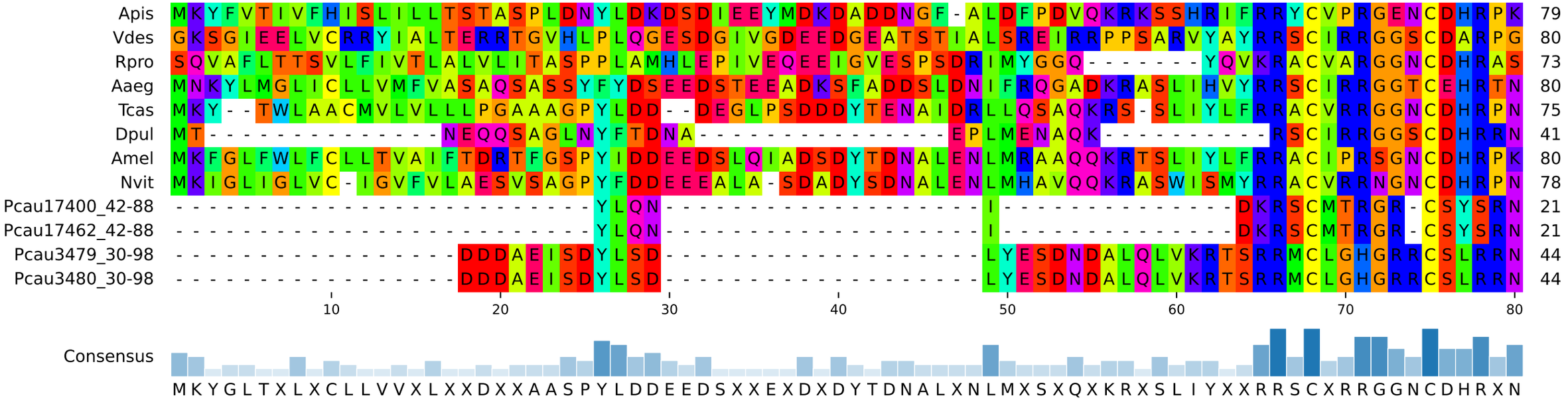
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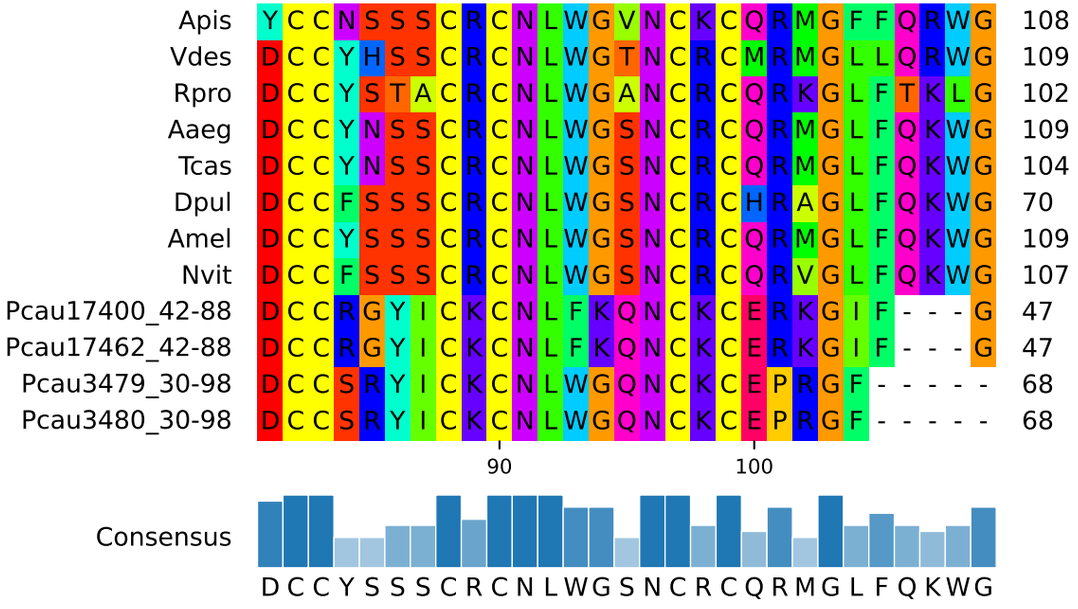
Vdes GKSGIEELVCRRYIALTERRTGVHLPLQGESDGIVGDEEDGEATSTIALSREIRRPPSARVYAYRRSCIRRGGSCDARPG 80
Rpro SQVAFLTTSVLFIVTLALVLITASPPLAMHLEPIVEQEEIGVESPSDRIMYGGQ-------YQVKRACVARGGNCDHRAS 73
Aaeg MNKYLMGLICLLVMFVASAQSASSYFYDSEEDSTEEADKSFADDSLDNIFRQGADKRASLIHVYRRSCIRRGGTCEHRTN 80
Tcas MKY--TWLAACMVLVLLLPGAAAGPYLDD--DEGLPSDDDYTENAIDRLLQSAQKRS-SLIYLFRRACVRRGGNCDHRPN 75
Dpul MT----------NEQQSAGLNYFTDNA----------EPLMENAQK----------RSCIRRGGSCDHRRN 41
Amel MKFGLFWLFCLLTVAIFTDRTFGSPYIDDEEDSLQIADSDYTDNALENLMRAAQQKRTSLIYLFRRACIPRSGNCDHRPK 80
Nvit MKIGLIGLVC-IGVFVLAESVSAGPYFDDEEEALA-SDADYSDNALENLMHAVQQKRASWISMYRRACVRRNGNCDHRPN 78
Pcau17400_42-88 ----------YLQN----------I----------DKRSCMTRGR-CSYSRN 21
Pcau17462_42-88 ----------YLQN----------I----------DKRSCMTRGR-CSYSRN 21
Pcau3479_30-98 ----------DDDAEISDYLSD----------LYESDNDALQLVKRTSRRMCLGHGRRCSLRRN 44
Pcau3480_30-98 ----------DDDAEISDYLSD----------LYESDNDALQLVKRTSRRMCLGHGRRCSLRRN 44
10 20 30 40 50 60 70 80
Consensus
MKYGLTXLXCLLVVXLXXDXXAASPYLDDEEDSXXEXDXDYTDNALXNLMXSXQXKRXSLIYXXRRSCXRRGGNCDHRXN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Vdes DCCYHSSCRCNLWGTNCRCMRMGLLQRWG 109
Rpro DCCYSTACRCNLWGANCRCQRKGLFTKLG 102
Aaeg DCCYNSSCRCNLWGSNCRCQRMGLFQKWG 109
Tcas DCCYNSSCRCNLWGSNCRCQRMGLFQKWG 104
Dpul DCCFSSSCRCNLWGSNCRCHRAGLFQKWG 70
Amel DCCYSSSCRCNLWGSNCRCQRMGLFQKWG 109
Nvit DCCFSSSCRCNLWGSNCRCQRVGLFQKWG 107
Pcau17400_42-88 DCCRGYICKCNLFKQNCKCERKGIF---G 47
Pcau17462_42-88 DCCRGYICKCNLFKQNCKCERKGIF---G 47
Pcau3479_30-98 DCCSRYICKCNLWGQNCKCEPRGF----- 68
Pcau3480_30-98 DCCSRYICKCNLWGQNCKCEPRGF----- 68
90 100
Consensus
DCCYSSSCRCNLWGSNCRCQRMGLFQKWG