176 175 177 171 128 139 135 127 127 147 78 --TALQKH VAFFDQNKDG ||YPWETYKG FRXLGFGF|T --LTLSEX Ca<sup>2+</sup> binding EF Hand motif QKXARTCTDG VMPWETYR Heme binding and kinase phosphorylation domain ODG XXPKKFEQIF ONO 245 243 243 243 236 195 P 195 P 210 188 192 Histidine DSDTYDTDGR TALOKH Histidine KNIHKGKHGS FEQIAKKRAS C-terminal kinase phosphorylation domain N-terminal H caleosin domain XIRASYDGSL | PSPLLP | Y \* Proline knot FLSYPTQPSK DPEK GEWKFLX-LA XXPLQR-VR----XINL T L P L QQ Lipid-binding domain 4 - -LKLSXXNRXG FDPVGXXASK STXSAF Arclo3 Arclo3 Arclo3 Arclo4 Arclo6 Arclo6 Arclo6 Arclo6 Consensus PDA Consensus Atclos Atclos Atclos Atclos Atclos Atclos DL13 PDA DF50 Consensus AICLO2
AICLO2
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AICLO3
AICLO3
AICLO4
AICLO6 PDA PS1159\_g7126.t1\_PF05042 PS1159\_g7126.t1\_PF05042 **DF**50 PS1159 g7126.t1 PF05042 DL13