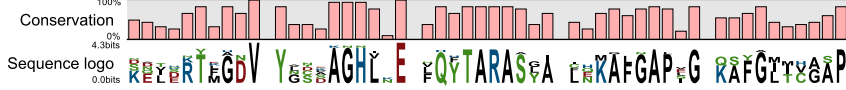


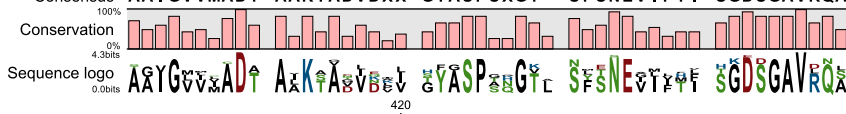




218363708: SEIERTMGDV YGSSAGHL-E FQYTARASYA LNKA GAP I G KSFGMT CASP 282  
 218425442: SEIERTMGDV YGSSAGHL-E FQYTARASYA LNKA GAP I G KSFGMT CASP 282  
 115511419: SEIERTMGDV YGSSAGHL-E FQYTARASYA LNKA GAP I G KSFGMT CASP 282  
 26111730: SEIERTMGDV YGSSAGHL-E FQYTARASYA LNKA GAP I G KSFGMT CASP 203  
 83574254: NEVHRTMGDV YGTPAGHL-E FQYTARASGA LNKA FGAP LG QAF A I T V GAP 310  
 90103542: SEVQRTMGDV YGTPAGHL-E FQYTARASYA LQKA FGAP LG QAF G I T V GAP 294  
 166852915: KELRRTFGDV YVNEAGHL-E FQYTARASYA LQKA FGAP LG KAF G L I V GAP 292  
 219567067: KQTDKY LGNV YLCDAGHL-E VQYTARASLI FEKAF GAP SG QAF G I MHAAP 326  
 152206095: KQTDKY LGNV YLCDAGHL-E VQYTARASLI FEKAF GAP SG QAF G I MHAAP 326  
 1072\_3: KQTDKY LGNV YLCDAGHL-E VQYTARASLI FEKAF GAP SG QAF G I MHAAP 319  
 29335721: DNL SRT FGDV YNSAAGHL-E LQFTARASGA CHMA FGAP EG KAY G L I CGAP 304  
 37542641: DNL SRT FGDV YNSAAGHL-E LQFTARASGA CHMA FGAP EG KAY G L I CGAP 304  
 116098028: DNL SRT FGDV YNSAAGHL-E LQFTARAAGA CHMA FGAP EG KAY G L I CGAP 192  
 111075047: KELDRTFGDV YAGDAGHL-E LQYTARASLA IQKAFNAPV G KAF G L I V GAP 186  
 118133308: KALERTFGDV YGCDAGHL-E LHYTARASYA LEKGF GAP V G KSF G I I V GAP 211  
 169119423: KD - - - TKA - V - - - DKAGHVN - 213  
 152933790: KD - - - TKA - V - - - DKAGHVN - 213  
 169405180: KDVDNTEH - V - - - DTKNNKE - 193



218363708: AA GLV I ADA AAKSAVIDPV GYASPSQGT - SFSNEV I FT F SGDSGAVRQA 331  
 218425442: AA GLV I ADA AAKSAVIDPV GYASPSQGT - SFSNEV I FT F SGDSGAVRQA 331  
 115511419: AA GLV I ADA AAKSAVIDPV GYASPSQGT - SFSNEV I FT F SGDSGAVRQA 331  
 26111730: AA GLV I ADA AAKSAVIDPV GYASPSQGT - SFSNEV I FT F SGDSGAVRQA 252  
 83574254: AA GVM I ADT AAKAATVQAV GYASPGNGT - SFSNEV I FM F TGDSDGAVRQA 359  
 90103542: AA GVV I ADT AAKAATVQAV GYASPGNGT - SFSNEV I FM F SGDSGAVRQS 343  
 166852915: AA GVL CDT AVKAAEVEV I GYASPAKGT - SMTNEA I LF F SGDSGAVRQA 341  
 219567067: AGVGM I ADT ALKTADV KLI TYGSP TNGVL SYTNE L I T I SGDSGAVLQS 376  
 152206095: AGVGM I ADT ALKTADV KLI TYGSP TNGVL SYTNE L I T I SGDSGAVLQS 376  
 1072\_3: AGVGM I ADT ALKTADV KLI TYGSP TNGVL SYTNE L I T I SGDSGAVLQS 369  
 29335721: TG I GVM ADT A I KTAGV N L SFASPAHGT - SFSNEGMV H I SGDSGAVRQA 353  
 37542641: AG I GVM ADT A I KTAGV N L SFASPAHGT - SFSSEGMV H I SGDSGAVRQA 353  
 116098028: SG I GVM ADT A I KTAGV N L TFASPGHGT - SFSNEGI V H I SGDSGAVRQA 241  
 111075047: AA I GVL MADT A I K T A N V D I V GYASPAAGT - SFSNEV I L M V TGDSDGAVRQS 235  
 118133308: AA I GVM ADT A I K T A N V E M I SYASPSQGT A N - SNEV I I T I TGDSDGAVRQS 260  
 169119423: - - - - - D - - - - - VD LDK I H - - - - - KL NLEN - - - - - L HKDD - - - - - V DNL 236  
 152933790: - - - - - D - - - - - VD LDK I H - - - - - KL NLEN - - - - - L HKDD - - - - - V DNL 236  
 169405180: - - - - - D - - - - - GD LDK I H - - - - - KL NLEN - - - - - L HKED - - - - - V DNL 216



218363708: V I AAREVGLK LLSTLD - - PV - E I KSTT - - - - 355  
 218425442: V I AAREVGLK LLSTLD - - PV - E I KSTT - - - - 355  
 115511419: V I AAREVGLK LLSTLD - - PV - E I KSTT - - - - 355  
 26111730: V I AAREVGLK LLSTLD - - PV - E I KSTT - - - - 276  
 83574254: V I AARDV GKT LLATLD - - PS - E I KSTT - - - - 383  
 90103542: V I AARDV GKR LLATLD - - PA - E I KSTT - - - - 367  
 166852915: I I AAREVGLK LLSTLGEAP - - - - KSLSGEP Y 368  
 219567067: LTAARKAGLS ILRSMGQDPV - SMSKPT - - - - F 403  
 152206095: LTAARKAGLS ILRSMGQDPV - SMSKPT - - - - F 403  
 1072\_3: LTAARKAGLS ILRSMGQDPV - SMSKPT - - - - F 396  
 29335721: V I AGREVGLK LLAE LGDTPV NDFPS - - - - Y 379  
 37542641: V I AGREVGLK LLAE LGDTPV NDFPS - - - - Y 379  
 116098028: V I AGREVGLK LLAQ I GENPV NDFPS - - - - Y 267  
 111075047: V I AAREL GKK LLEAMA - GPA PSVTK - - - - - 259  
 118133308: VMAAREVGLG ILRSMGQNPV - - - - STTEP - - - - - 285  
 169119423: V - - - RKNGL E KA - - - - - - - - - - - - - - - 245  
 152933790: V - - - RKNGL E KA - - - - - - - - - - - - - - - 245  
 169405180: V - - - RKNGL E - - - - - - - - - - - - - - - - 222

