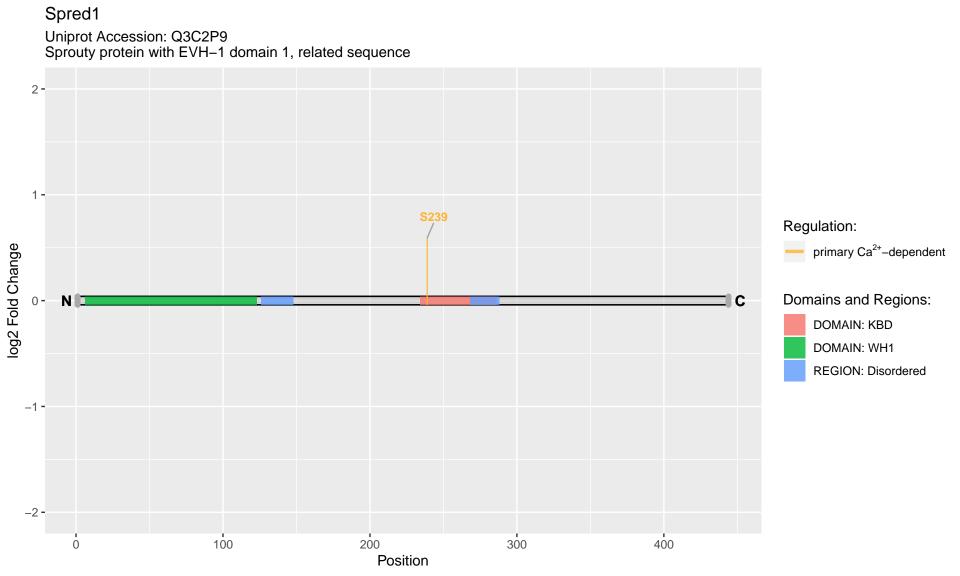


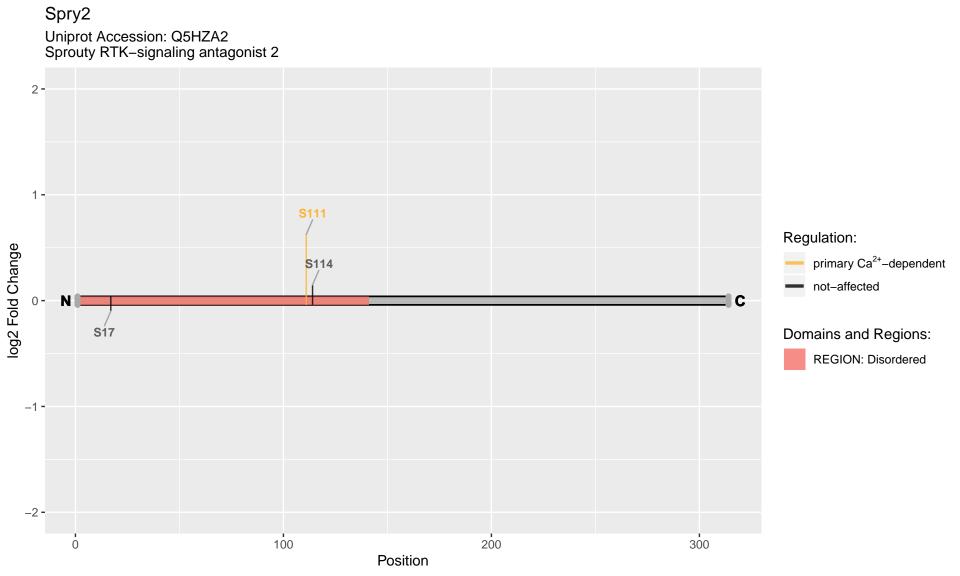


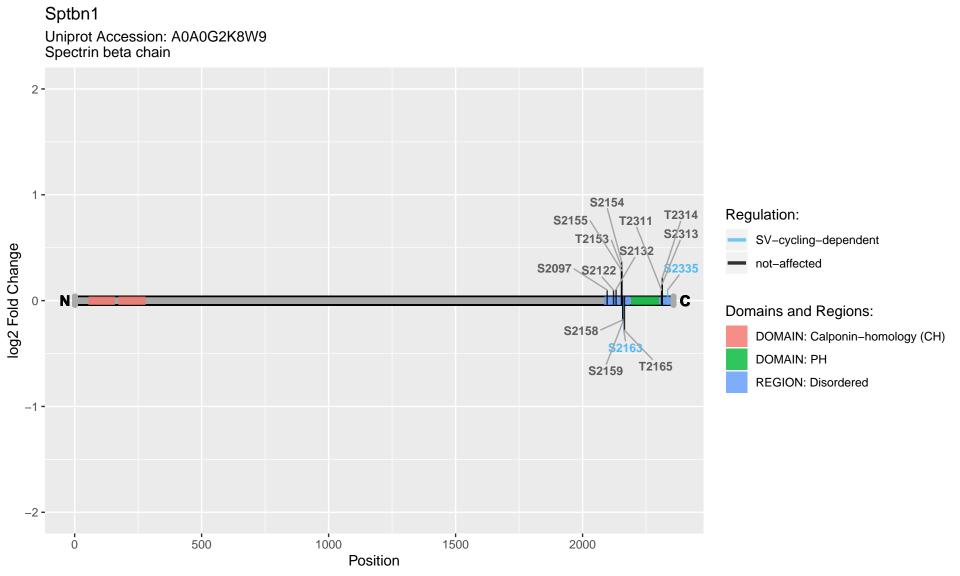


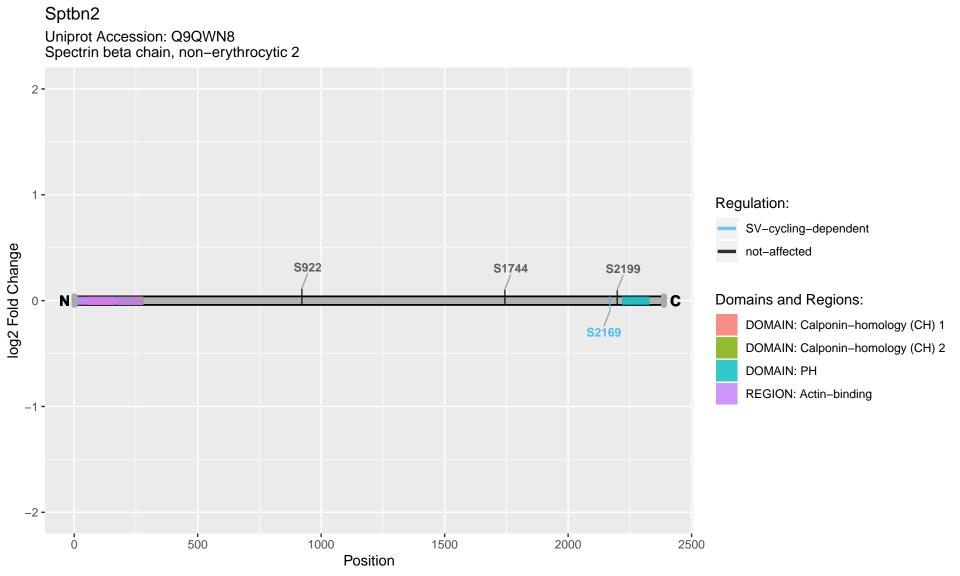


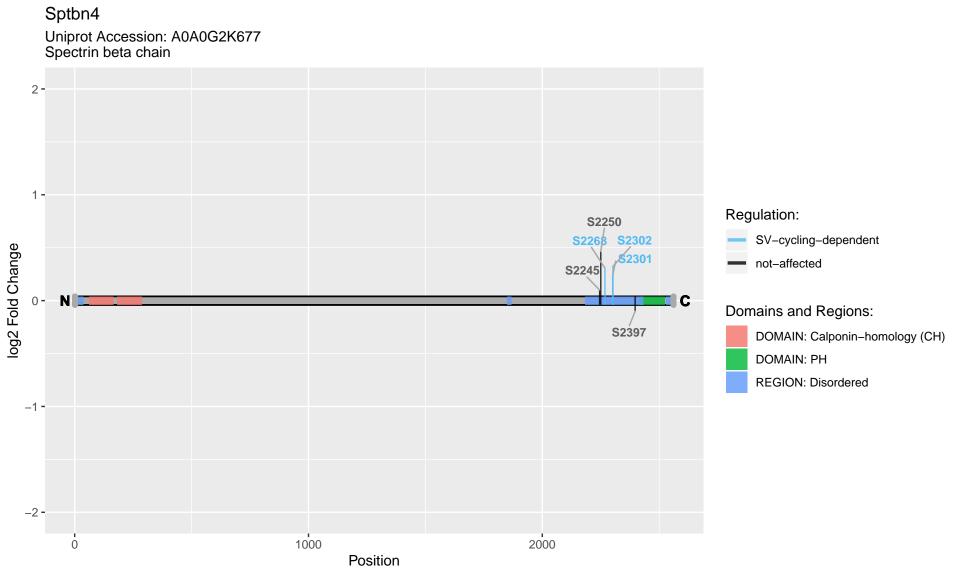


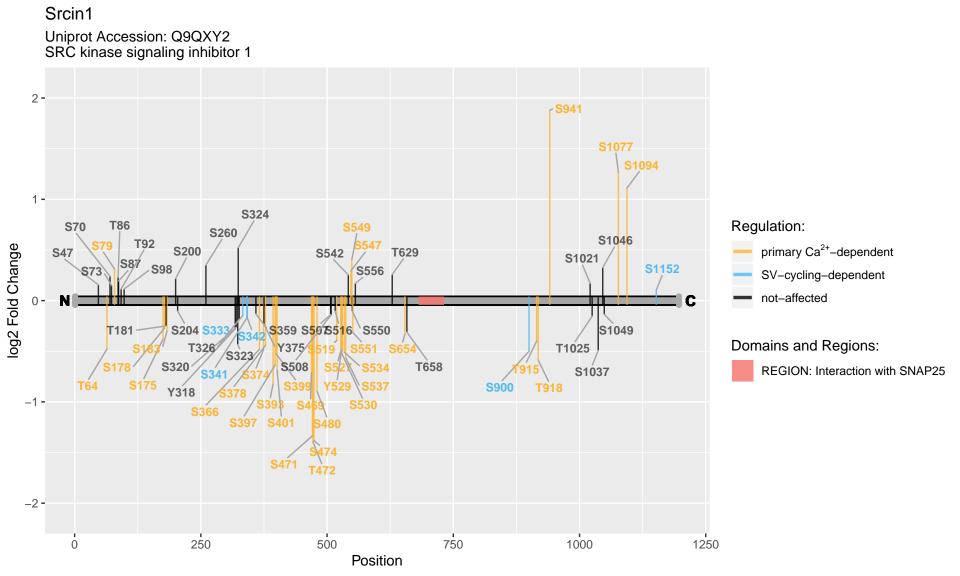


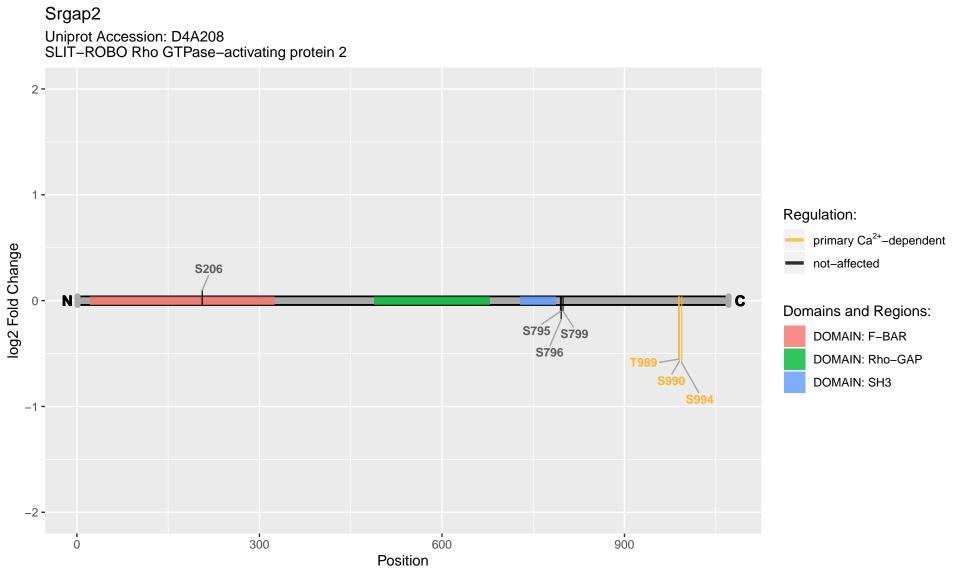


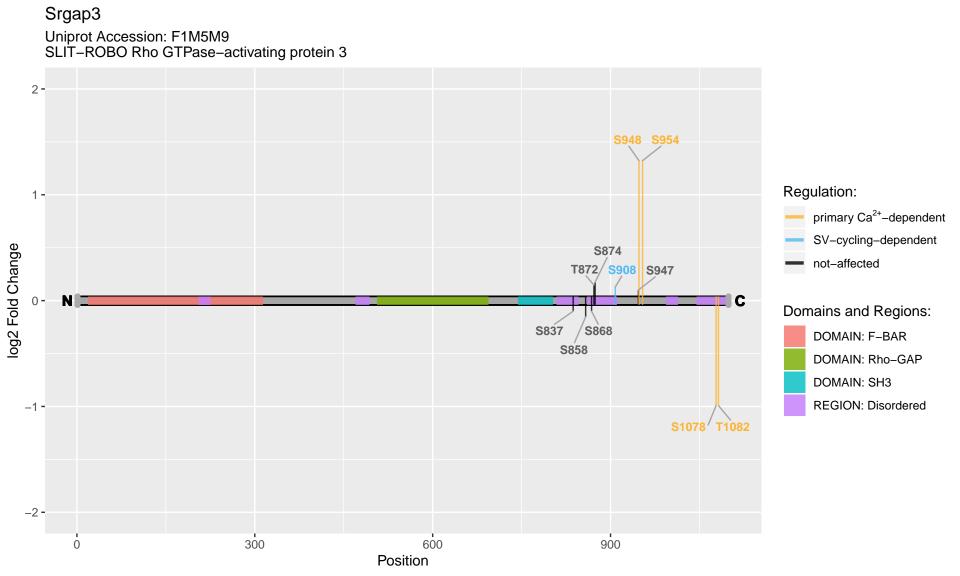


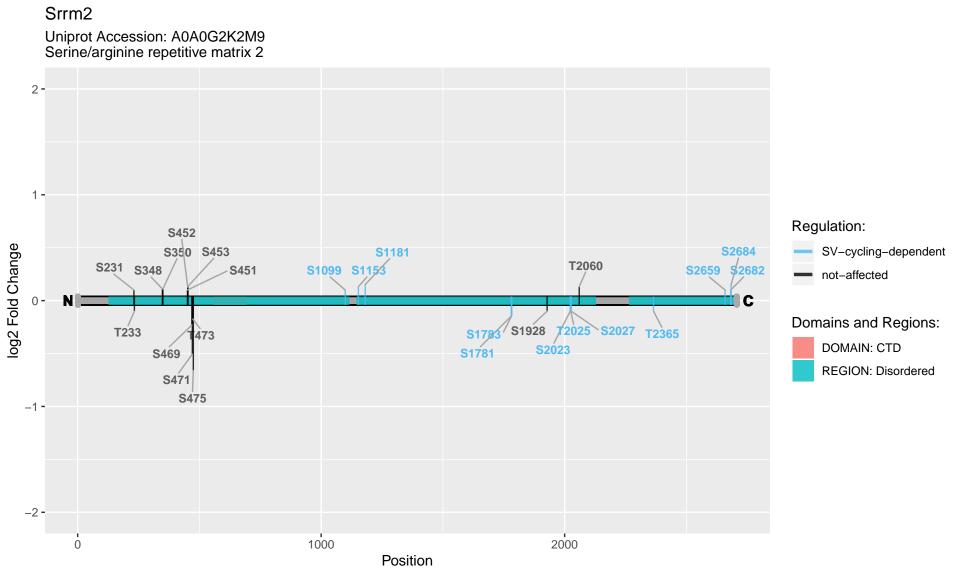


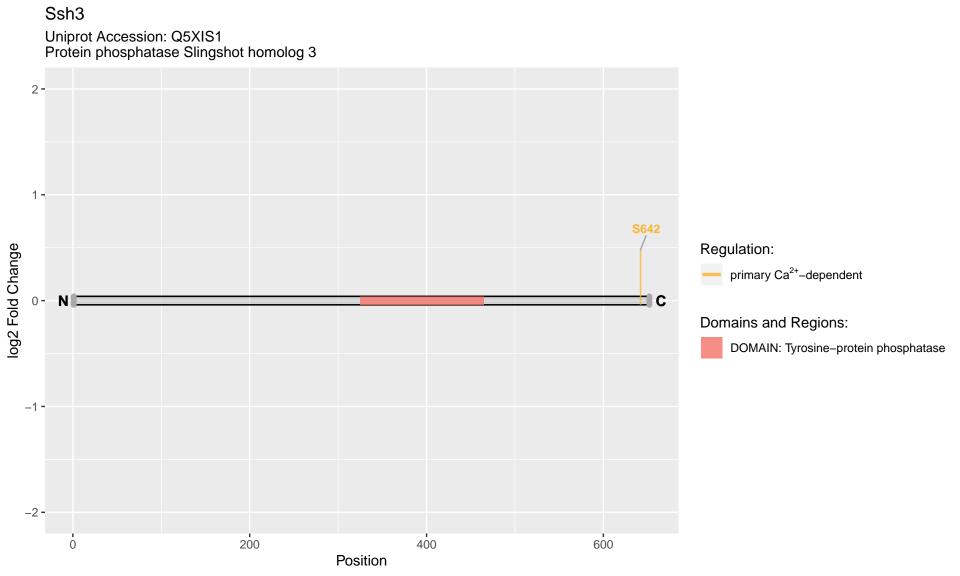


