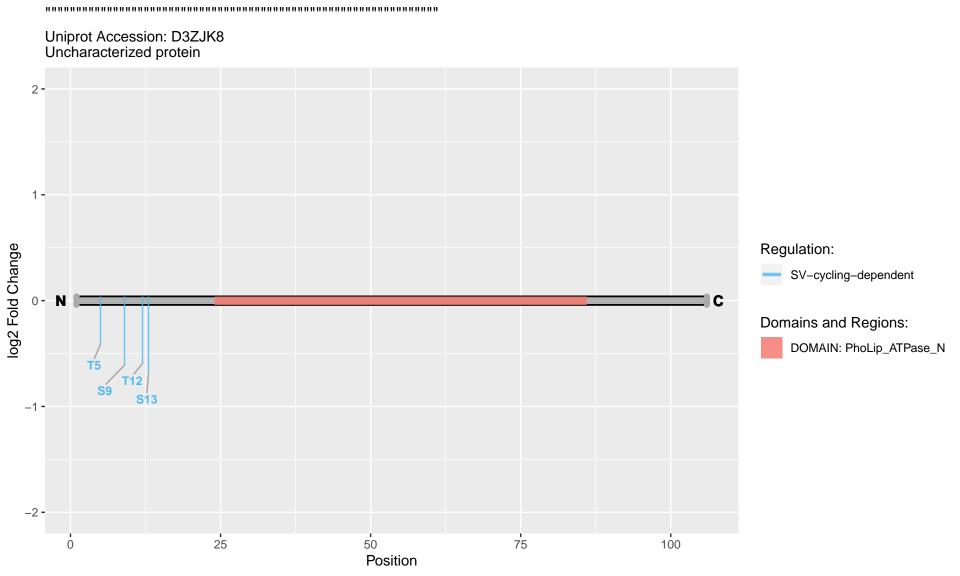
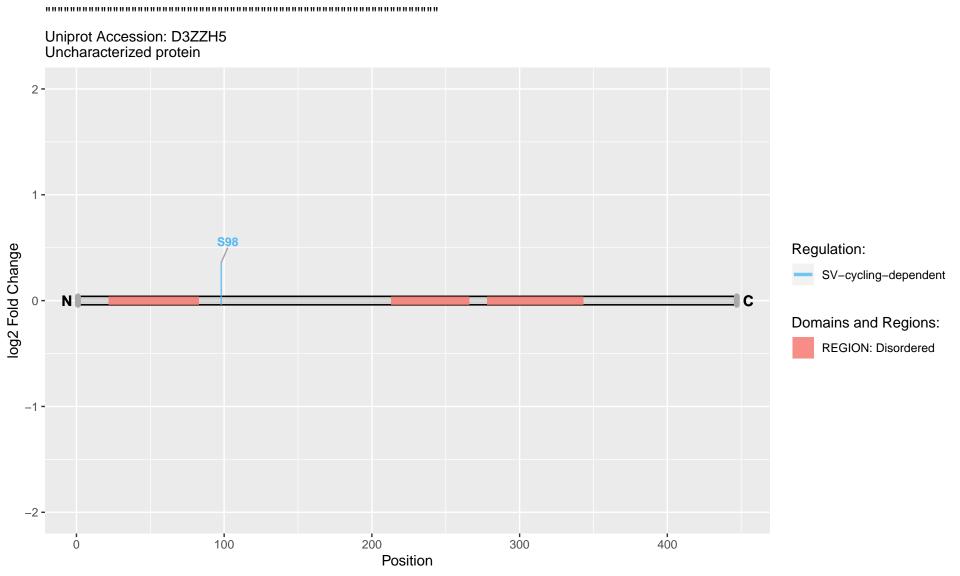


Uniprot Accession: A0A0G2JW65 Uncharacterized protein 2 -Regulation: primary Ca²⁺-dependent log2 Fold Change not-affected **S748** Domains and Regions: DOMAIN: DH S717 S725 DOMAIN: N-terminal Ras-GEF DOMAIN: PH **REGION: Disordered** -1 **-**-2 **-**200 400 600 800 Position

Uniprot Accession: A0A0G2JZ27 Uncharacterized protein 2 -Regulation: S416 S424 log2 Fold Change S412 S420 SV-cycling-dependent **S500 S727** S418 not-affected C Domains and Regions: T477 **S636 S380** S483 DOMAIN: FH2 **S384 REGION: Disordered** -1 **-**-2 **-**250 500 750 1000 1250 Position



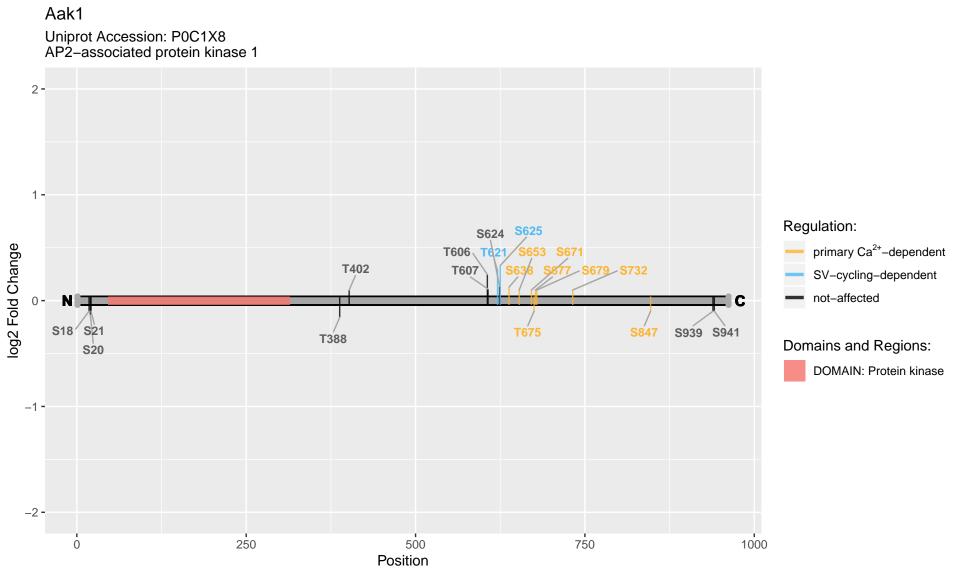


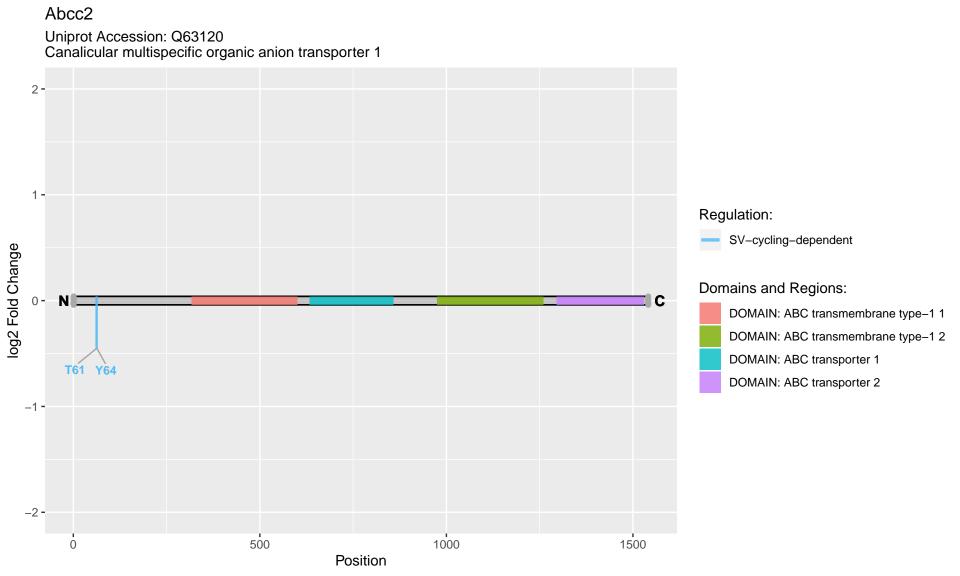
Uniprot Accession: M0R970 Uncharacterized protein 2 -Regulation: log2 Fold Change primary Ca²⁺-dependent S42 S46 not-affected Domains and Regions: REGION: Disordered -1 **-**-2 **-**75 25 100 Position

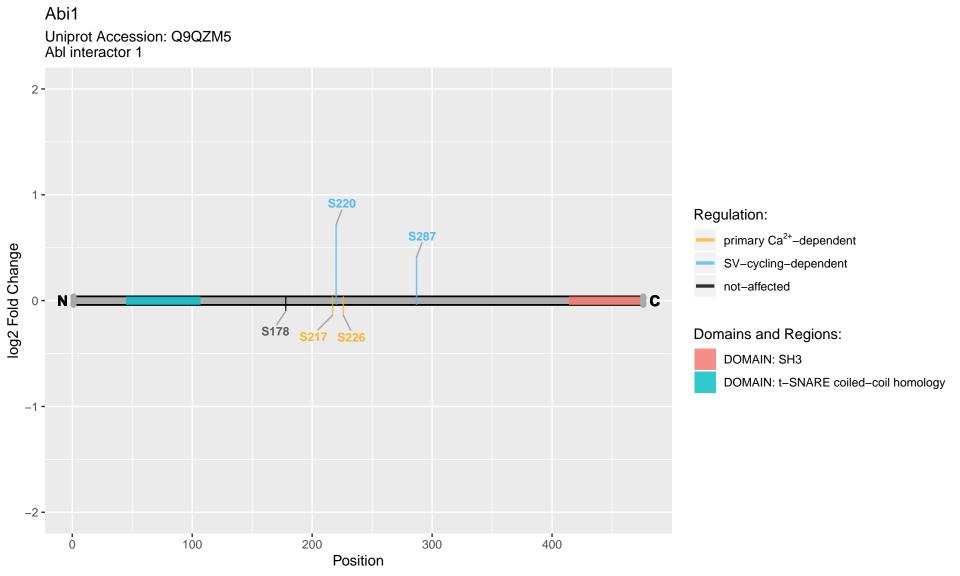
Uniprot Accession: M0RDY2 Uncharacterized protein 2 log2 Fold Change Regulation: SV-cycling-dependent **S**36 -1 **-**-2 **-**50 100 150 Position

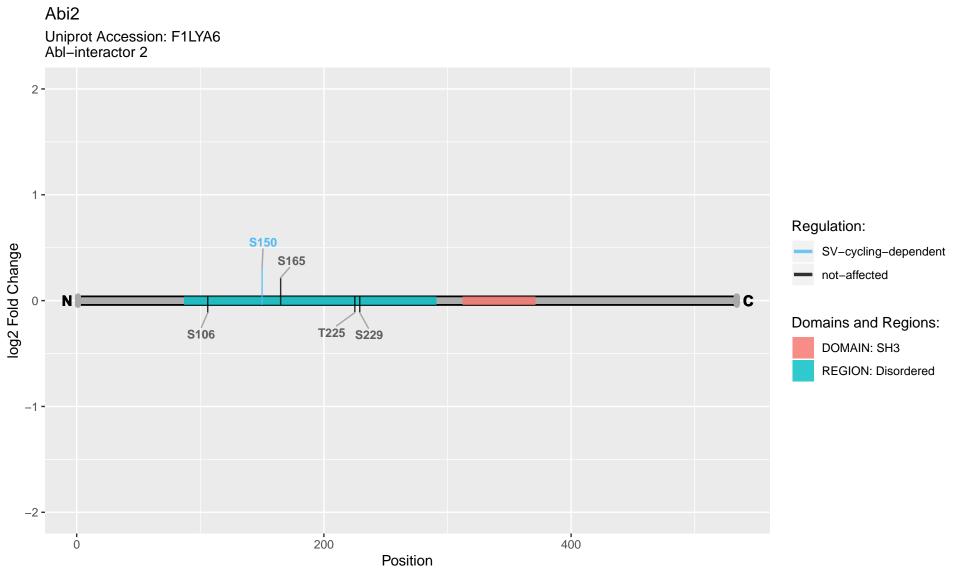
Uniprot Accession: O08654 UPF0183 protein C16orf70 homolog 2 log2 Fold Change Regulation: SV-cycling-dependent S270 S272 -1 **-**-2 **-**200 300 400 100 Position

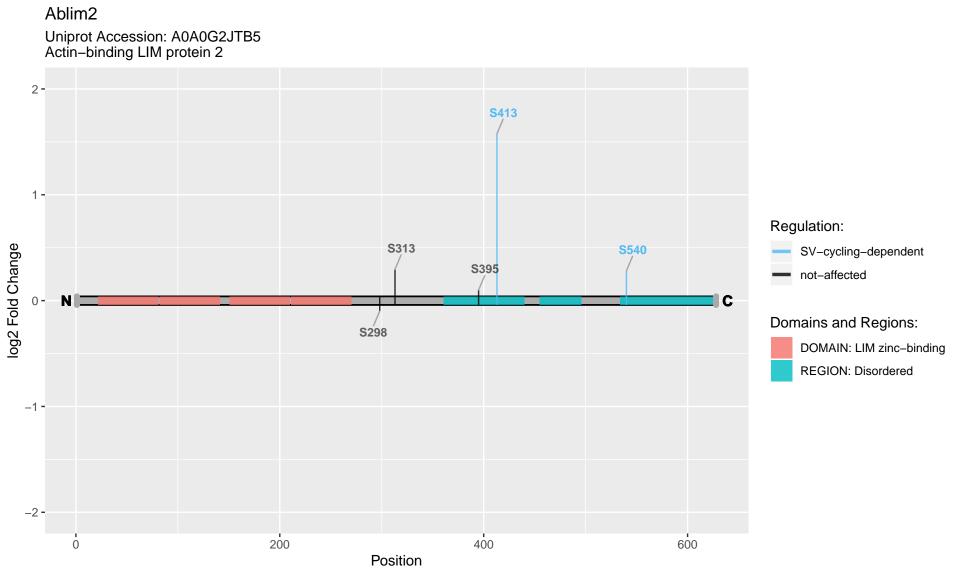
Uniprot Accession: Q63003 5E5 antigen 2 -**S251 S690** log2 Fold Change **S695** Regulation: SV-cycling-dependent C not-affected -1 **-**-2 **-**200 600 400 800 Position

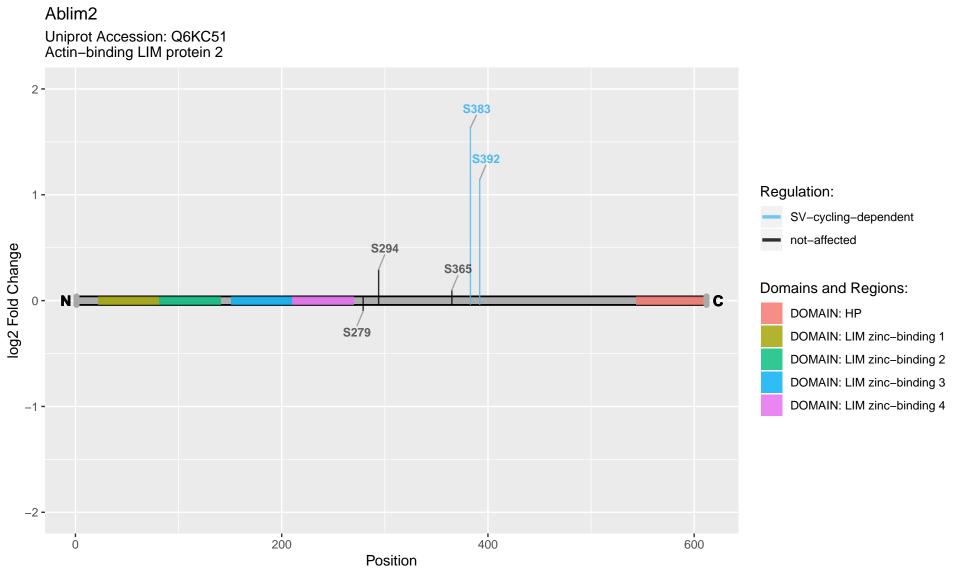


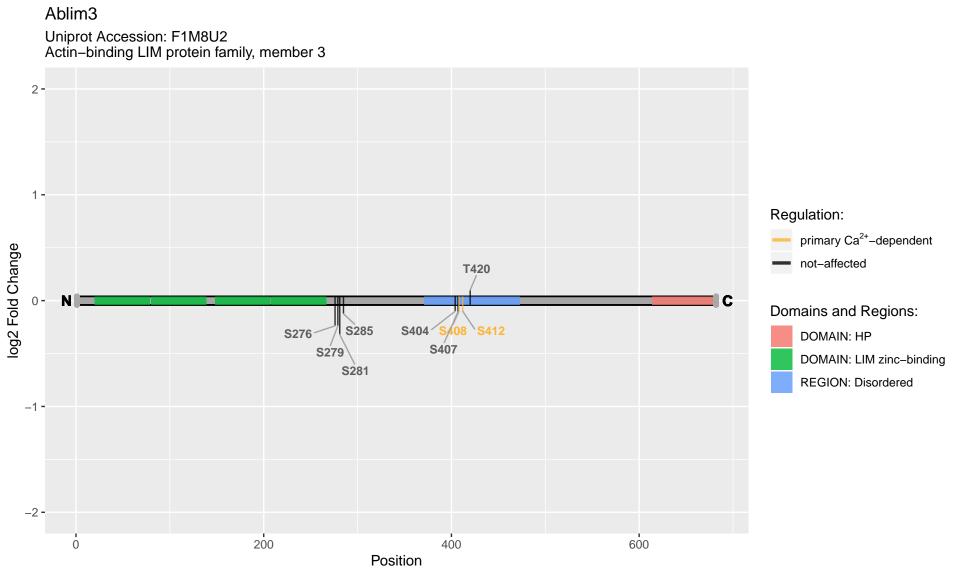


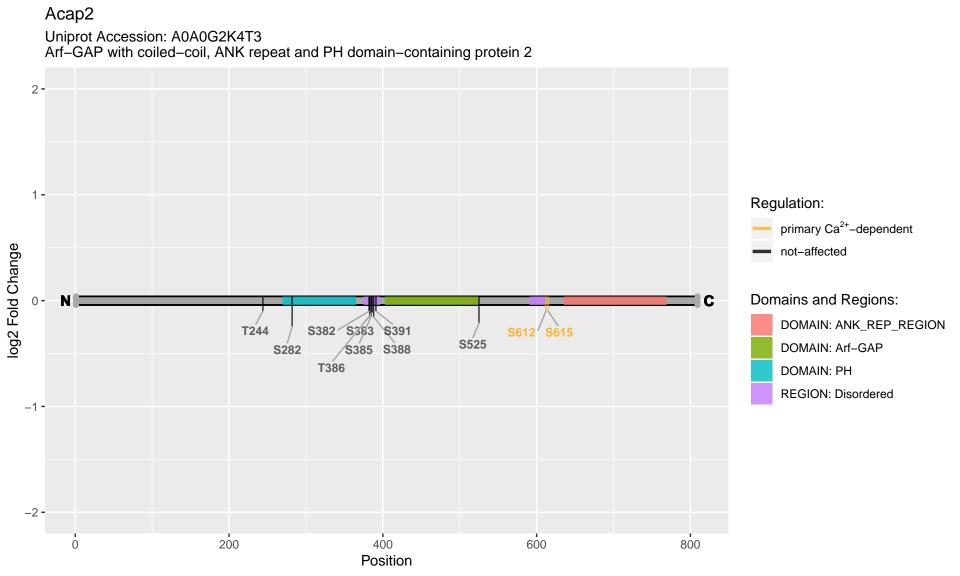


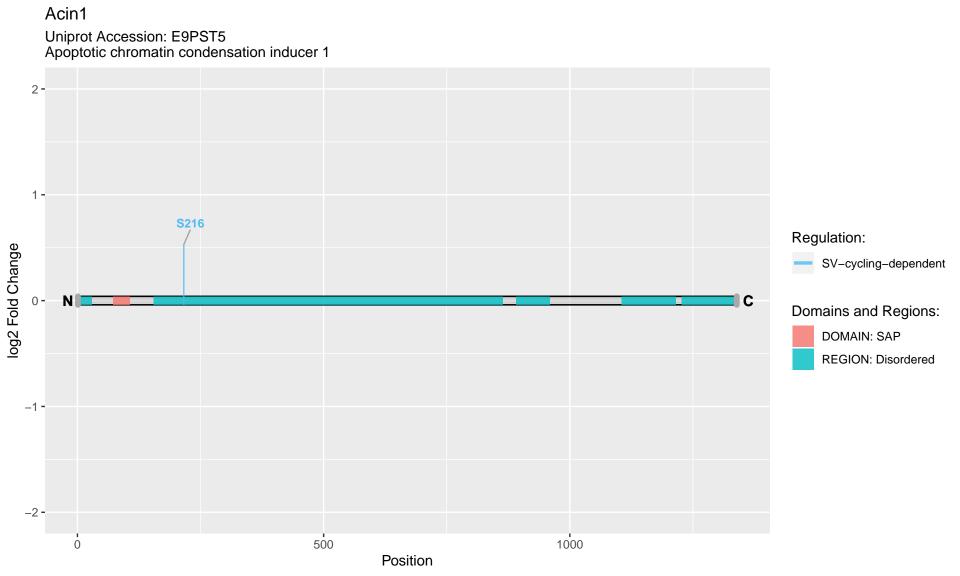


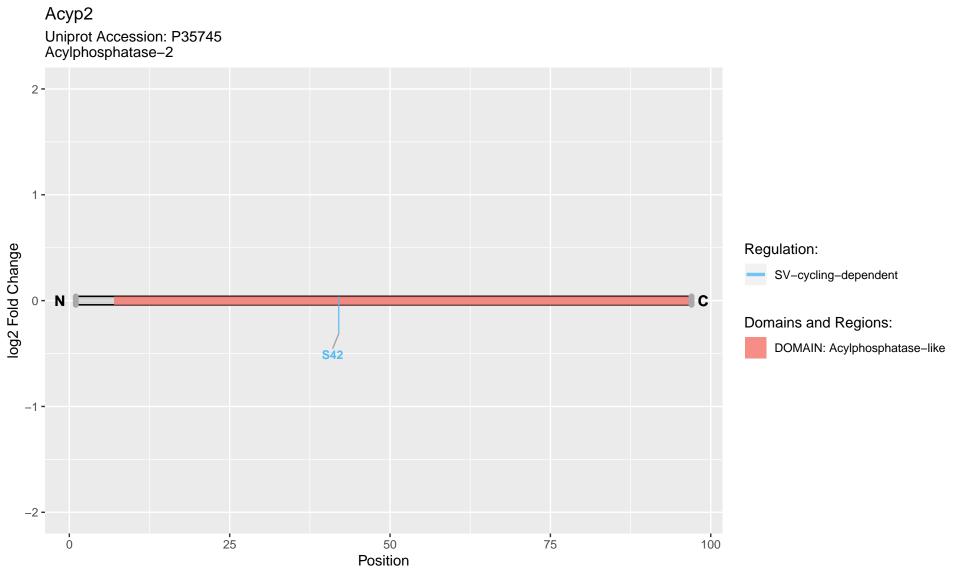


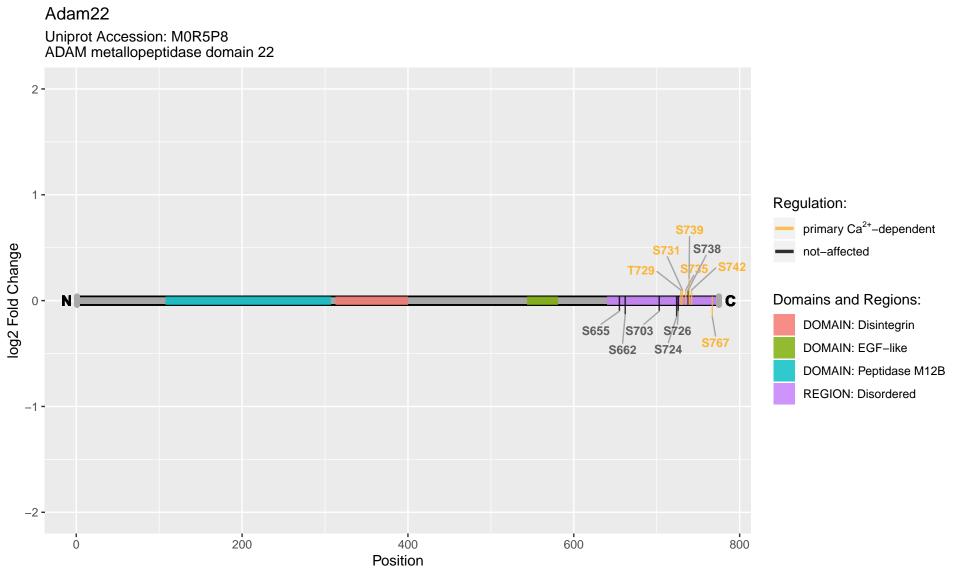


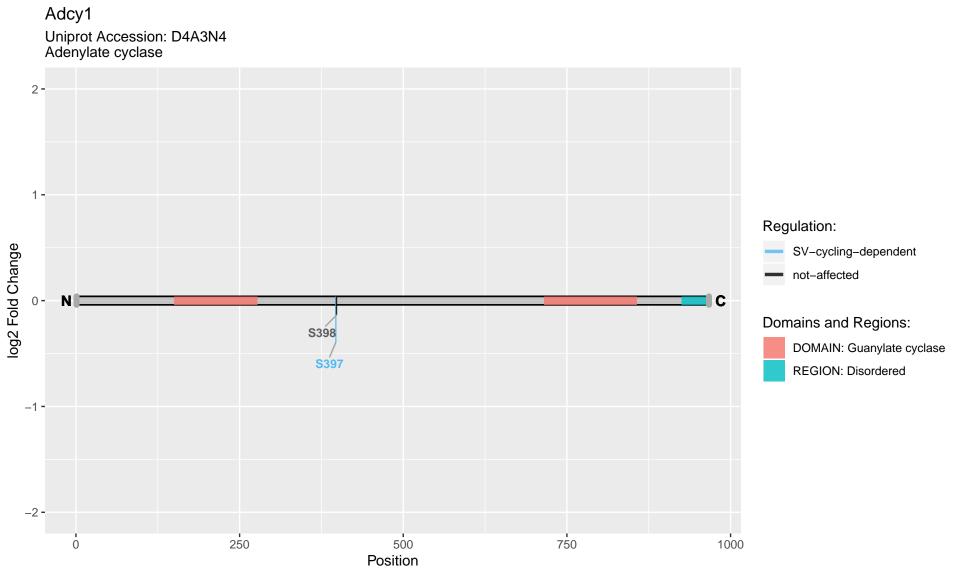


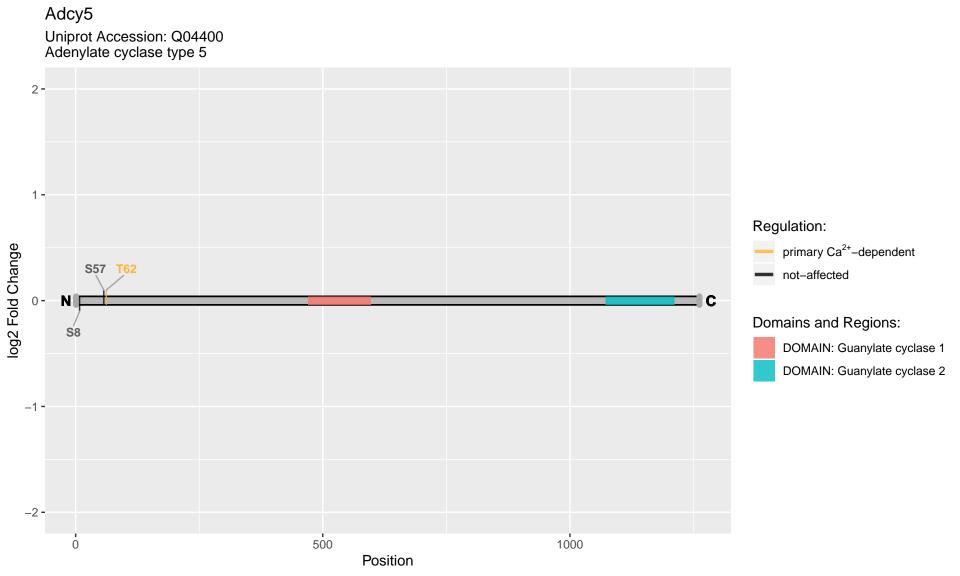


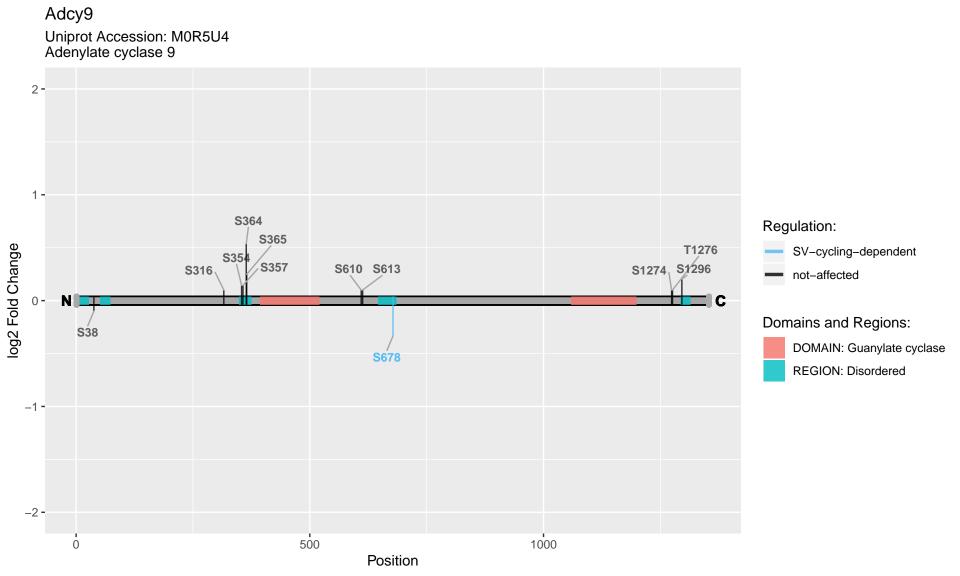


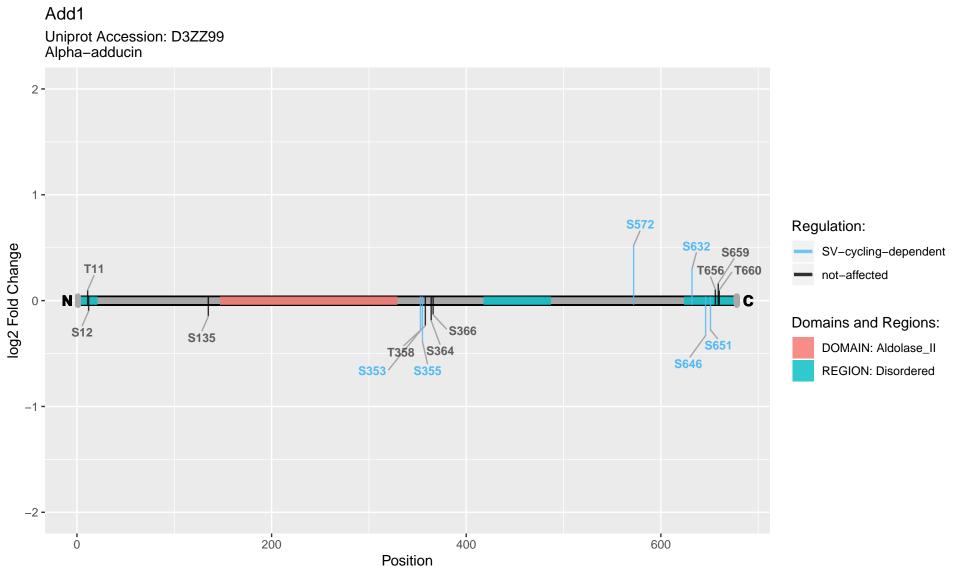


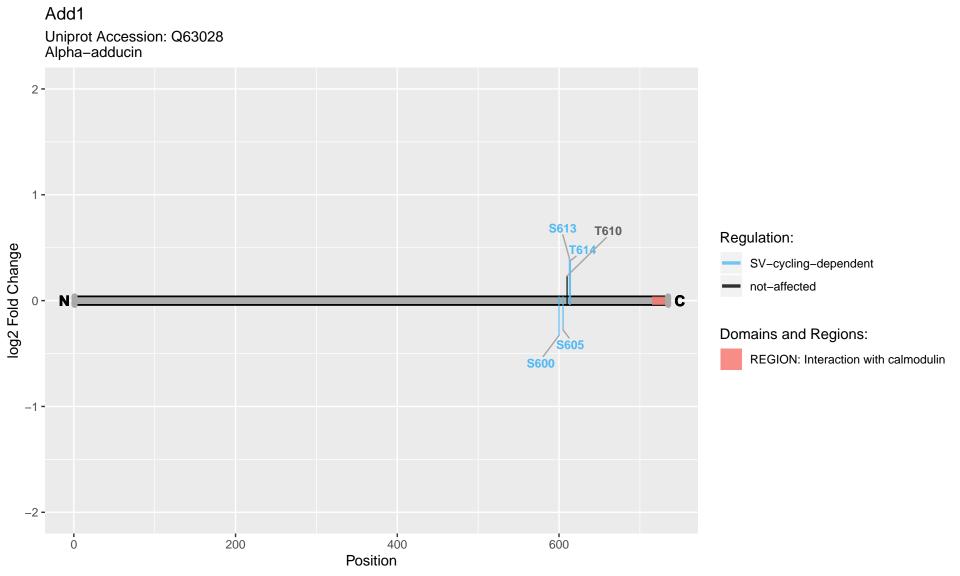


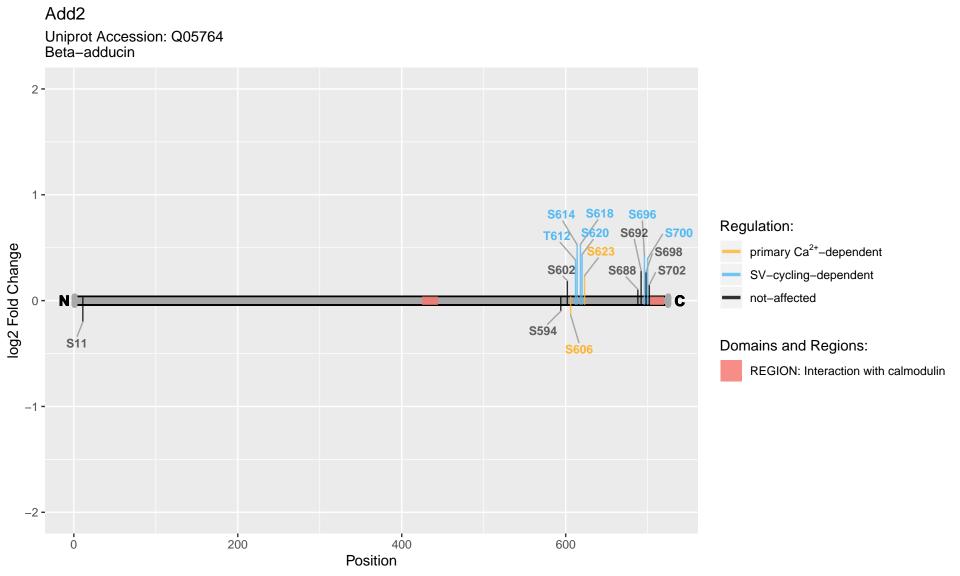


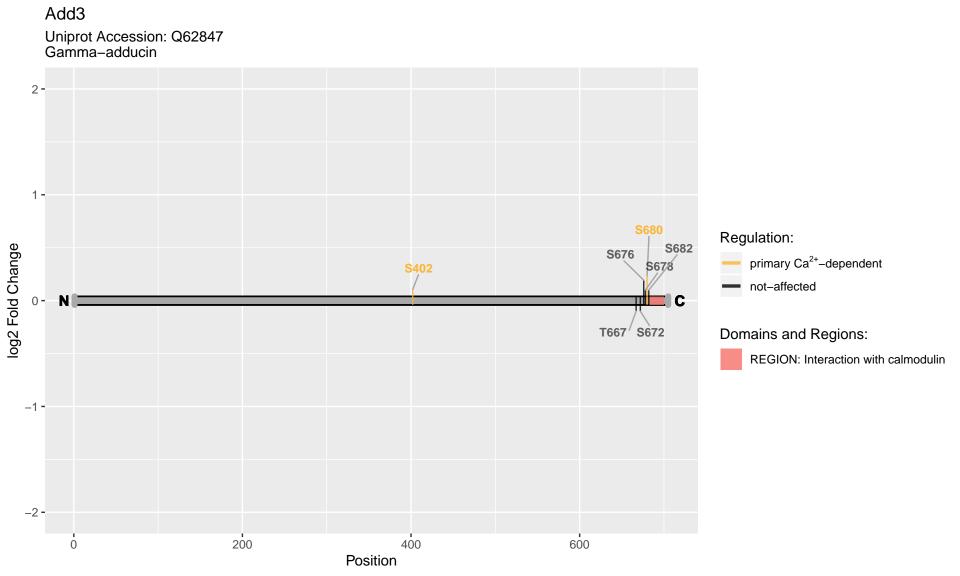


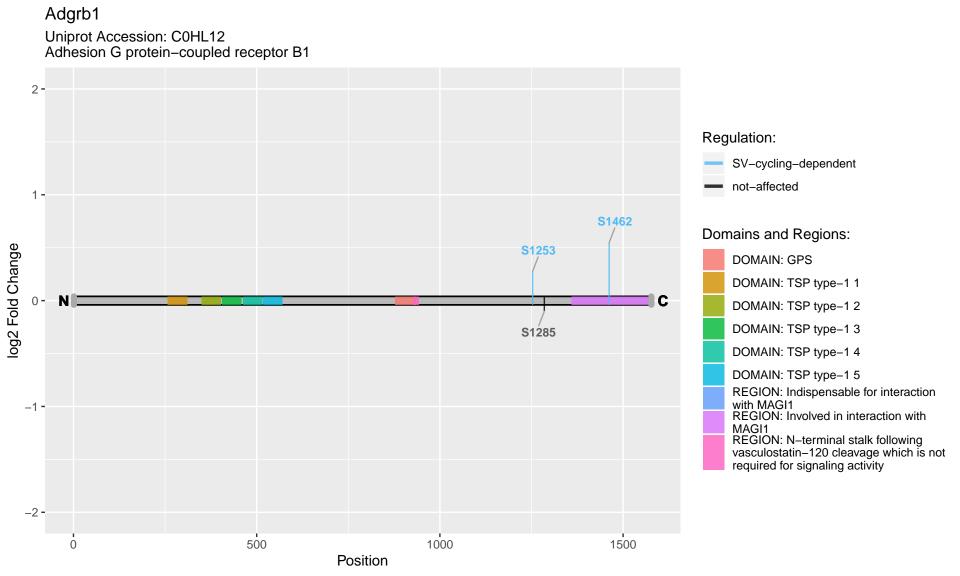


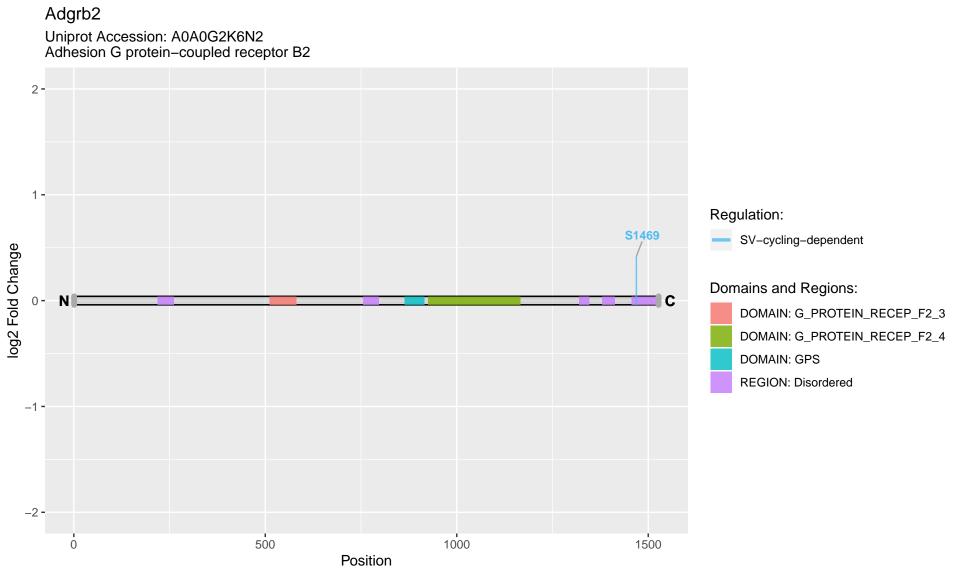


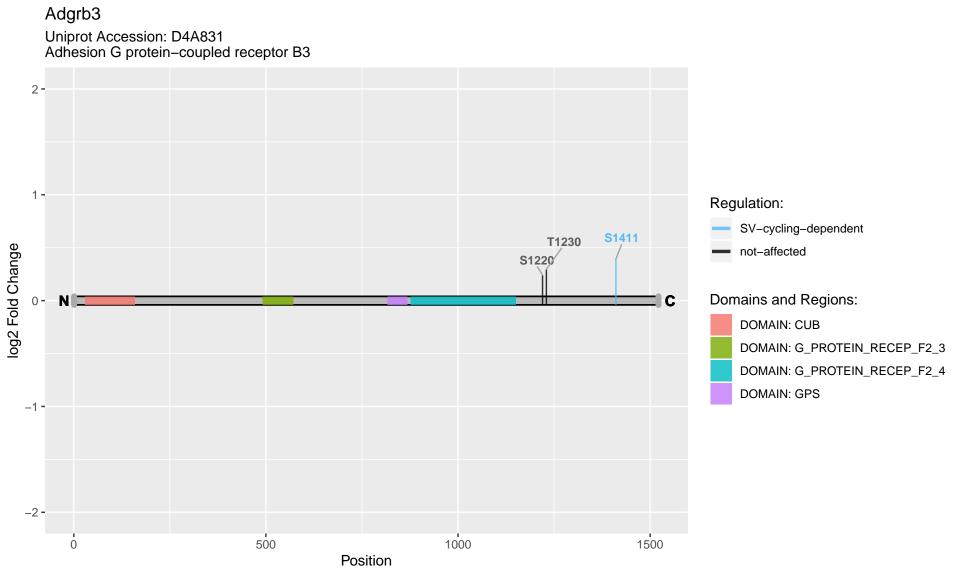


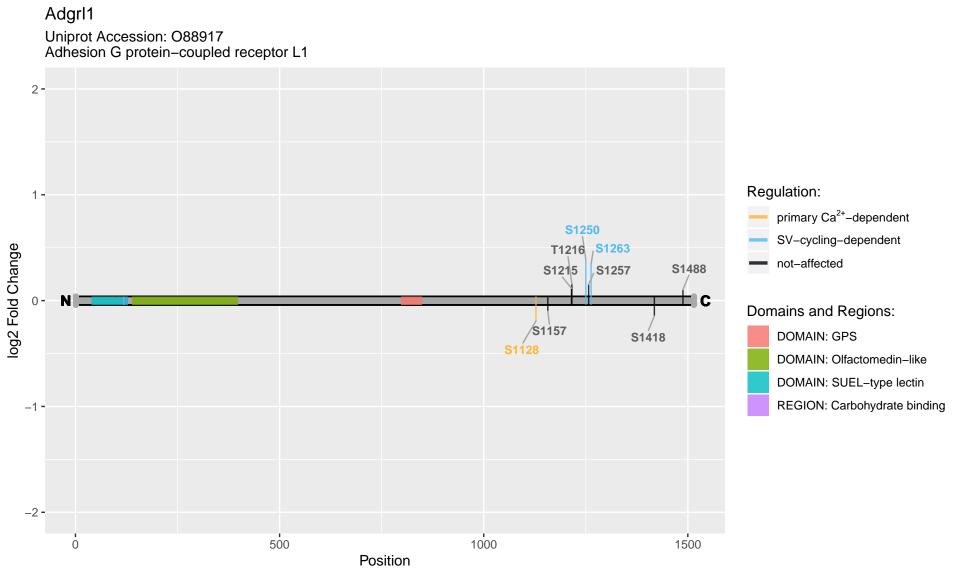


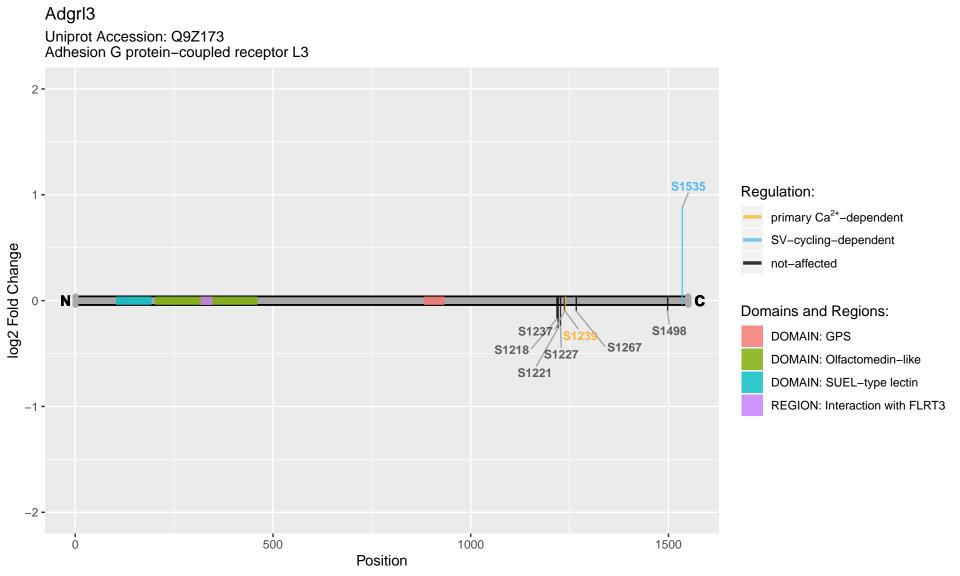


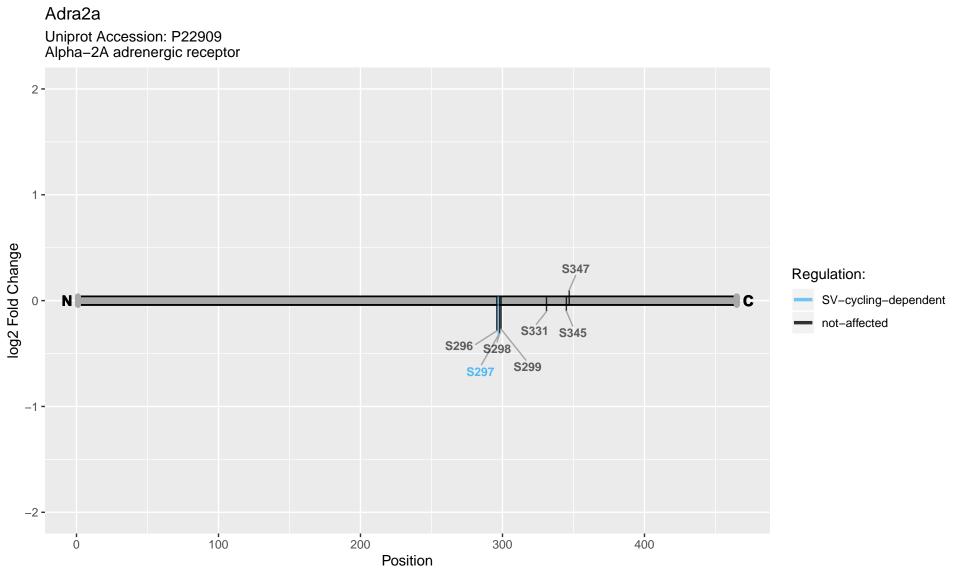


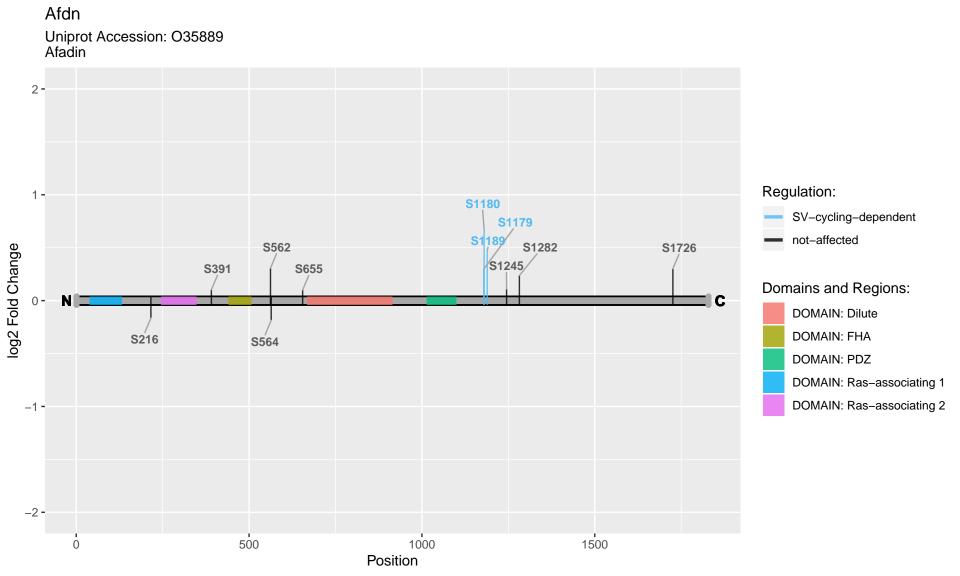


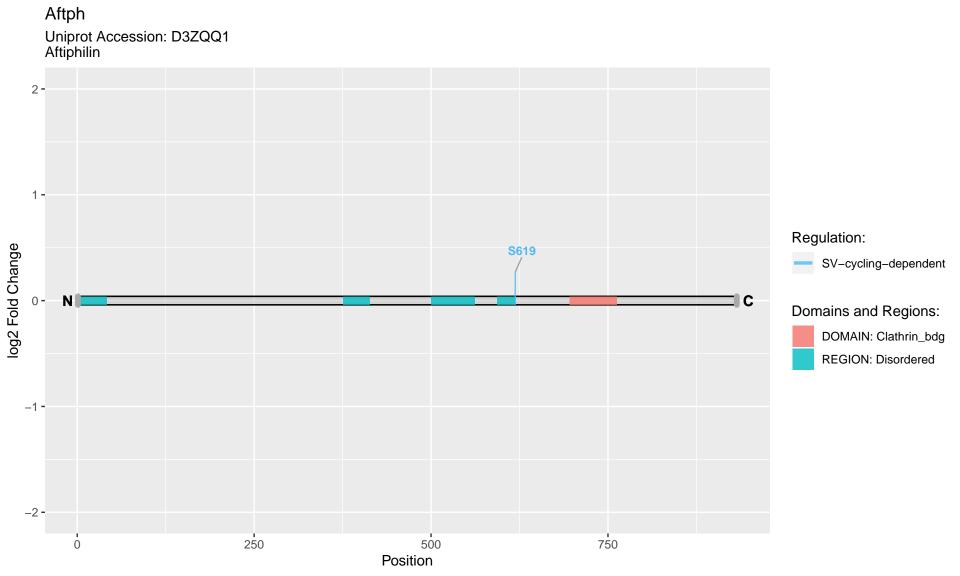




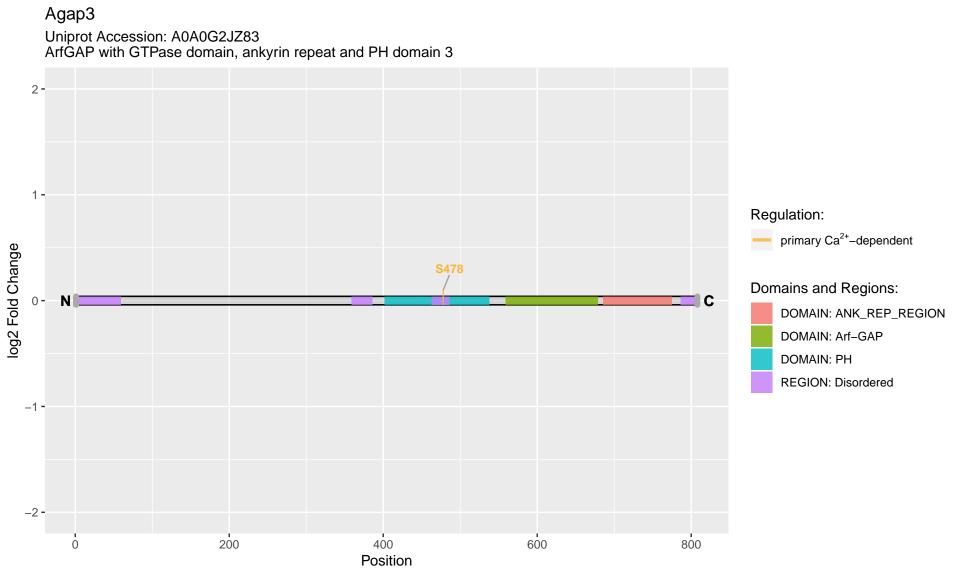


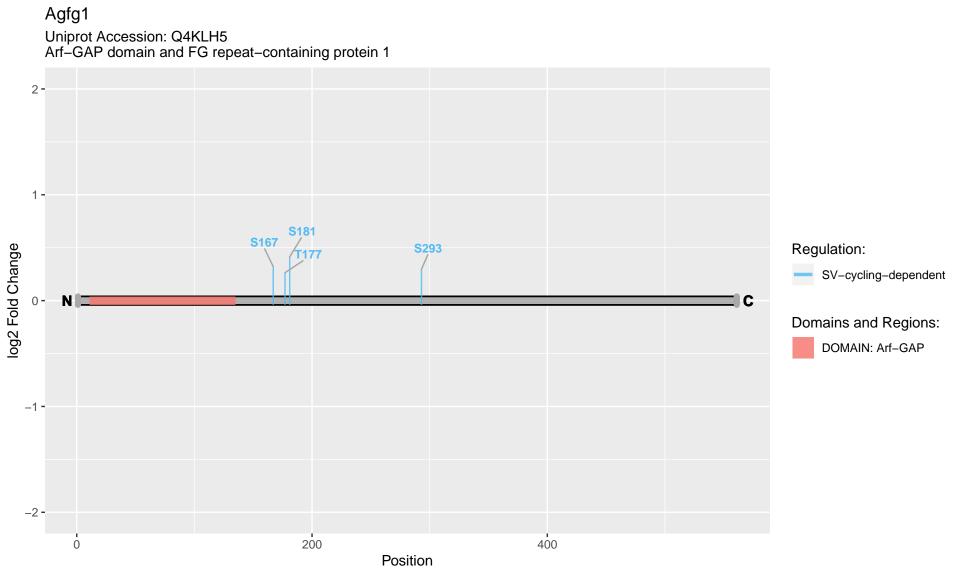


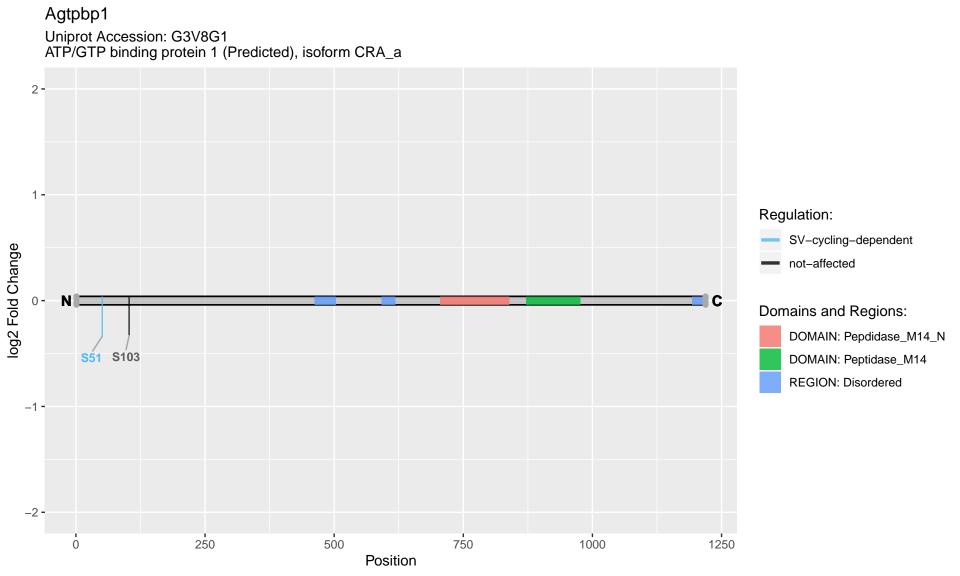


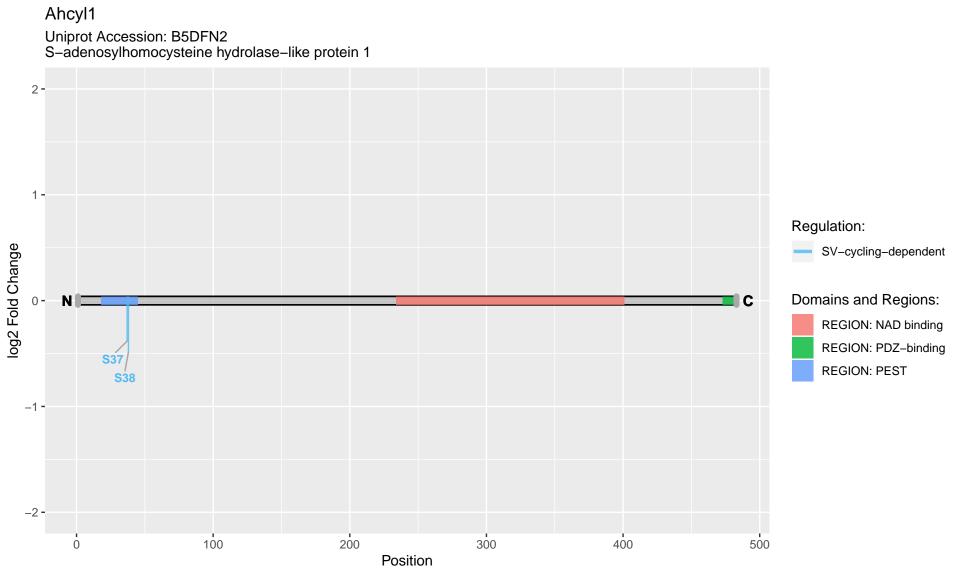


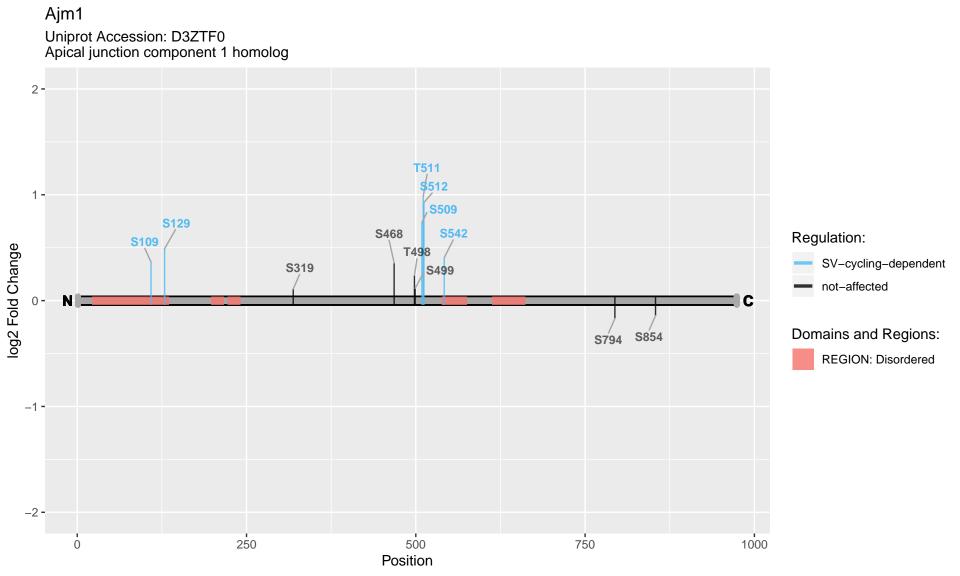
Agap2 Uniprot Accession: Q8CGU4 Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 2 2 -**S650** Regulation: primary Ca²⁺-dependent 1 -SV-cycling-dependent **S1171** not-affected S1175 log2 Fold Change T173 T838 \$659 S168 /S175 Domains and Regions: DOMAIN: Arf-GAP S632 **S167** DOMAIN: PH **S921** S642 REGION: G domain T641 **REGION: Interaction with EPB41L1 REGION: Interaction with PLCG1** _1 **-**REGION: Interactions with HOMER1 and NF2 -2 **-**250 500 750 1000 Position

