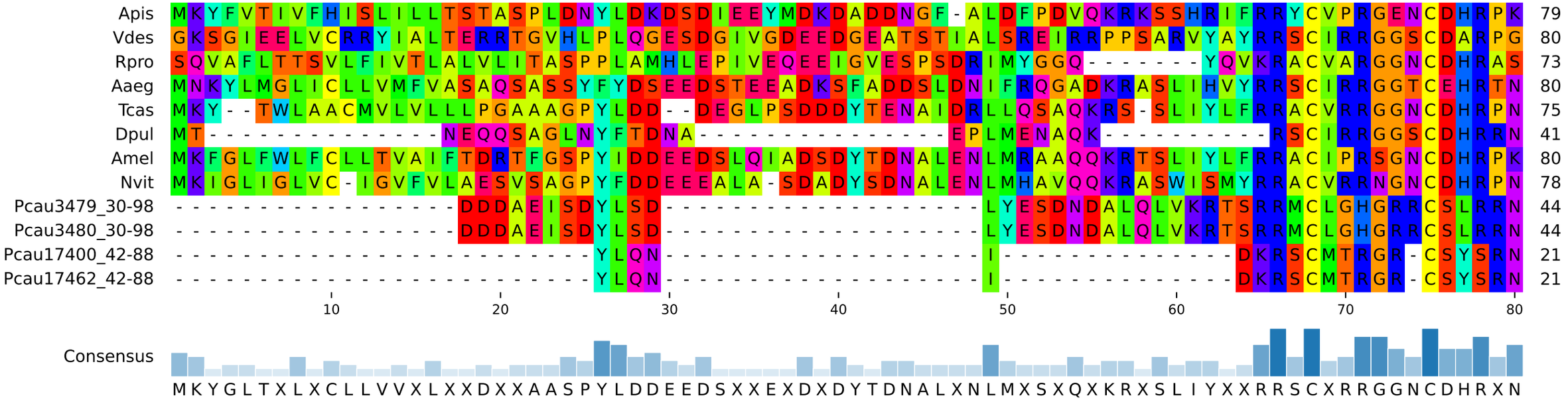
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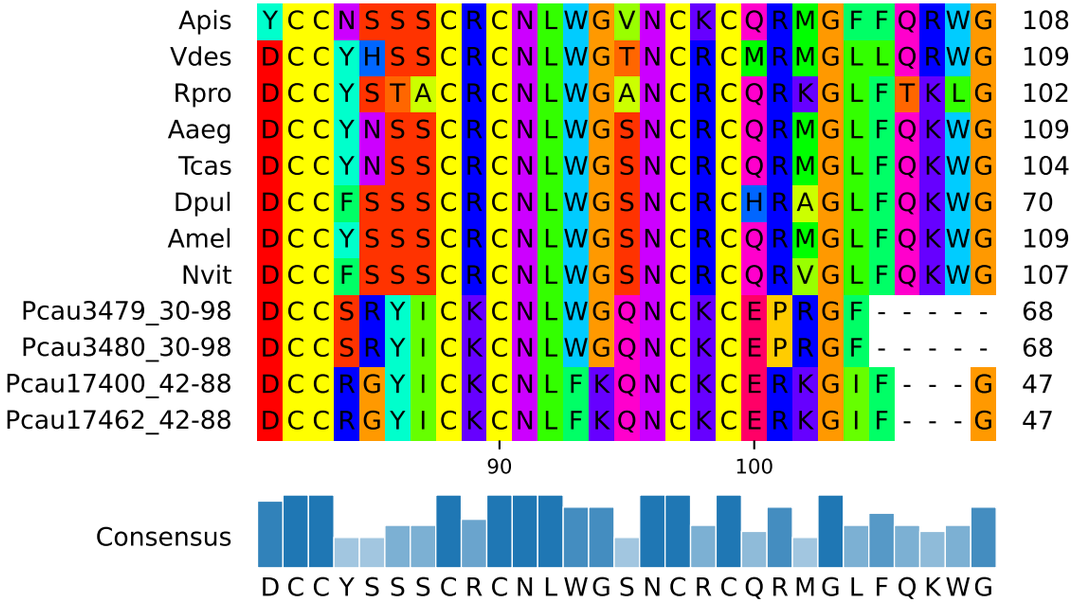
Rpro SQVAFLTTSVLFIVTLALVLITASPPLAMHLEPIVEQEEIGVESPSDRIMYGGQ-------YQVKRACVARGGNCDHRAS 73
Aaeg MNKYLMGLICLLVMFVASAQSASSYFYDSEEDSTEEADKSFADDSLDNIFRQGADKRASLIHVYRRSCIRRGGTCEHRTN 80
Tcas MKY--TWLAACMVLVLLLPGAAAGPYLDD--DEGLPSDDDYTENAIDRLLQSAQKRS-SLIYLFRRACVRRGGNCDHRPN 75
Dpul MT----------NEQQSAGLNYFTDNA----------EPLMENAQK----------RSCIRRGGSCDHRRN 41
Amel MKFGLFWLFCLLTVAIFTDRTFGSPYIDDEEDSLQIADSDYTDNALENLMRAAQQKRTSLIYLFRRACIPRSGNCDHRPK 80
Nvit MKIGLIGLVC-IGVFVLAESVSAGPYFDDEEEALA-SDADYSDNALENLMHAVQQKRASWISMYRRACVRRNGNCDHRPN 78
Pcau3479_30-98 ----------DDDAEISDYLSD----------LYESDNDALQLVKRTSRRMCLGHGRRCSLRRN 44
Pcau3480_30-98 ----------DDDAEISDYLSD----------LYESDNDALQLVKRTSRRMCLGHGRRCSLRRN 44
Pcau17400_42-88 ----------YLQN----------I----------DKRSCMTRGR-CSYSRN 21
Pcau17462_42-88 ----------YLQN----------I----------DKRSCMTRGR-CSYSRN 21
10 20 30 40 50 60 70 80
Consensus
M K Y G L T X L X C L L V V X L X X D X X A A S P Y L D D E E D S X X E X D X D Y T D N A L X N L M X S X Q X K R X S L I Y X X R R S C X R R G G N C D H R X N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Tcas DCCYNSSCRCNLWGSNCRCQRMGLFQKWG 104
Dpul DCCFSSSCRCNLWGSNCRCHRAGLFQKWG 70
Amel DCCYSSSCRCNLWGSNCRCQRMGLFQKWG 109
Nvit DCCFSSSCRCNLWGSNCRCQRVGLFQKWG 107
Pcau3479_30-98 DCCSRYICKCNLWGQNCKCEPRGF----- 68
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Pcau17400_42-88 DCCRGYICKCNLFKQNCKCERKGIF---G 47
Pcau17462_42-88 DCCRGYICKCNLFKQNCKCERKGIF---G 47
90 100
Consensus
D C C Y S S S C R C N L W G S N C R C Q R M G L F Q K W G