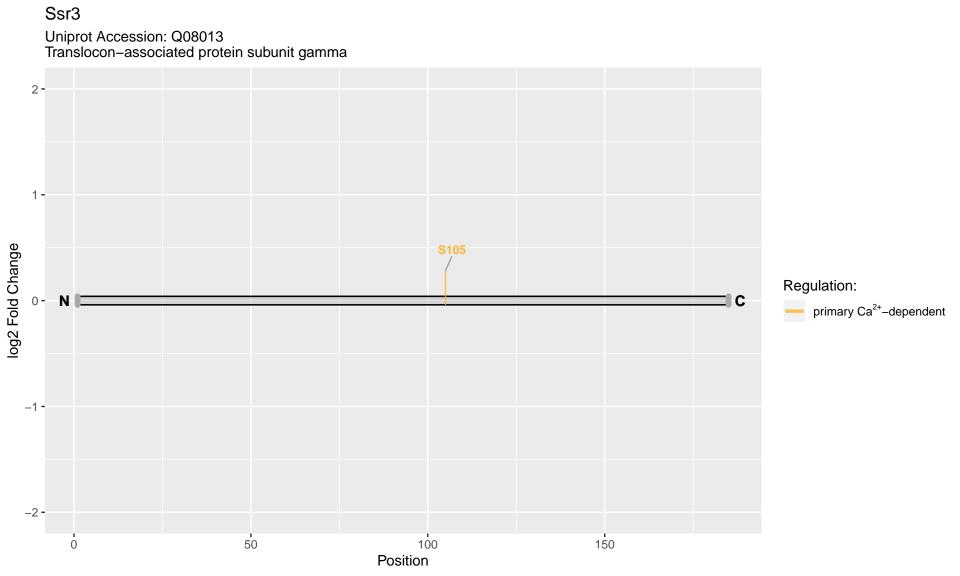


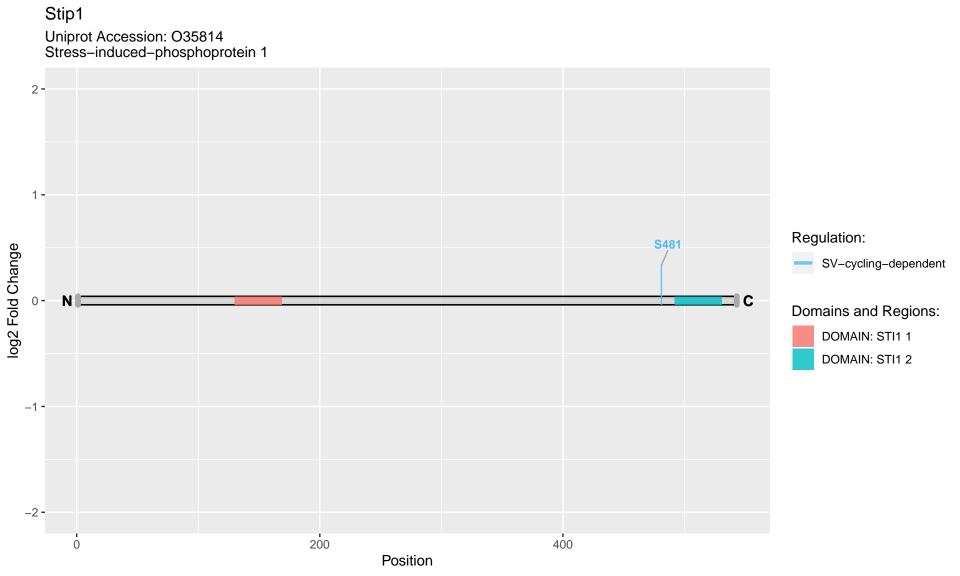


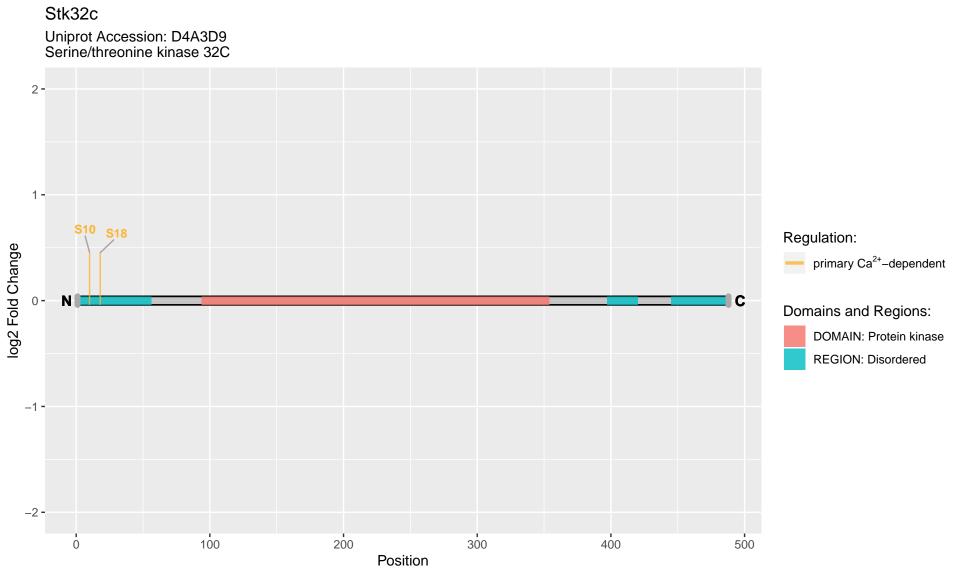


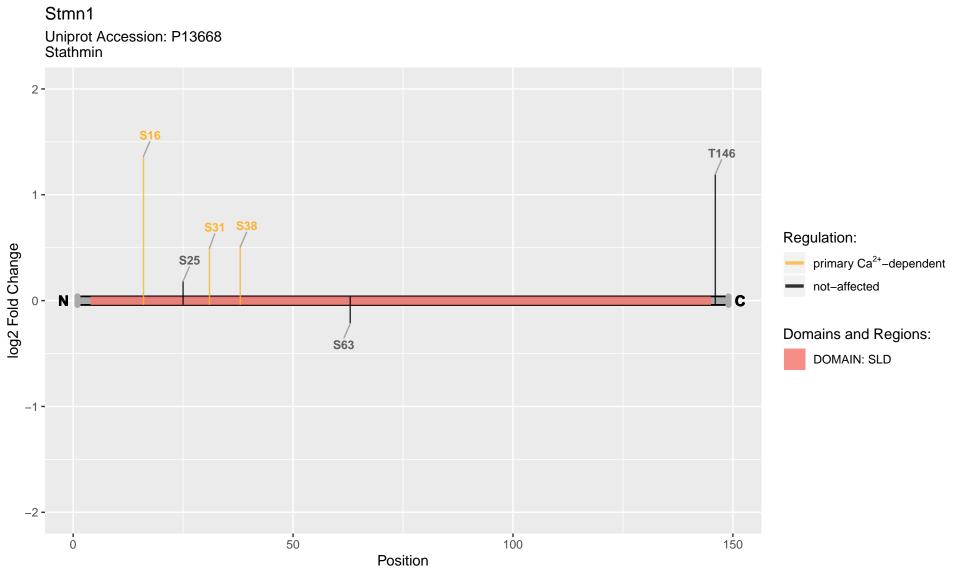


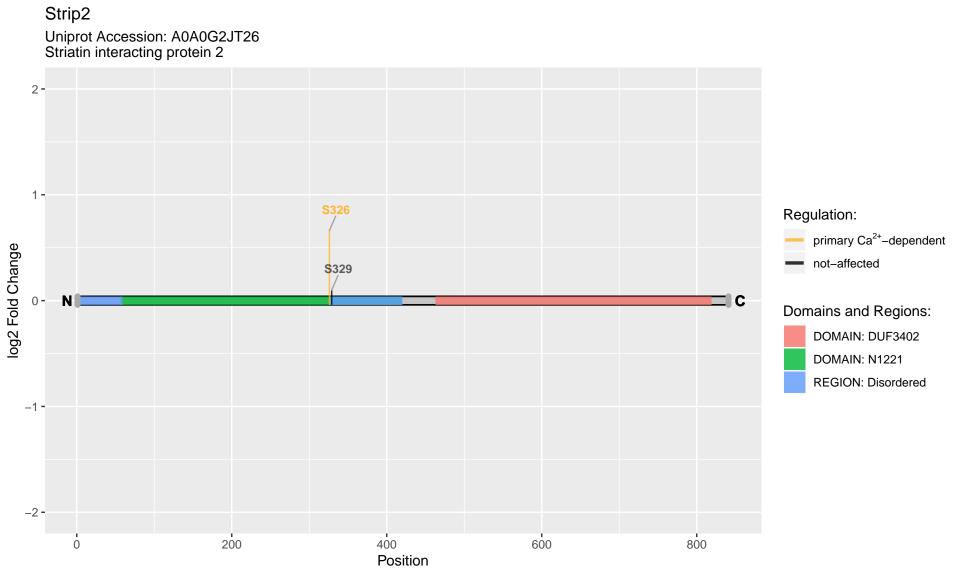


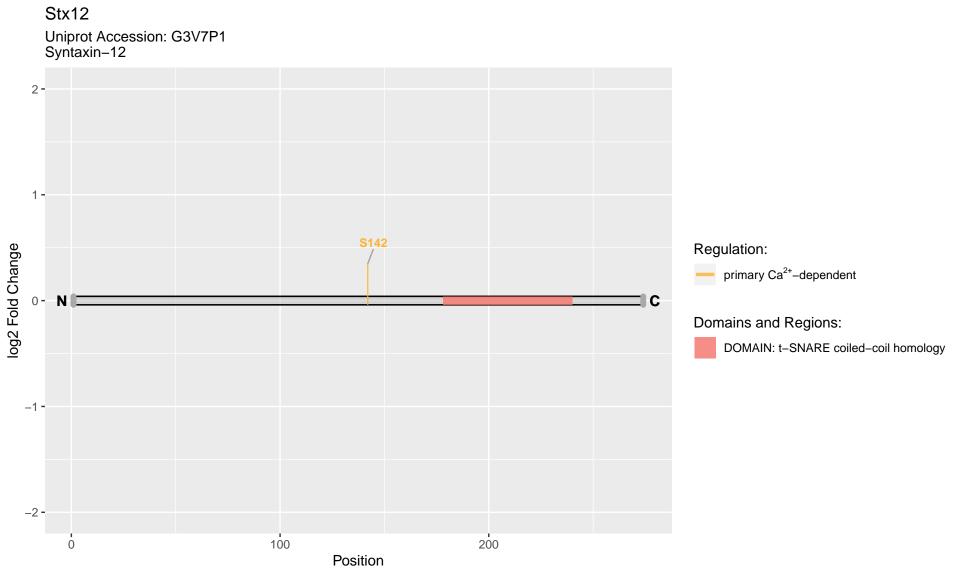


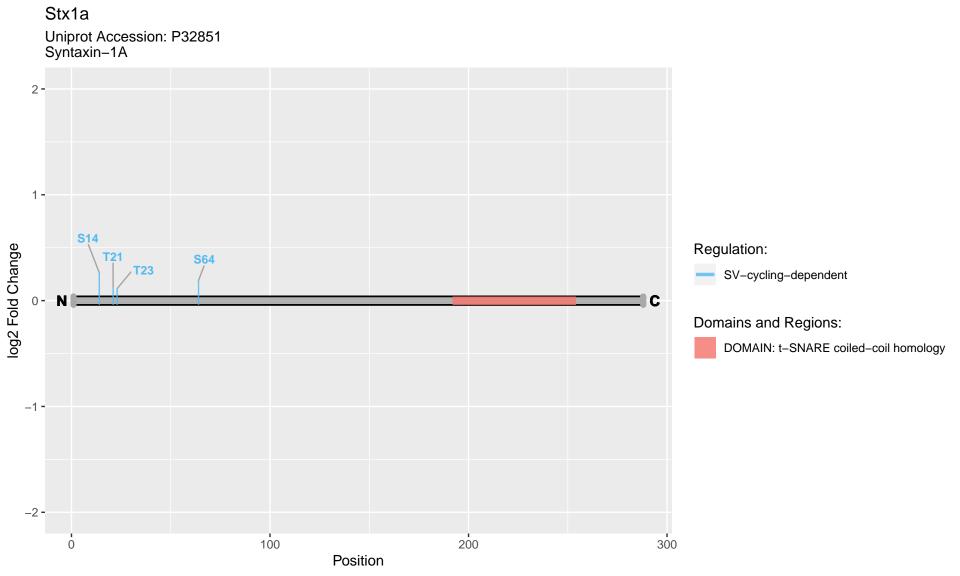


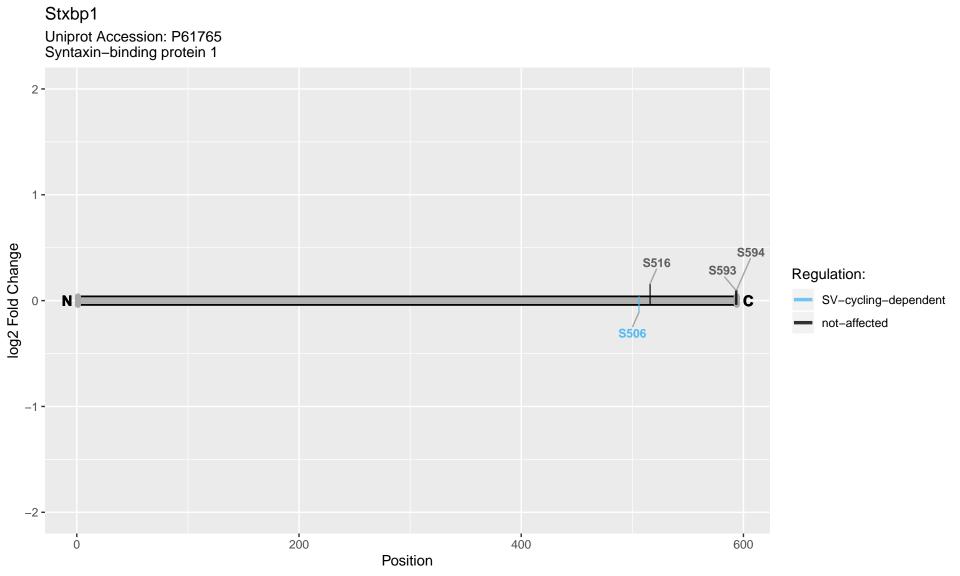


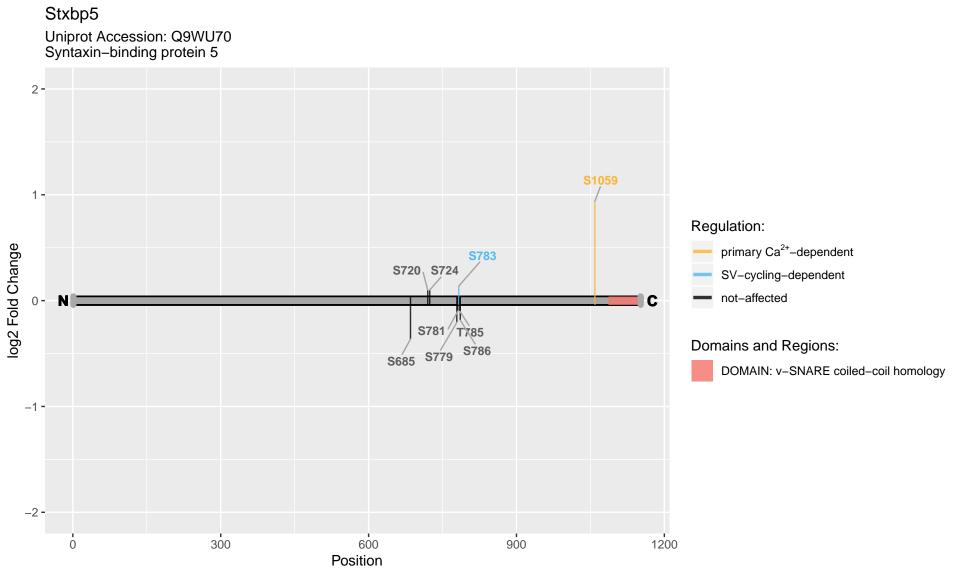


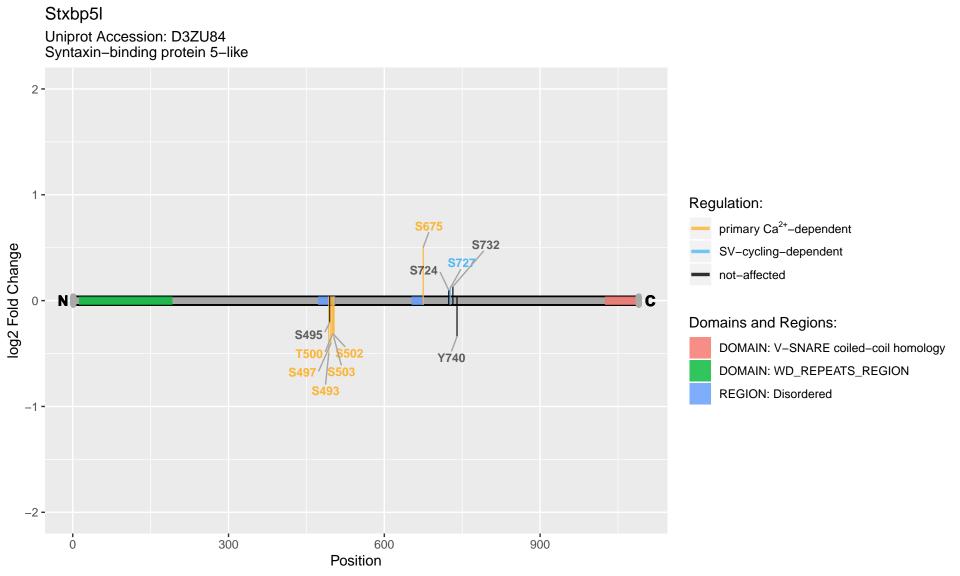


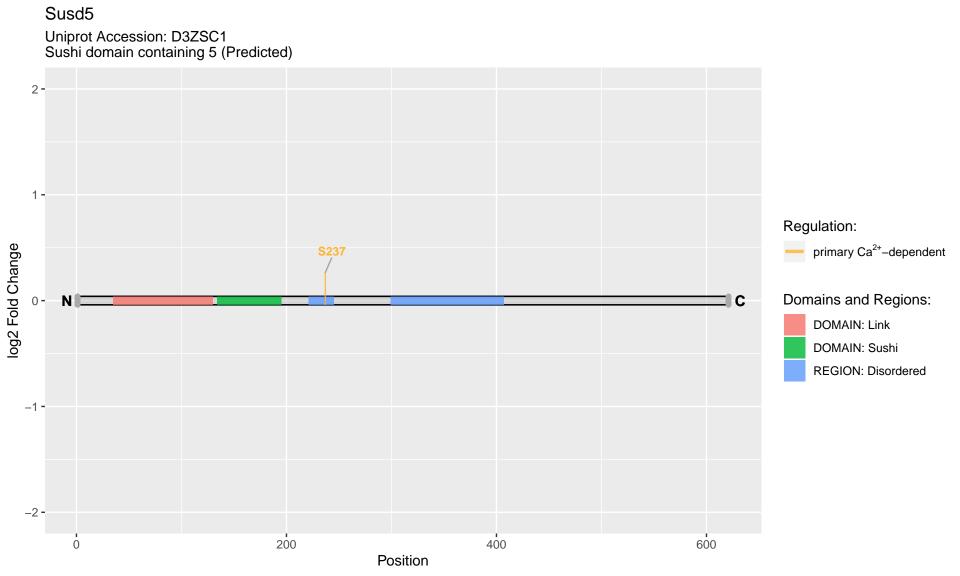