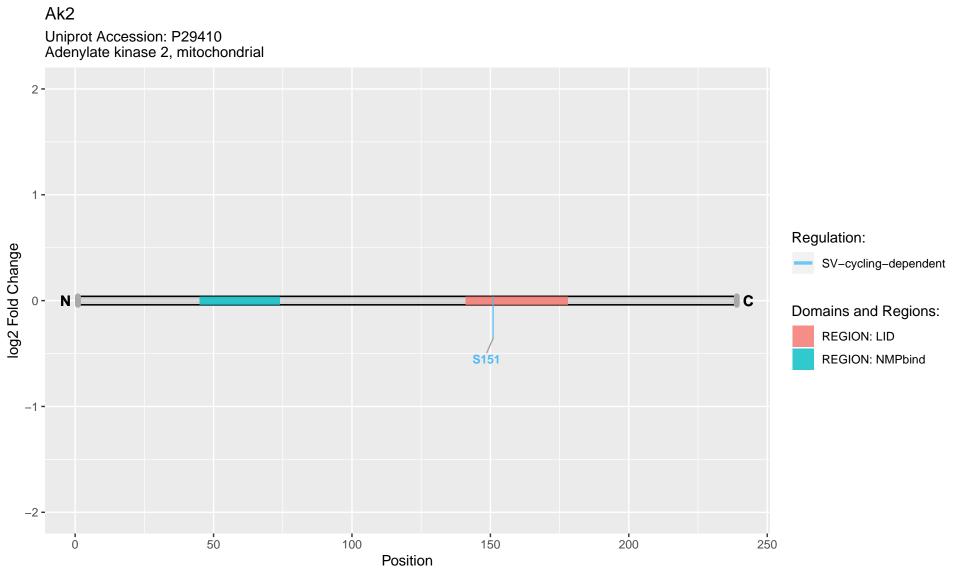


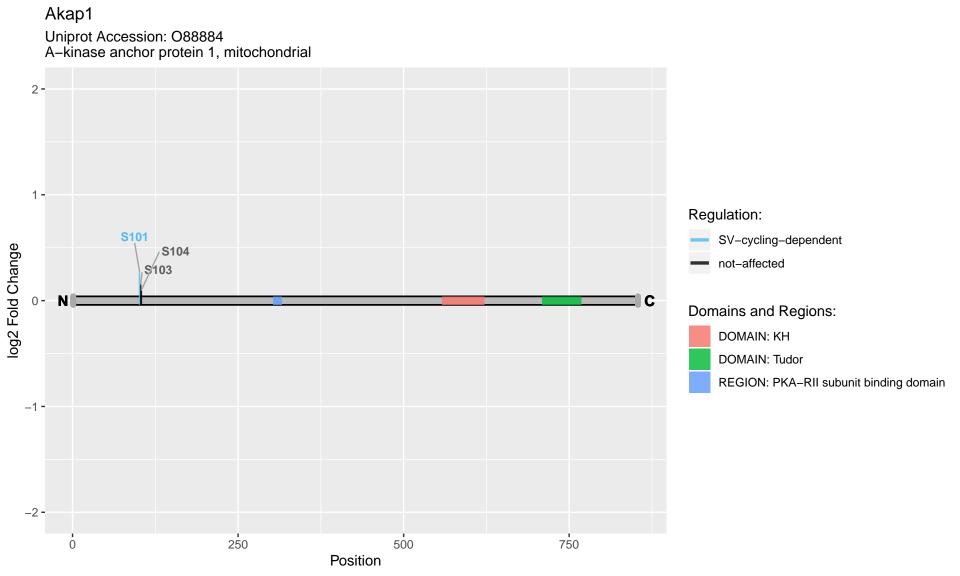


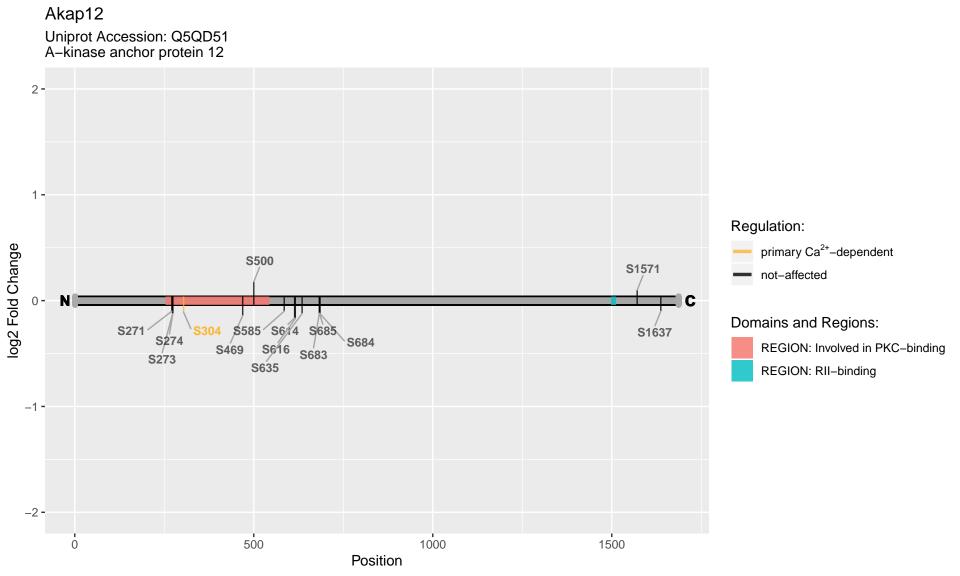


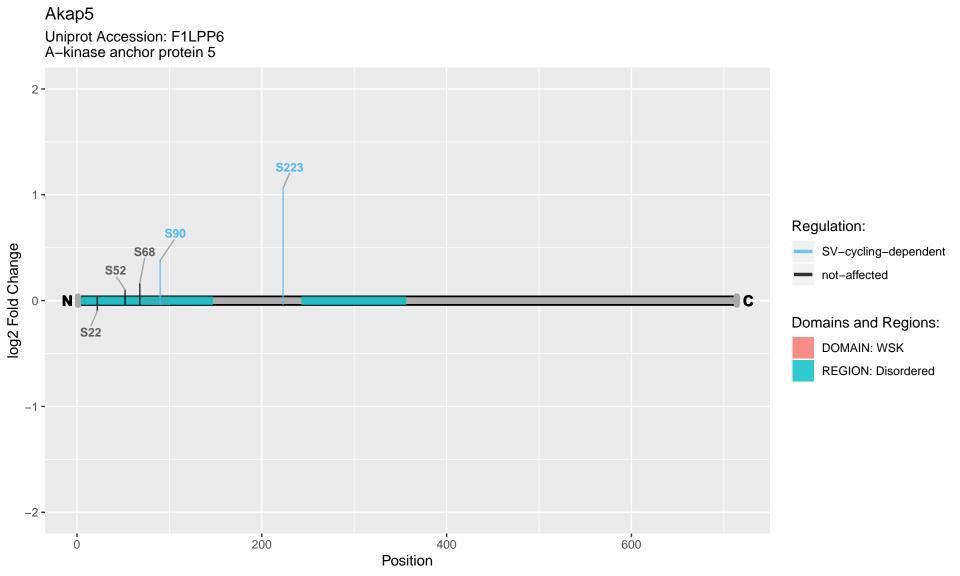


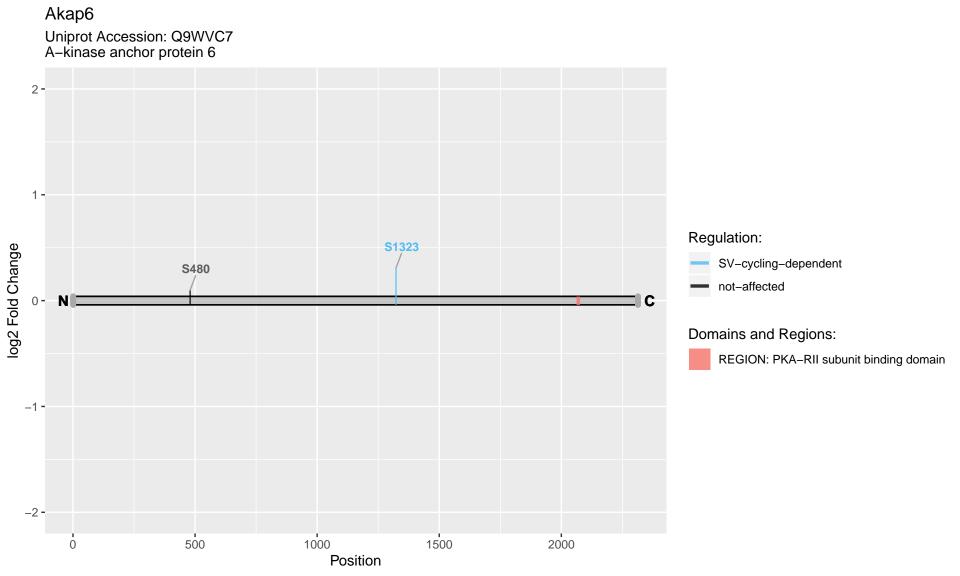


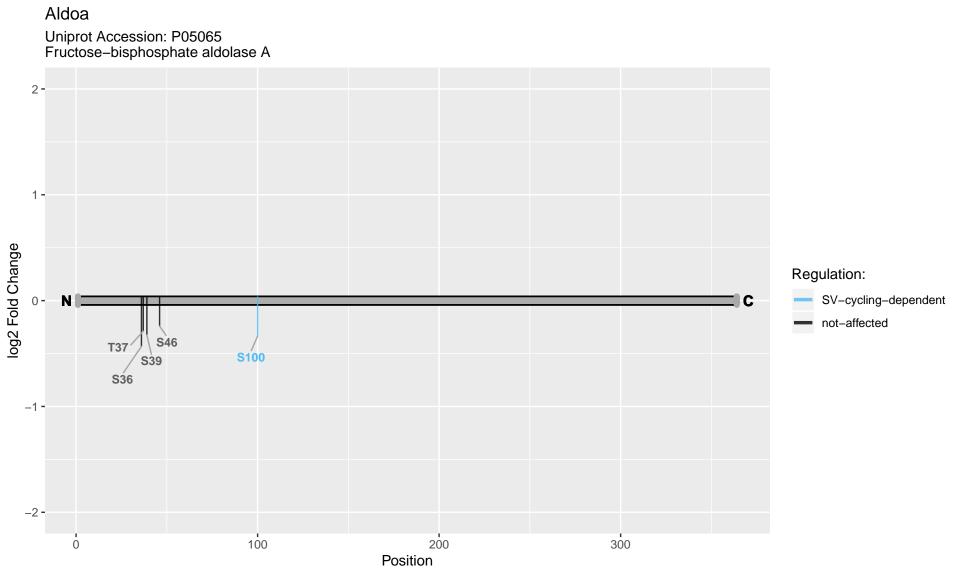


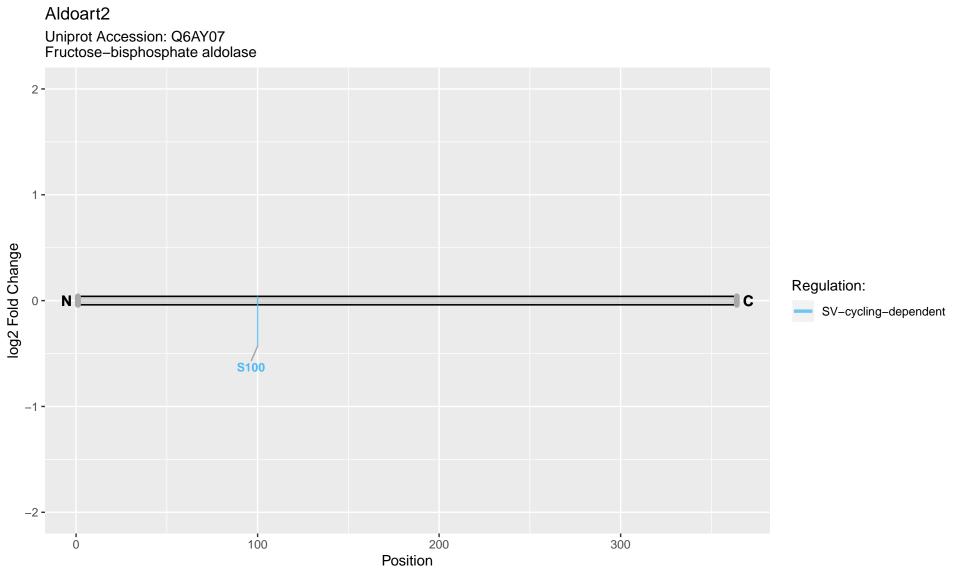


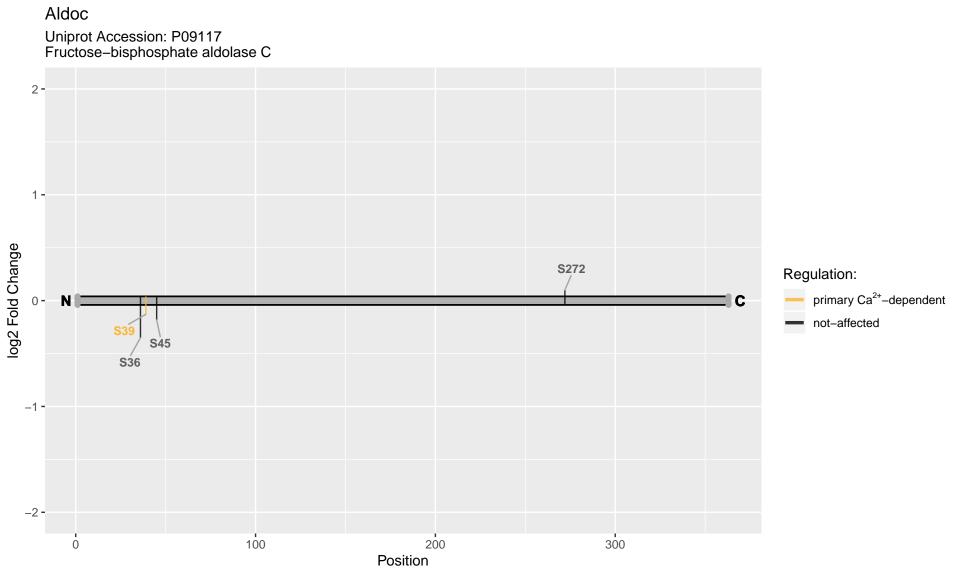


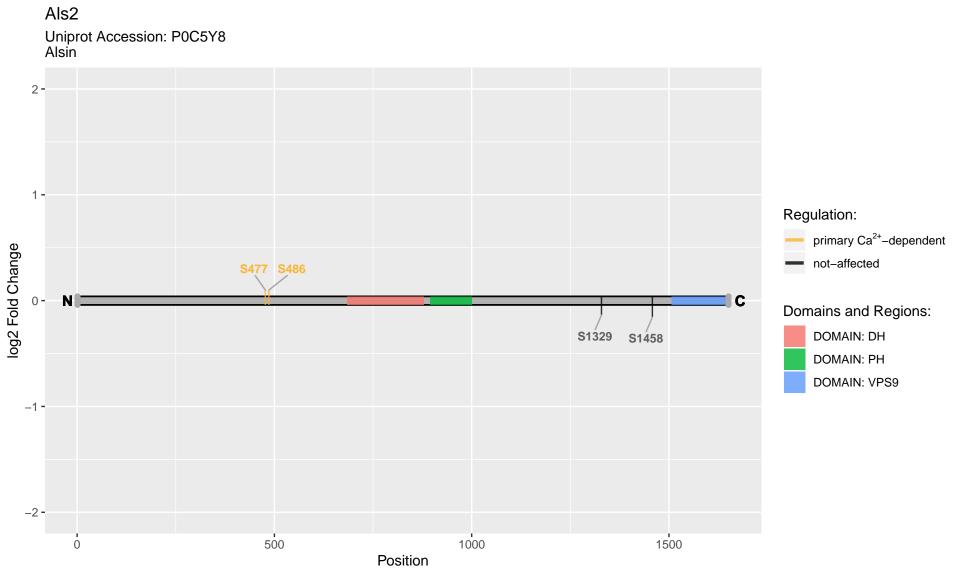


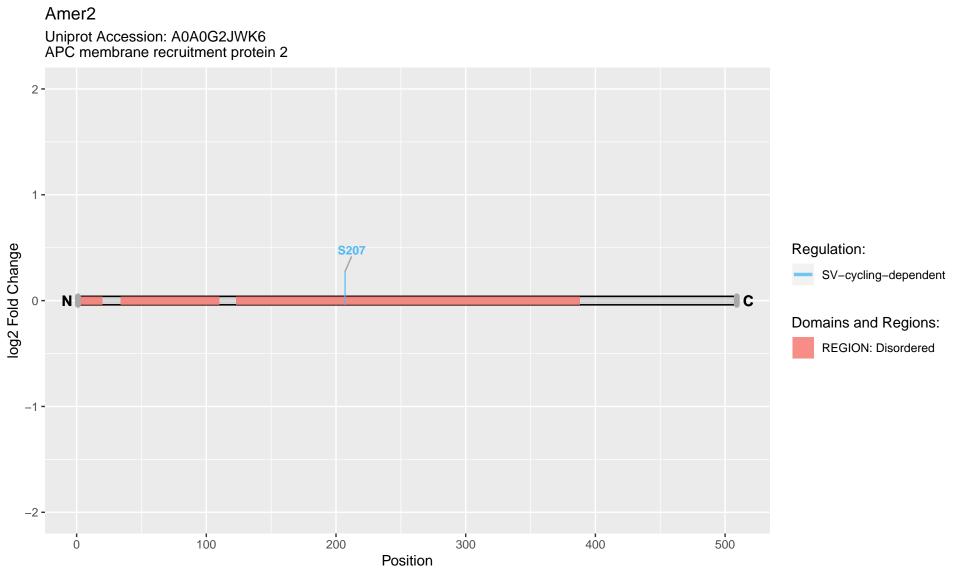


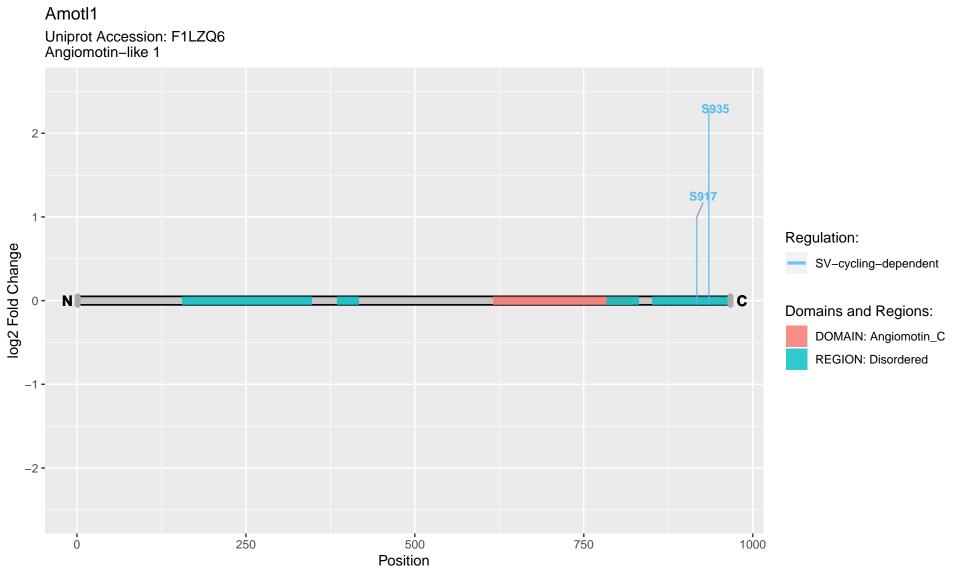


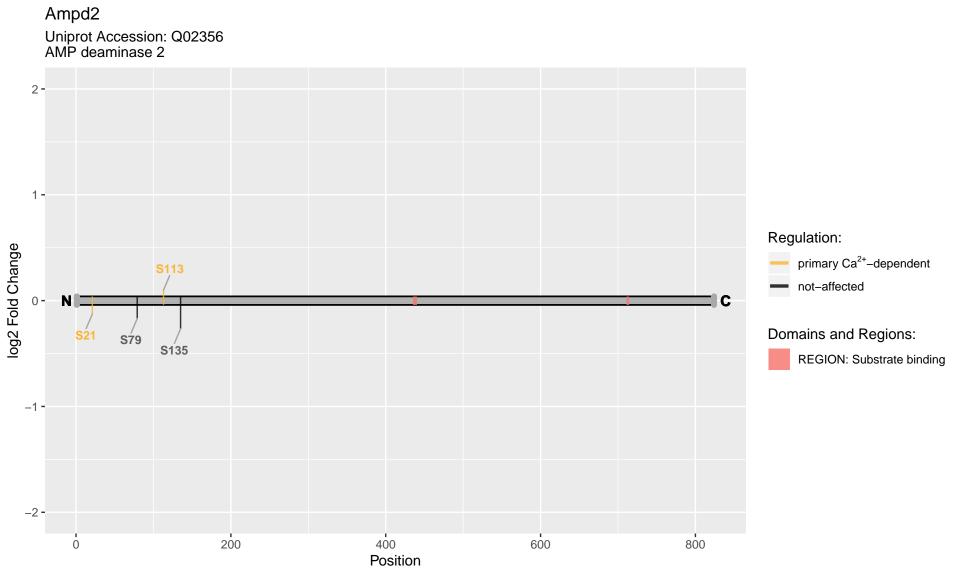


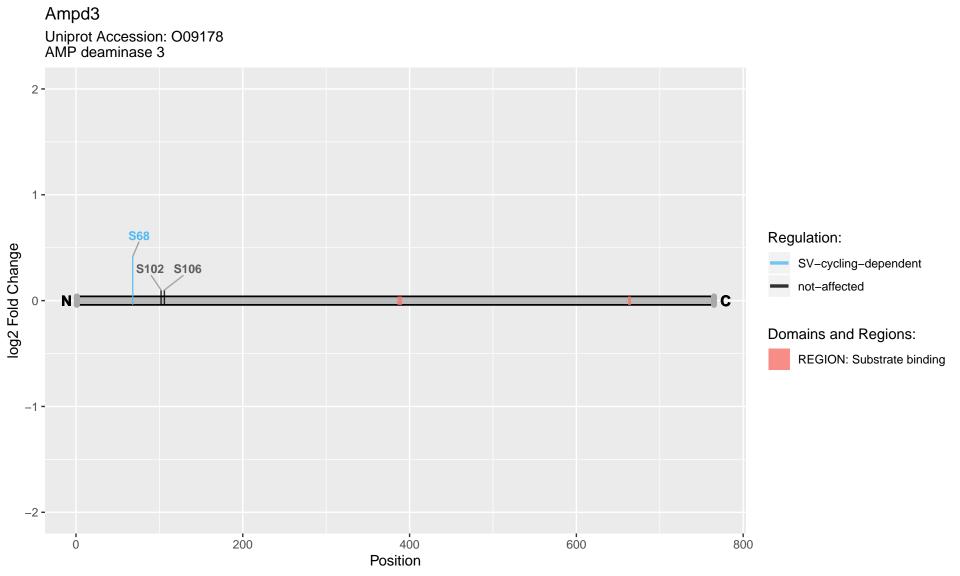


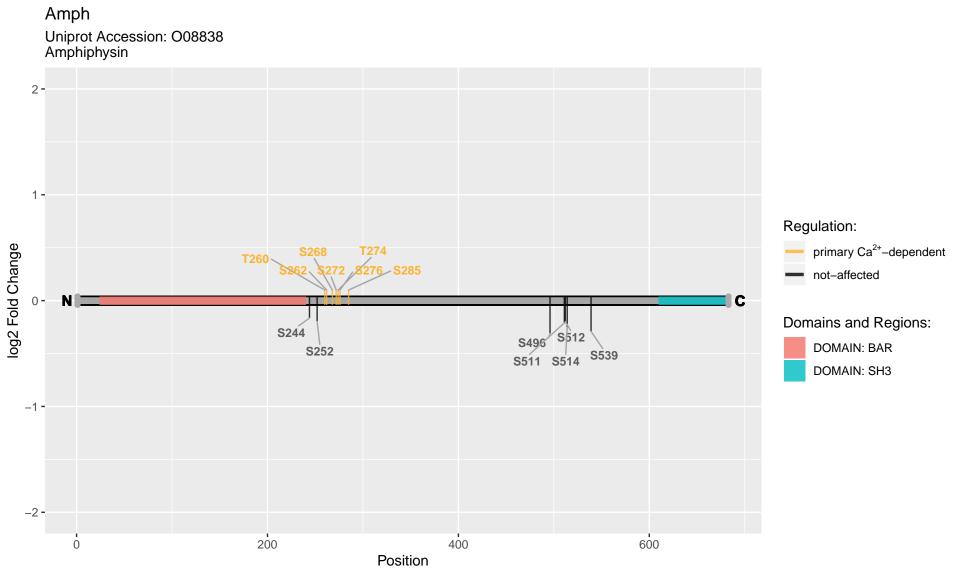


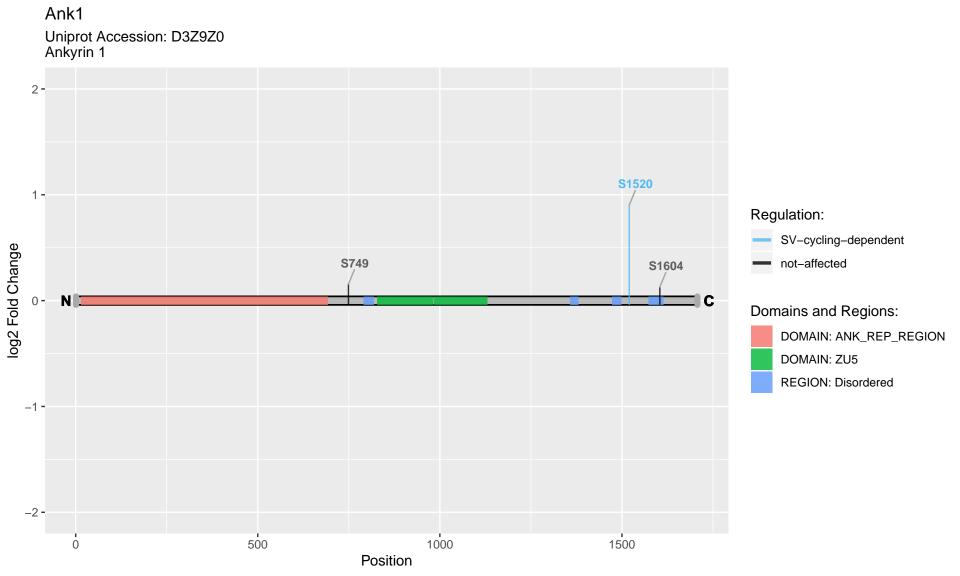


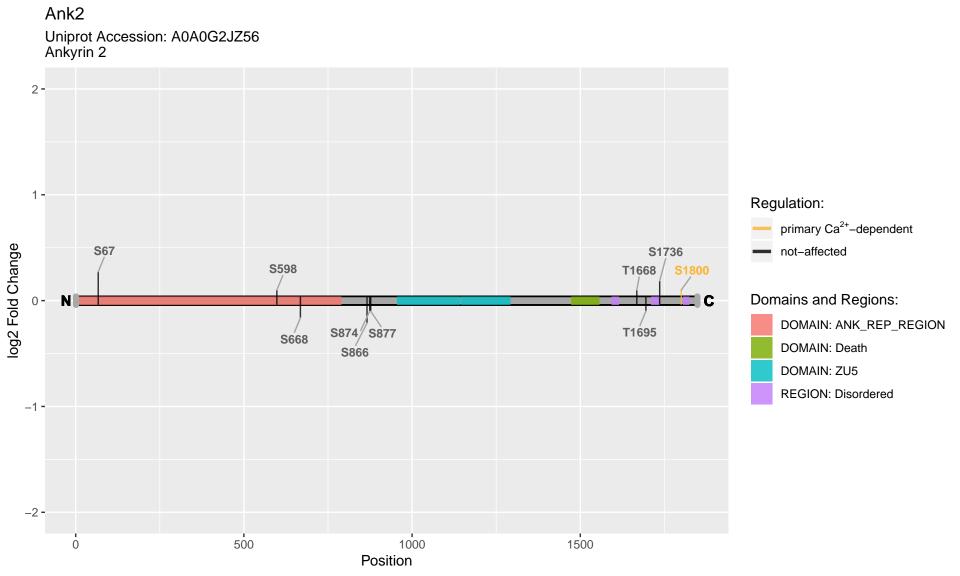


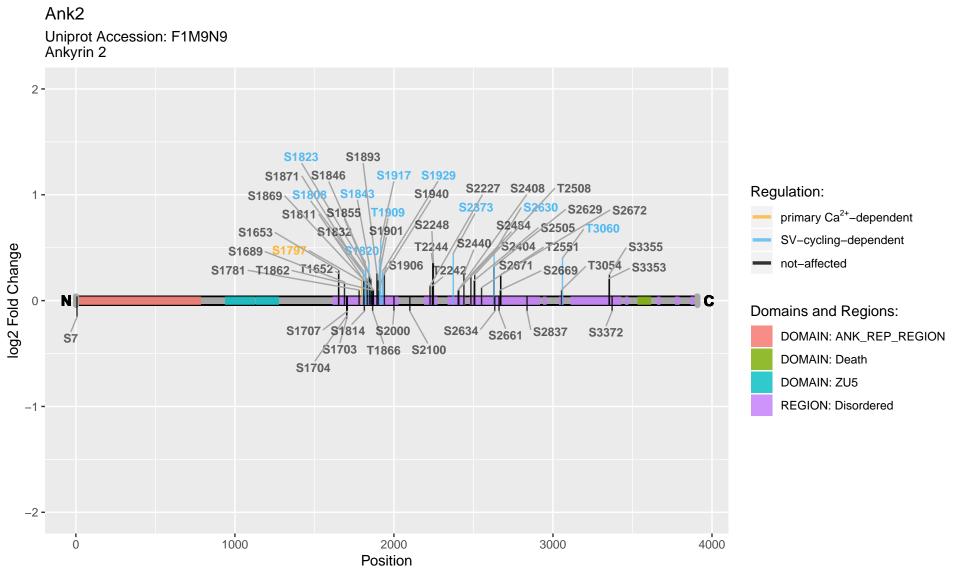


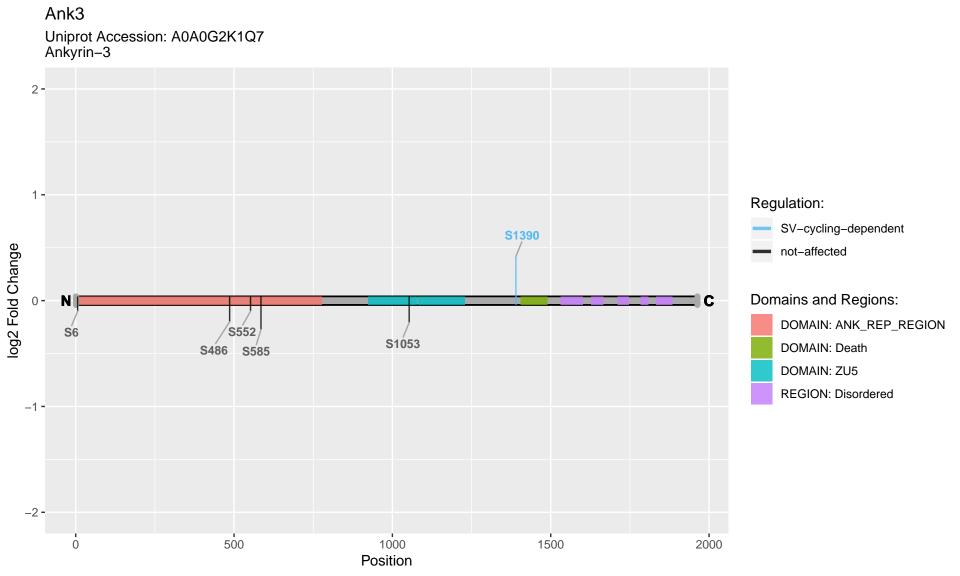


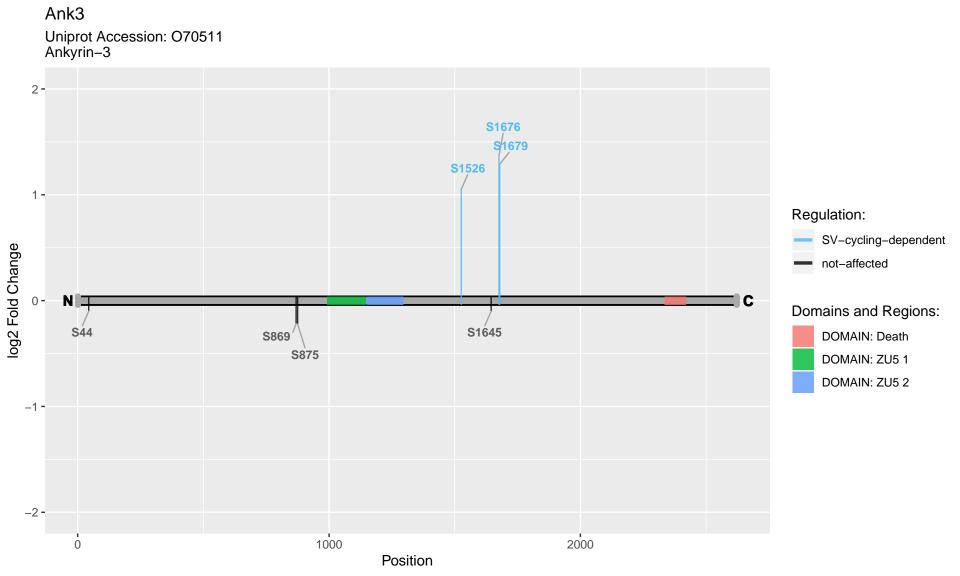


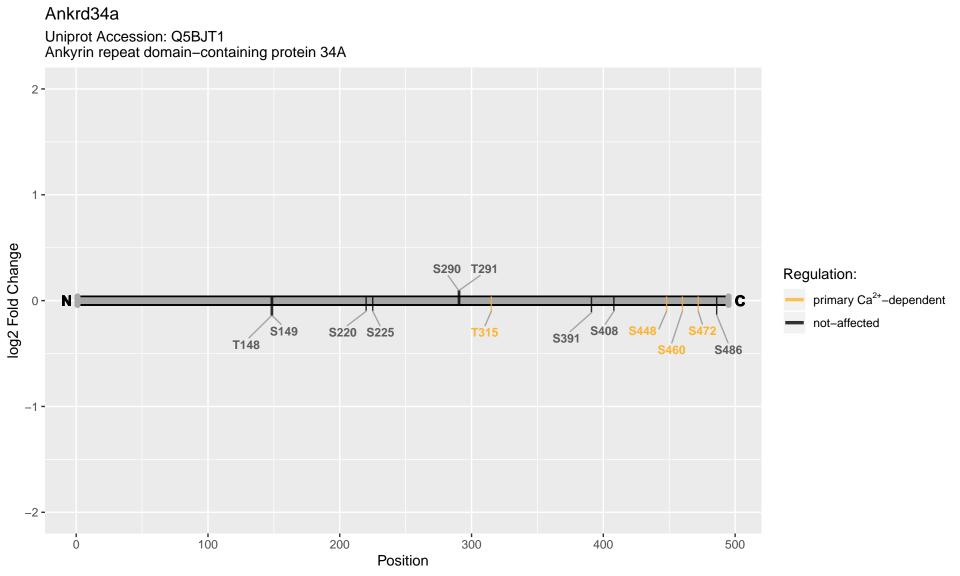


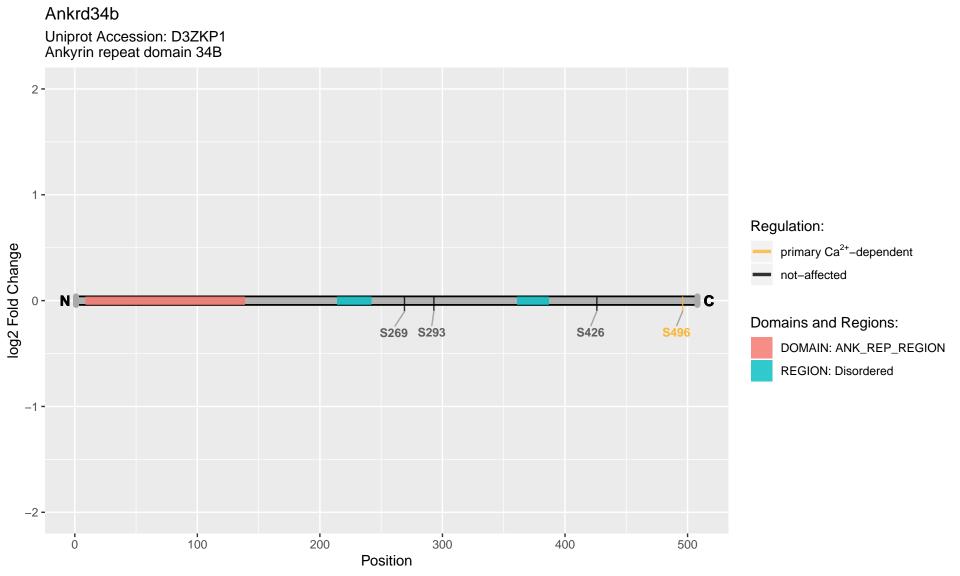


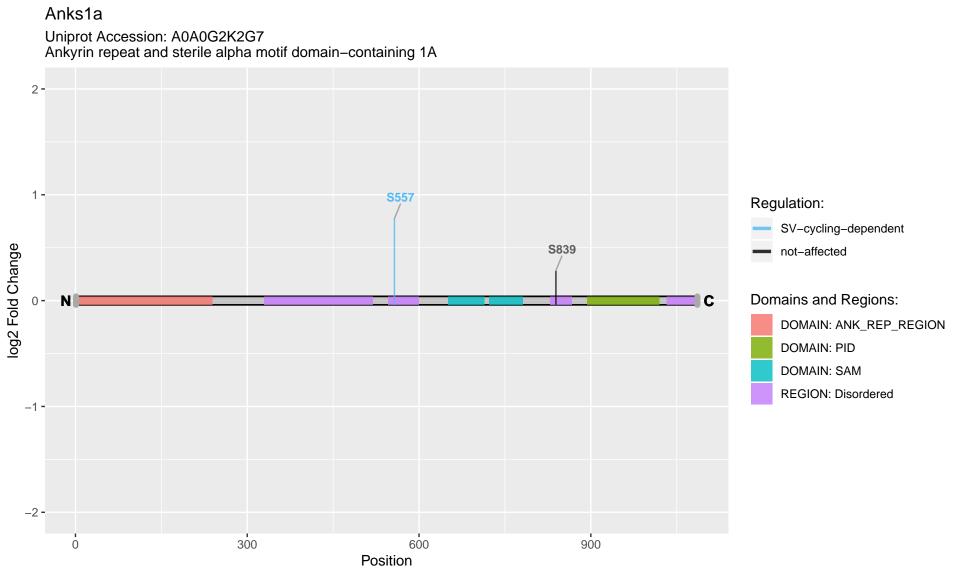


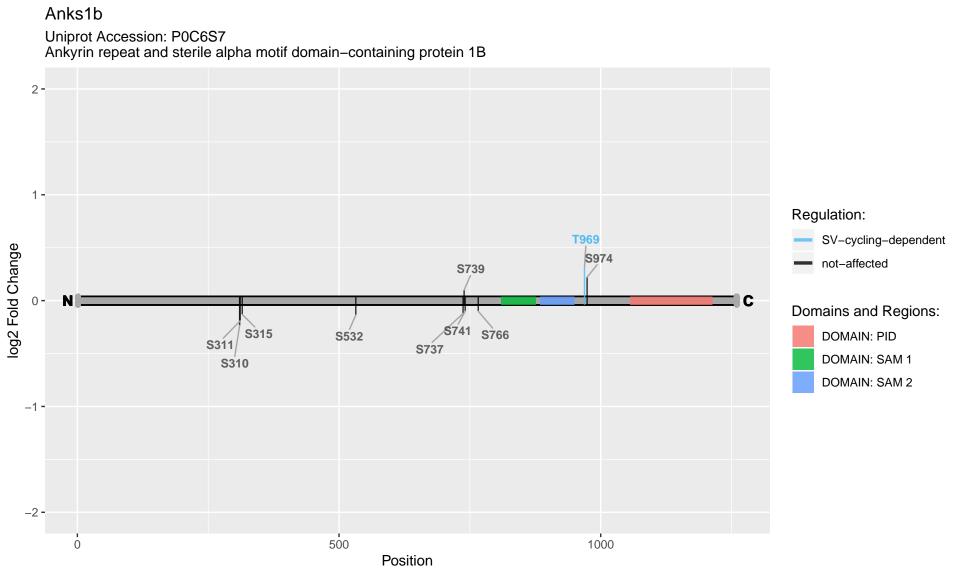


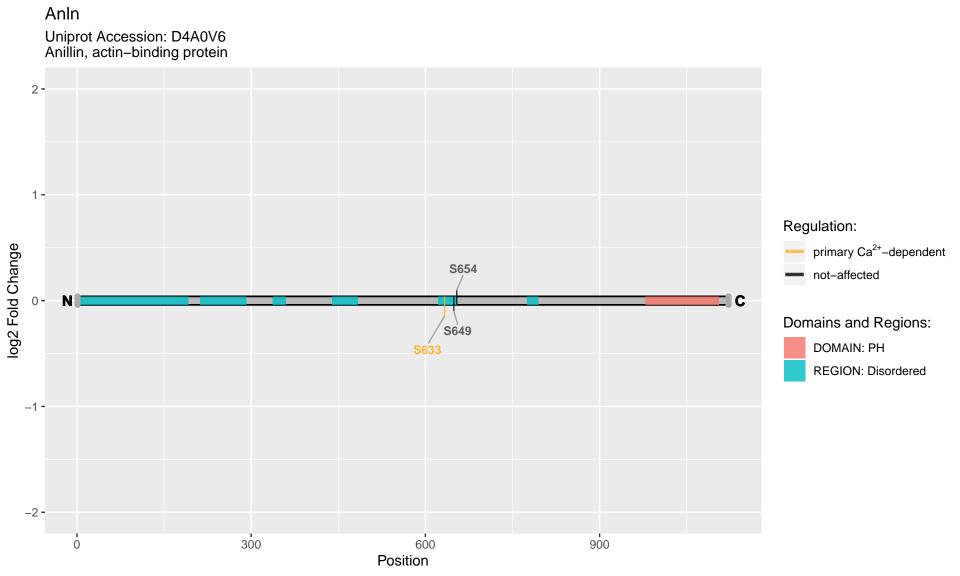


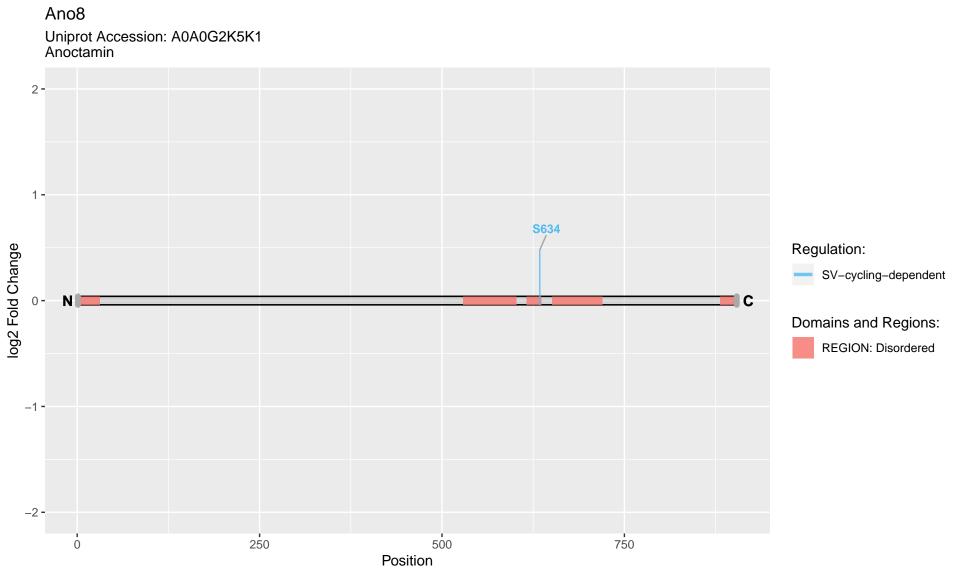


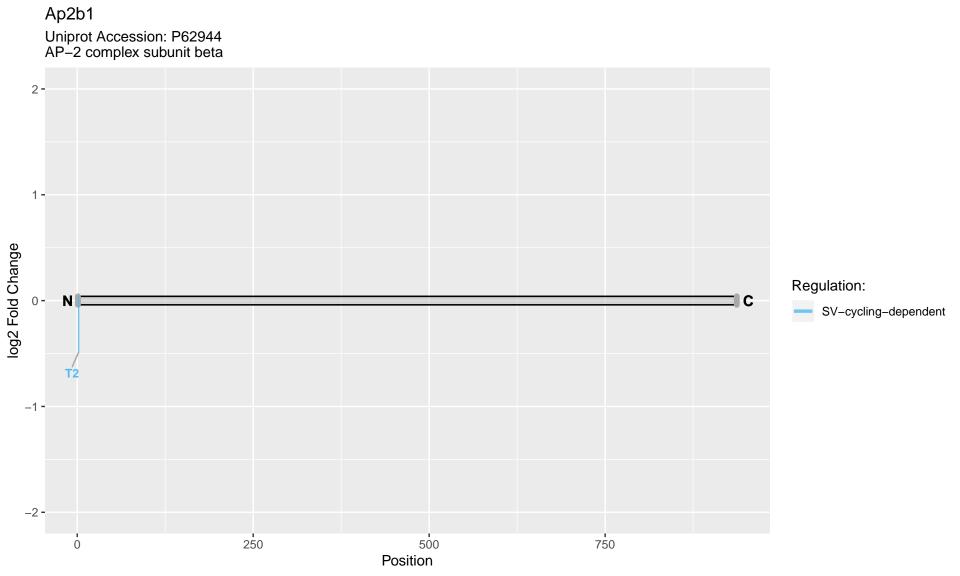


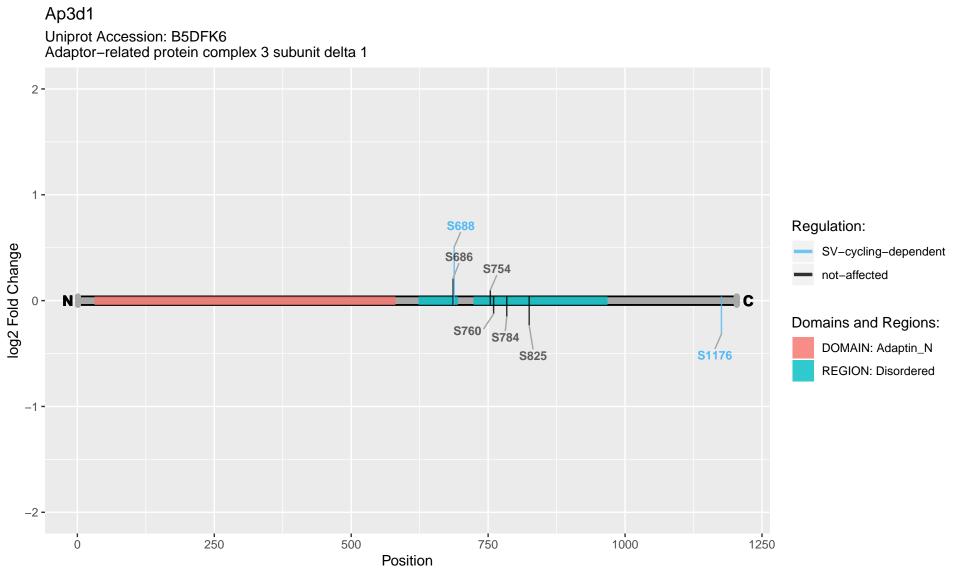


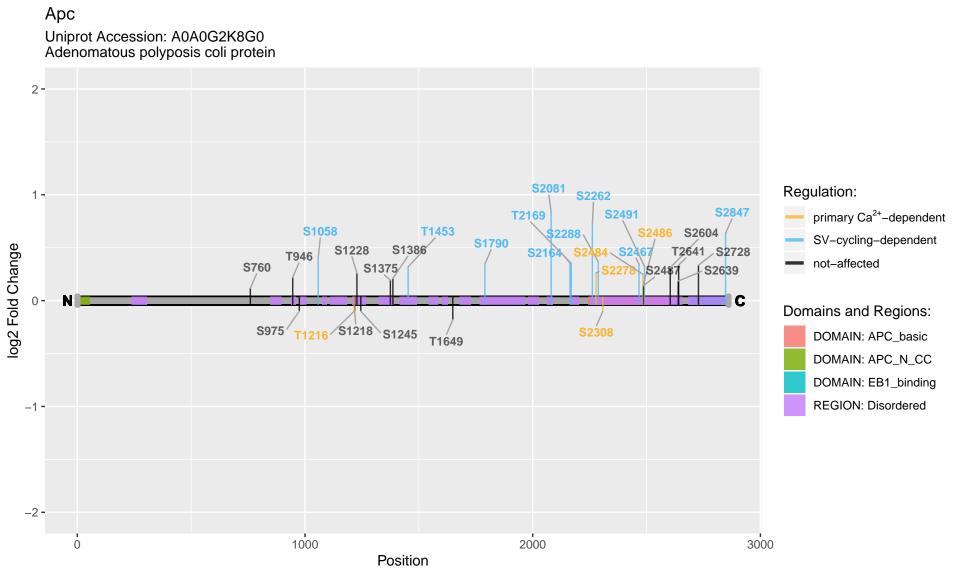


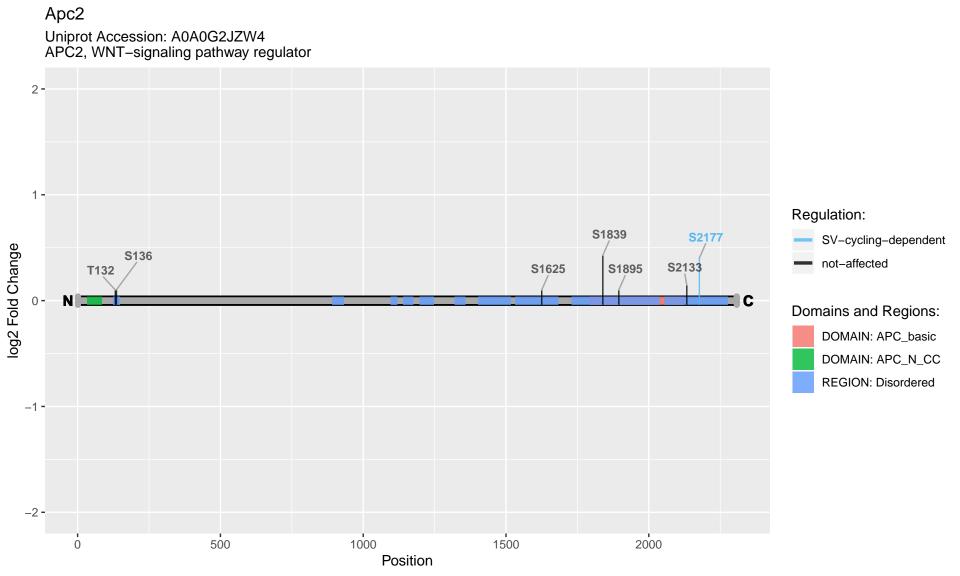


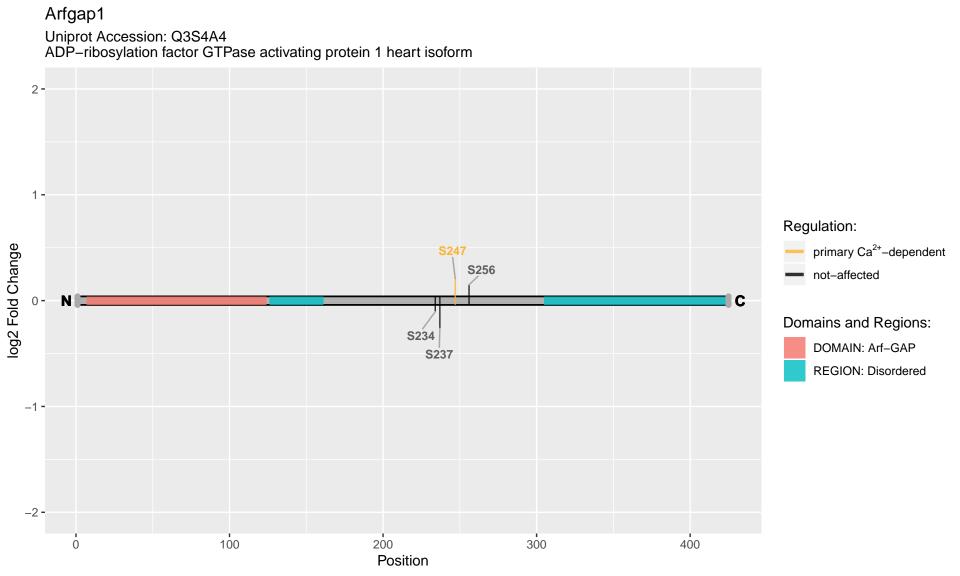


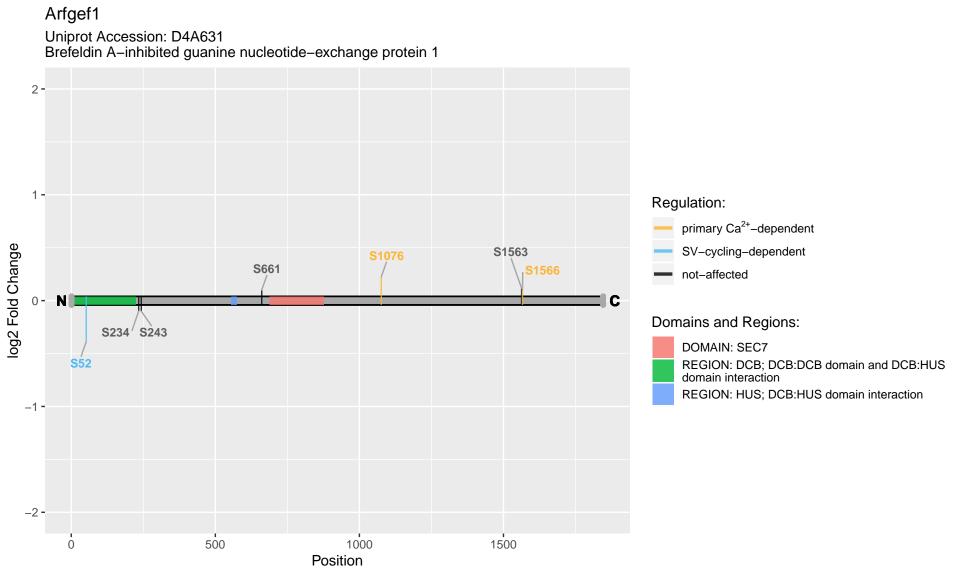


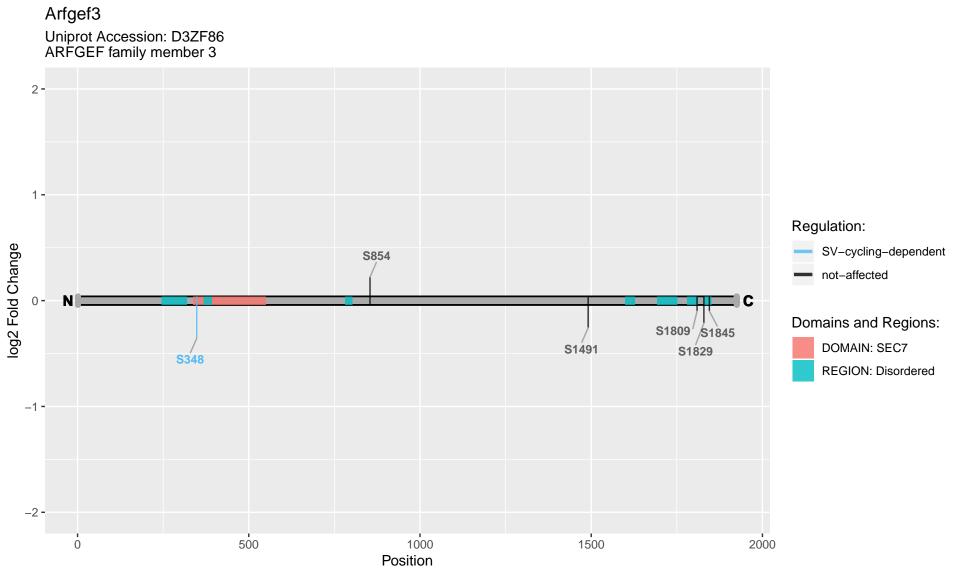


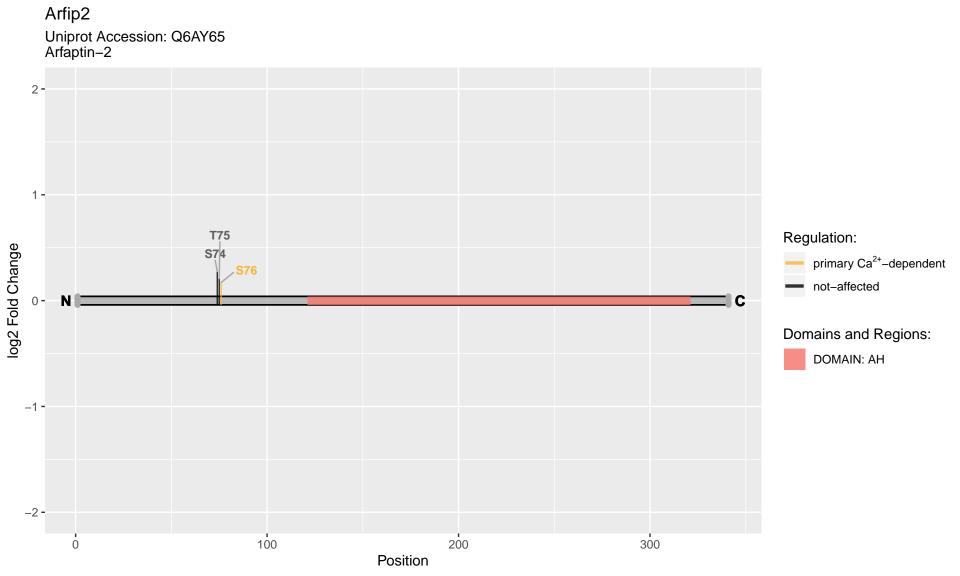


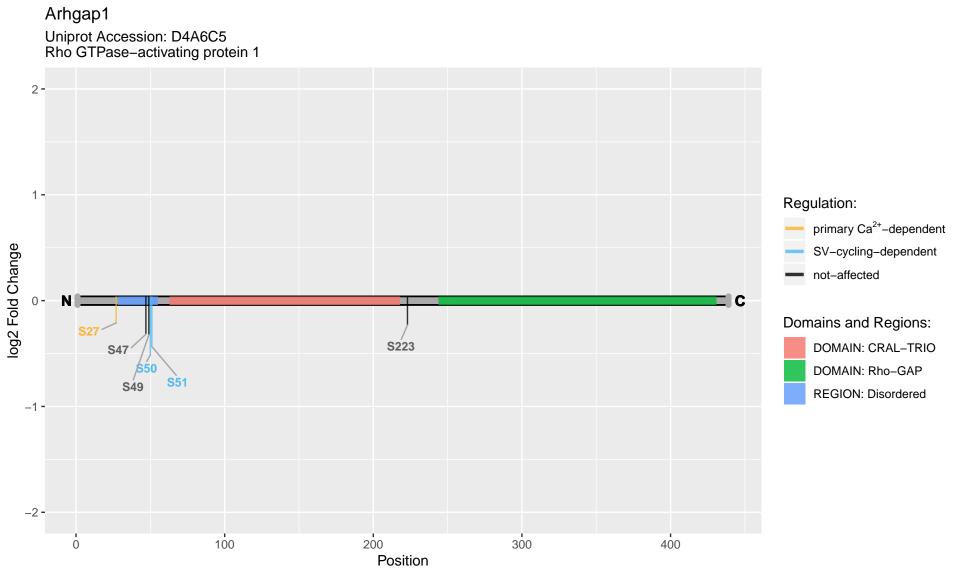


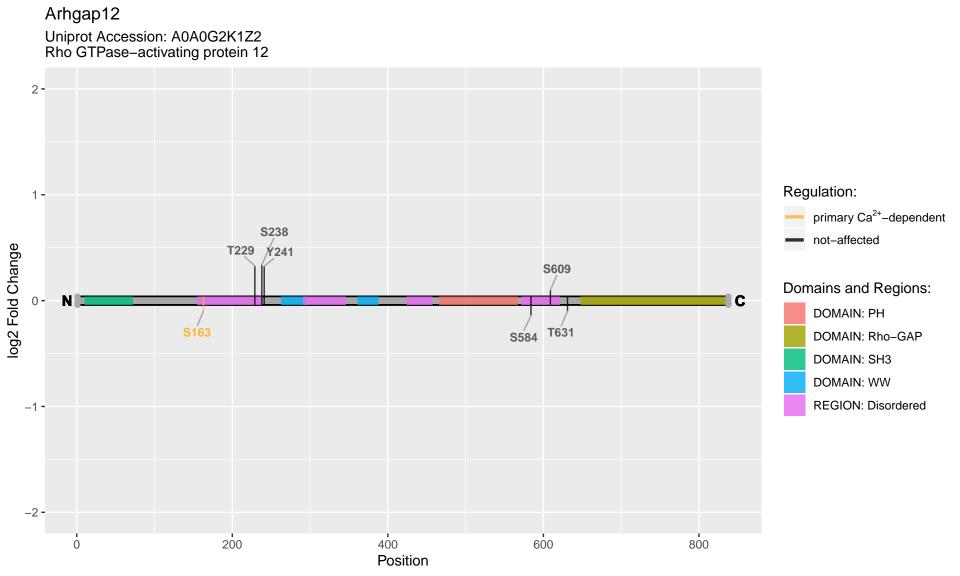


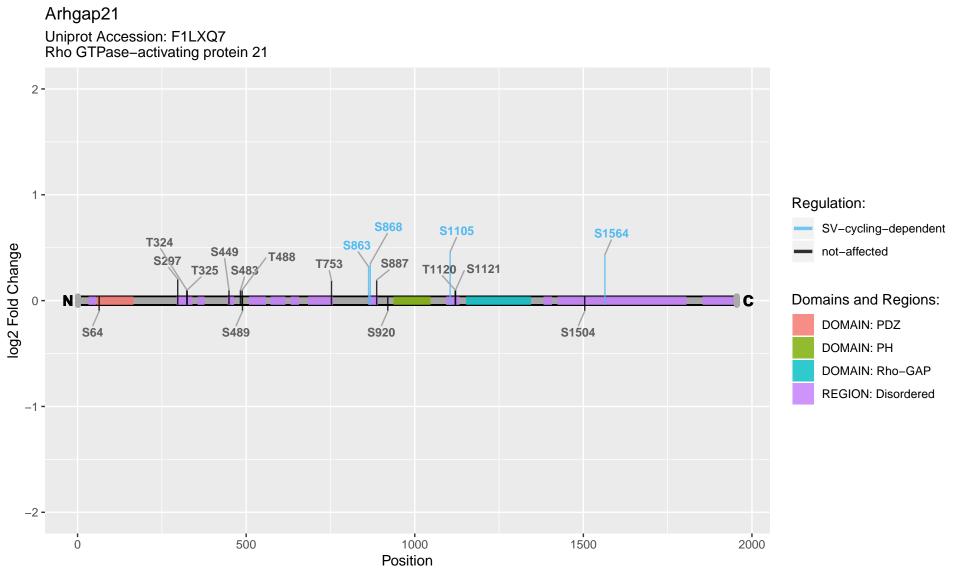


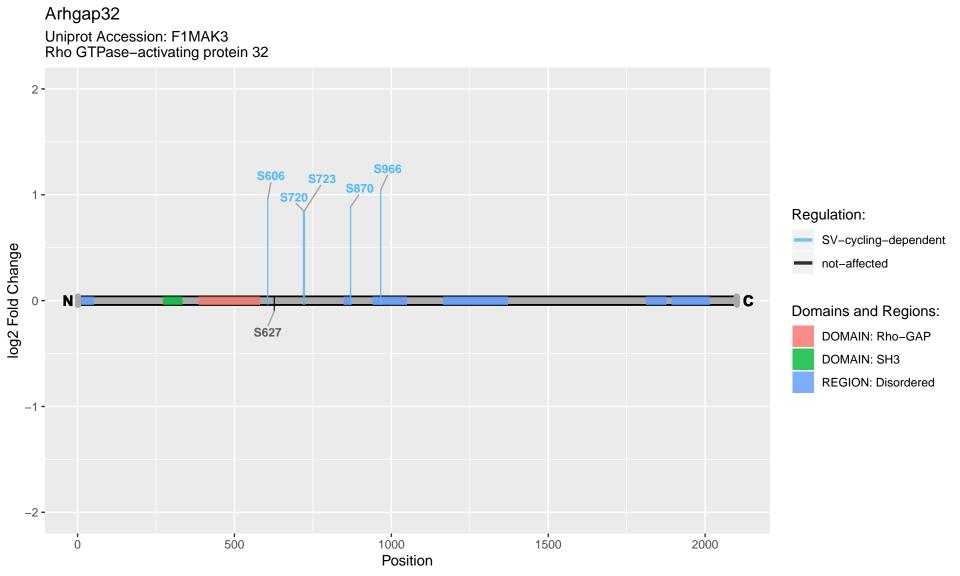


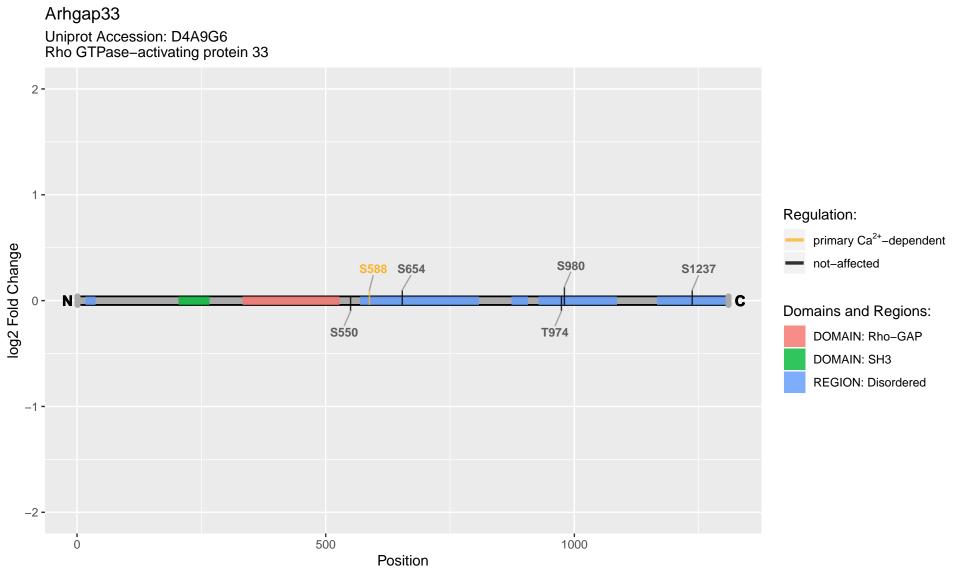


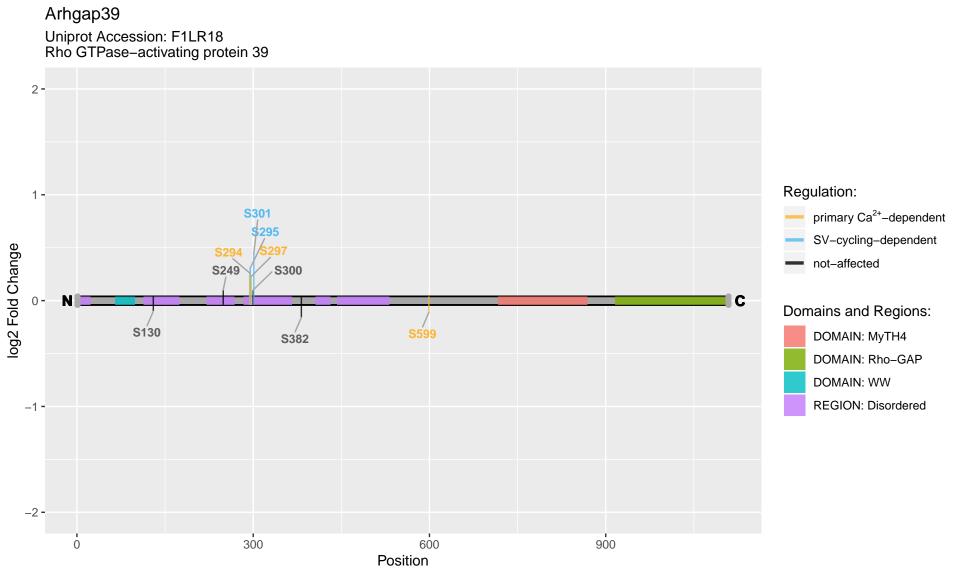


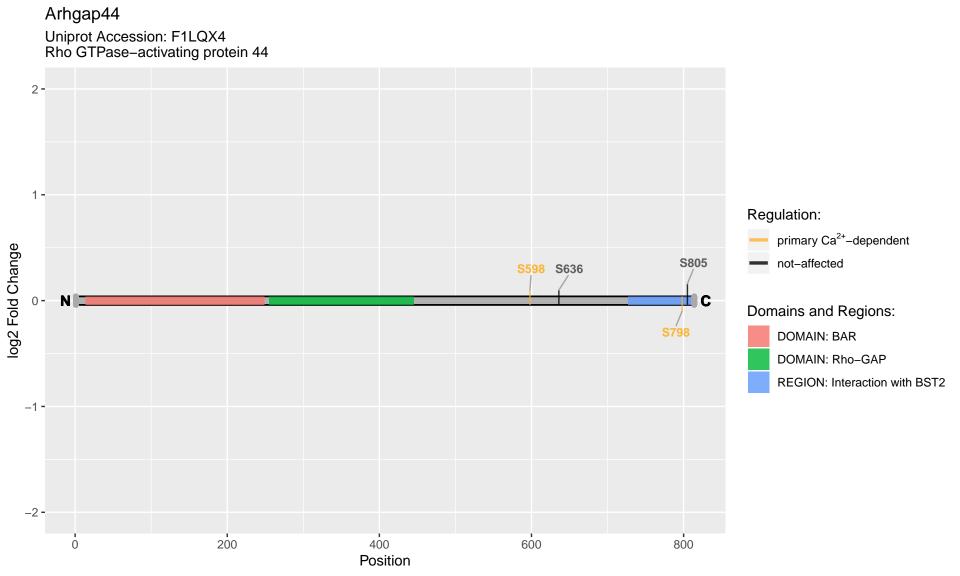


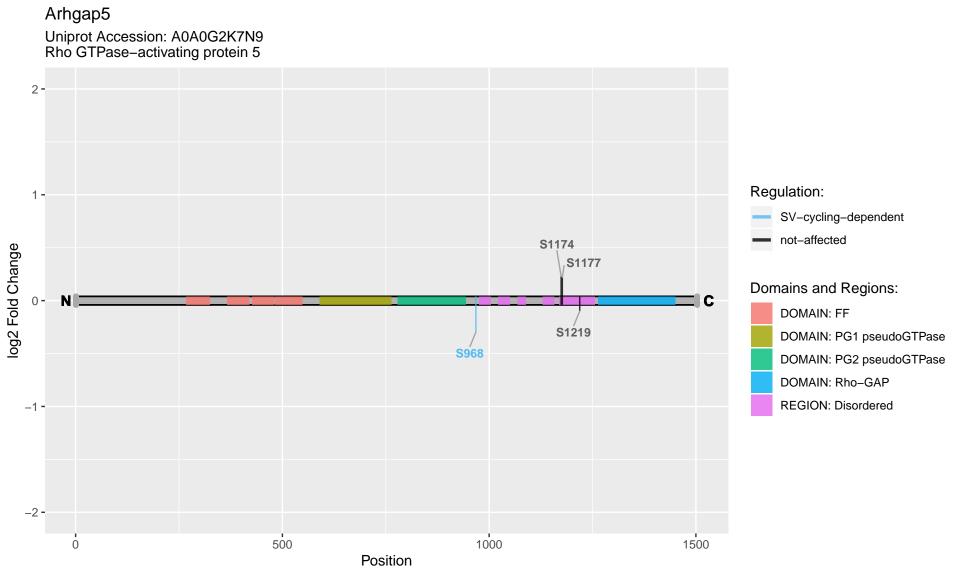


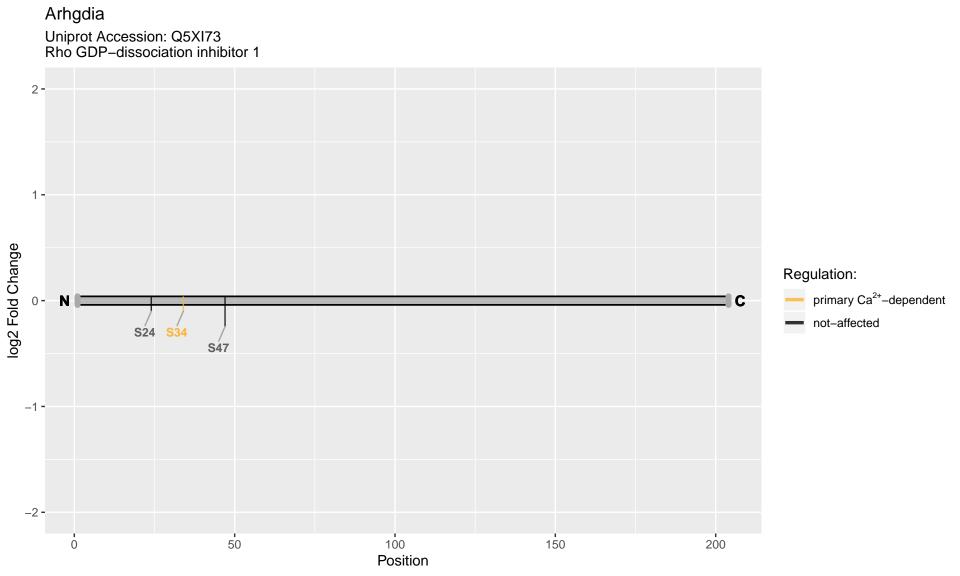


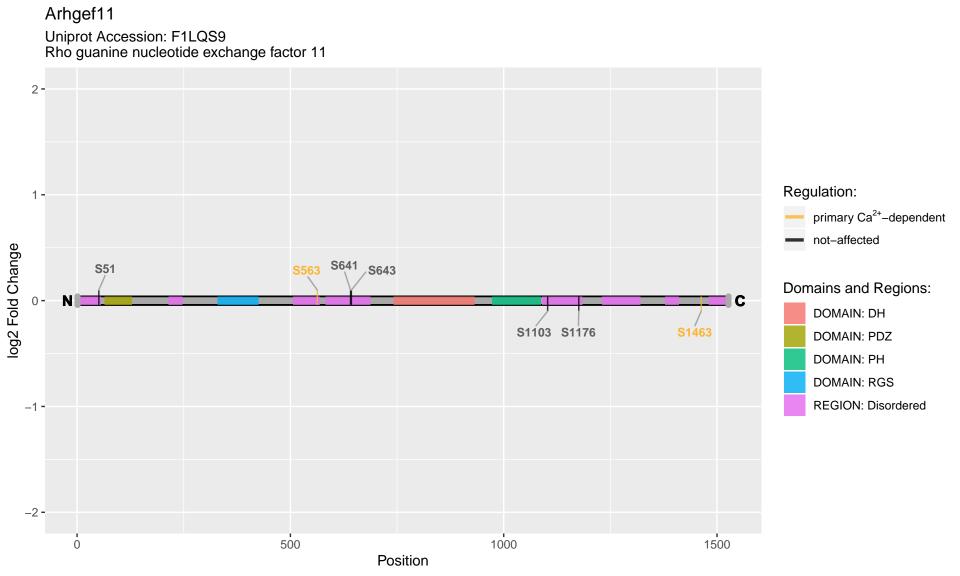


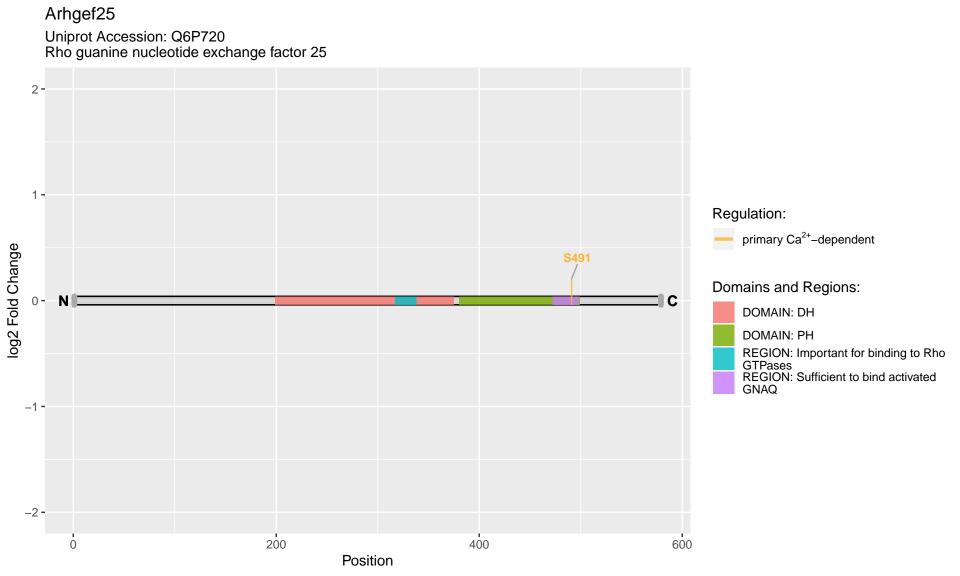


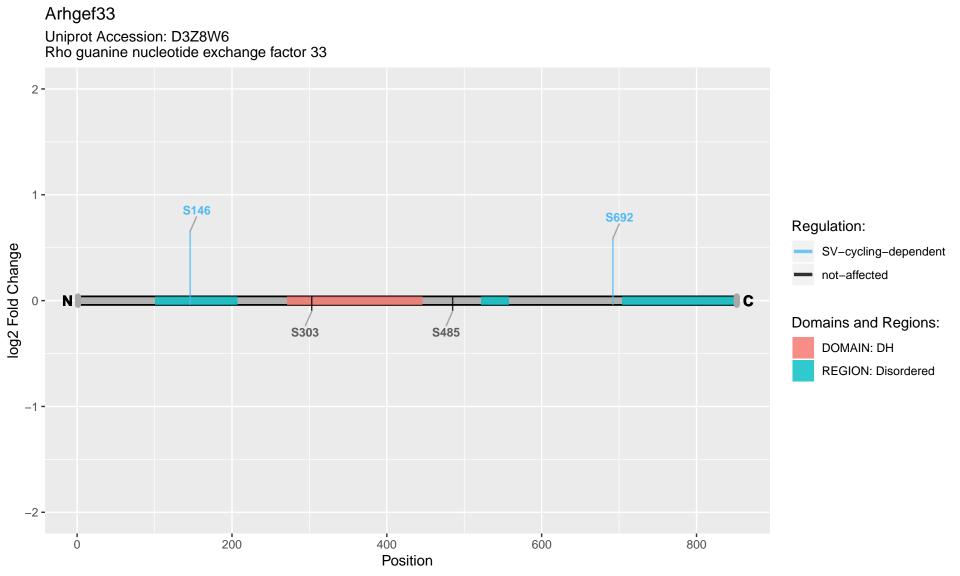


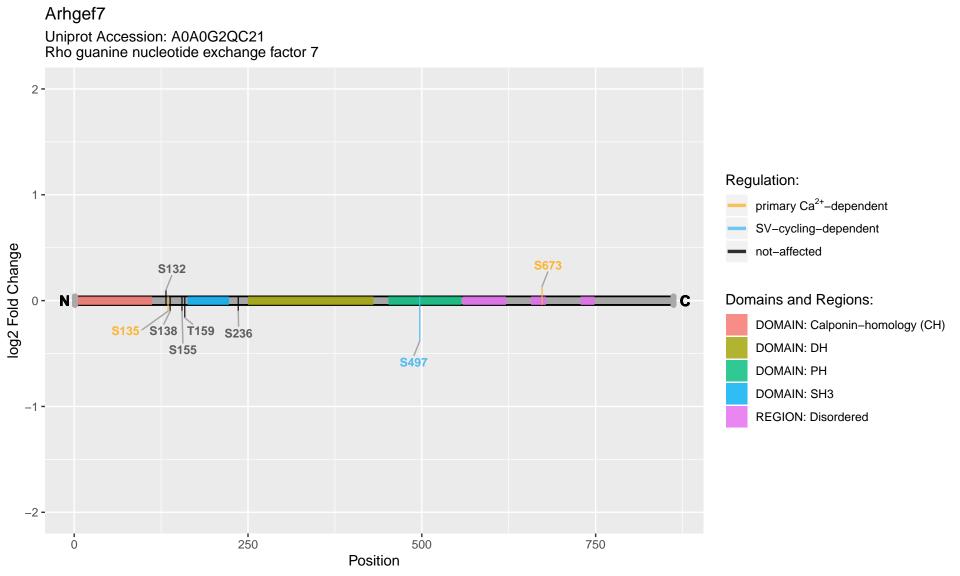


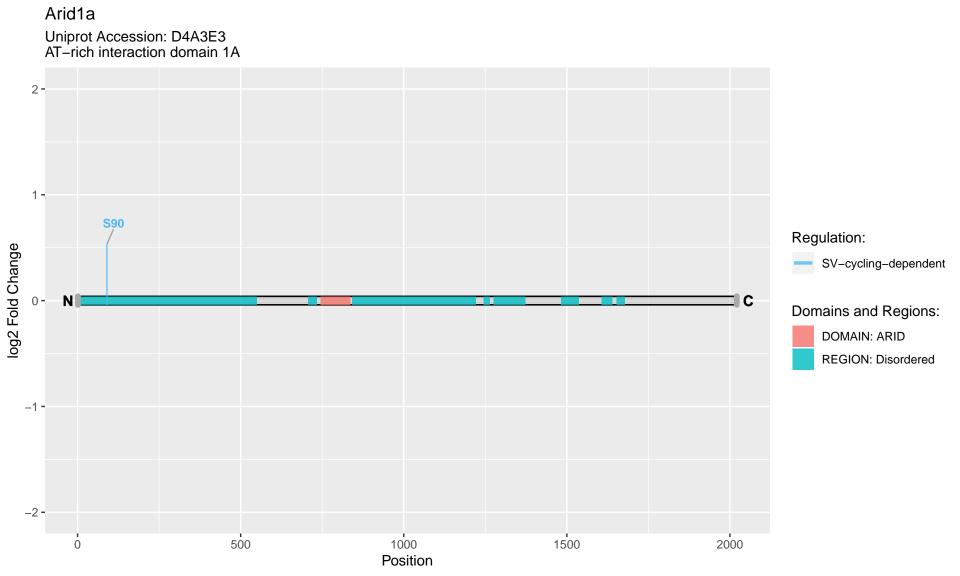


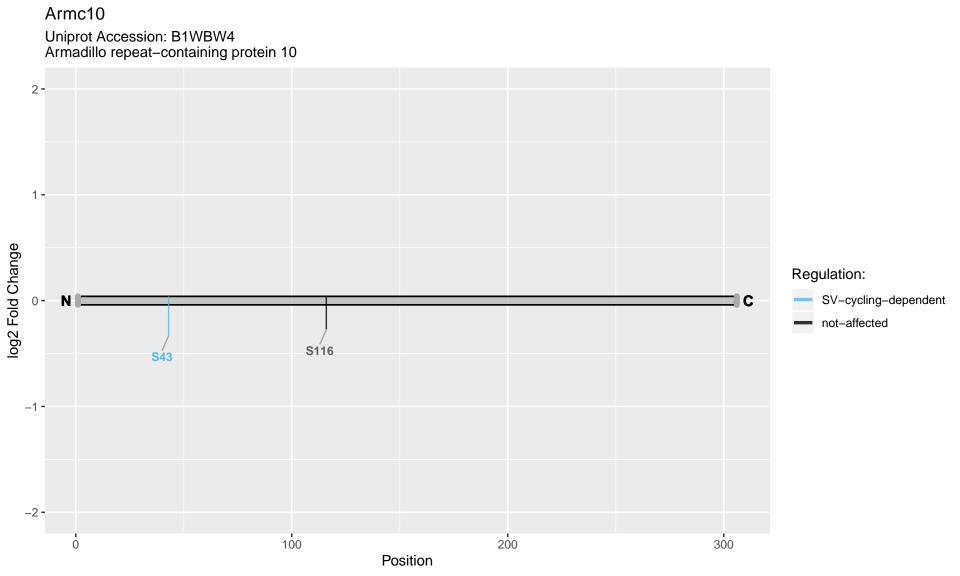


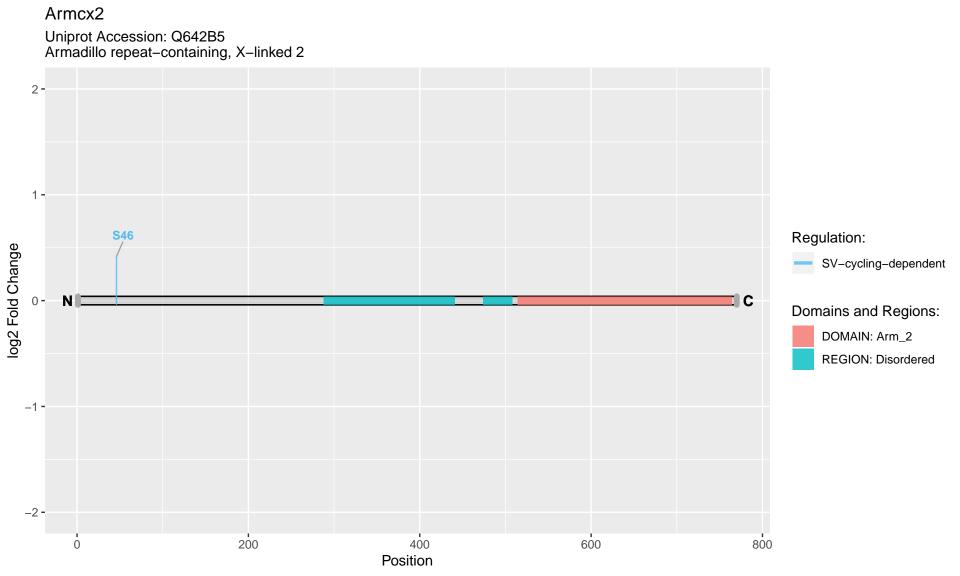


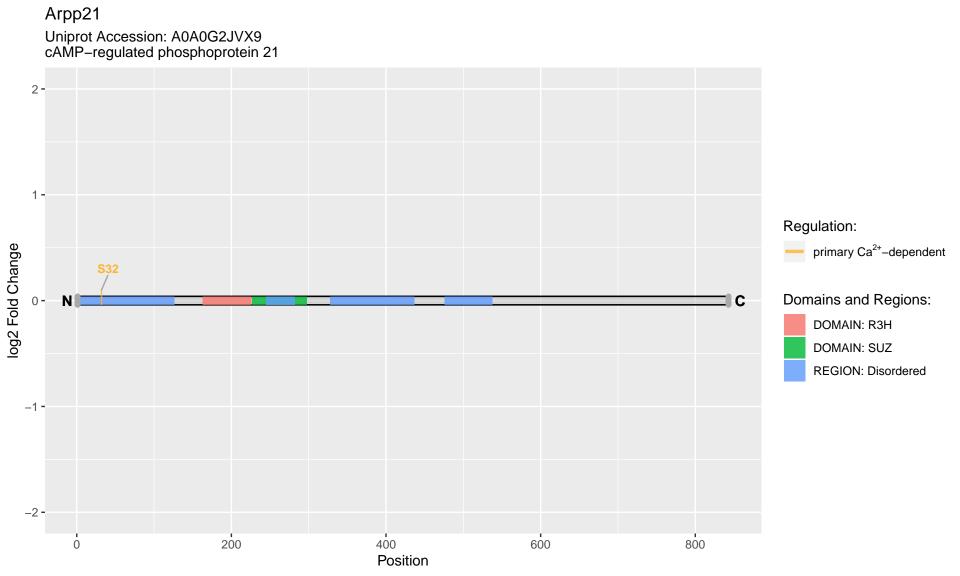


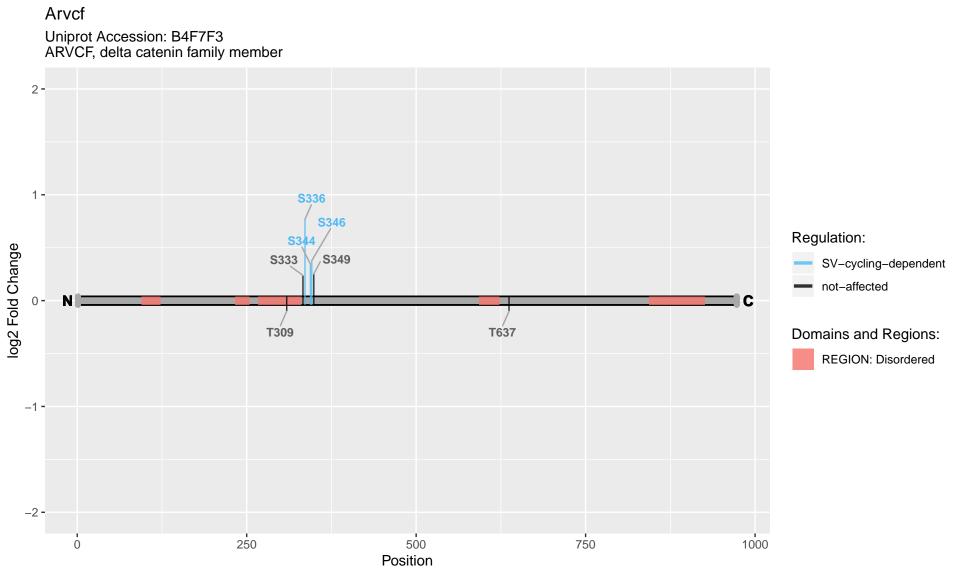


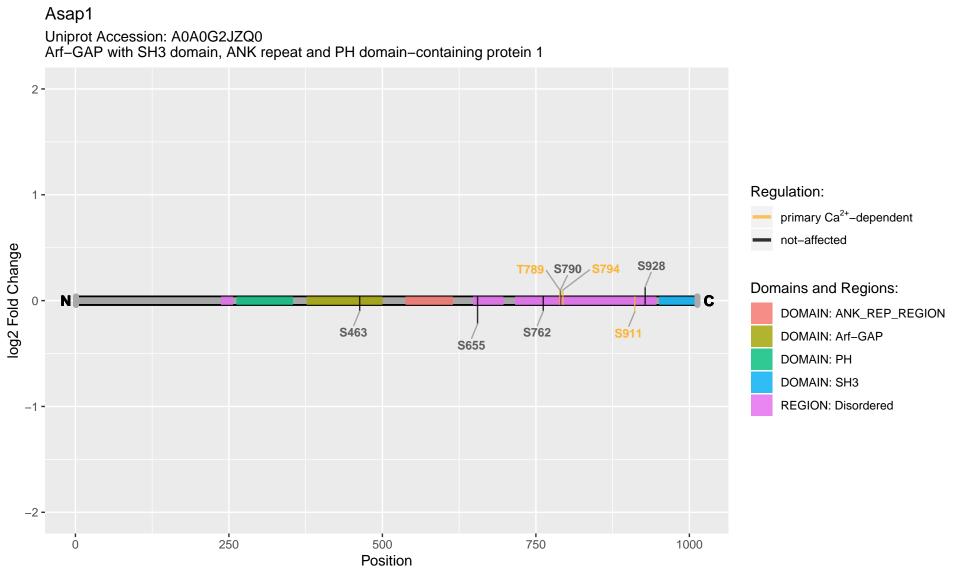


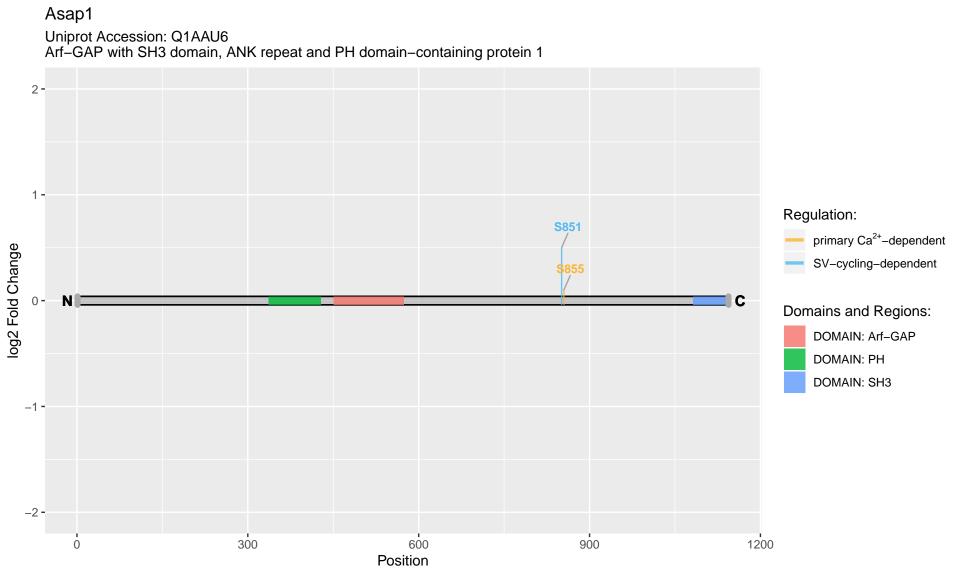


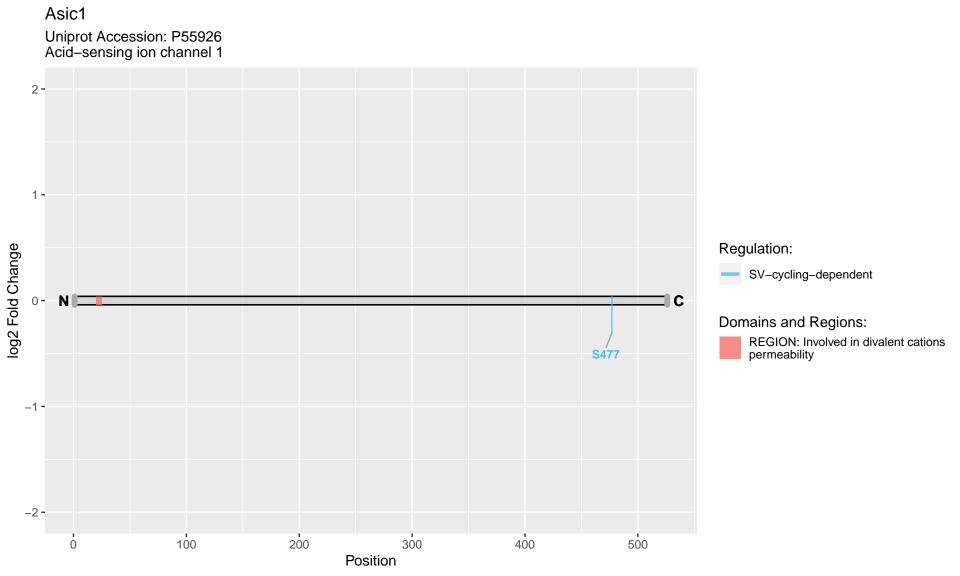


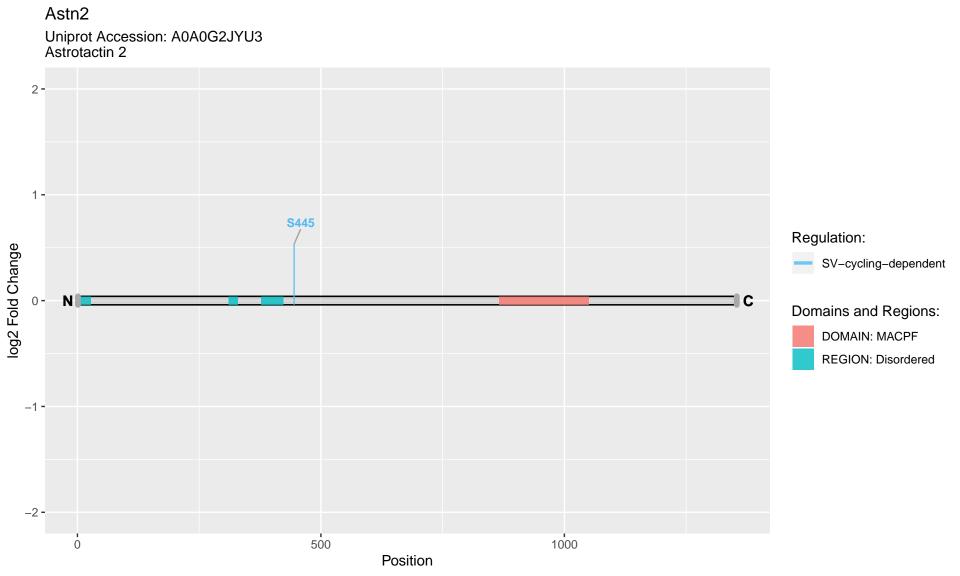


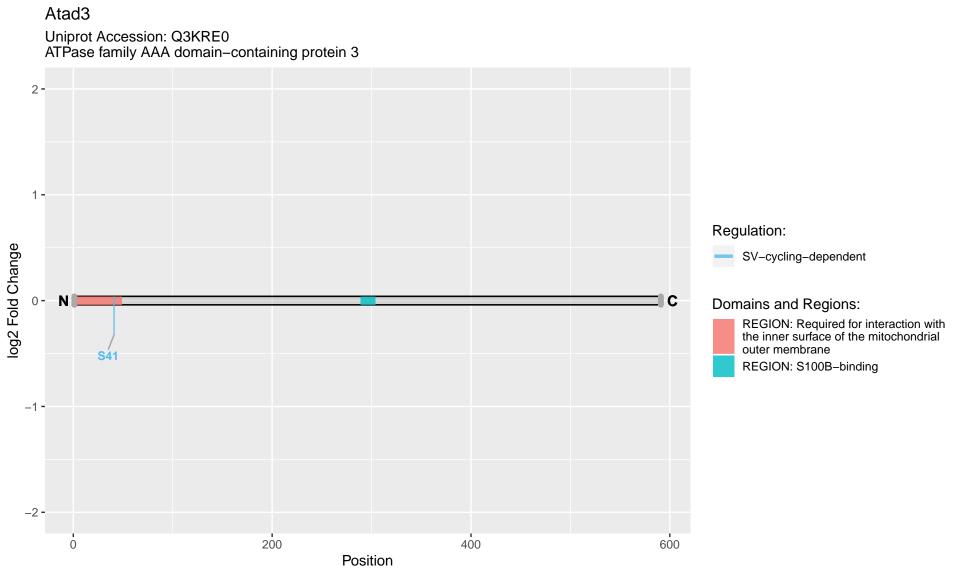


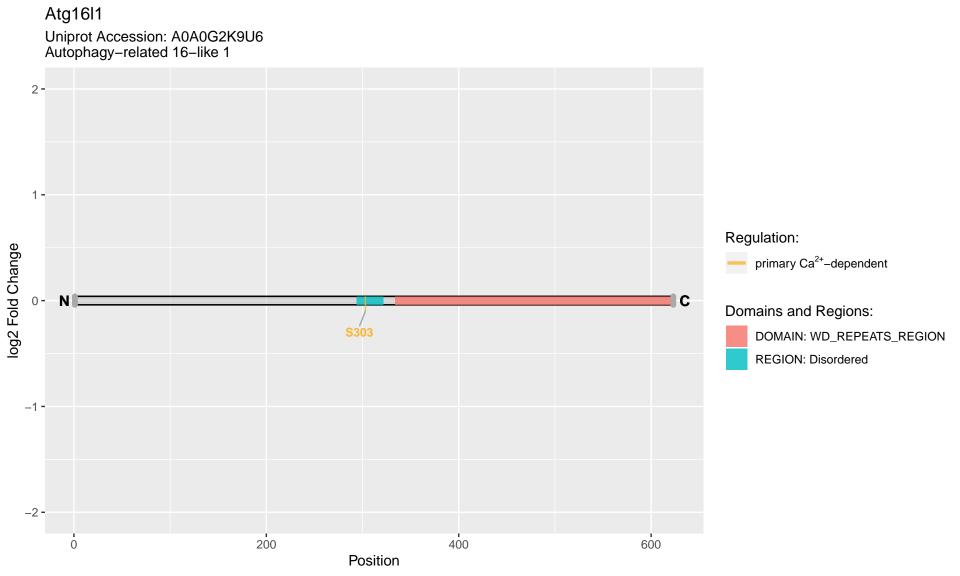


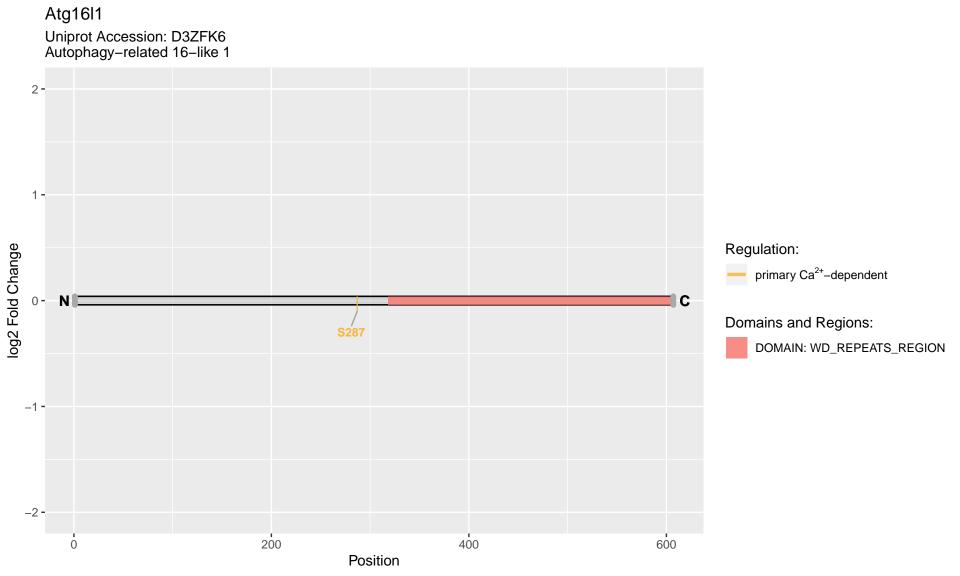


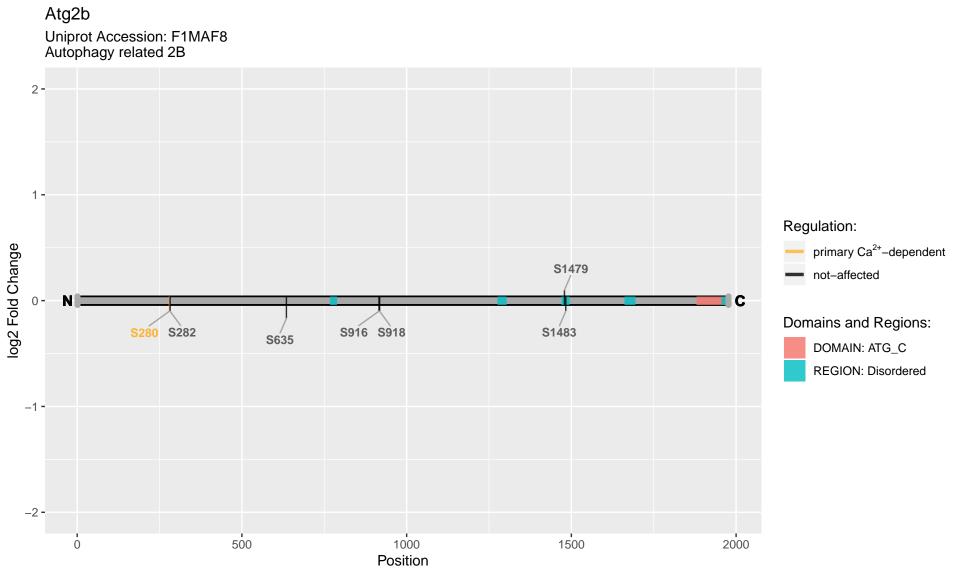


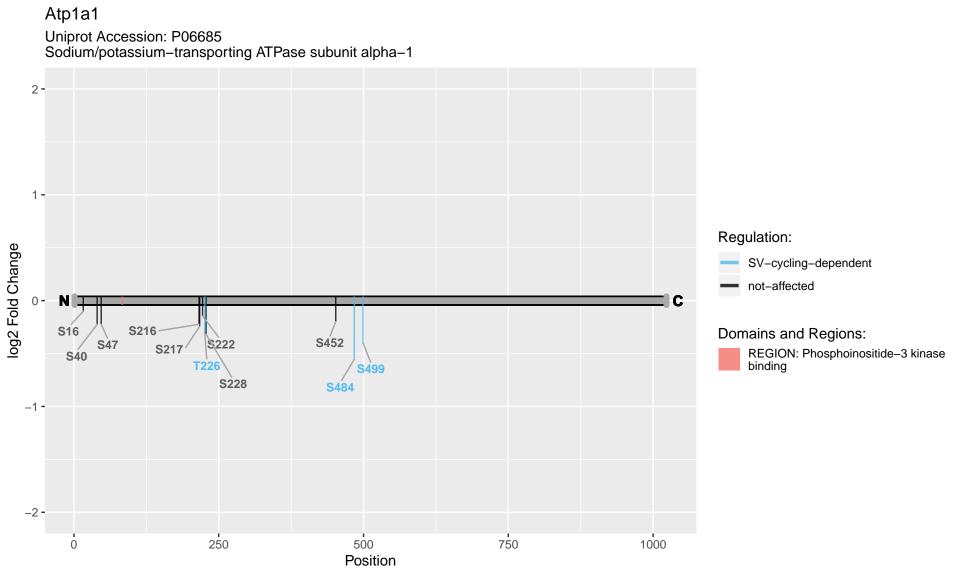


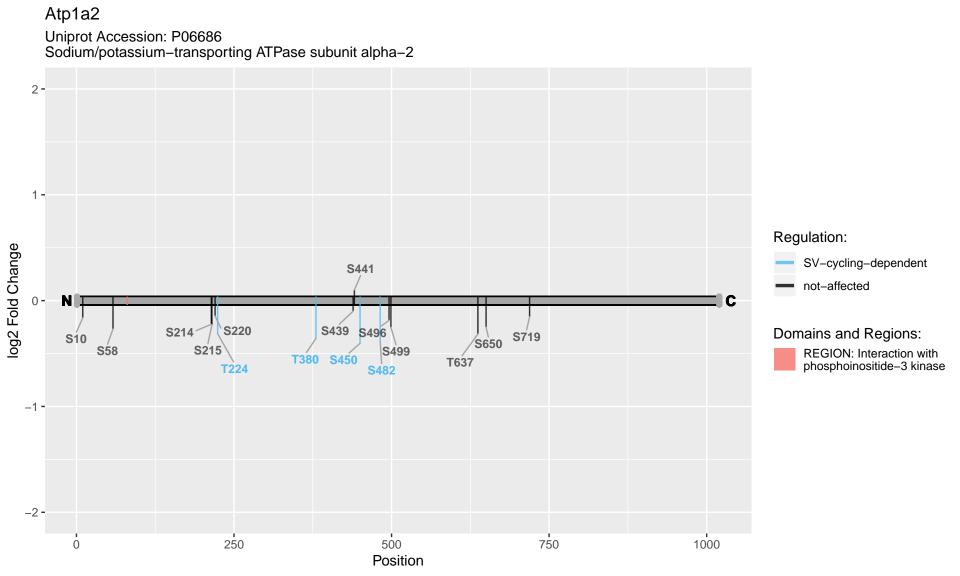


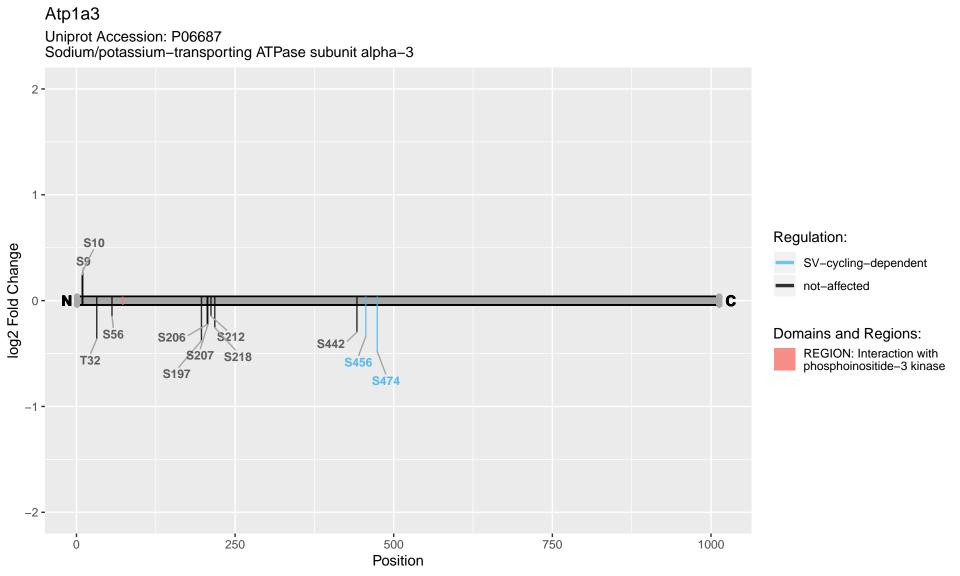


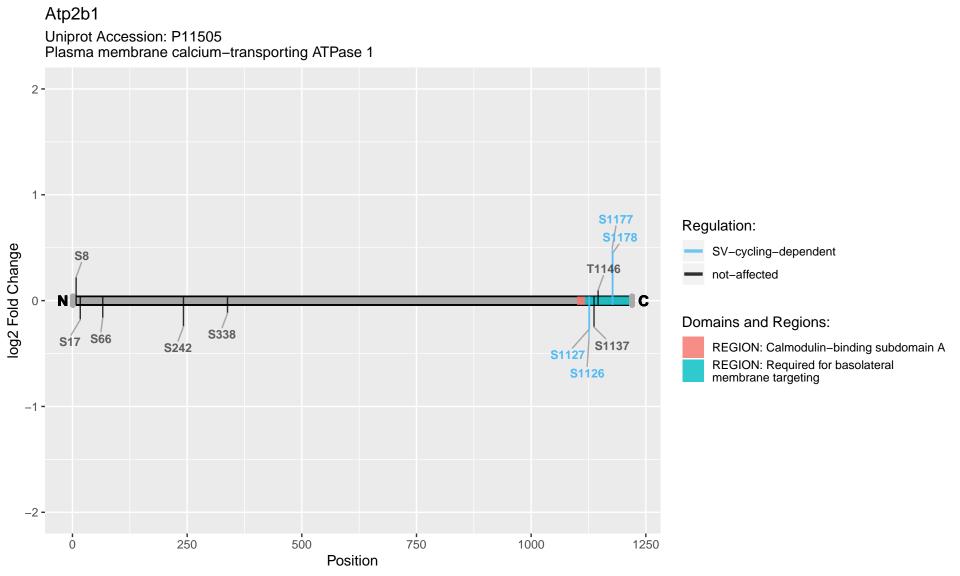


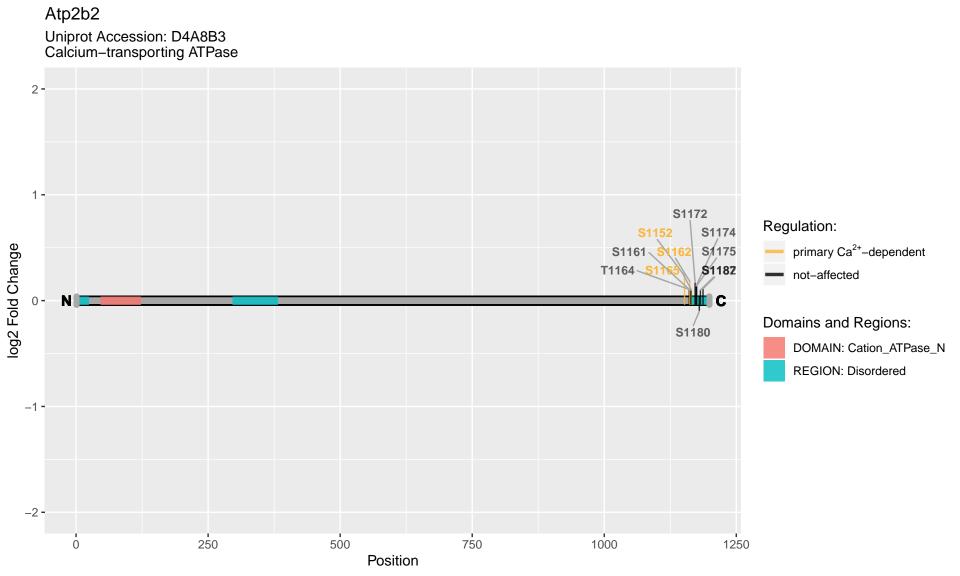


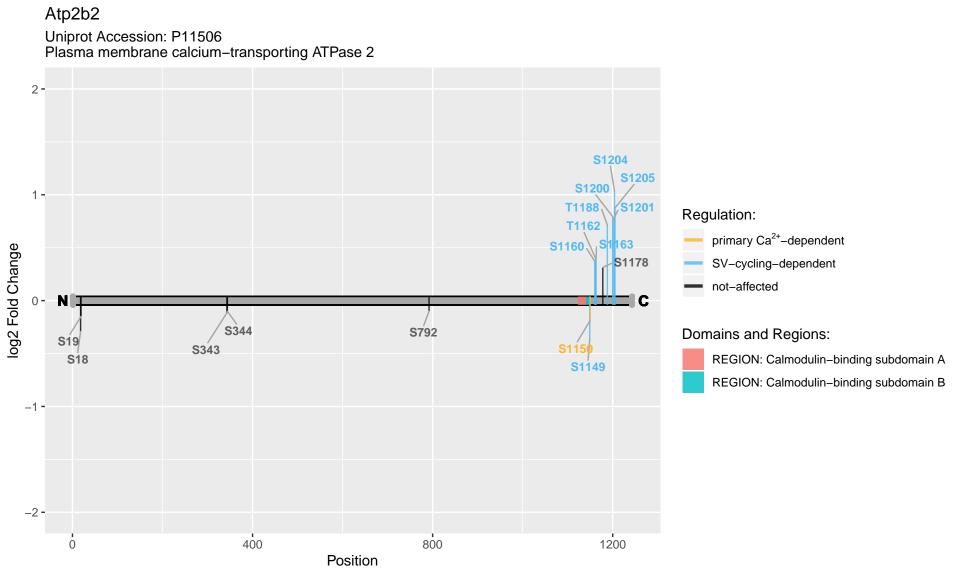


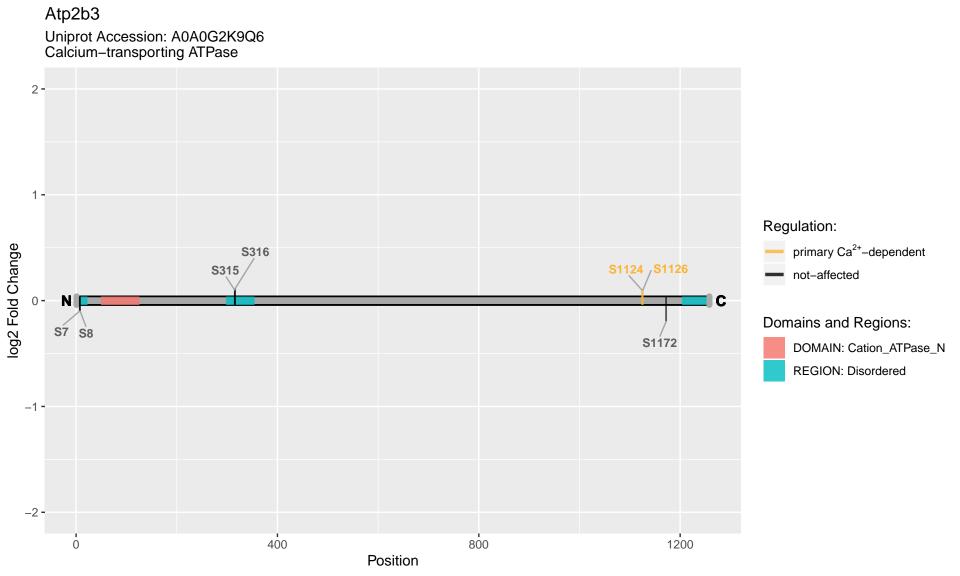


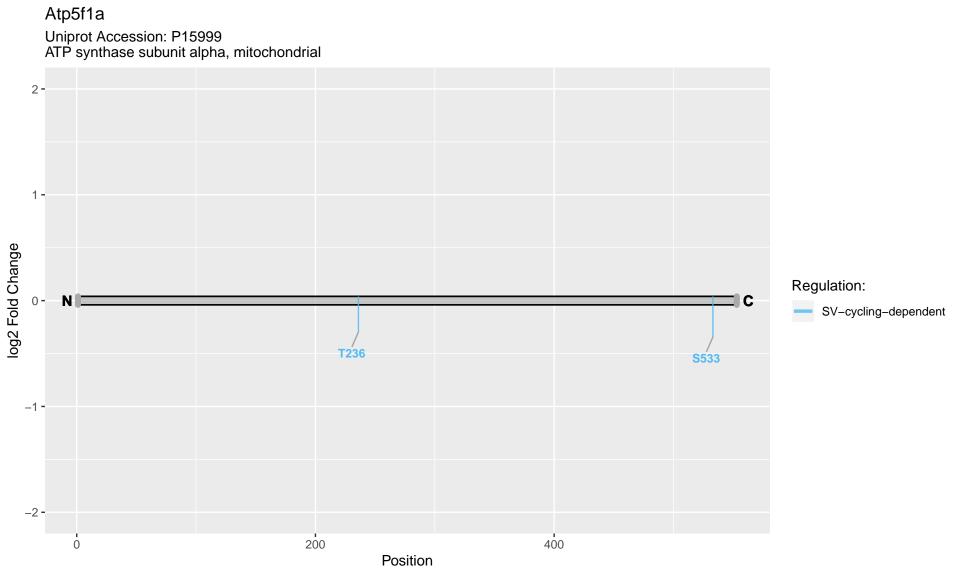


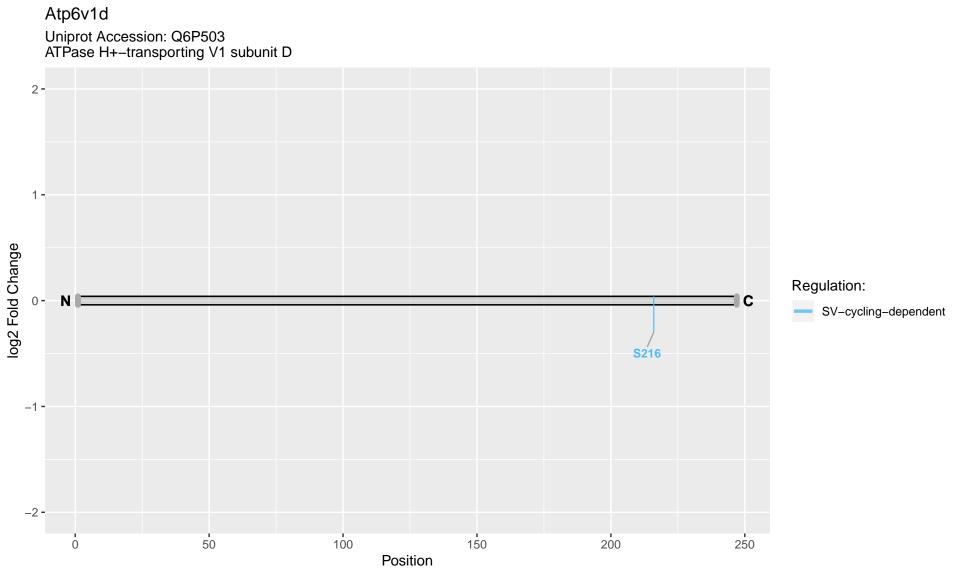


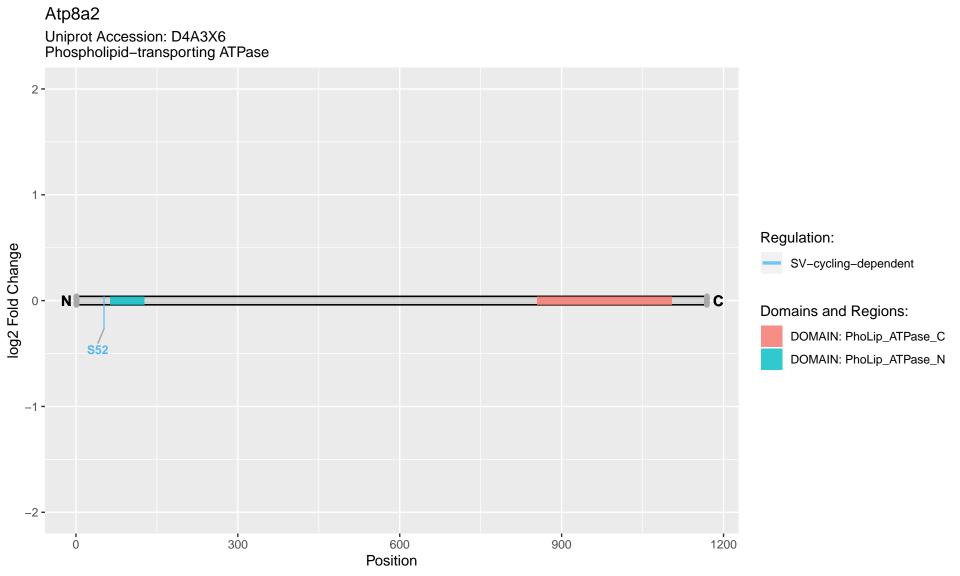


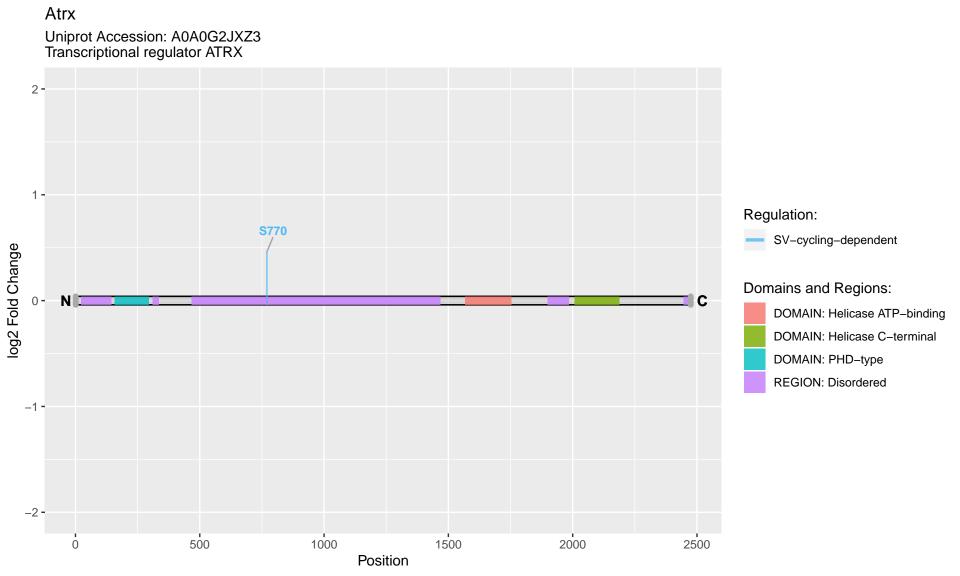


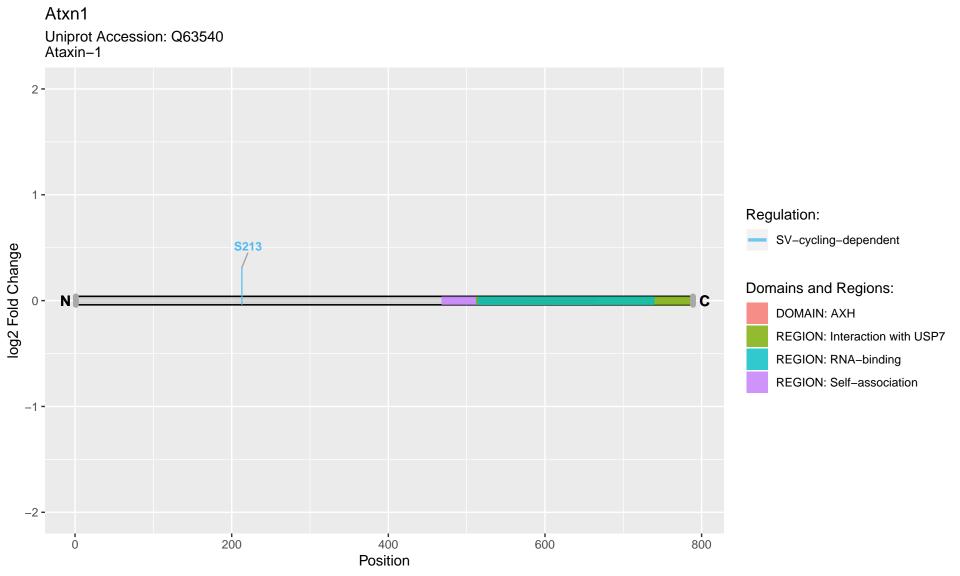


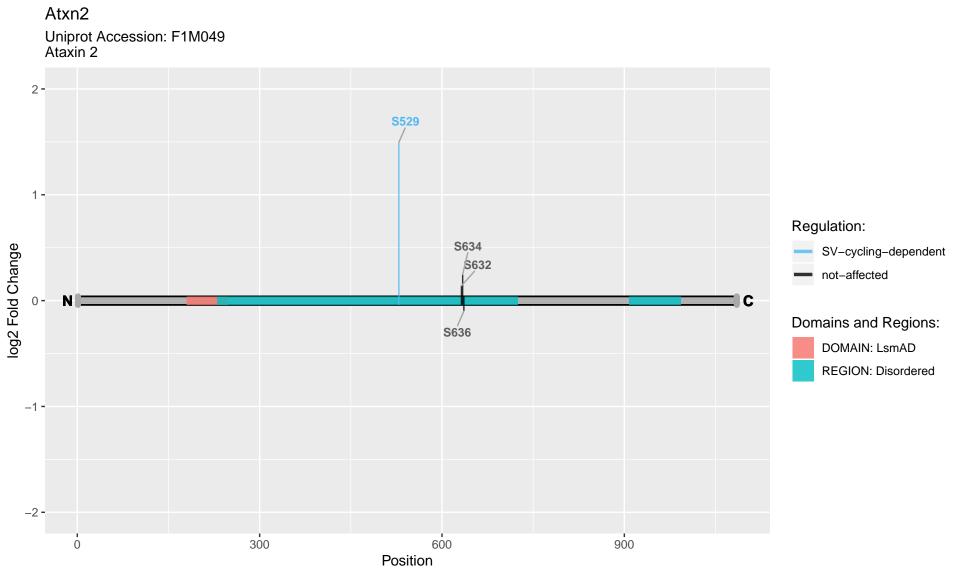


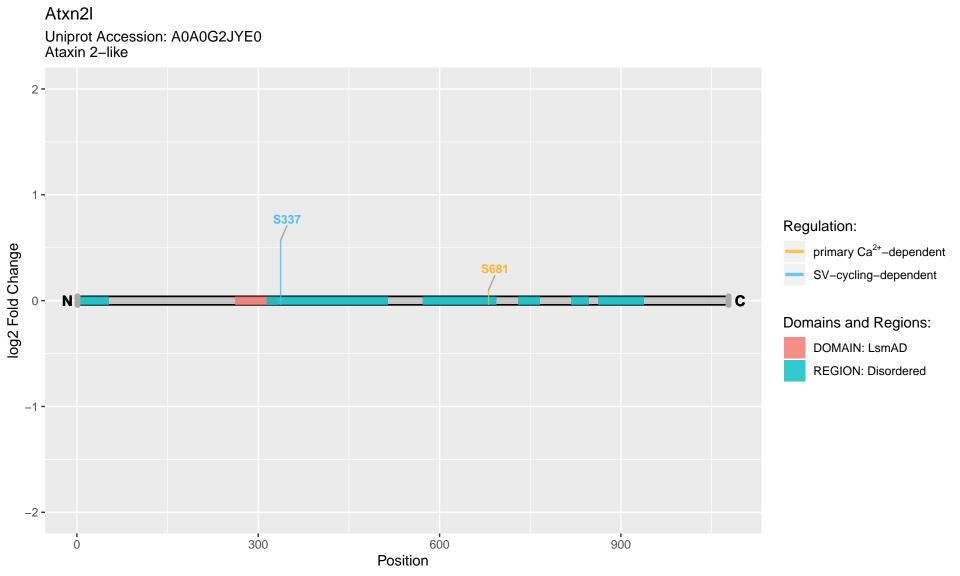


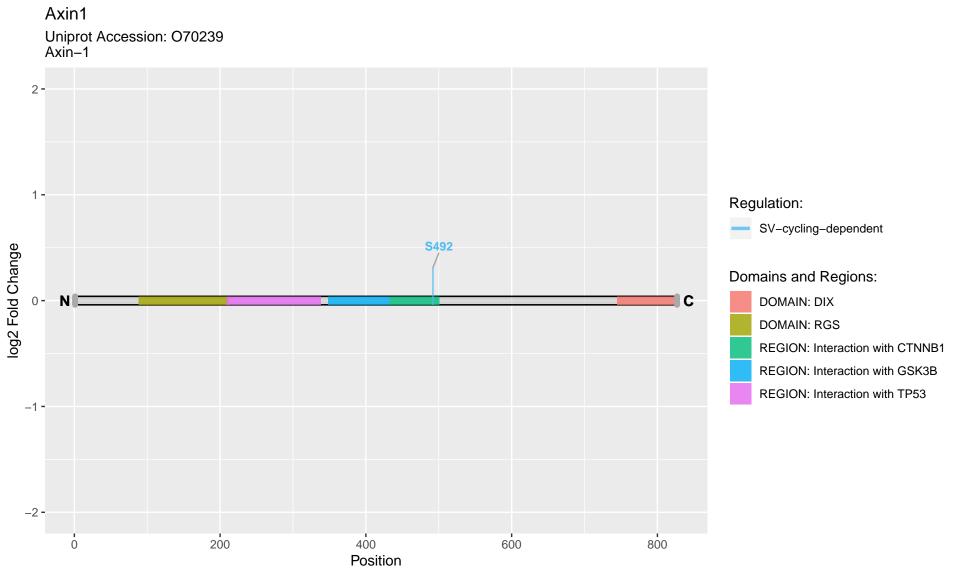


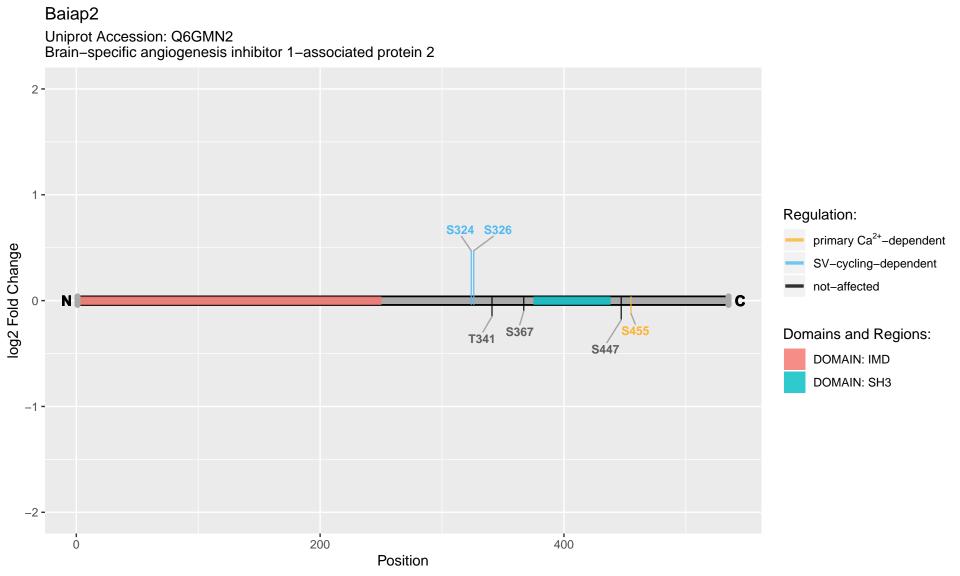


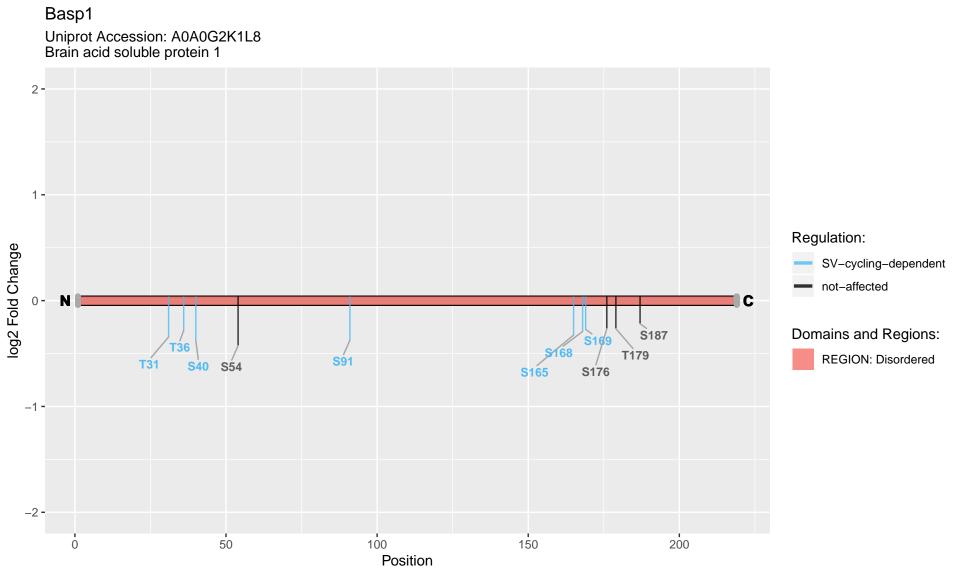


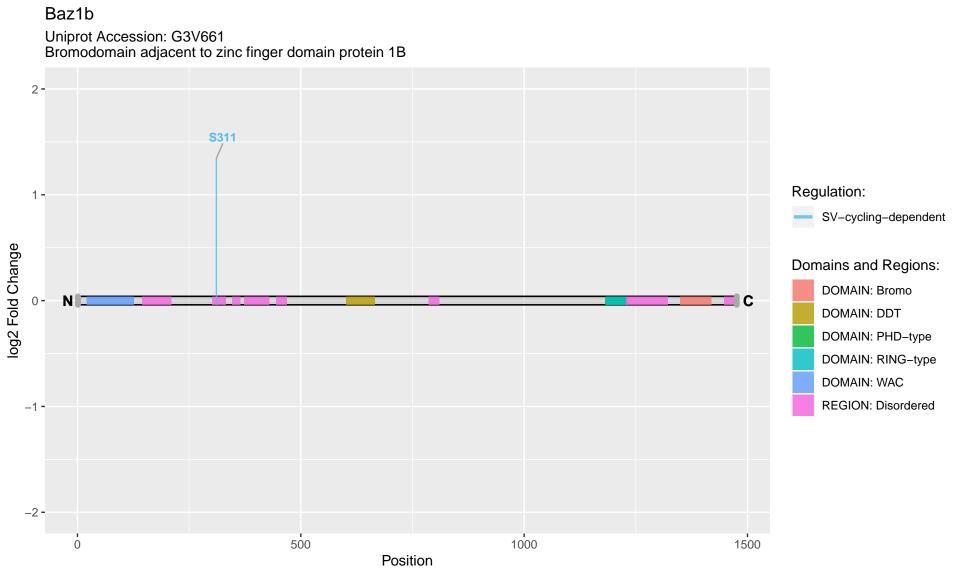


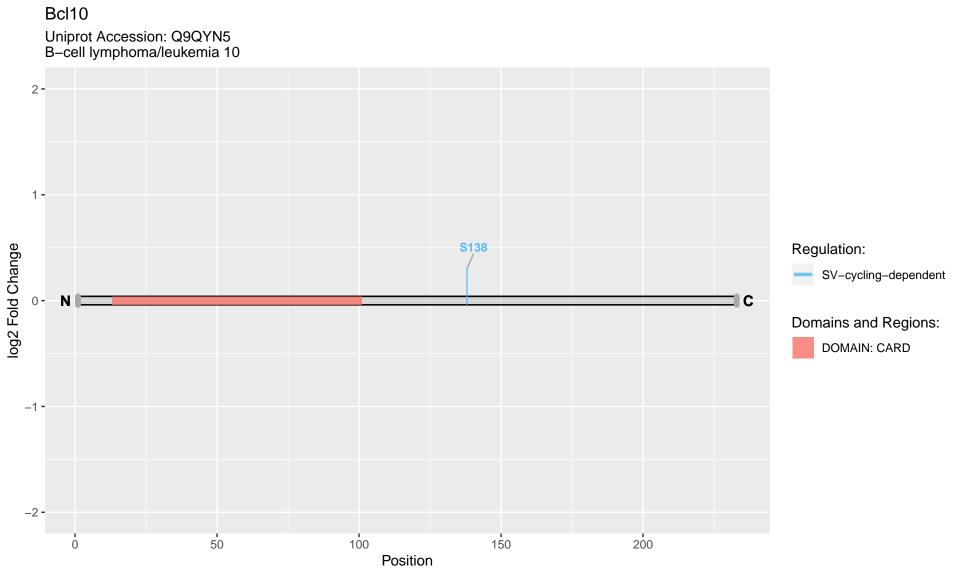


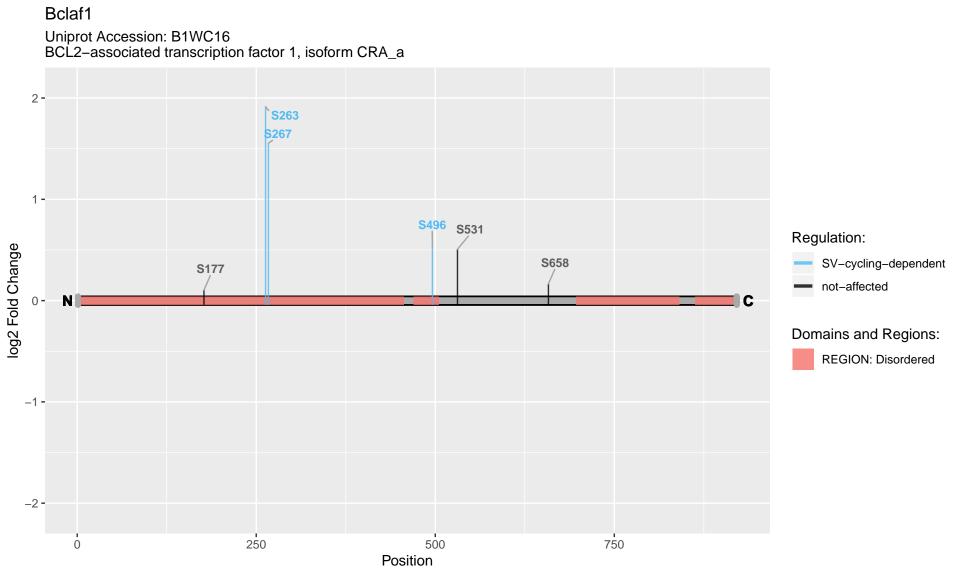


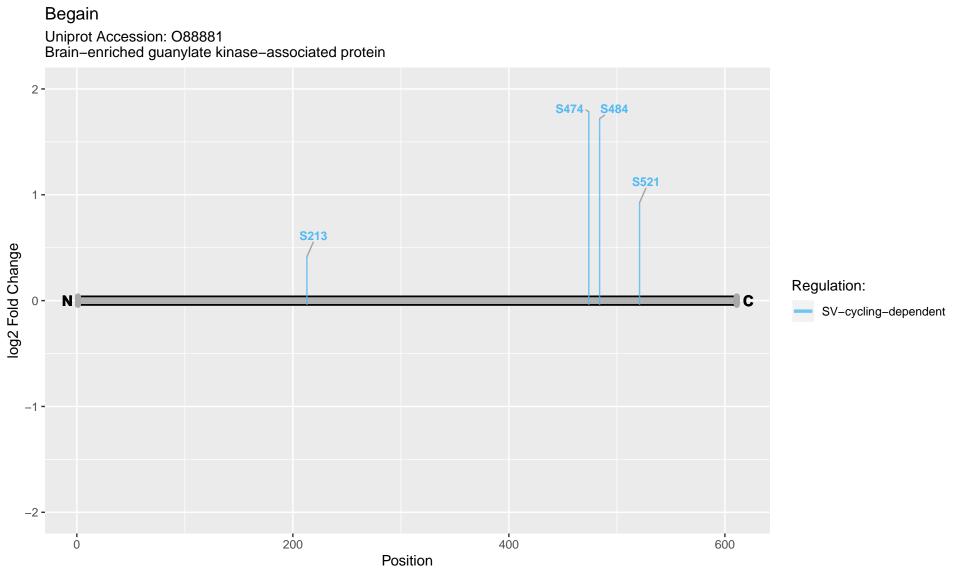


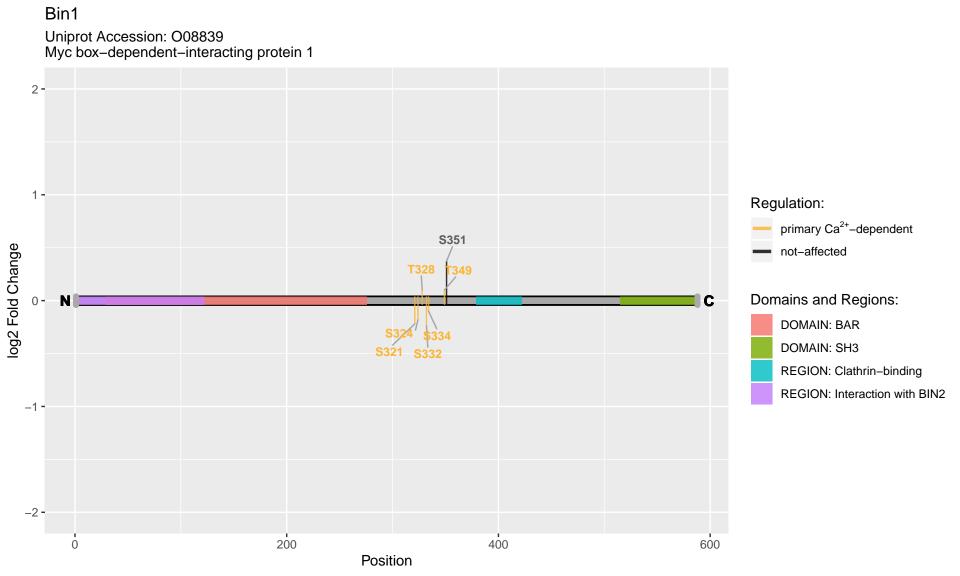


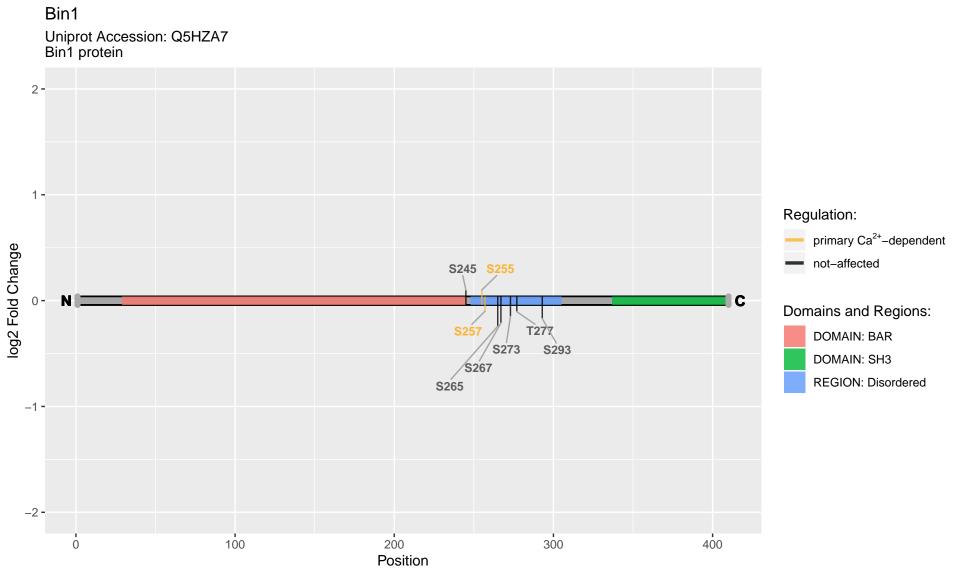


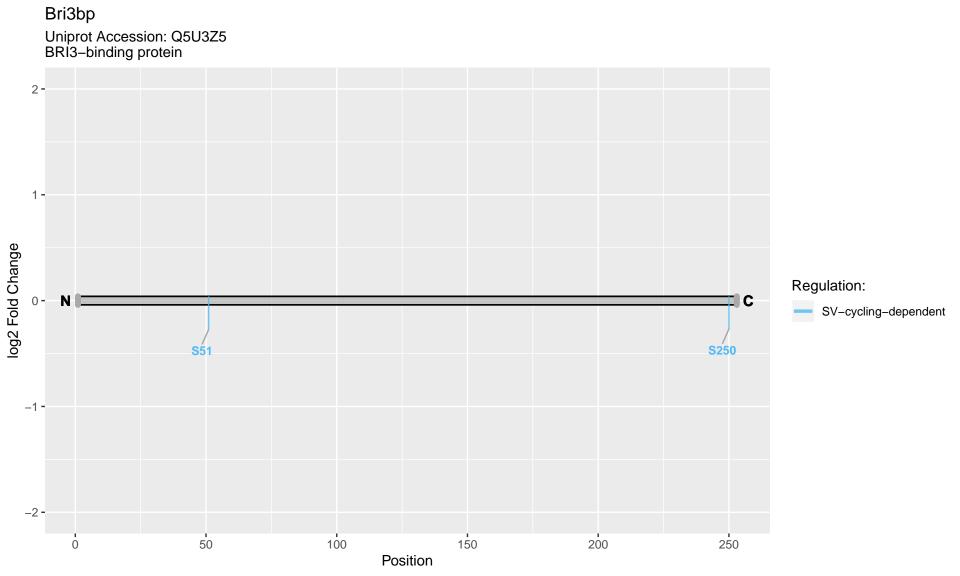


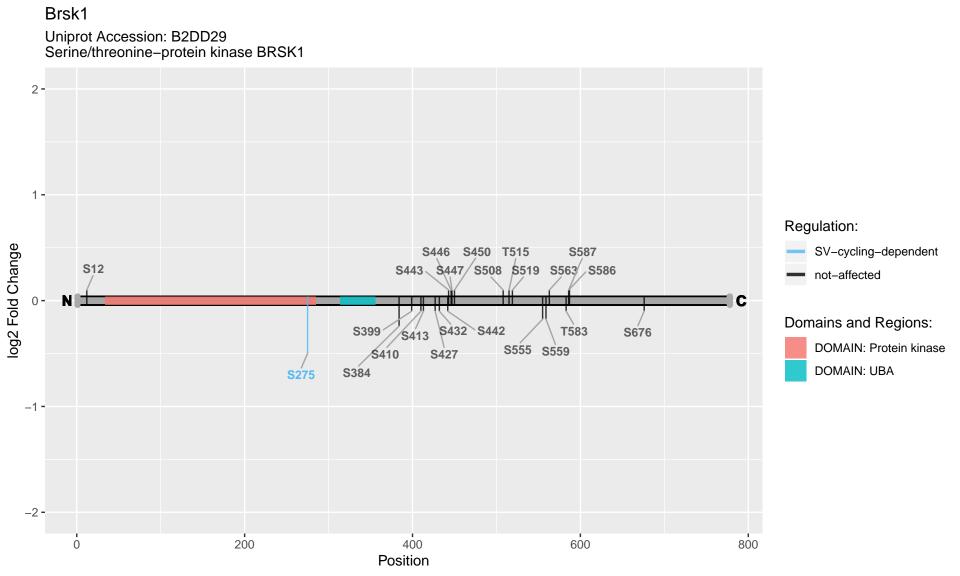


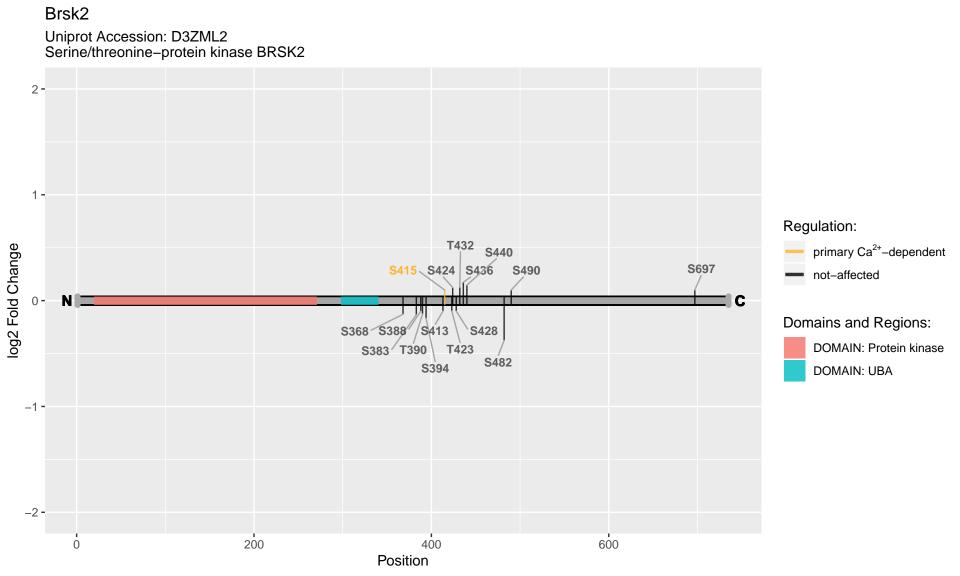


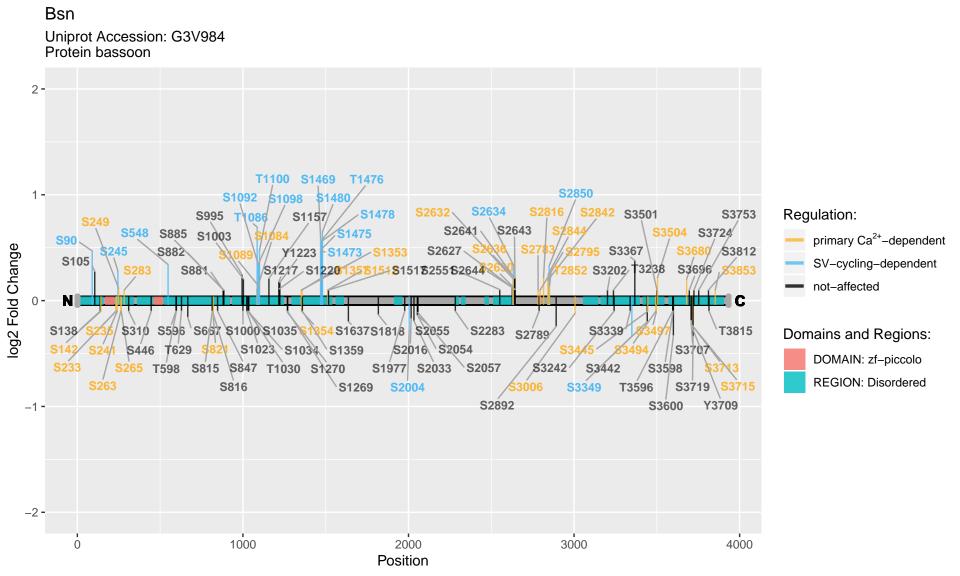


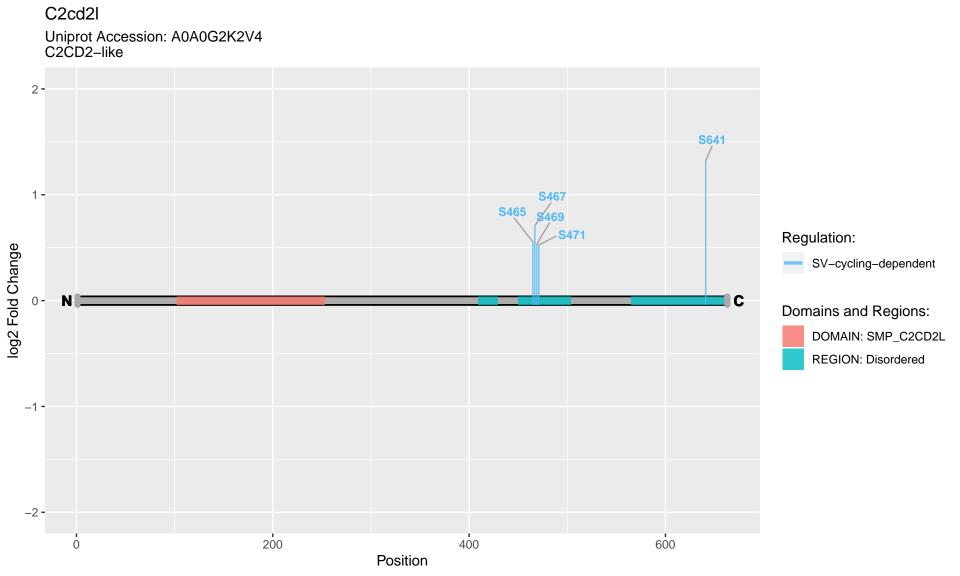


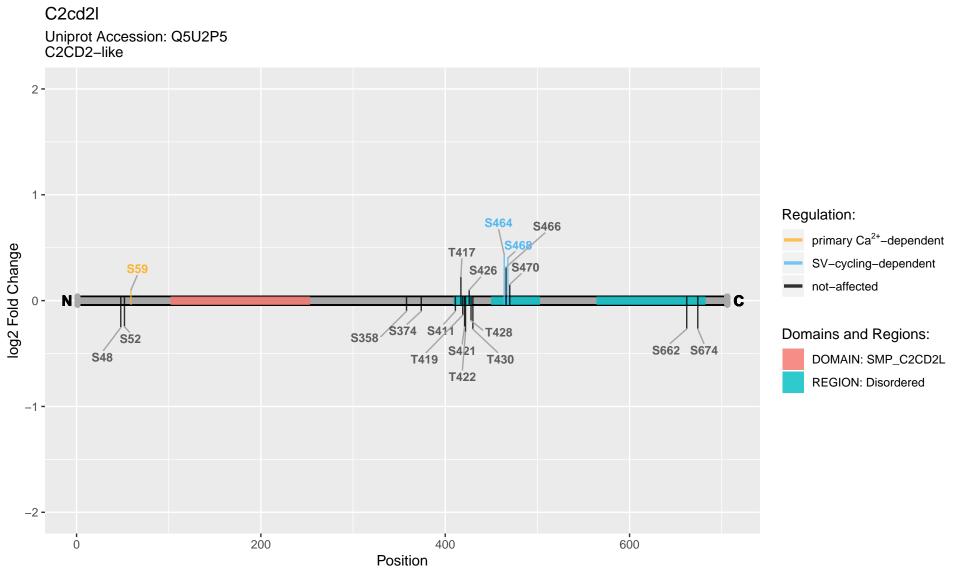


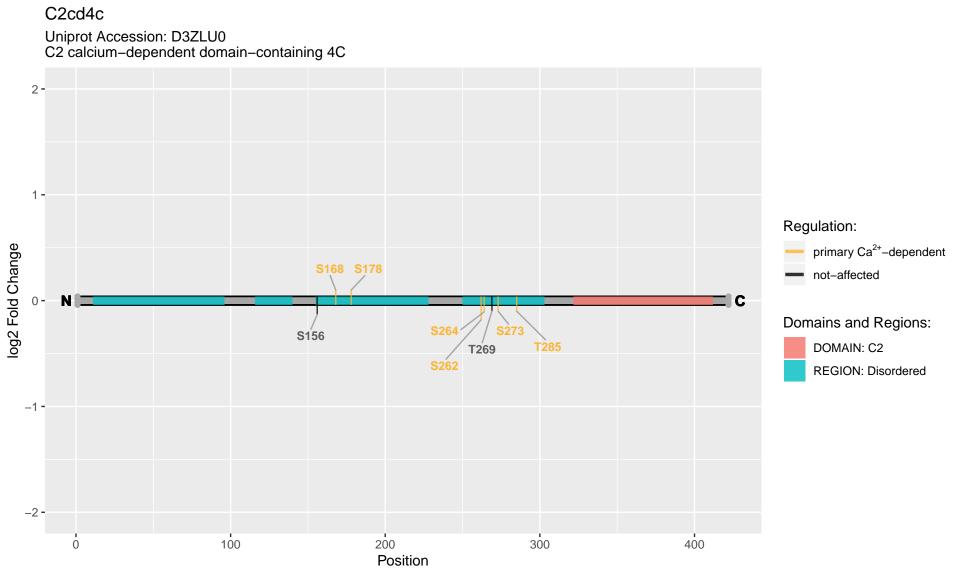


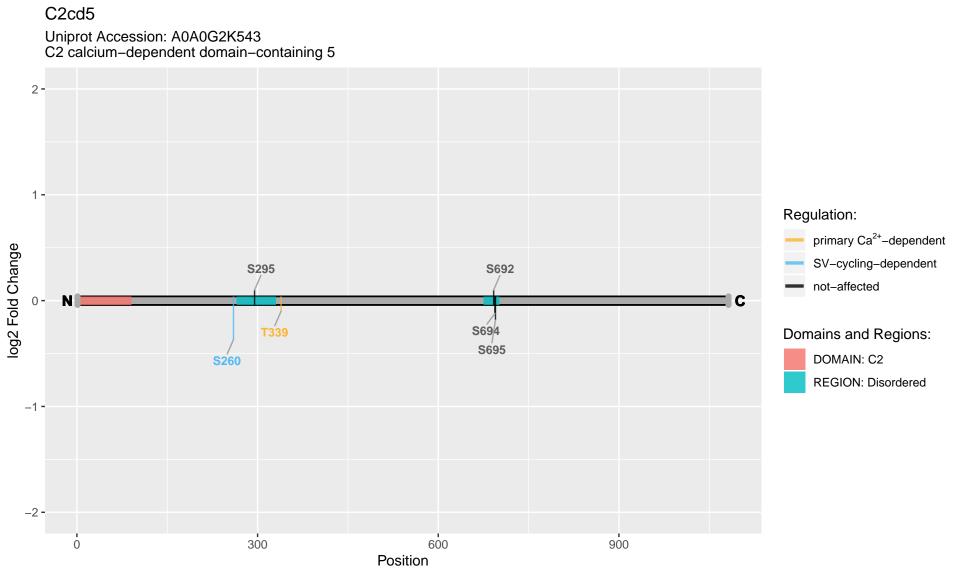


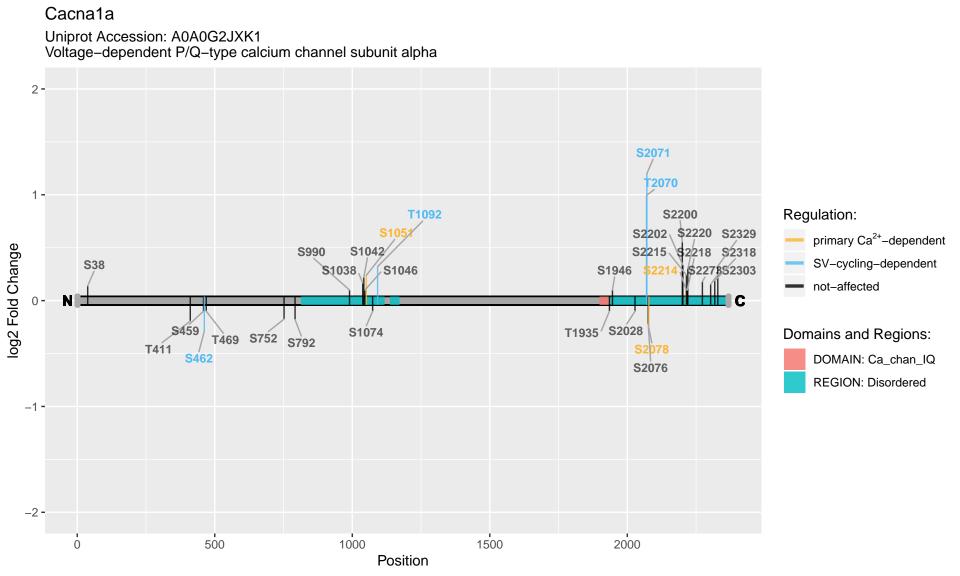


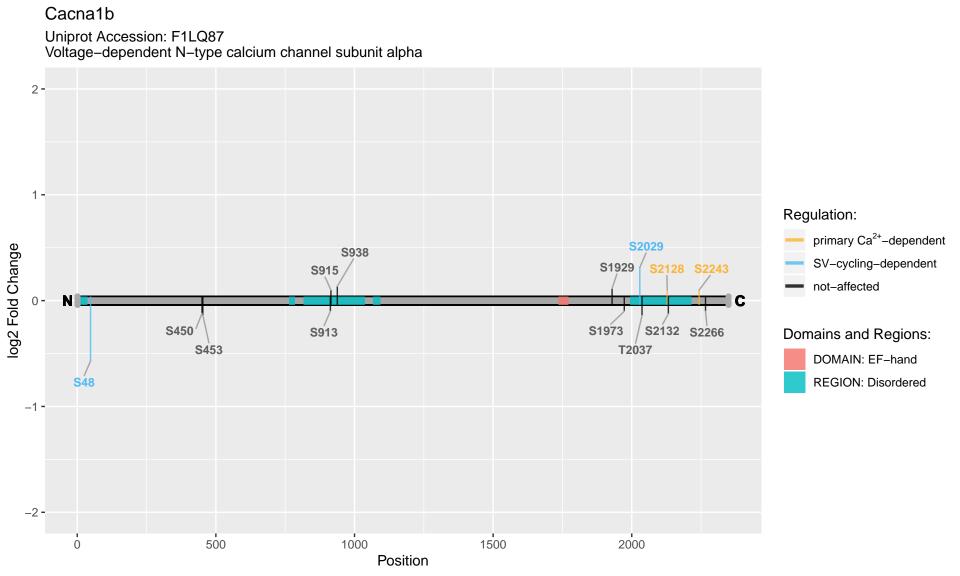


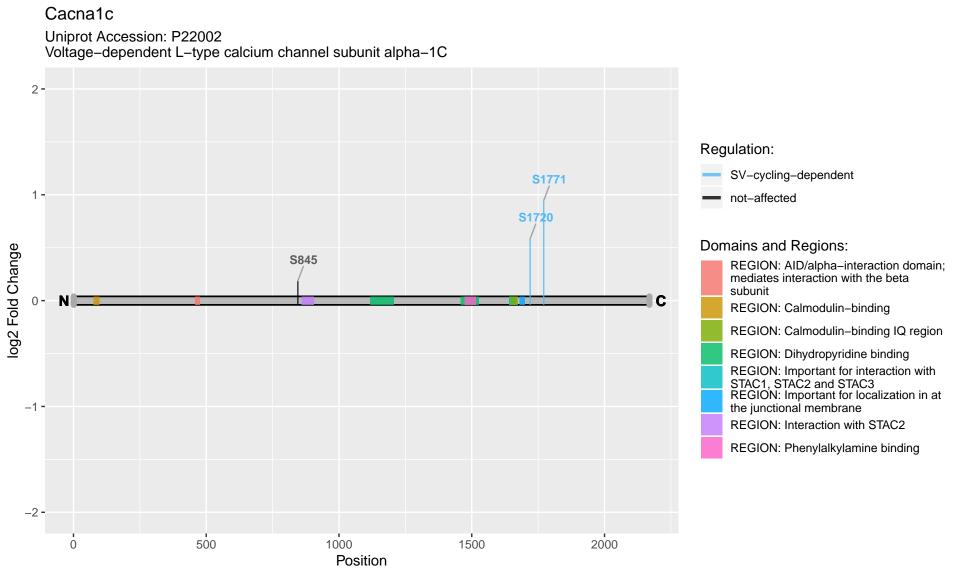


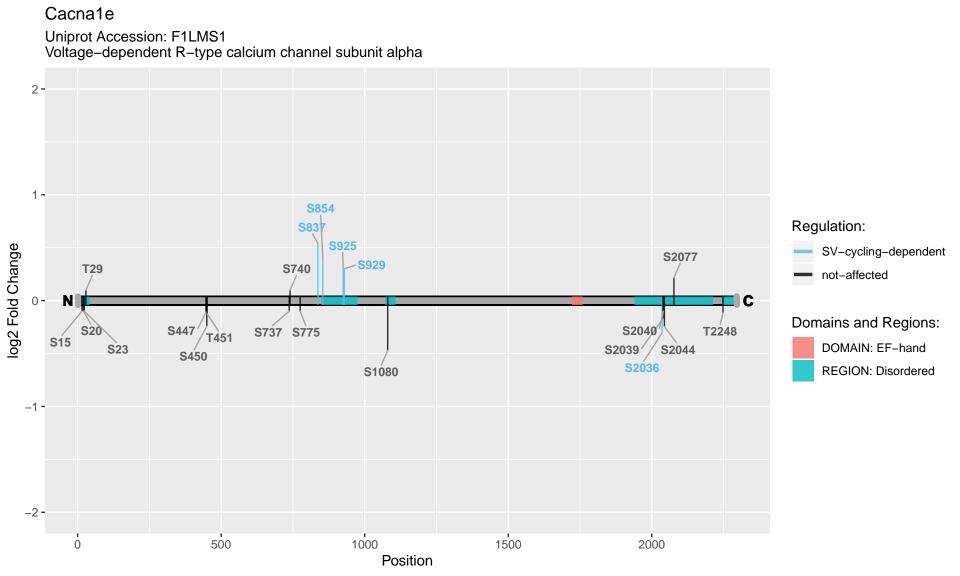


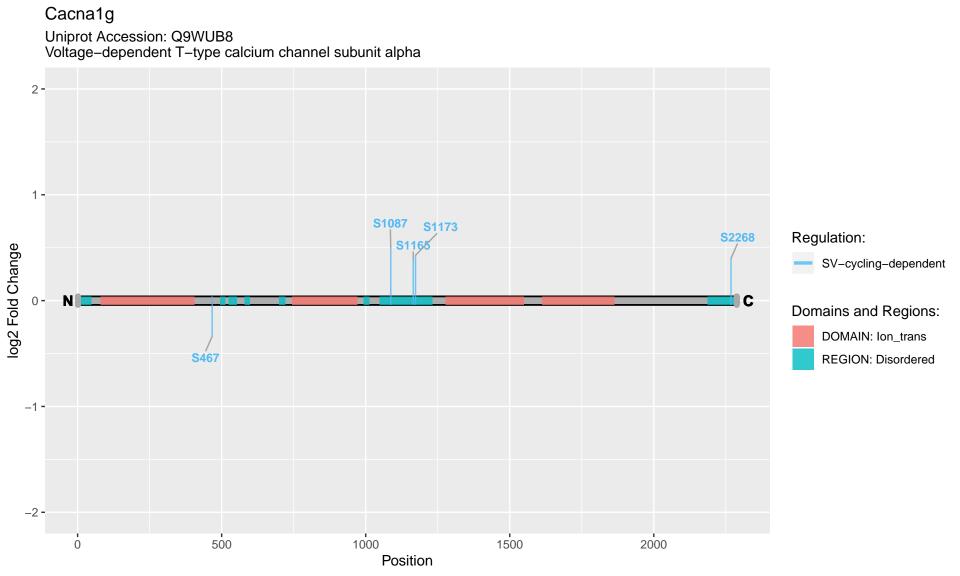


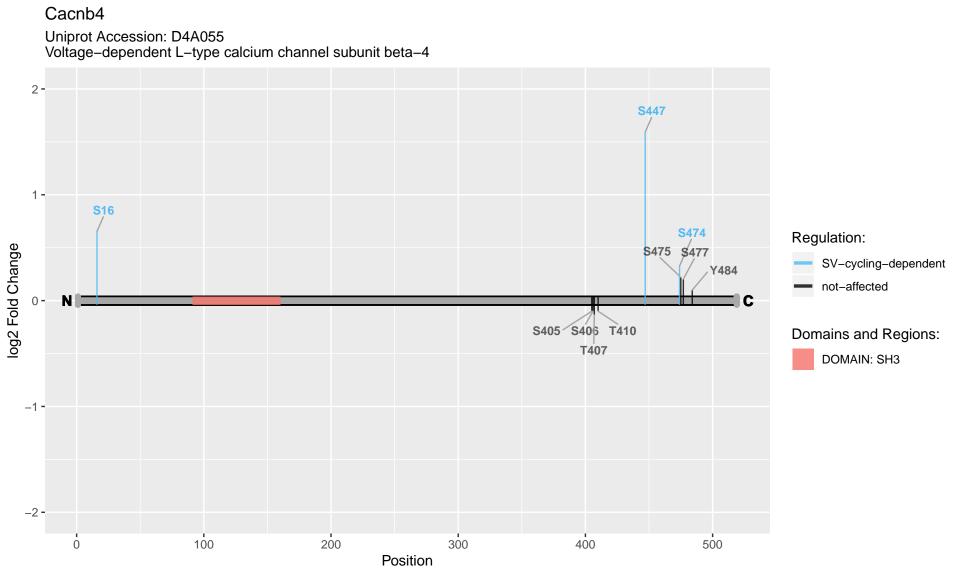


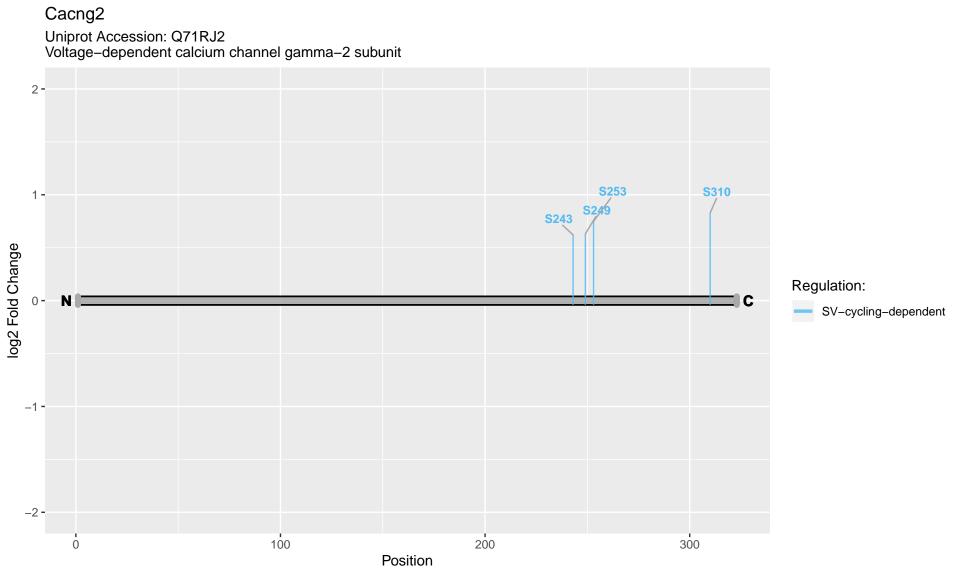


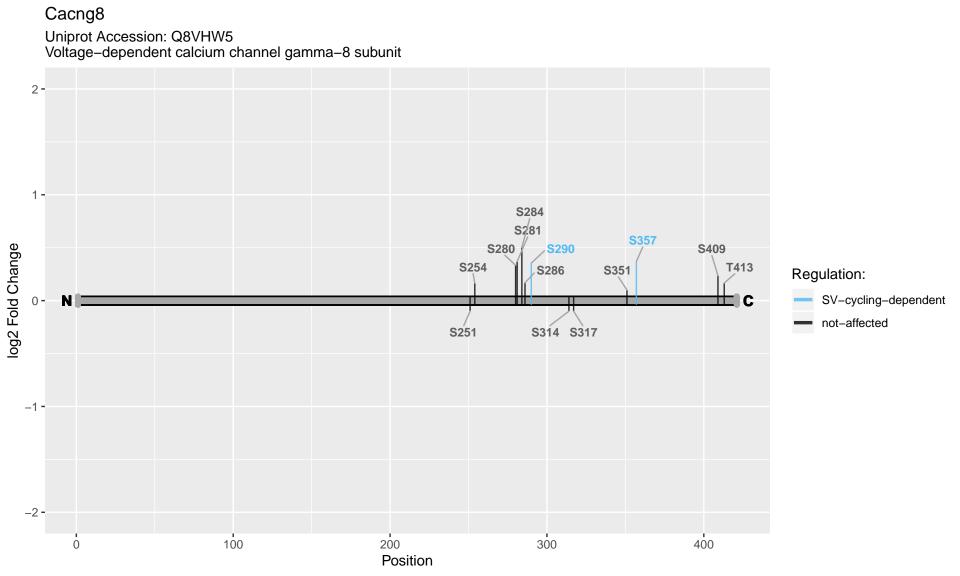


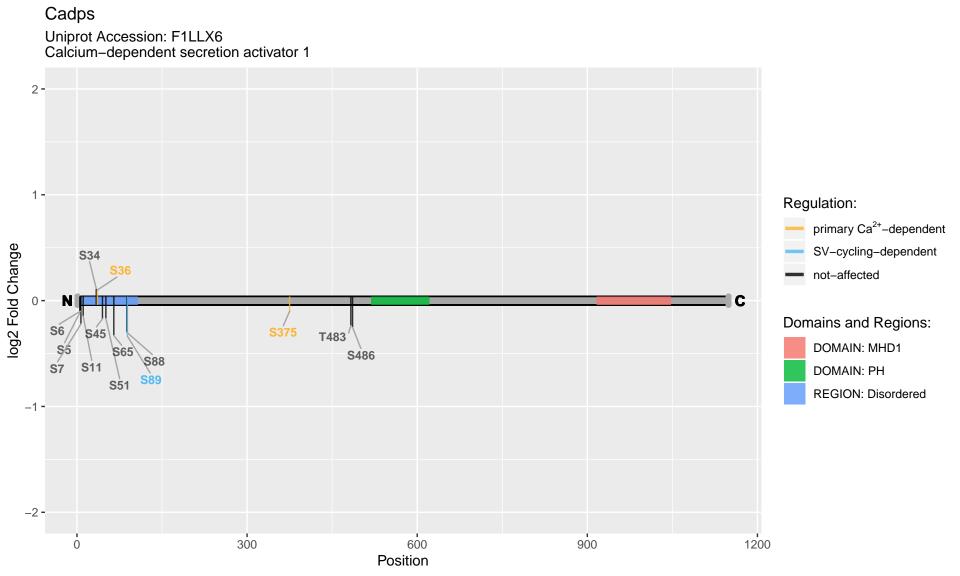


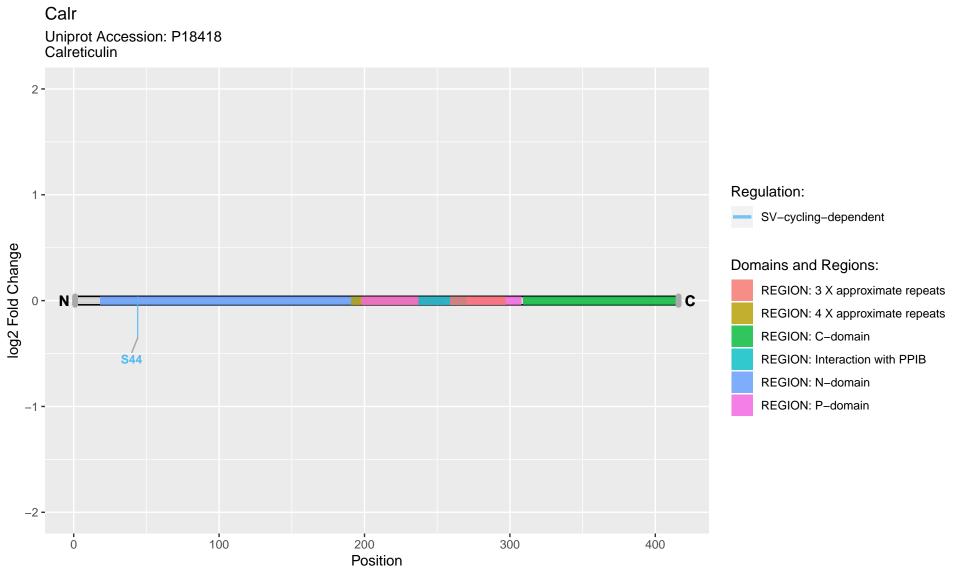


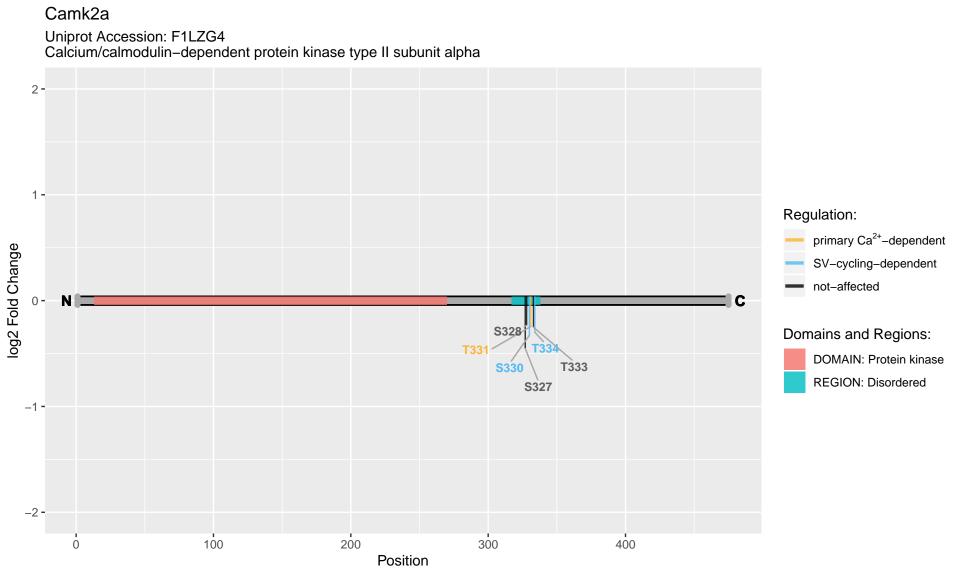


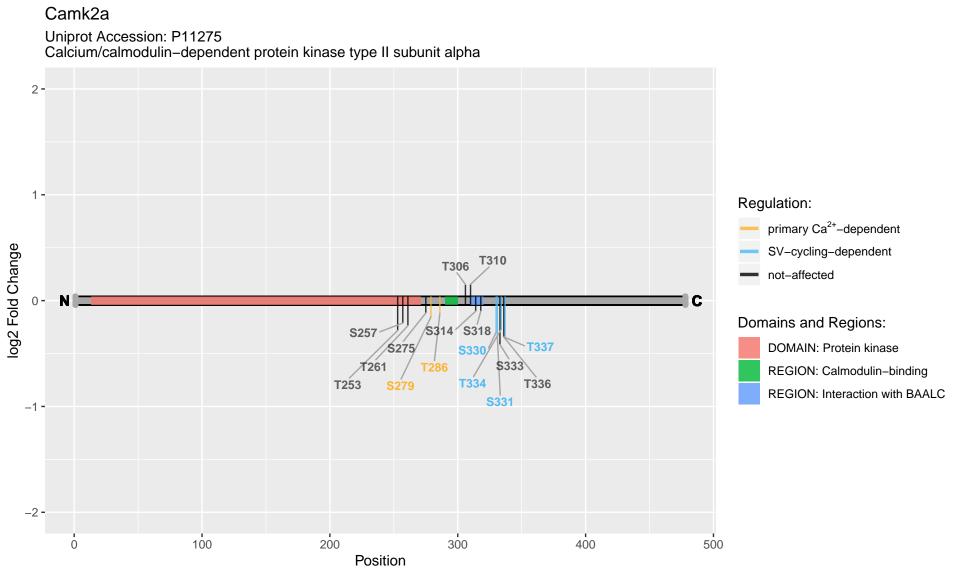


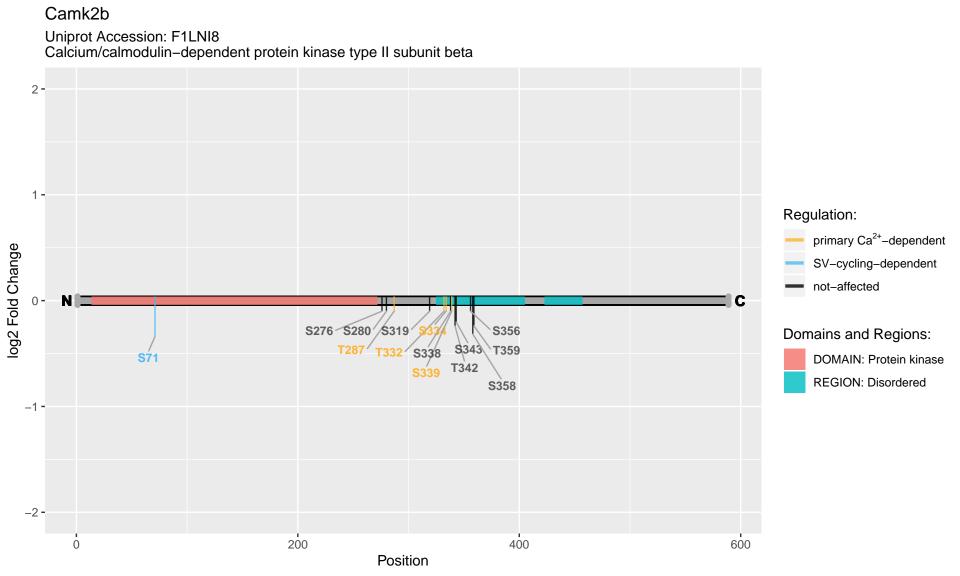


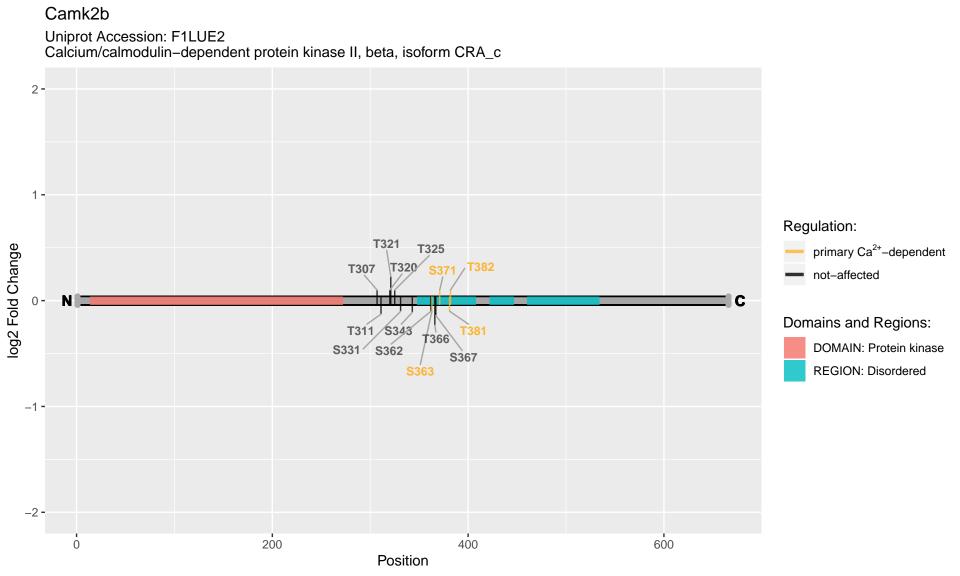


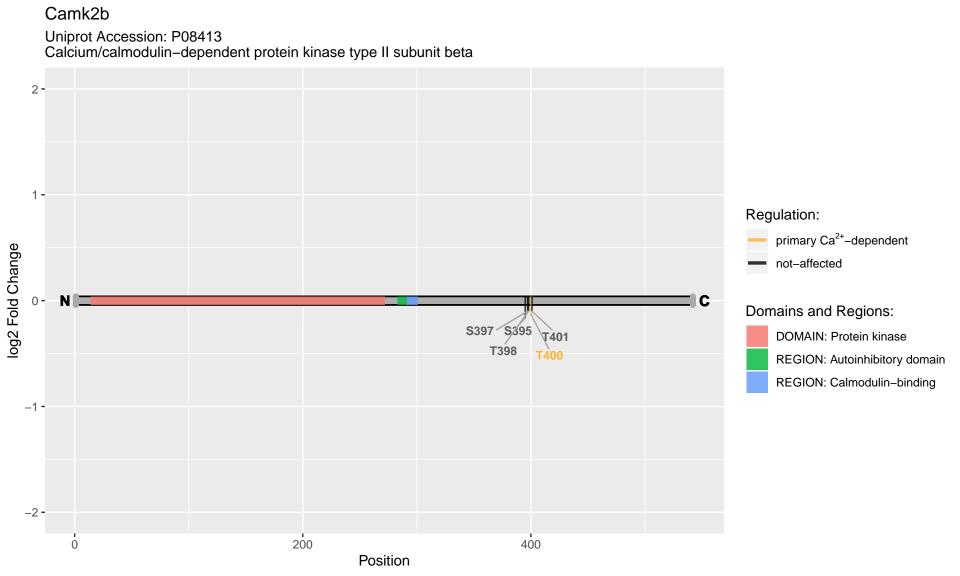


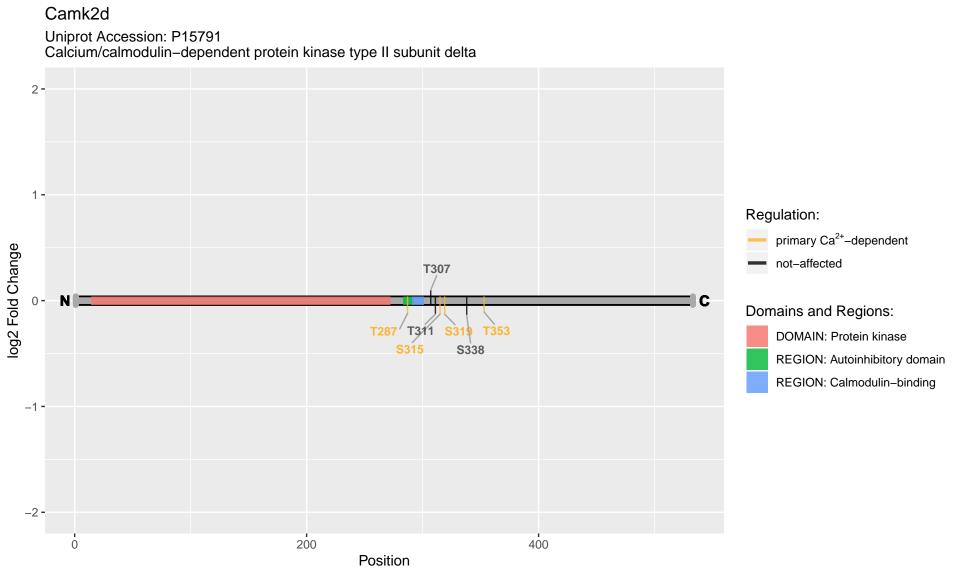


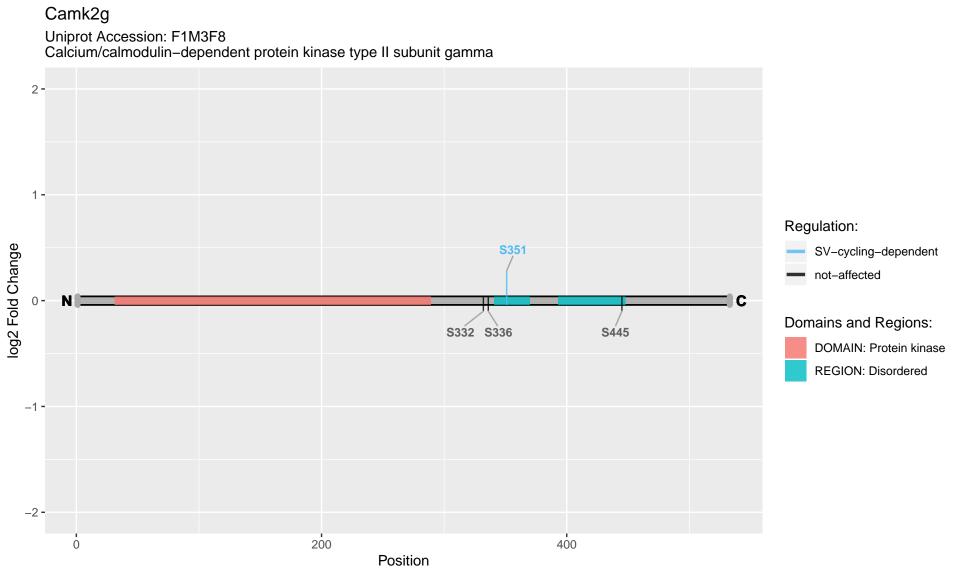


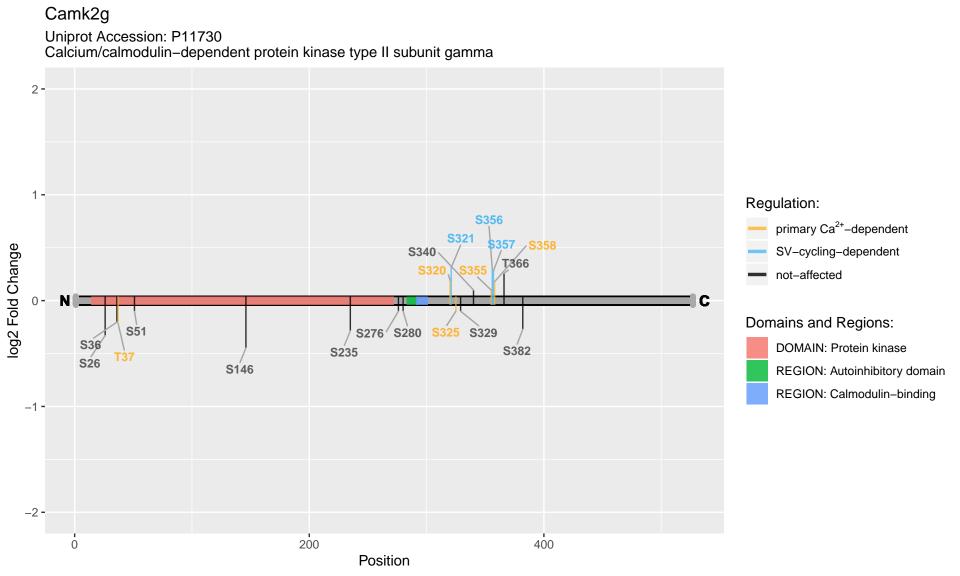


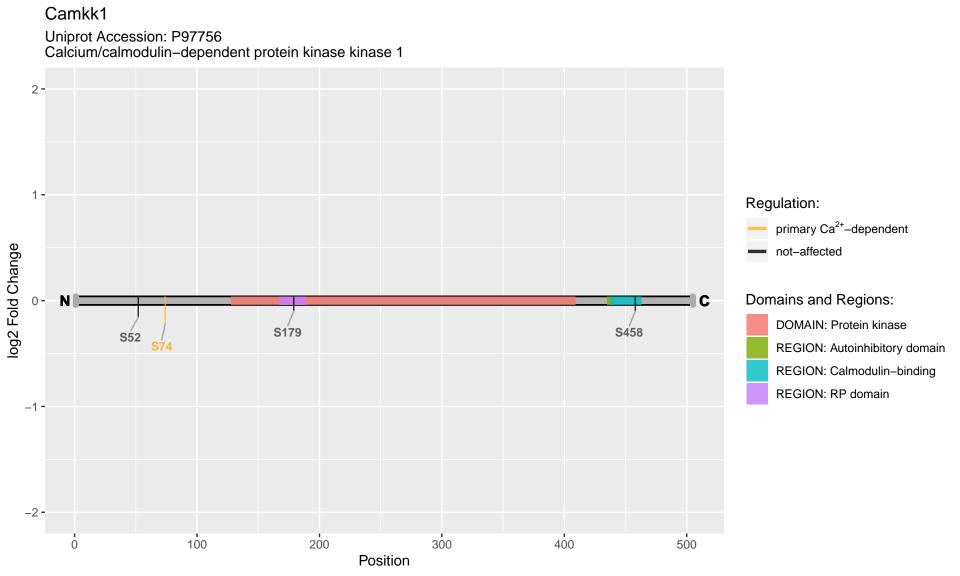


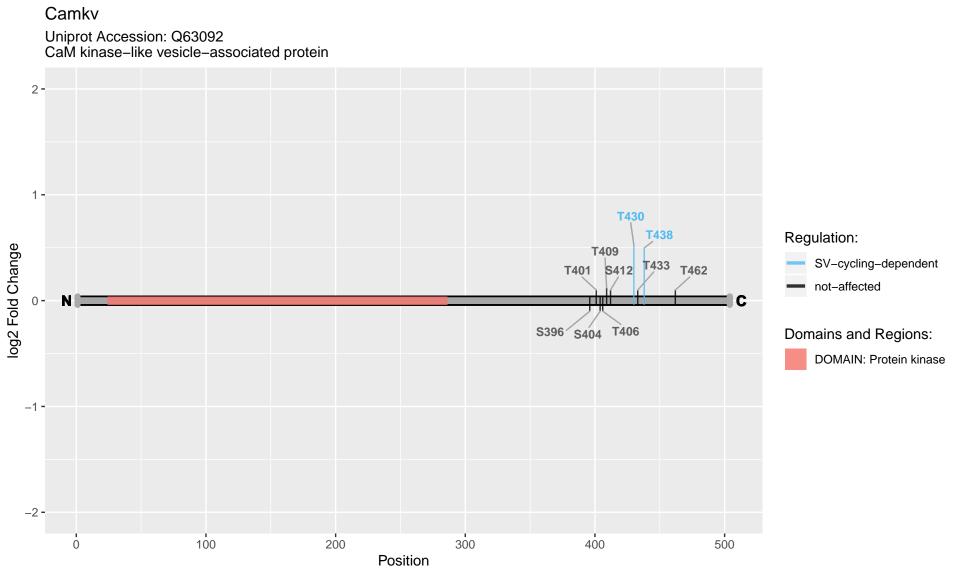


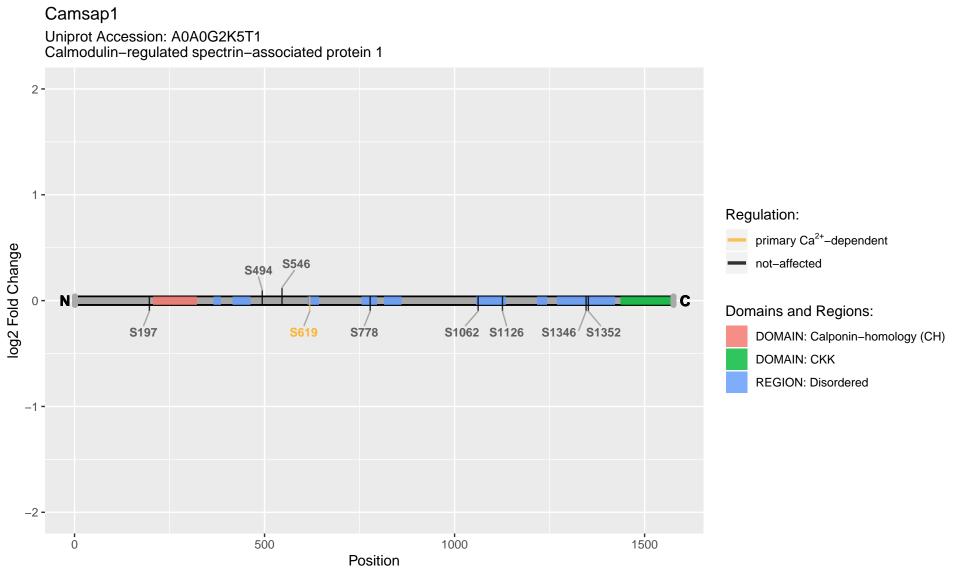


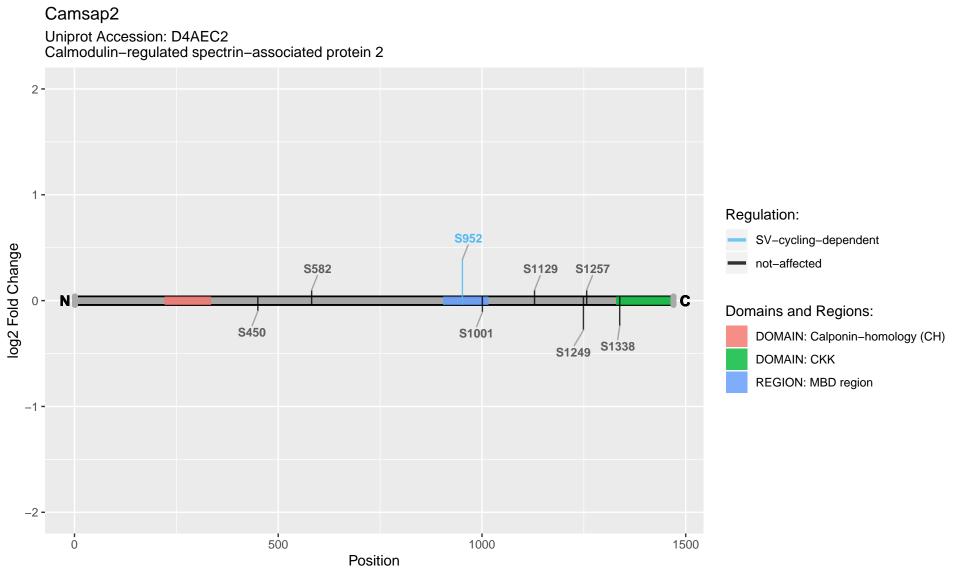


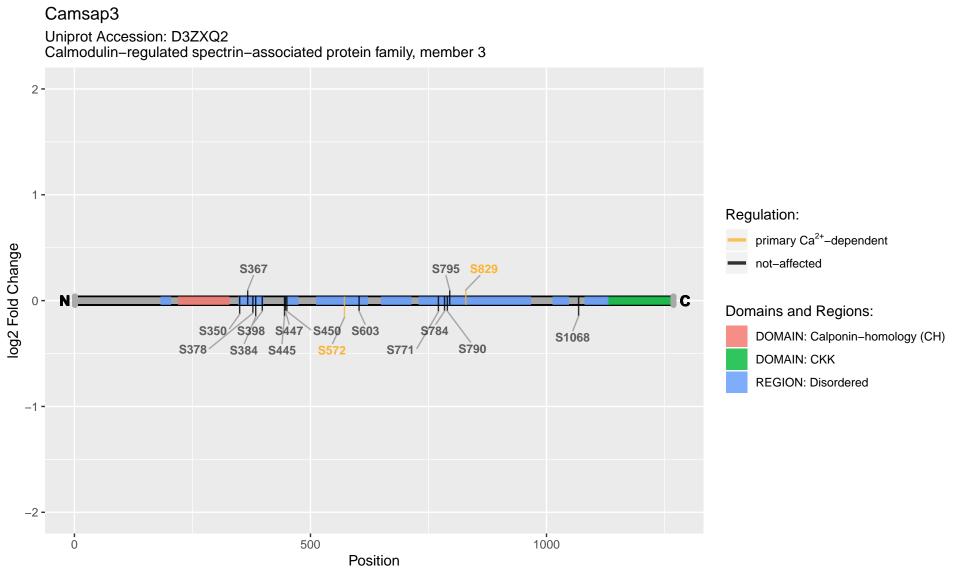


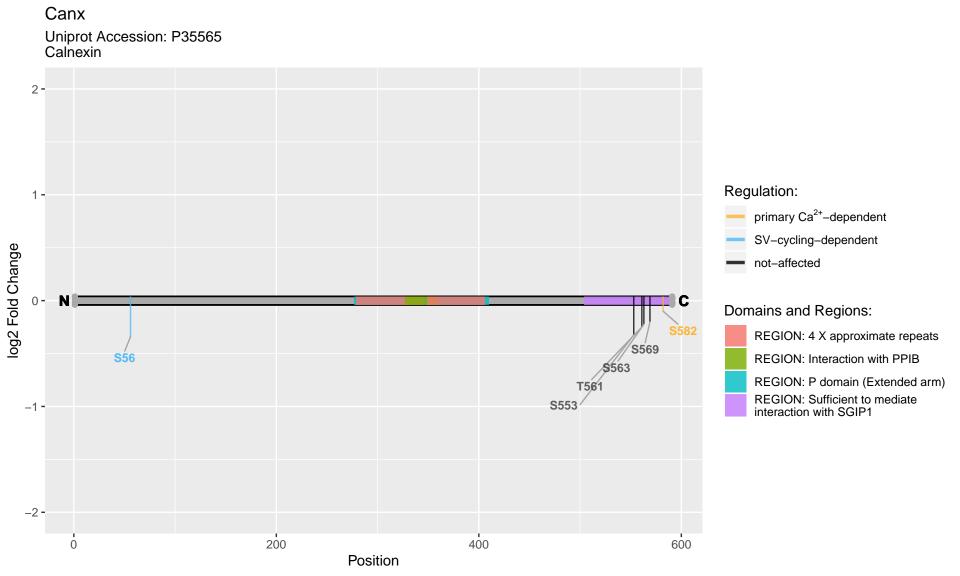


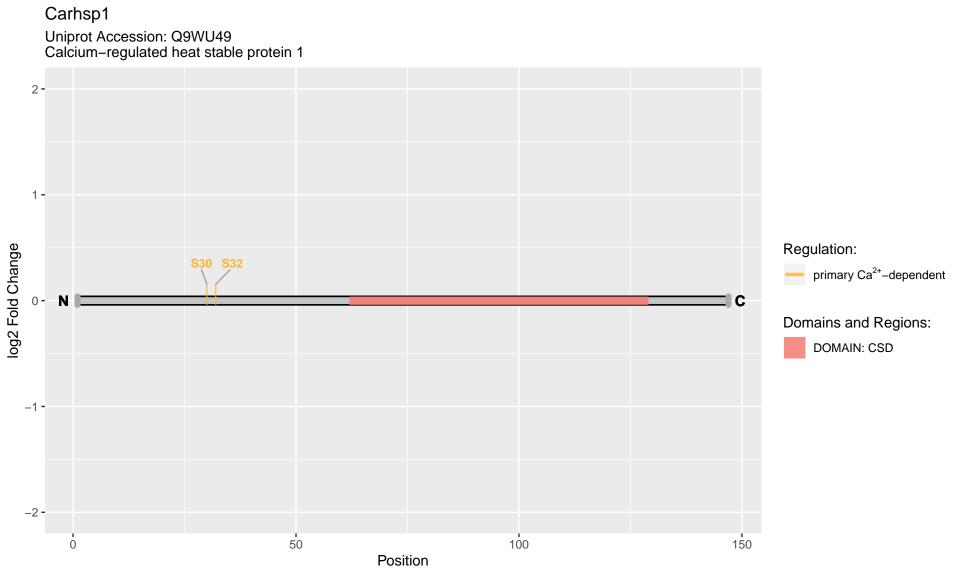


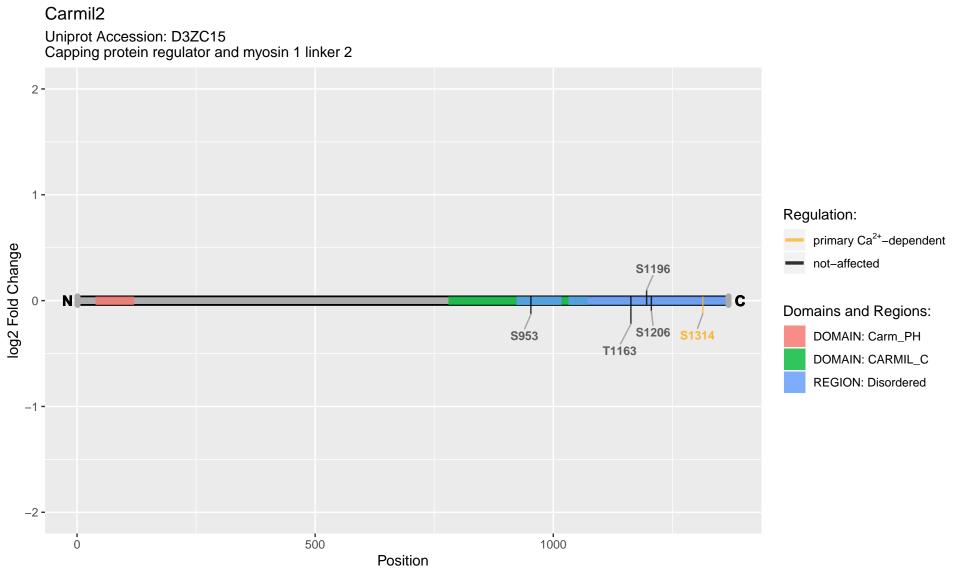


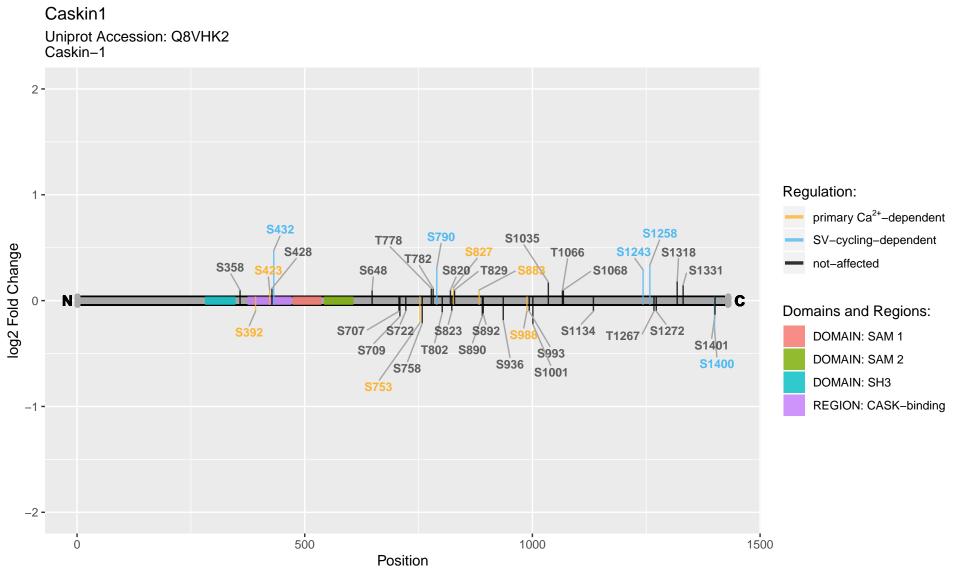


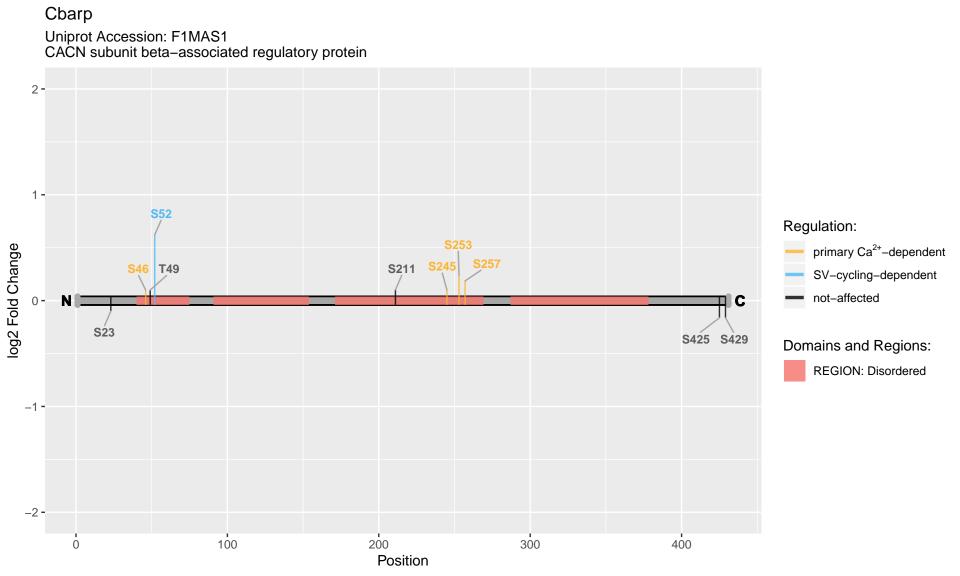


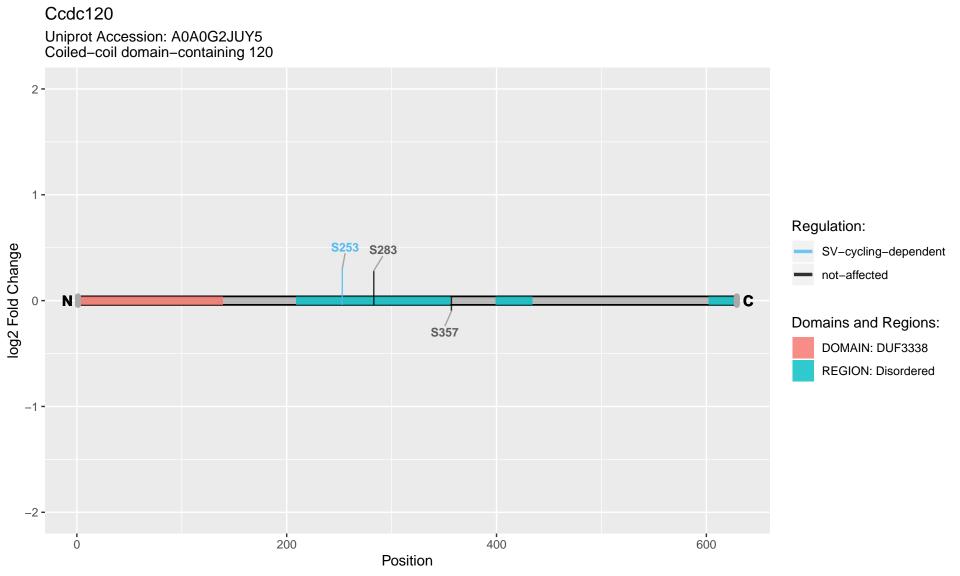


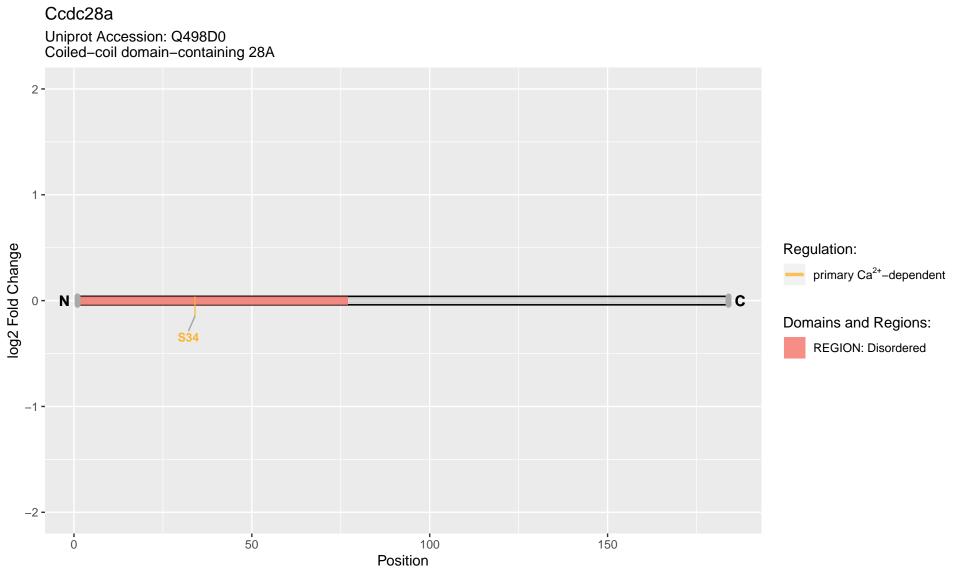


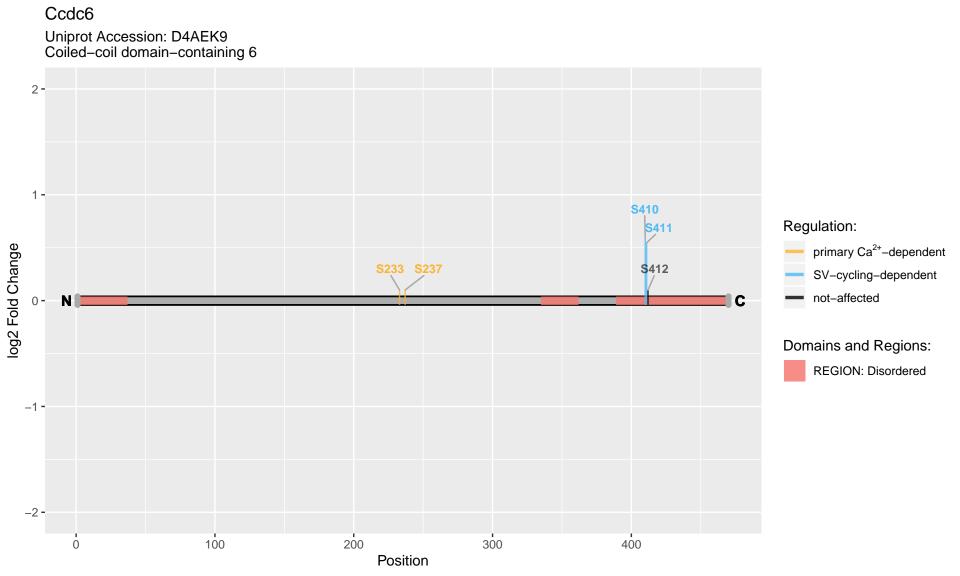


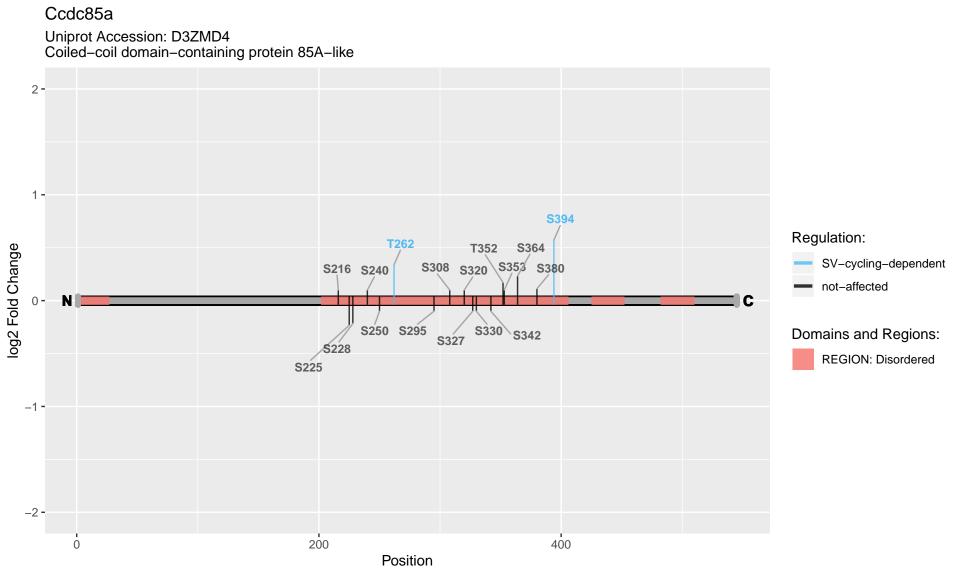


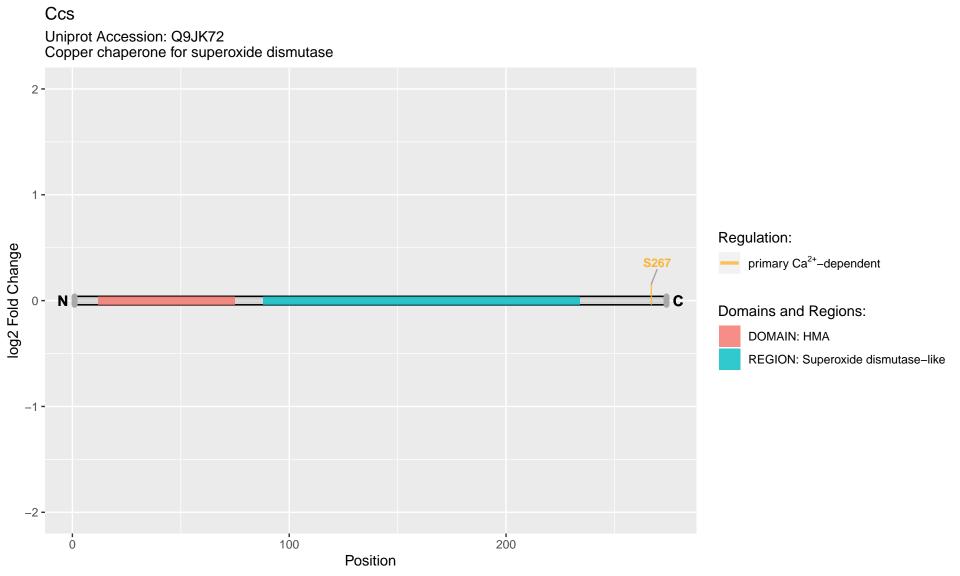


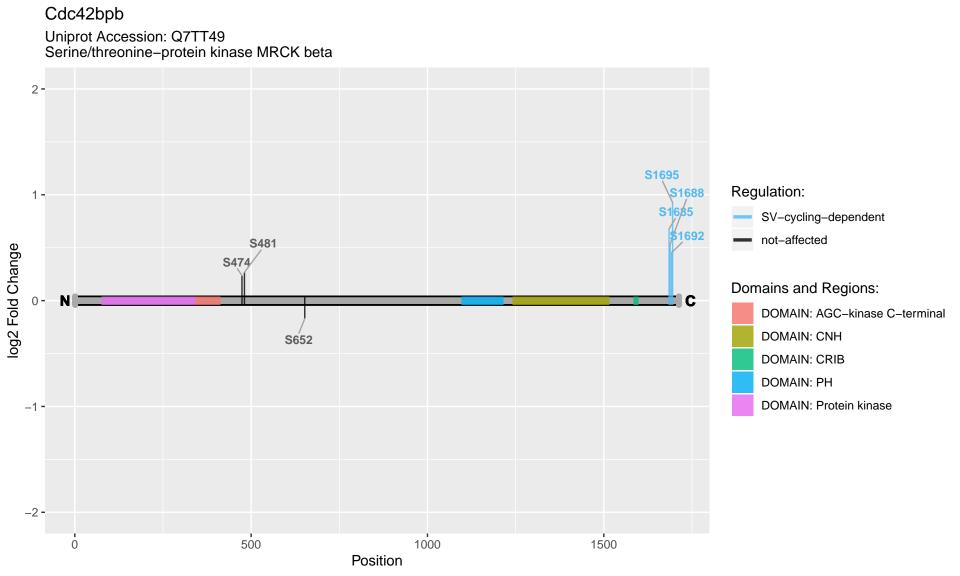


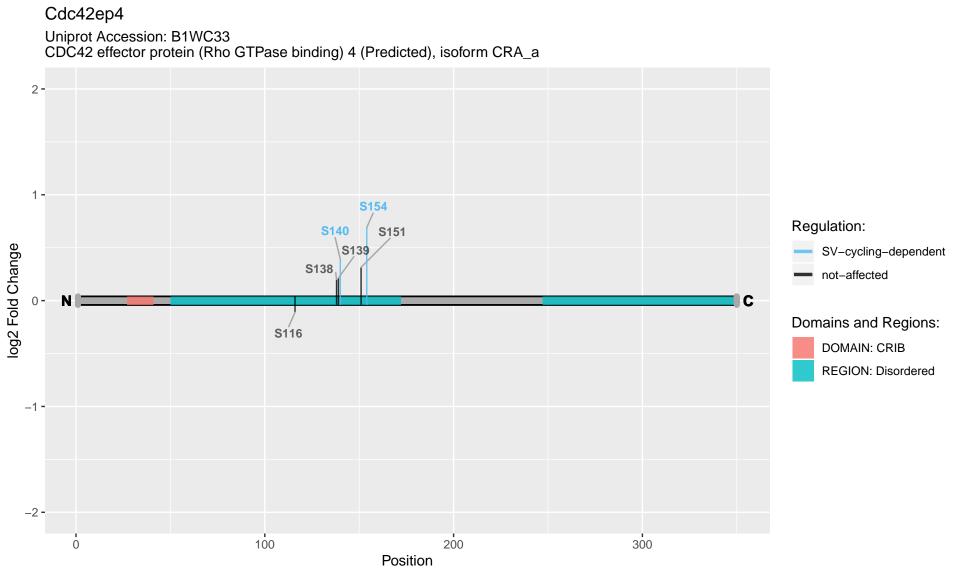


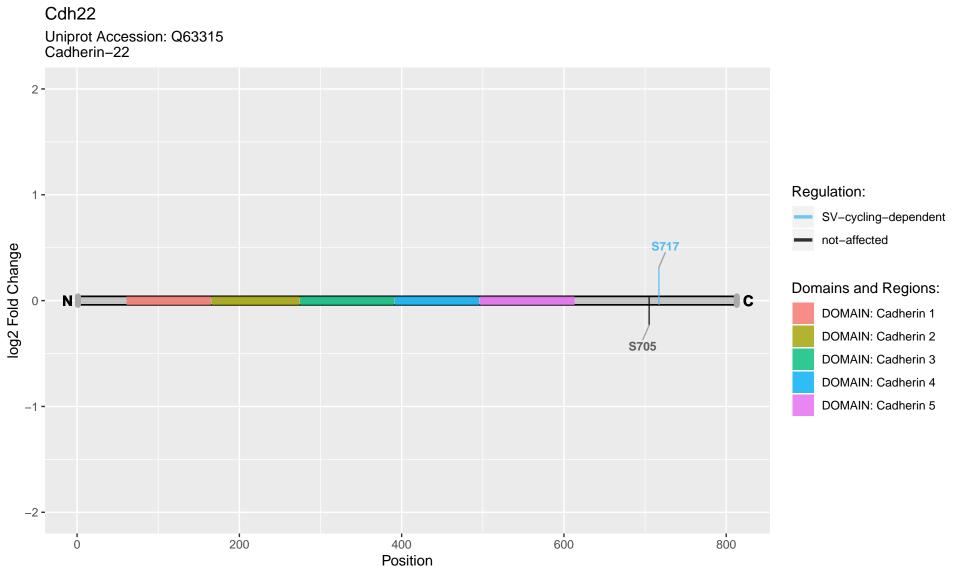


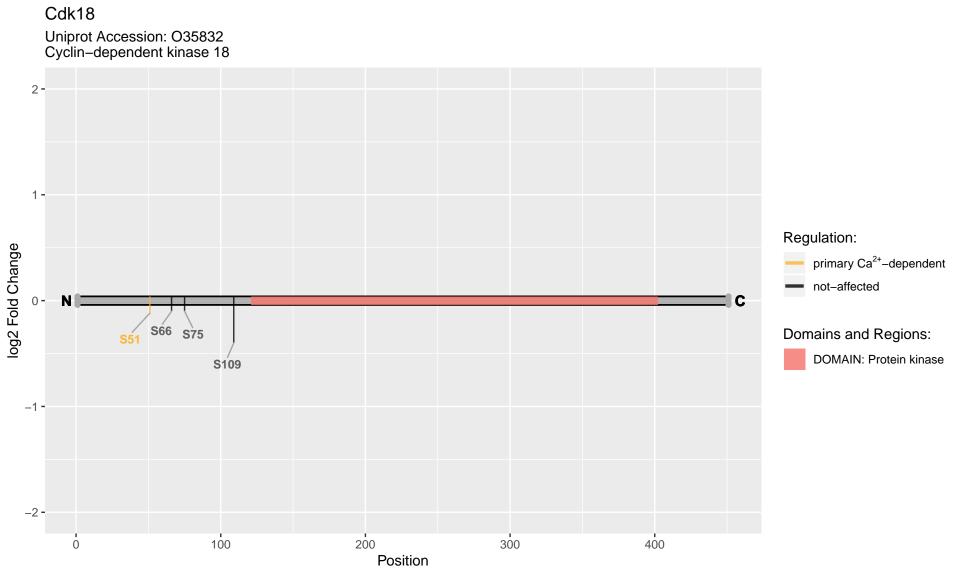


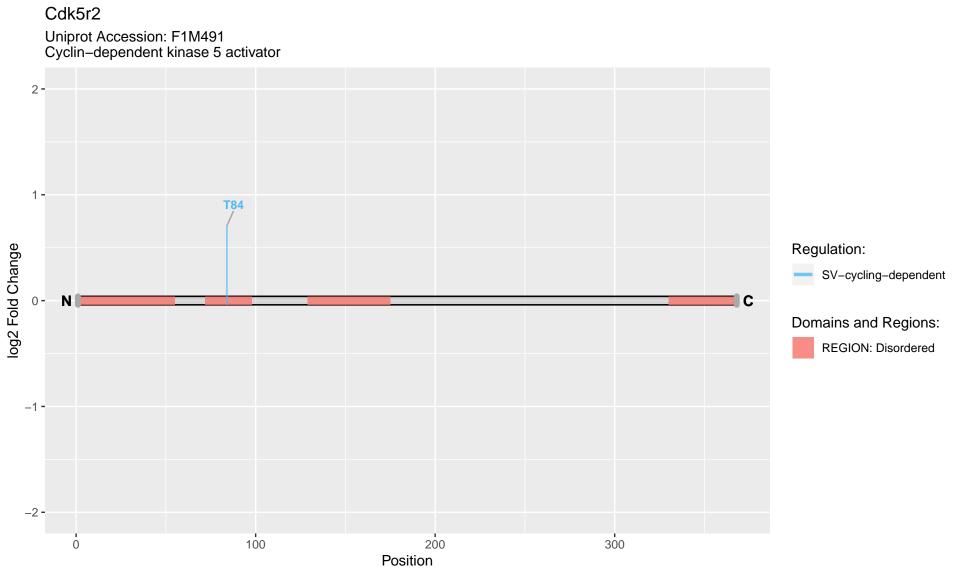


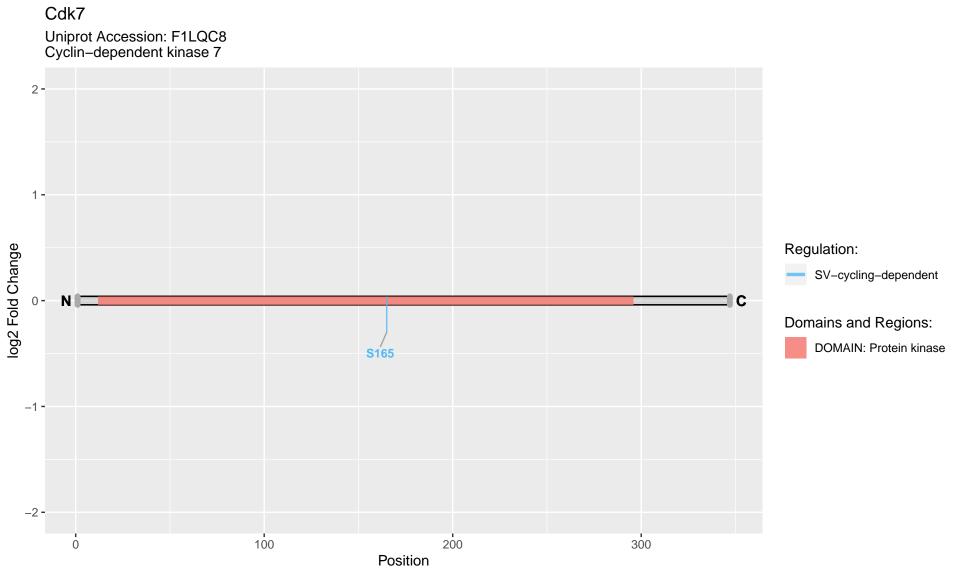


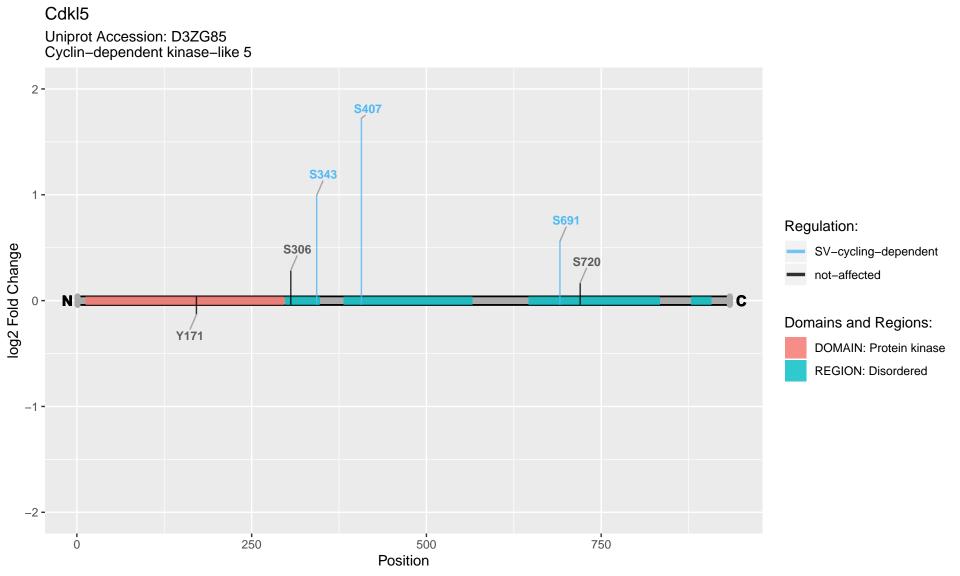


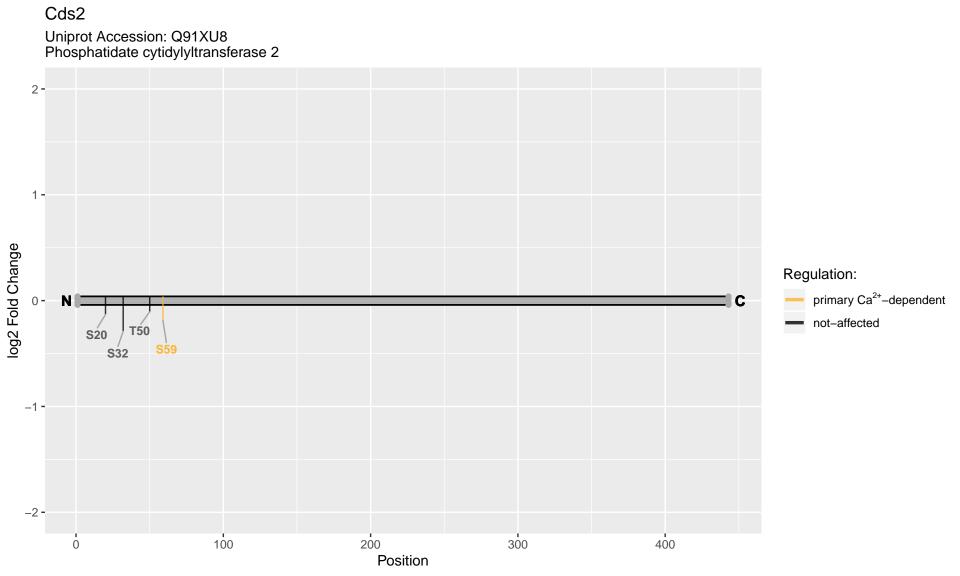


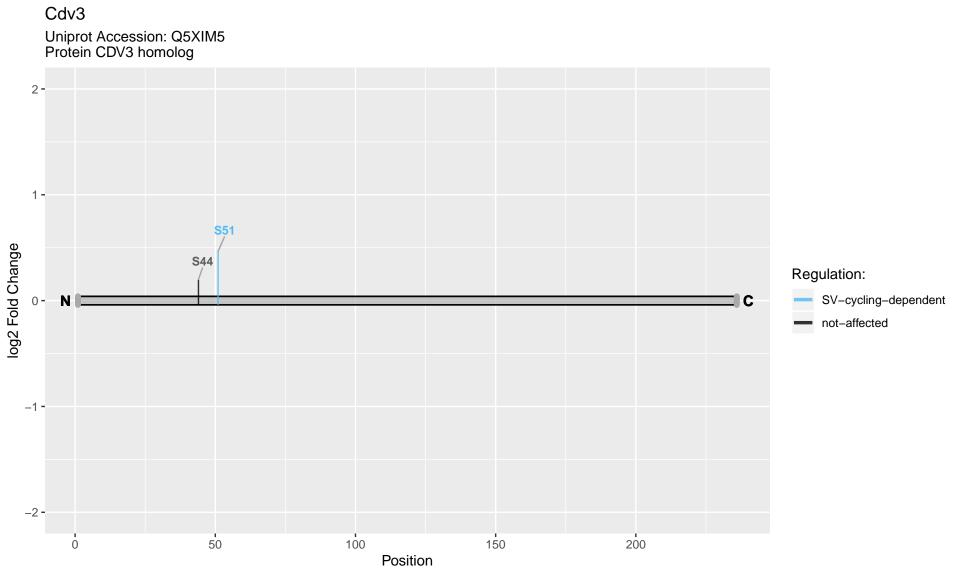


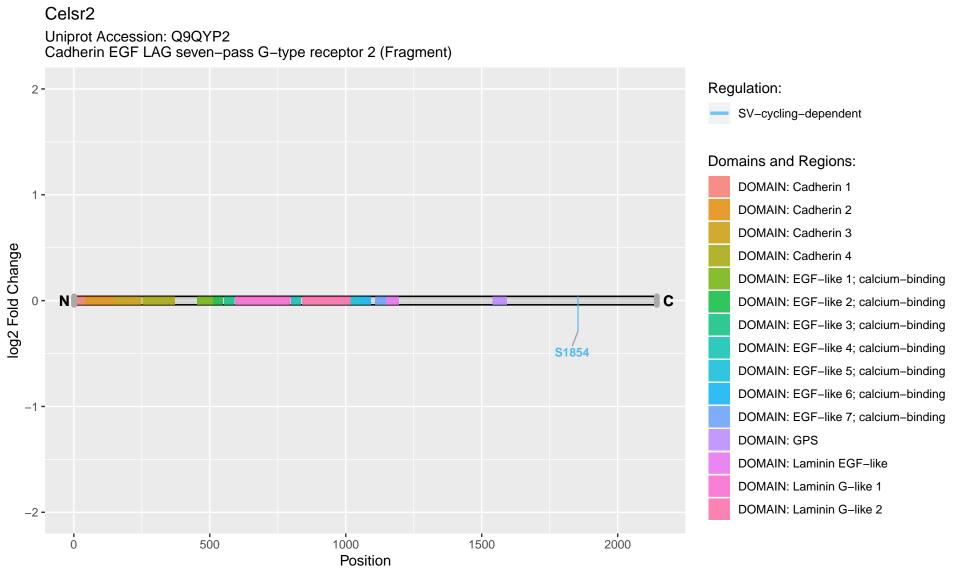


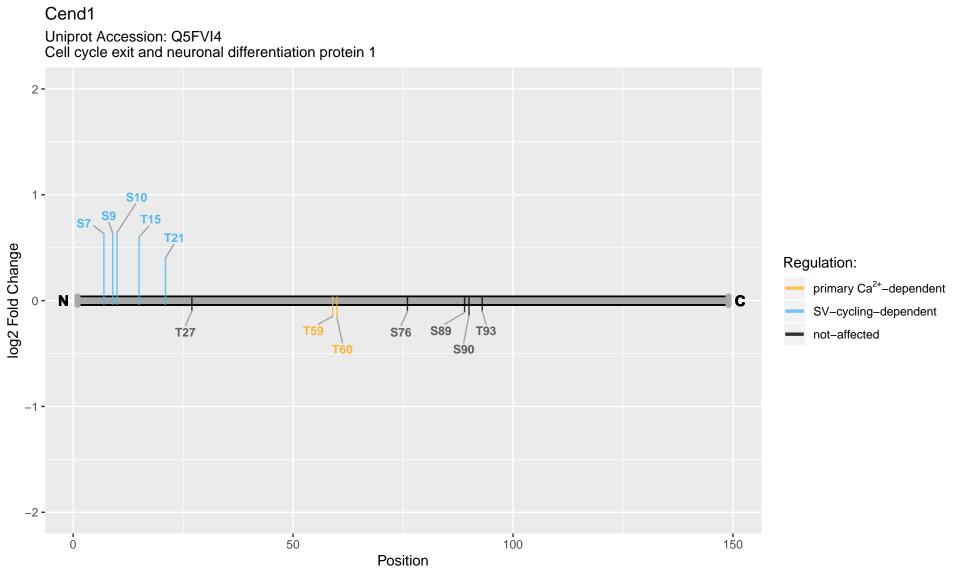


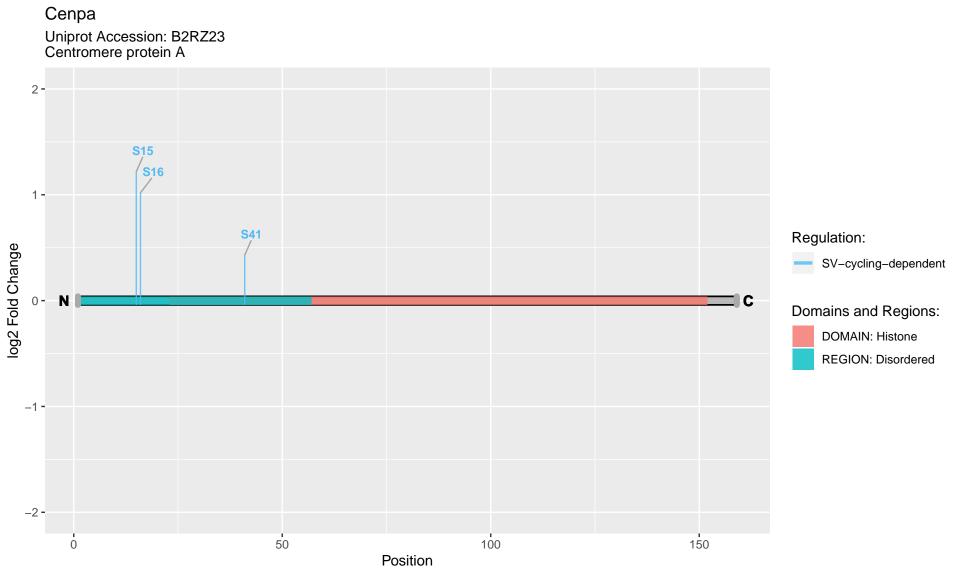


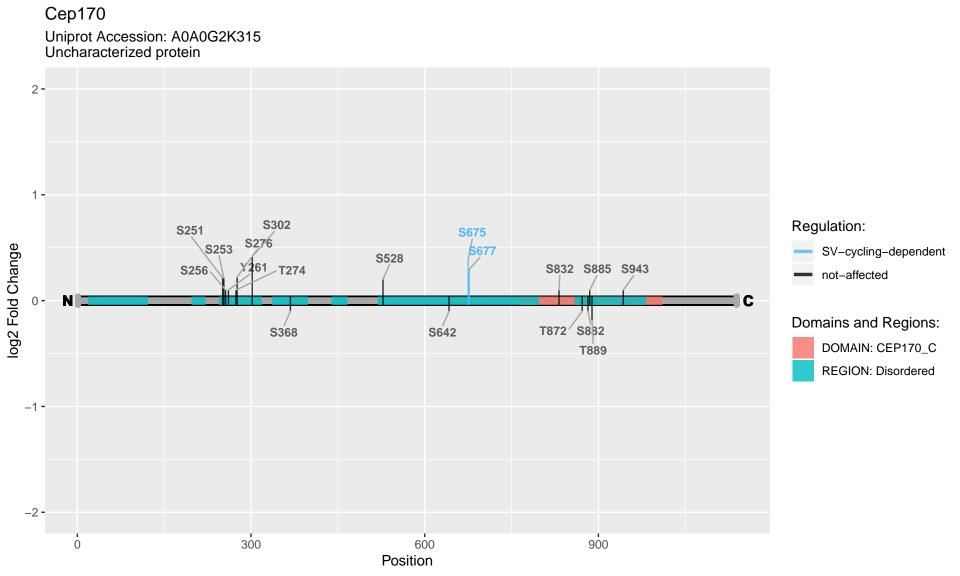


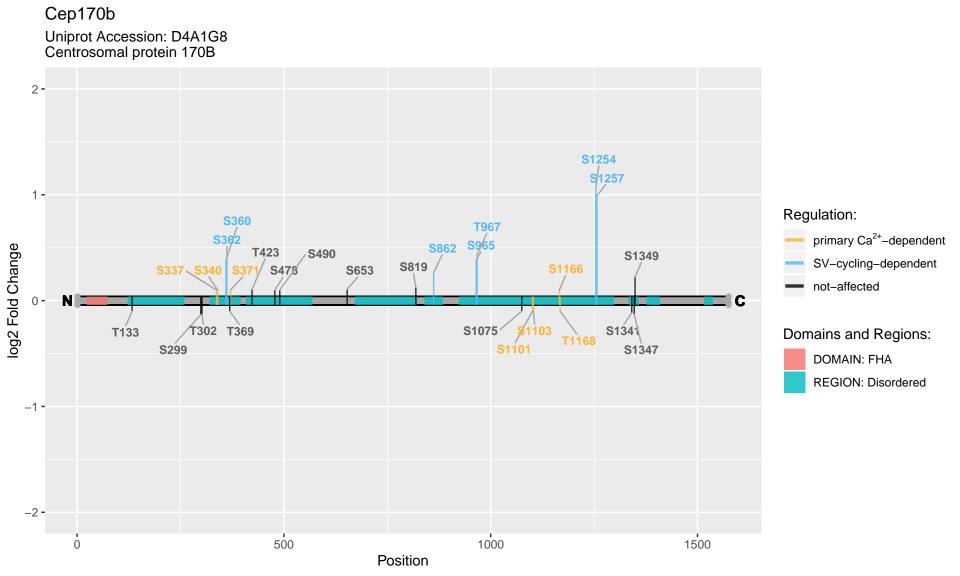


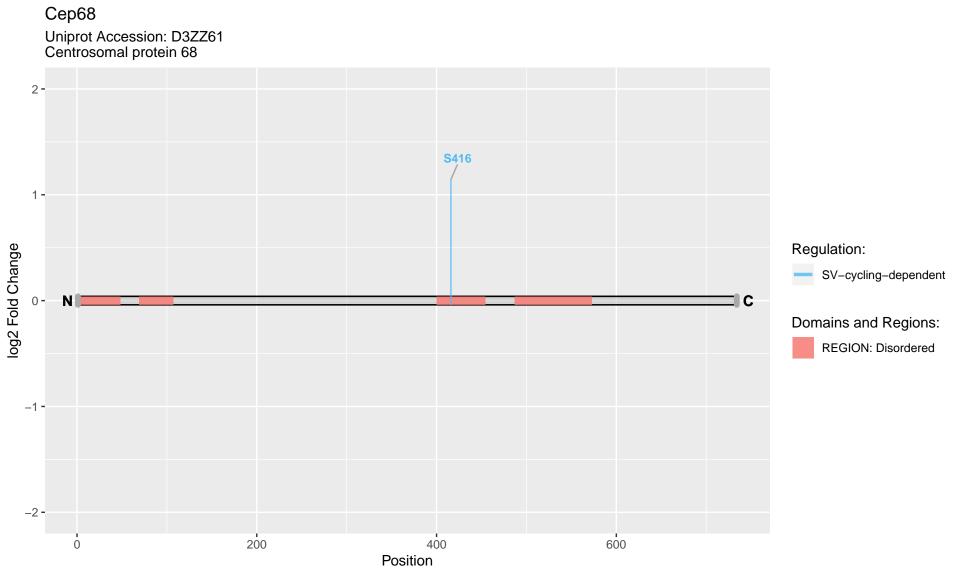


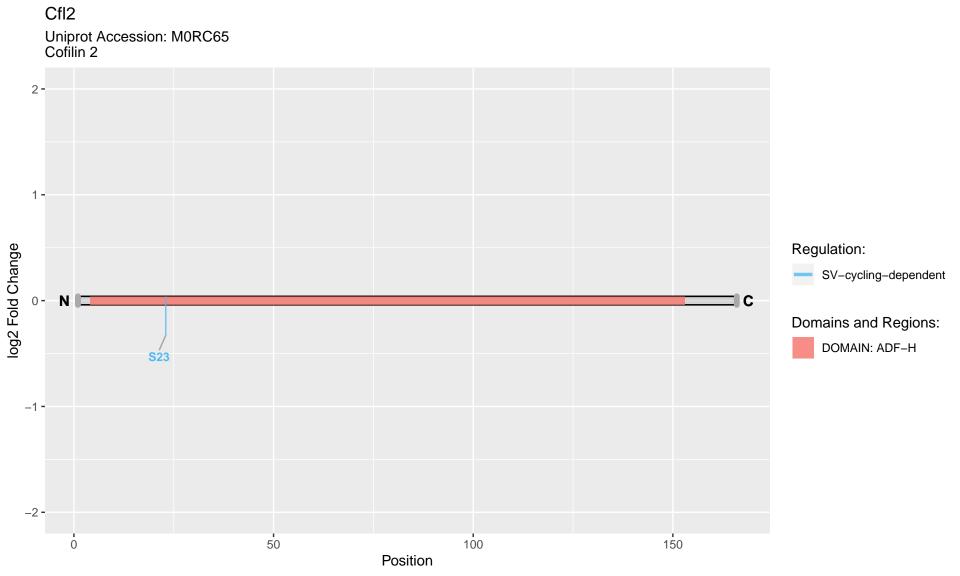


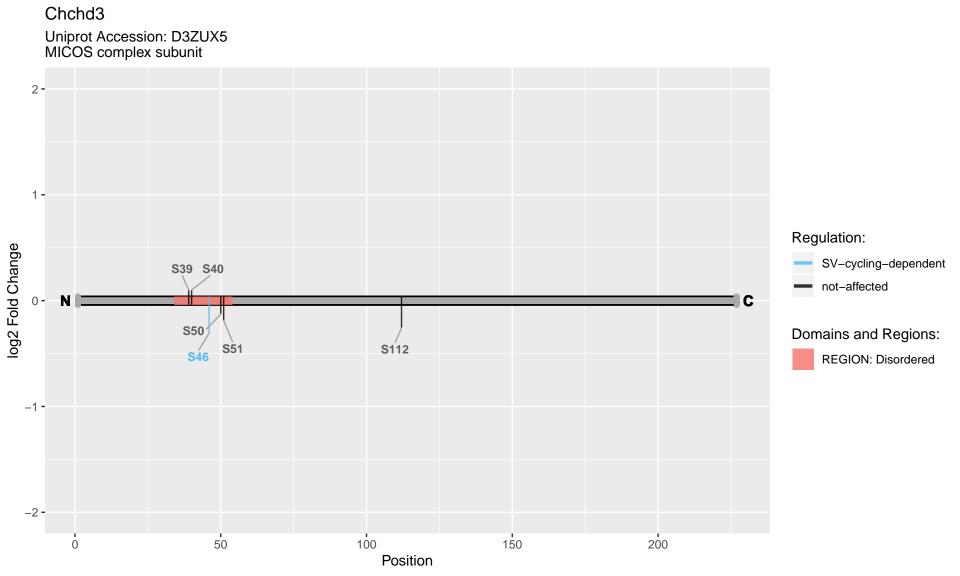


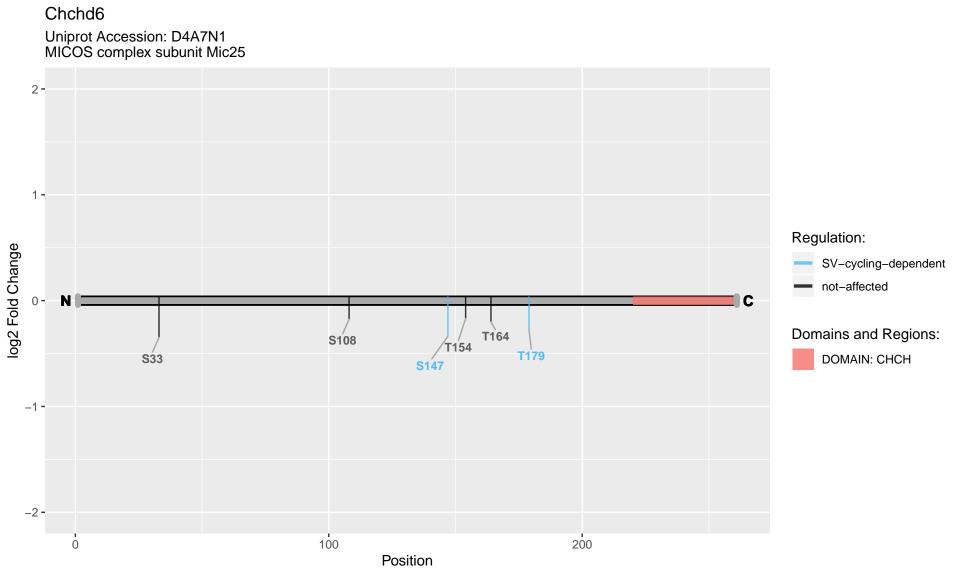


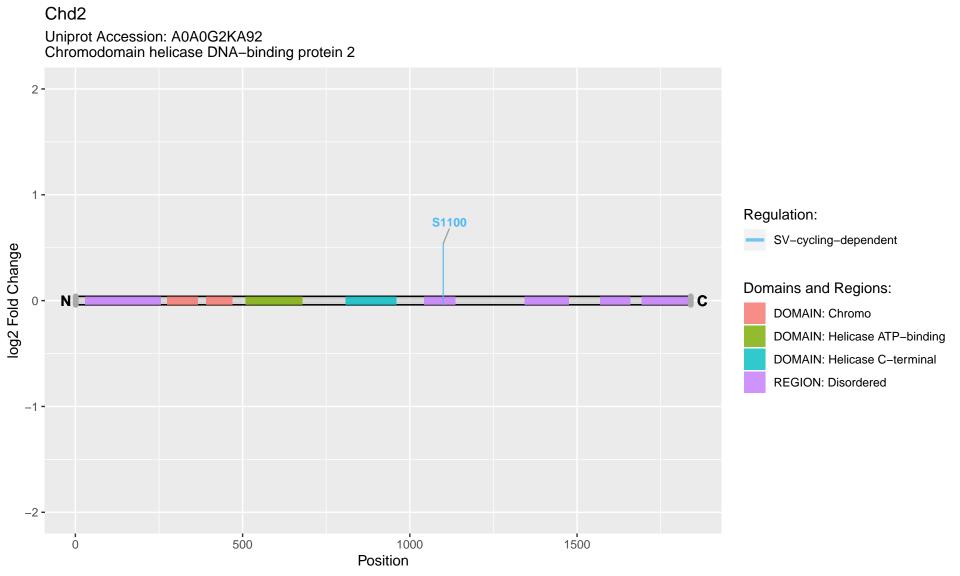


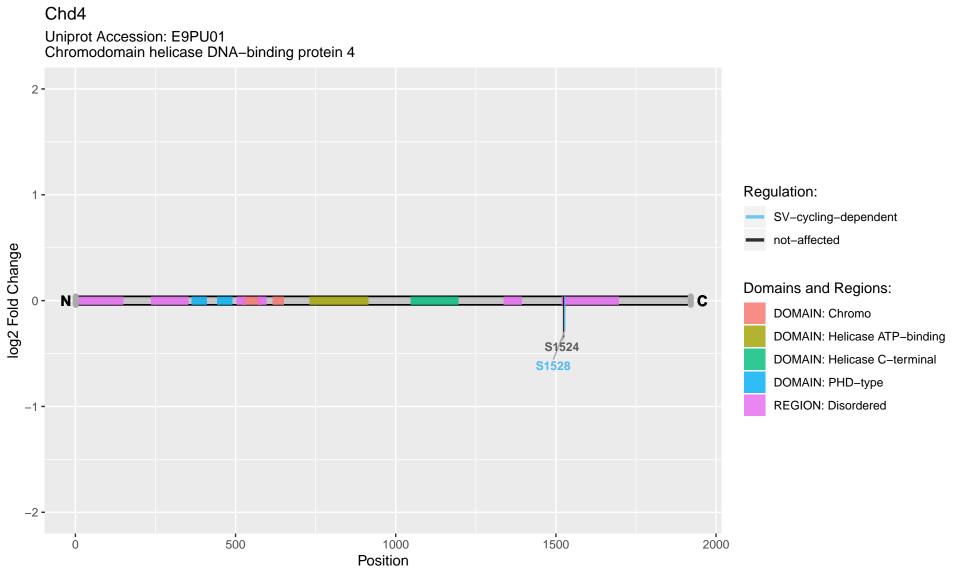


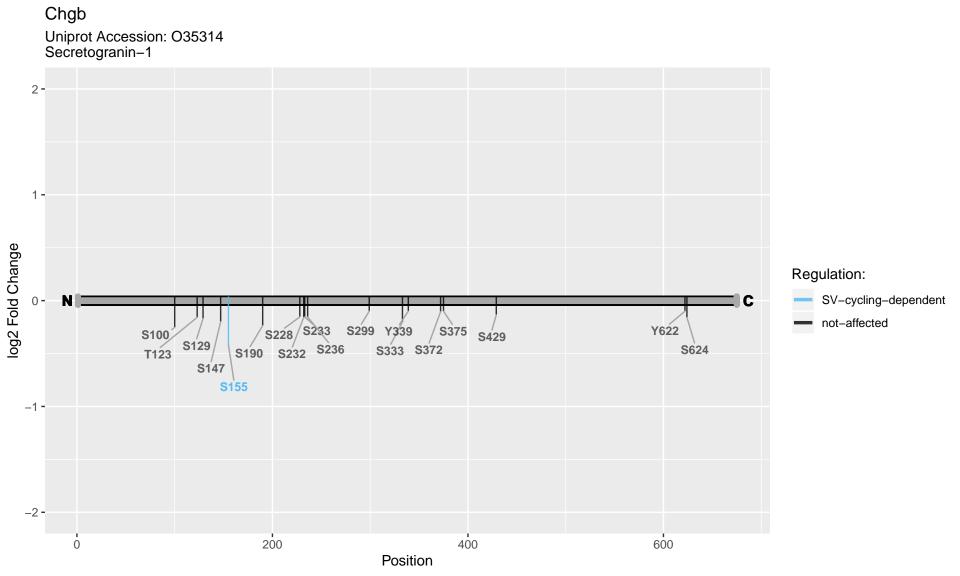


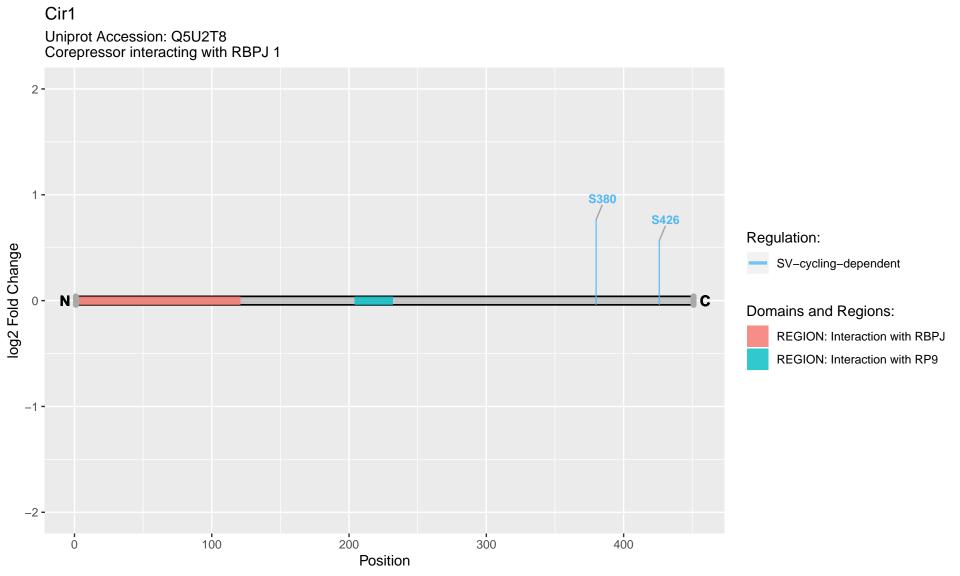


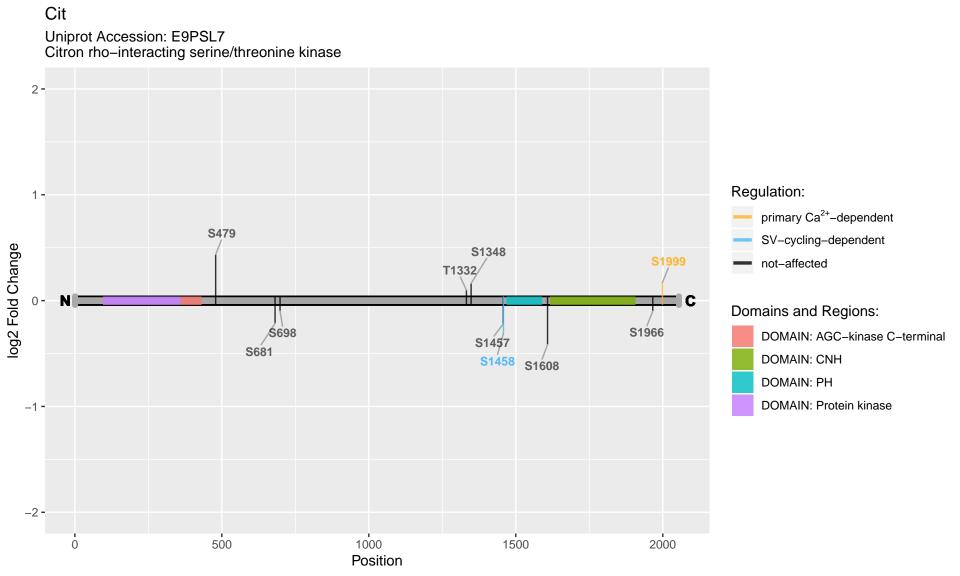


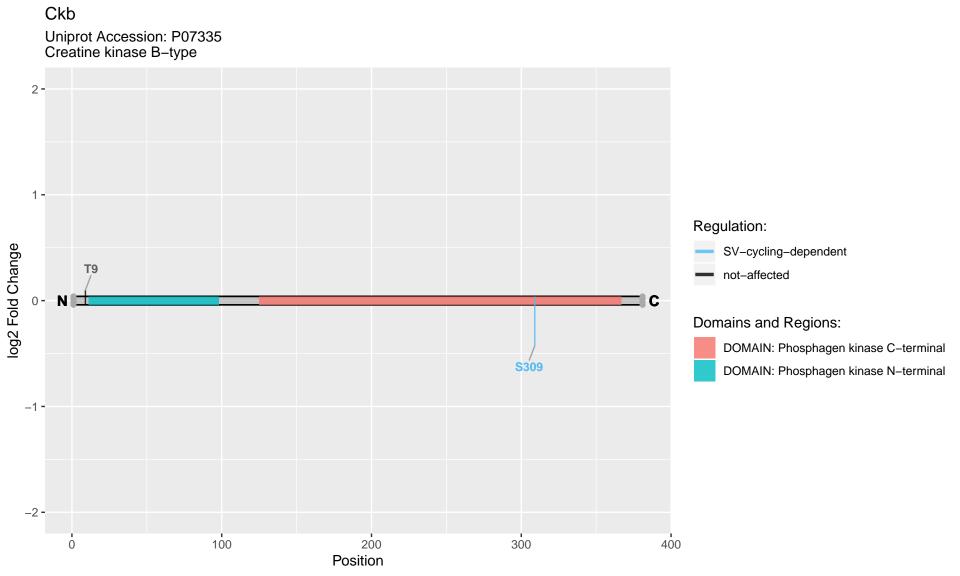


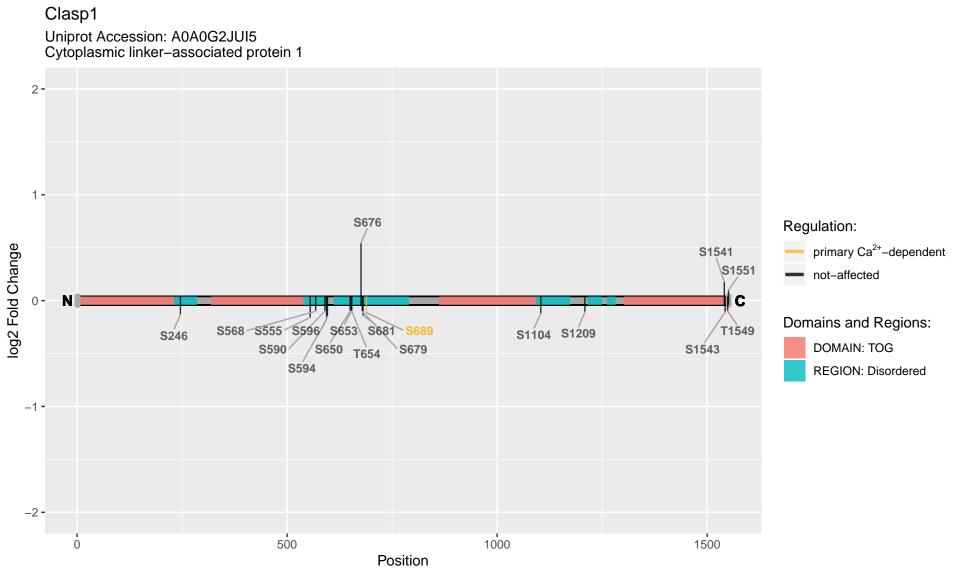


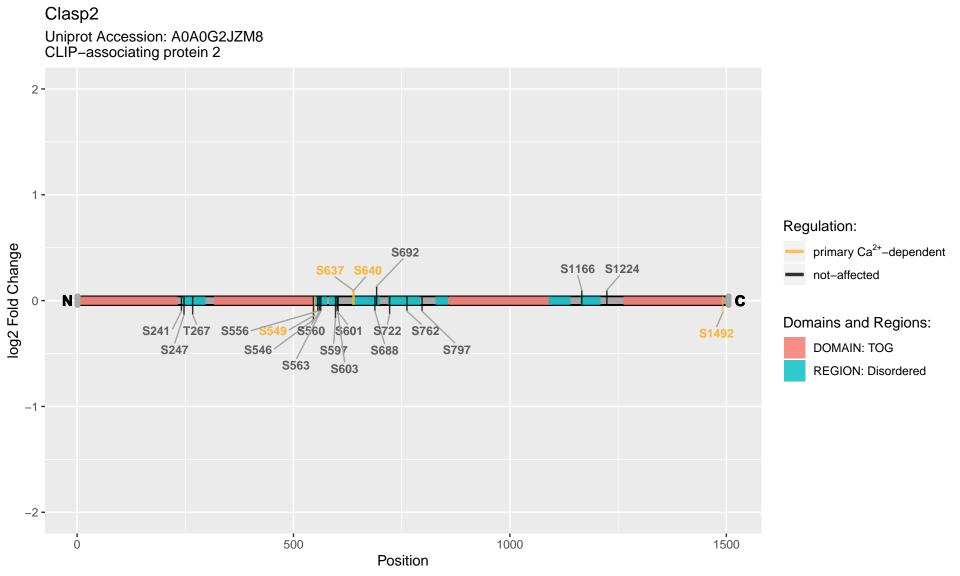


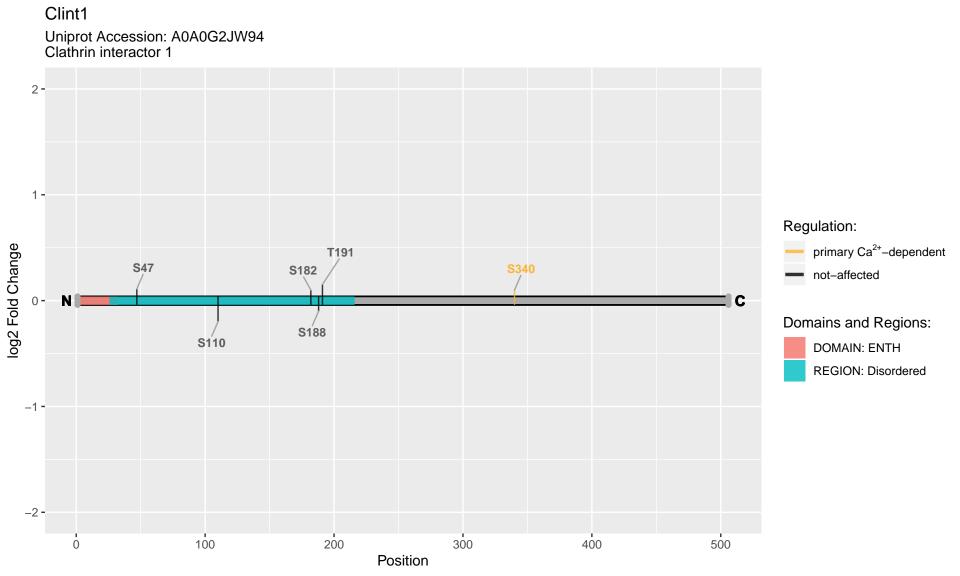


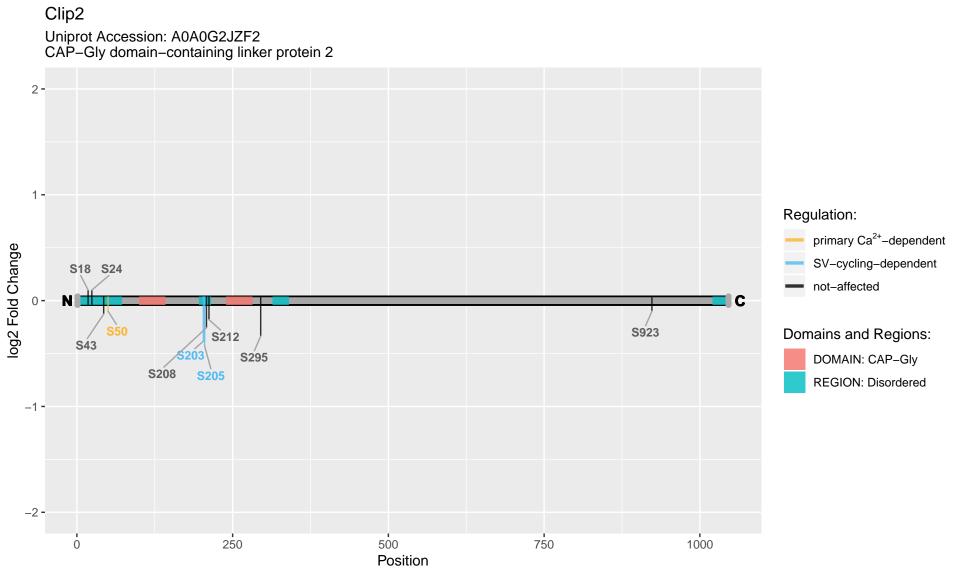


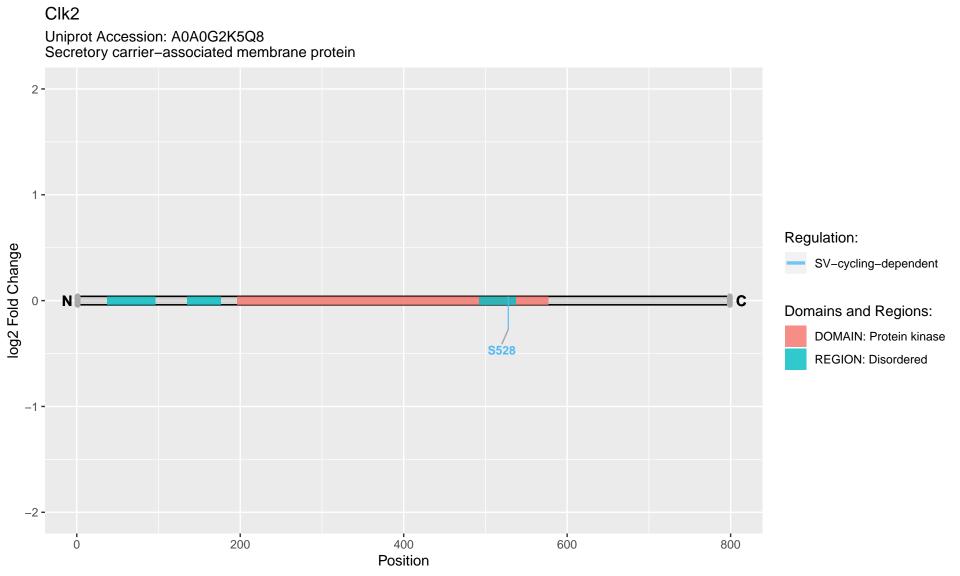


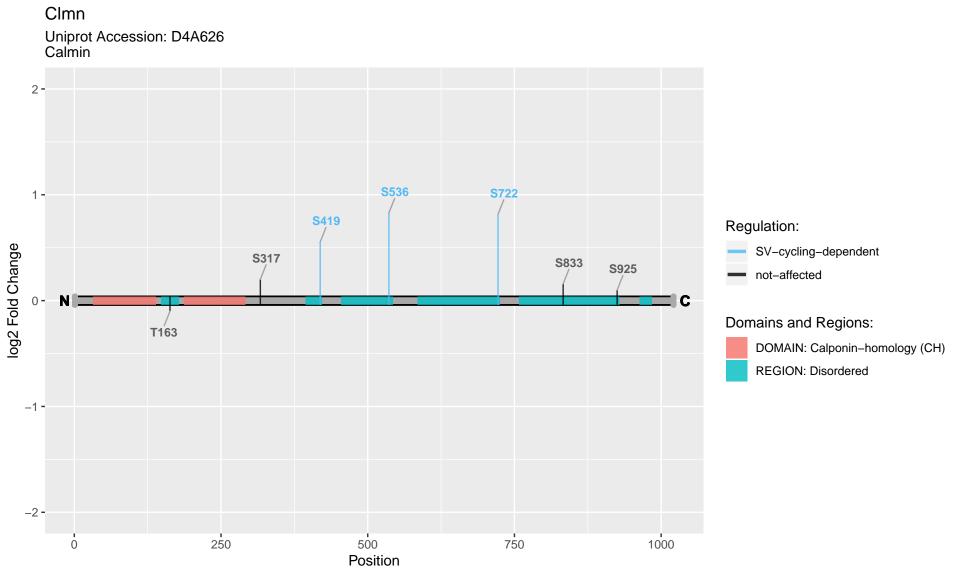


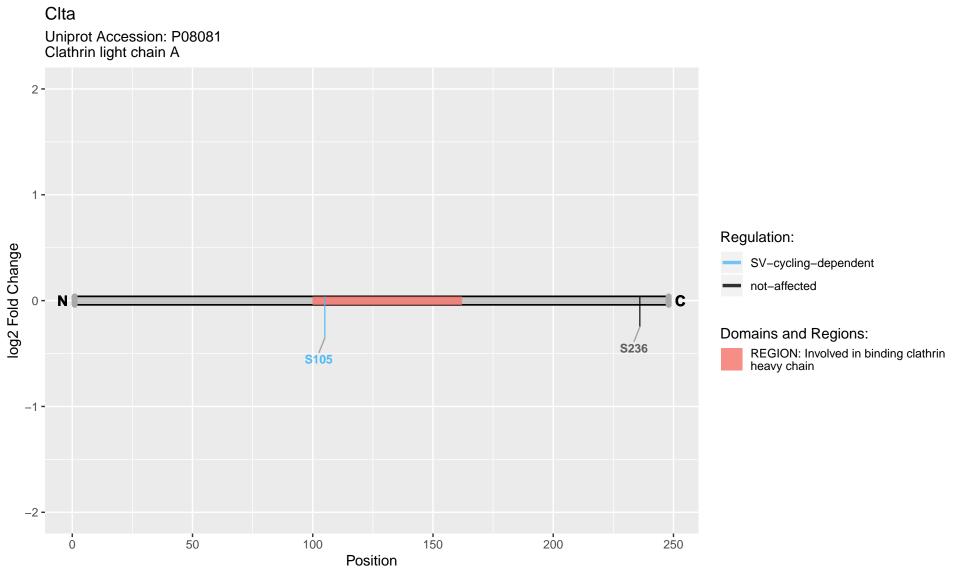


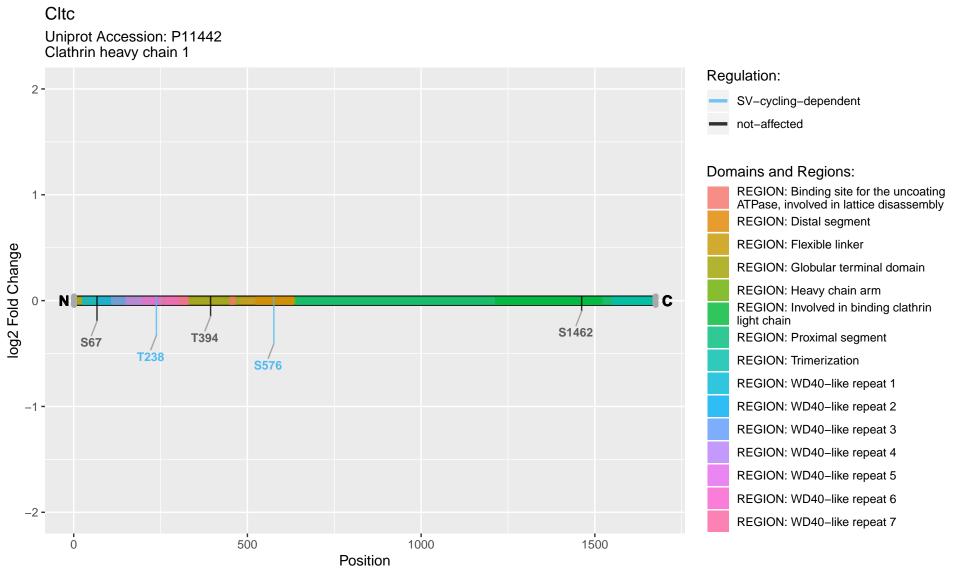


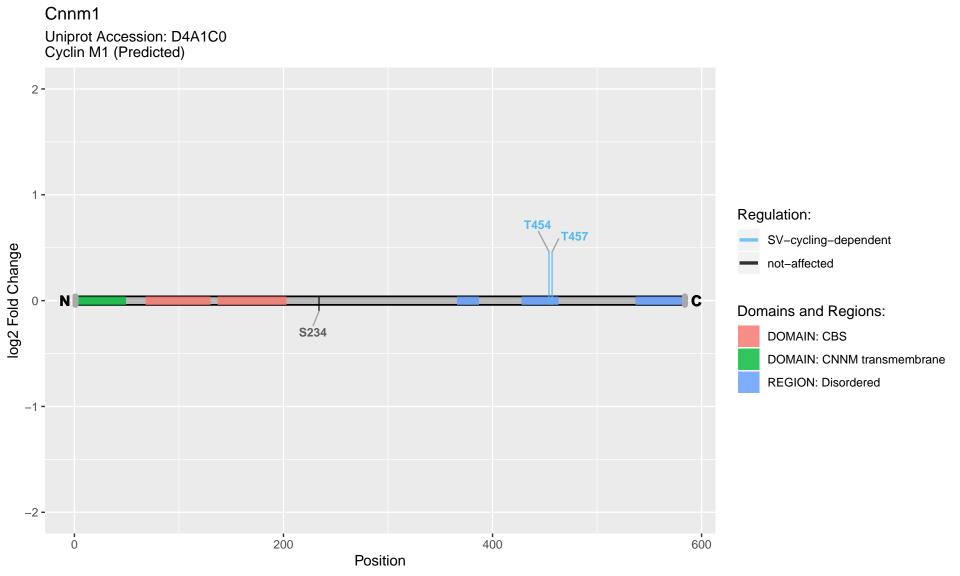


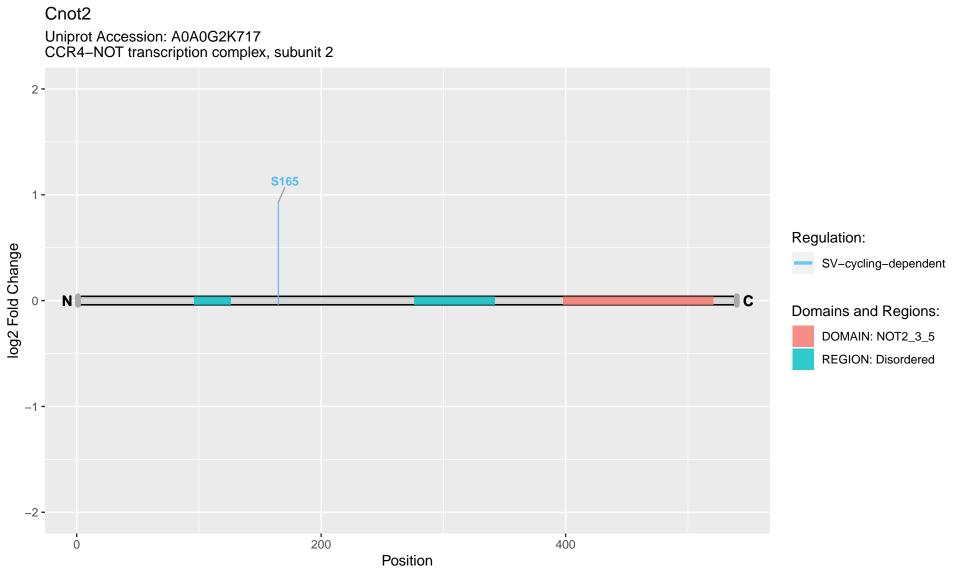


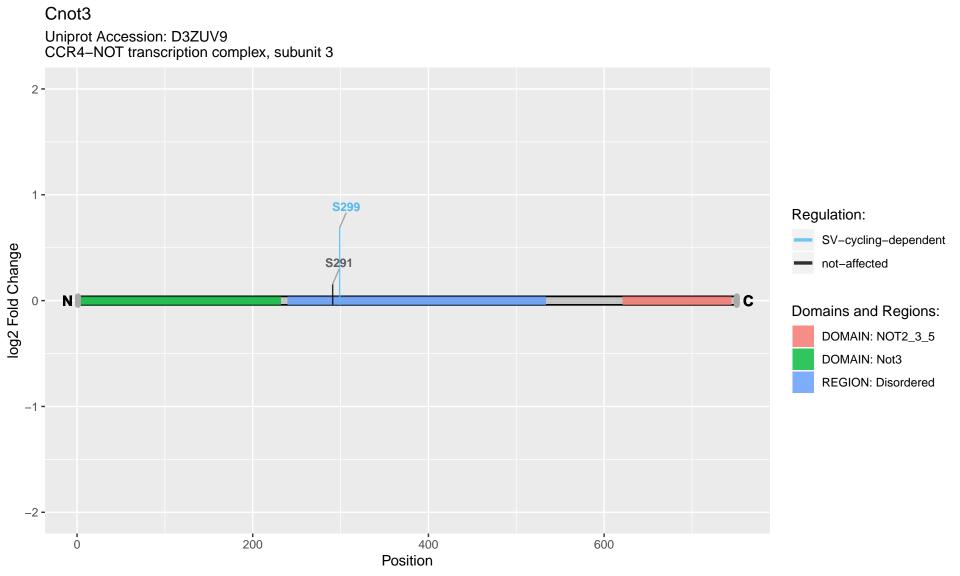


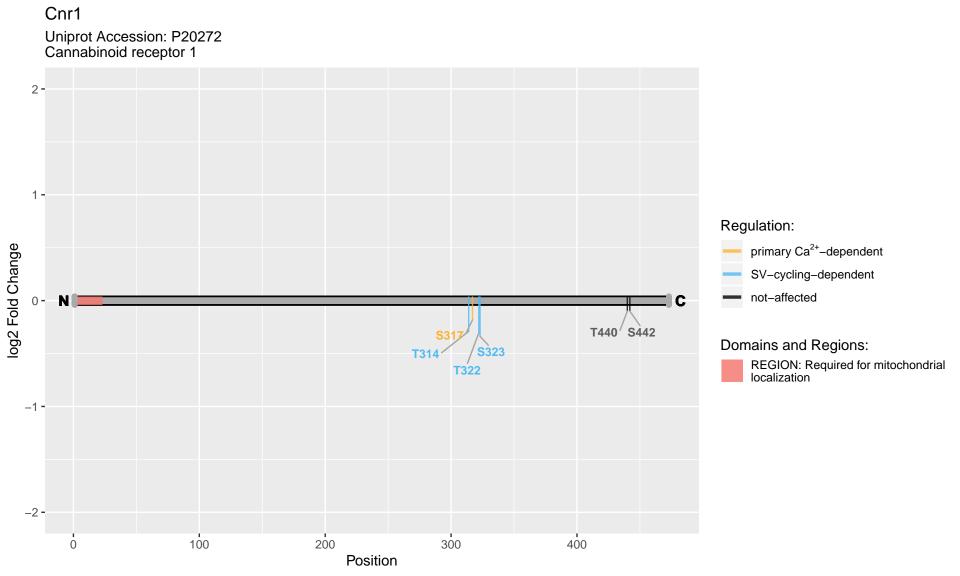


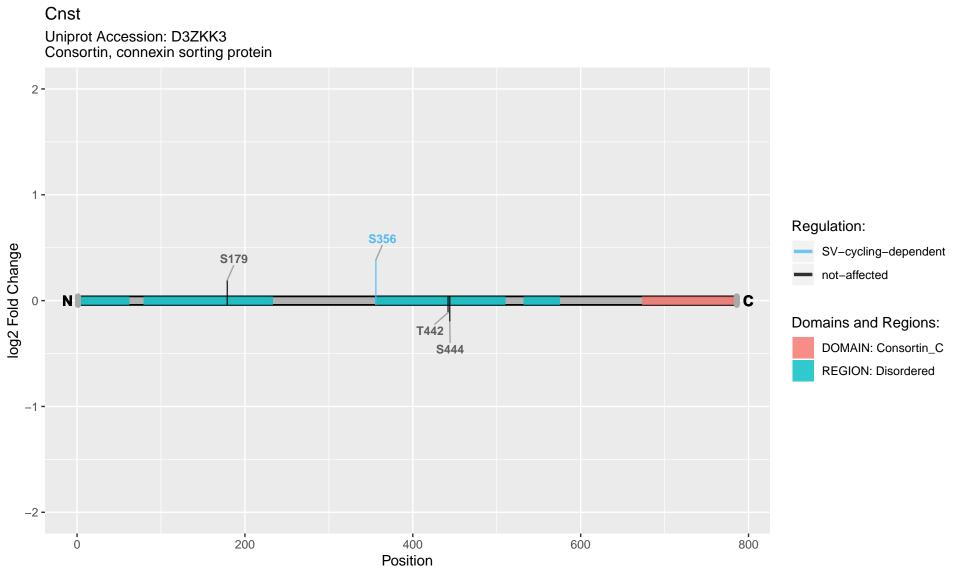


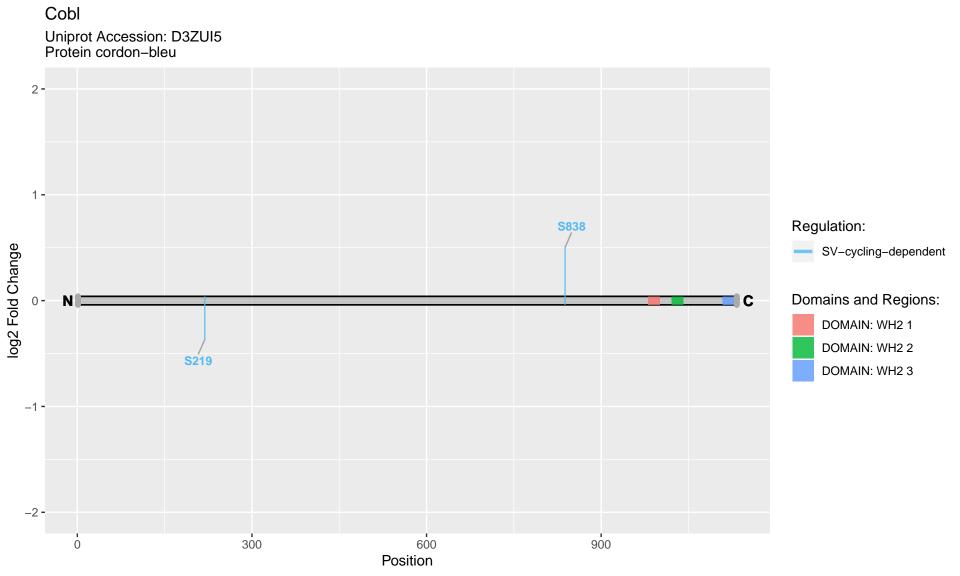


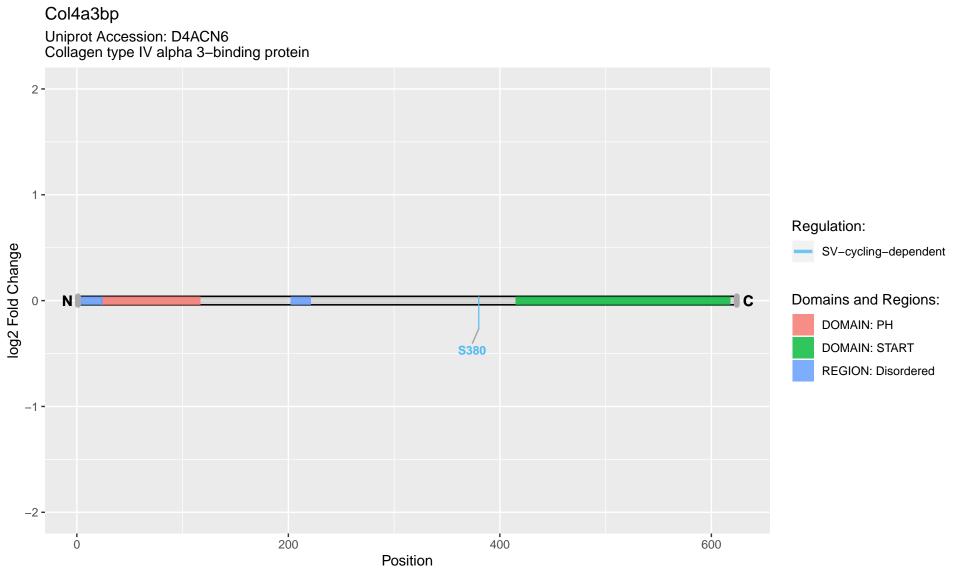


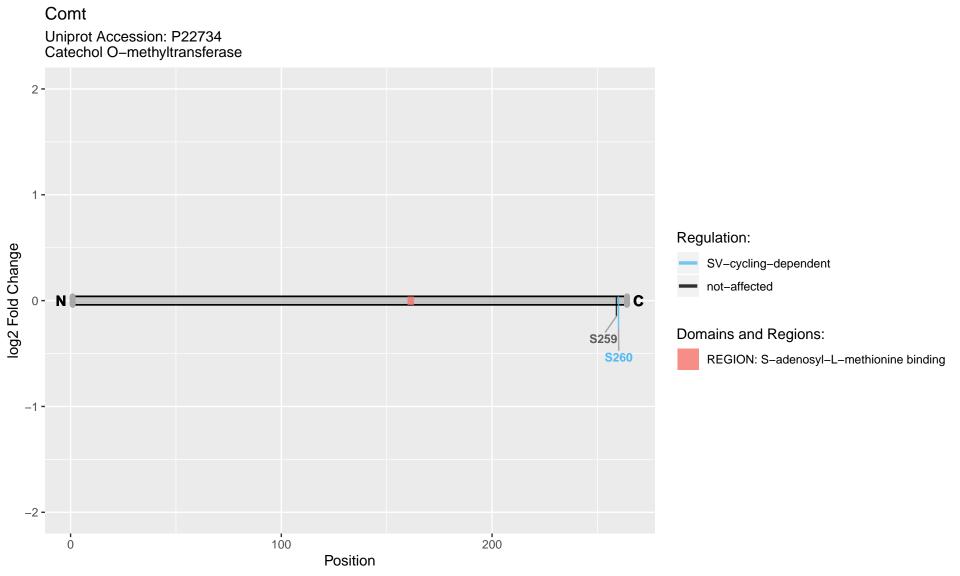


