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gi|6912534|ref|NP_036474.1|      ------------------------------------MDRHSSYIFIWLQLELCAMAVLLTKGEIRCYCDAAHCVATGYMCKSELSACFSRLLDPQNSNSPLTHGCLDSLASTTDICQAKQARNHSGTTIPTLECCHEDMCNYRGLHDV   150
gi|114629876|ref|XP_001150397.1| MRHLTGAFRERGKNKGITCRITCKTCEEEEEEEKLALQFYTPPTFYDFPFGLKEIDFGKQTTNCEIRCYCDAAHCVATGYMCKSELSACFSRLLDPQNSNSPLTHGCLDSLASTTDICQAKQARNHSGTTMPTLECCHEDMCNYRGLHDV   150
gi|33468995|ref|NP_080781.1|     ------------------------------------MDRHSSYFFIWLQLELCAMAVLLTKGEIRCYCDAAHCVATGYMCKSELSACFSRLLDPQNTNSPLTHGCLDSLASTADICRAKQAQNHSGPAMPTLECCHEDMCNYRGLHDV   150
gi|20806113|ref|NP_620782.1|     ------------------------------------MDRHSSYIFIWLQLELCAMAVLLTKGEIRCYCDAAHCVATGYMCKSELSACFSRLLDPQNTNSPLTHGCLDSLASTADICRAKQAQNHSGPTMPTLECCHEDMCNYRGLHDV   150
gi|118085621|ref|XP_425974.2|    ------------------------------------MDRHSSYIFIWLQLELCAMAVLLTRGEIRCYCDAAHCVATGYMCKSELSACFSRLLDPQNTHSPLTHGCLDSIASTADICQAKQAQNHSGTTVSTLECCHEDMCNYRGLHDV   150
gi|57039467|ref|XP_544209.1|     ------------------------------------MDRHSSYIFIWLQLELCAMAVLLSRGEIRCYCDAAHCVATGYMCKSELSACFSRLLDPQNTNSPLTHGCLDSLANTADICQAKQARNHSGTTMPTLECCHEDMCNYRGLHDV   150
gi|114052651|ref|NP_001039774.1| ------------------------------------MDRHSSYIFIWLQLELCAMAVLLTKGEIRCYCDAAHCVATGYMCKSELSACFSRLLDPQNINSPLTHGCLDSLASTADICQARQARNHSGSPLPSLECCHEDMCNYRGLQDV   150
gi|18858339|ref|NP_571859.1|     ------------------------------------MDRLVS---LWFQLELCAMAVLLTKGEIRCYCDAPHCVATGYMCKSELNACFTKVLDPLNTNSPLTHGCVDSLLNSADVCSSKNVDISSGSSSP-VECCHDDMCNYRGLHDL   150
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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gi|6912534|ref|NP_036474.1|      LSPPRGEASGQGNRYQHDGSRNLITKVQELTSSKELWFRAAVIAVPIAGGLILVLLIMLALRMLRSENKRLQDQRQQMLSRLHYSFHG-HHSKKGQVAKLDLECMVPVSGHENCCLTCDKMRQADLSN------DKILSLVHWGMYSGHG   300
gi|114629876|ref|XP_001150397.1| LSPPRGEASGQGNRYQHDGSRNLITKVQELTSSKELWFRAAVIAVPIAGGLILVLLIMLALRMLRSENKRLQDQRQQMLSRLHYSFHG-HHSKKGQVAKLDLECMVPVSGHENCCLTCDKMRQADLSN------DKILSLVHWGMYSGHG   300
gi|33468995|ref|NP_080781.1|     LSPSKSEASGQGNRYQHDSSRNLITKMQELTSSKELWFRAAVIAVPIAGGLILVLLIMLALRMLRSENKRLQDERQQMLSRLHYSFHG-HHSKKGQVAKLDLECMVPVSGQENCCLTCDKMRQAELSN------EKILSLVHWGMYSGHG   300
gi|20806113|ref|NP_620782.1|     LSPPKSEASGQGNRYQHDSSRNLITKVQELTSSKELWFRAAVIAVPIAGGLILVLLIMLALRMLRSENKRLQDQRQQMLSRLHYSFHG-HHSKKGQVAKLDLECMVPVSGQENCCLTCDKMRQADLSN------EKILSLVHWGMYSGHG   300
gi|118085621|ref|XP_425974.2|    LSPSKGETSGQGSRYQHDS-KNLITKVQELTSSKELWFRAAVIAVPIAGGLILVLLIMLALRMLRSENKRLQDQRQQMLSRLHYSFHG-HHSKKGQVAKLDLECMVPVTGHENCCMTCDKMRHSDLSN------DKILSLVHWGMYSGHG   300
gi|57039467|ref|XP_544209.1|     LAPPKGEASGQGNRYQHDGSRNLITKVQELTSSKELWFRAAVIAVPIAGGLILVLLIMLALRMLRSENKRLQDQRQQMLSRLHYSFHG-HHSKKGQVAKLDLECMVPVSGHENCCLTCDKMRQADLSN------EKILSLVHWGMYSGHG   300
gi|114052651|ref|NP_001039774.1| LTPPKGEASGQGNRYQHDGNRNLITKVQELTSSKELWFRAAVIAVPIAGGLILVLLIMLALRMLRSENKRLQEQRQQMLSRLHYSFHG-HHSKKGQVAKLDLECMVPVSGHENCCLTCDKMRQADLSH------DRILSLVHWGMYSGHG   300
gi|18858339|ref|NP_571859.1|     THP-RGDST---DRY-HSSNQNLITRVQELASAKEVWFRAAVIAVPIAGGLILVLLIMLALRMLRSENKRLQAQRQQMLSRLHYSFHGHHHAKKGHVAKLDLECMVPVTGHENCCLGCDKLRQTDLCTGGGSGGERLLSLVHWGMYTGHG   300
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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                                 ****:
gi|6912534|ref|NP_036474.1|      KLEFV   305
gi|114629876|ref|XP_001150397.1| KLEFV   305
gi|33468995|ref|NP_080781.1|     KLEFI   305
gi|20806113|ref|NP_620782.1|     KLEFV   305
gi|118085621|ref|XP_425974.2|    KLEFV   305
gi|57039467|ref|XP_544209.1|     KLEFV   305
gi|114052651|ref|NP_001039774.1| KLEFV   305
gi|18858339|ref|NP_571859.1|     KLEFV   305
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