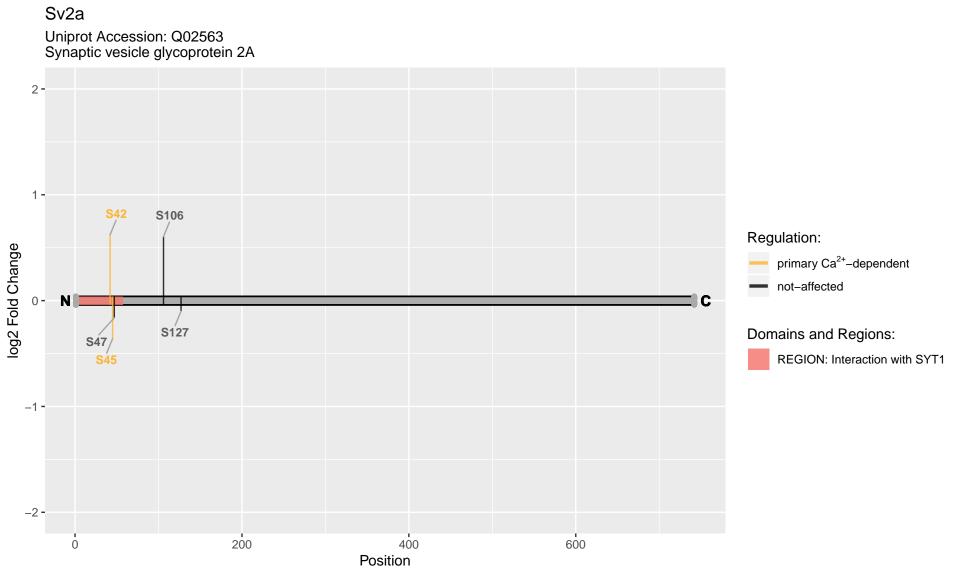


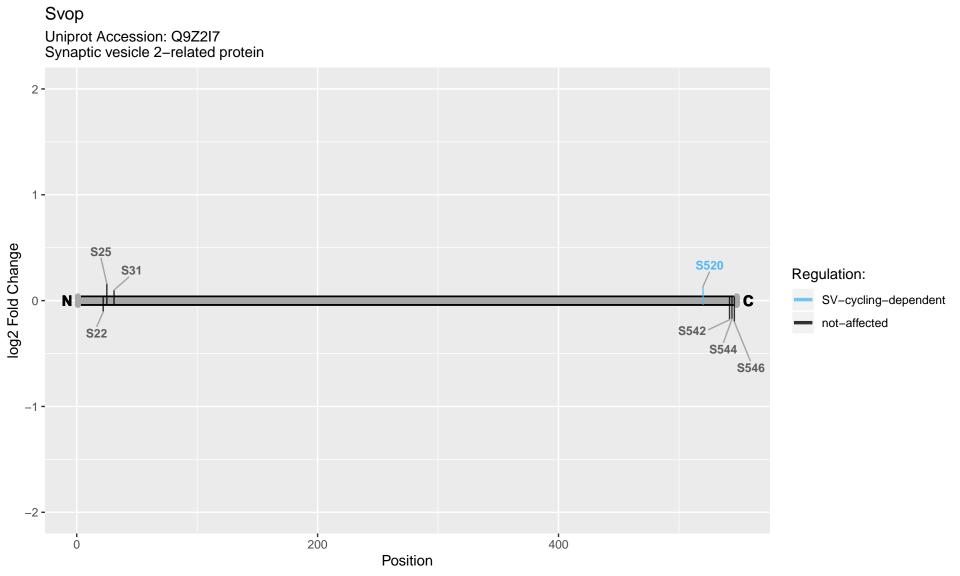


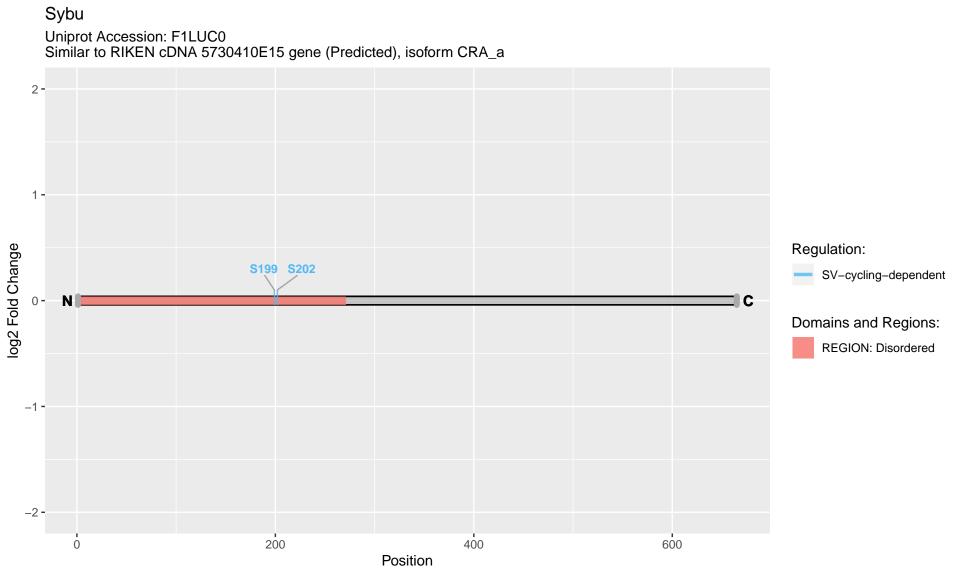


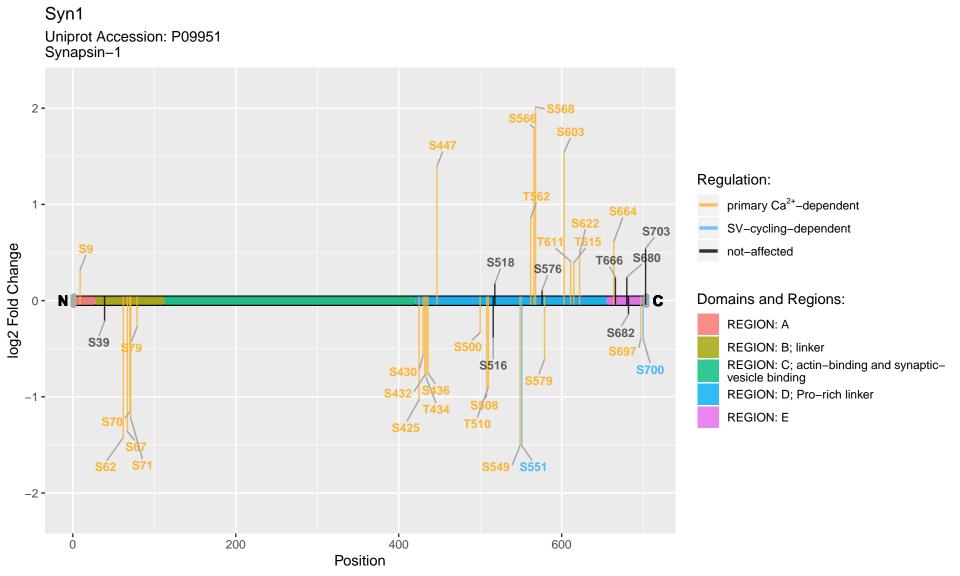


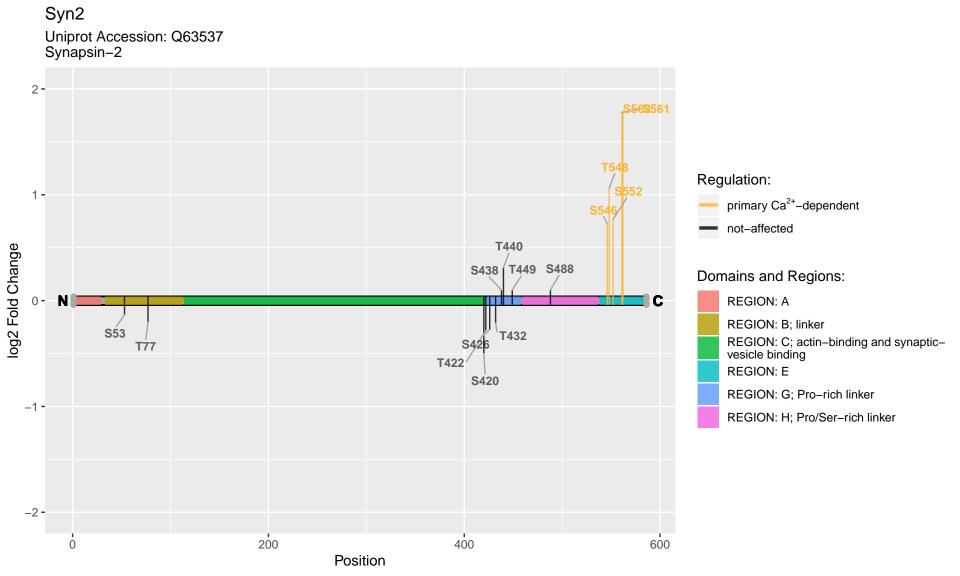


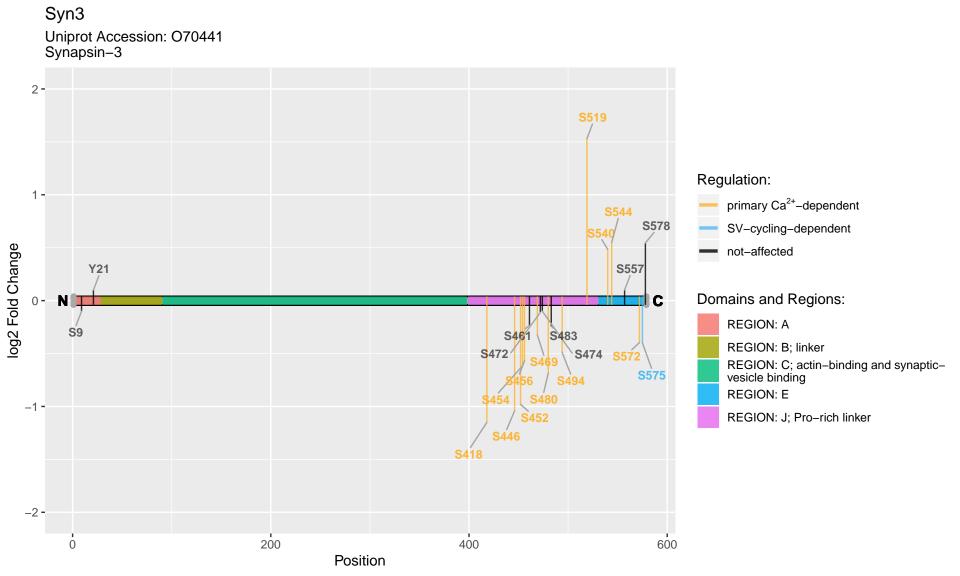


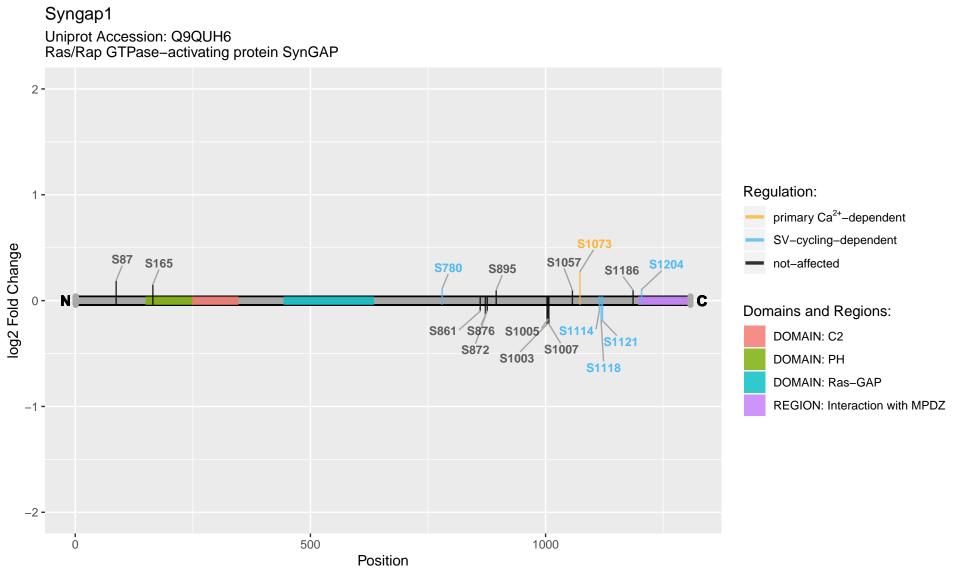


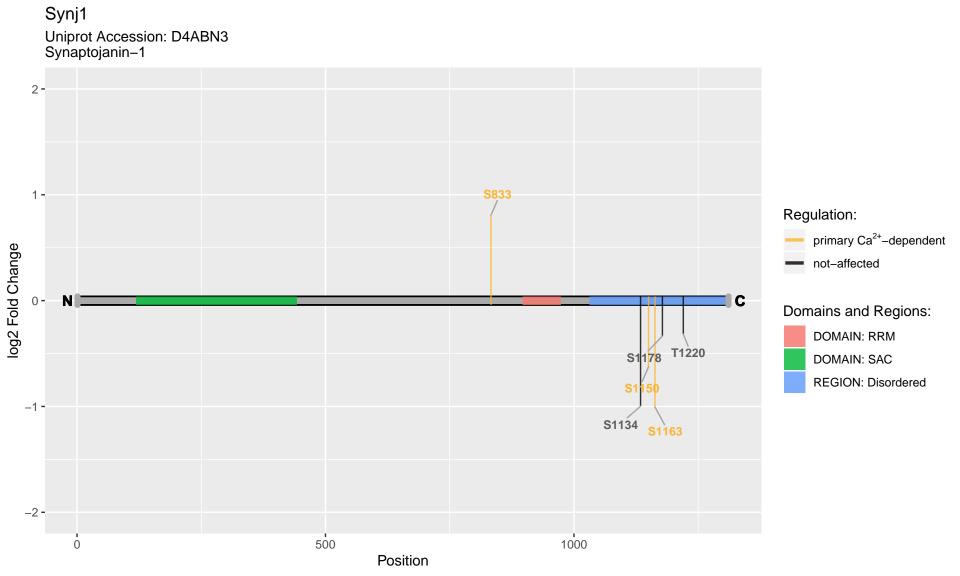


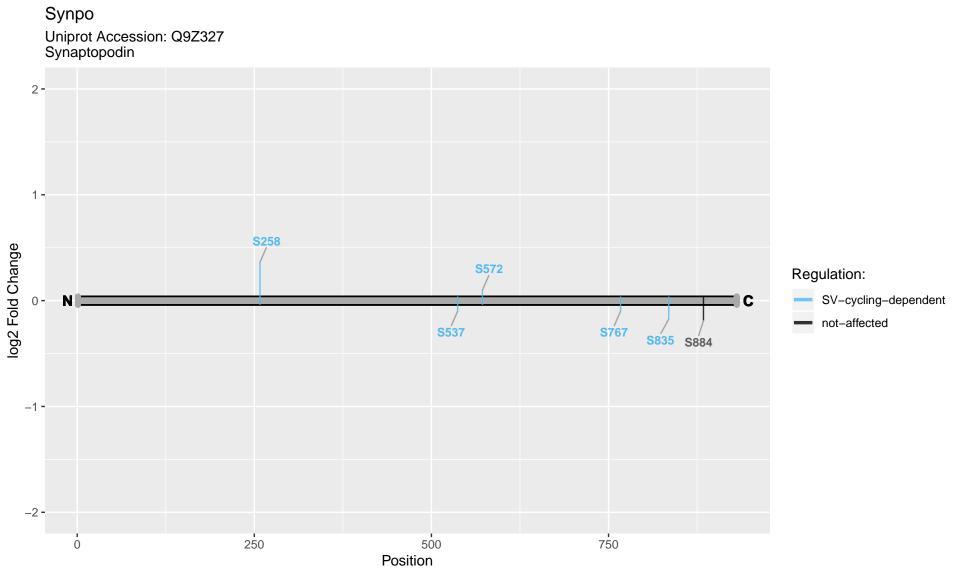


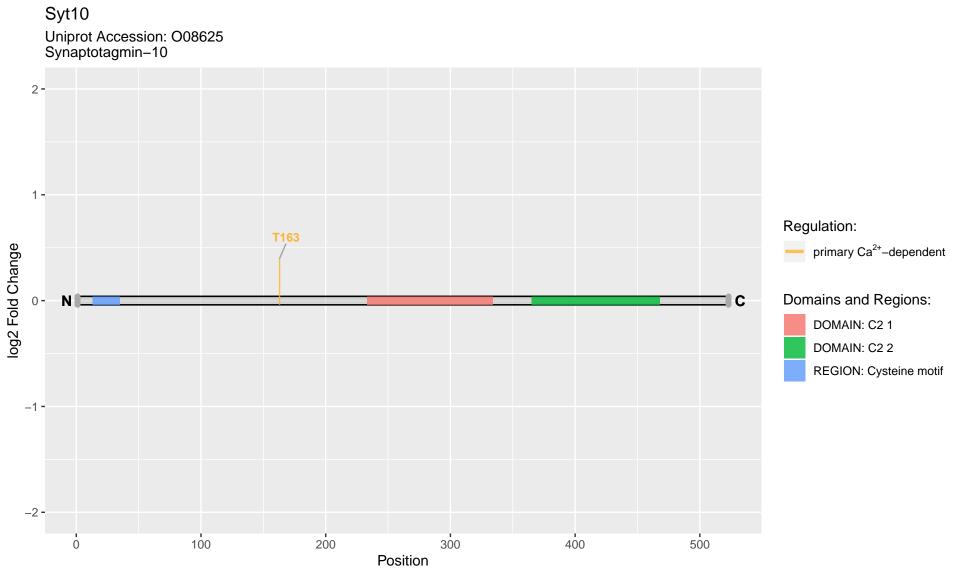