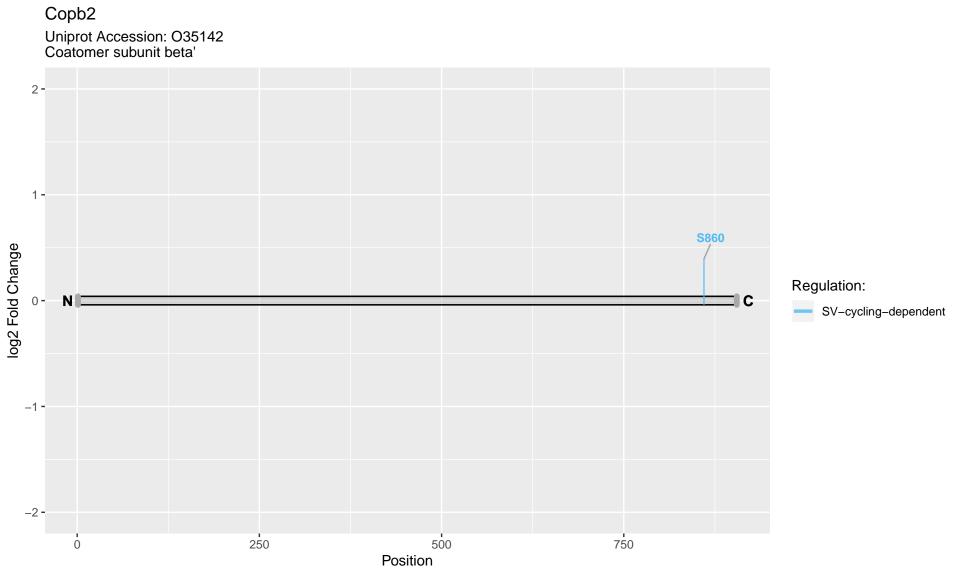


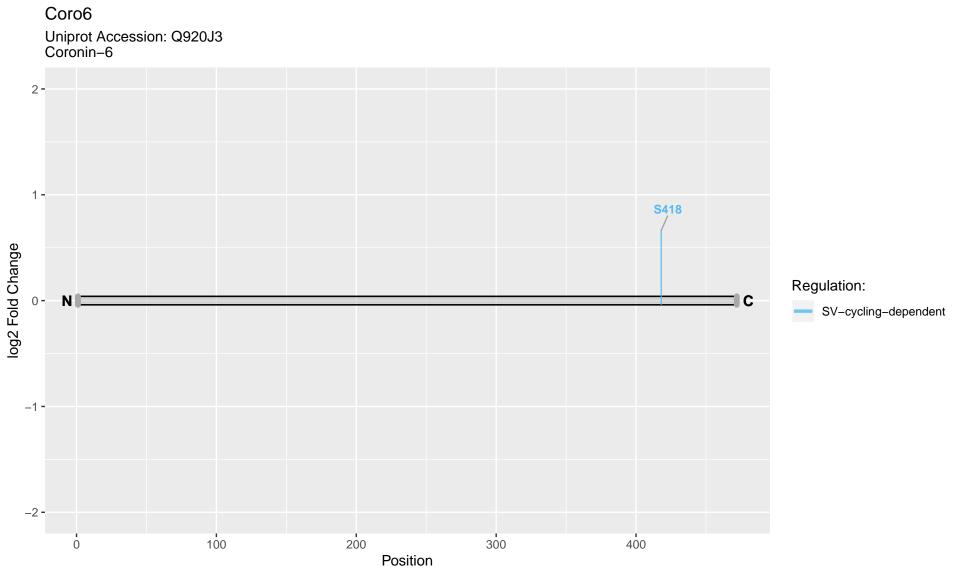


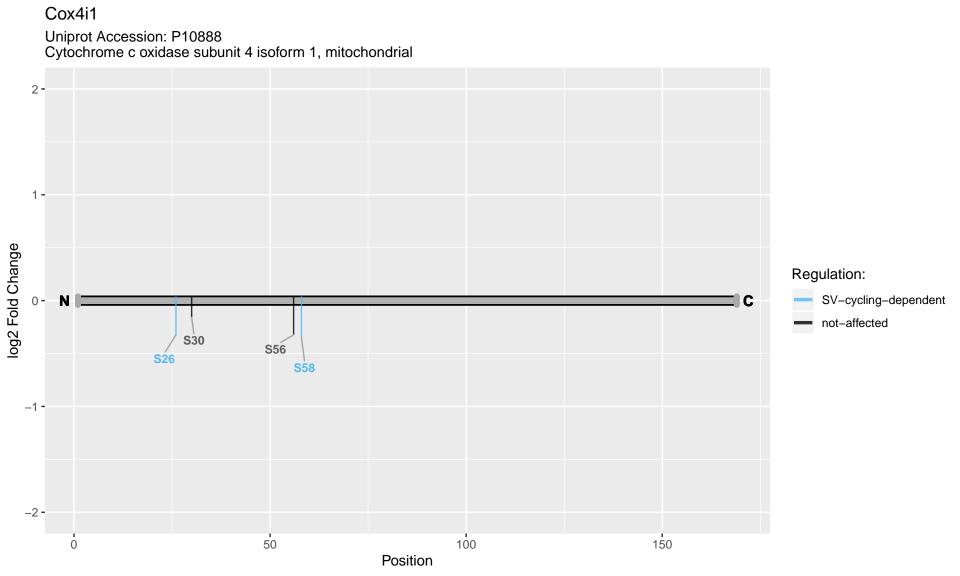


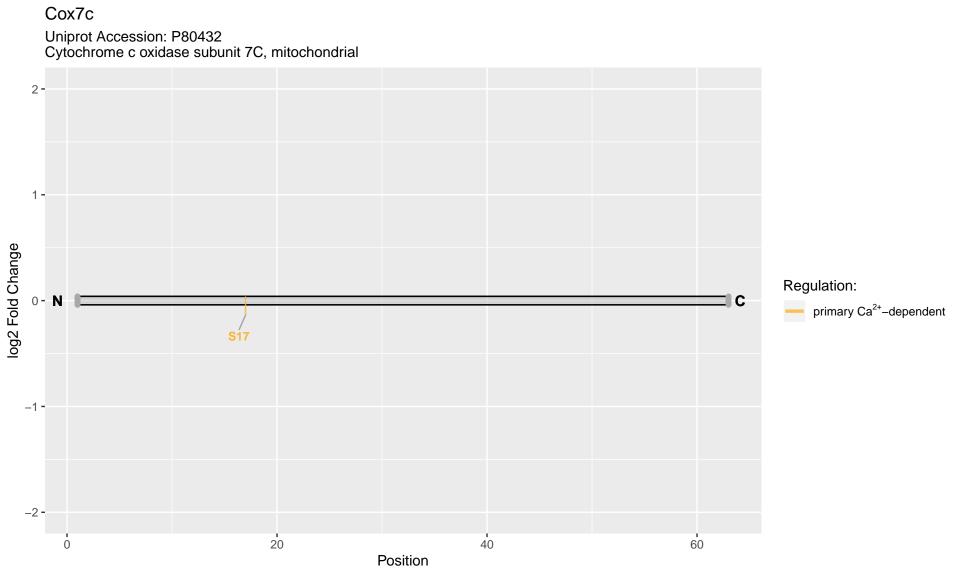


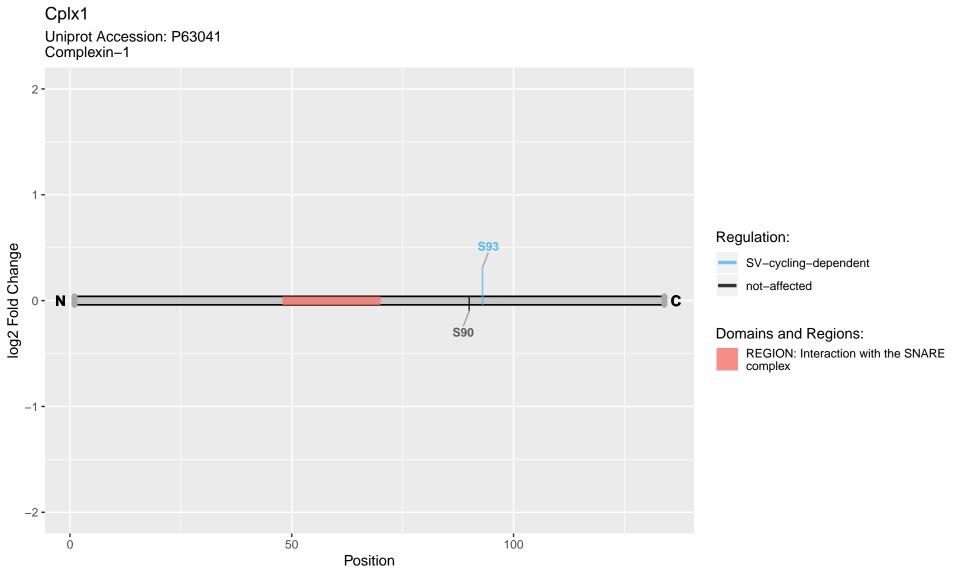


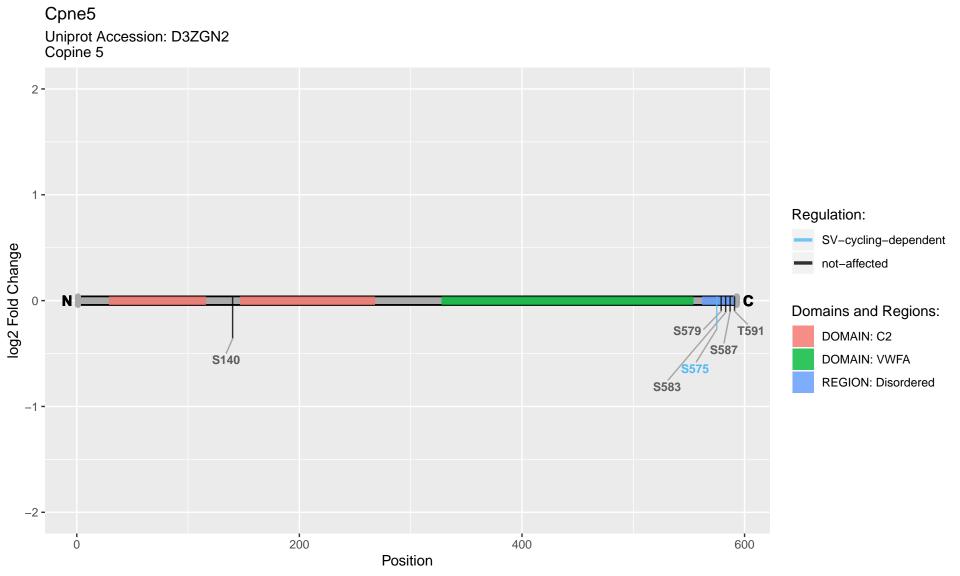


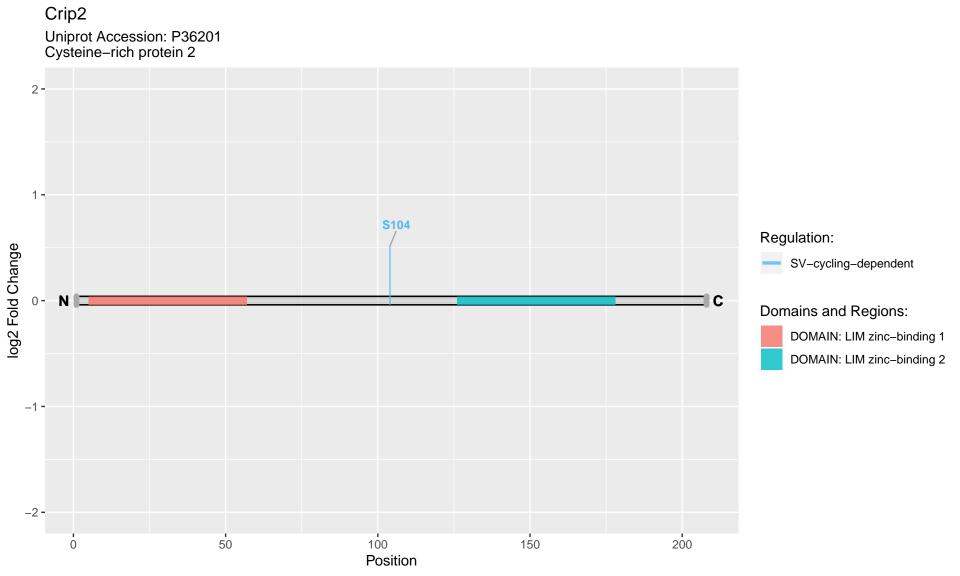


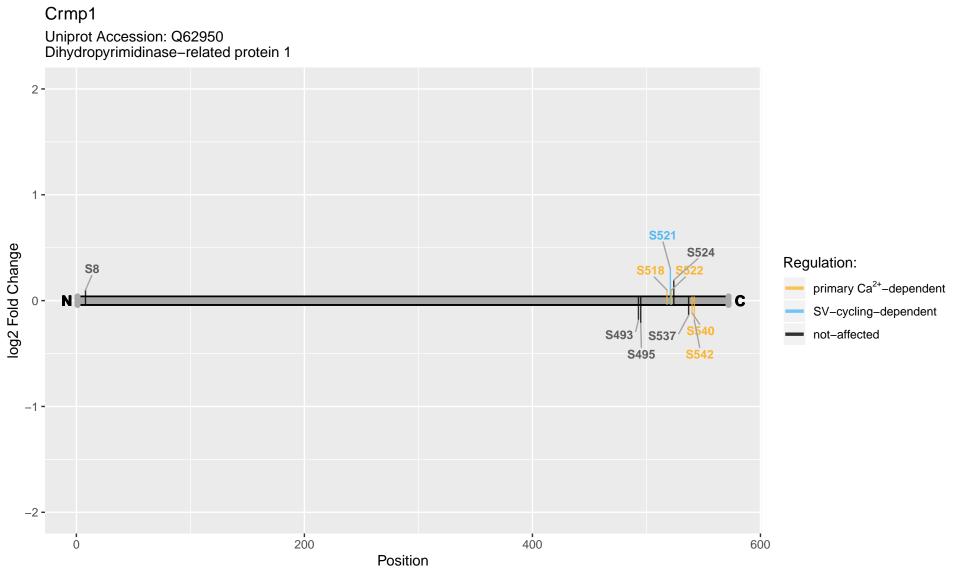


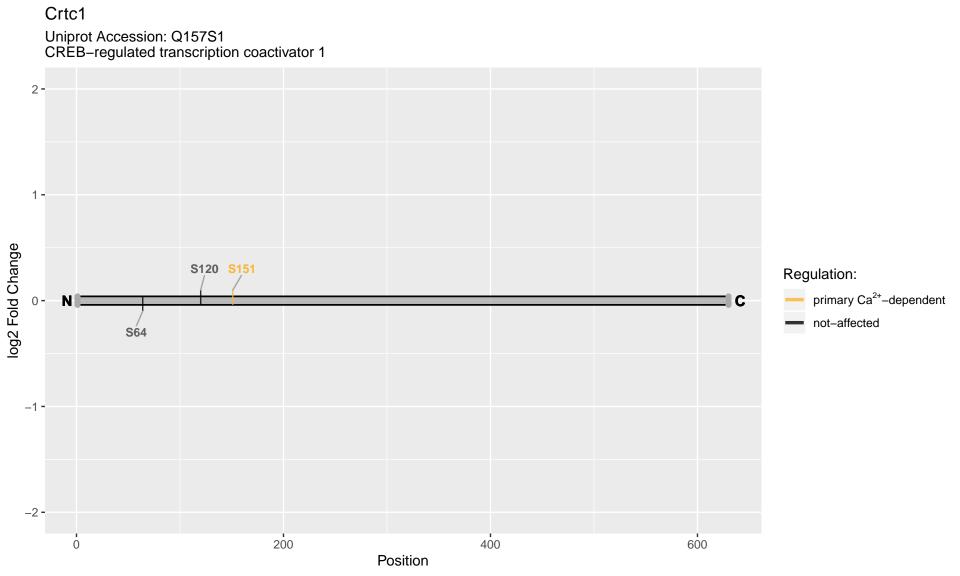


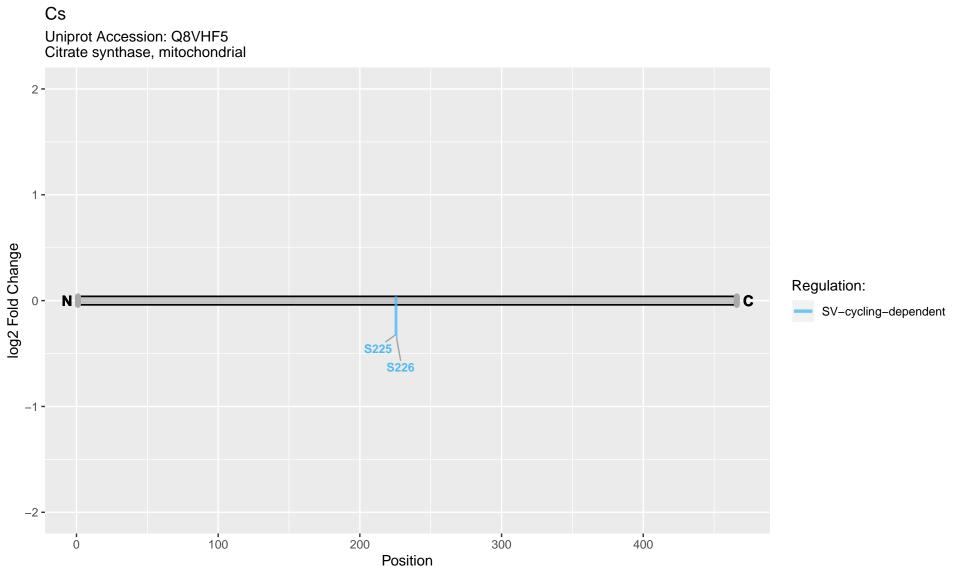


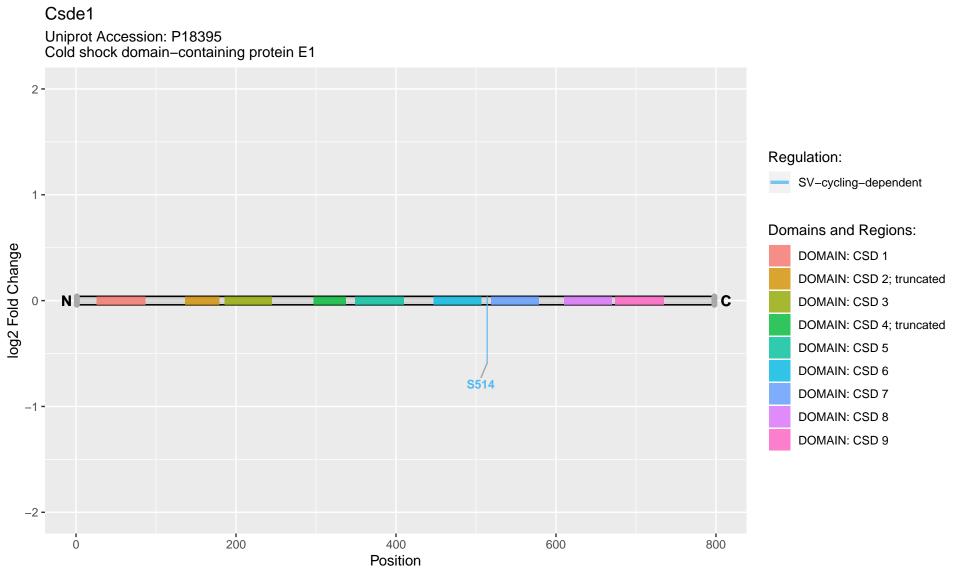


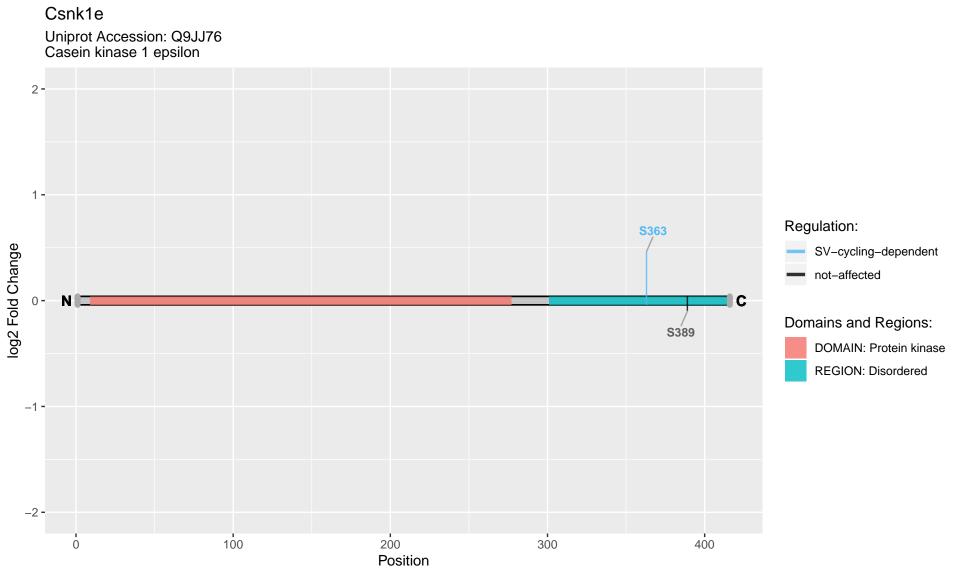


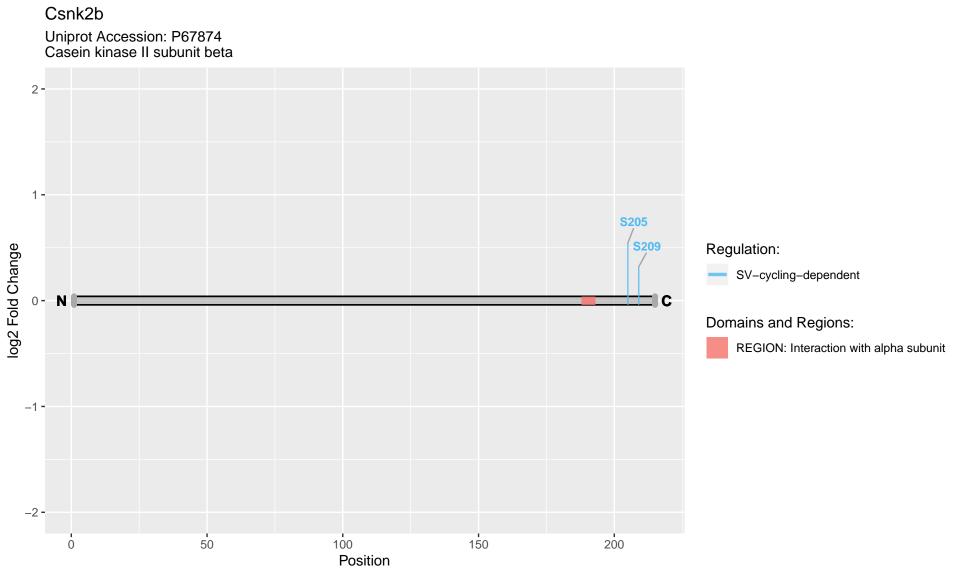


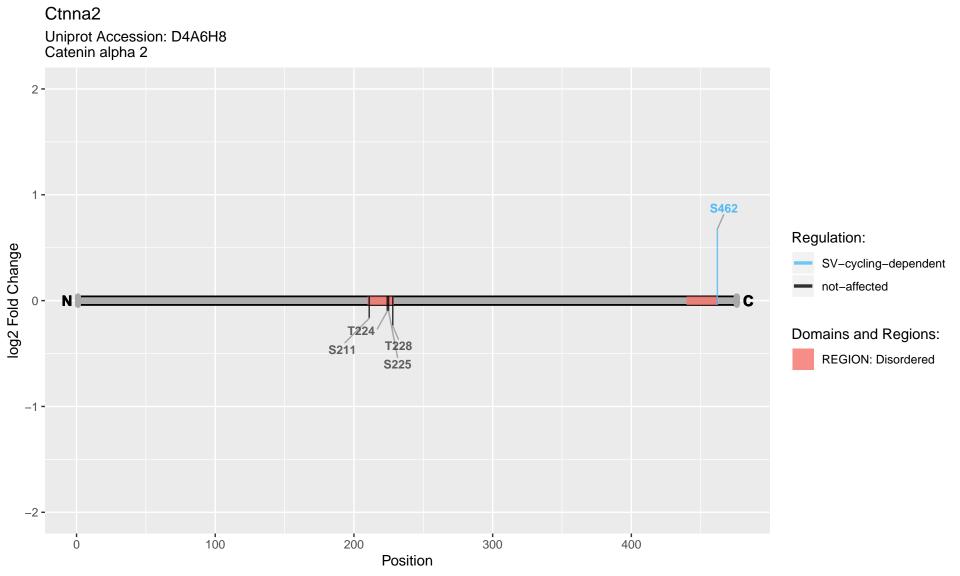


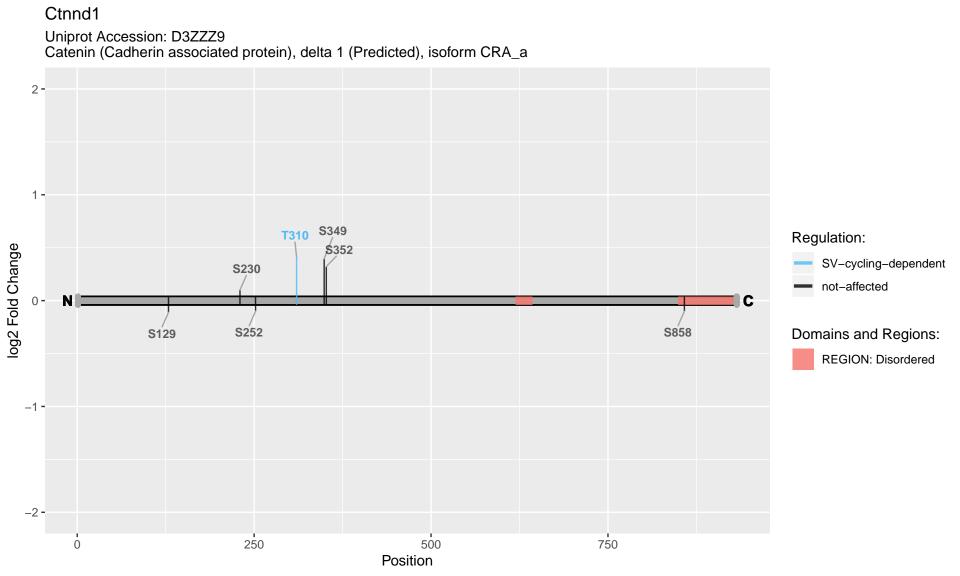


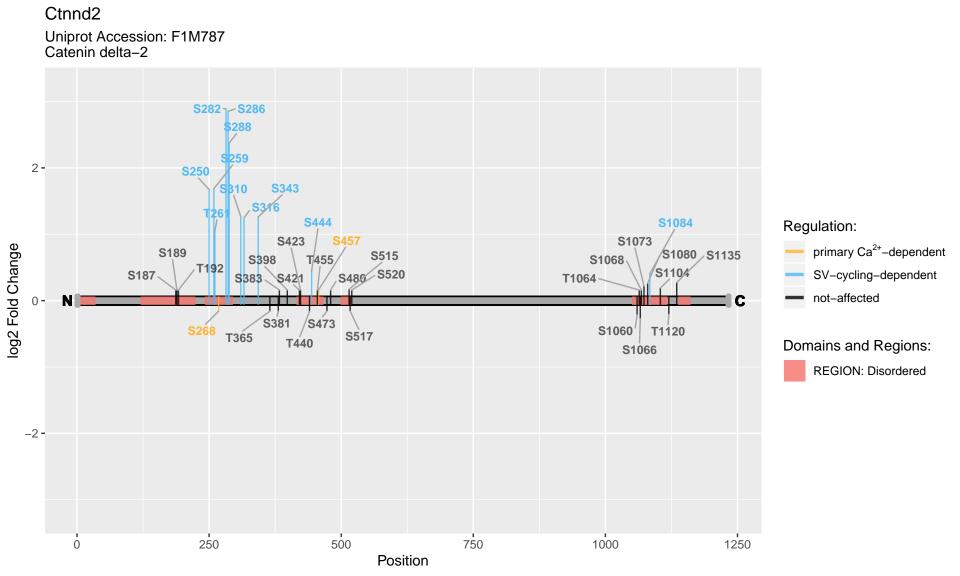


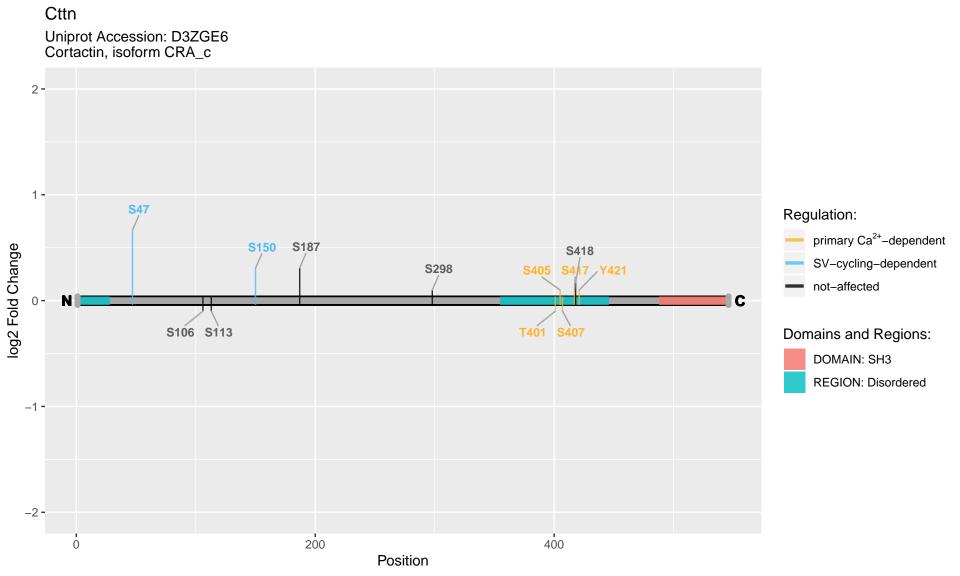


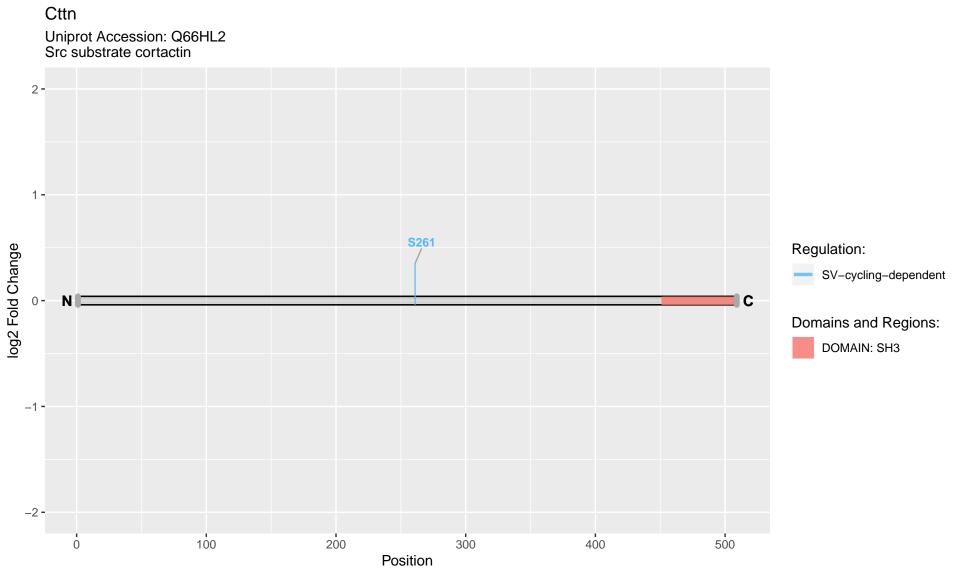


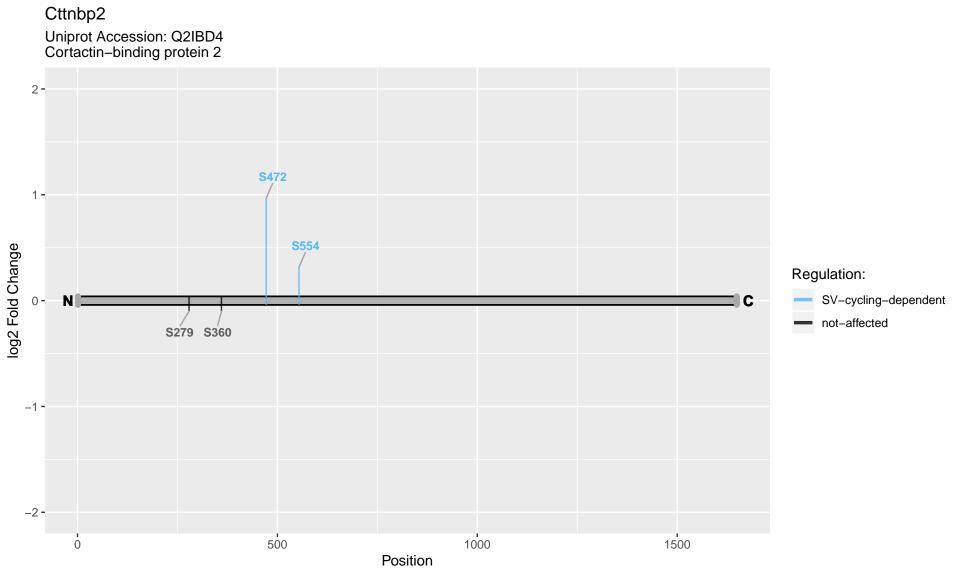


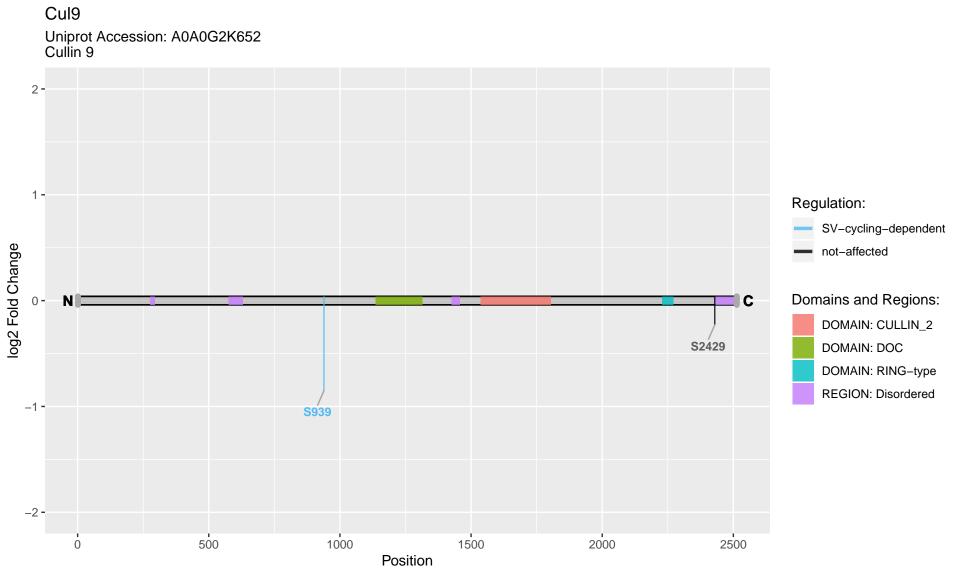


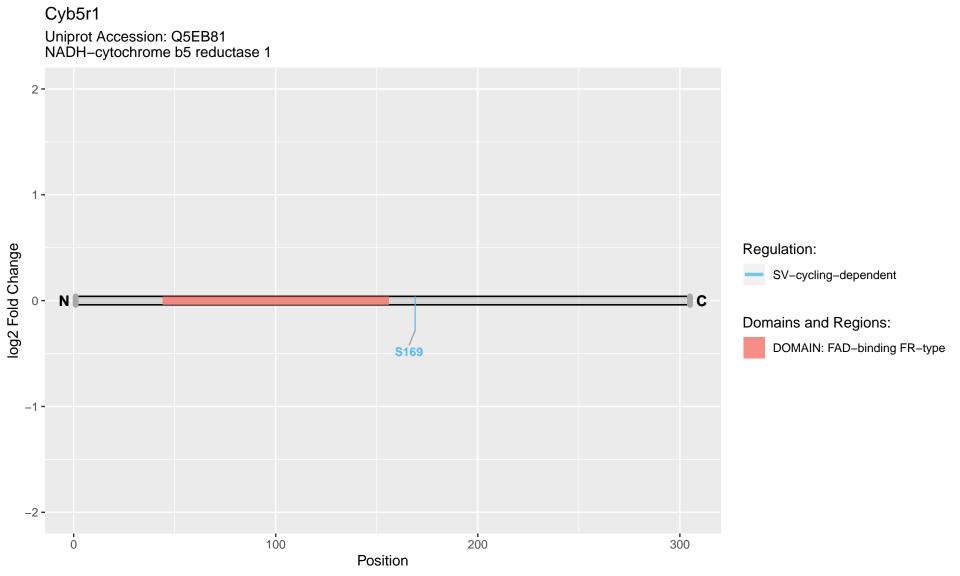


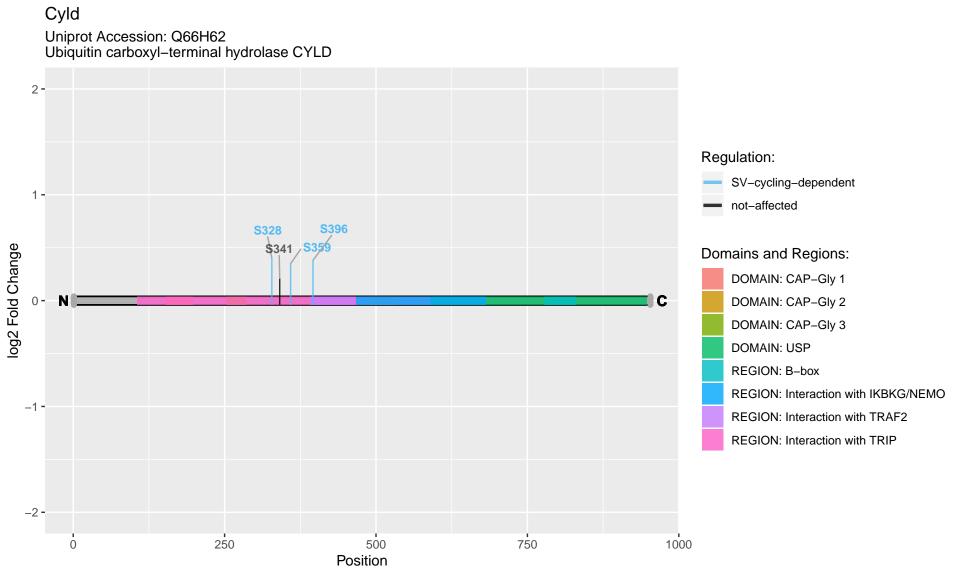


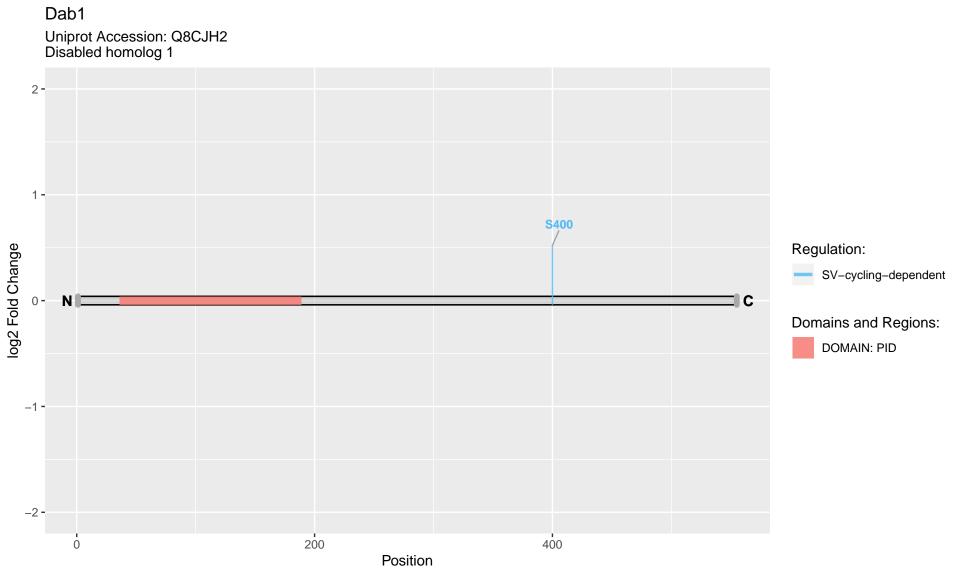


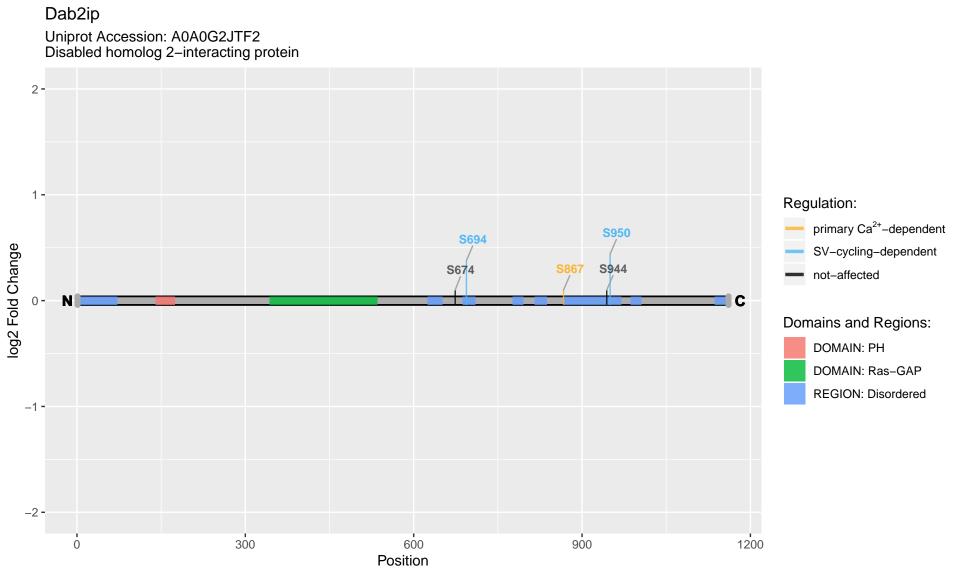


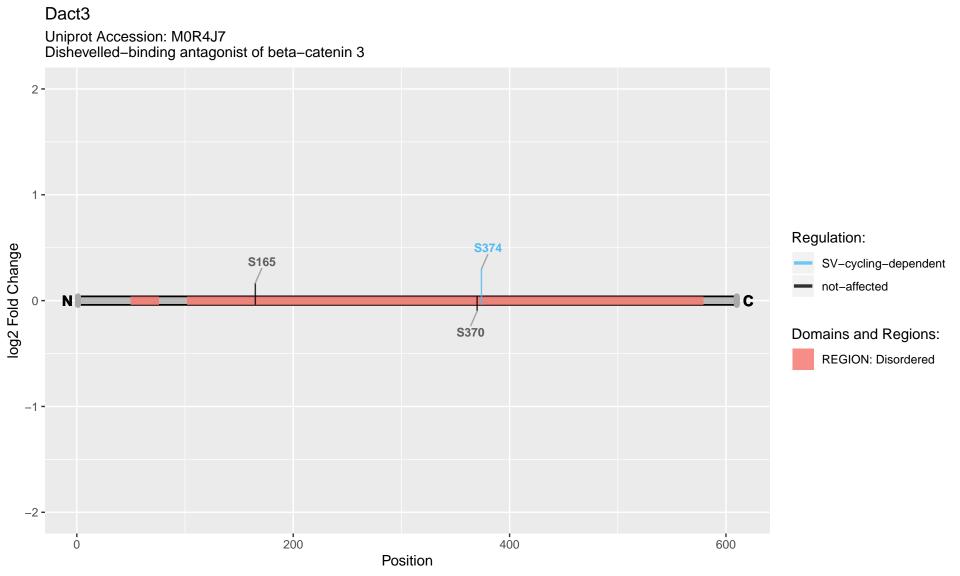


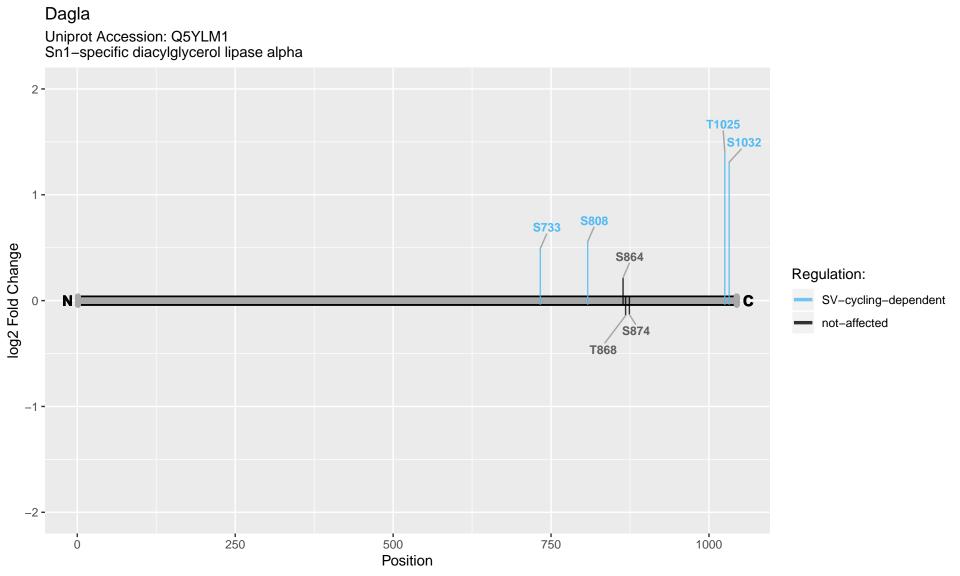


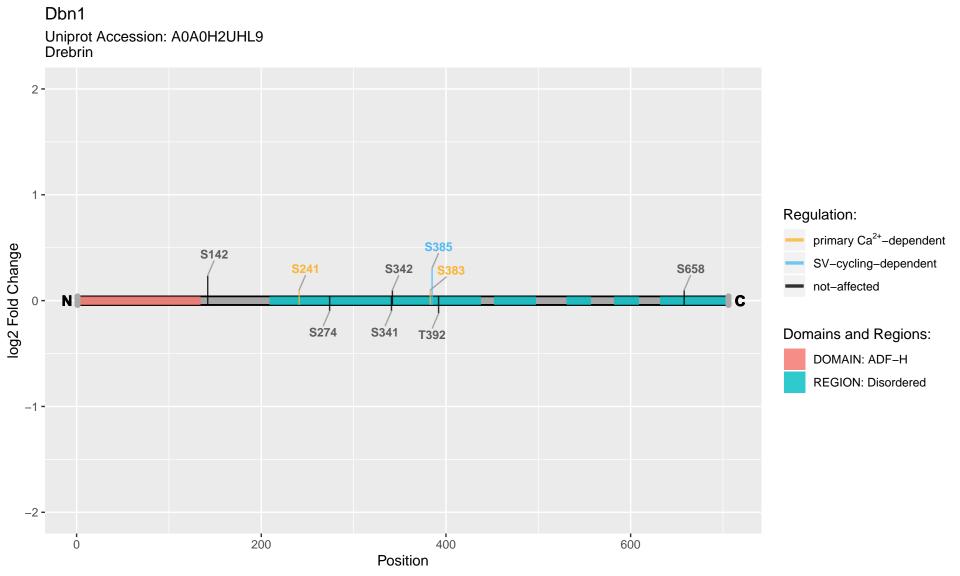


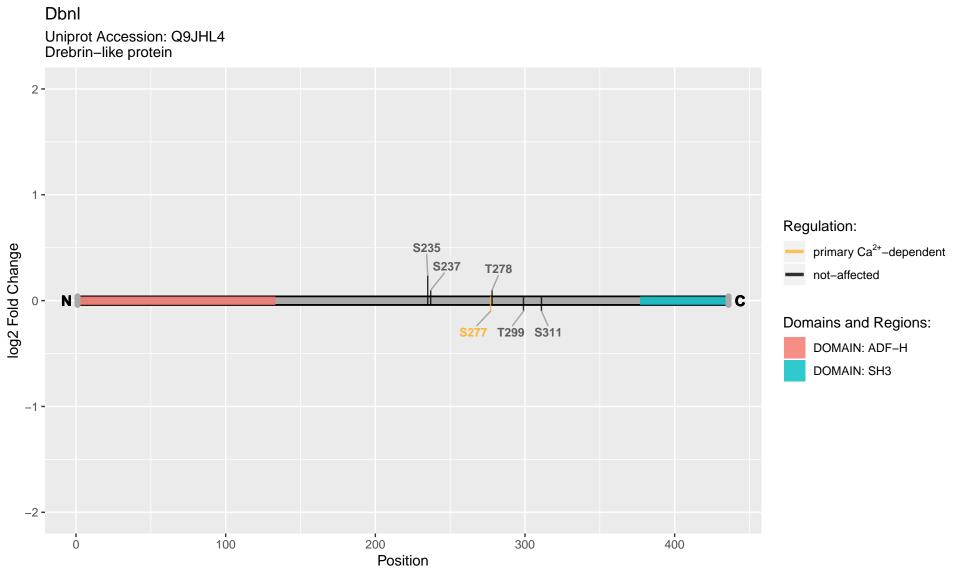


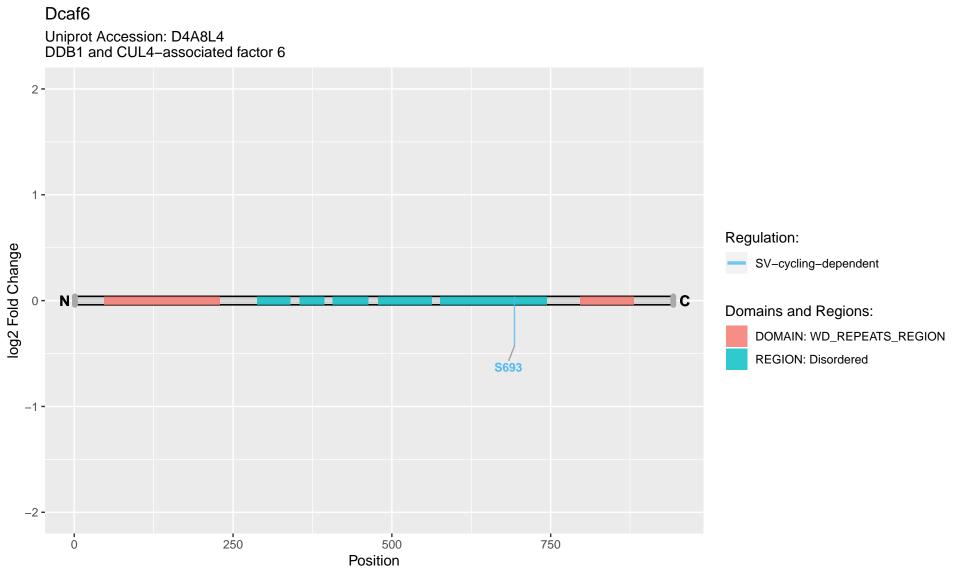


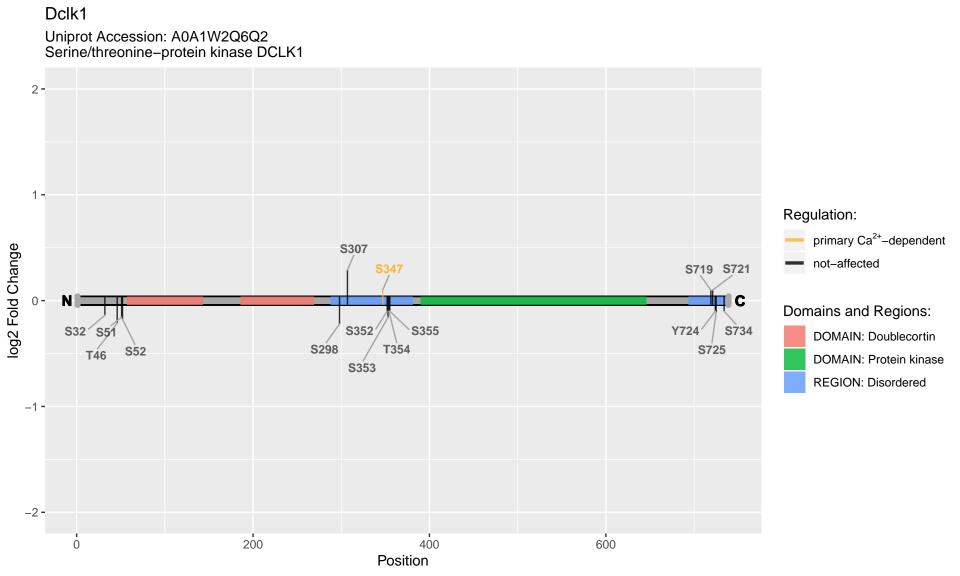


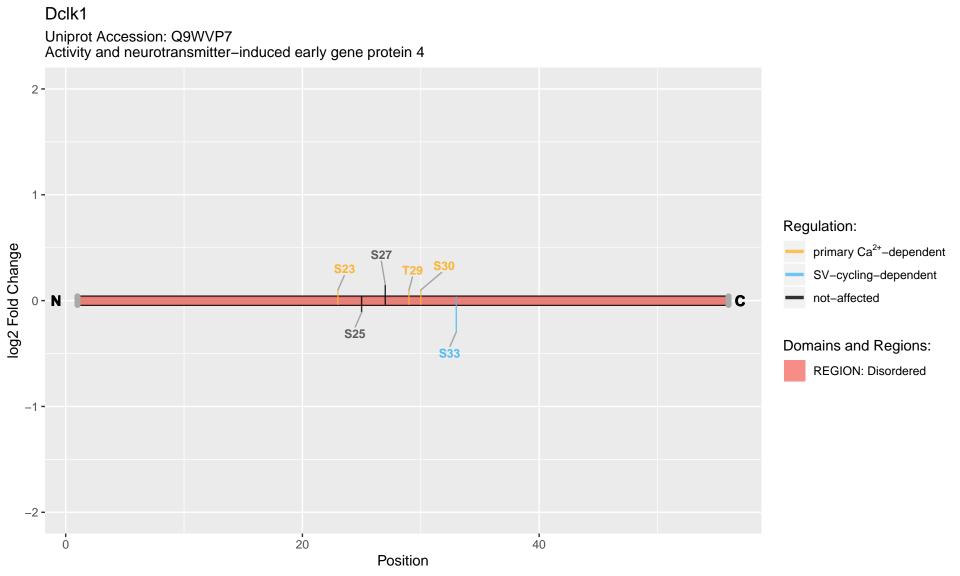


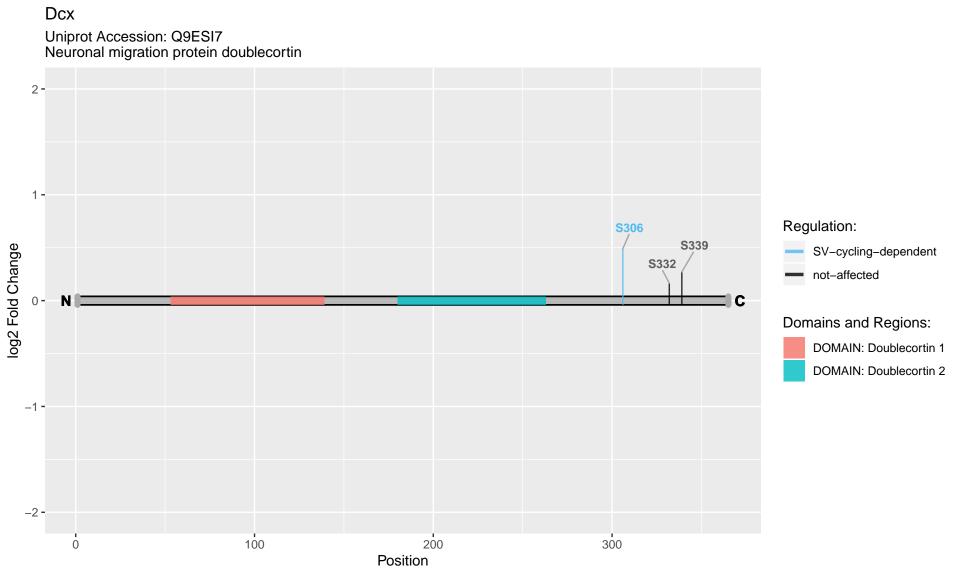


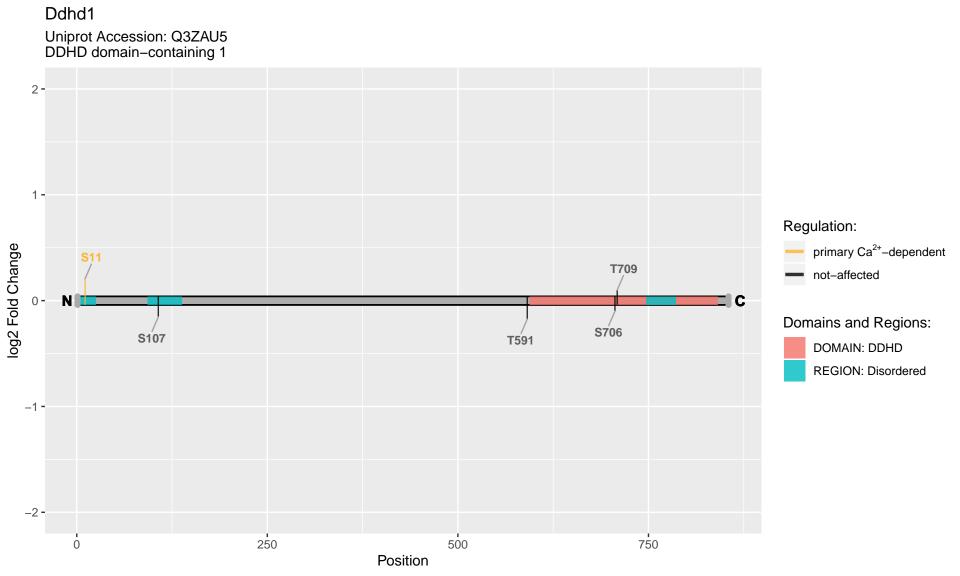


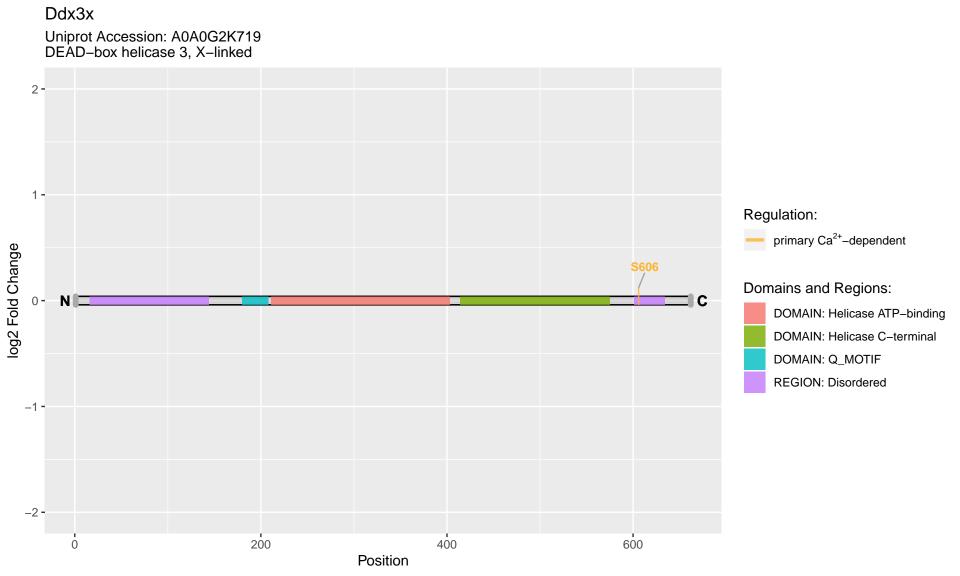


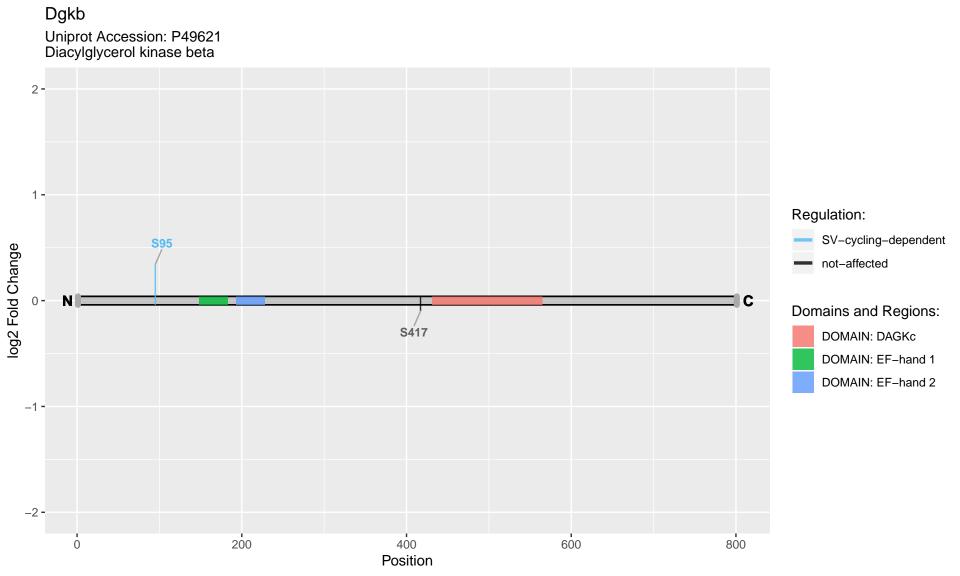


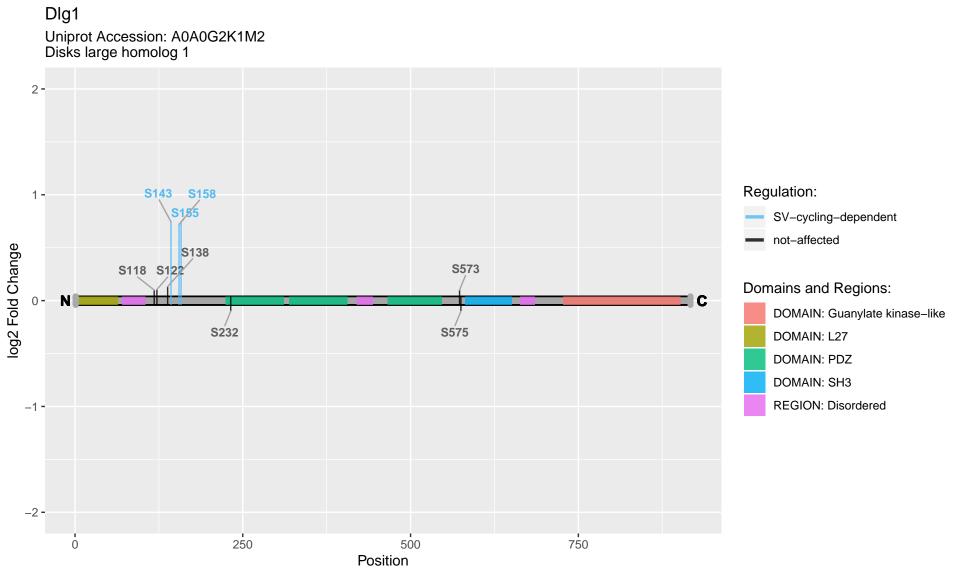


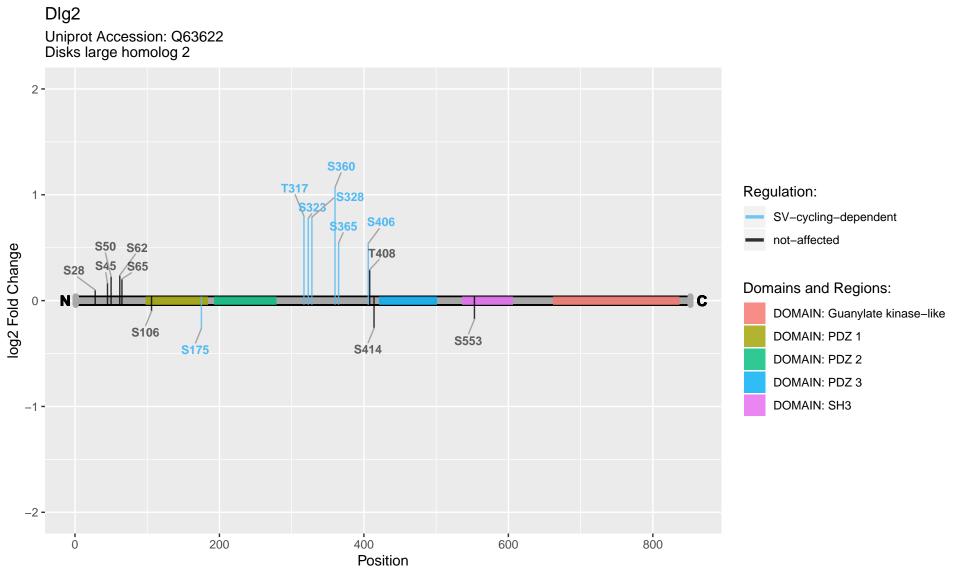


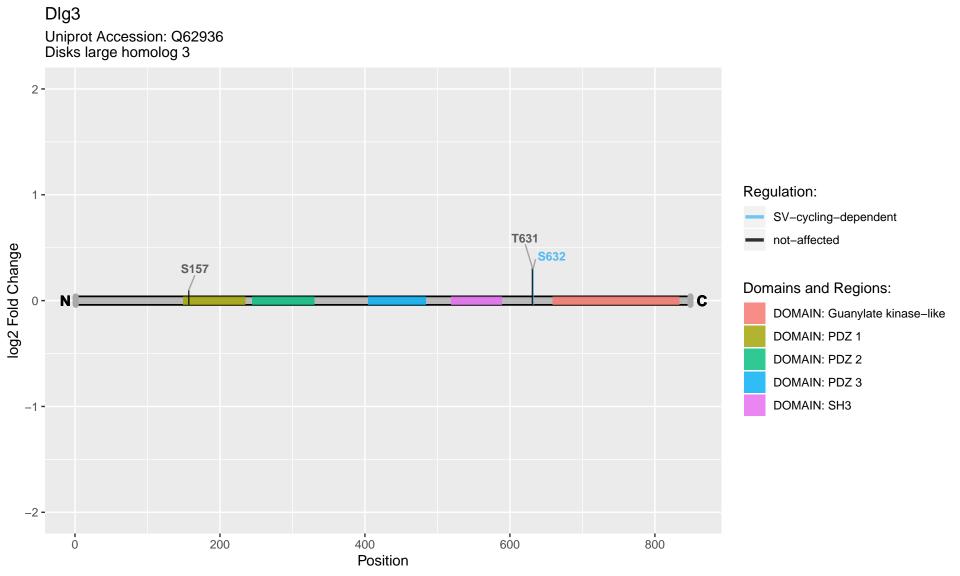


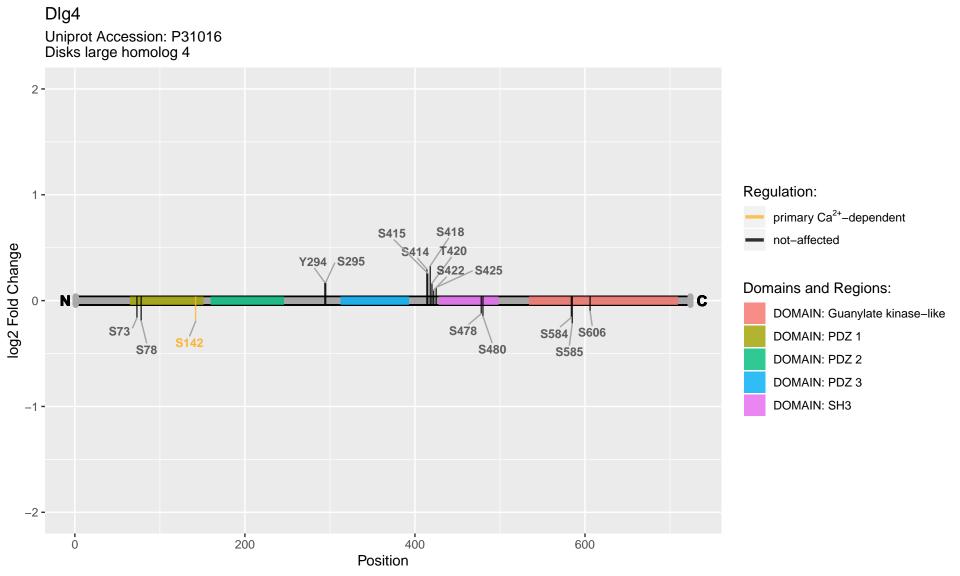


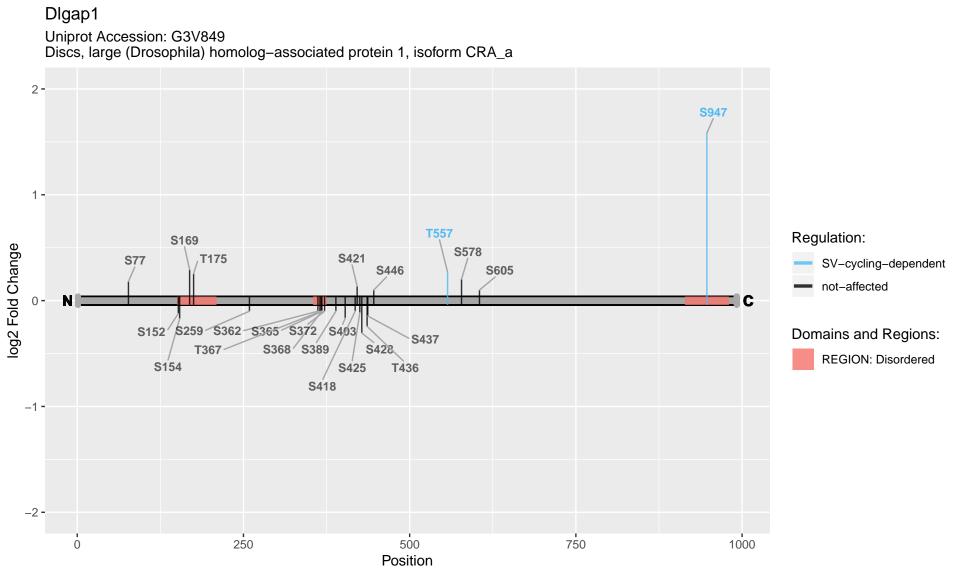


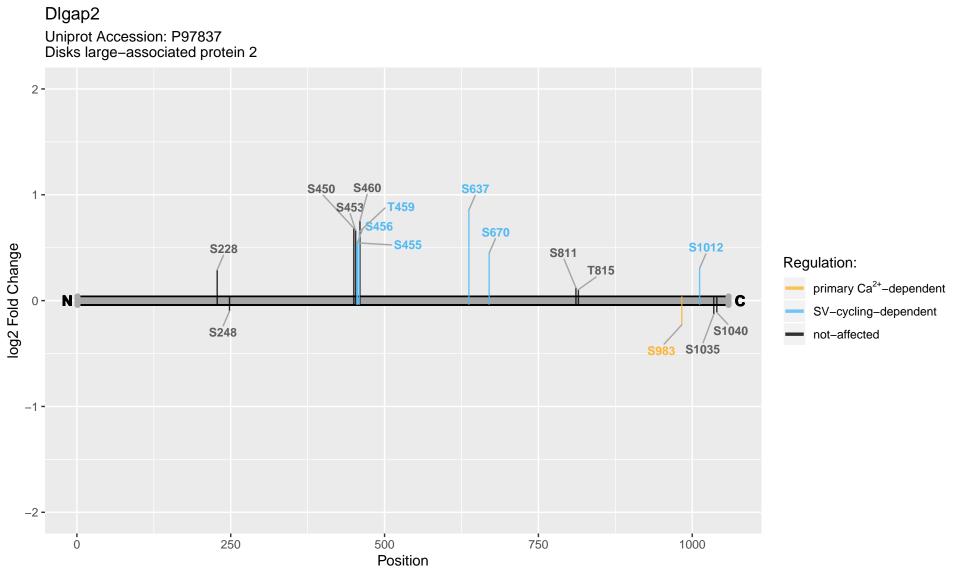


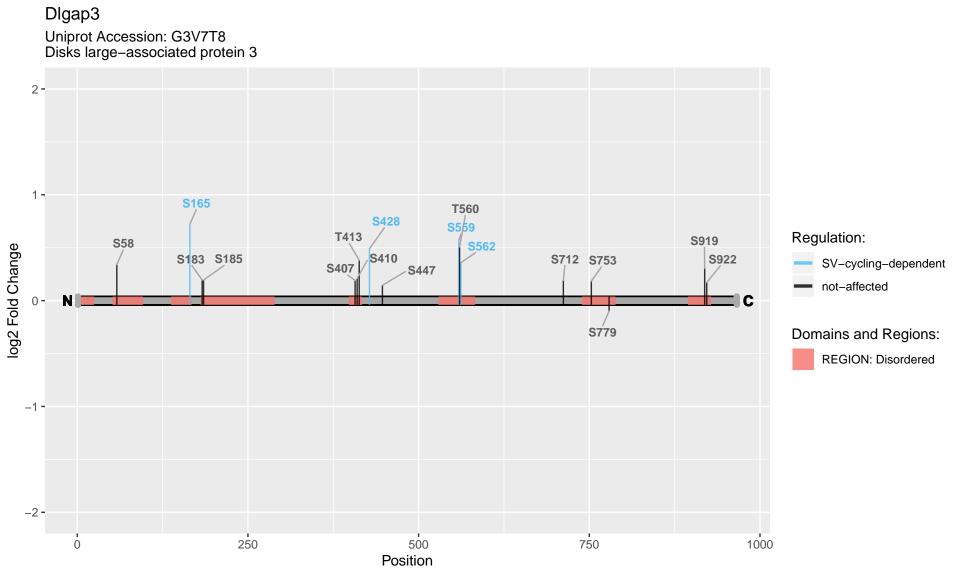


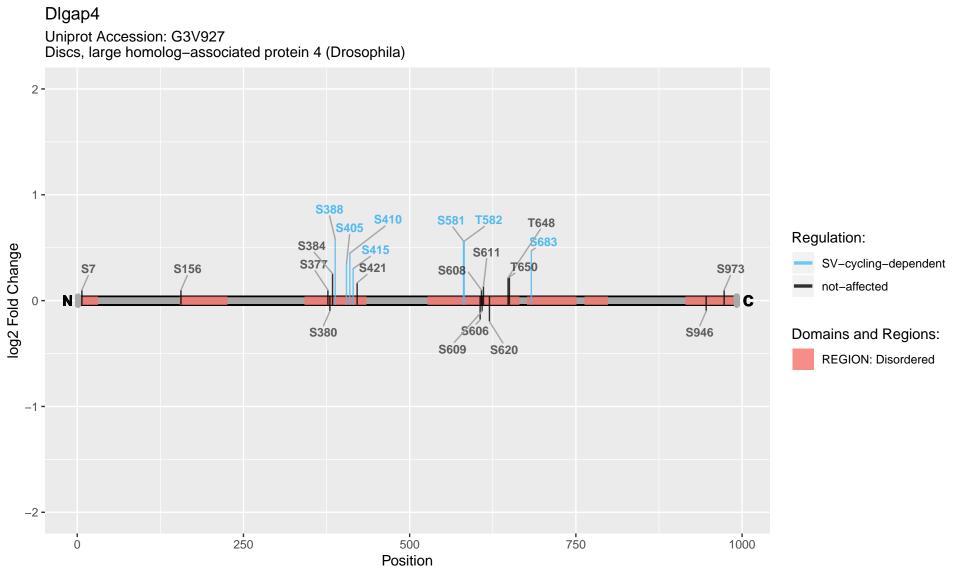


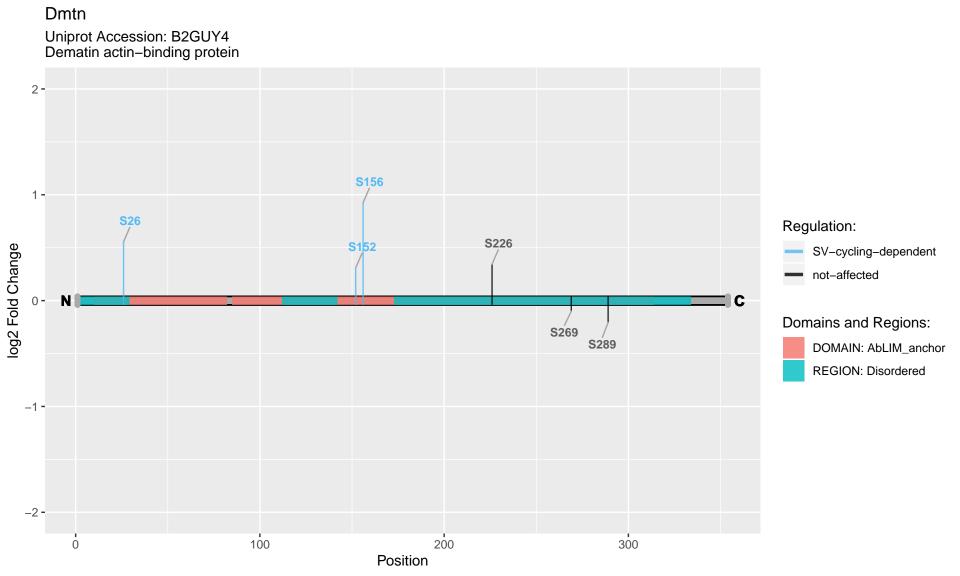


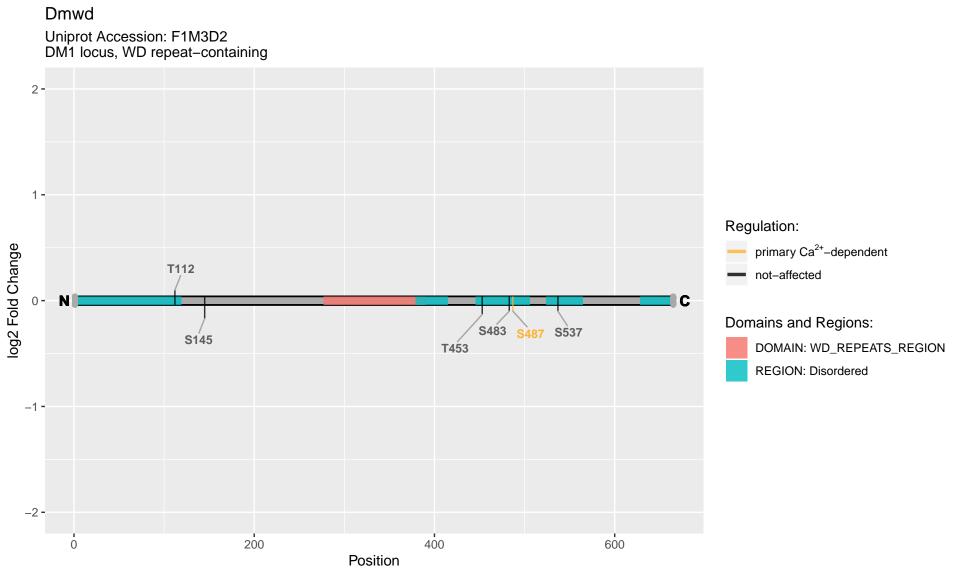


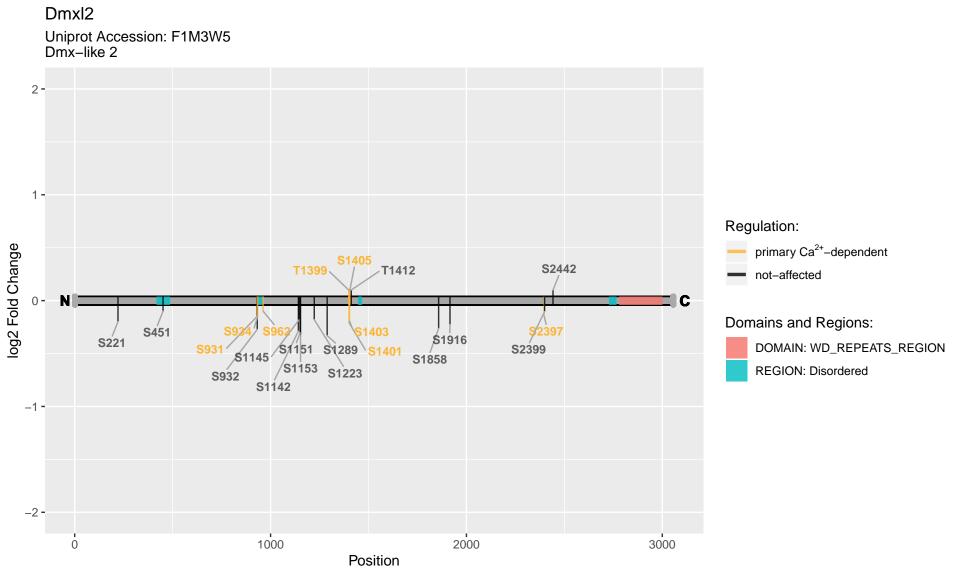


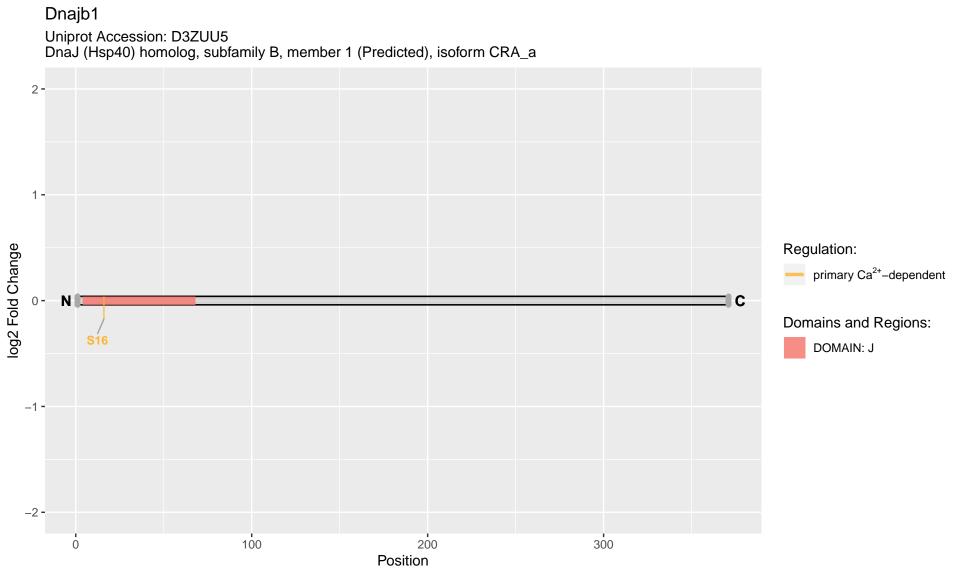


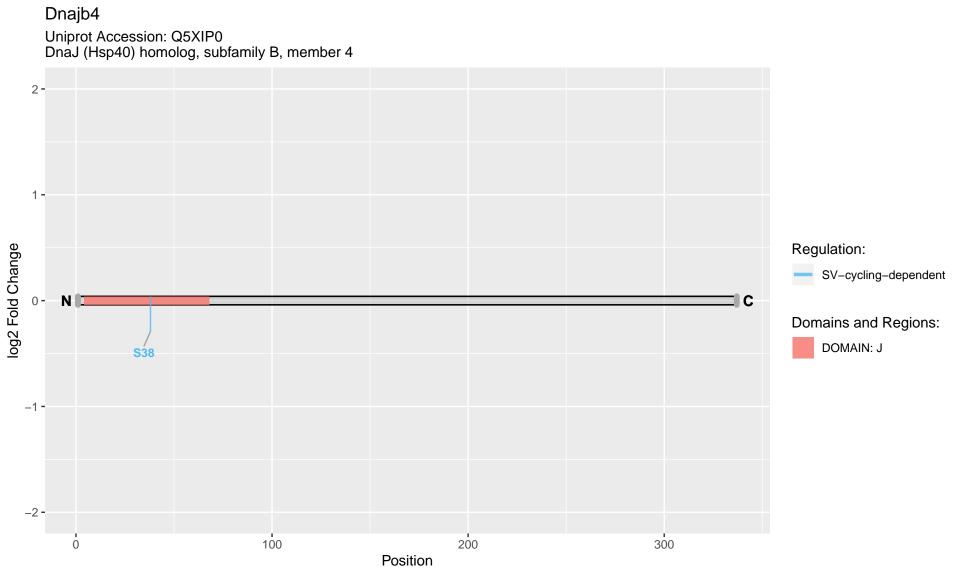


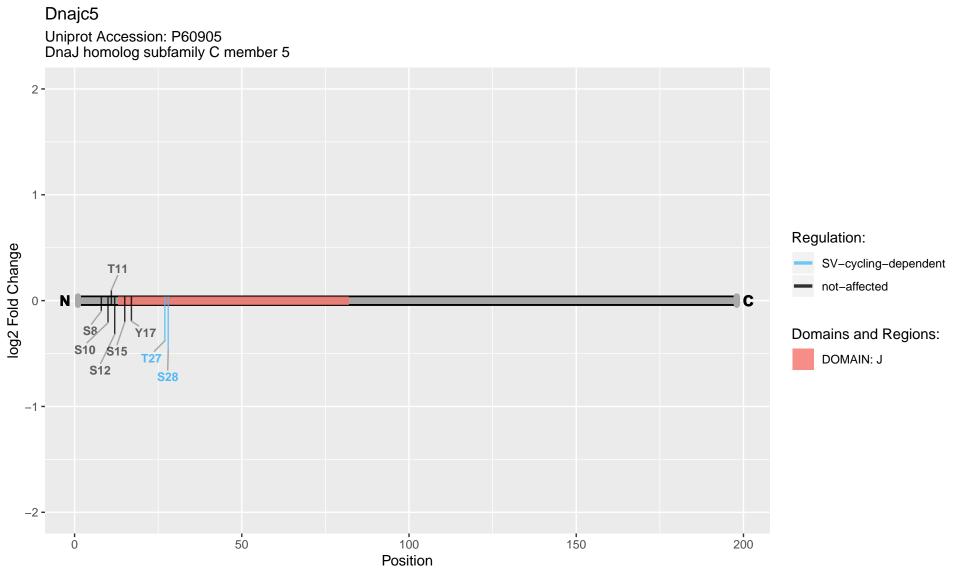


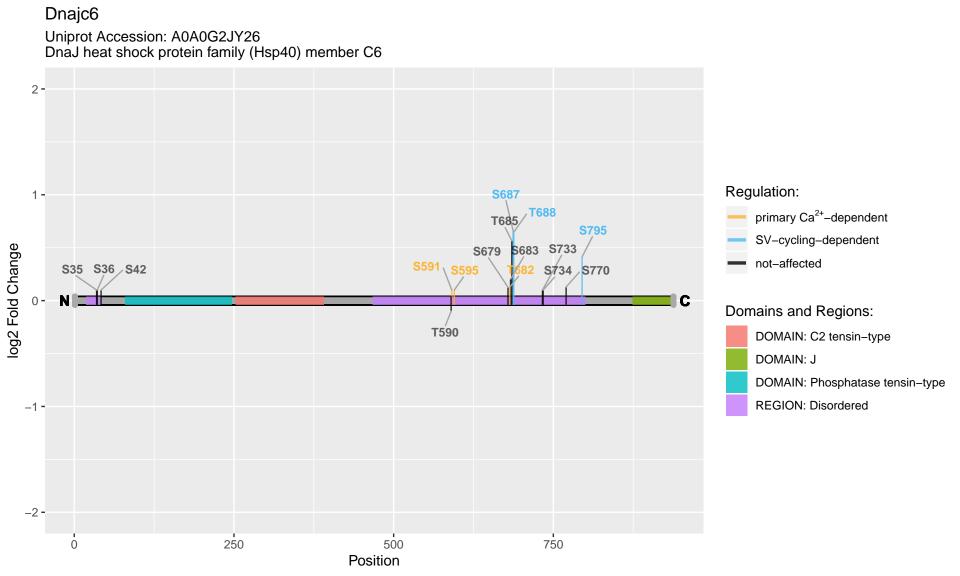


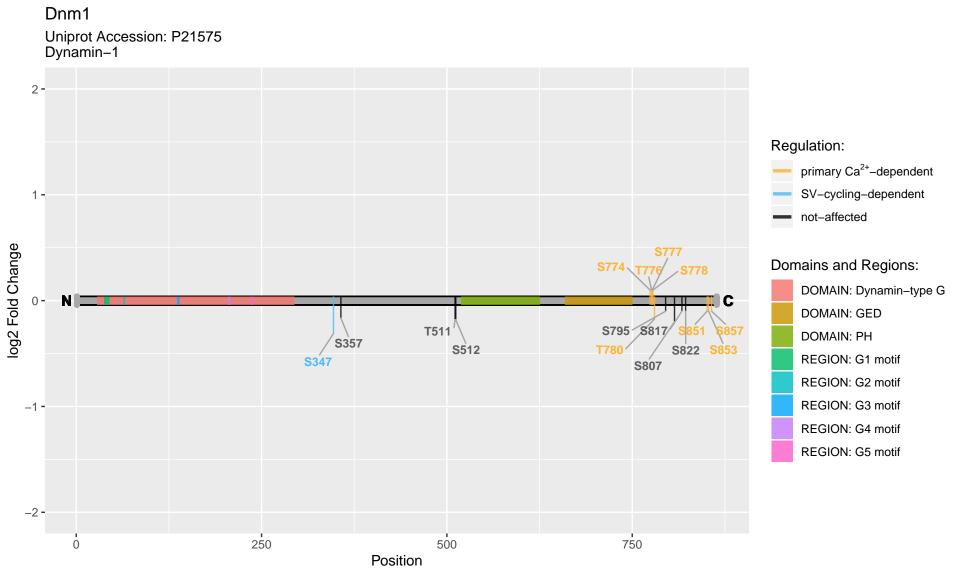


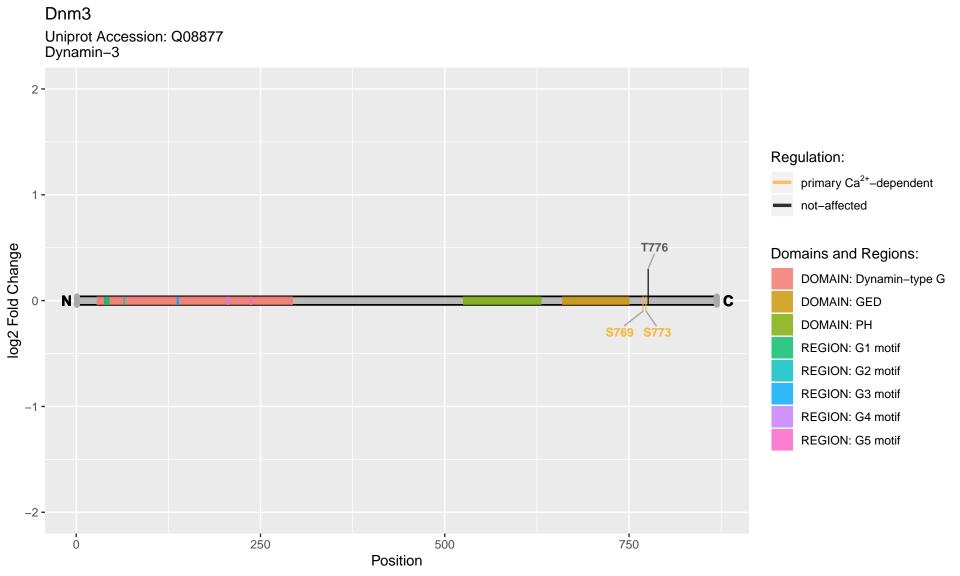


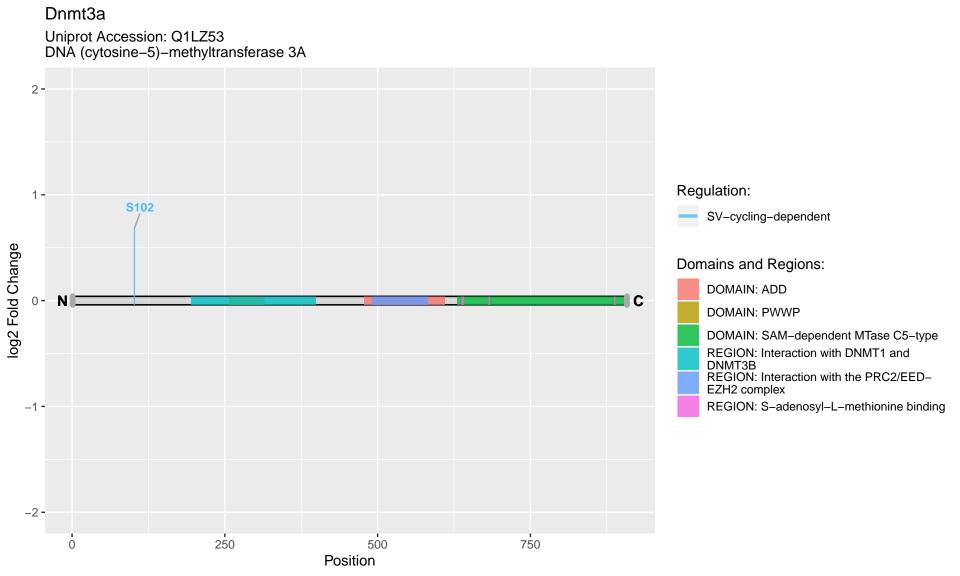


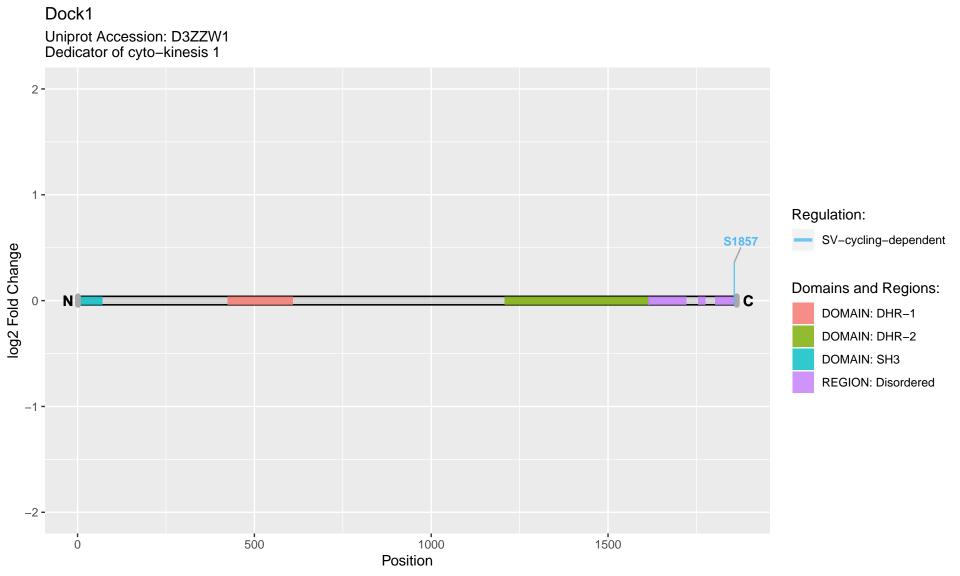


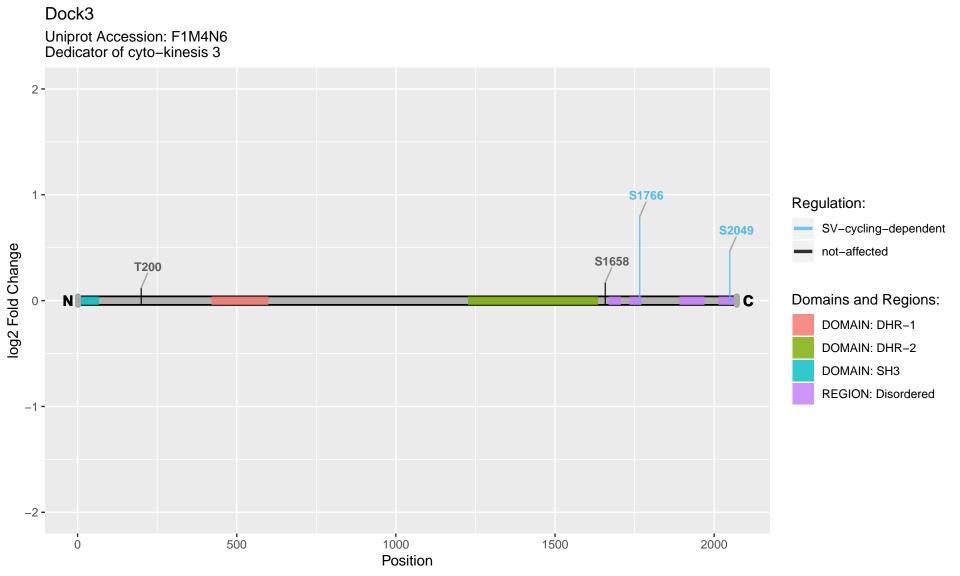


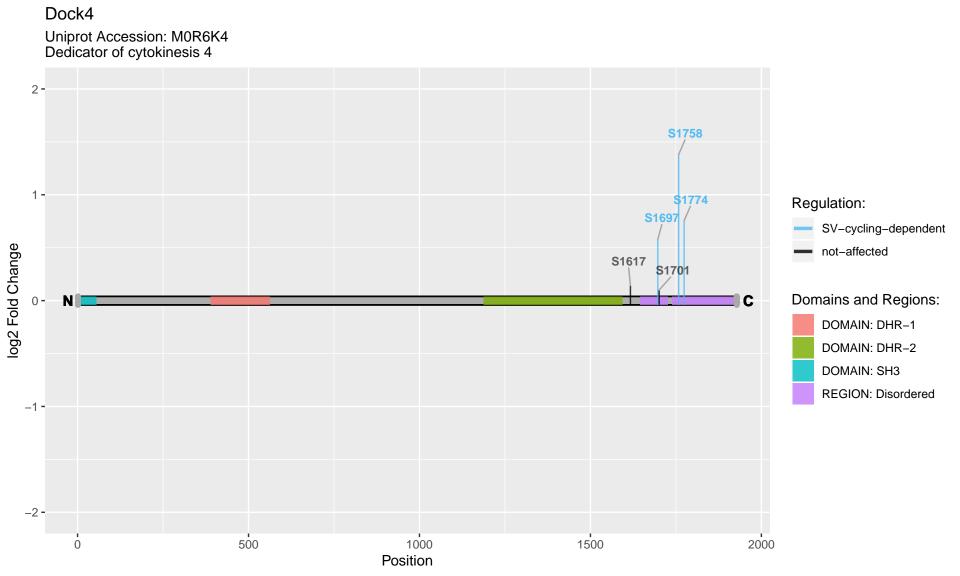


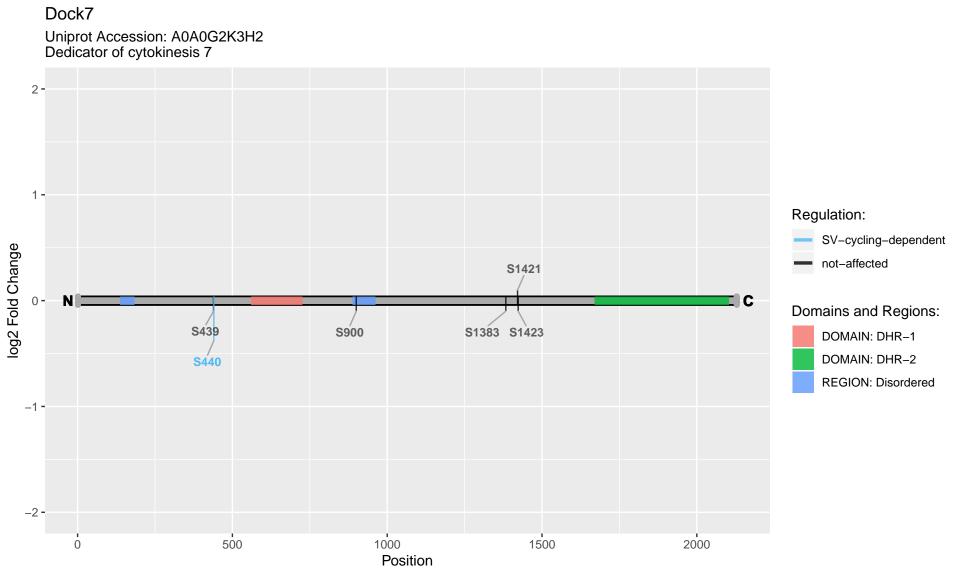


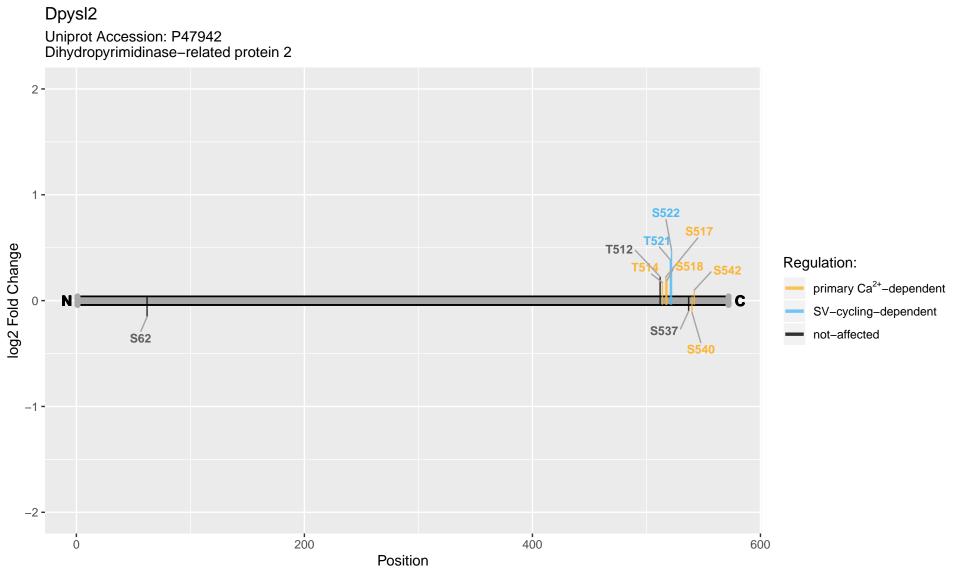


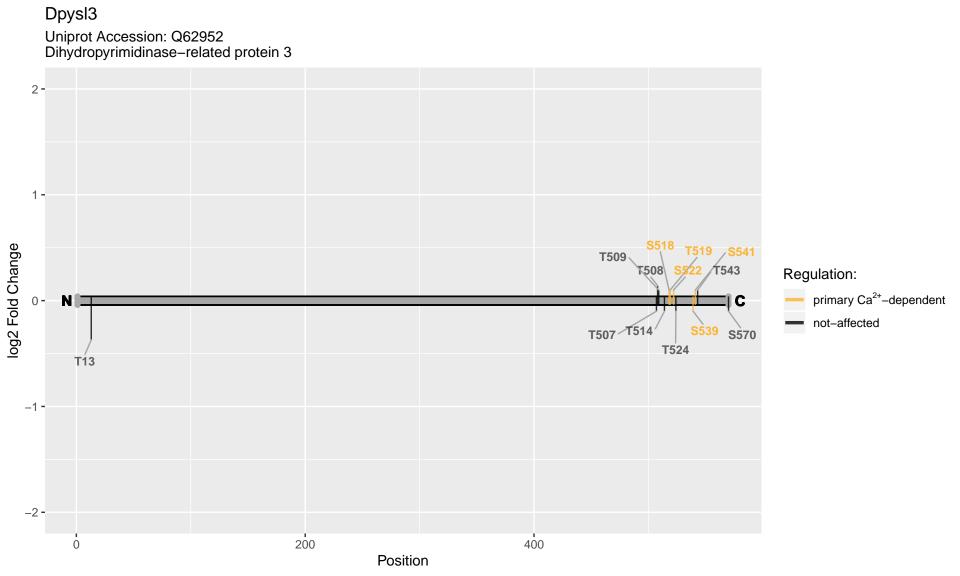


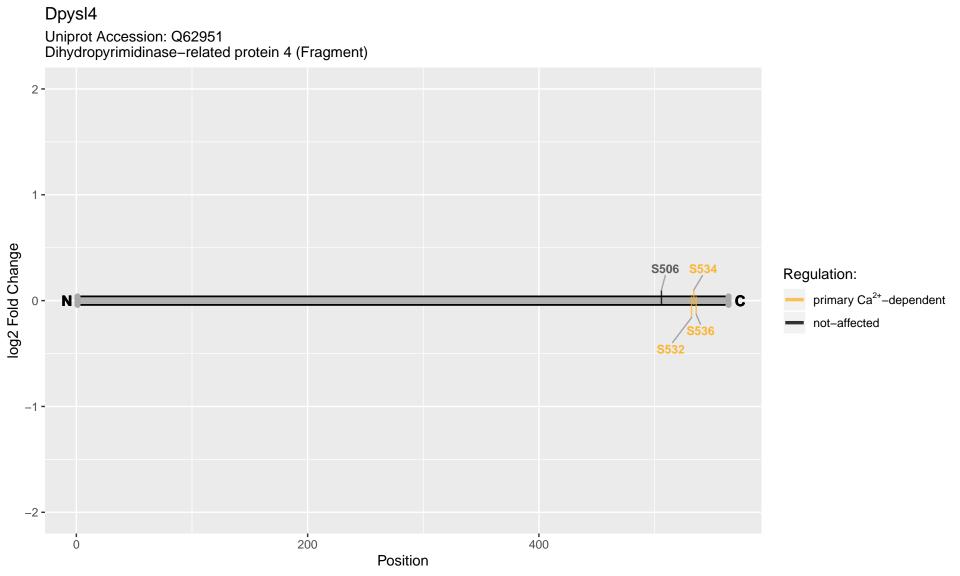


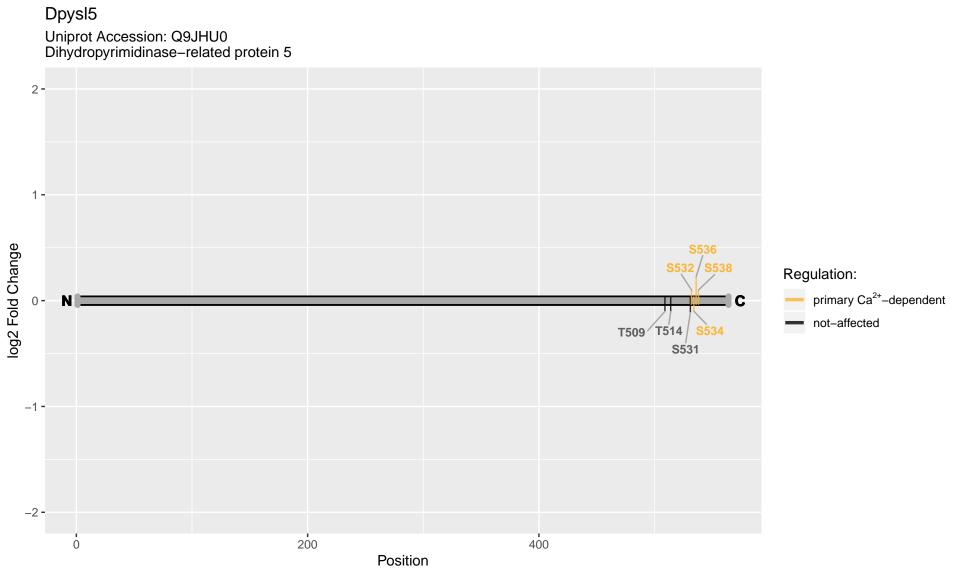


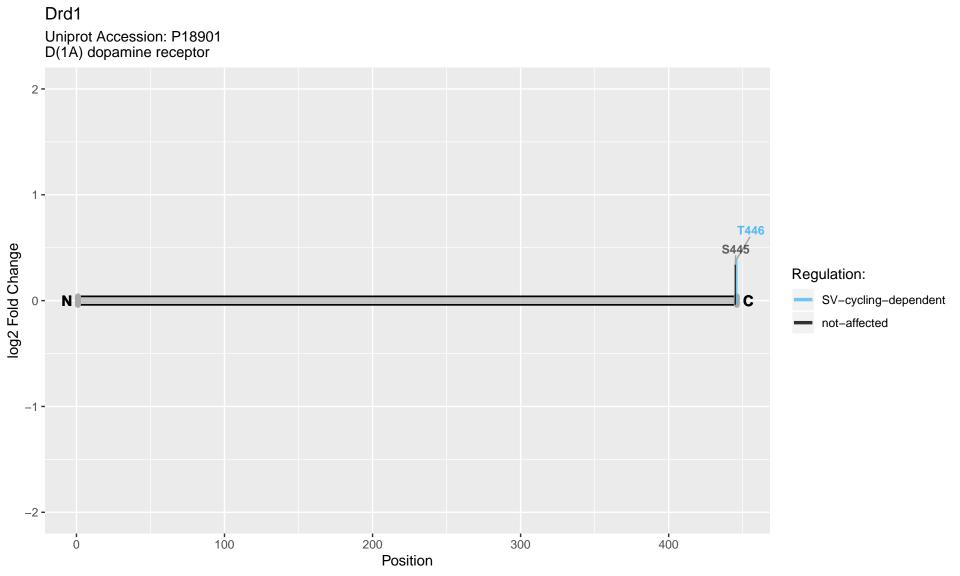


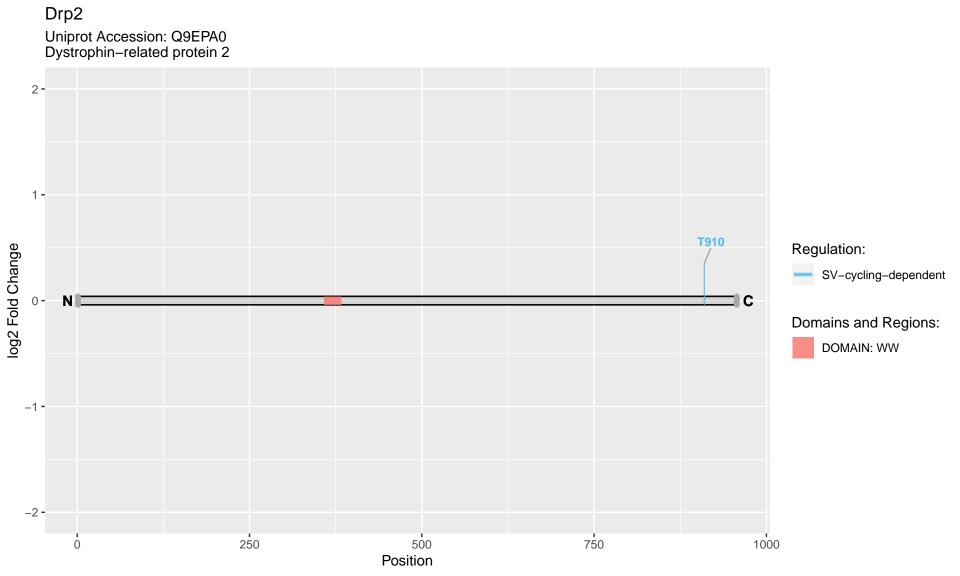


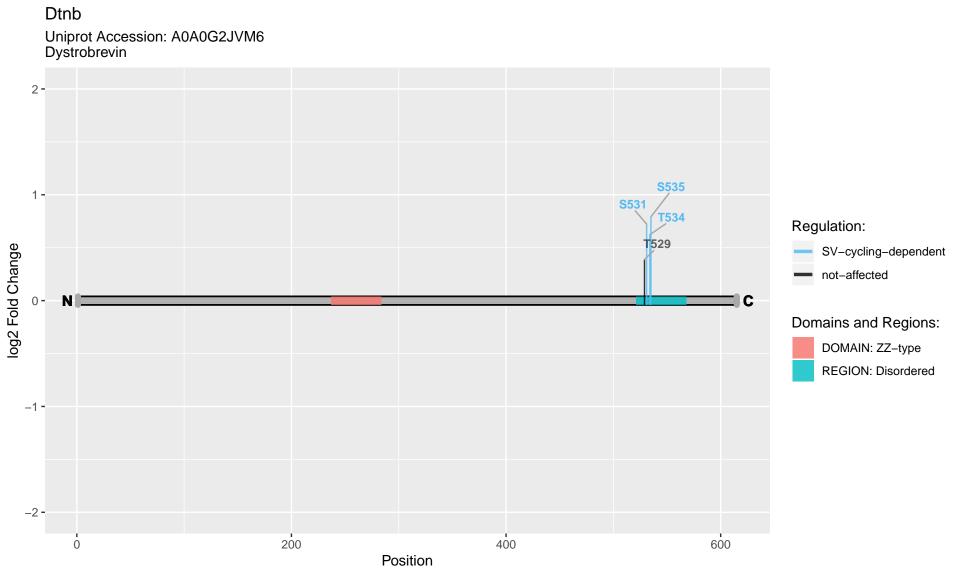


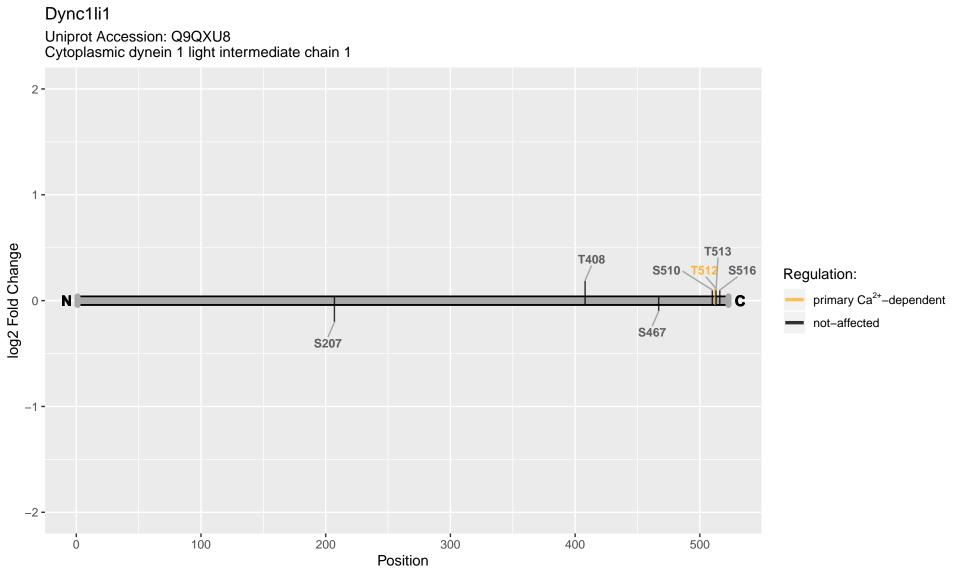


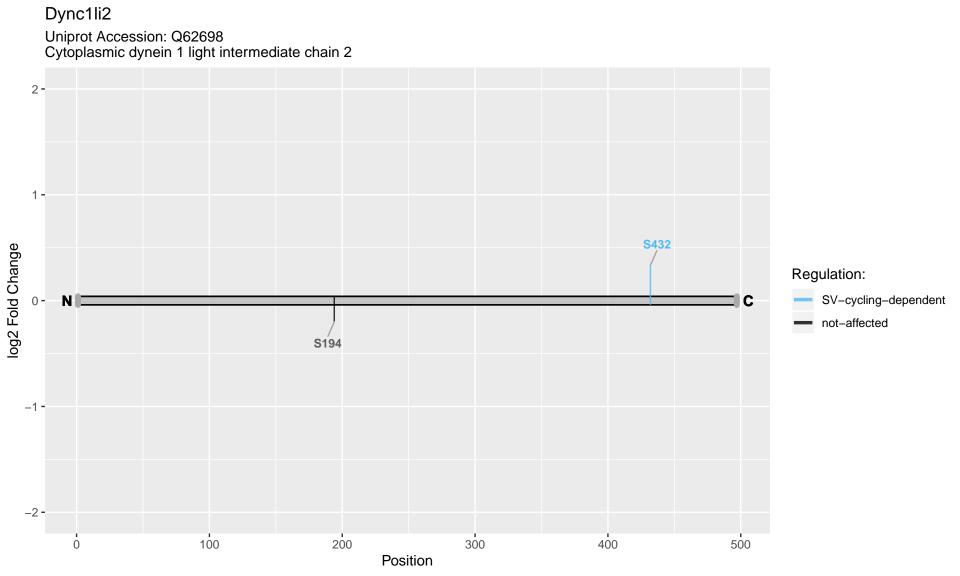


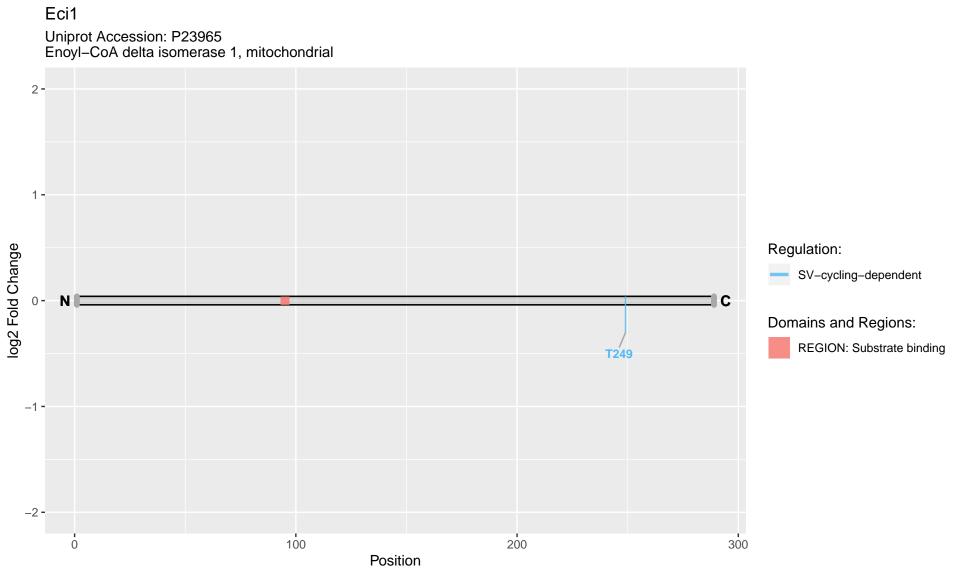


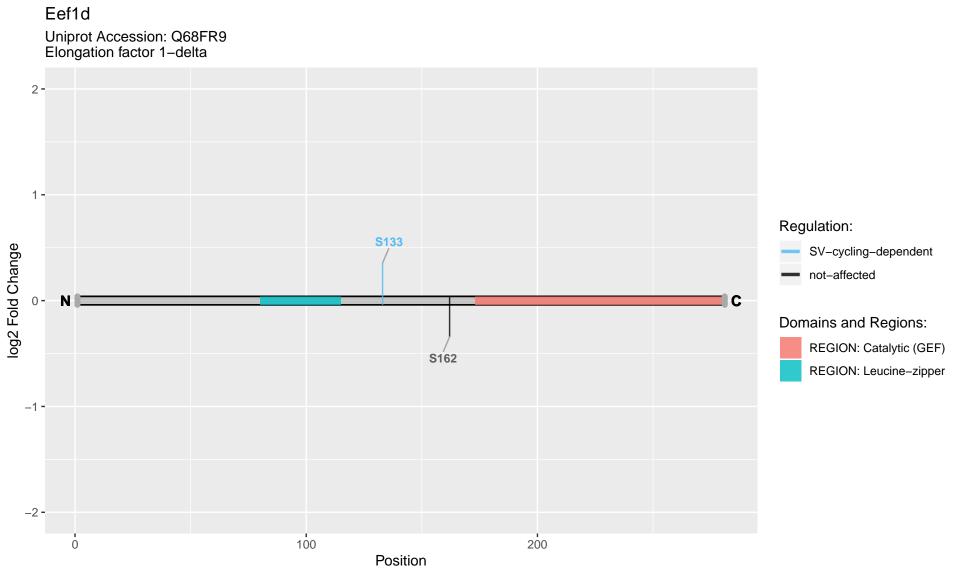


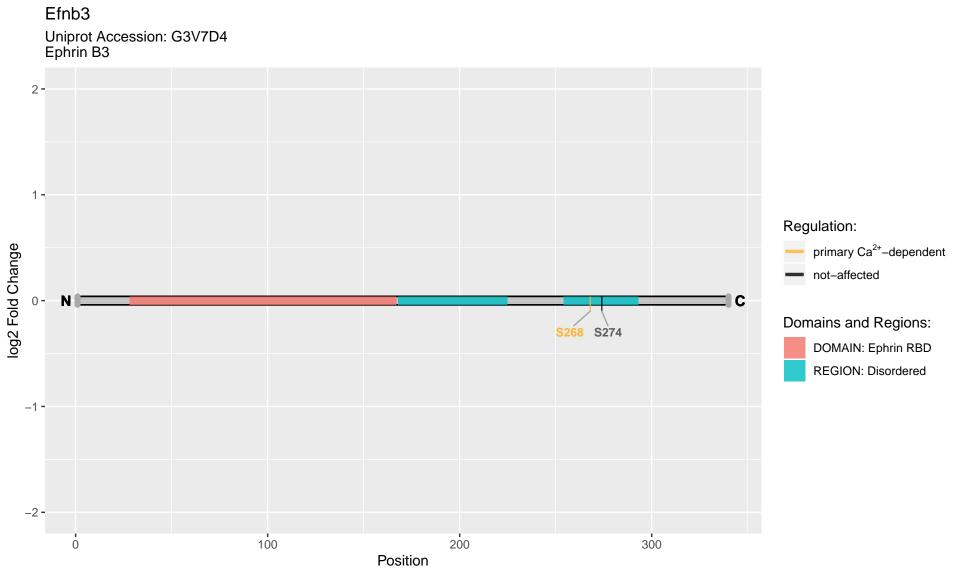


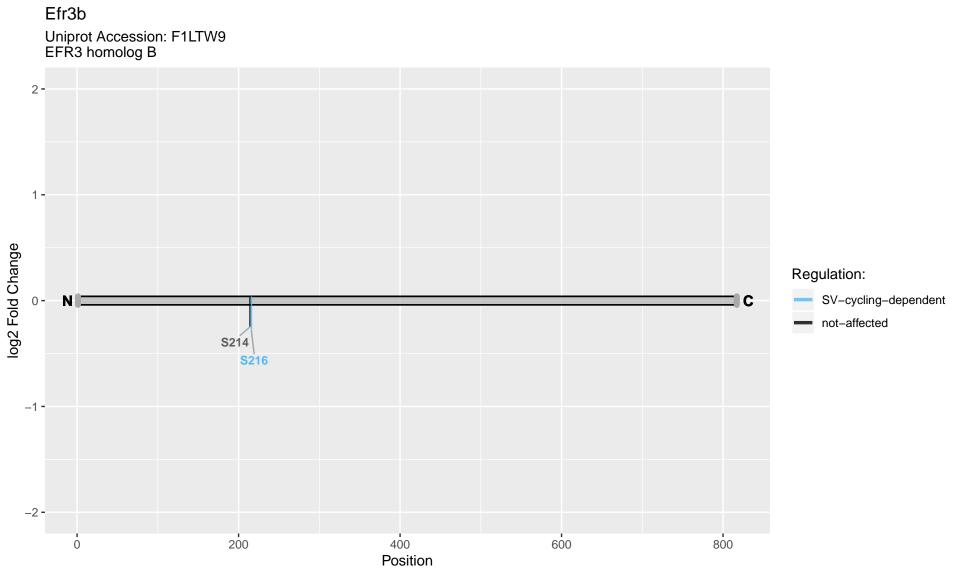


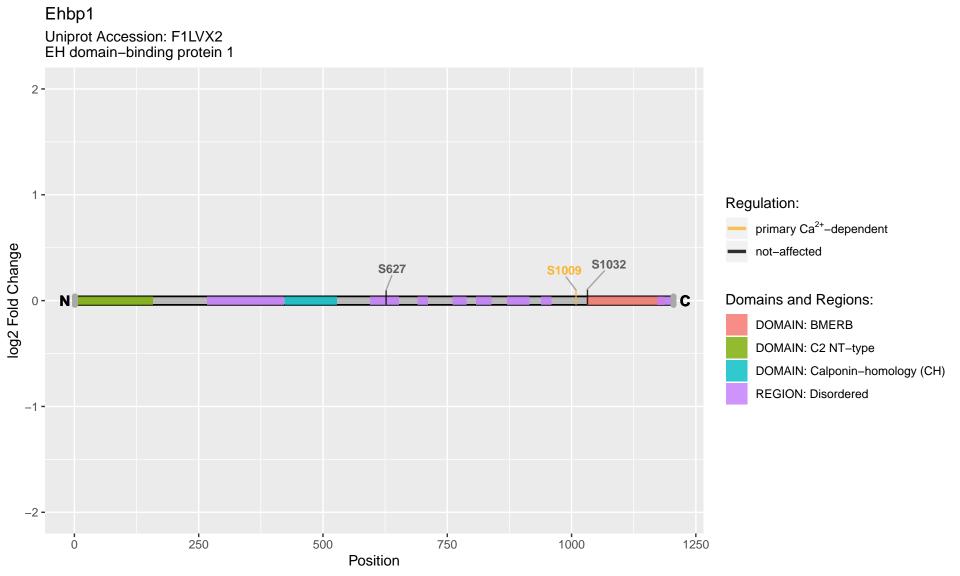


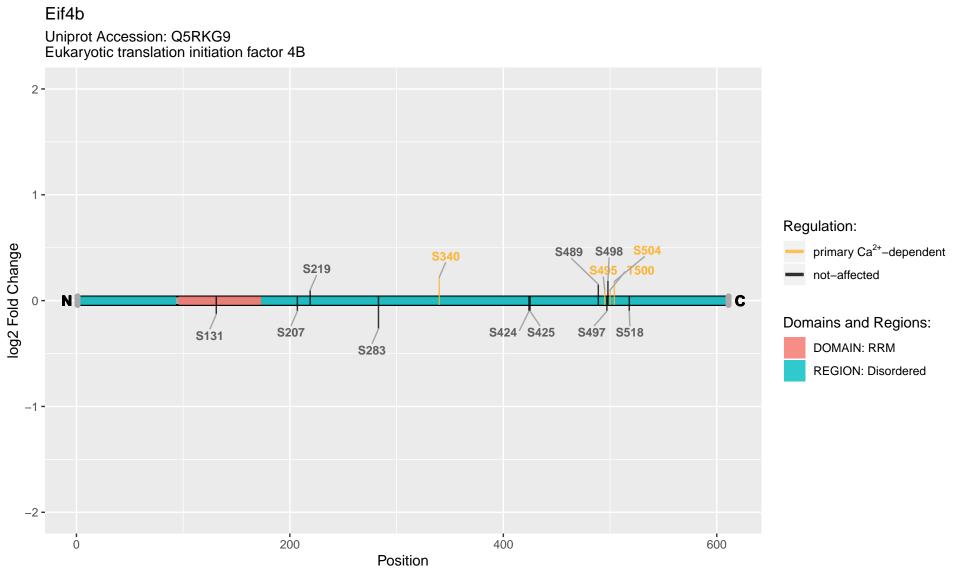


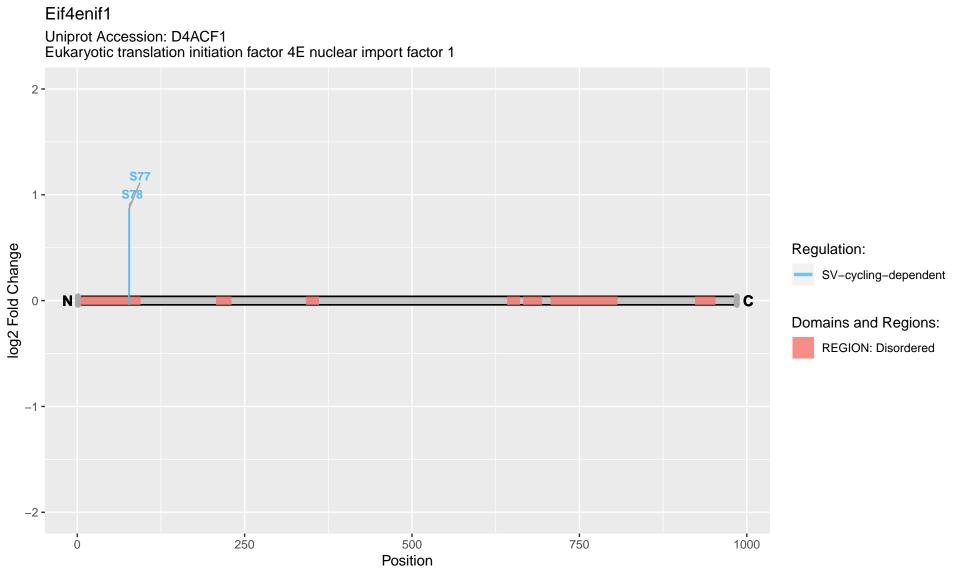






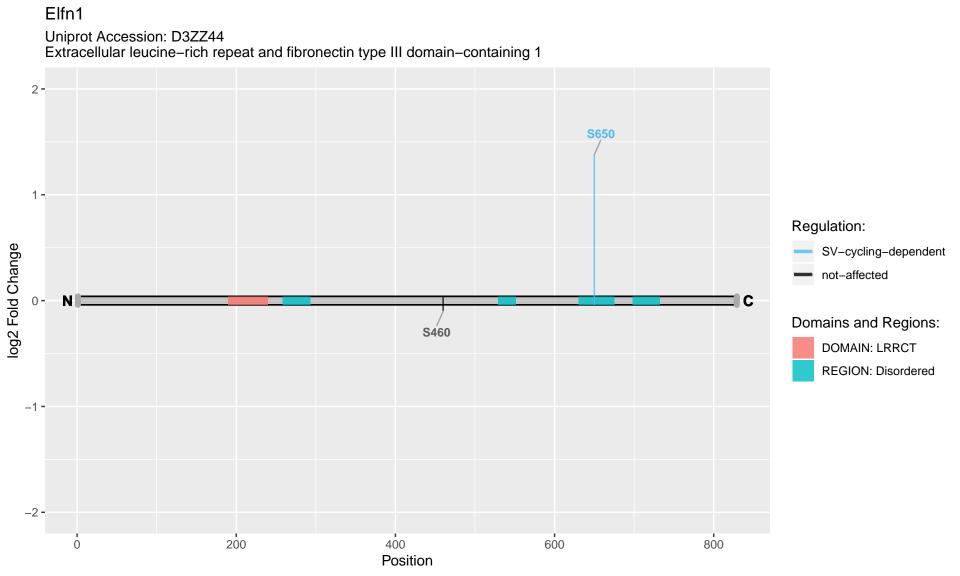


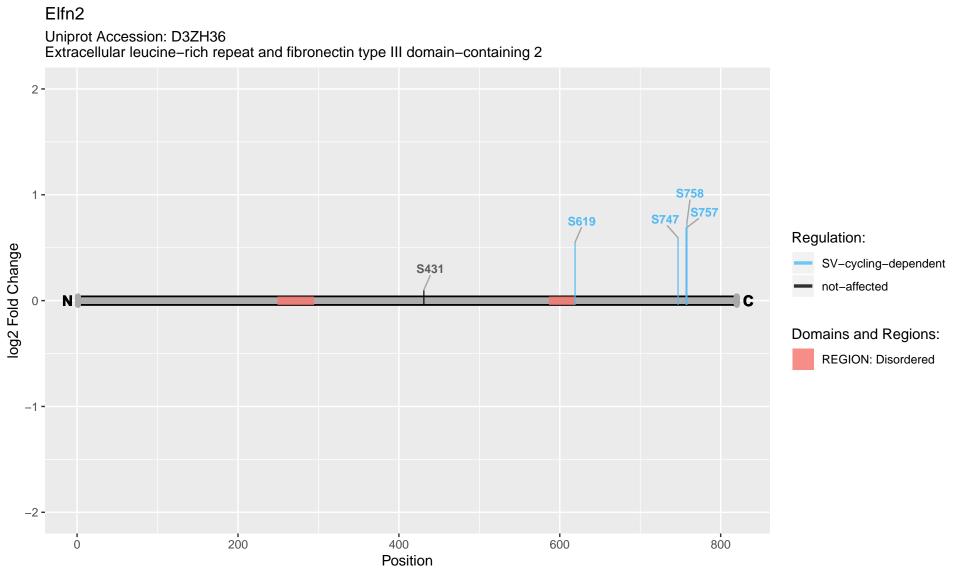


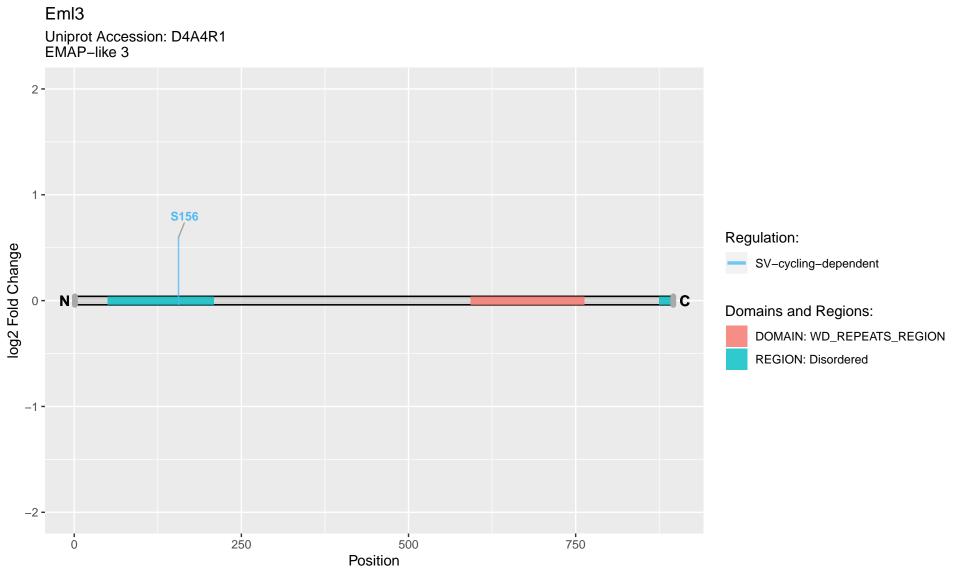


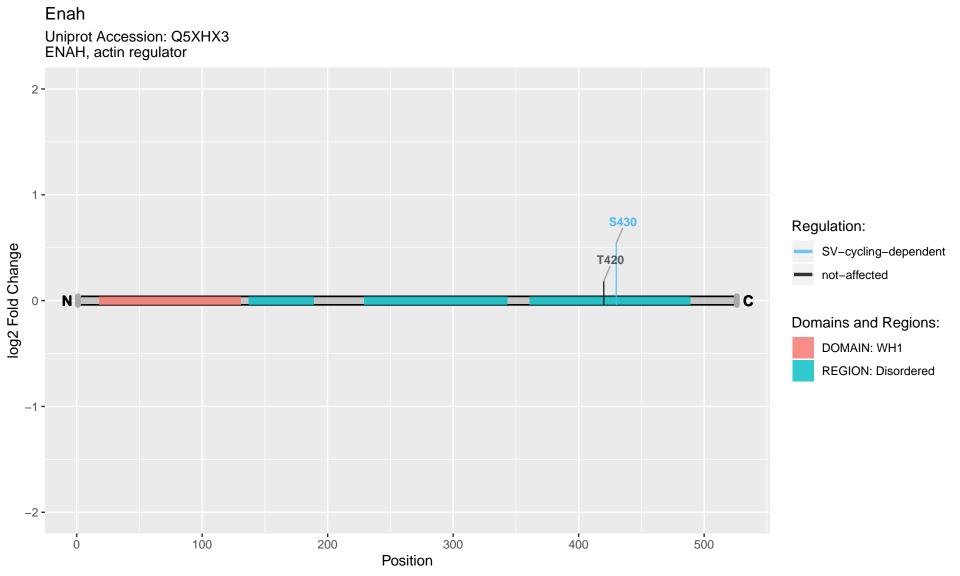
Eif4g1 Uniprot Accession: D3ZU13 Eukaryotic translation initiation factor 4 gamma, 1 2 -Regulation: **S1185** SV-cycling-dependent log2 Fold Change S1187 T1211 not-affected **\$1209** C Domains and Regions: S1079 DOMAIN: MI DOMAIN: W2 **REGION: Disordered** -1 **-**-2 **-**500 1000 1500 Position

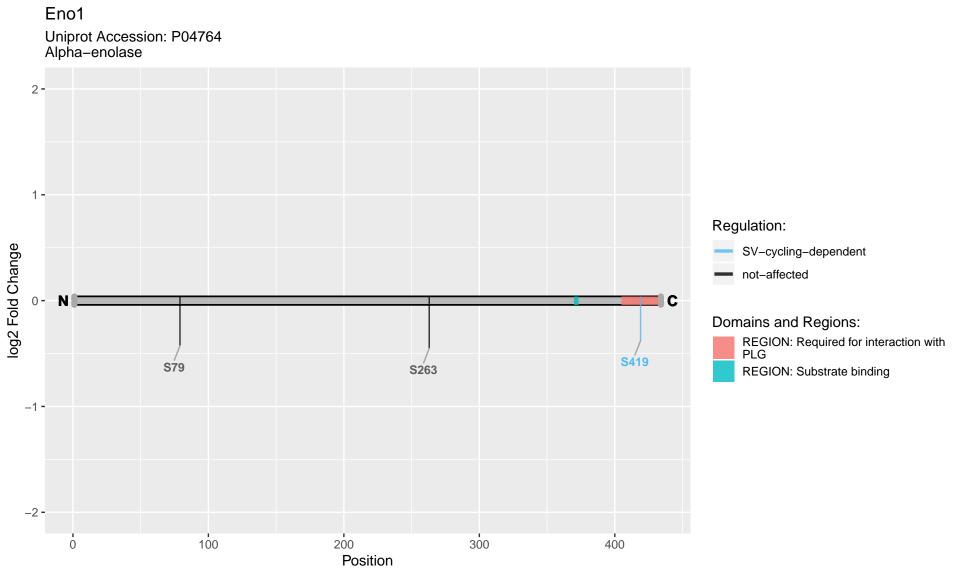
Eif4g3 Uniprot Accession: A0A0G2JY73 Eukaryotic translation initiation factor 4 gamma, 3 2 -Regulation: **S526 S322** primary Ca²⁺-dependent log2 Fold Change **S1186** SV-cycling-dependent Domains and Regions: DOMAIN: MI DOMAIN: W2 **REGION: Disordered** -1 **-**-2 **-**500 1000 1500 Position

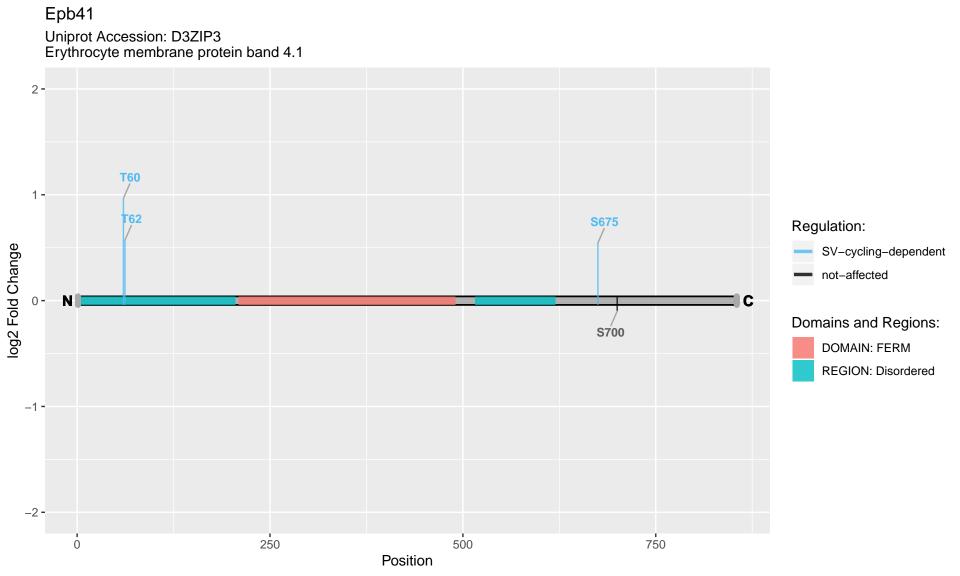




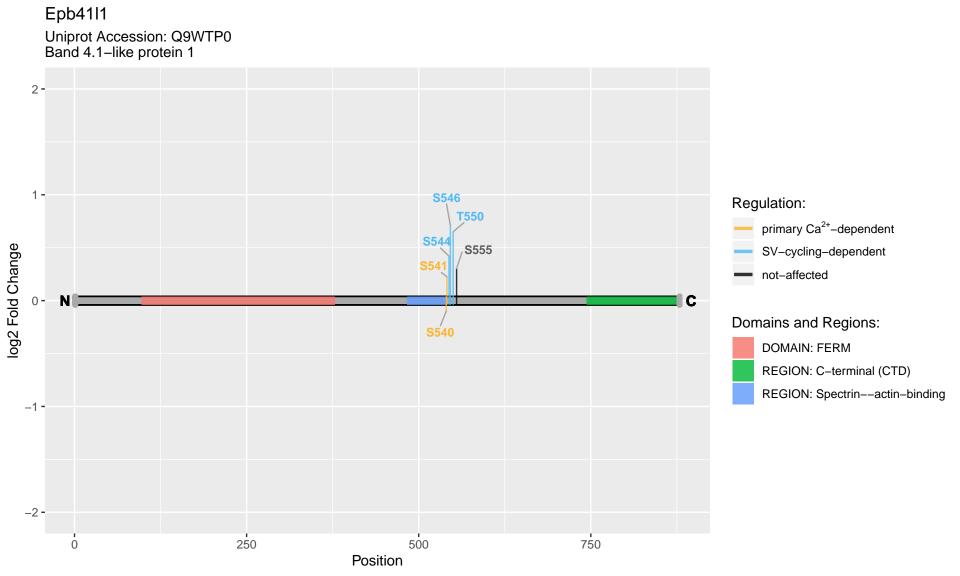




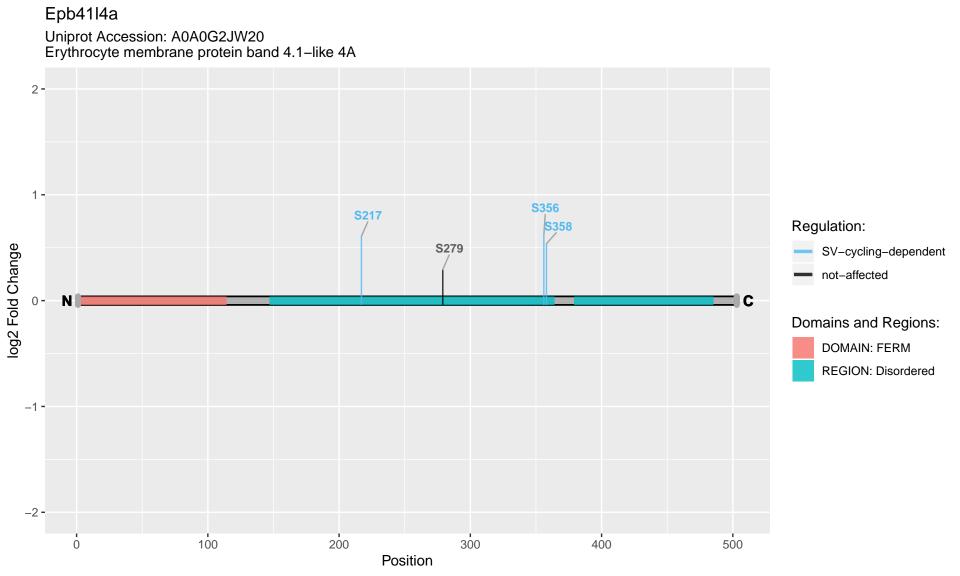


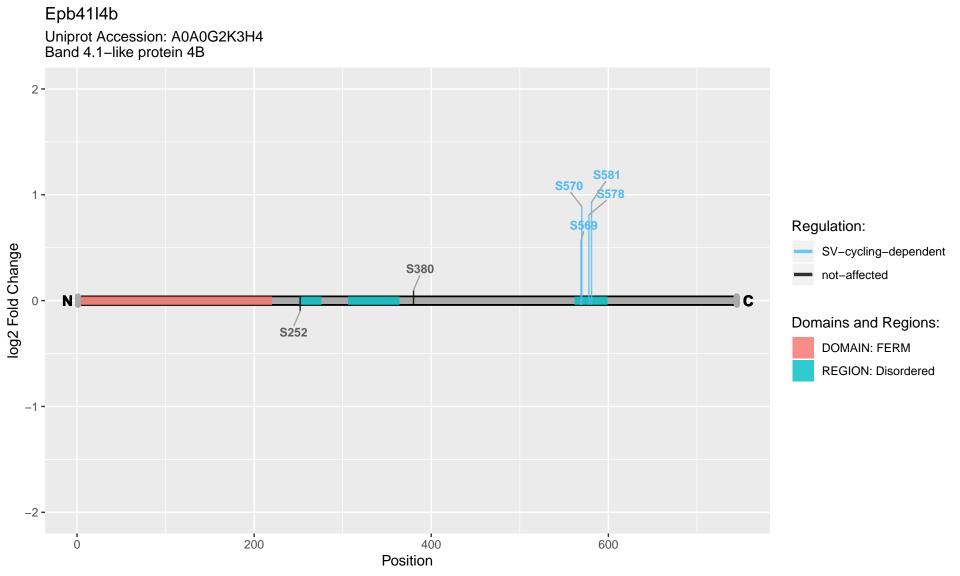


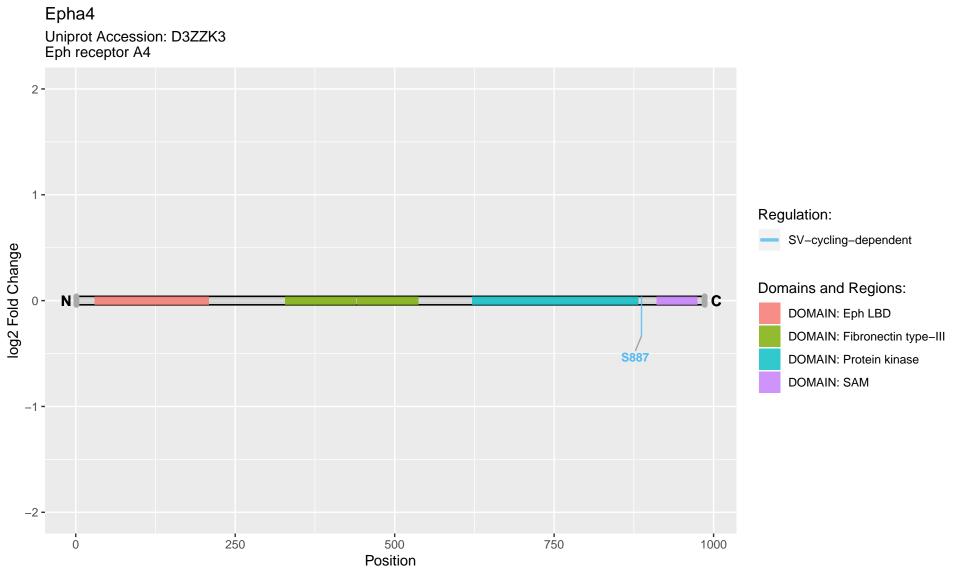
Epb41I1 Uniprot Accession: A0A0G2K0F3 Band 4.1–like protein 1–like 2 -T488 T489 T550 1 -S546 Regulation: **S1223 S**915 T475 S1322 primary Ca²⁺-dependent log2 Fold Change S1236 S1320/ SV-cycling-dependent S437 \$510 S1311 / T1324 S1452 T29 T30 T33 not-affected T1252 S1393 S430 Domains and Regions: S1349 S378 DOMAIN: FERM **REGION: Disordered** -1 **-**-2 **-**500 1000 1500 Position

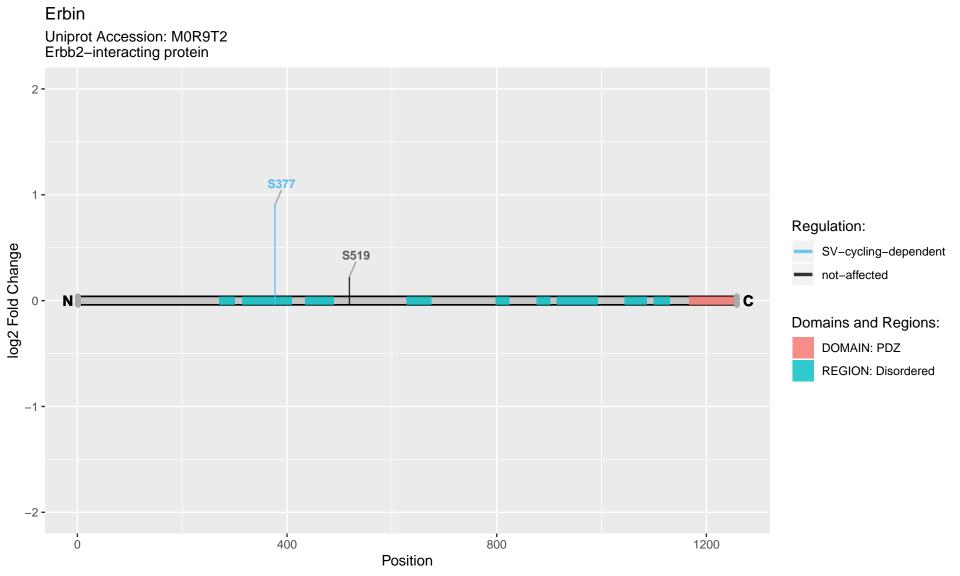


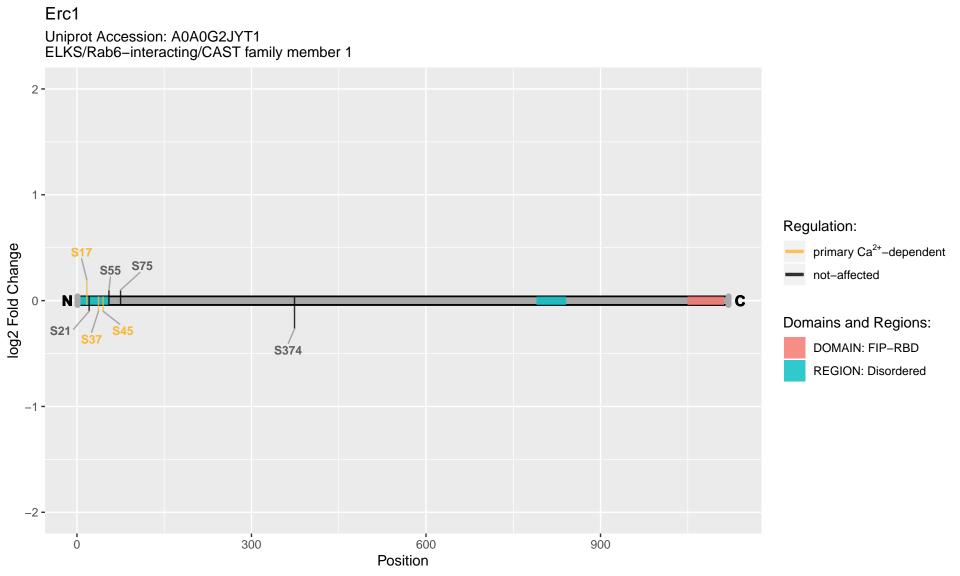
Epb41I3 Uniprot Accession: G3V874 Erythrocyte membrane protein band 4.1-like 3 2 -**S91 S578** 1 -**S508** Regulation: Y82 **S94** primary Ca²⁺-dependent T495 T469 log2 Fold Change **S66** S102 S576 **S838 J470** SV-cycling-dependent **S743 S907 T**472 T577 **\$100** not–affected Domains and Regions: S801 S412 S812 **S766** DOMAIN: FERM S808 **REGION: Disordered** -1 **-**-2 **-**250 750 500 1000 Position

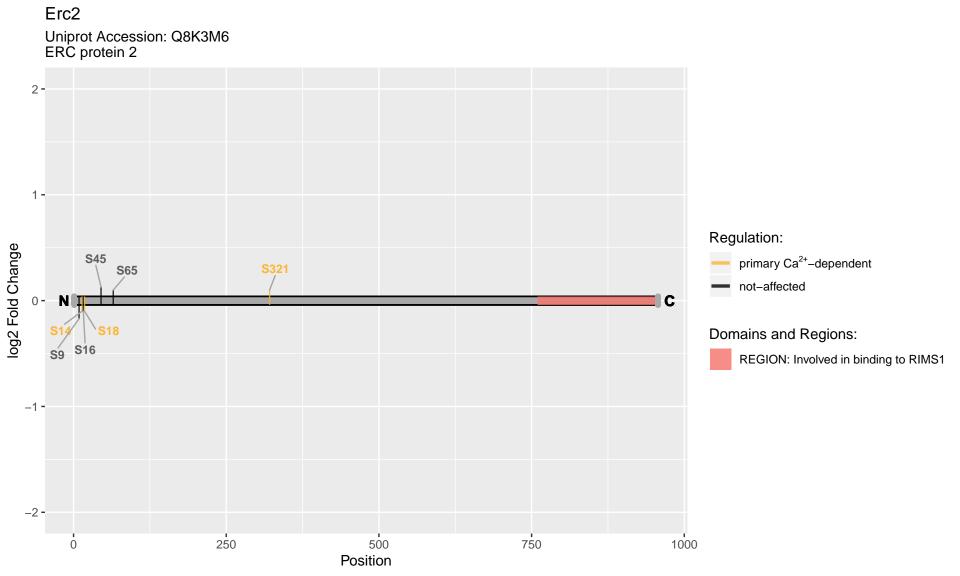


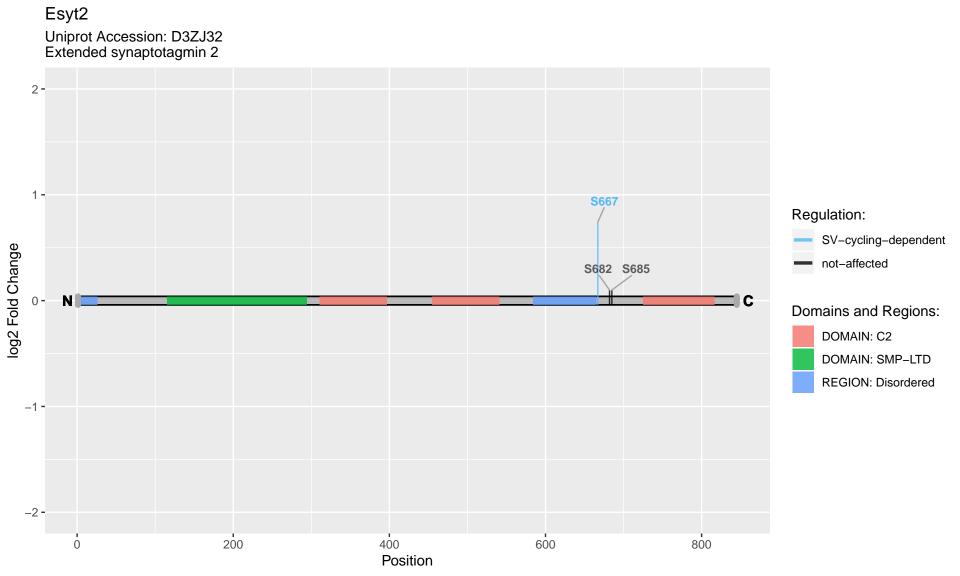


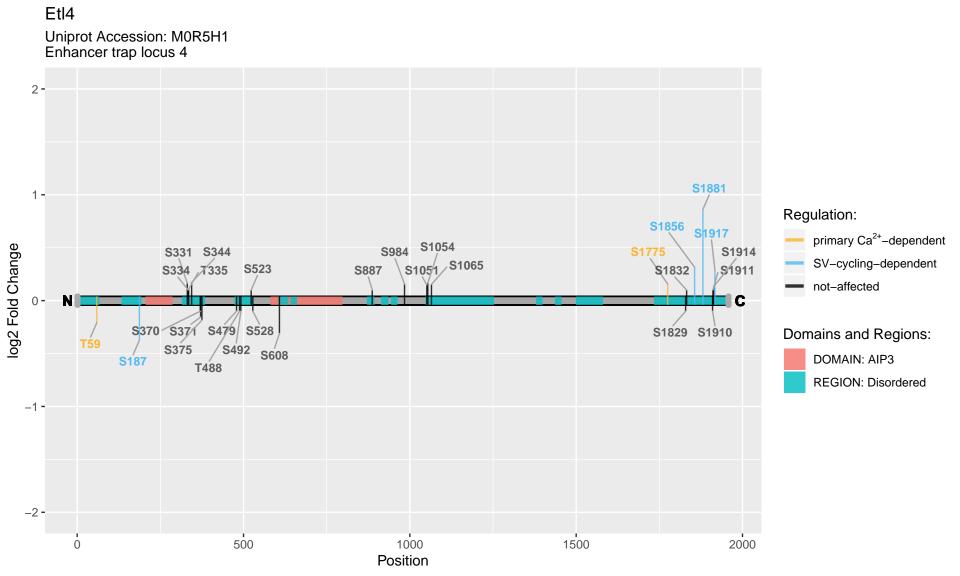


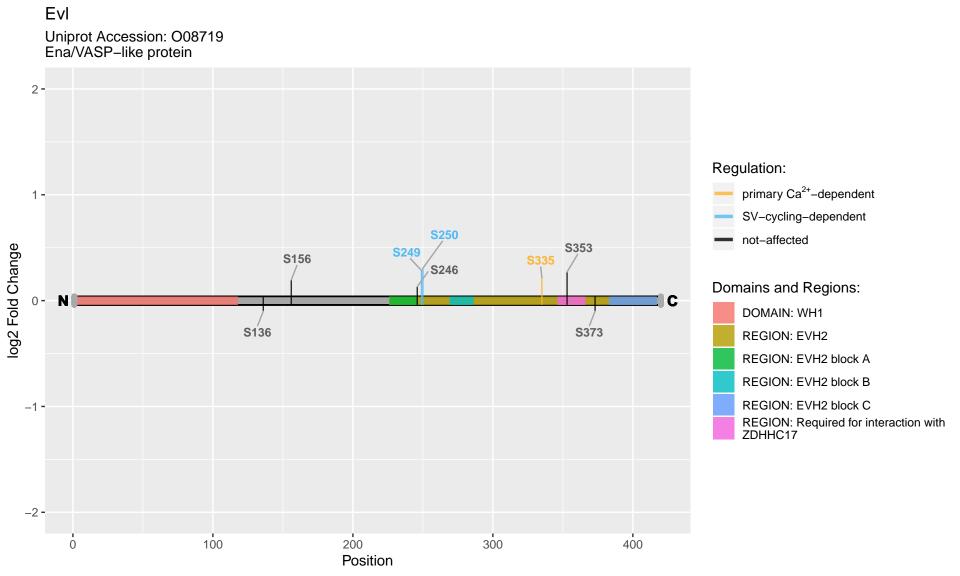


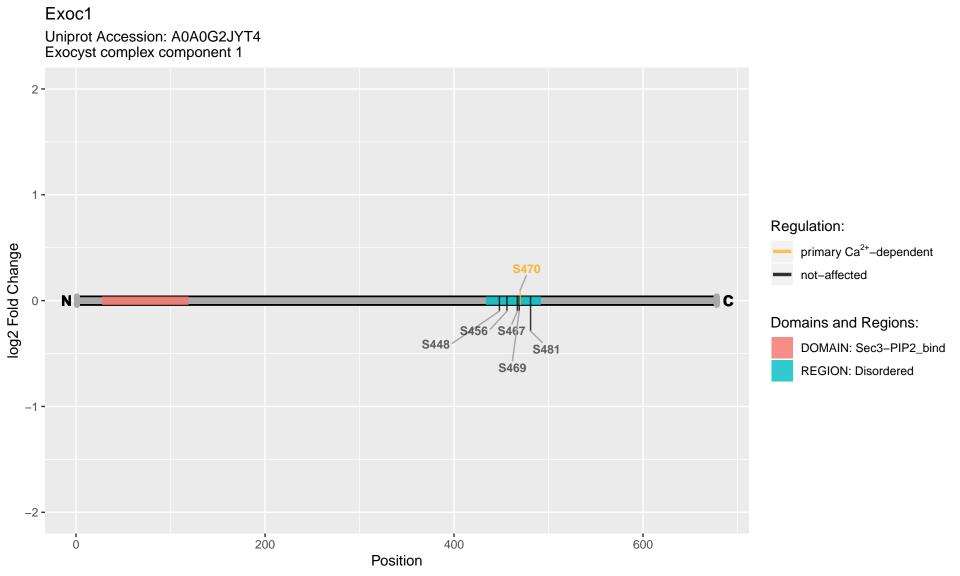


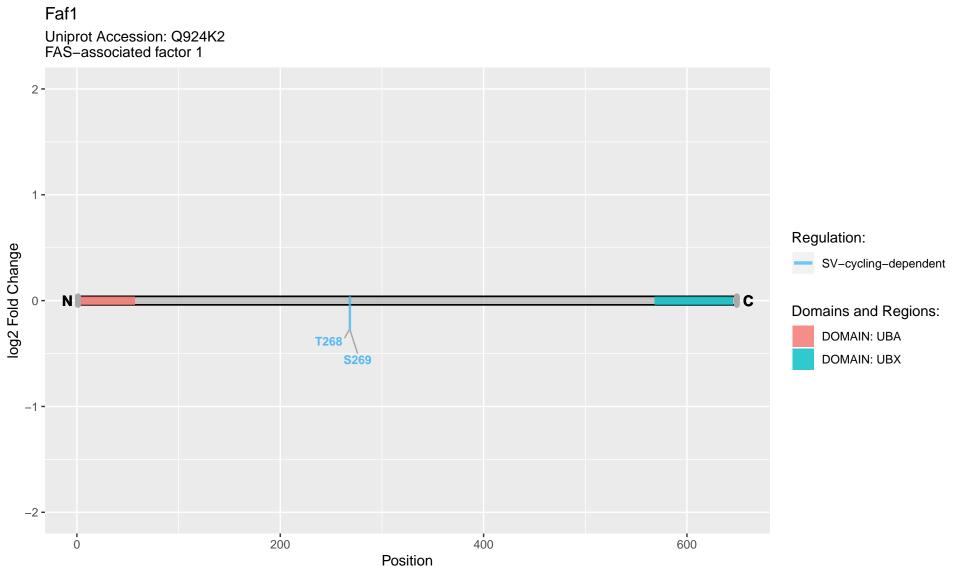


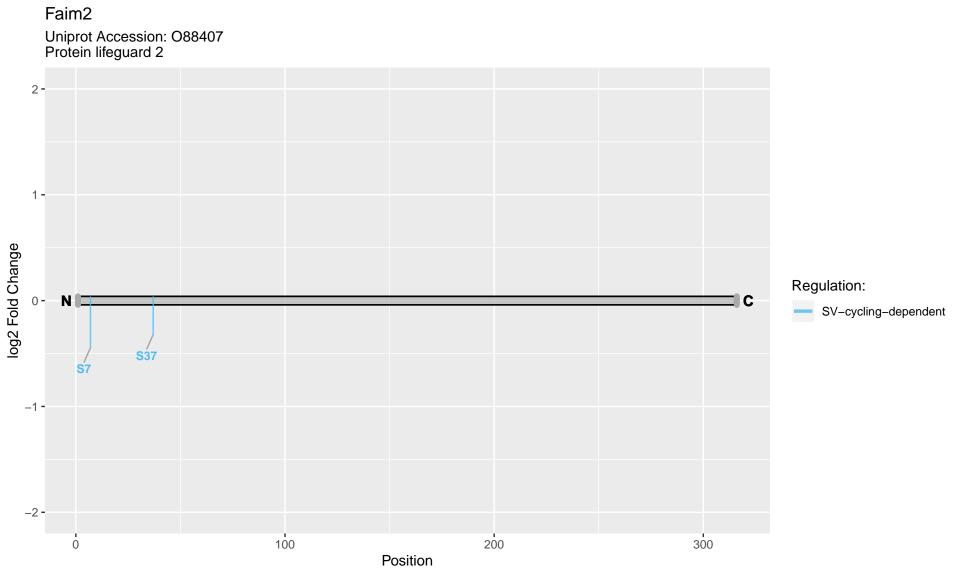




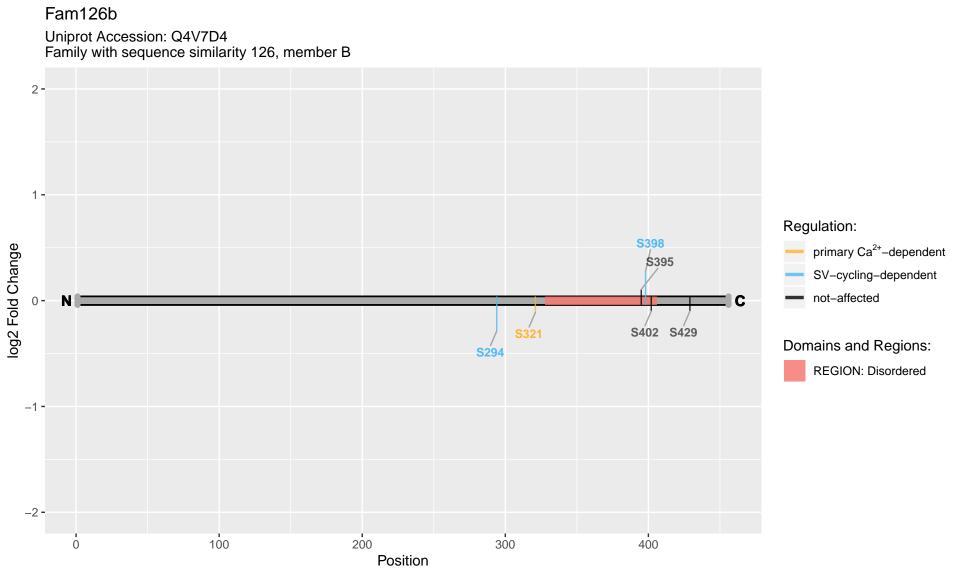


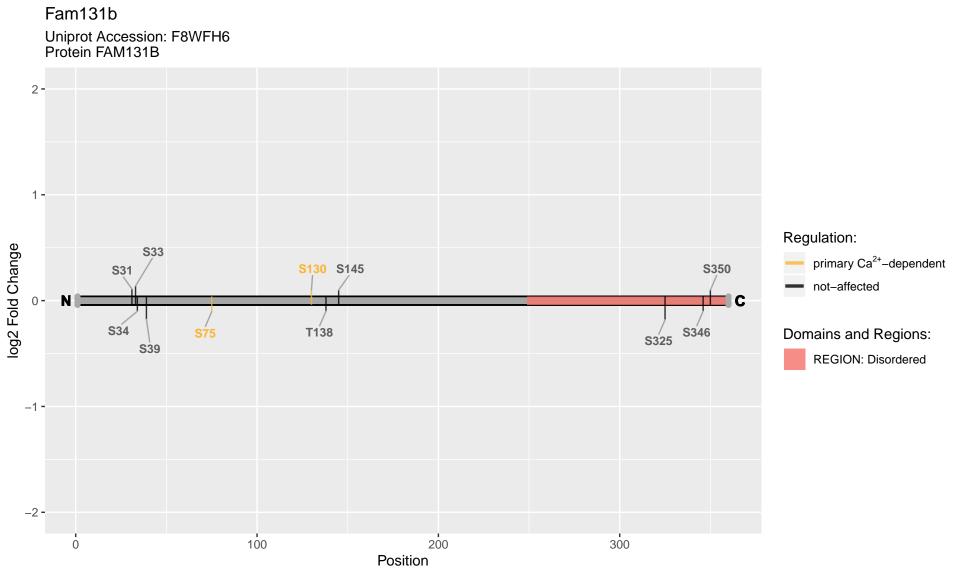


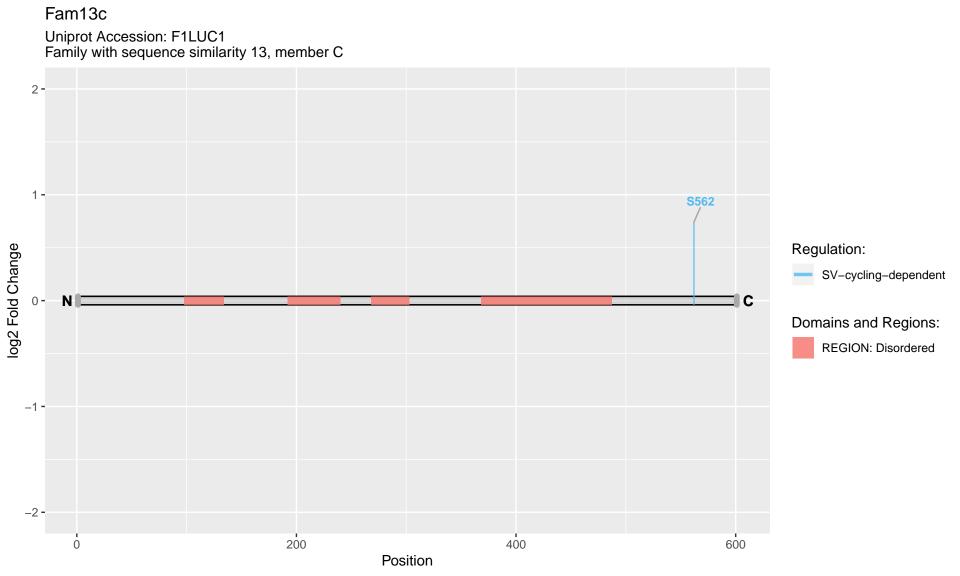




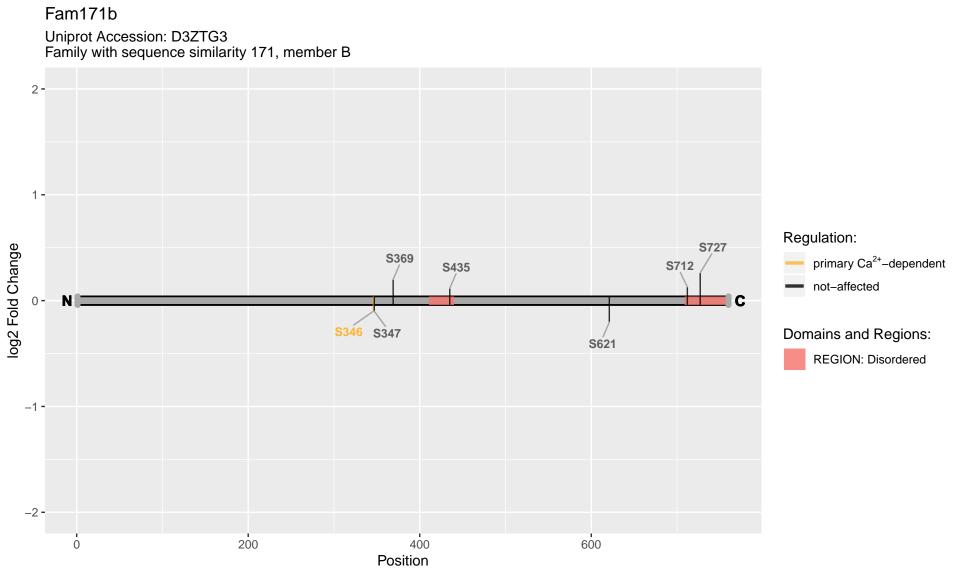
Fam117b Uniprot Accession: F1M8D5 Amyotrophic lateral sclerosis 2 (Juvenile) chromosome region, candidate 13 (Predicted) 2 -**S160** Regulation: log2 Fold Change SV-cycling-dependent **S205** not-affected Domains and Regions: **REGION: Disordered** -1 **-**-2 **-**100 200 300 Position

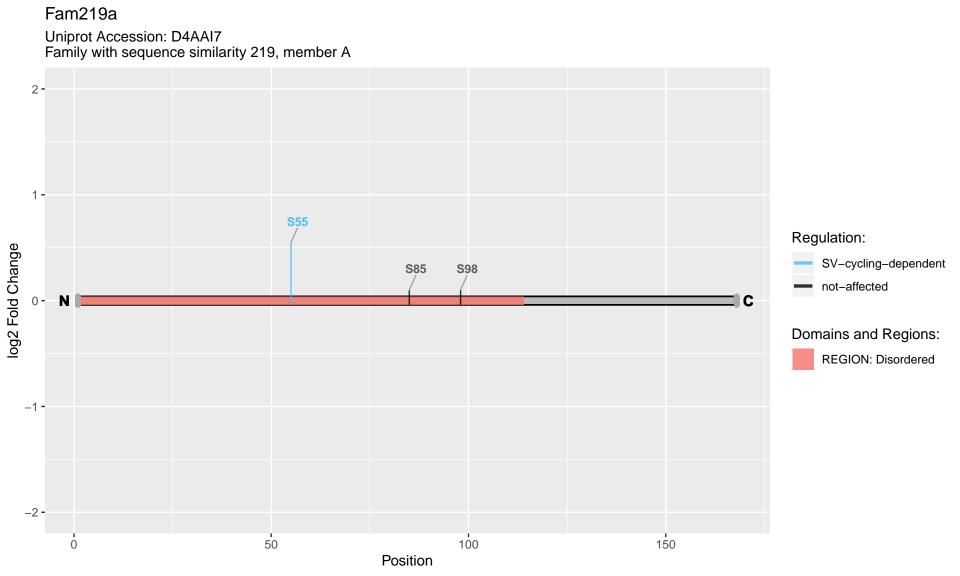




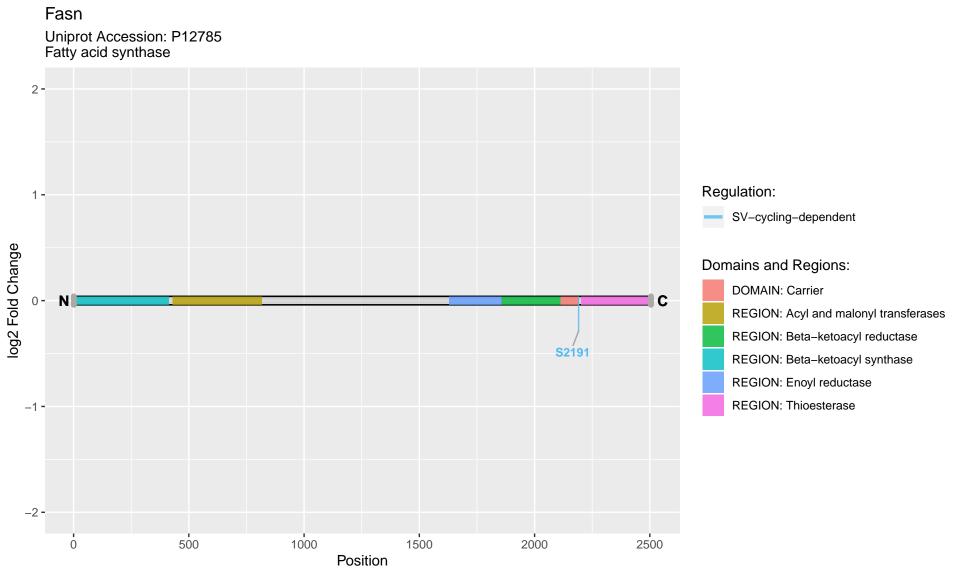


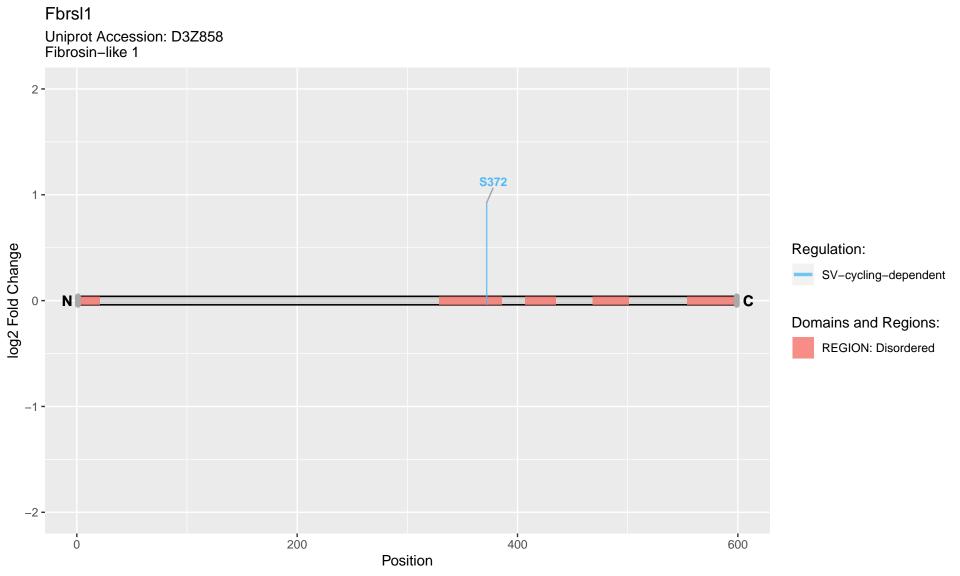
Fam171a1 Uniprot Accession: D4A7Y4 Family with sequence similarity 171, member A1 2 -Regulation: **S793** log2 Fold Change SV-cycling-dependent S340 not-affected Domains and Regions: **REGION: Disordered** -1 **-**-2 **-**250 750 500 Position

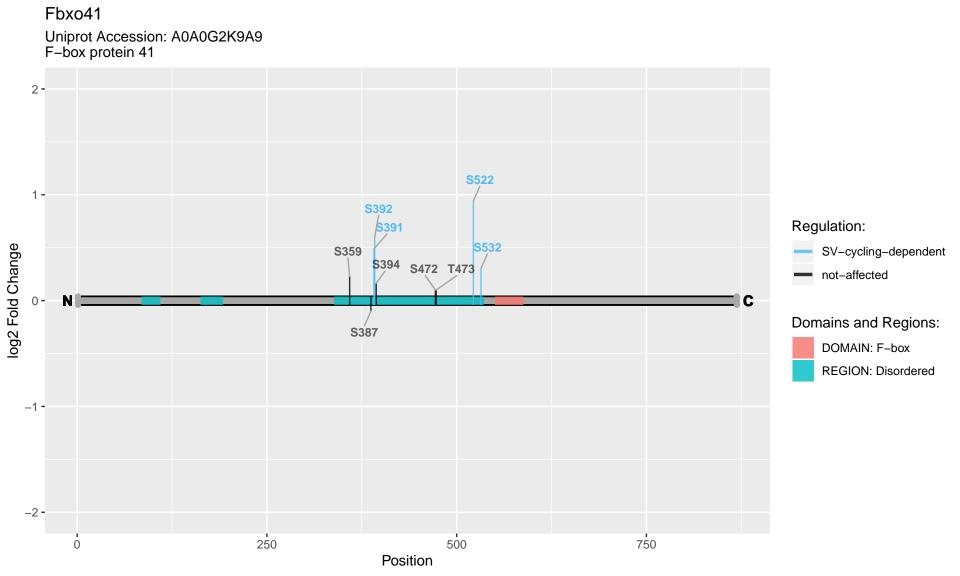


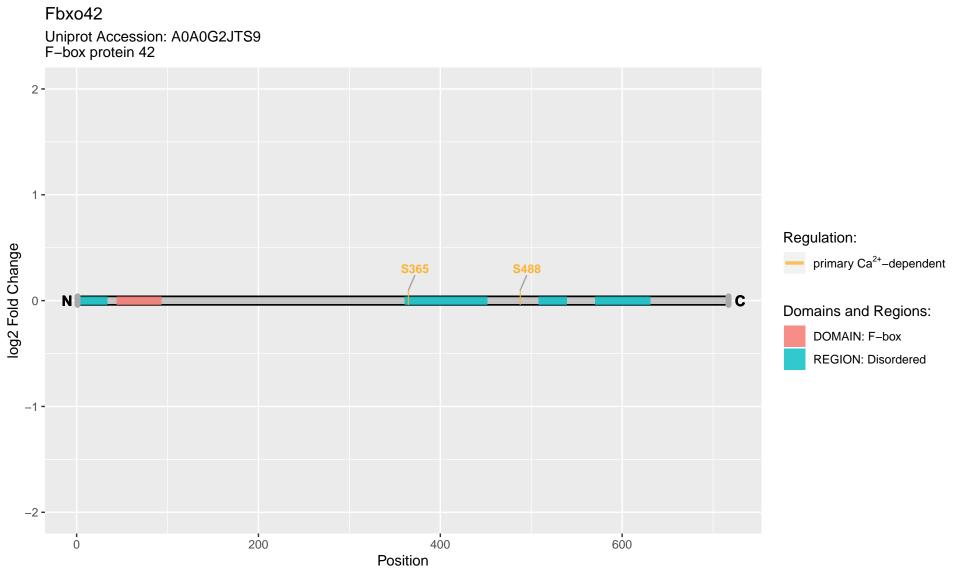


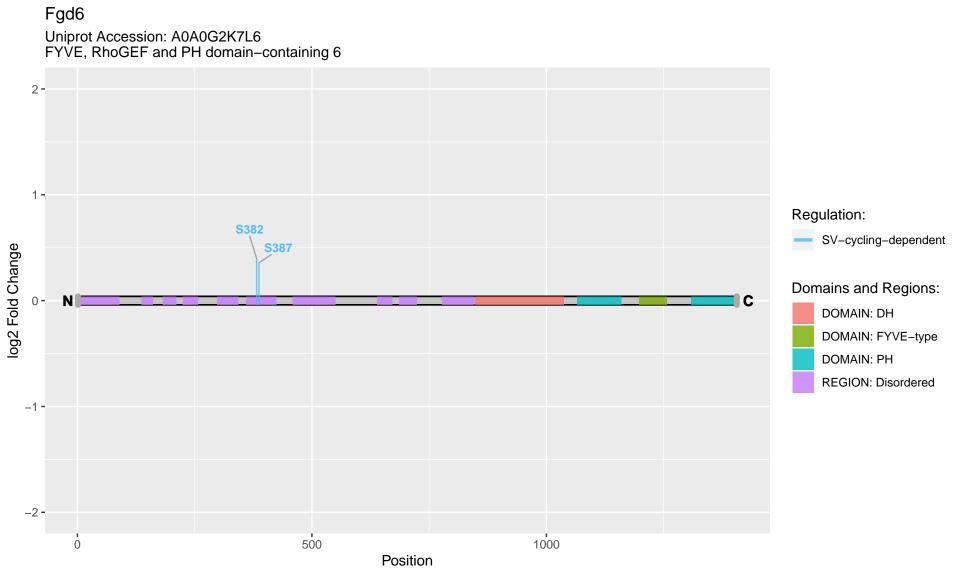
Farp1 Uniprot Accession: F1LYQ8 FERM, ARHGEF and pleckstrin domain–containing protein 1 2 -**S427** 1 -Regulation: SV-cycling-dependent log2 Fold Change not-affected Domains and Regions: II C DOMAIN: DH S875 T34 DOMAIN: FERM **S837** DOMAIN: PH 1 DOMAIN: PH 2 -1 **-**-2 **-**250 500 750 1000 Position



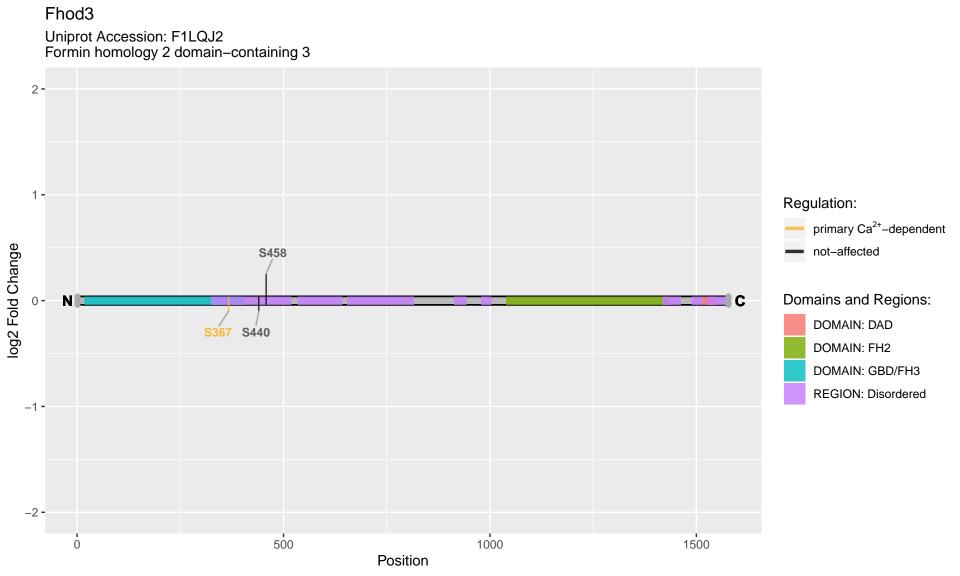


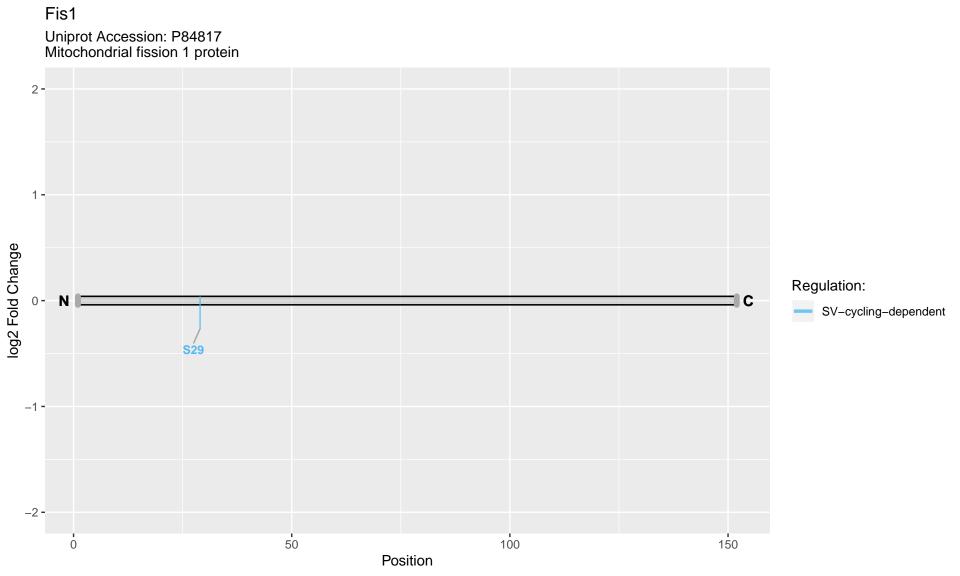


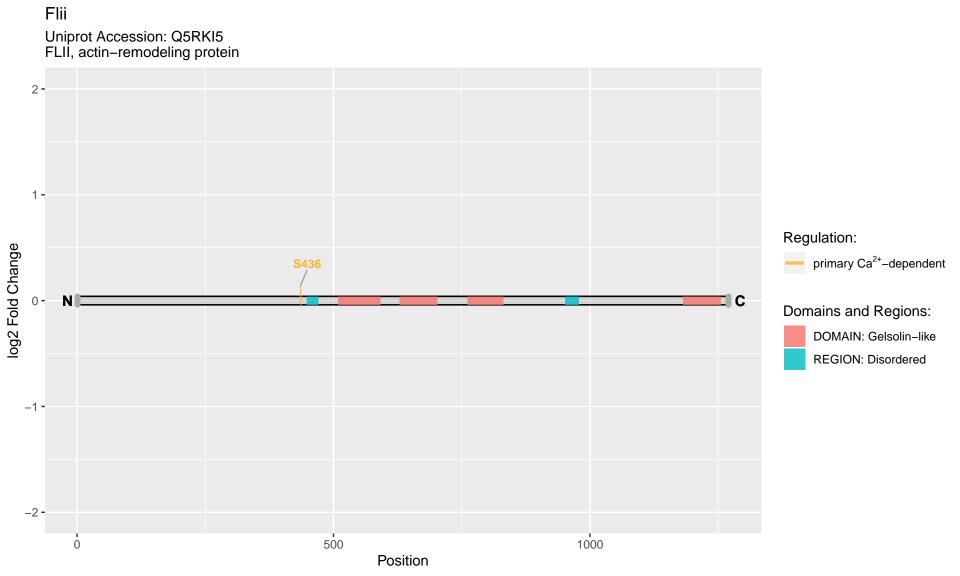


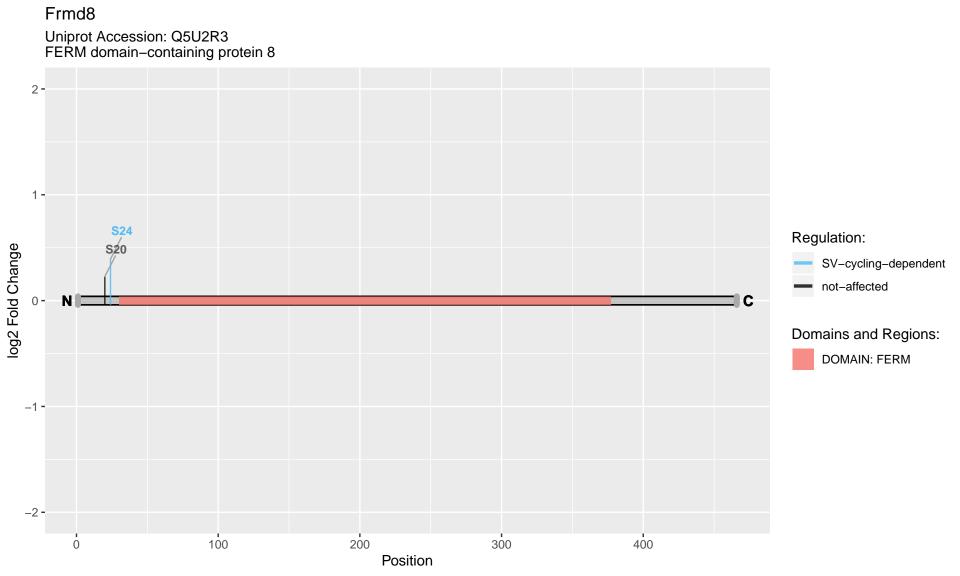


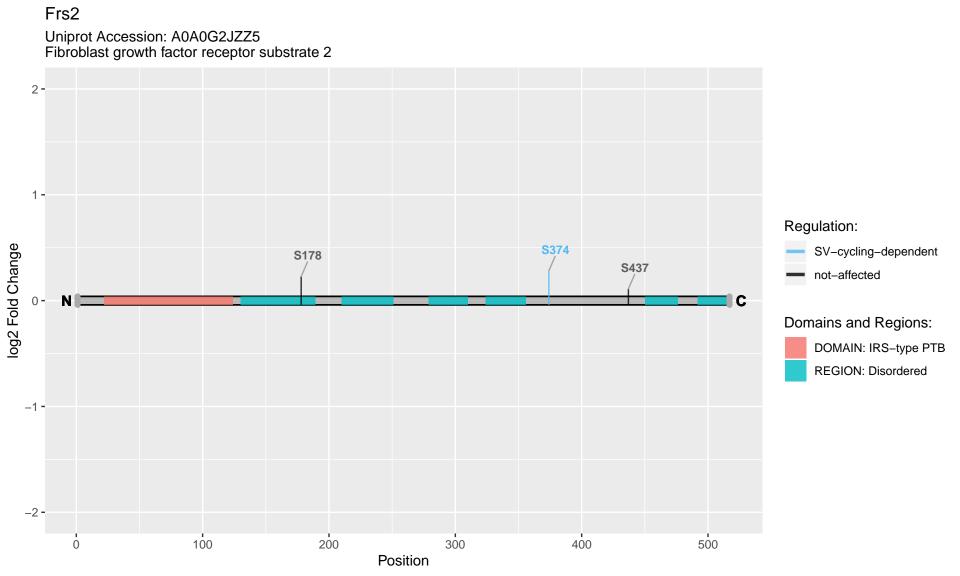
Fgf14 Uniprot Accession: Q8R5L7 Fibroblast growth factor 14 2 log2 Fold Change Regulation: SV-cycling-dependent **S210** -1 **-**-2 **-**50 150 200 100 250 Position

