>Ppa\_COSA-1

MSLMQLPVFANISCDASGSQSLLVDANFAEKTGTLHKDYIGDWVAELKSLNKTRMDECDDYGQIYLTRETVEYMFTLCIRLRMPIEVRFMATSIFDRFMRVHTQQMIDFLANIDMNSTKKREEWDGVETNMSRQLTLRICSAIQIASKIVSYHDSLSTNQICKCLRMLGTPYTKSAILKSEIRLLKAVDYEIPPTQVVYAESILKLFSLTKRTNIKVNSVWSFMCILLDVVLMEGDTIYNNLIRTVLDDISIVSQTQRNRLKSDWILLATALVCAGCCCHYGFQVGDSVSVELEDICQIPAKDTSELAIAILEVARGKEDLLRPSINRQVTPPPTKRFAVPQLNPRDGSIPFGVPMHDHPRERTTYPNRDHRSNYPL

>Cele\_COSA-1

MSSSRSHRKNTSTLGTPAVSAANQTVKNPNLKKNEPKSDNEPPKTLVSMEPDFYDPRGACHMIYWTDCIAQMAVDIRERQNAANQSDFDFMKPKLVEYVFTVCVRLRLPNEVRFTAALILNSFMLRHLCSLHDFMERQEMSIQRKKREWENLESNMERQIPLRILTAIQISSKFHSYHDSLSSRQVVNTLRKIGLPYTISAVLESEQRVFKLIGFKMPDSPLDACEMALKVLTFTMKKRGMIDEEKYNDLWQHTLIVLDVCFINHIELYERFIRKCPAICRTEERLNISKFKWDIQLLAAATVQTAYILLLGTSQIANVSVIINNLLRCDNAYVEPLKQSIIELACAKKNESIPECSTSS

>Hsap\_CNTD1

MDGPMRPRSASLVDFQFGVVATETIEDALLHLAQQNEQAVREASGRLGRFREPQIVEFVFLLSEQWCLEKSVSYQAVEILERFMVKQAENICRQATIQPRDNKRESQNWRALKQQLVNKFTLRLVSCVQLASKLSFRNKIISNITVLNFLQALGYLHTKEELLESELDVLKSLNFRINLPTPLAYVETLLEVLGYNGCLVPAMRLHATCLTLLDLVYLLHEPIYESLLRASIENSTPSQLQGEKFTSVKEDFMLLAVGIIAASAFIQNHECWSQVVGHLQSITGIALASIAEFSYAILTHGVGANTPGRQQSIPPHLAARALKTVASSNT

>Mmus\_Cntd1

MNMEGPLRPRLVNCSDFQFGVVTTETIENALLHLAQQNEQAVKEAAGRTGSFRETRIVEFVFLLSEQWCLEKSVSYQAVEILERFMLKQAEDICRQATLQLRGKDTELQSWRAMKEQLVNKFILRLVSCVQLASKLSFHYKIVSNITVLNFLQALGYVHTKEELLESELDILKSLNFQINLPTPLAYVEMLLEVLGYNGCLVPATQLHATCLTLLDLVYLLHEPIYESLLRASIENSTPSQLQGEKFLSVKEDFMLLAVGIIAASAFIQNHECWSQVIGHLQSITGIASESIAEFSYAILTHSVGANTPGPQQPVPHKAARALRTAAAAASSNT