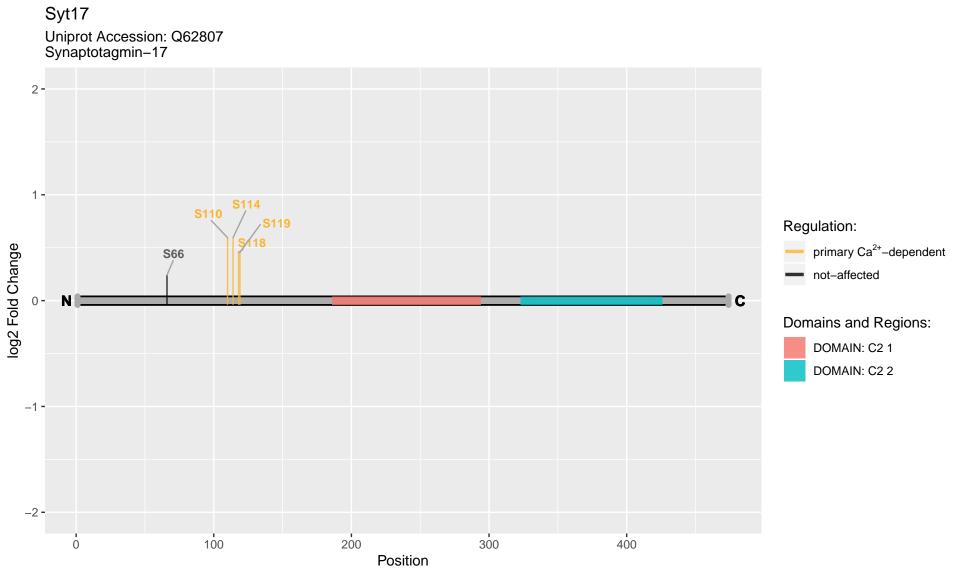


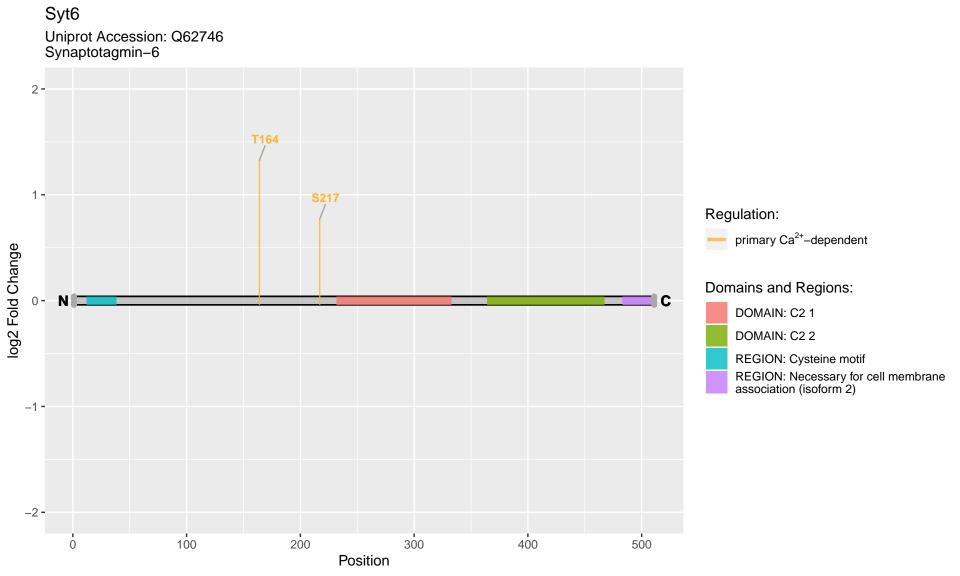


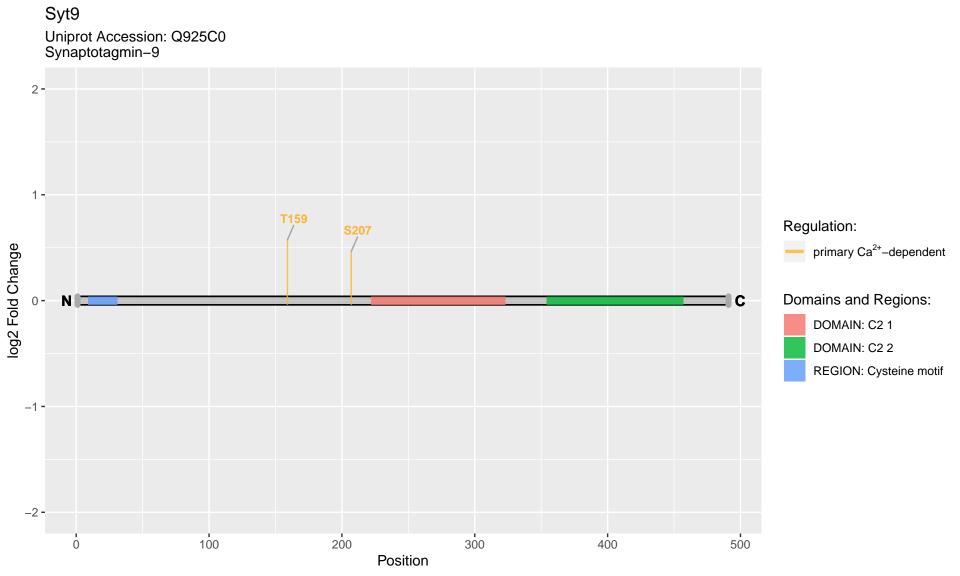


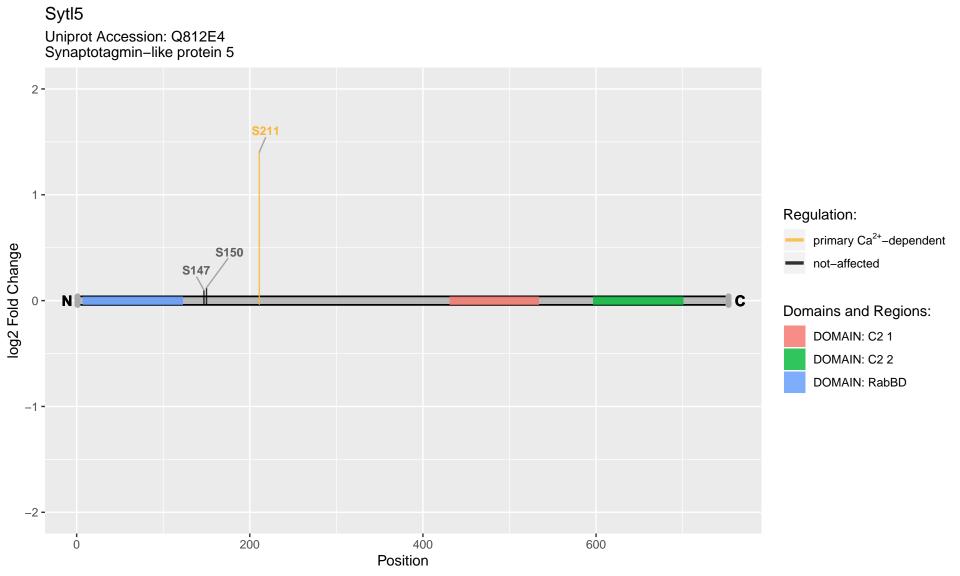


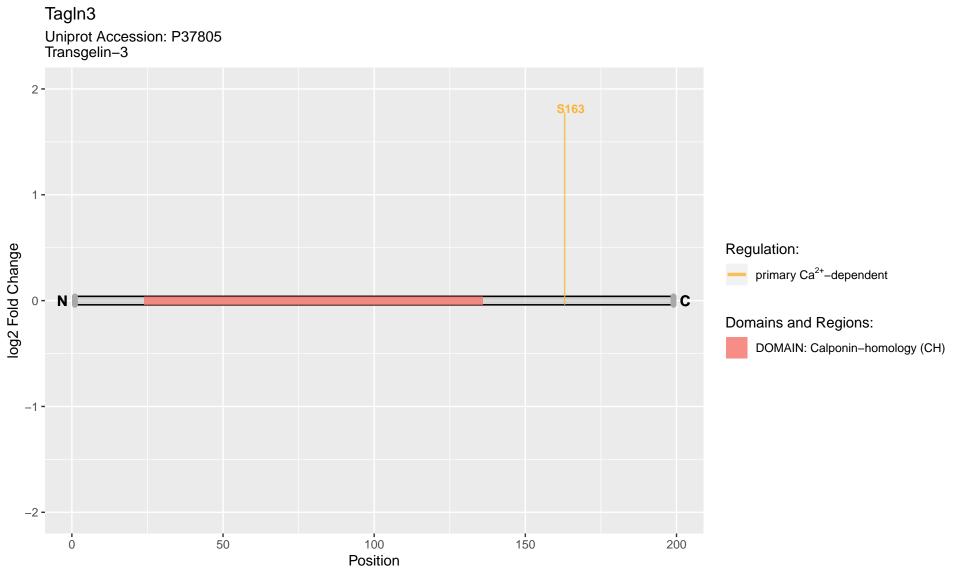


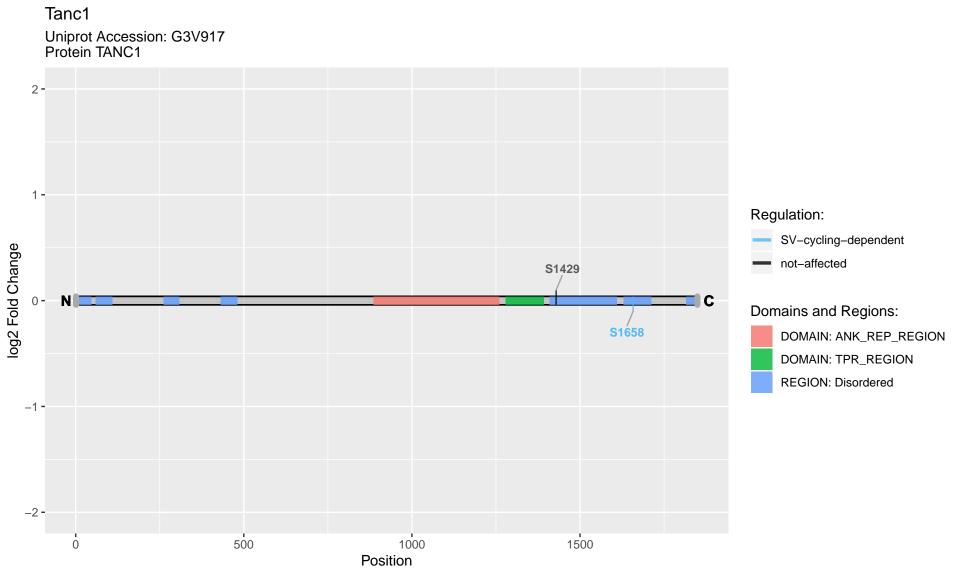




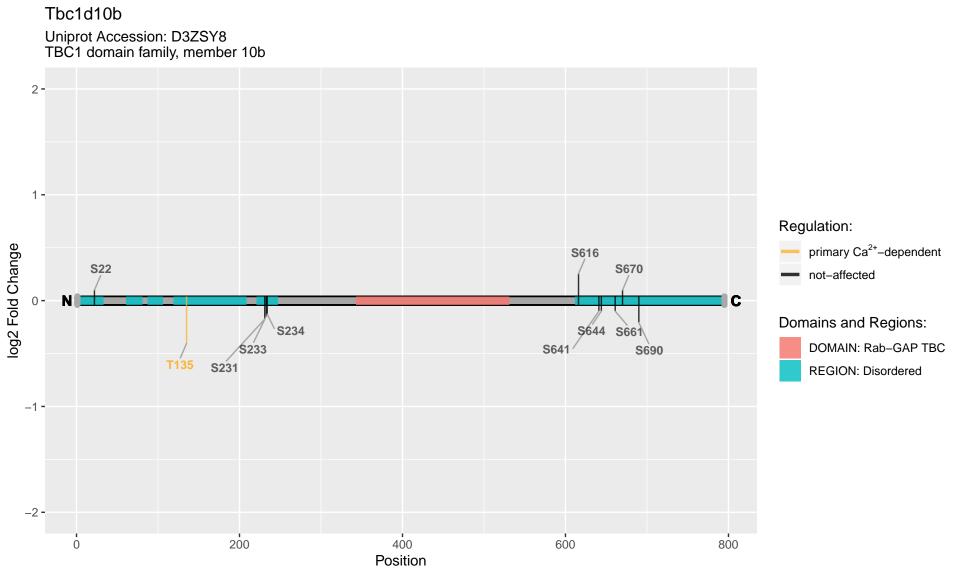


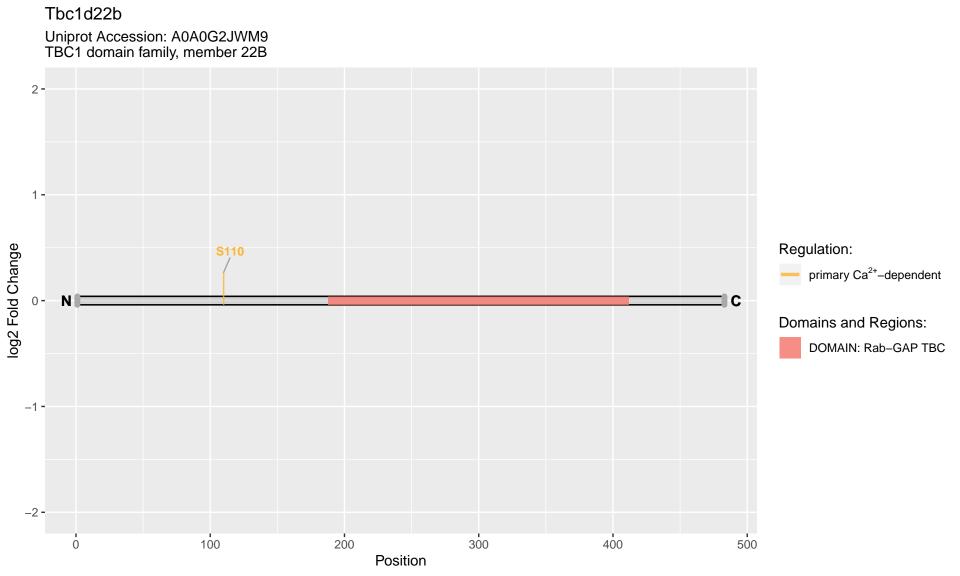


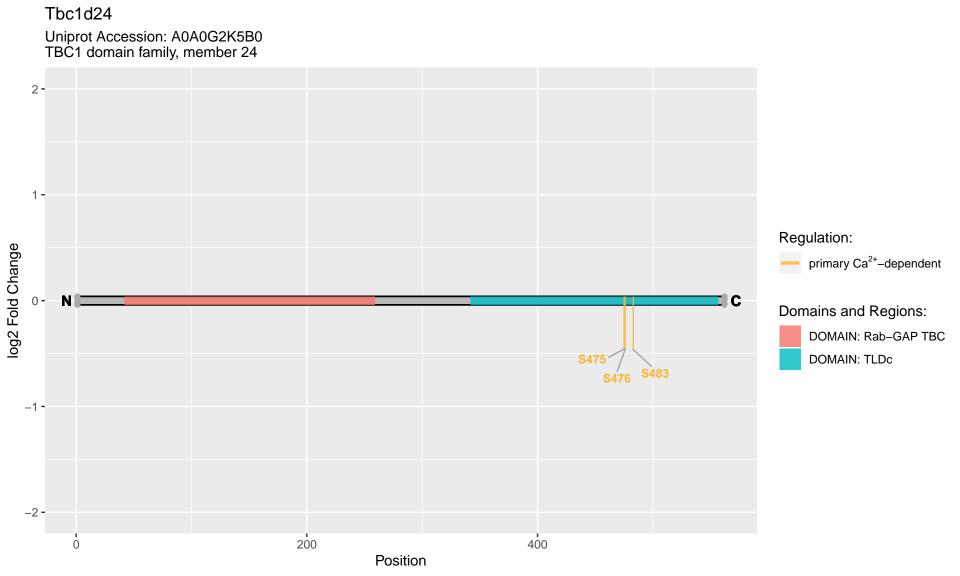


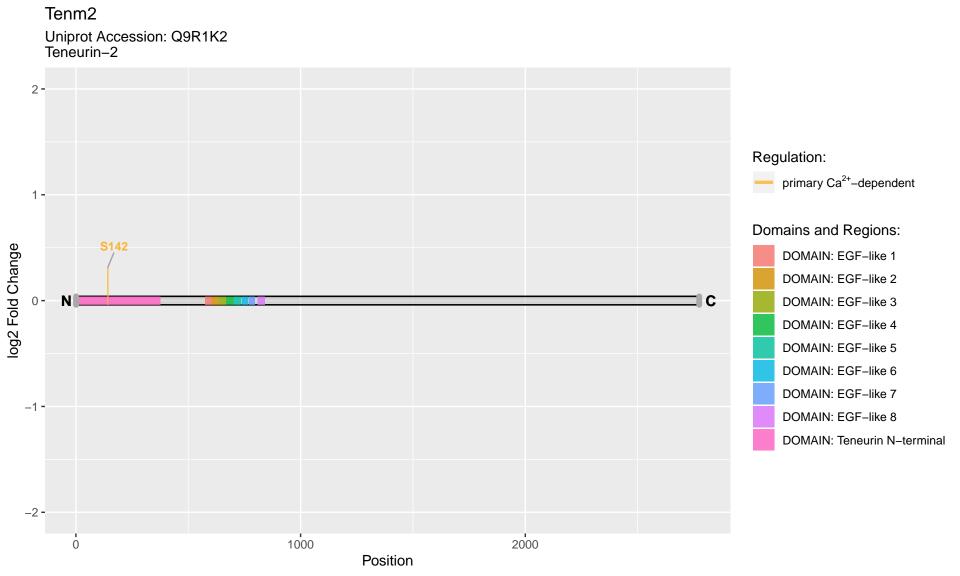