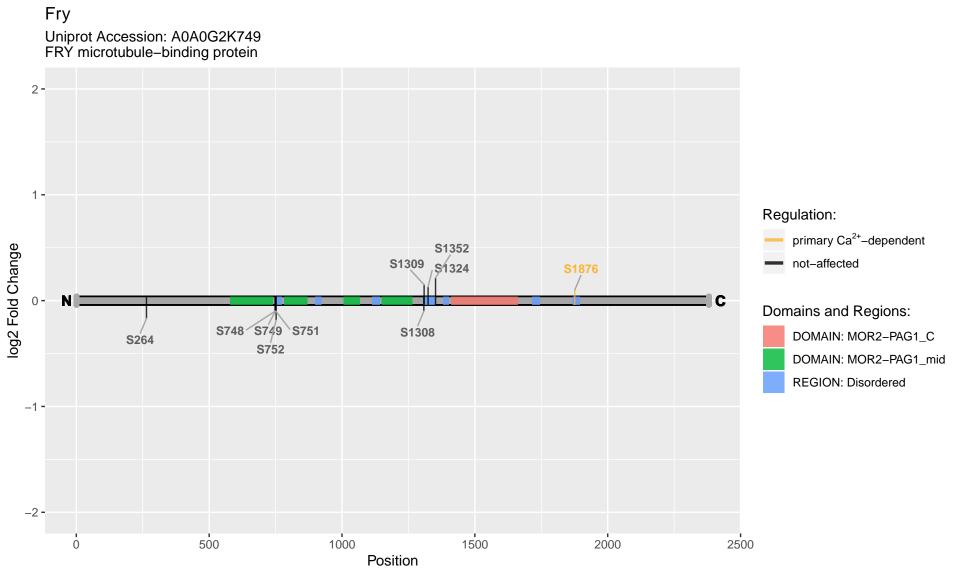


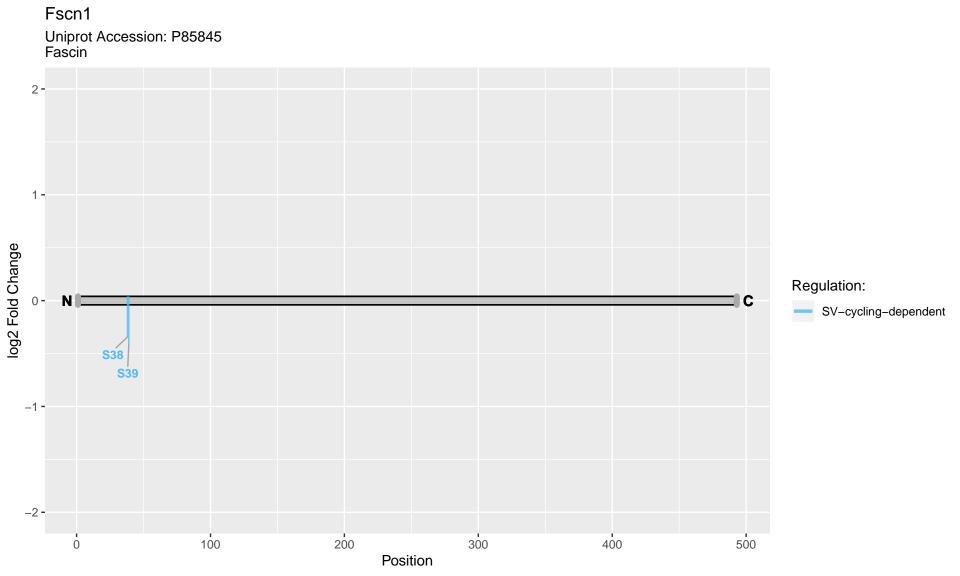


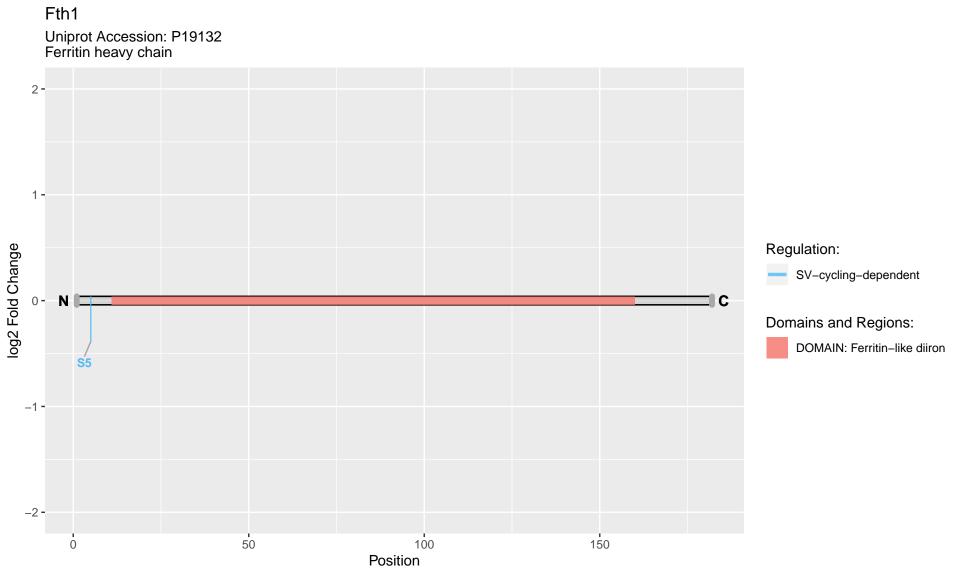


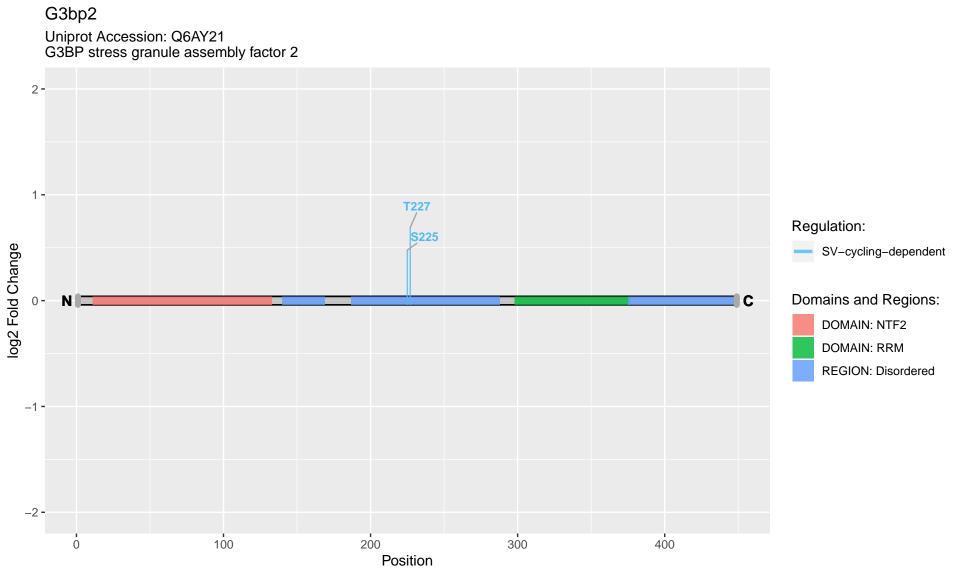


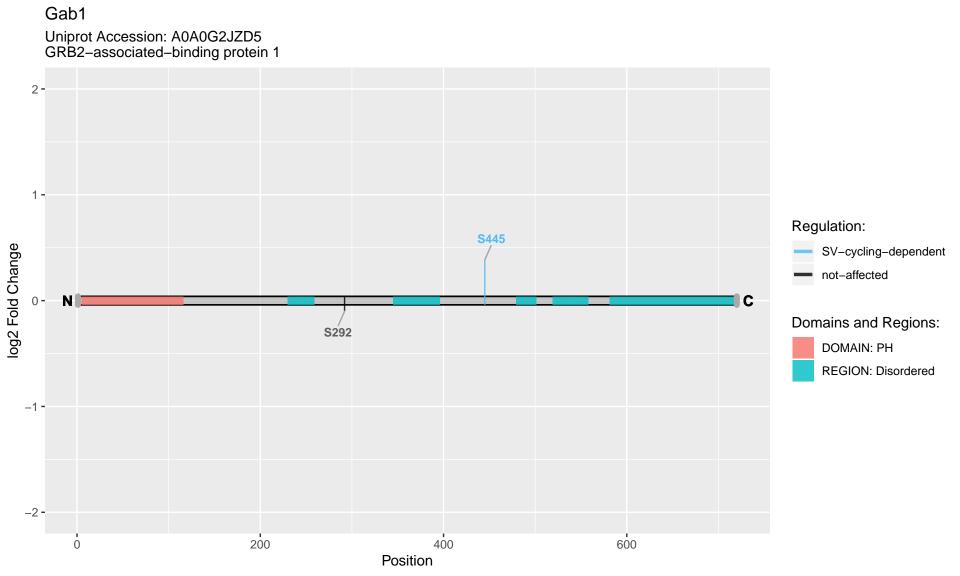


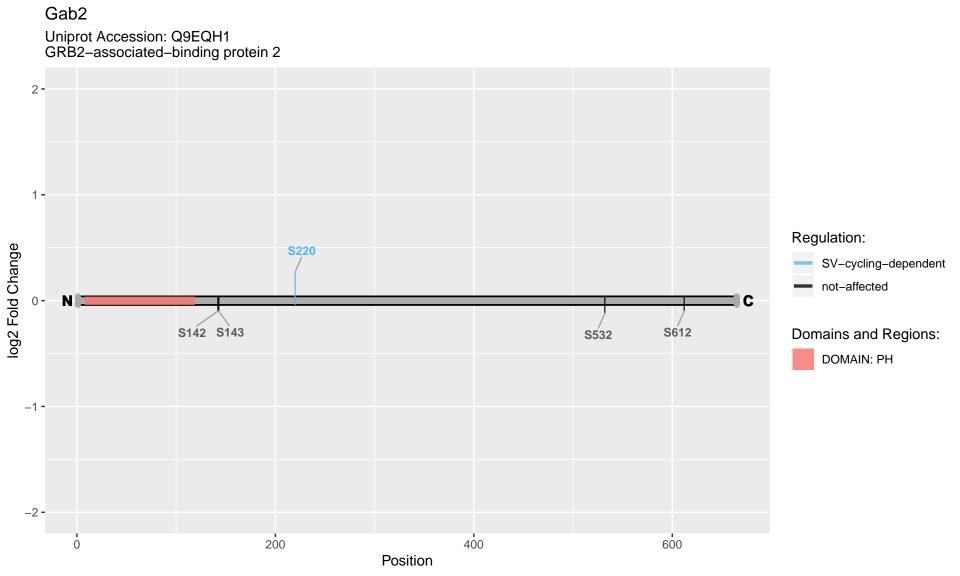


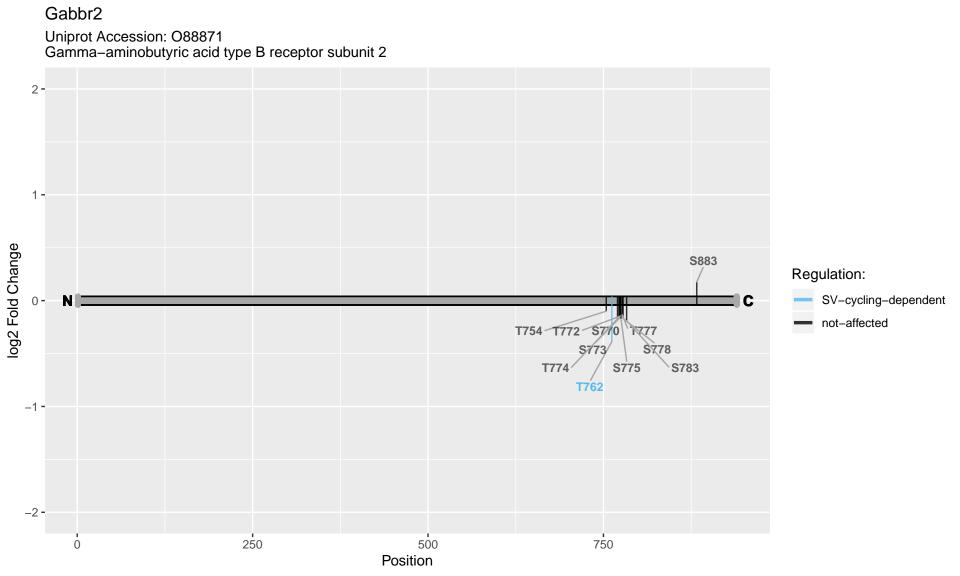


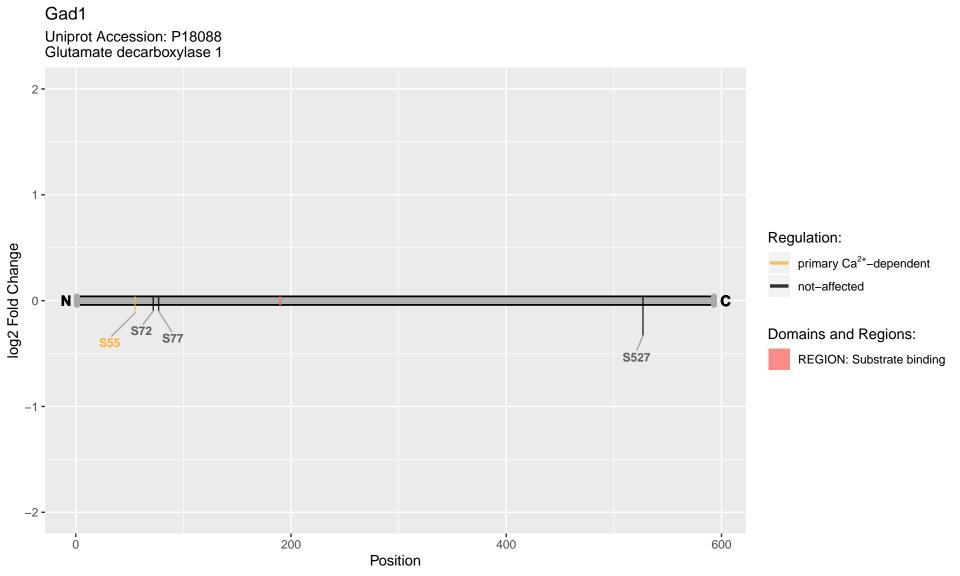


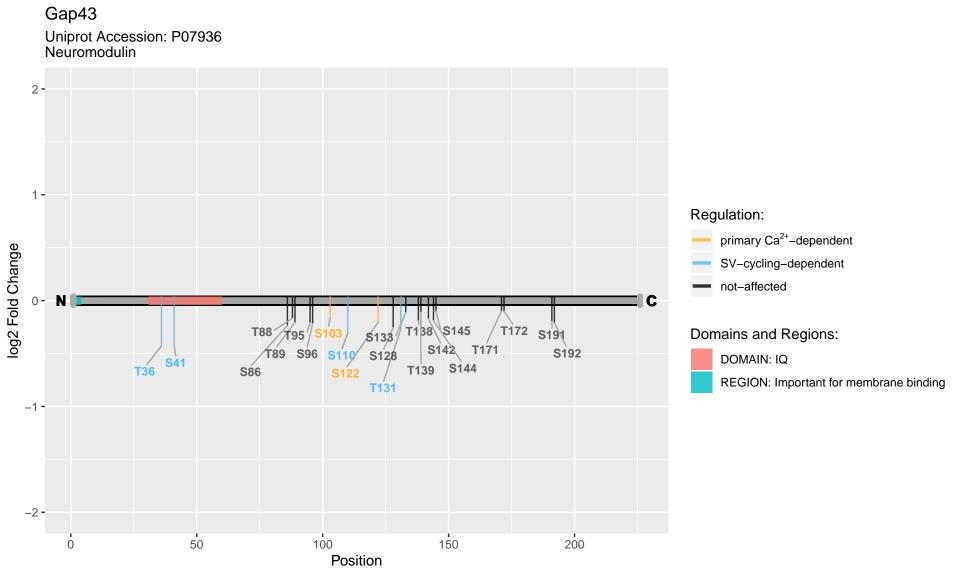


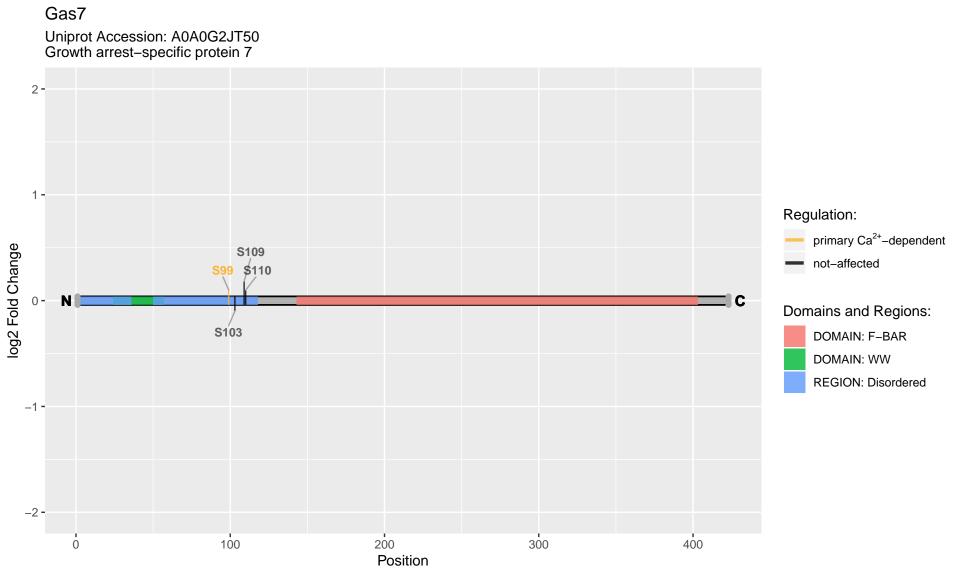


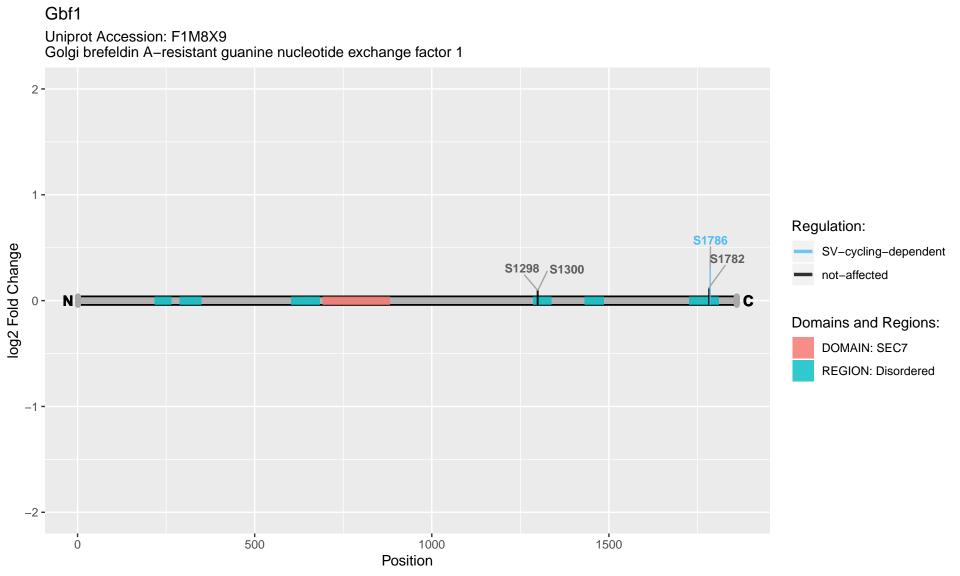


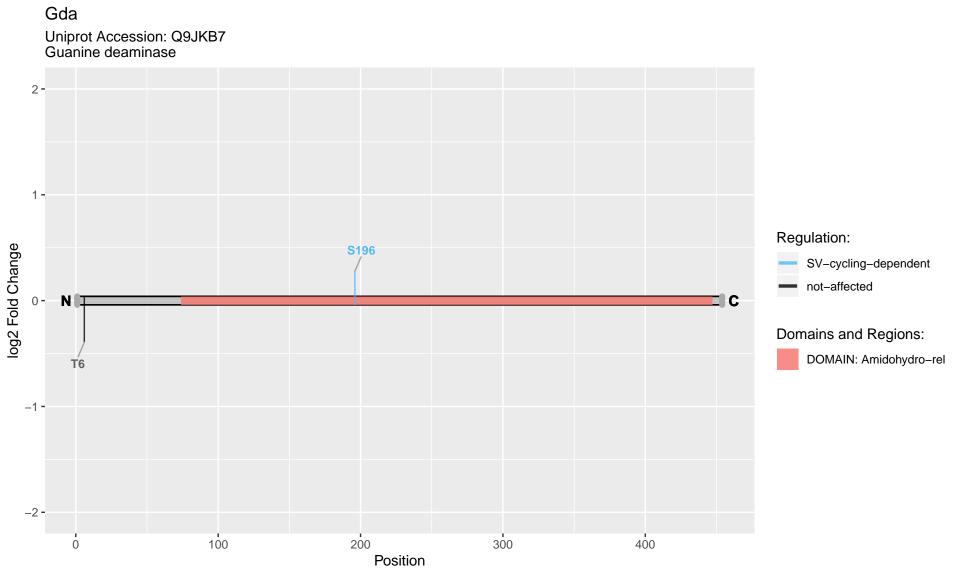


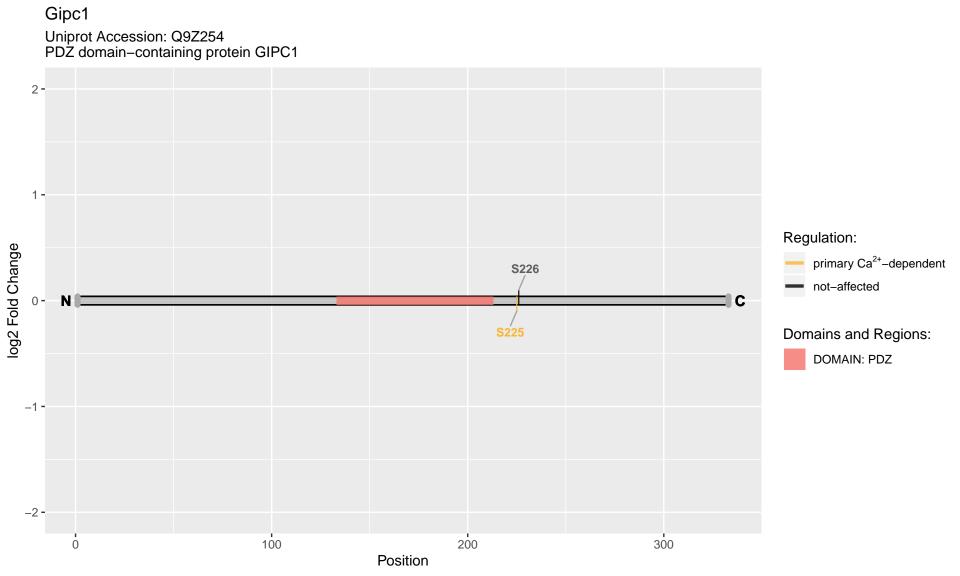


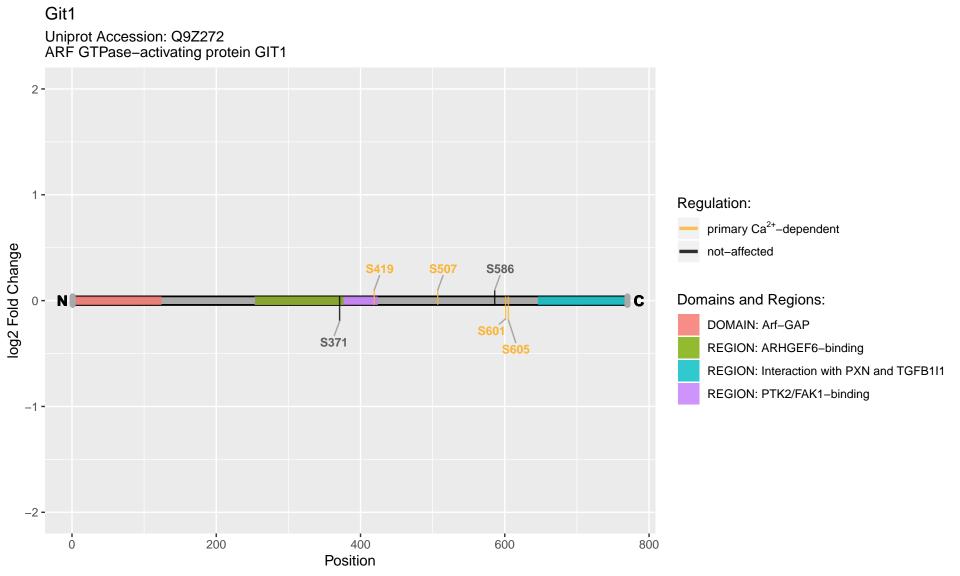


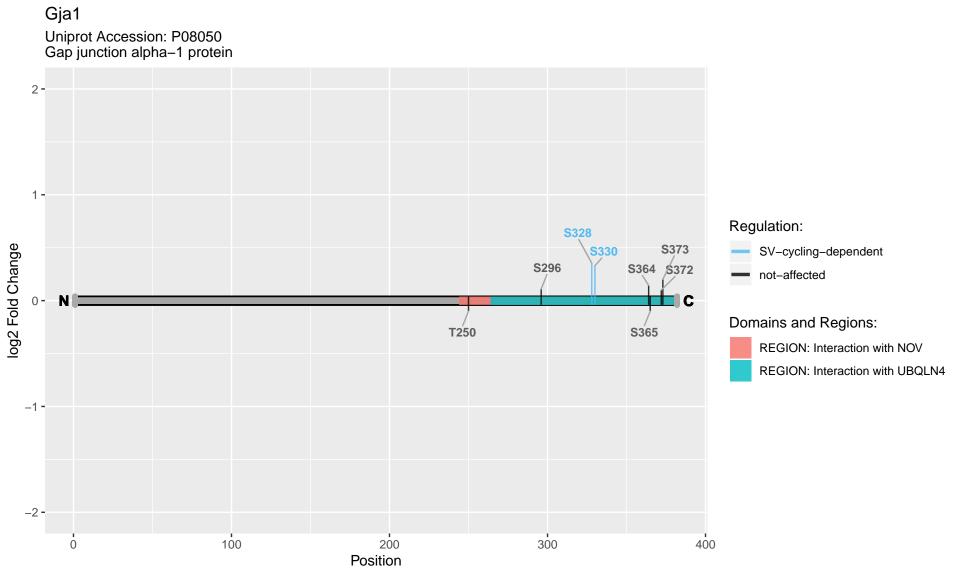


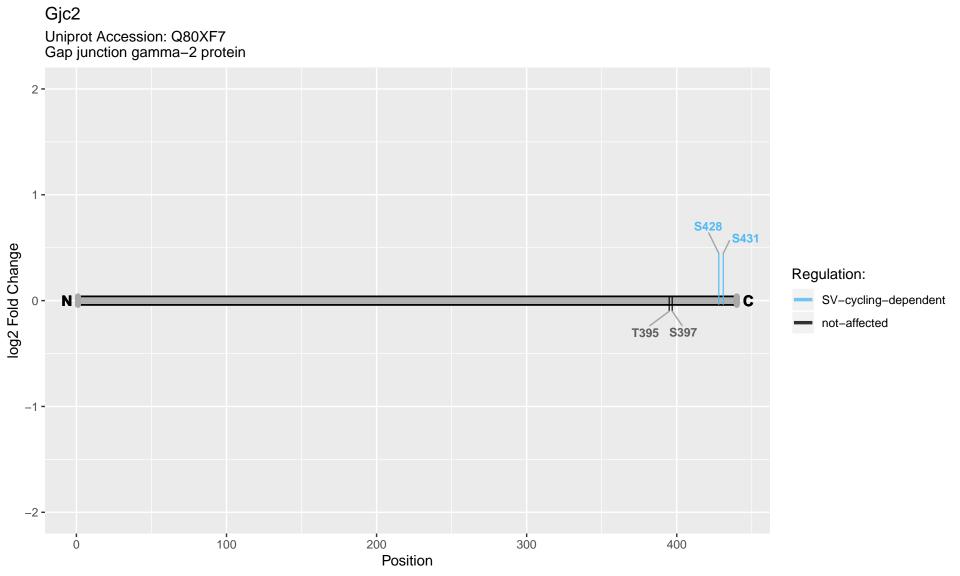


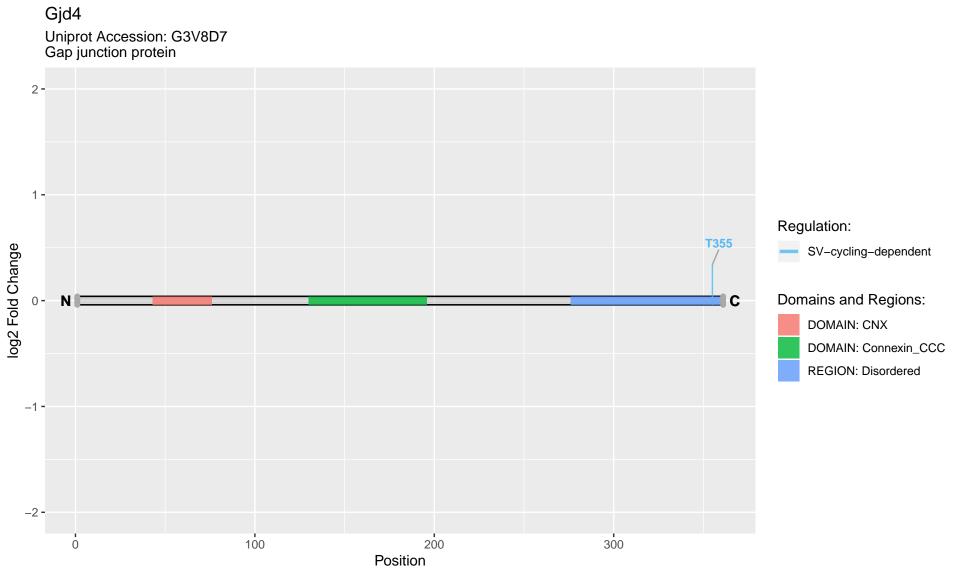


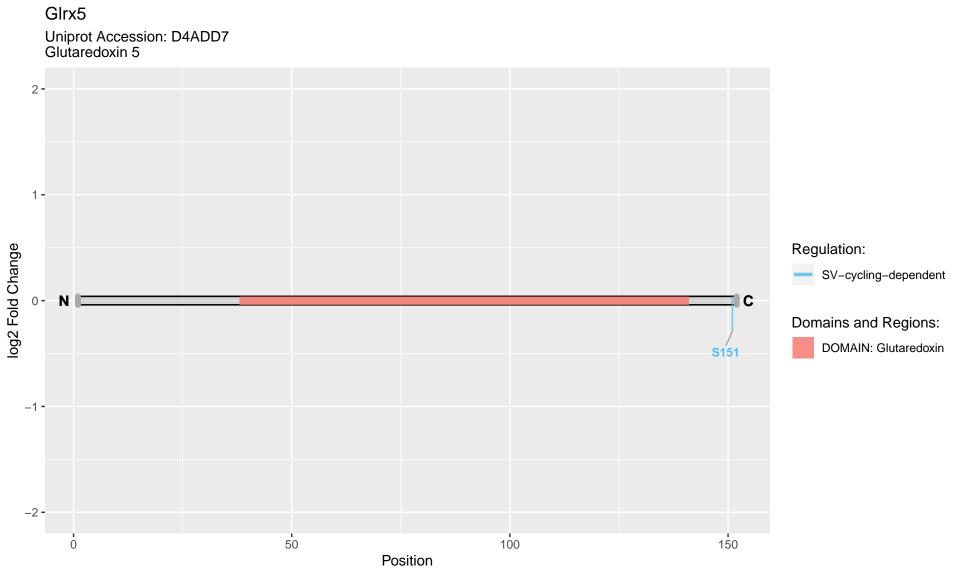


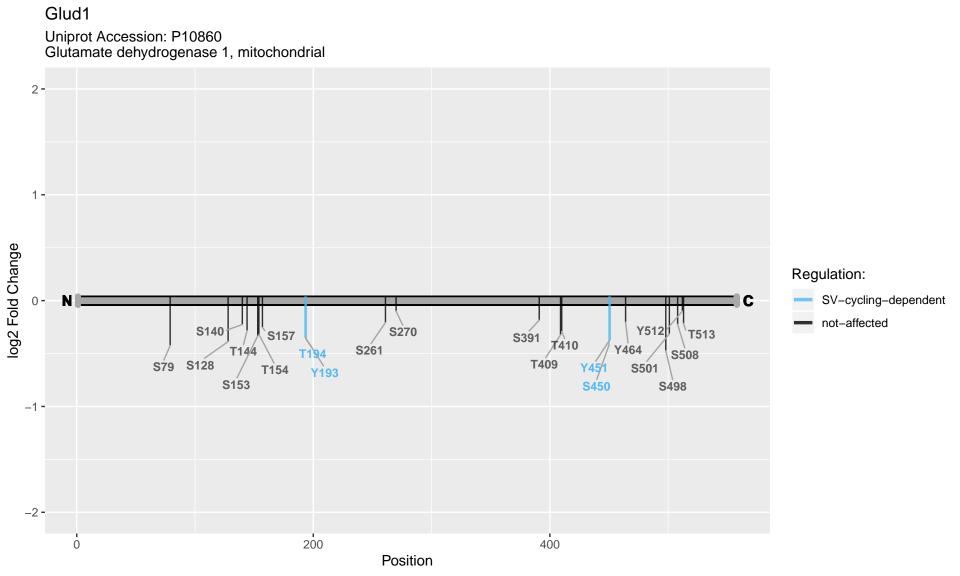


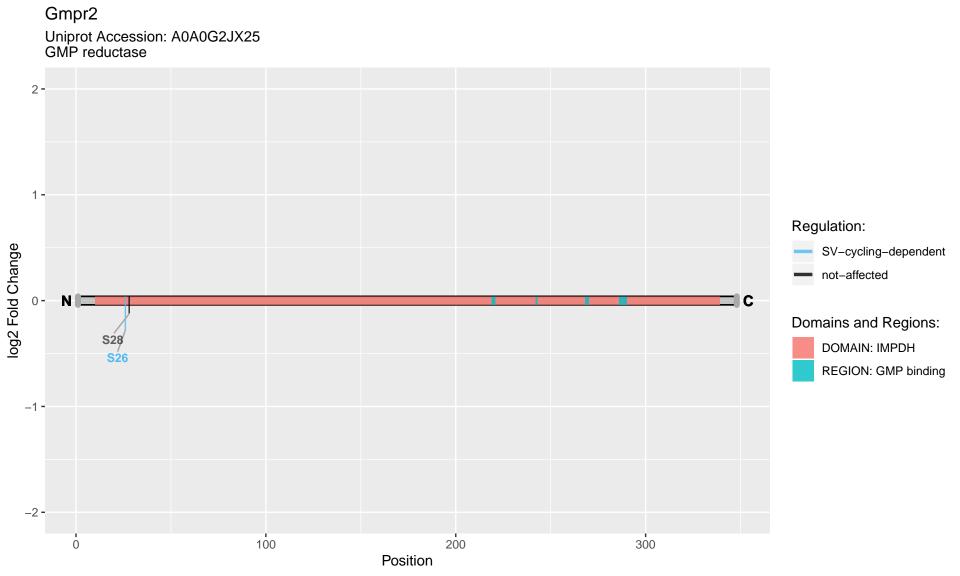


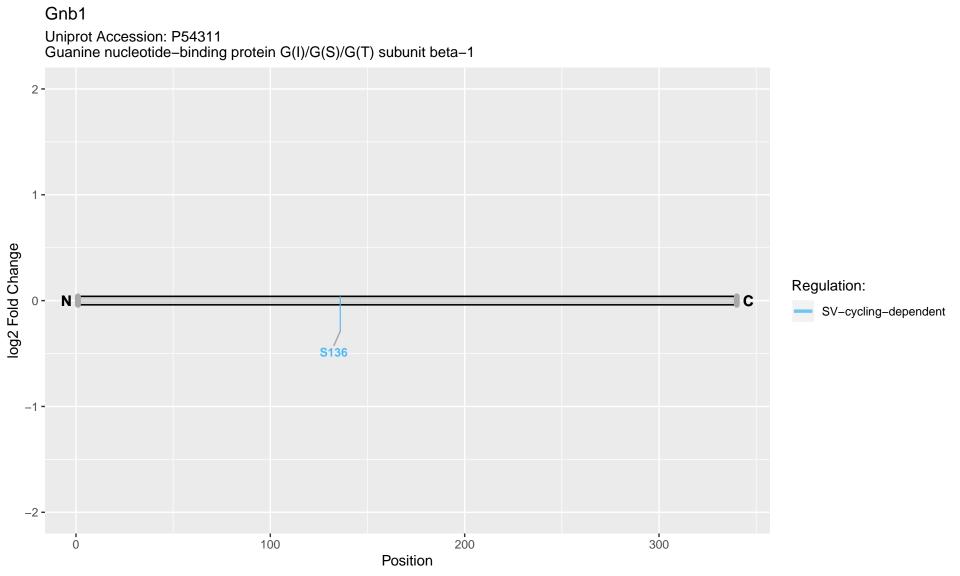


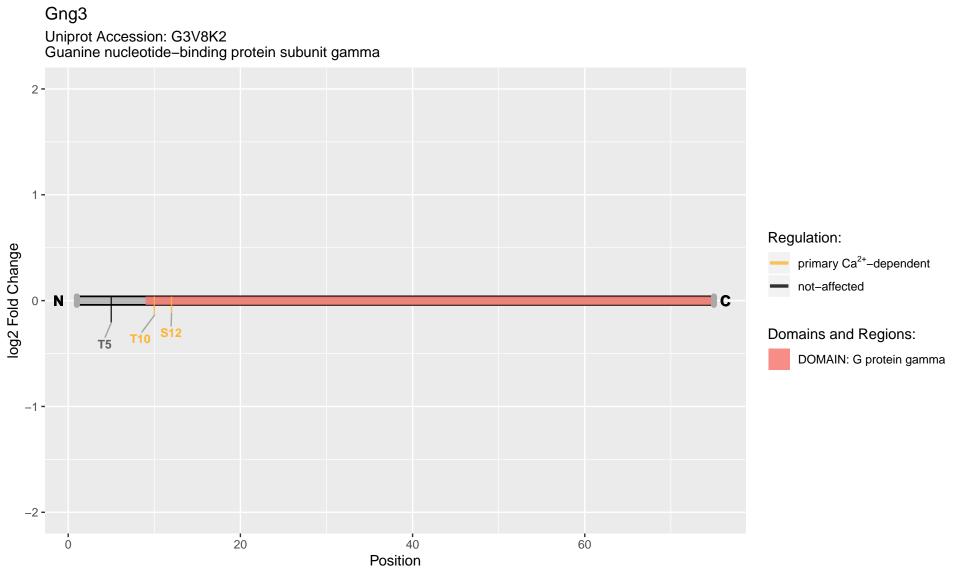


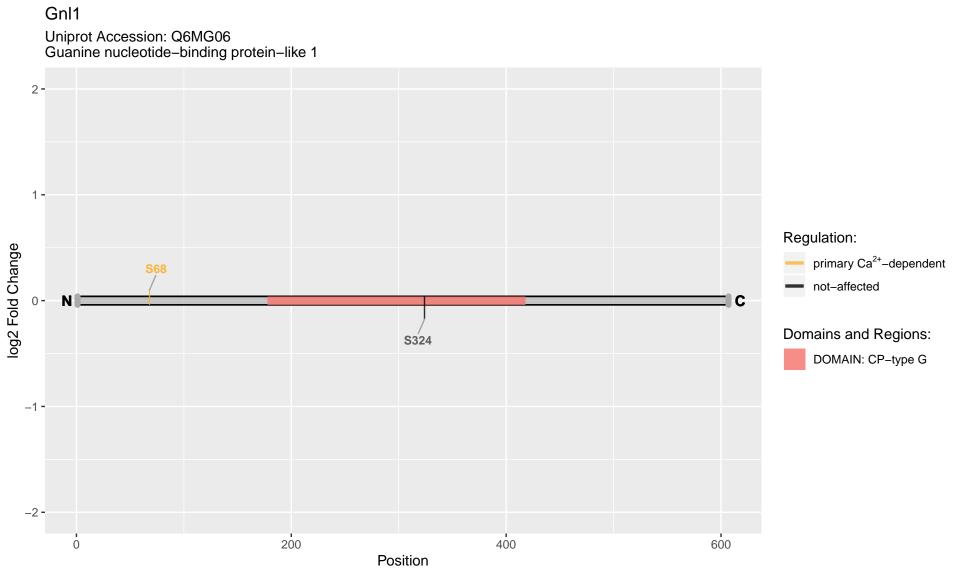


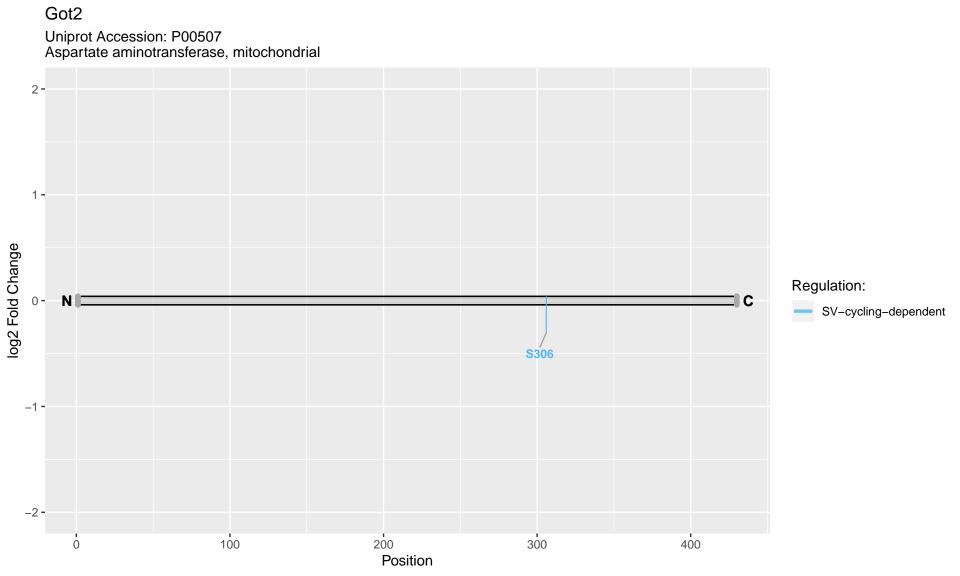


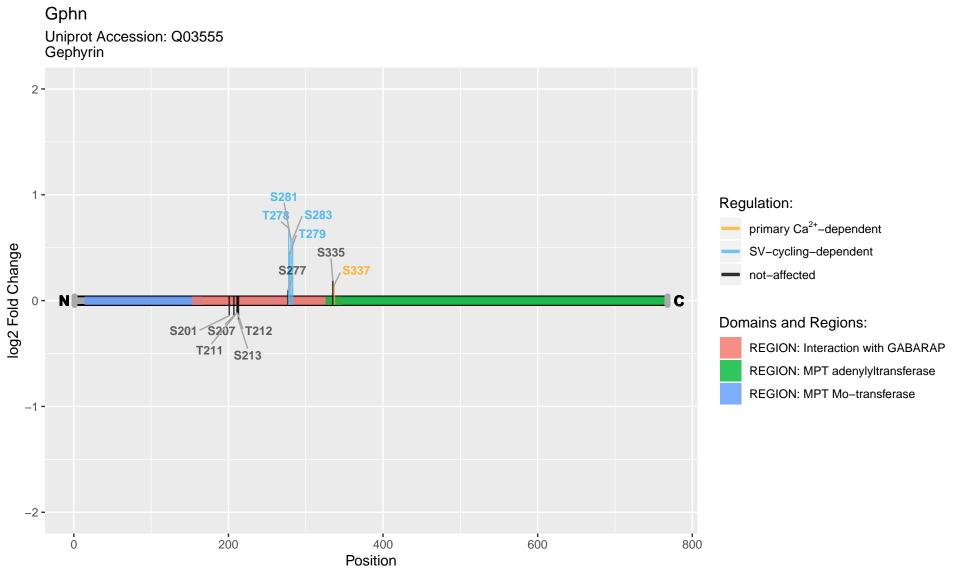


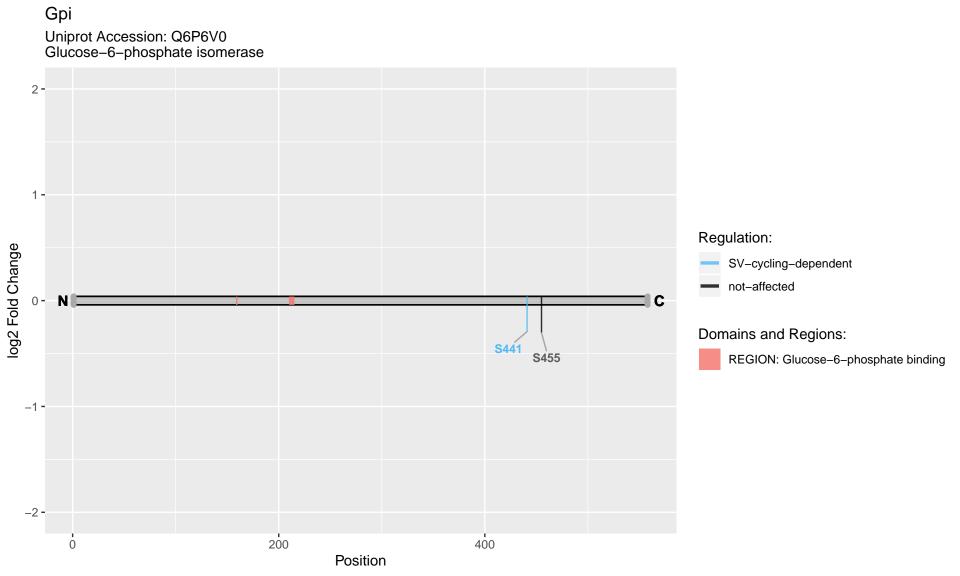


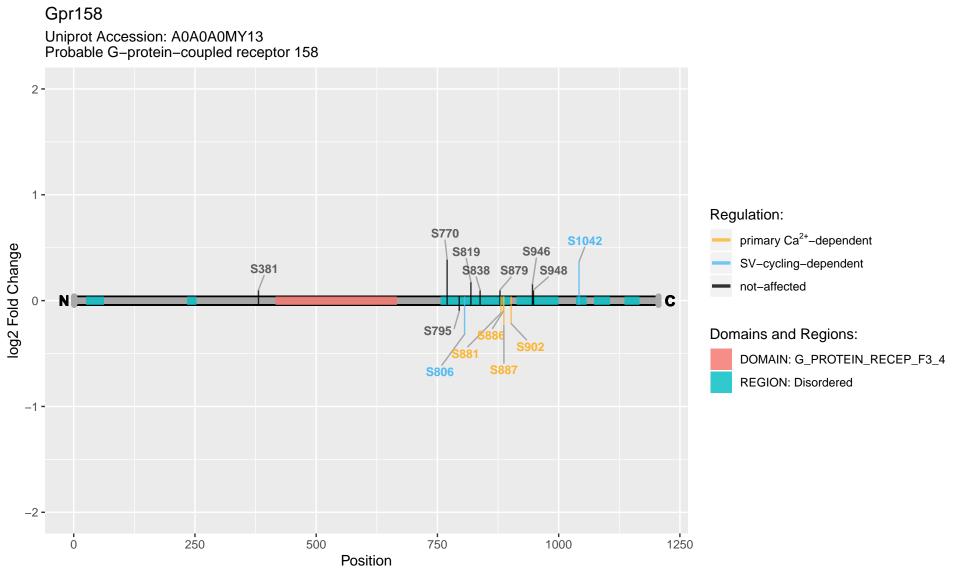


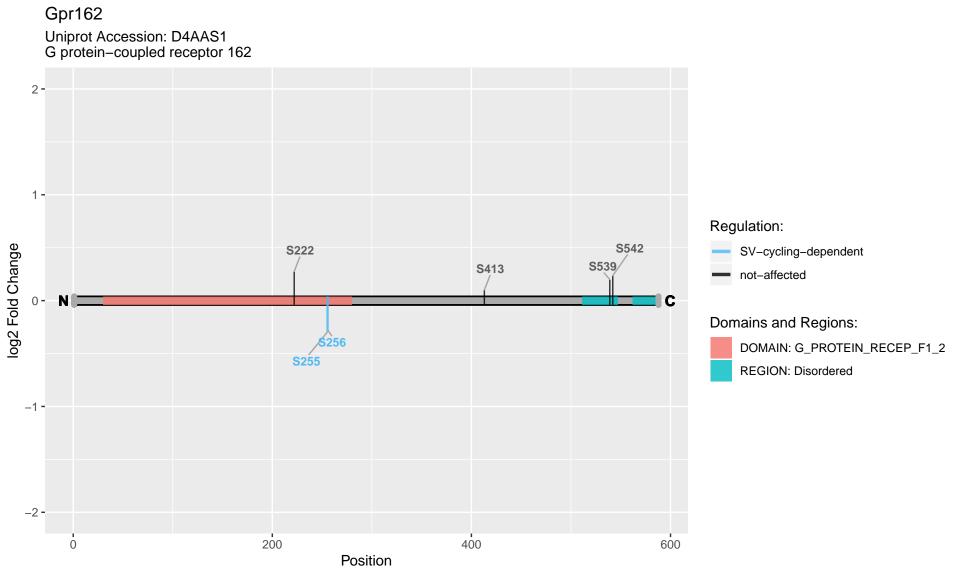


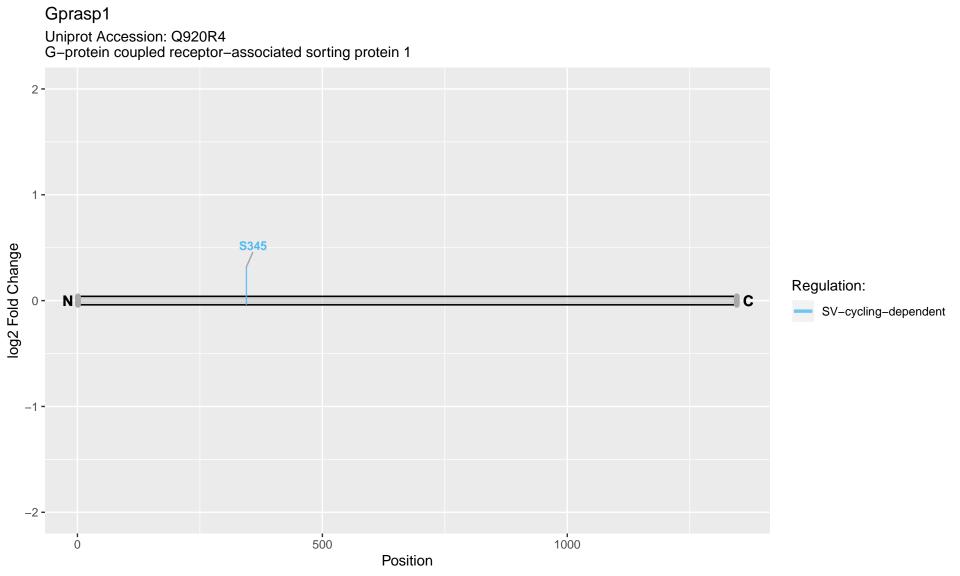


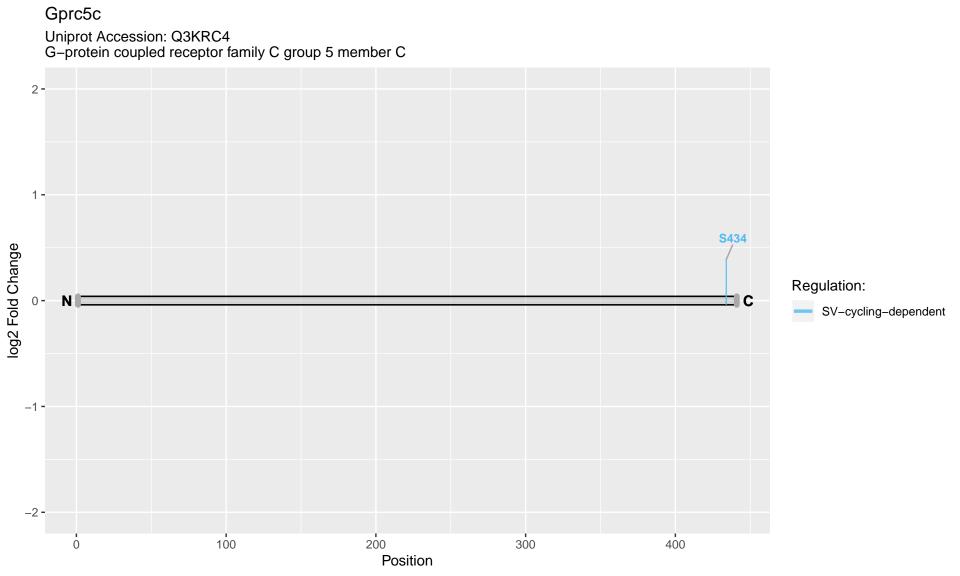


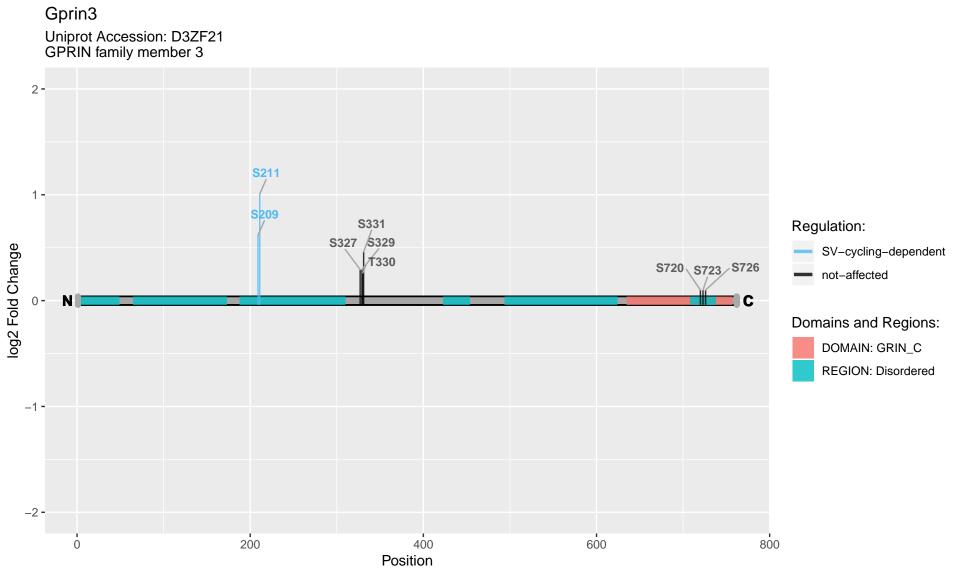


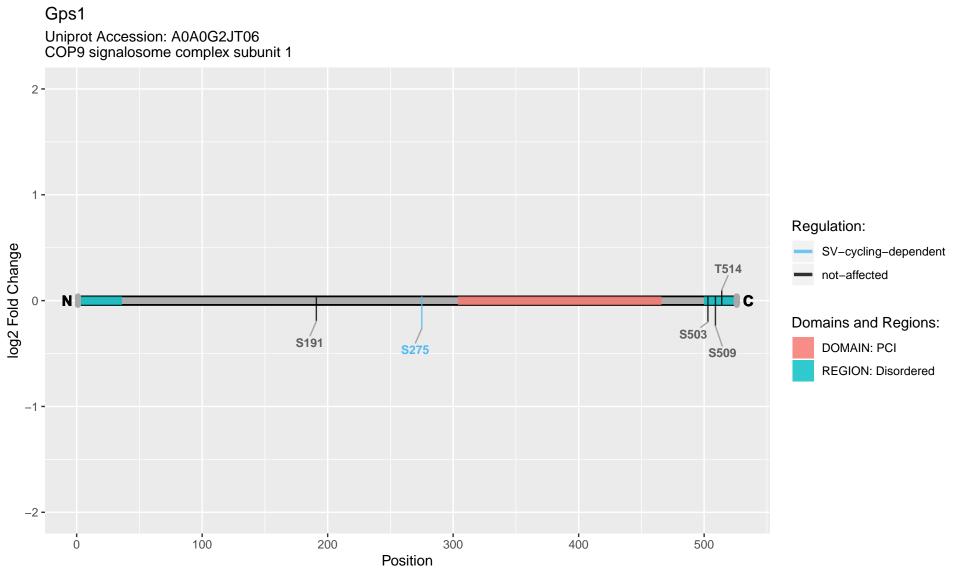


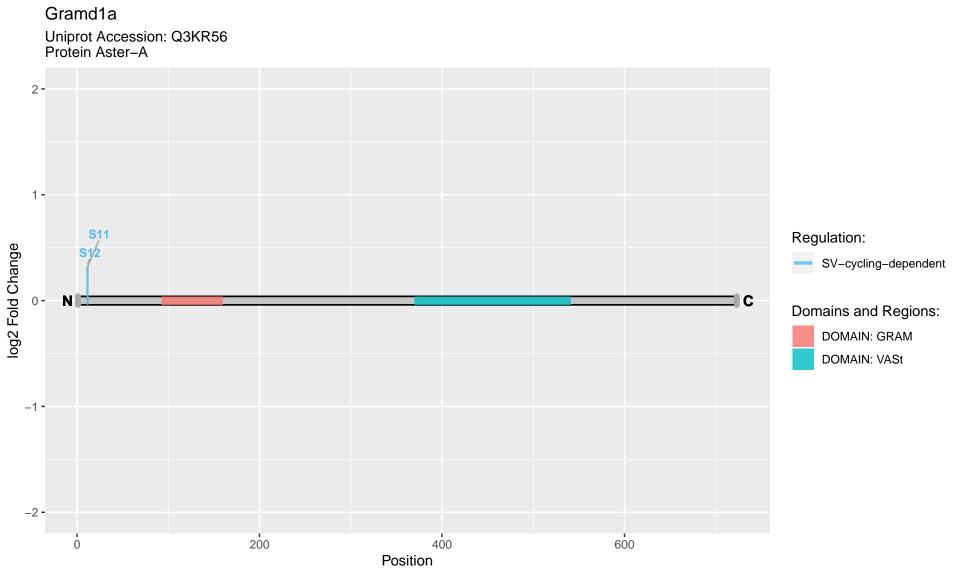


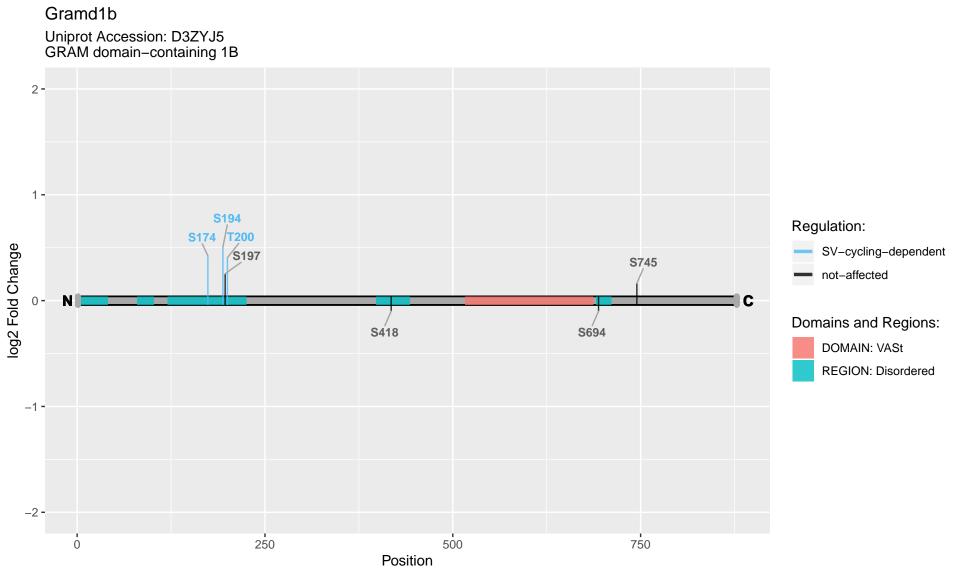


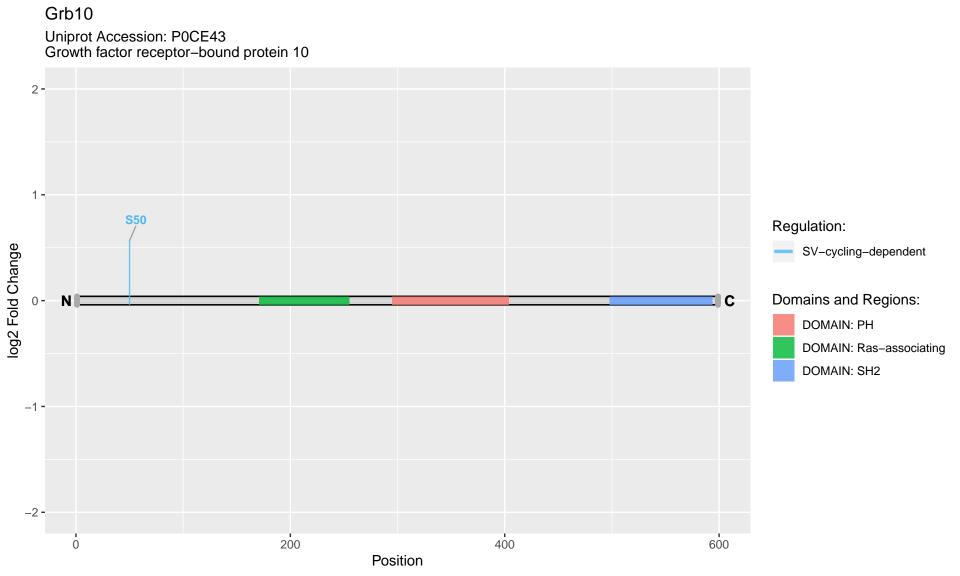


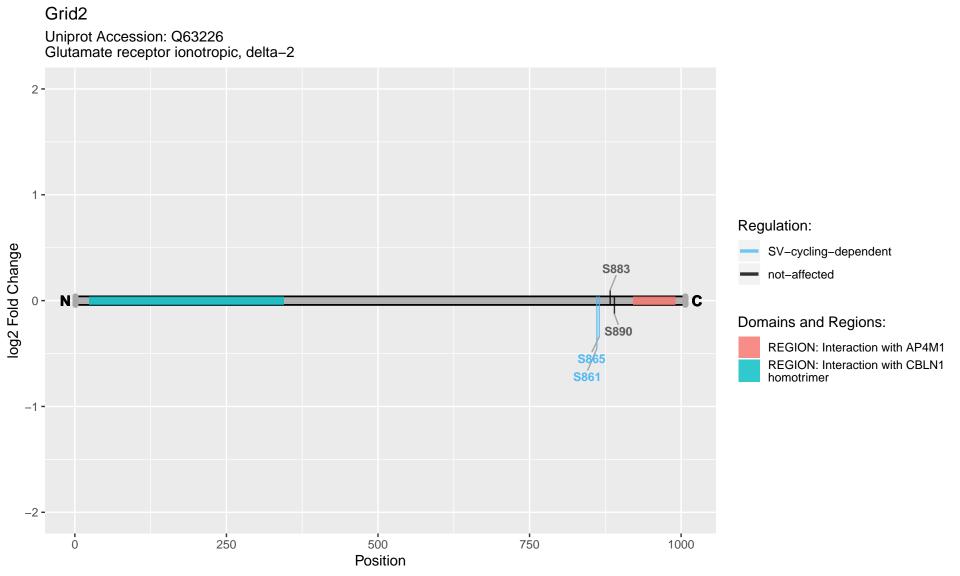


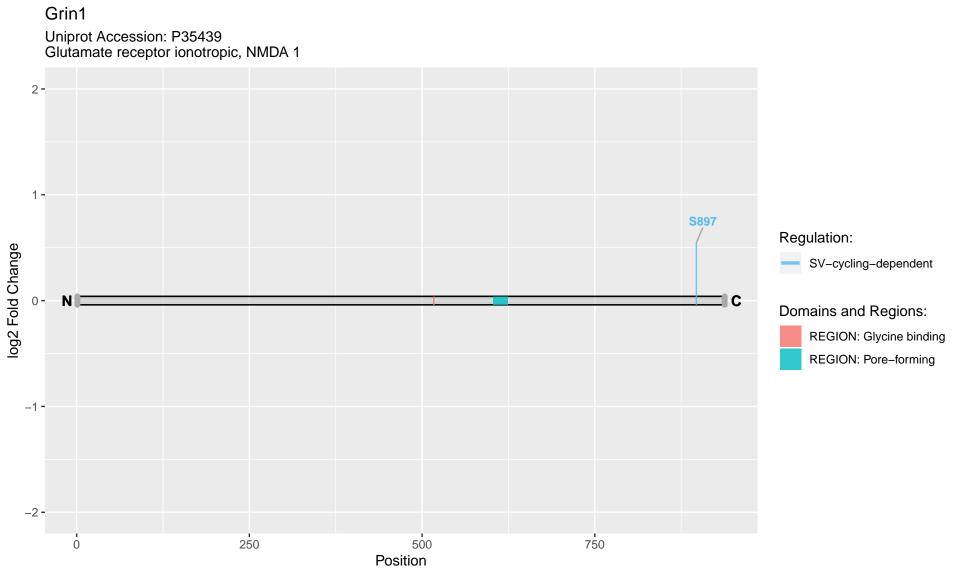


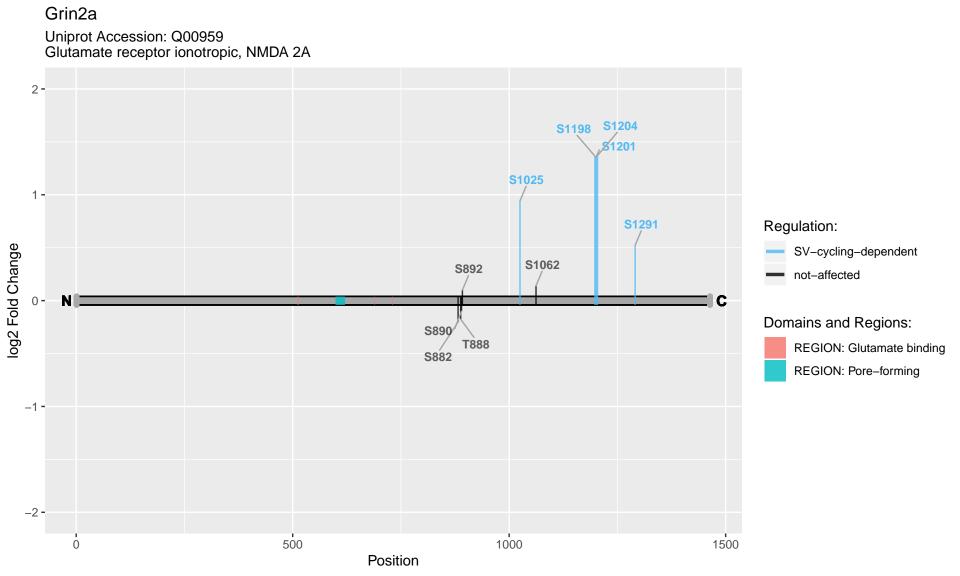


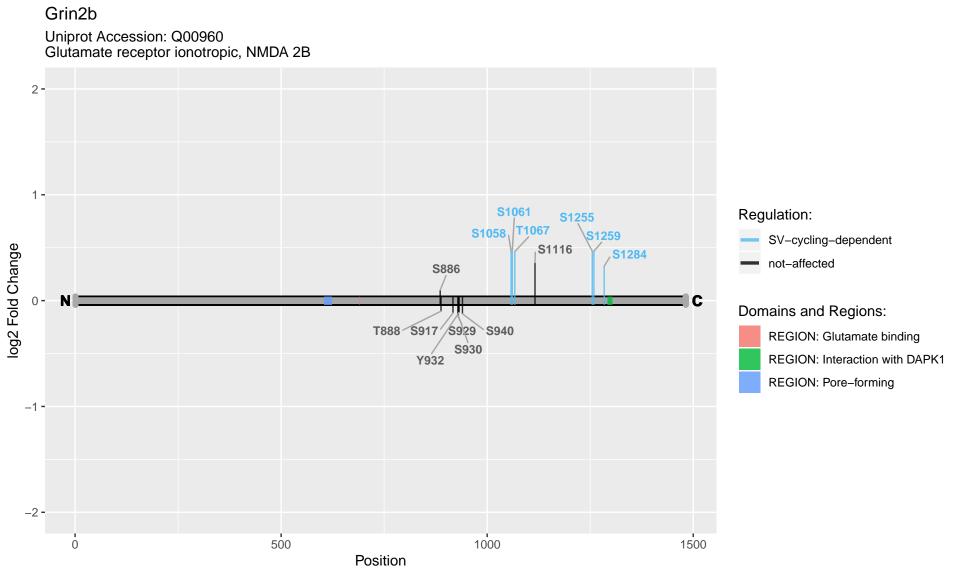


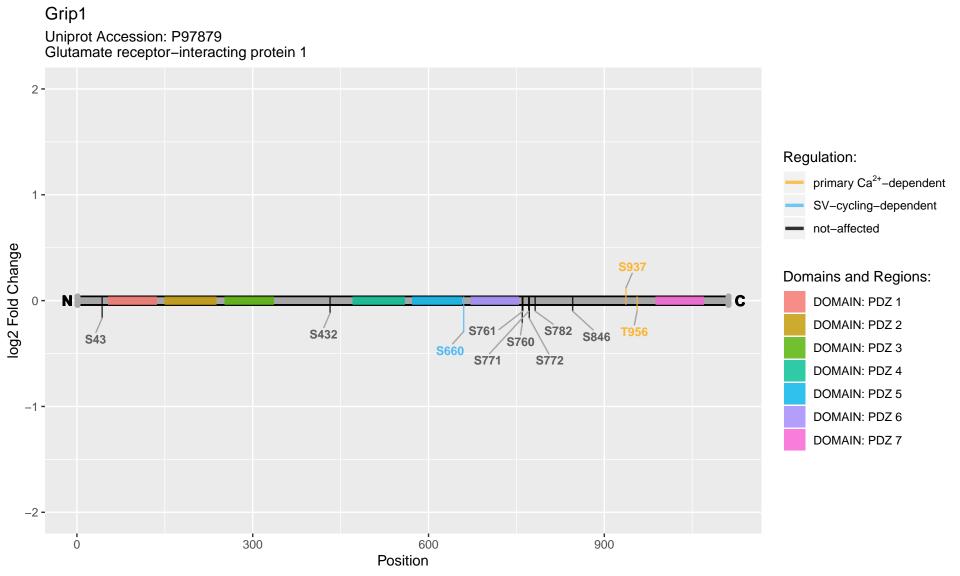


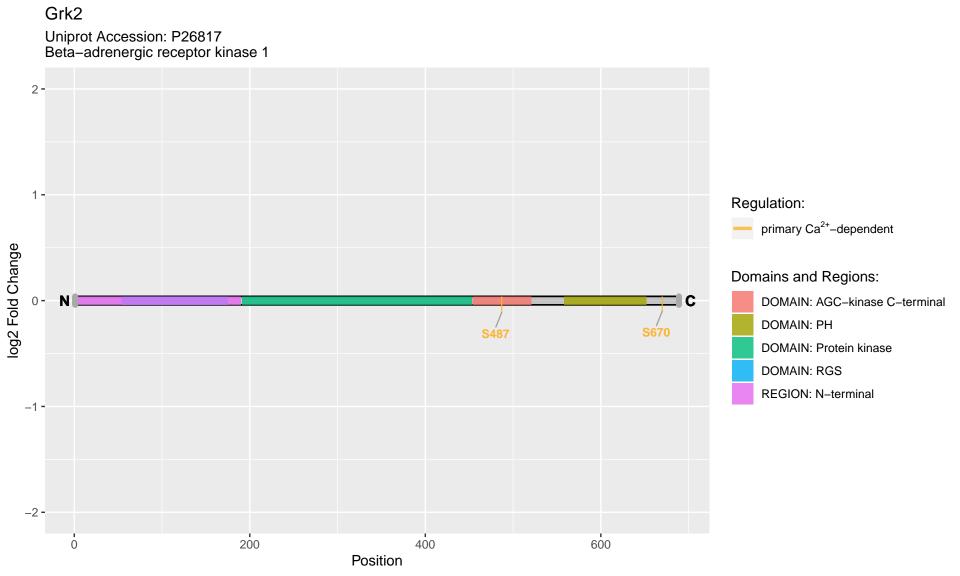


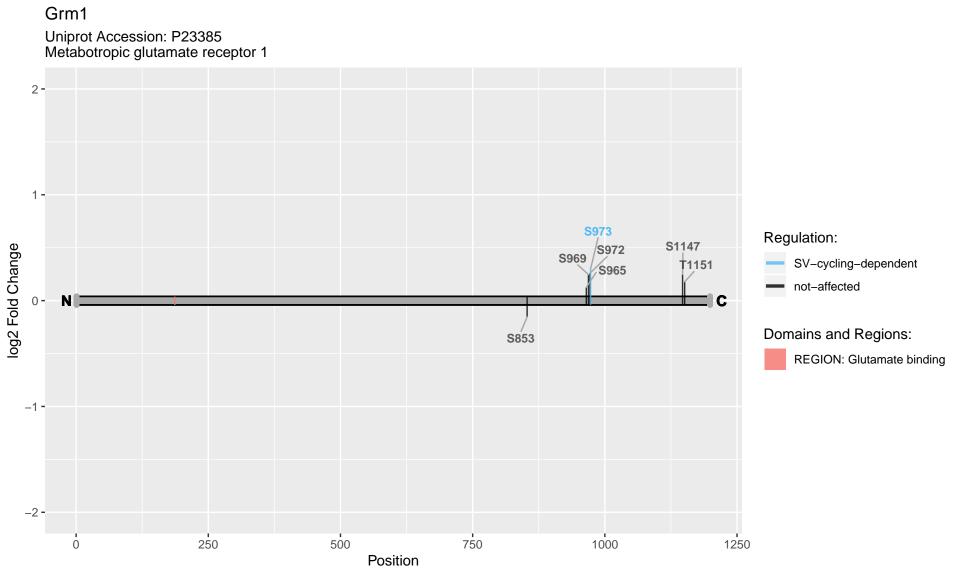


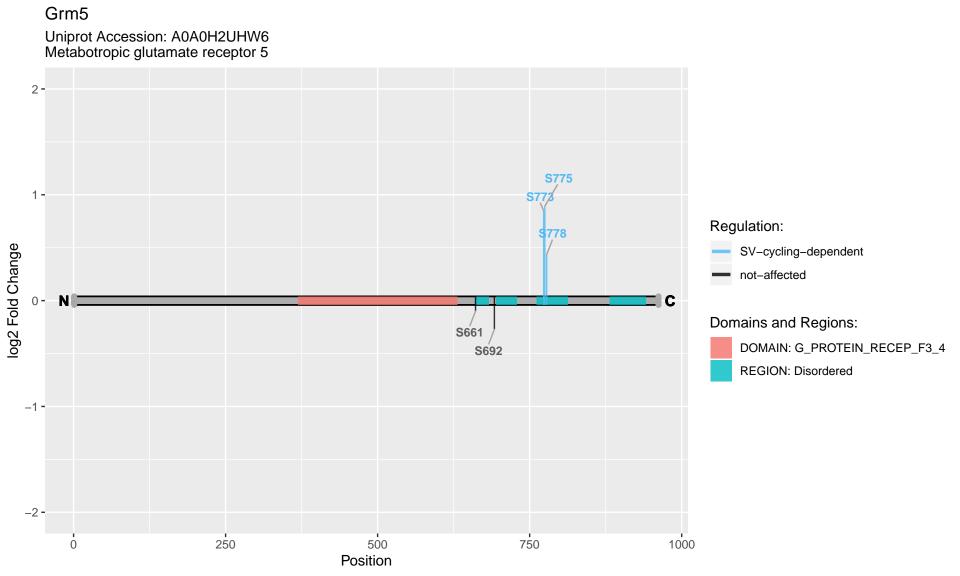


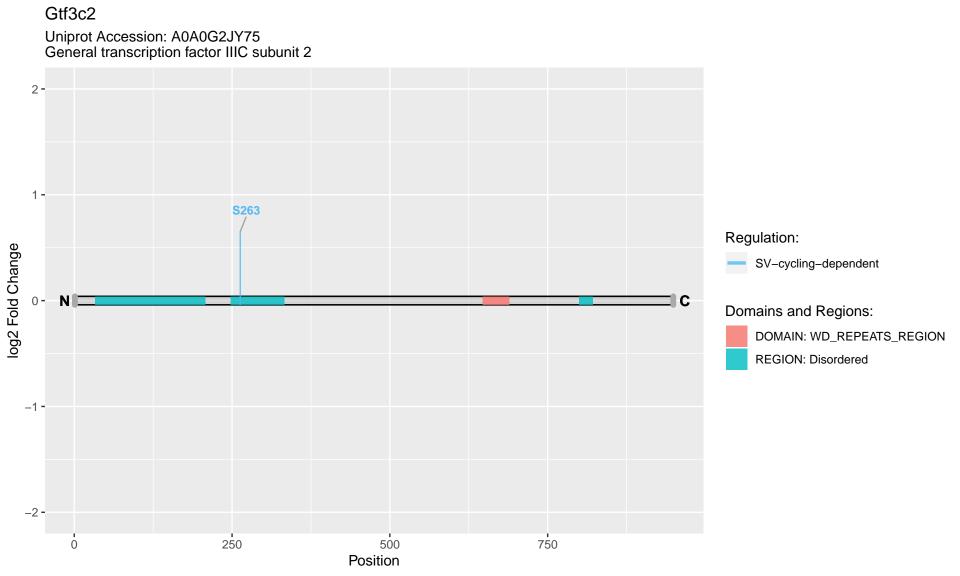


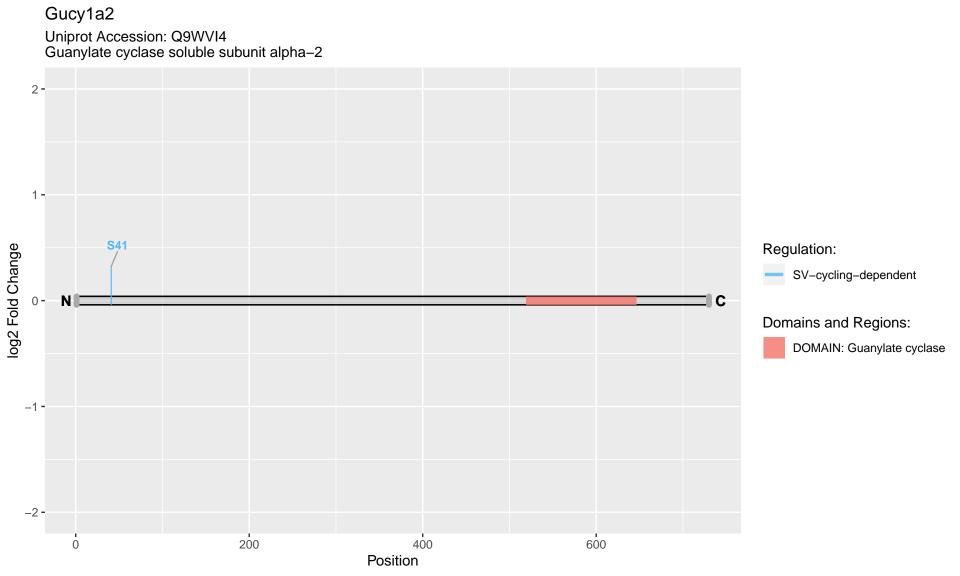


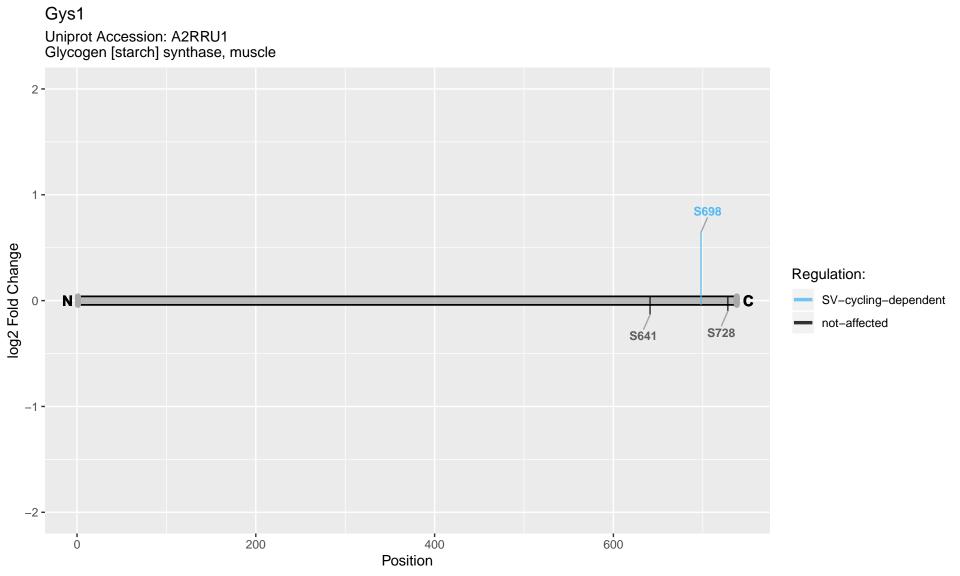


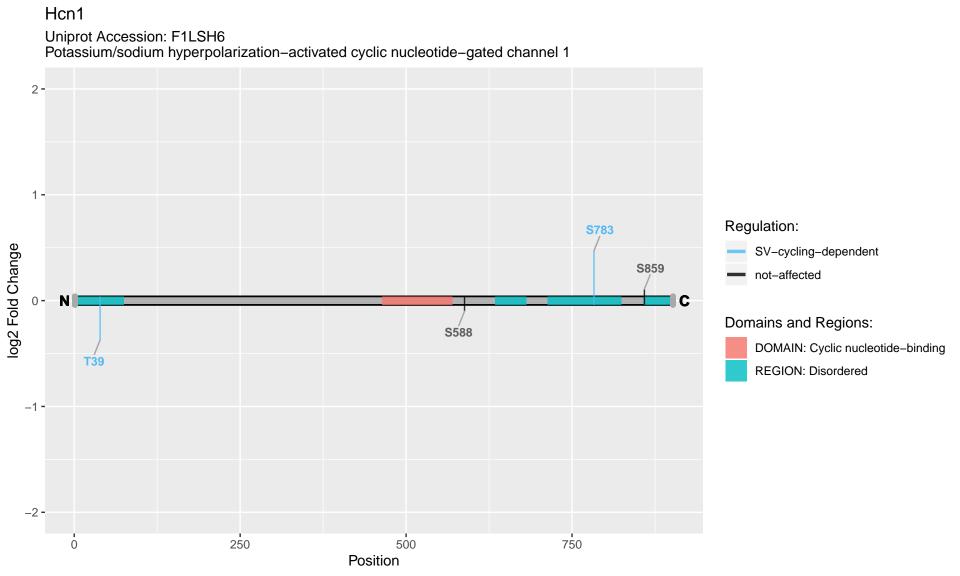


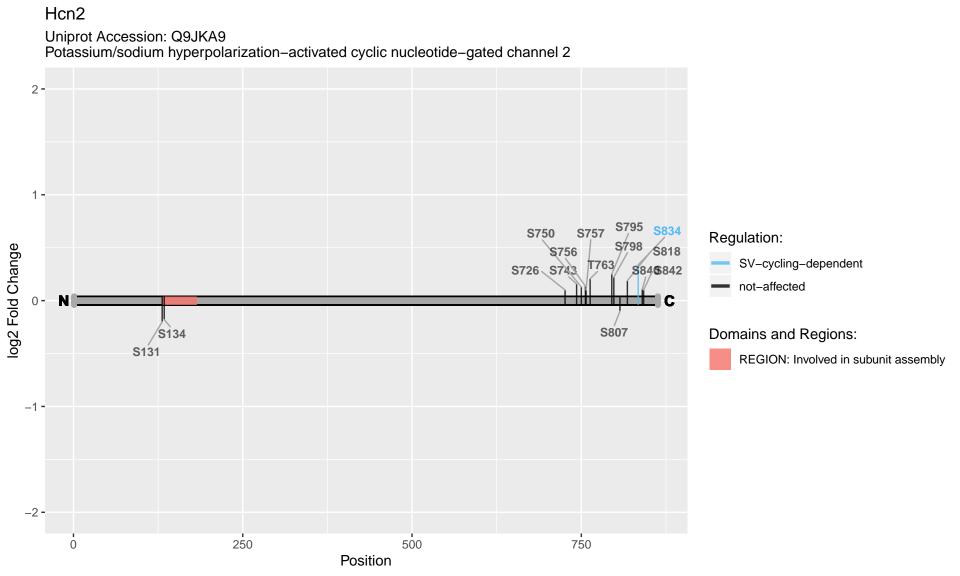


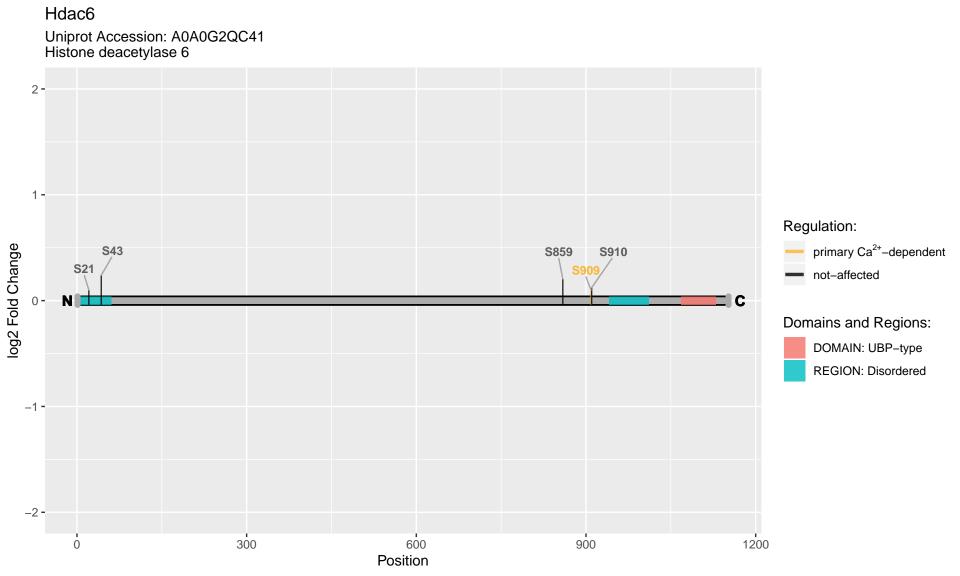


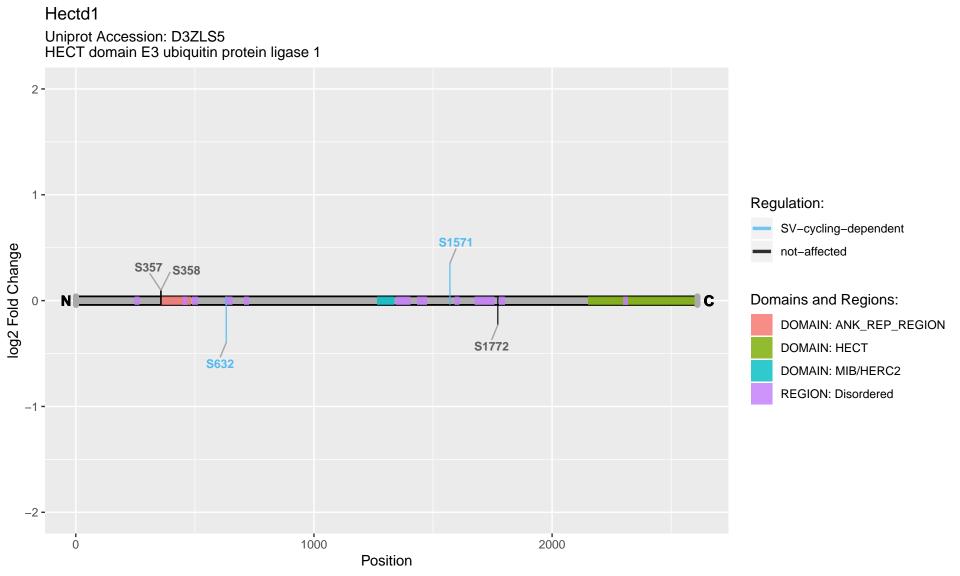


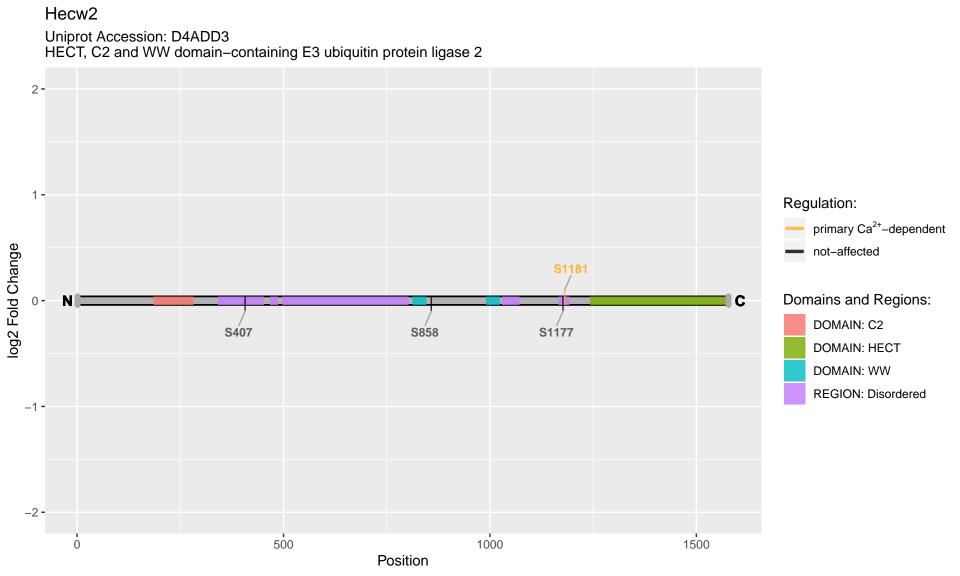


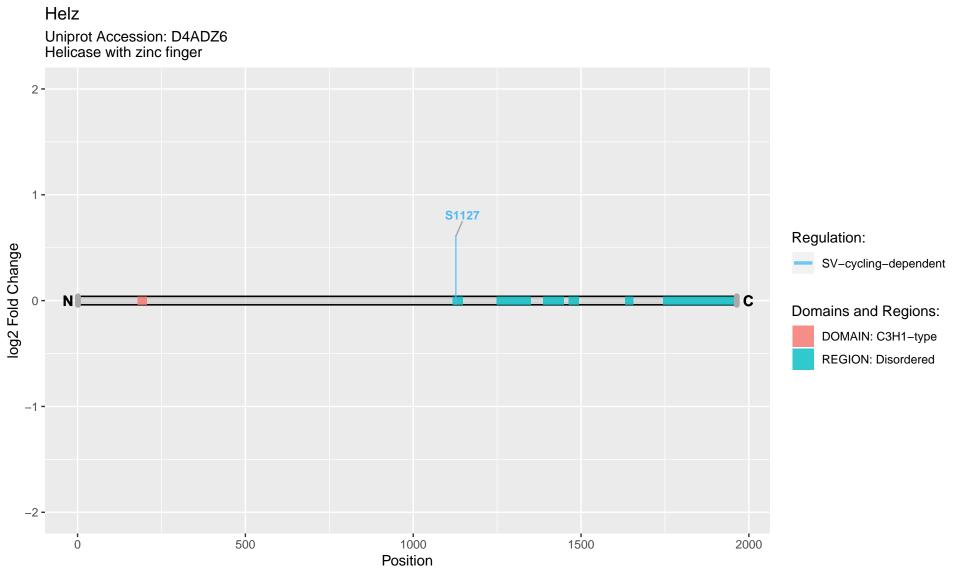


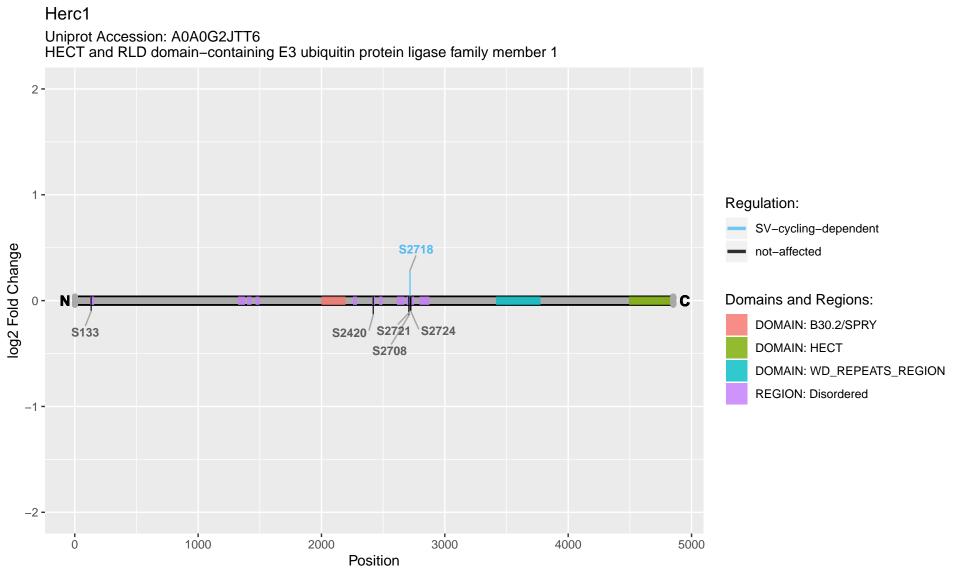


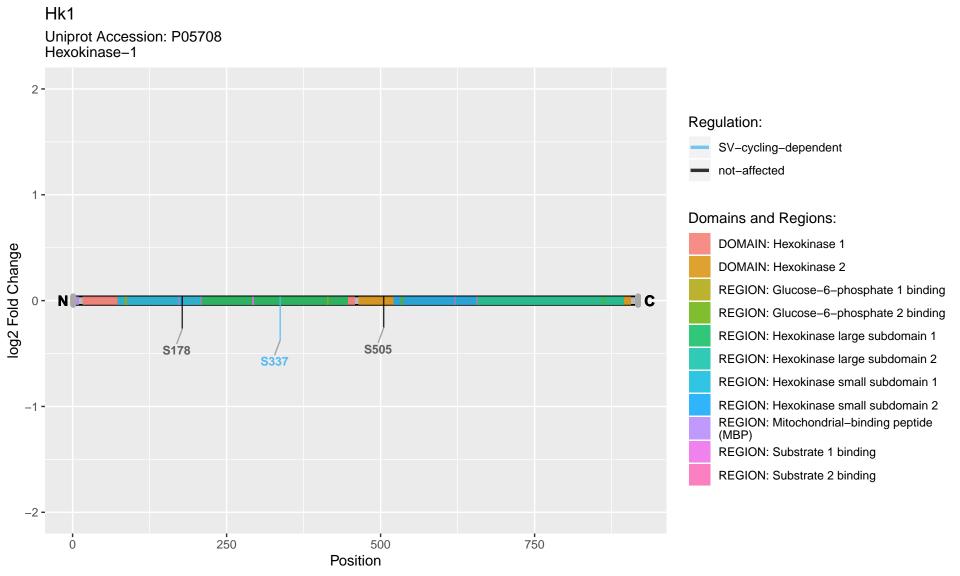


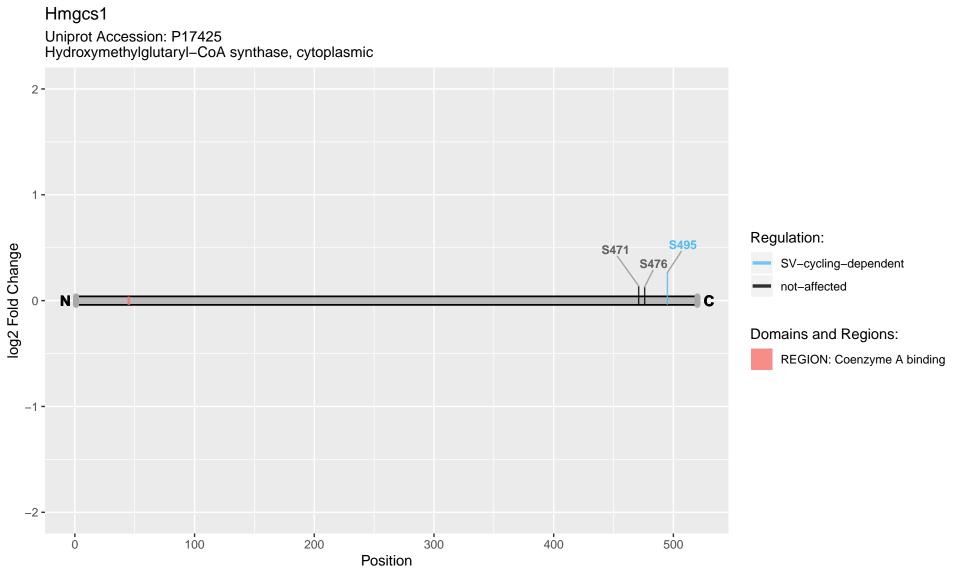


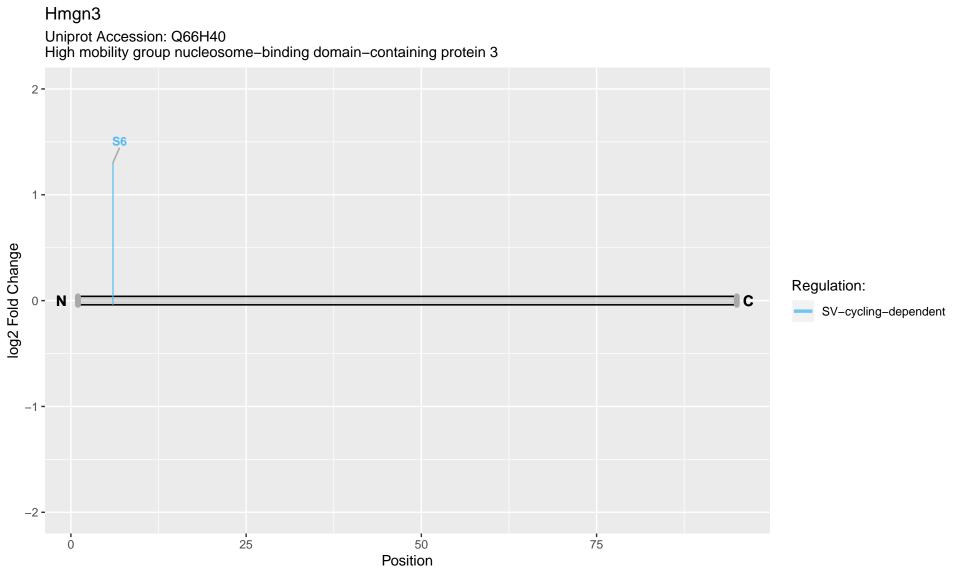


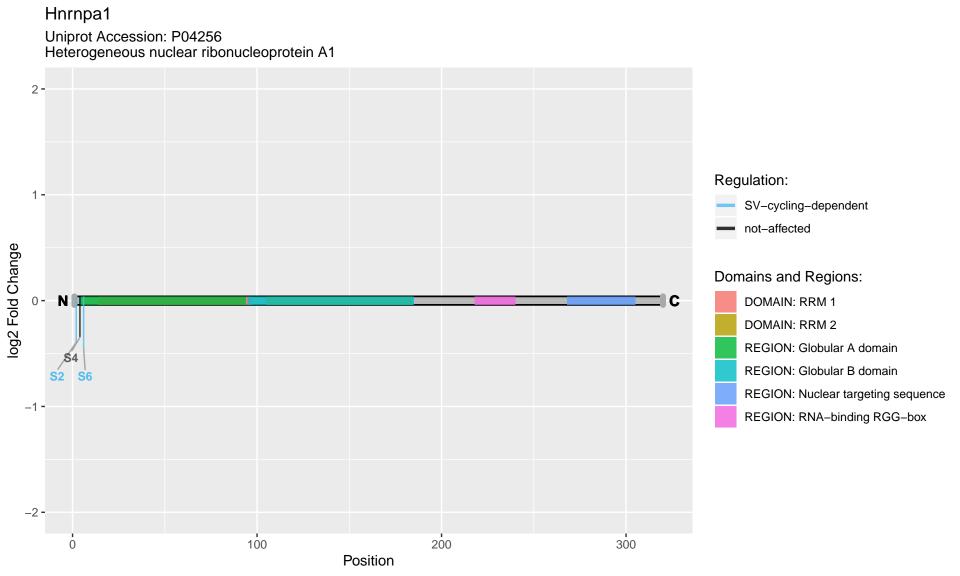


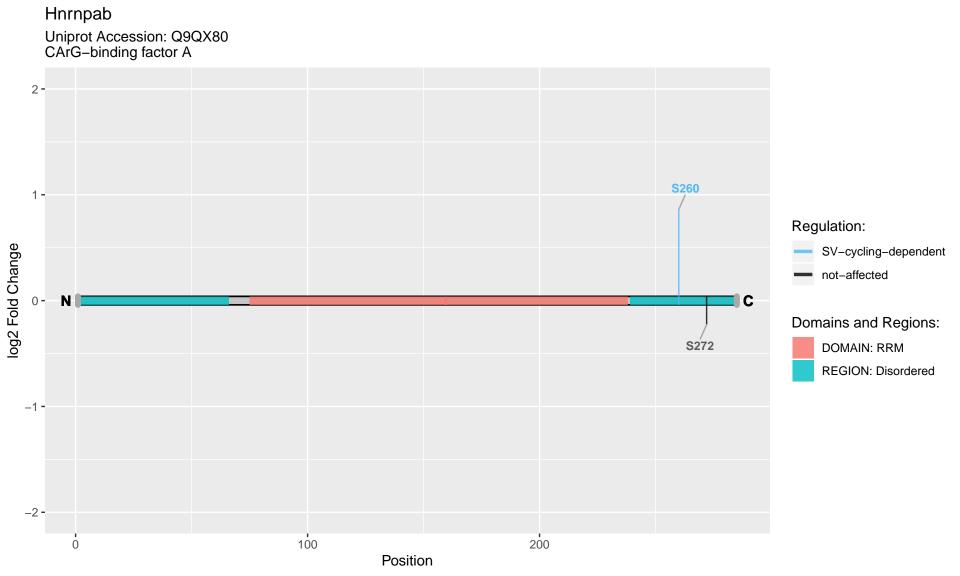


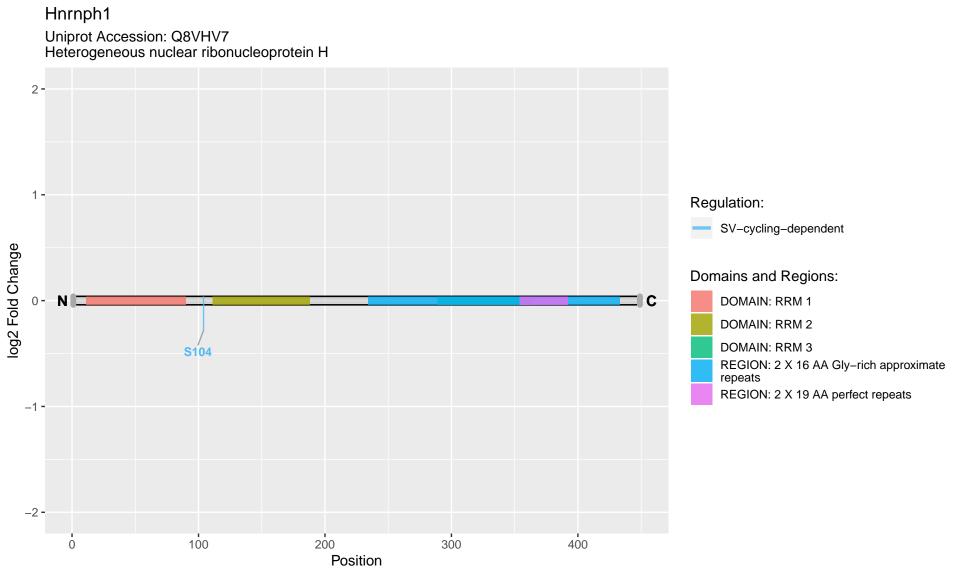


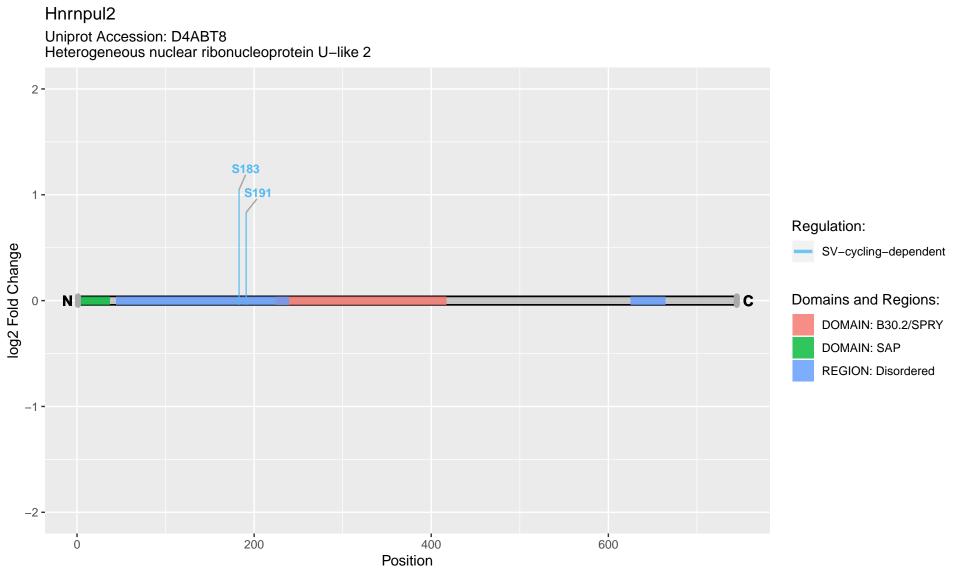


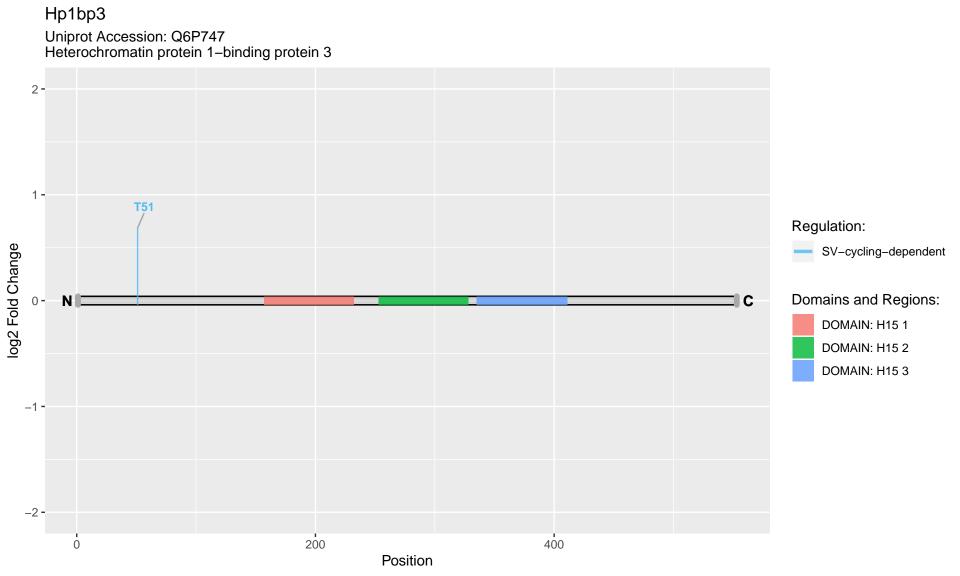


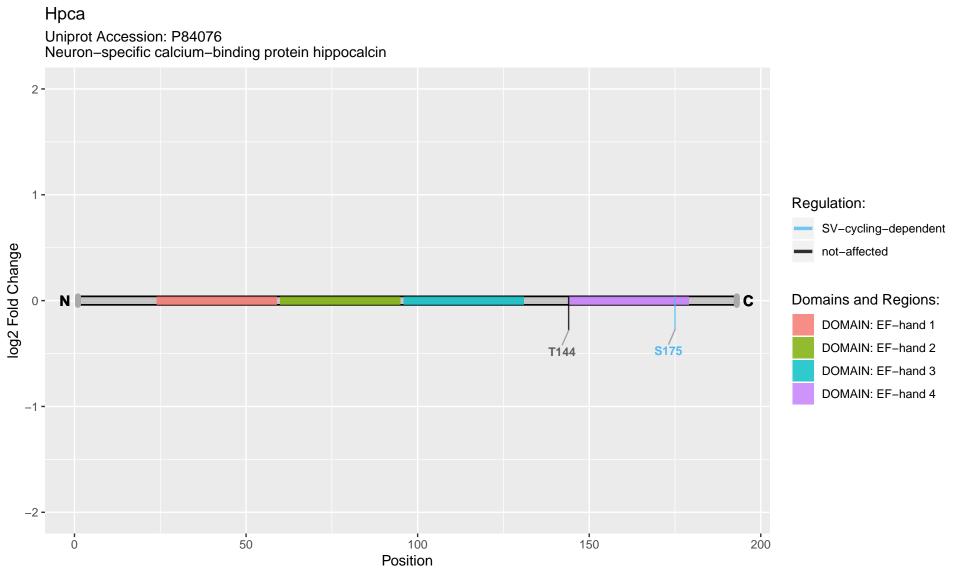


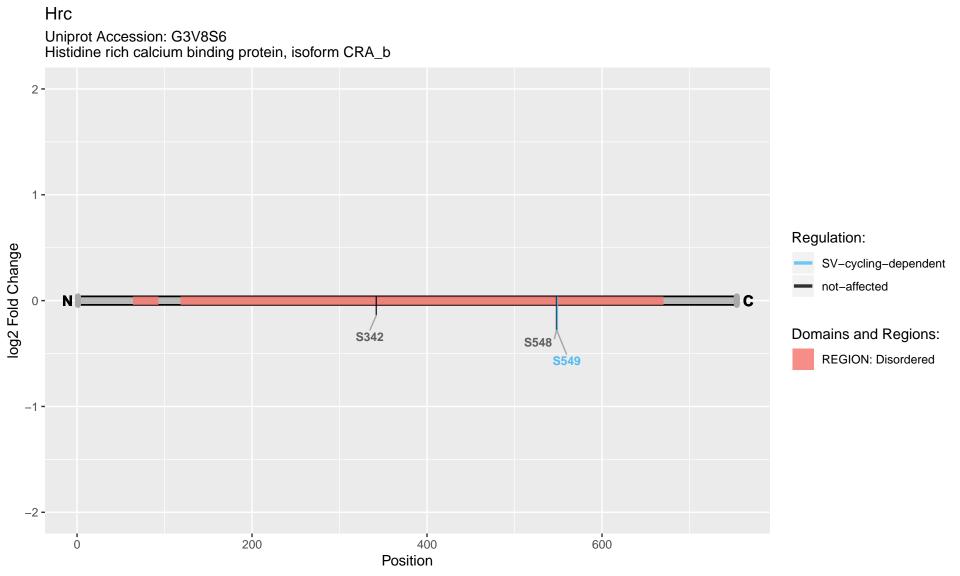


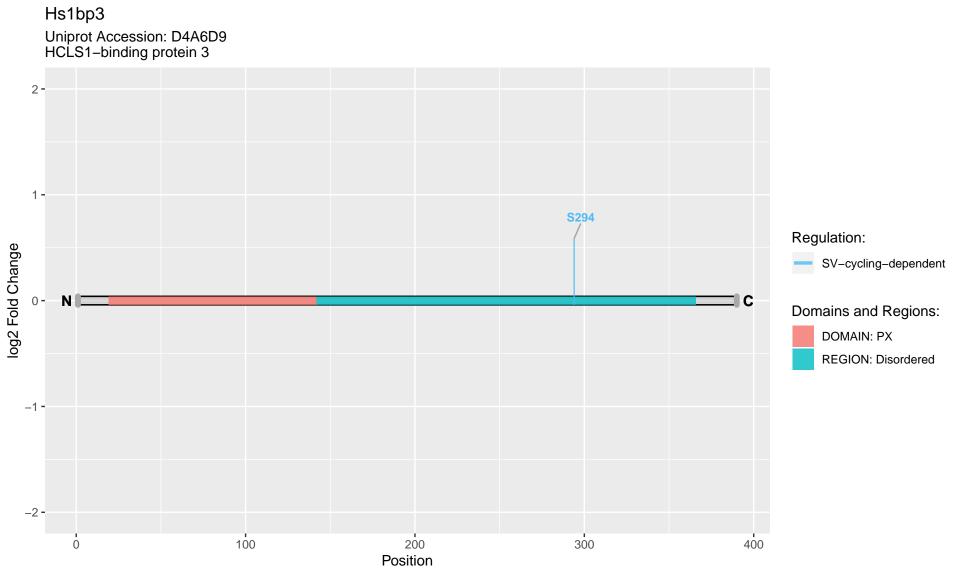


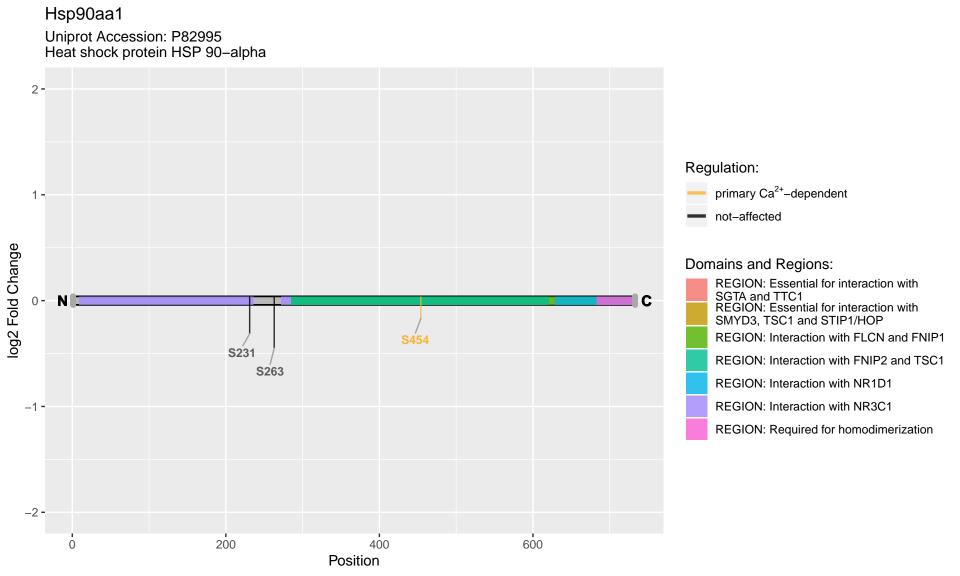


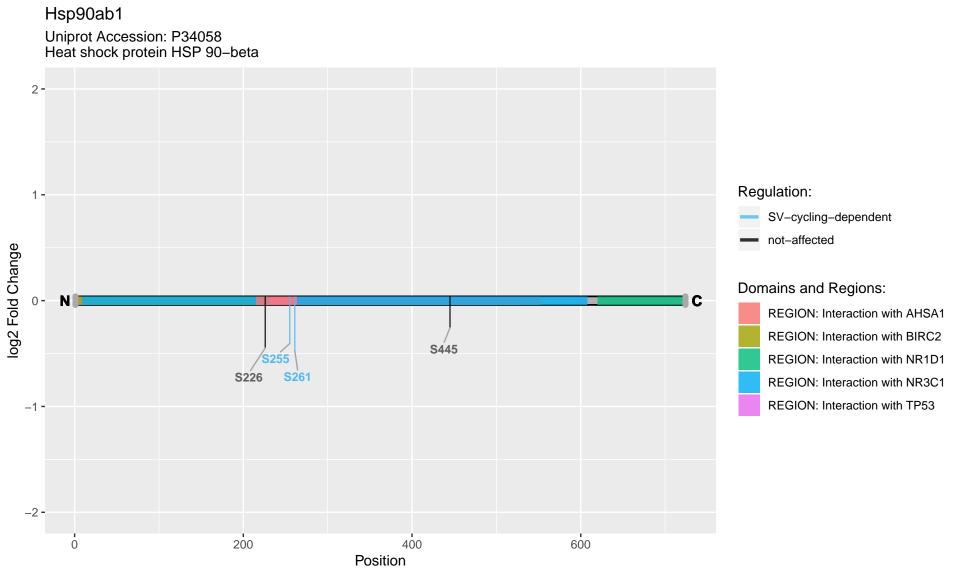


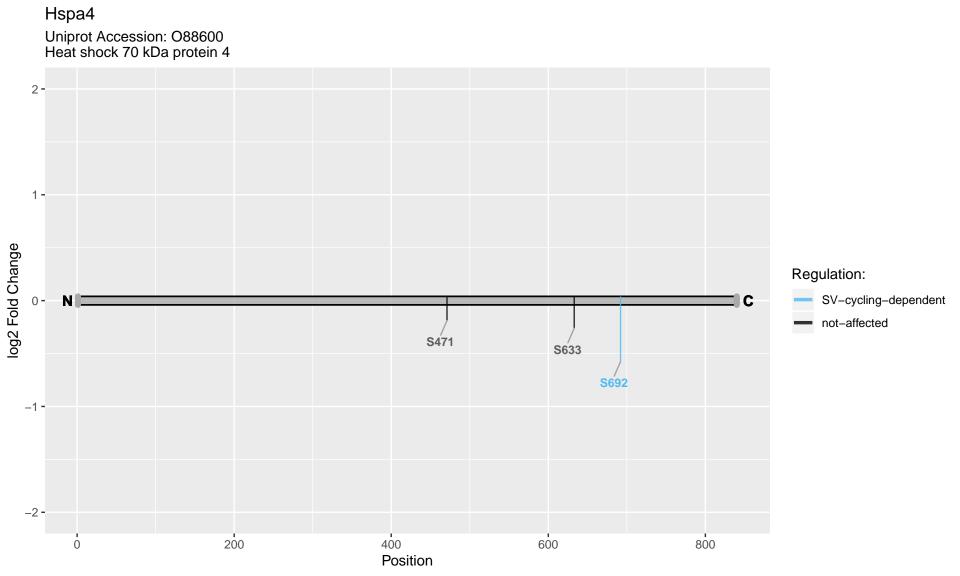


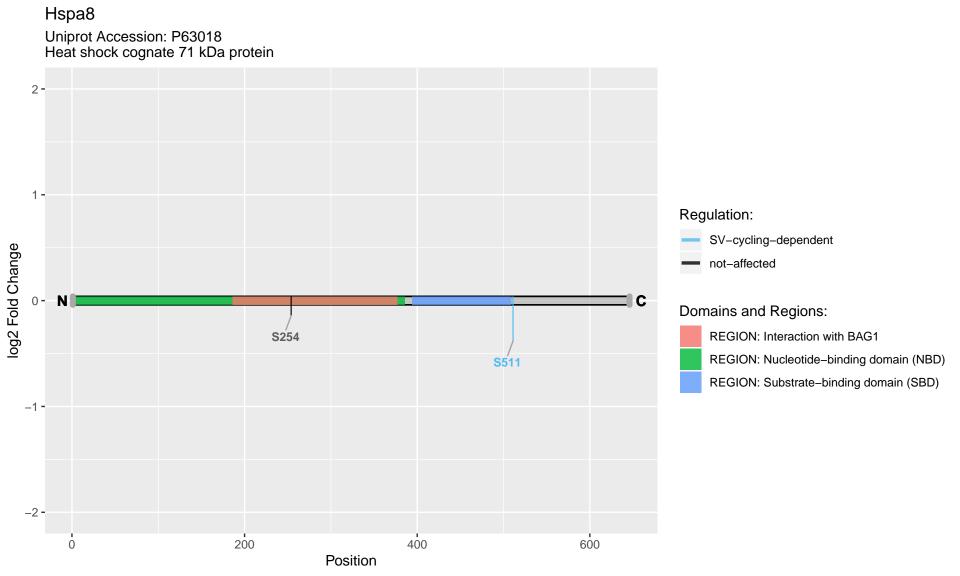


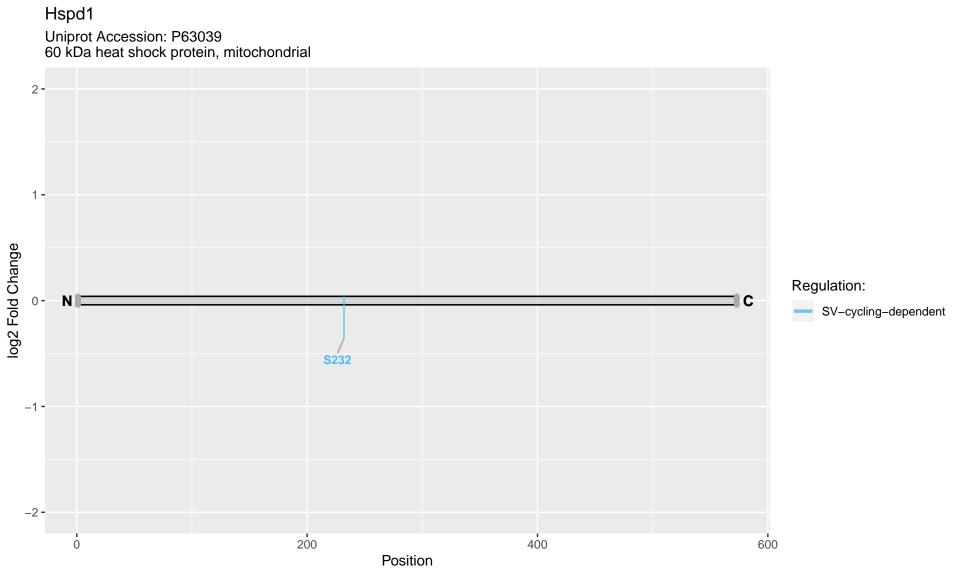


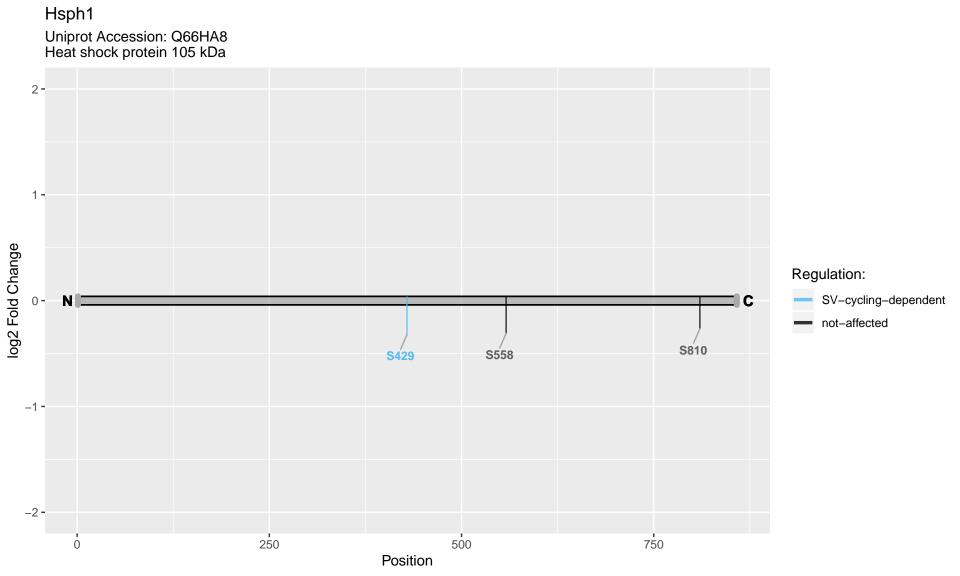


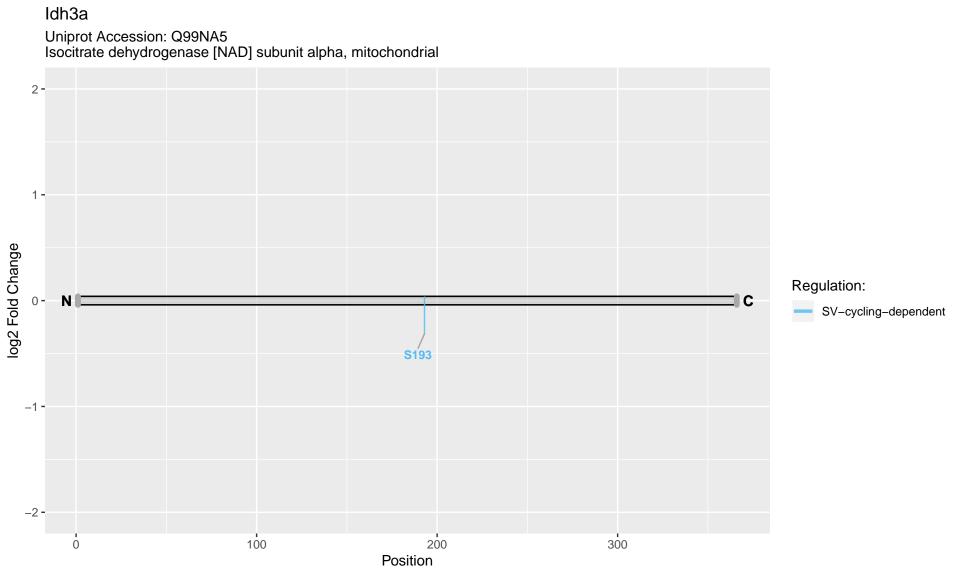


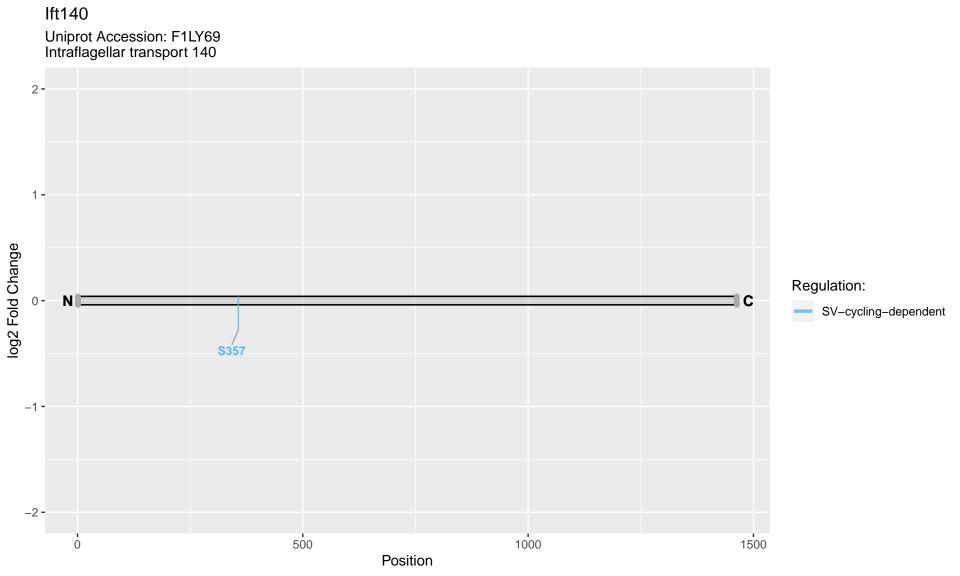


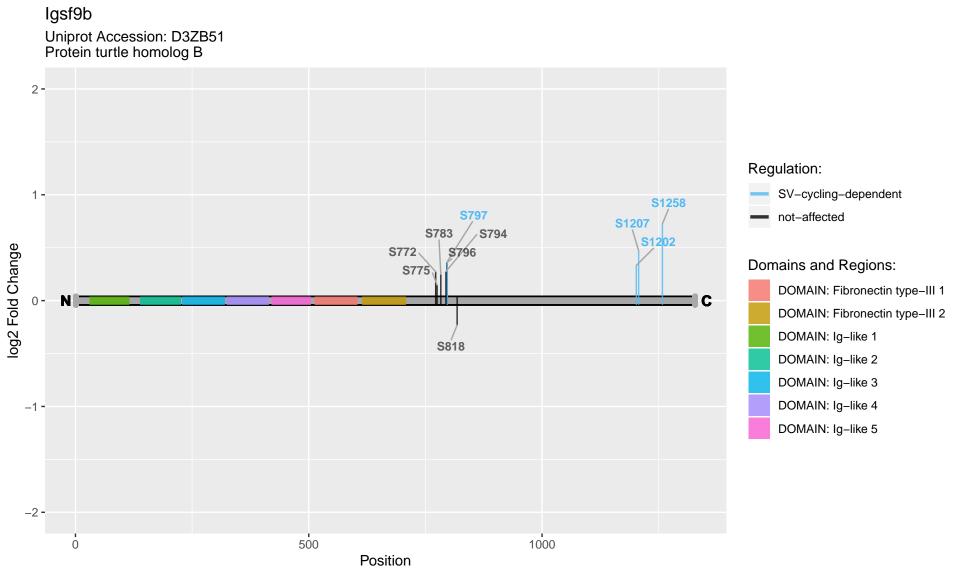


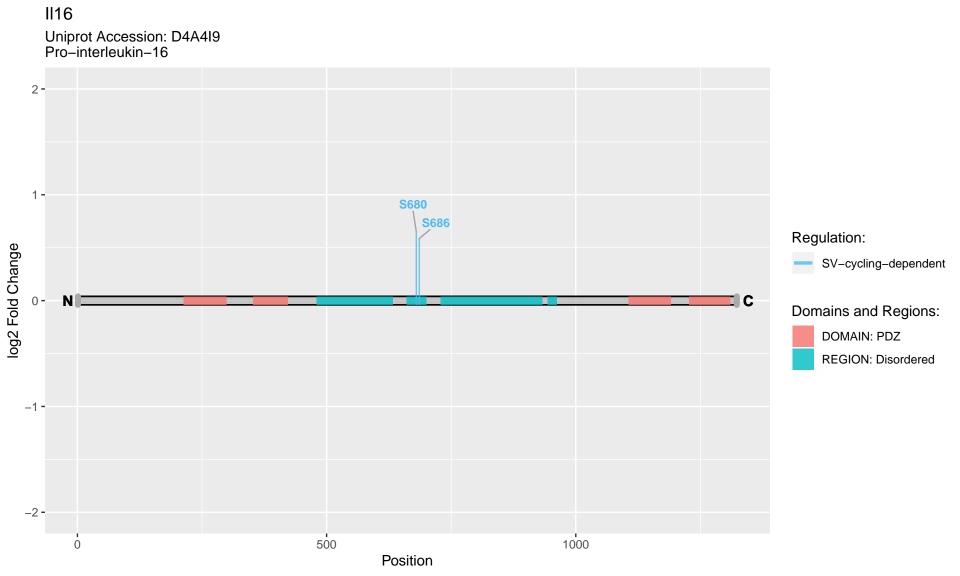


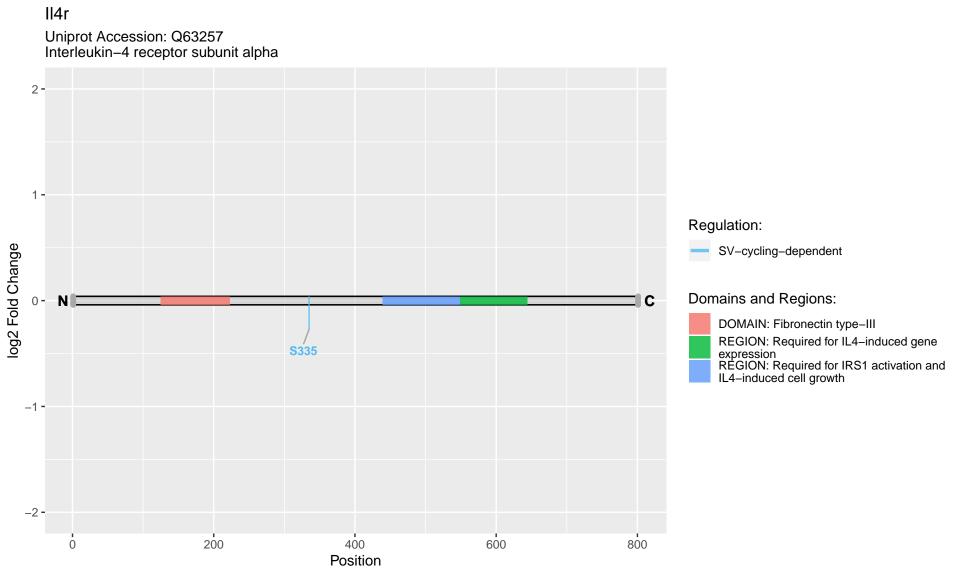


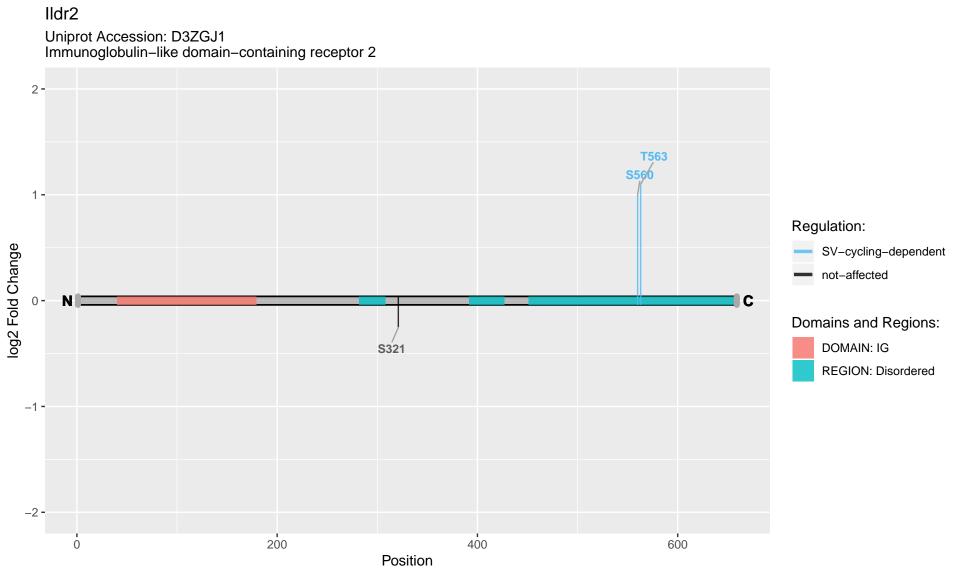


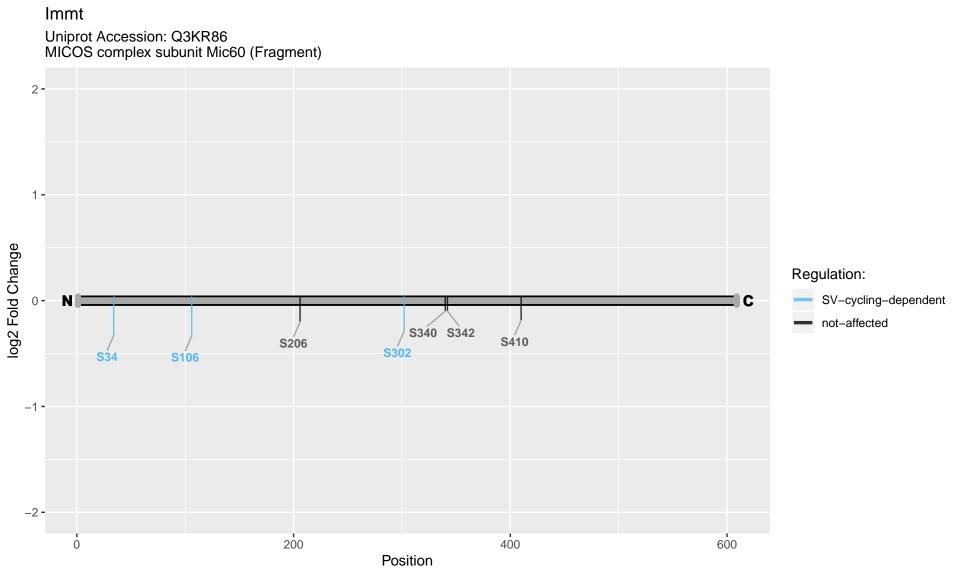


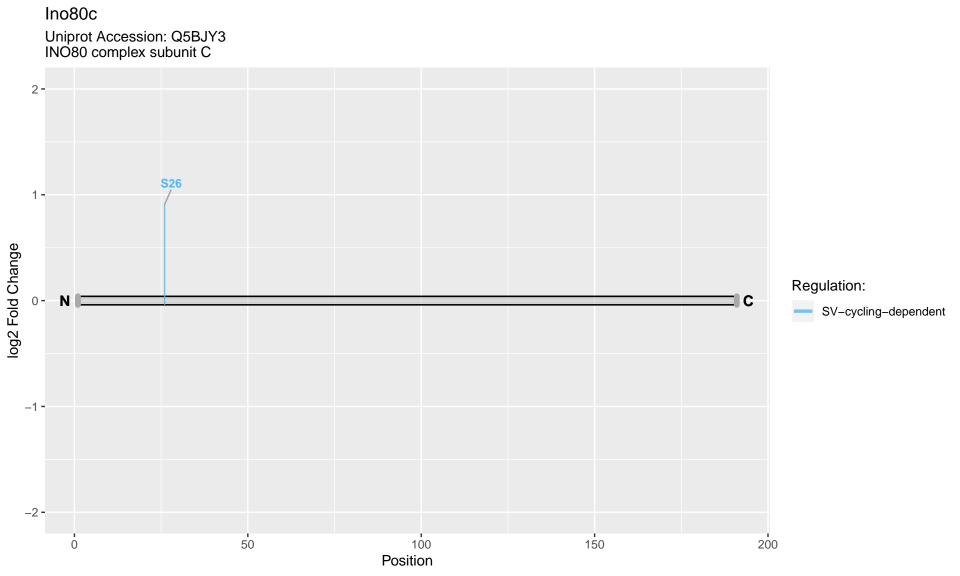


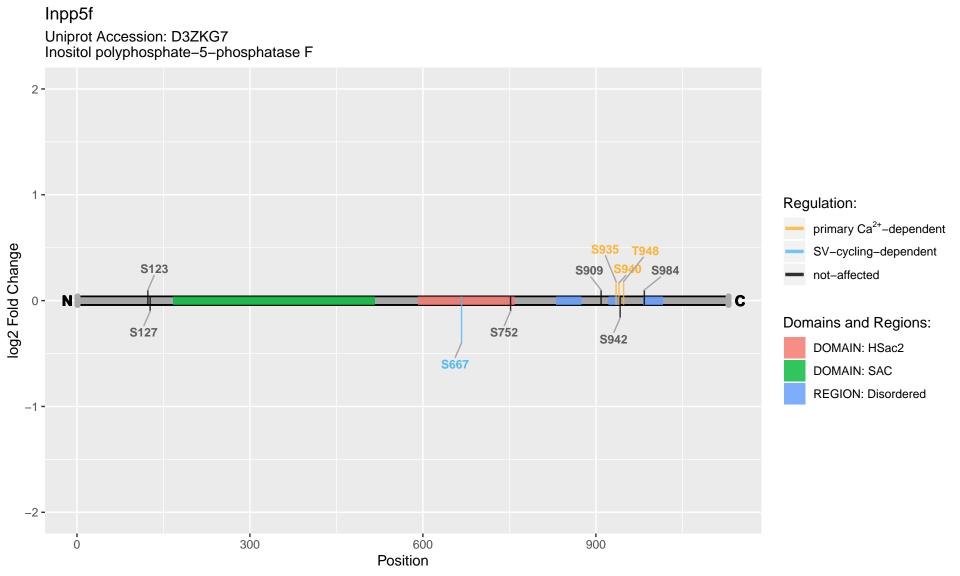


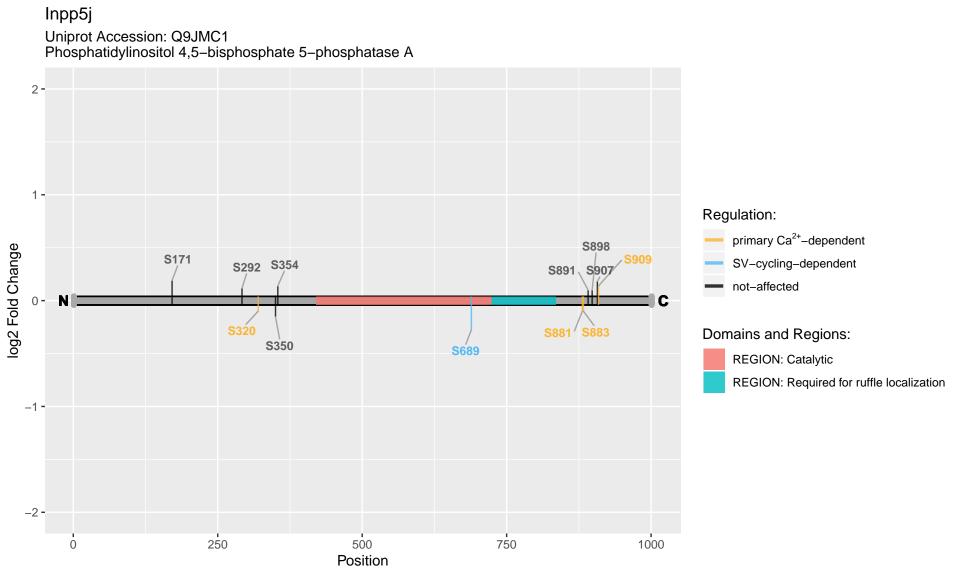


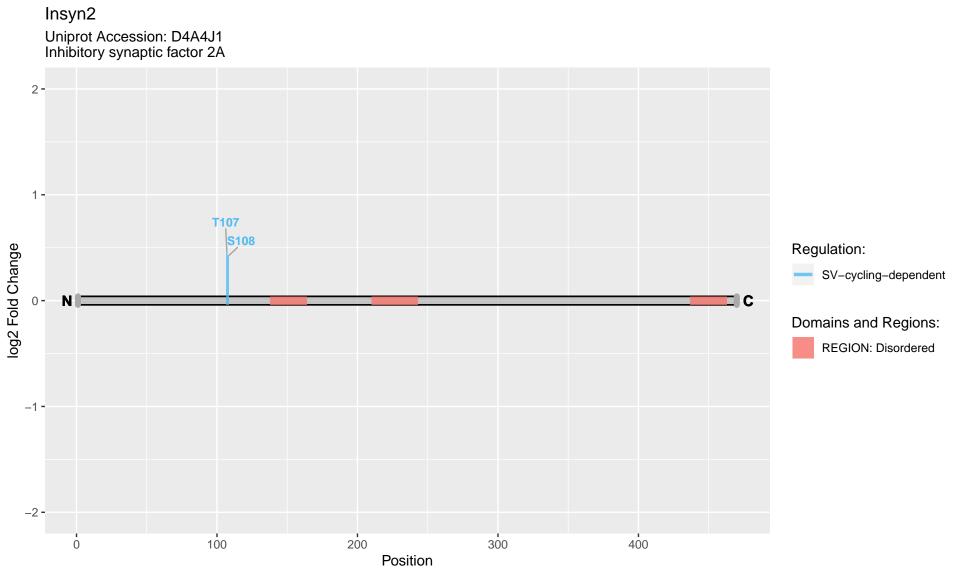


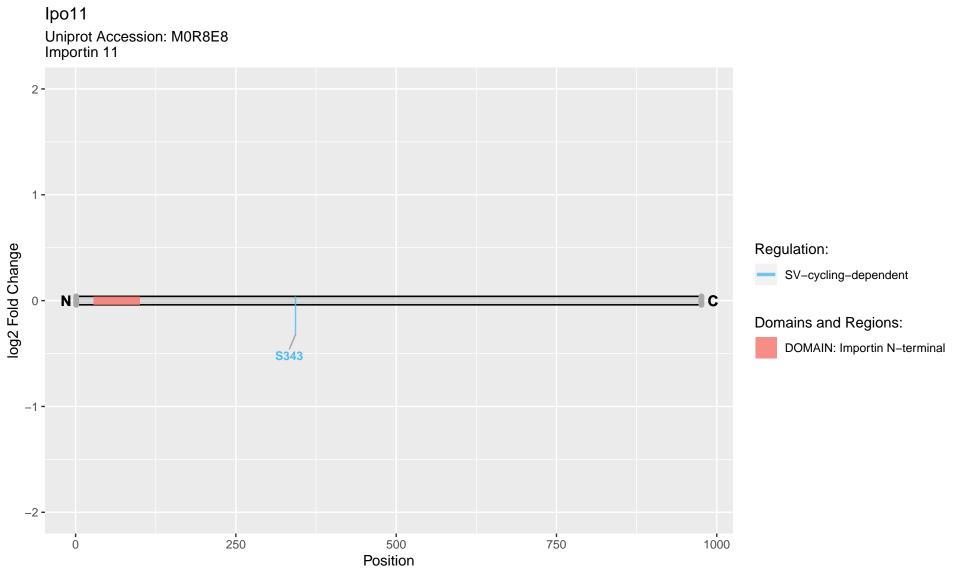


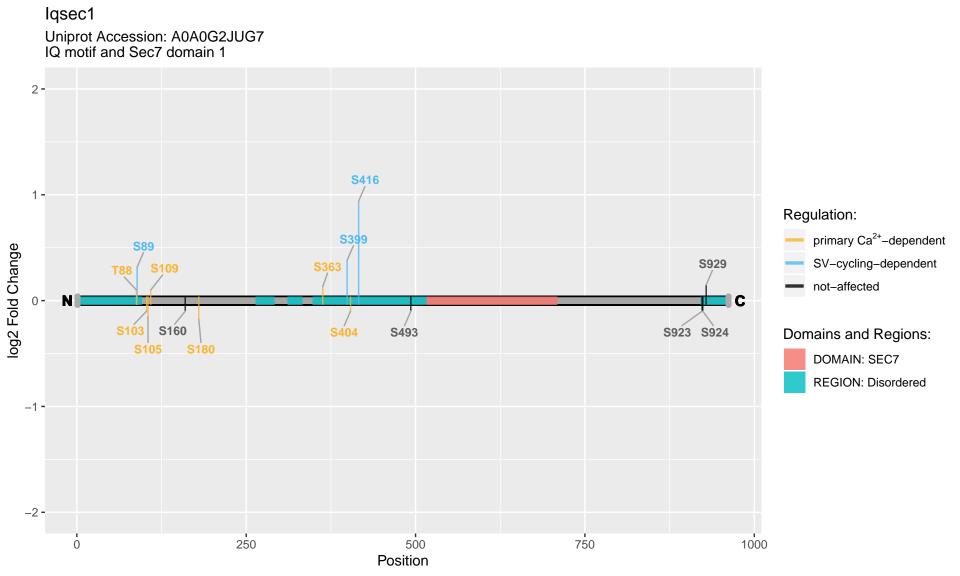


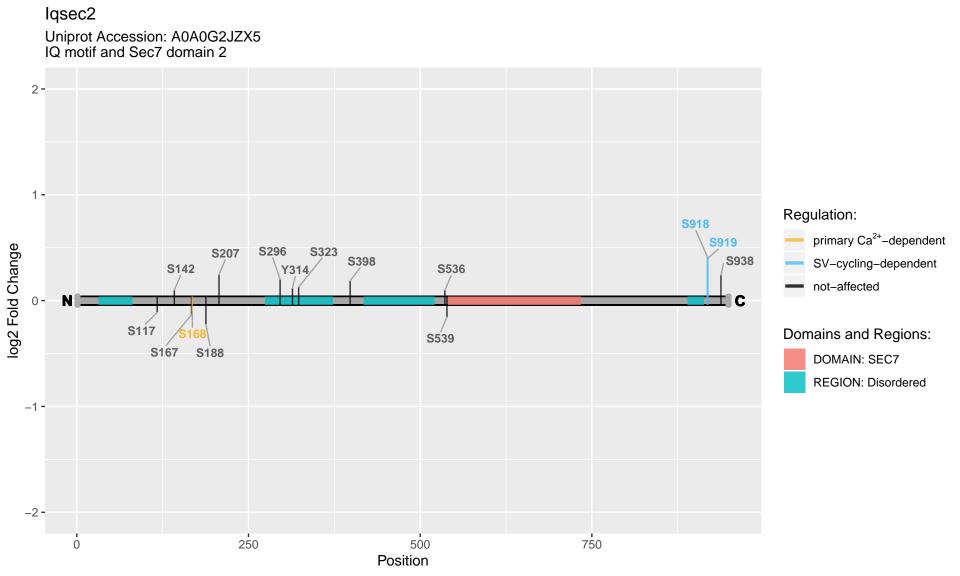


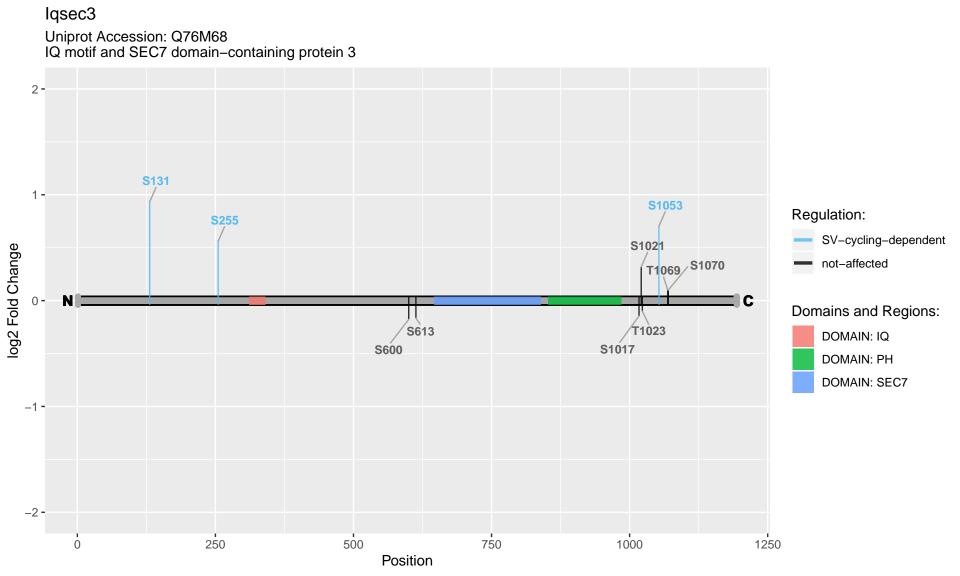


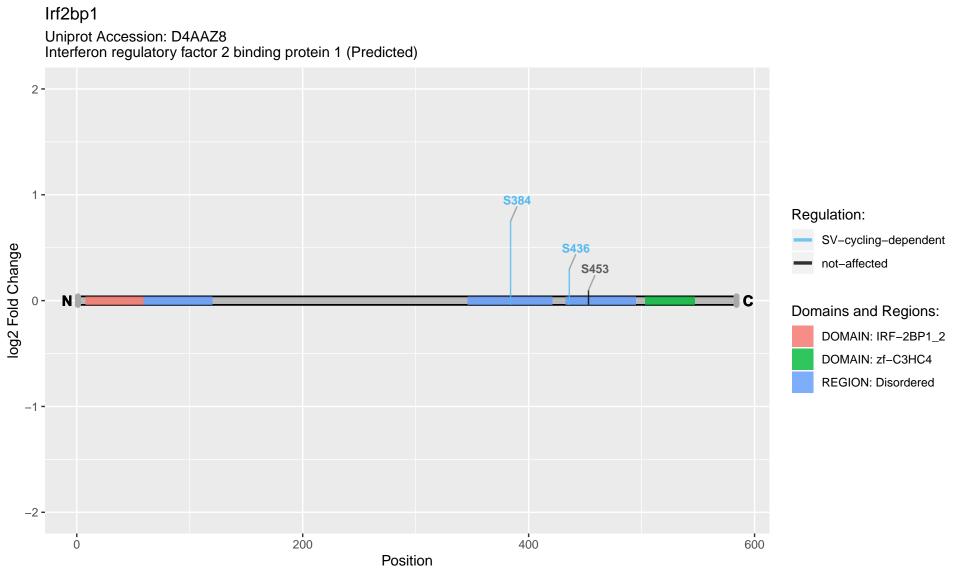


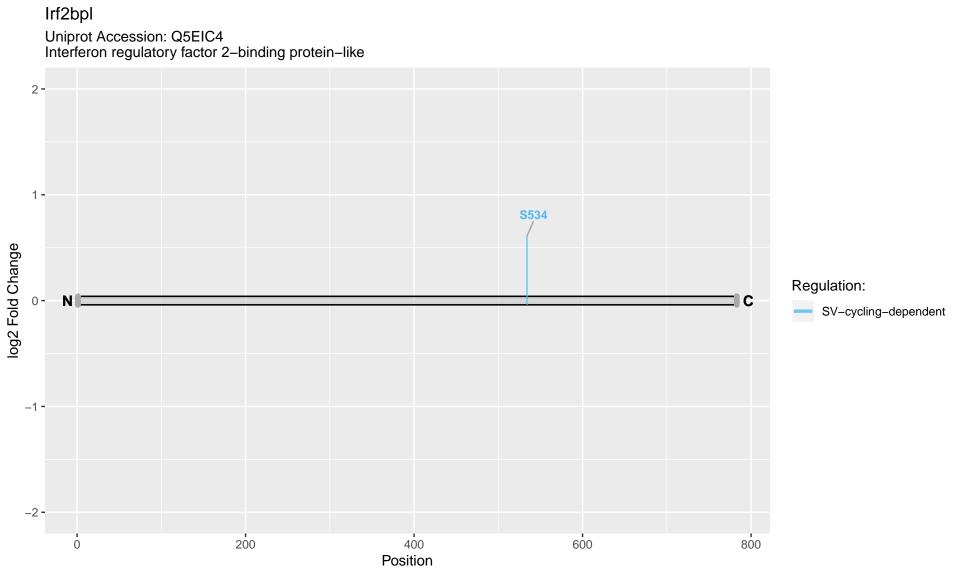


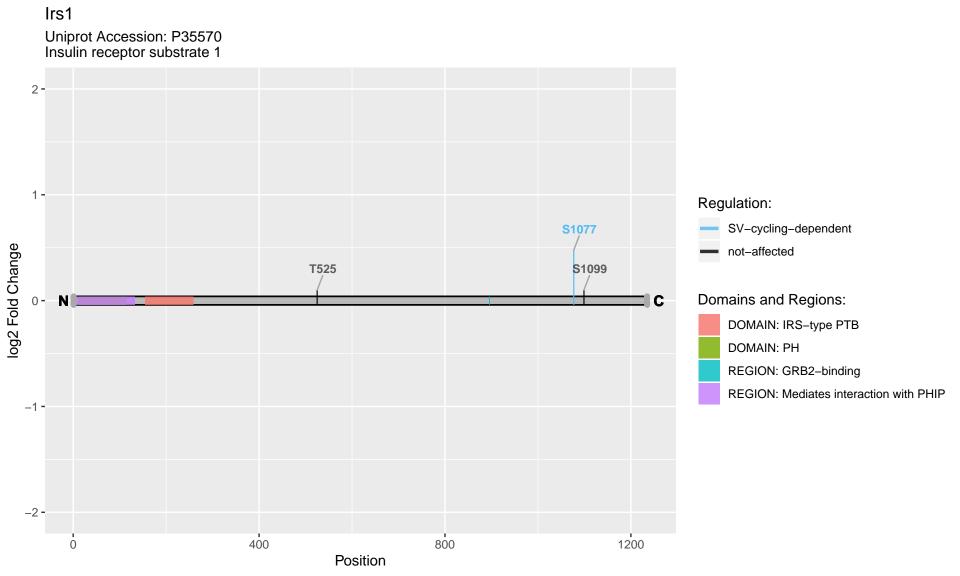


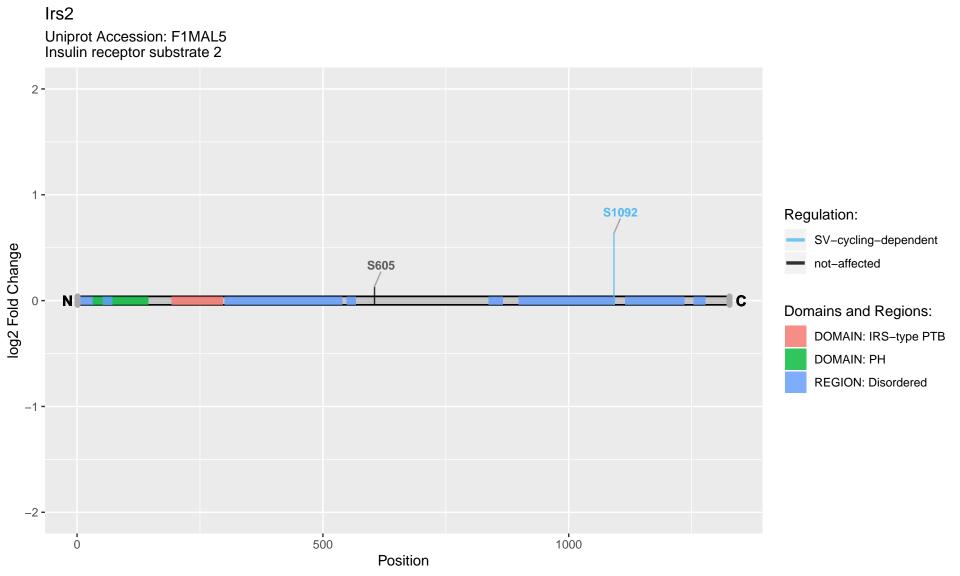


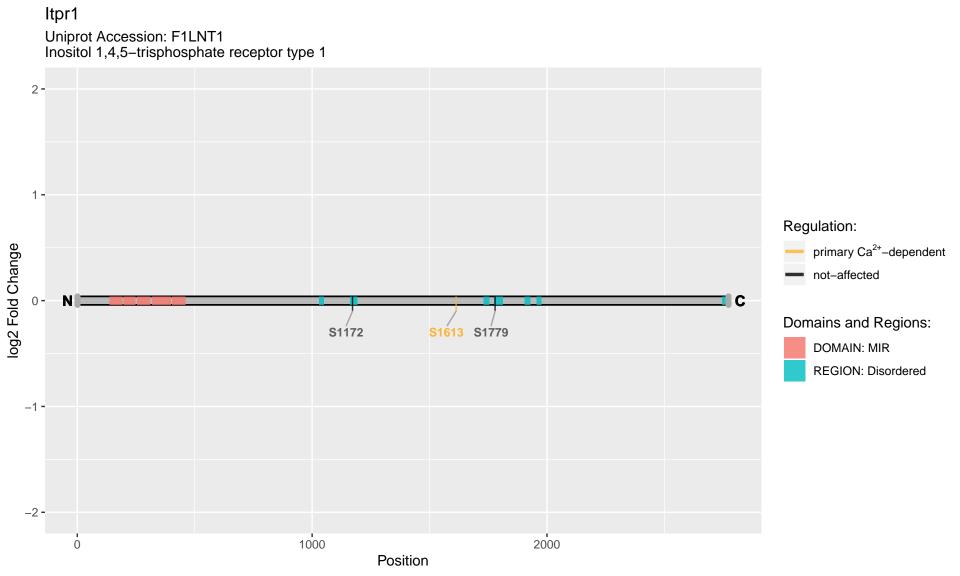


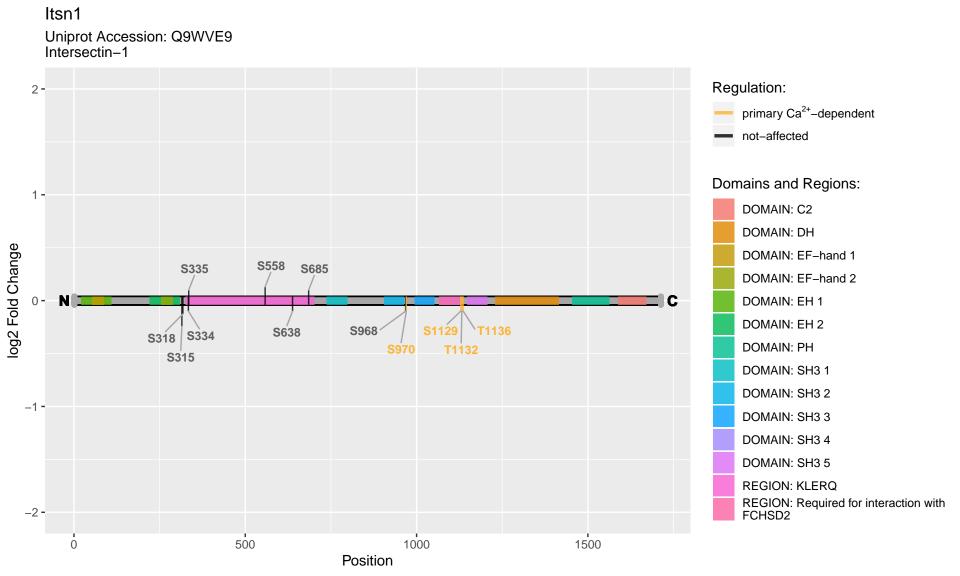


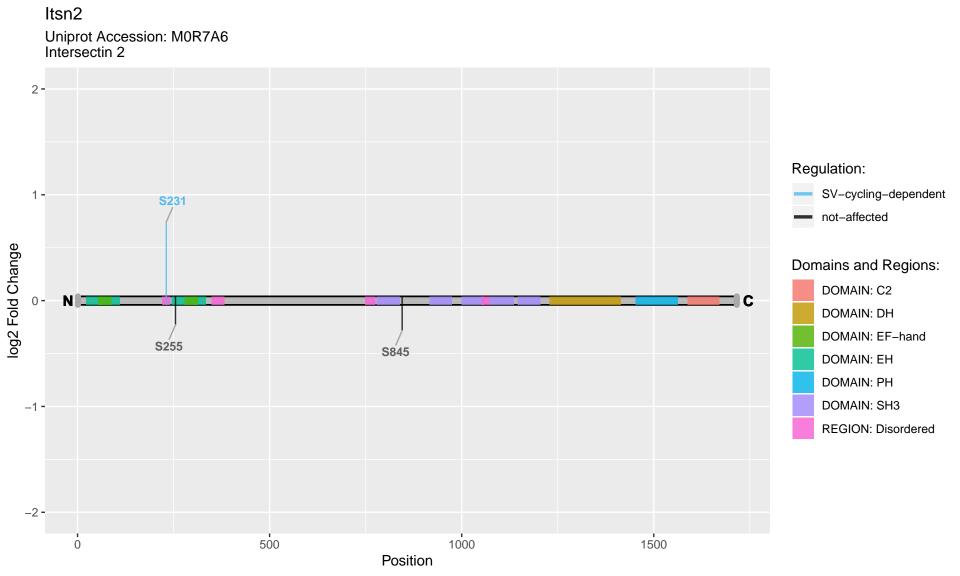


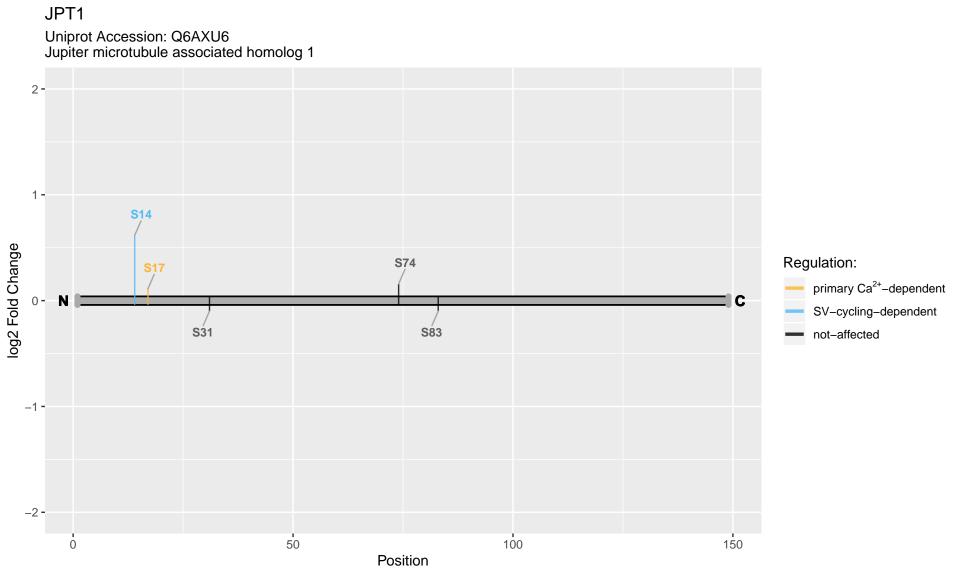


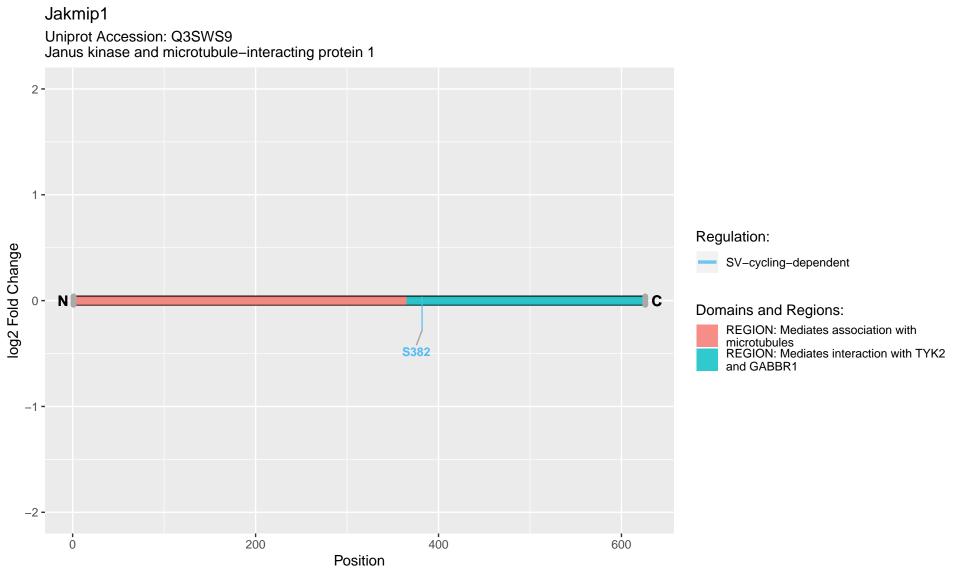


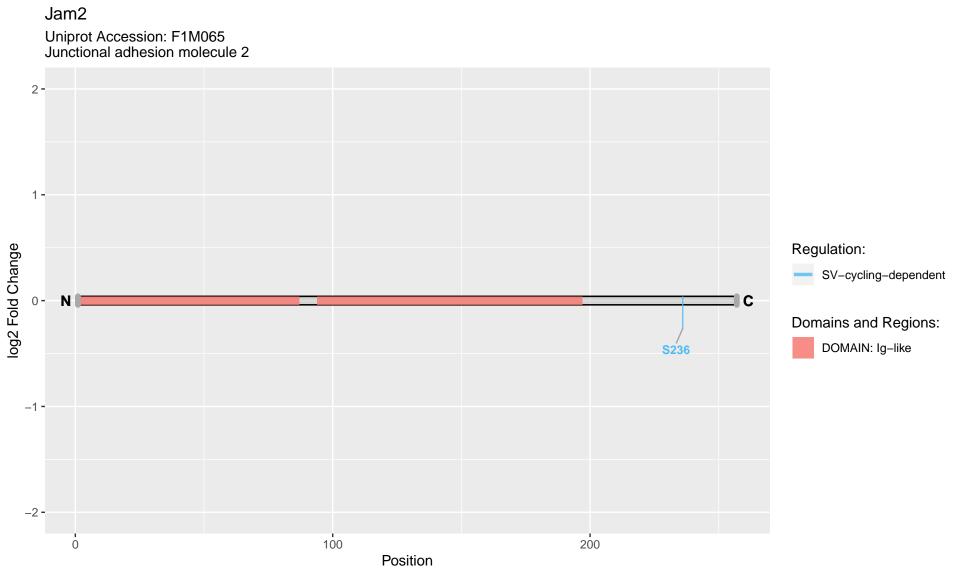


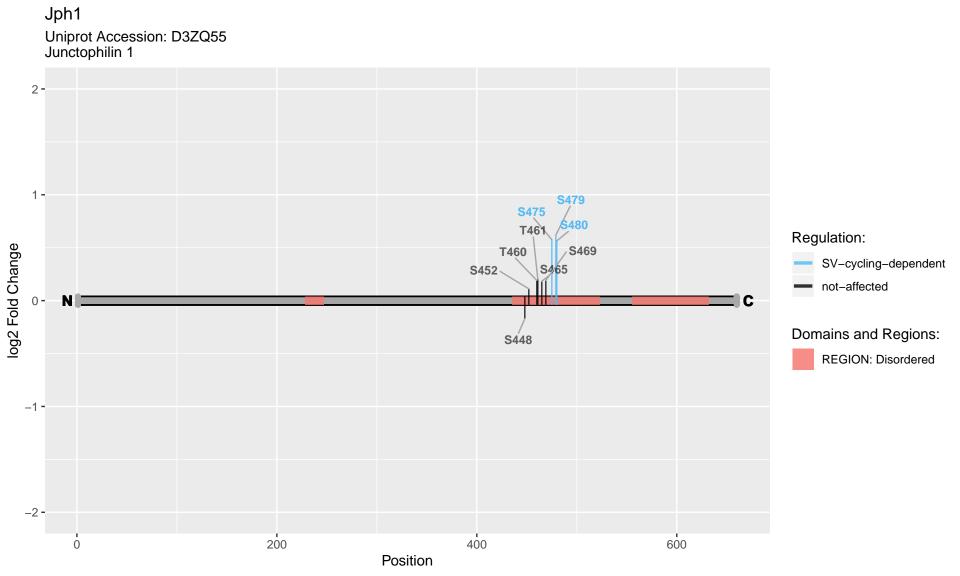


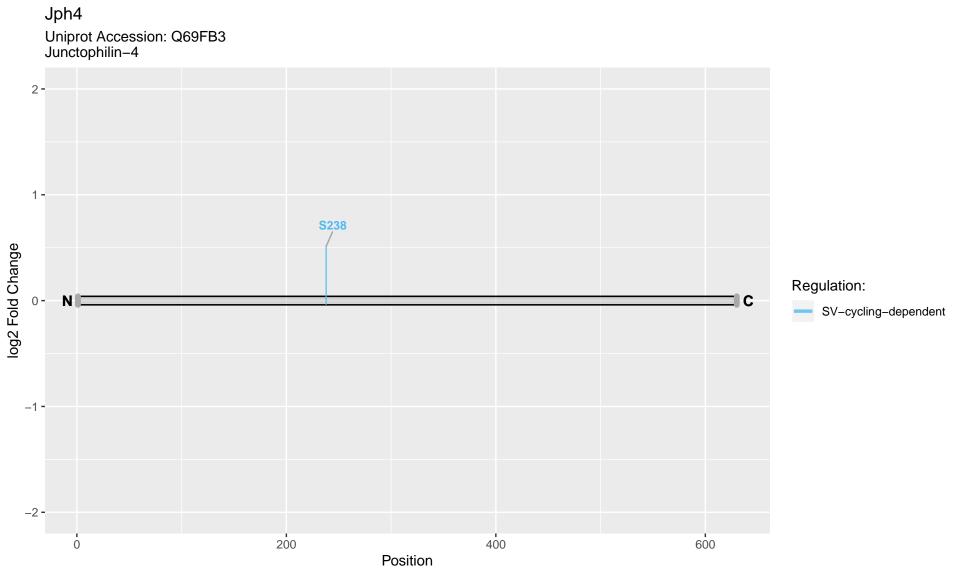


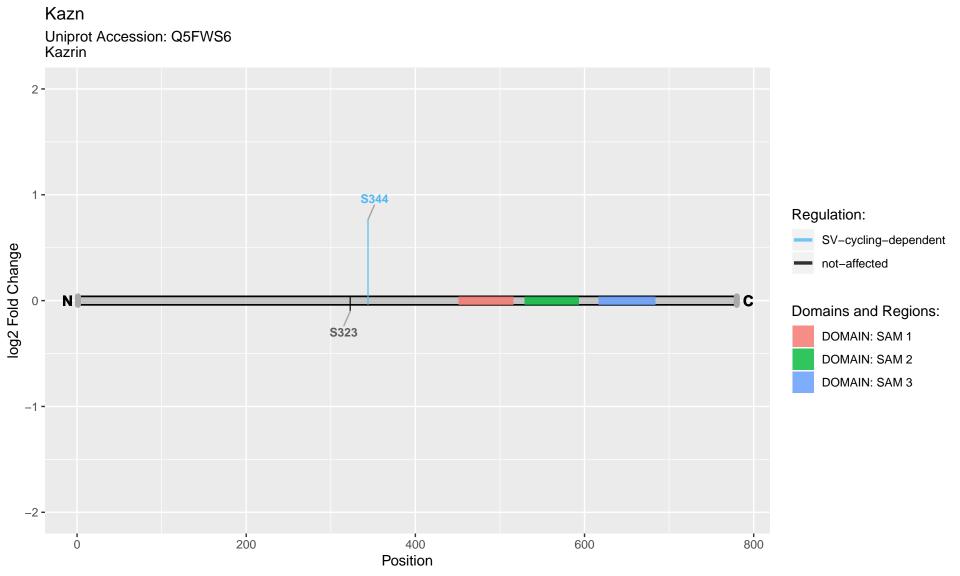


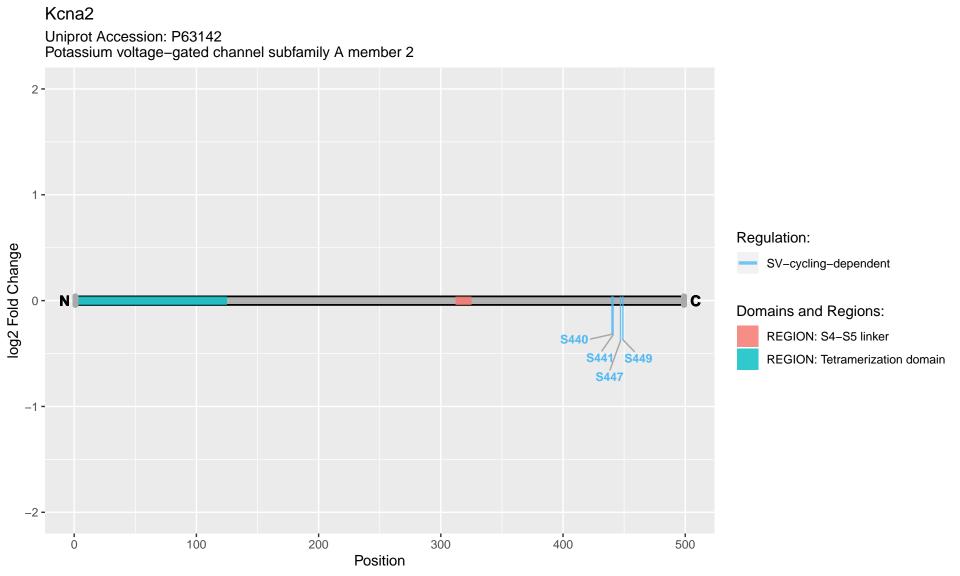


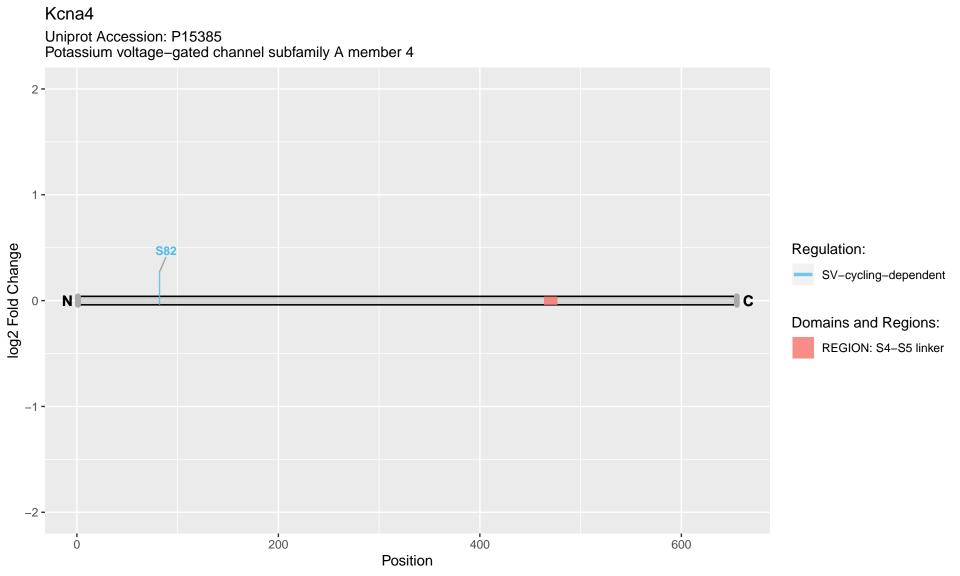


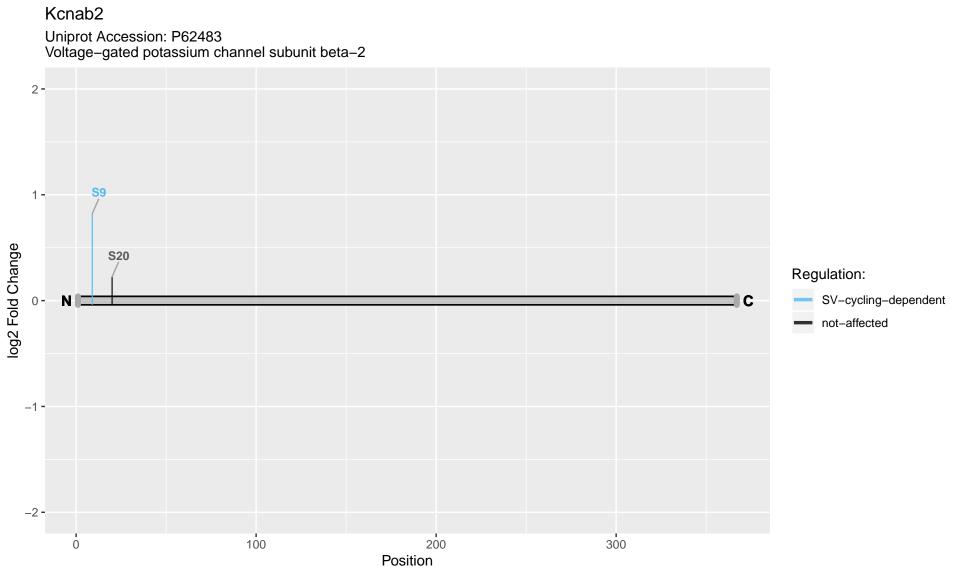


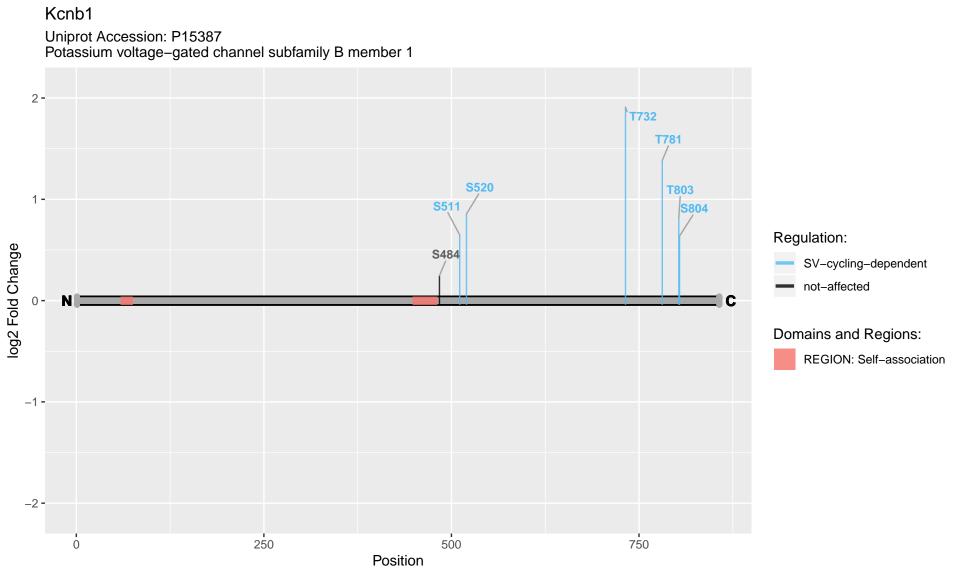


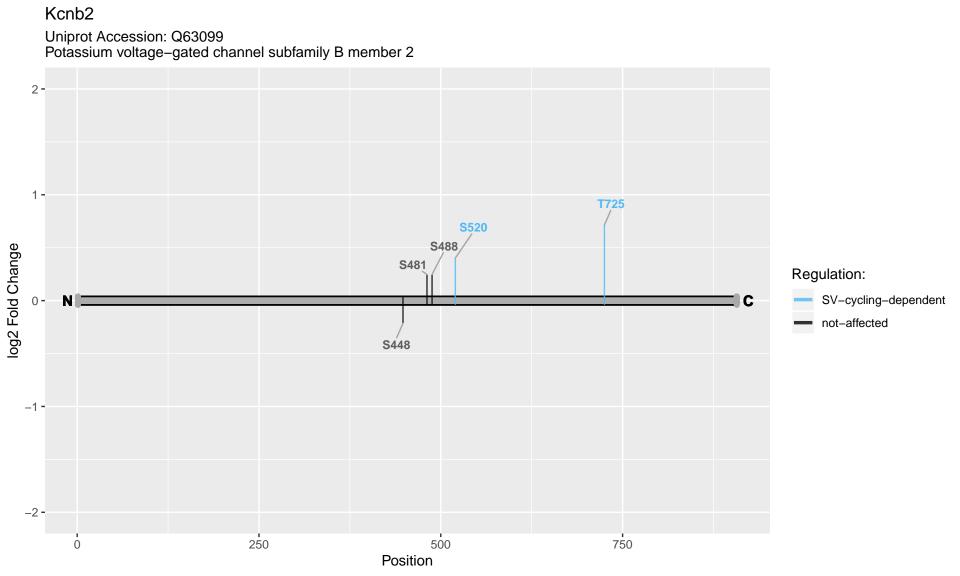


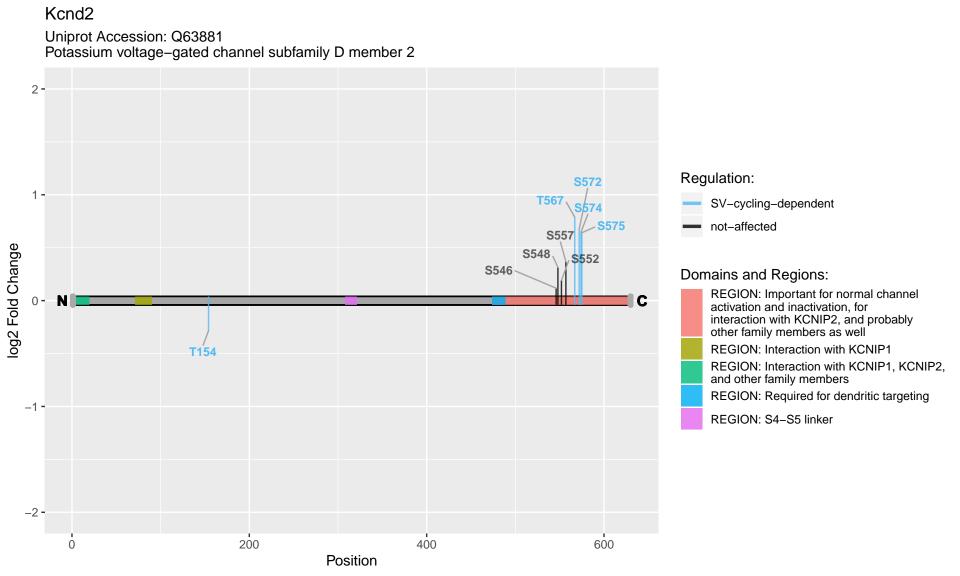


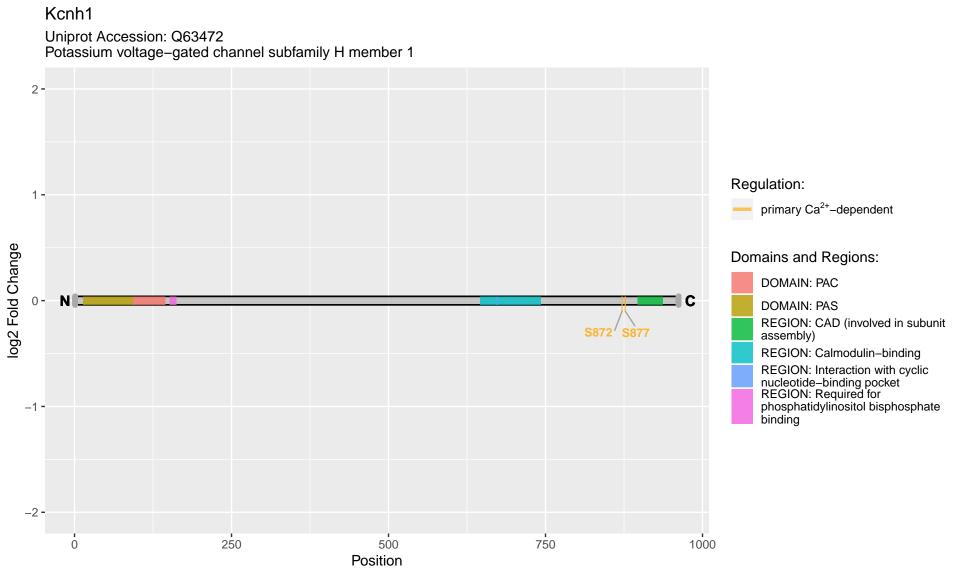


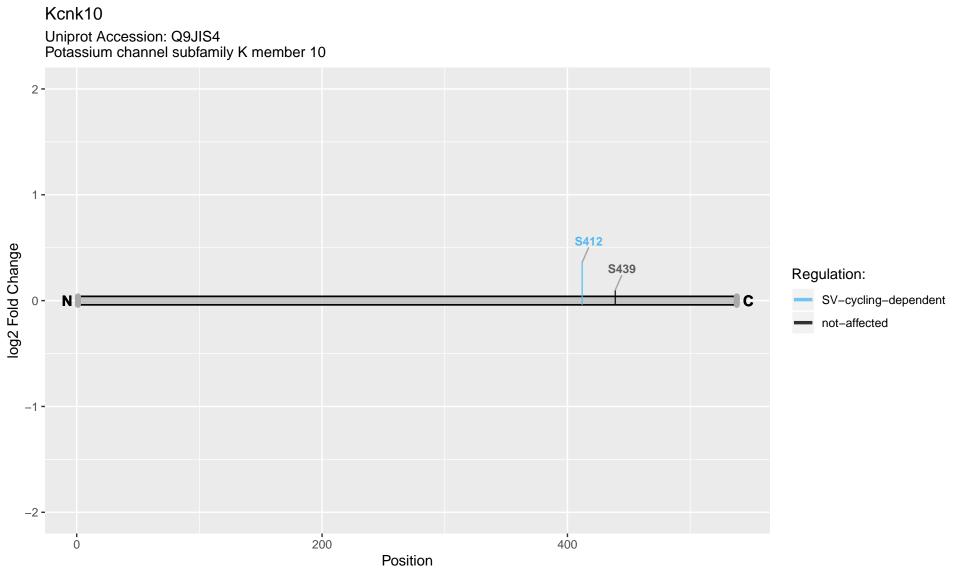


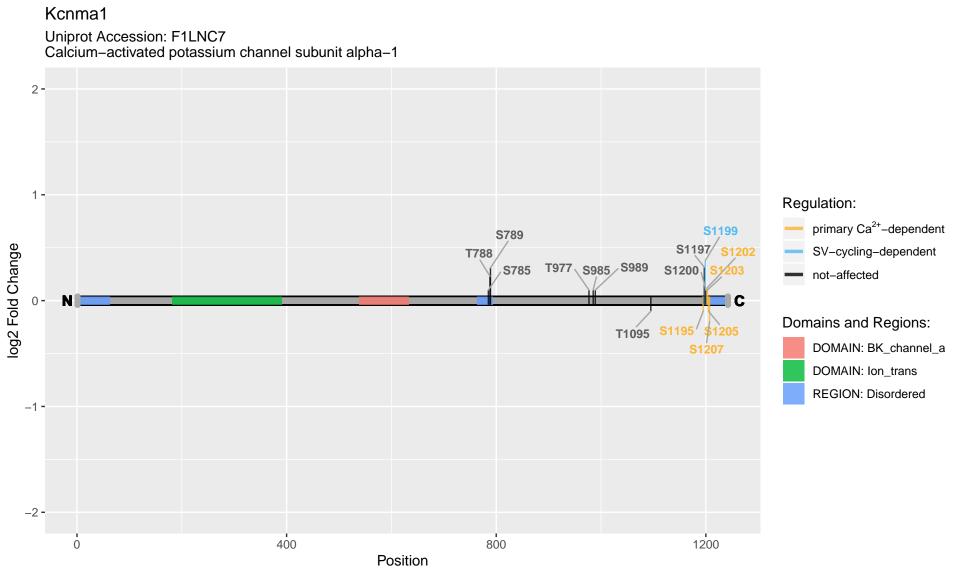


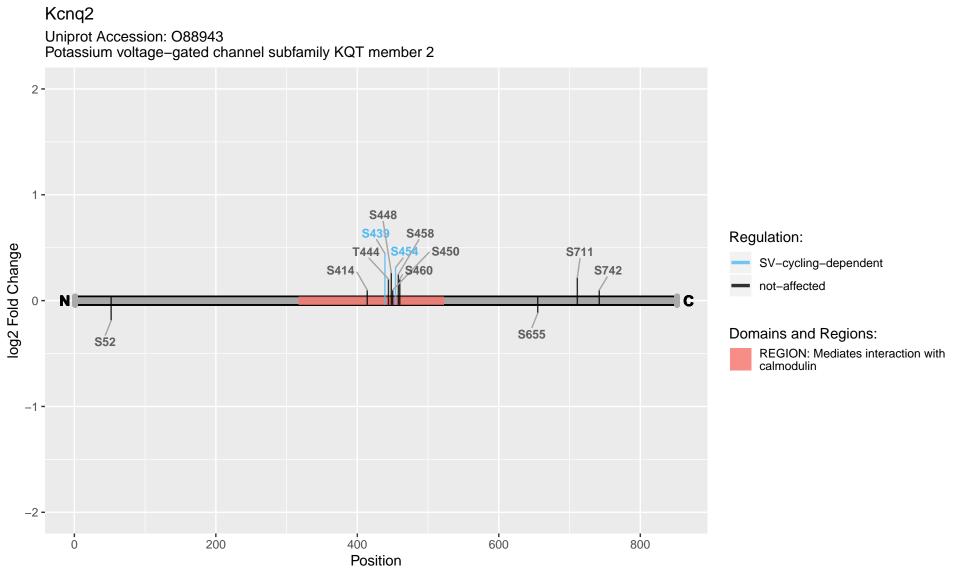


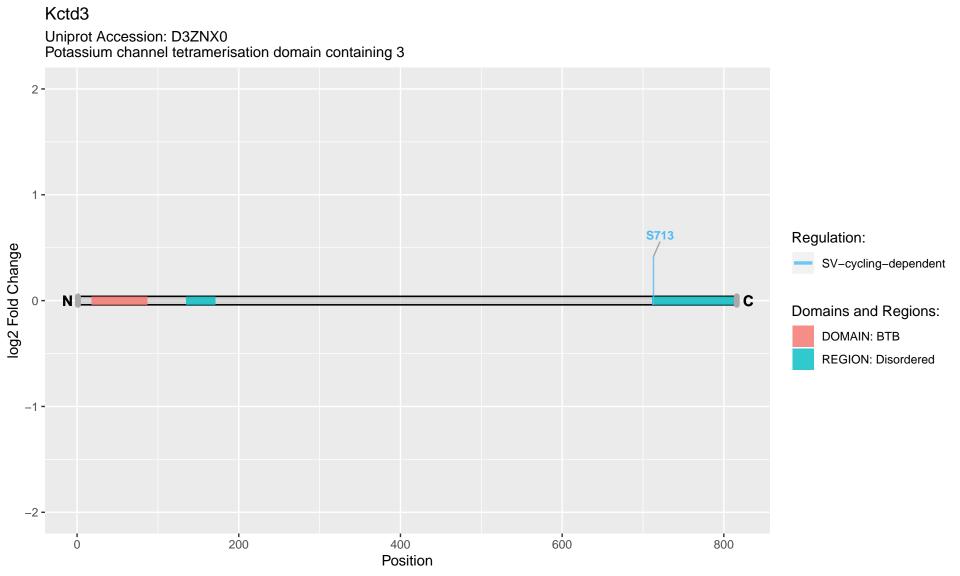


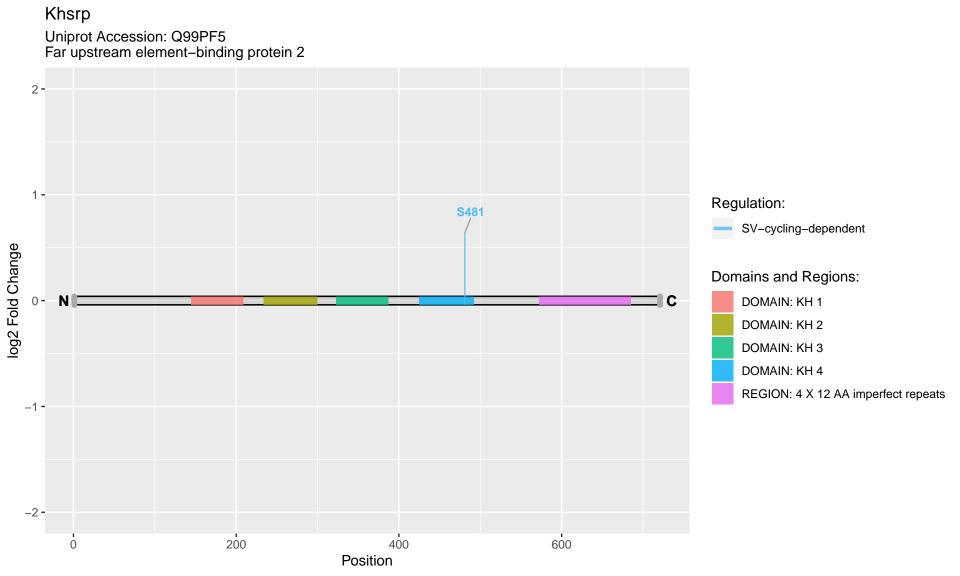


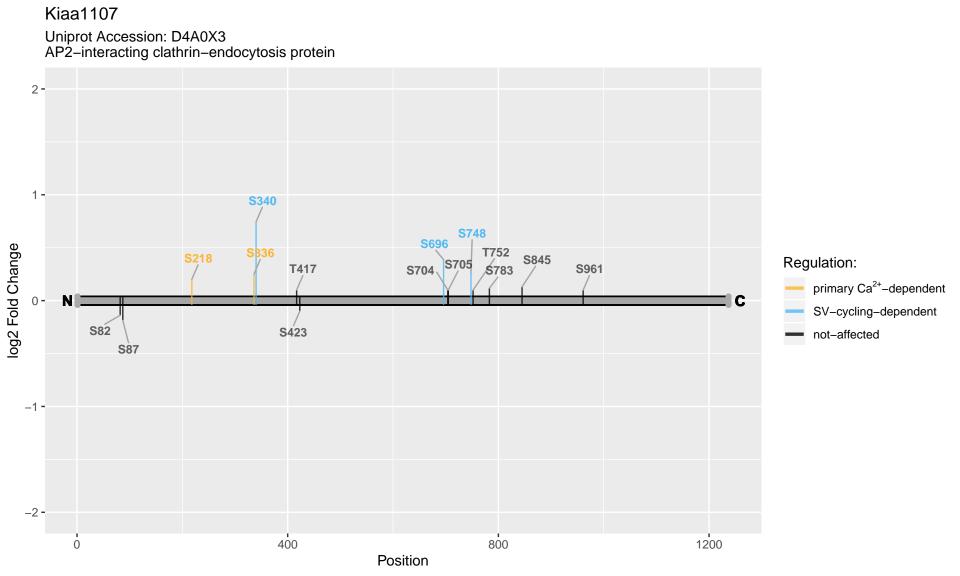


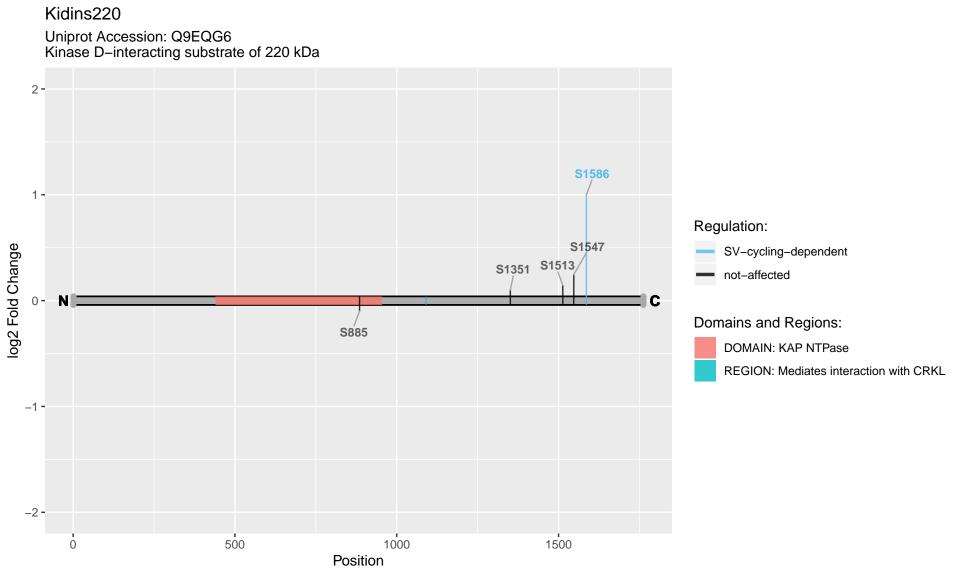


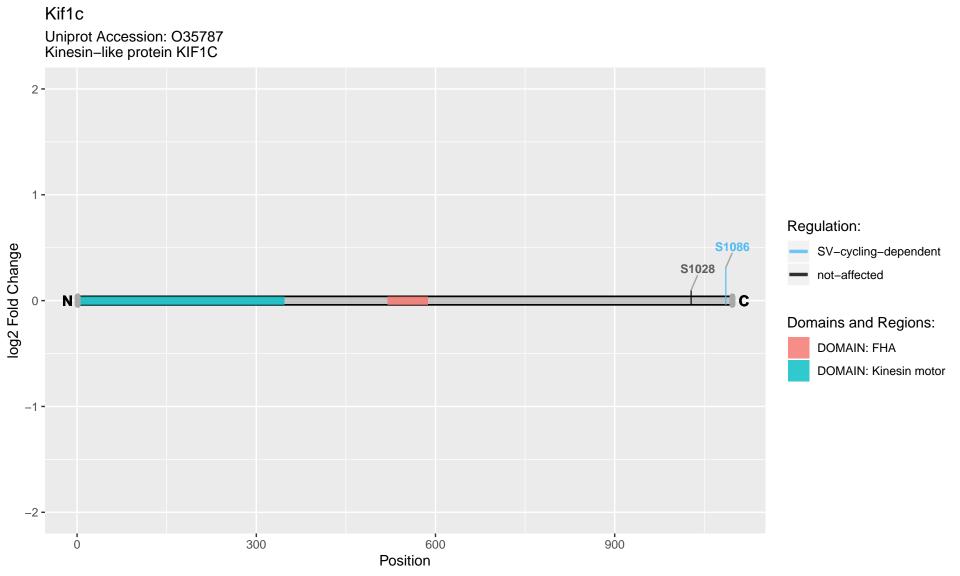


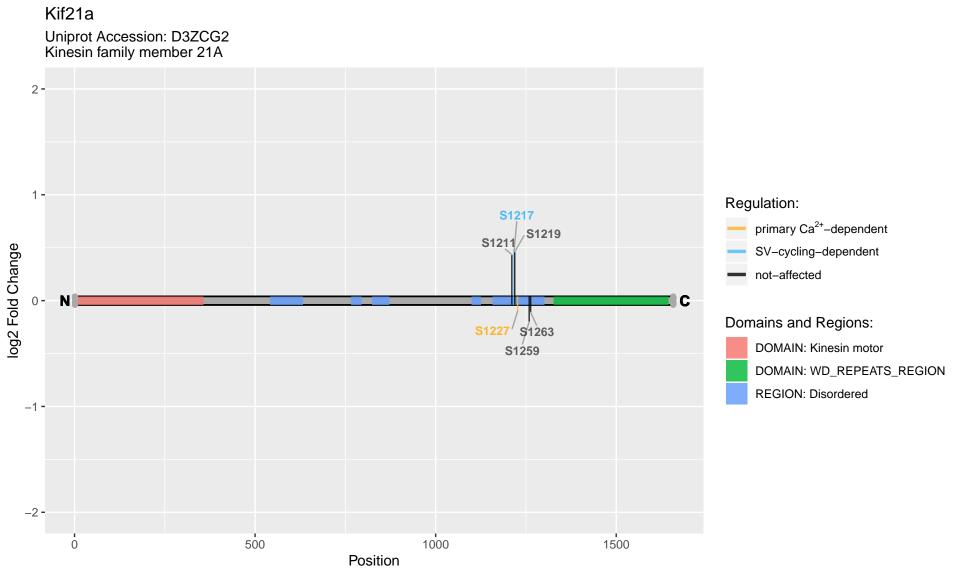


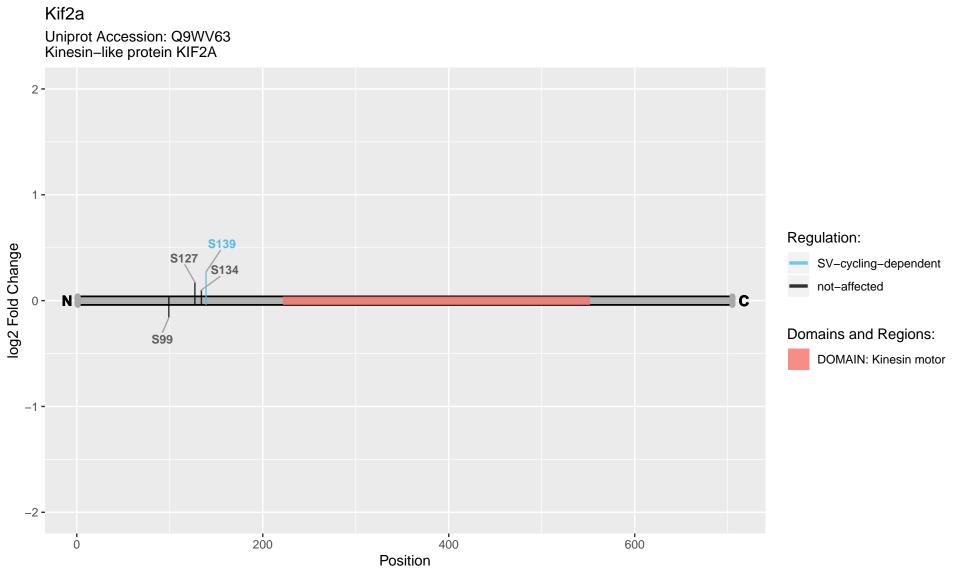


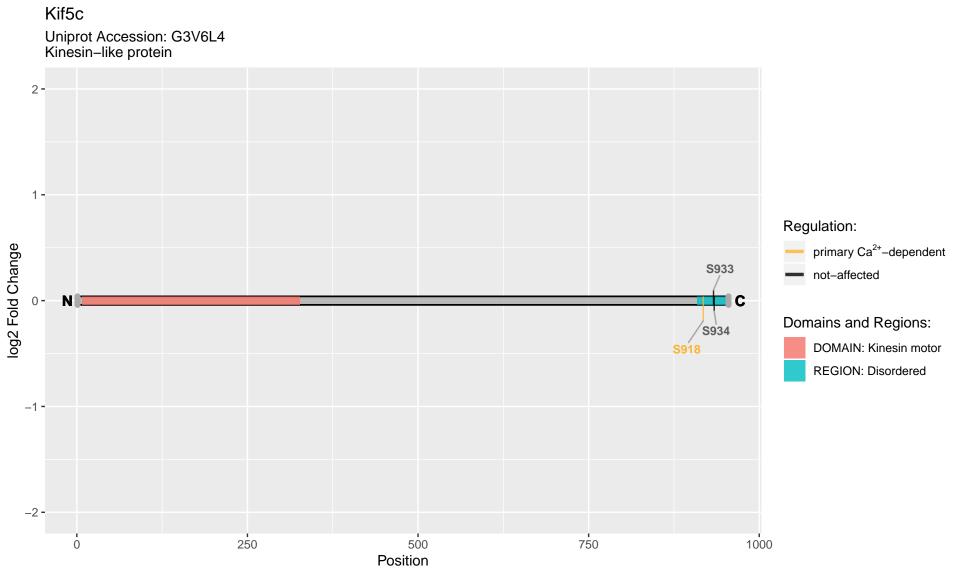


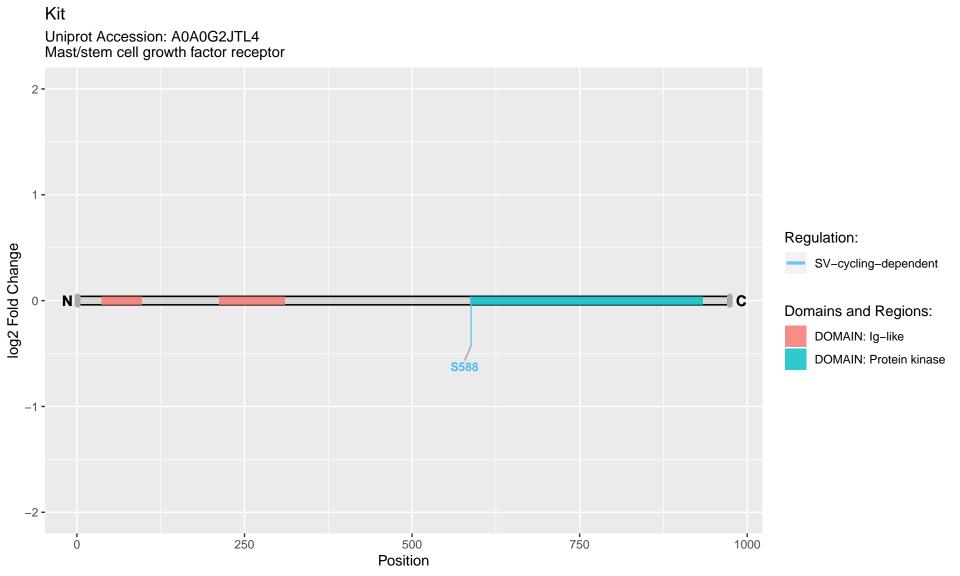


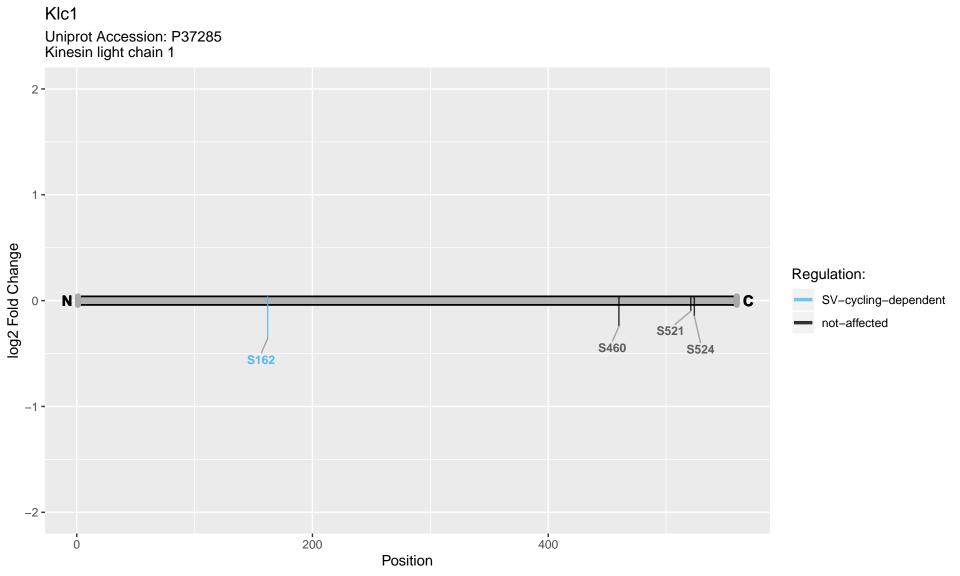


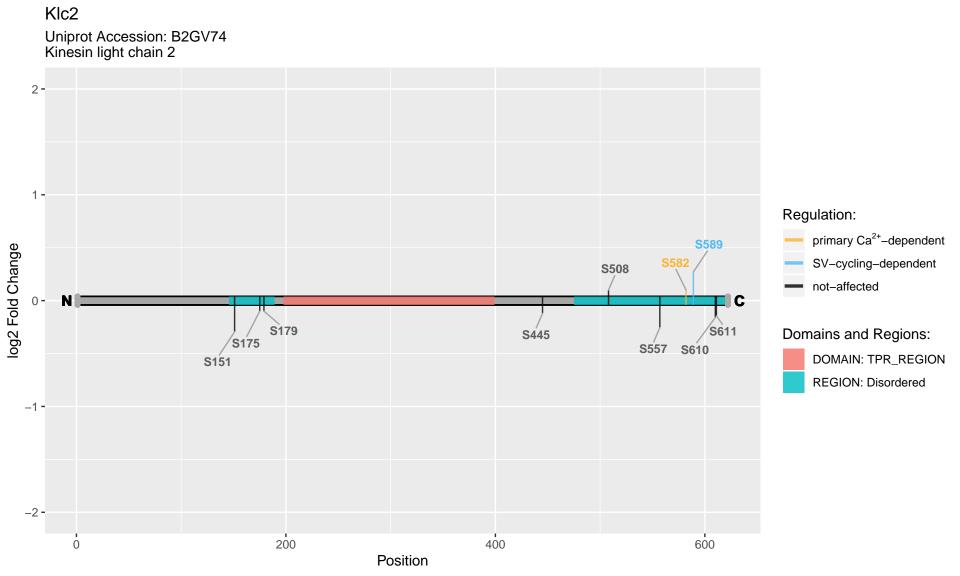


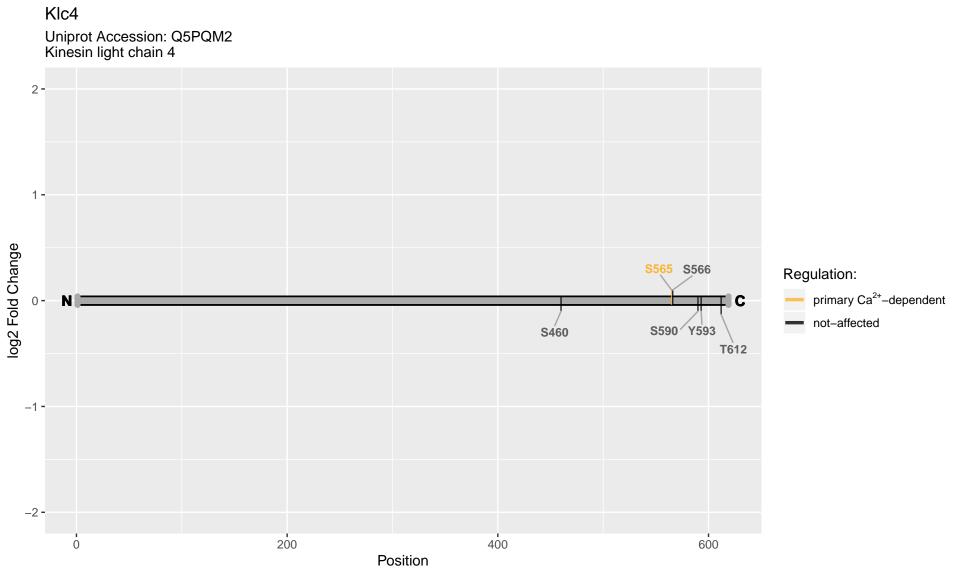


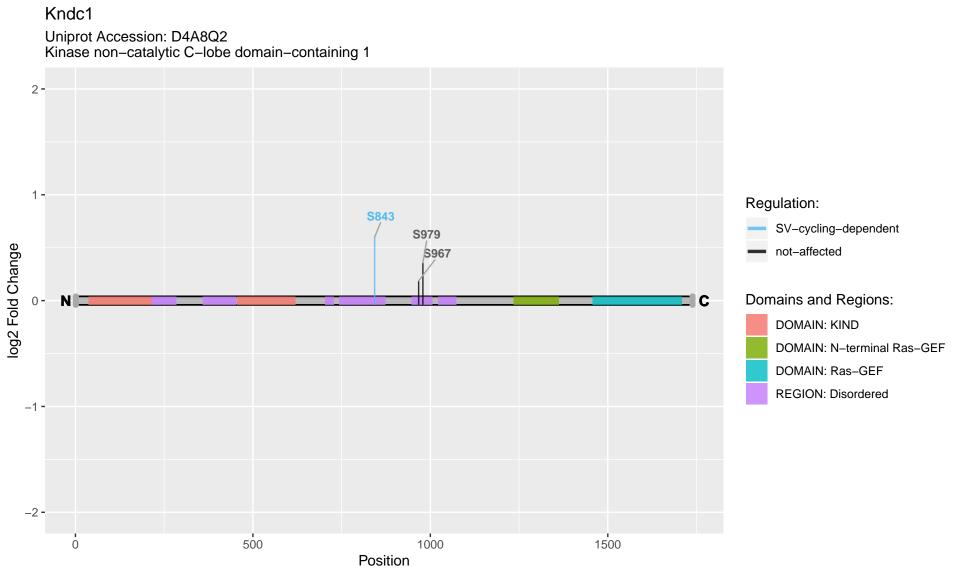


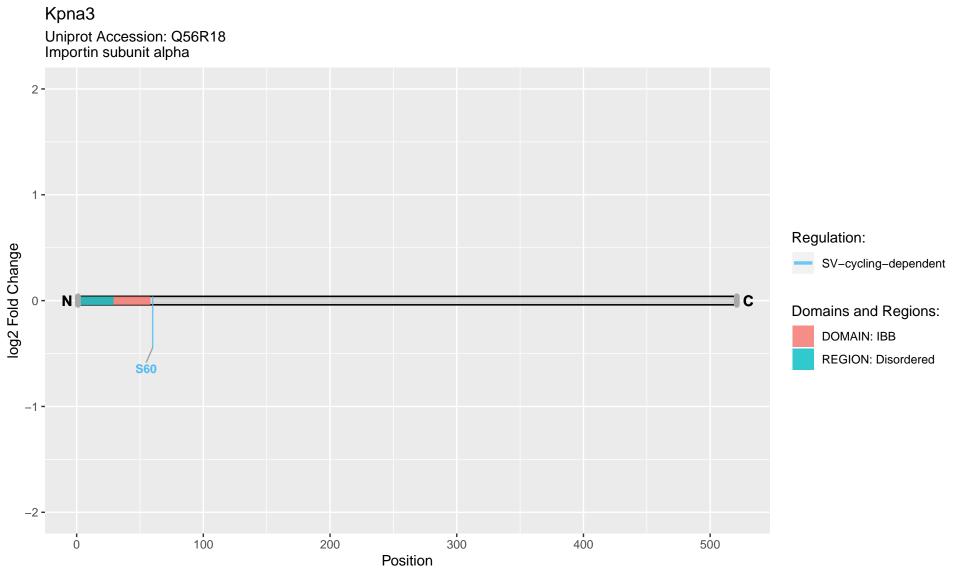


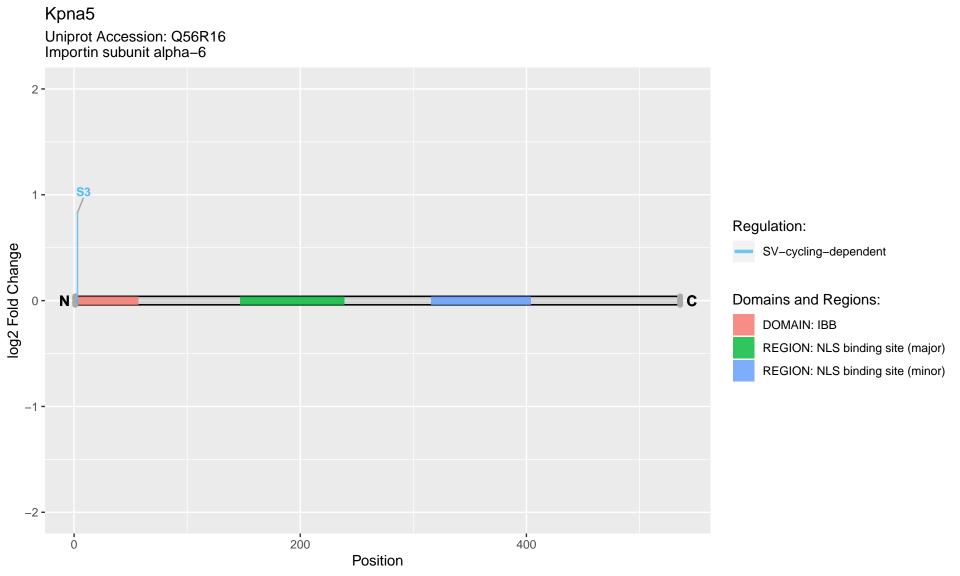