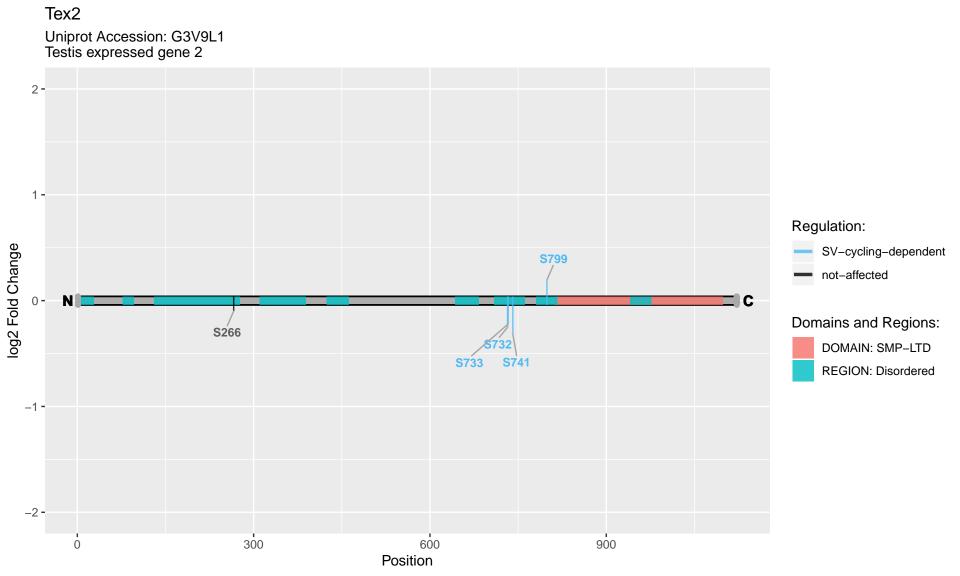
Tanc2 Uniprot Accession: A0A0G2K9J0 Tetratricopeptide repeat, ankyrin repeat and coiled-coil-containing 2 2 -1 -Regulation: primary Ca²⁺-dependent S1603 S1826 log2 Fold Change S1532 SV-cycling-dependent **S128 S474** S1528 S1646 not-affected Domains and Regions: S1562 /S1620 **S478** DOMAIN: ANK_REP_REGION S1616 **S2063** DOMAIN: TPR_REGION S84 S88 **REGION: Disordered** -1 **-**-2 **-**500 1000 1500 2000 **Position**

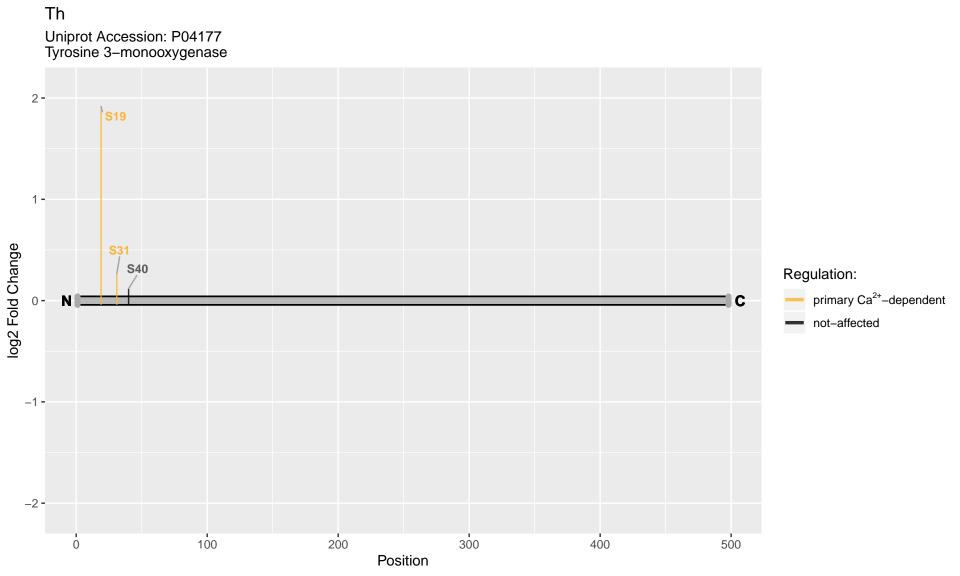






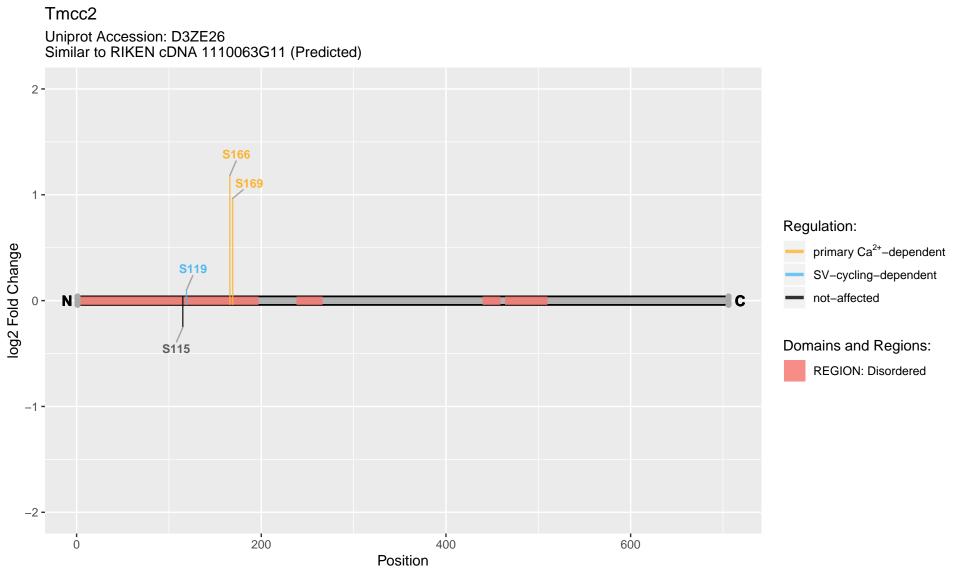


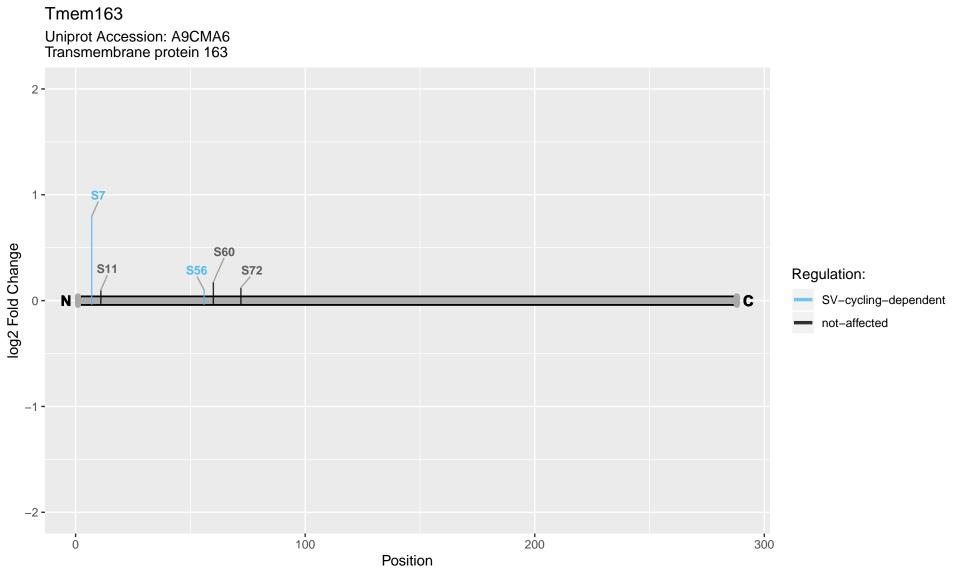


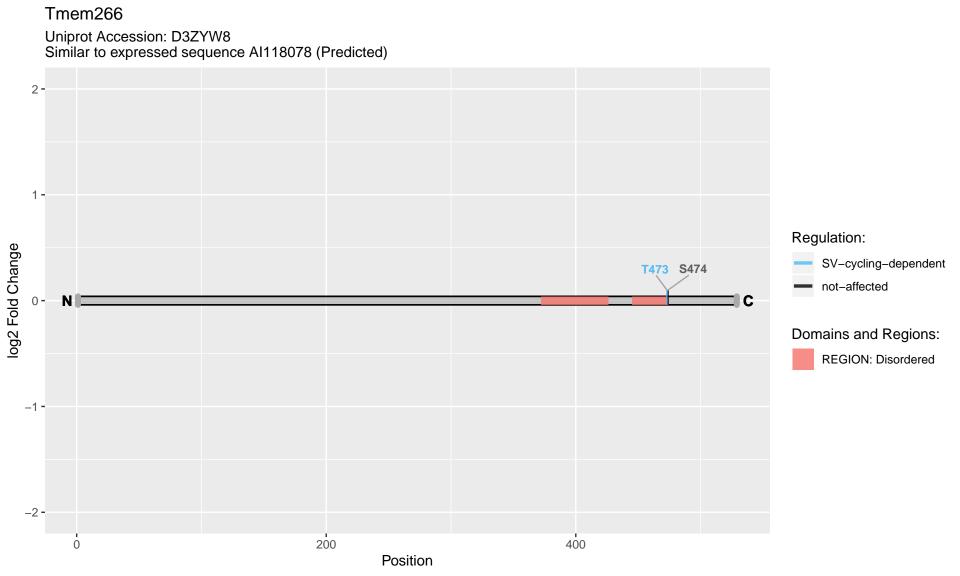


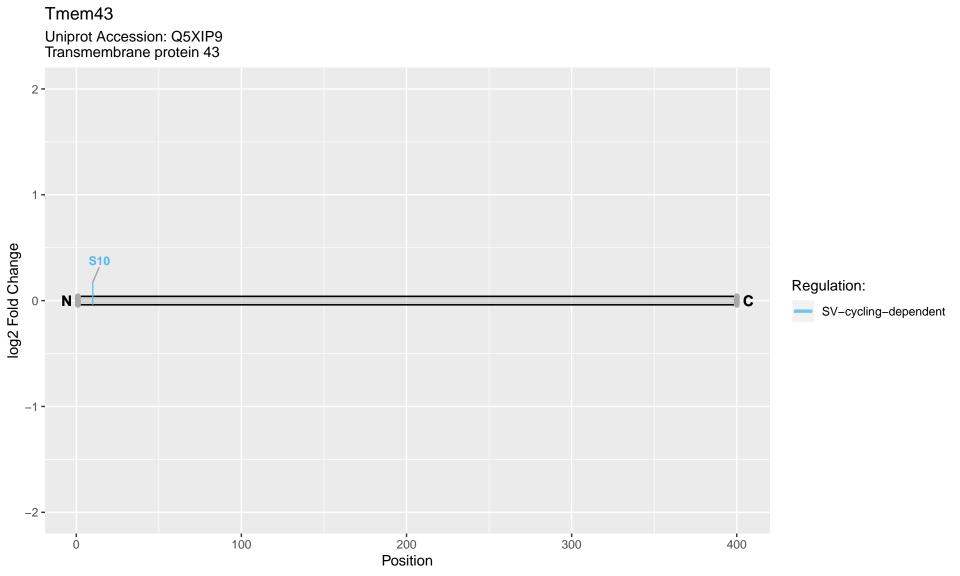
Tjp1 Uniprot Accession: A0A0G2K2P5 Tight junction protein ZO-1 2 -Regulation: SV-cycling-dependent 1 not-affected log2 Fold Change Domains and Regions: DOMAIN: Guanylate kinase-like C DOMAIN: PDZ 1 DOMAIN: PDZ 2 \$131 S280 \S303 S329 **S899** DOMAIN: PDZ 3 S284 Y132 DOMAIN: SH3 S277 DOMAIN: ZU5 -1 **-**REGION: Actin-binding region (ABR) REGION: Occludin (OCLN)-binding region -2 **-**500 1500 1000 **Position**

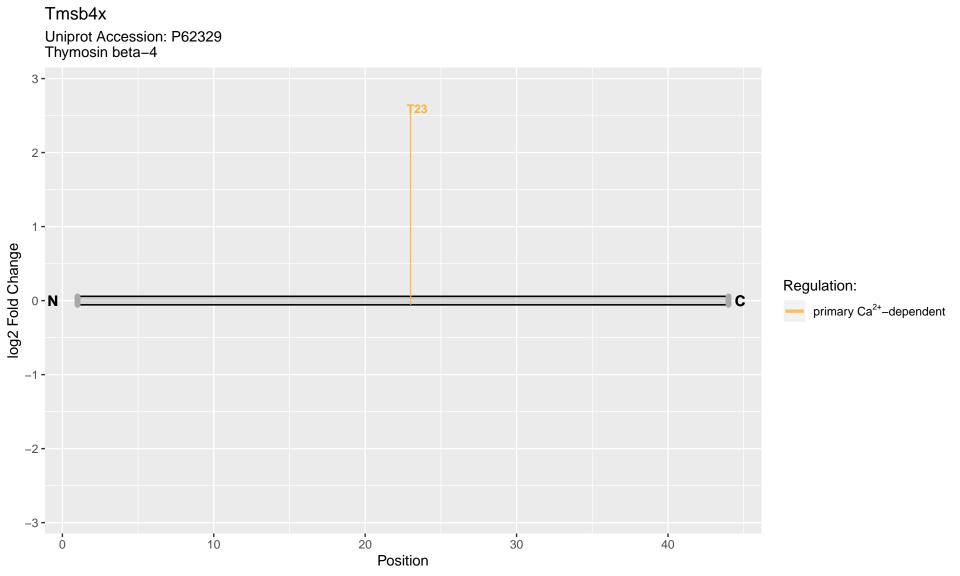
Tjp2 Uniprot Accession: Q3ZB99 Tight junction protein 2 2 -1 -Regulation: primary Ca²⁺-dependent log2 Fold Change not-affected S107 S421 C Domains and Regions: DOMAIN: Guanylate kinase-like S239 T267 S966 S380 DOMAIN: PDZ S263 S378 5411 S1129 S1132 DOMAIN: SH3 S270 S404 Y408 **S265 REGION: Disordered** -1 **-**T412 **S459** -2 **-**600 300 900 1200 Position