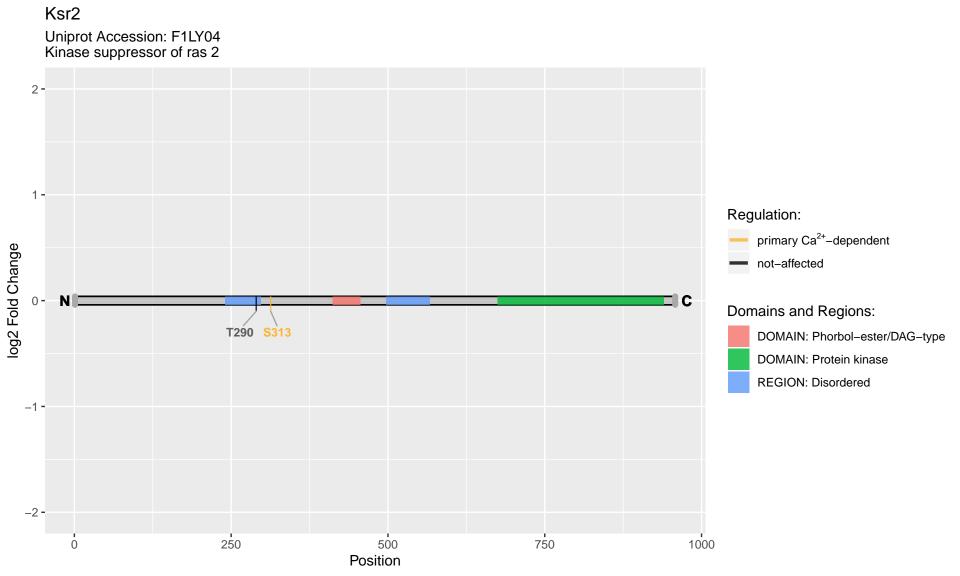


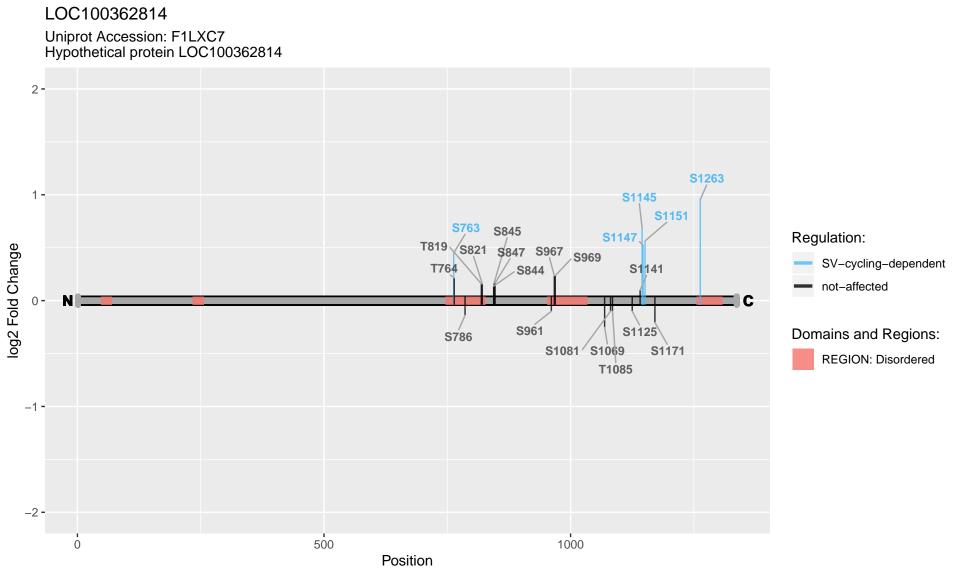


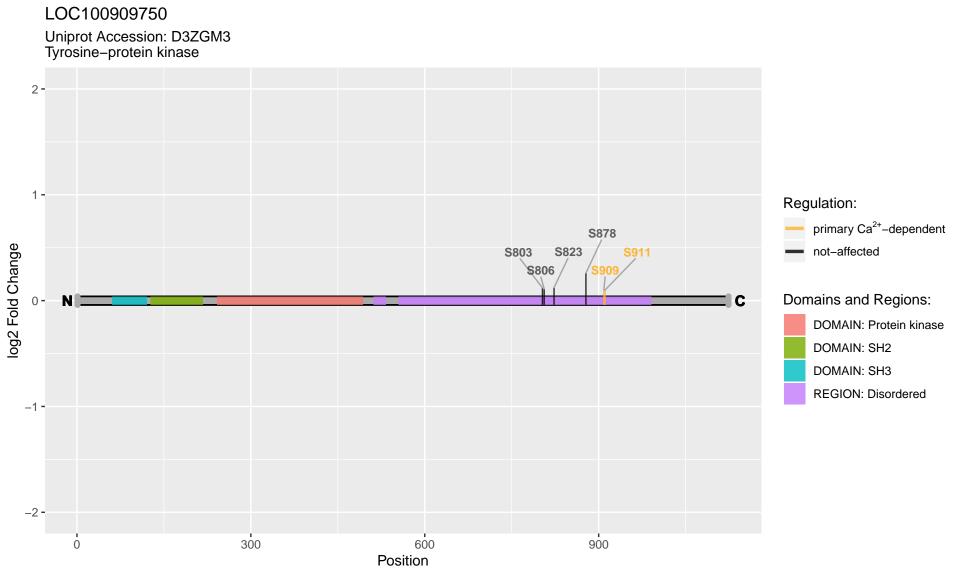


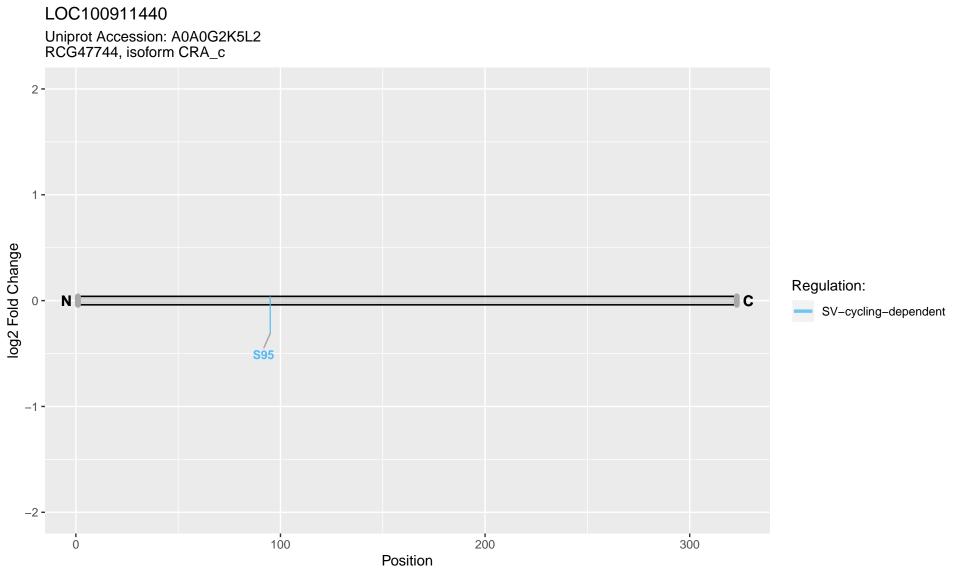


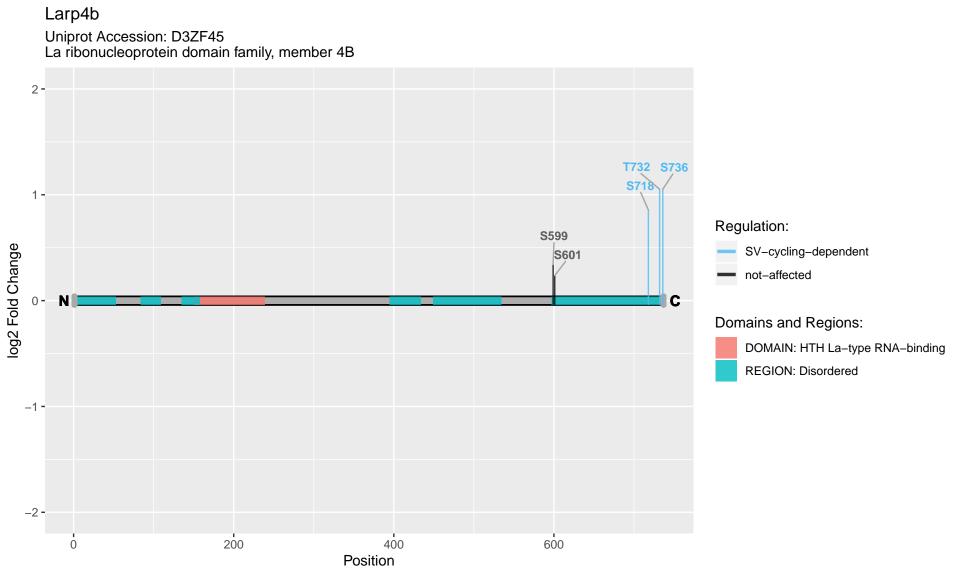


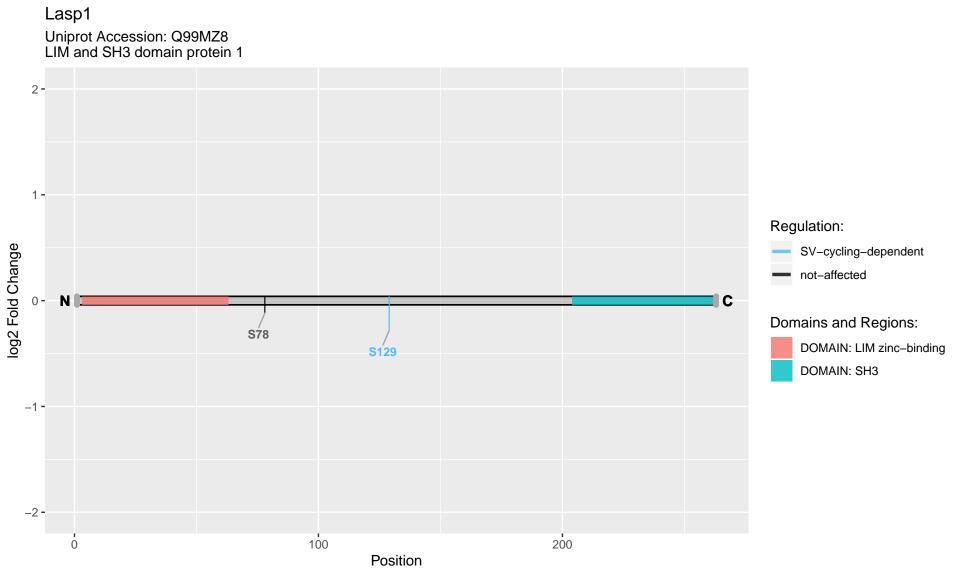


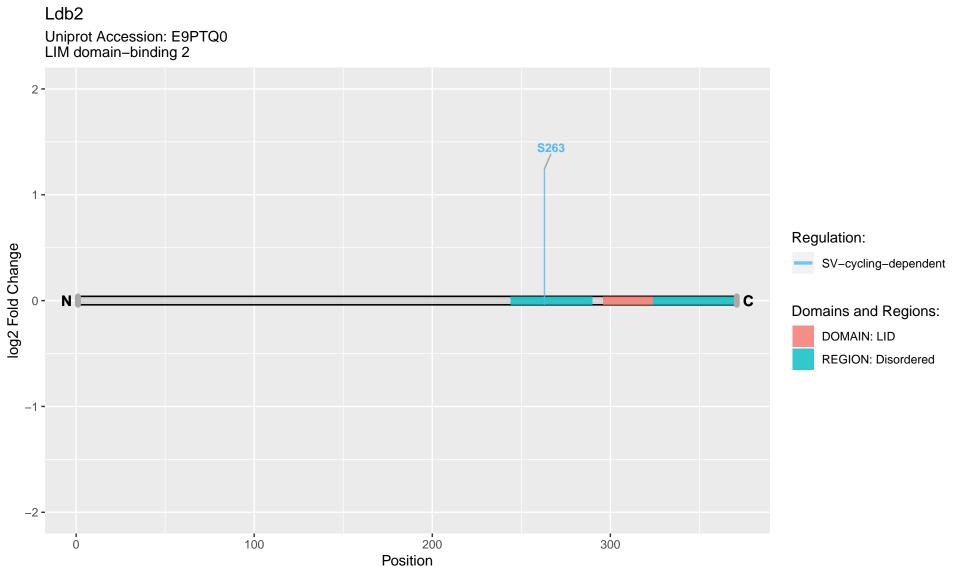


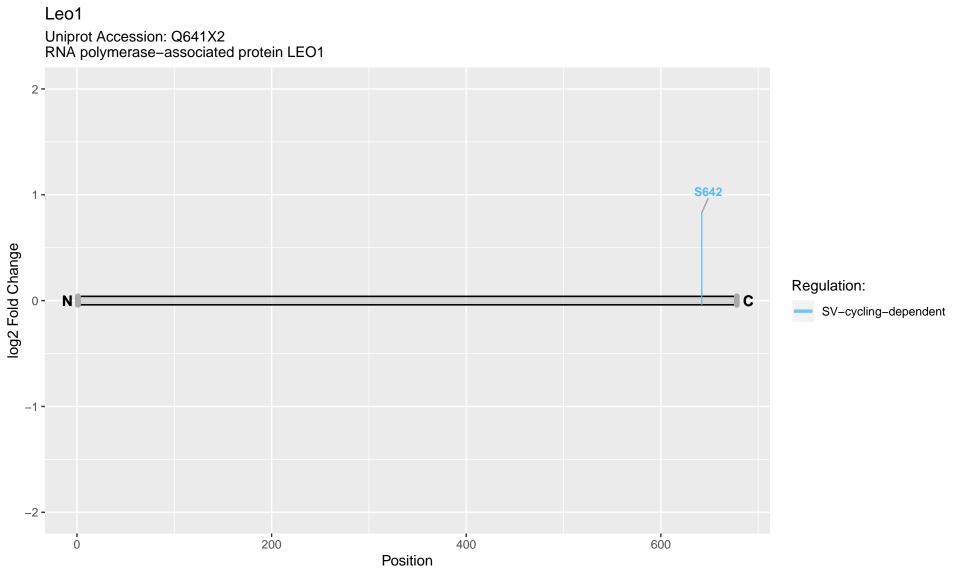


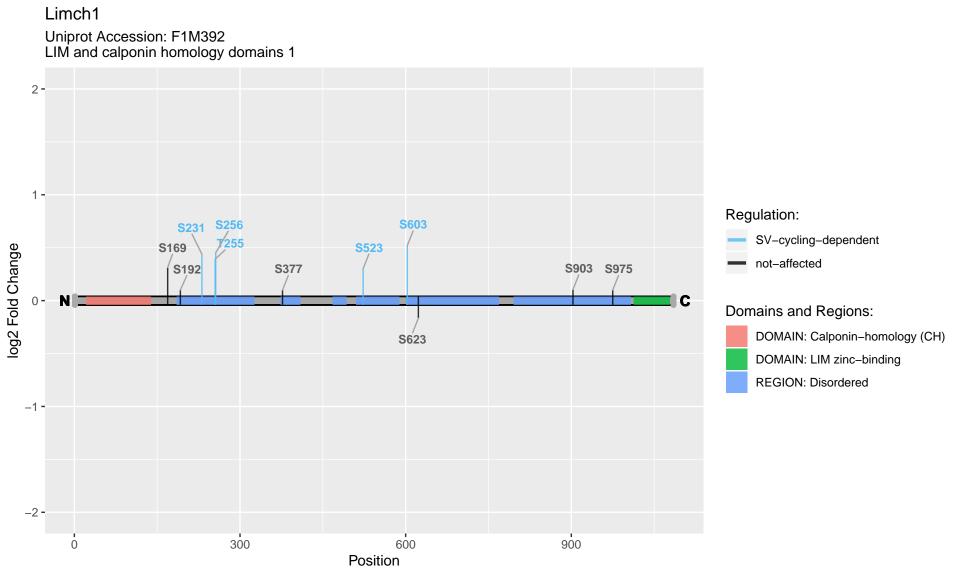


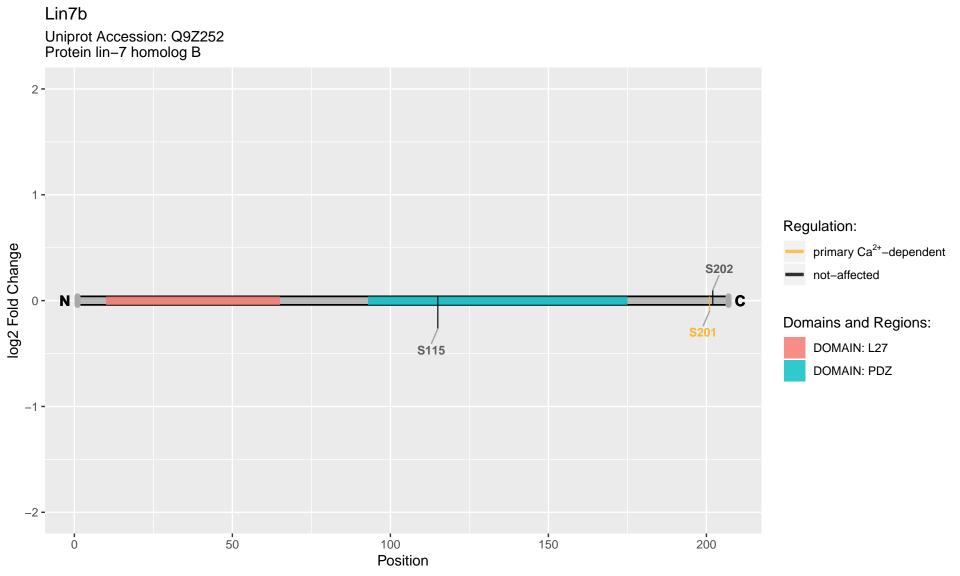


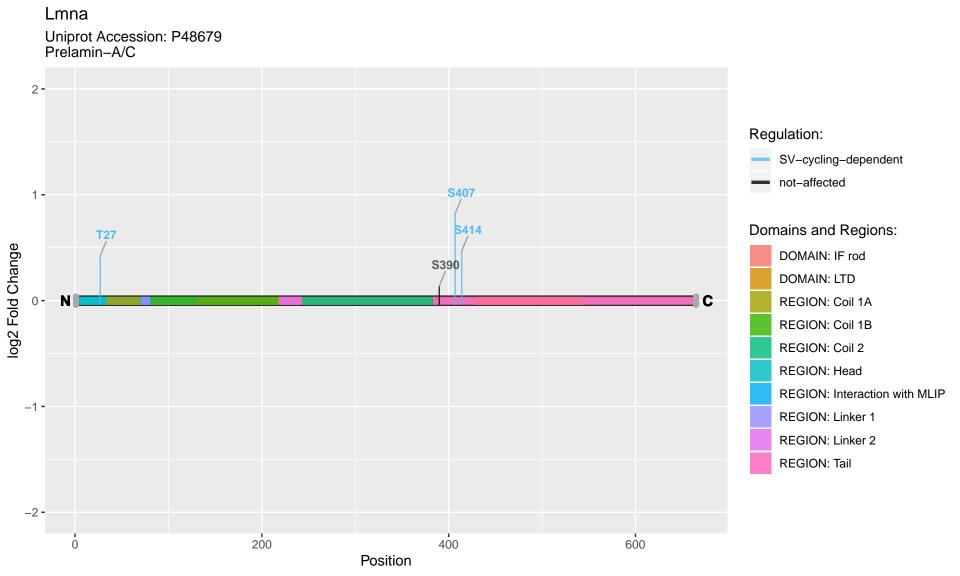


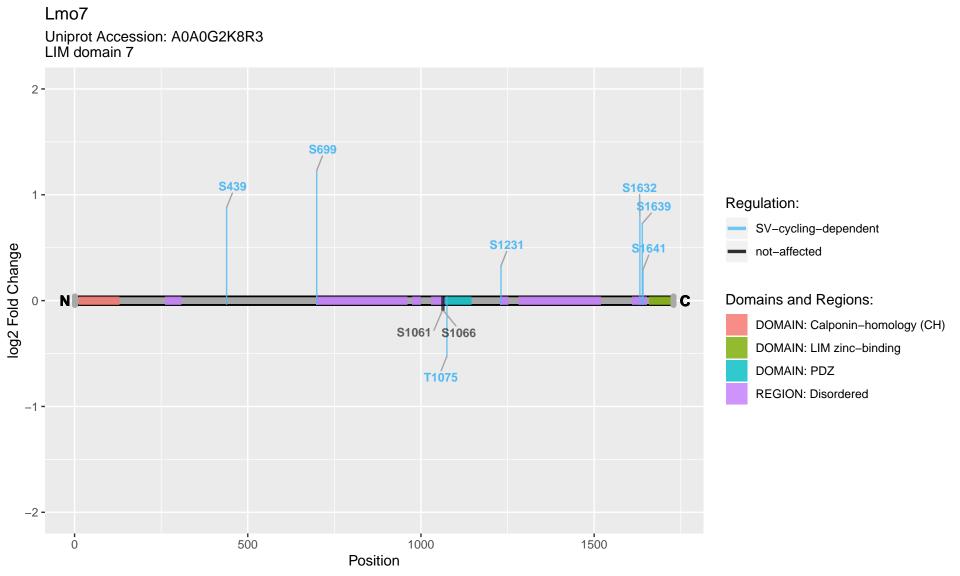


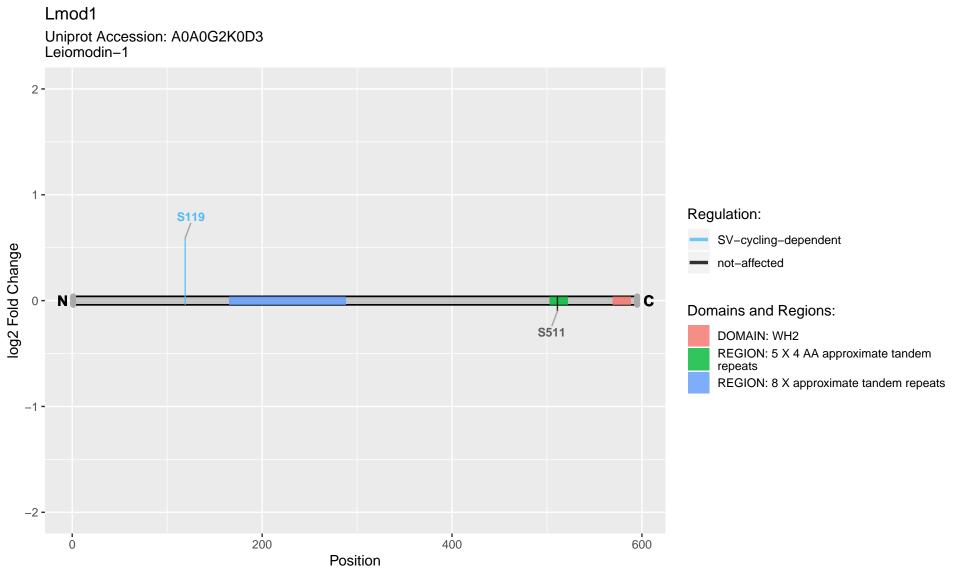


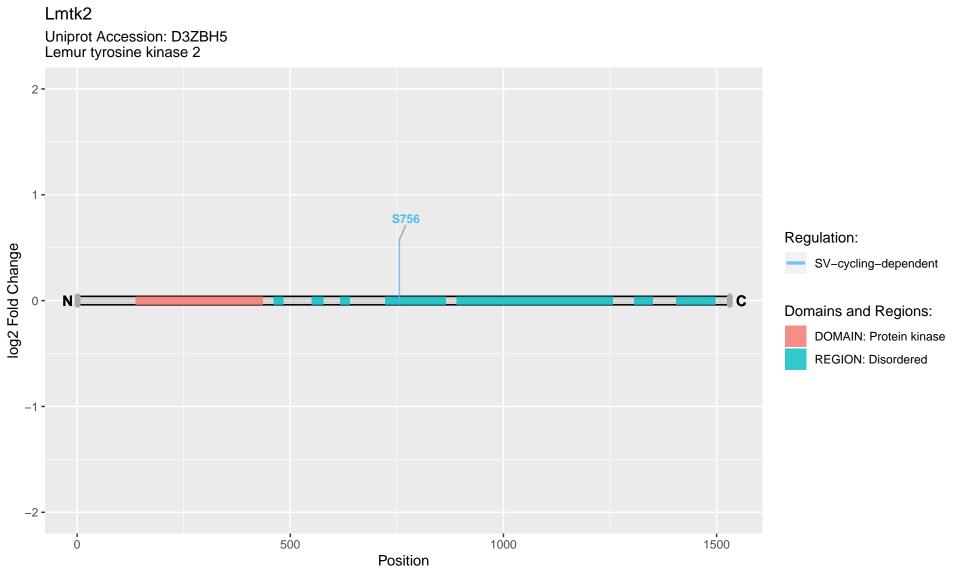


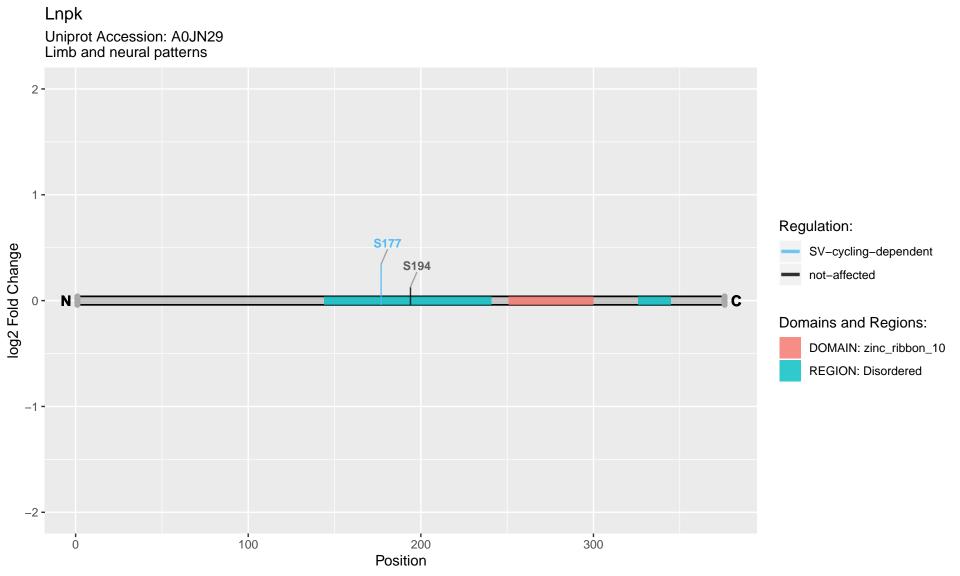


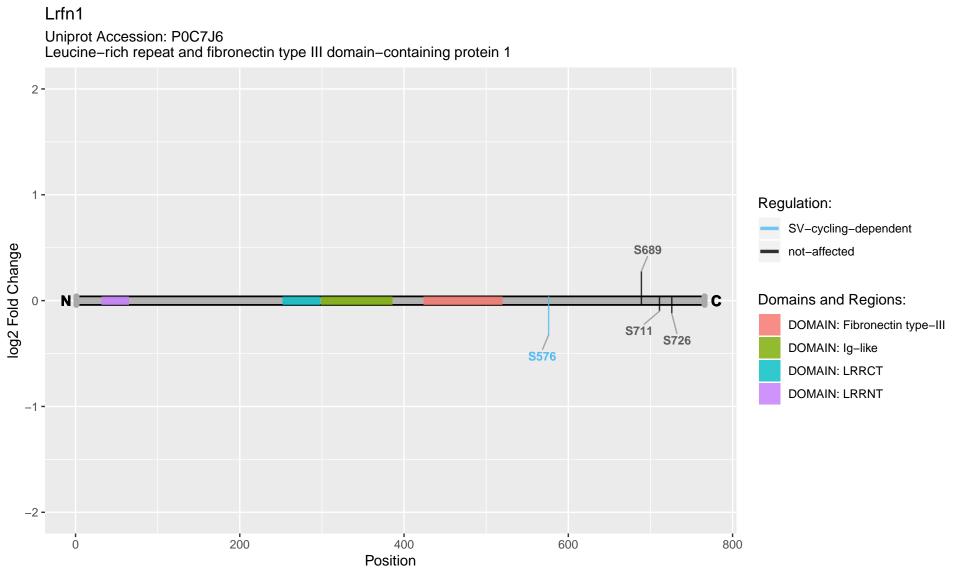


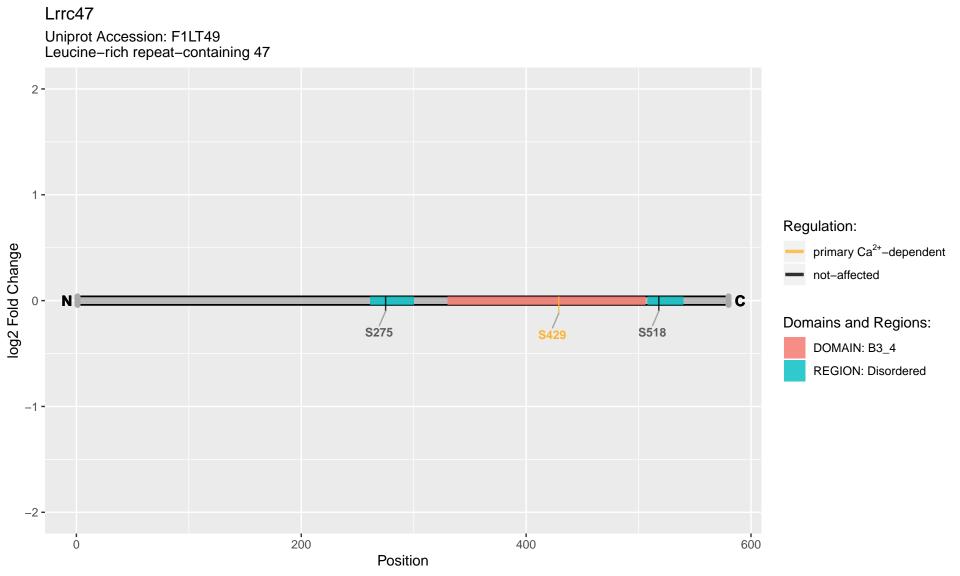


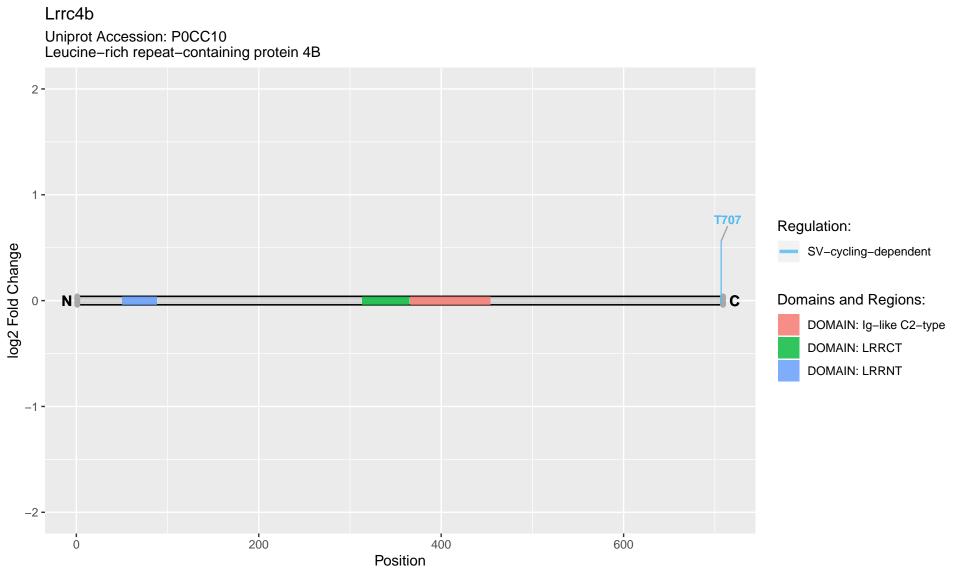


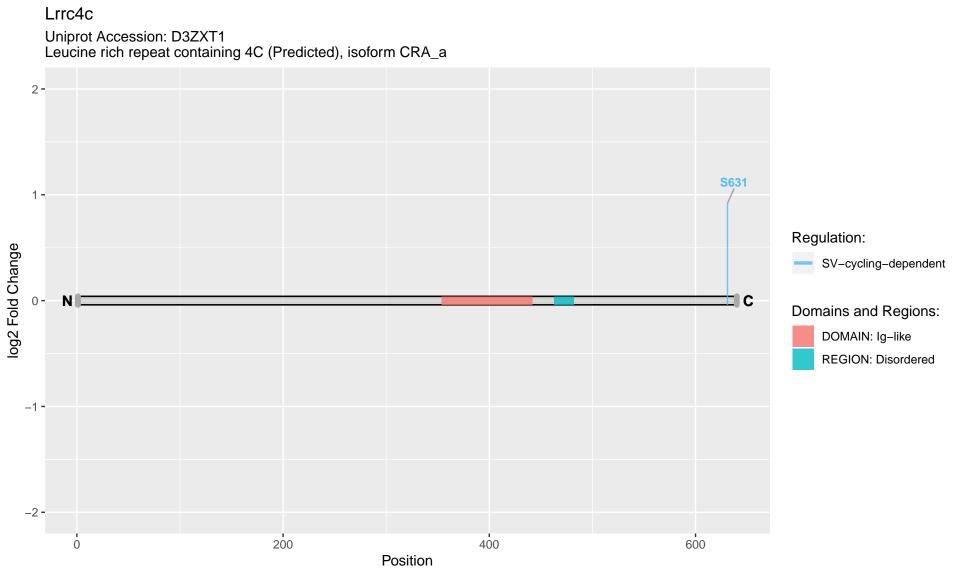


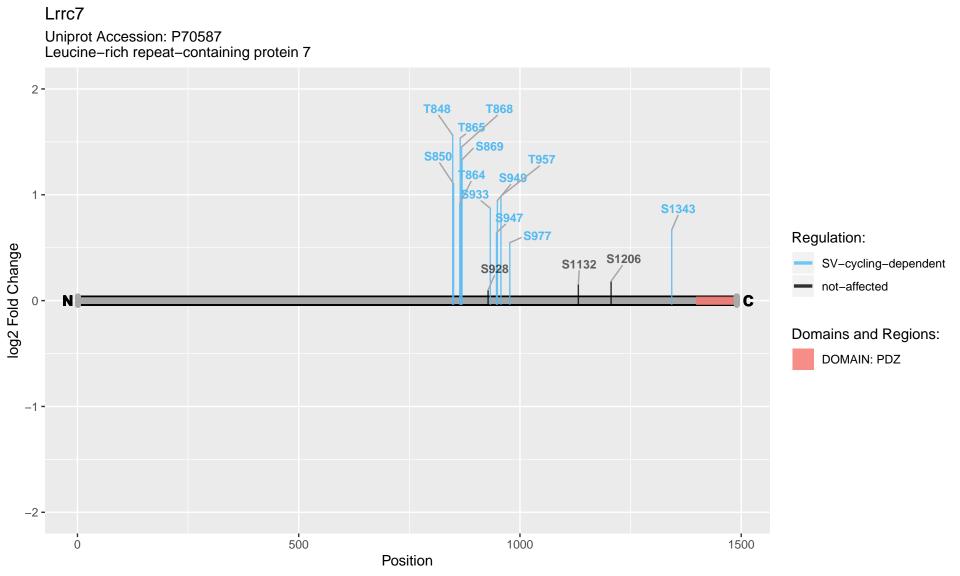


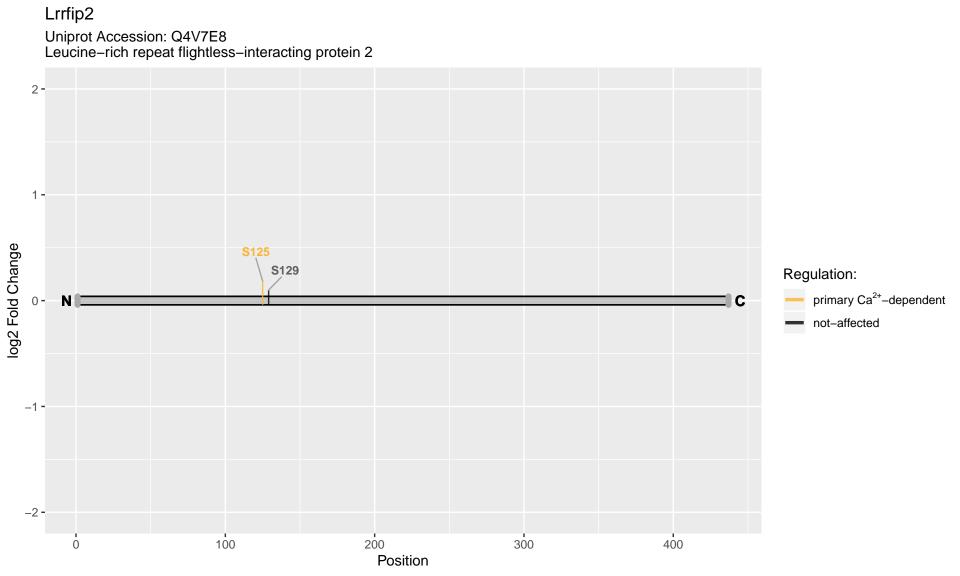


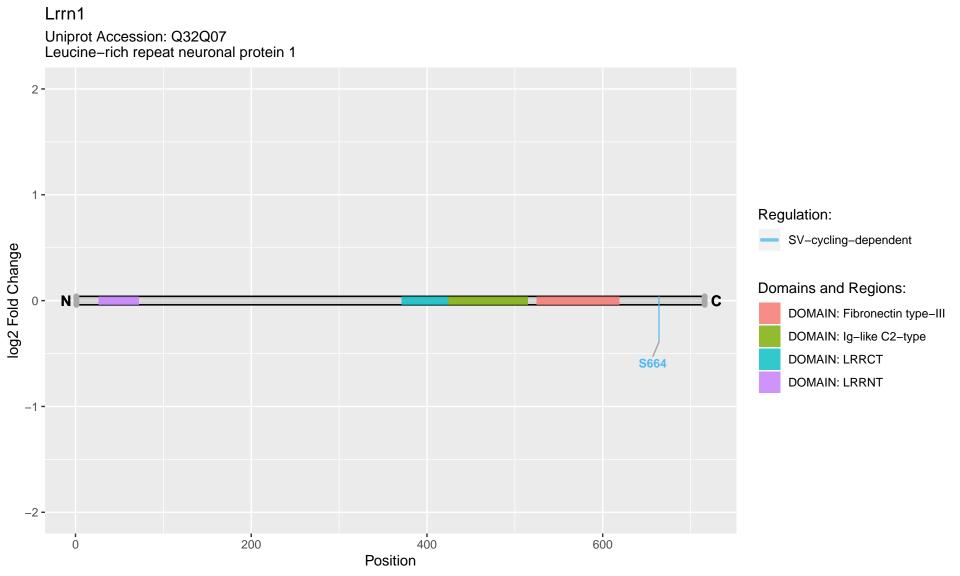


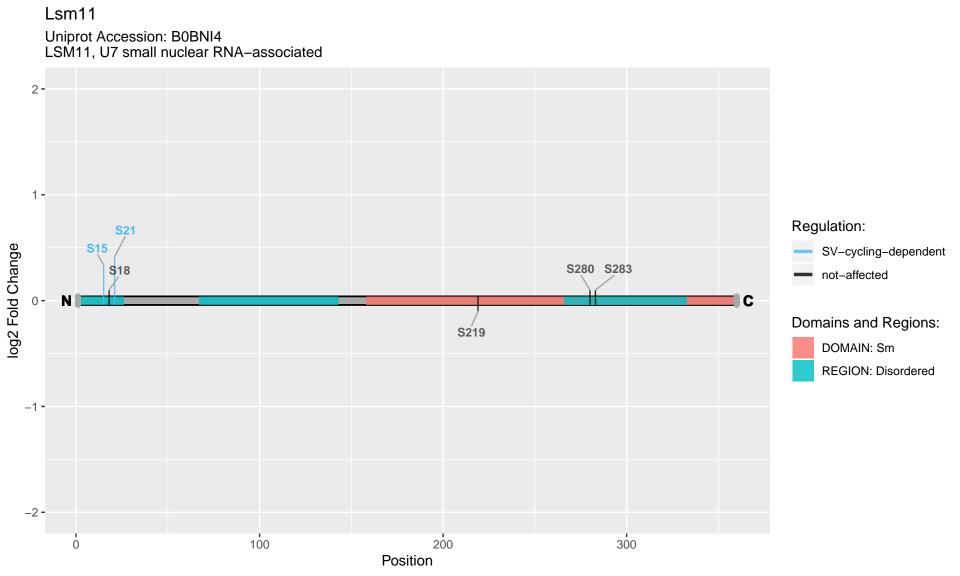


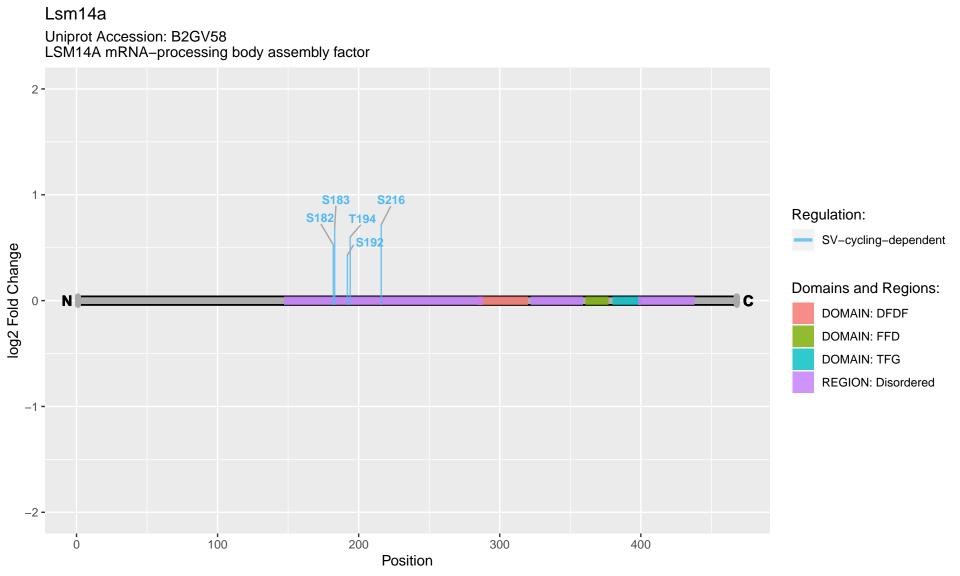


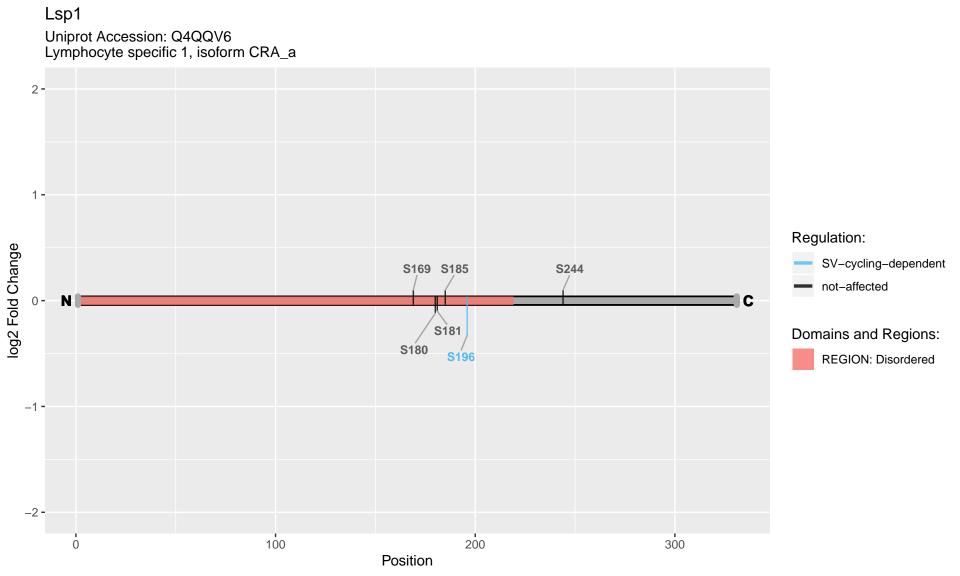


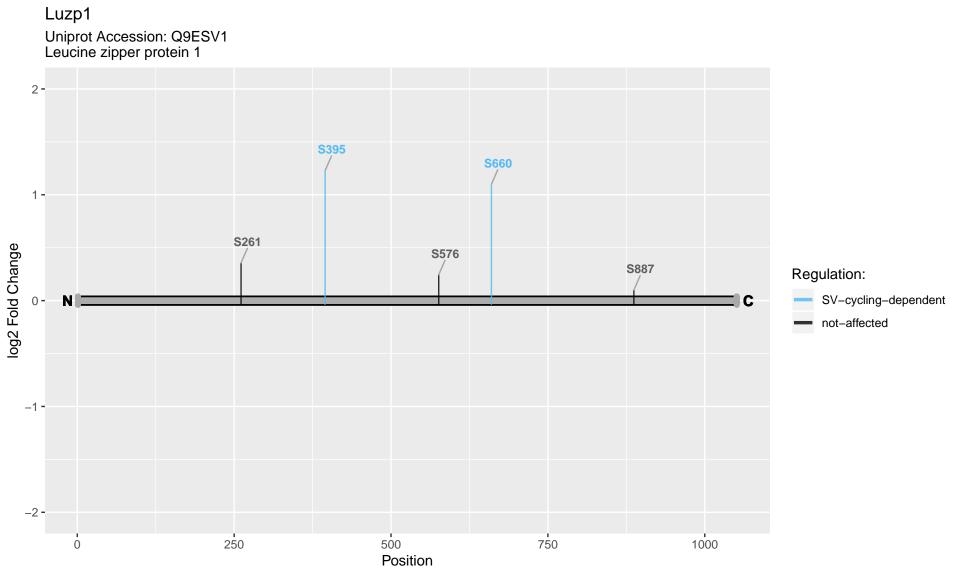


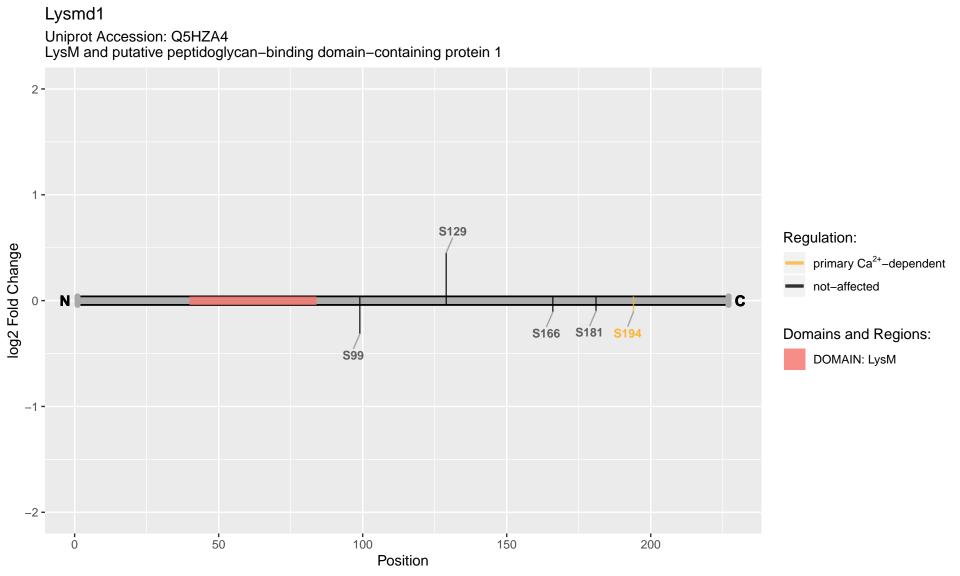


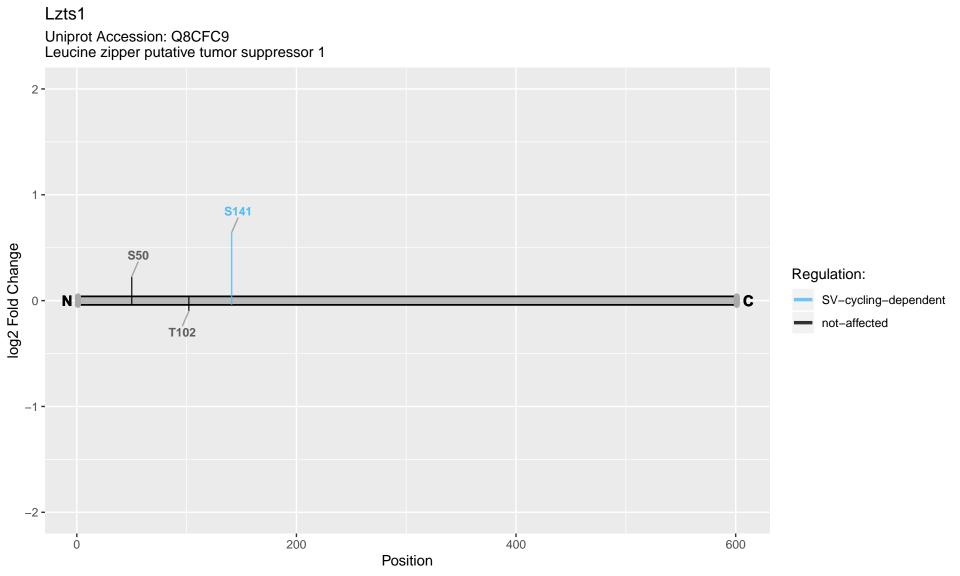


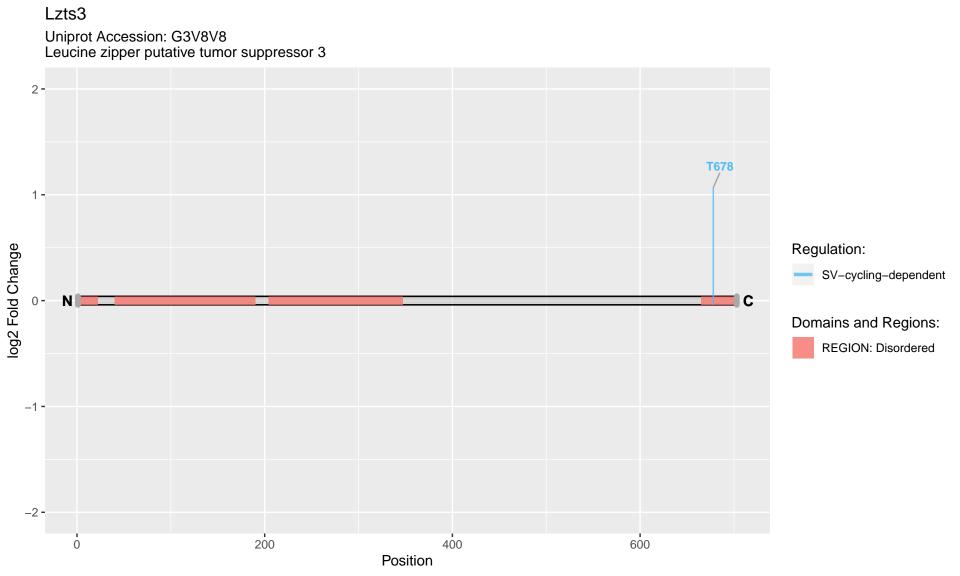


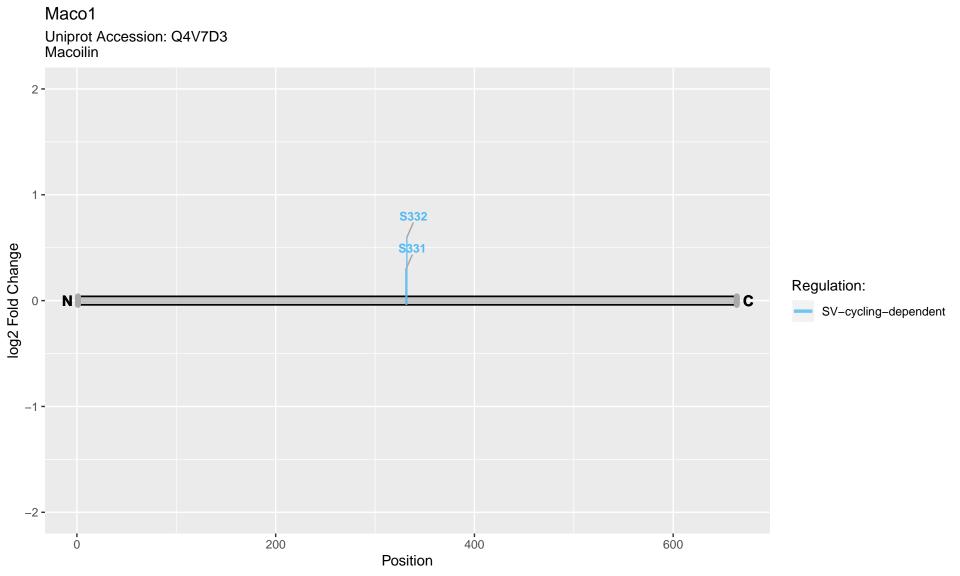


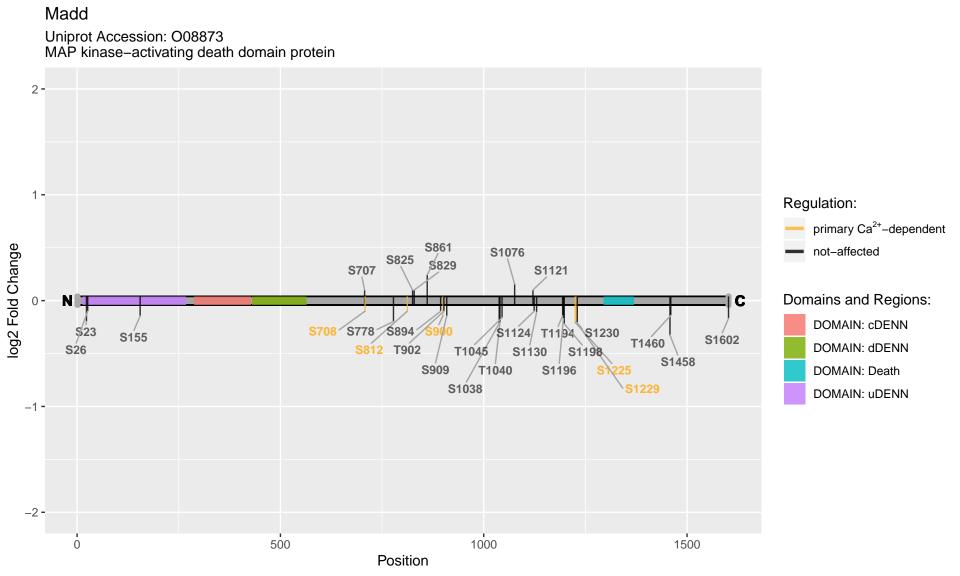


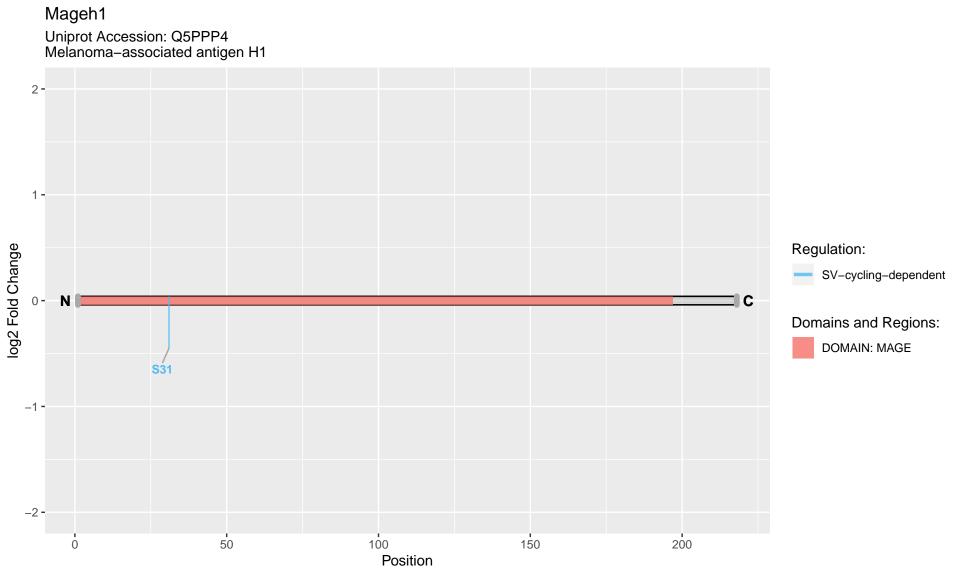


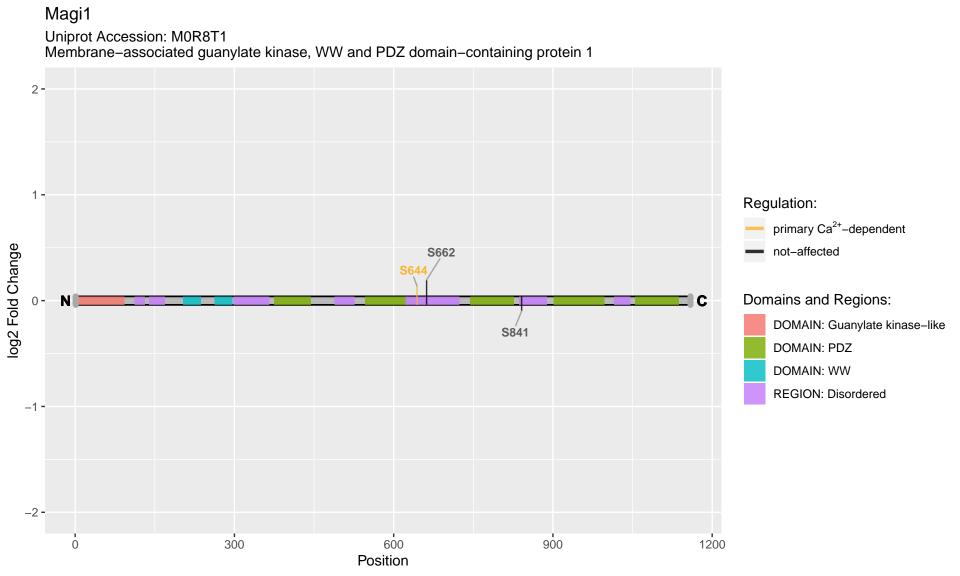


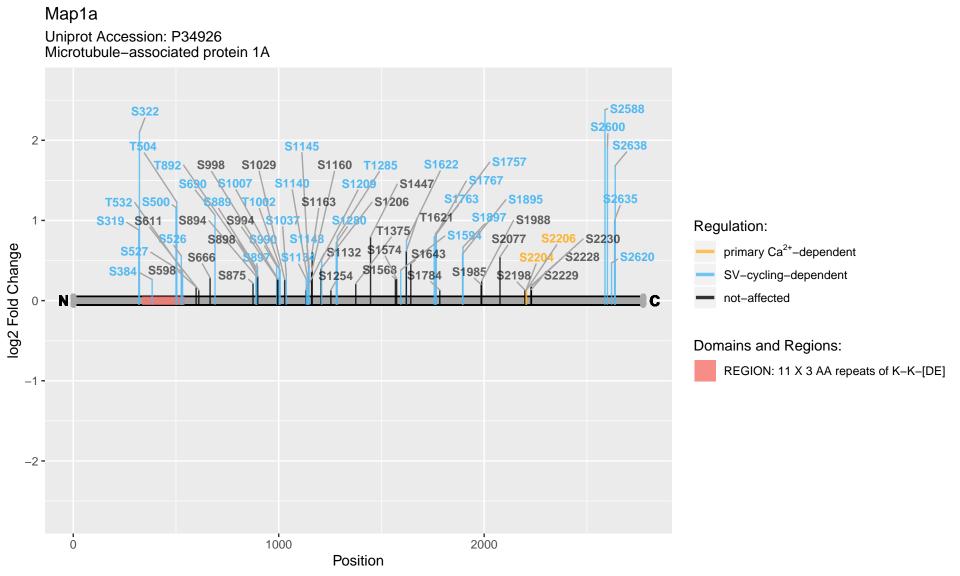


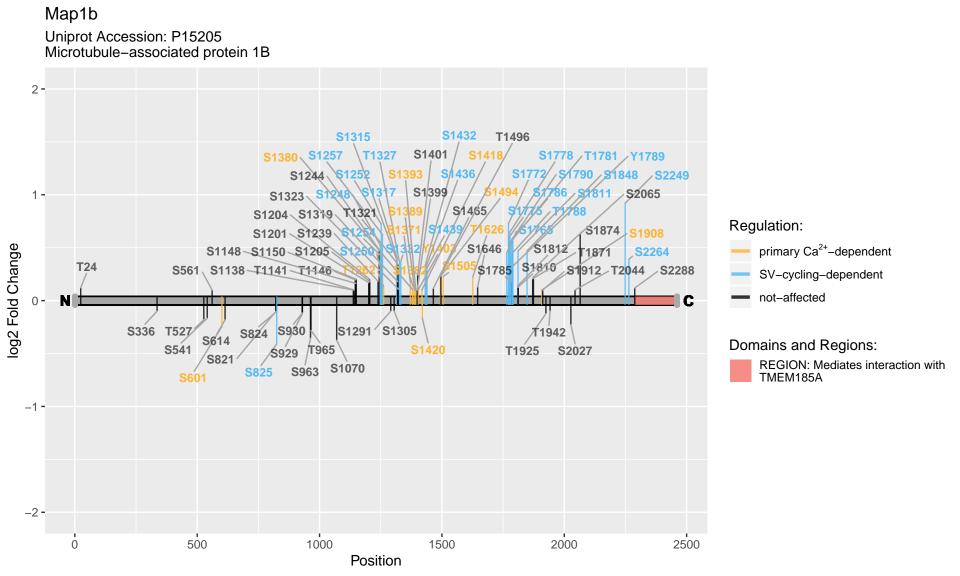


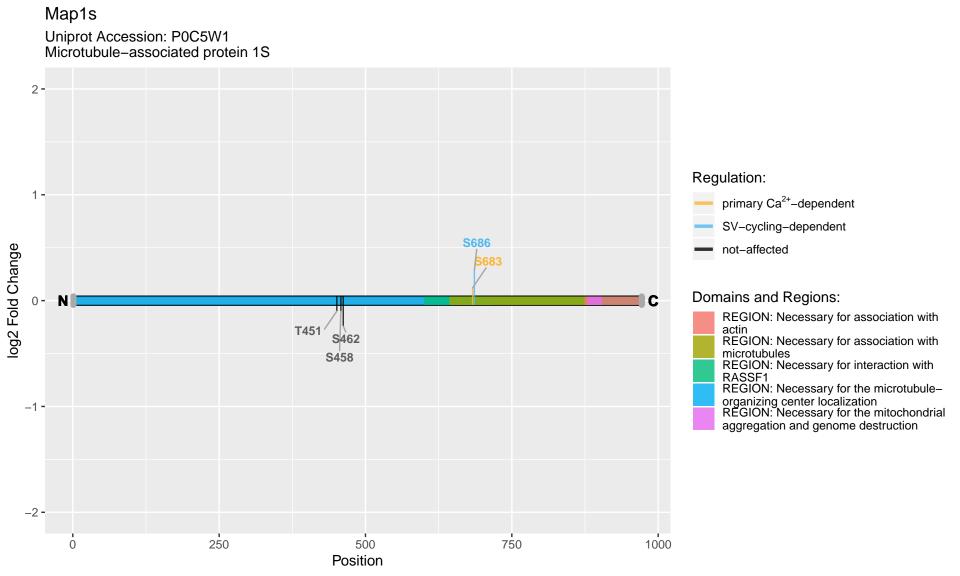


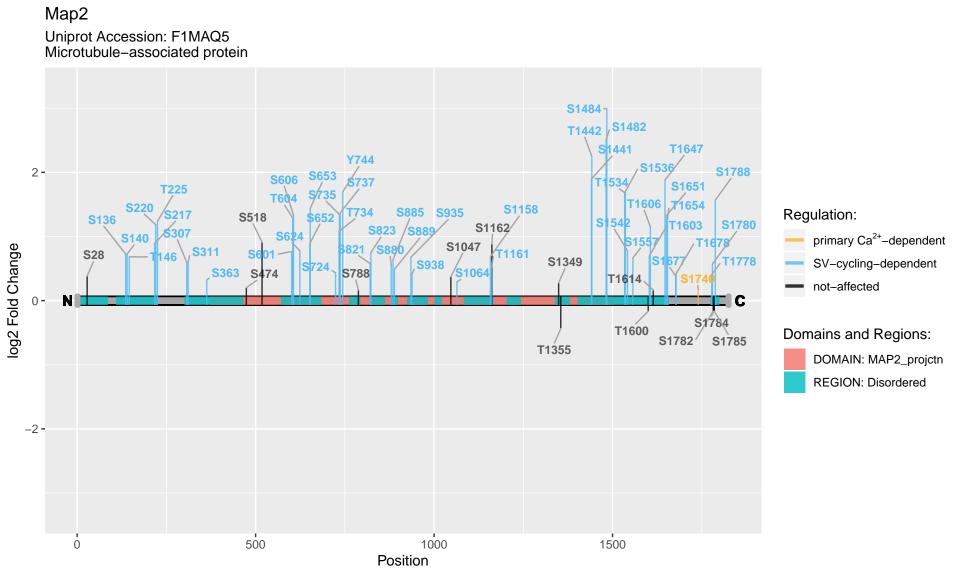


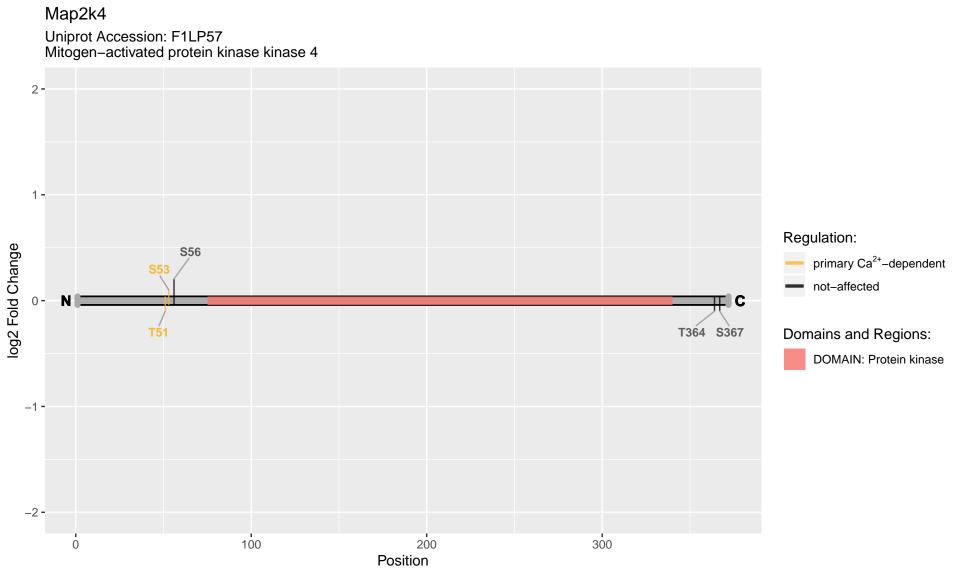


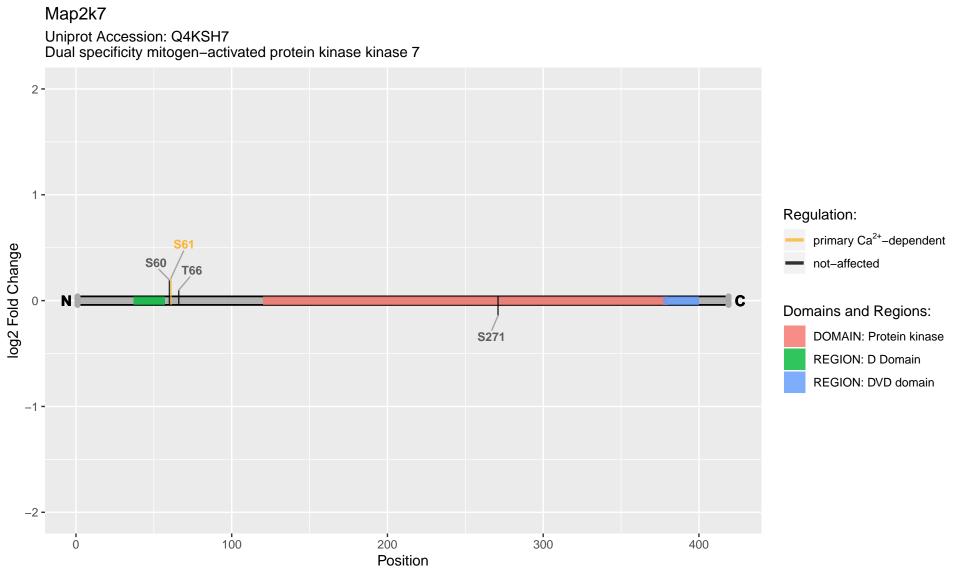


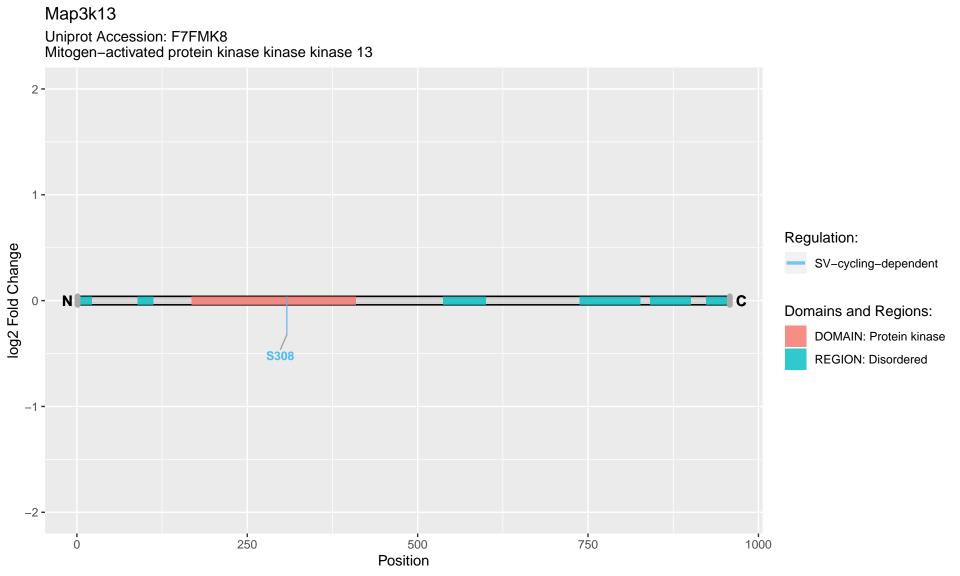


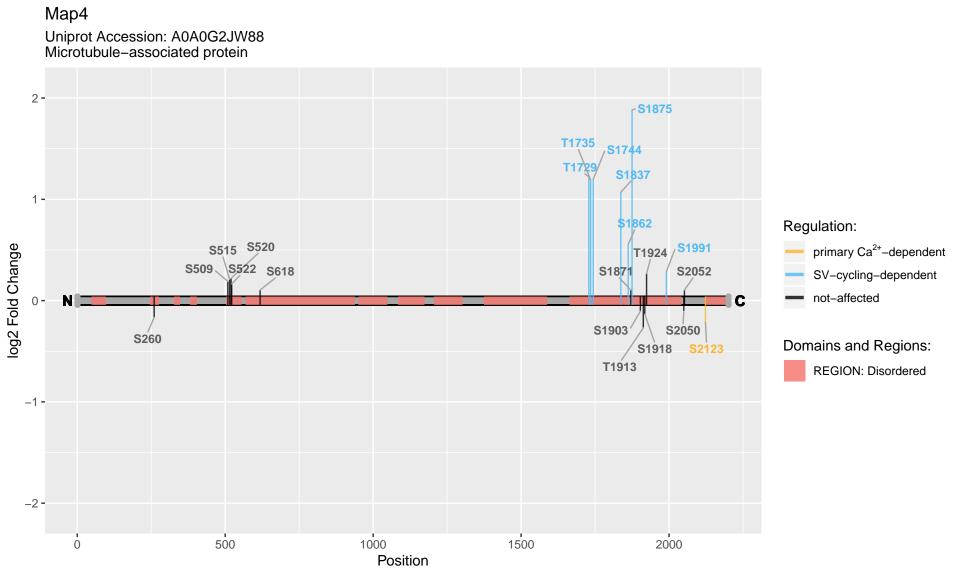


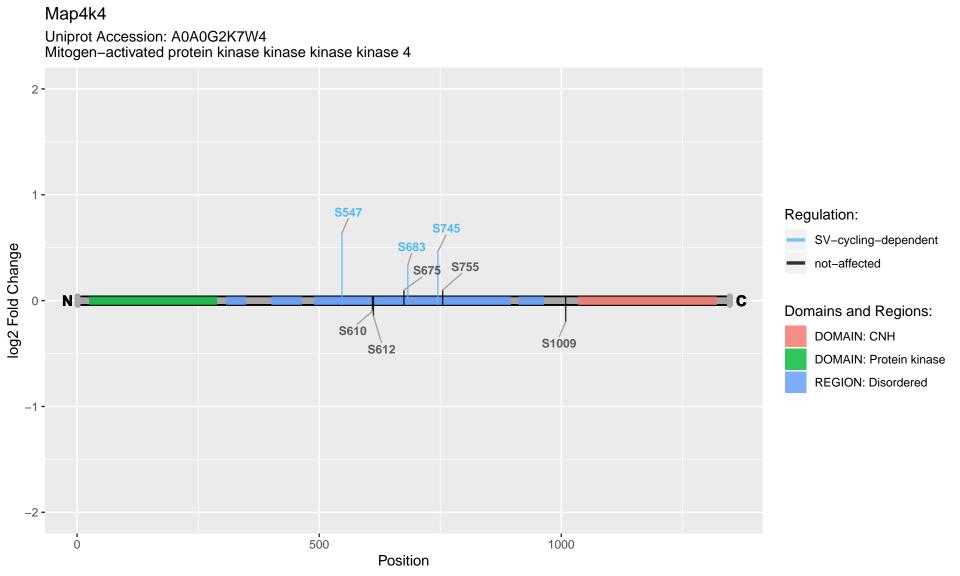


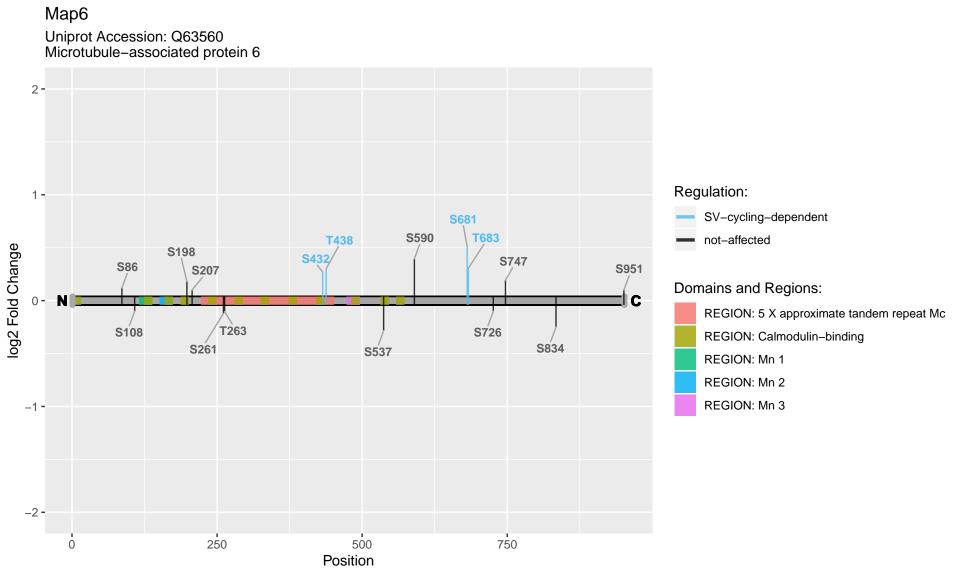


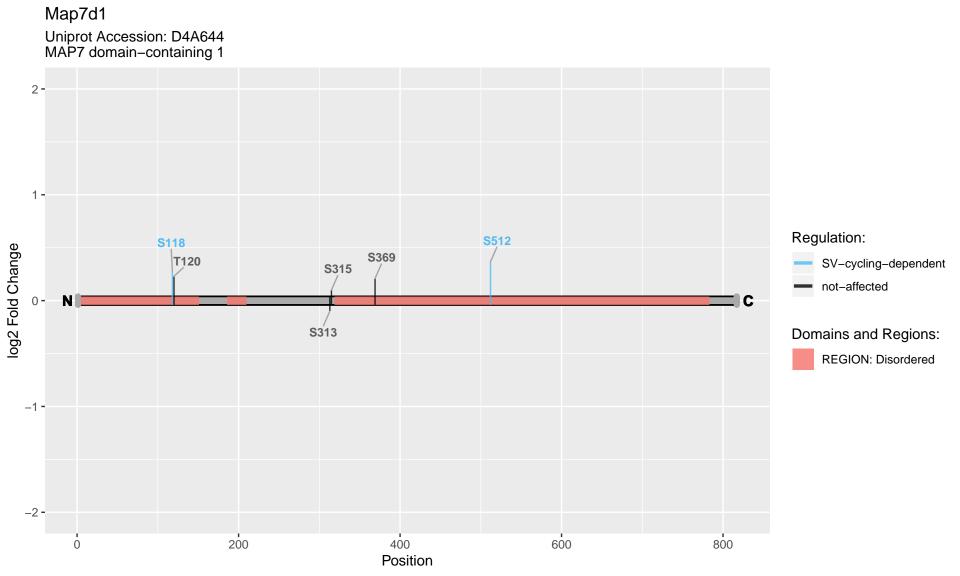


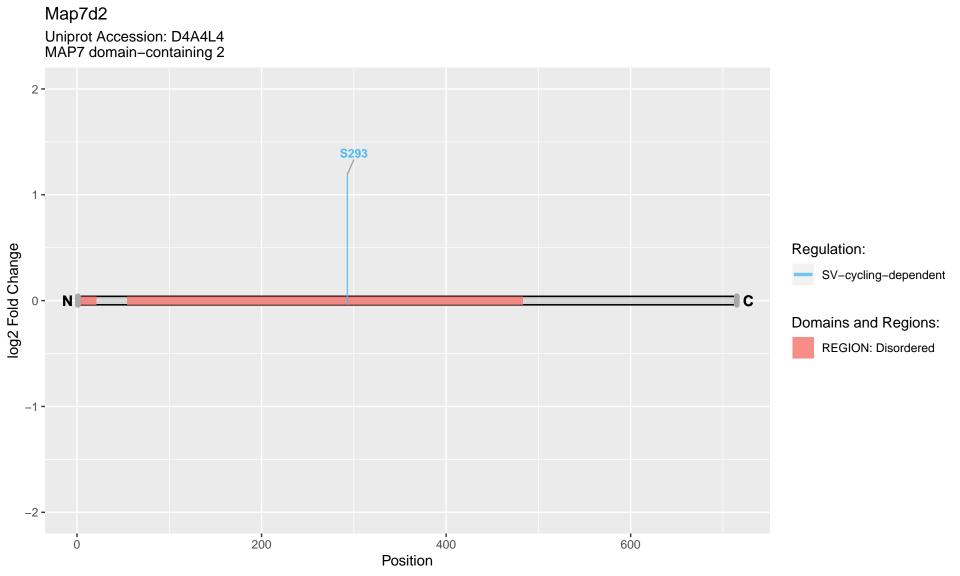


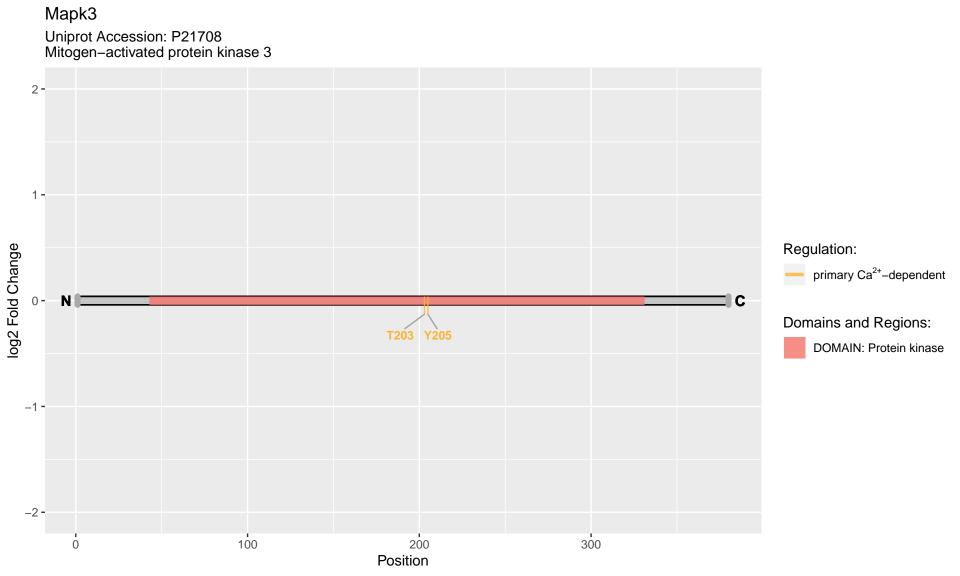


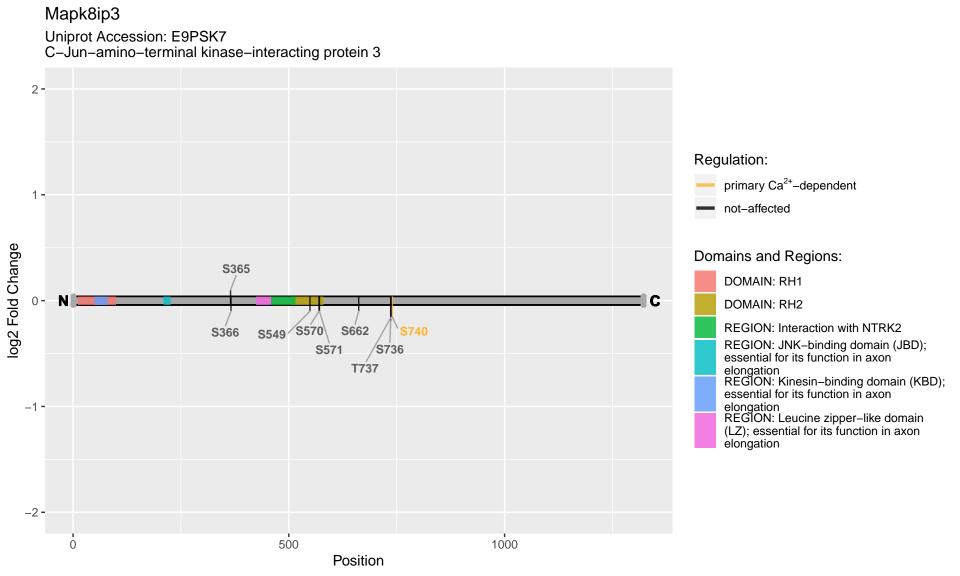


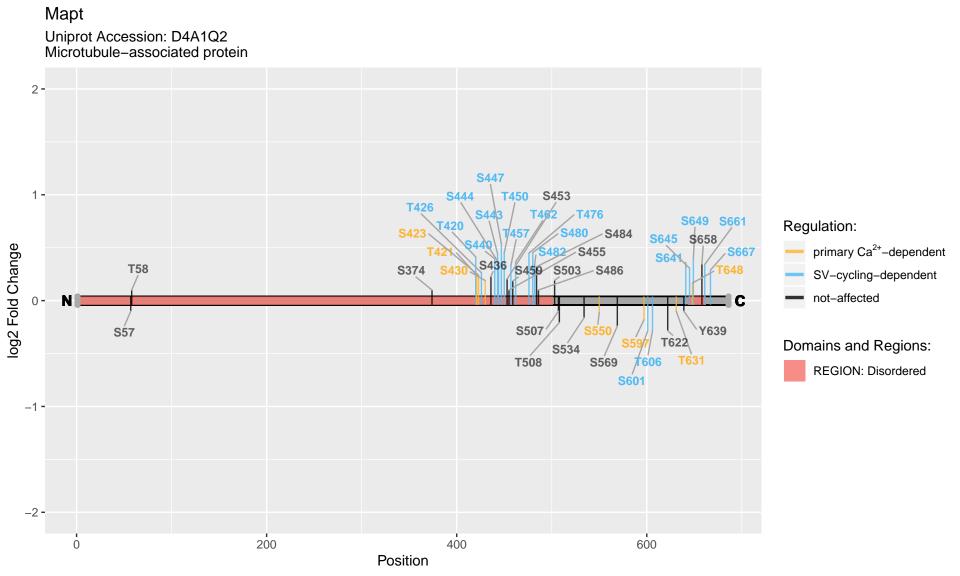


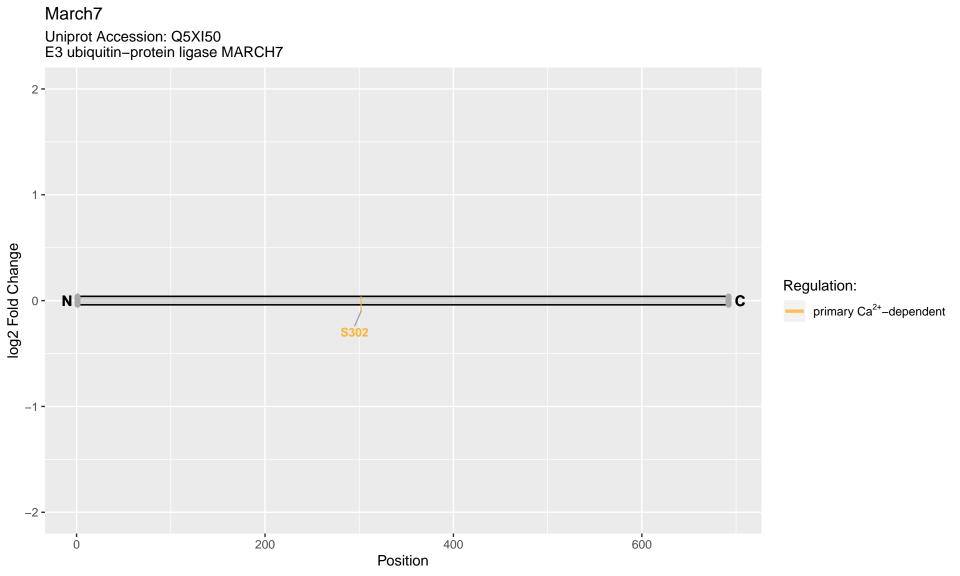


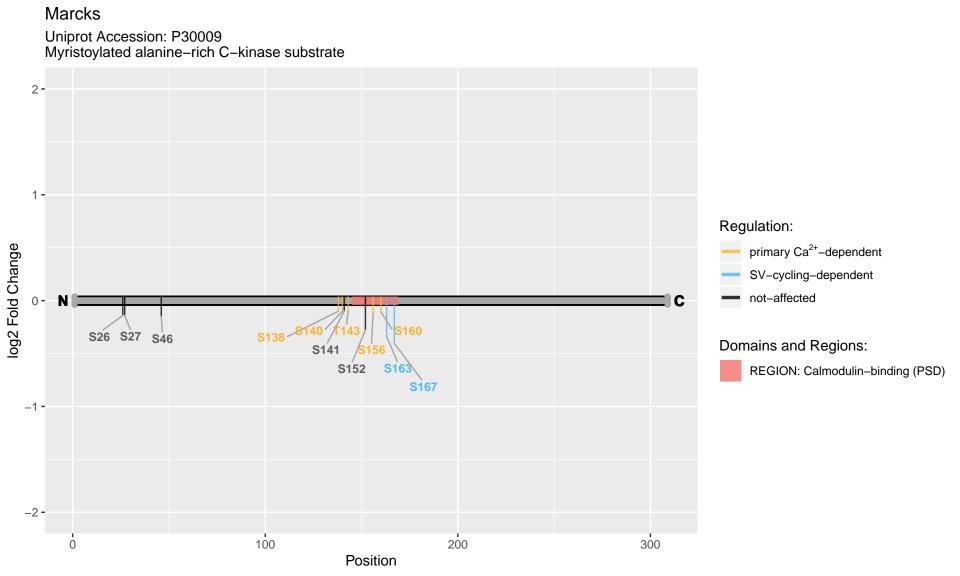


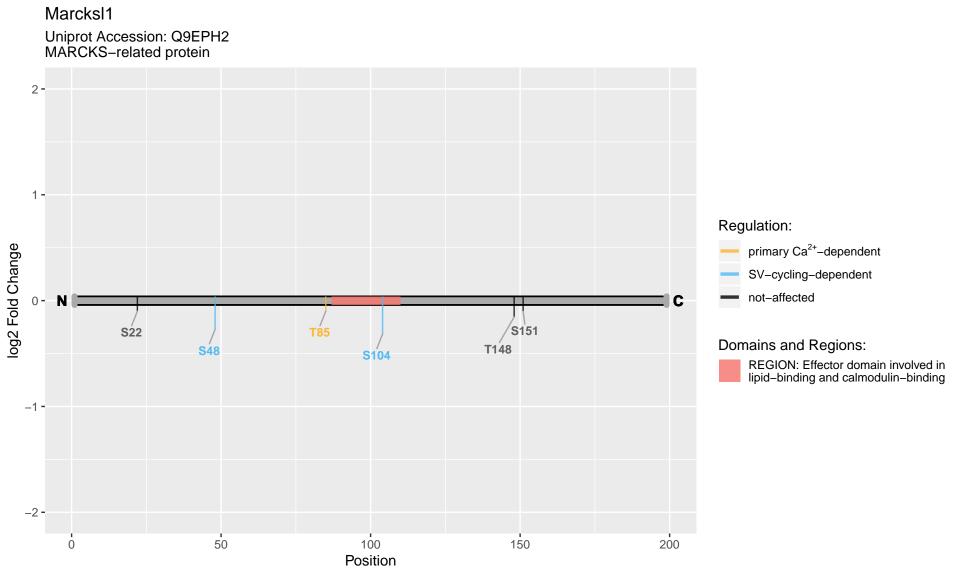


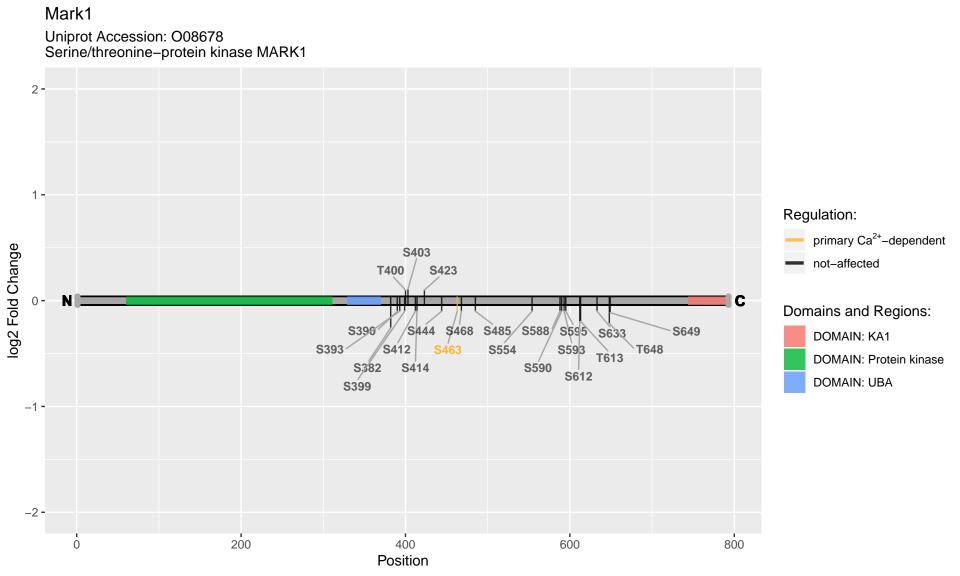


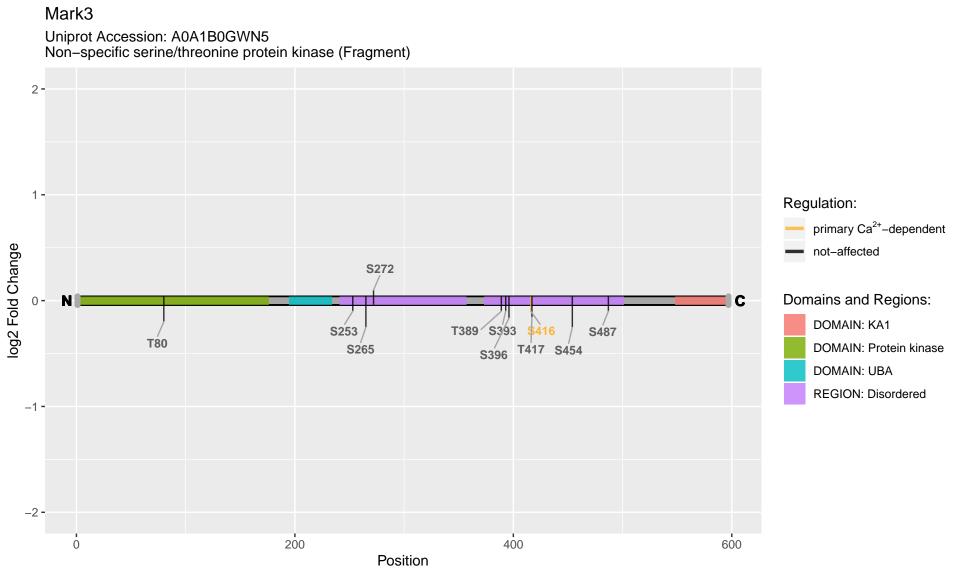


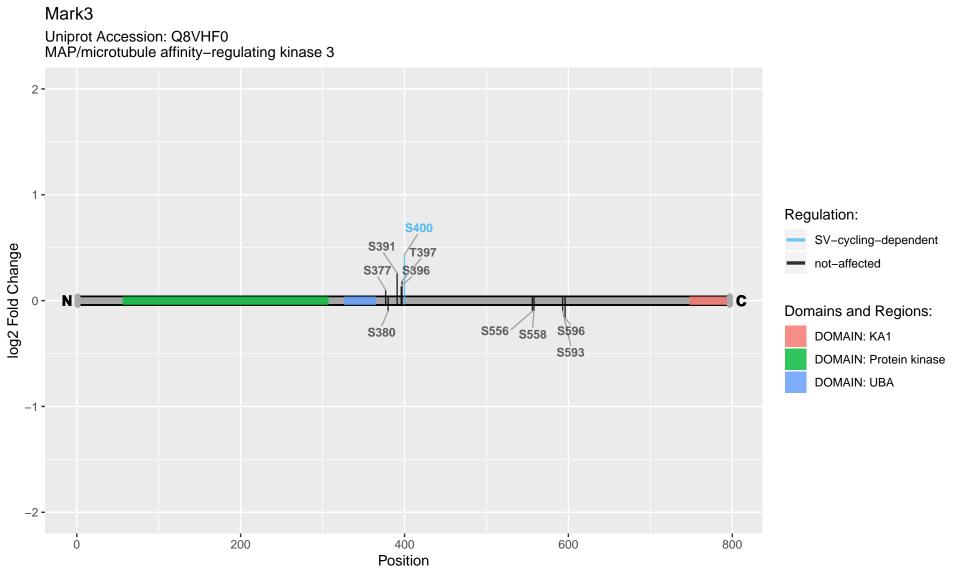


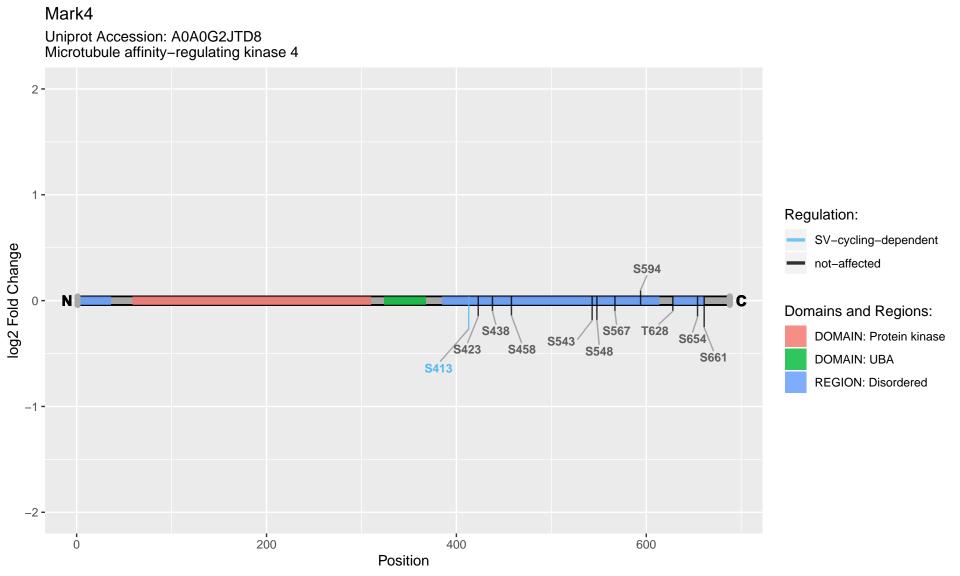


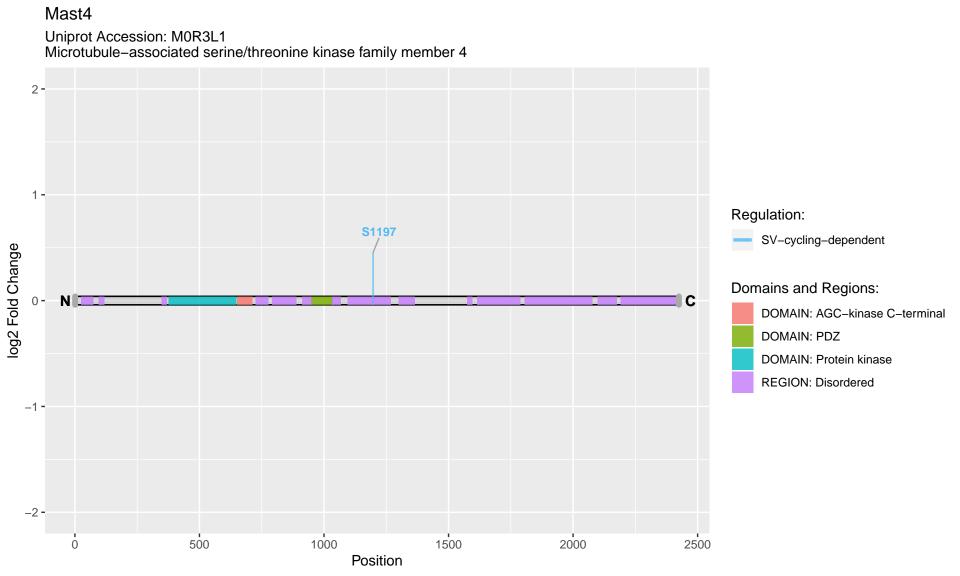


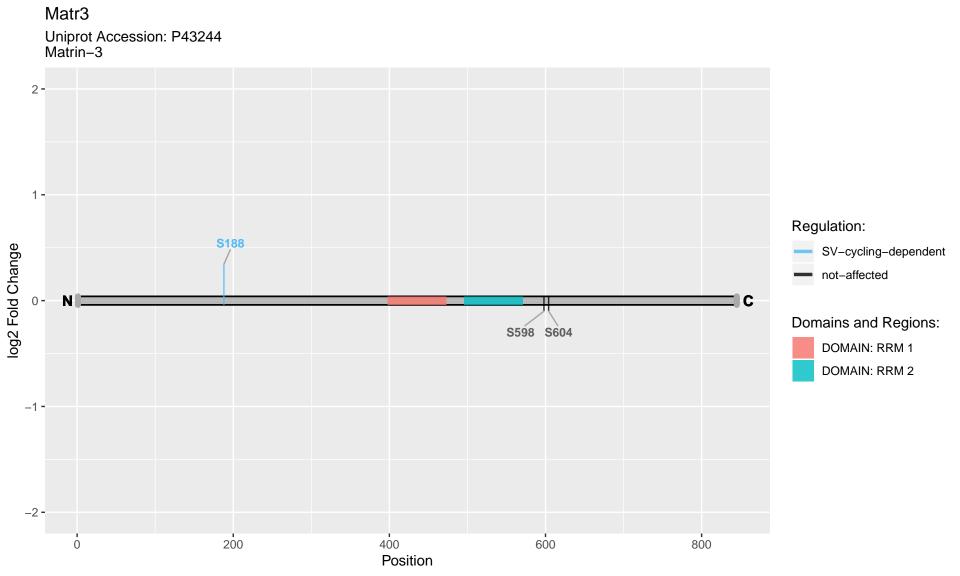


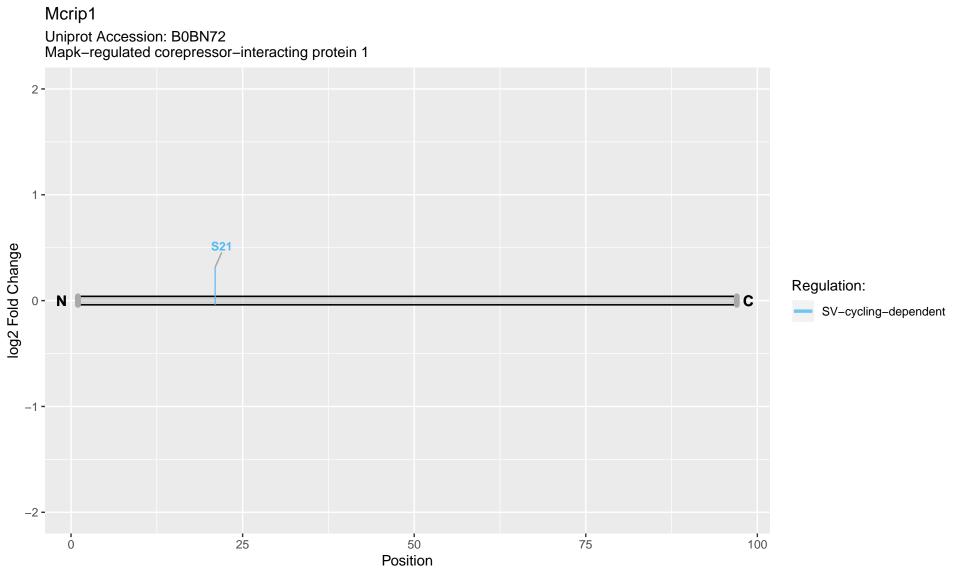


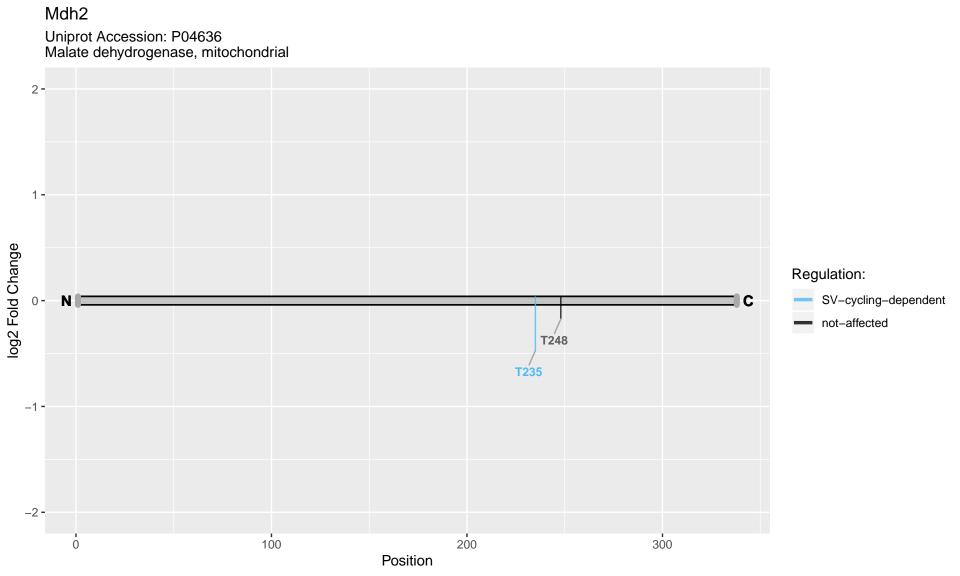


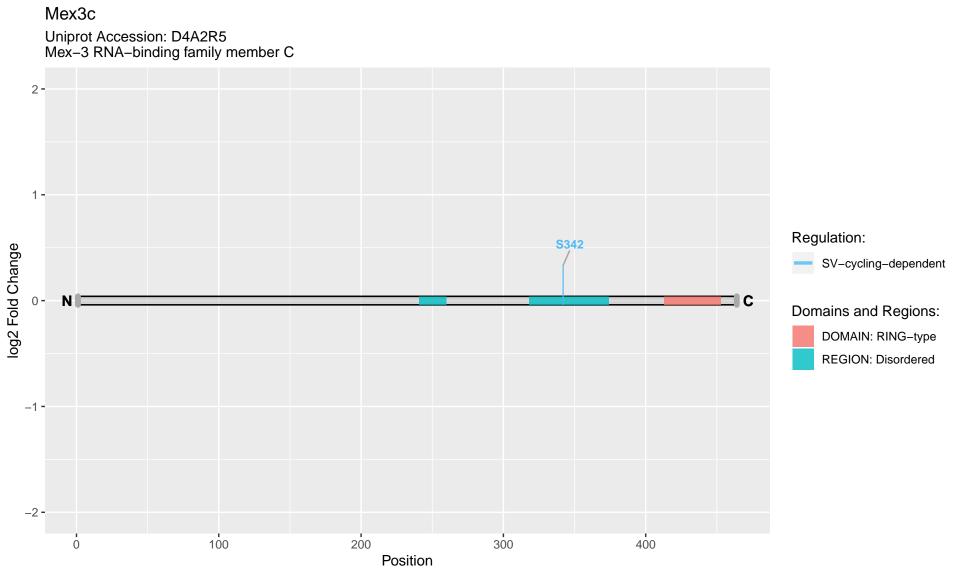


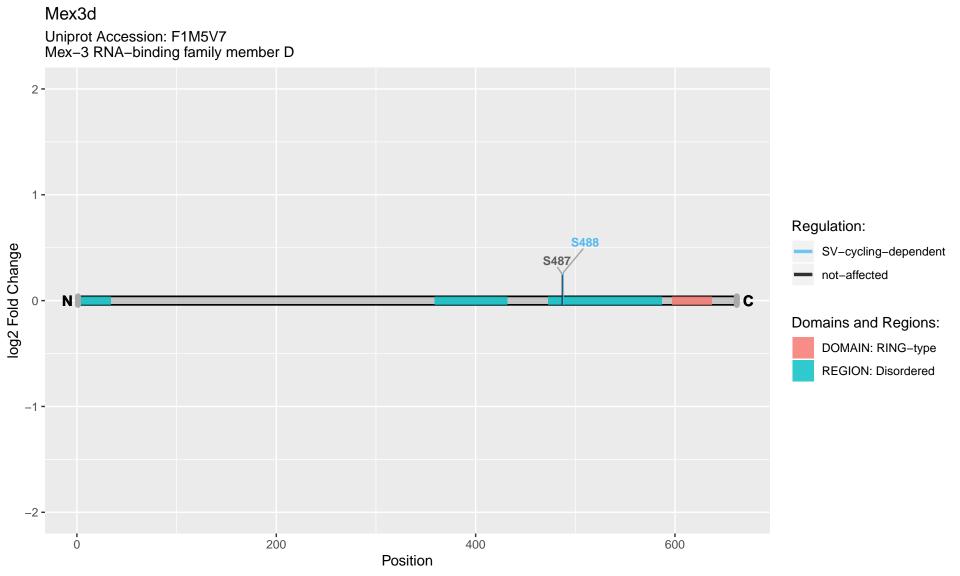


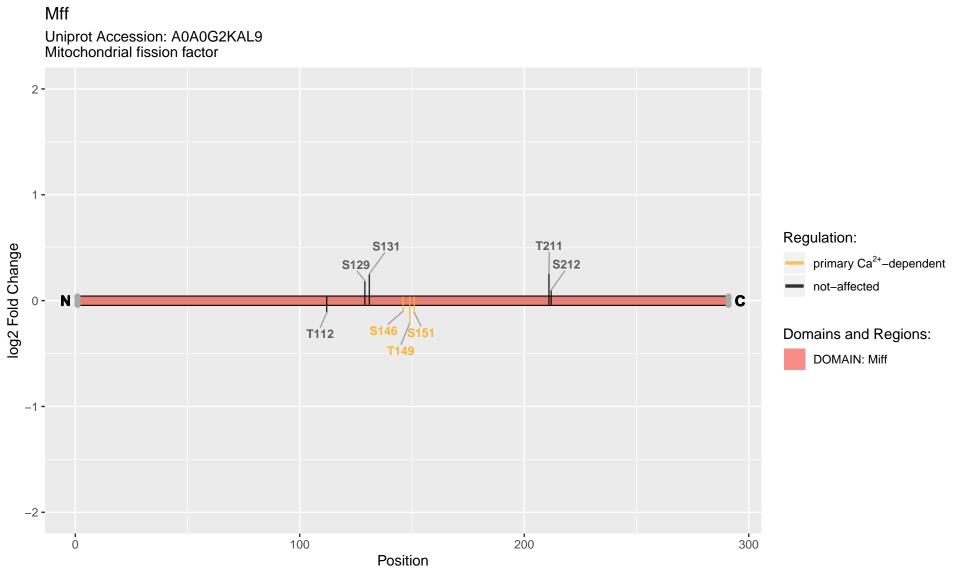


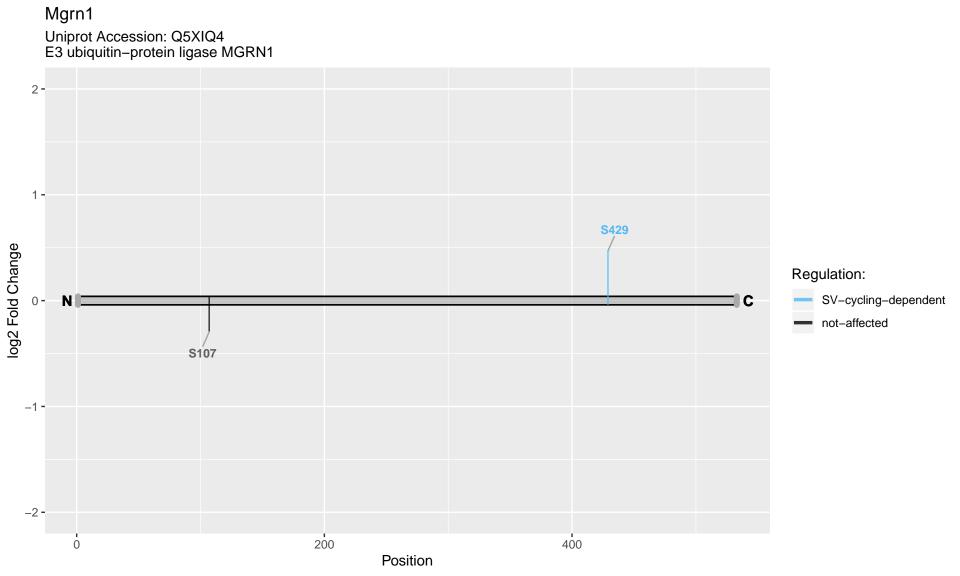


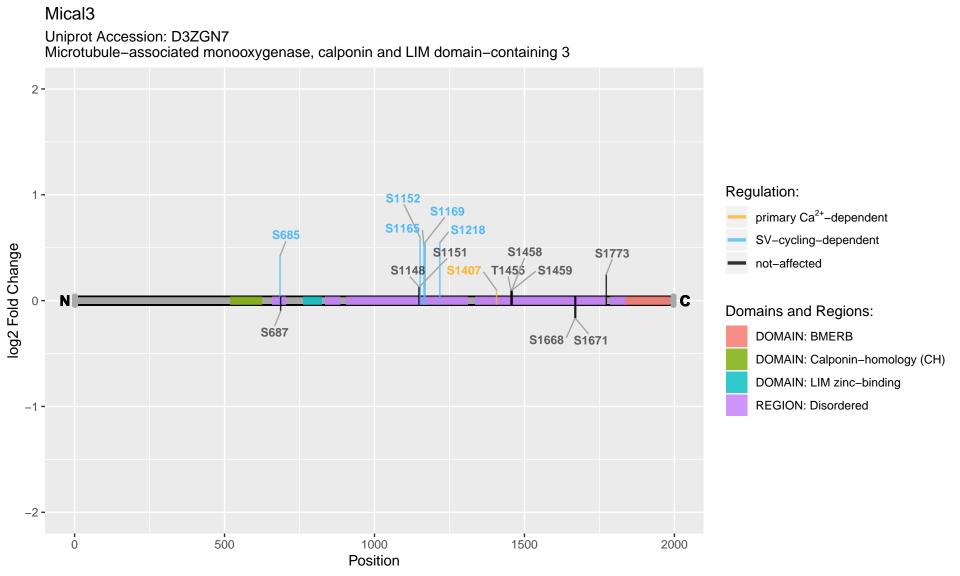


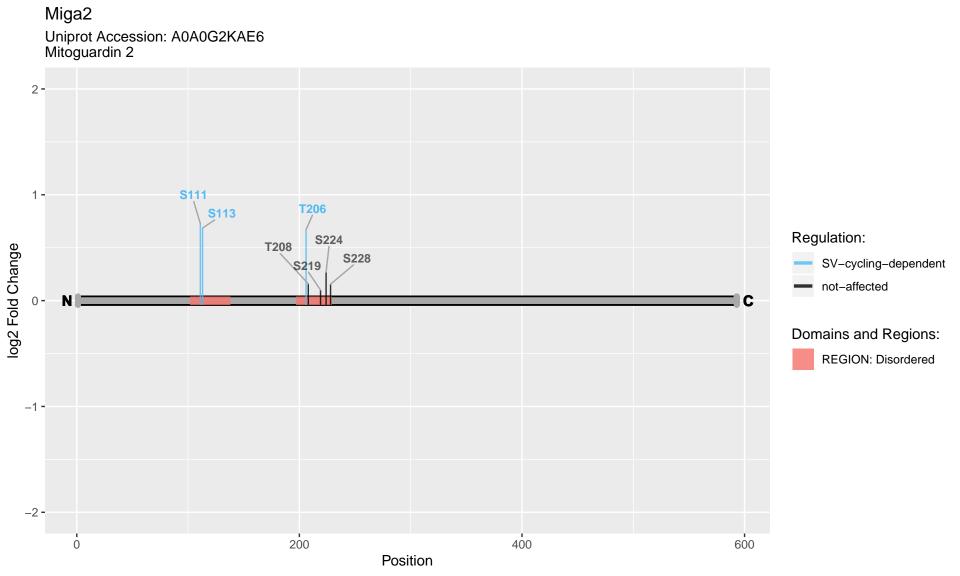


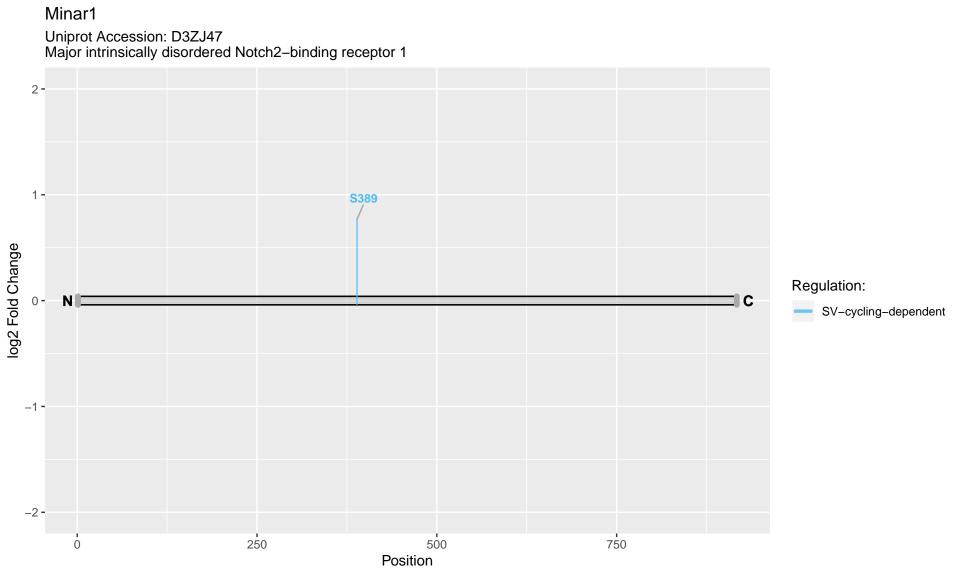


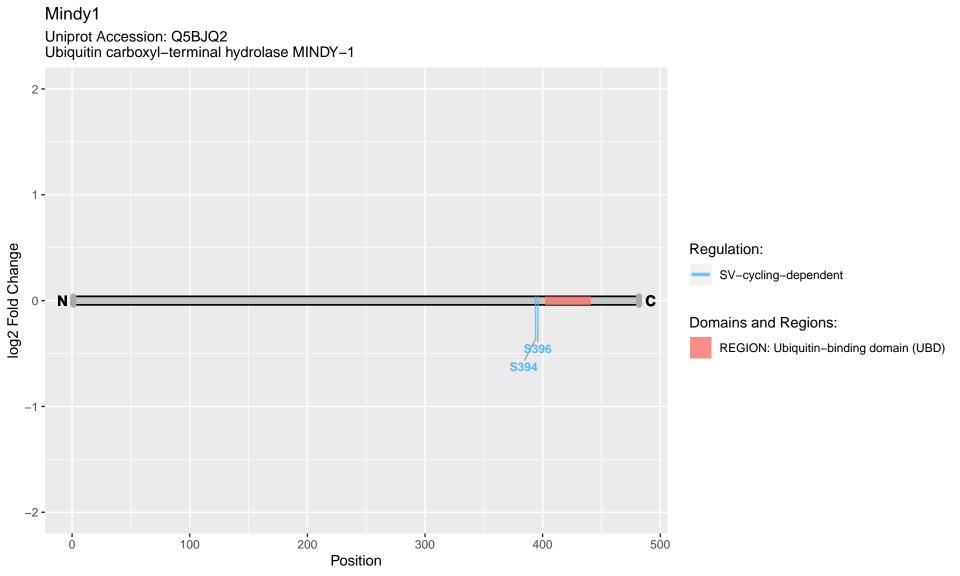


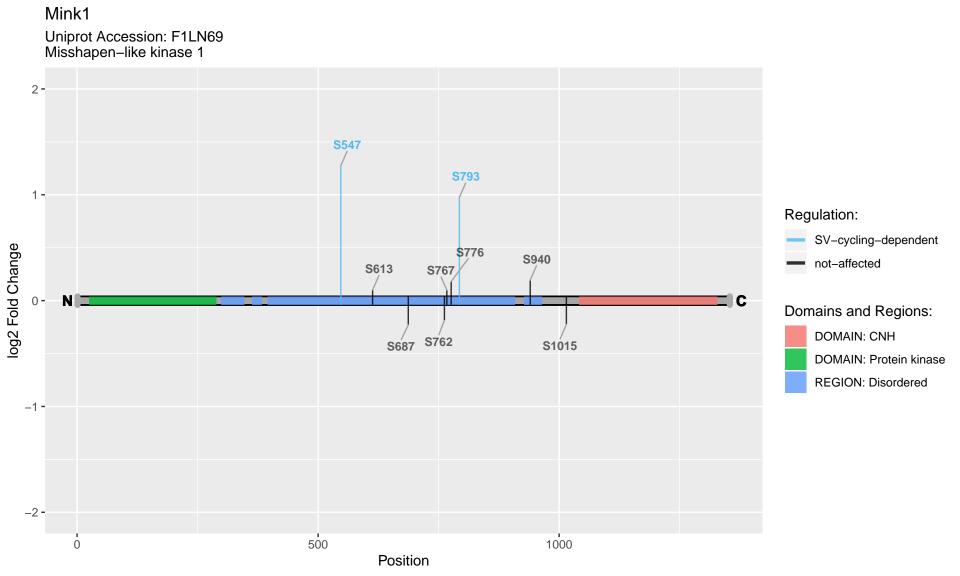


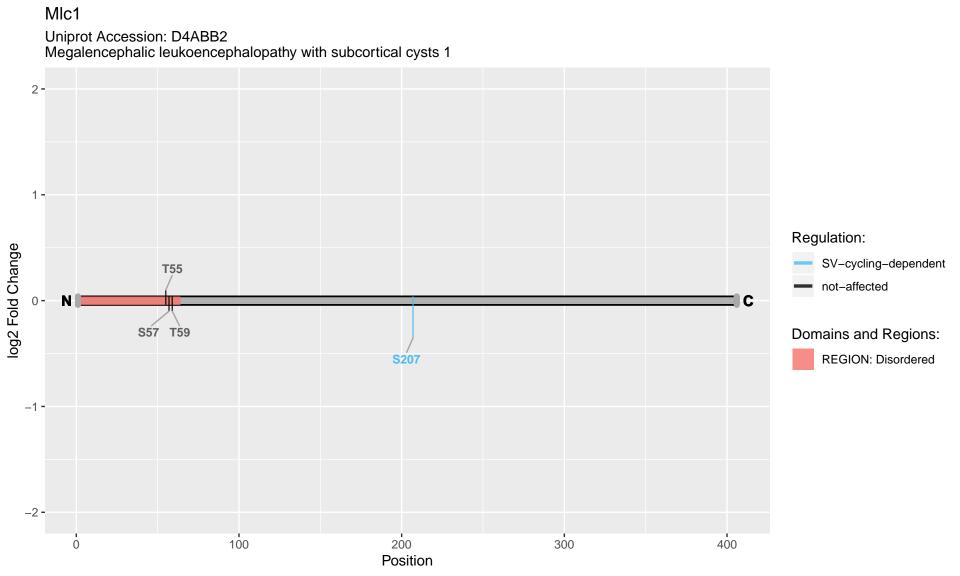


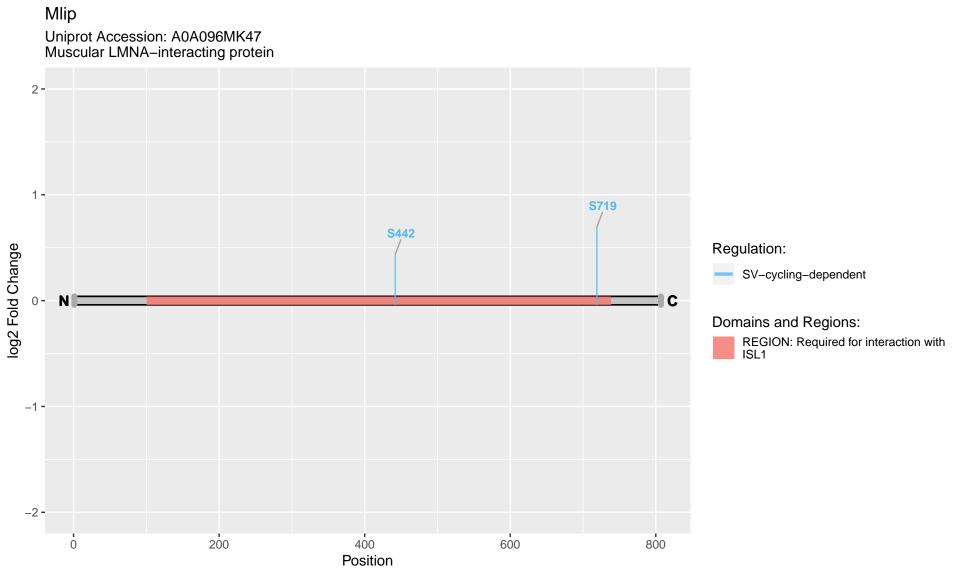


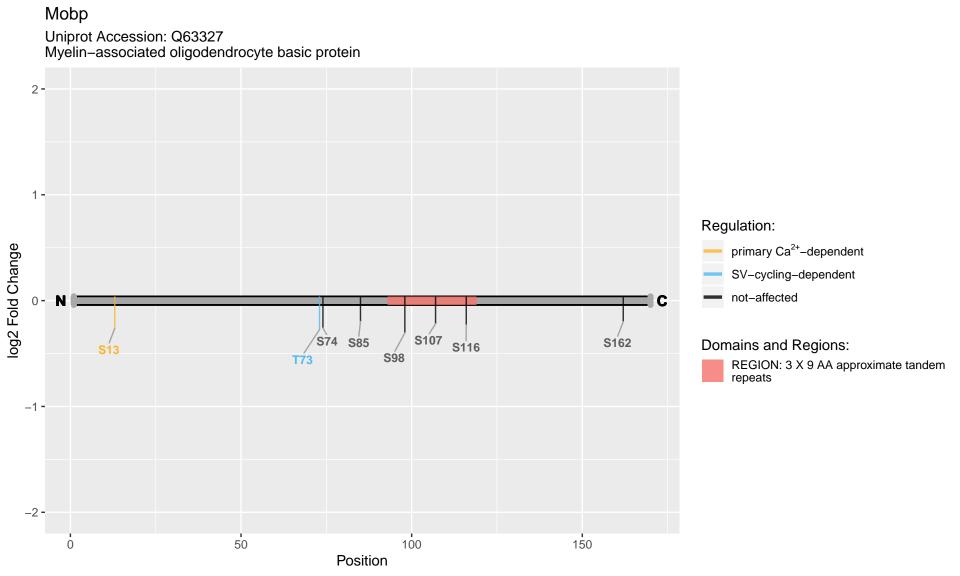


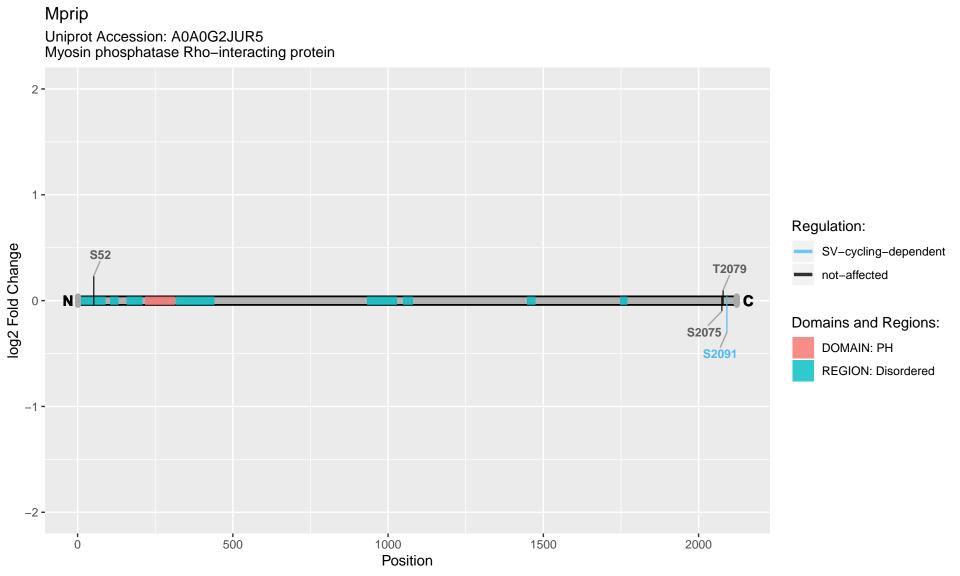


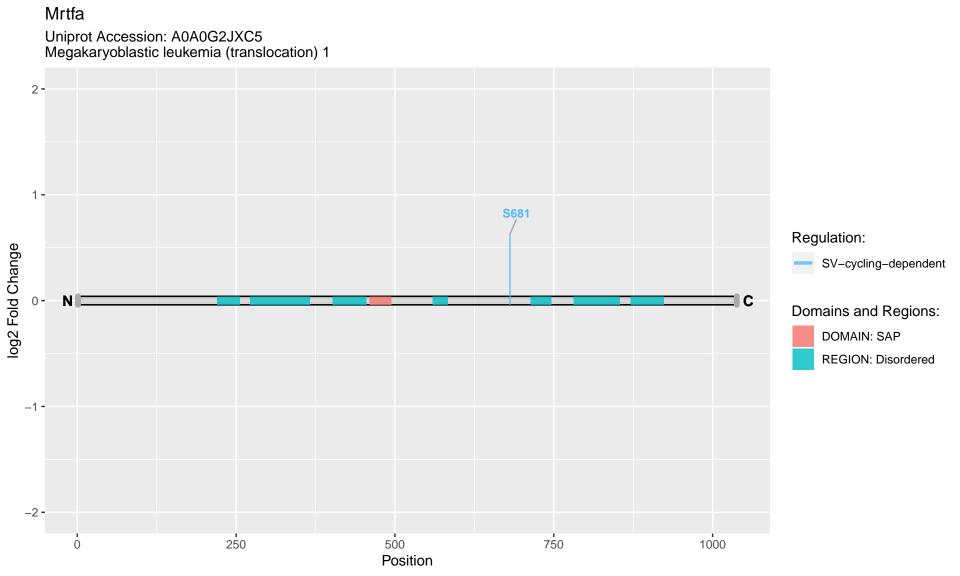


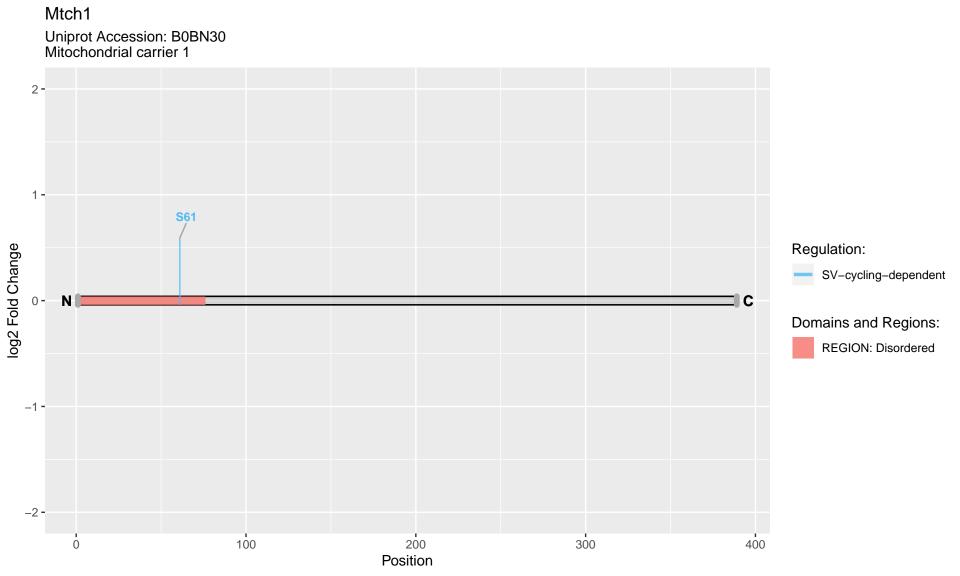


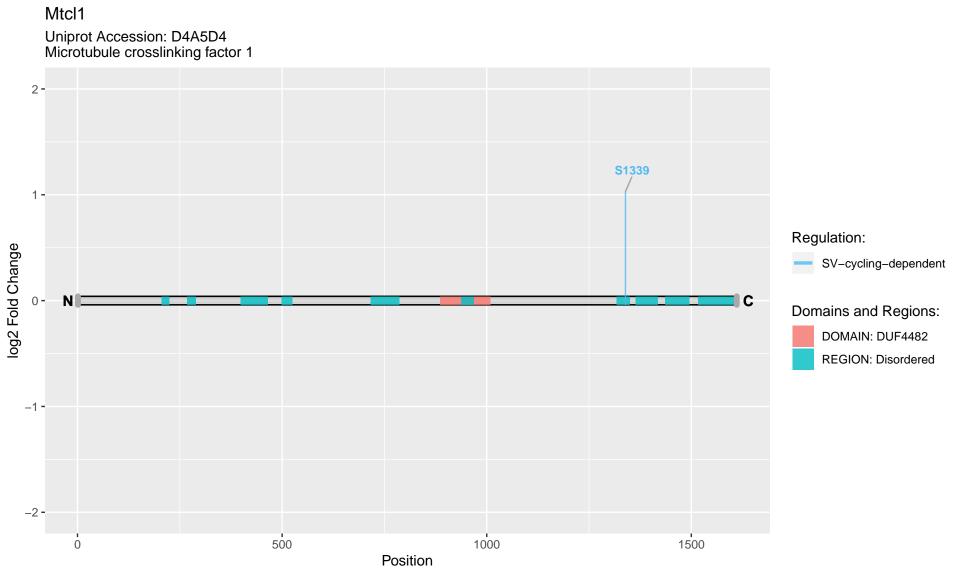


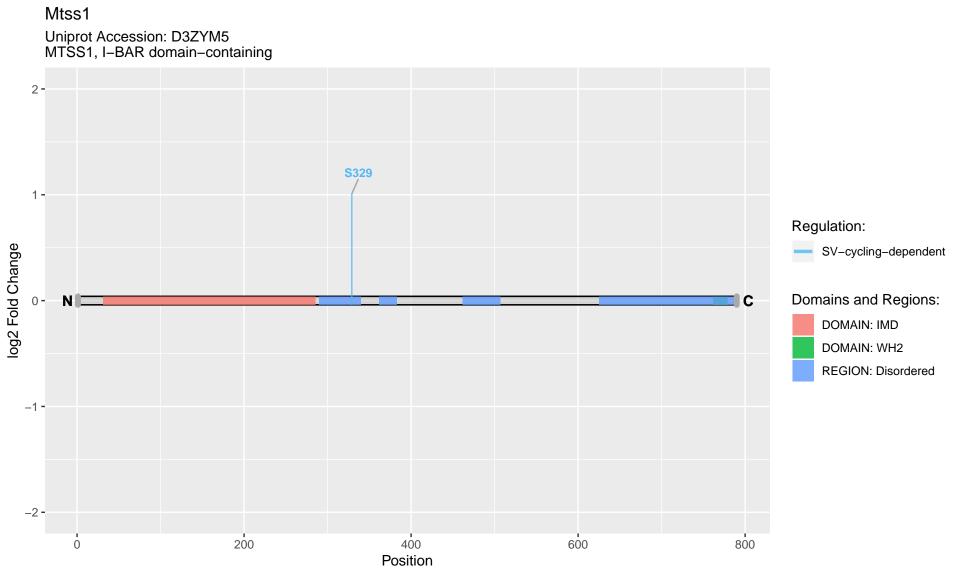


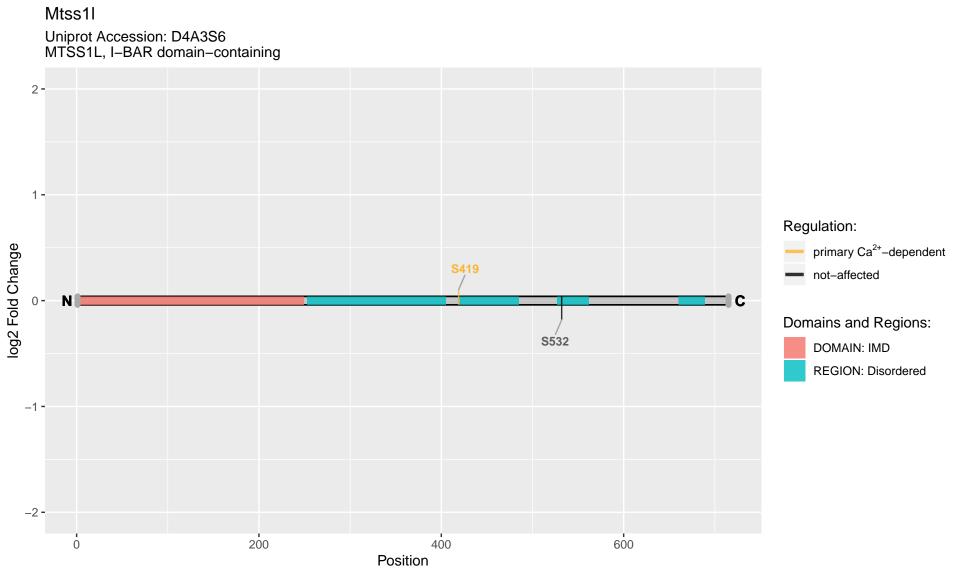


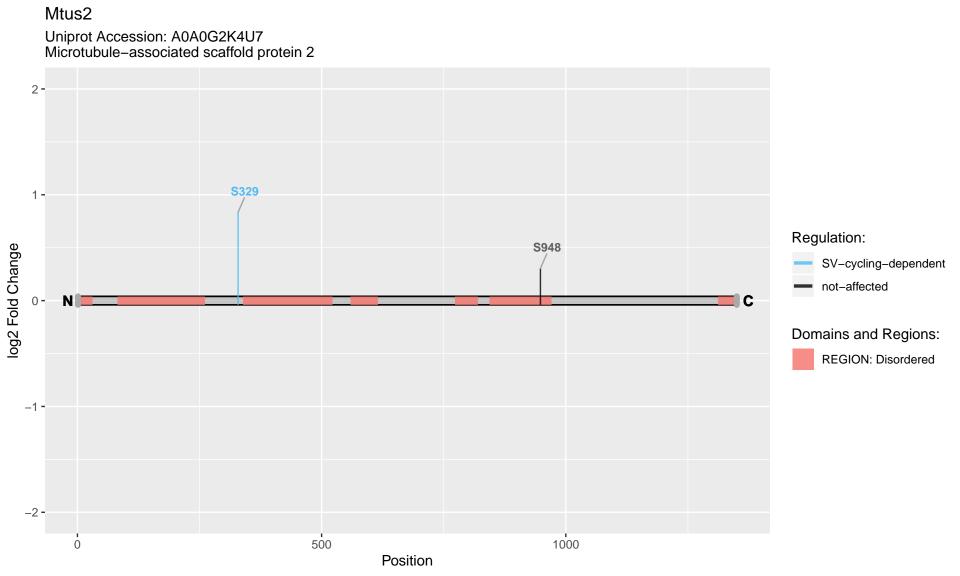


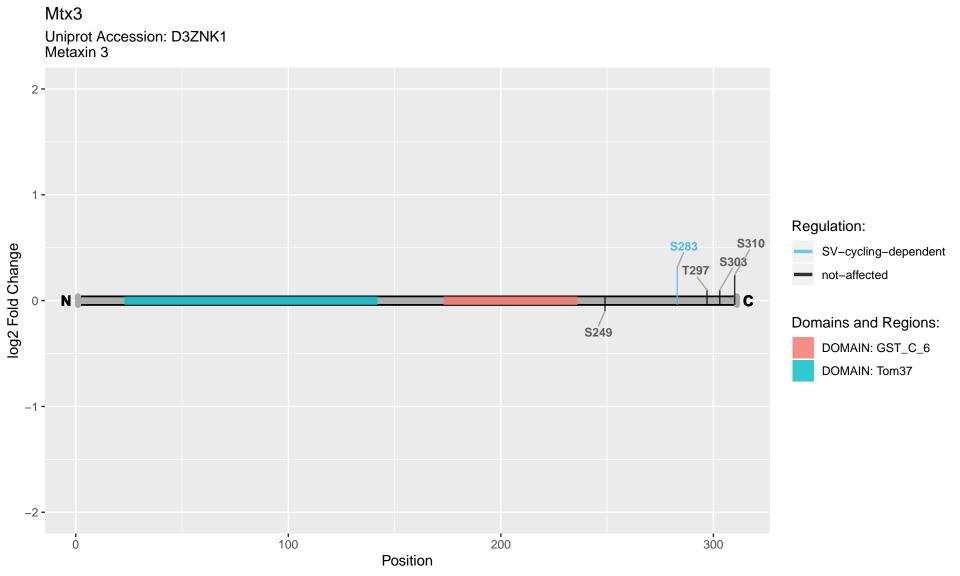


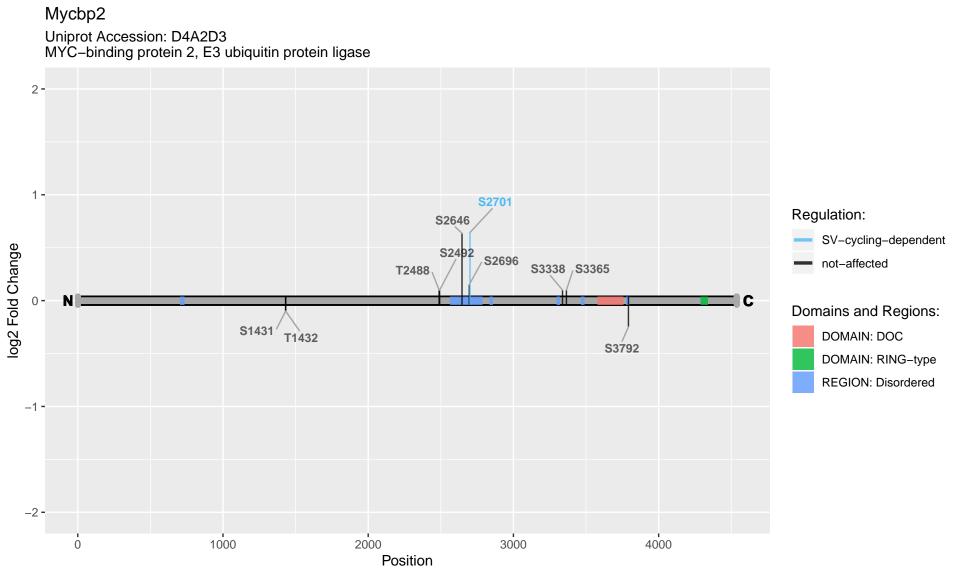


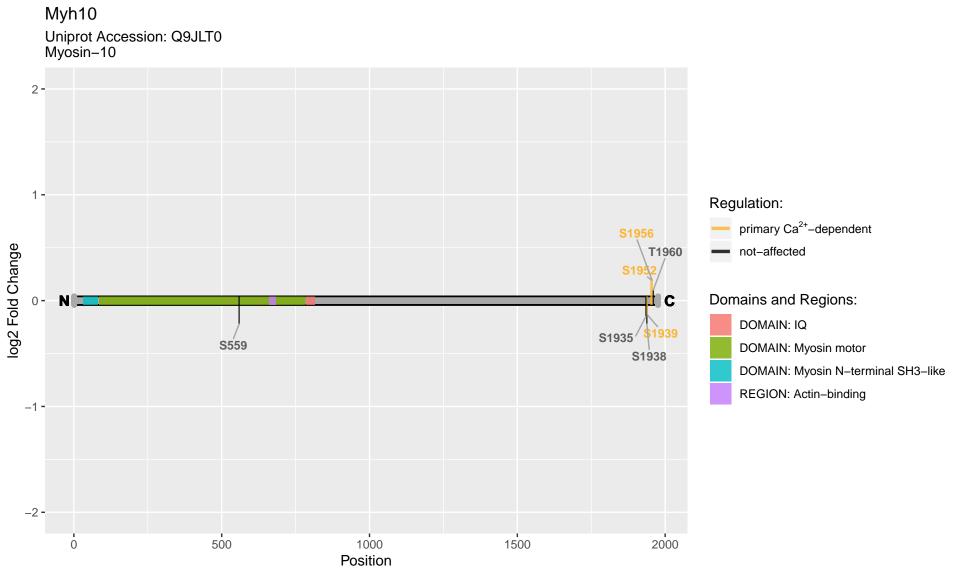


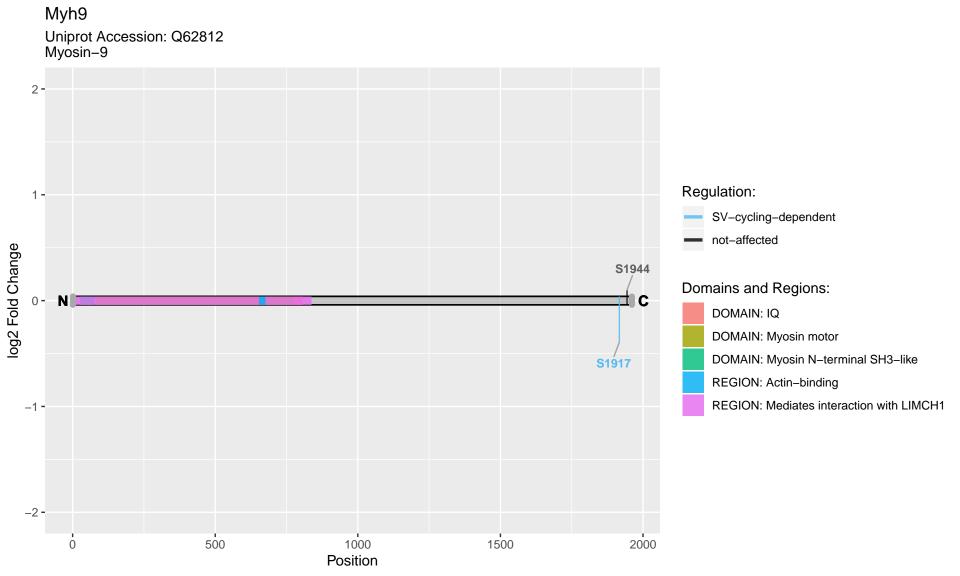


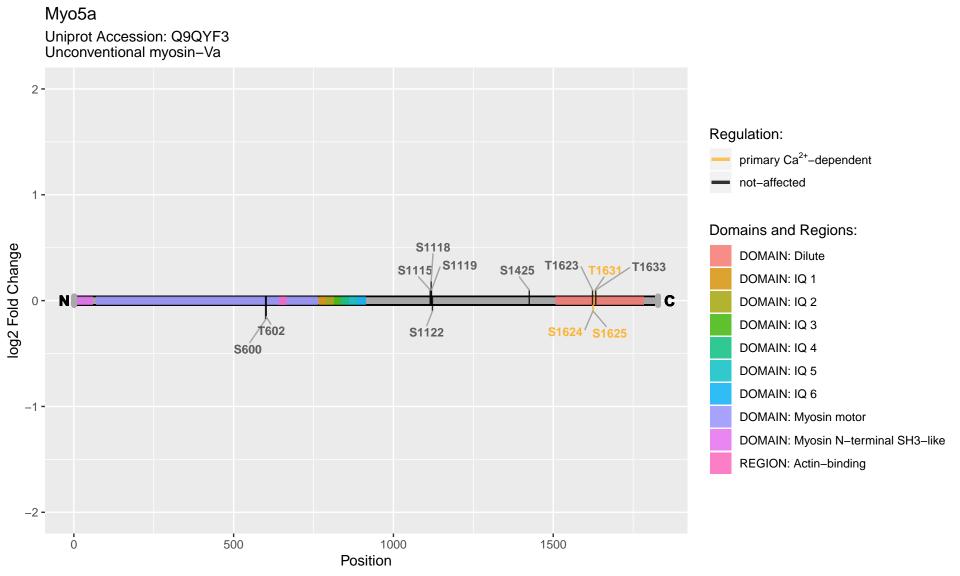


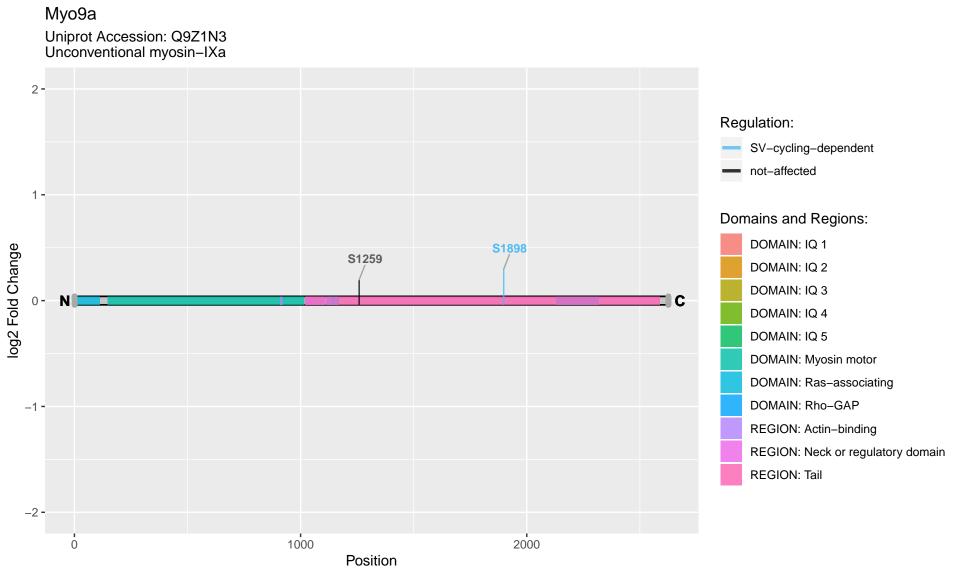


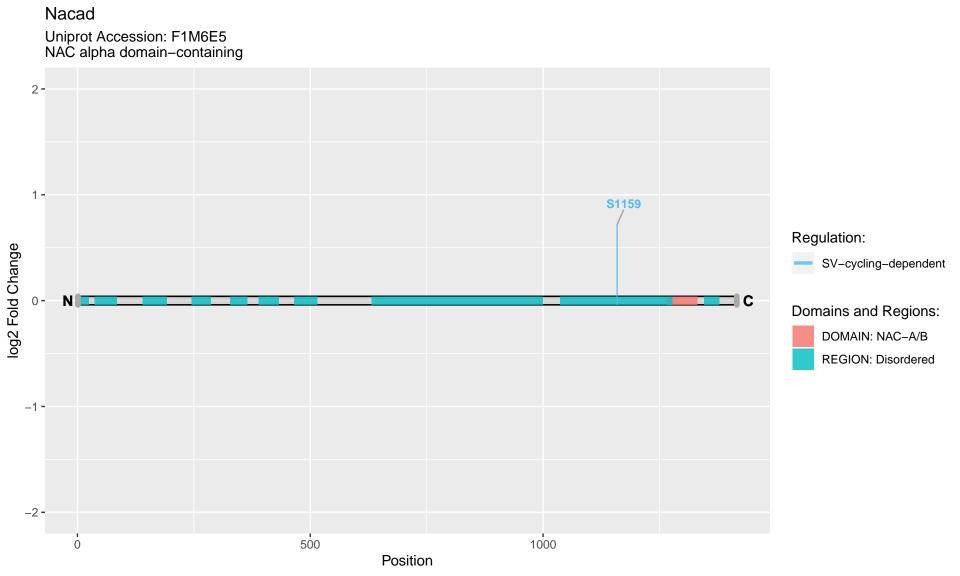


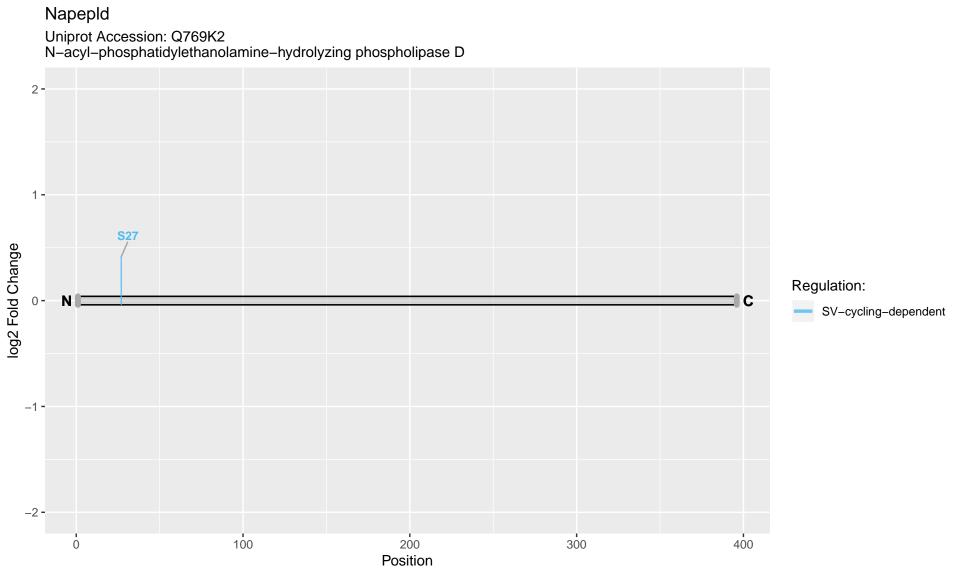


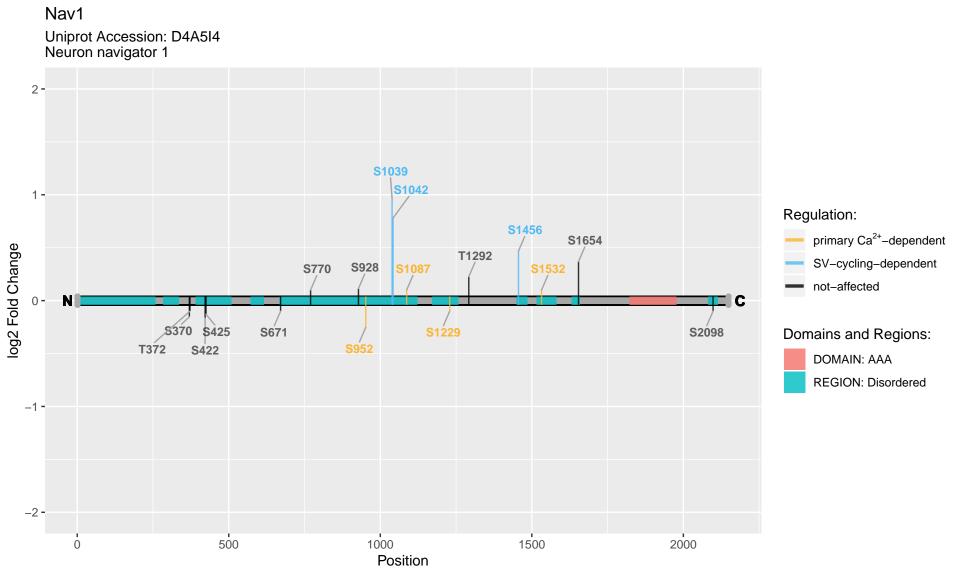


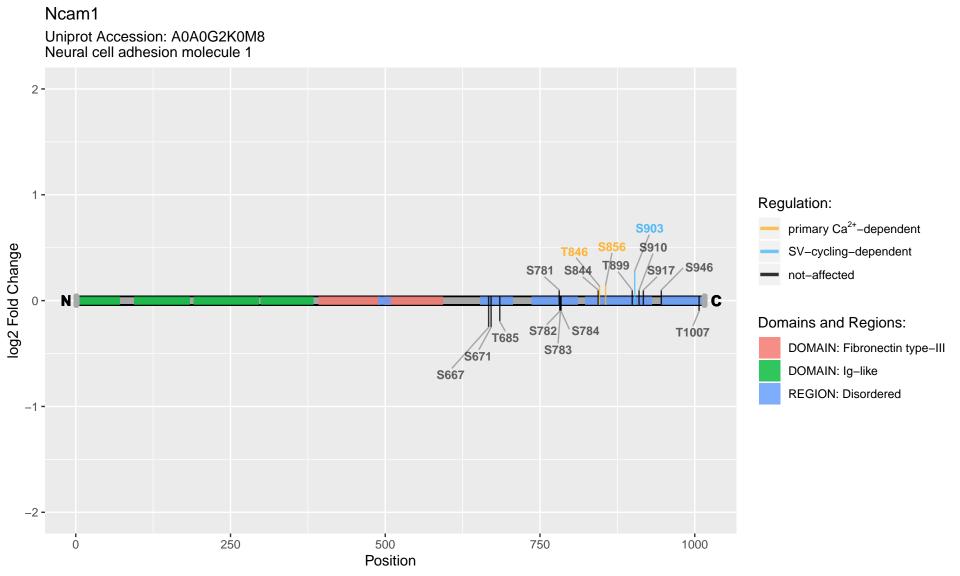


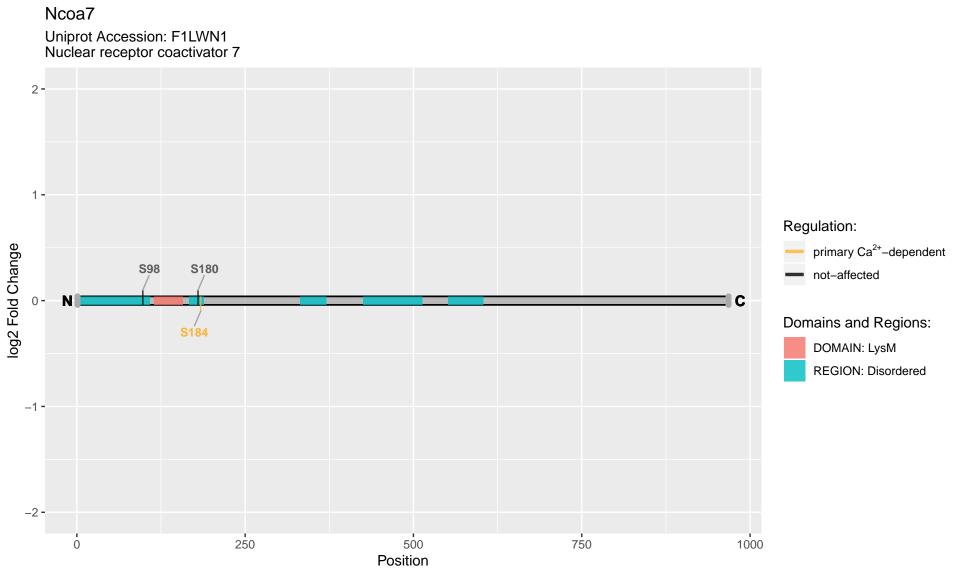


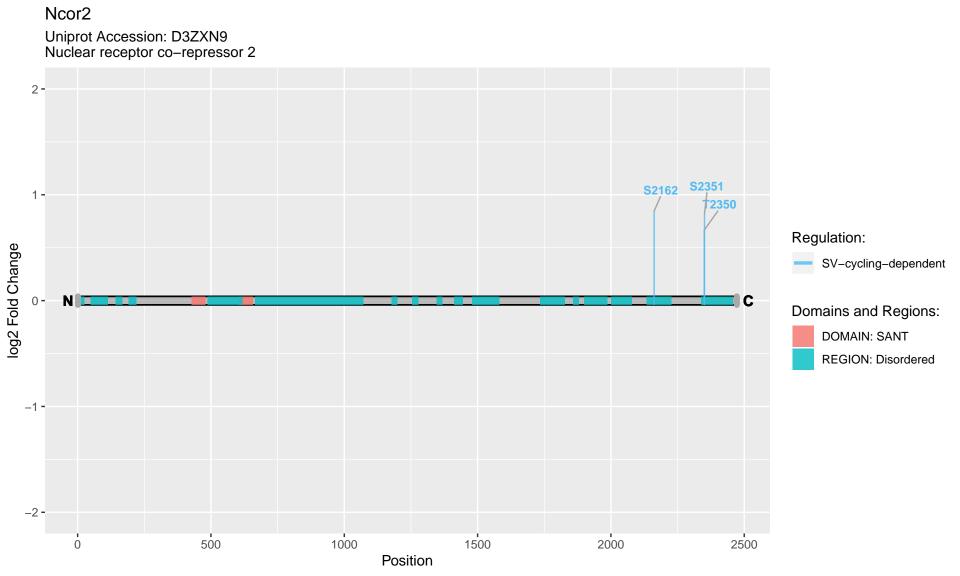


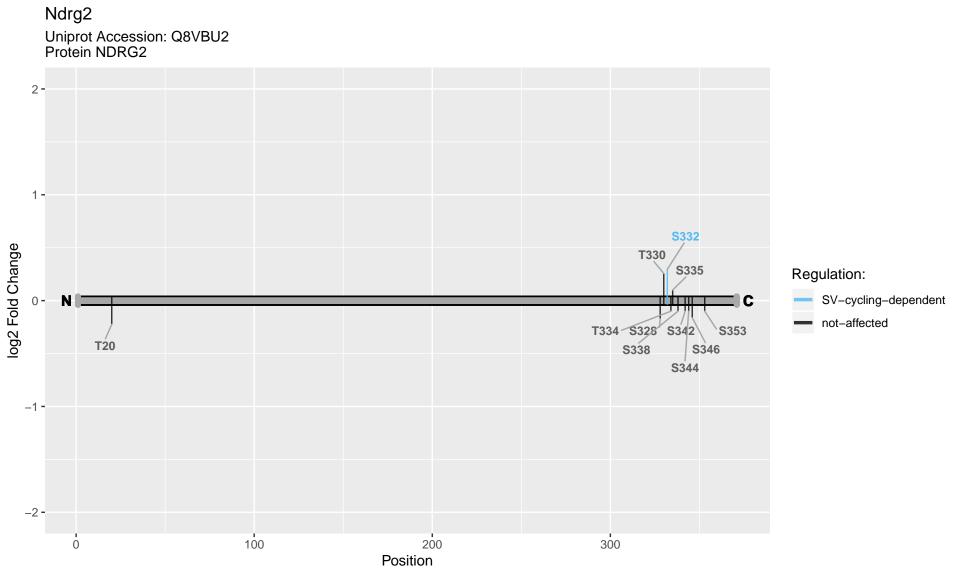


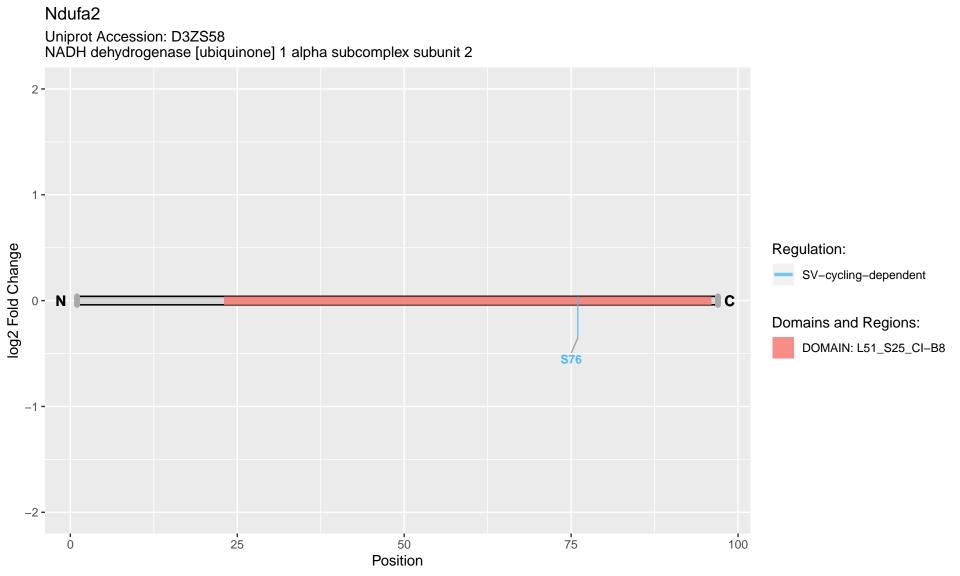


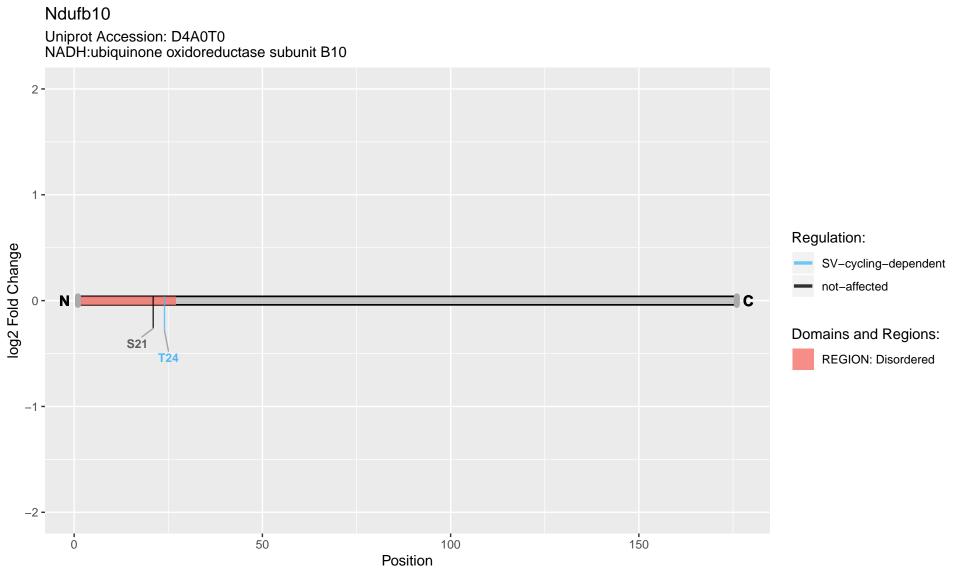


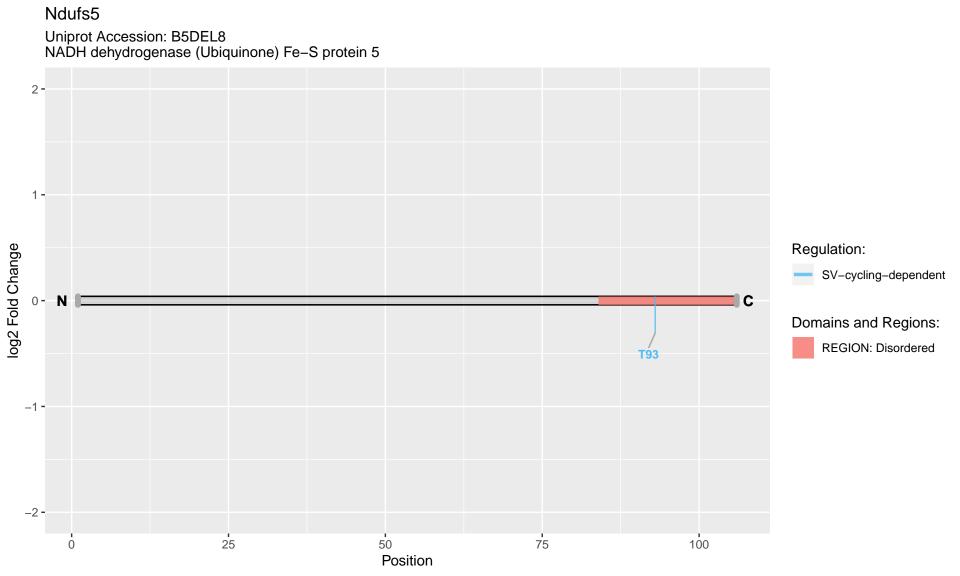


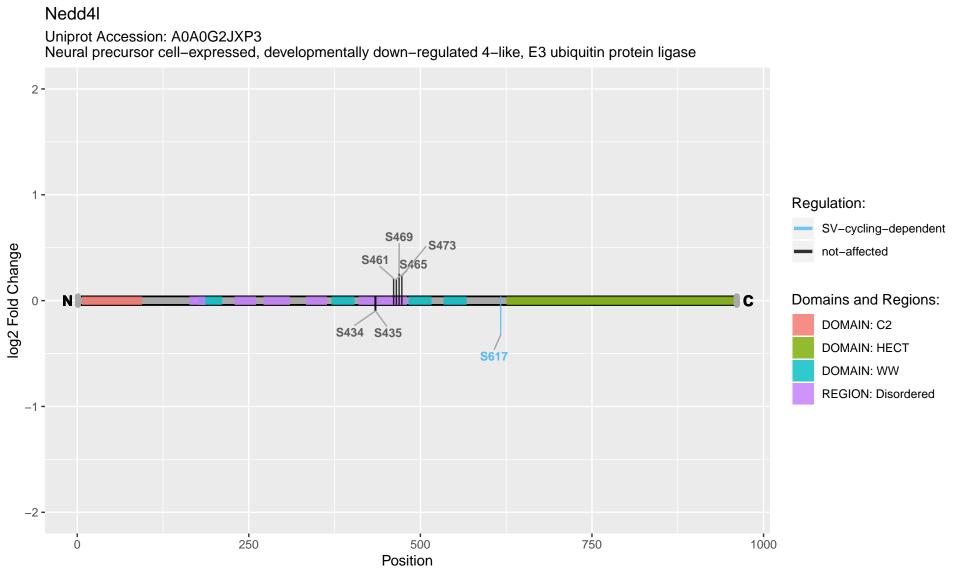


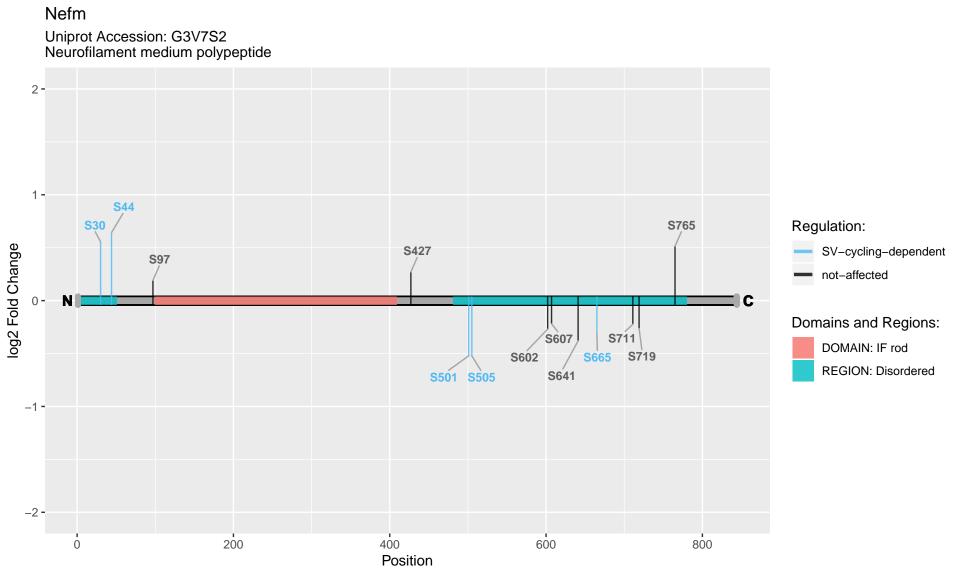


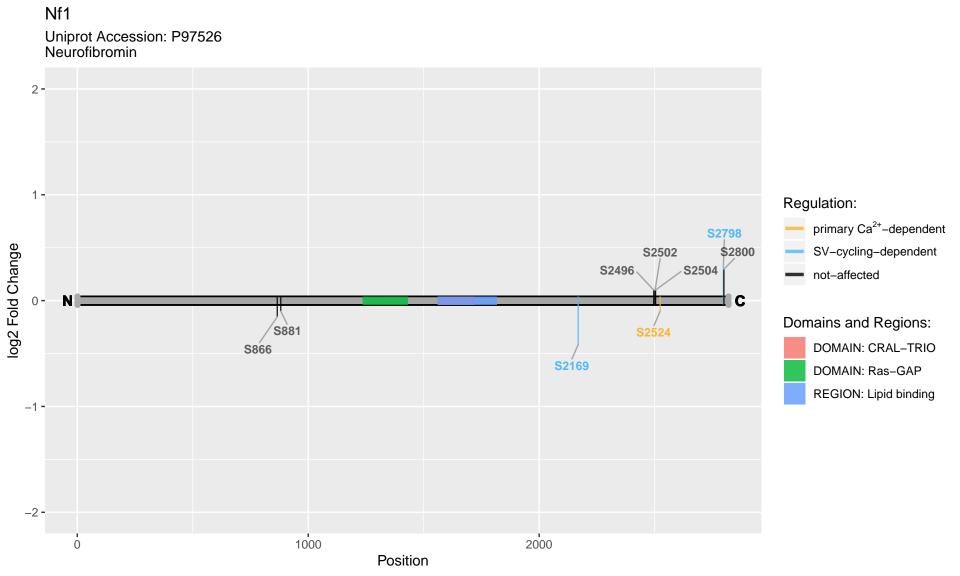


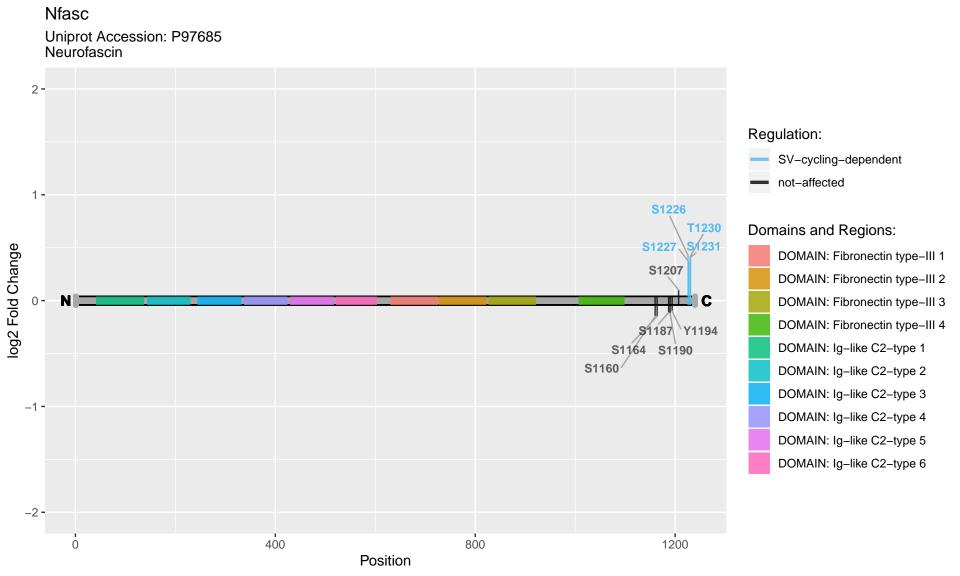


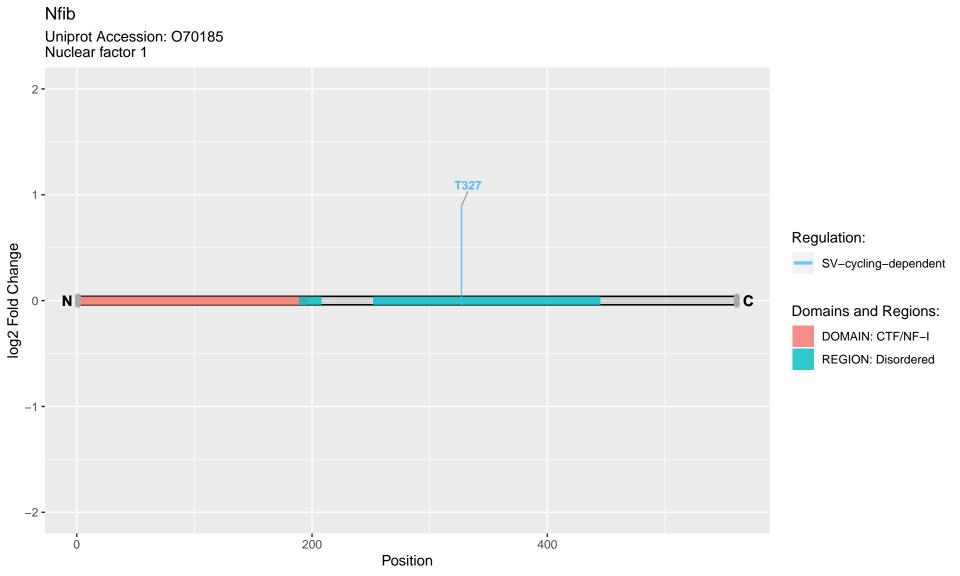


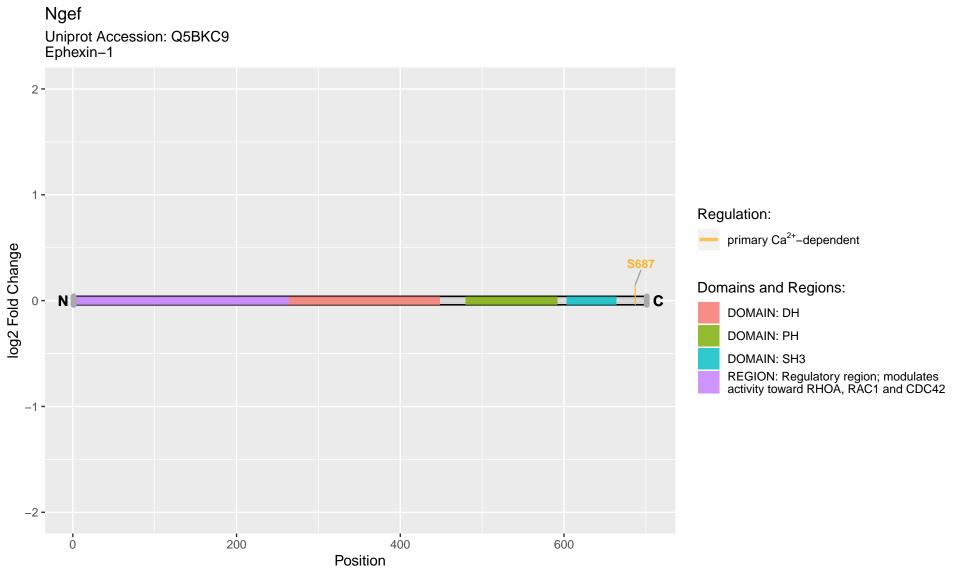


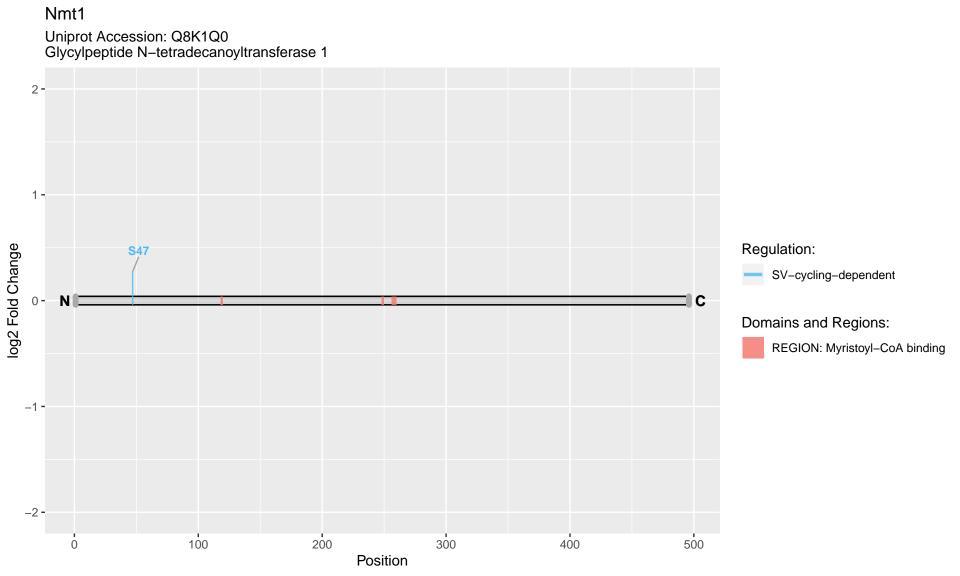


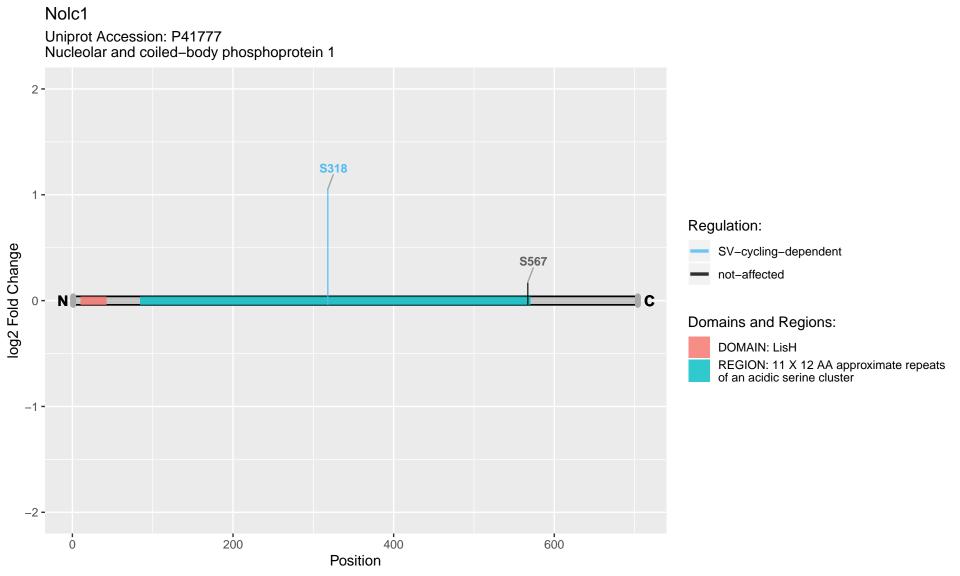


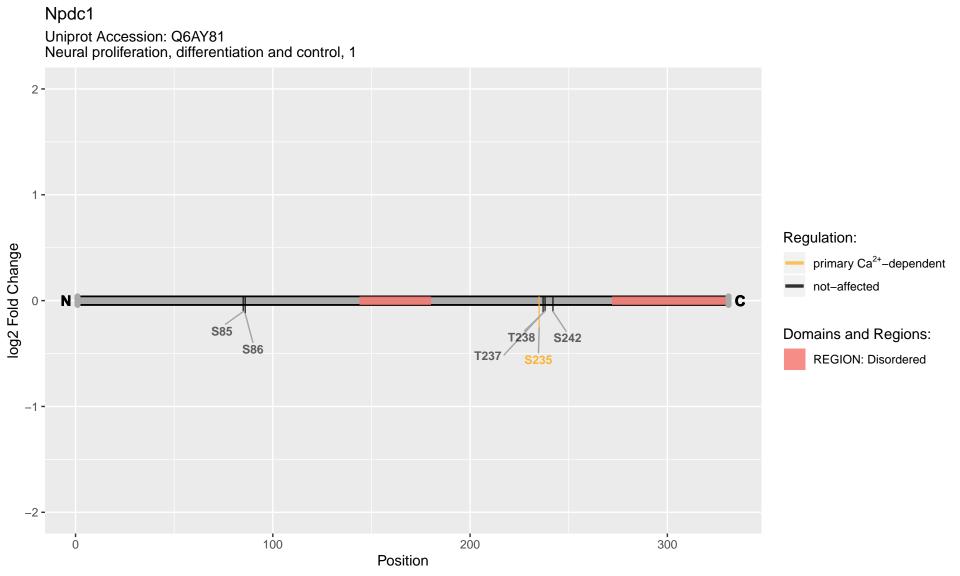


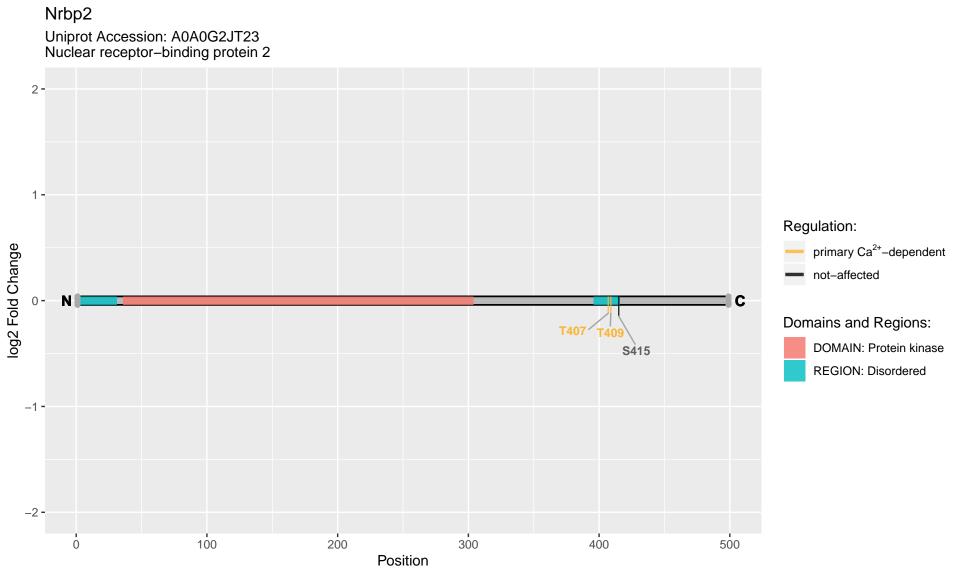


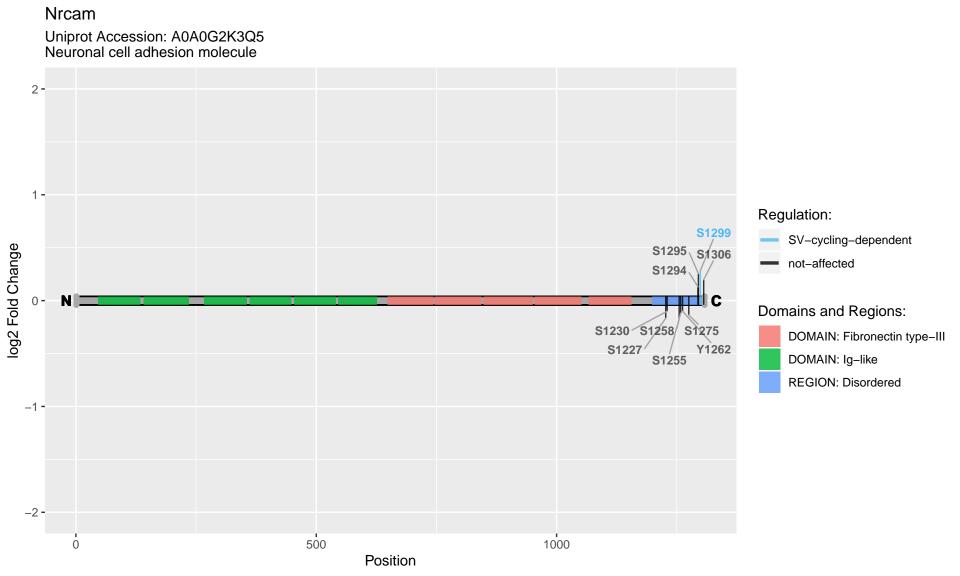


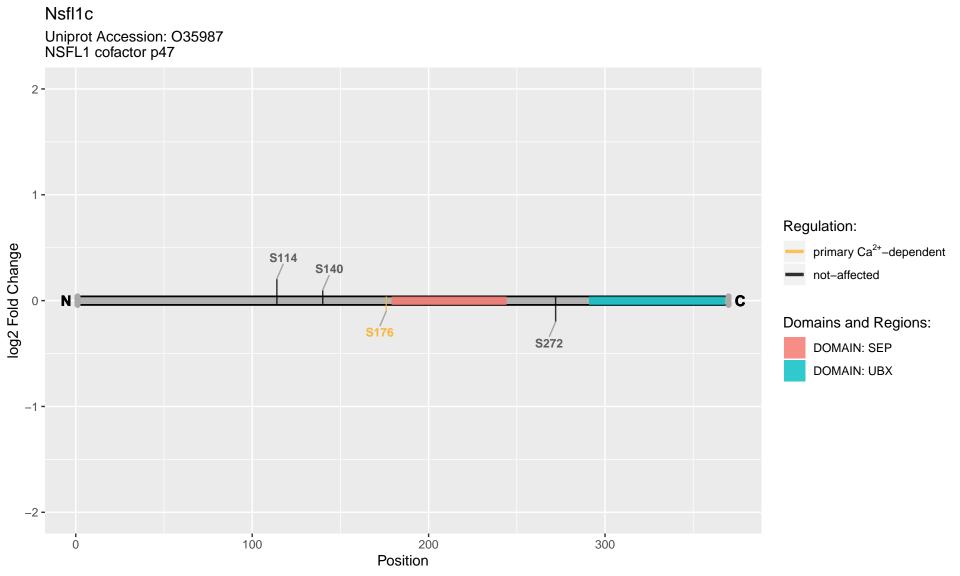


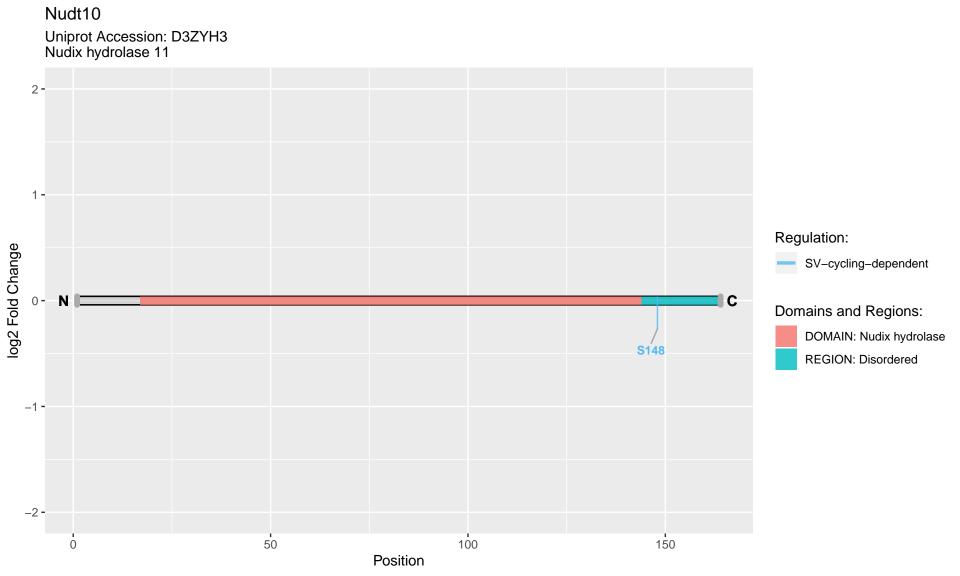


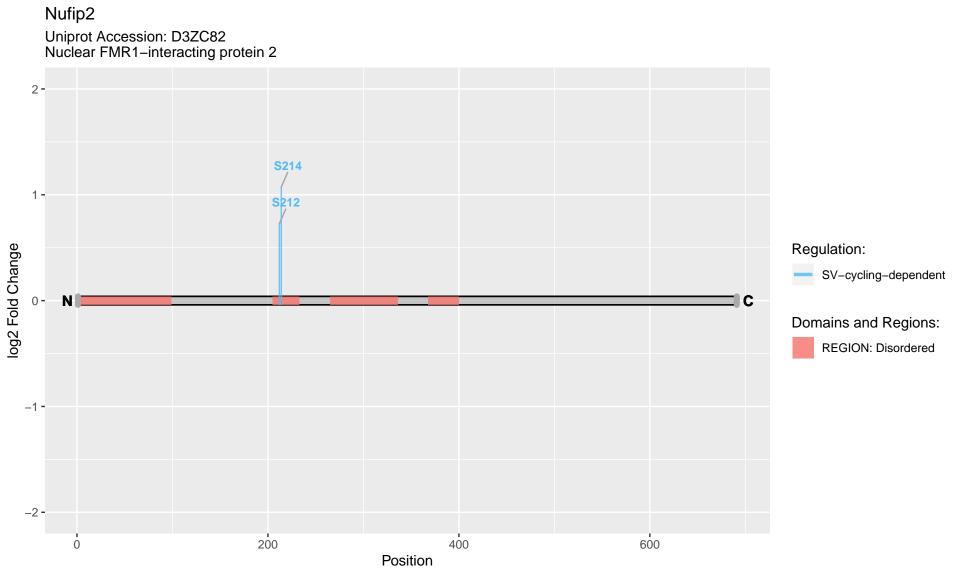


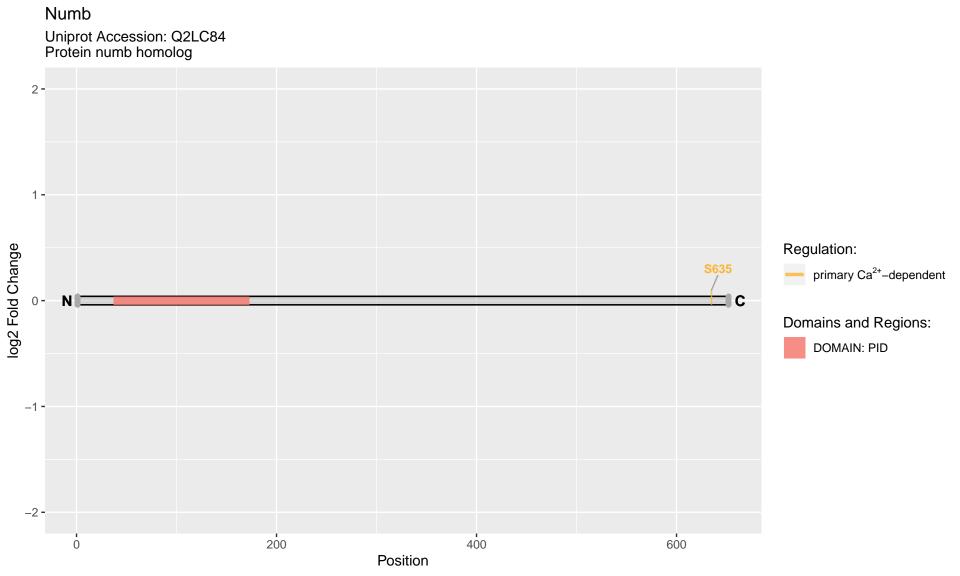


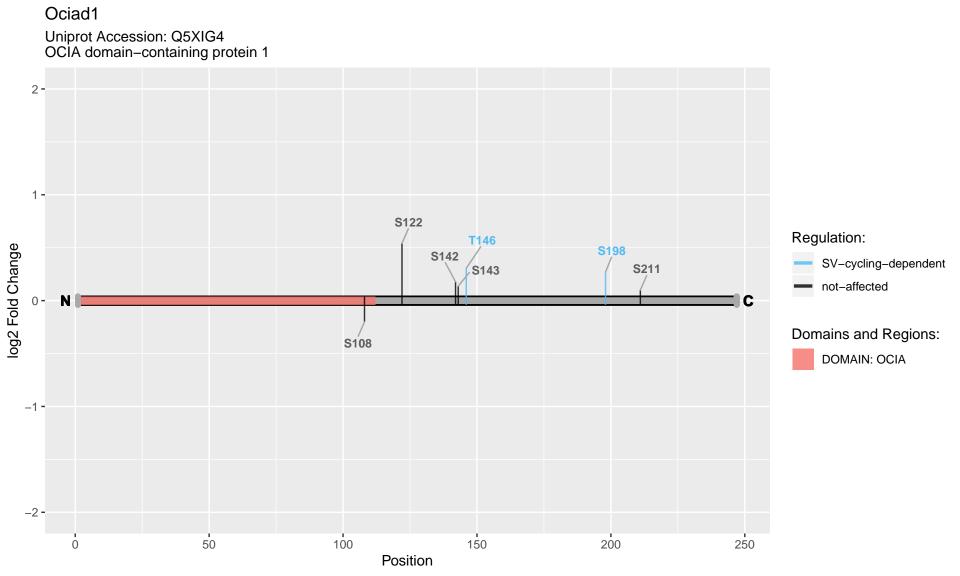


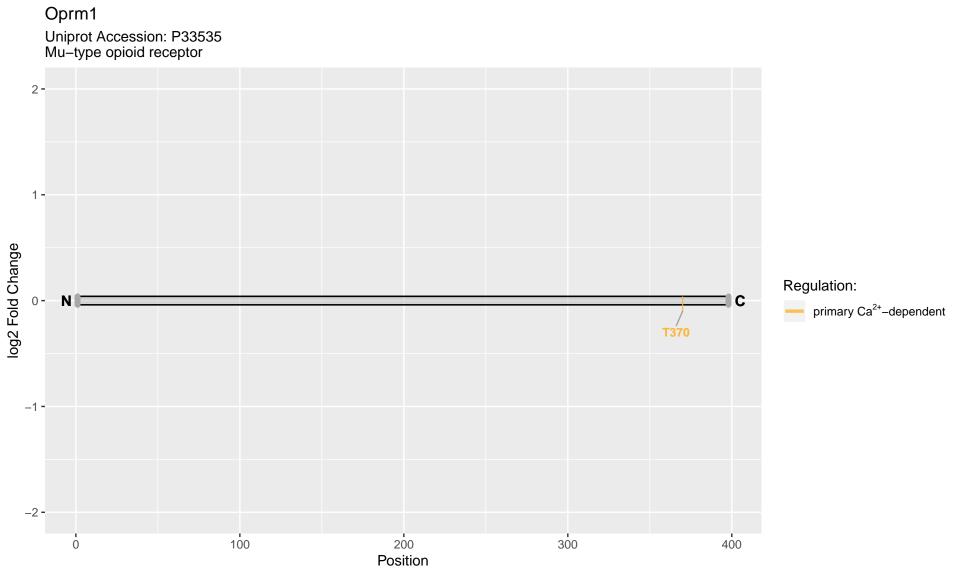


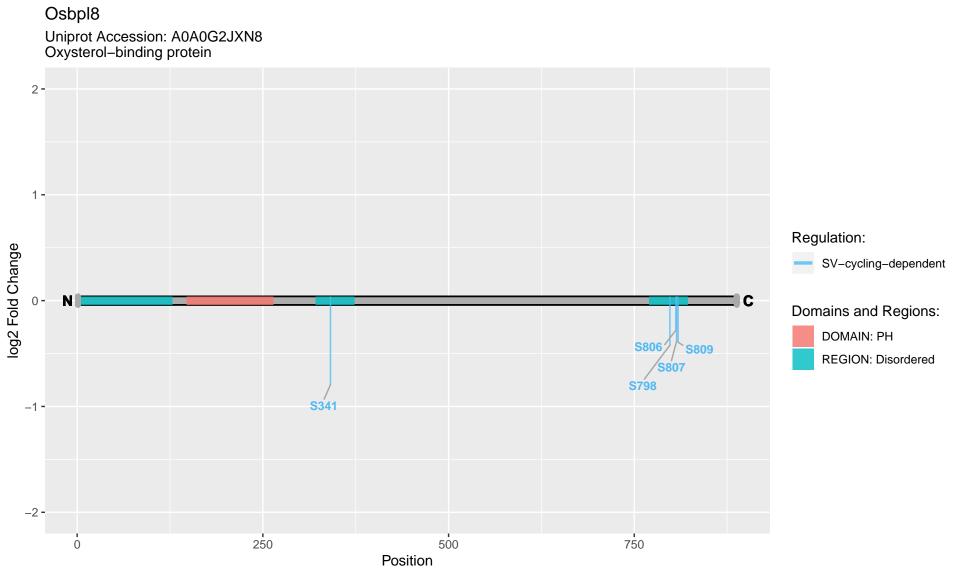


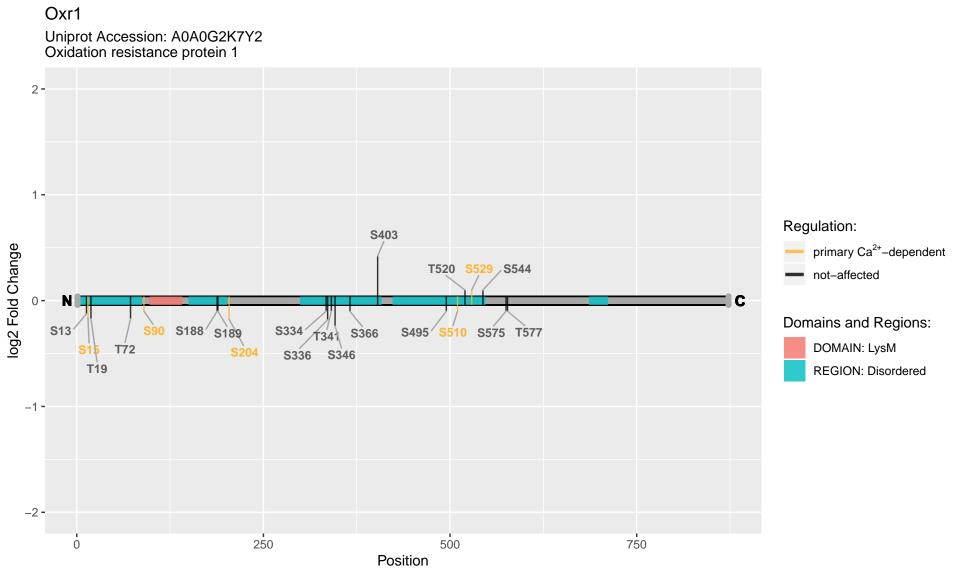


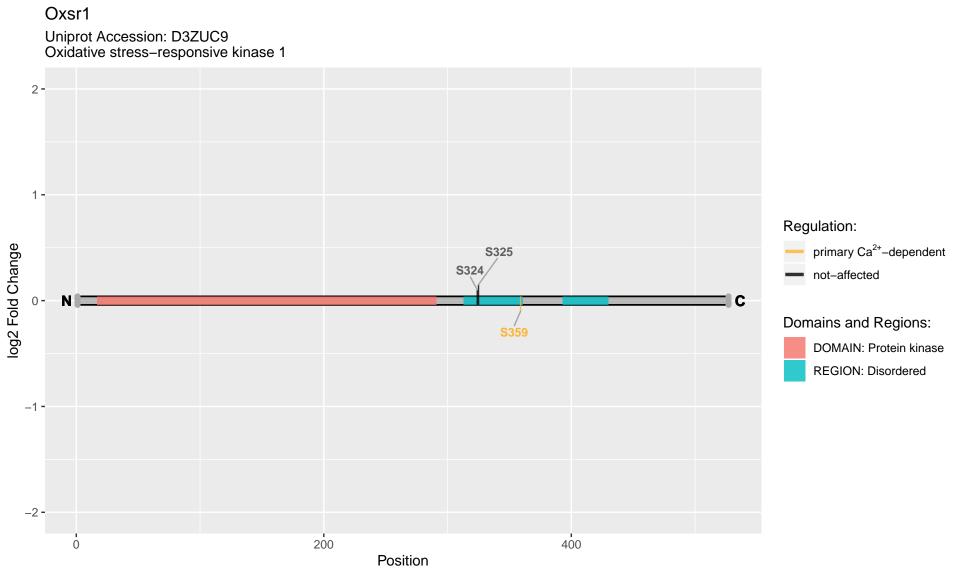


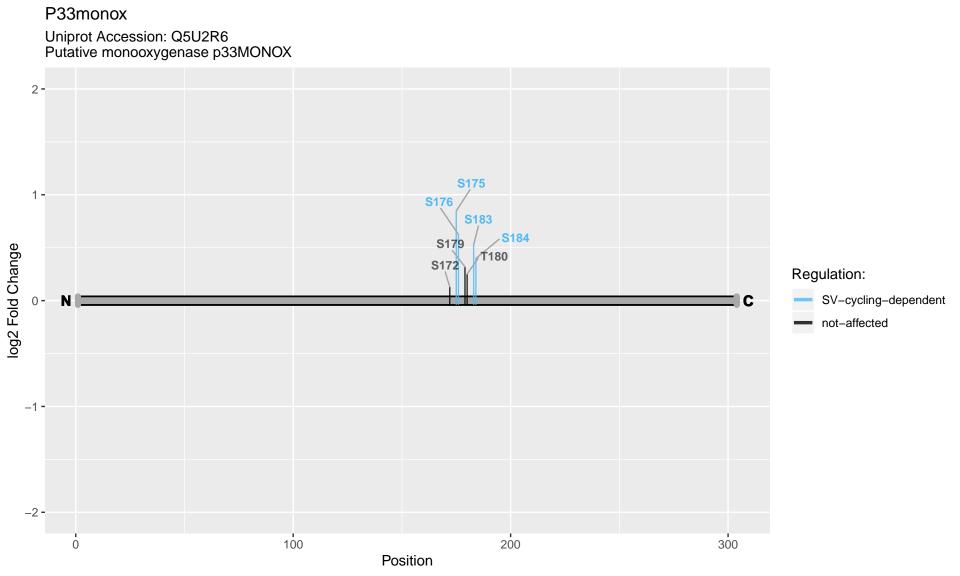


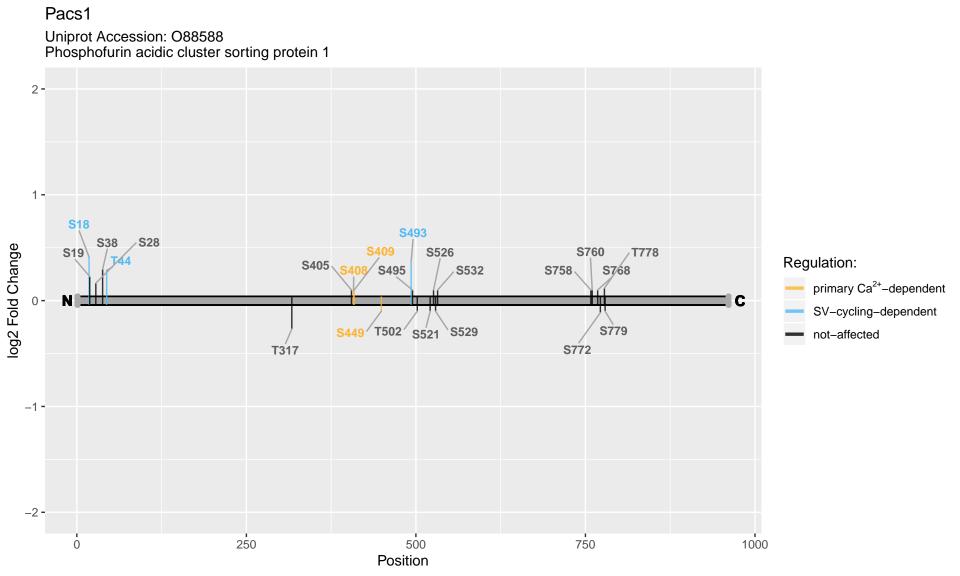


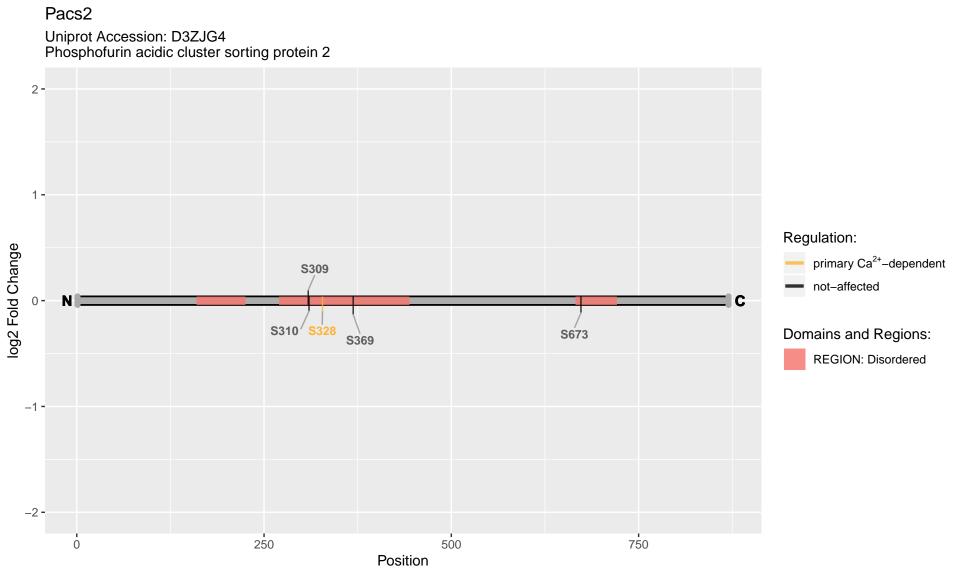


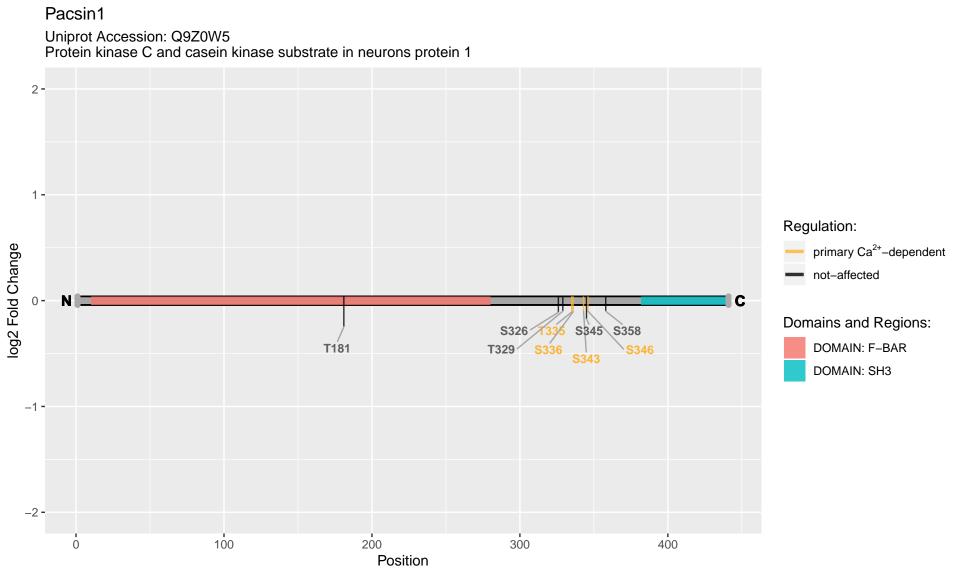


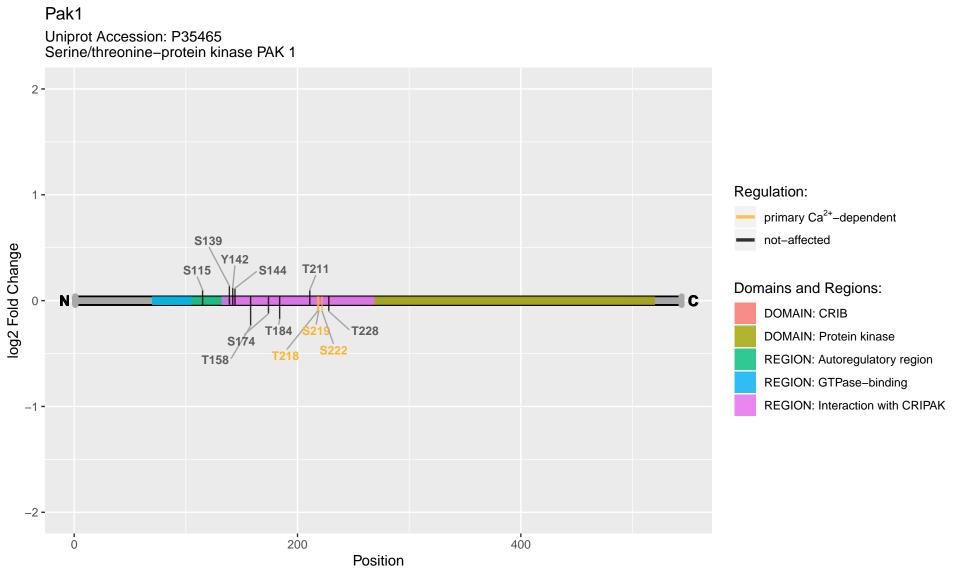


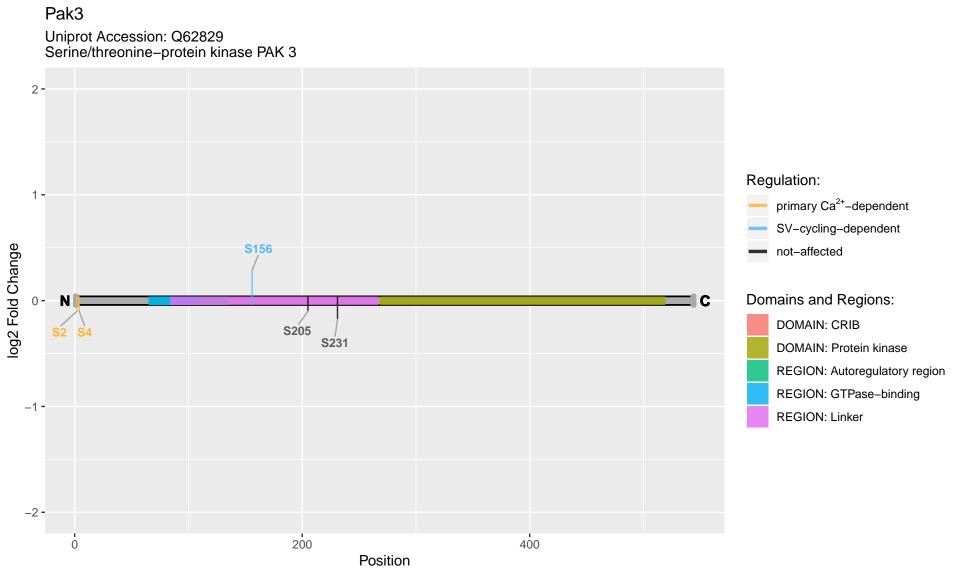


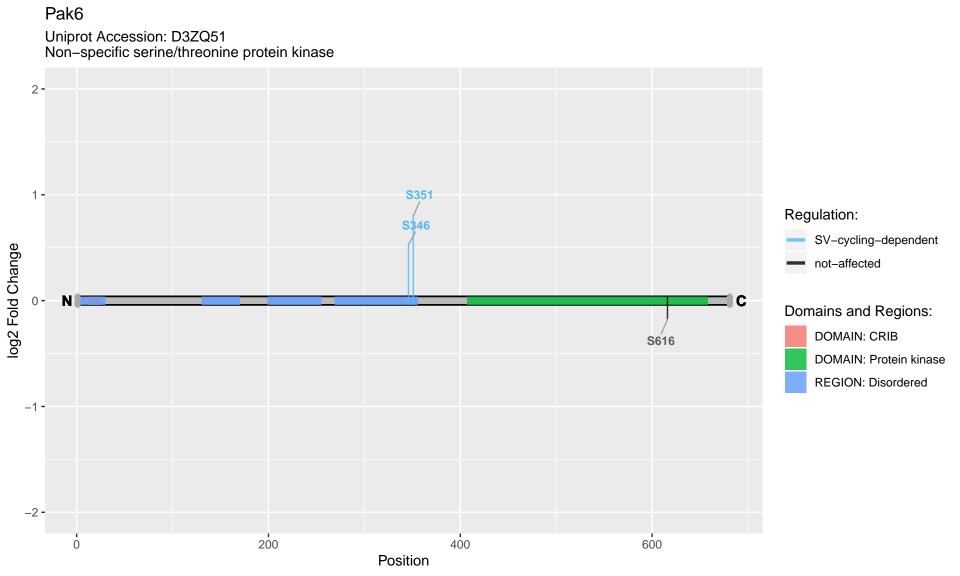


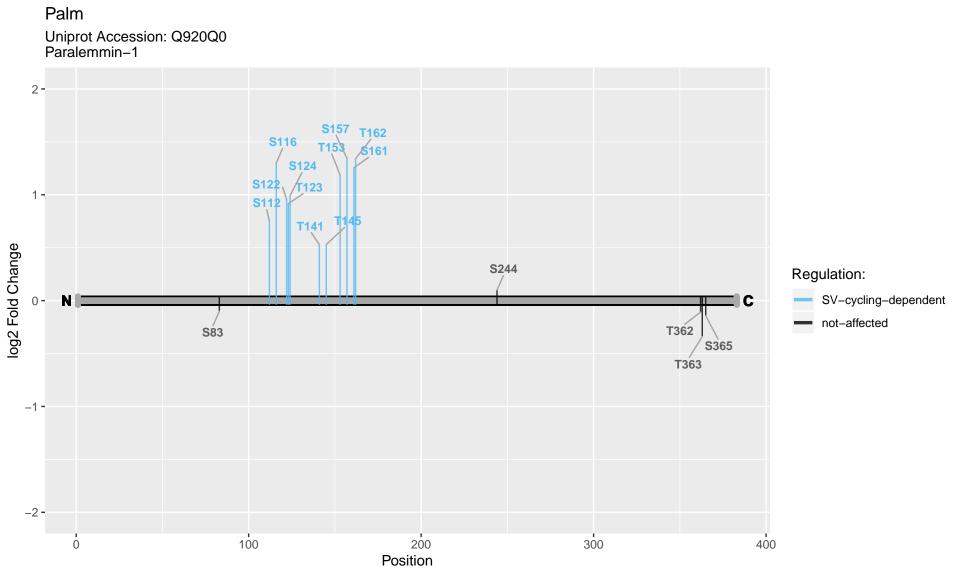


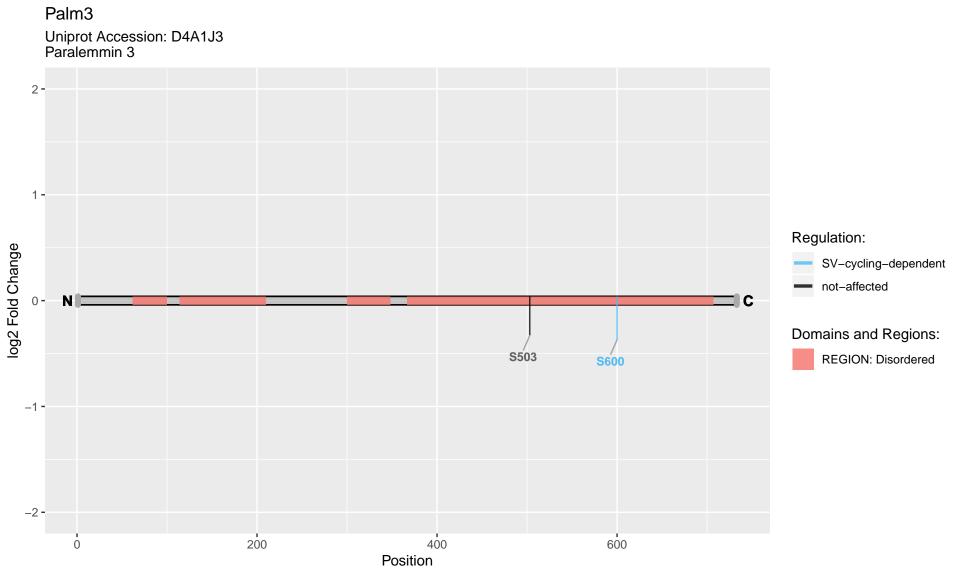


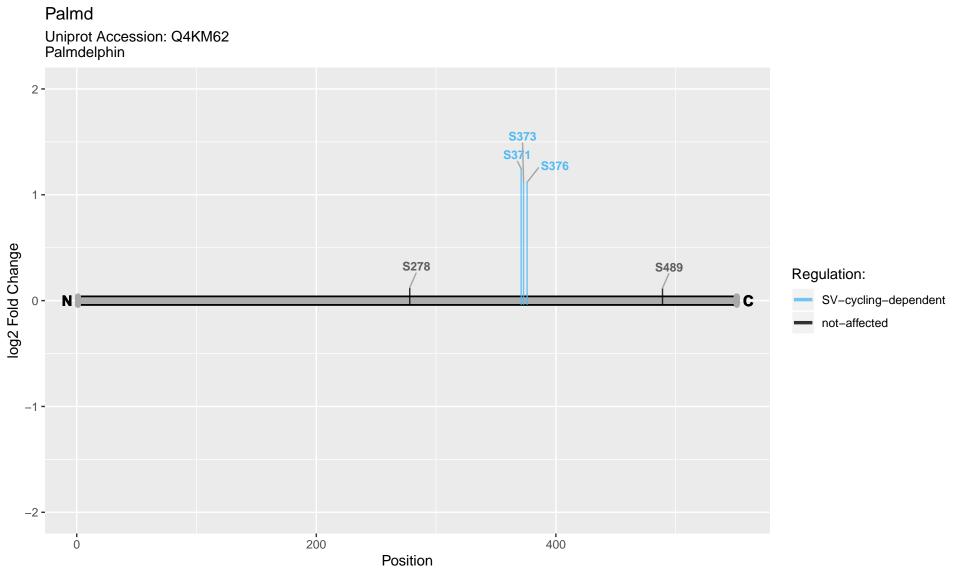