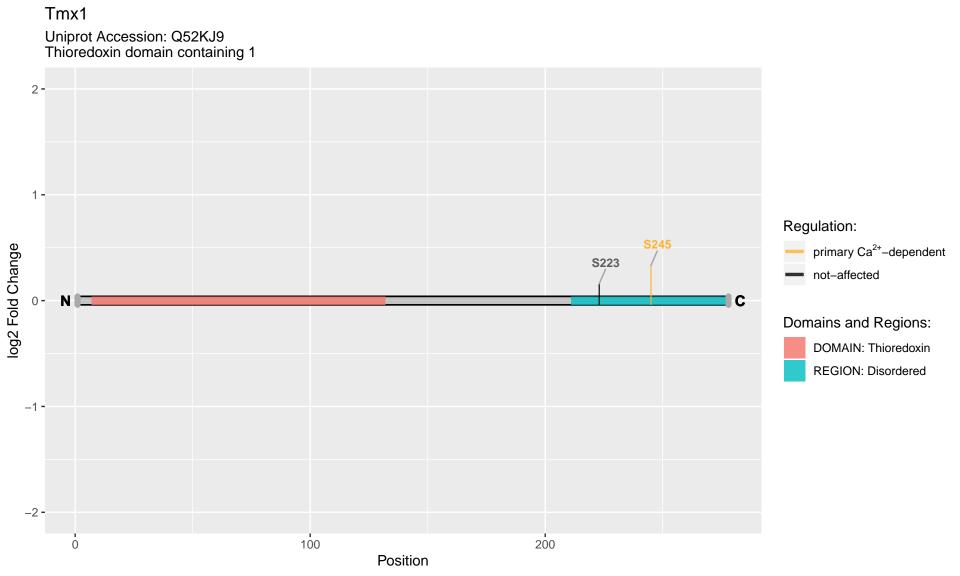


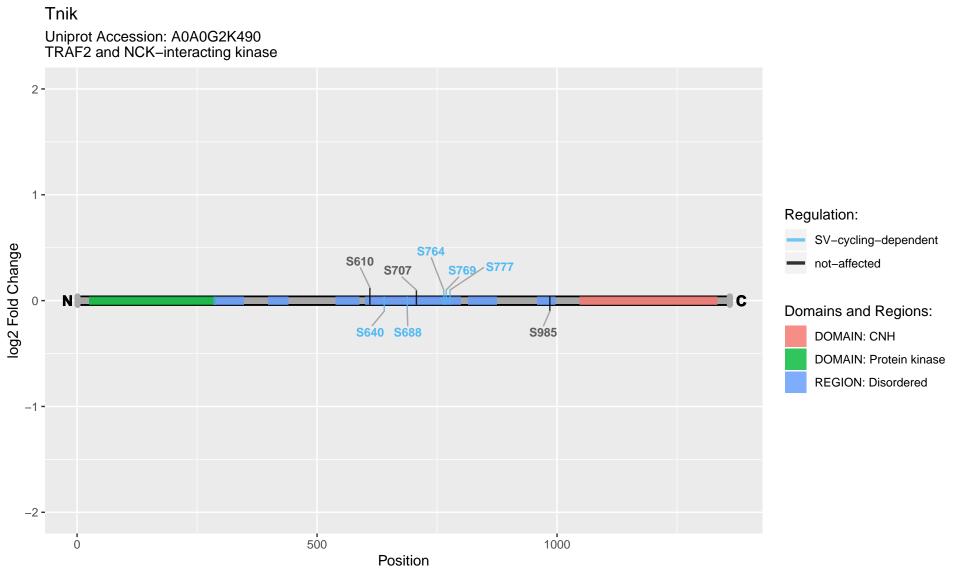


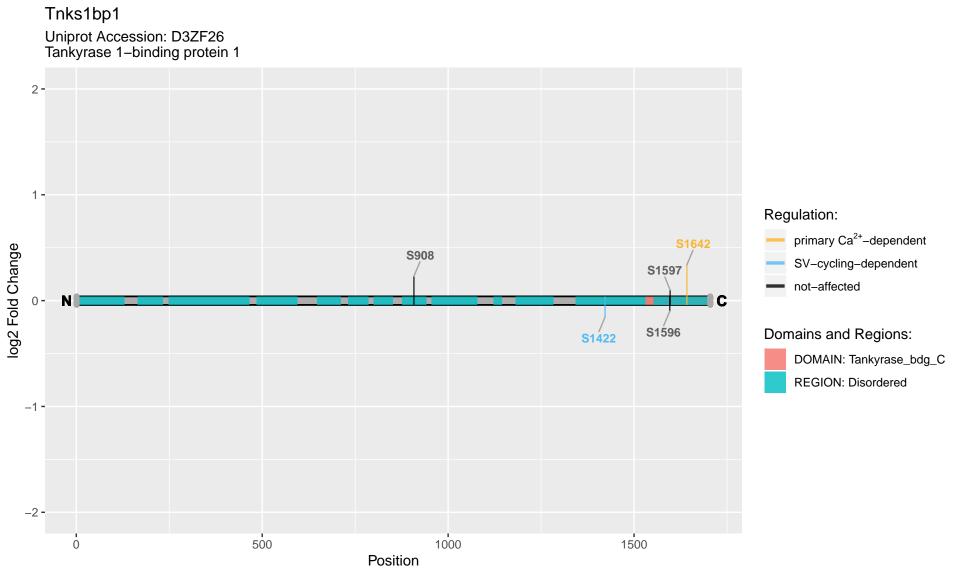


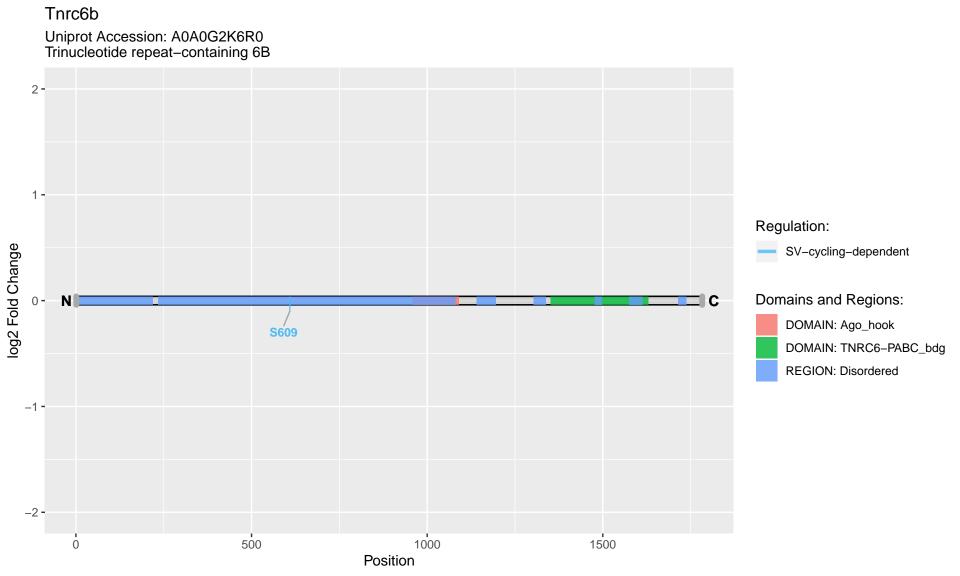


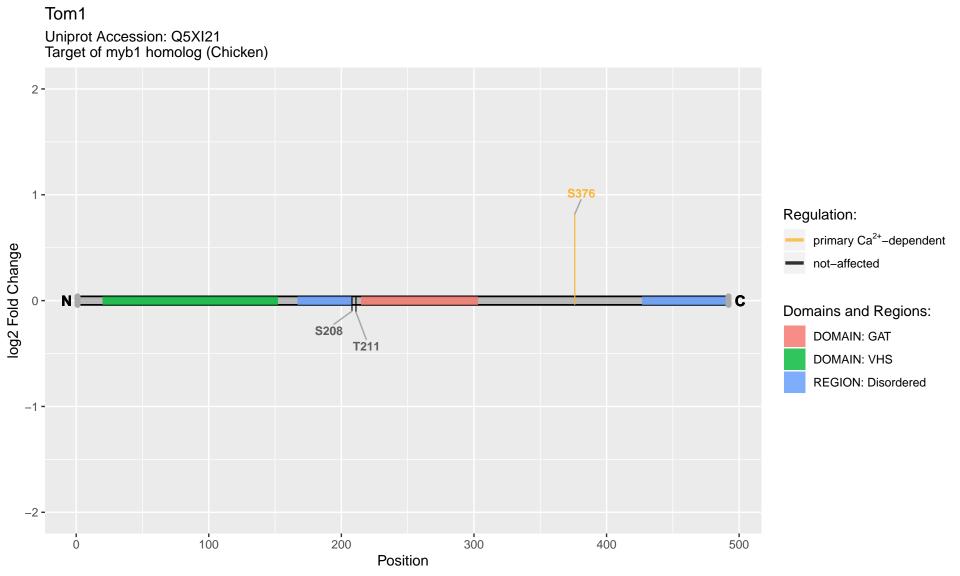


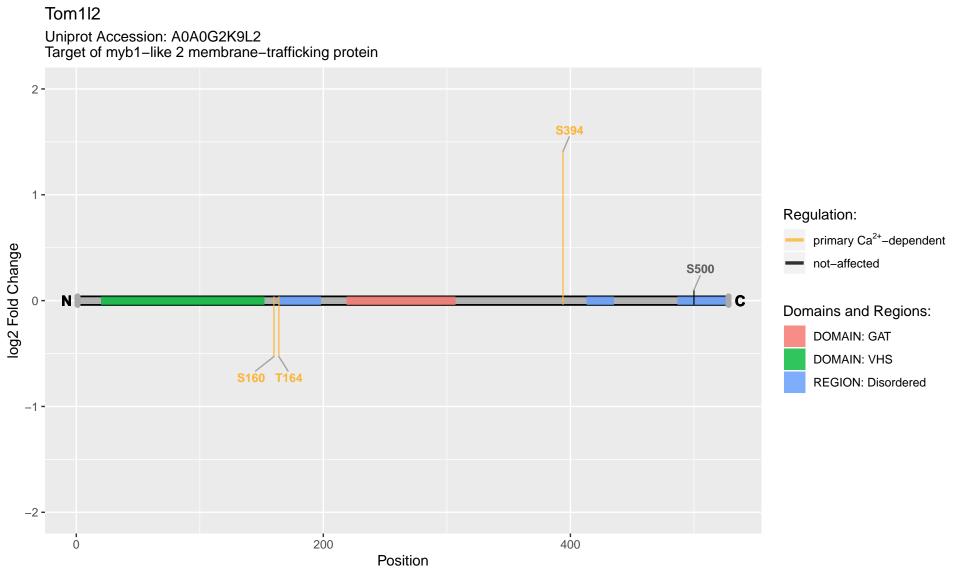


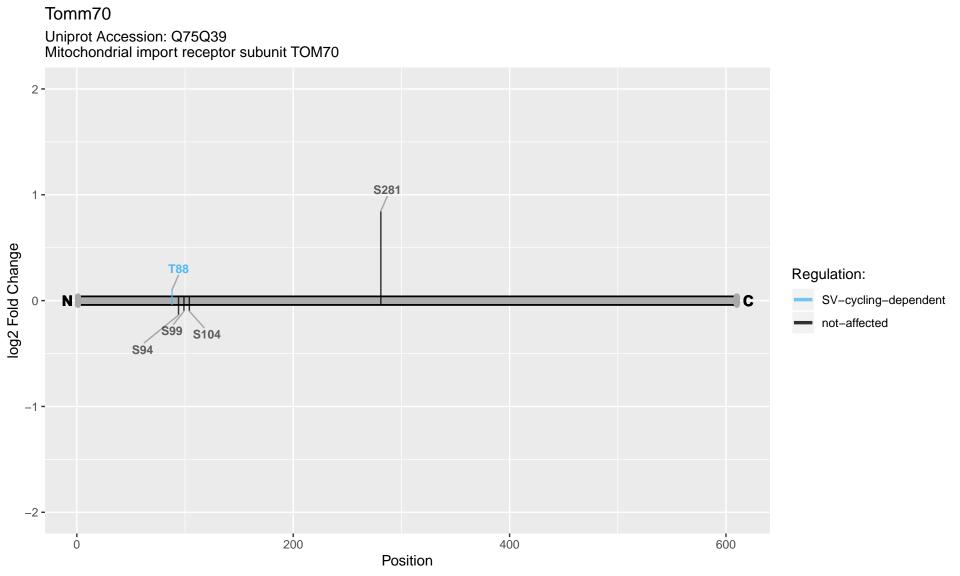


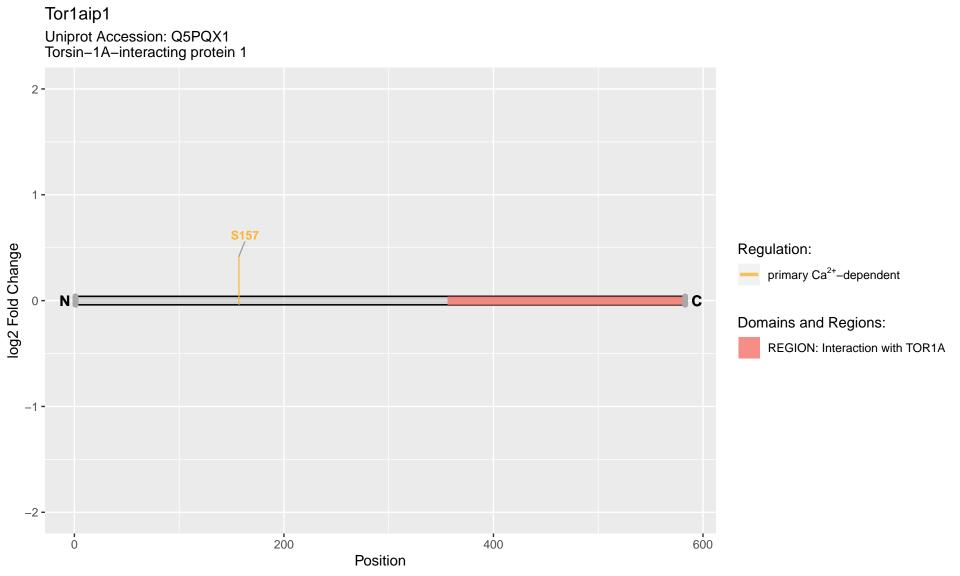


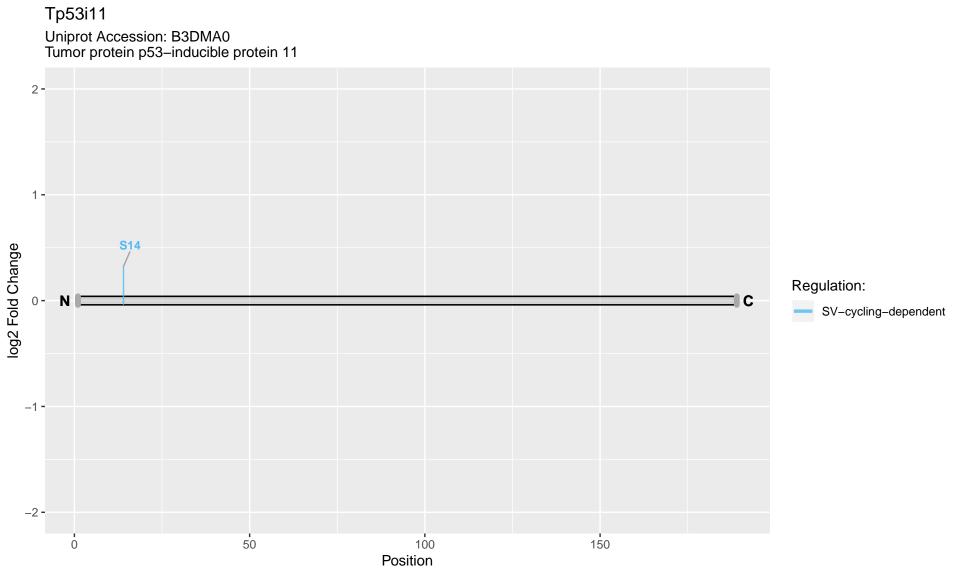