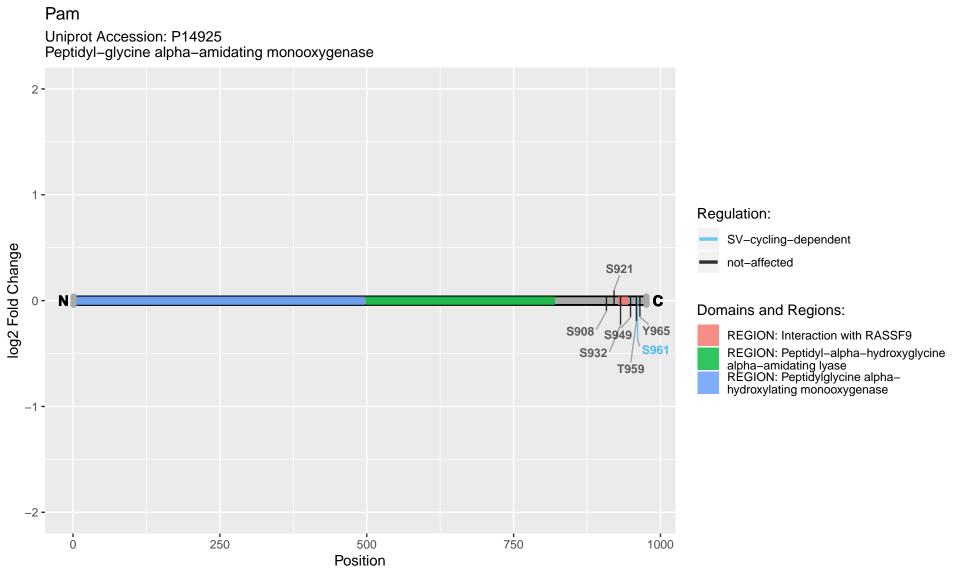


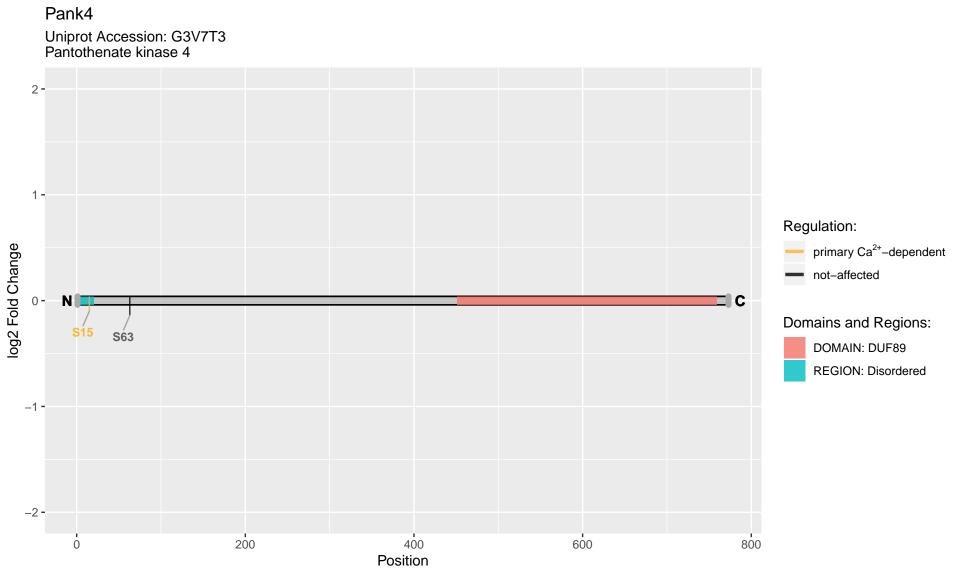


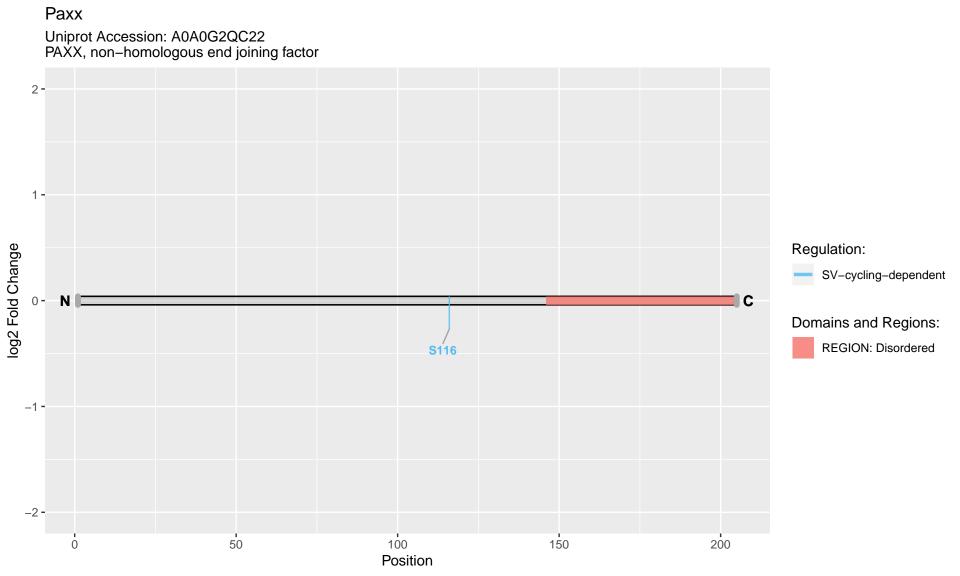


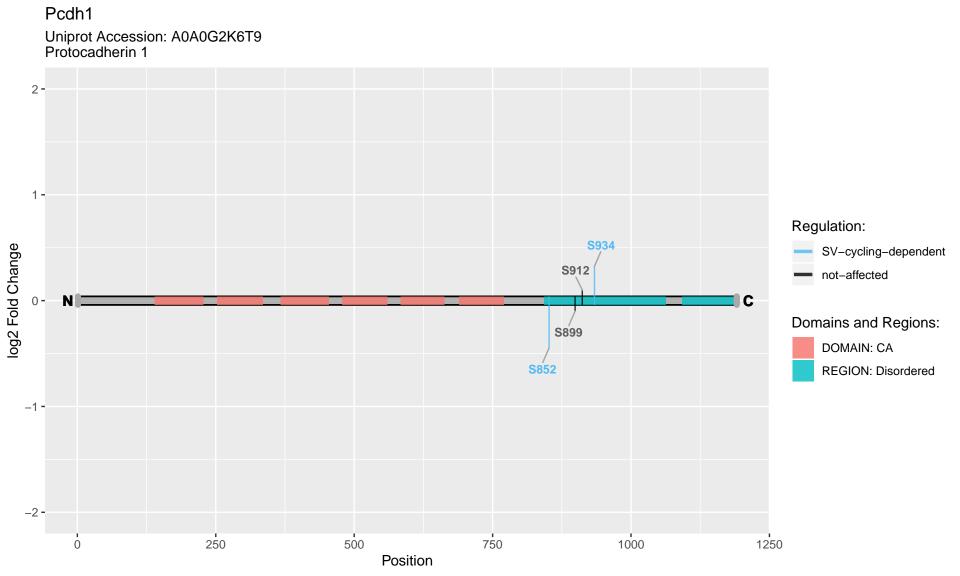


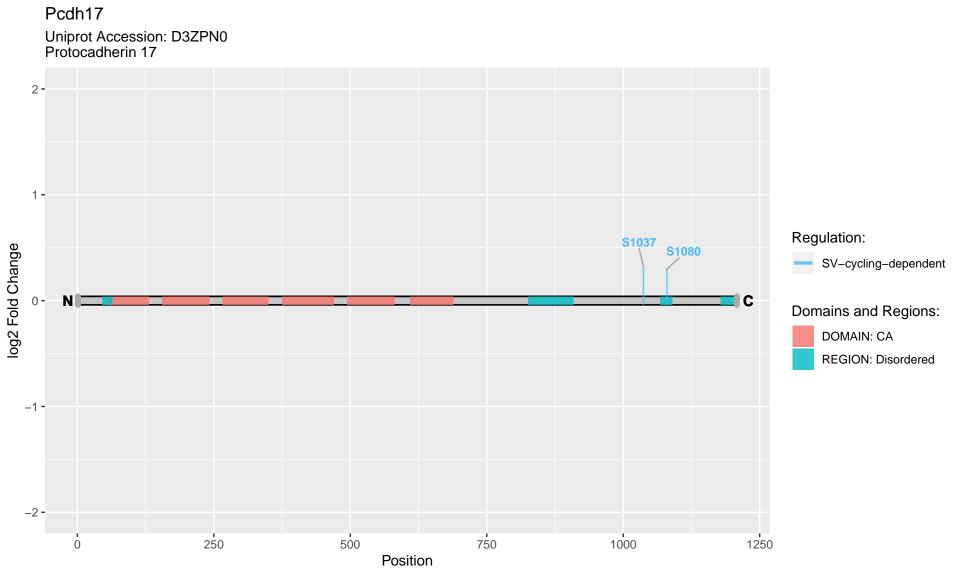


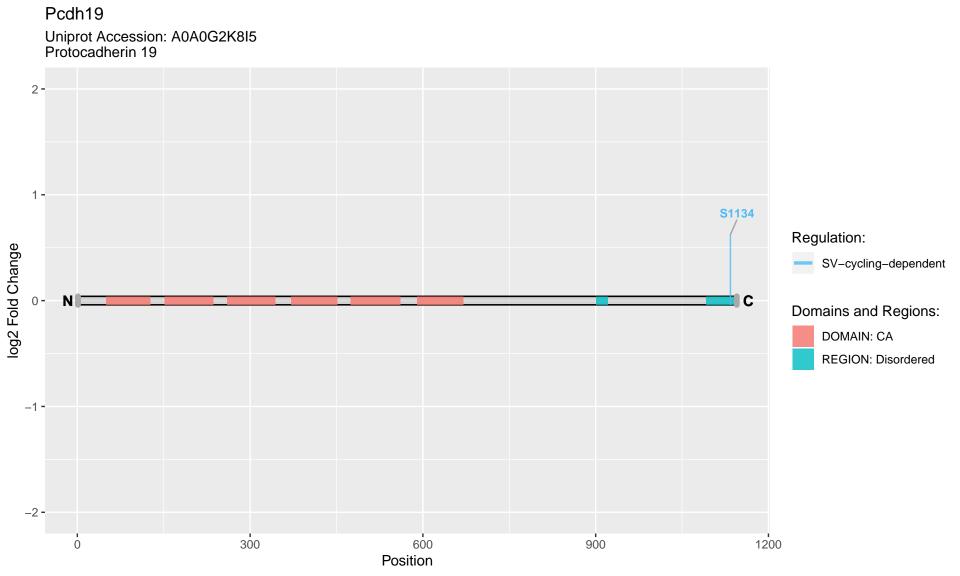


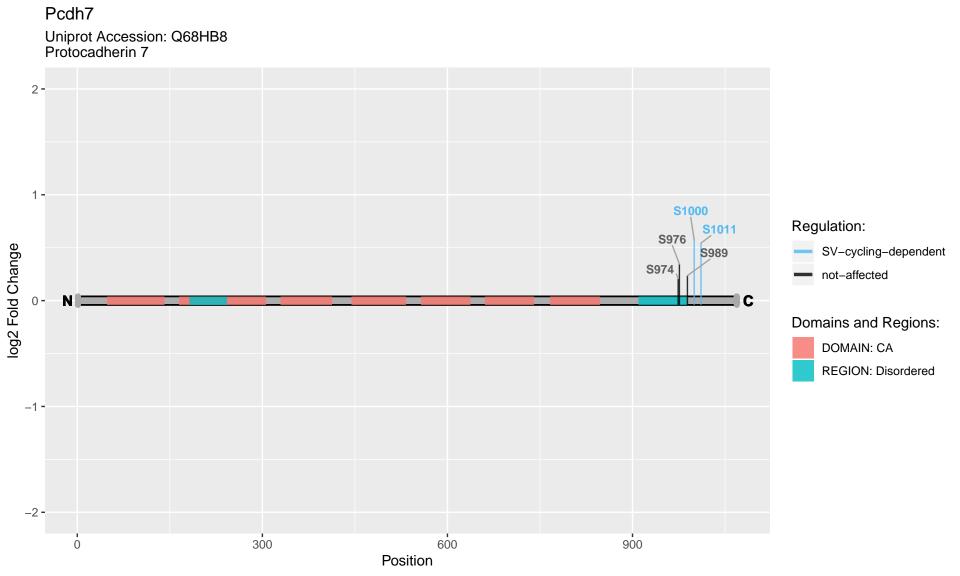


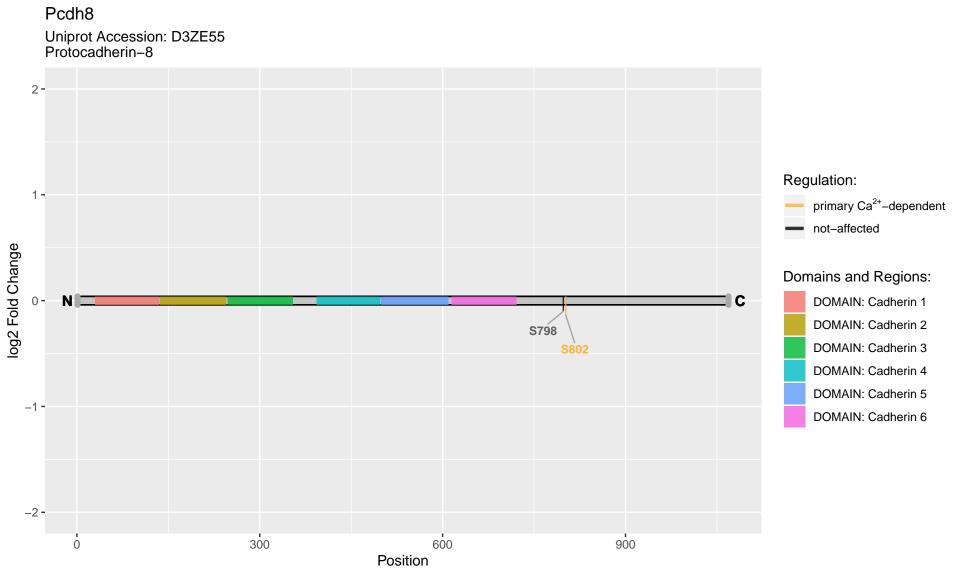


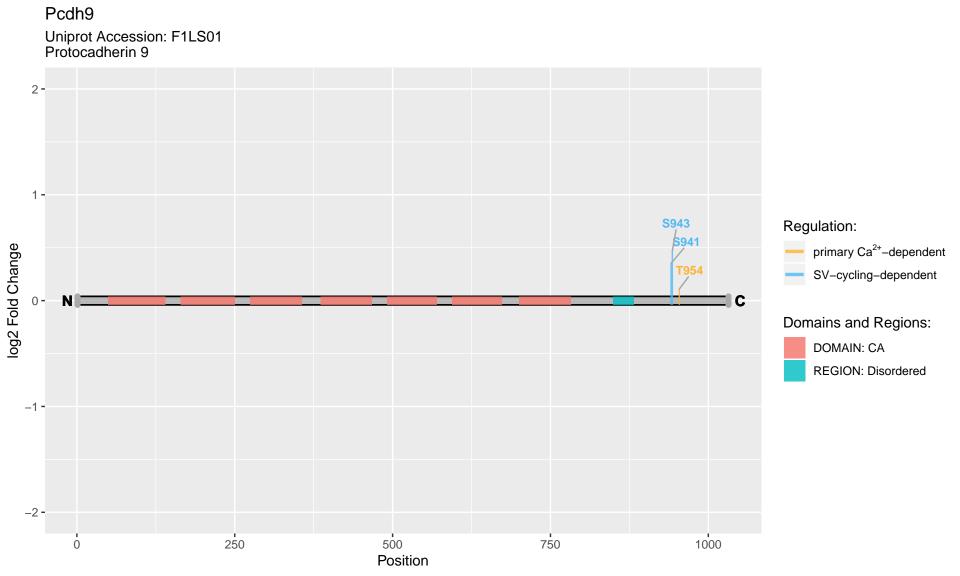


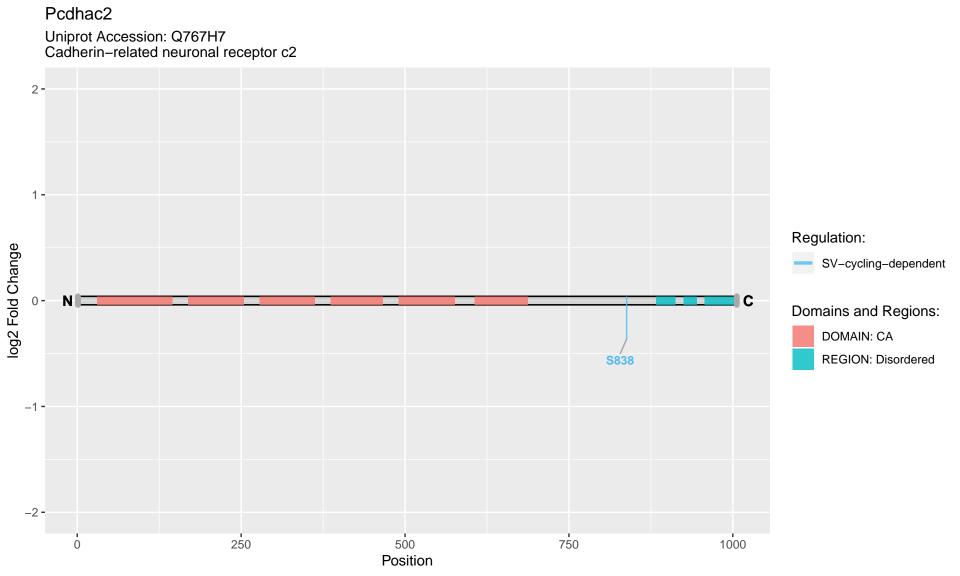


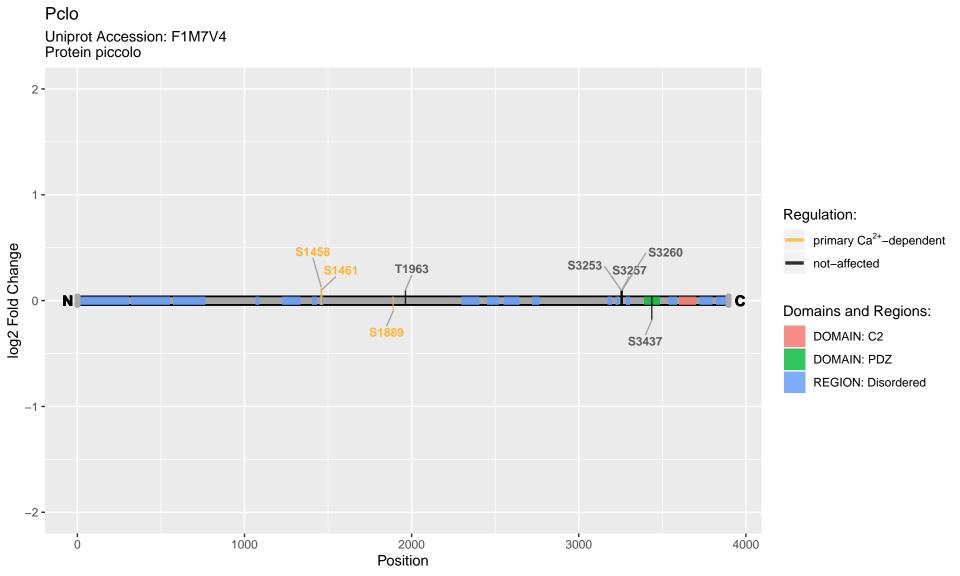


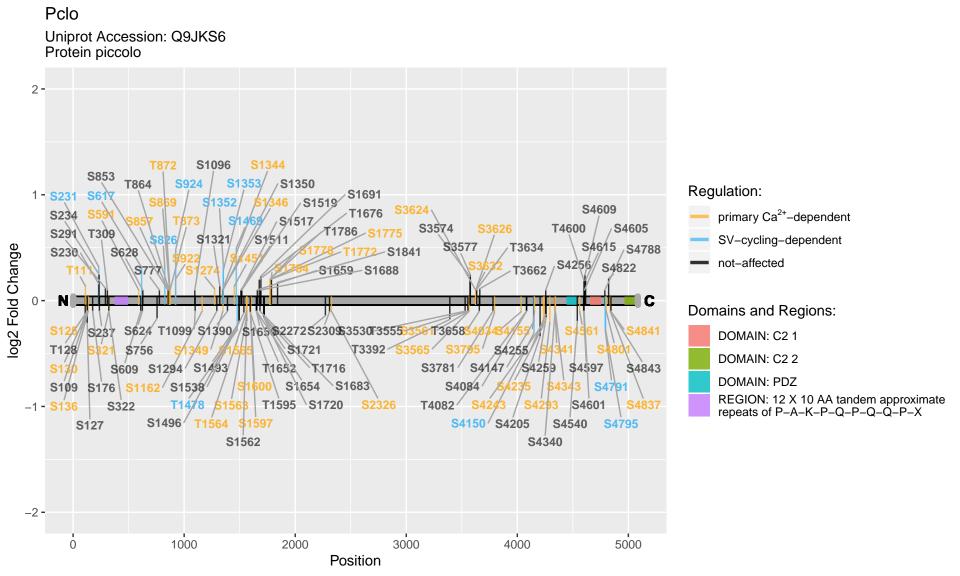


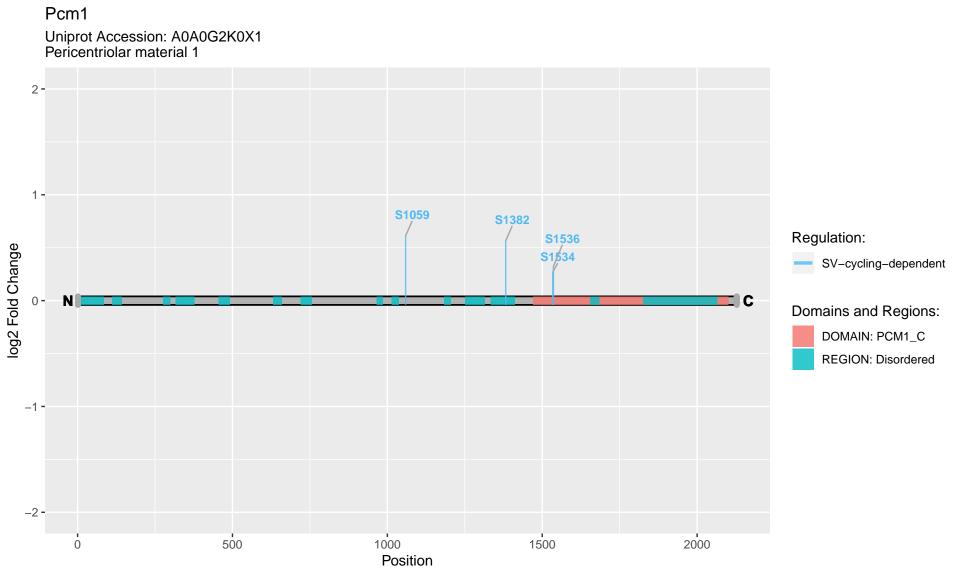


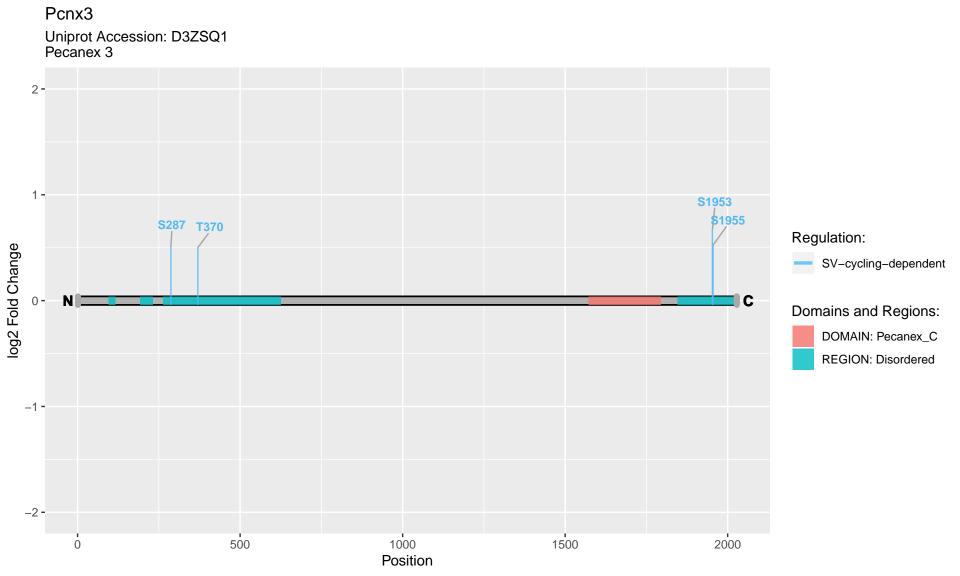


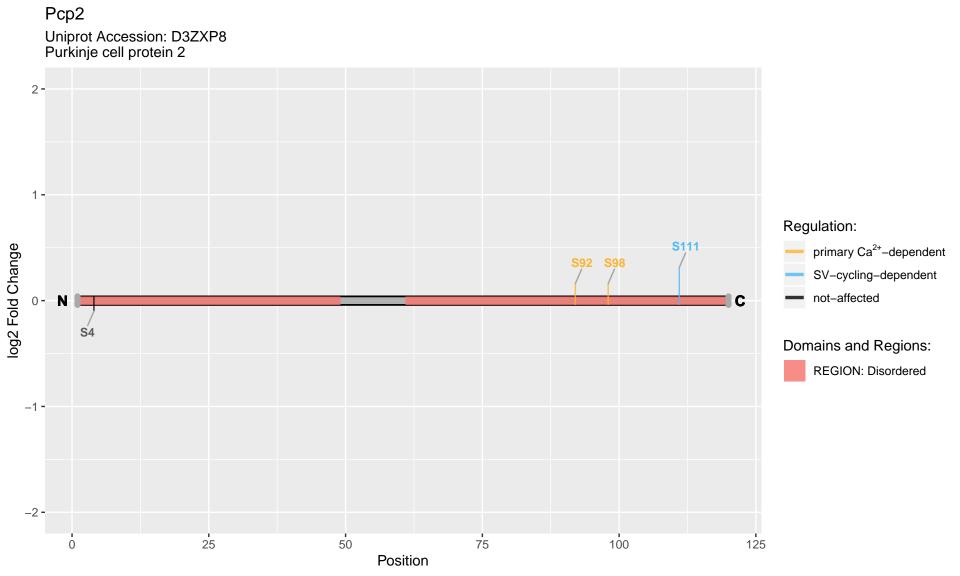


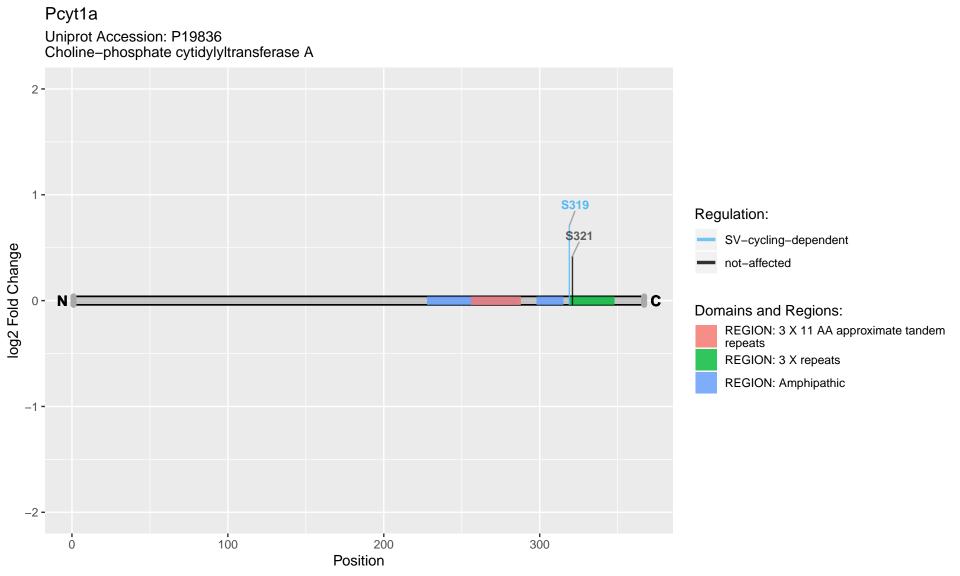


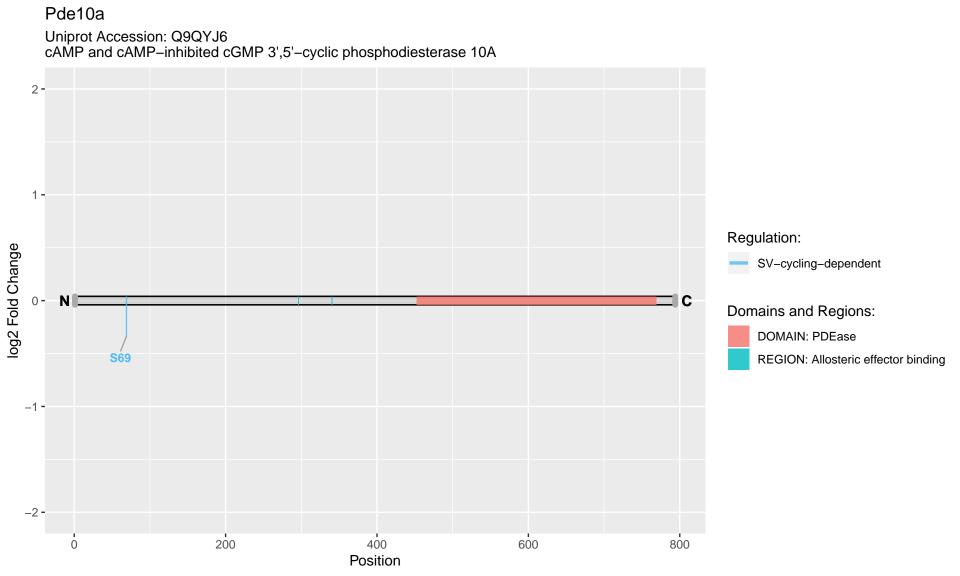


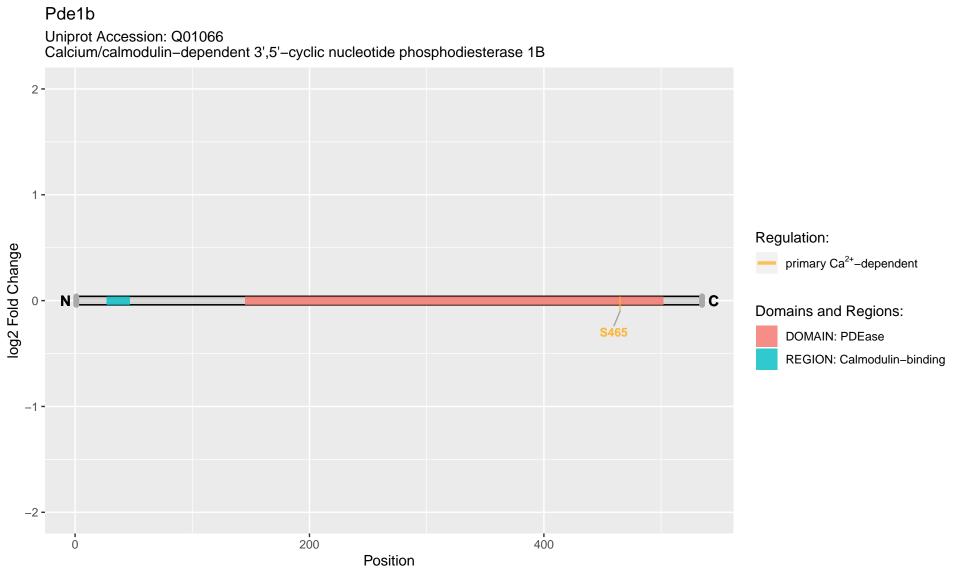


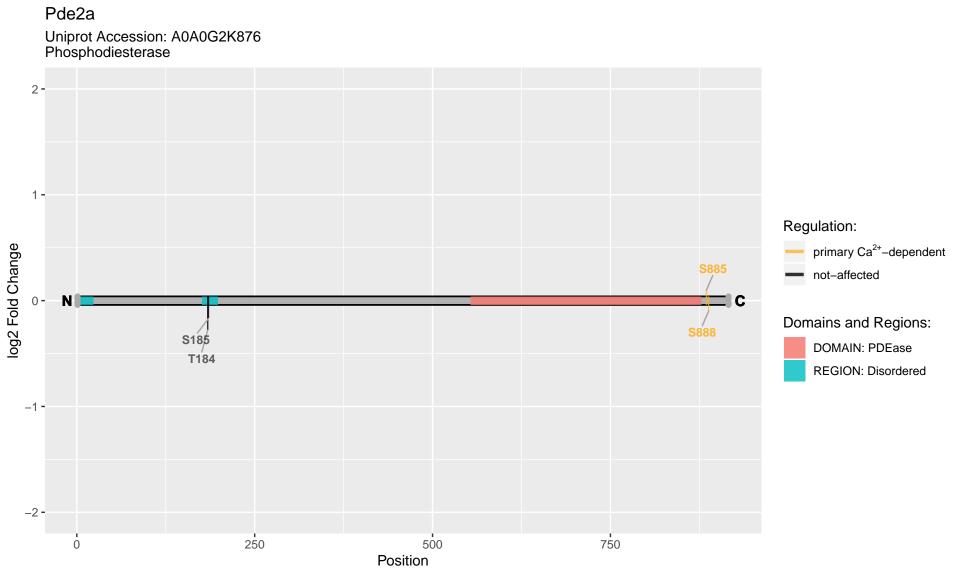


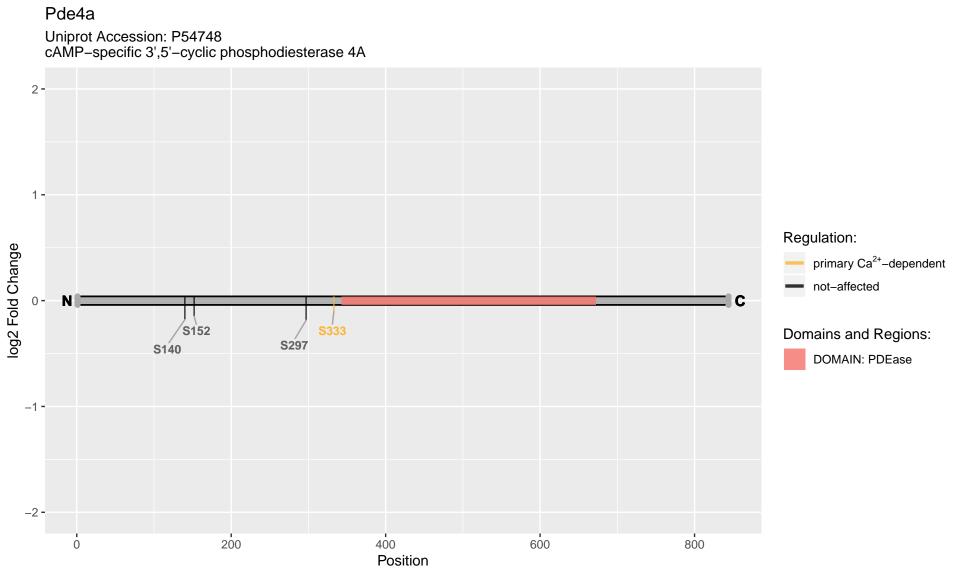


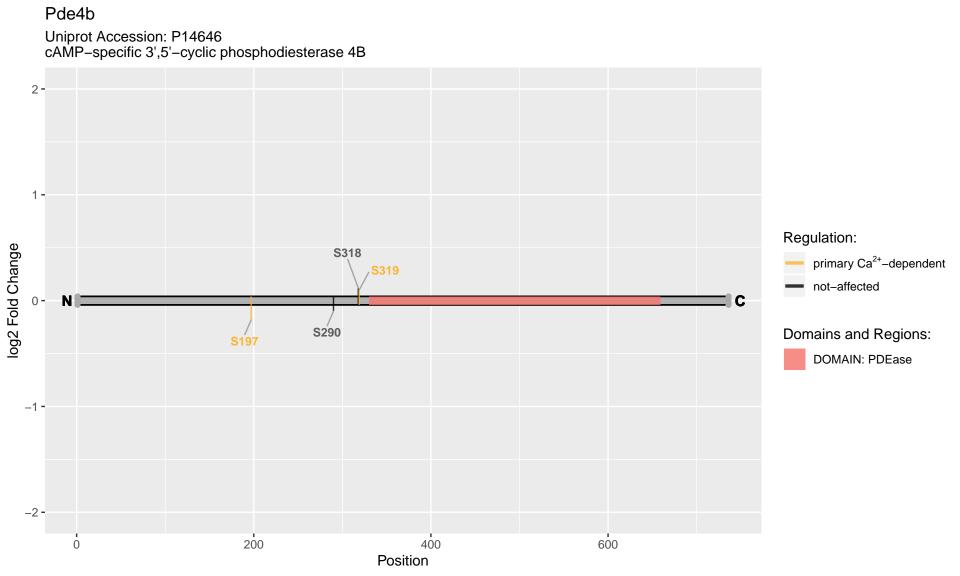


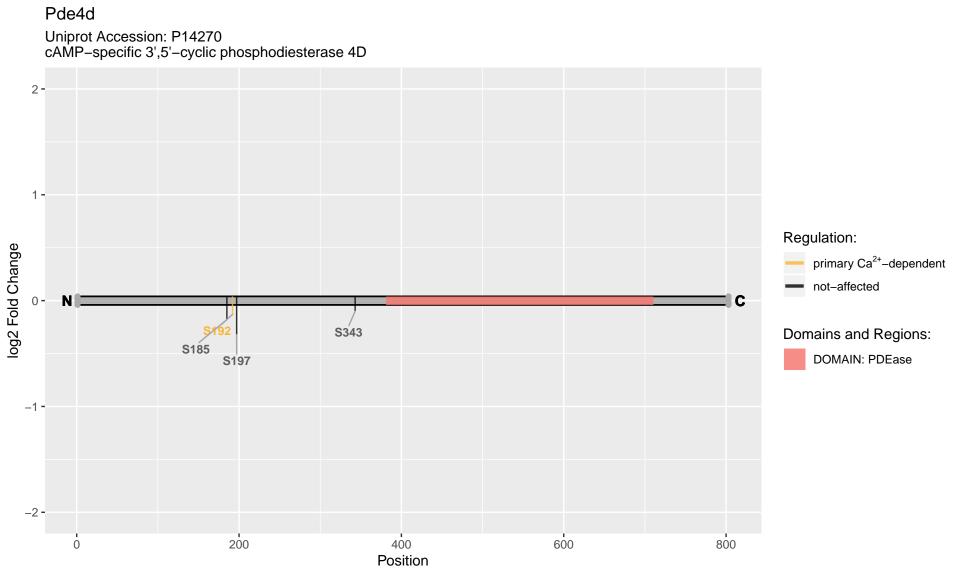


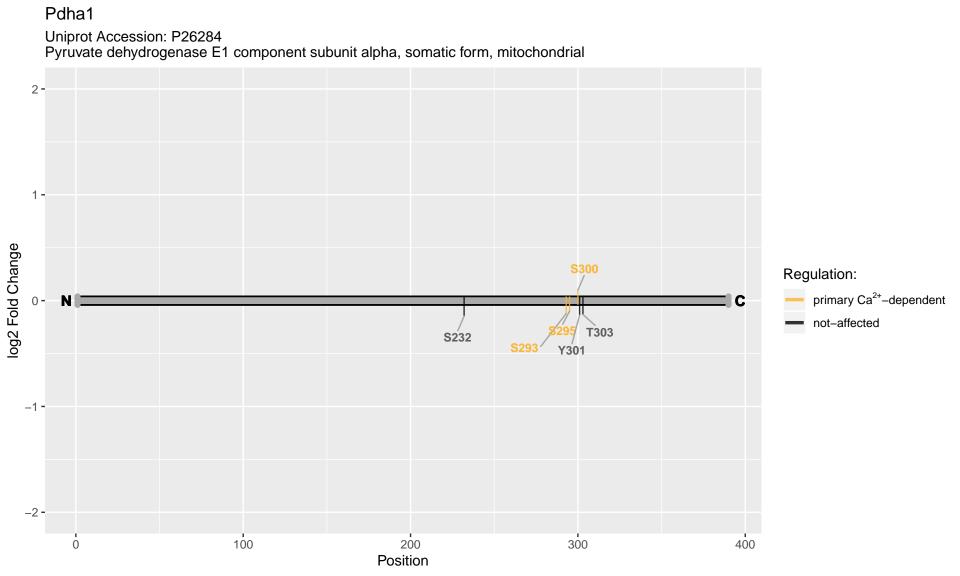


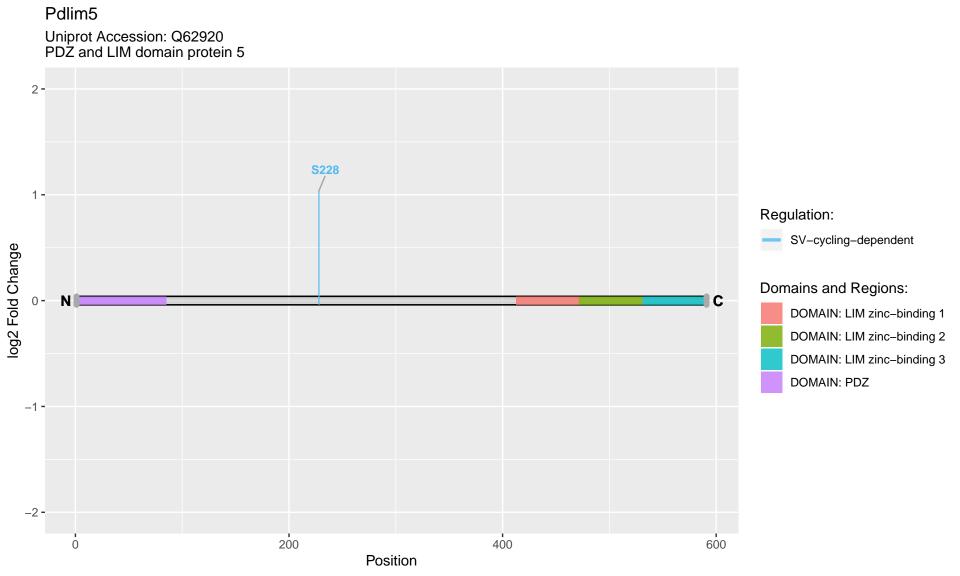


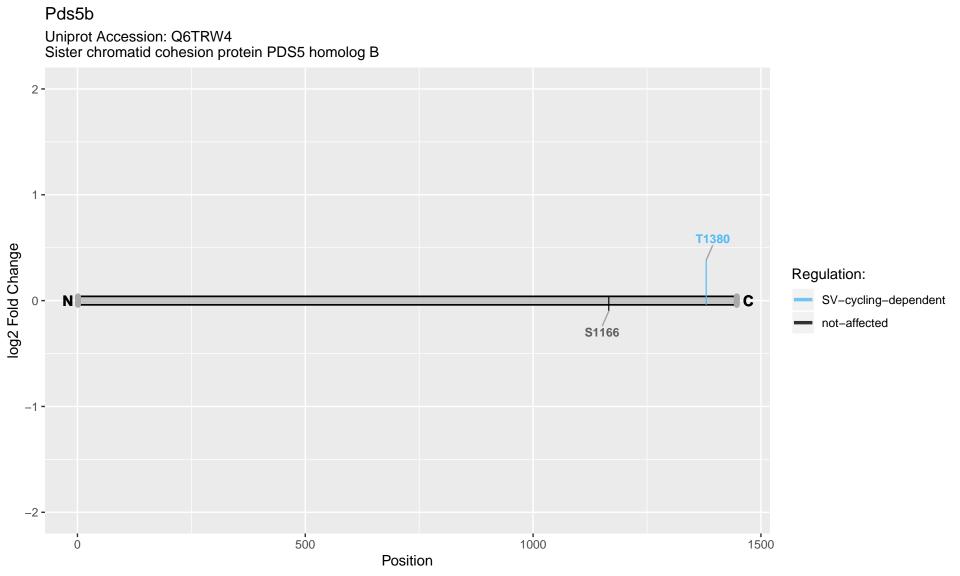


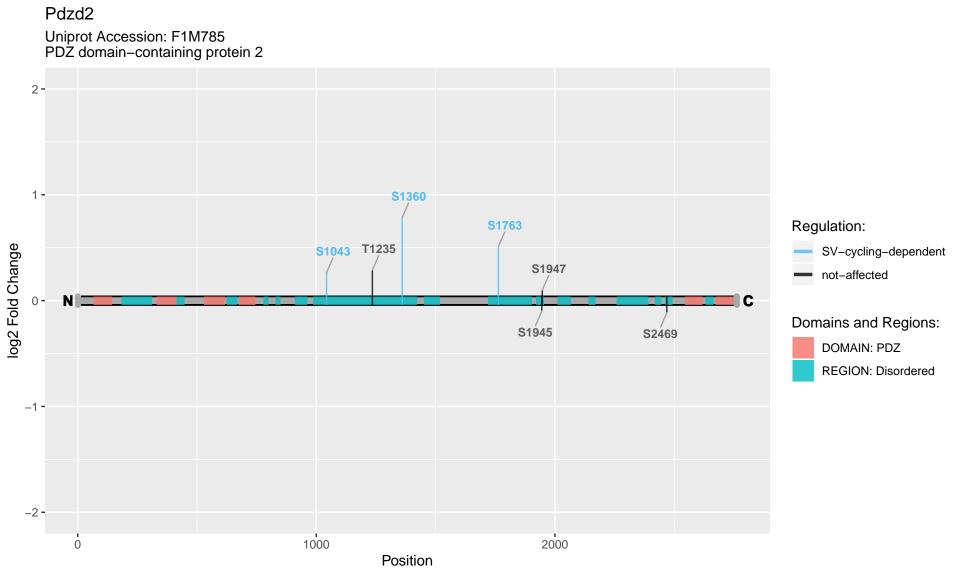


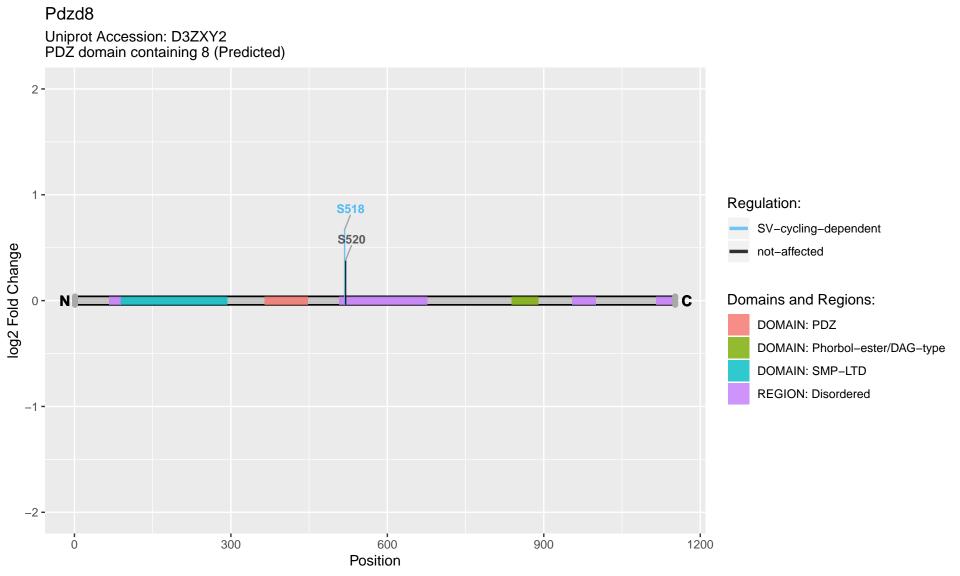


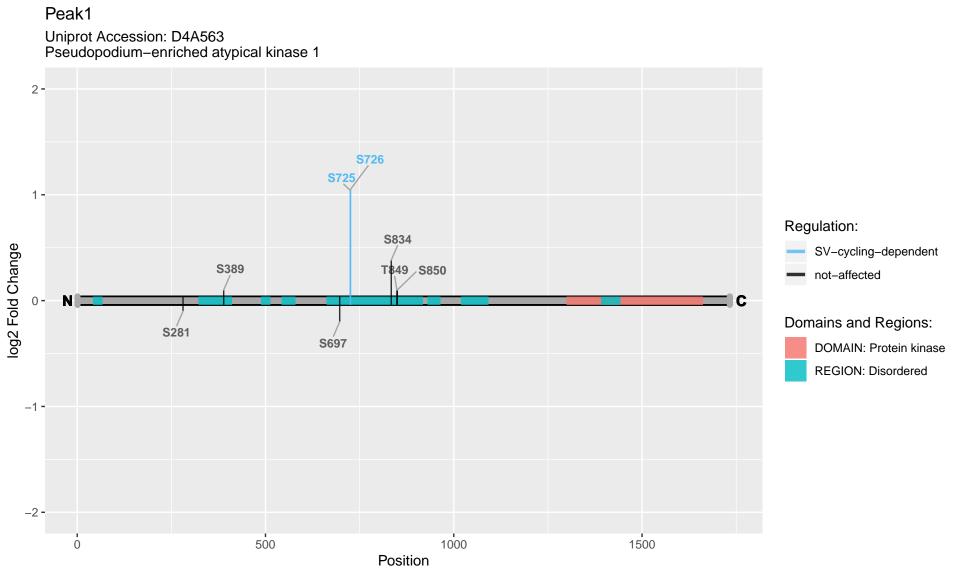


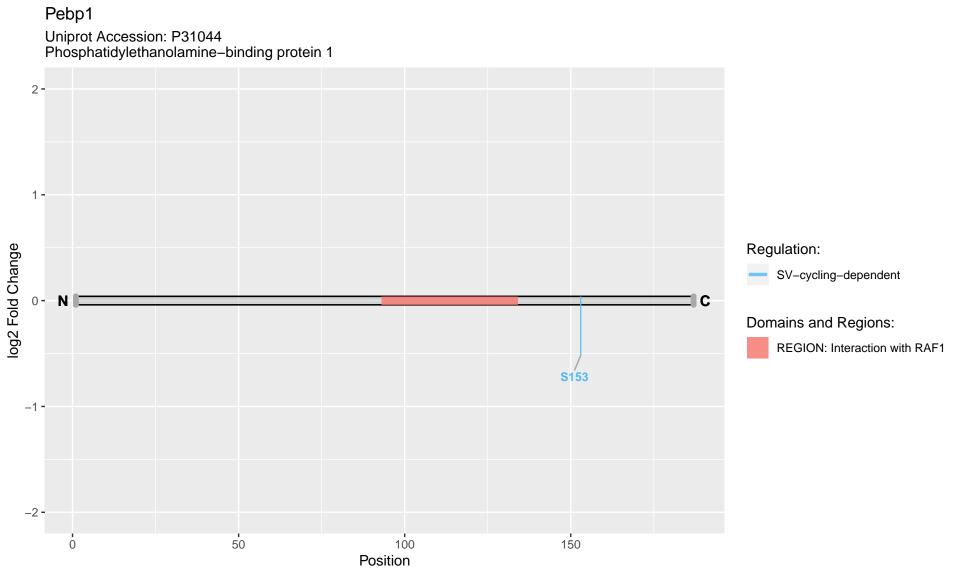


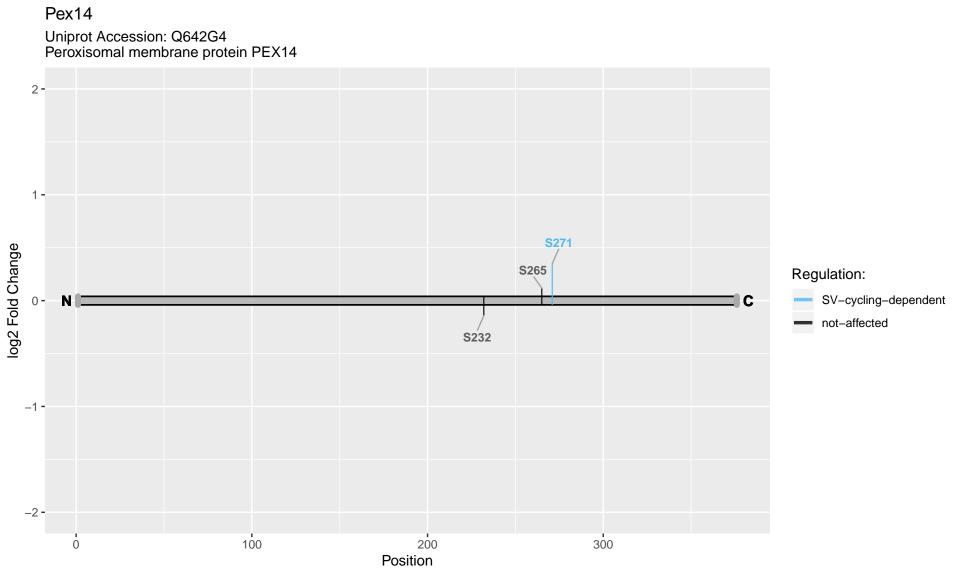


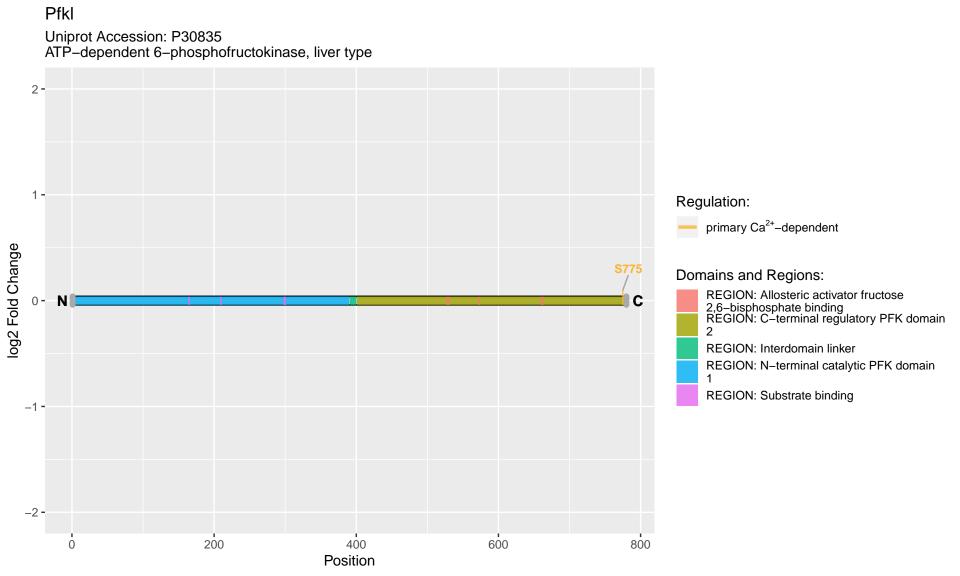


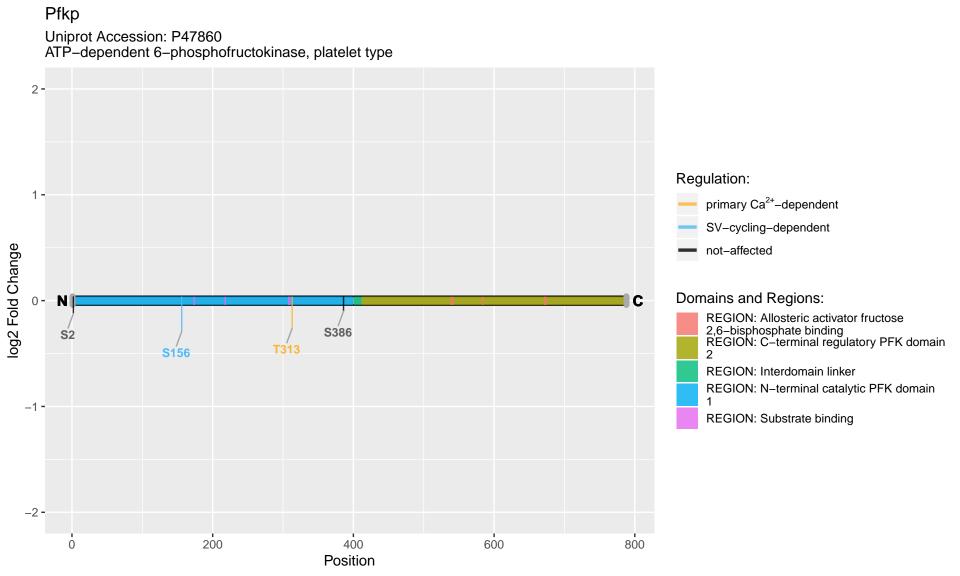


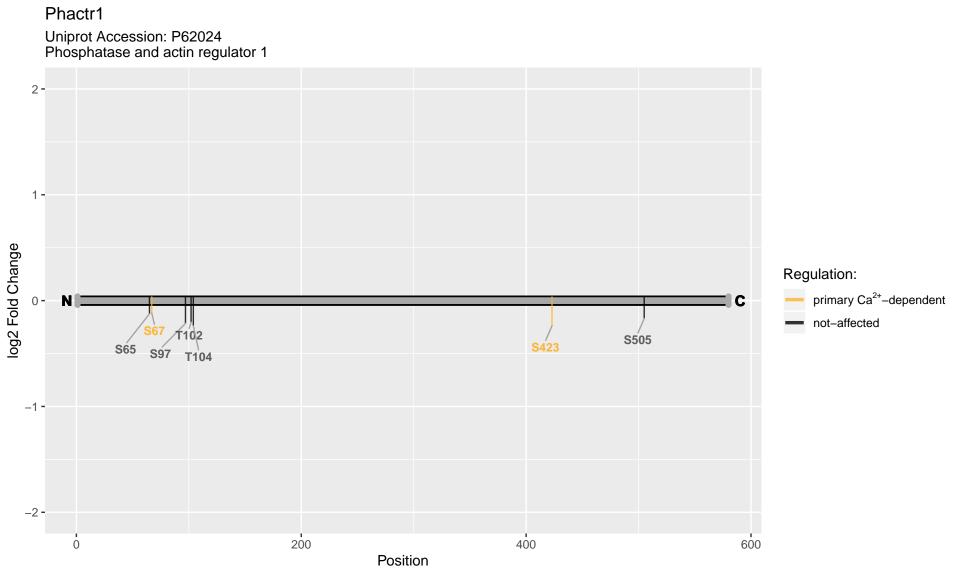


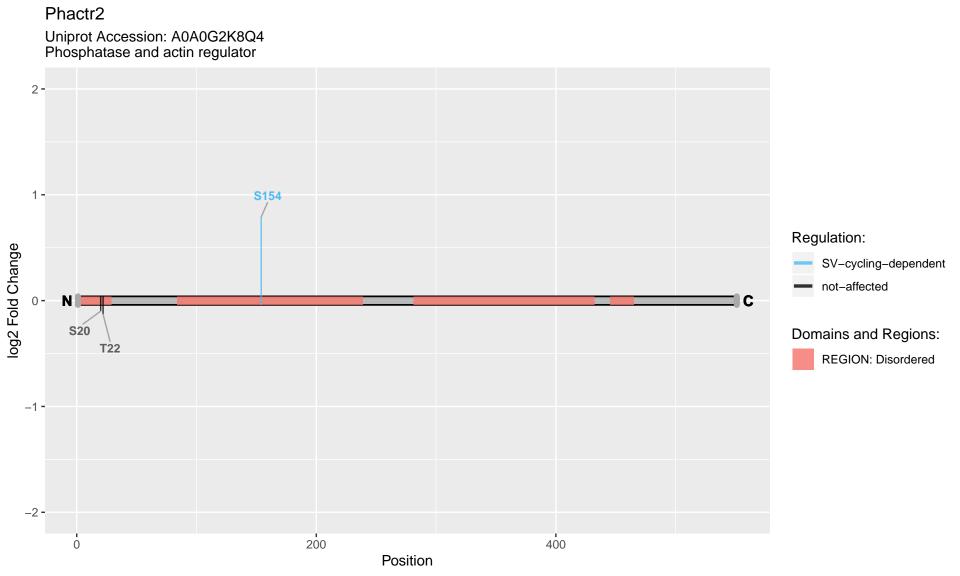


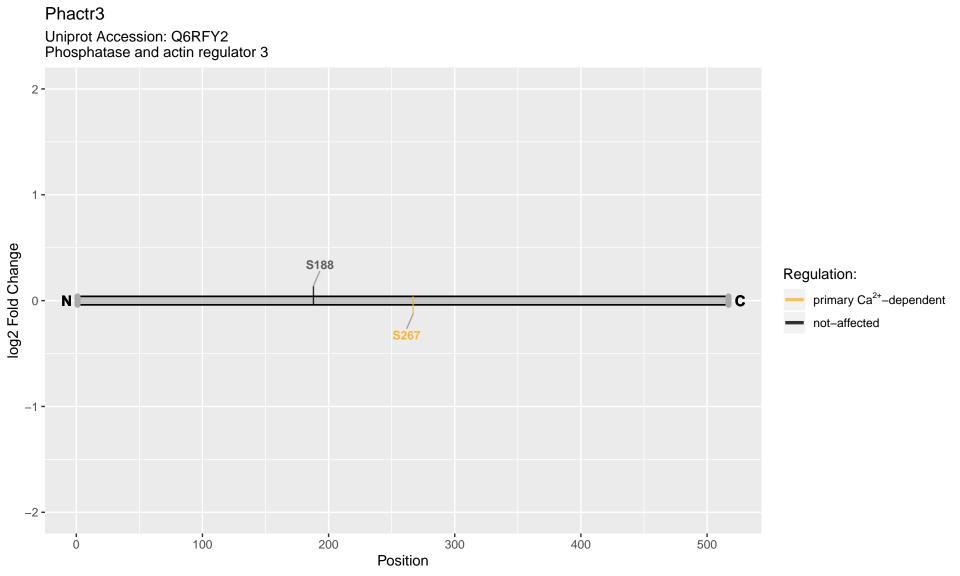


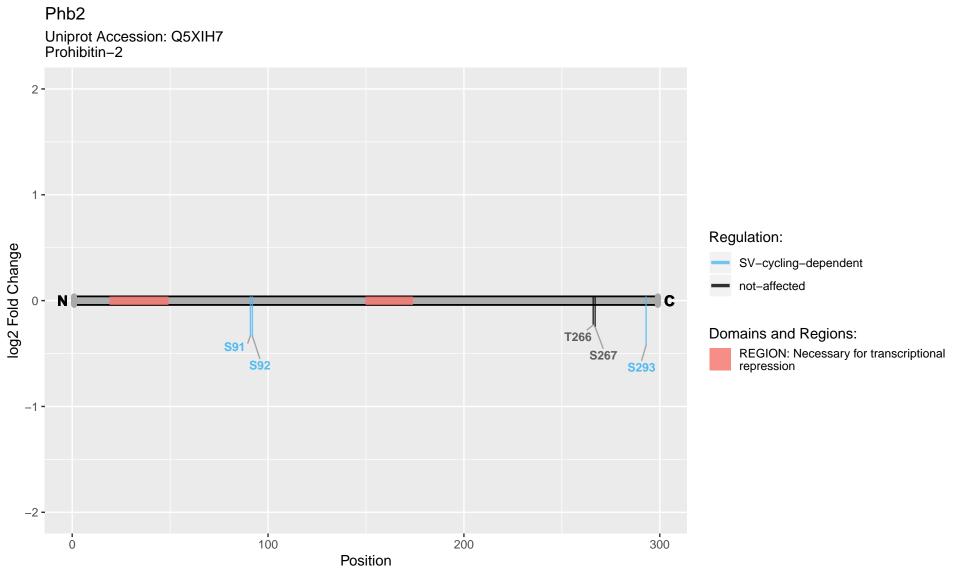


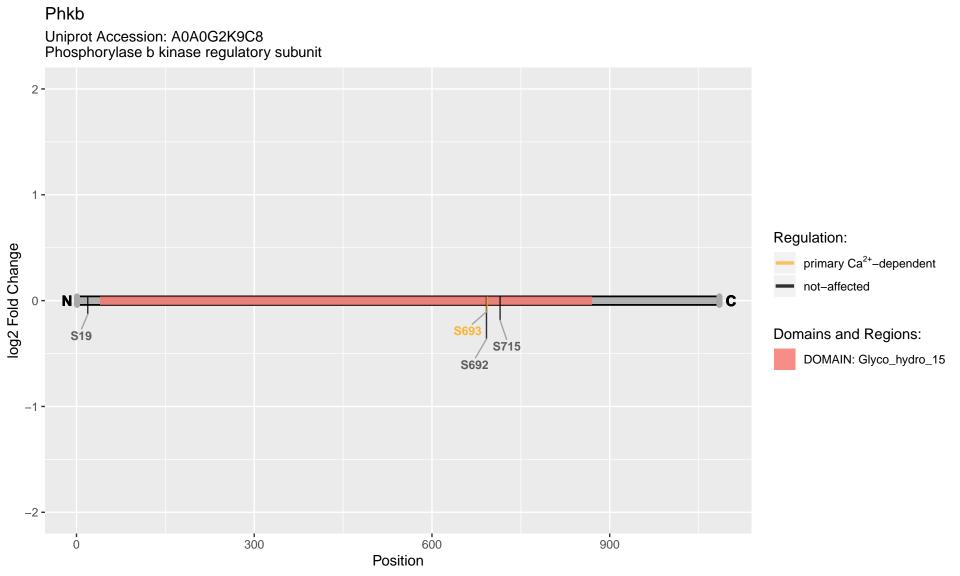


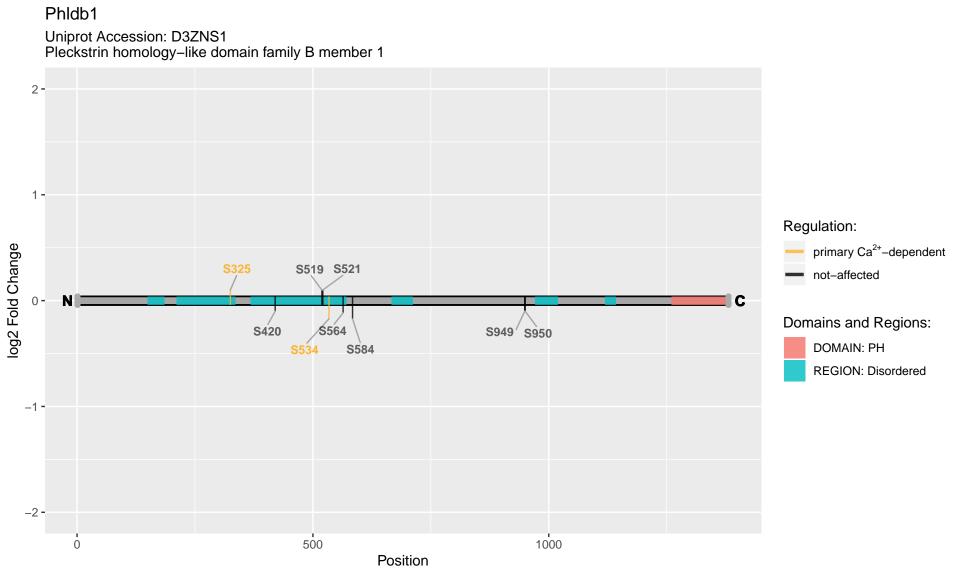


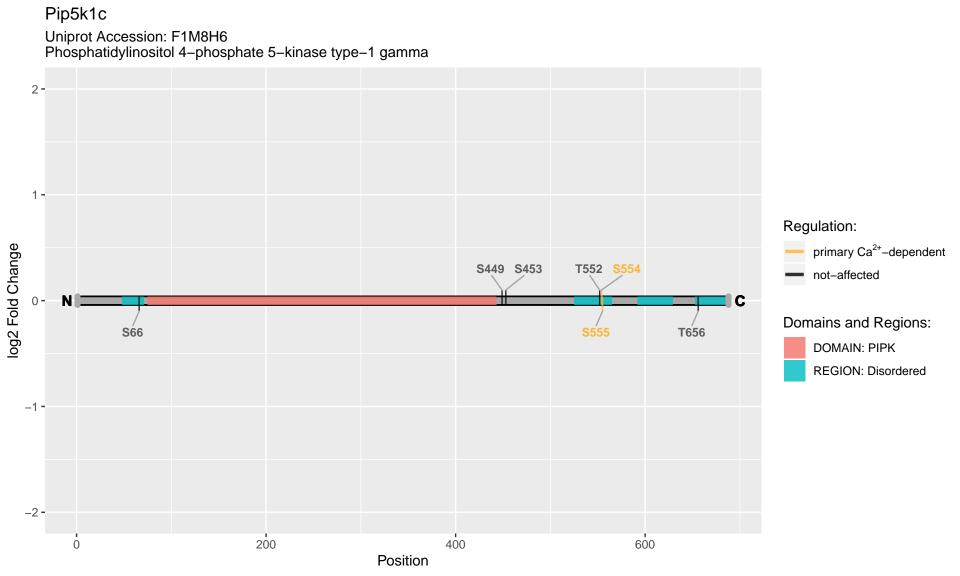


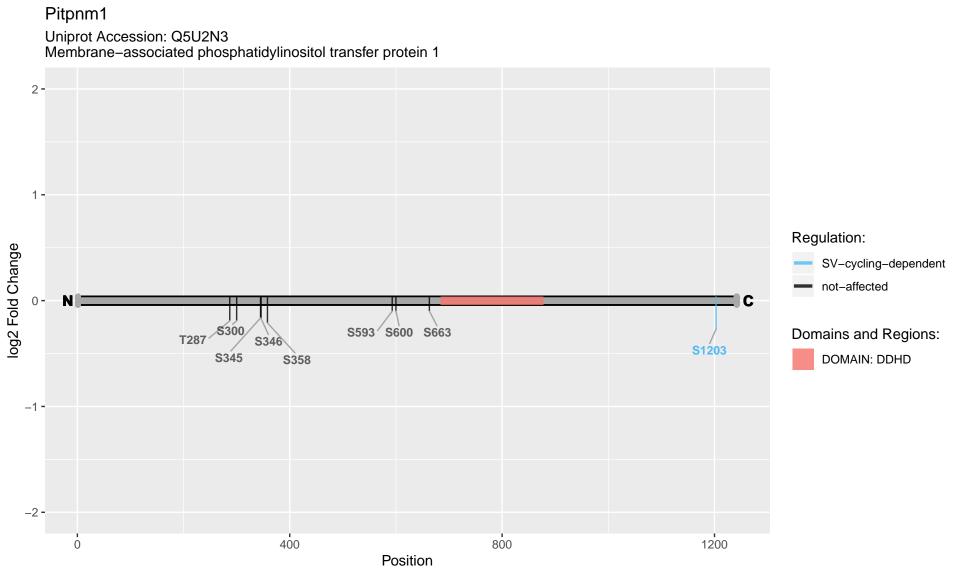


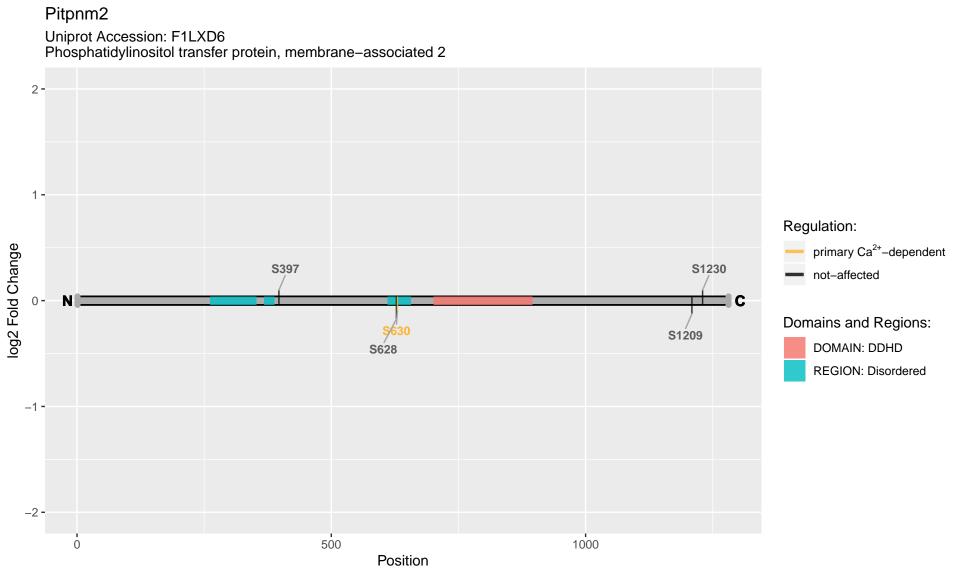


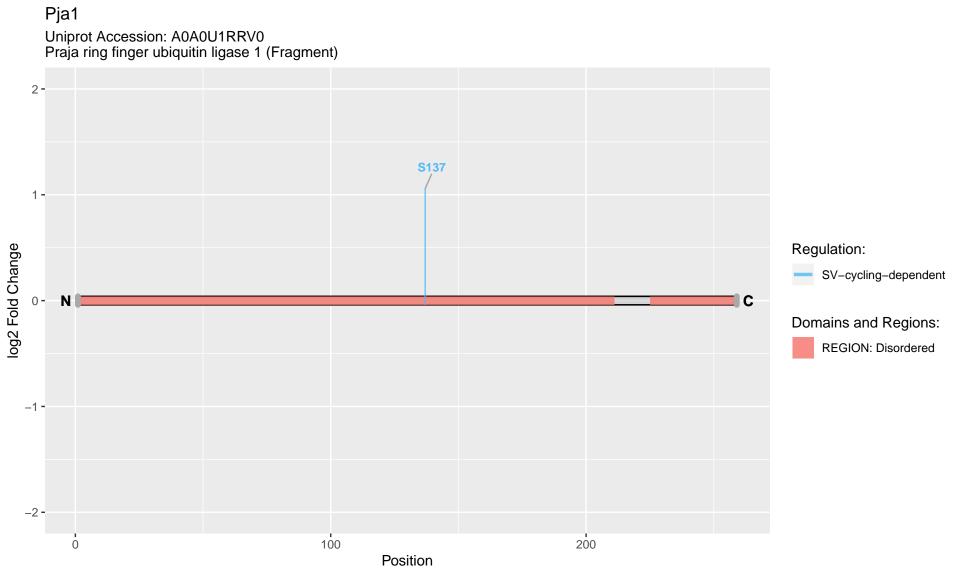


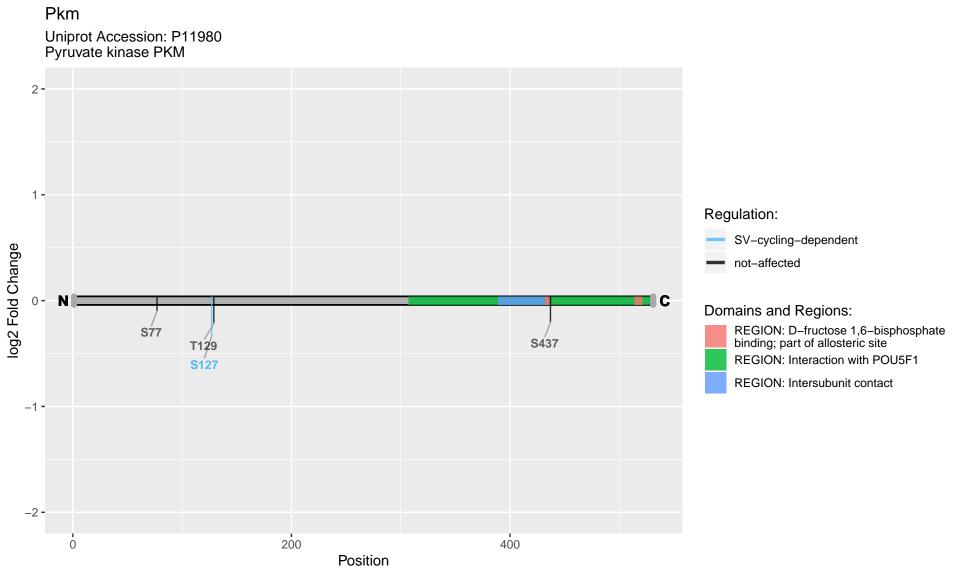


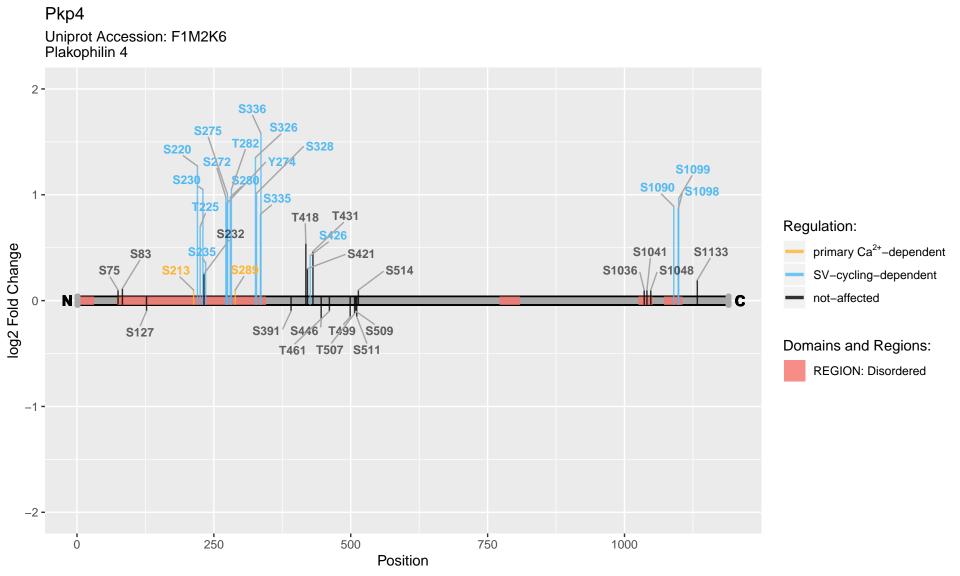


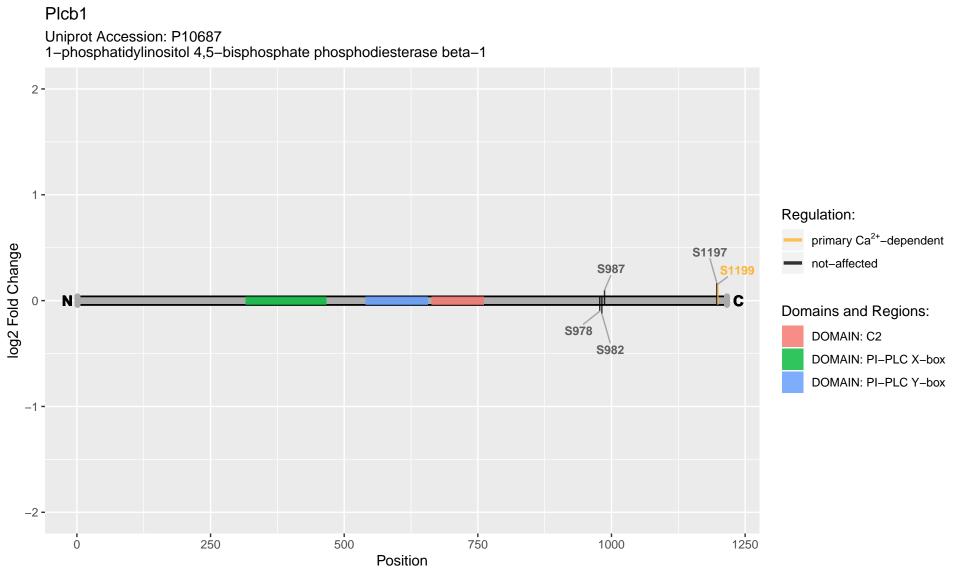


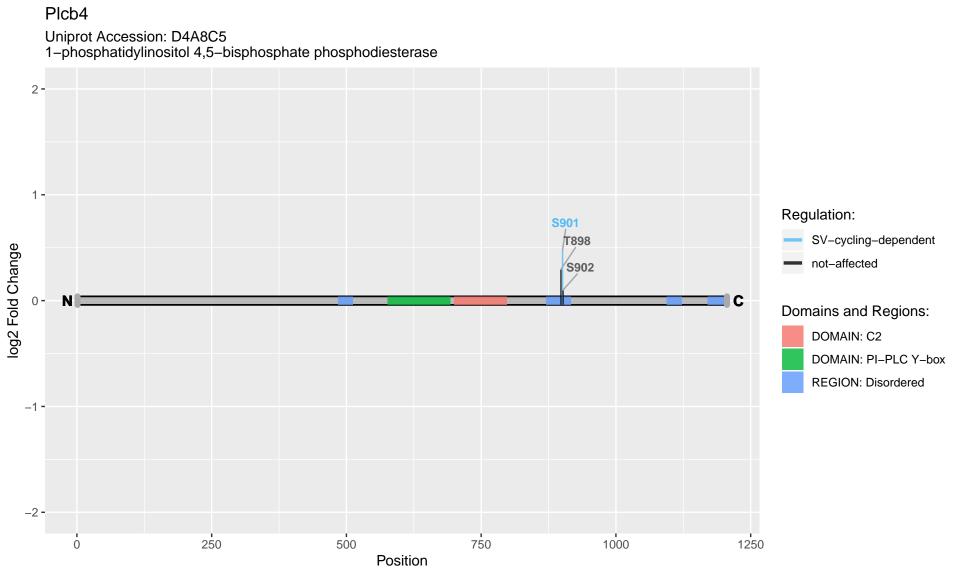


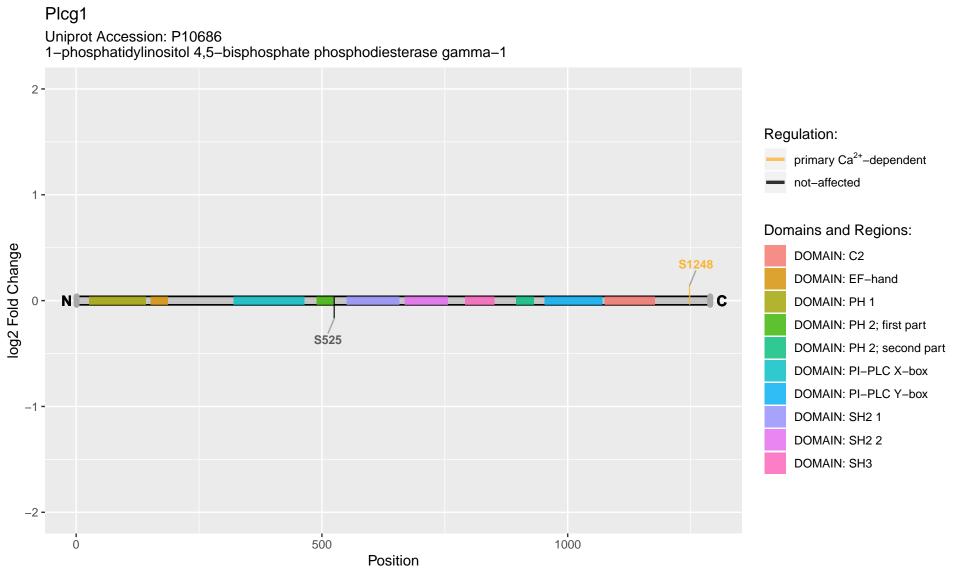


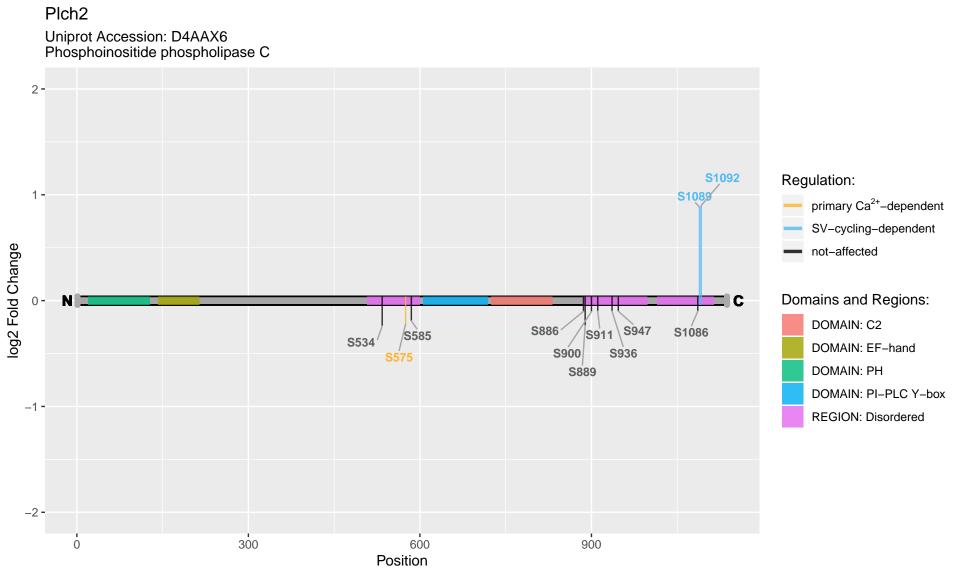


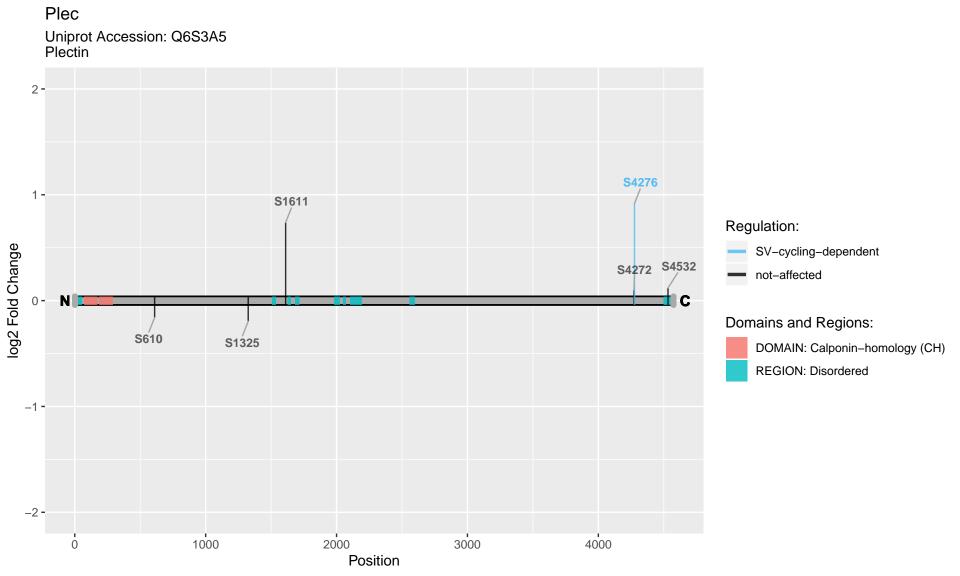


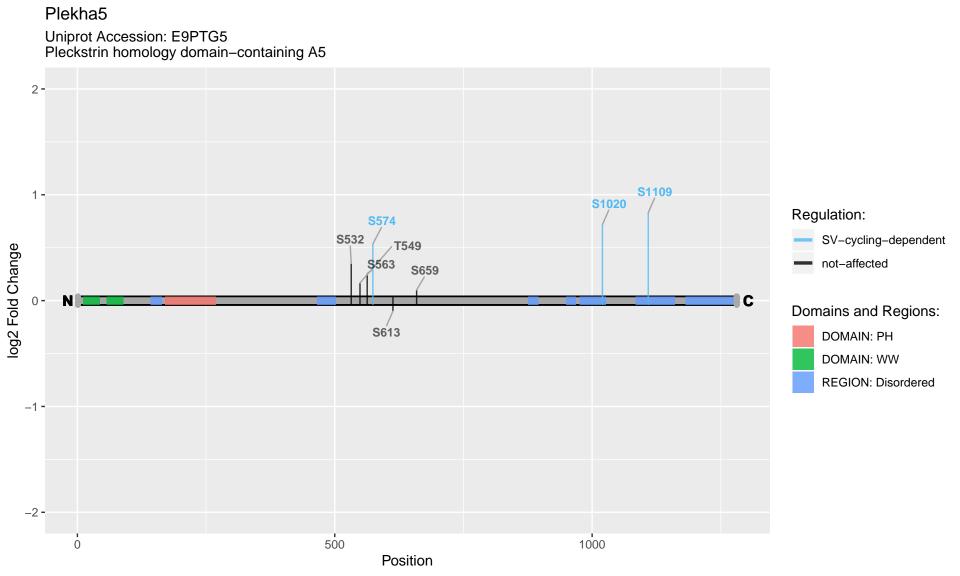


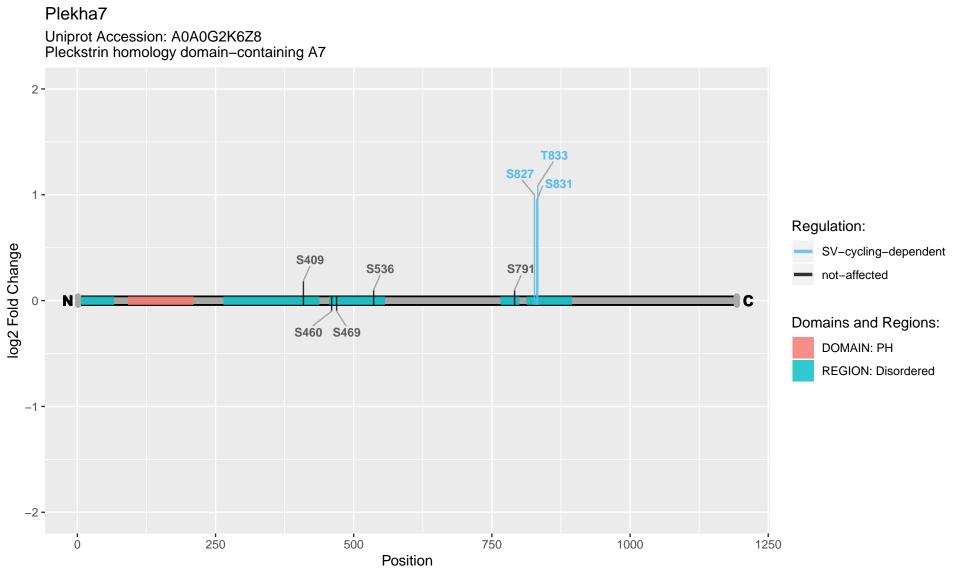


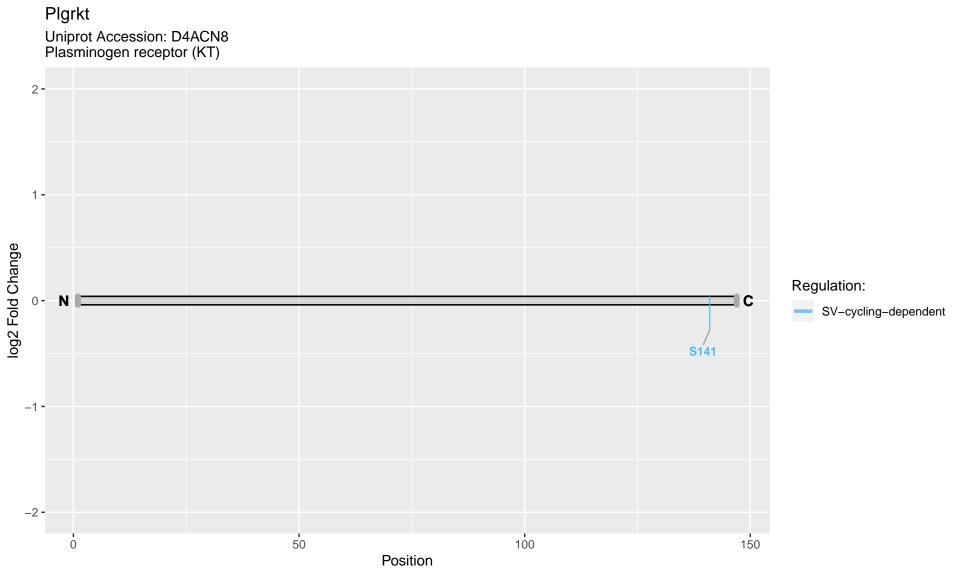


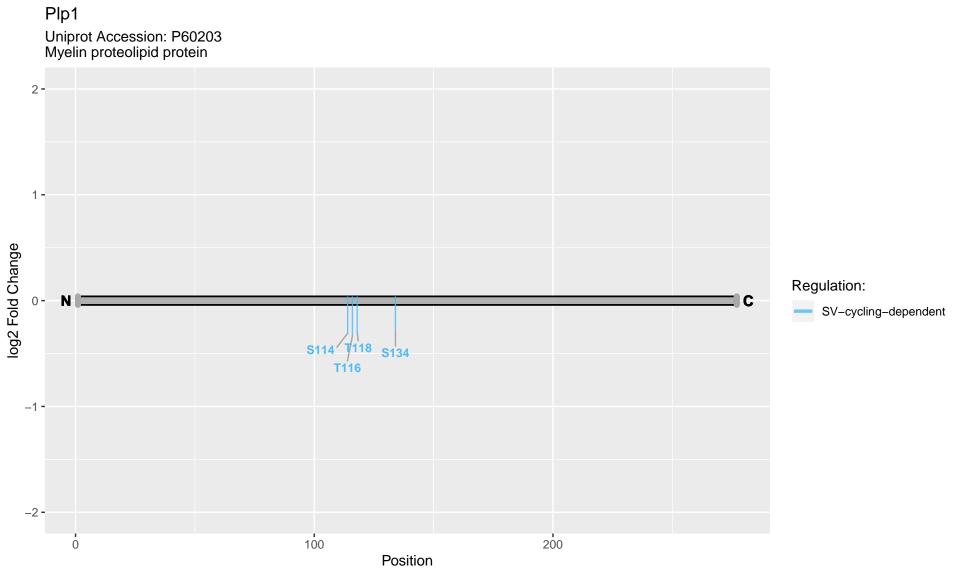


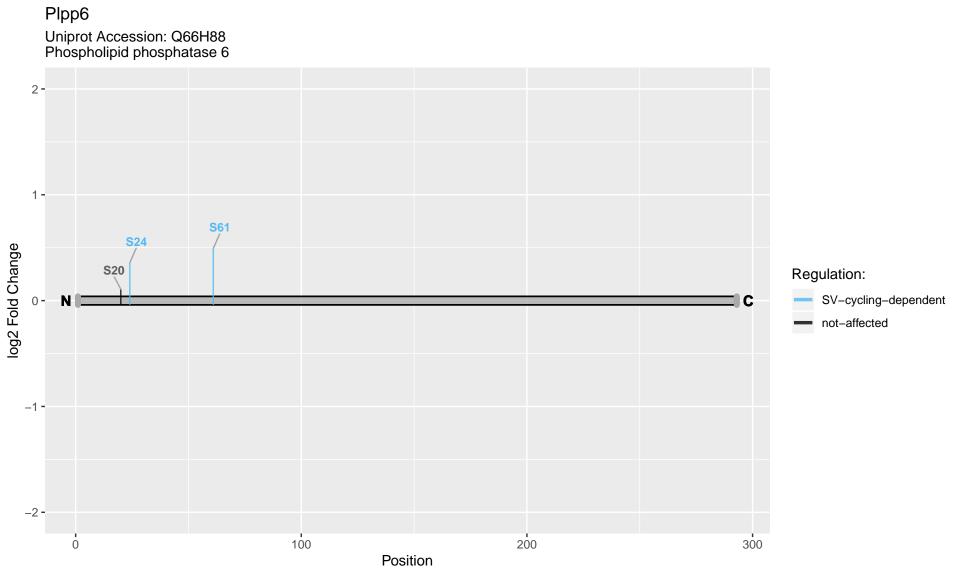


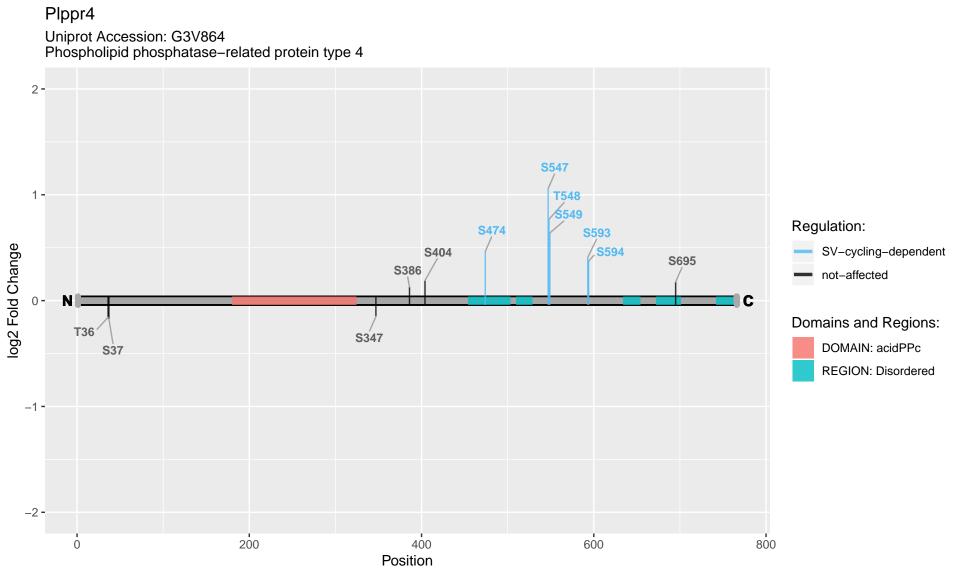


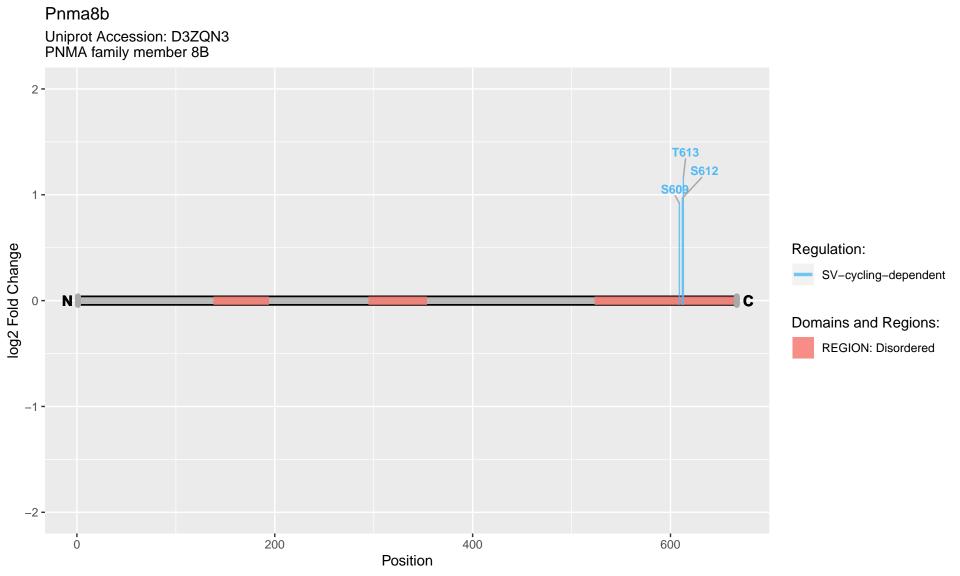


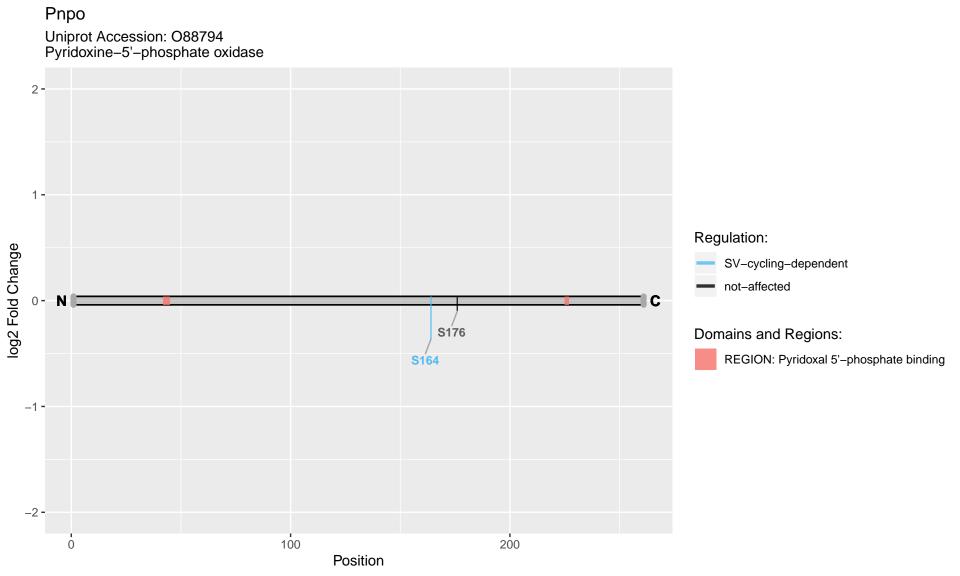


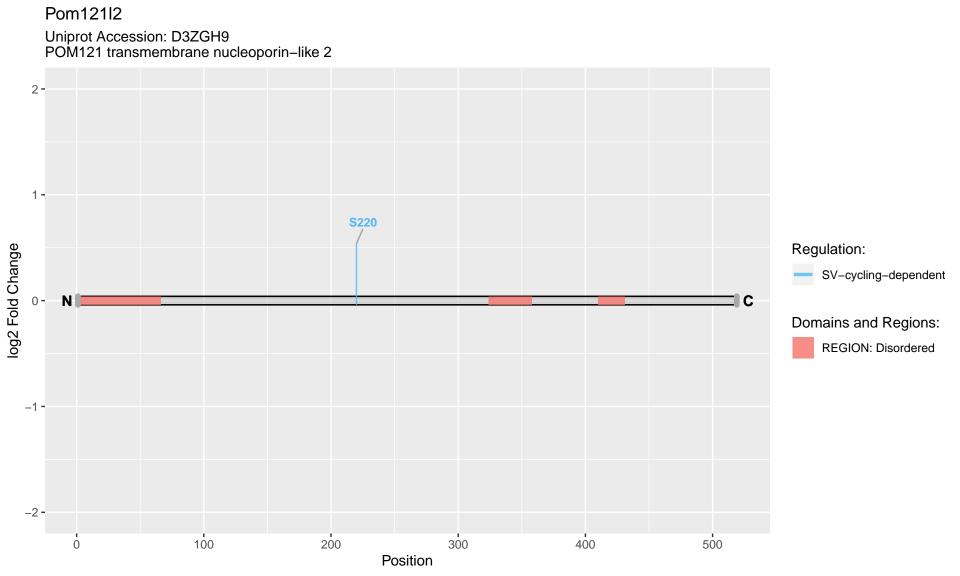


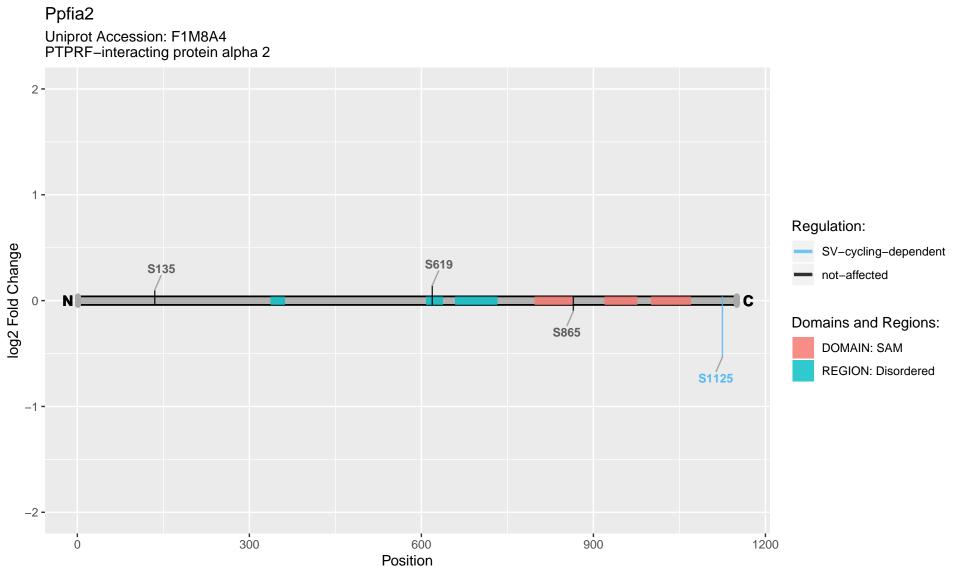


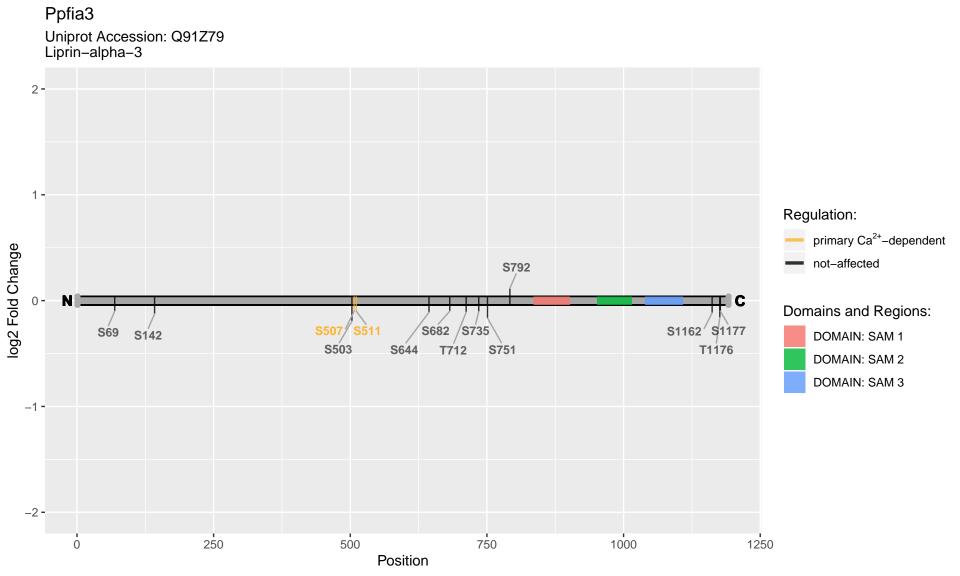


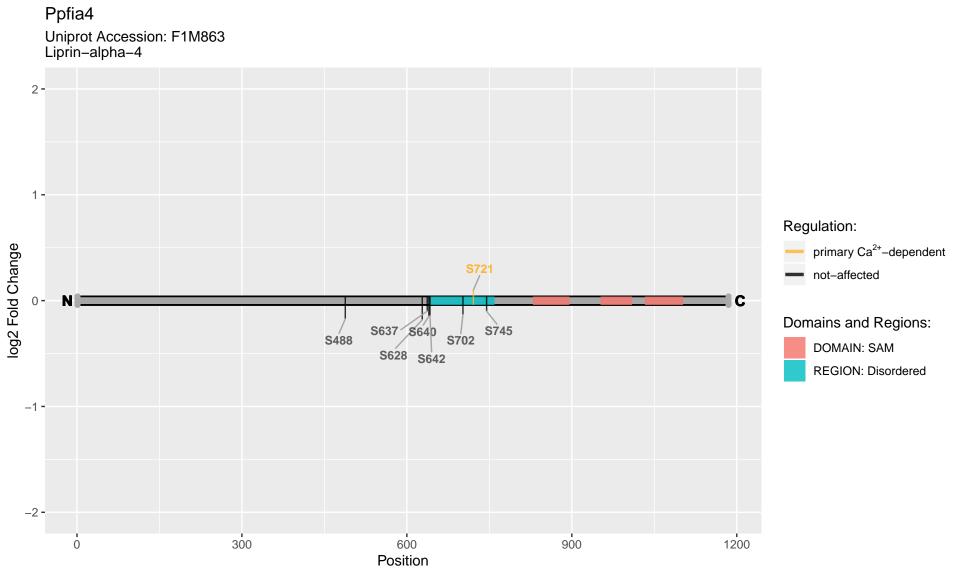


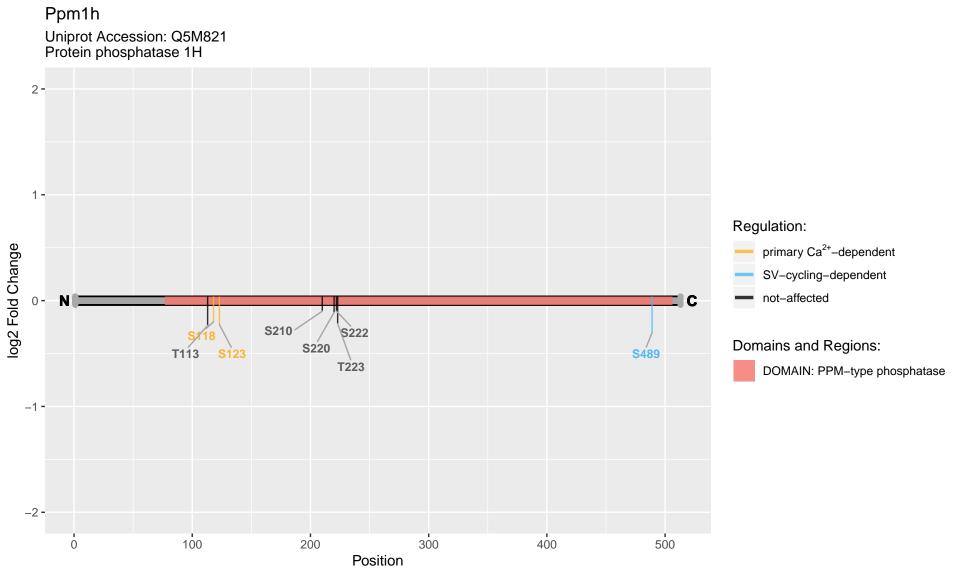


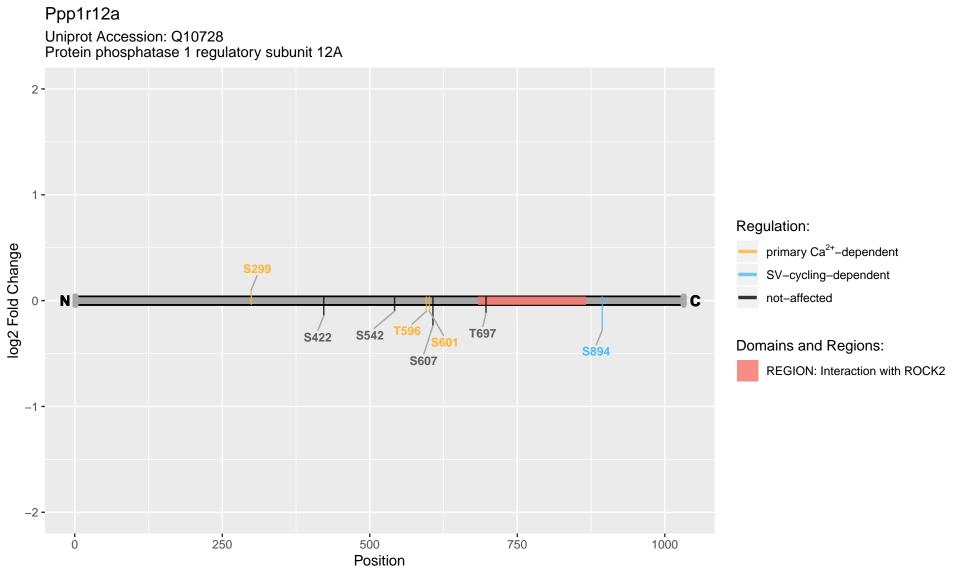


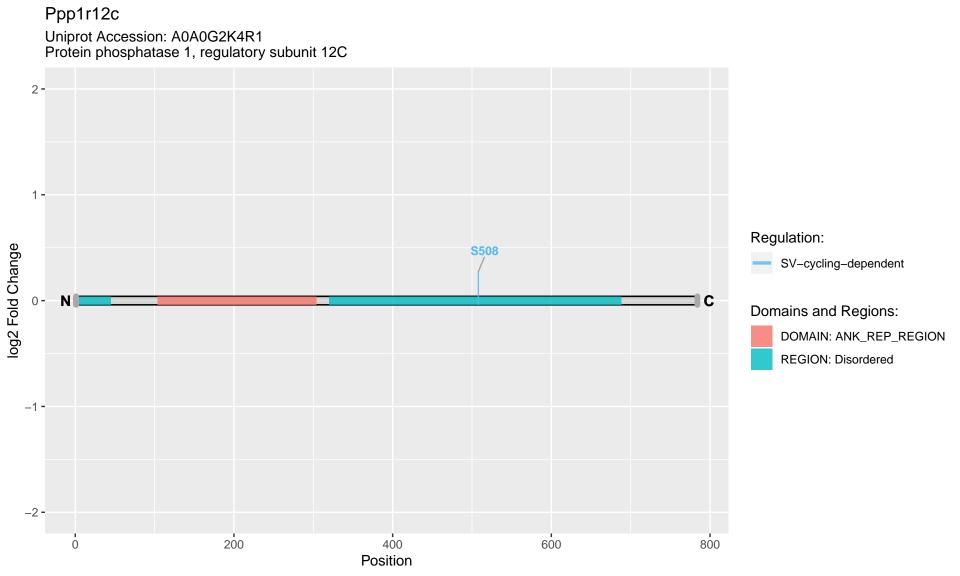


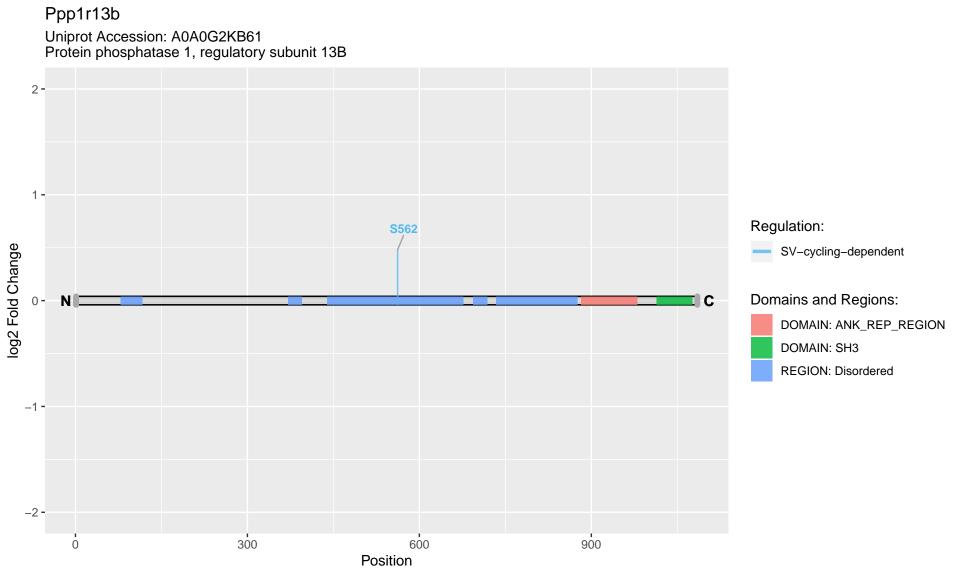


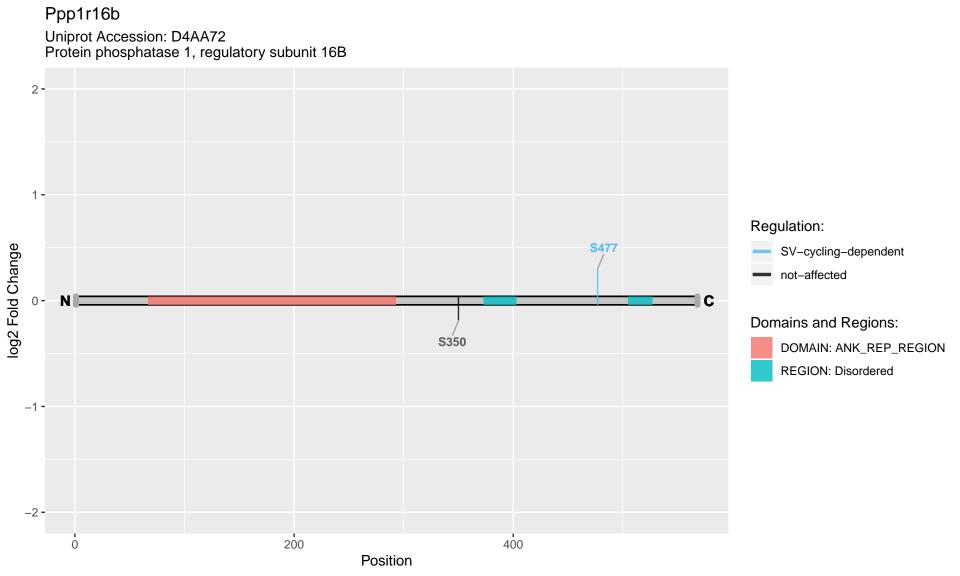


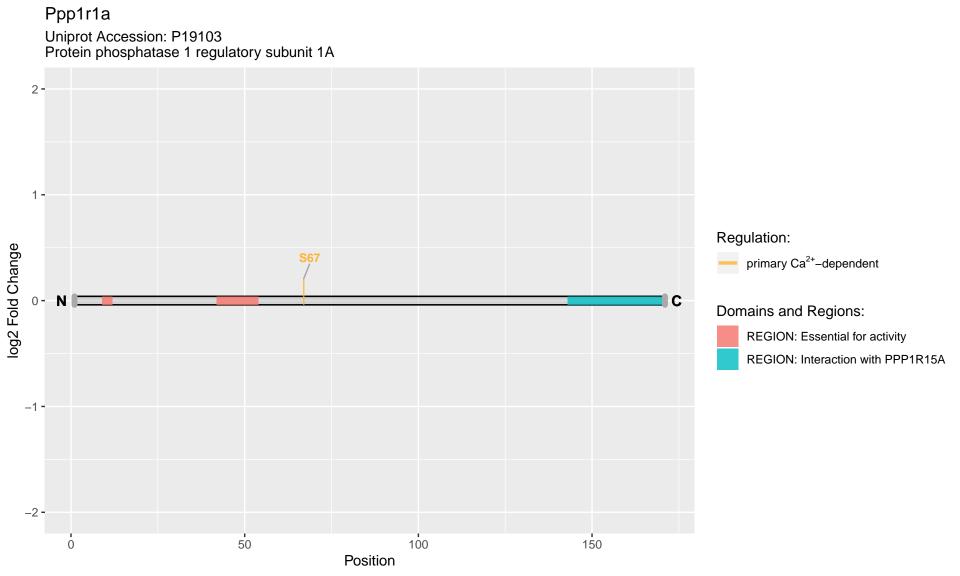


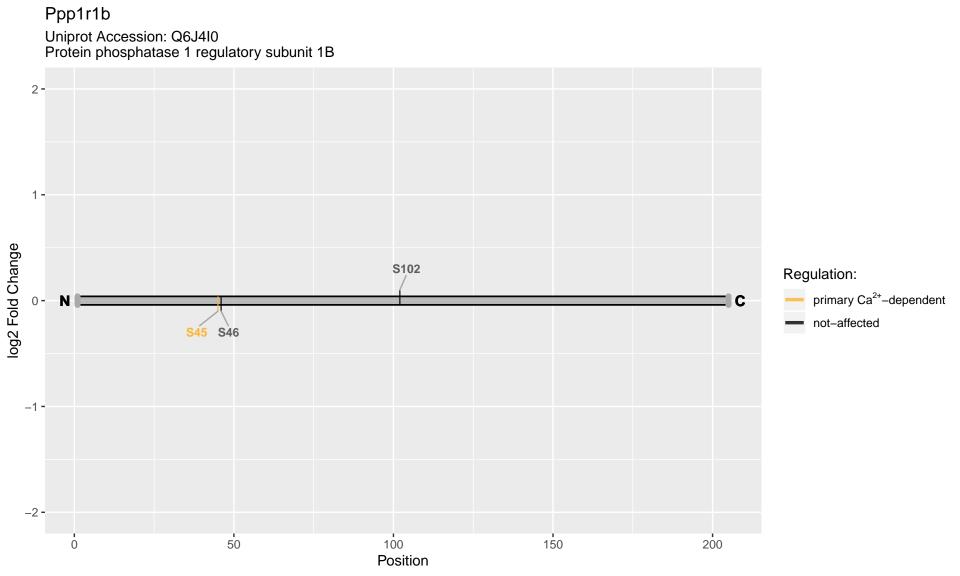


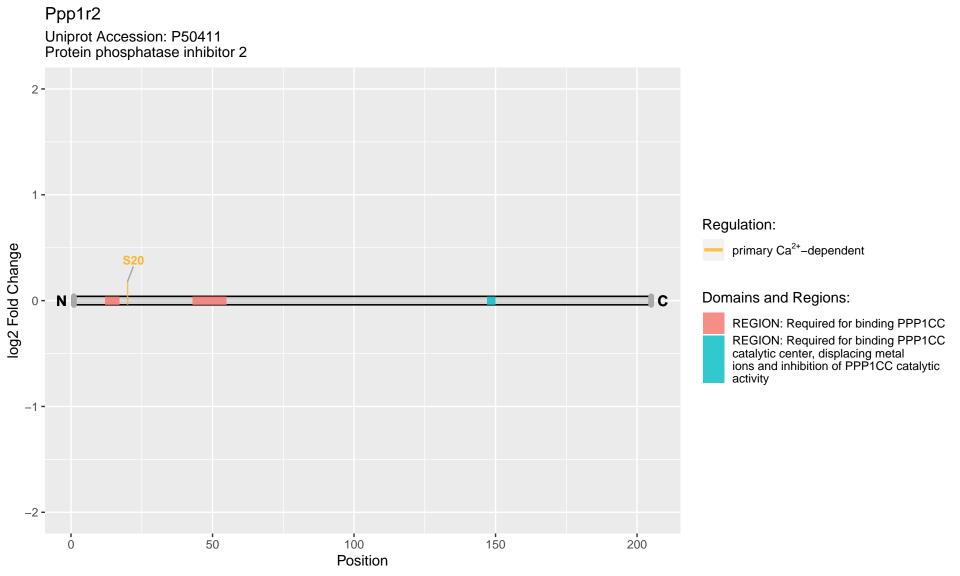


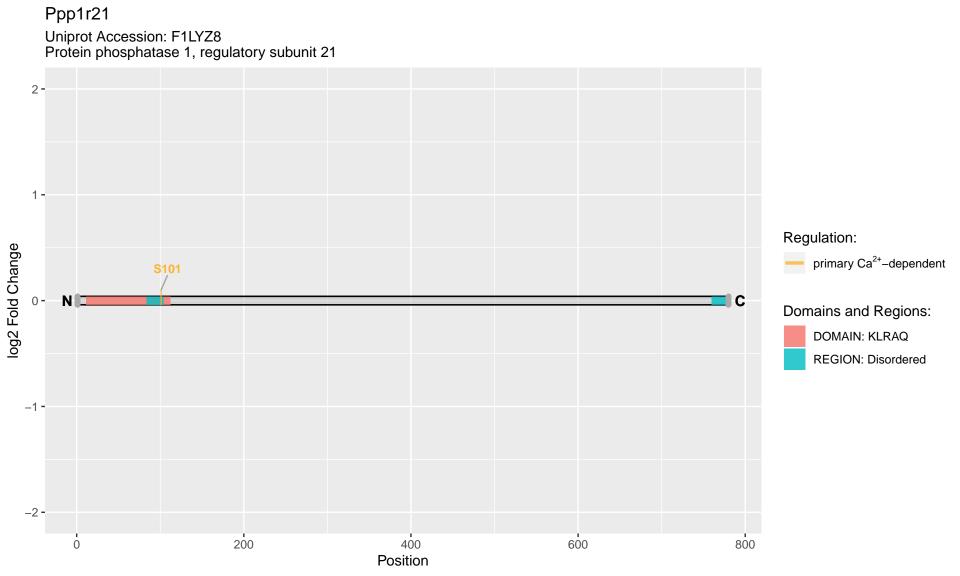


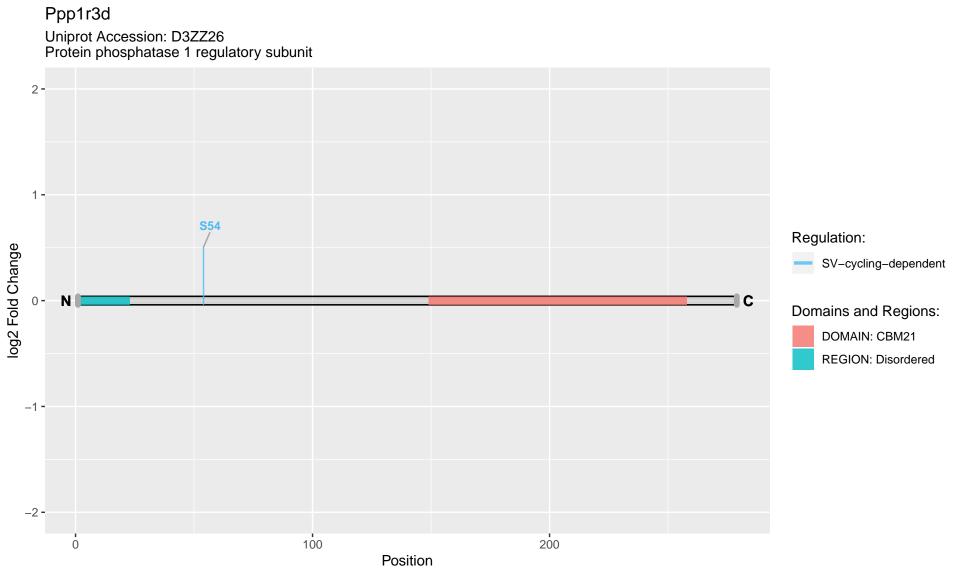


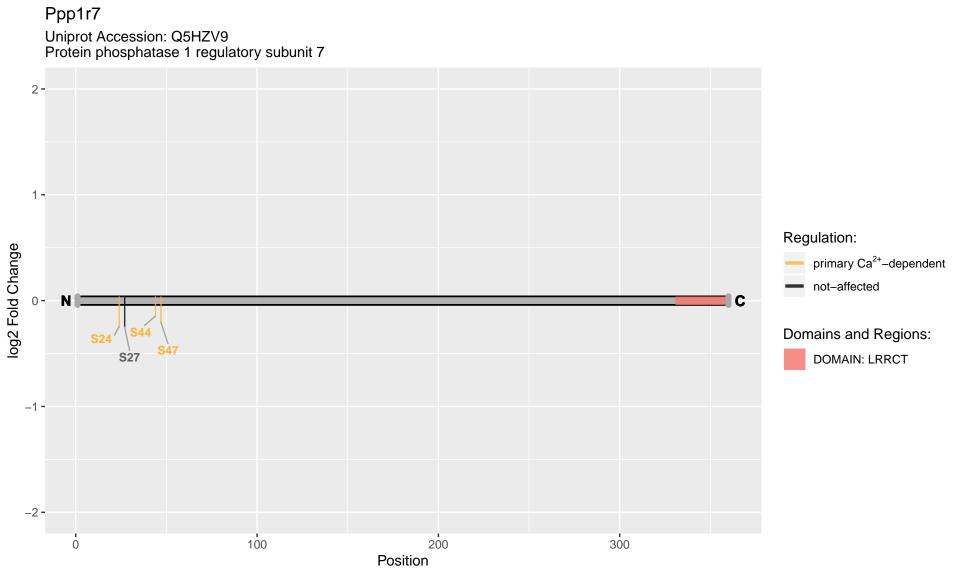


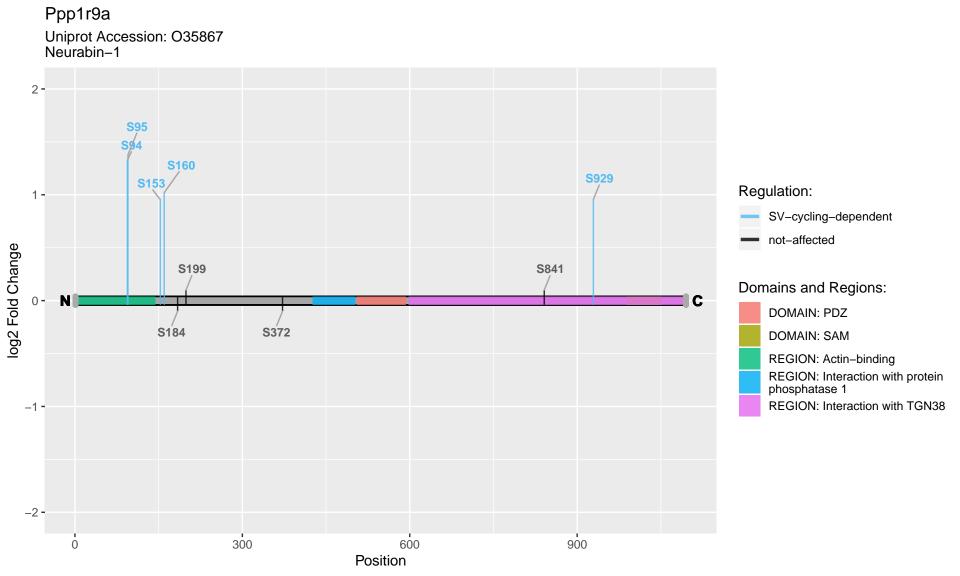


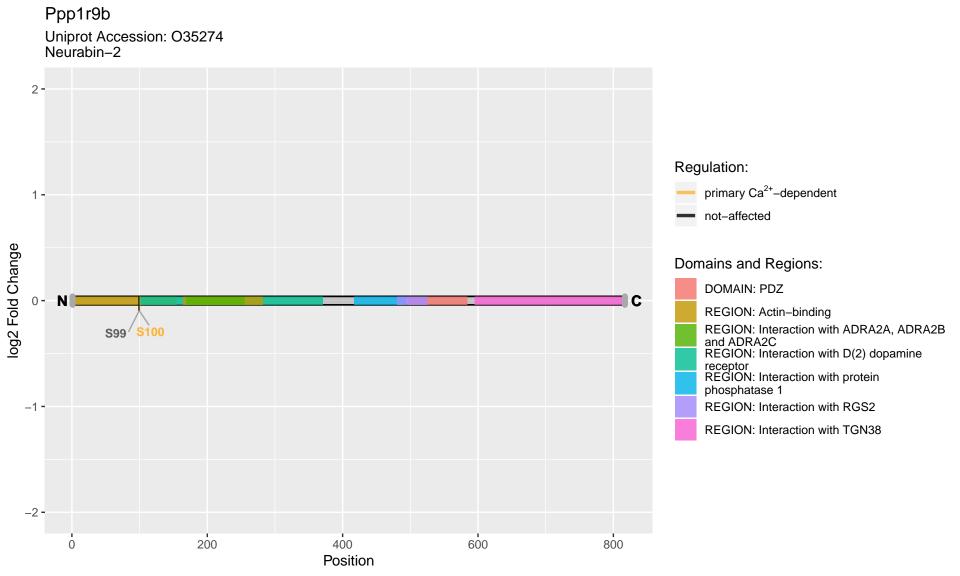


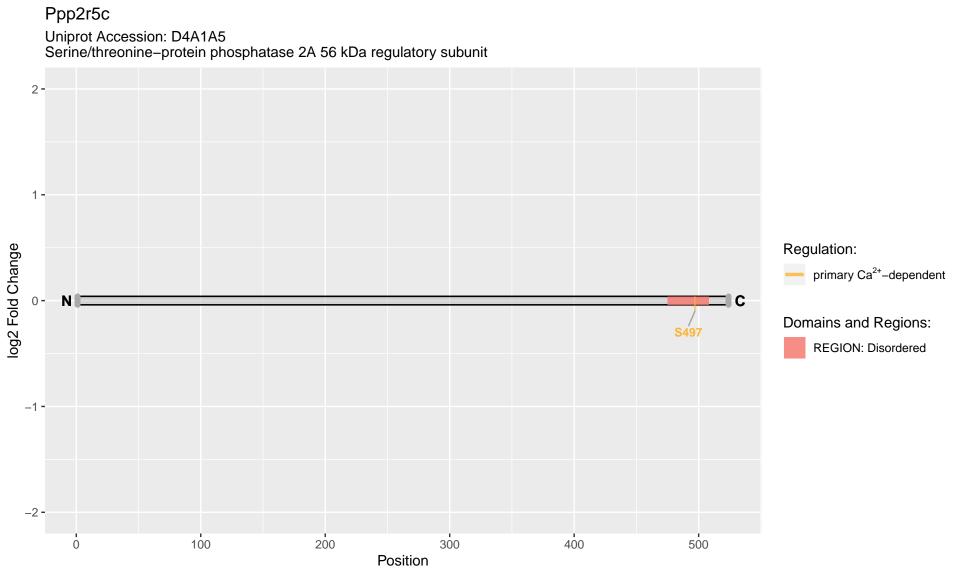


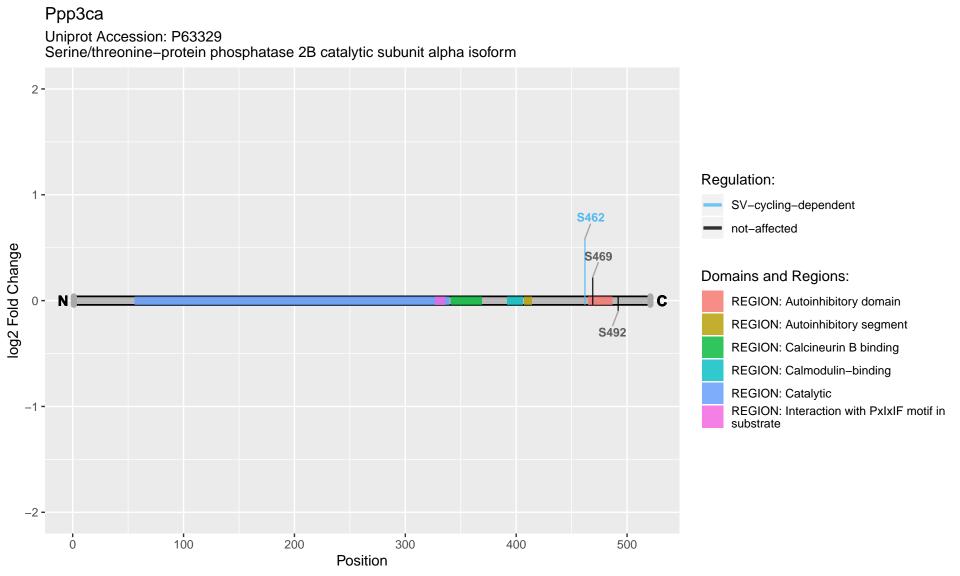


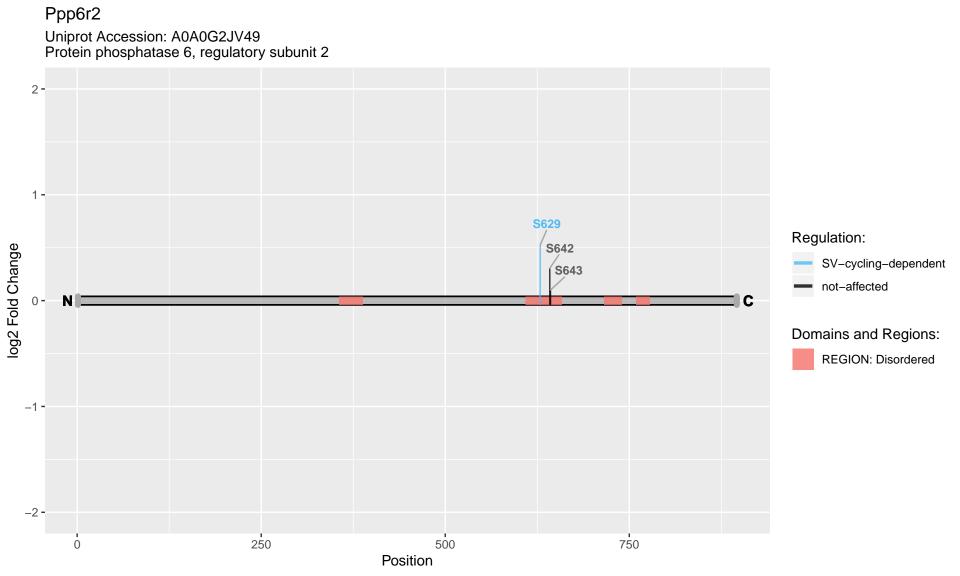


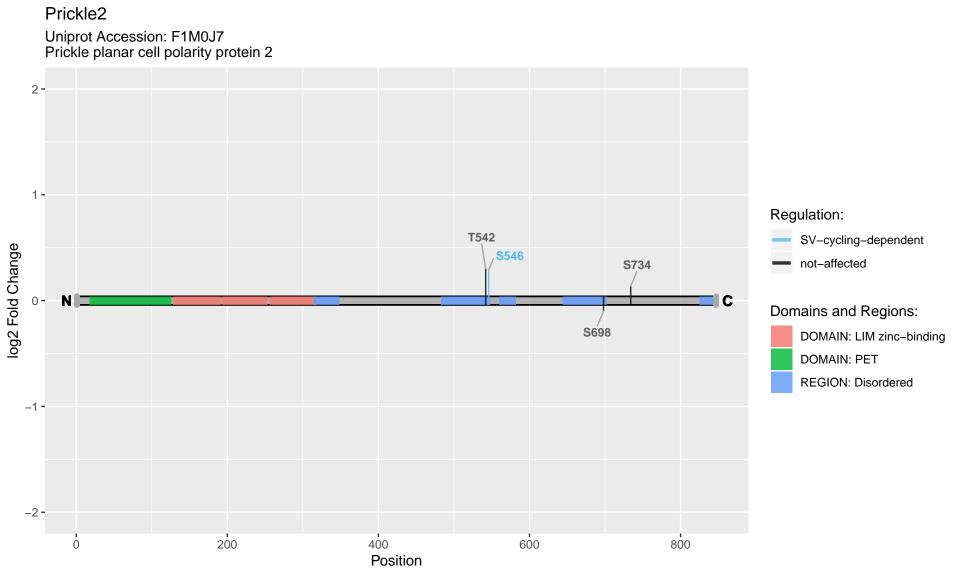


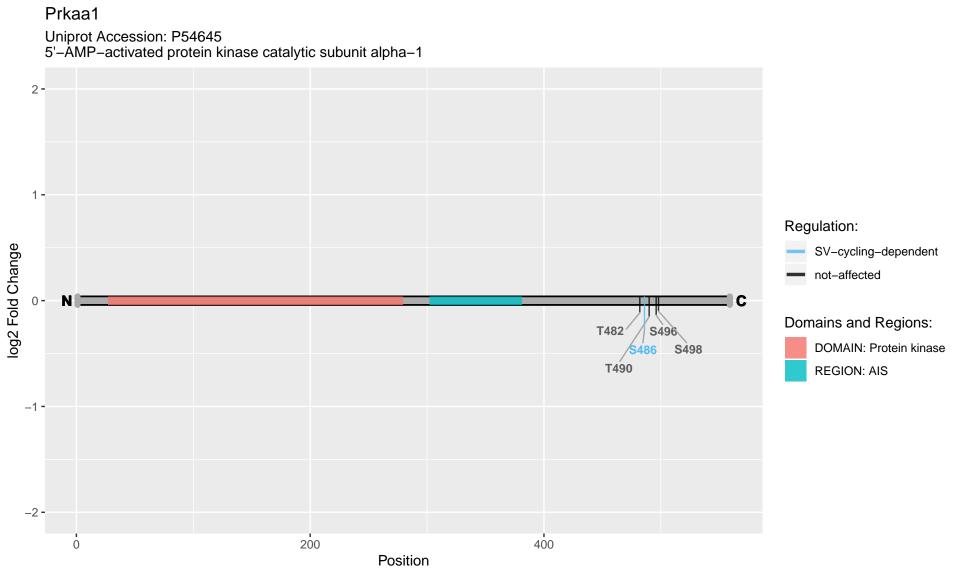


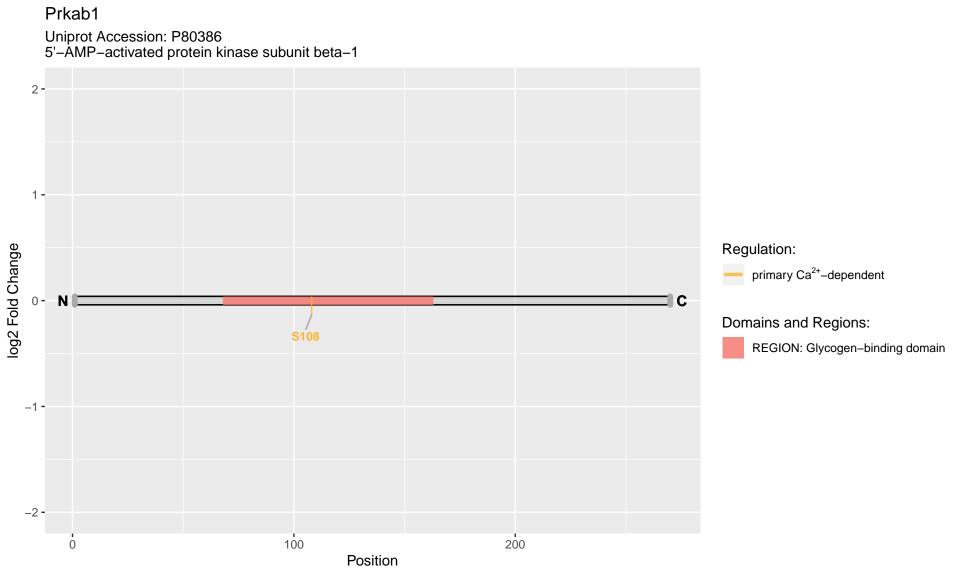


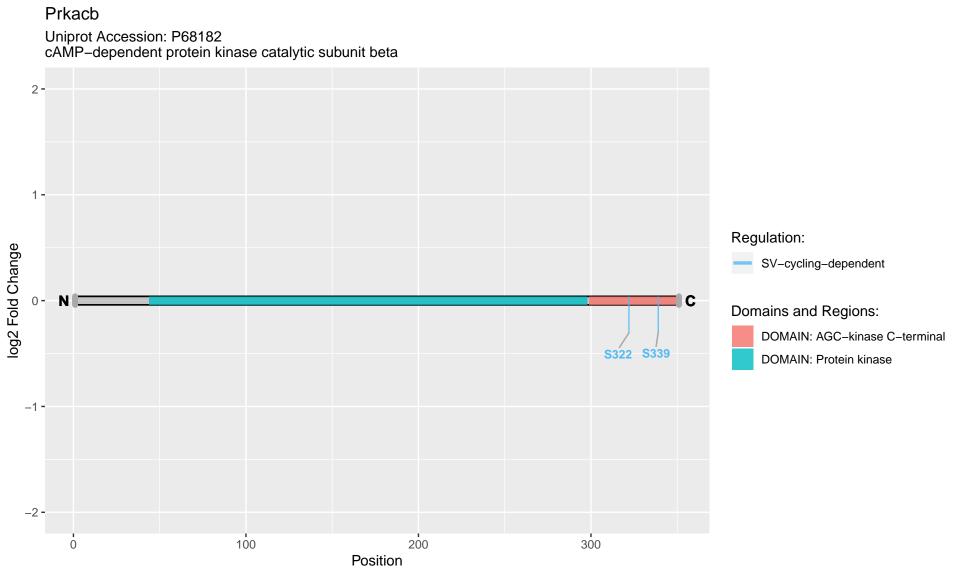


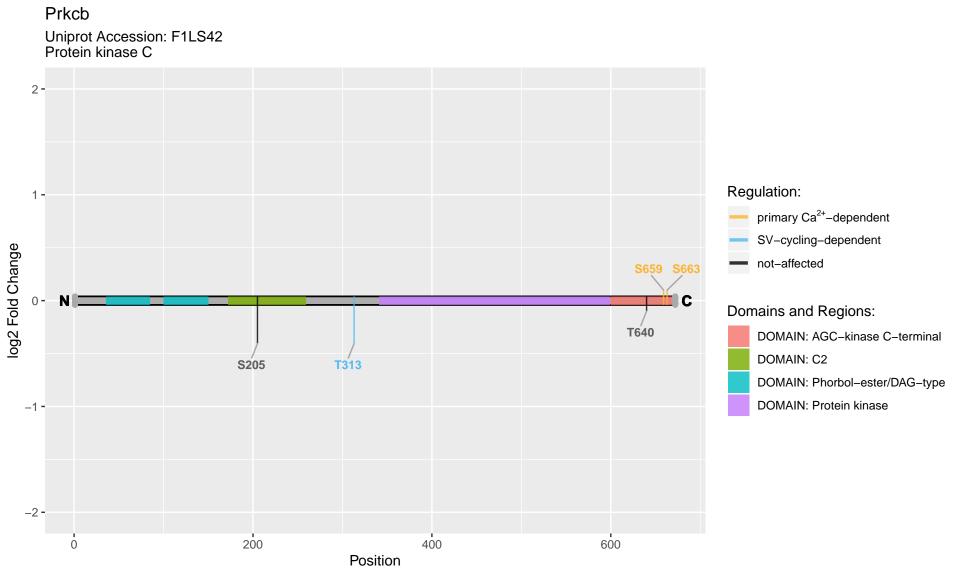


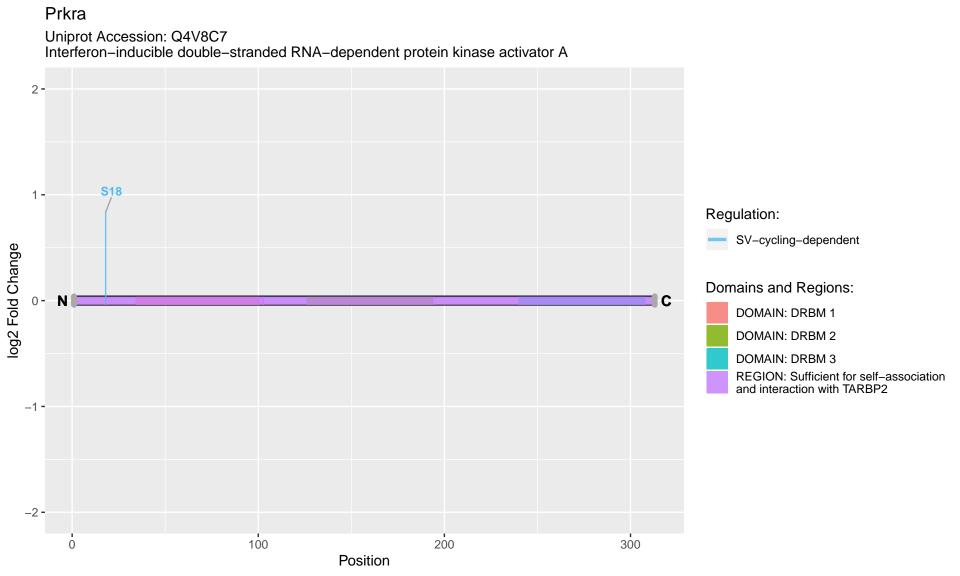


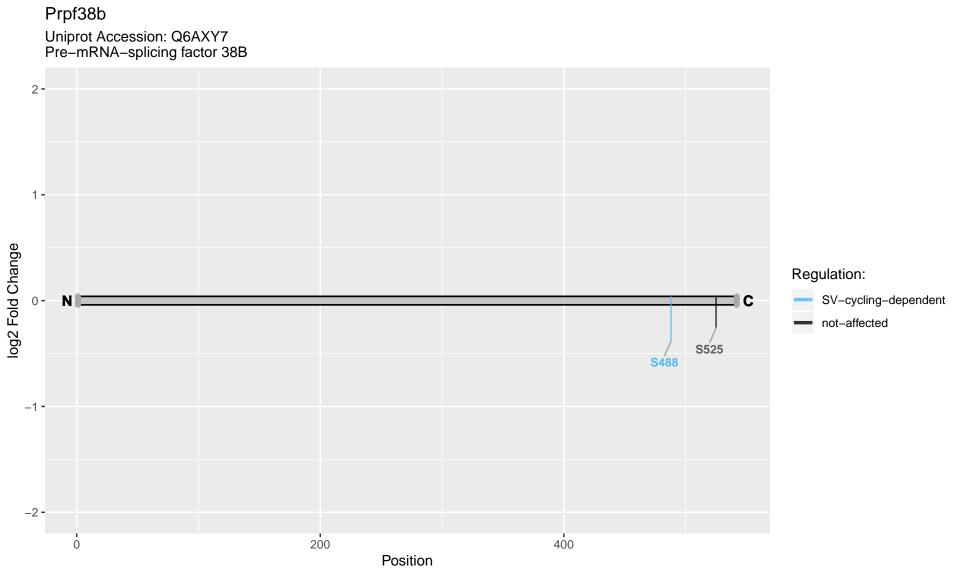


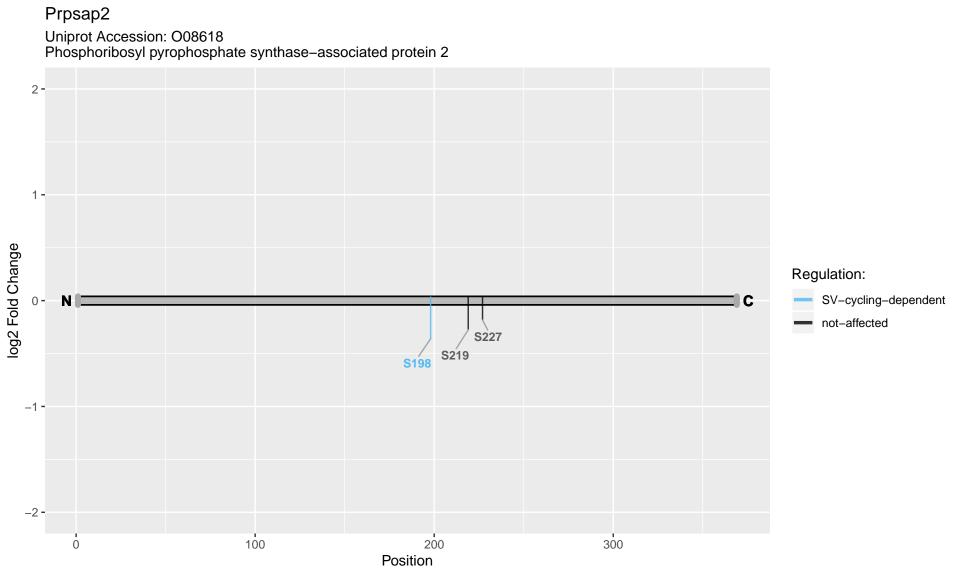


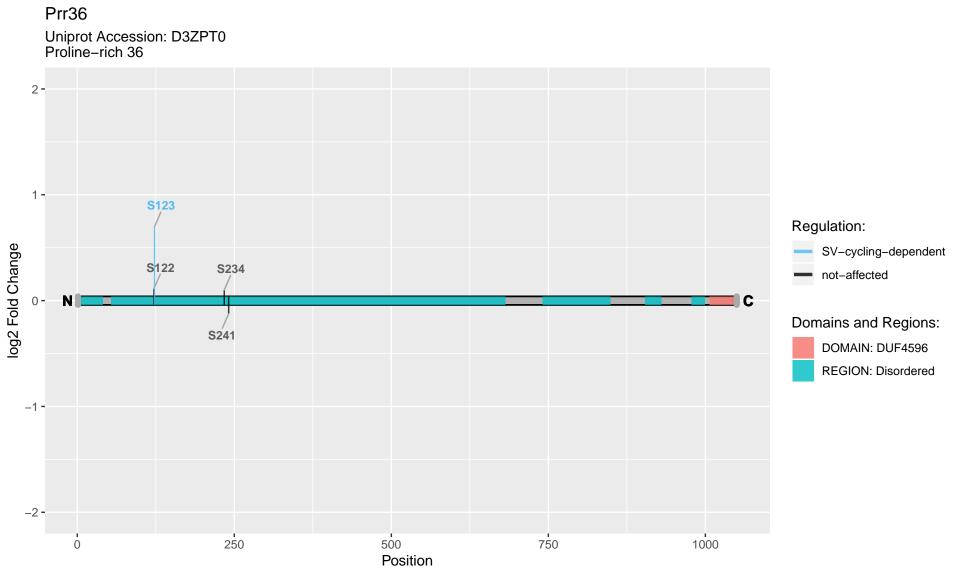


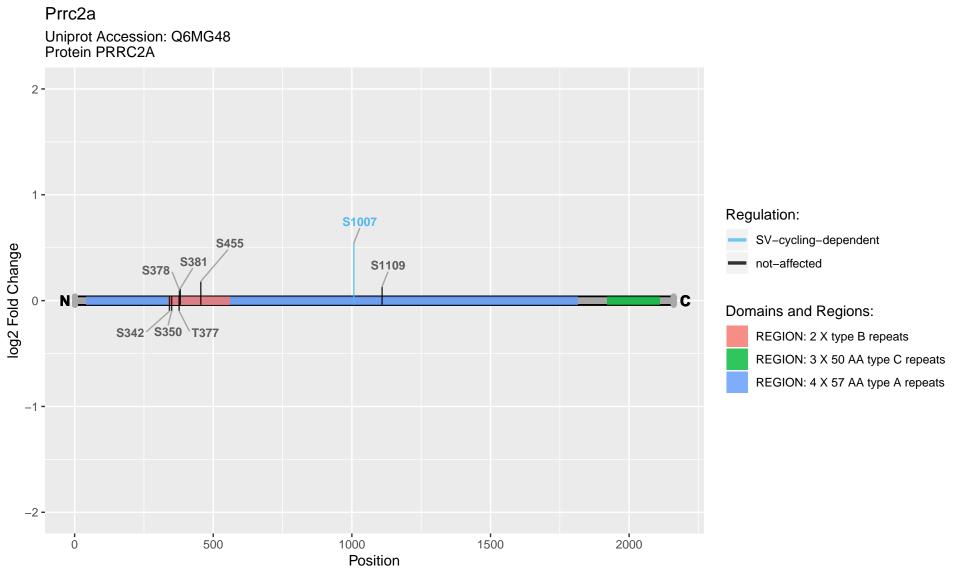


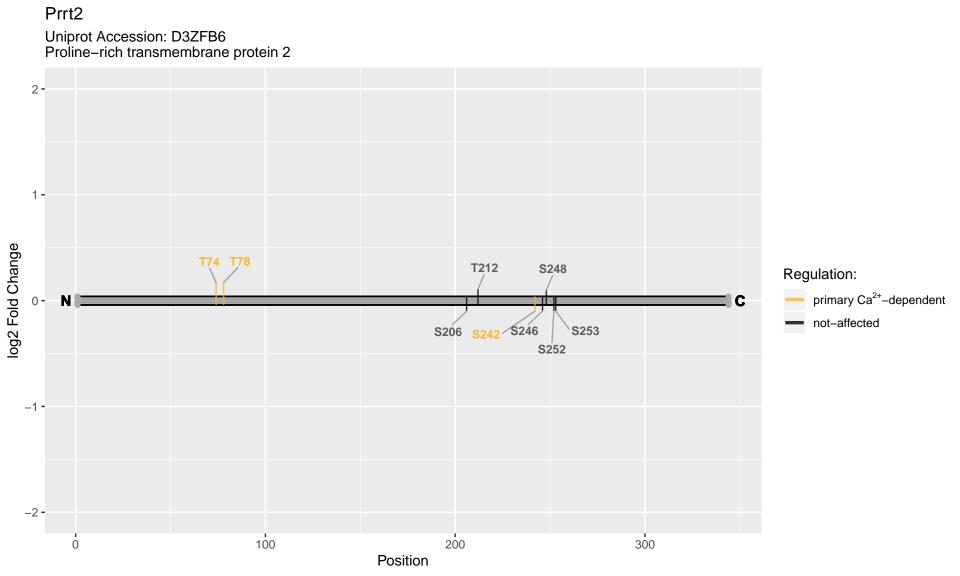


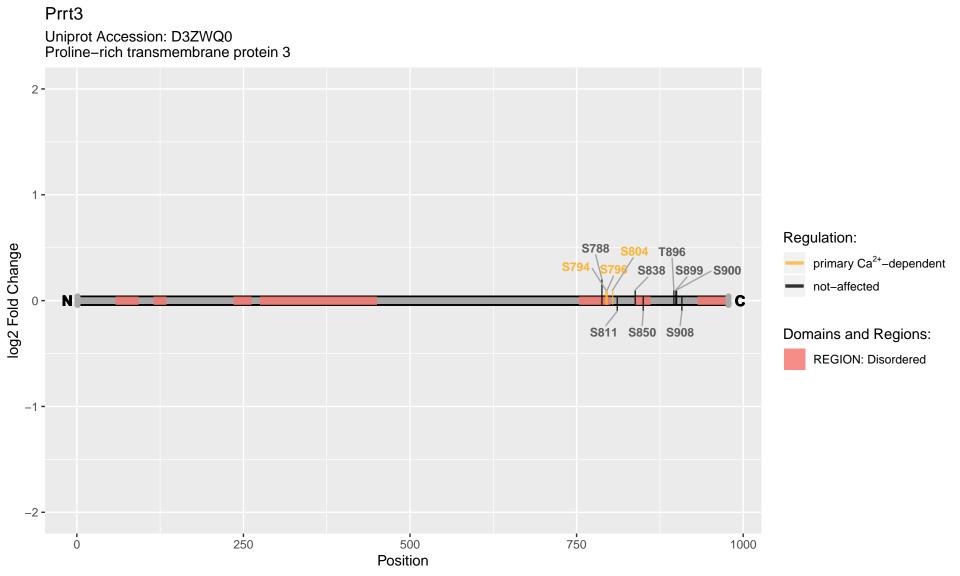


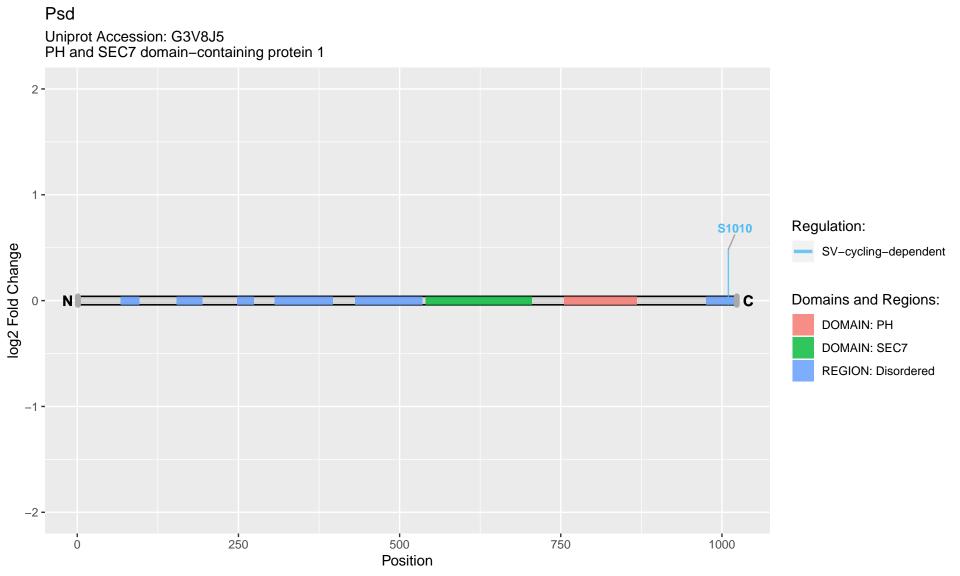


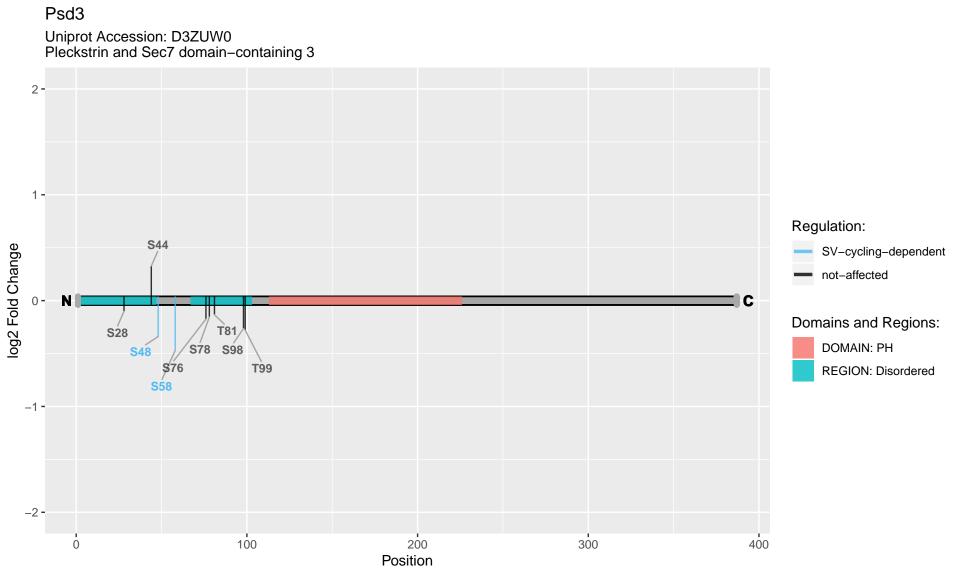


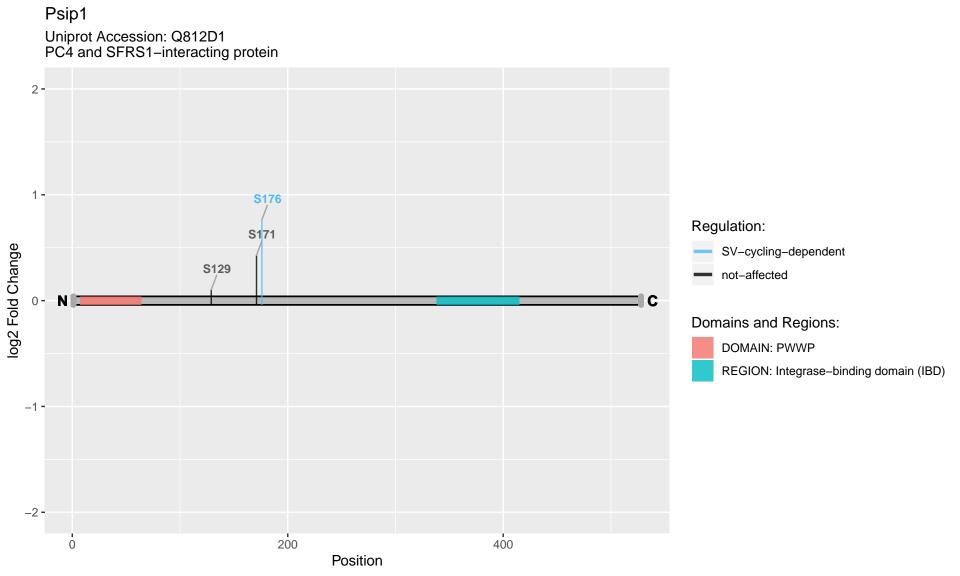


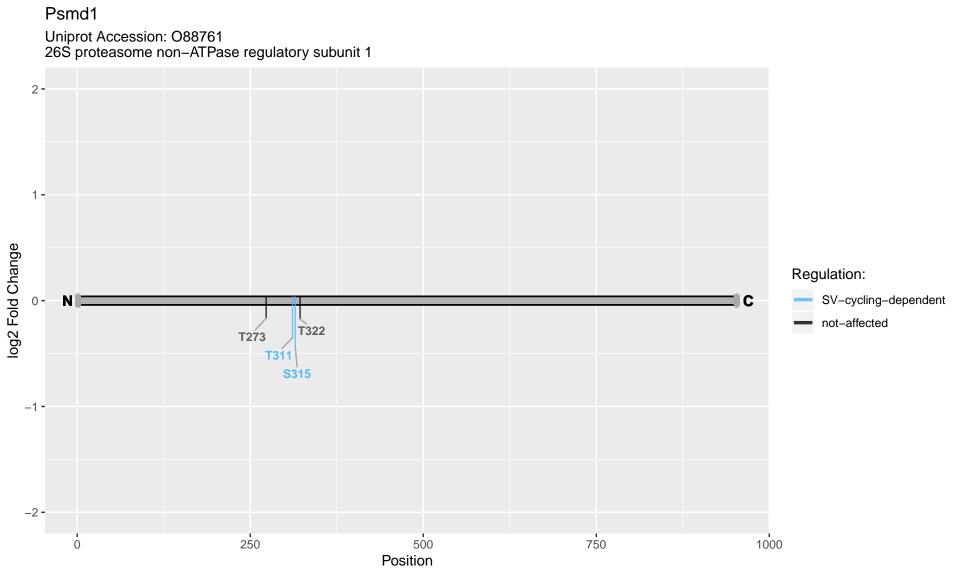


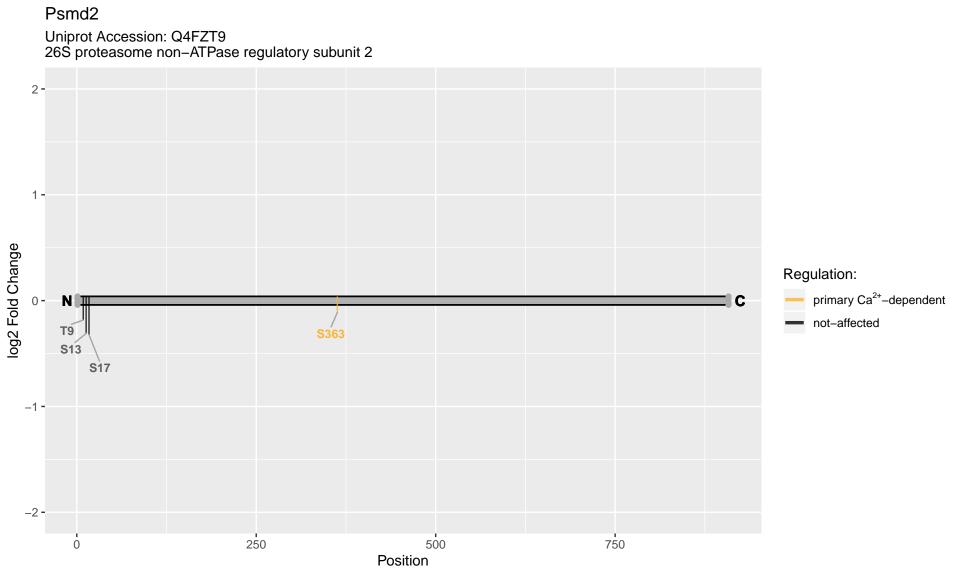


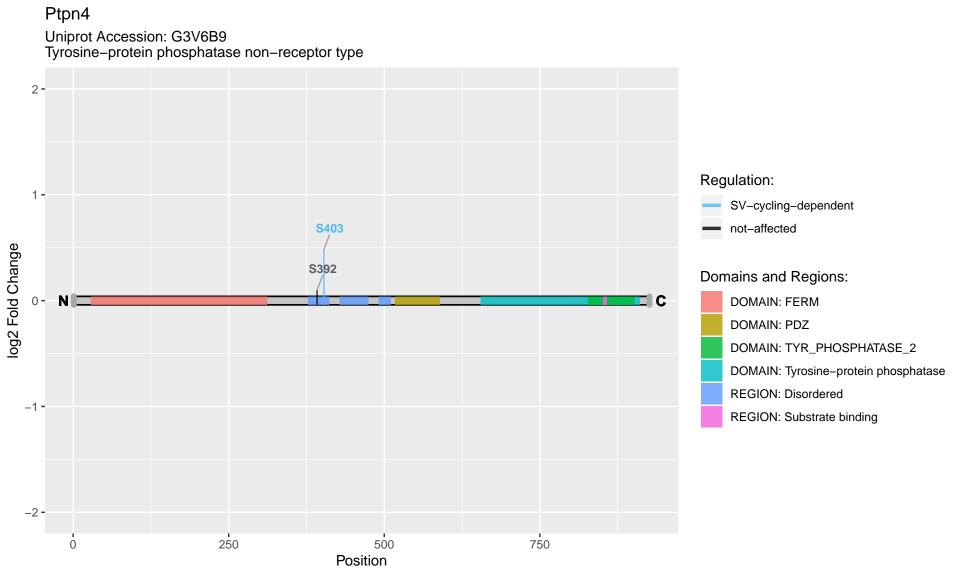


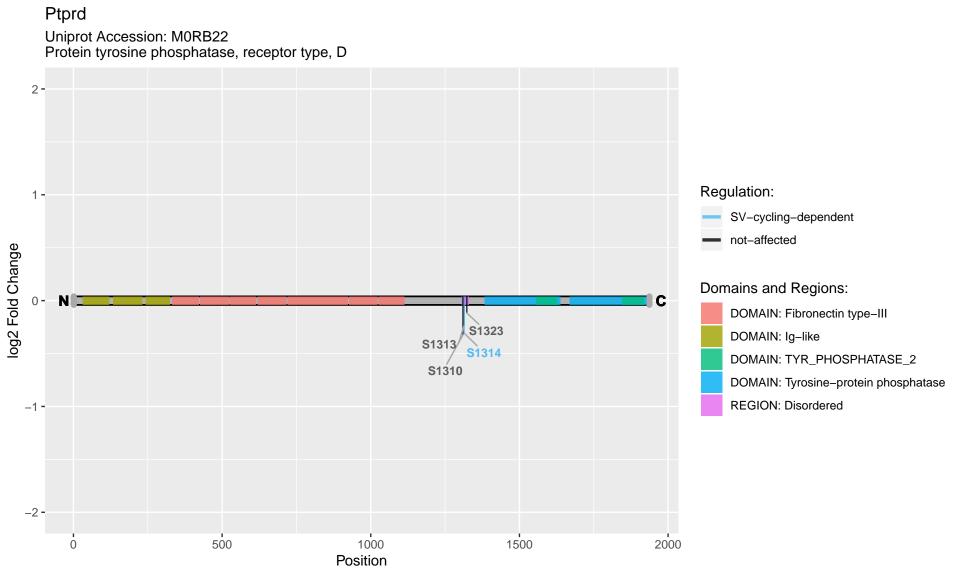


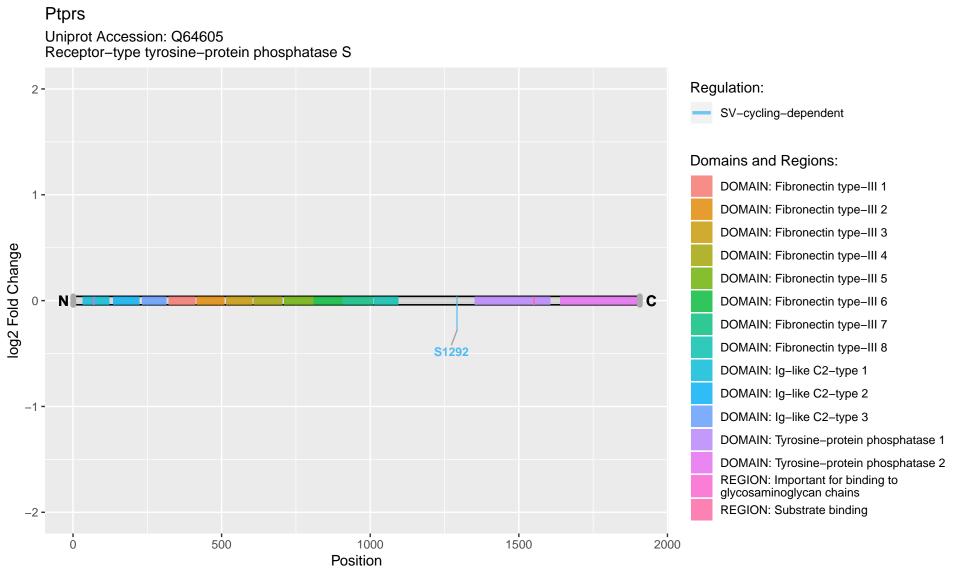


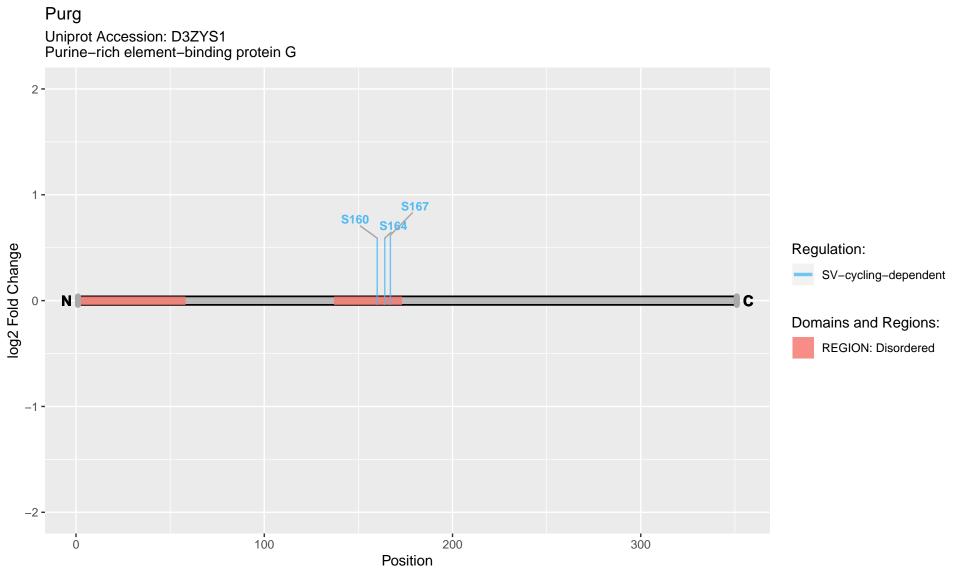


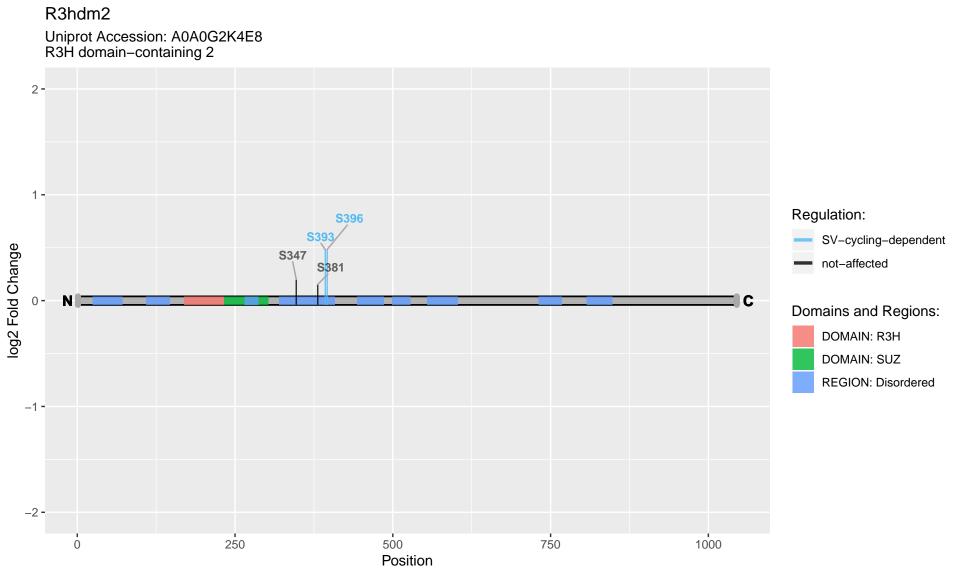


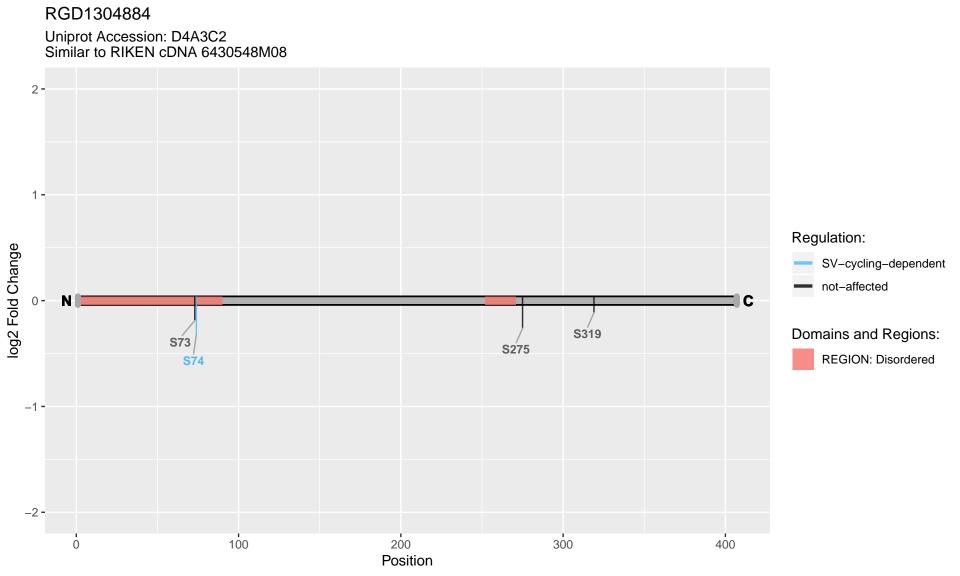


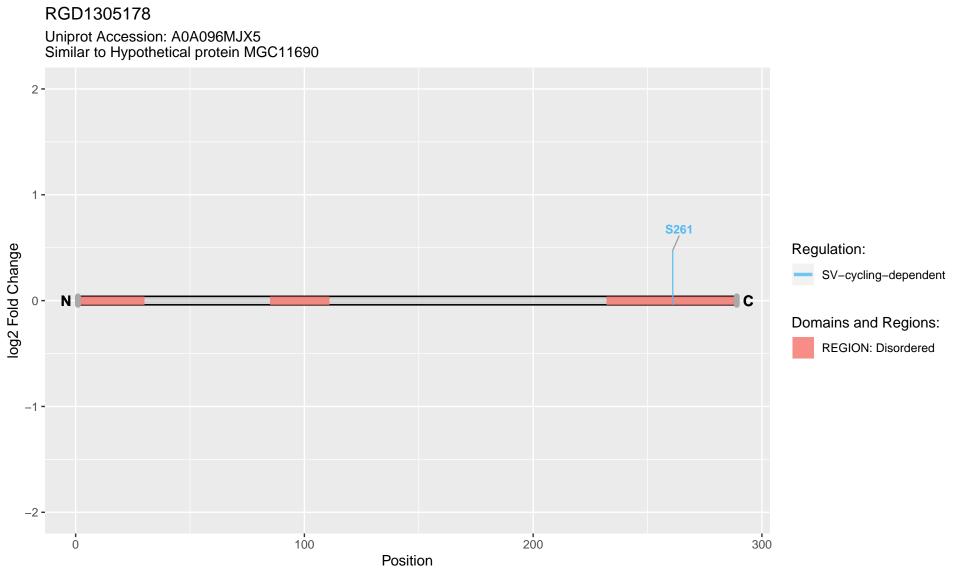


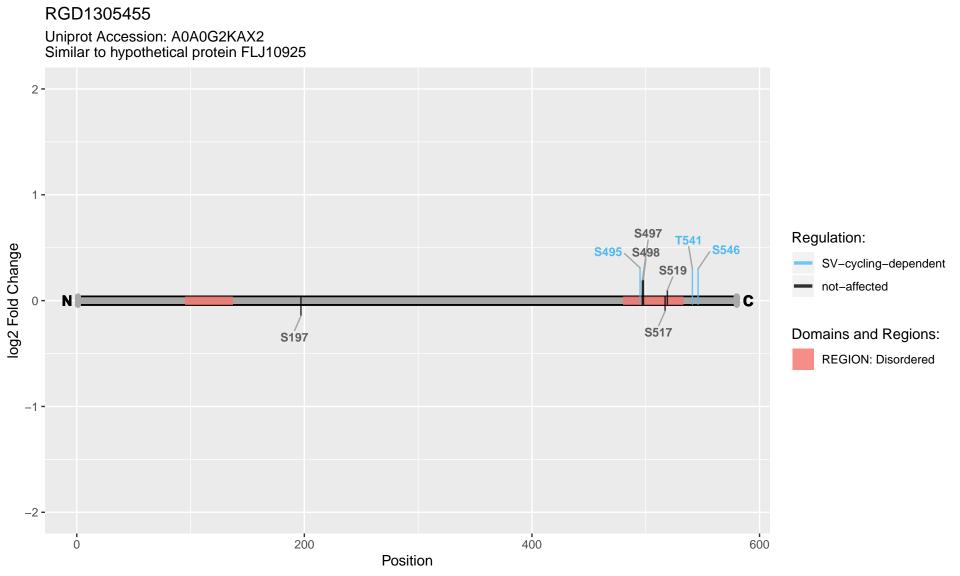


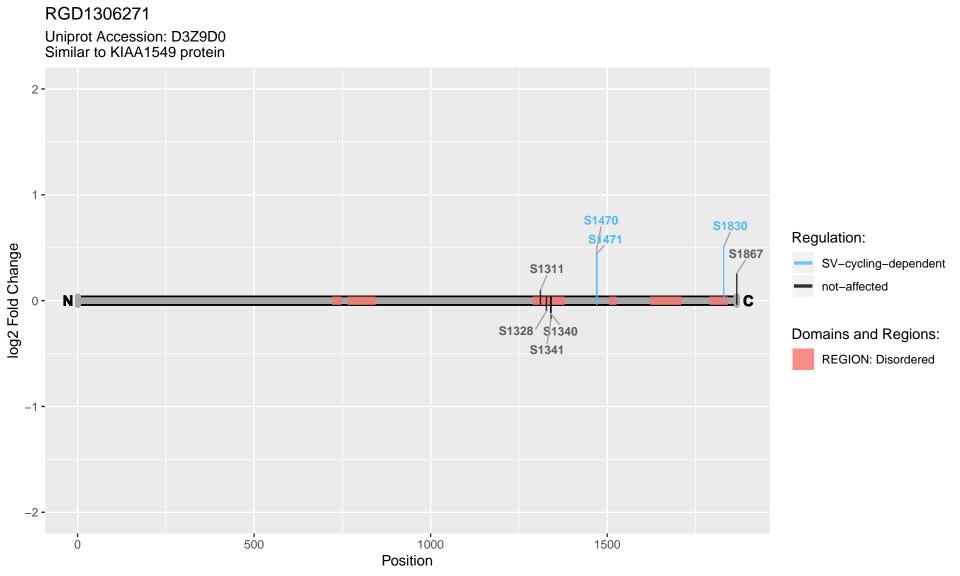


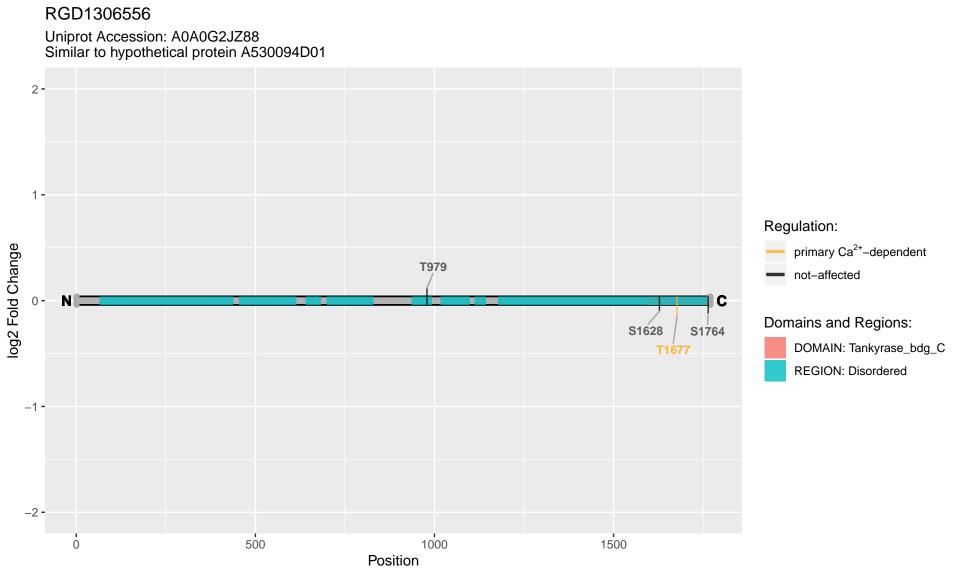


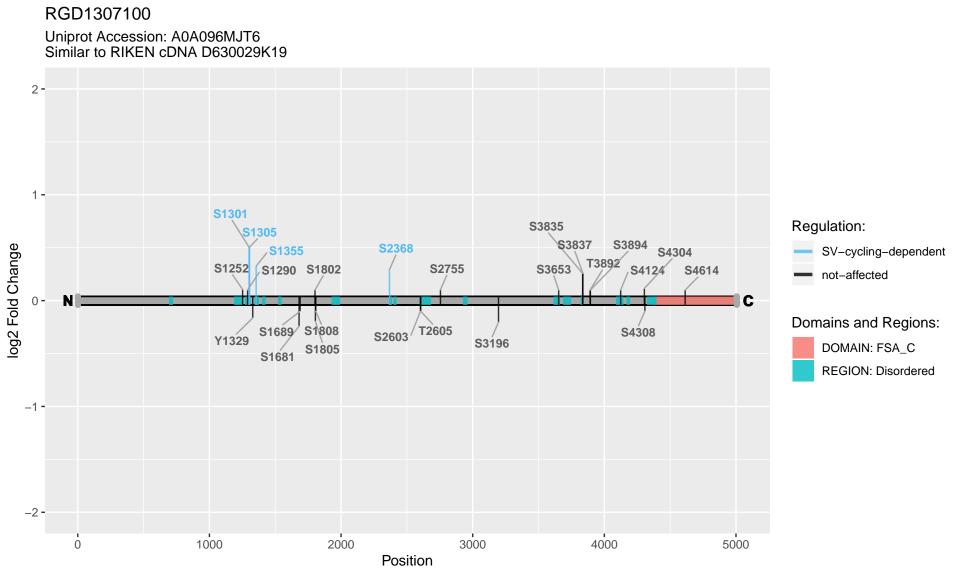


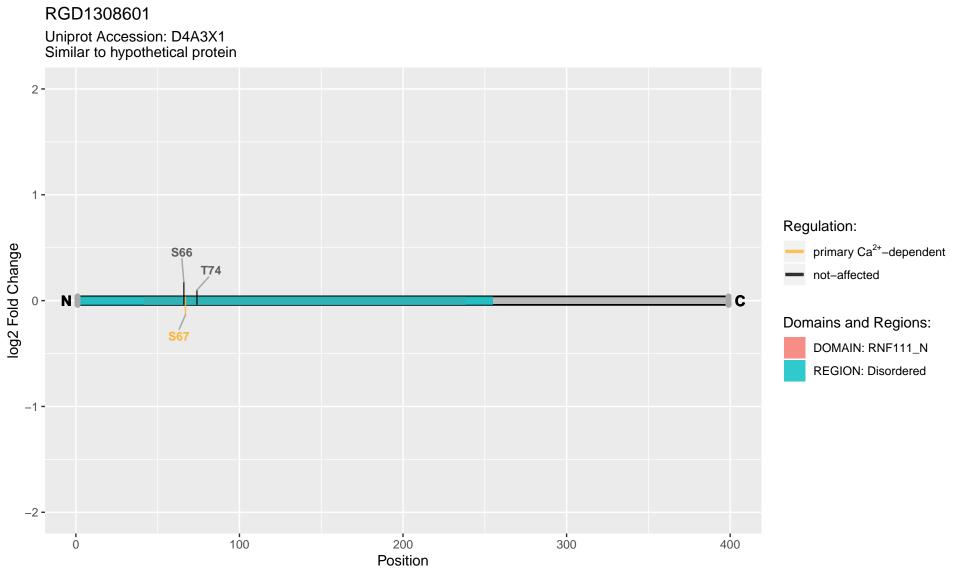


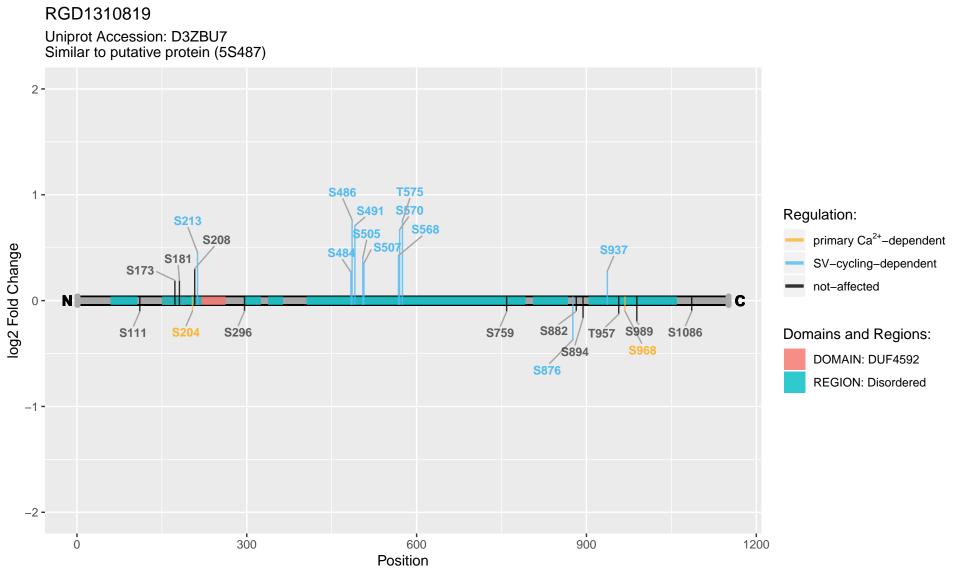


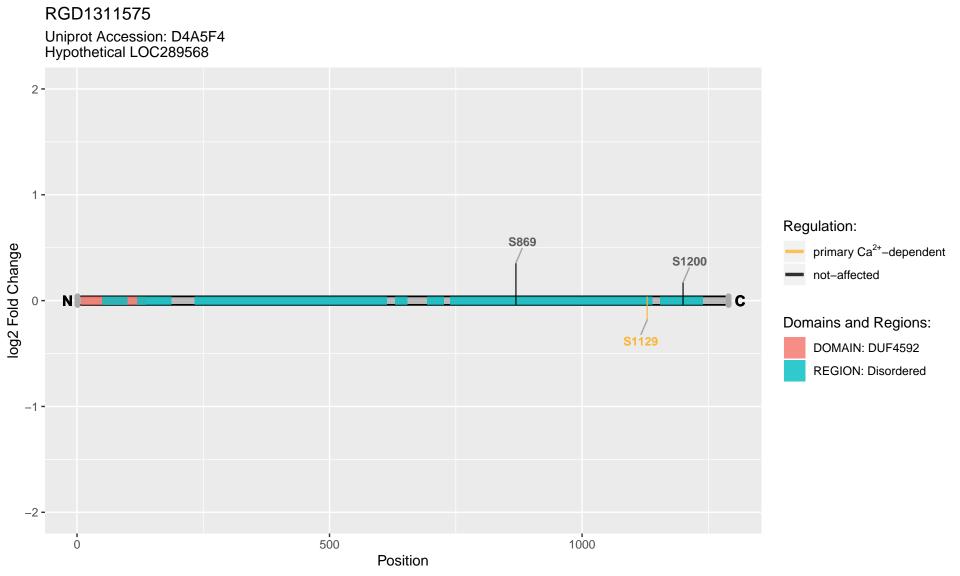


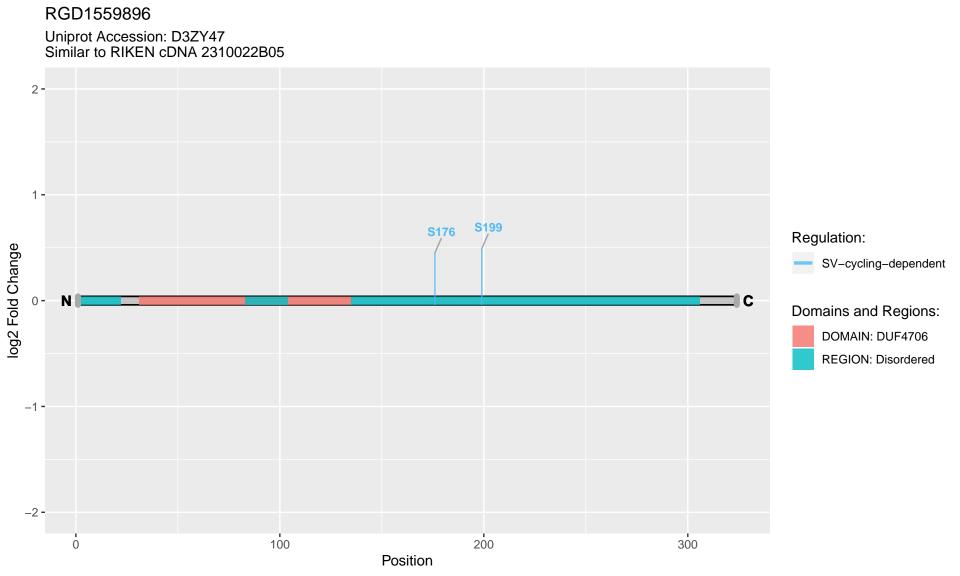


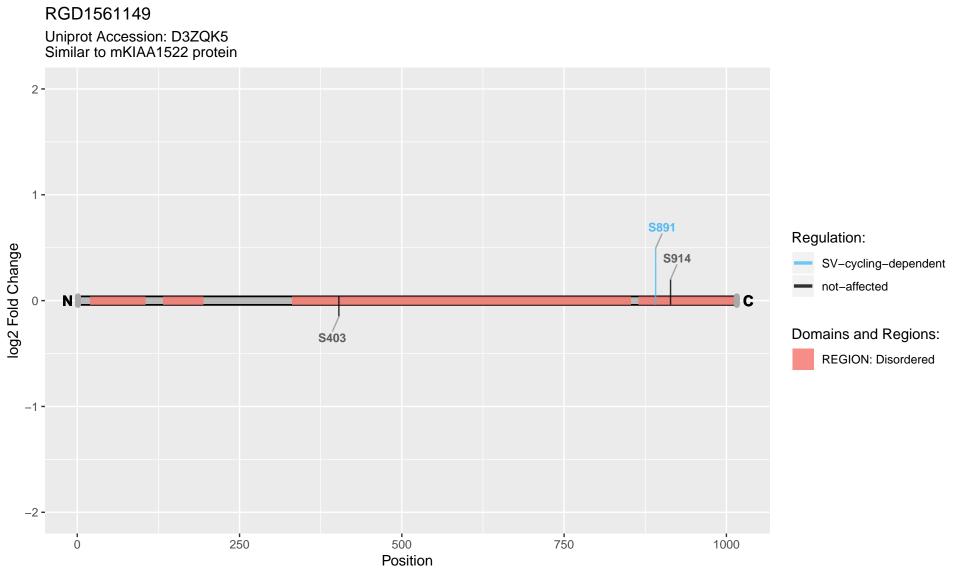


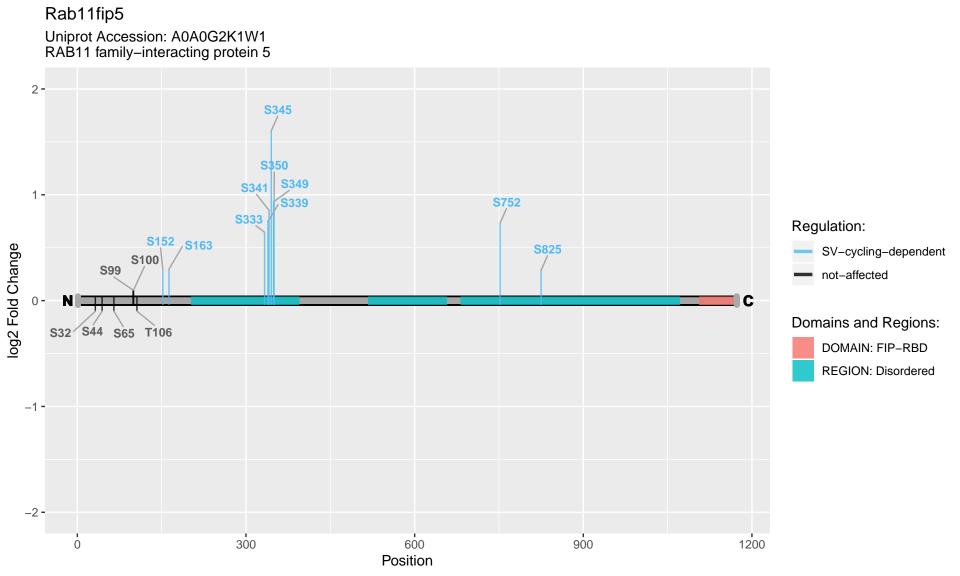


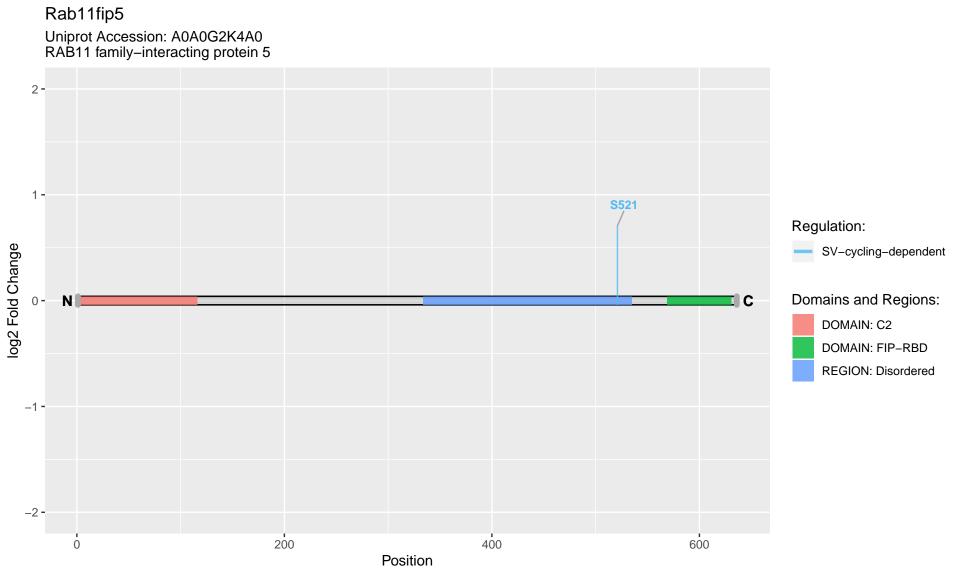


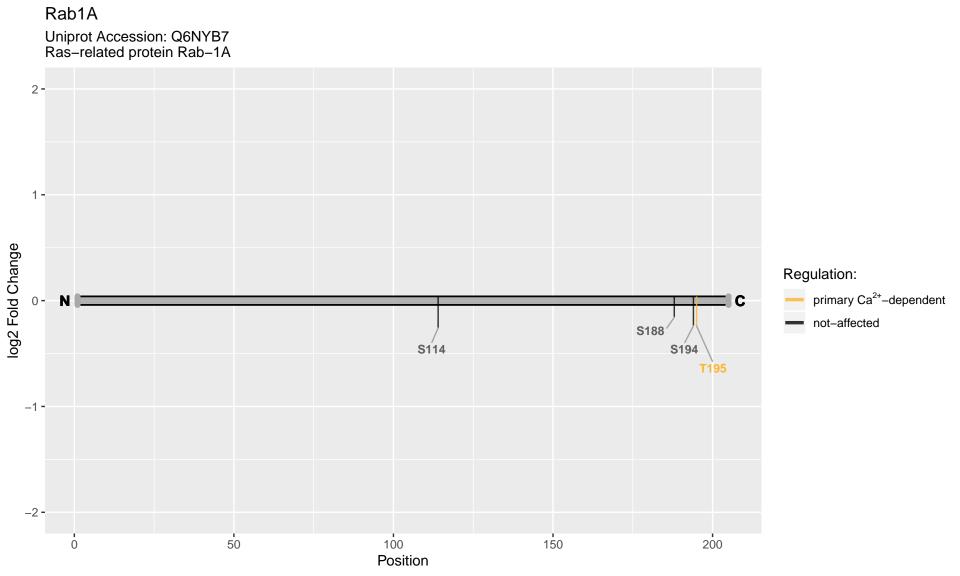


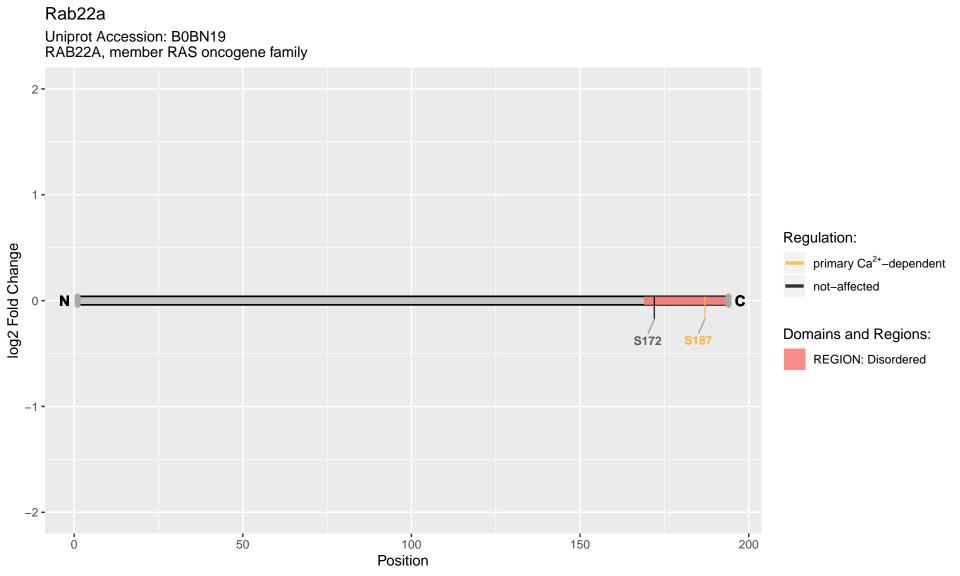


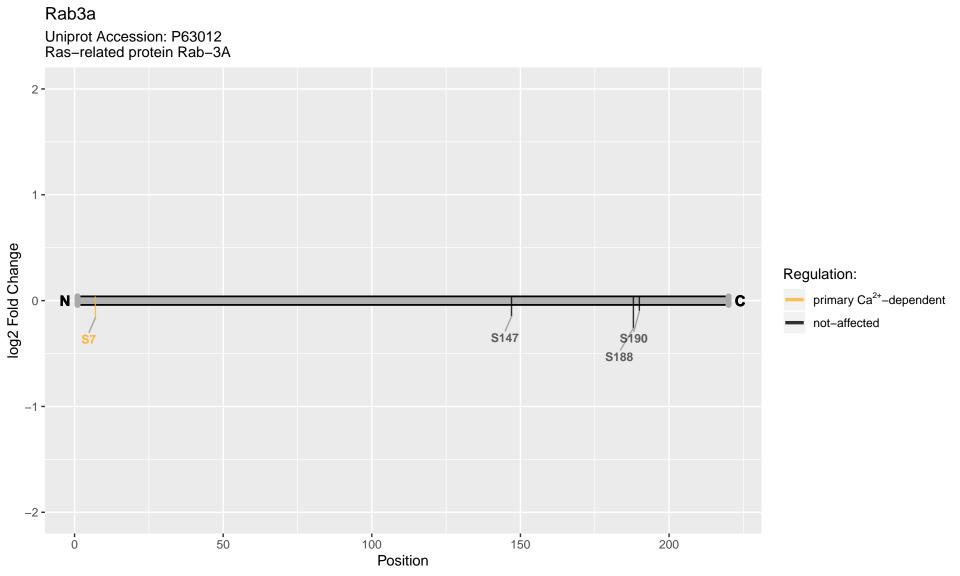


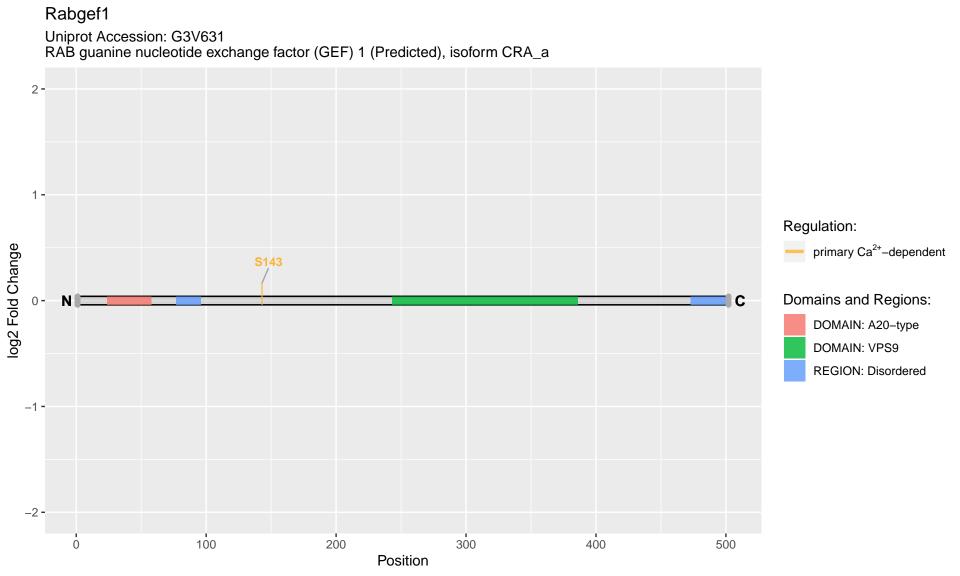


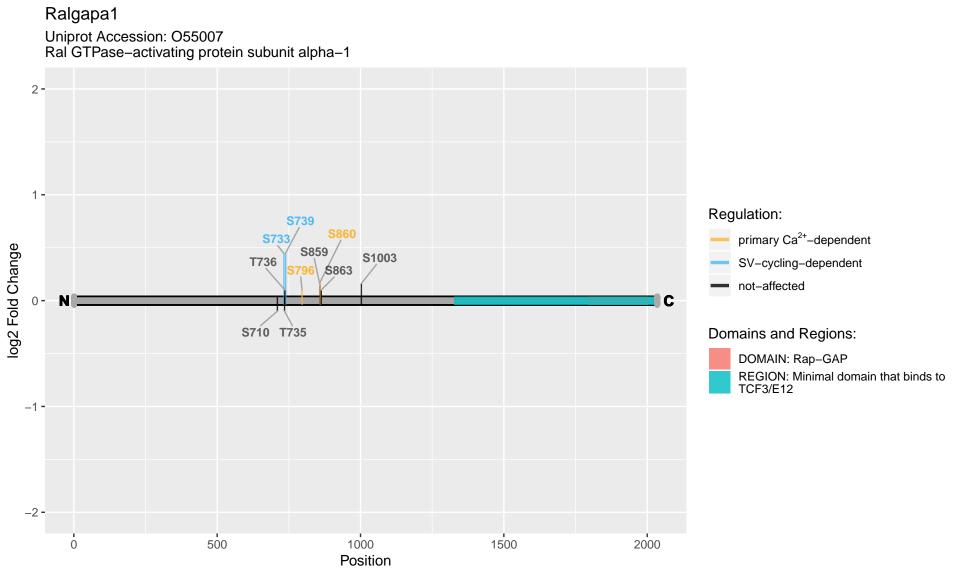


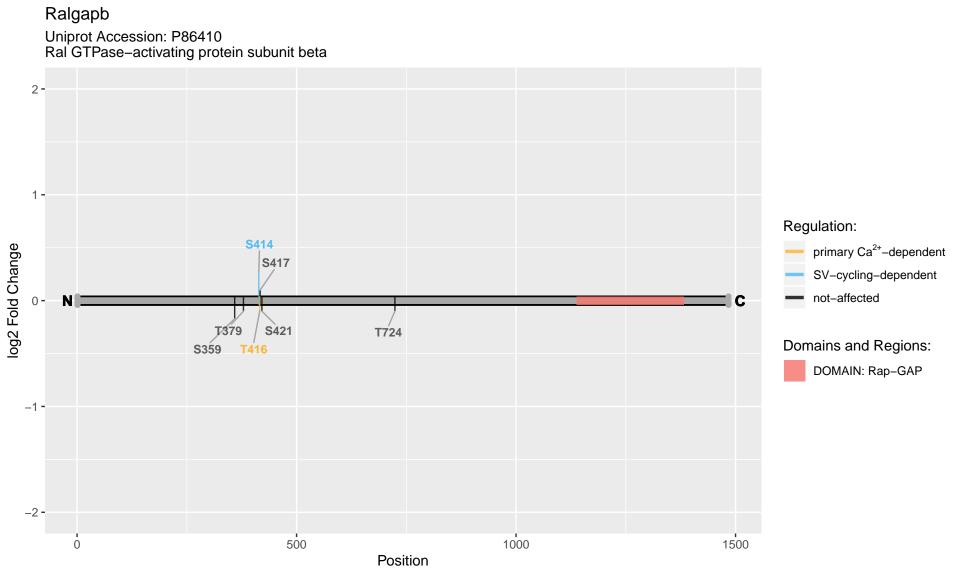


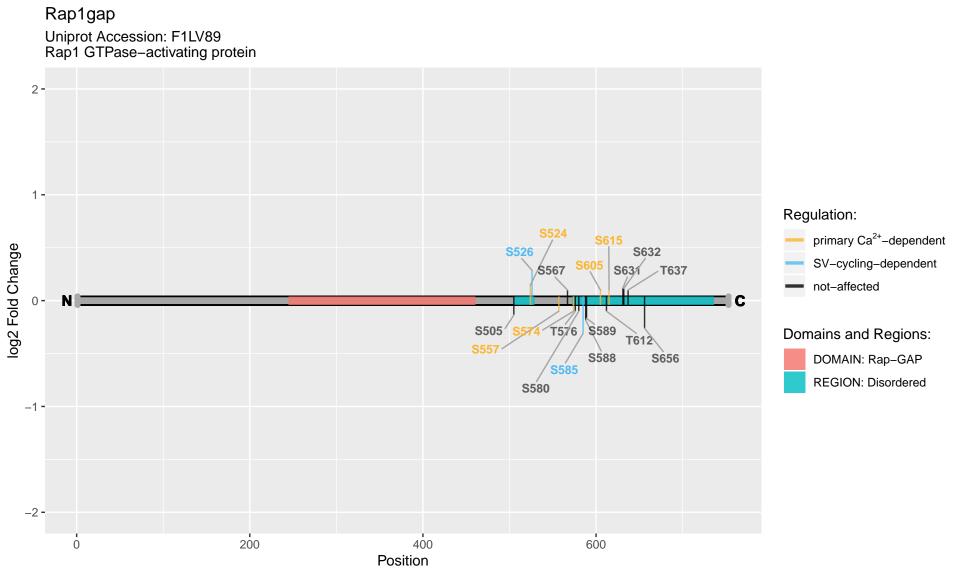


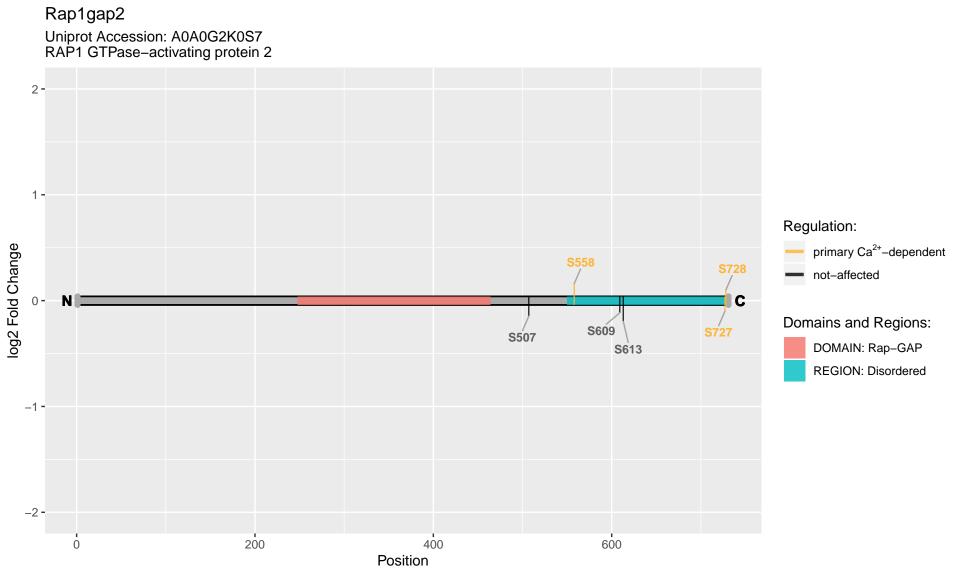


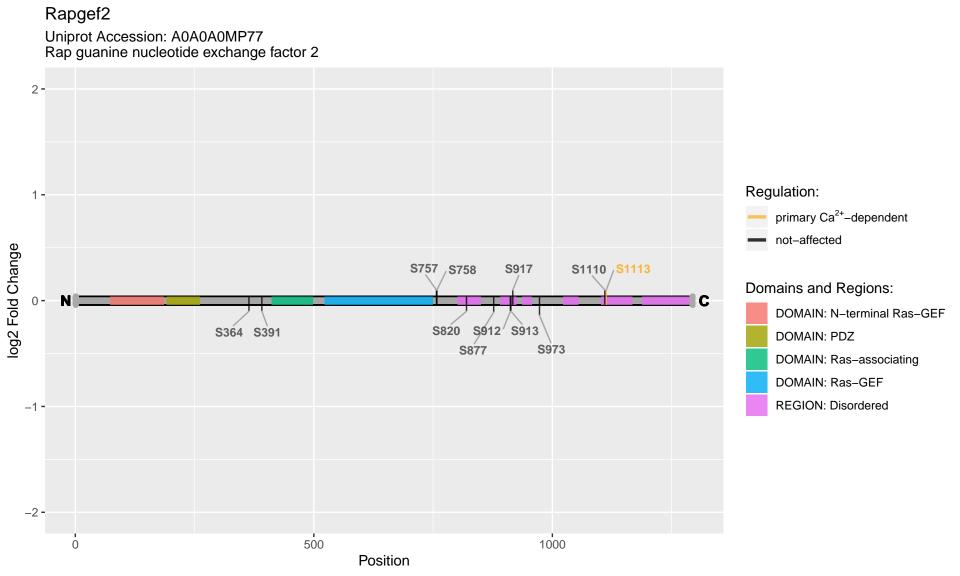


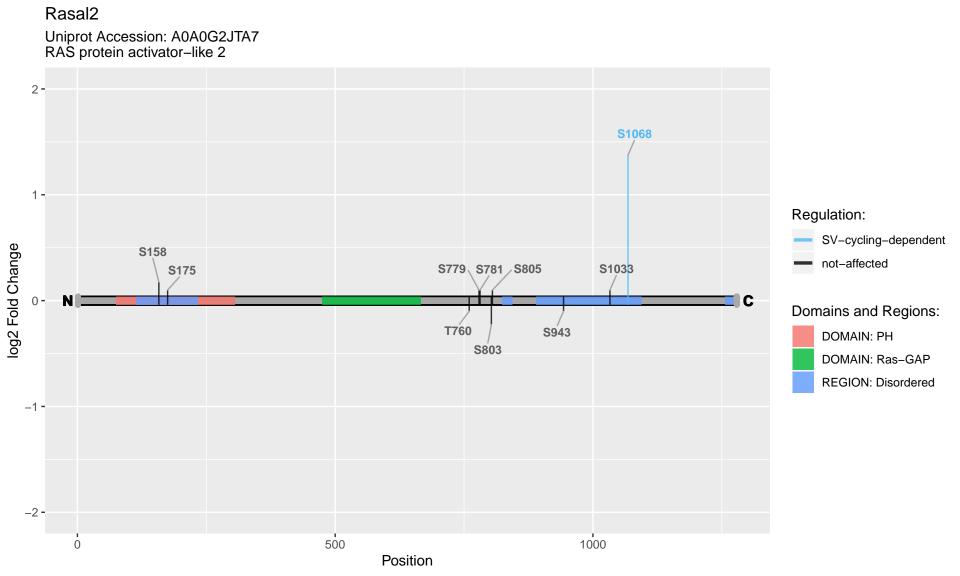


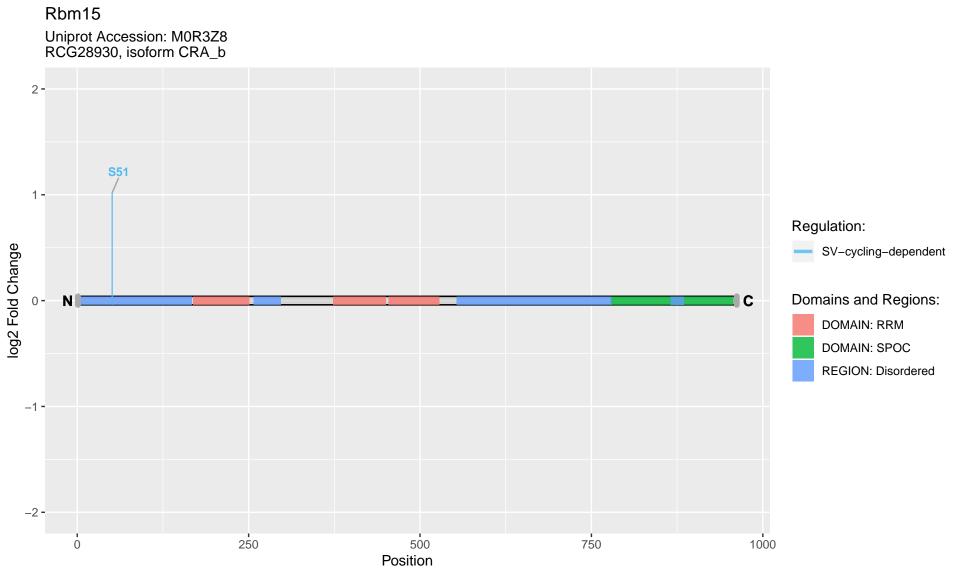