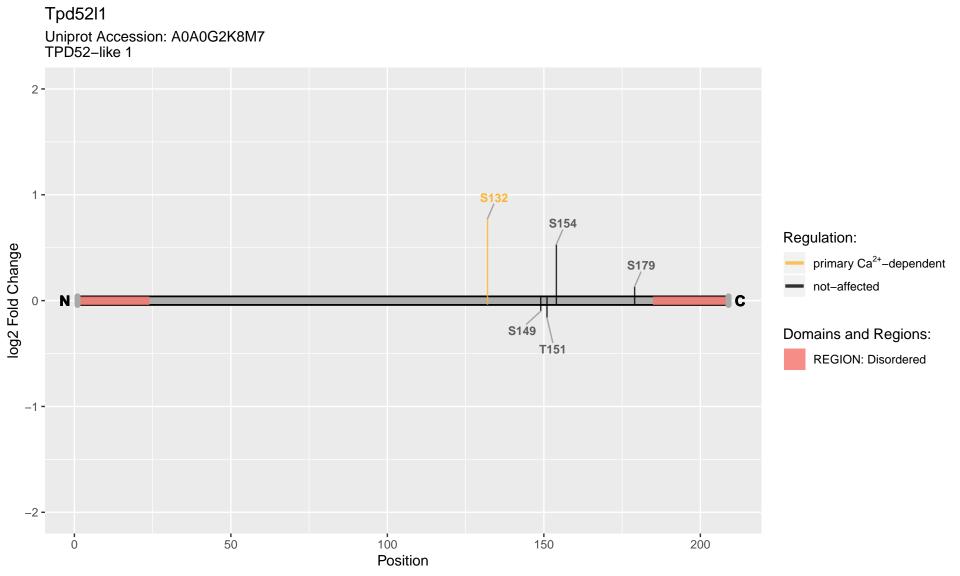


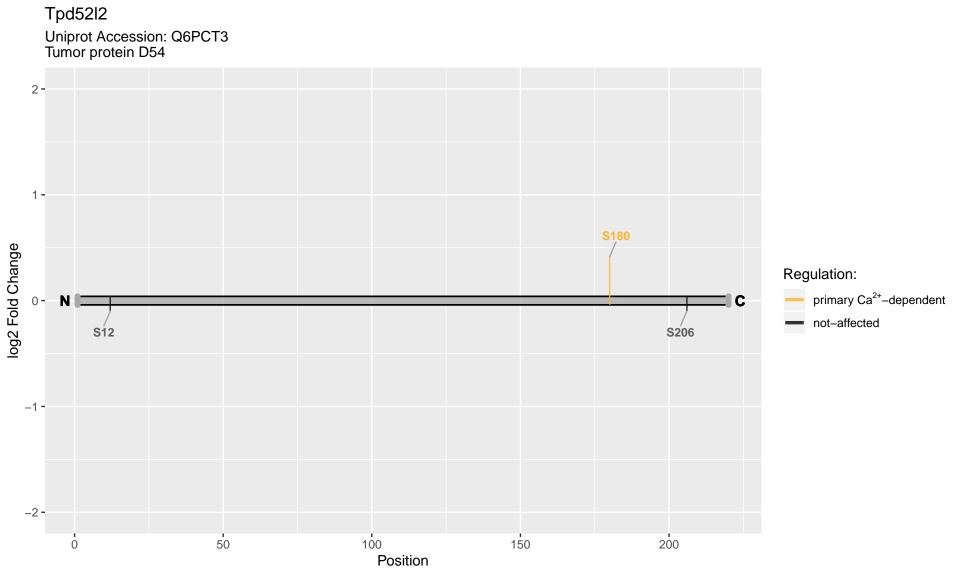


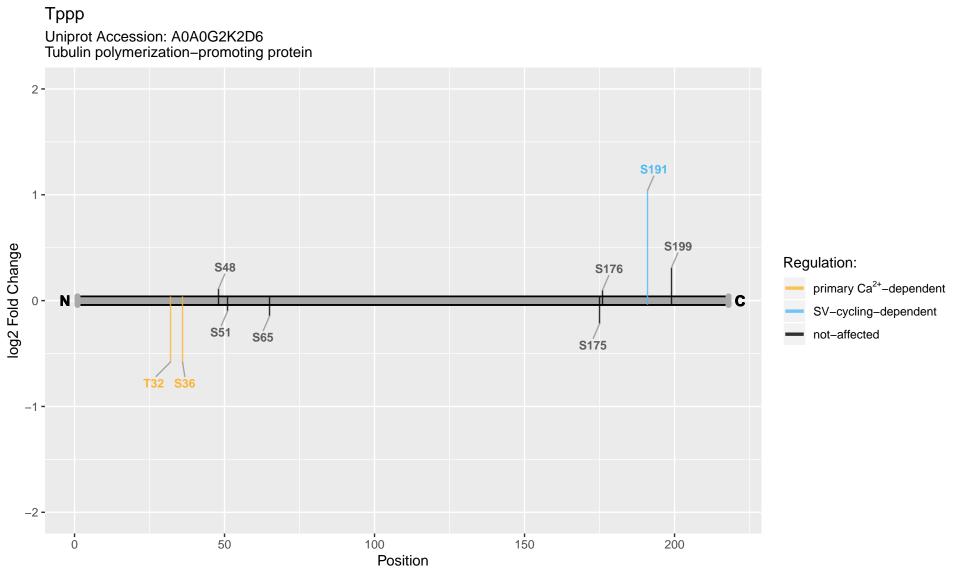












Trappc12 Uniprot Accession: D3ZE49 Trafficking protein particle complex 12 2 -1 -Regulation: log2 Fold Change primary Ca²⁺-dependent not-affected Domains and Regions: S128 S234 S125 DOMAIN: TPR_REGION **REGION: Disordered** -1 **-**-2 **-**200 400 600 800 Position