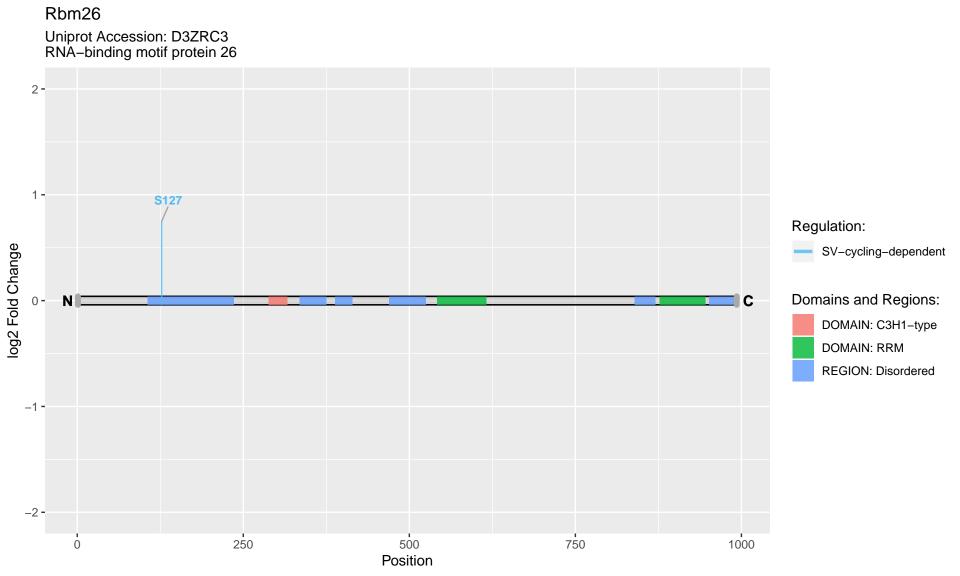


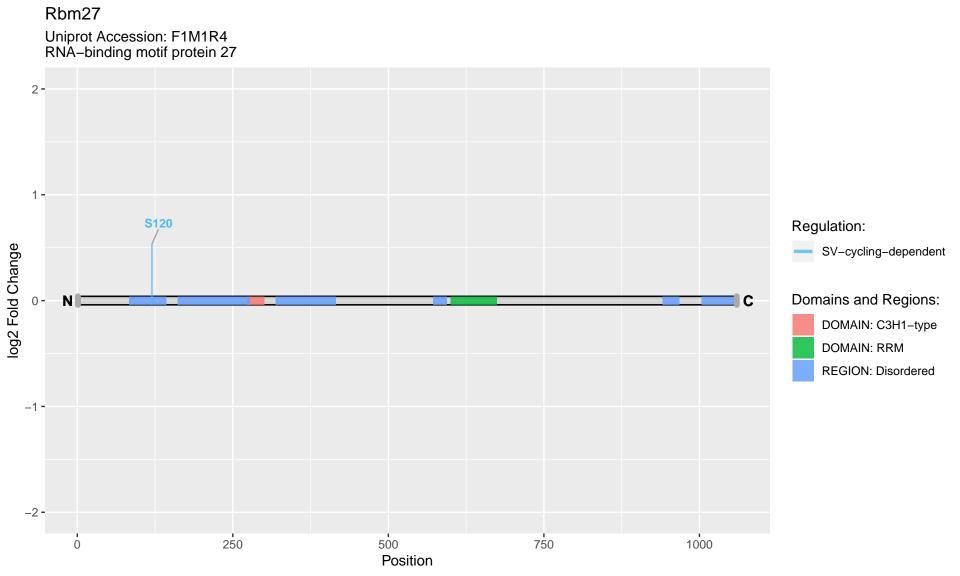


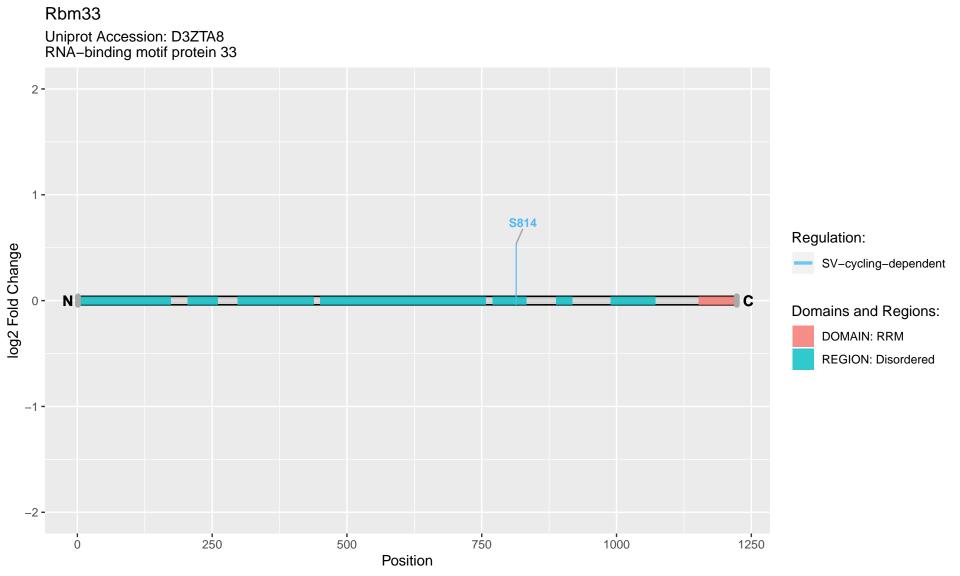


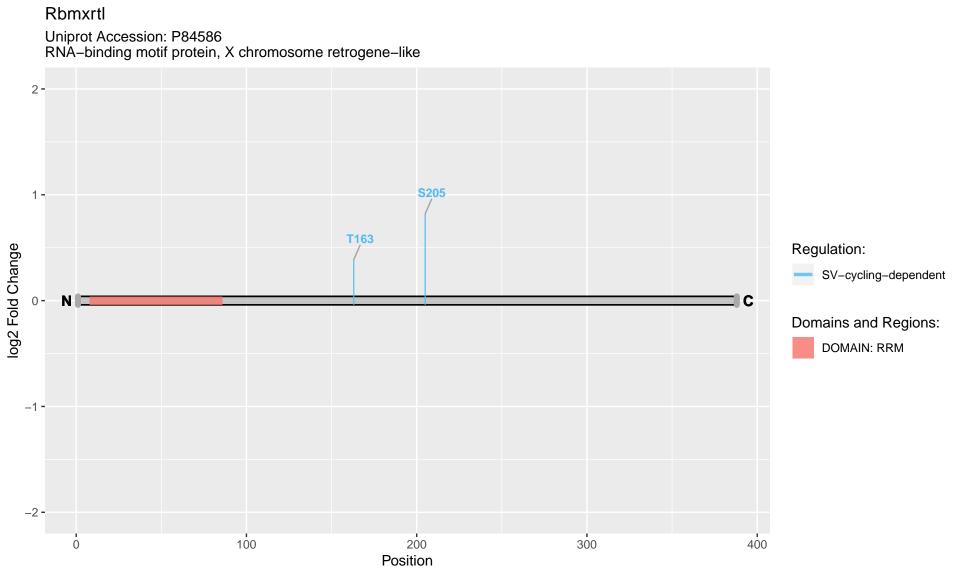


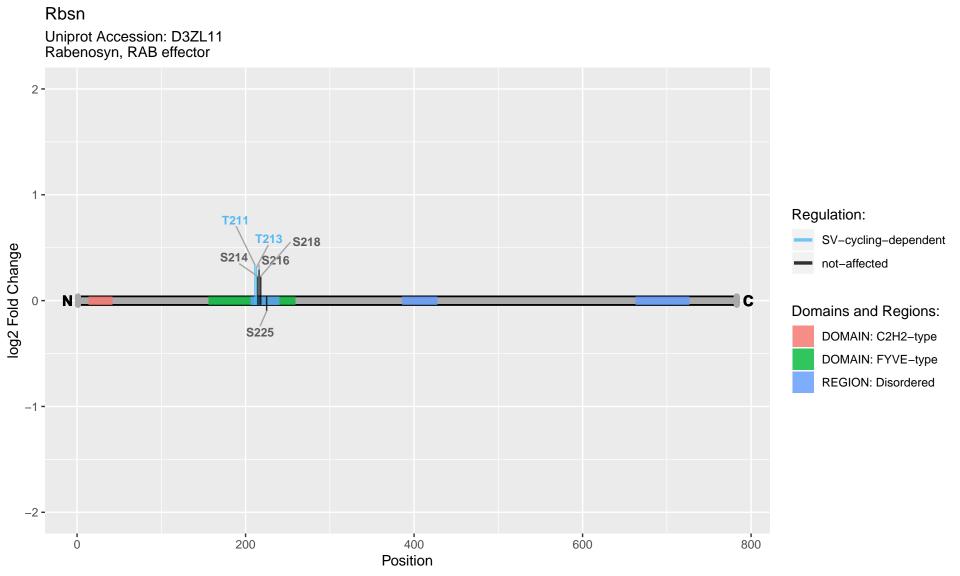


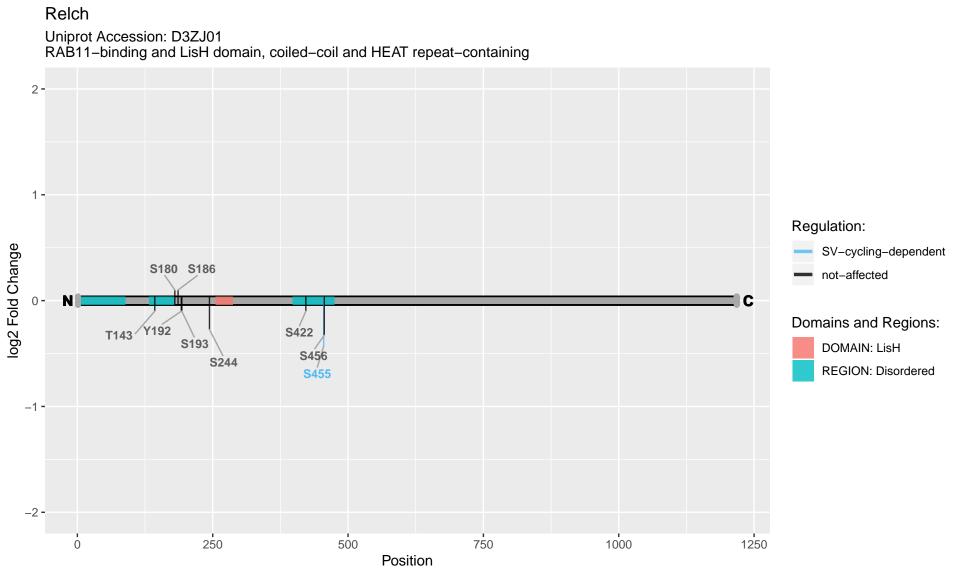


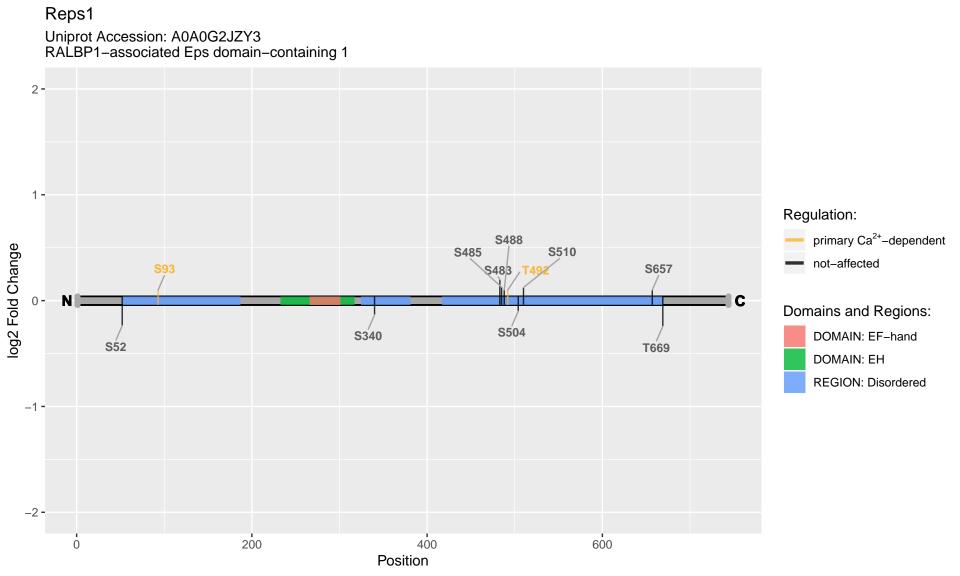


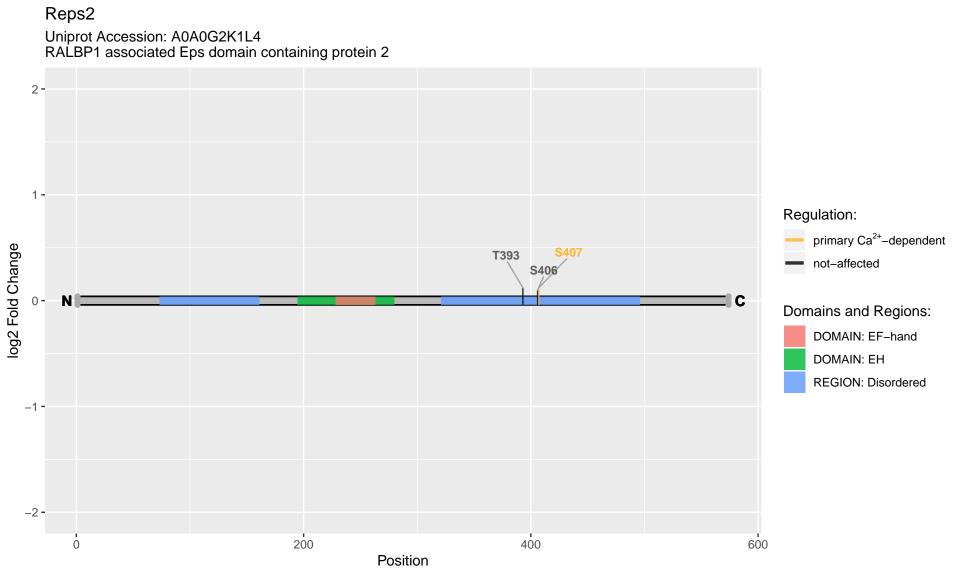


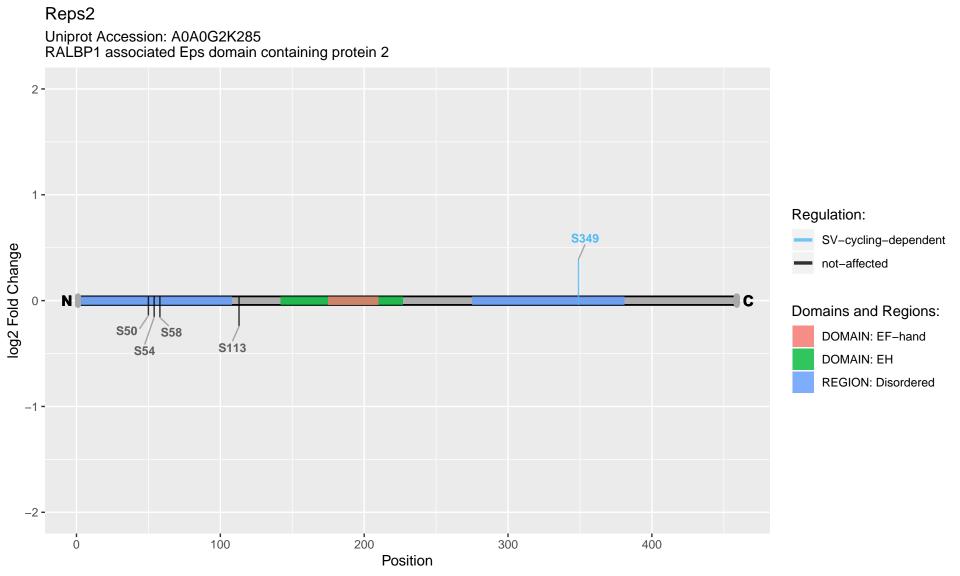


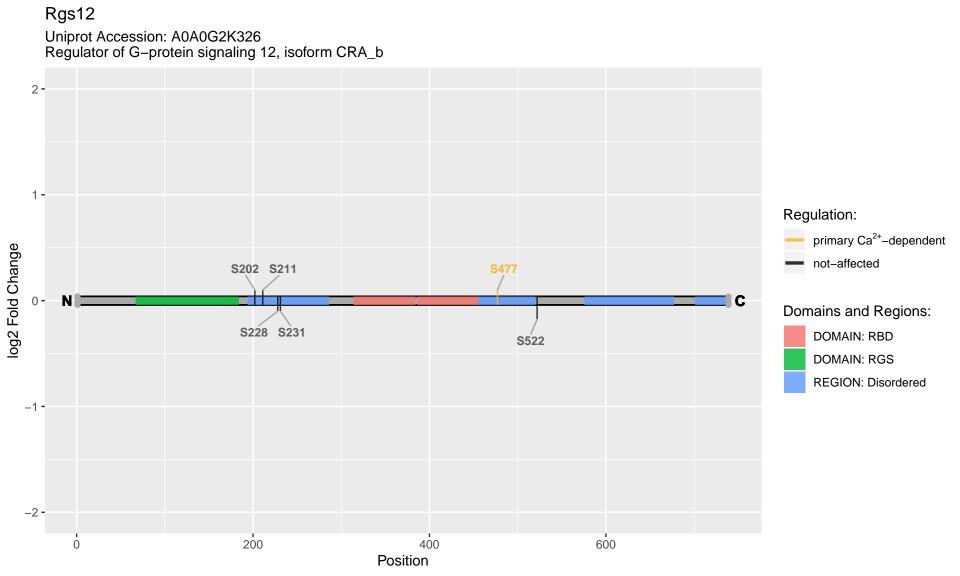


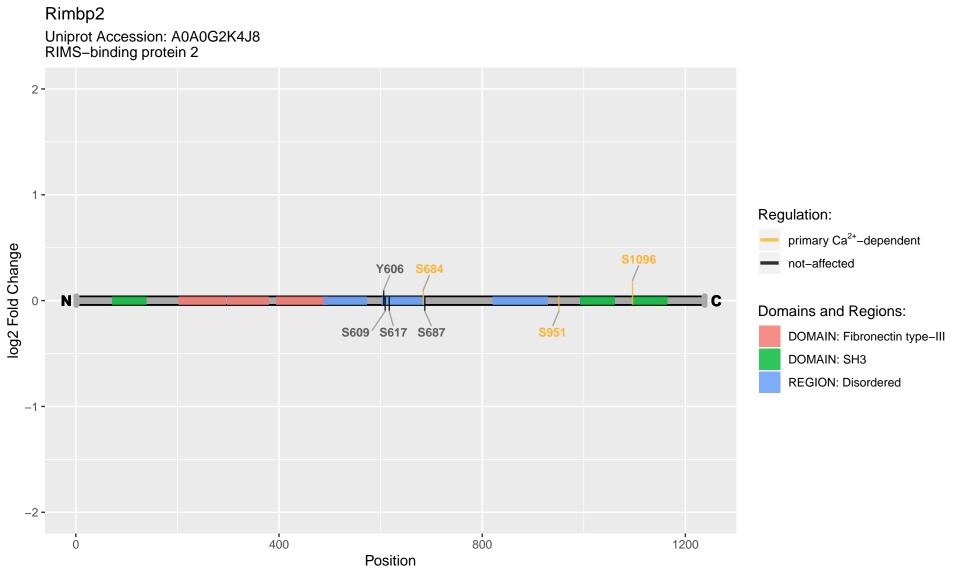


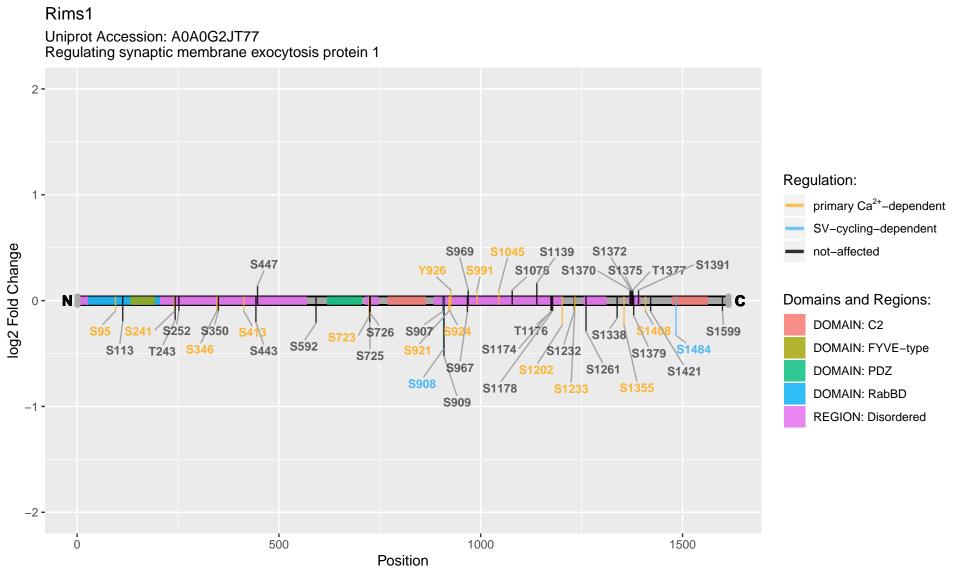


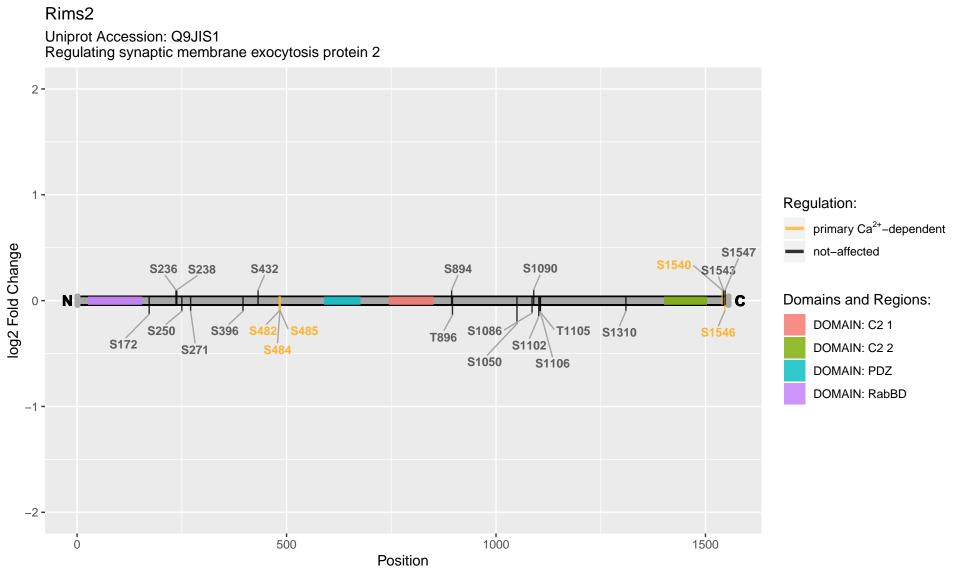


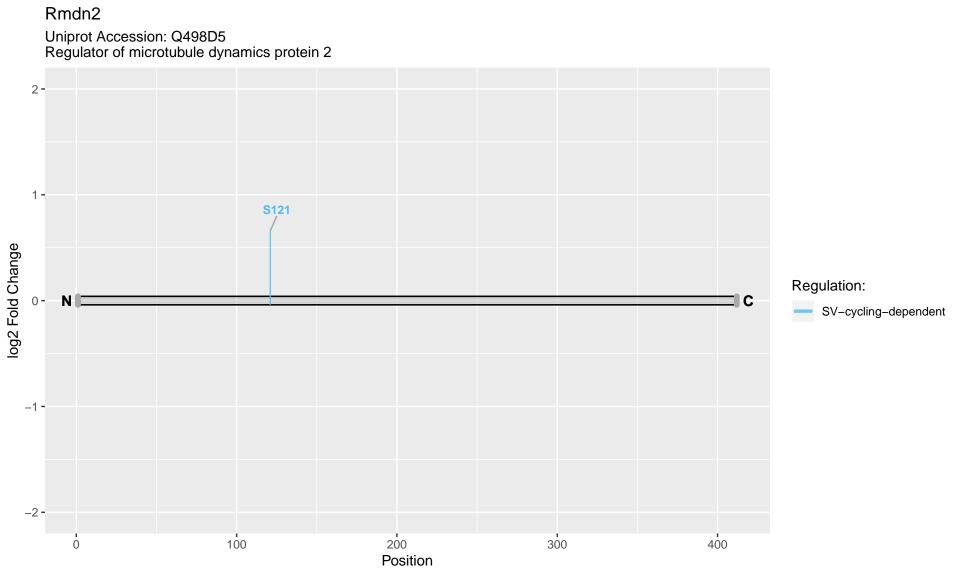


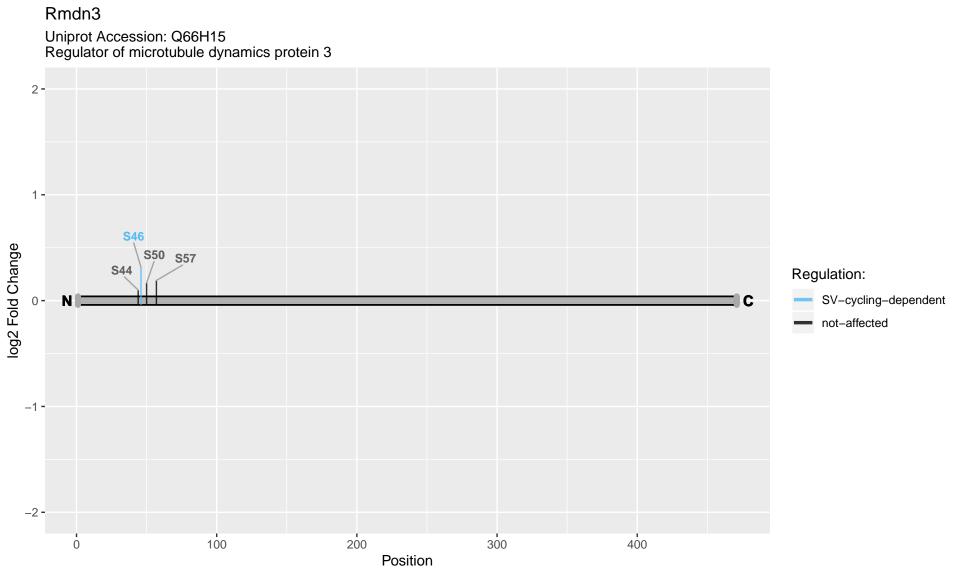


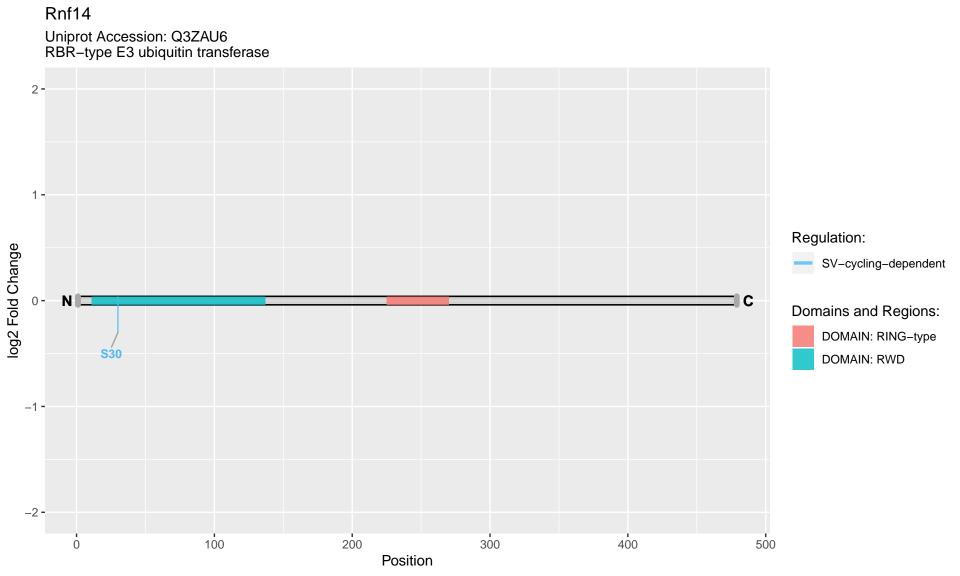


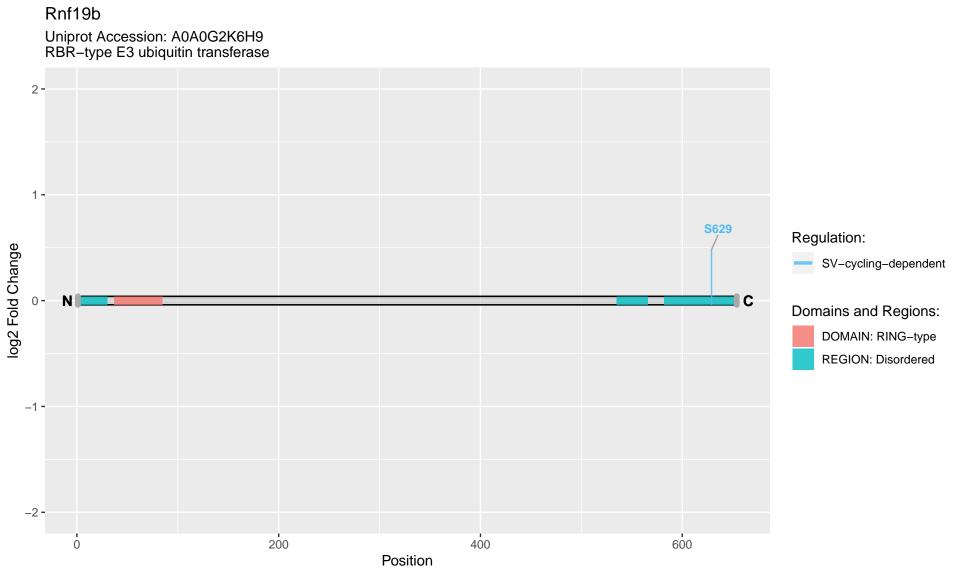


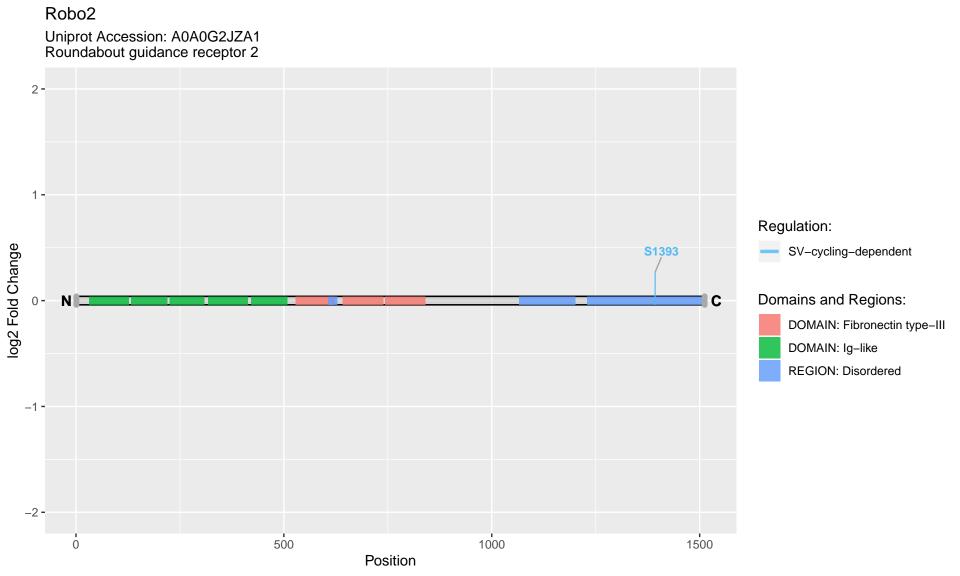


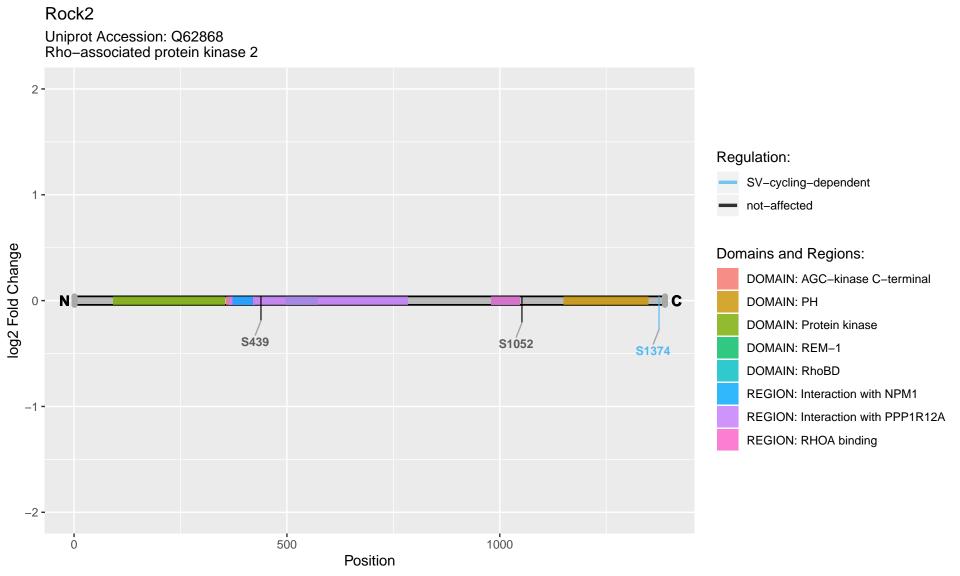


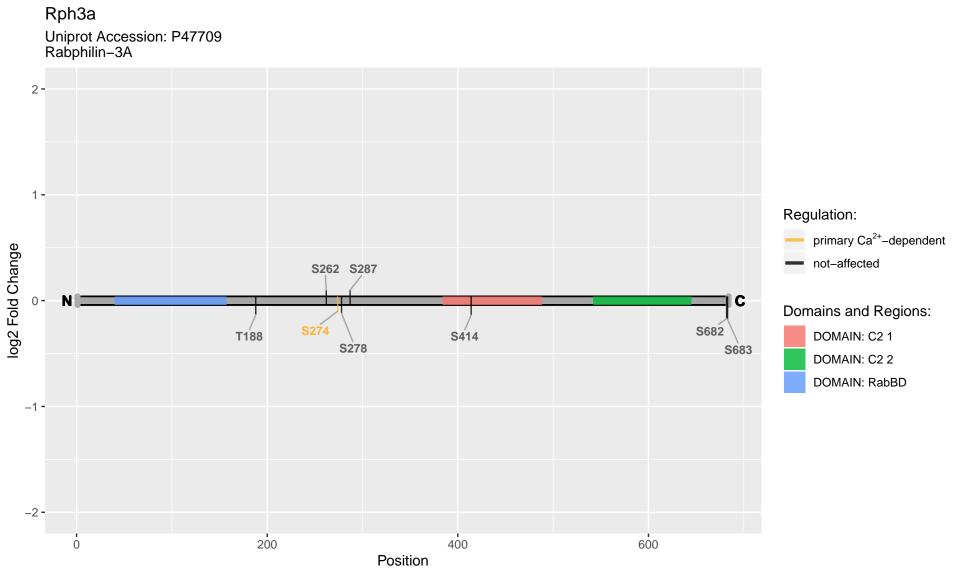


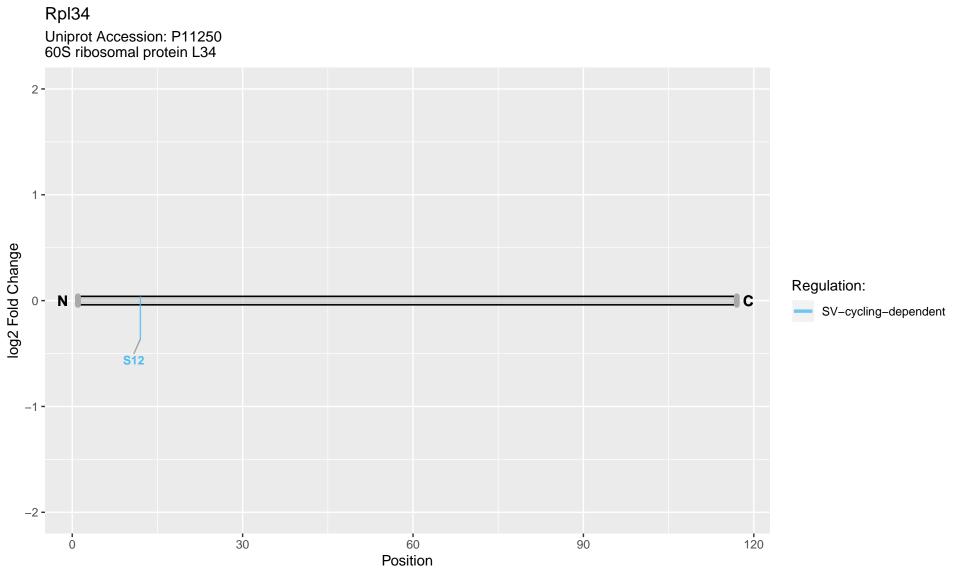


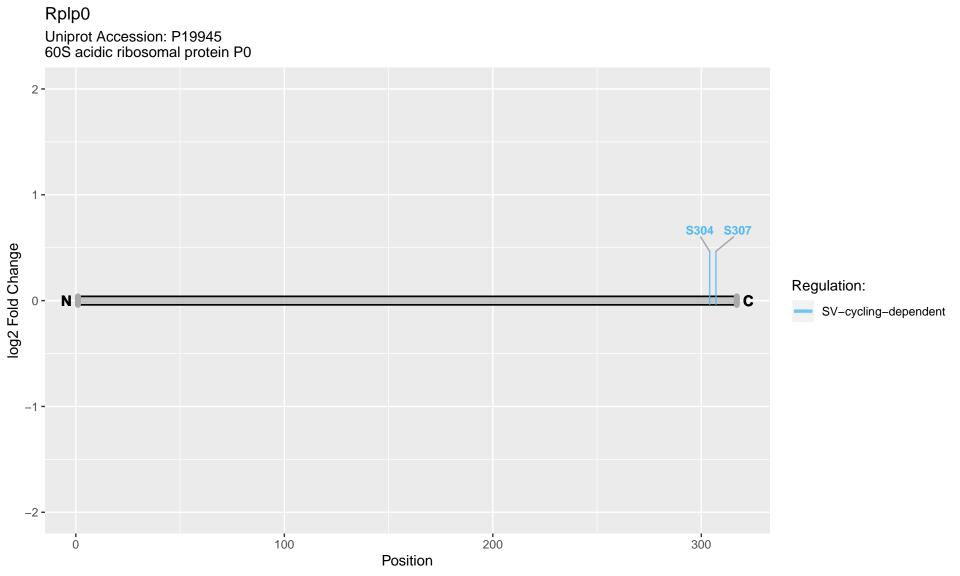


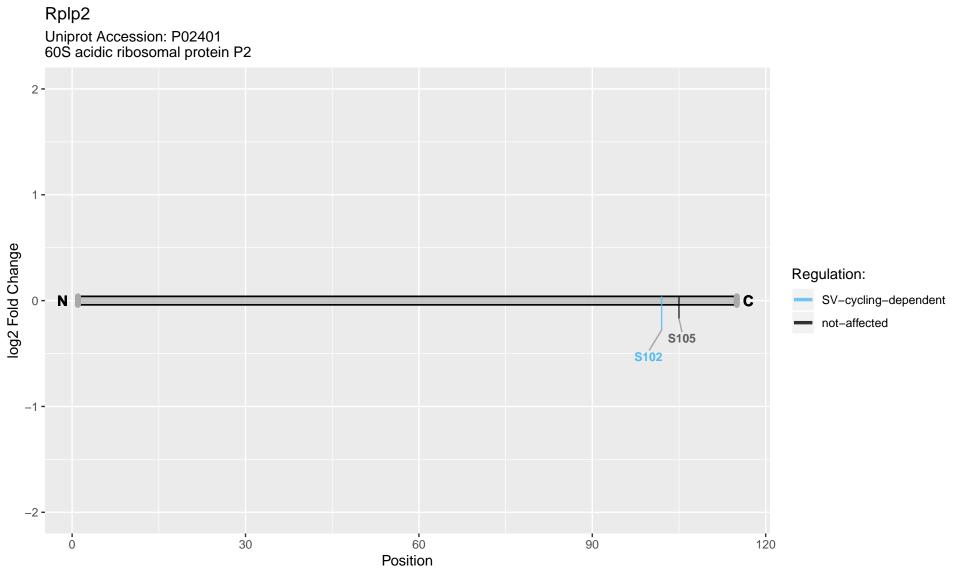


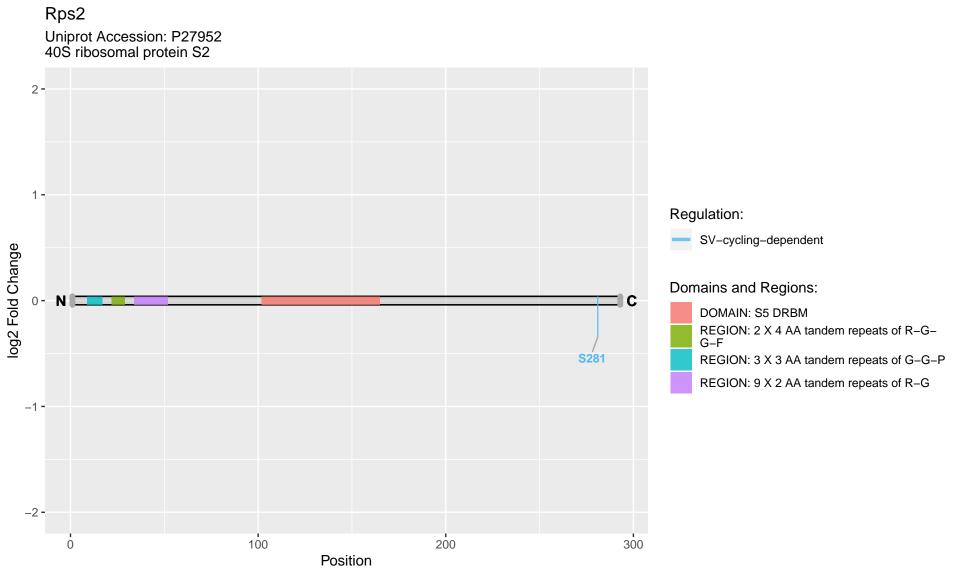


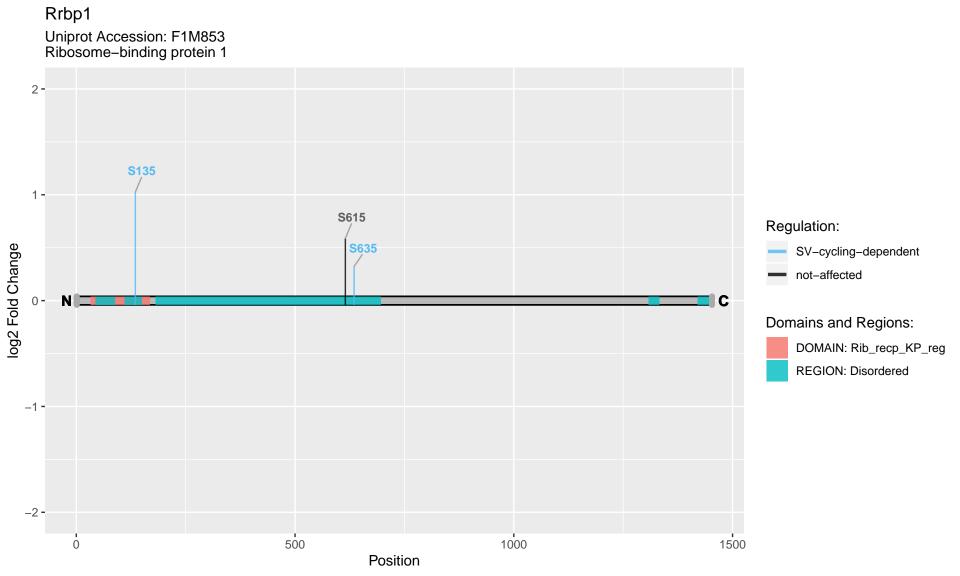


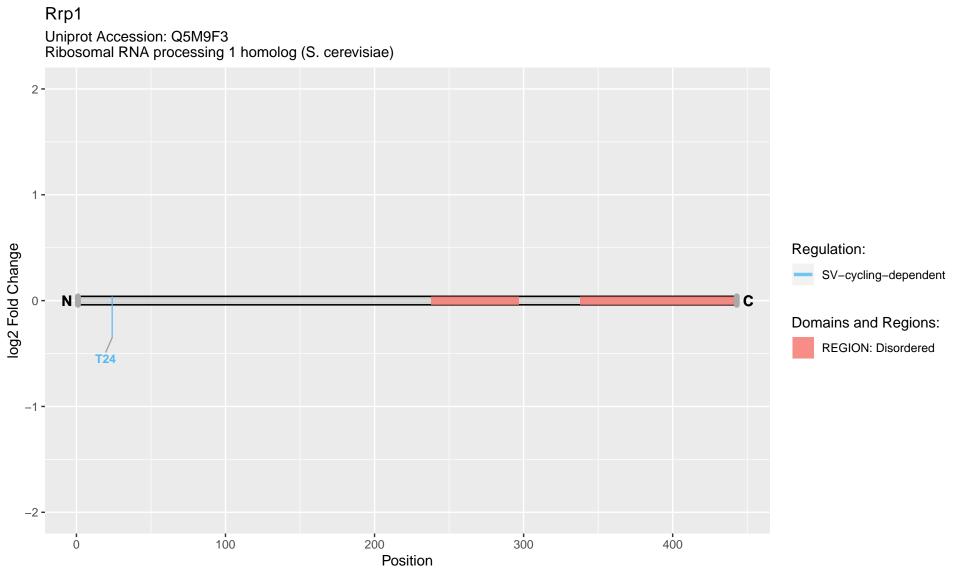


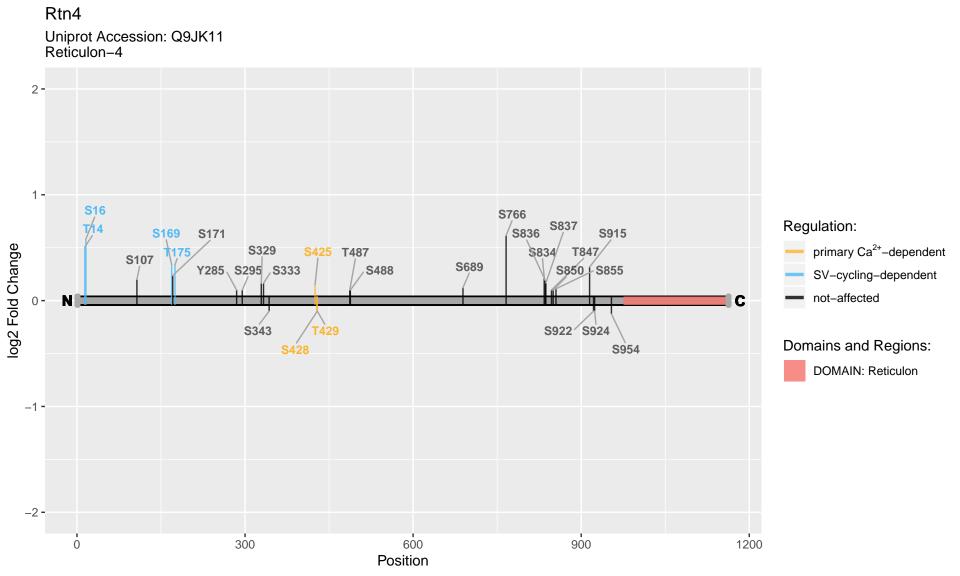


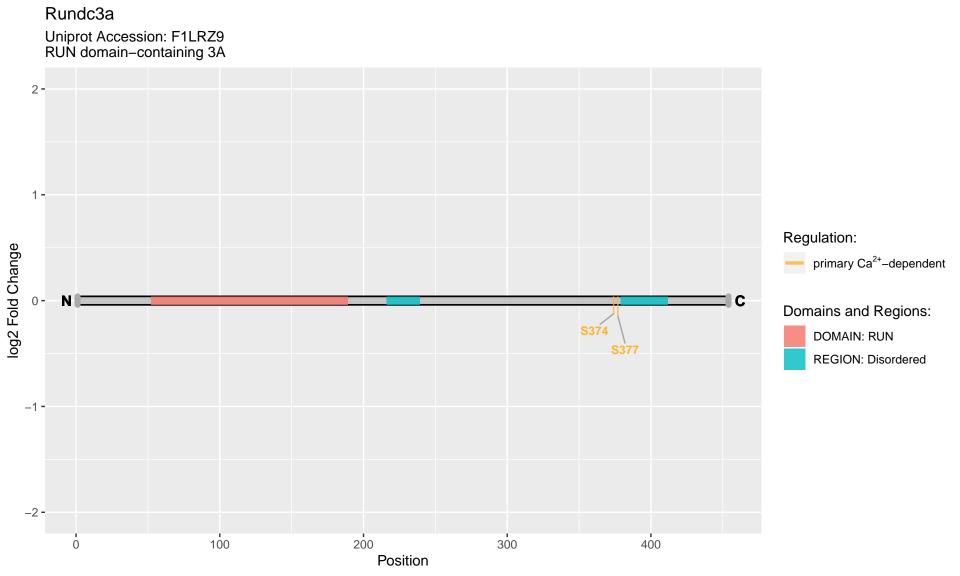


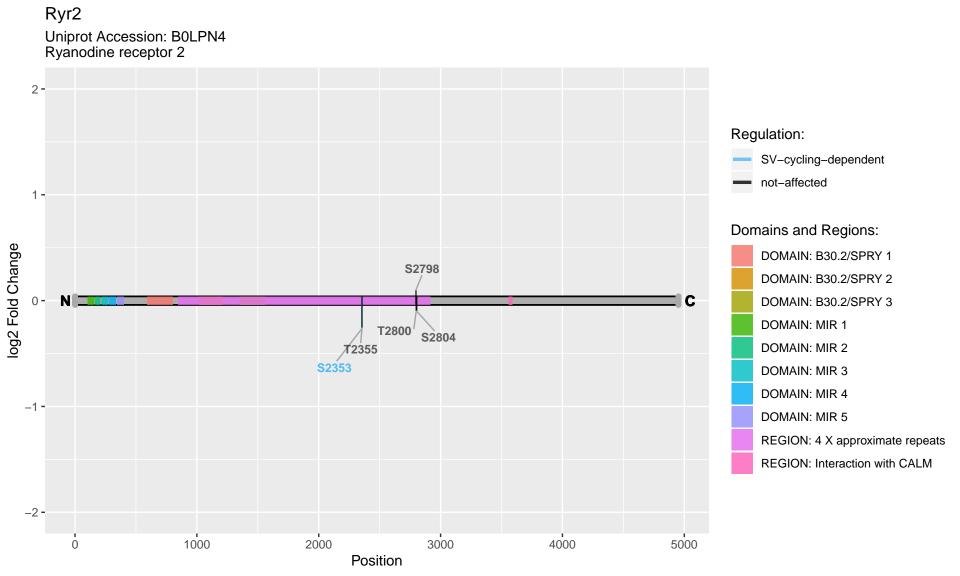


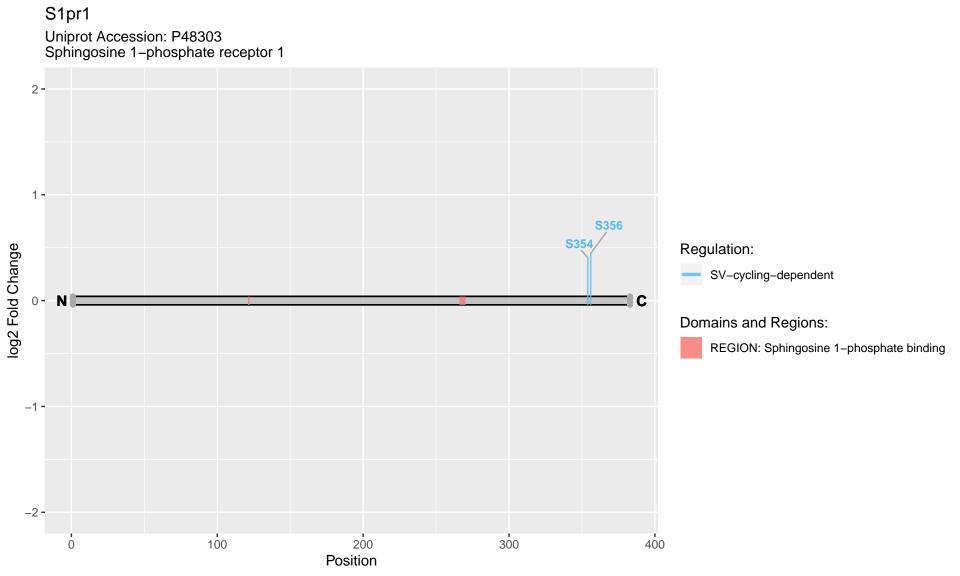


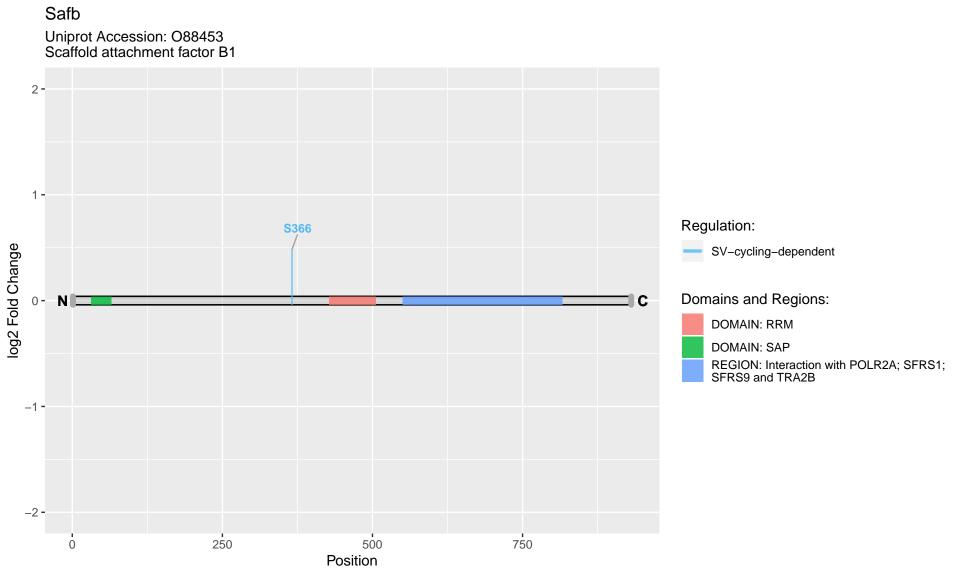


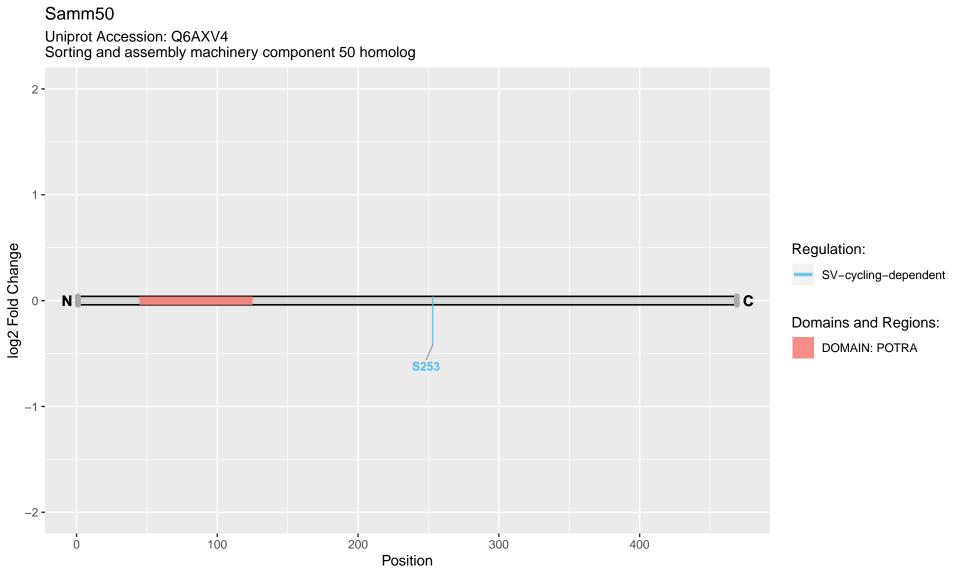


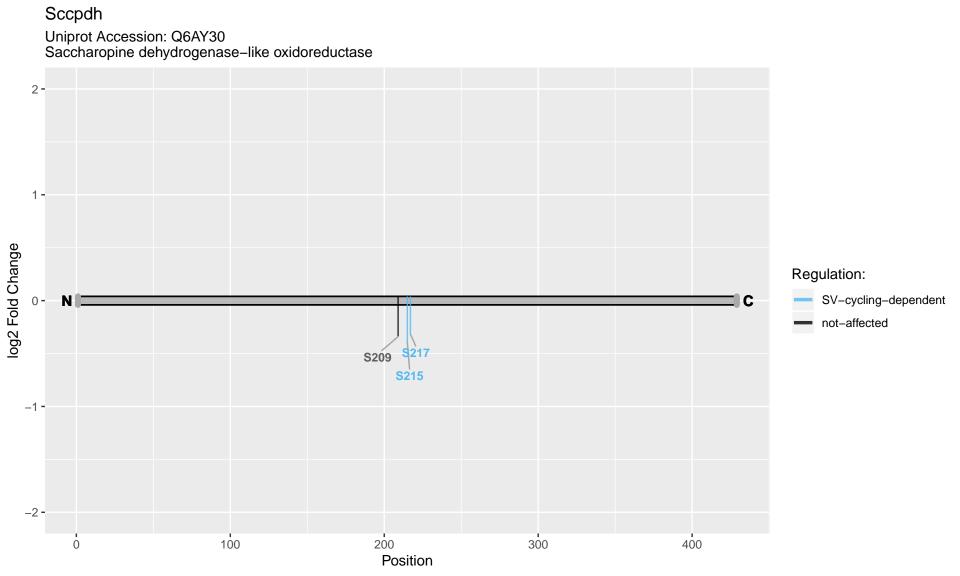


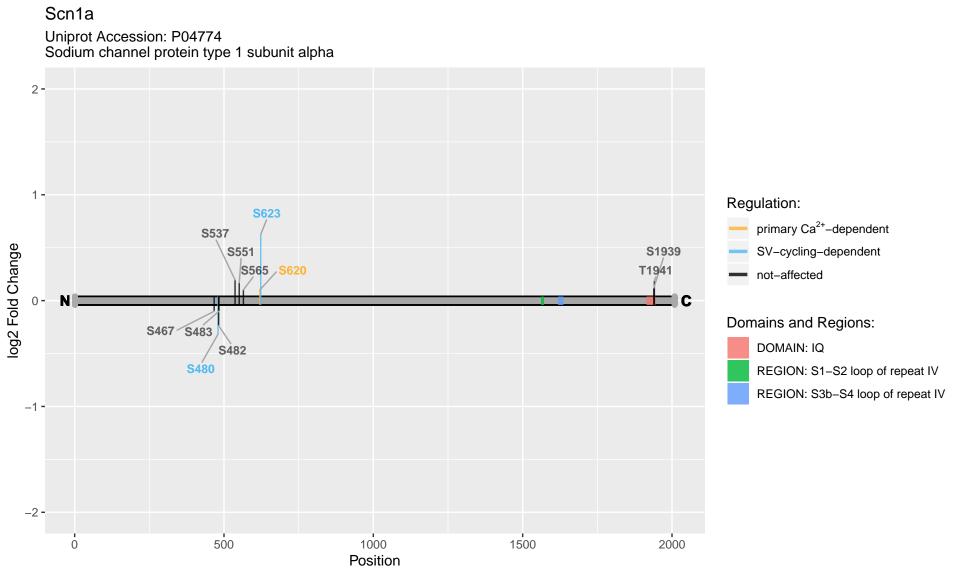


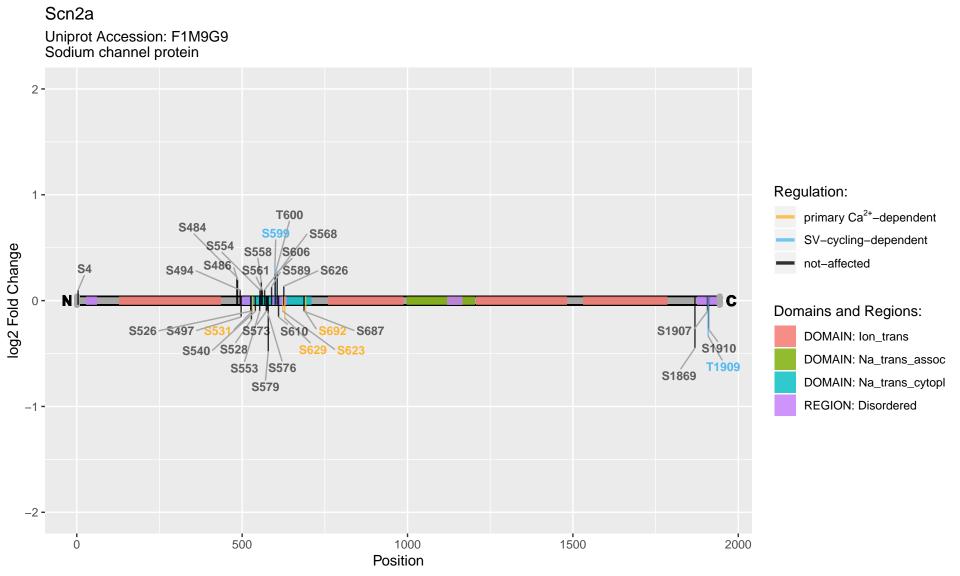


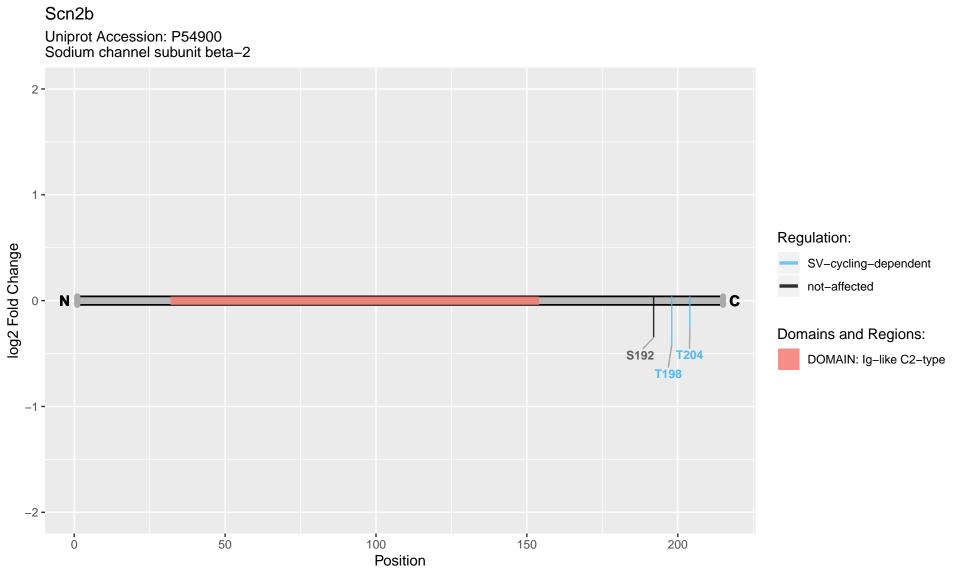


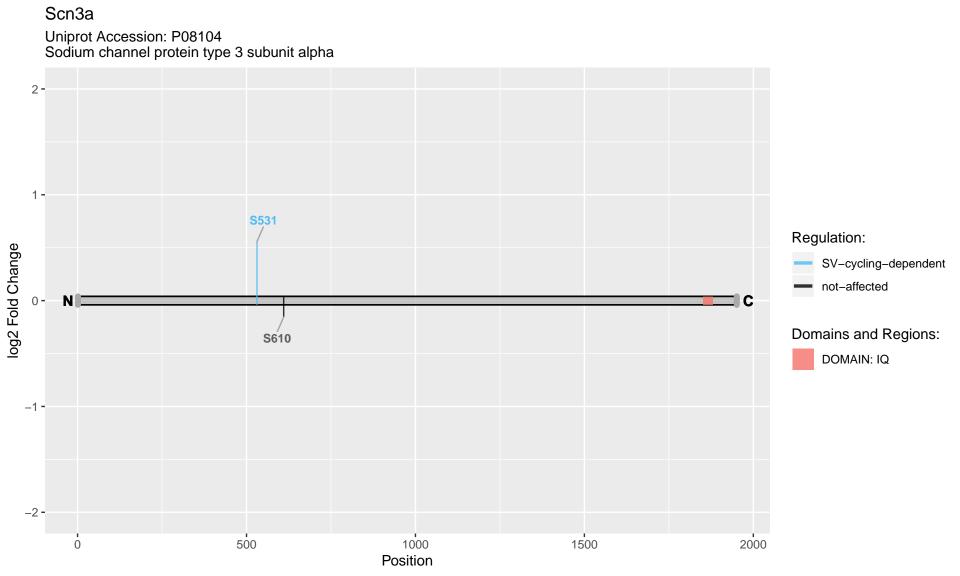


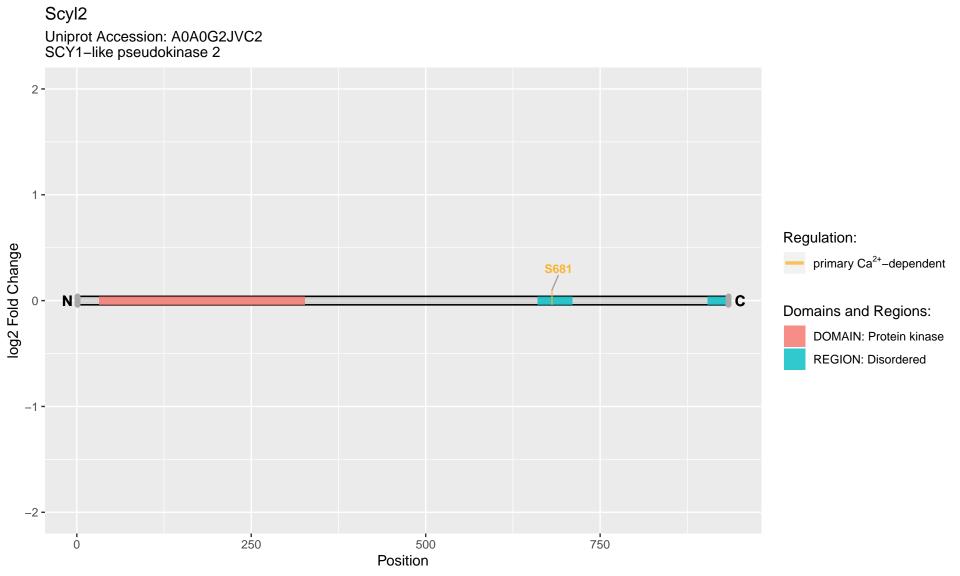


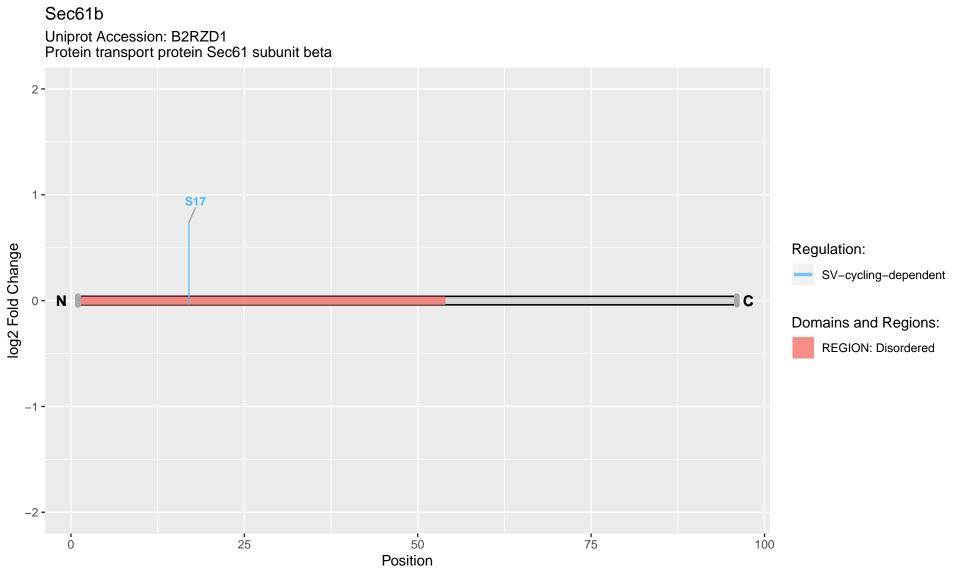


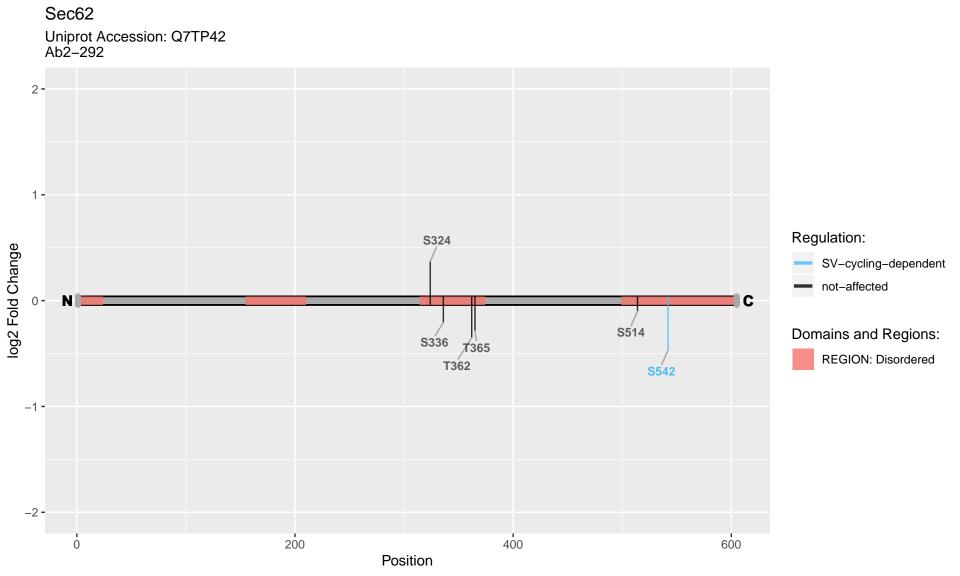


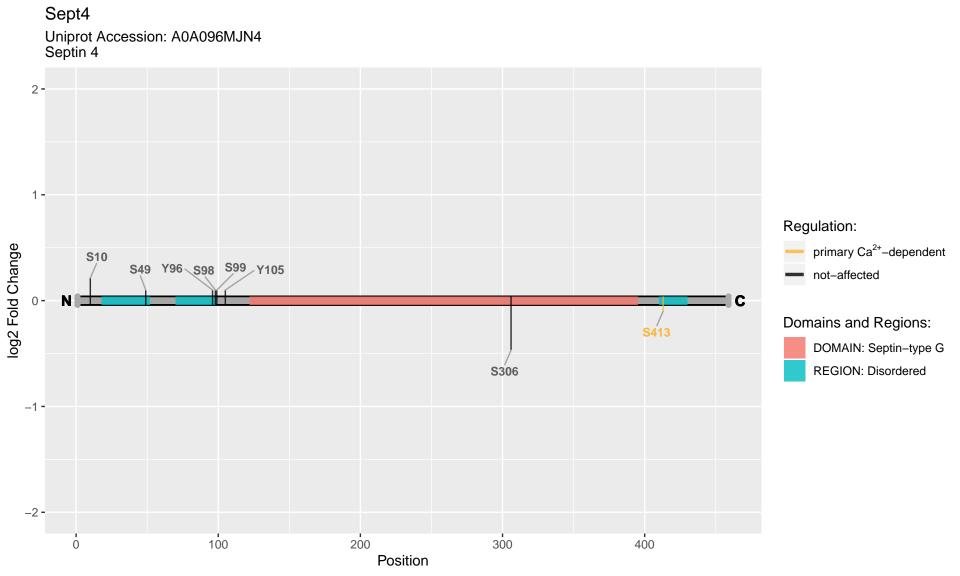


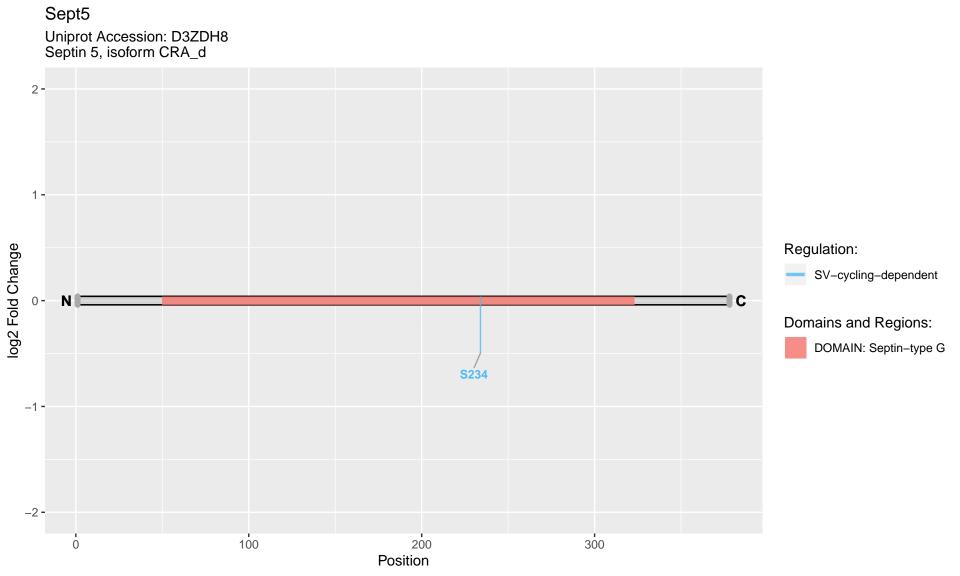


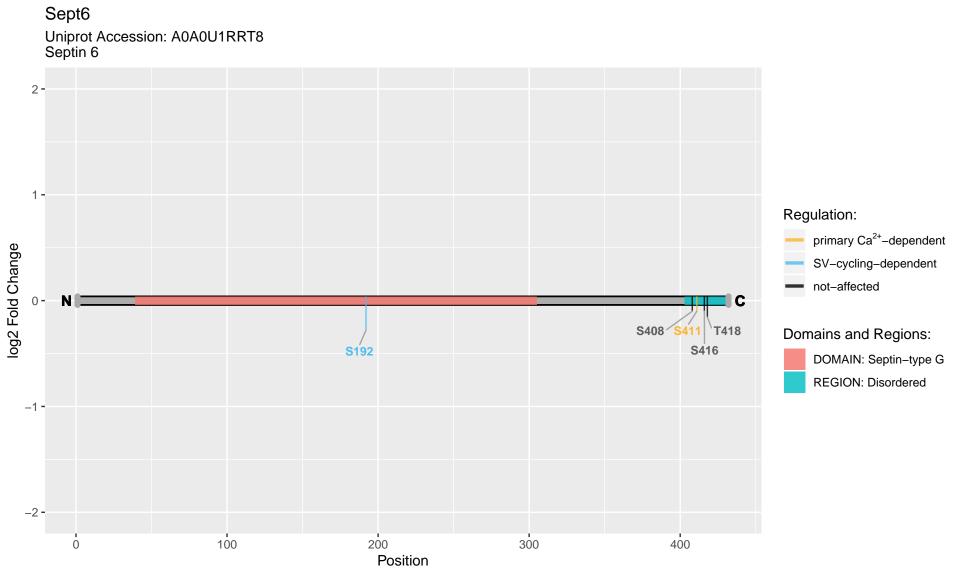


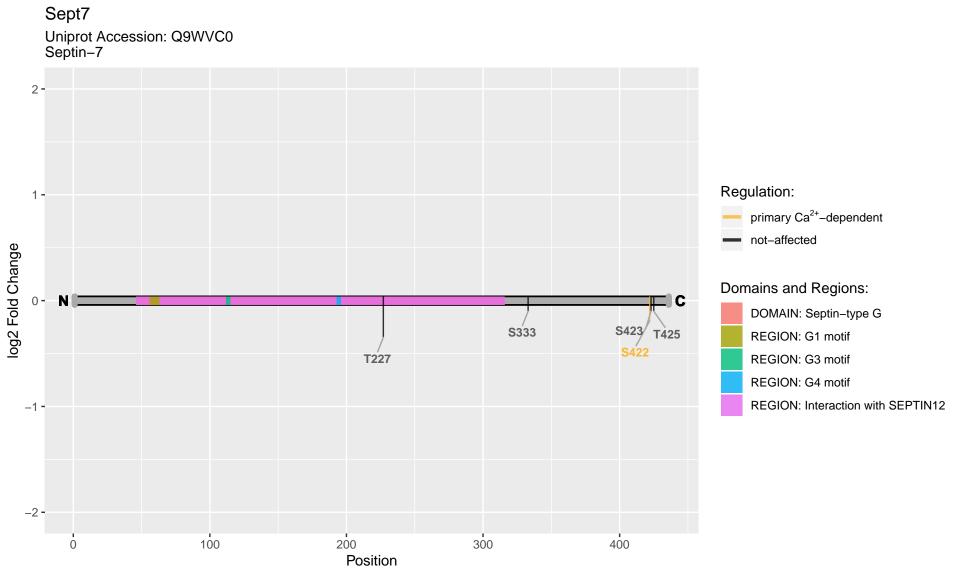


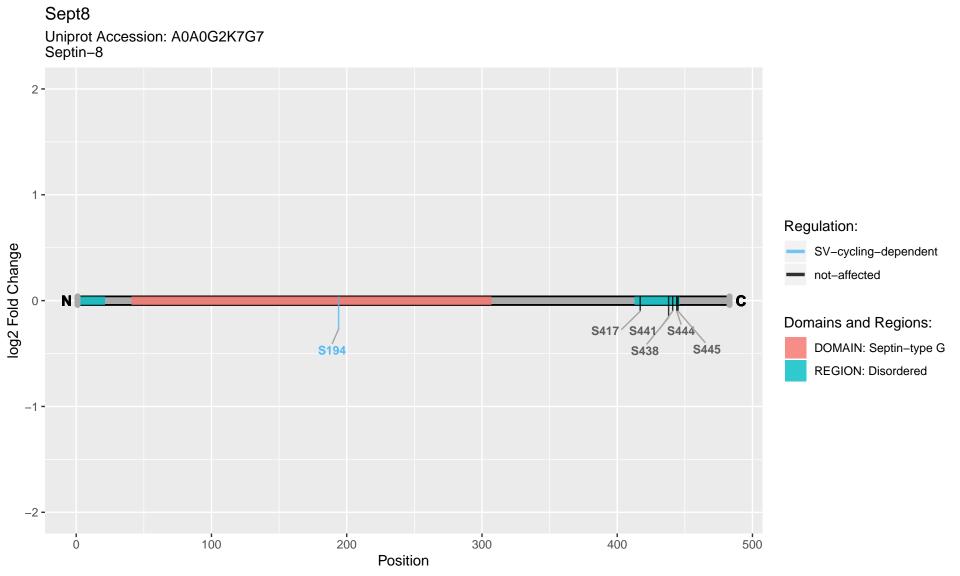


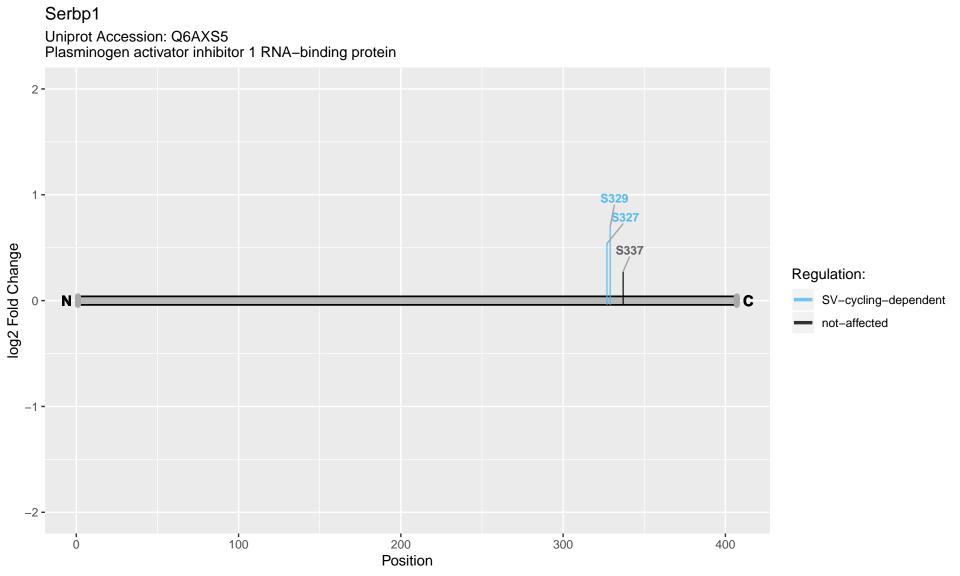


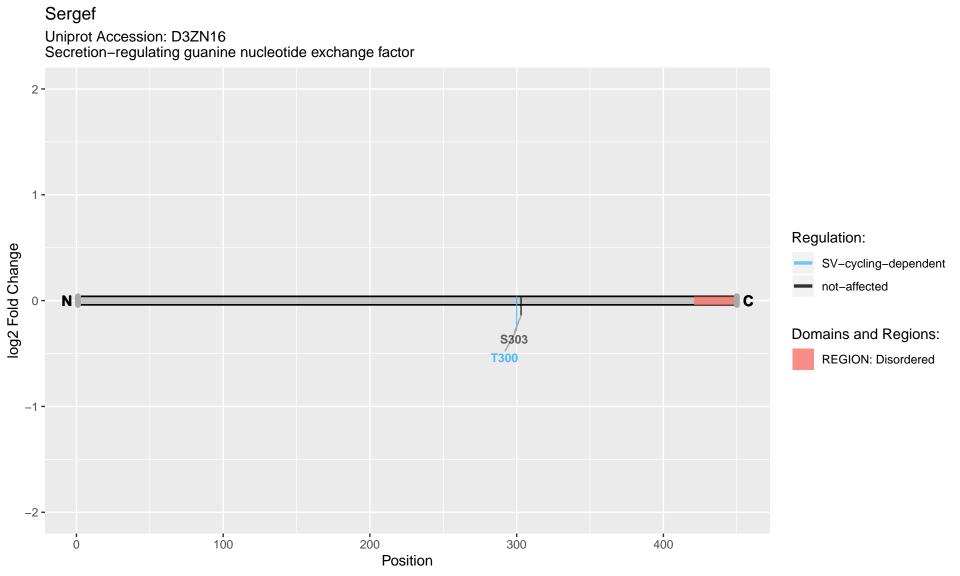


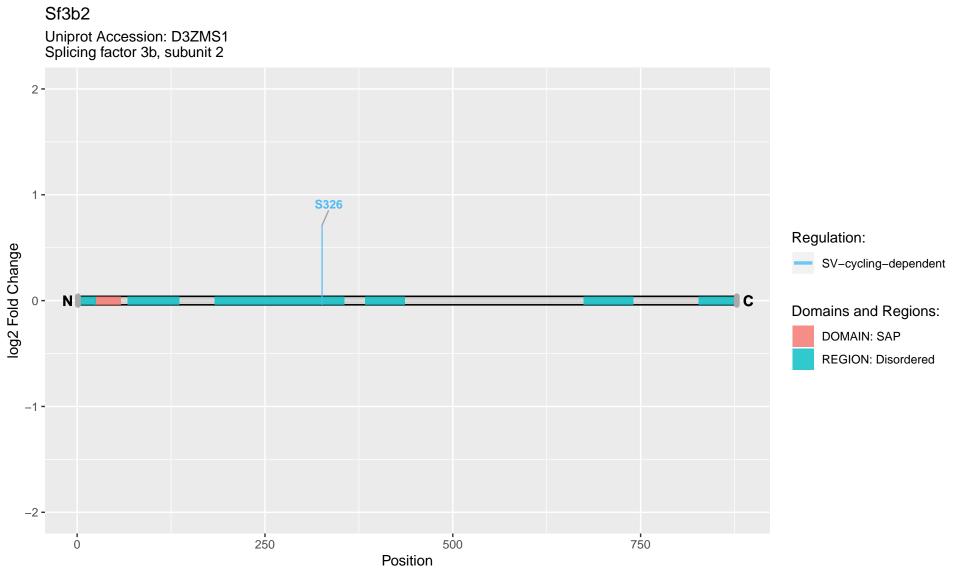


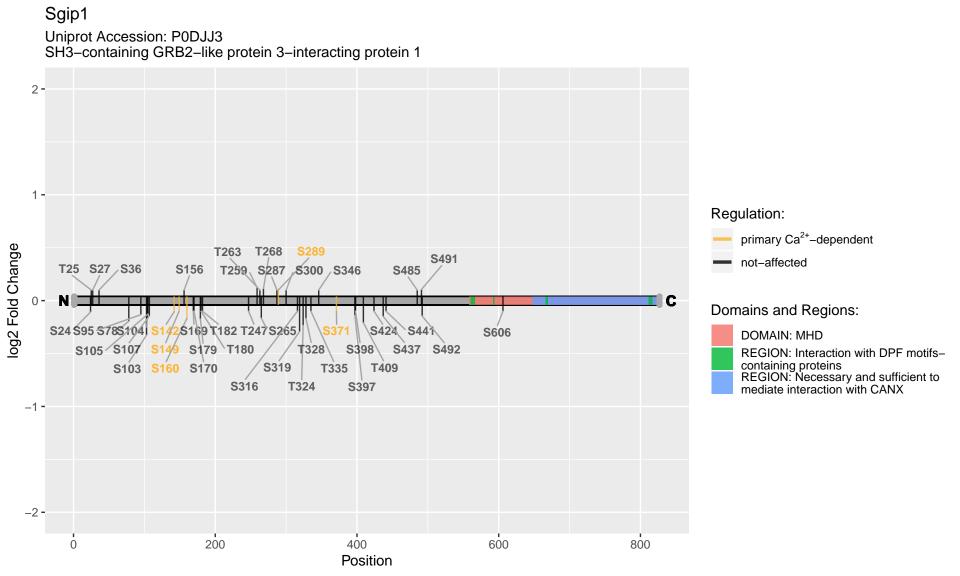


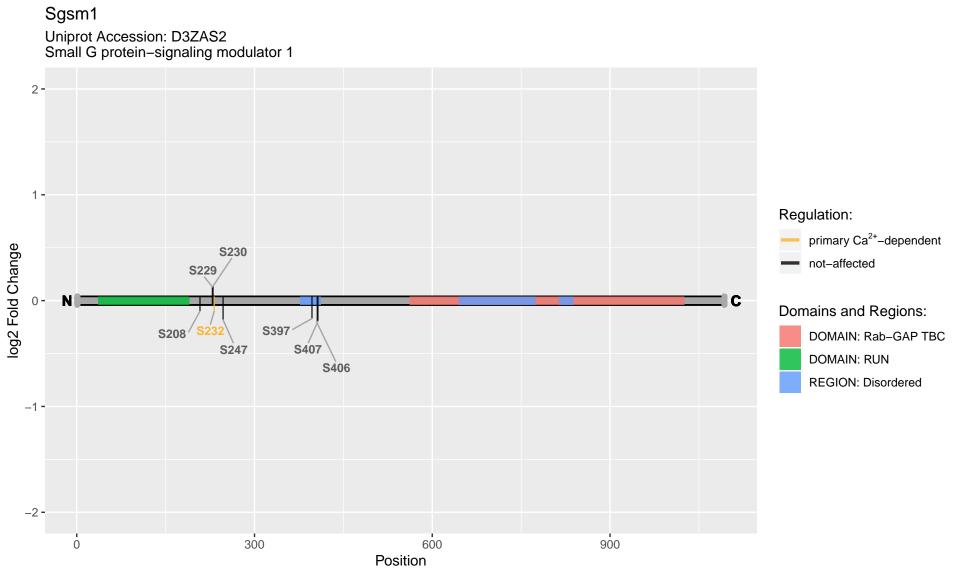


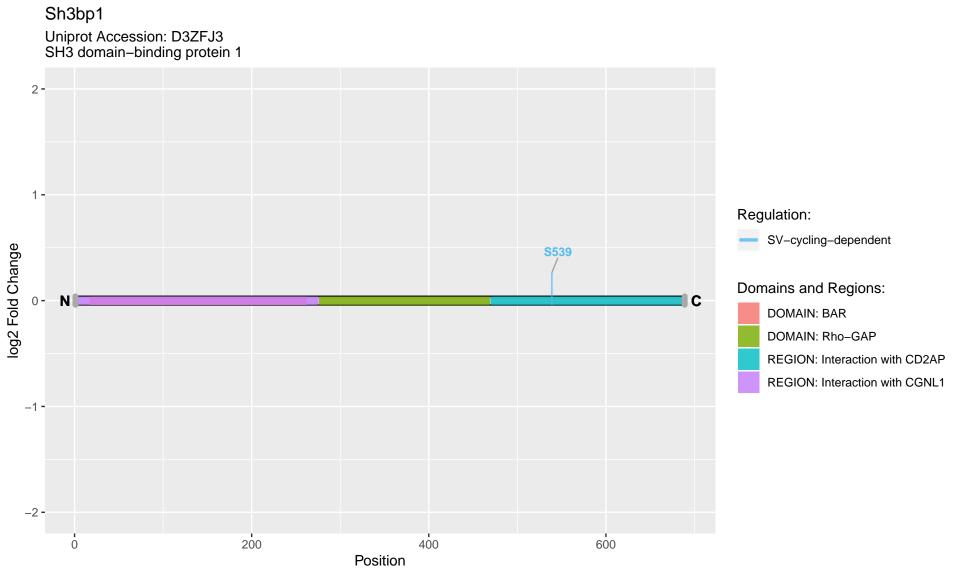


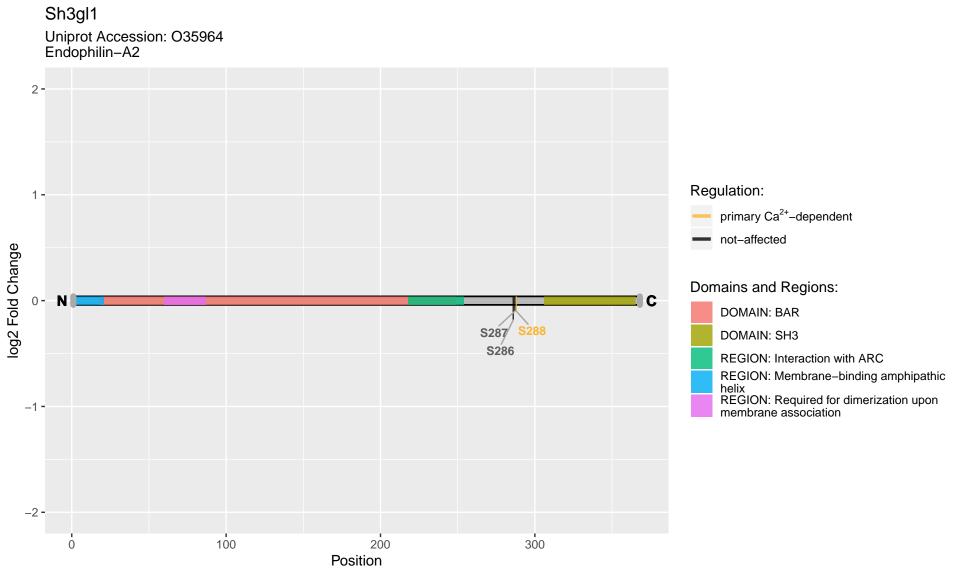


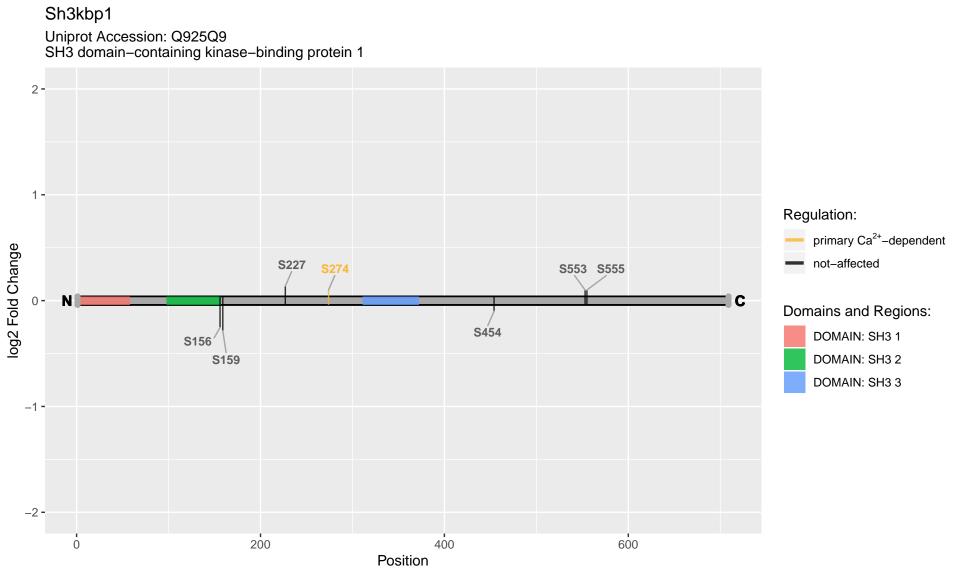


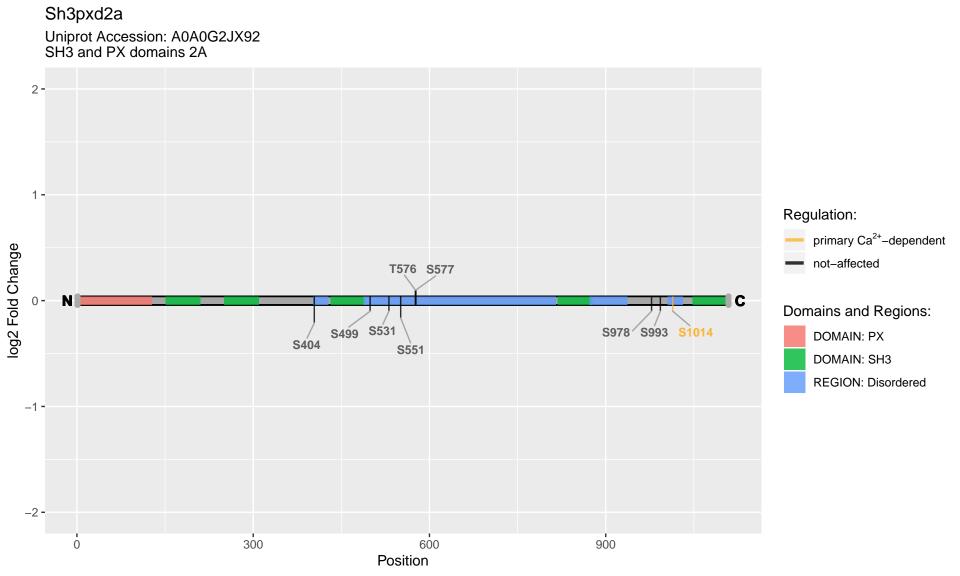


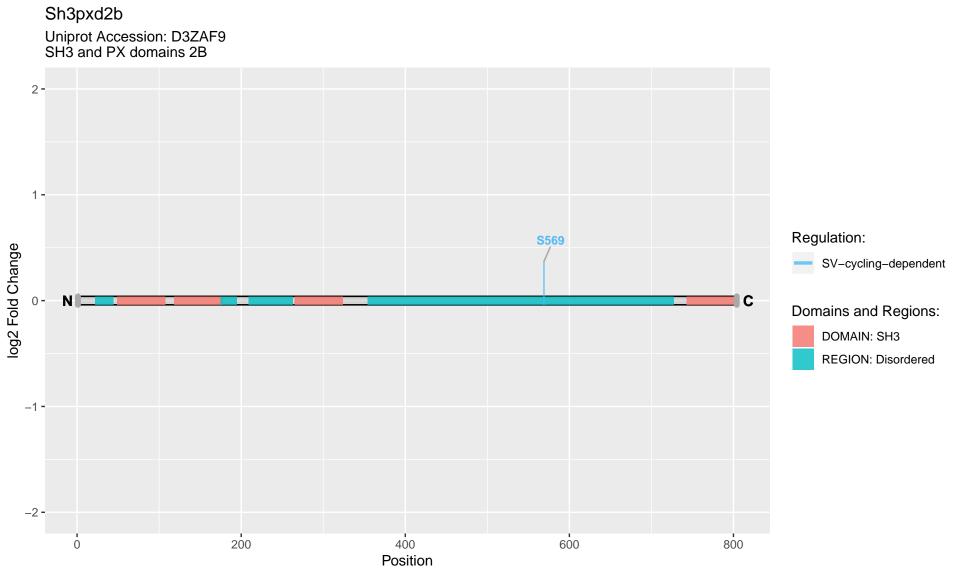


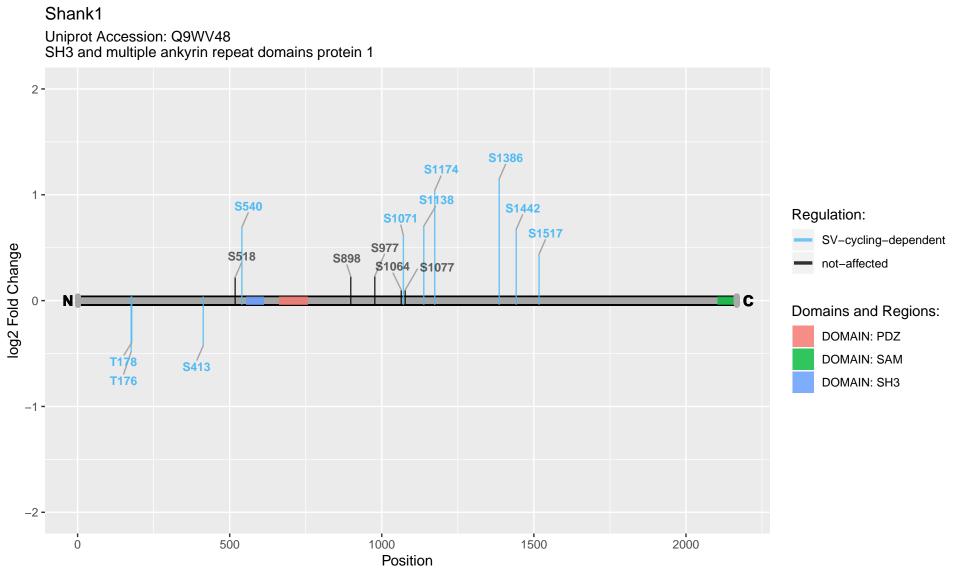


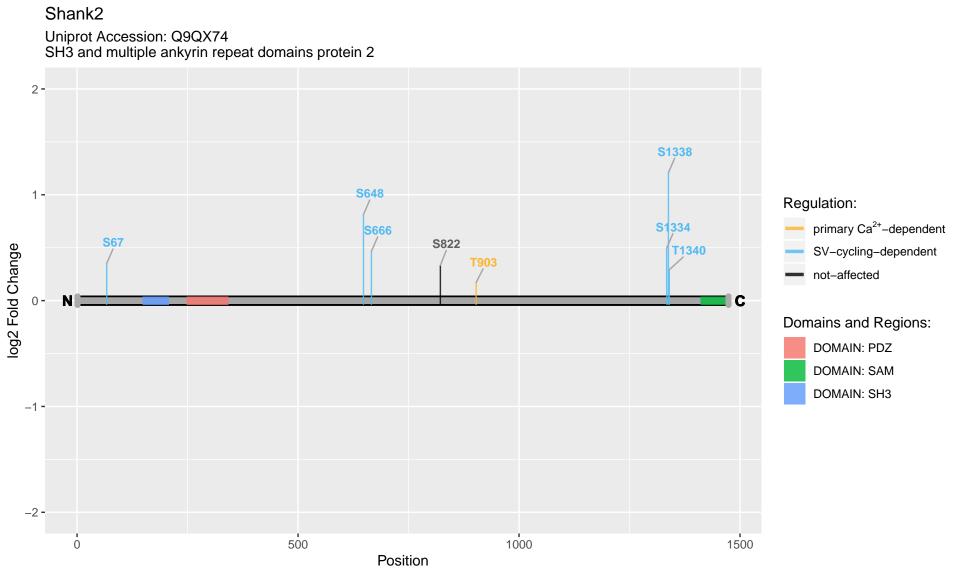




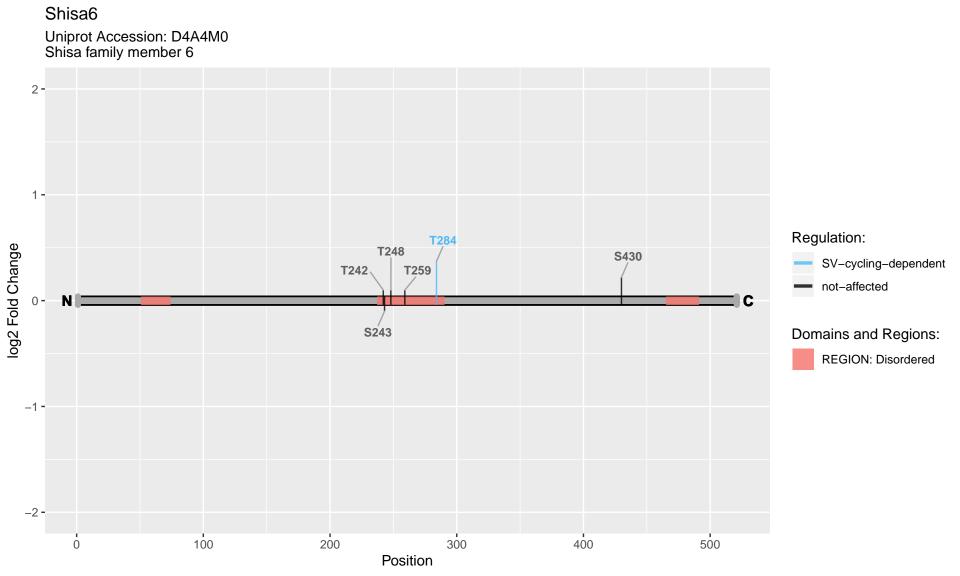


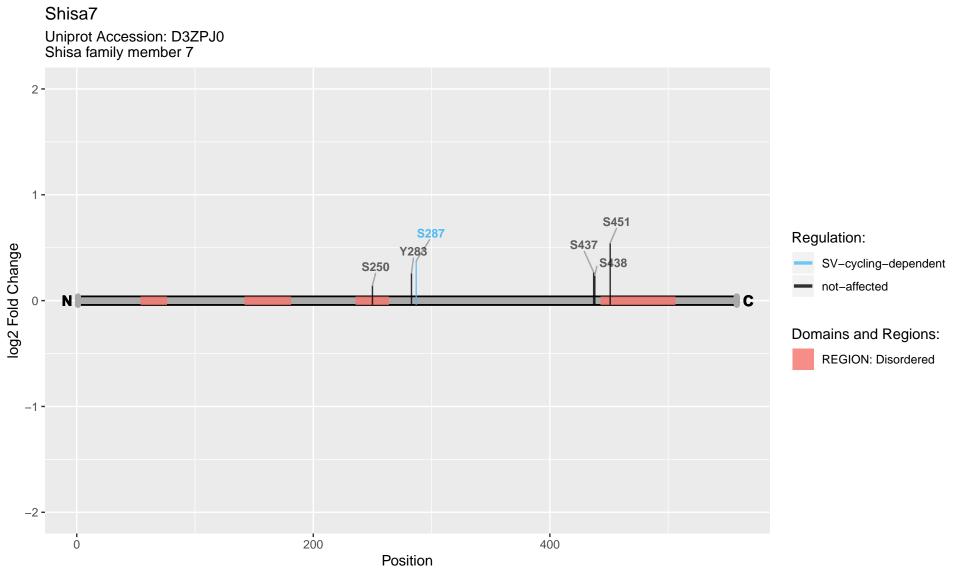


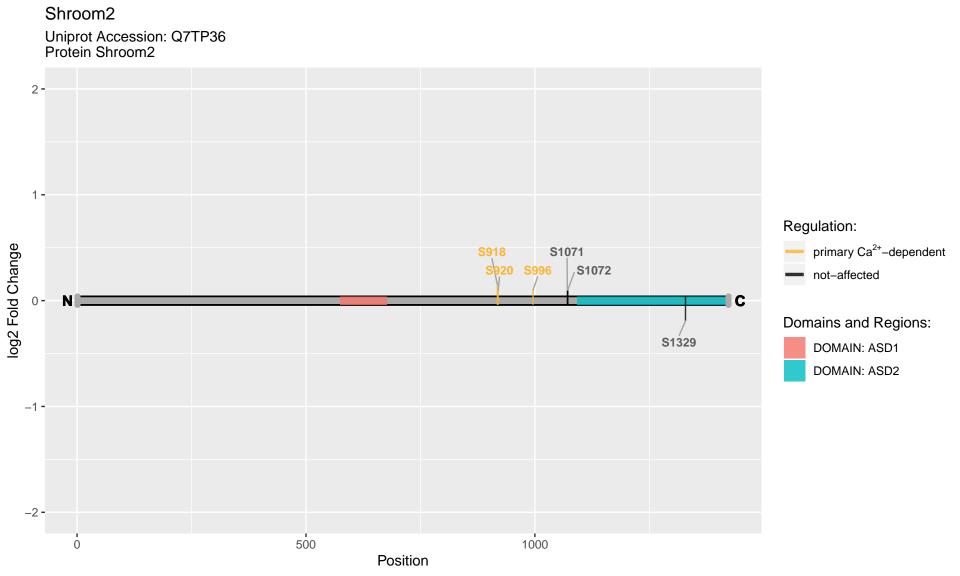


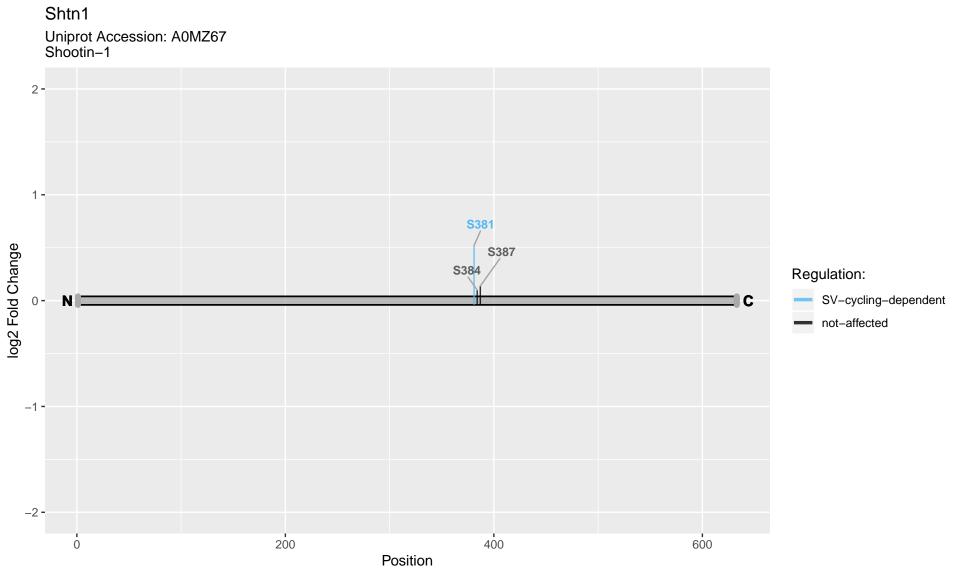


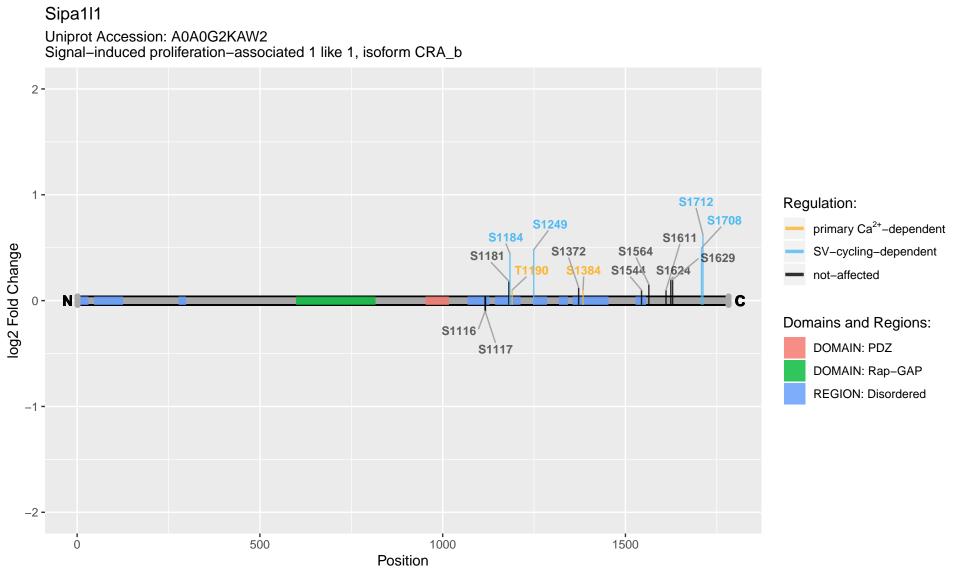
Shank3 Uniprot Accession: Q9JLU4 SH3 and multiple ankyrin repeat domains protein 3 2 -**S1189 S986** Regulation: 1 -S1135 SV-cycling-dependent S1511 not-affected S375 log2 Fold Change S434 S671 **S482 S685** Domains and Regions: DOMAIN: PDZ DOMAIN: SAM DOMAIN: SH3 **REGION:** Intramolecular interaction with the ANK repeats REGION: Required for interaction with _1 **-**ABI1 -2 **-**500 1000 1500 Position

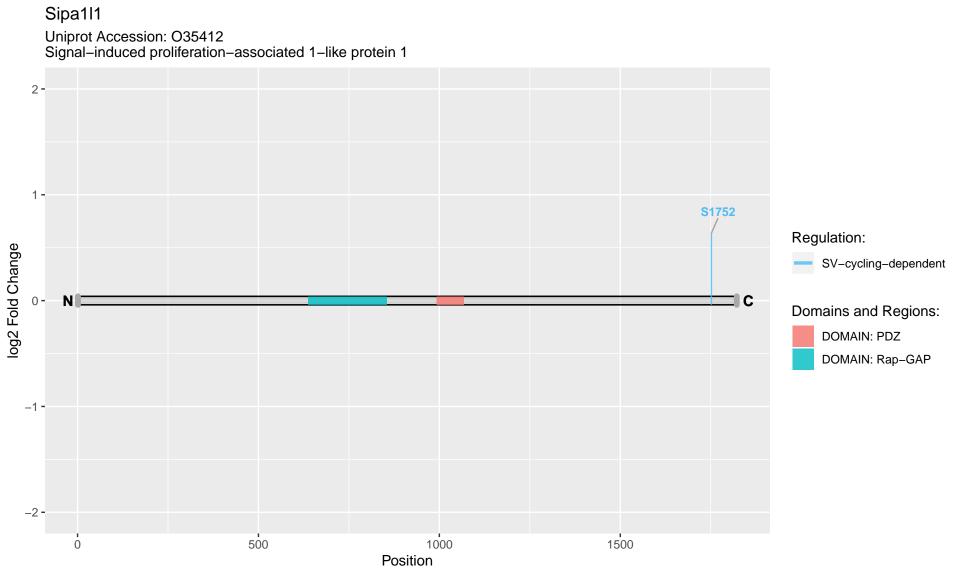


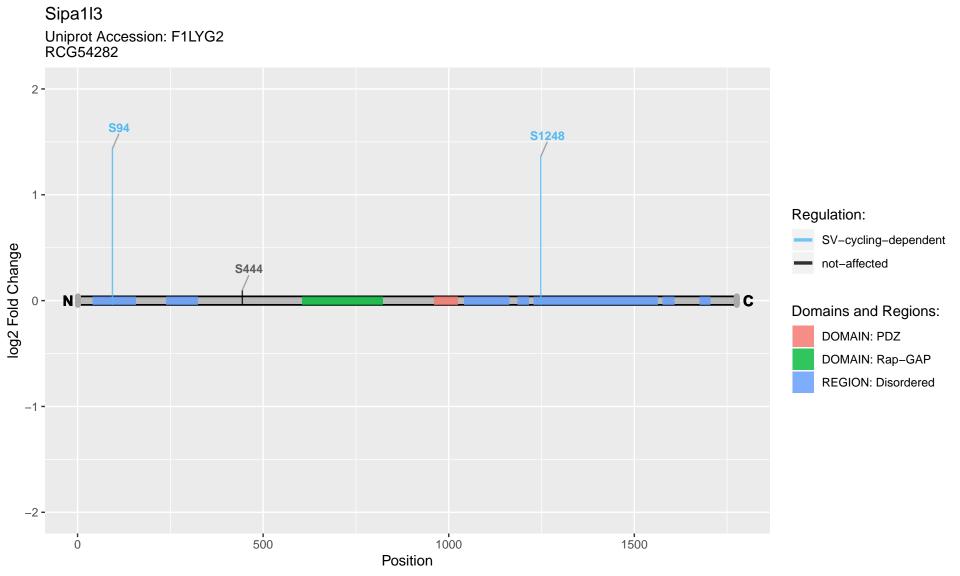


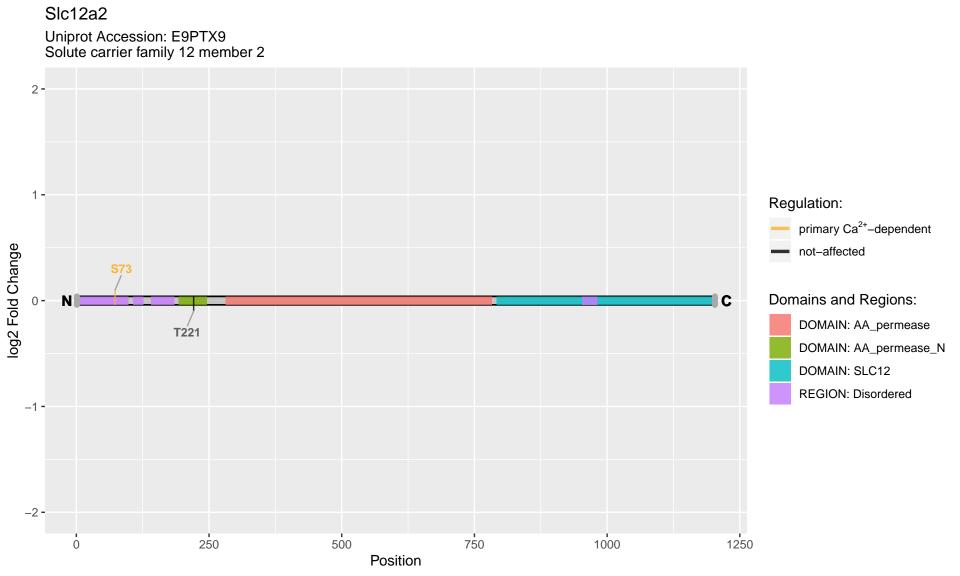


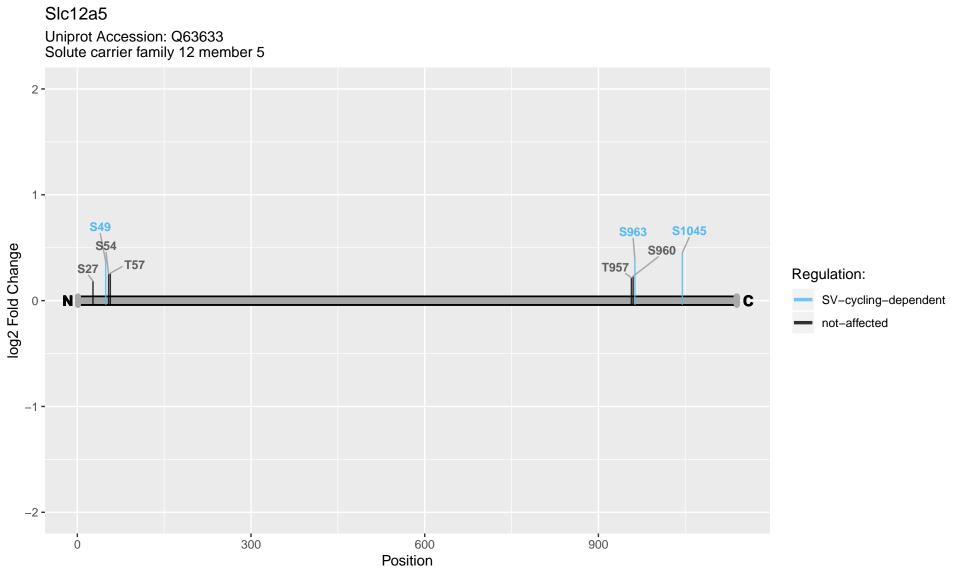


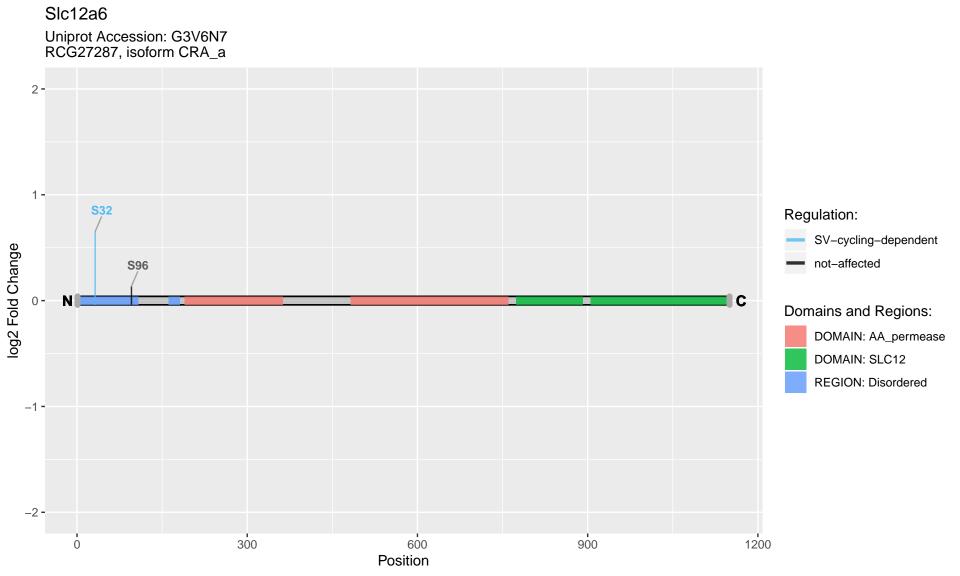


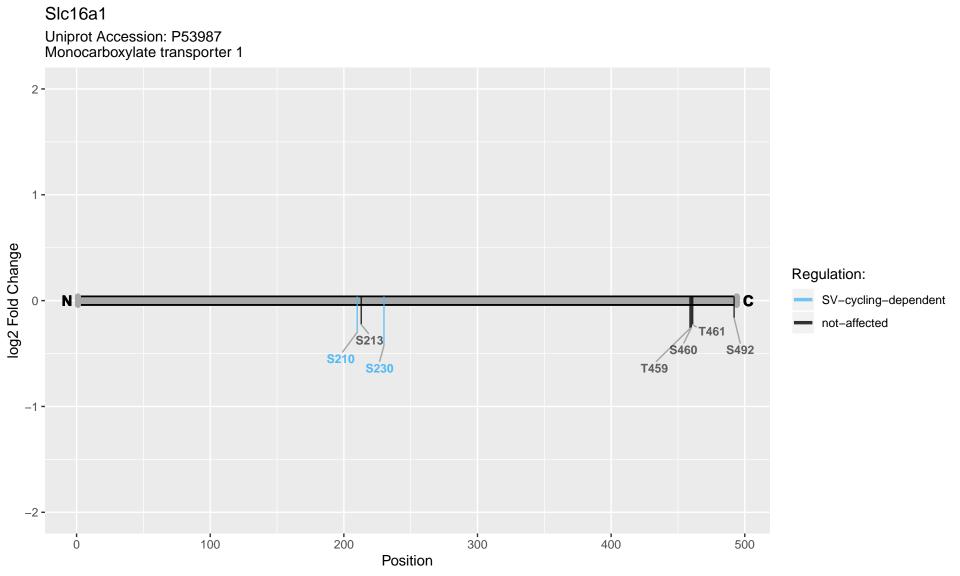


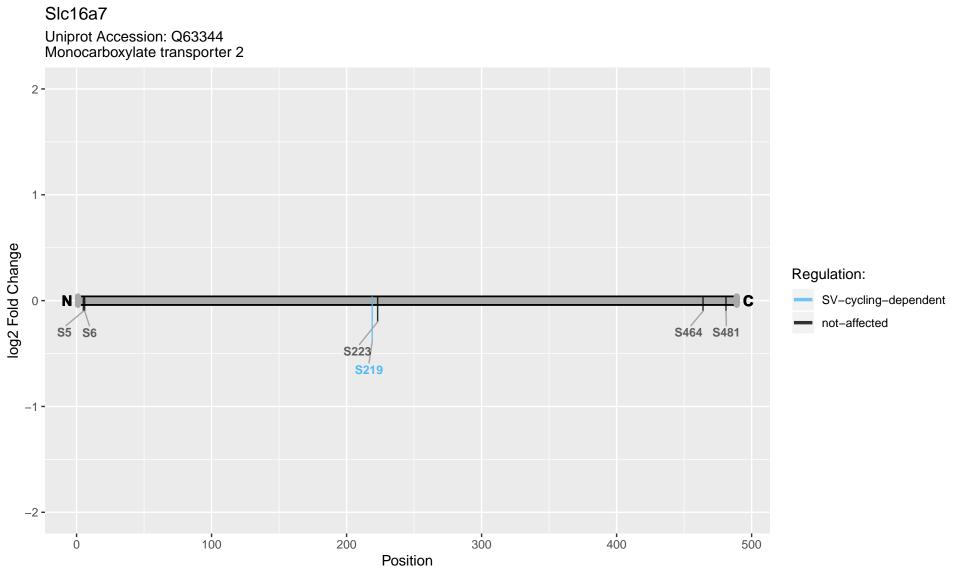


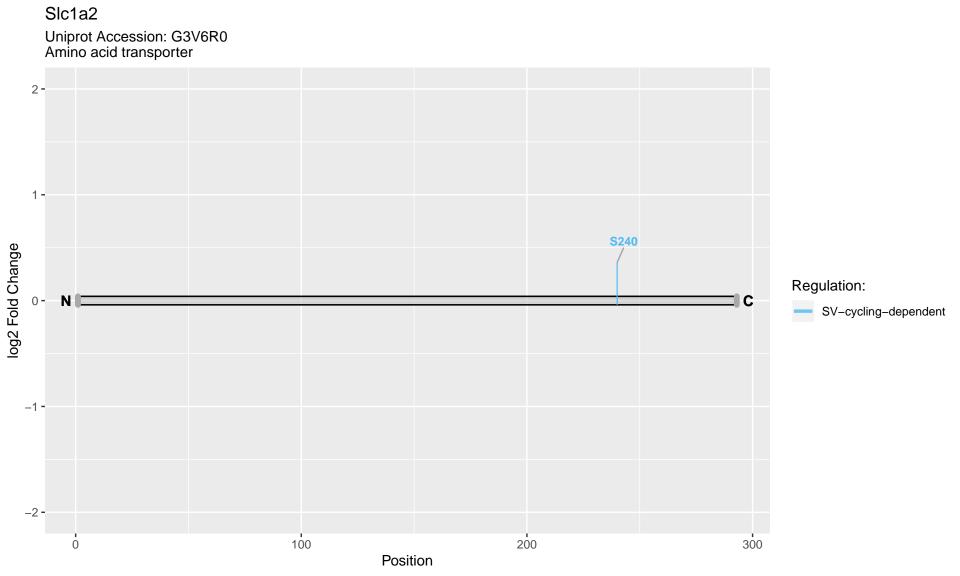


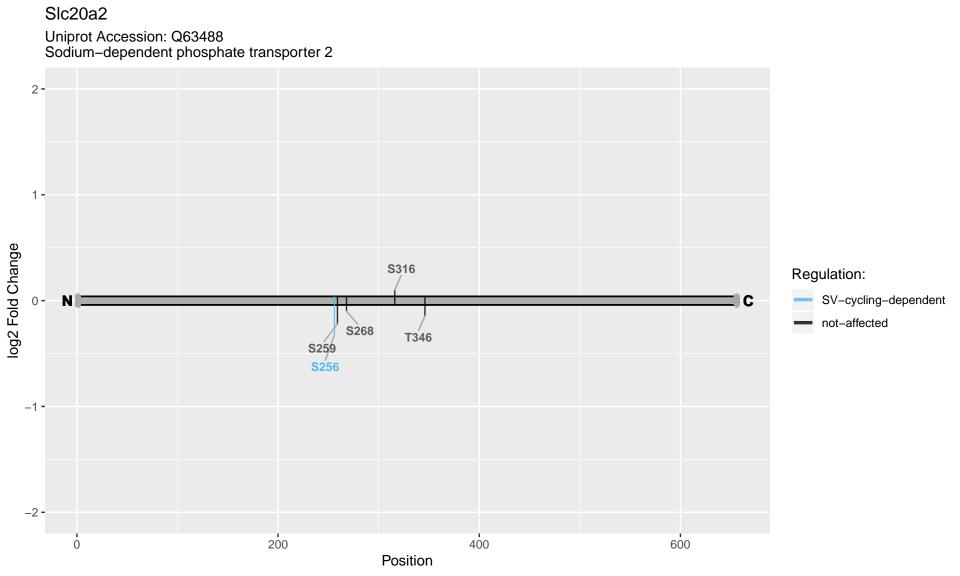


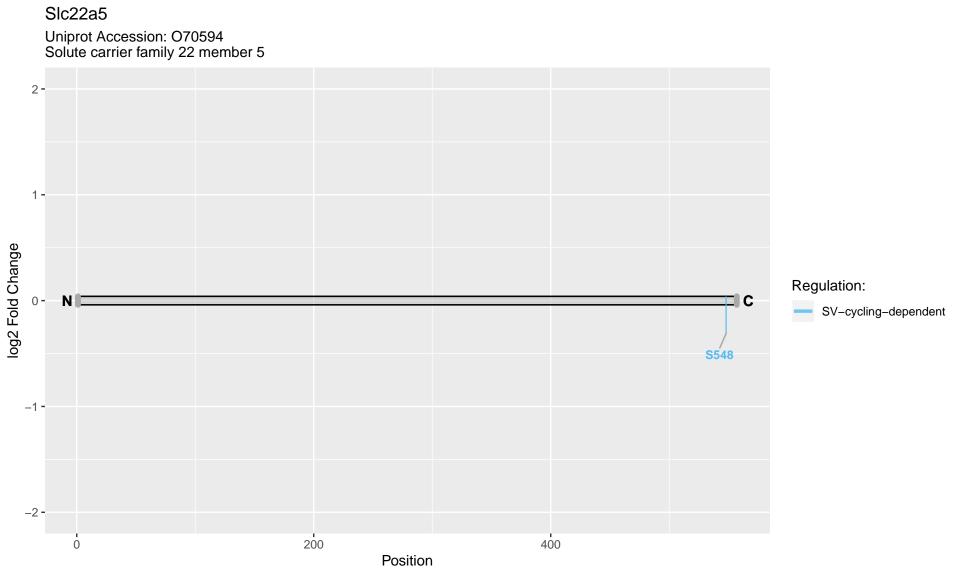


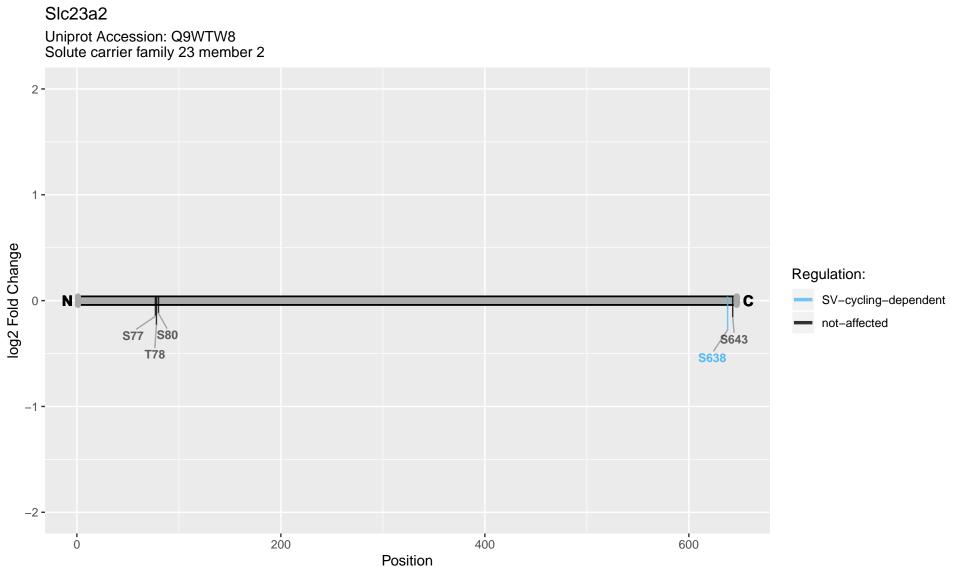


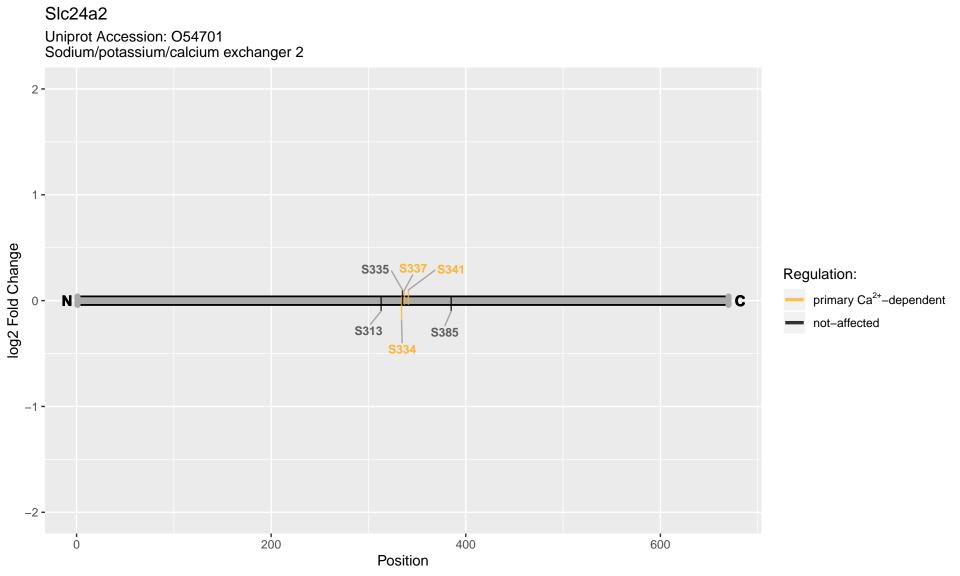


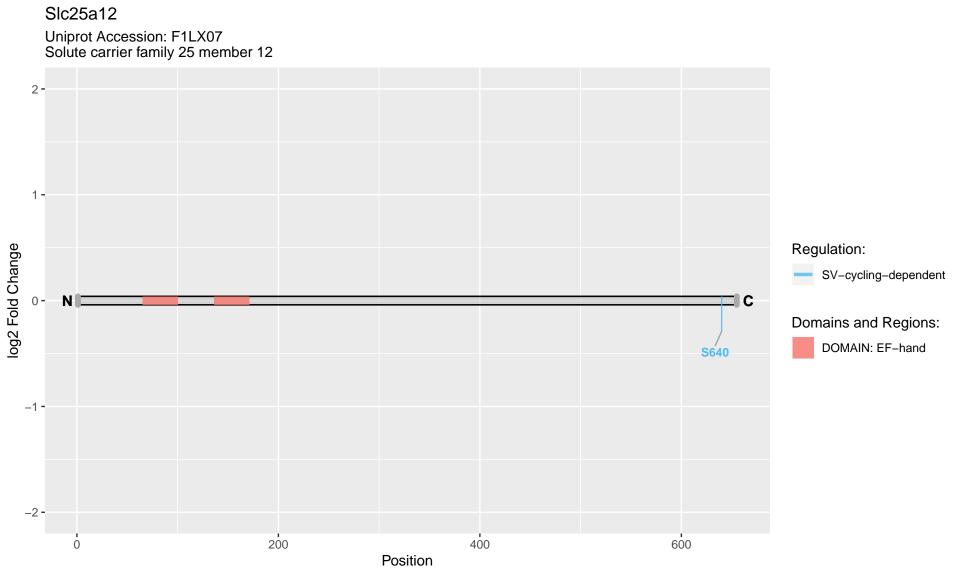


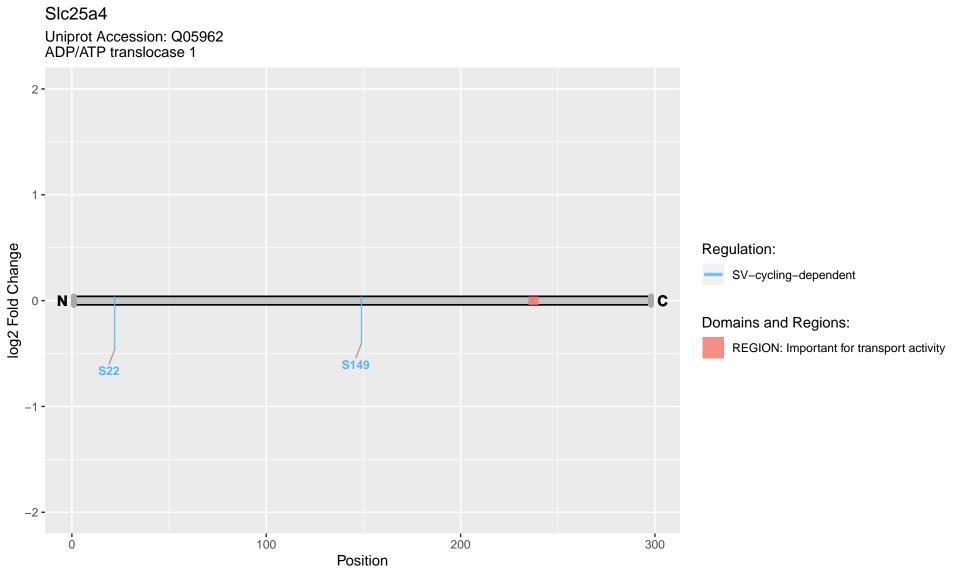


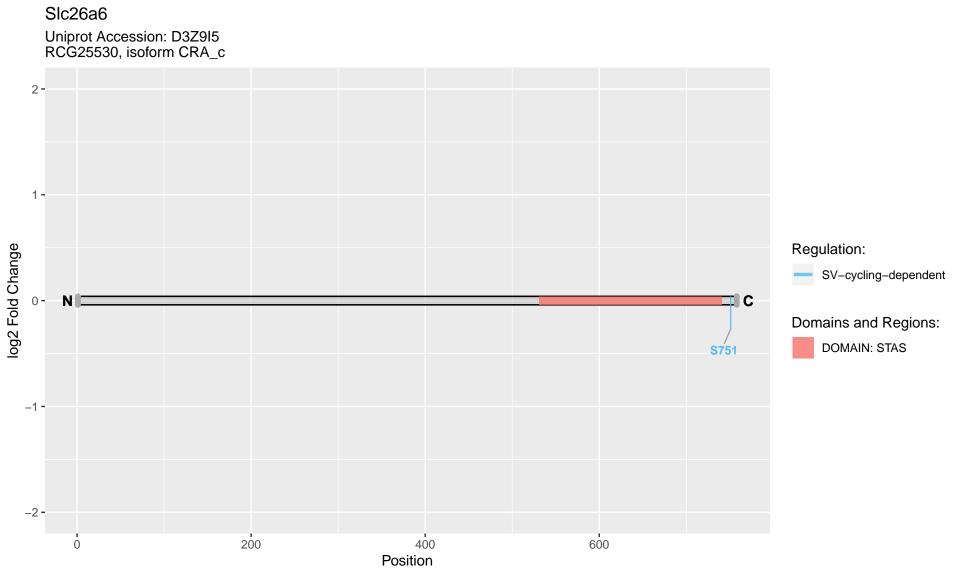


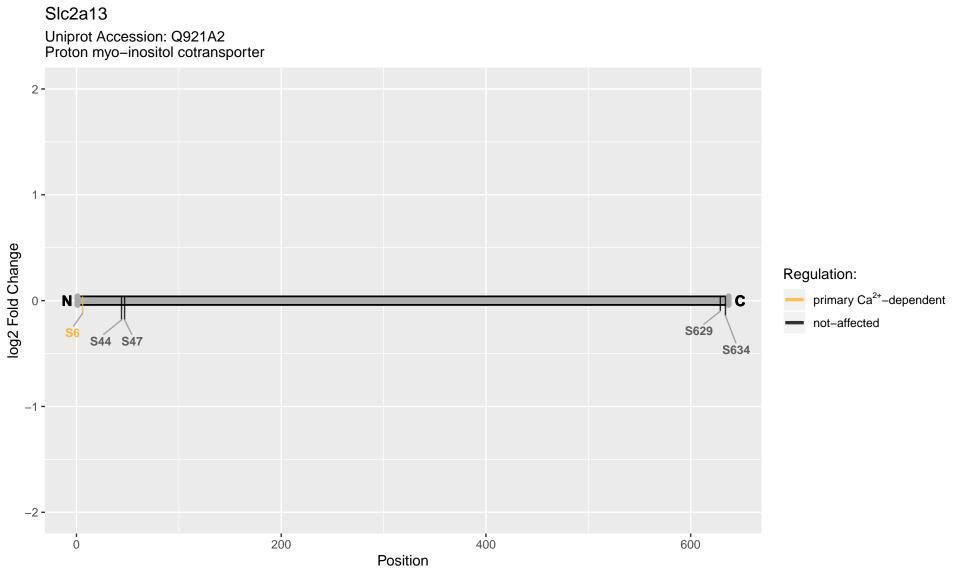


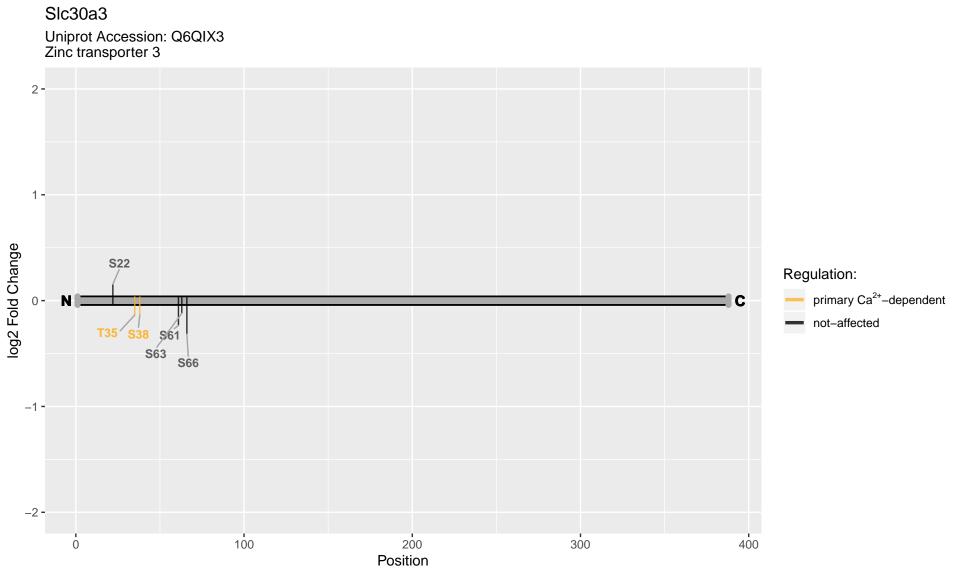


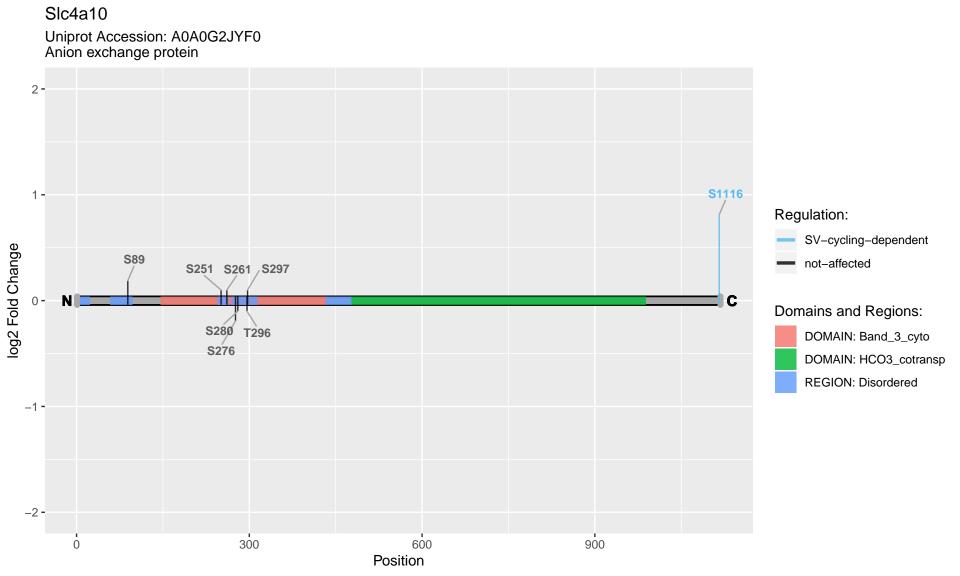


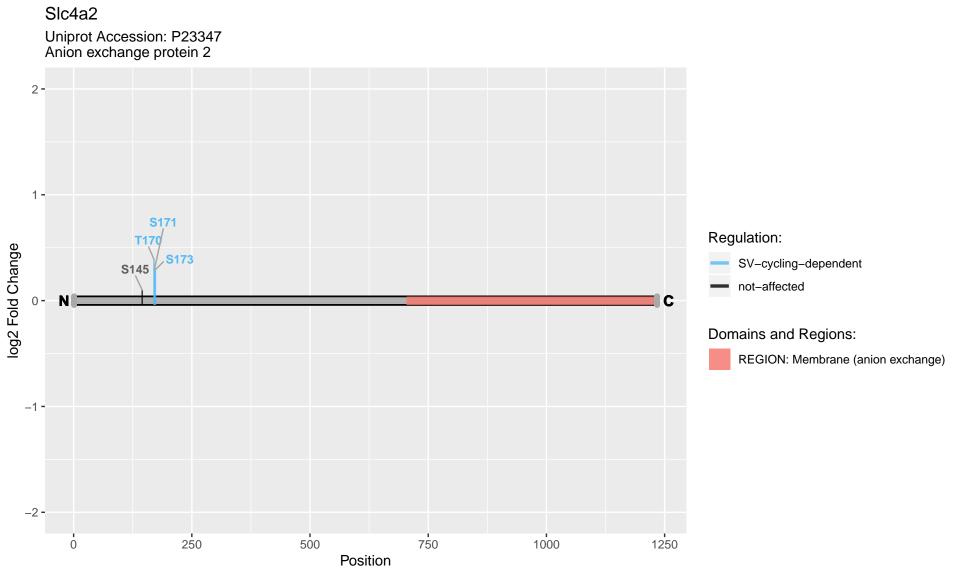


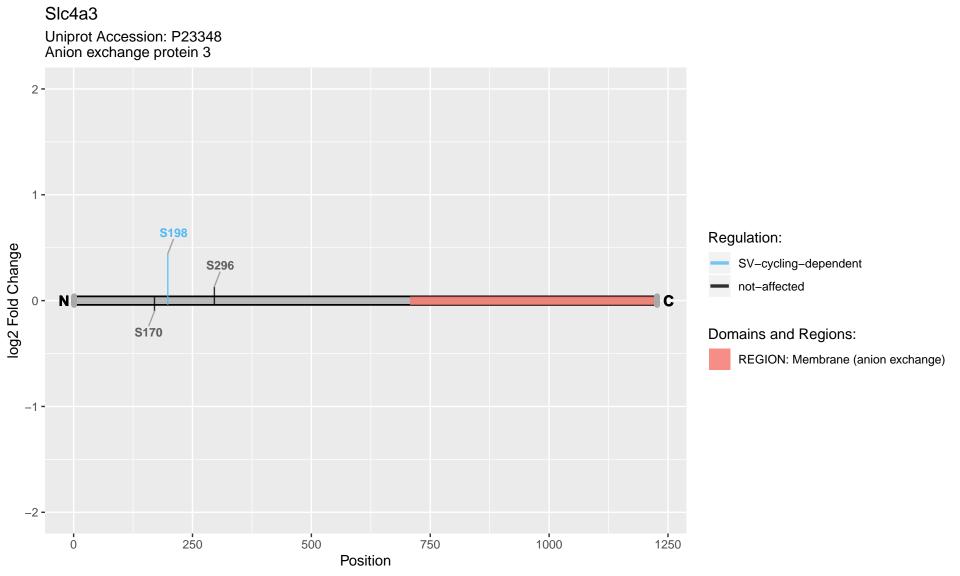


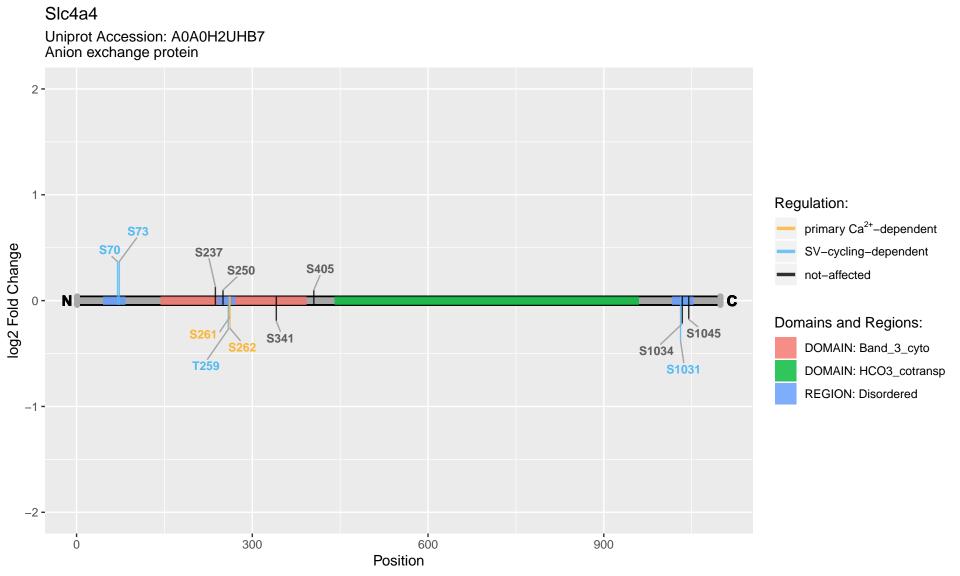


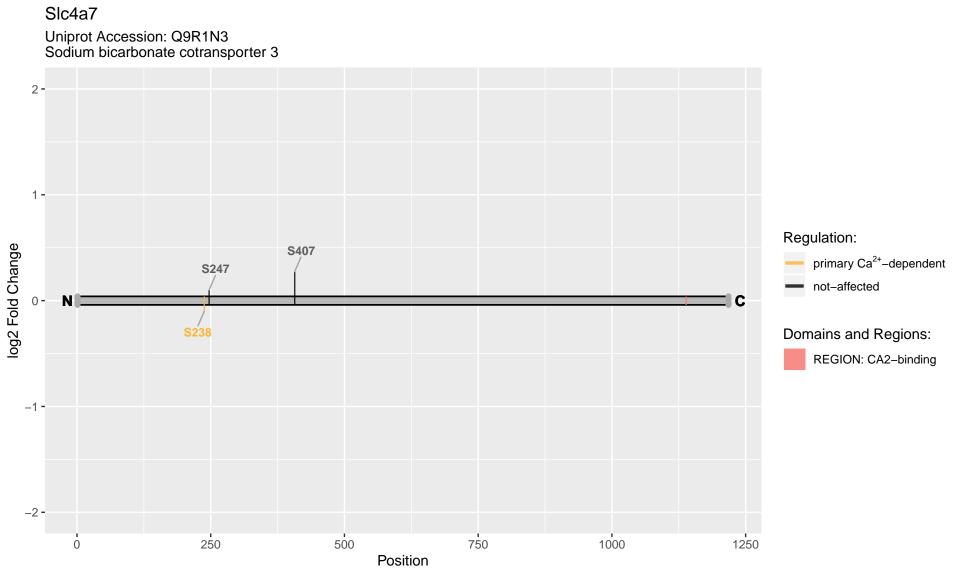


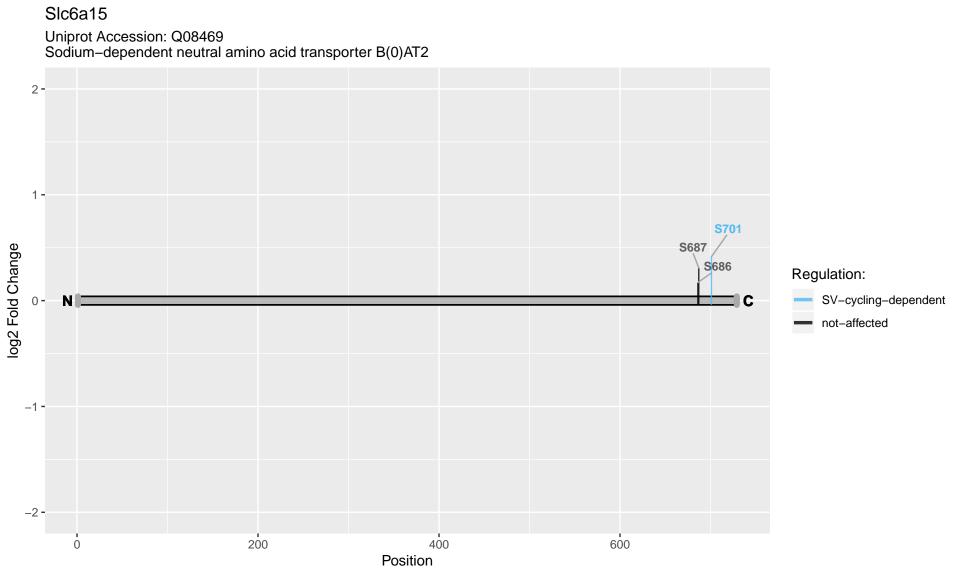


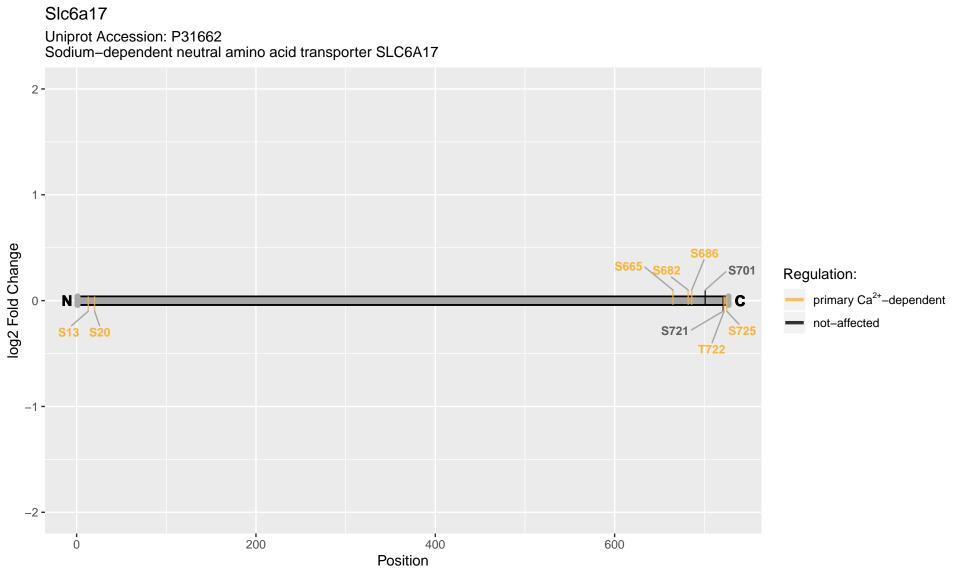


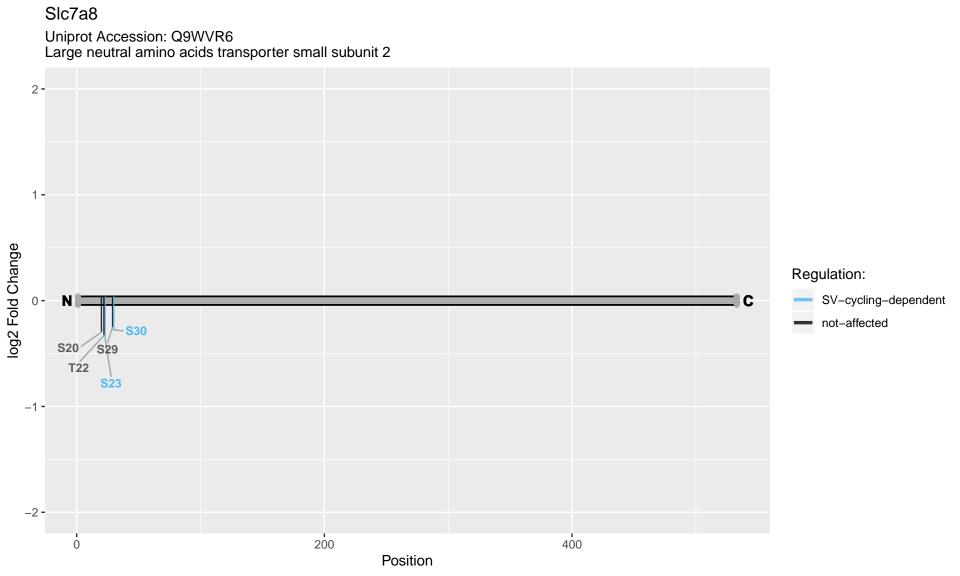


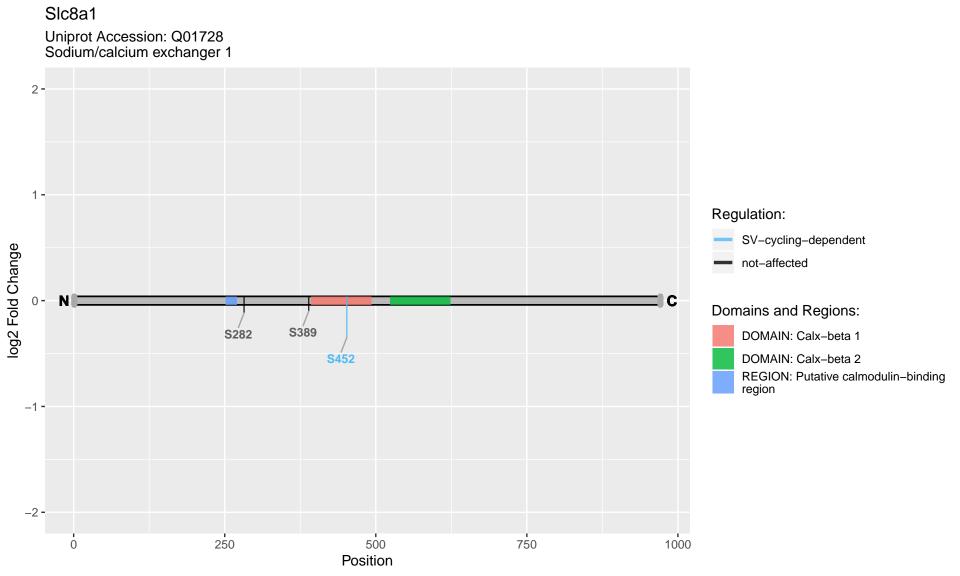


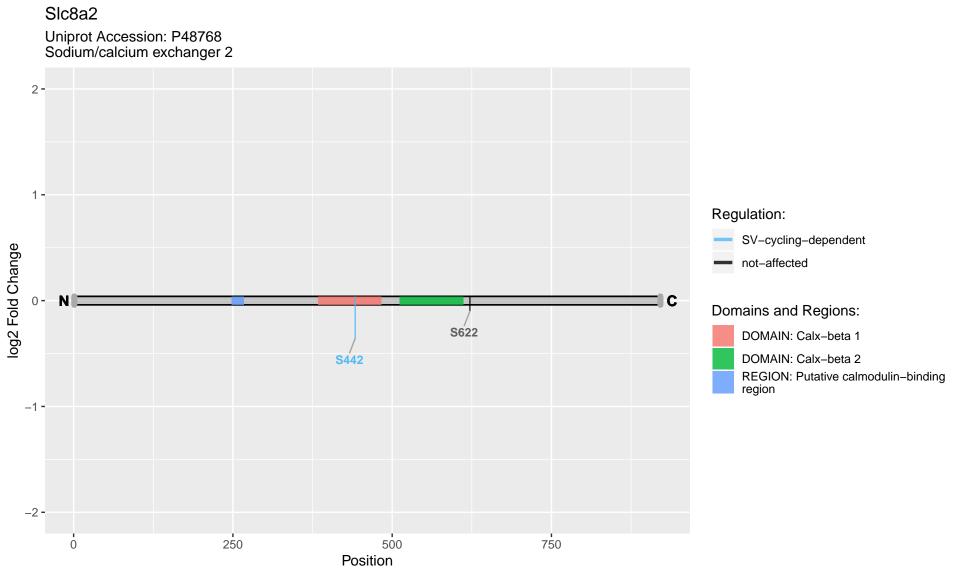


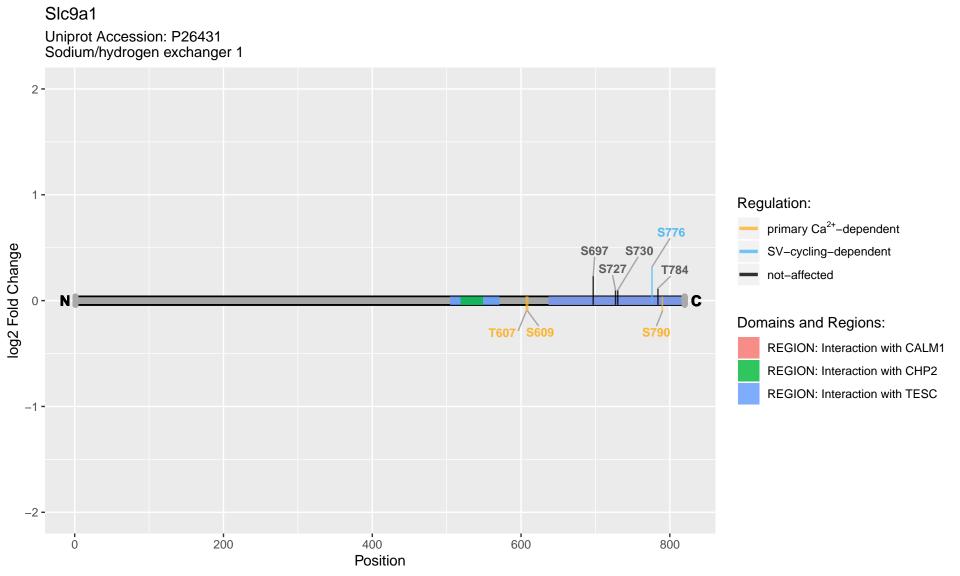


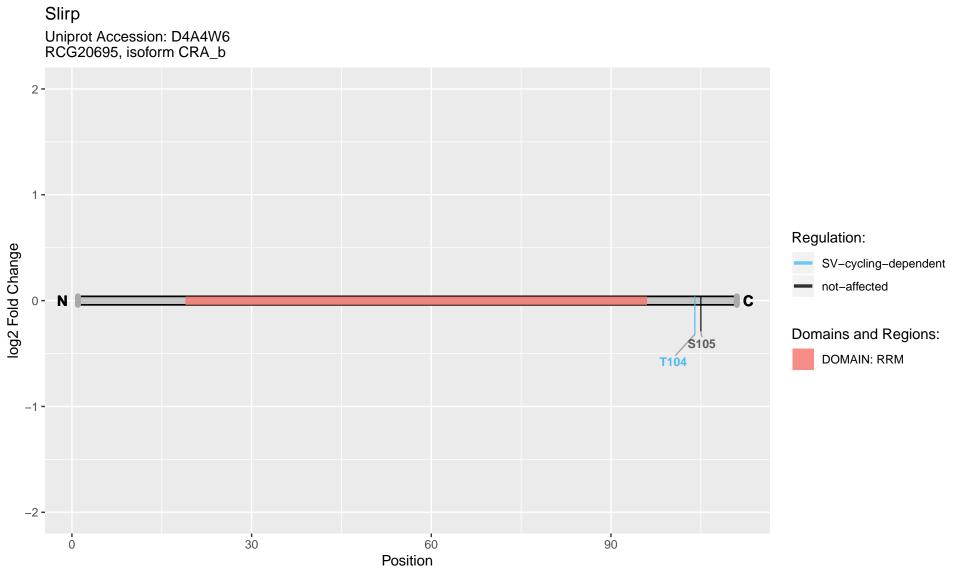


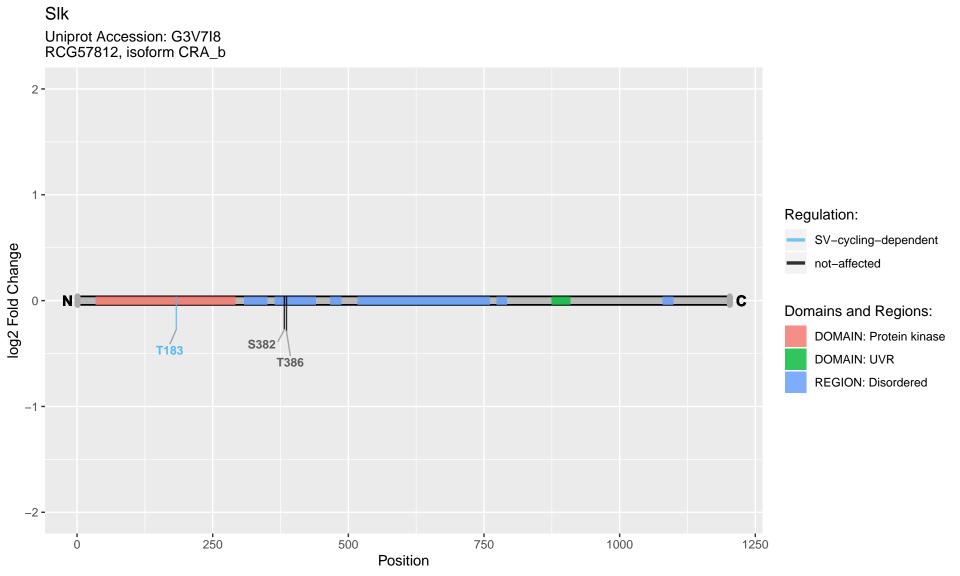


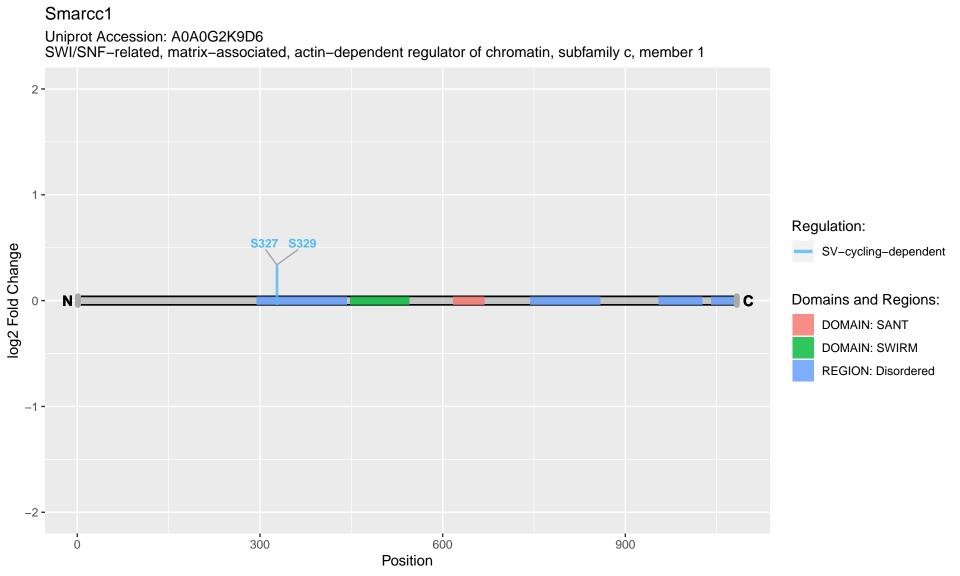


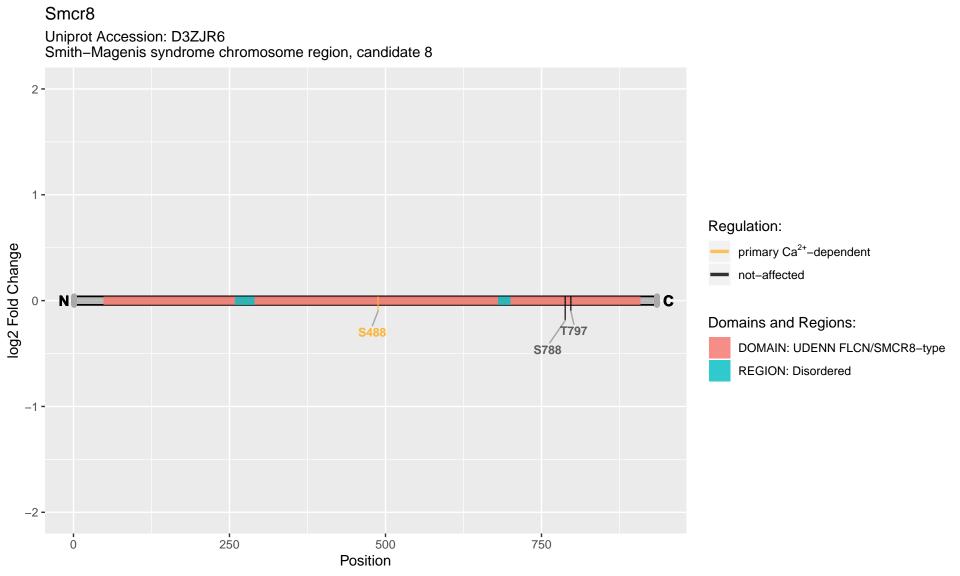


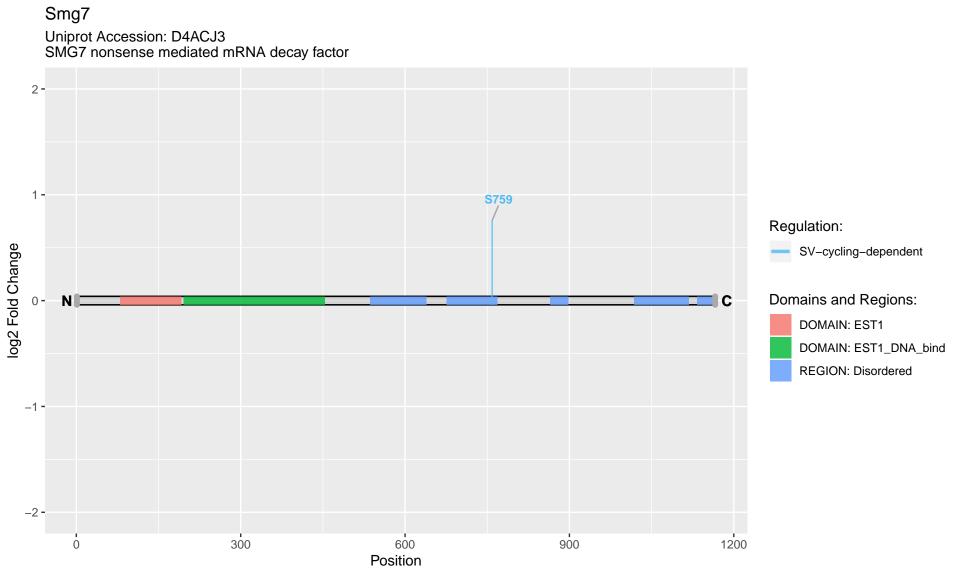


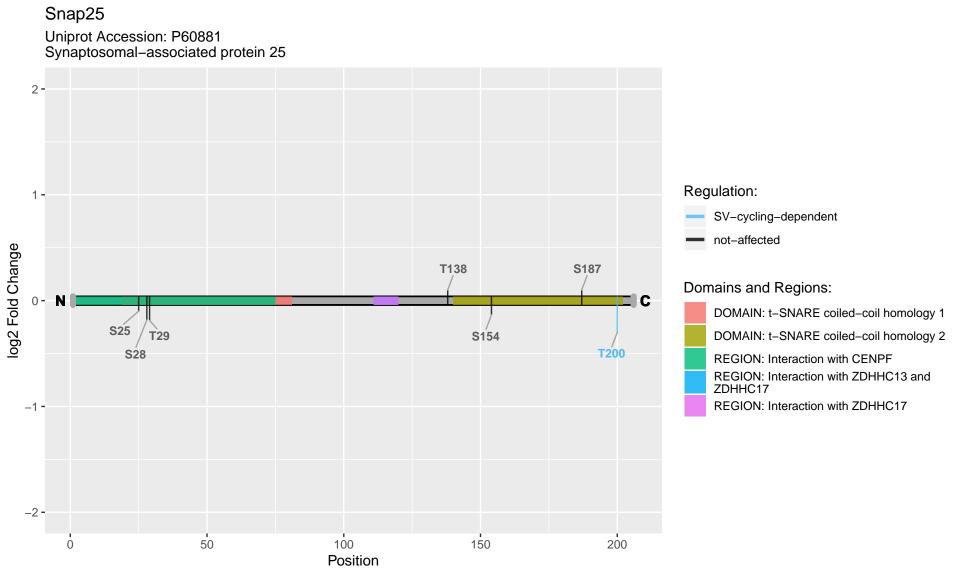


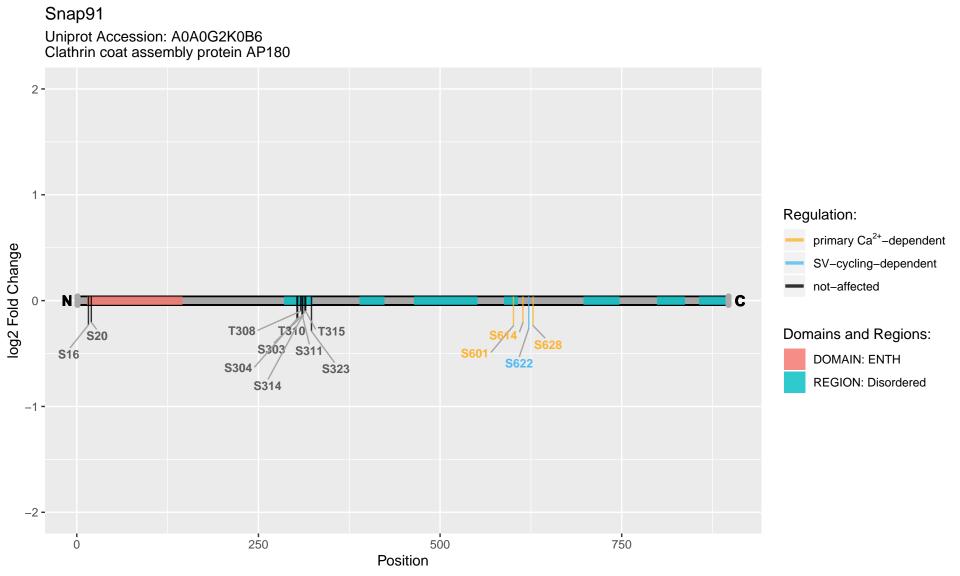


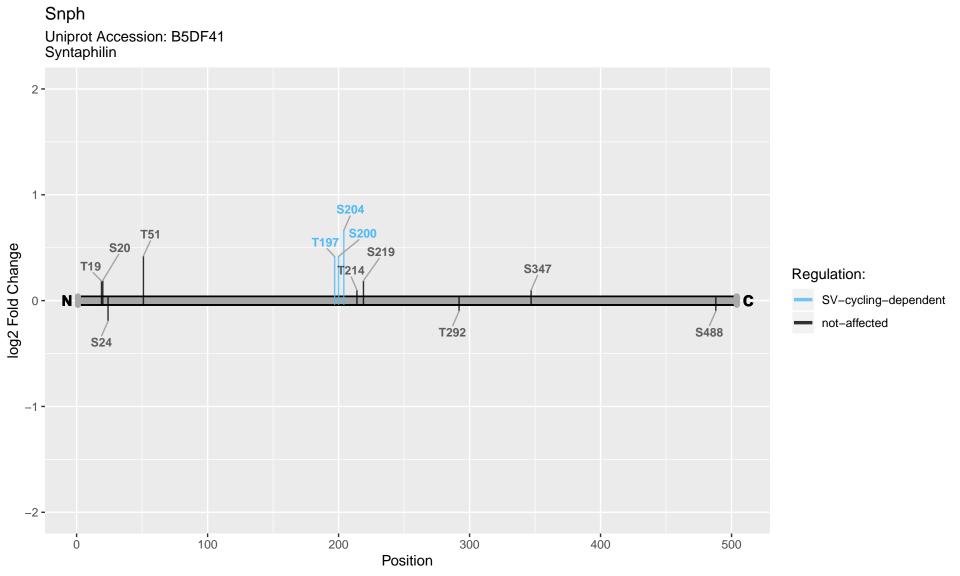


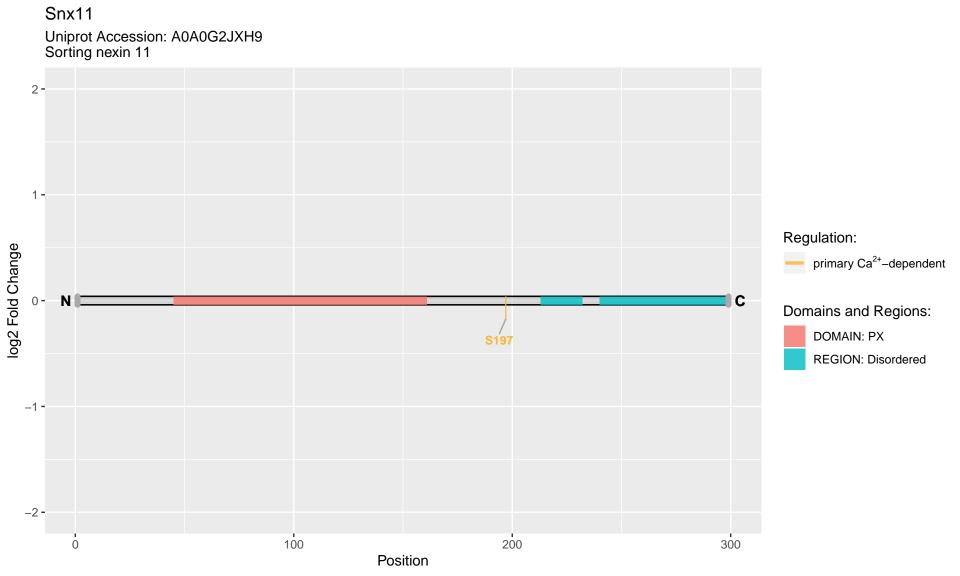


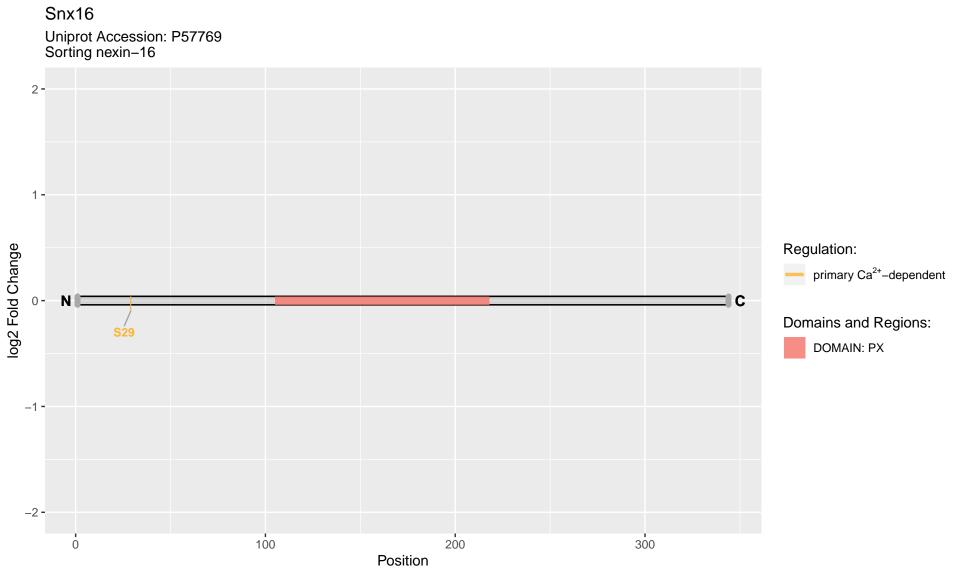


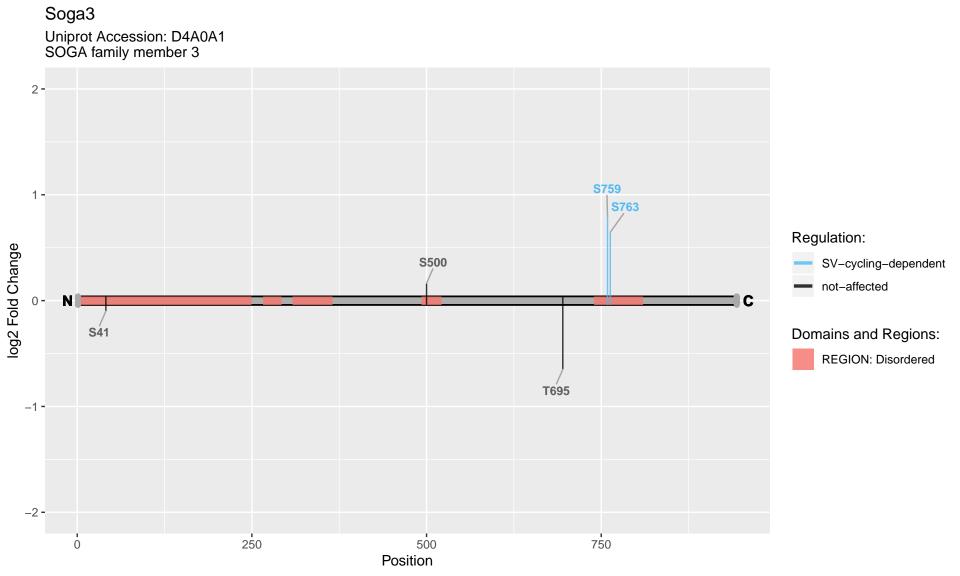




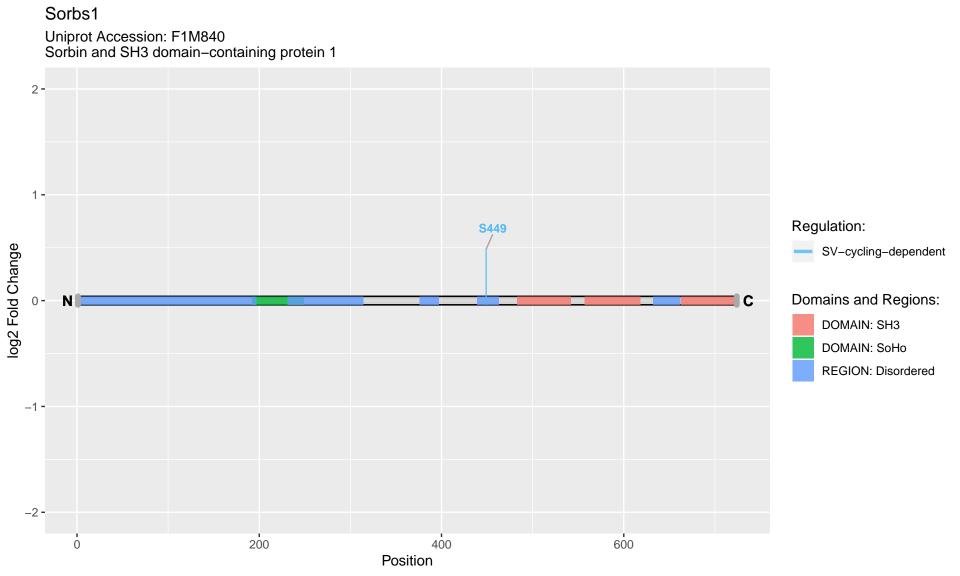


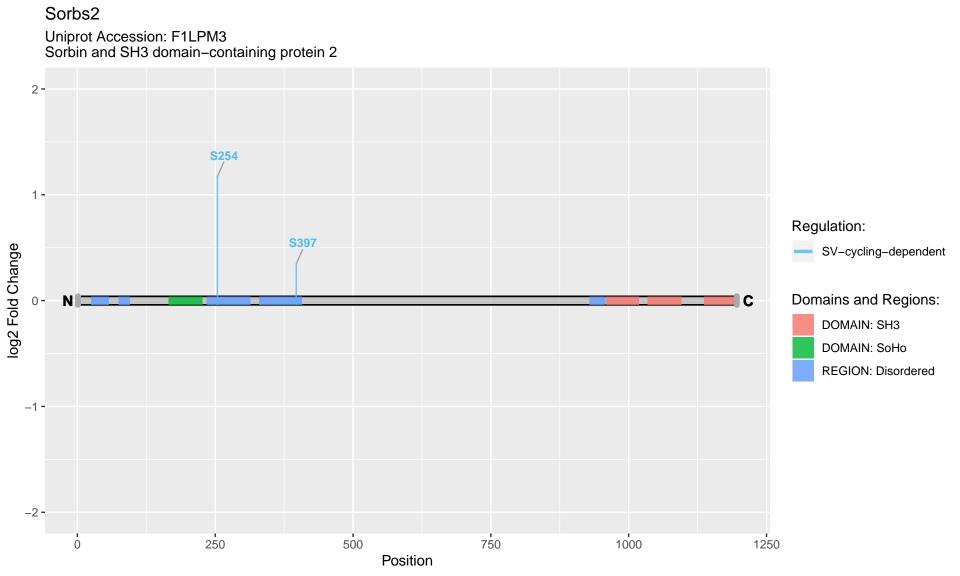


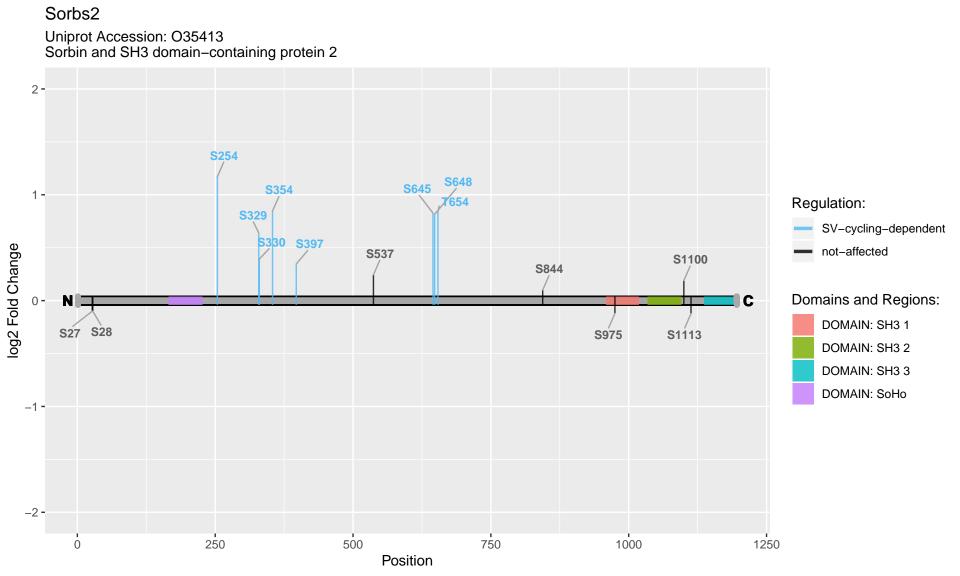


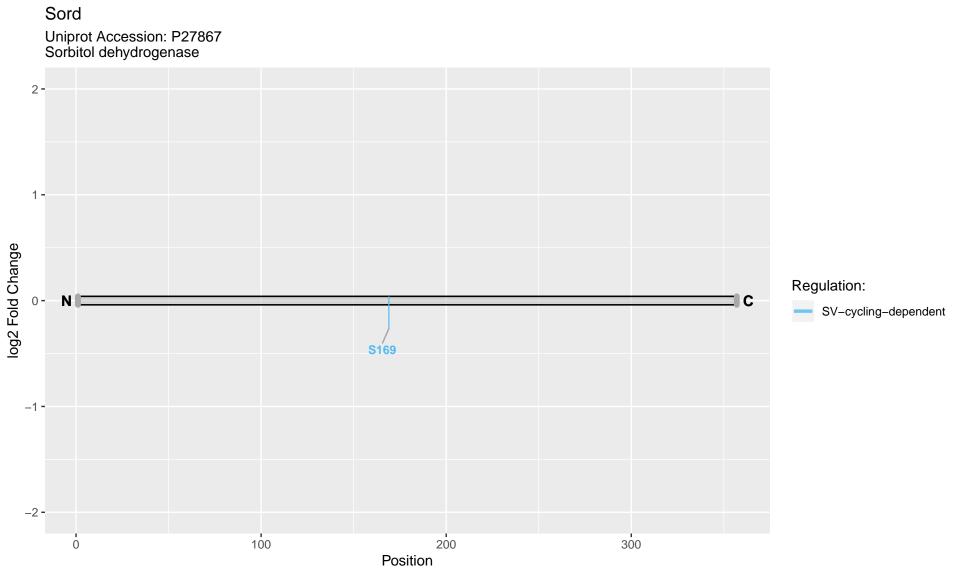


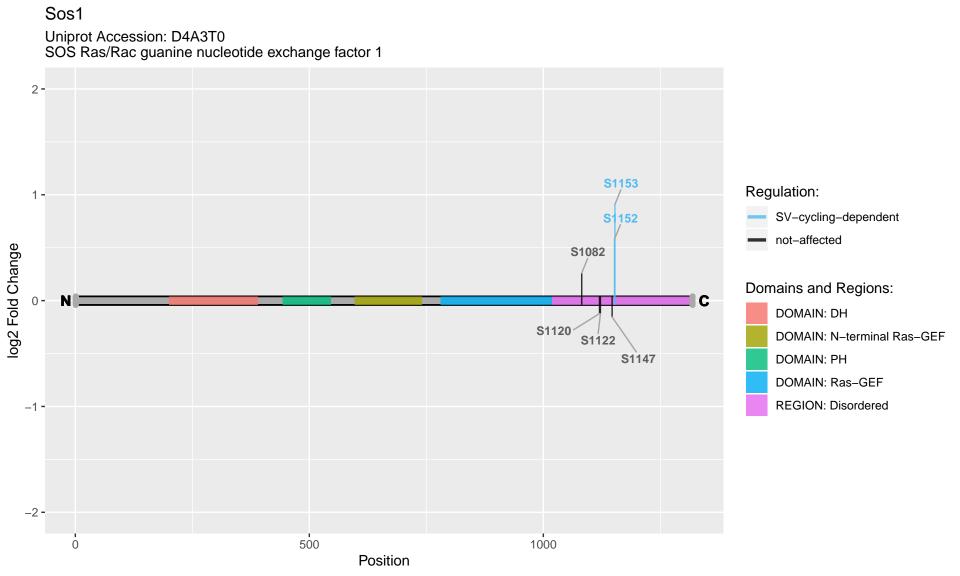
Sorbs1 Uniprot Accession: F1M820 Sorbin and SH3 domain-containing protein 1 2 -**S55 S62** Regulation: primary Ca²⁺-dependent **S470 S794 S707** log2 Fold Change **S268** SV-cycling-dependent S270 Y274 **S1209 S692** not-affected C Domains and Regions: T286 DOMAIN: SH3 DOMAIN: SoHo **REGION: Disordered** -1 **-**-2 **-**500 1000 Position

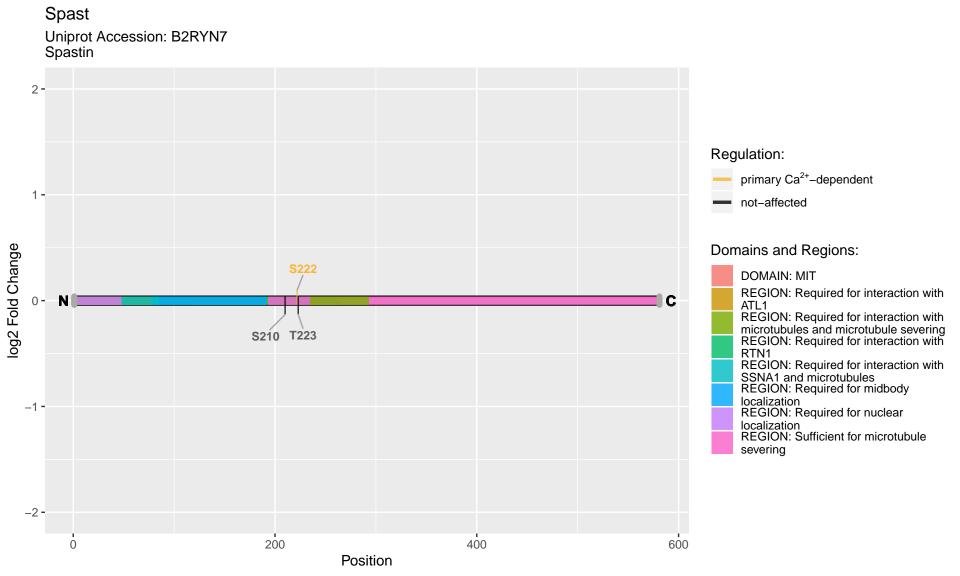


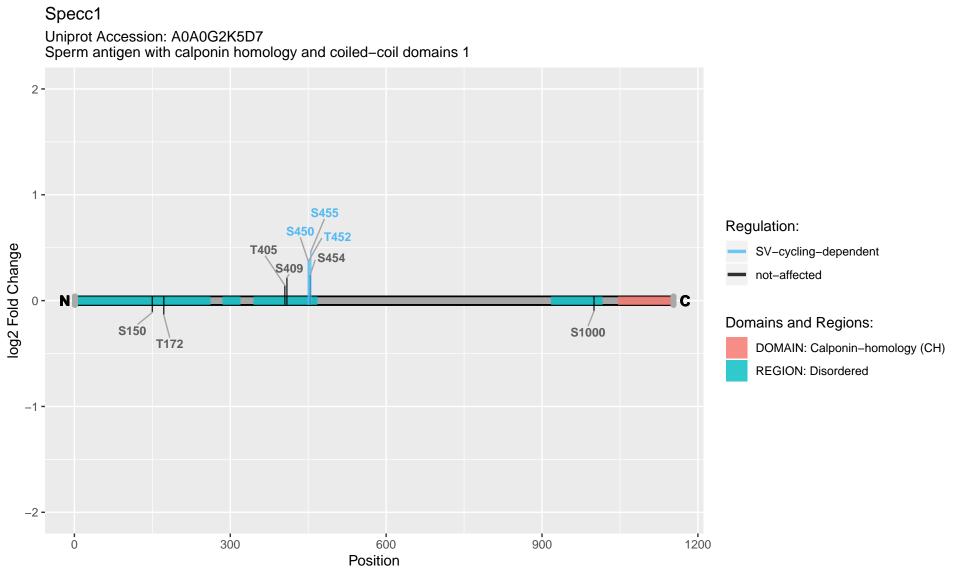


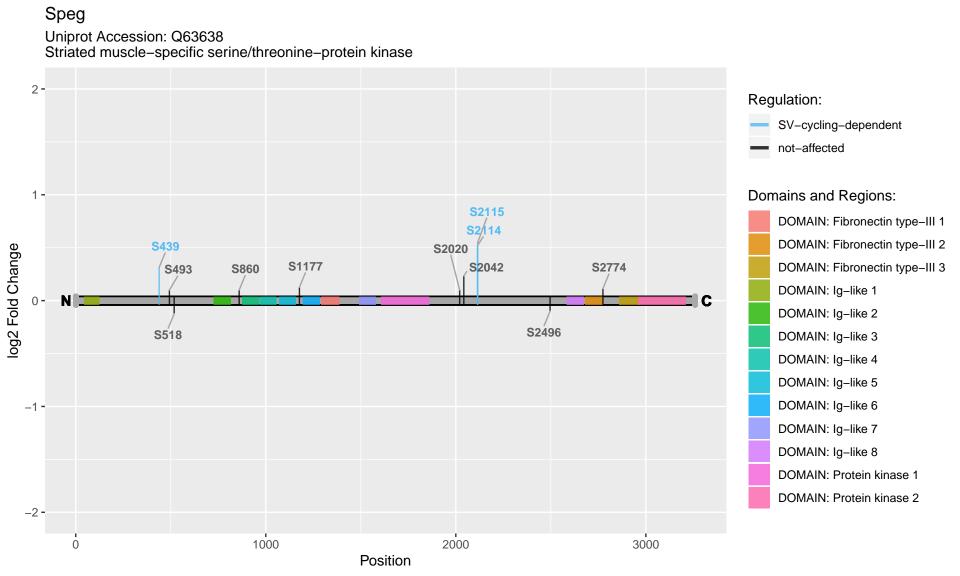


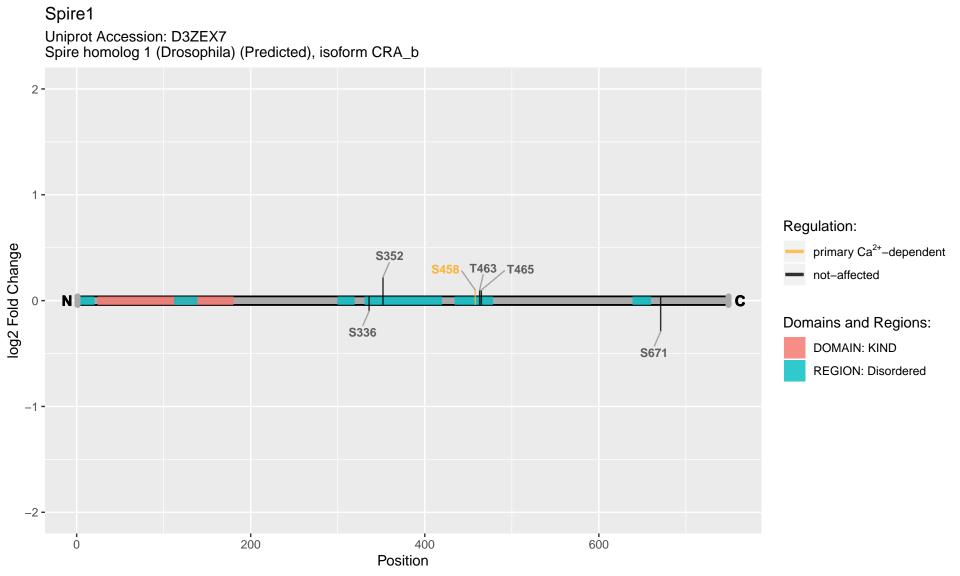


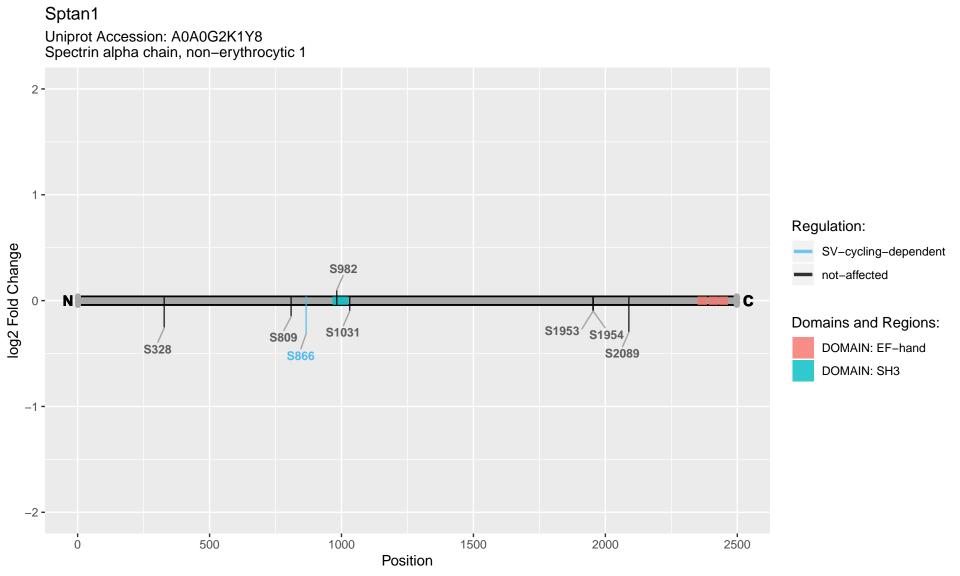


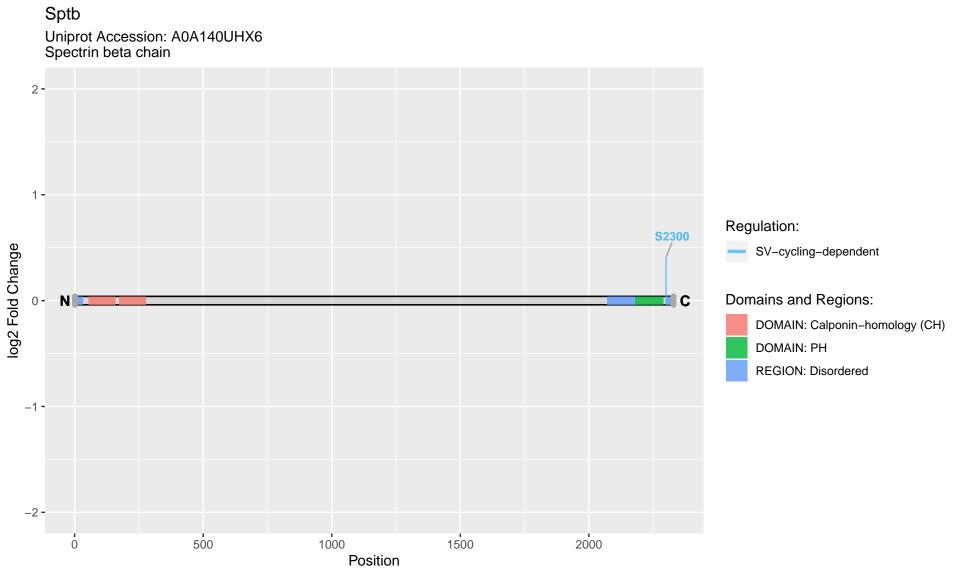


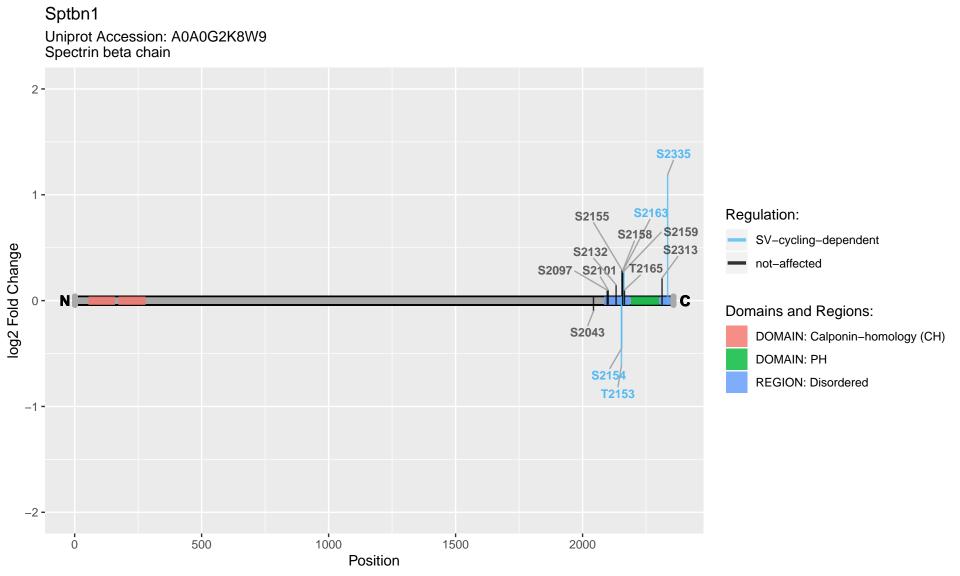


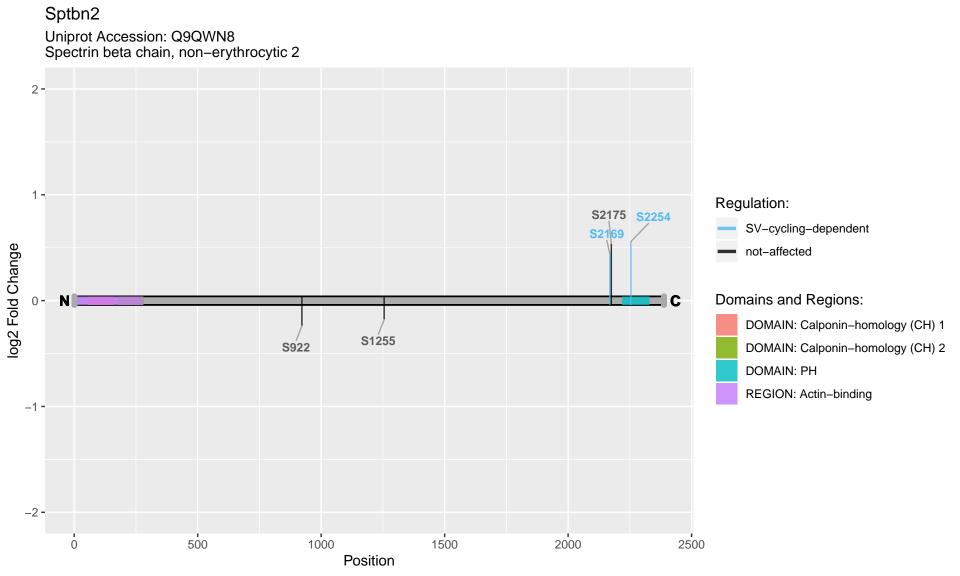


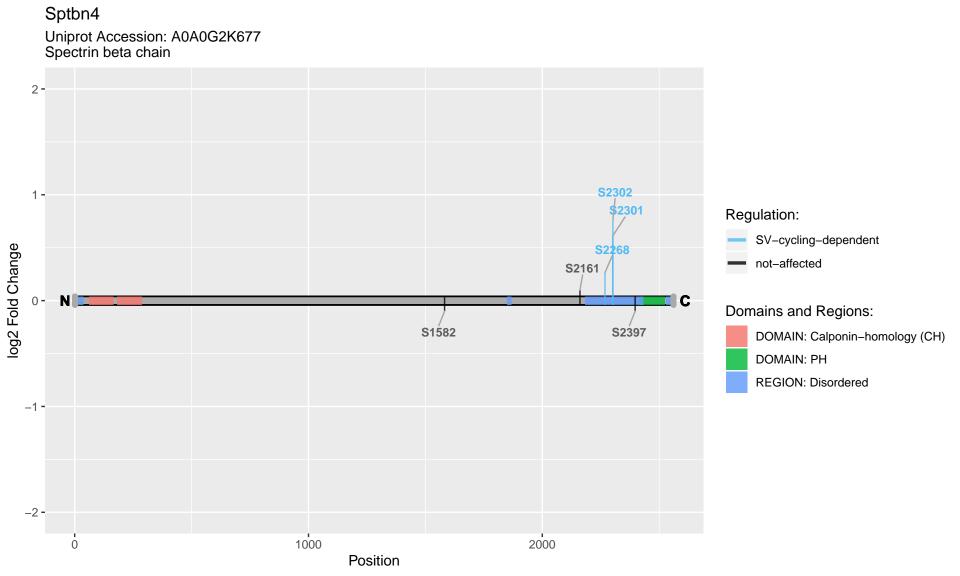


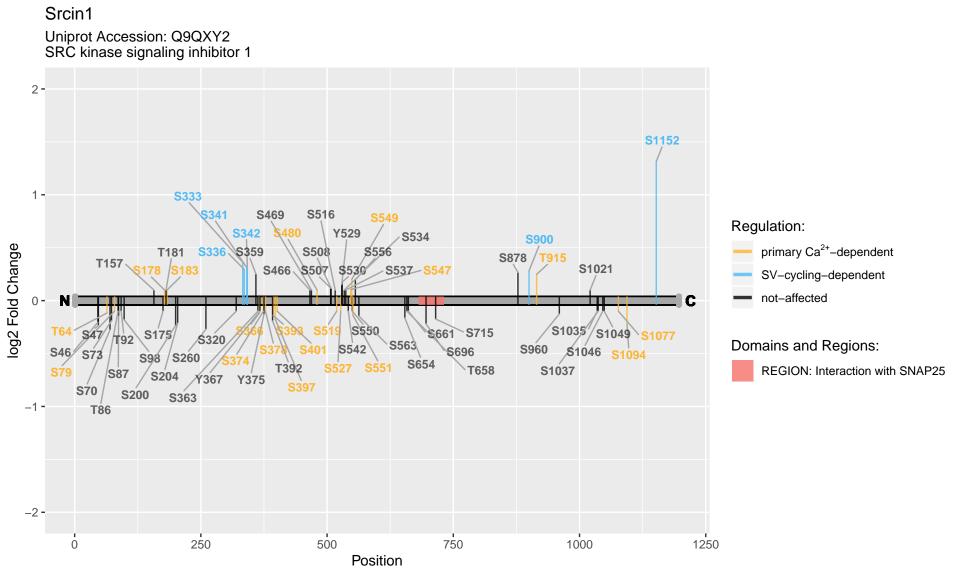


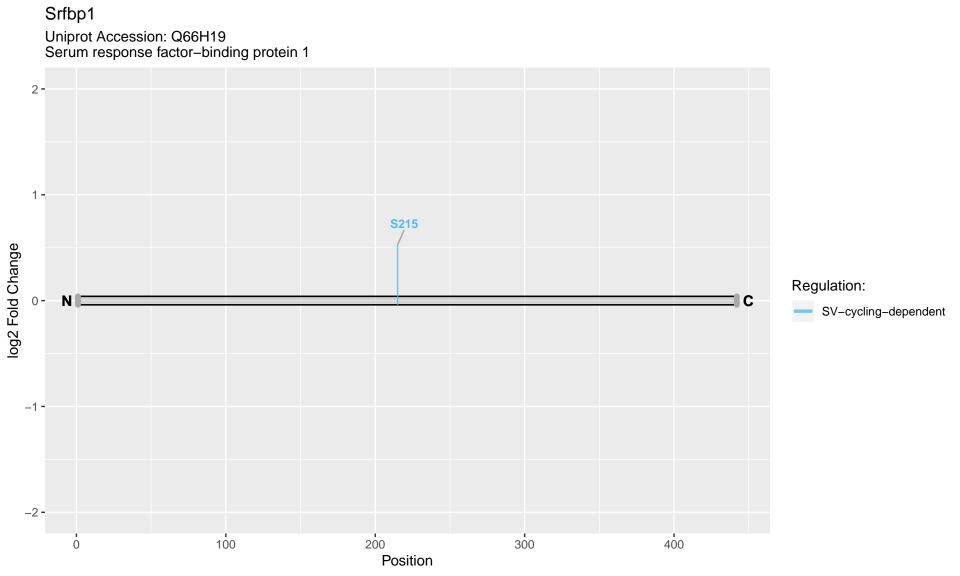


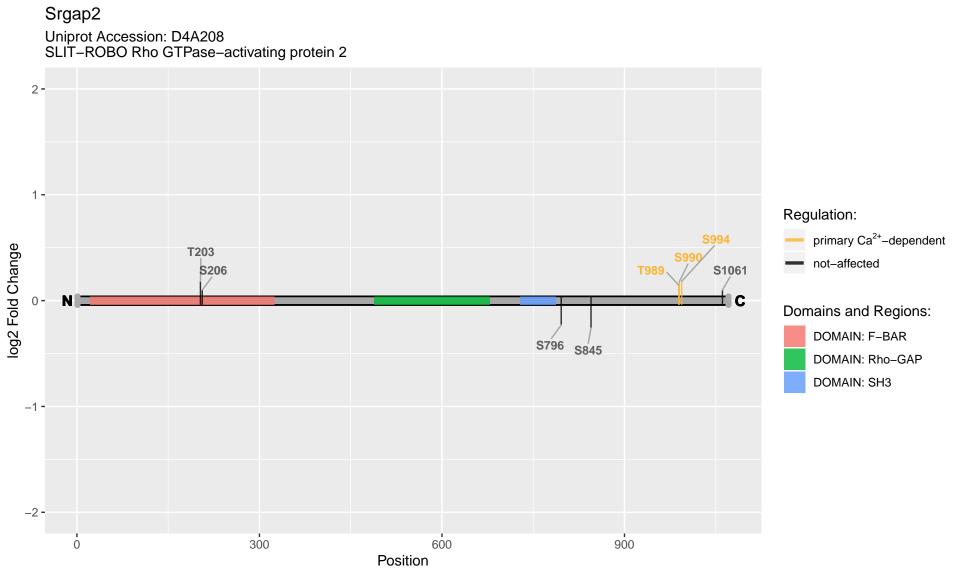


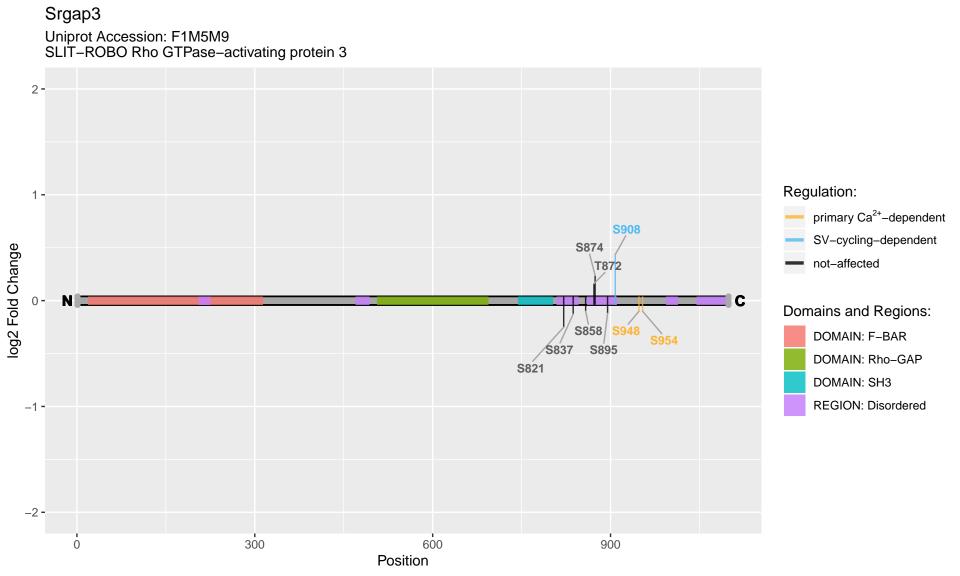


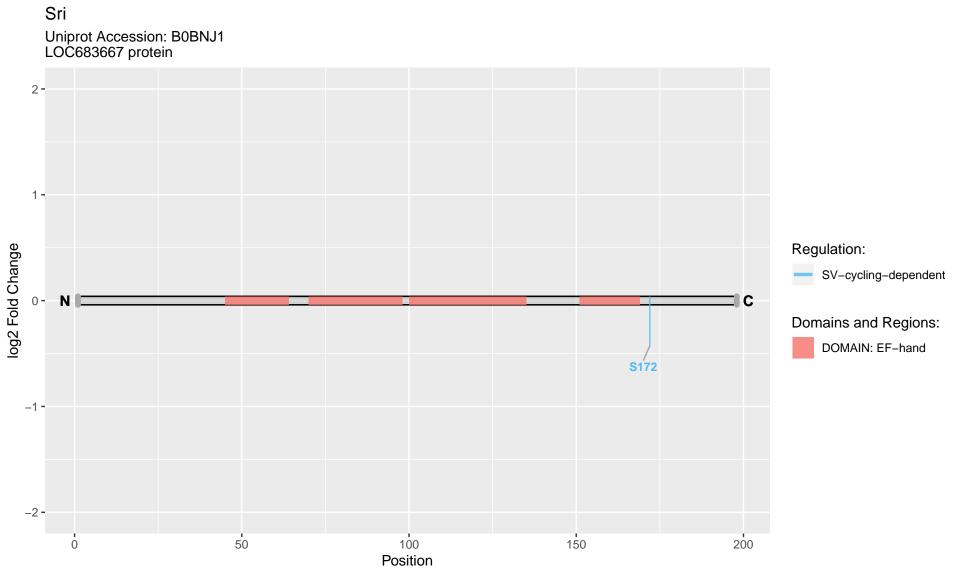


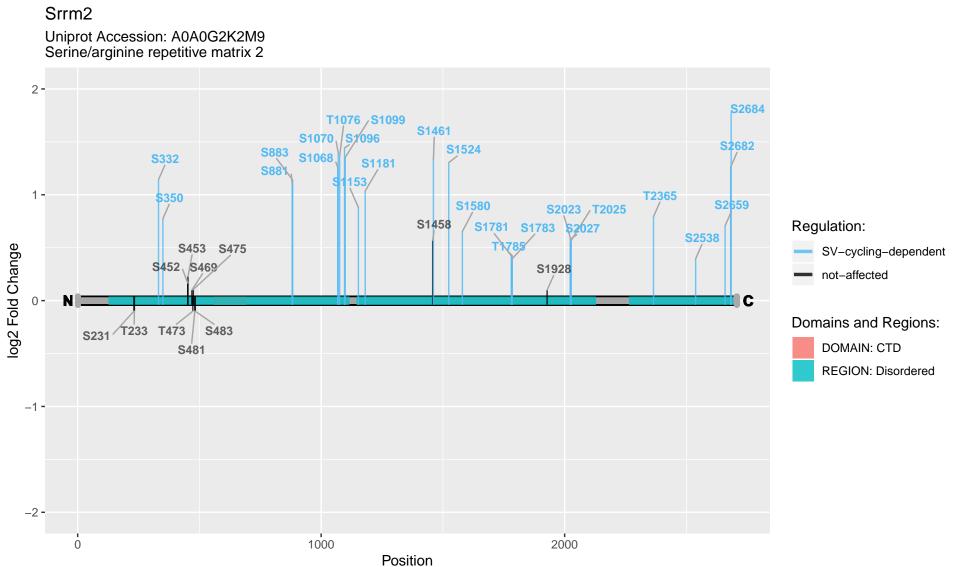


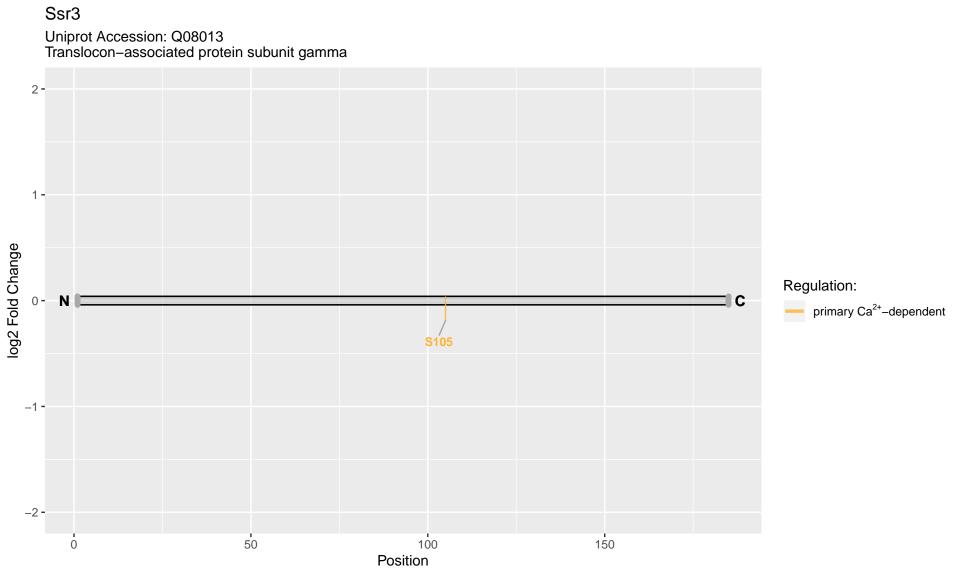


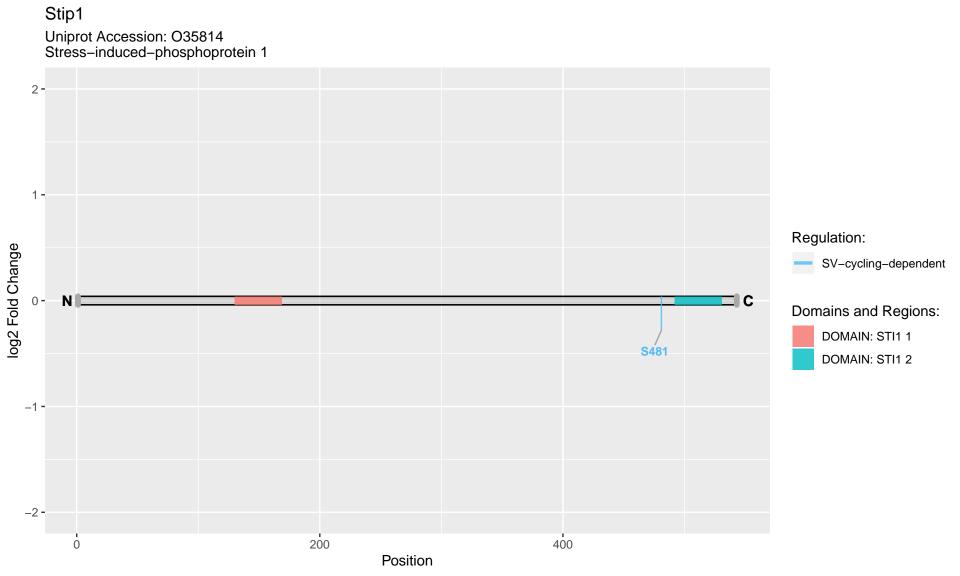


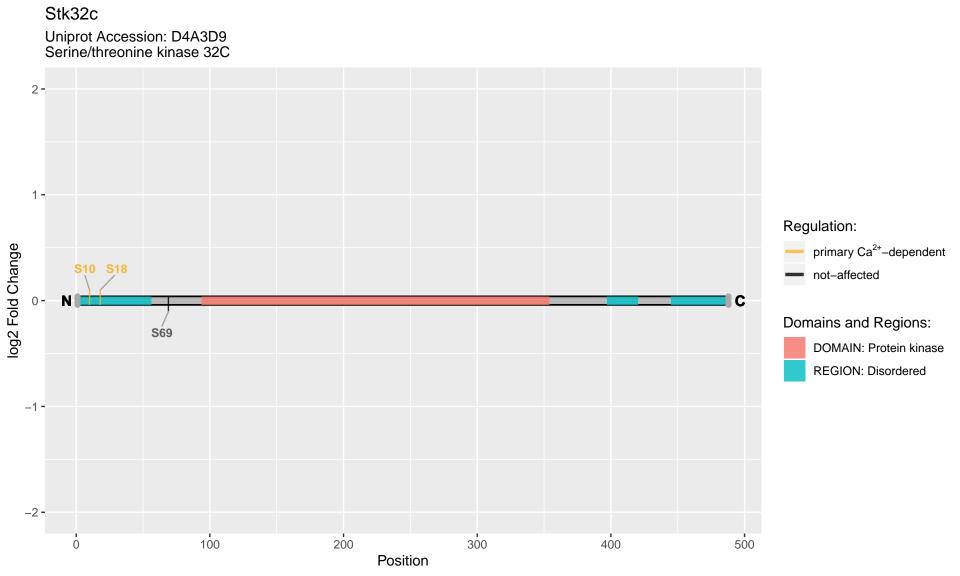


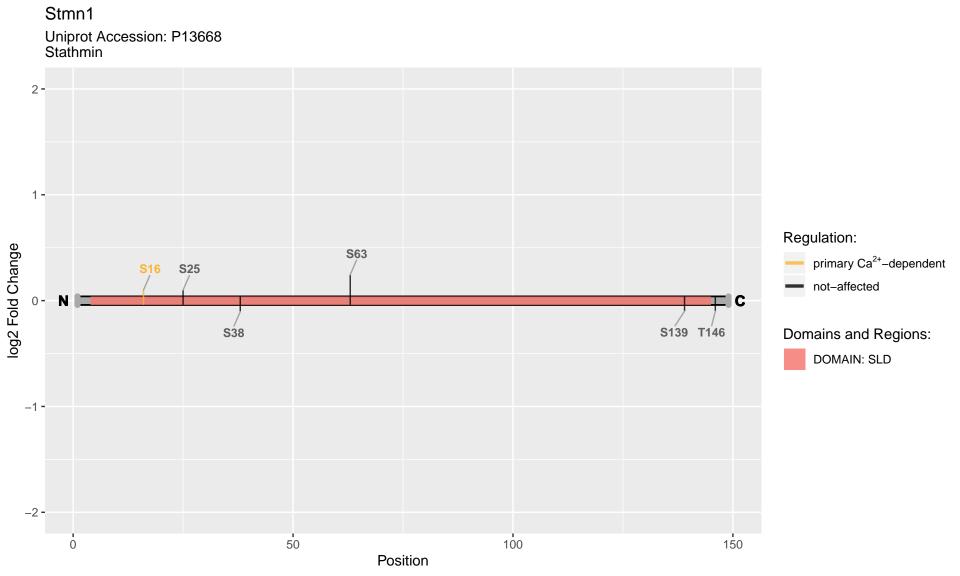


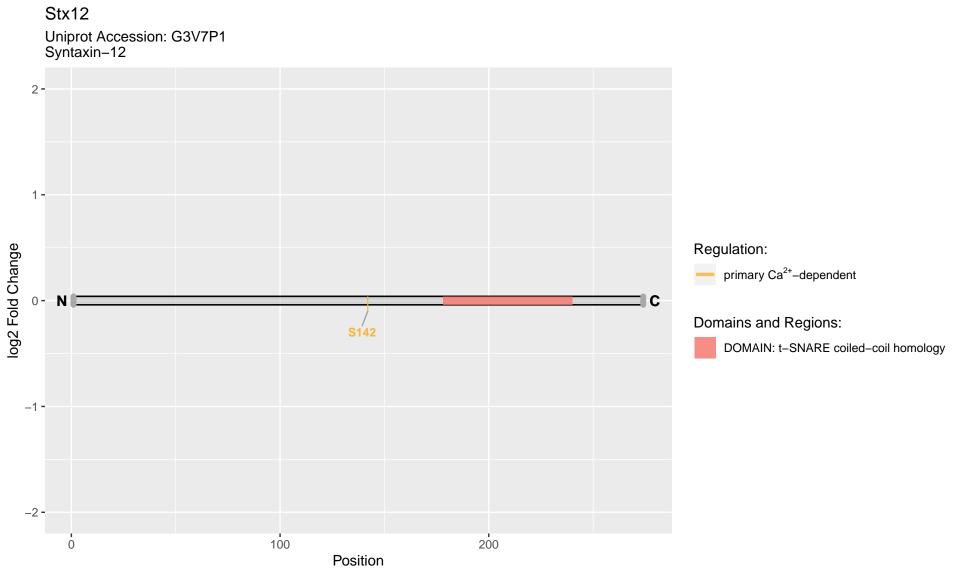


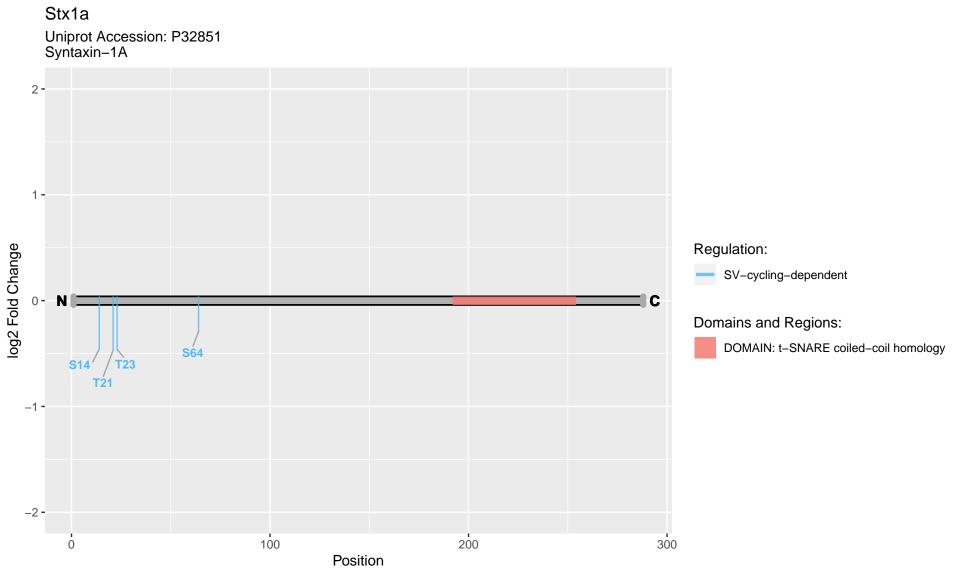


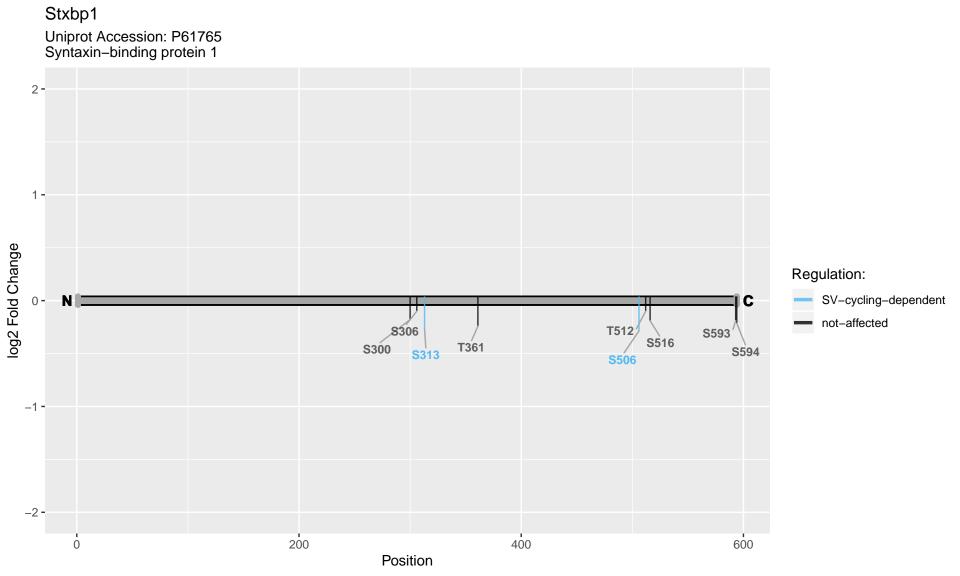


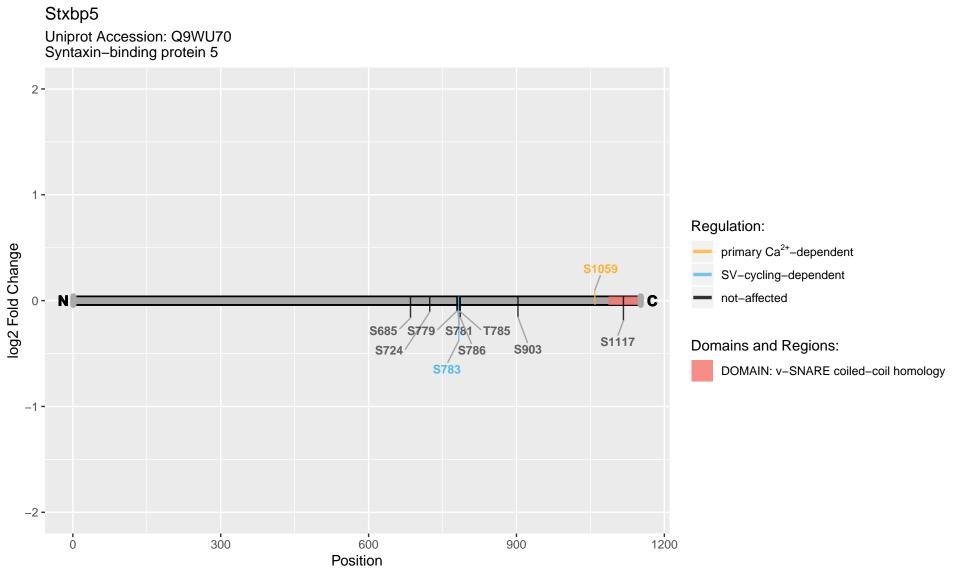


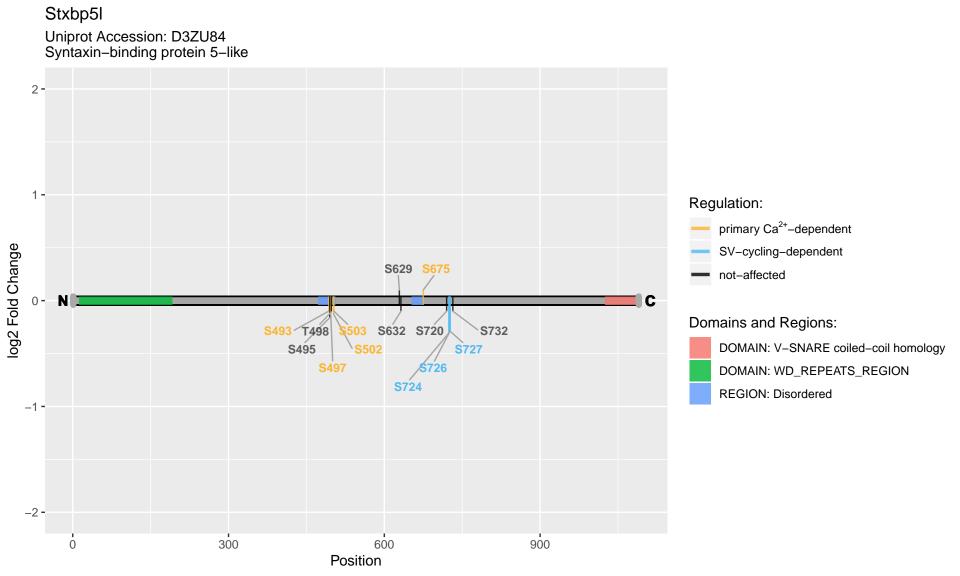


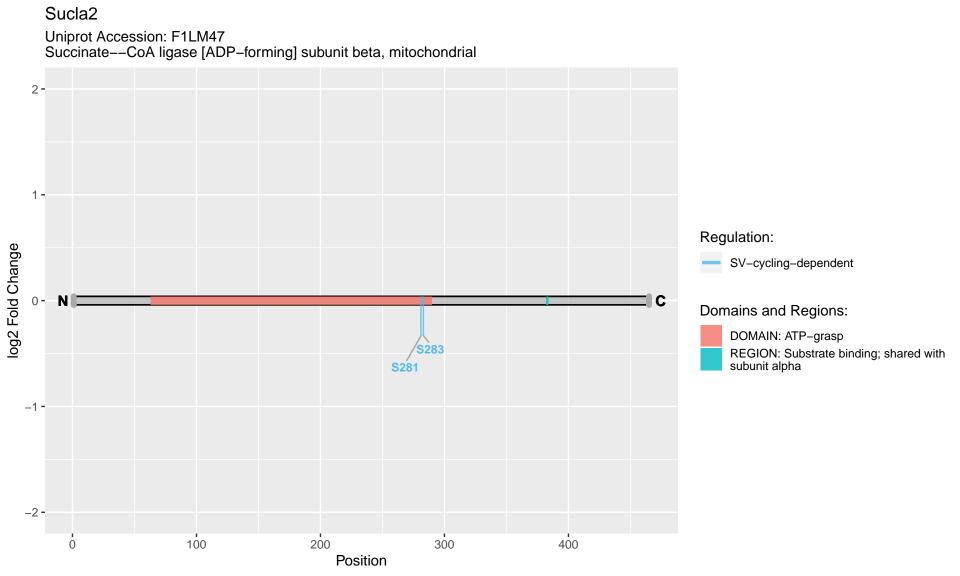


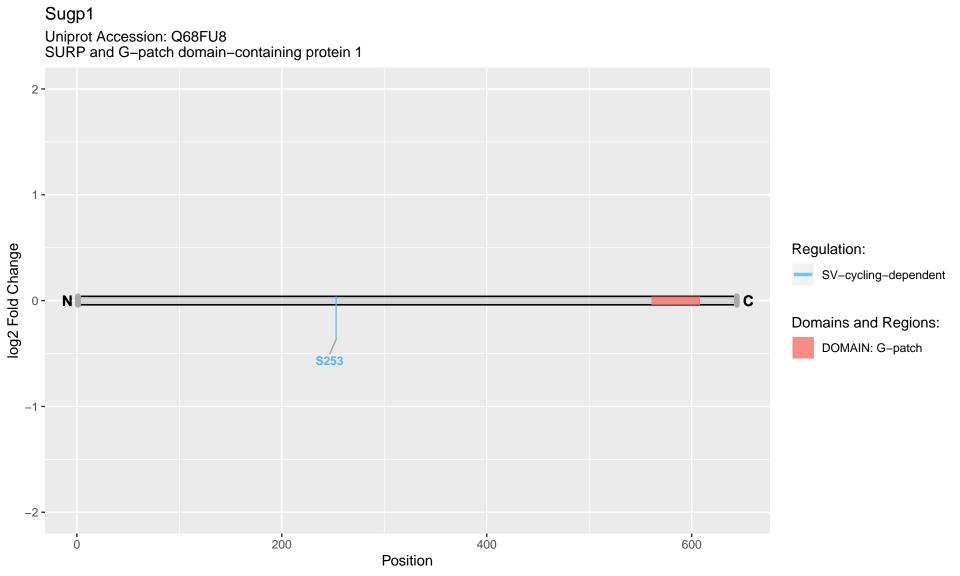


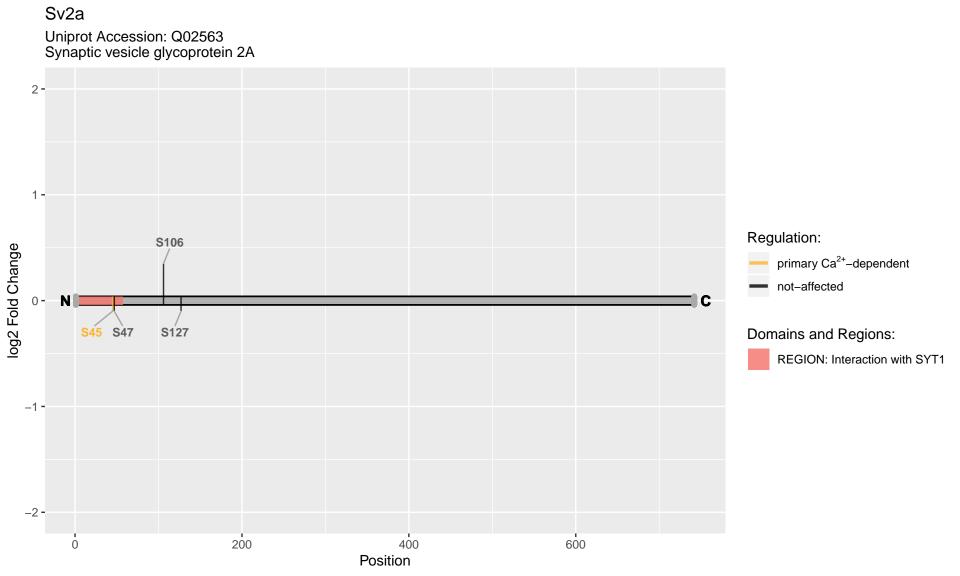


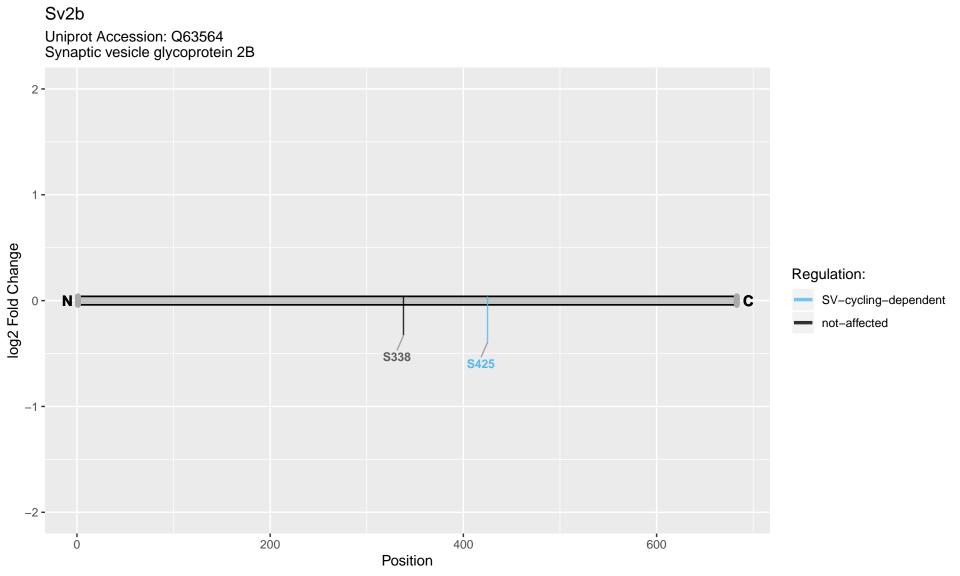


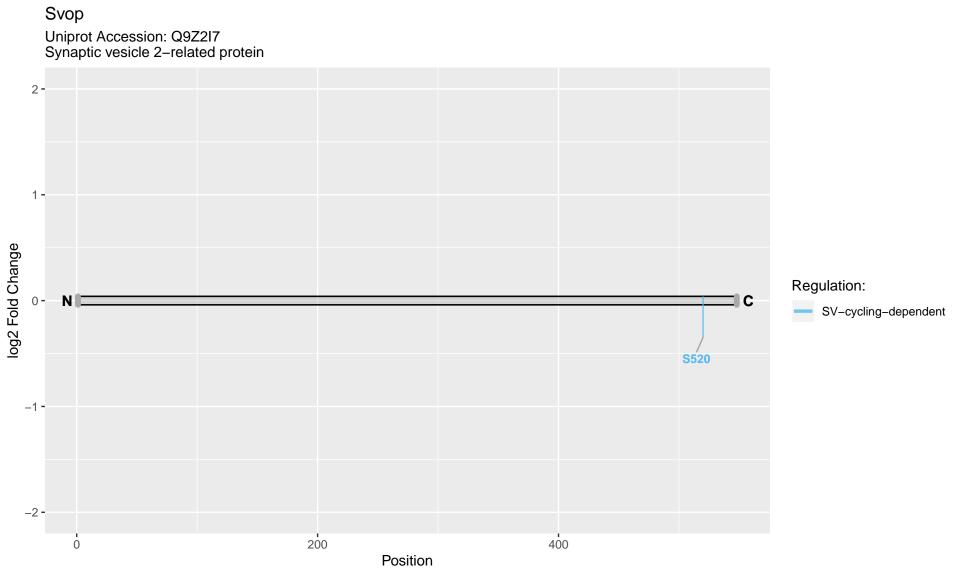


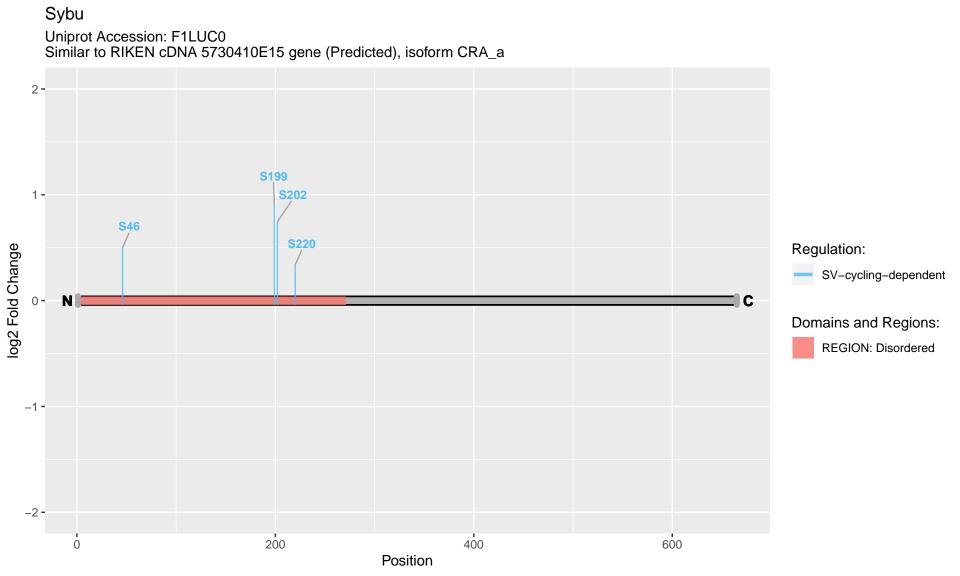


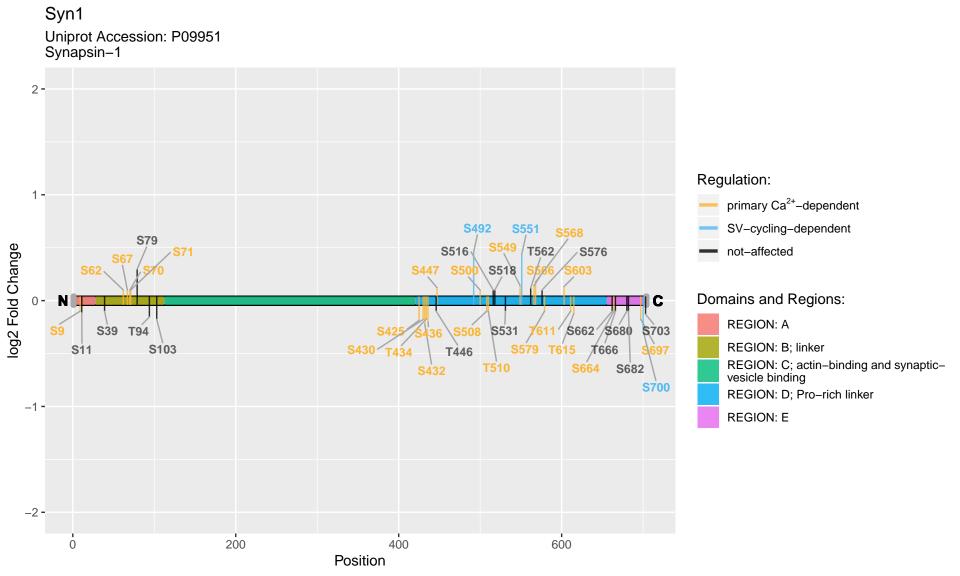


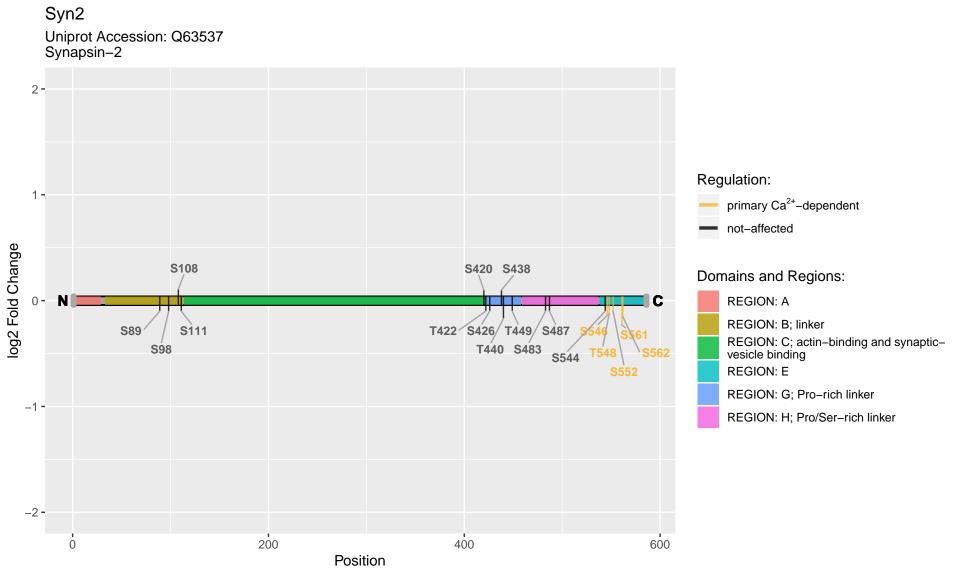


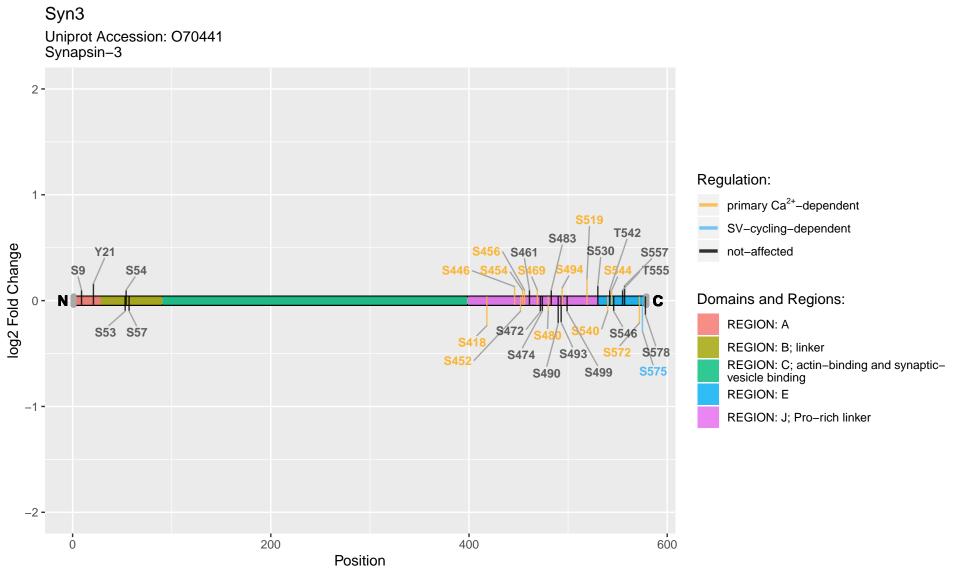


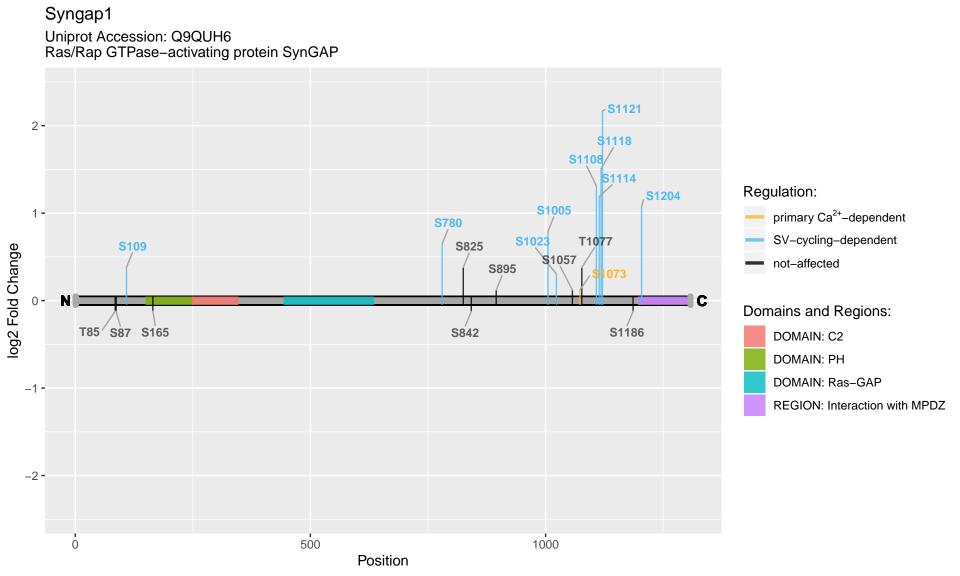


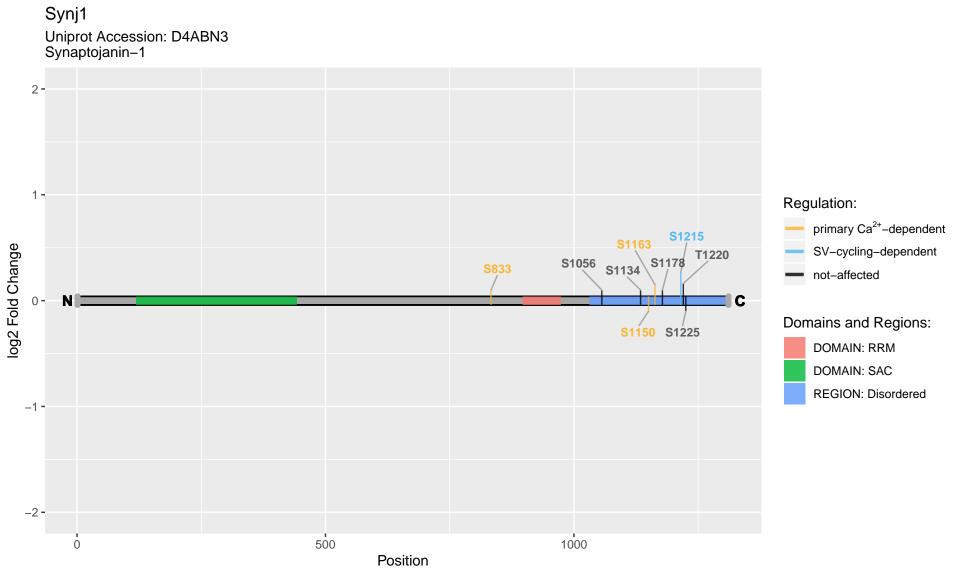


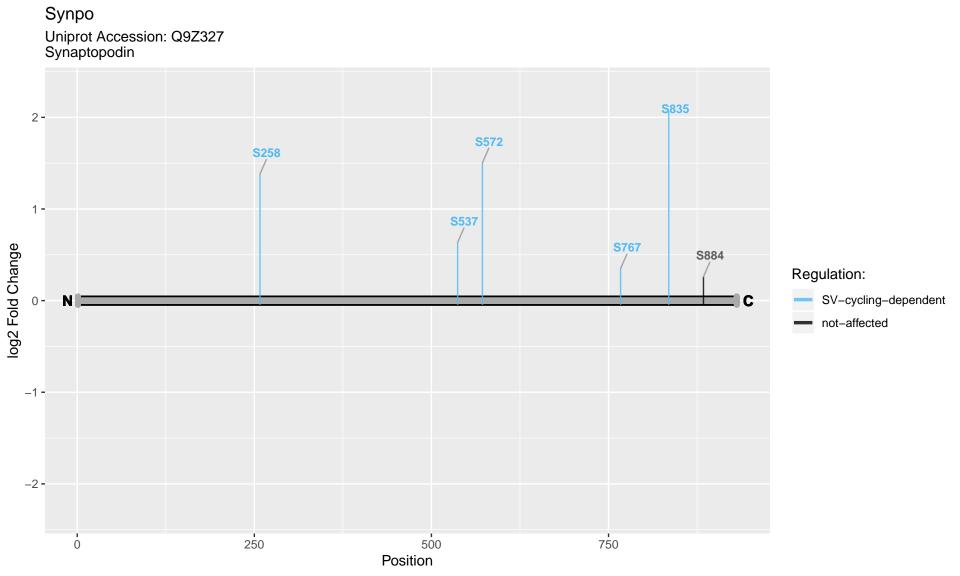


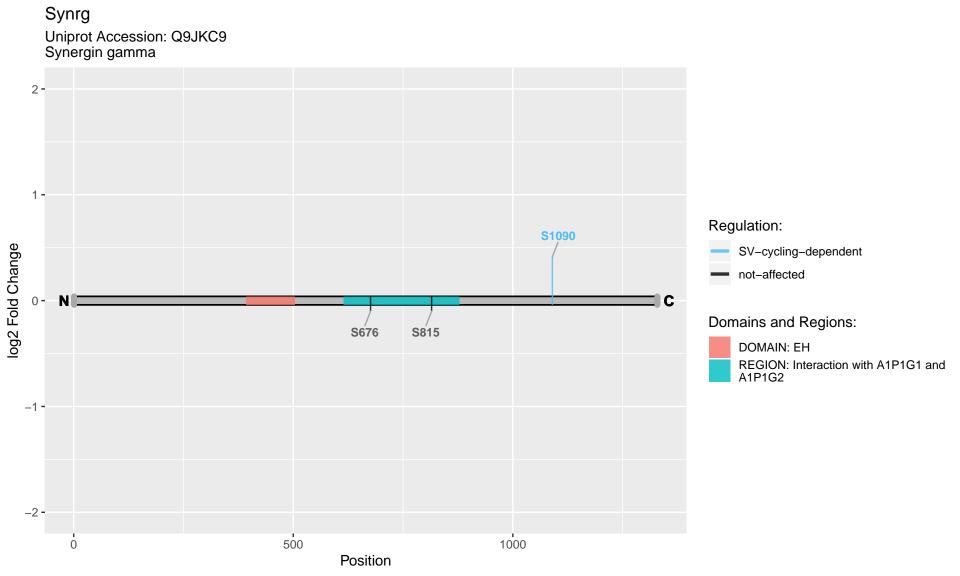


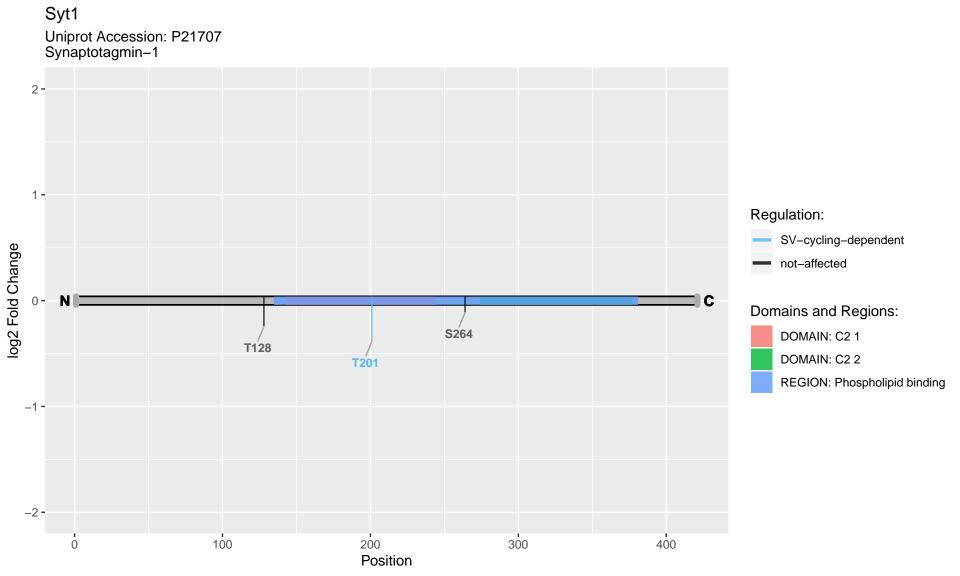


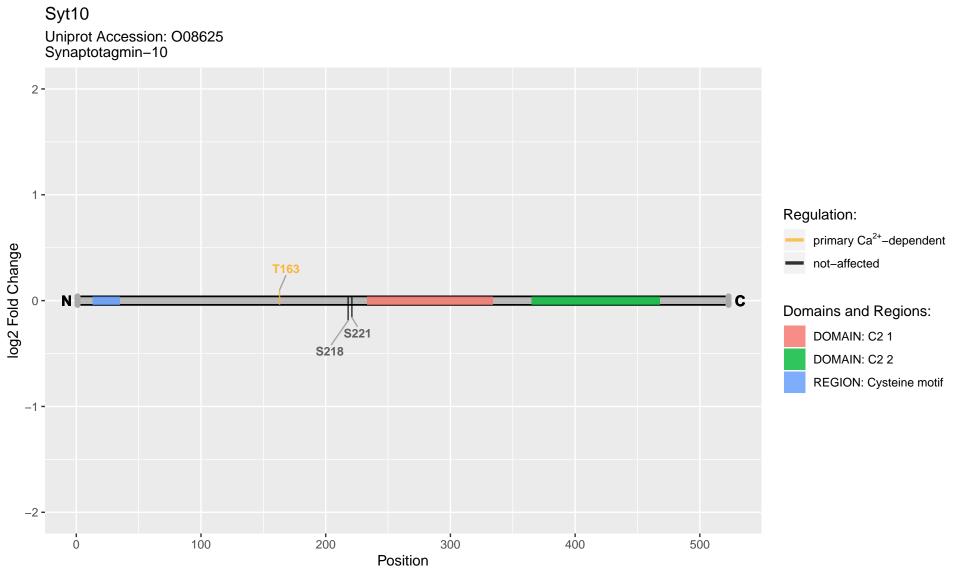


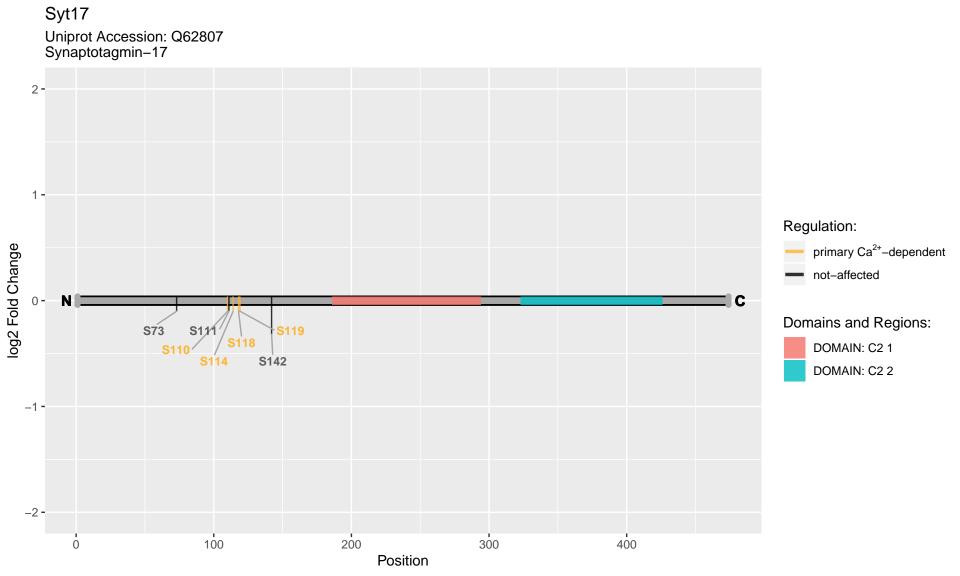


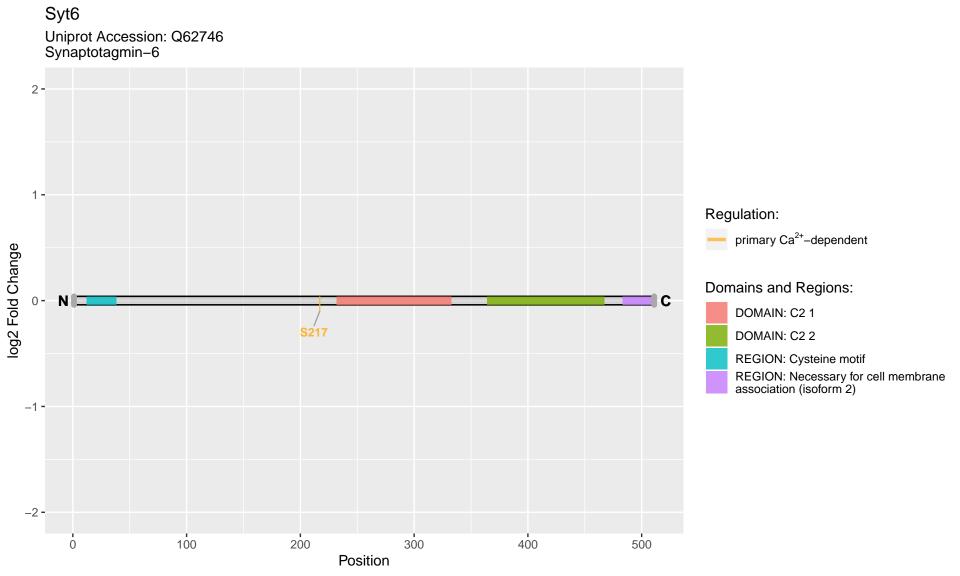


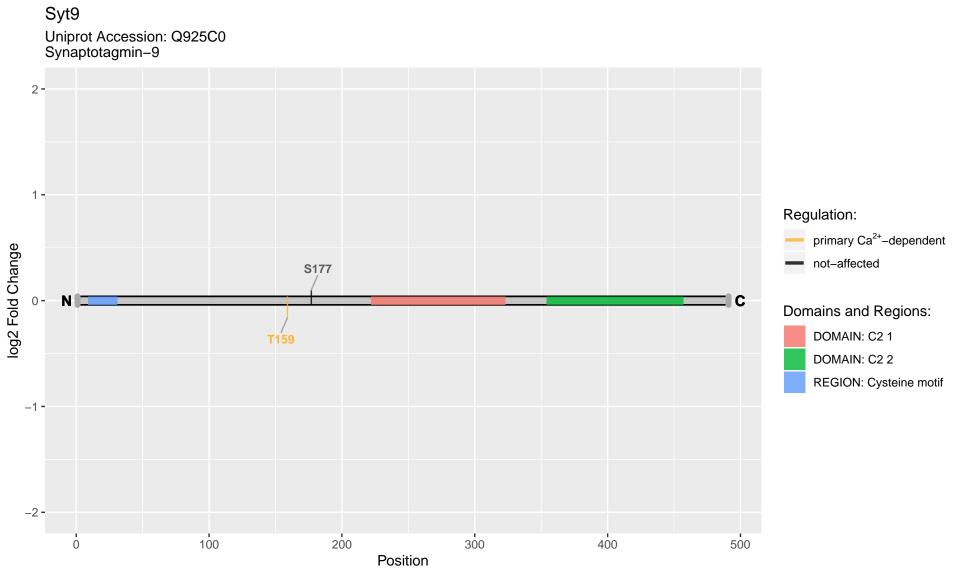


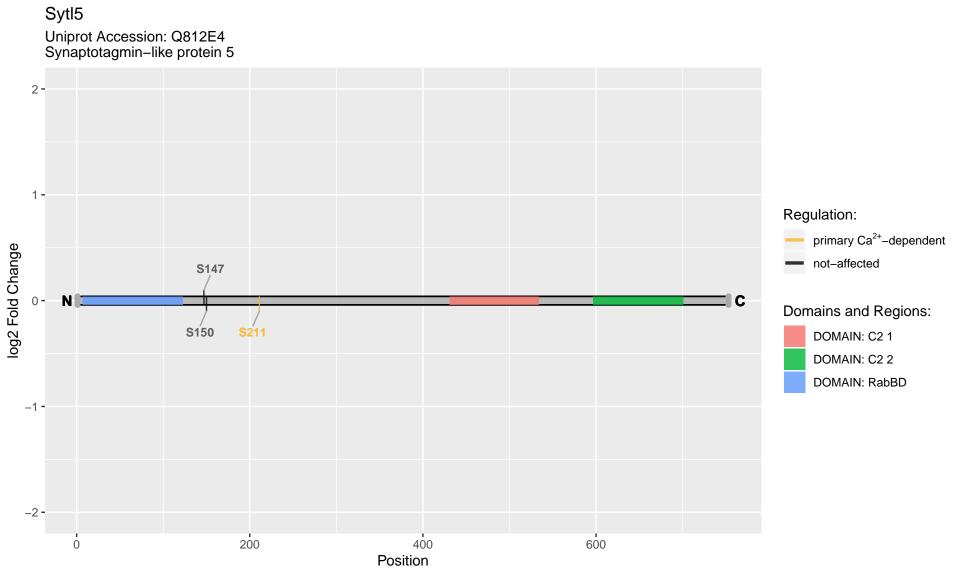


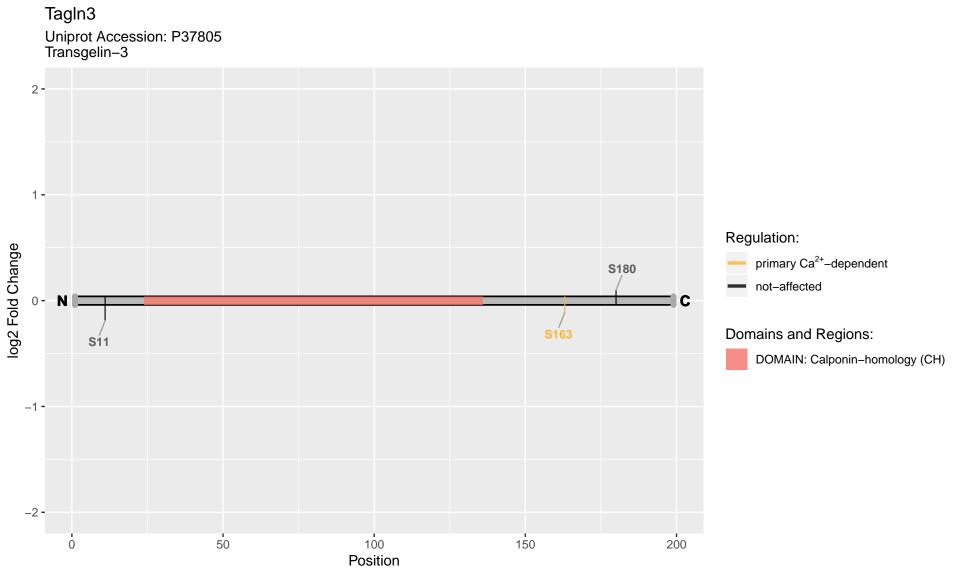


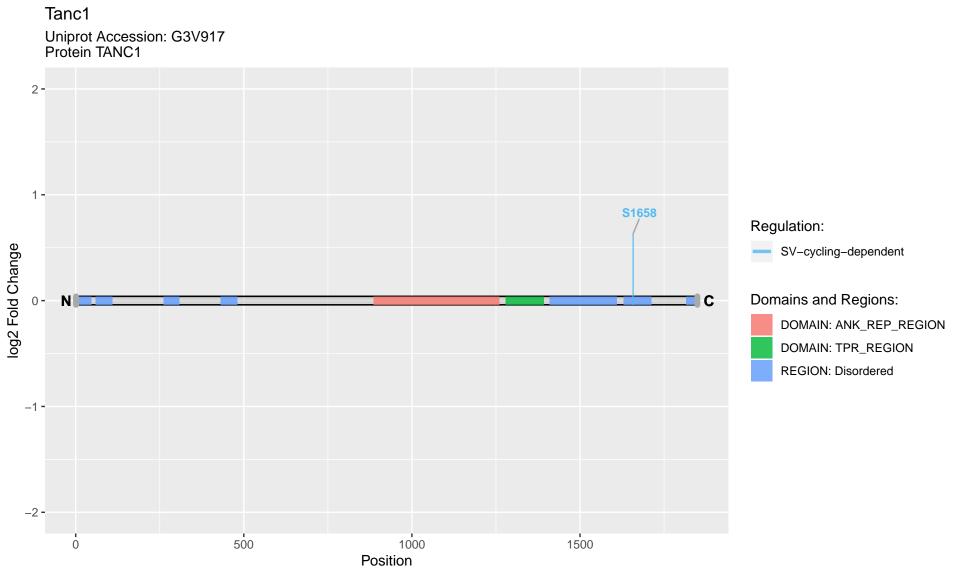




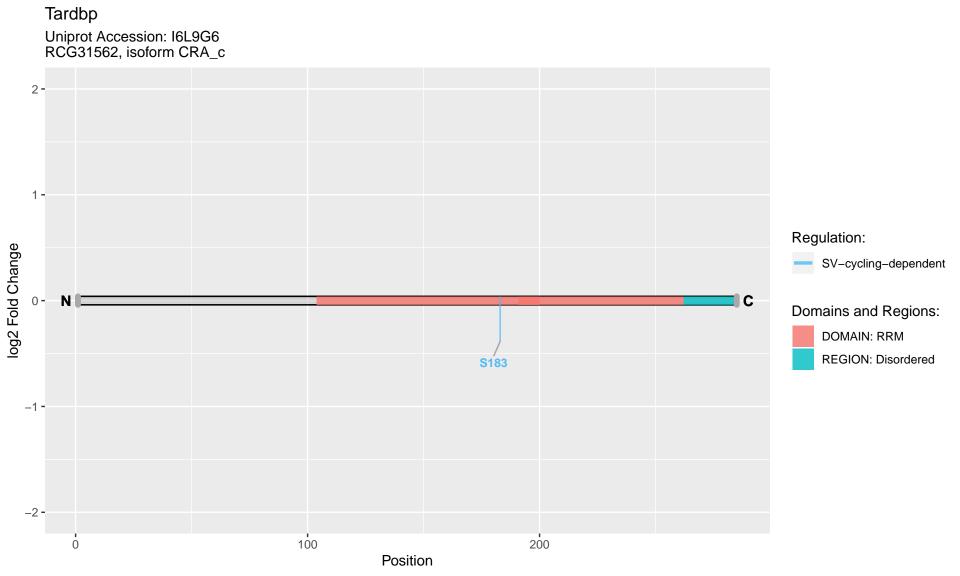


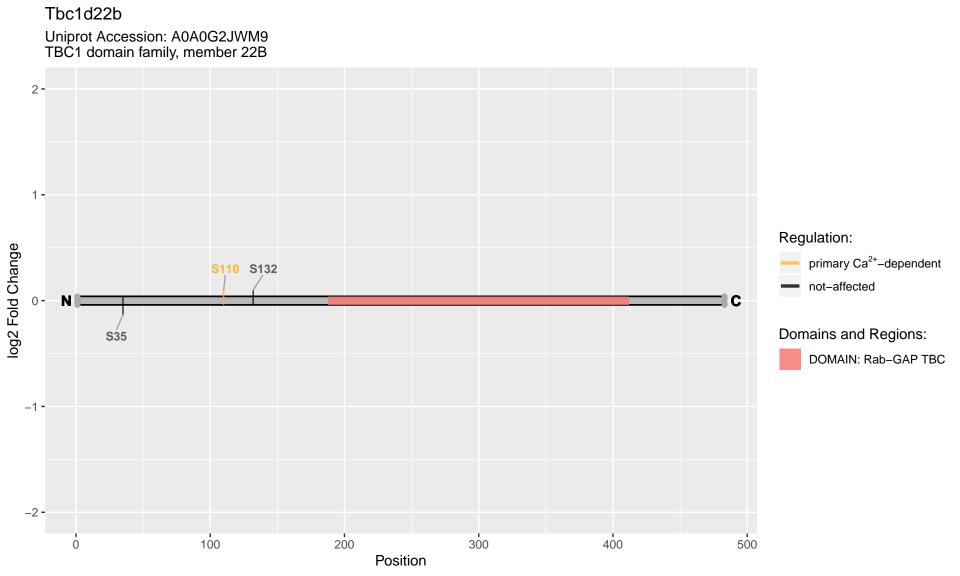


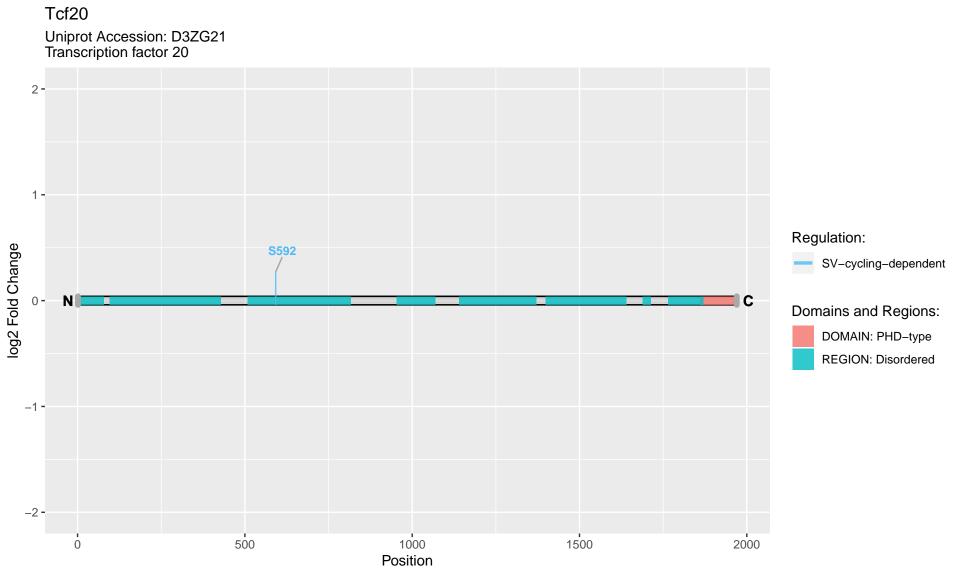


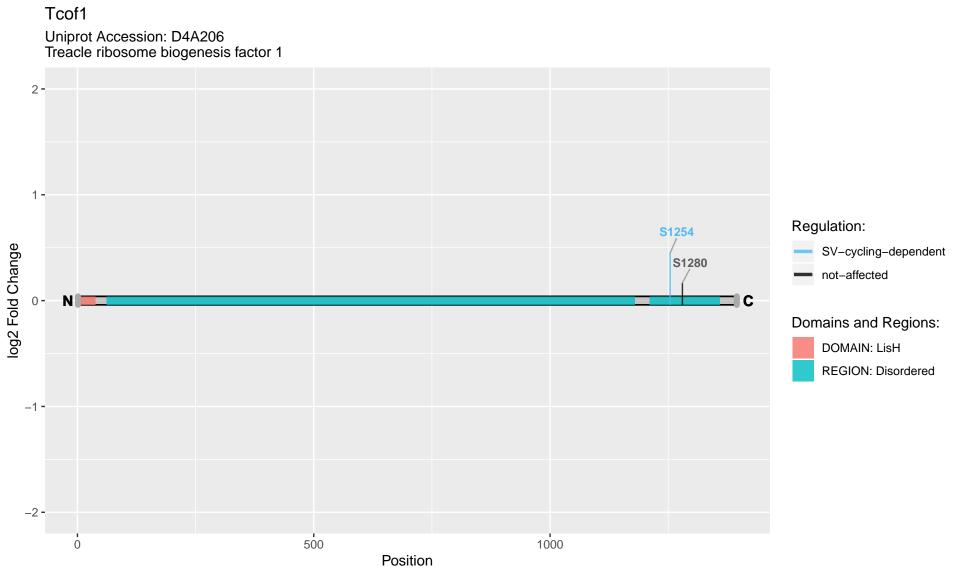


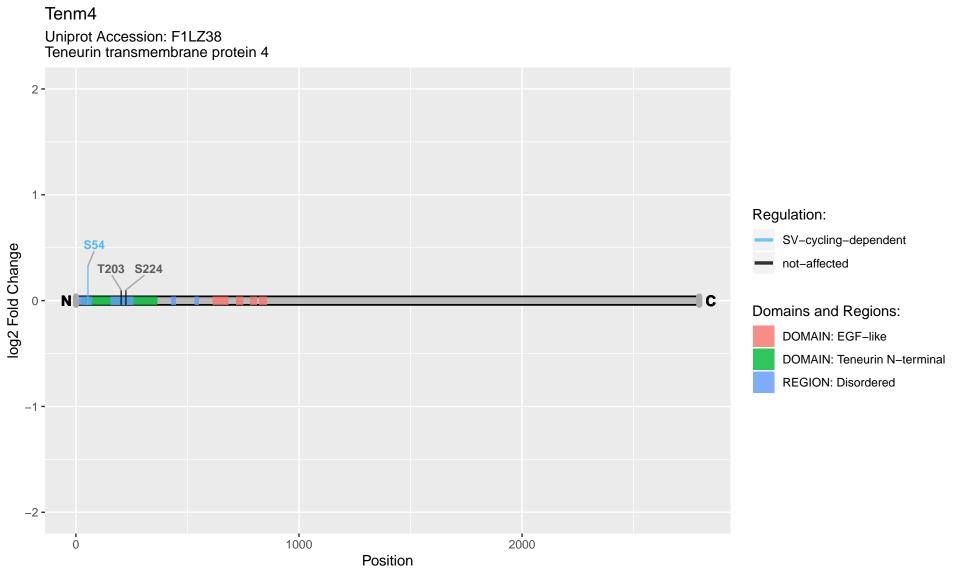
Tanc2 Uniprot Accession: A0A0G2K9J0 Tetratricopeptide repeat, ankyrin repeat and coiled-coil-containing 2 2 -**S2063** 1 -**S1646** Regulation: primary Ca²⁺-dependent **S1562** S1665 **S478** log2 Fold Change S1616/ SV-cycling-dependent S474 S472 S1603 S1620 not-affected C Domains and Regions: S88 S128 S243 S1532 \S1558 S1826 DOMAIN: ANK_REP_REGION S1528 DOMAIN: TPR_REGION **REGION: Disordered** -1 **-**-2 **-**500 1000 1500 2000 **Position**

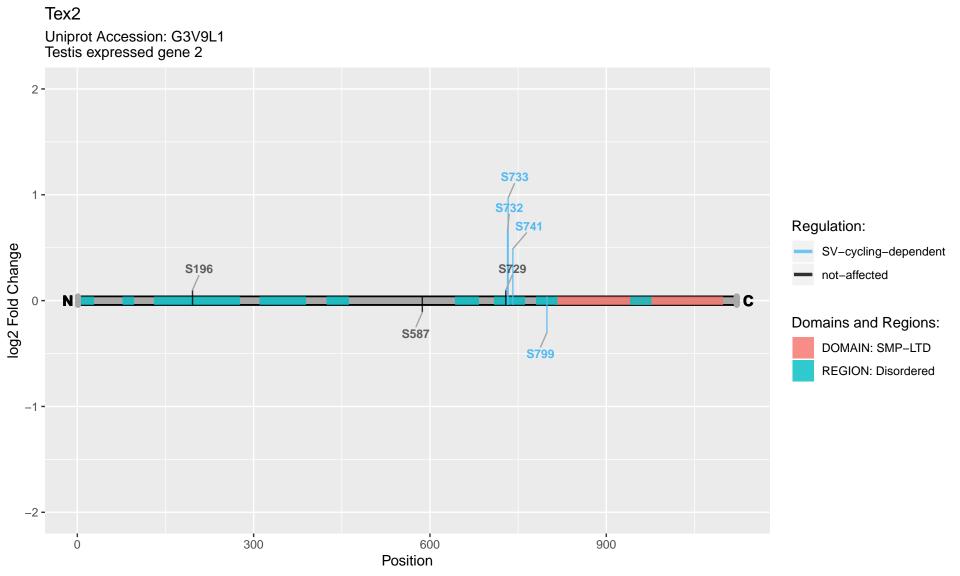


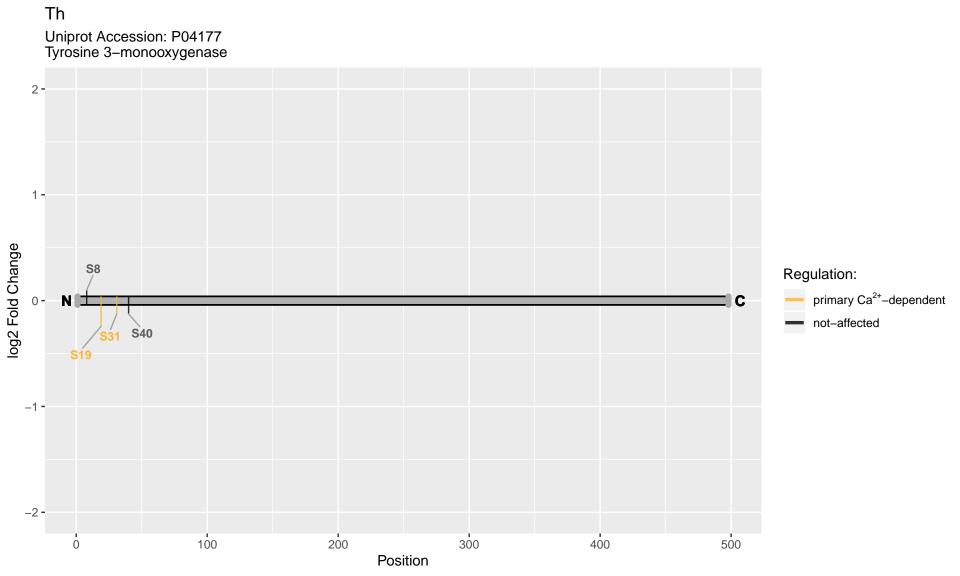


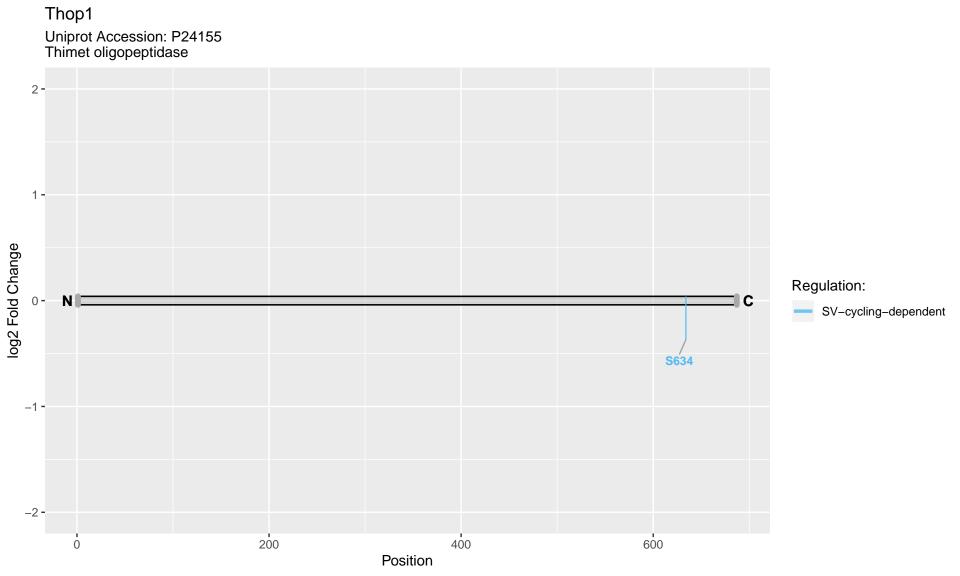


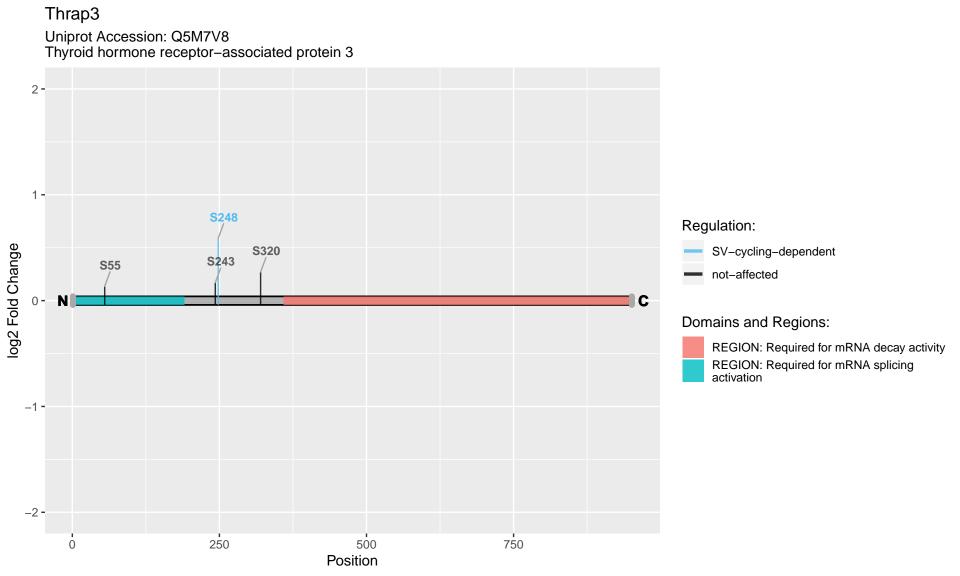




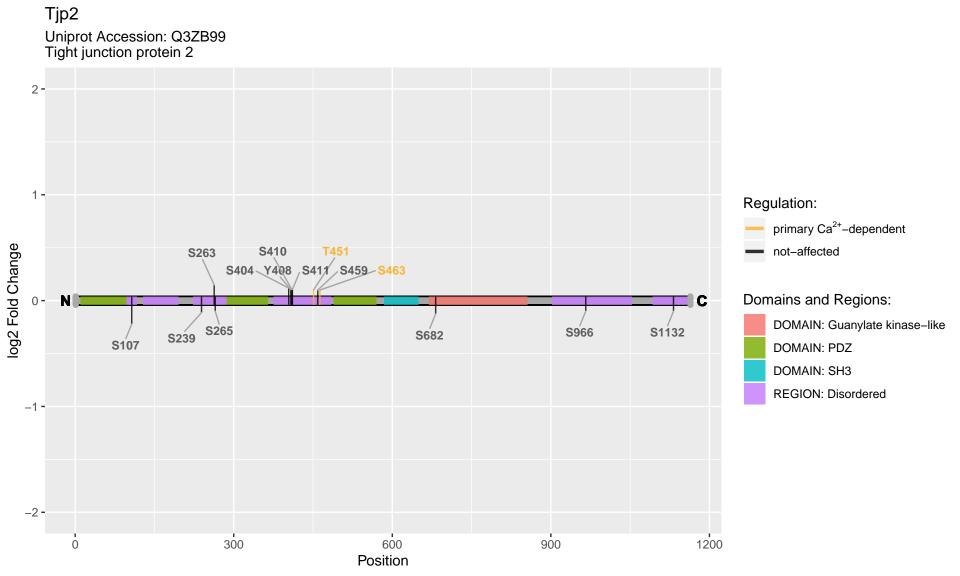


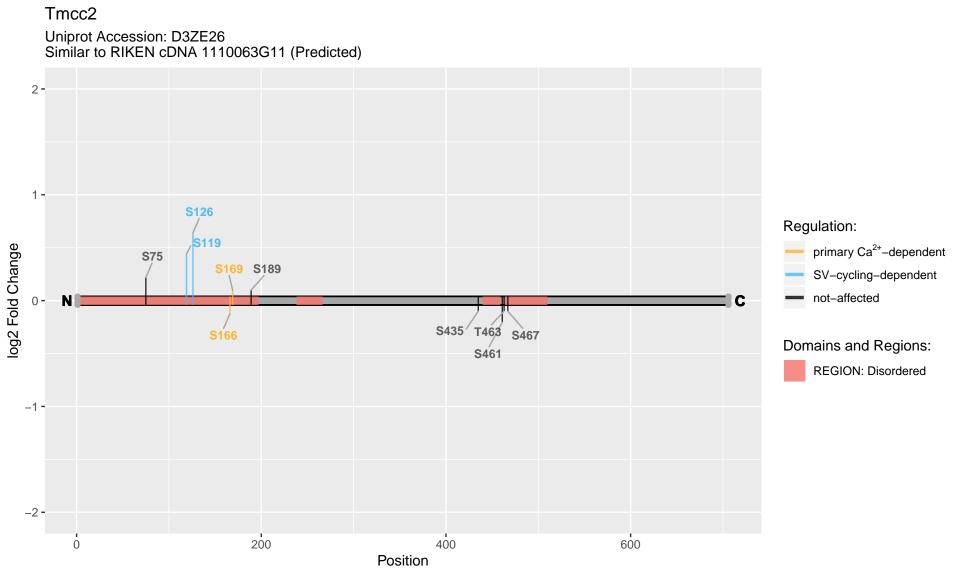


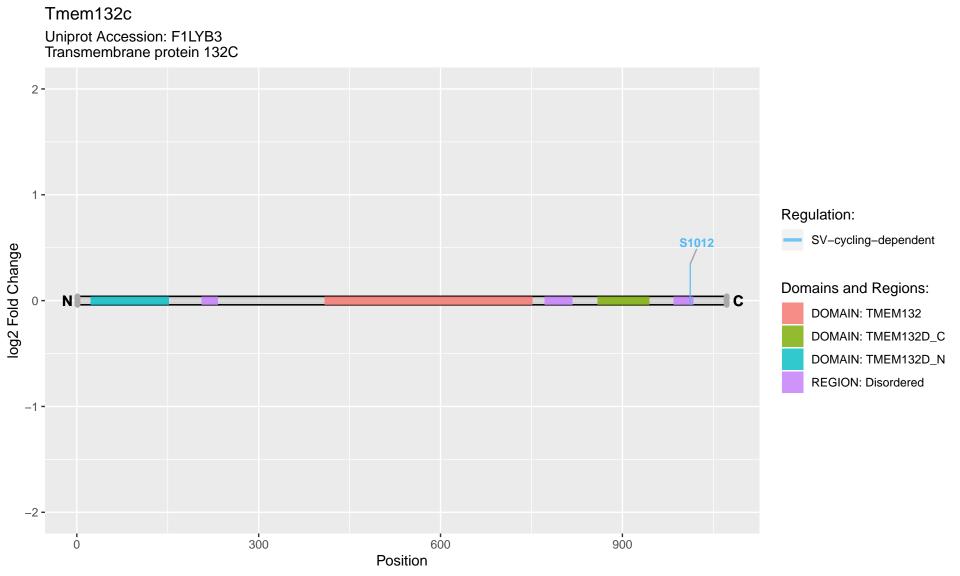


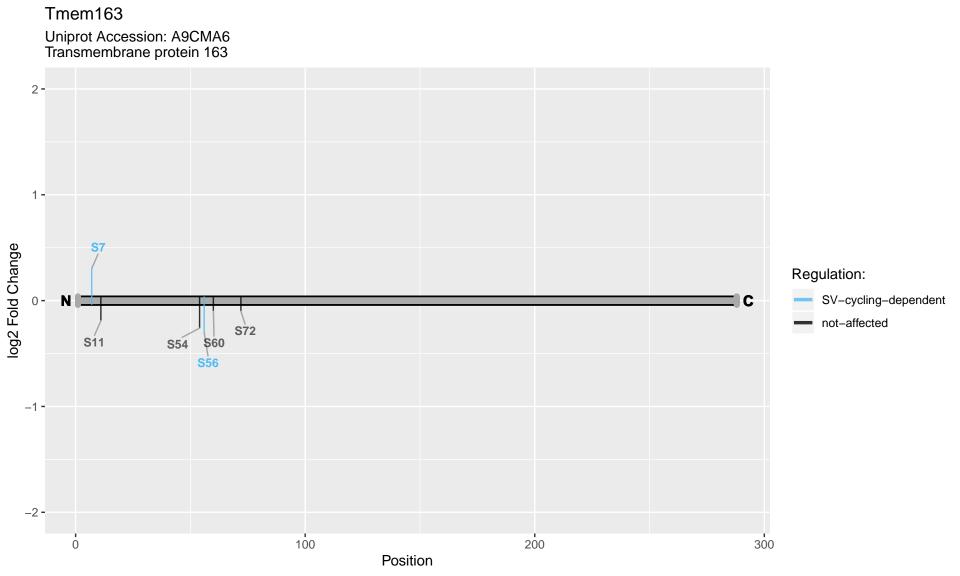


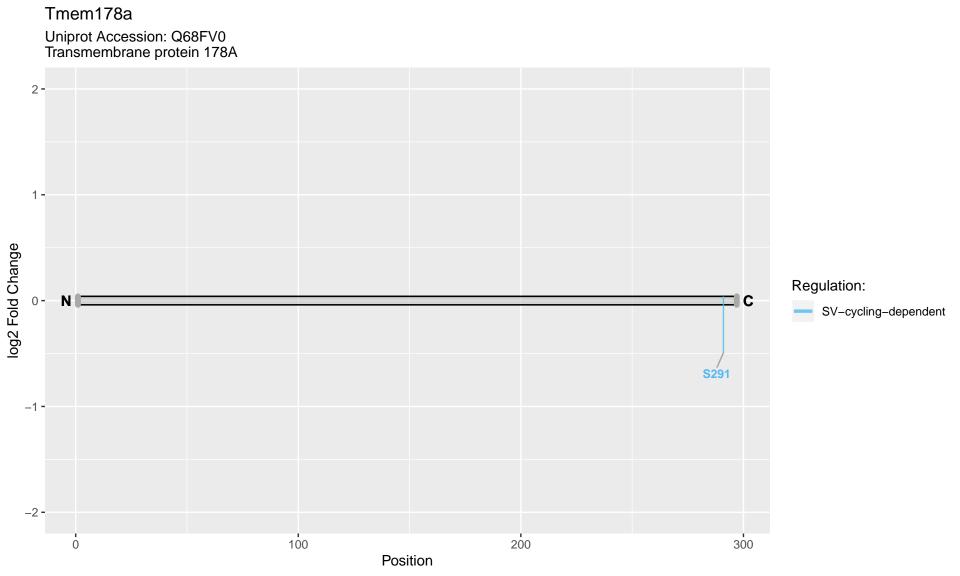
Tjp1 Uniprot Accession: A0A0G2K2P5 Tight junction protein ZO-1 2 -Regulation: SV-cycling-dependent 1 not-affected **S329** S303/ S131 log2 Fold Change Domains and Regions: S326 **S899** S125 / S179 DOMAIN: Guanylate kinase-like C DOMAIN: PDZ 1 DOMAIN: PDZ 2 Y132/ S178 S617 DOMAIN: PDZ 3 S175 S212 DOMAIN: SH3 DOMAIN: ZU5 -1 **-**REGION: Actin-binding region (ABR) REGION: Occludin (OCLN)-binding region -2 **-**500 1500 1000 **Position**

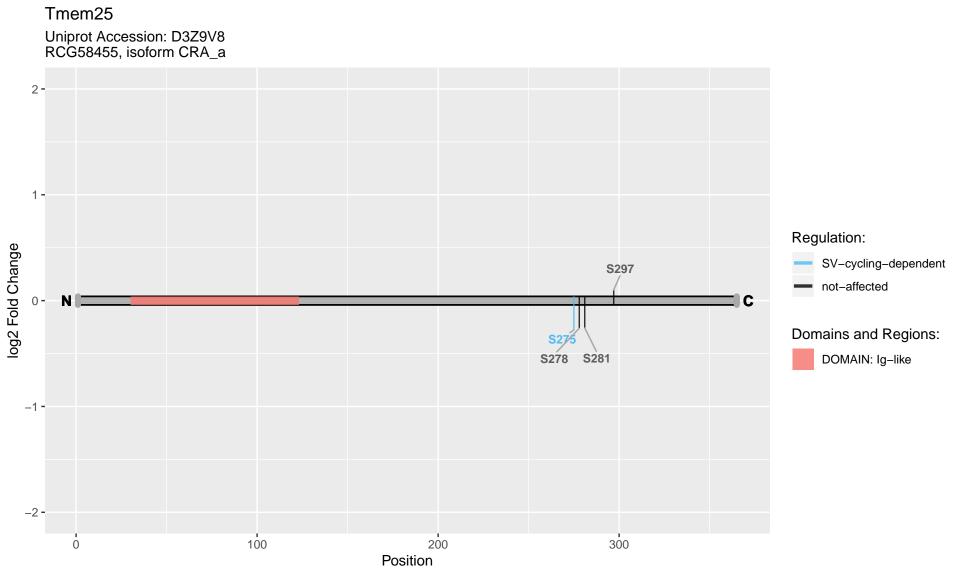


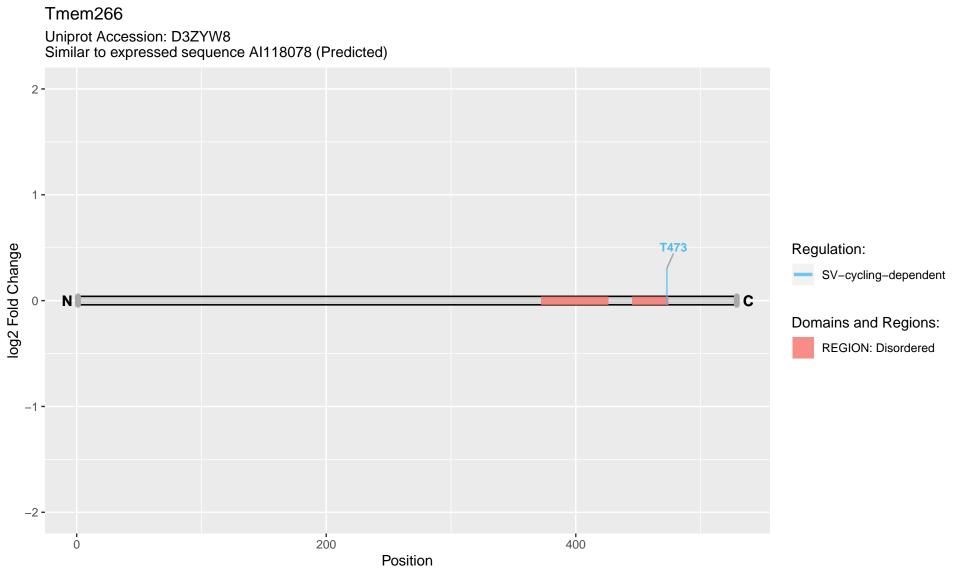


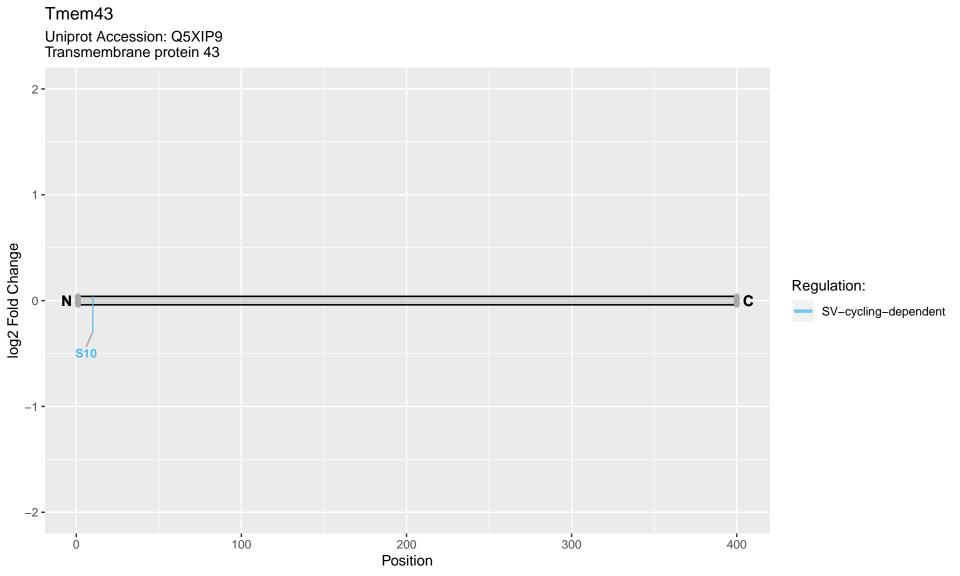


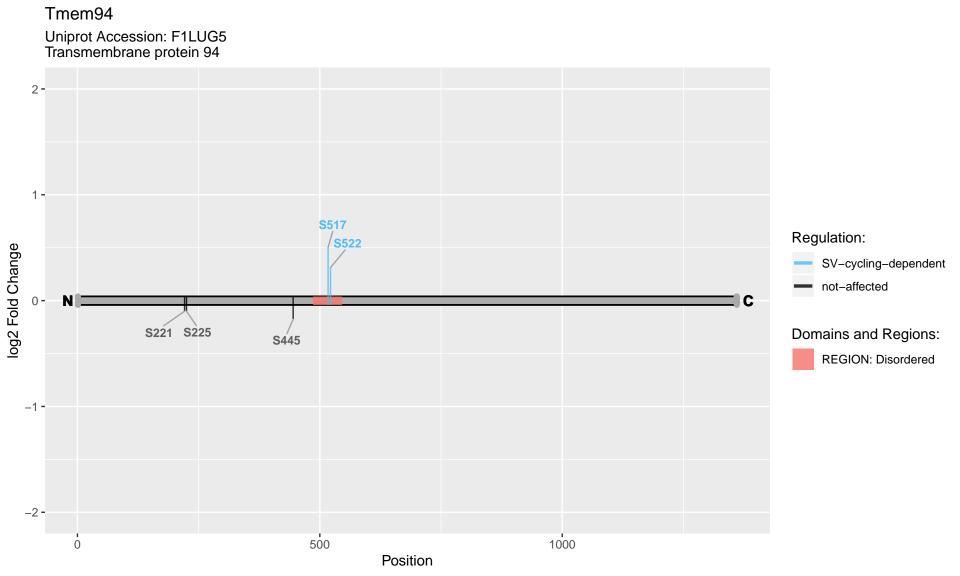


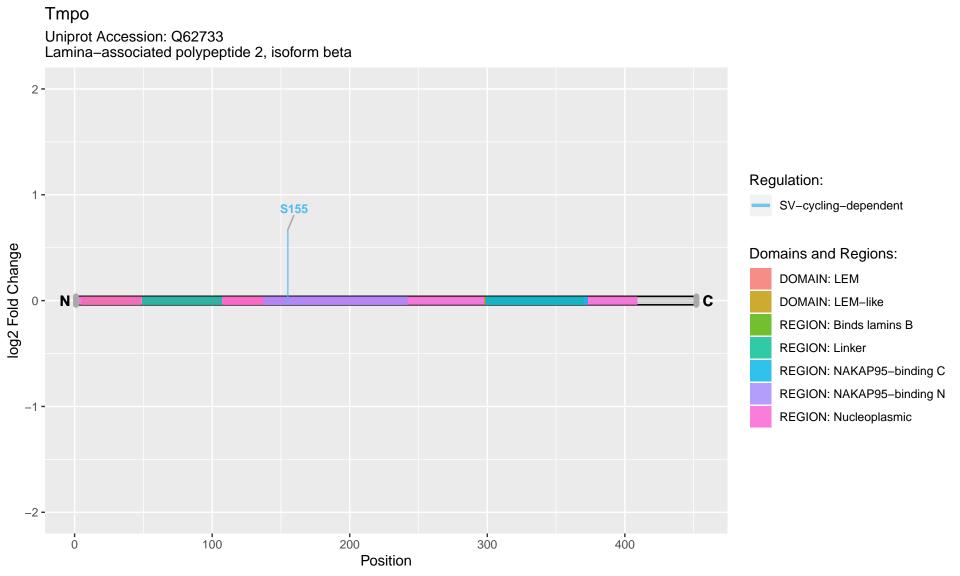


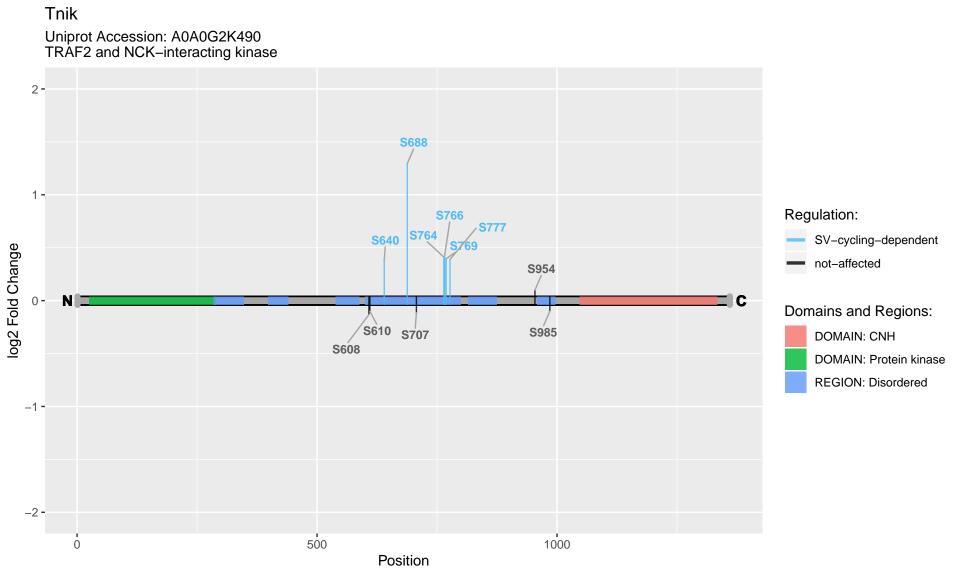


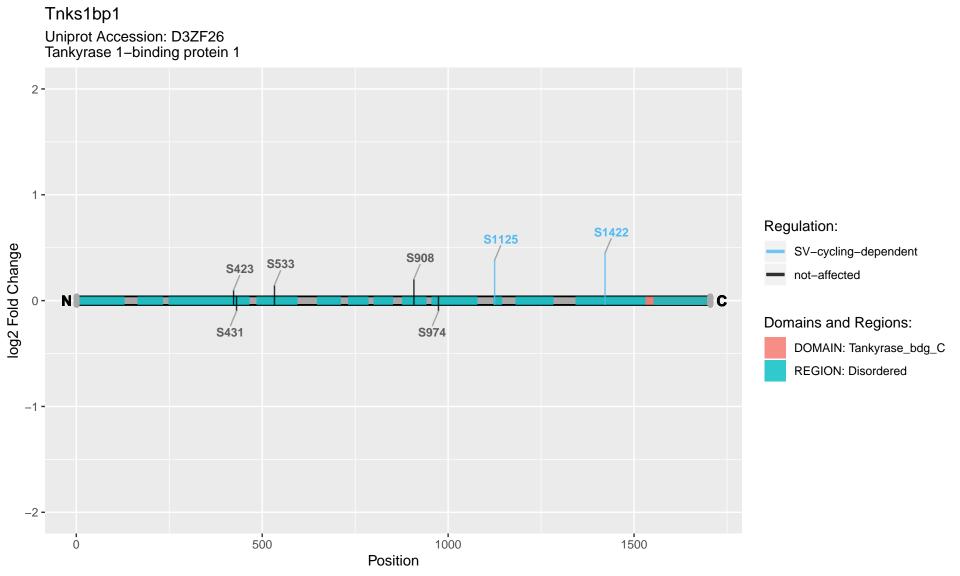


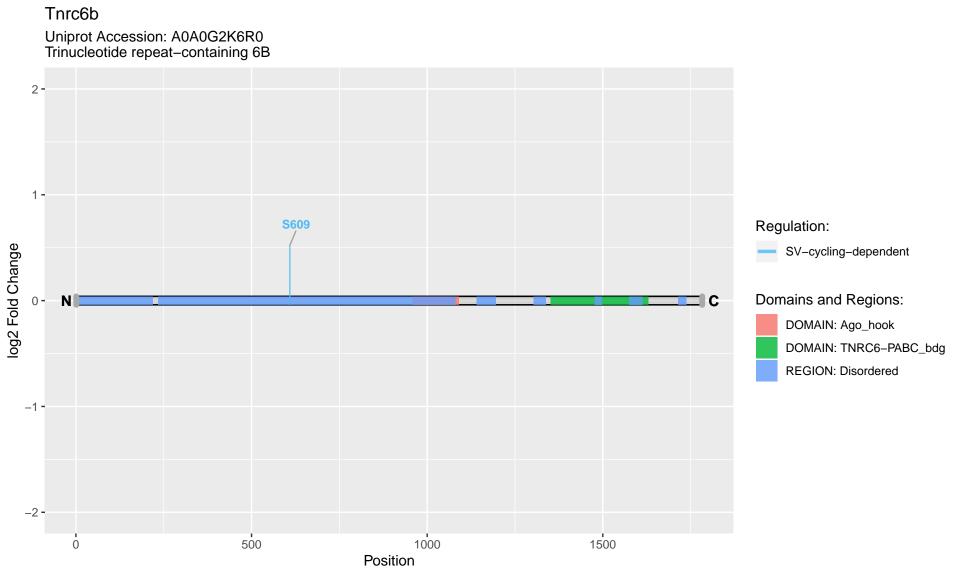


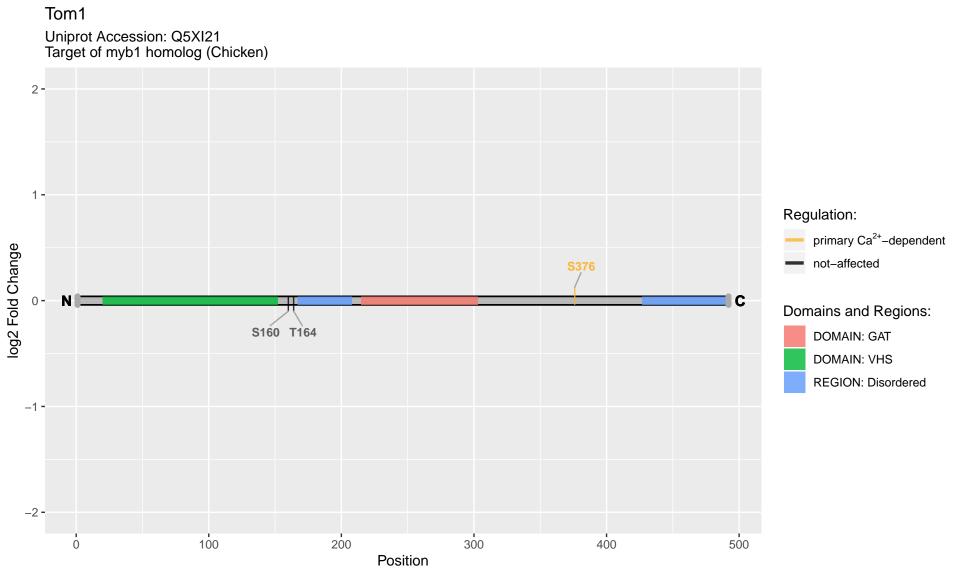


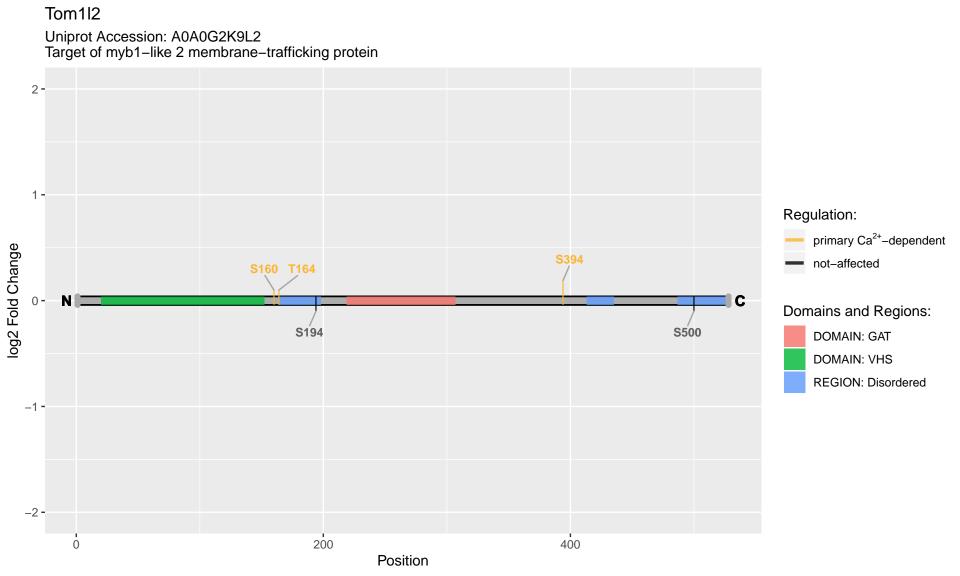


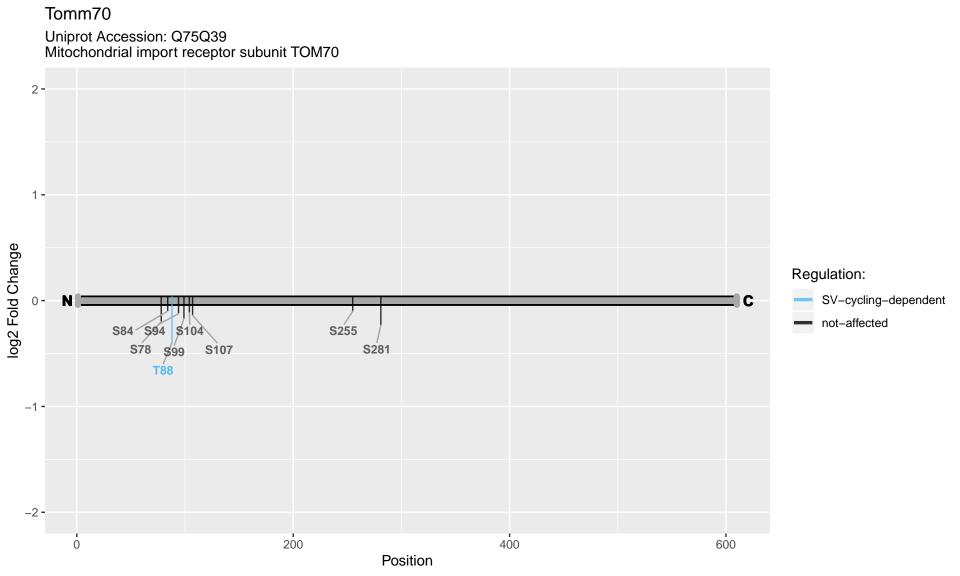


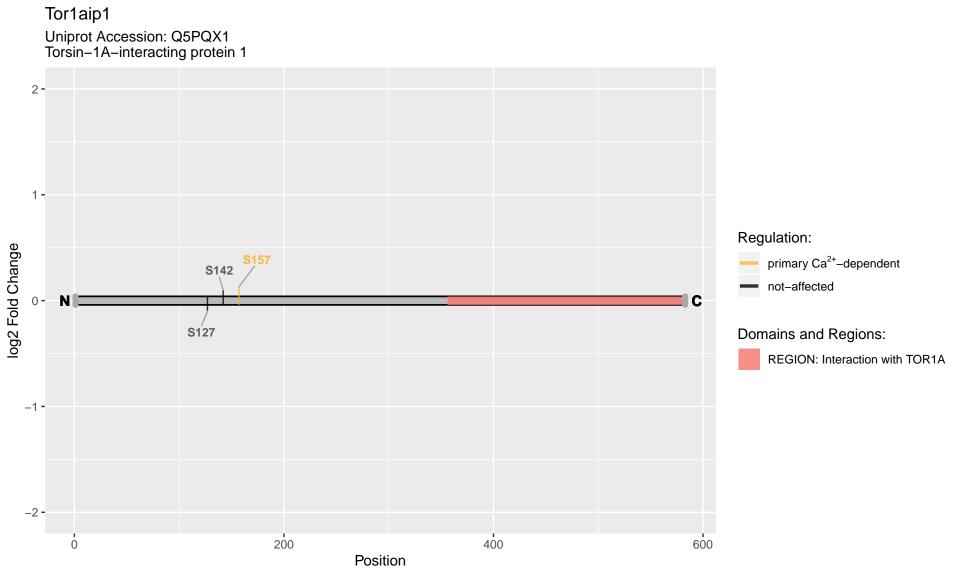


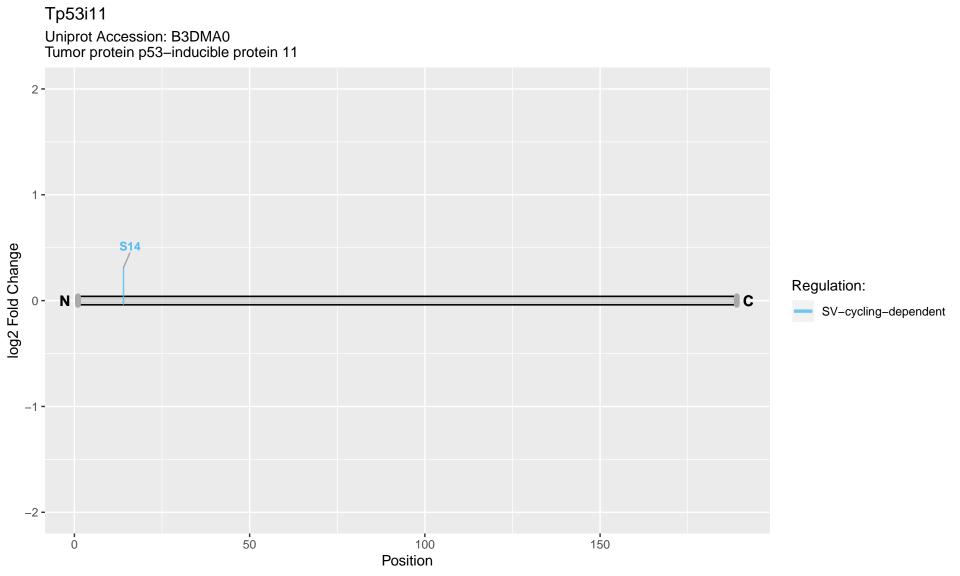


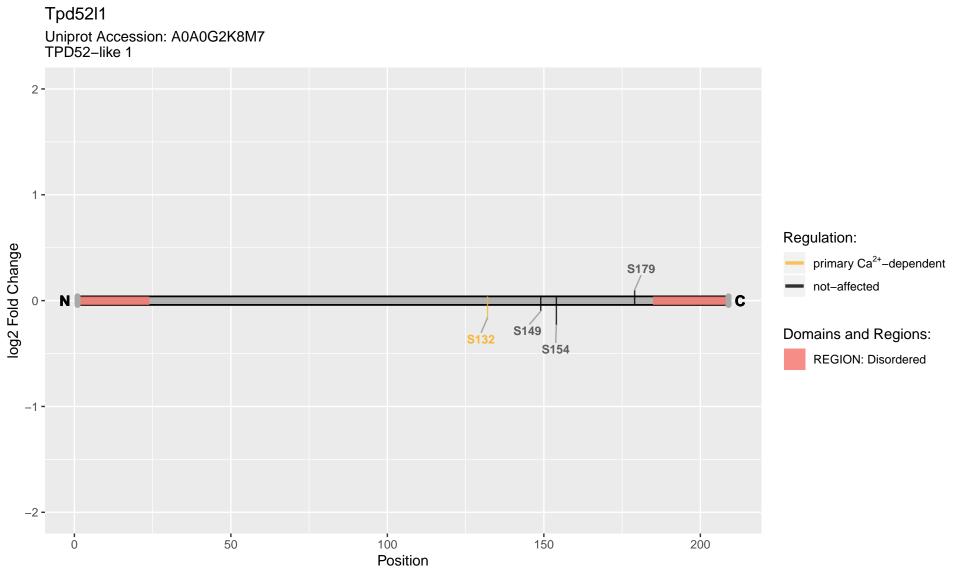


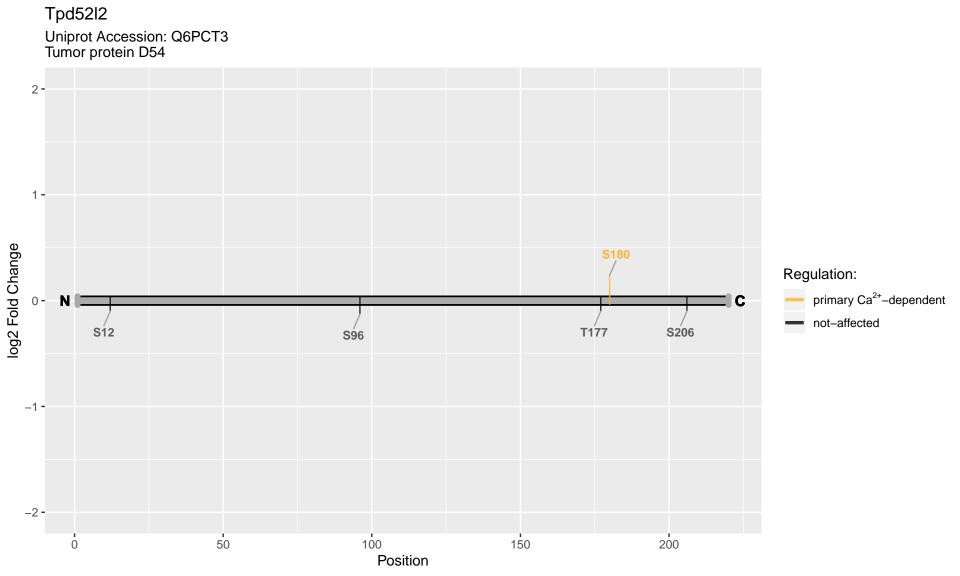


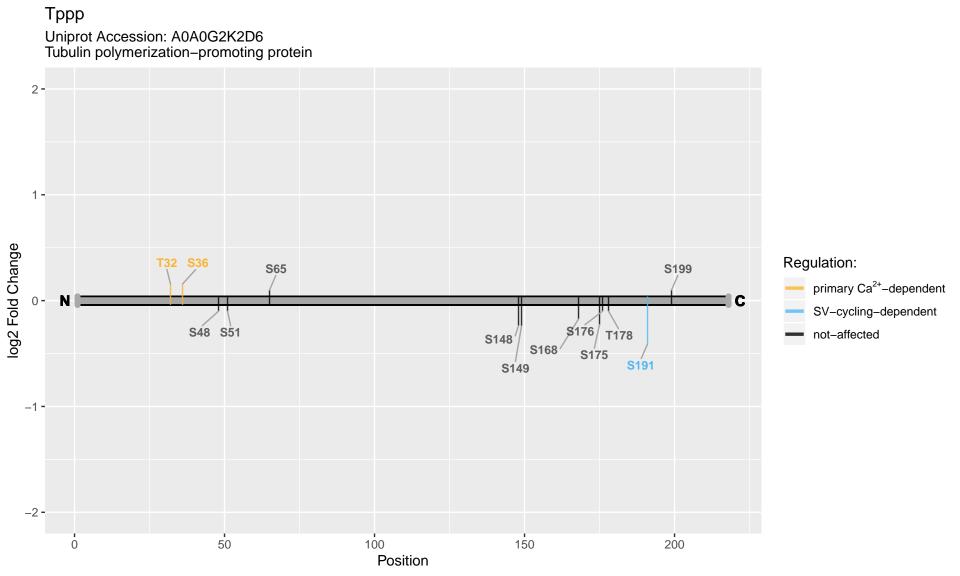


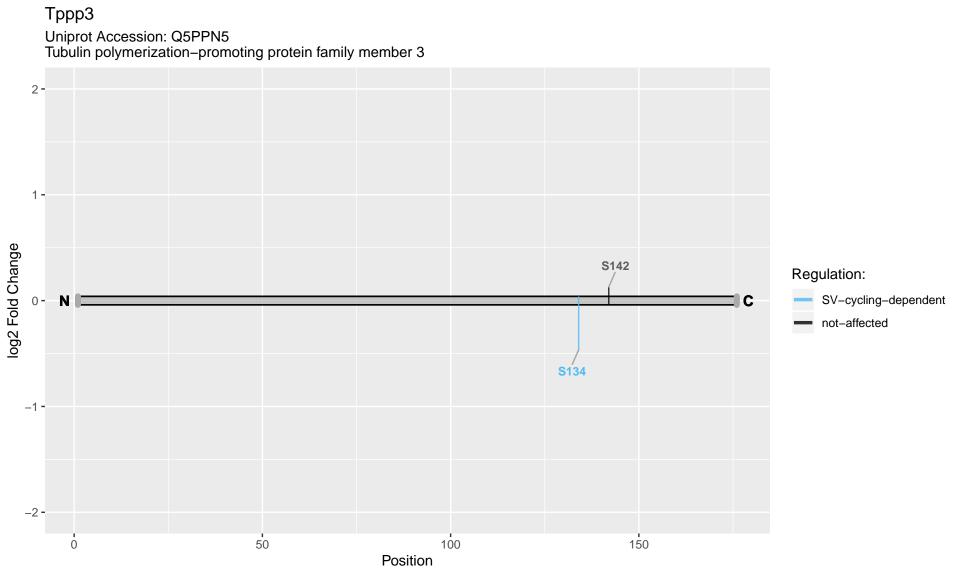


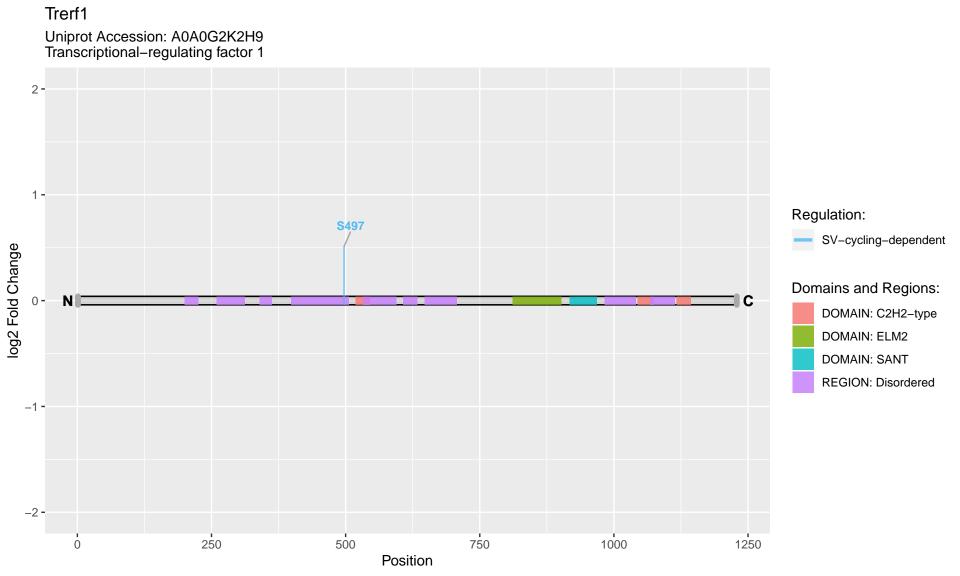


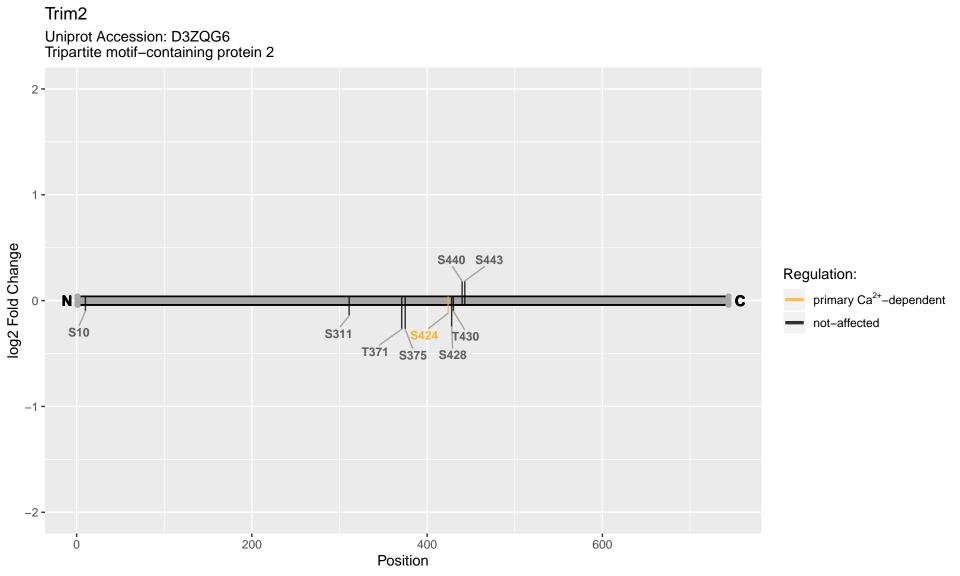


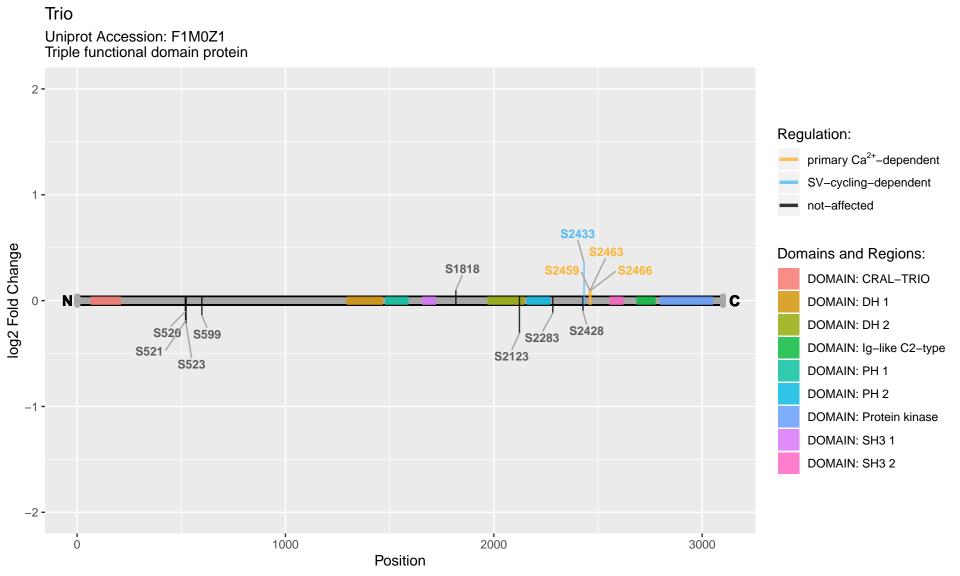


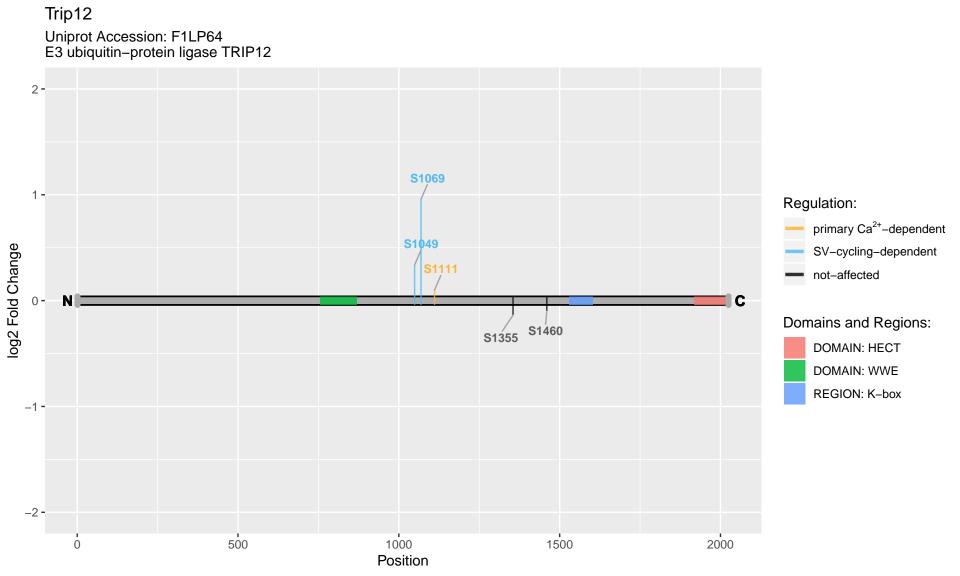


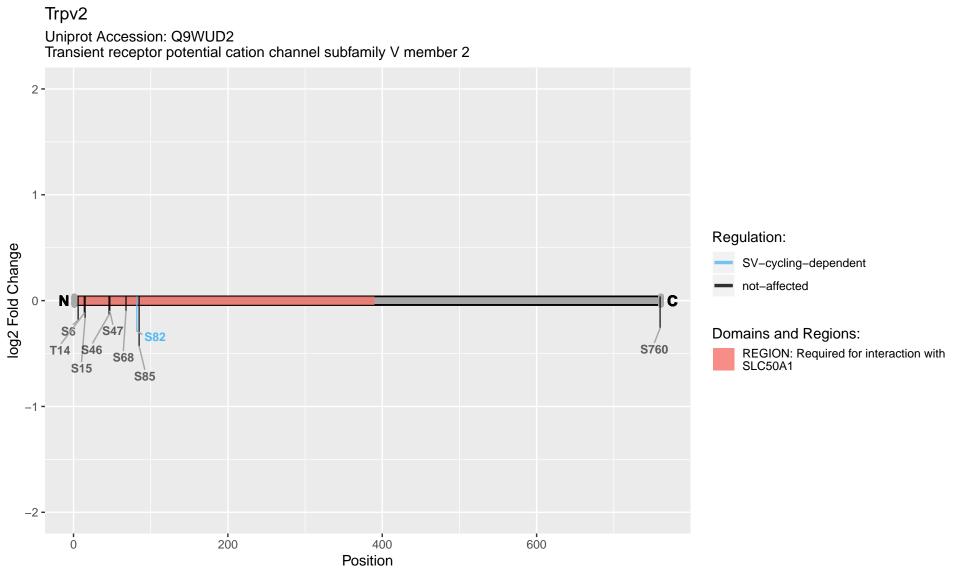


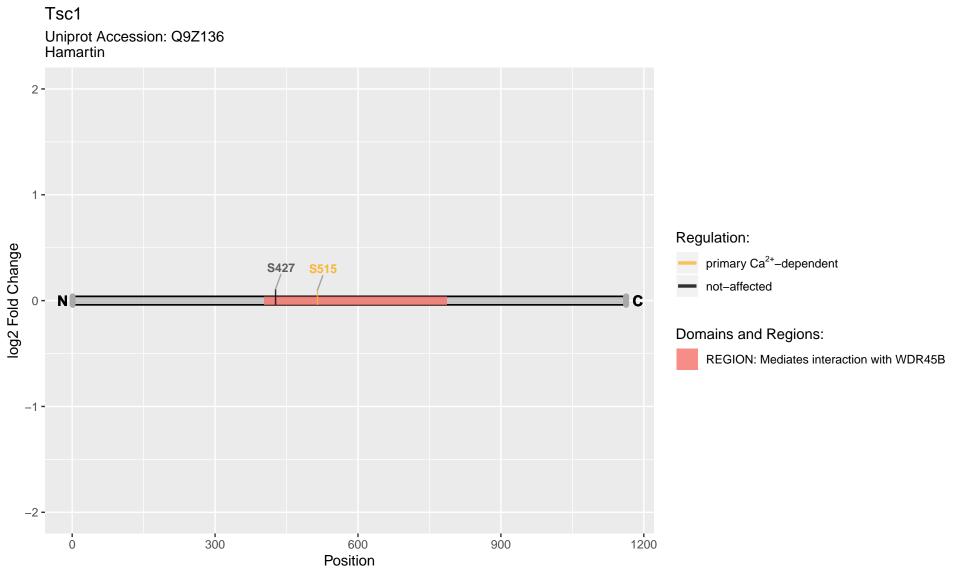


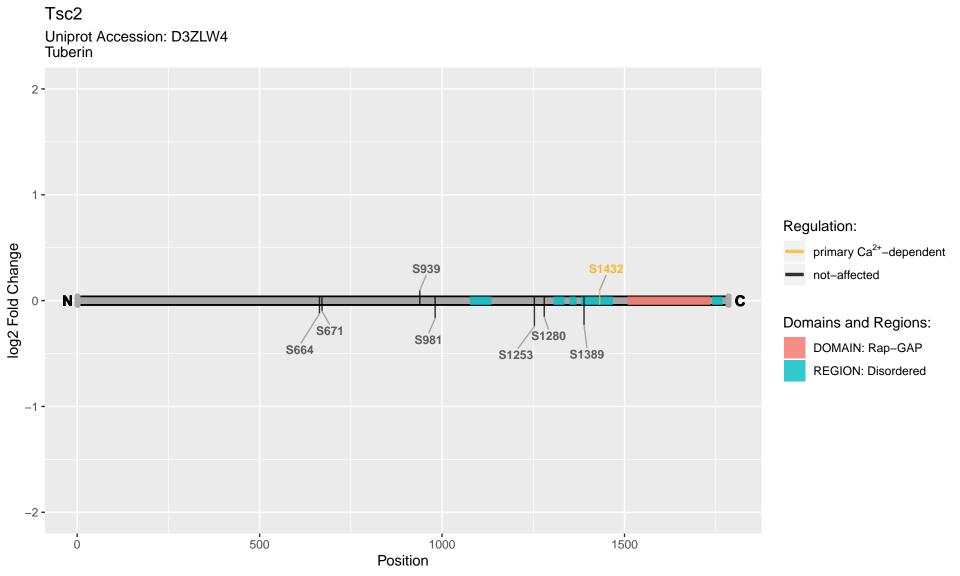


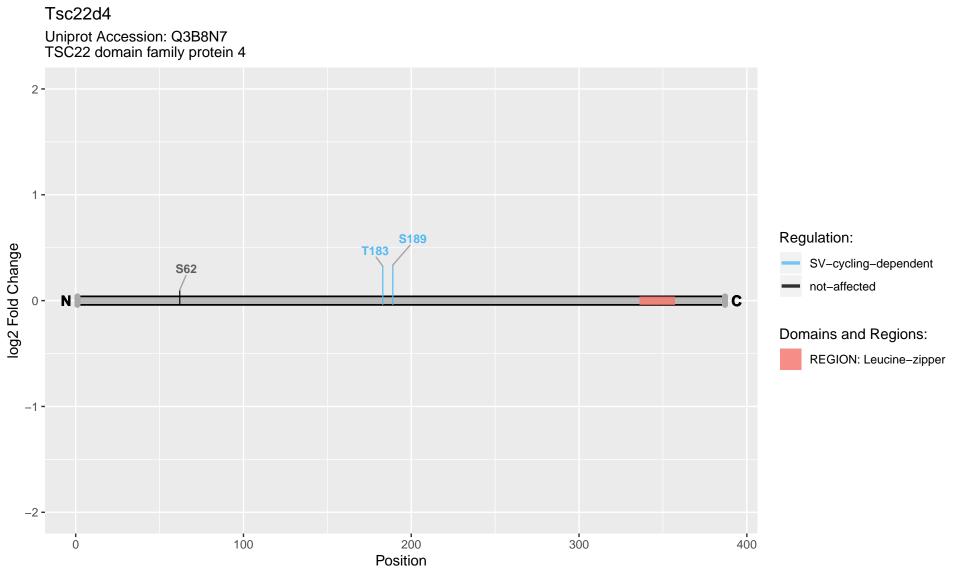


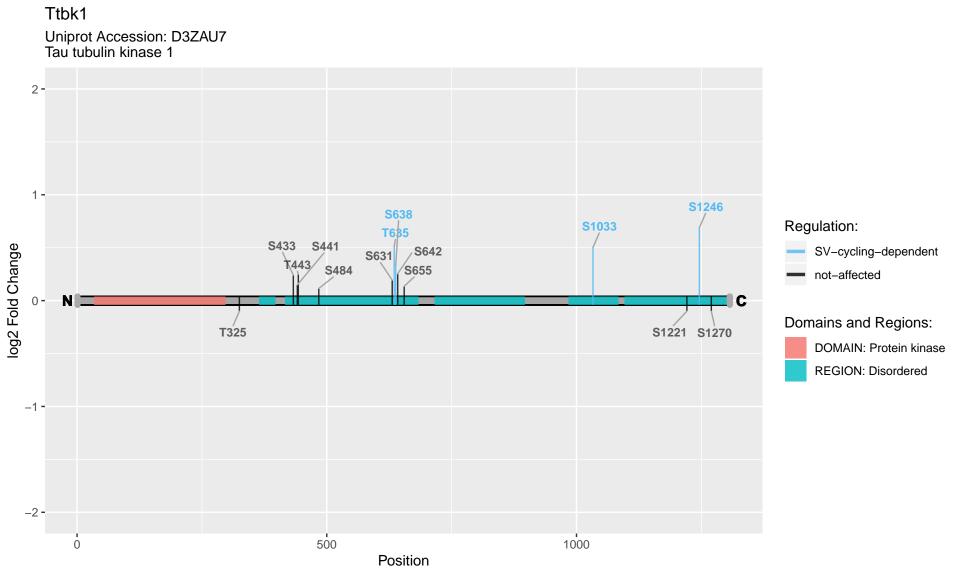


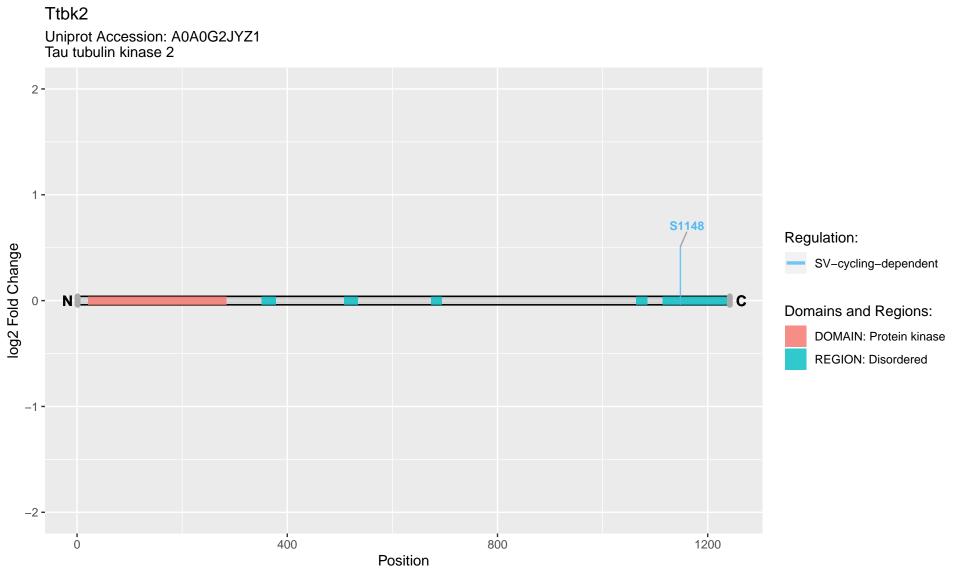


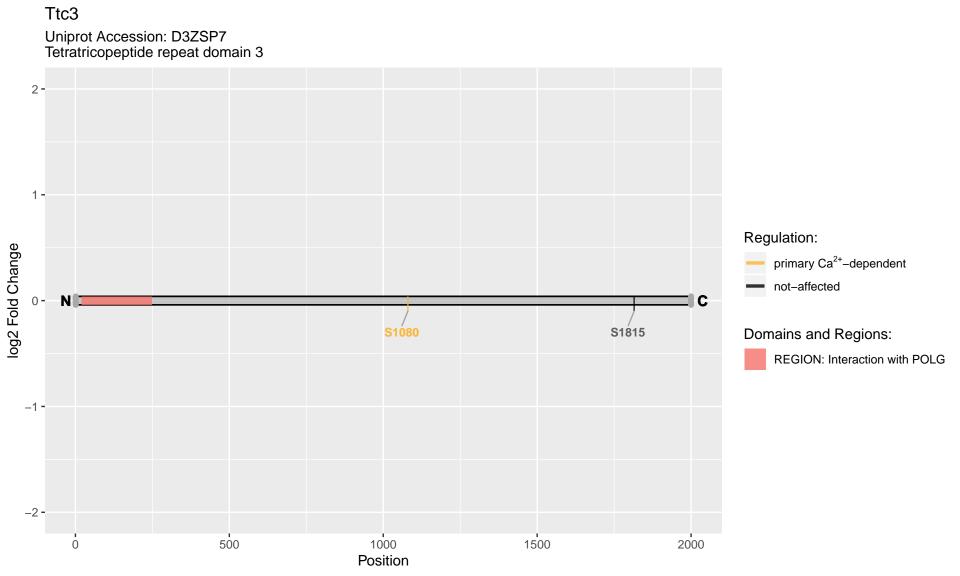


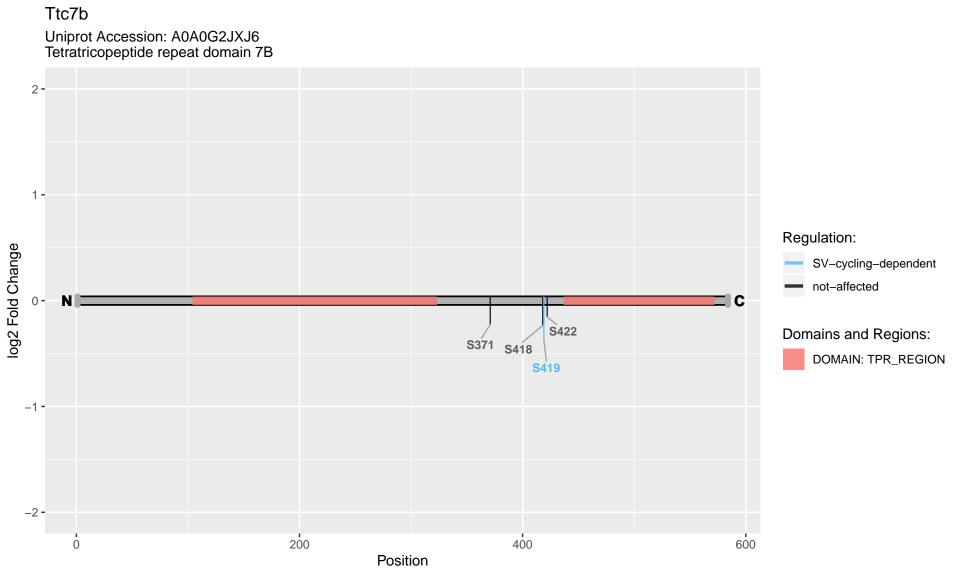


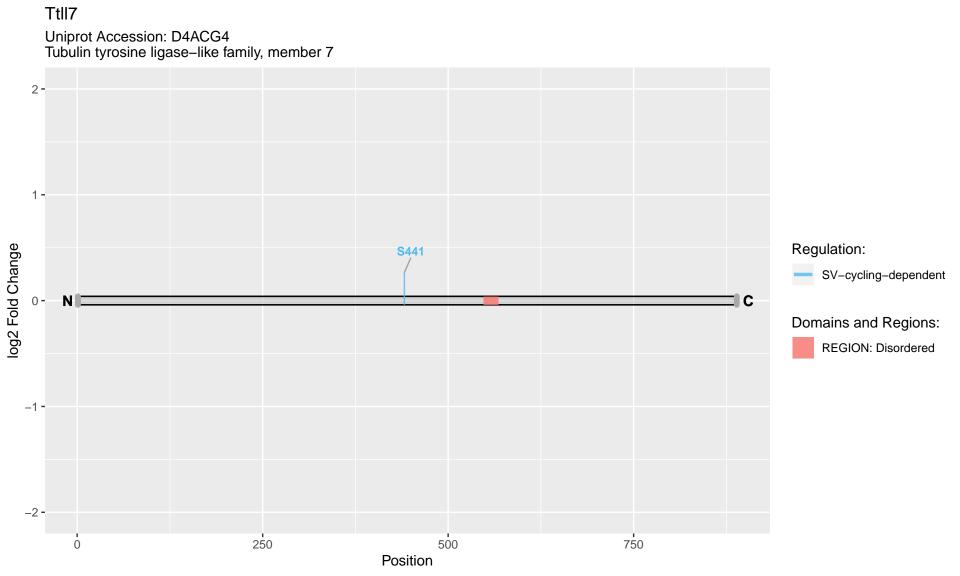


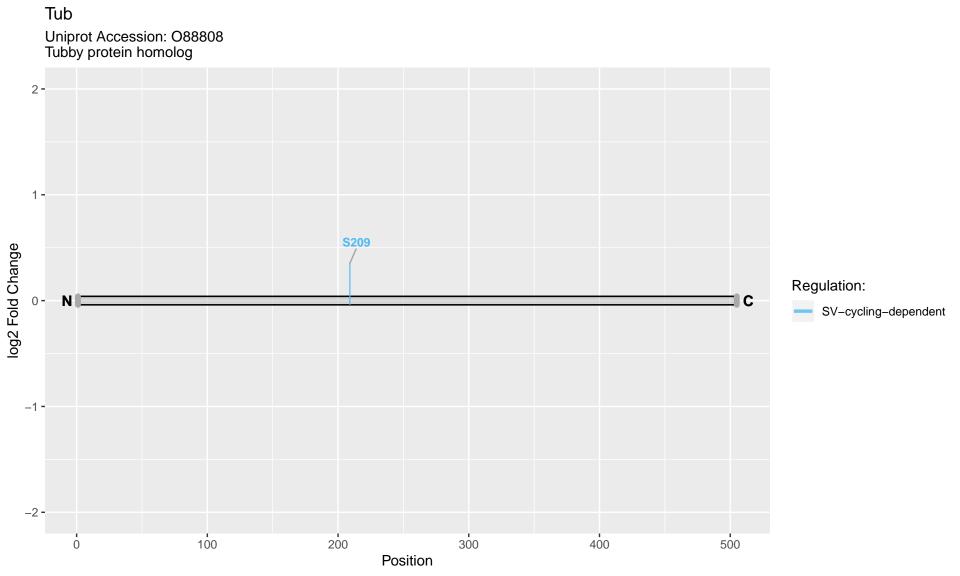


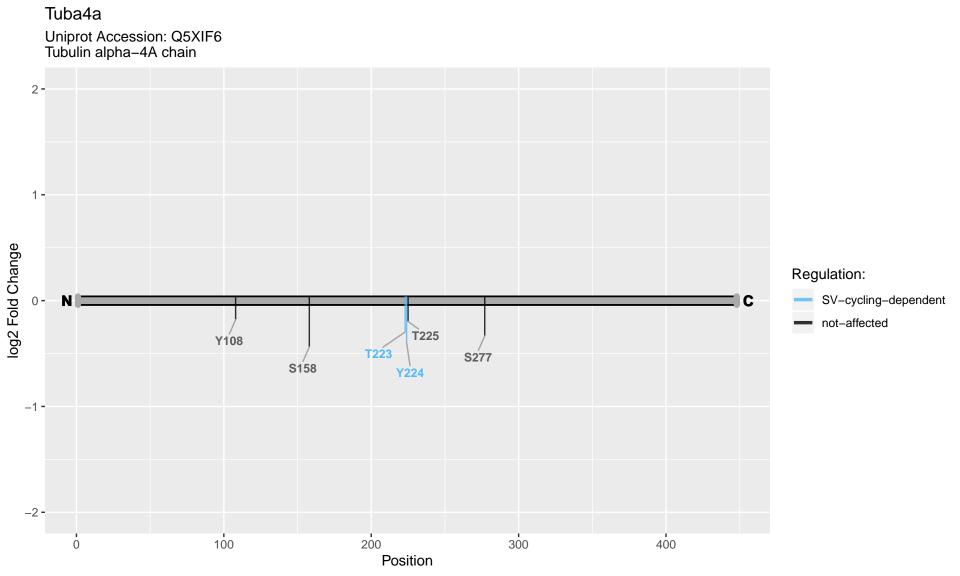


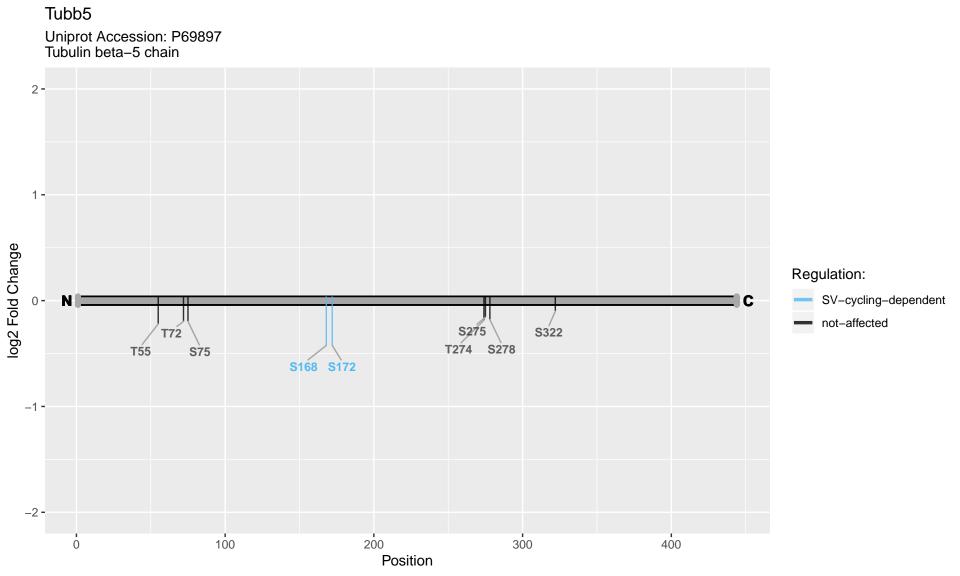


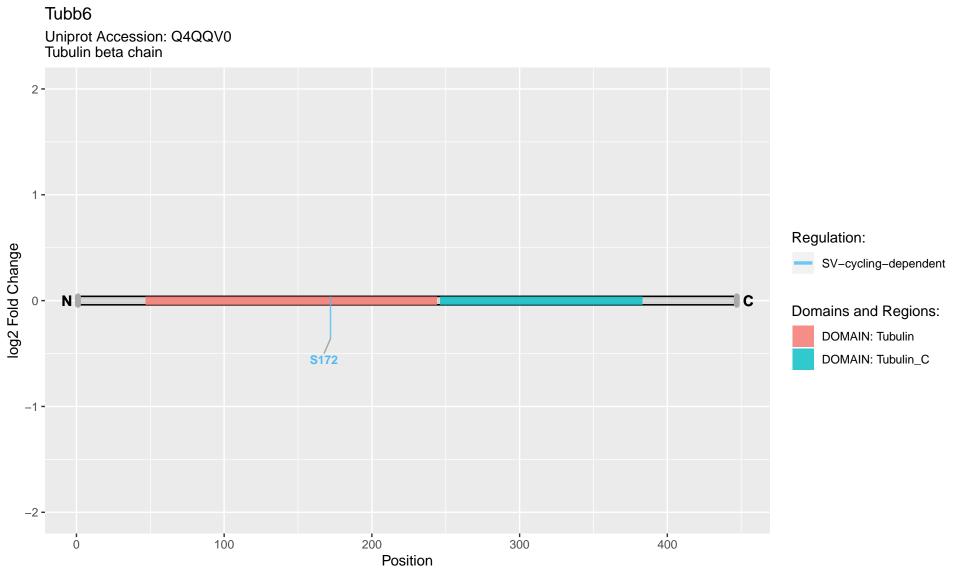


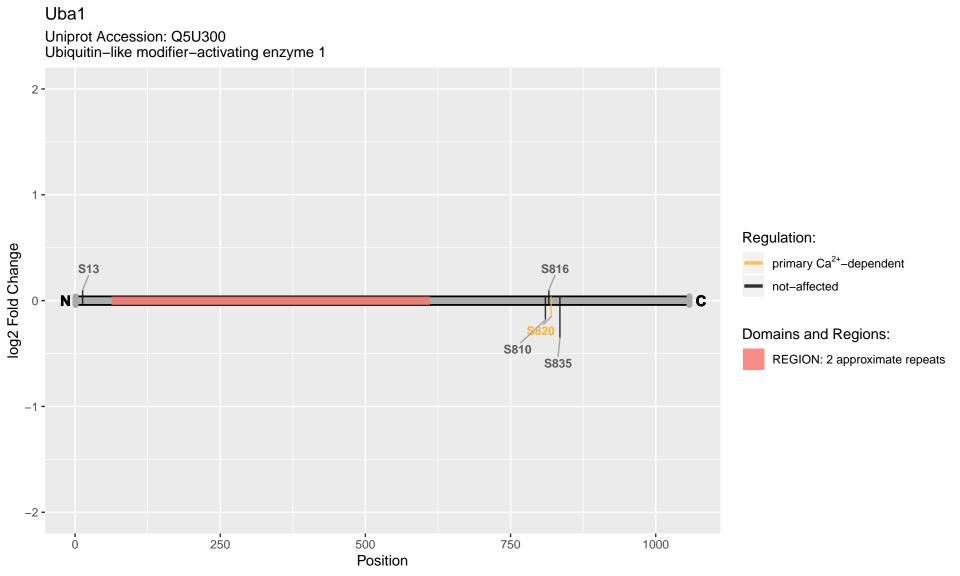


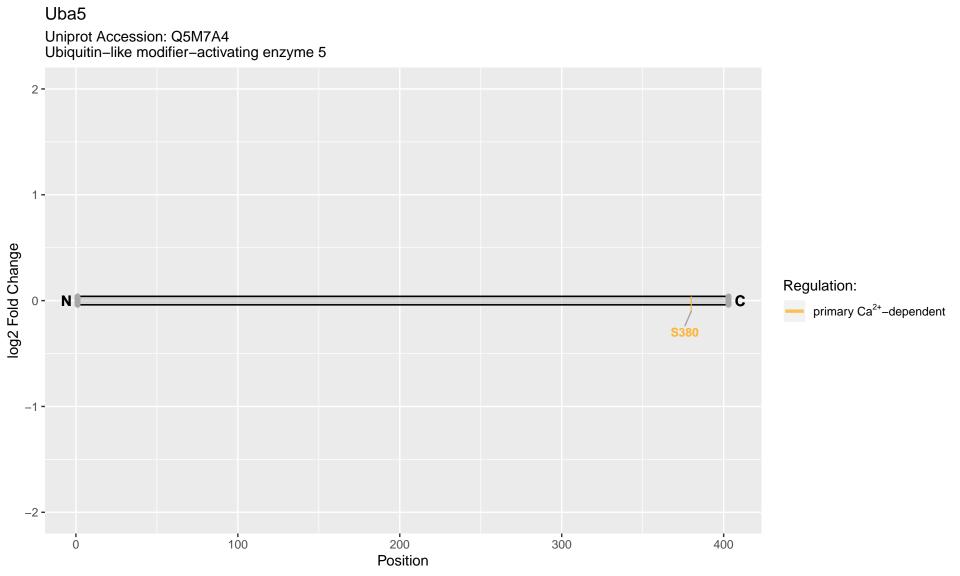


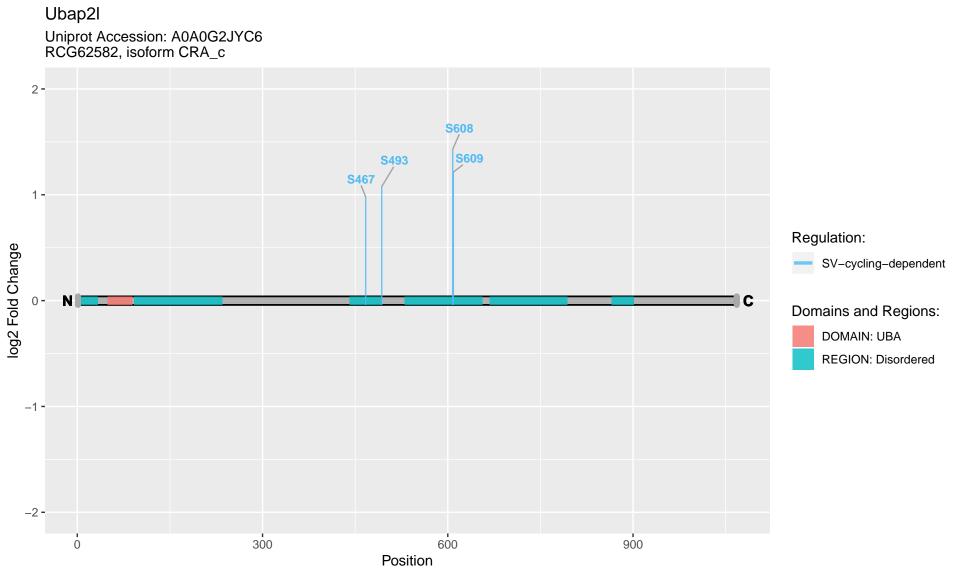


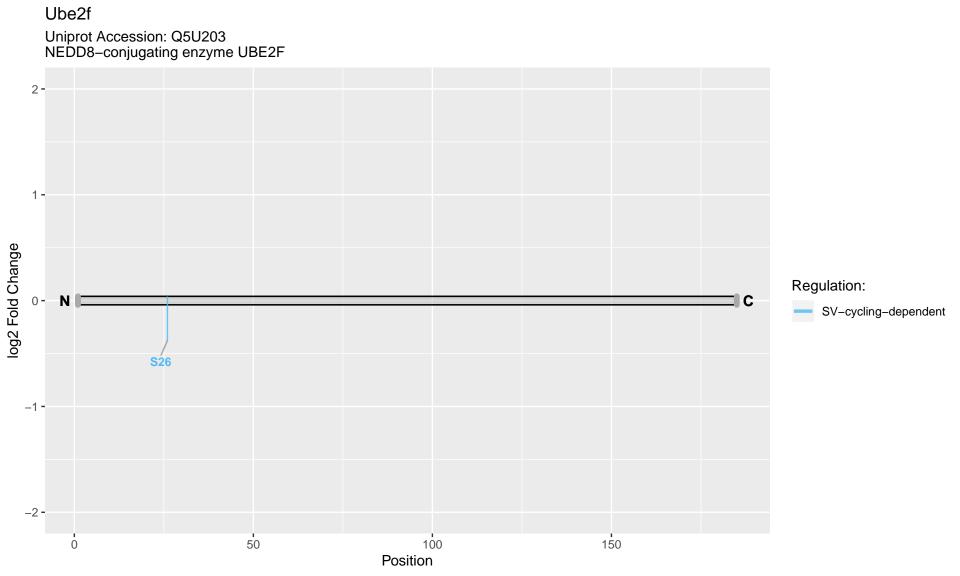


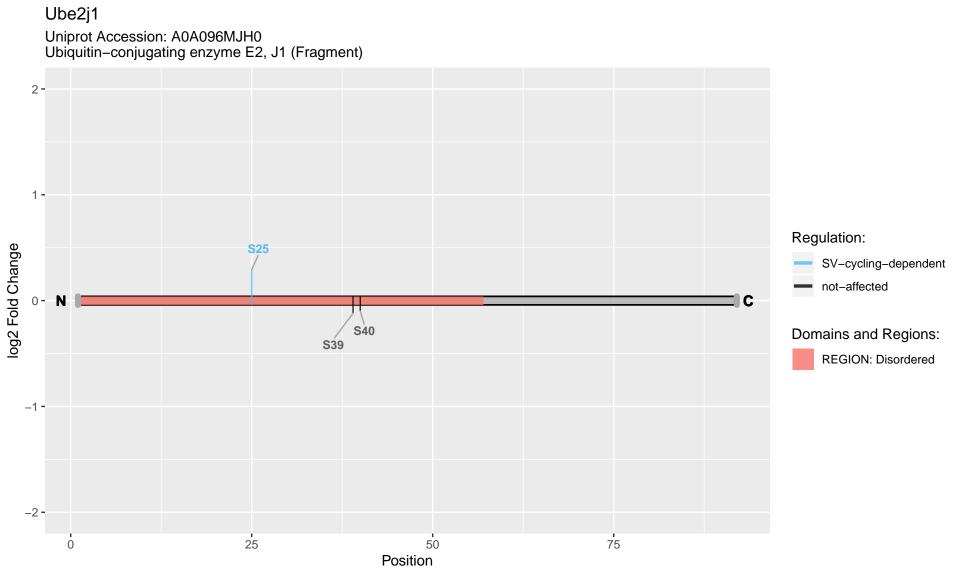


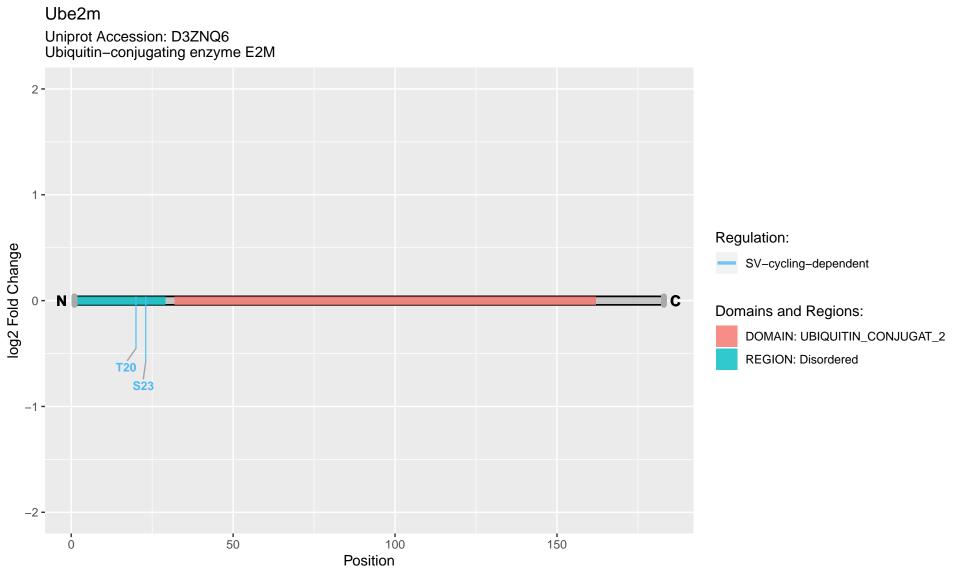


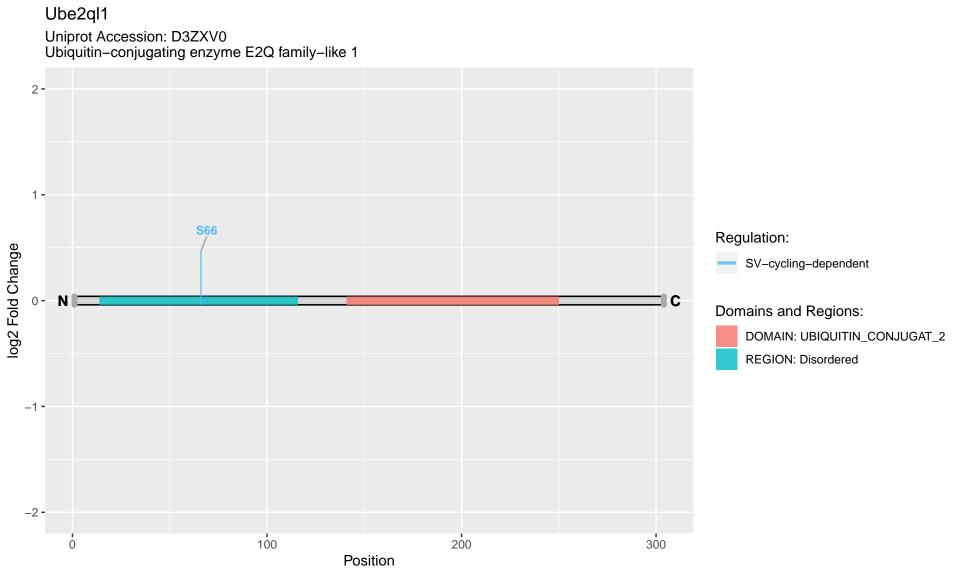


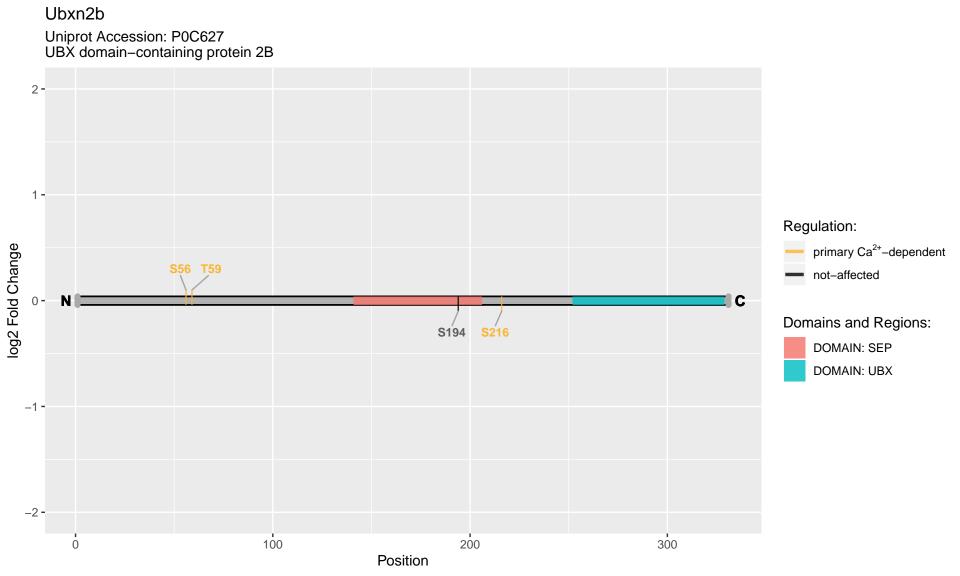


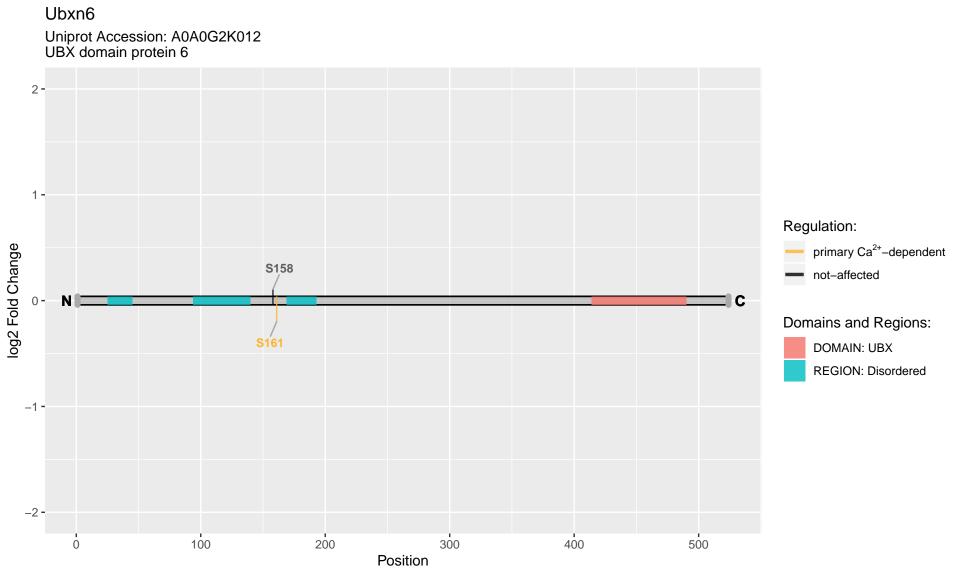


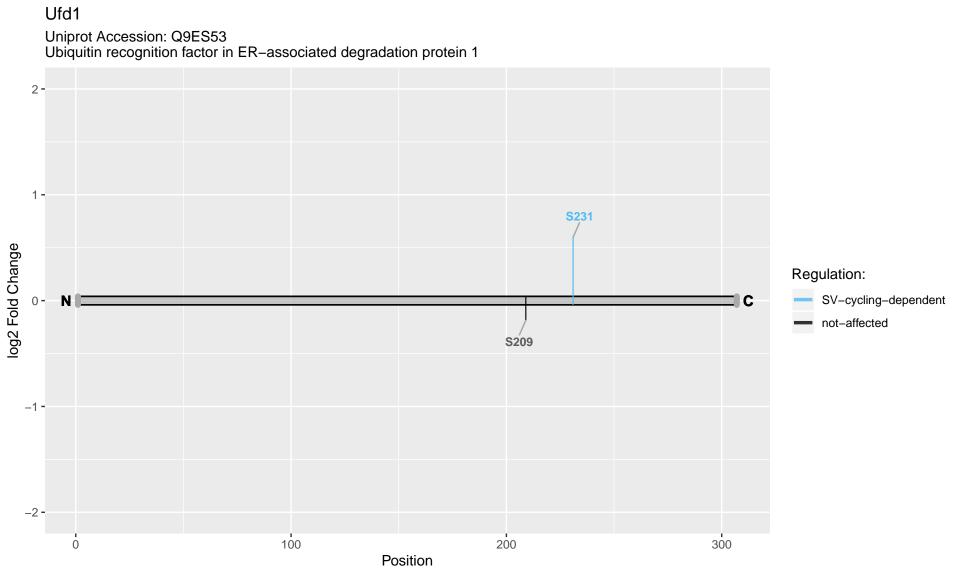


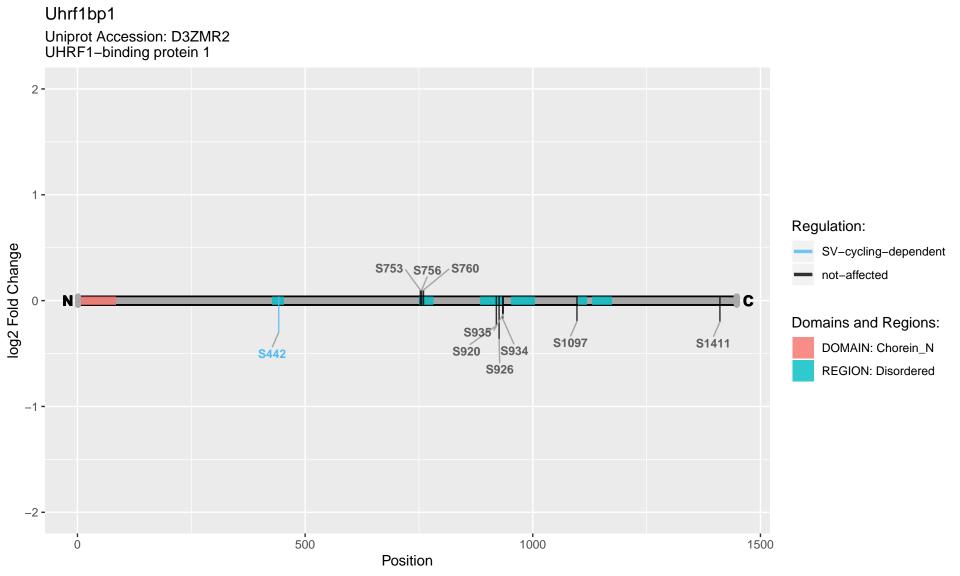


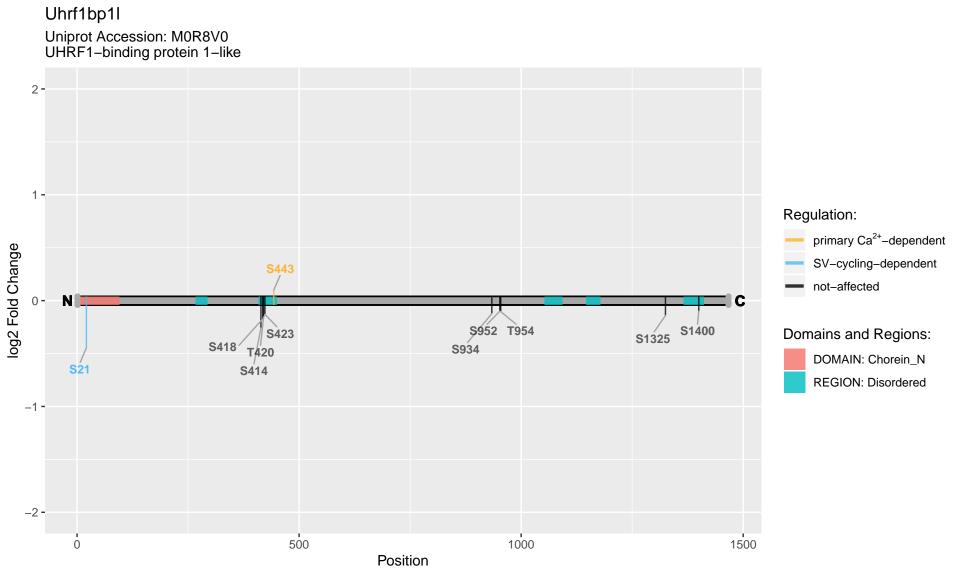


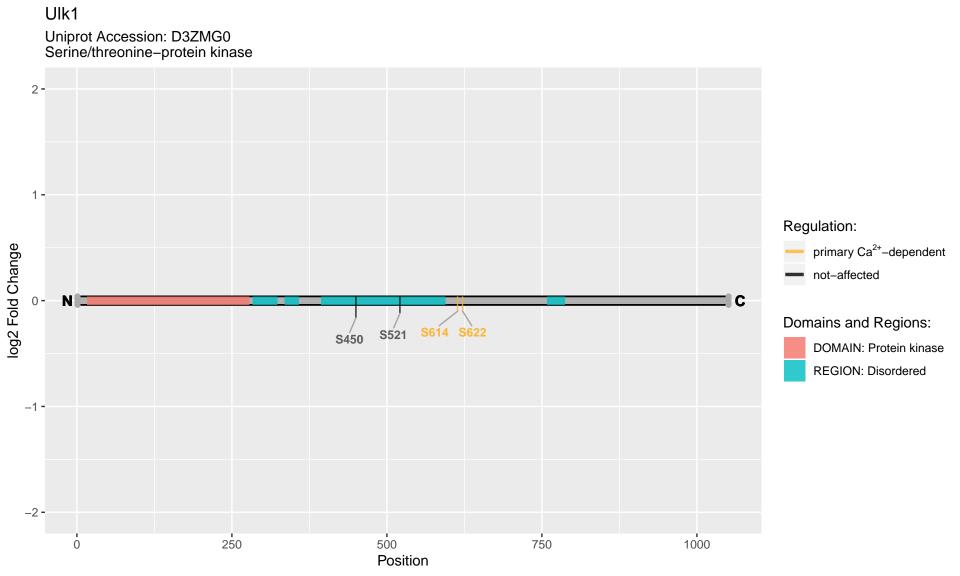


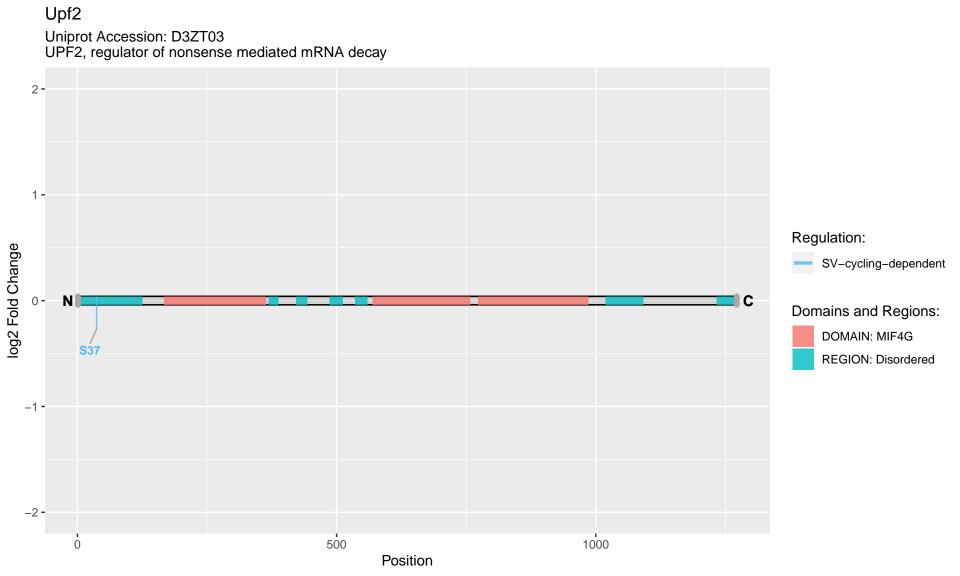


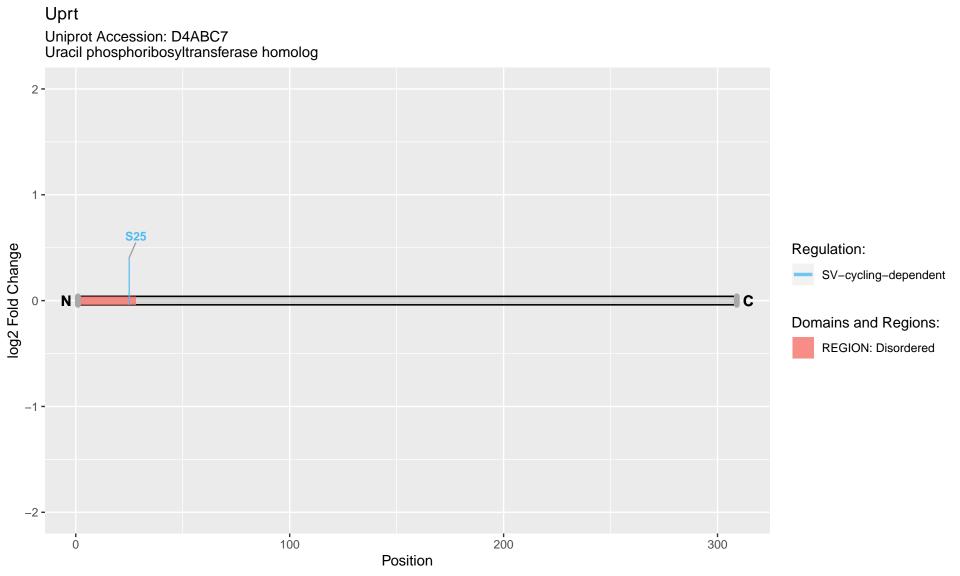


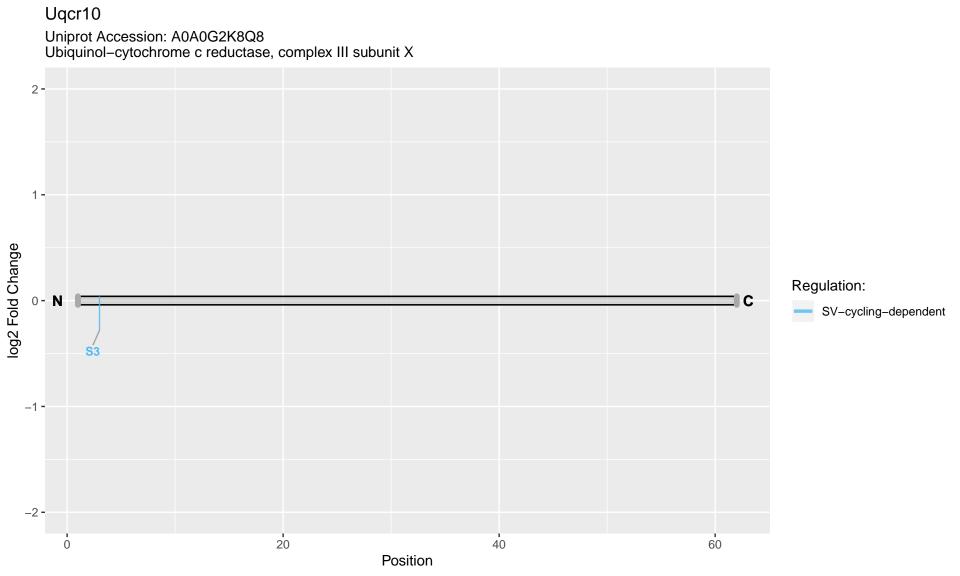


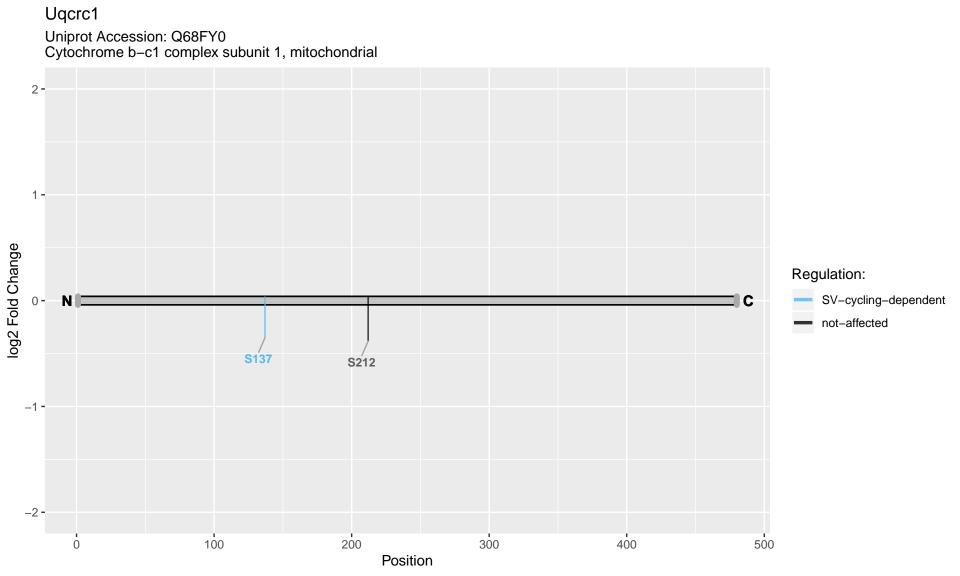


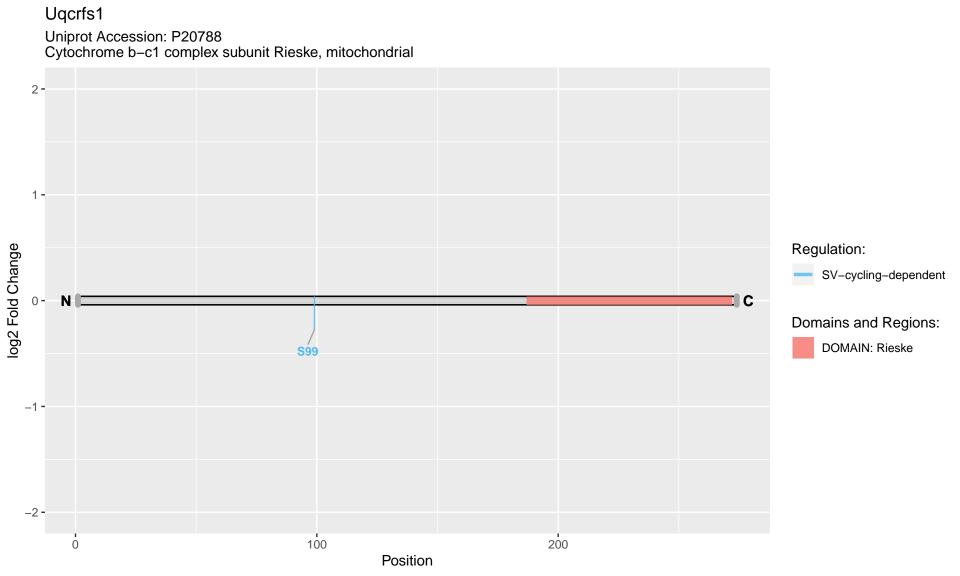


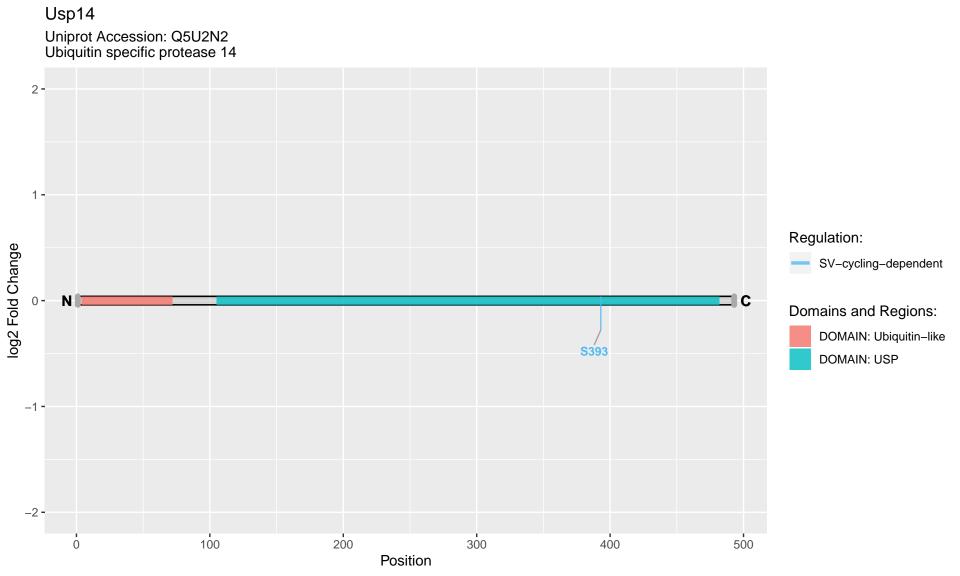


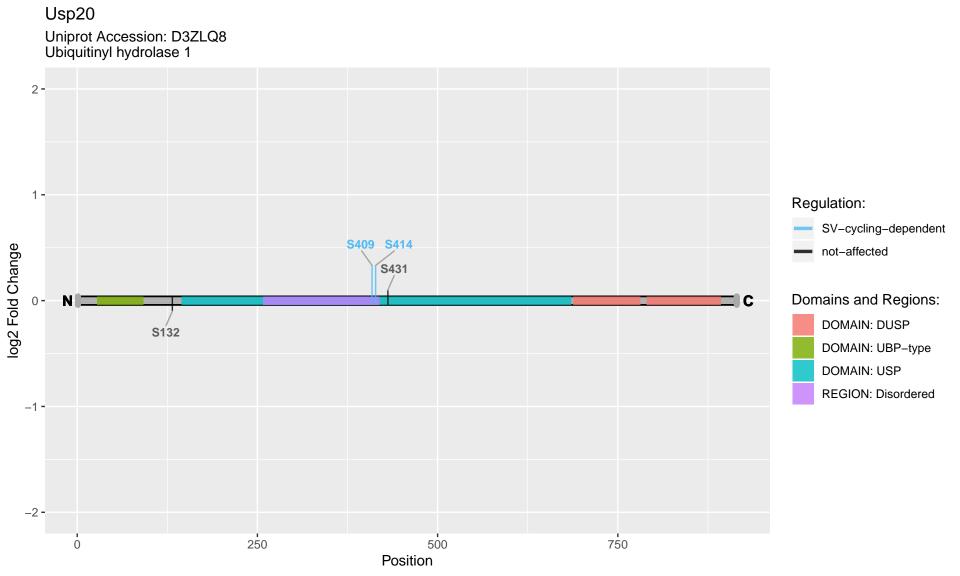


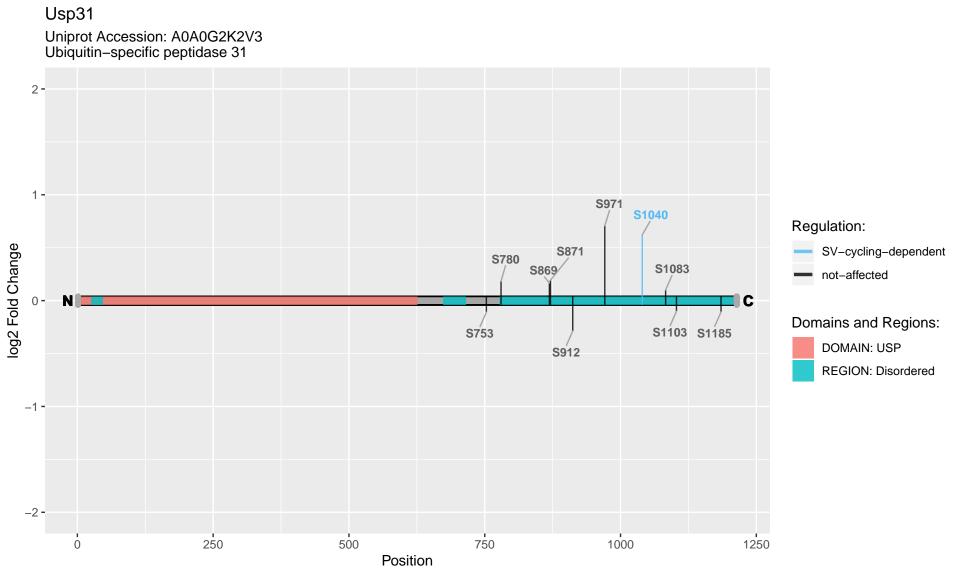


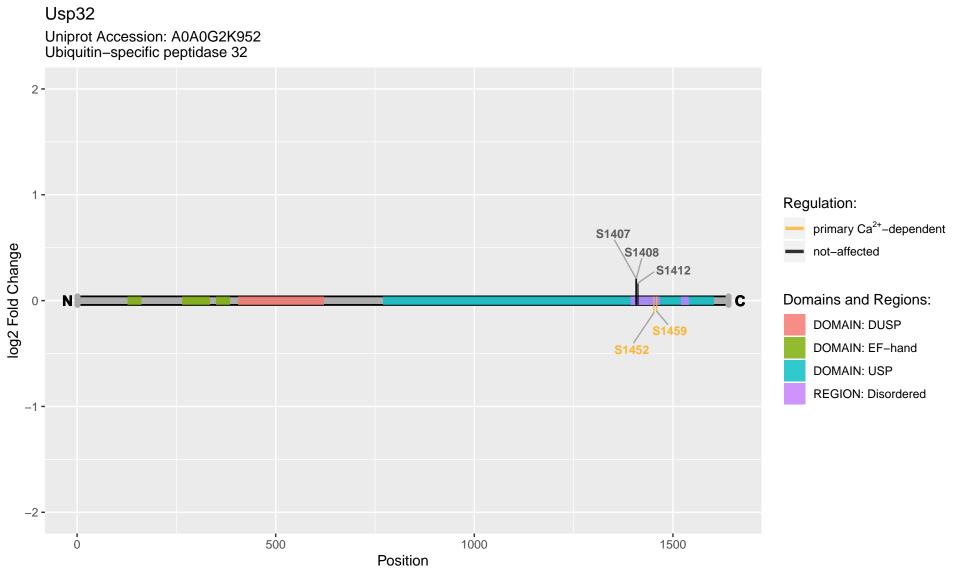


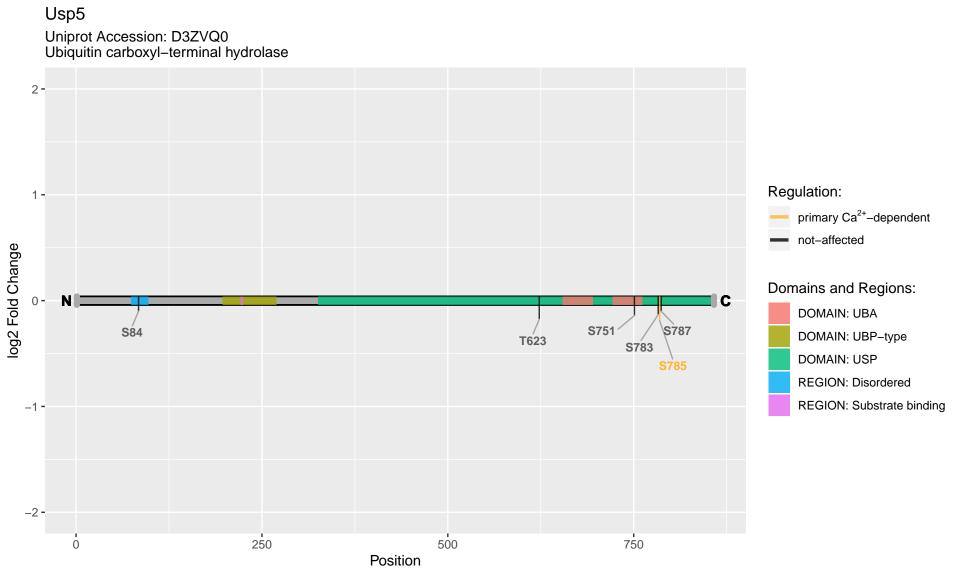


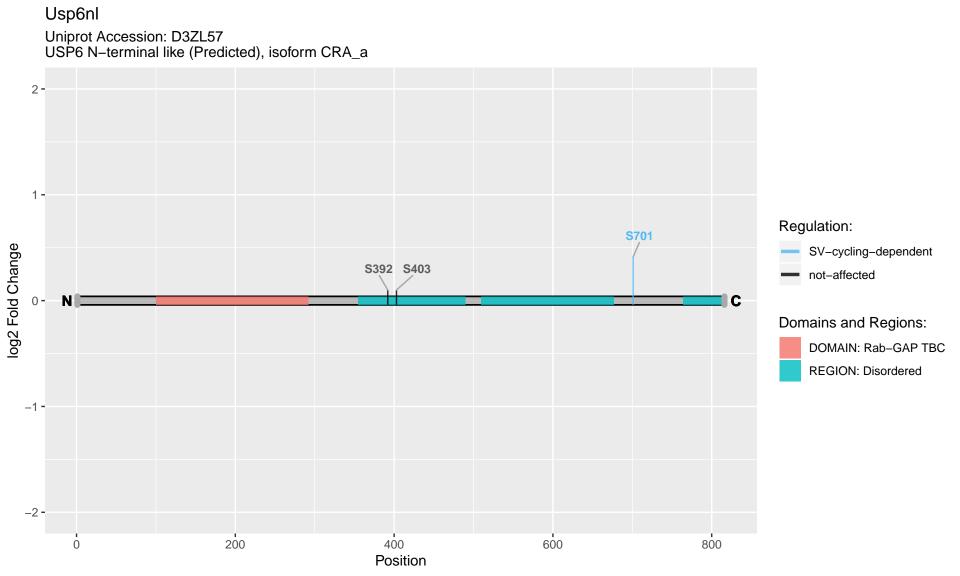


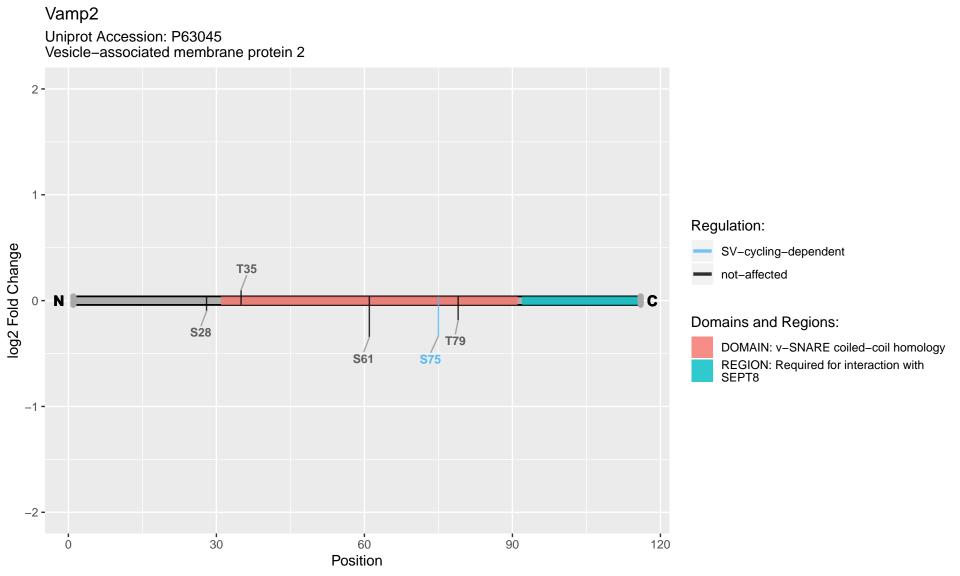


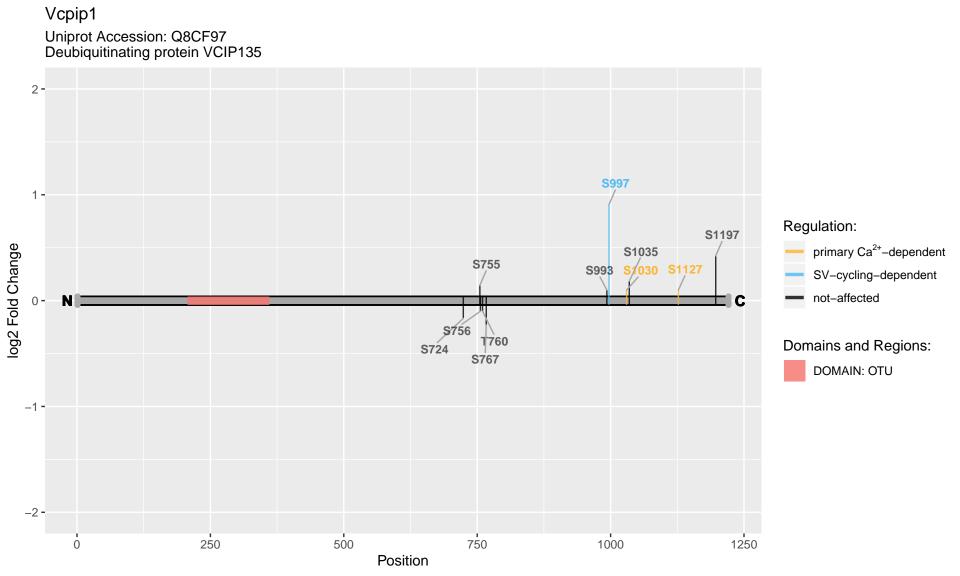


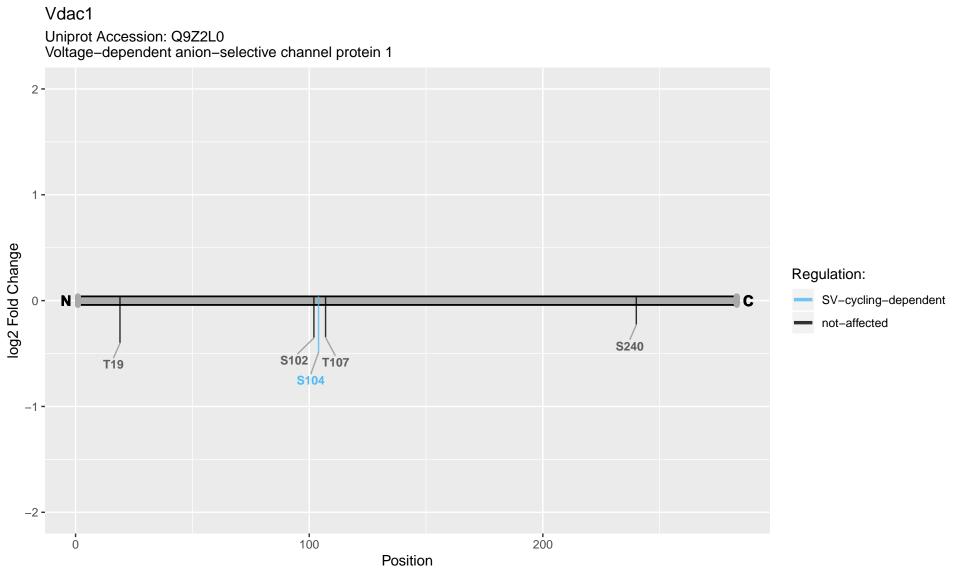


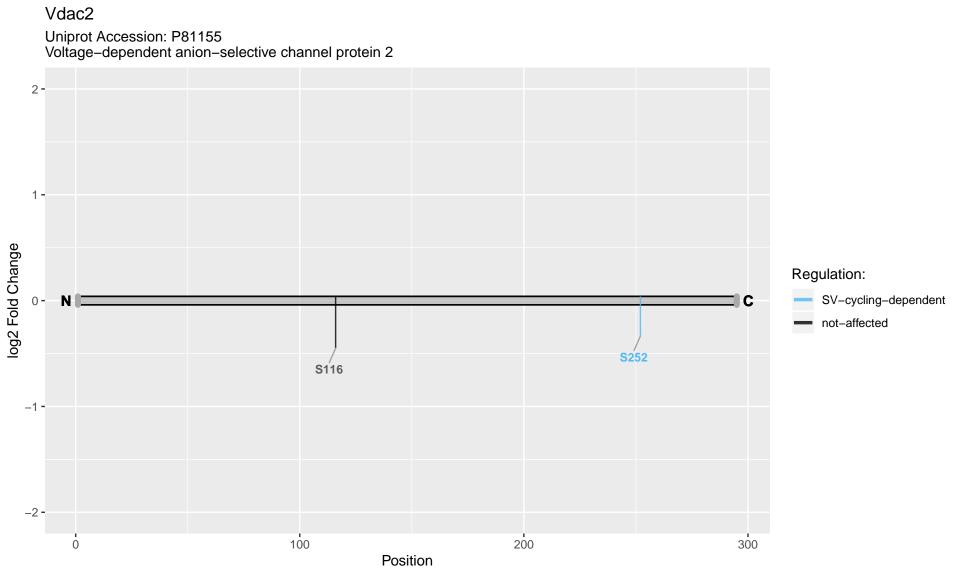


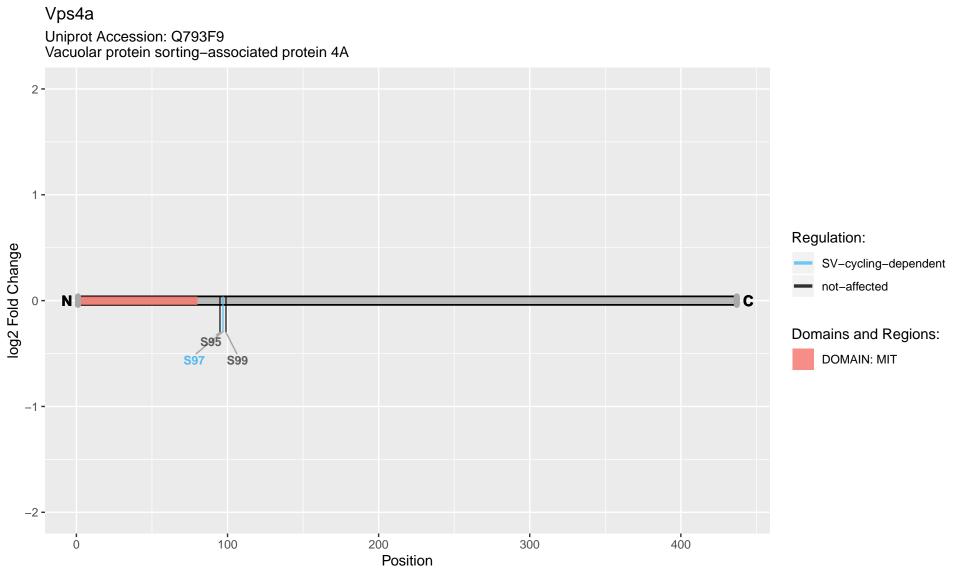


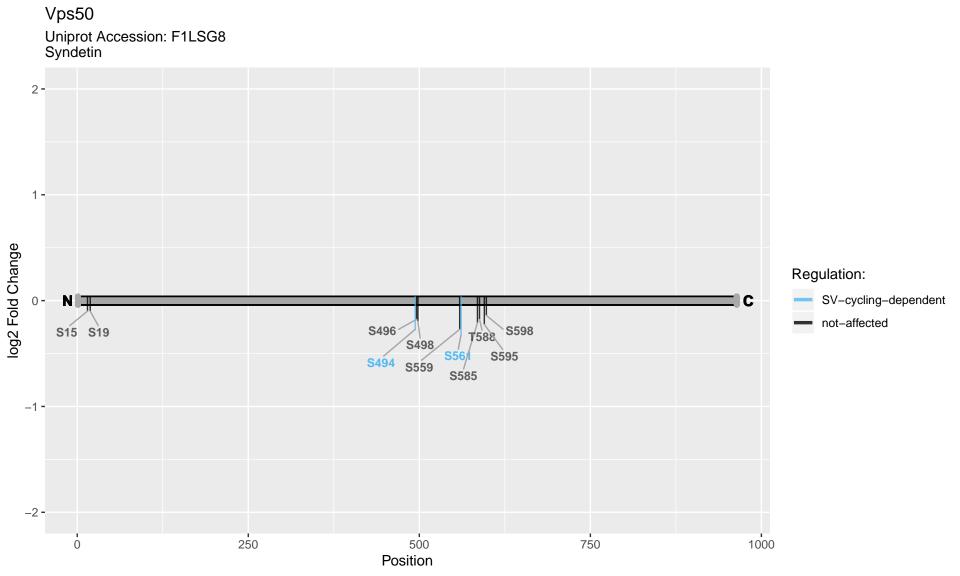


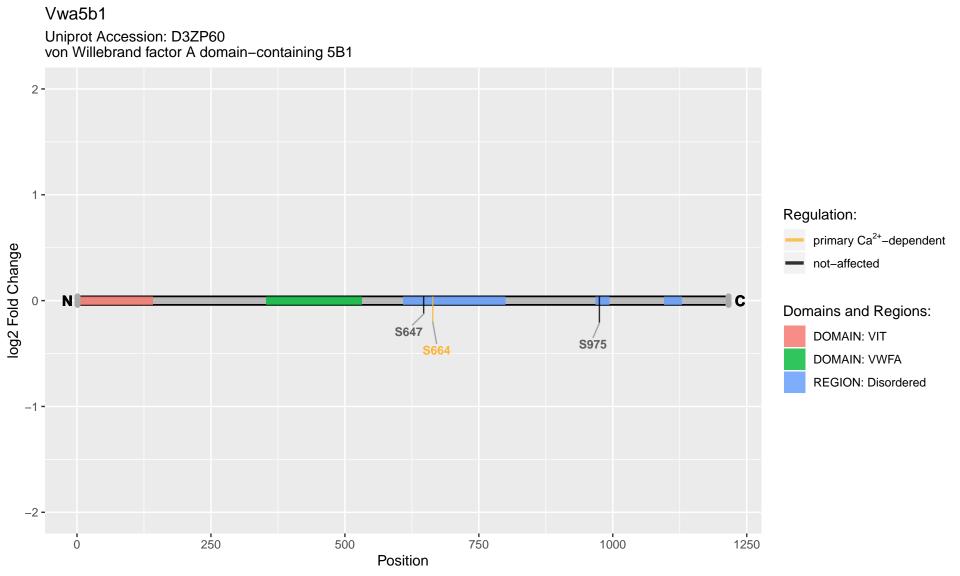


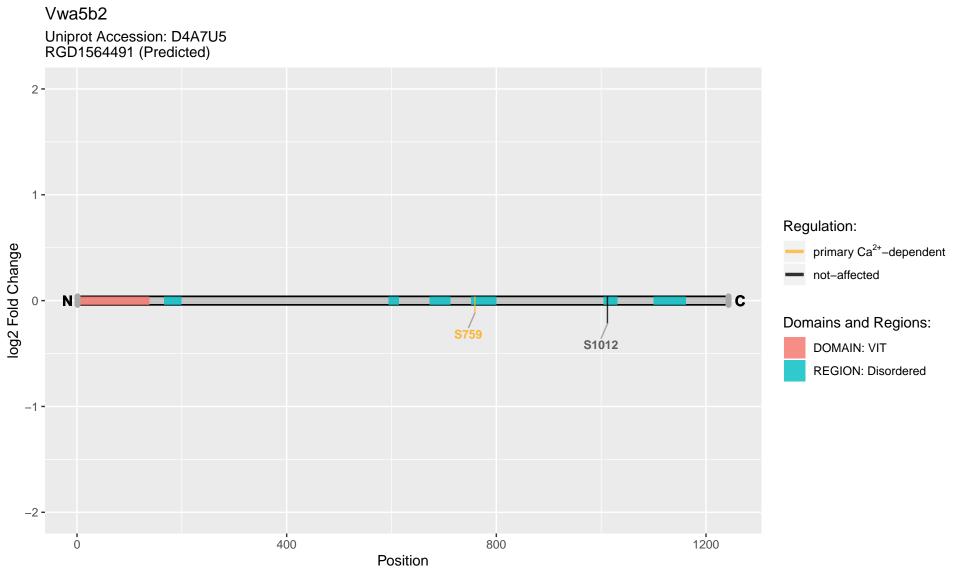


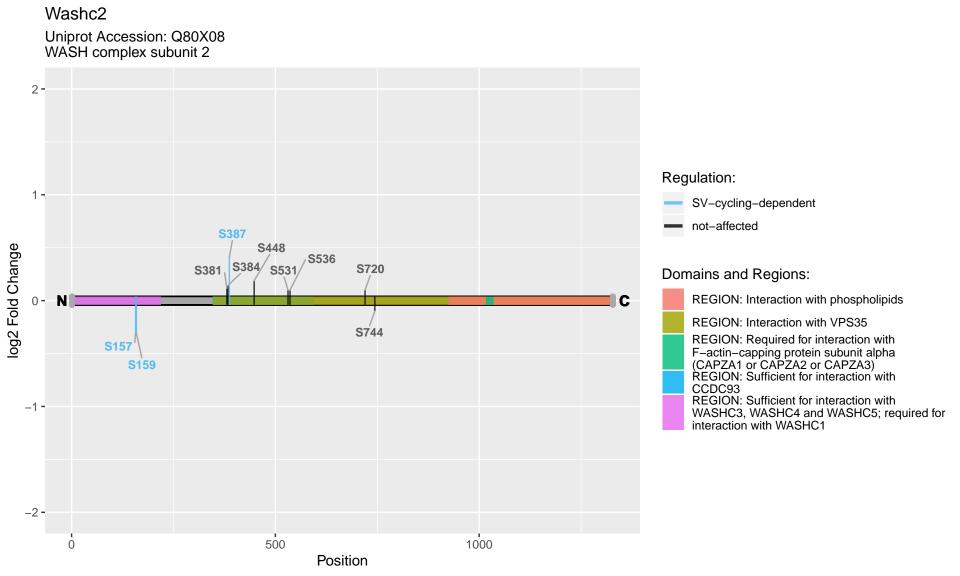


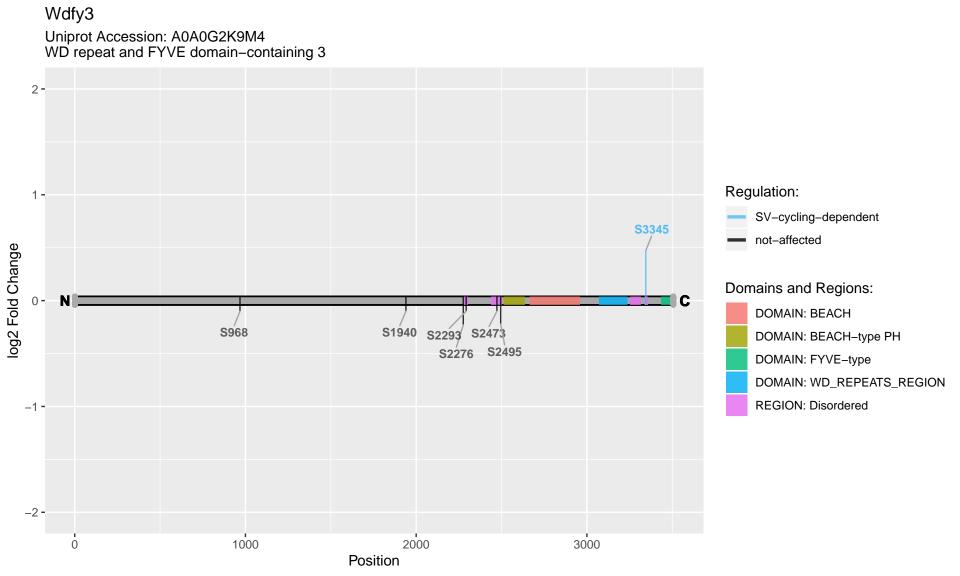


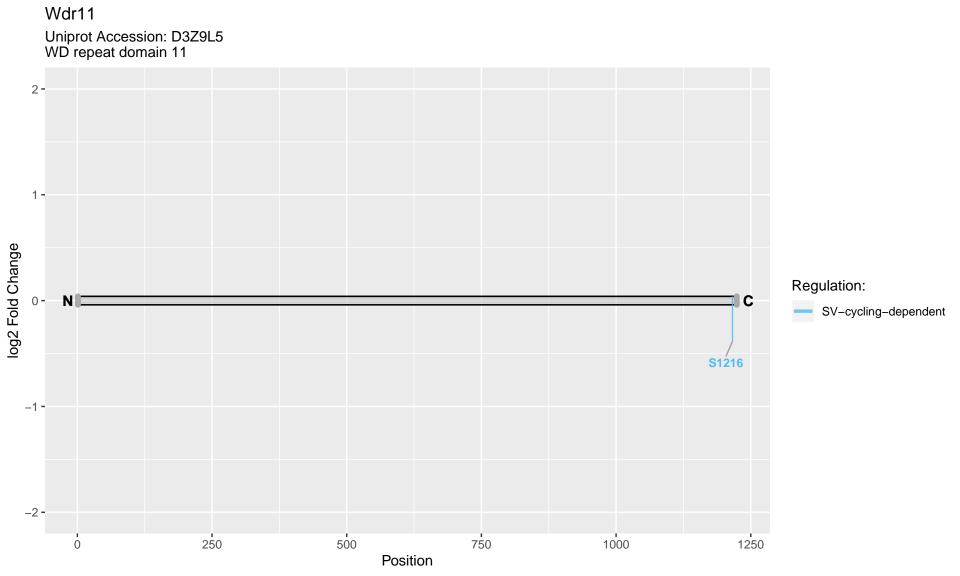


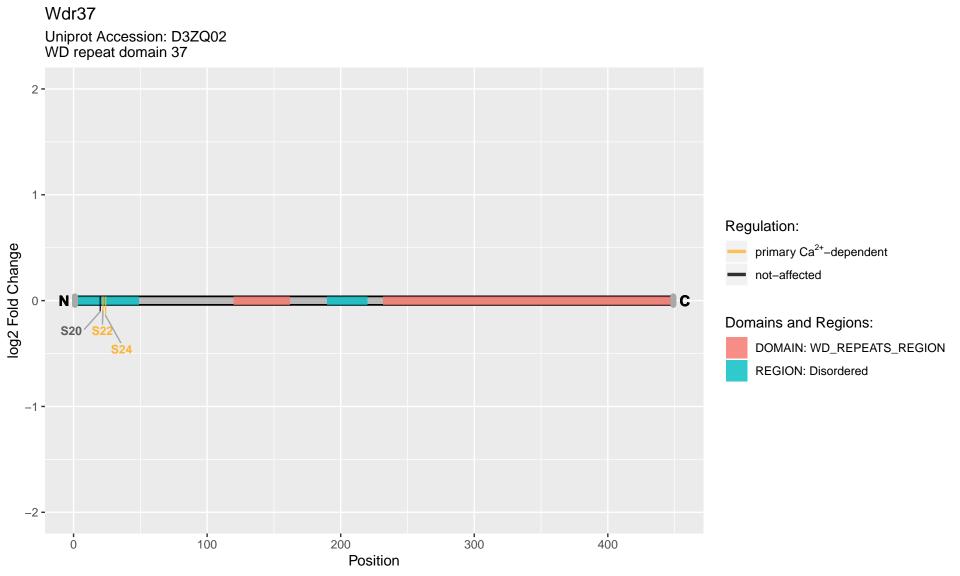


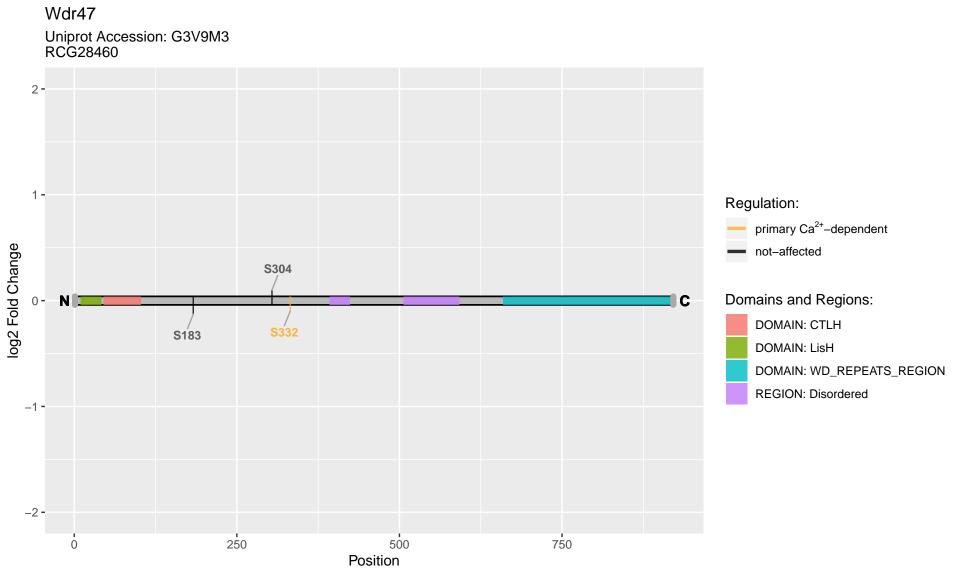


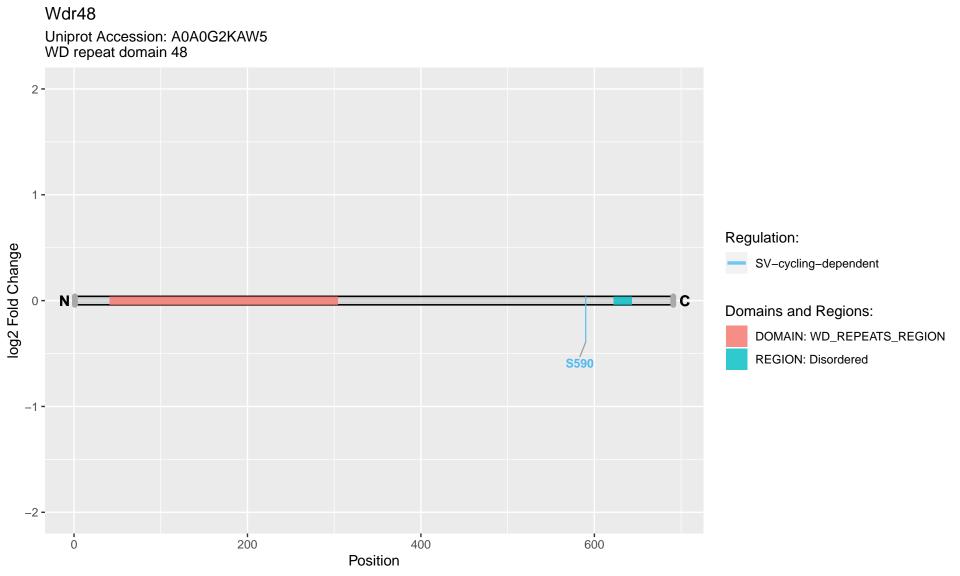


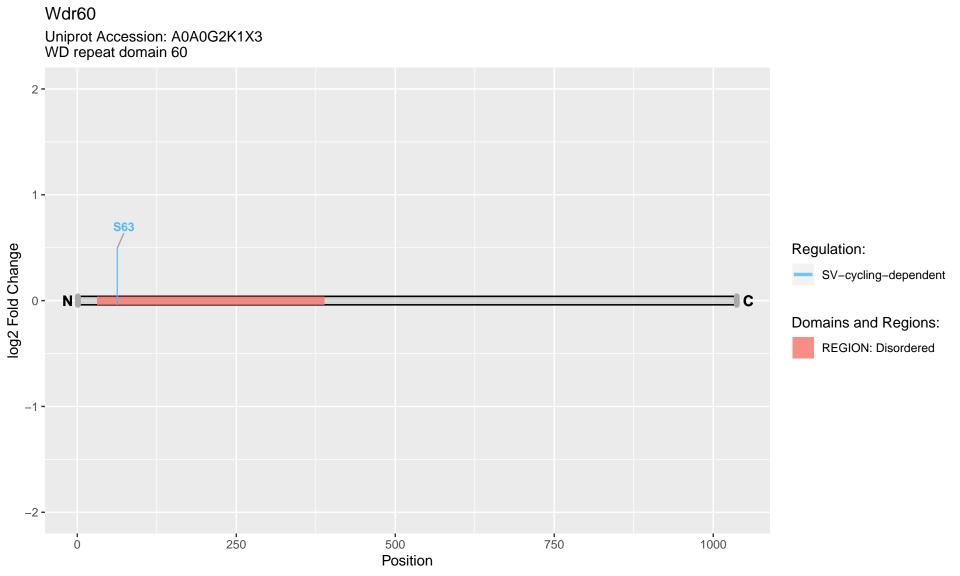


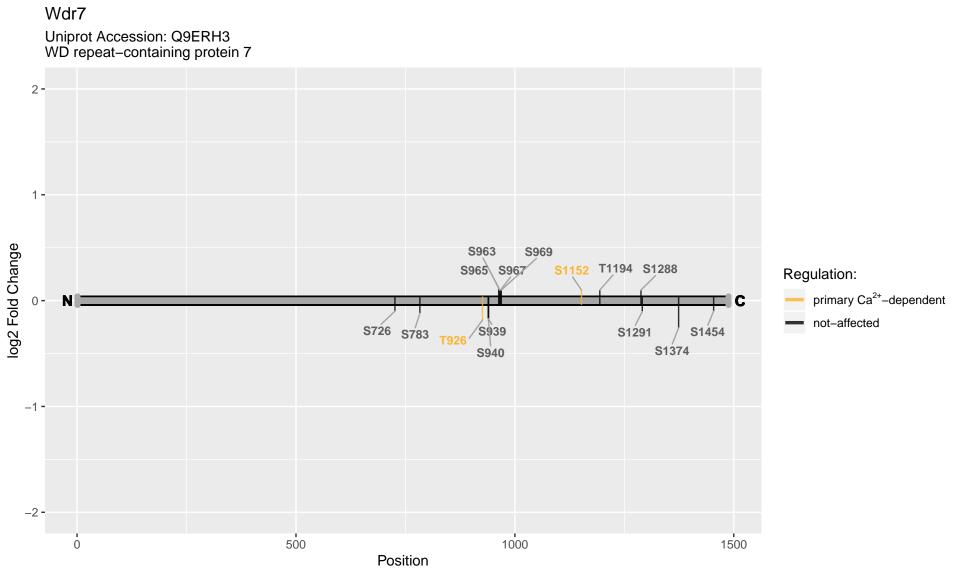


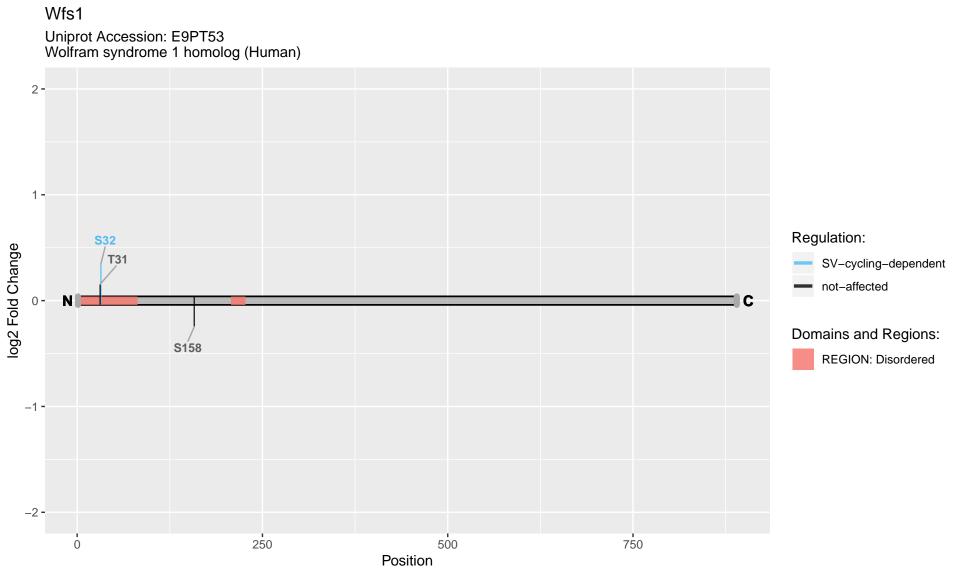


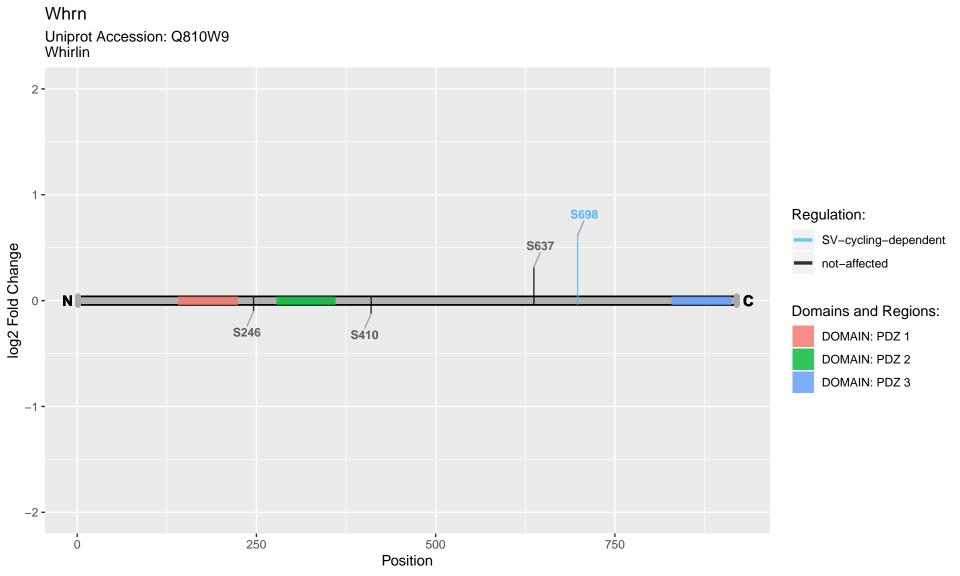


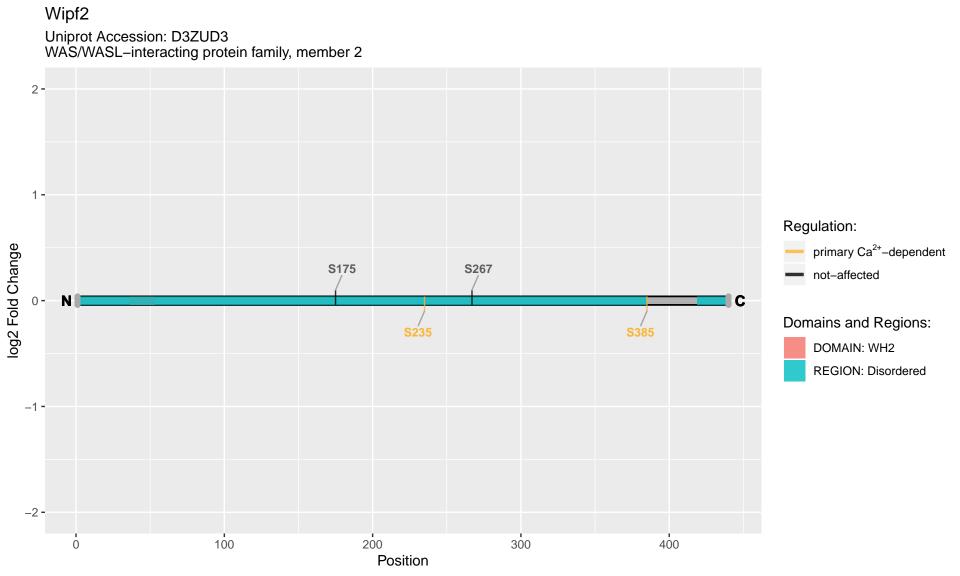


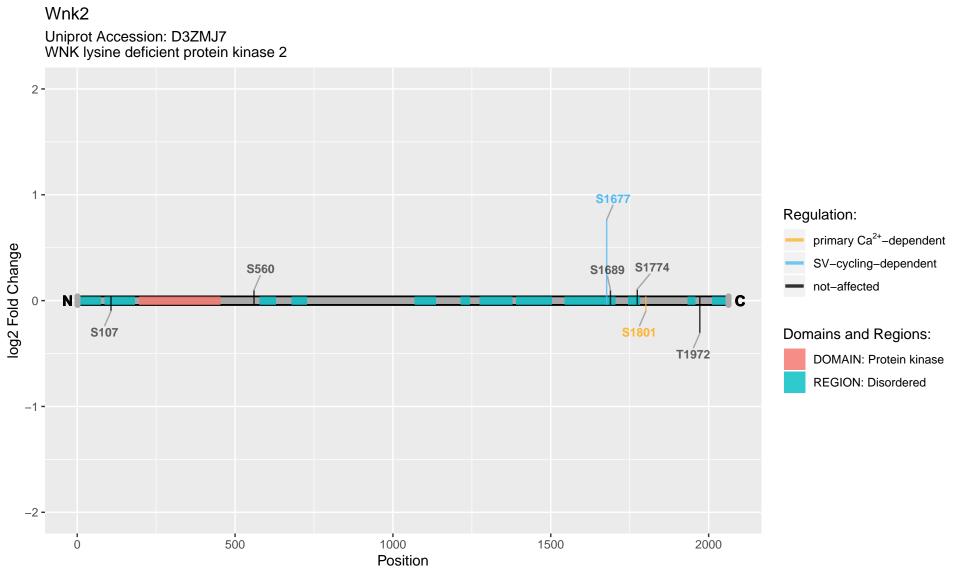


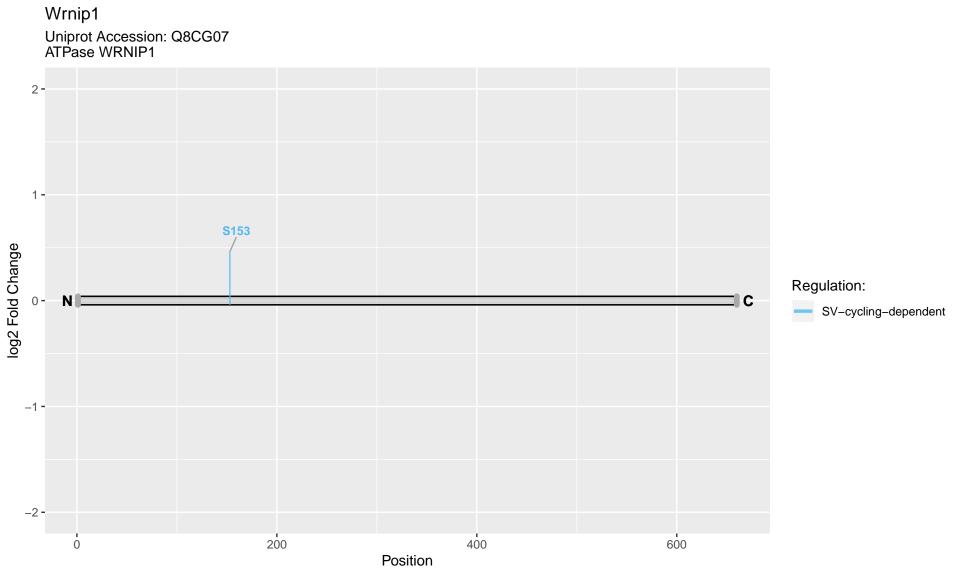


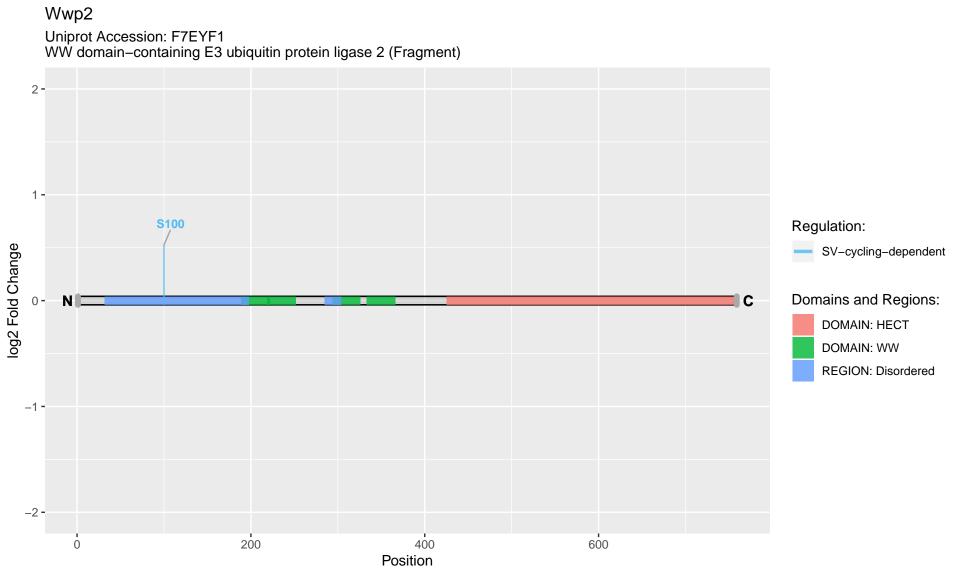


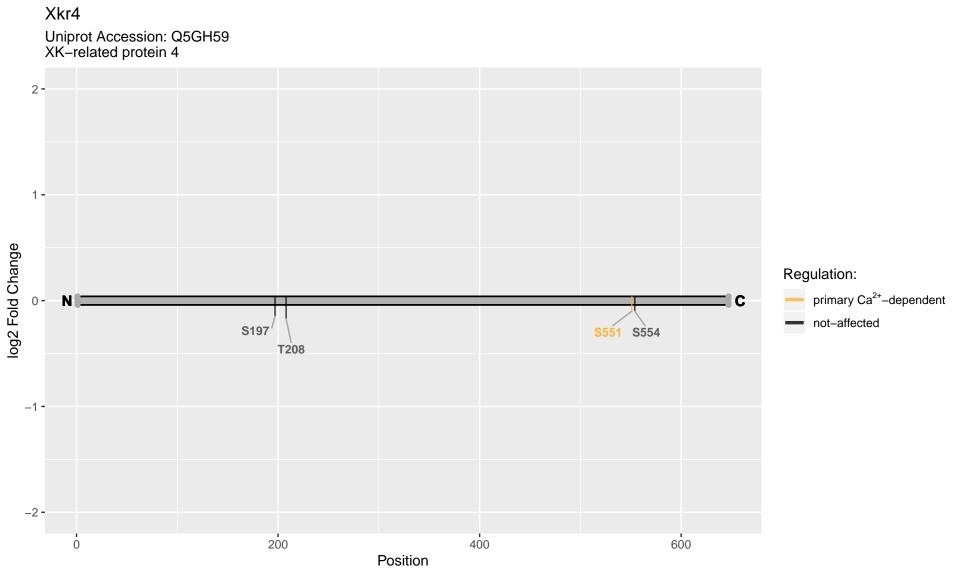


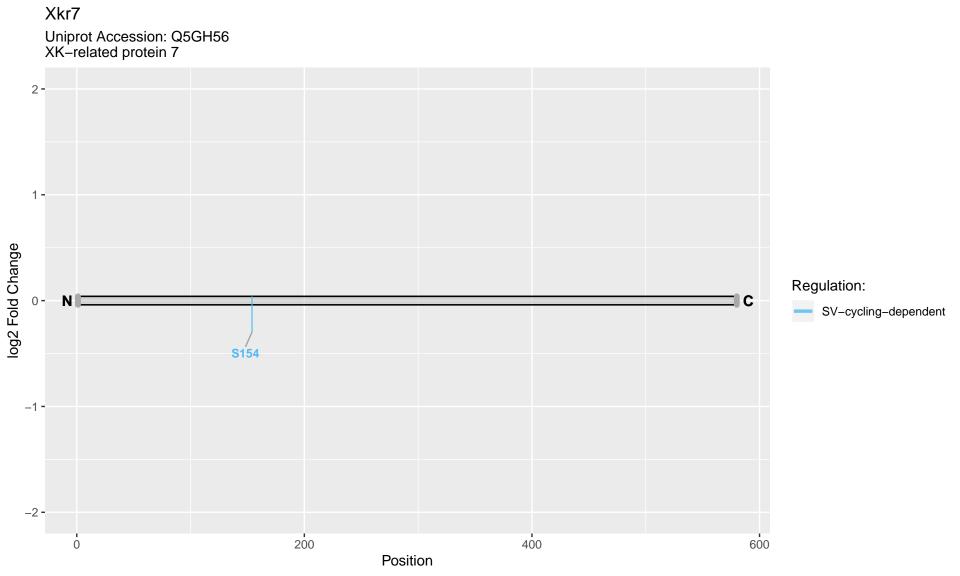


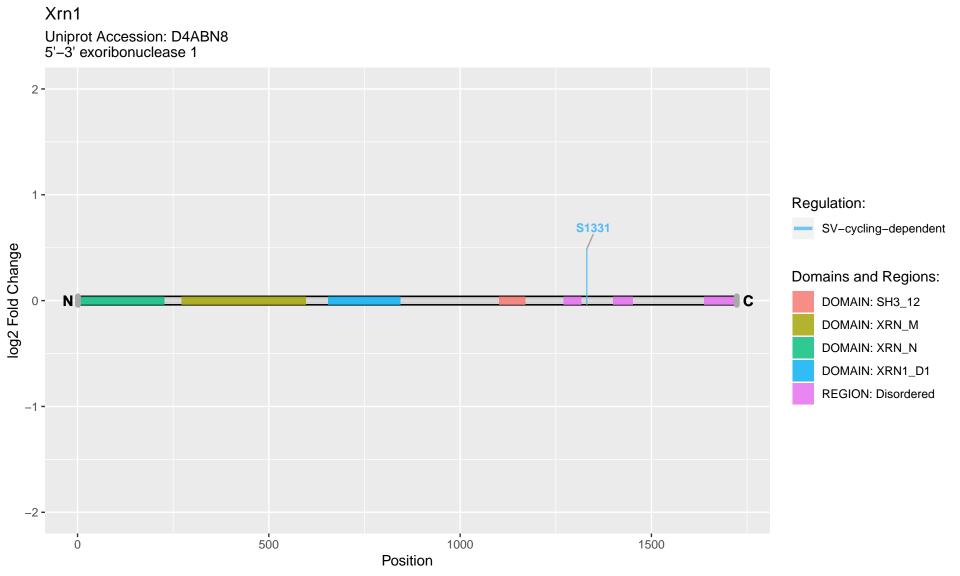


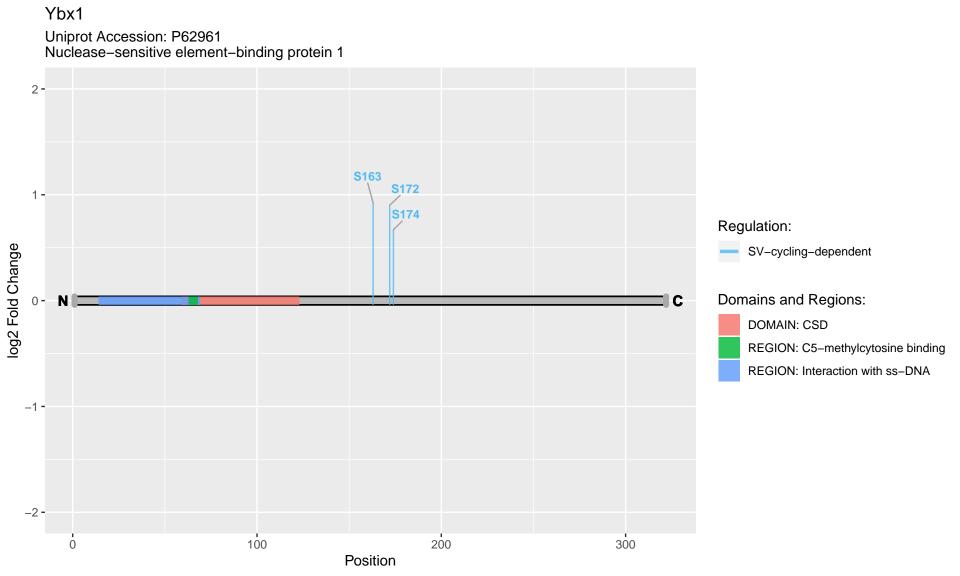


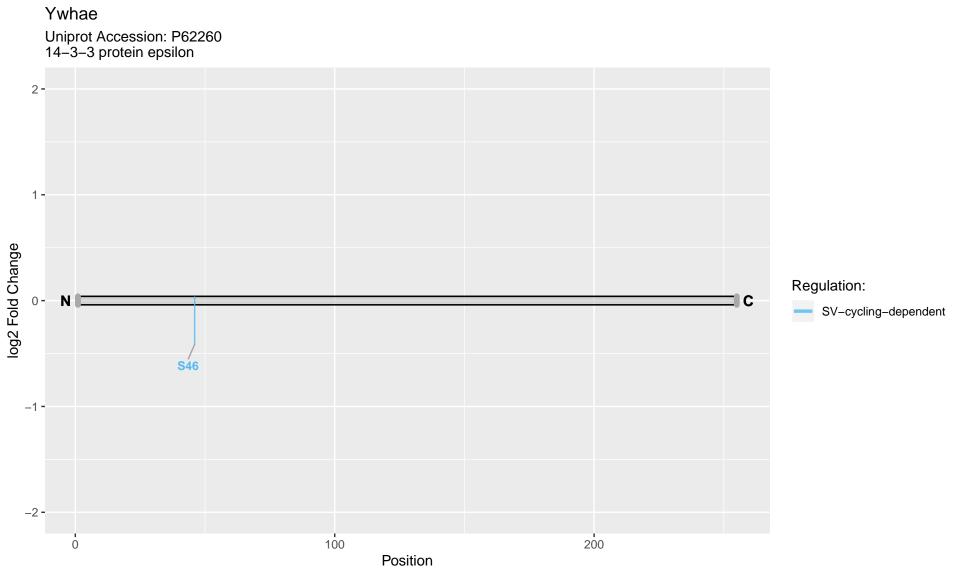


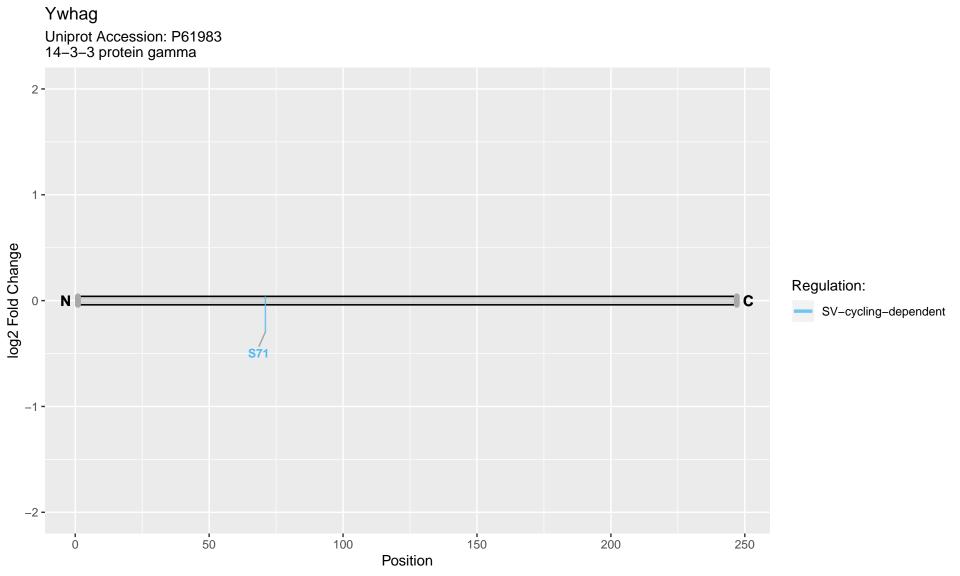


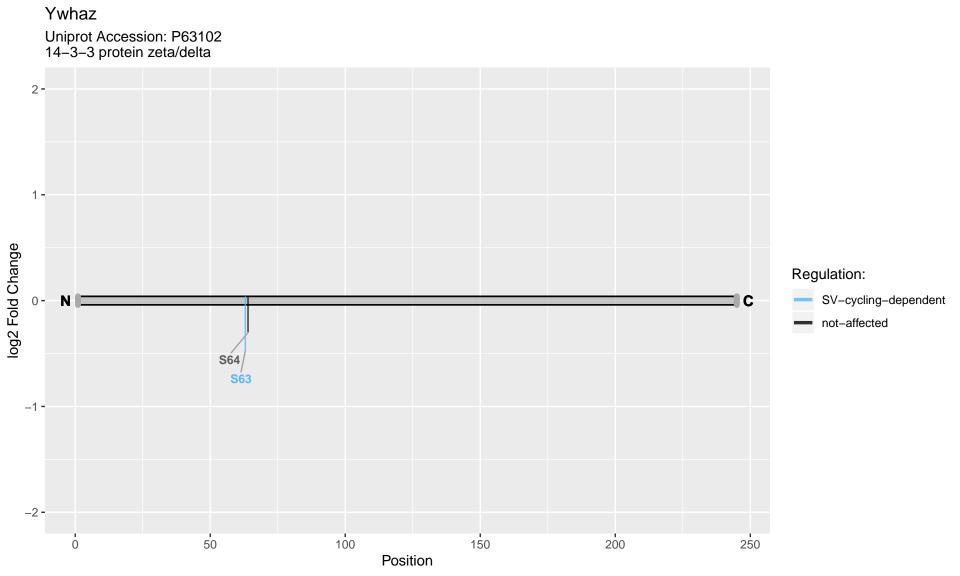












Zbtb16 Uniprot Accession: Q5S3S9 Promyelocytic leukemia zinc finger protein 2 -Regulation: SV-cycling-dependent log2 Fold Change T282 not-affected Domains and Regions: DOMAIN: BTB S302 S307 DOMAIN: C2H2-type **REGION: Disordered** -1 **-**-2 **-**200 400 600 Position

