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                                       1        10        20        30        40        50        60        70        80        90
  1 Hsap1_4AWN  ...................................LKIAAFNIQTFGETKMSNATLVSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLNQDA.PDTYHYVVSEPLGRNSYKPRYLFVYRPDQVS
    Hsap1       .........MRGMKLLGALLALAALLQGAVSLKIAAFNIQTFGETKMSNATLVSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLNQDA.PDTYHYVVSEPLGRNSYKPRYLFVYRPDQVS
    Xlae1       .........MAPARVMLLICGLTLILNLSDISALKIGAFNIRAFGDSKIKNPAVSSVLMKILPRYDIVVIQEVRDADHSAVKLLMQKINSLNTGPVYSHVISDTLGRDAYKEQYLFVYRNDKVT
    Rtem1       ...........MIRIII..GLTLALSSVSALKIGAFNIQAFGDSKMSNPEVTSIIMKILPRYDIVLIQEVRDTDLSAVETMMSELNSHCKKPQYSYVVSDSLGRDAYKERYLFVYRNDKVT
    Lcha1       .......MSATKLTVTLMALACALSTAESLKIGAFNVRALGDTKVSNATIANILVNIITMYDIAVIQEVRDADLSAVHHLMNLI.DRK.PDSYSYVISEPLGRSSYKEQYLFIYRNGQVS
    Ecal1       .........MLPKMTCLLV.LLLSSAPGVLCGLLIGAFNIKSFGDSKMSNATLADIIVKVVQRYDIILIQEVRDVDLTATNSLMKKLNSDS.AHVYQHVVSEPLGRSTYKERYLFVYRAKKVS
    Scan1       ......MHQLITALTLTACLLSAAYSIQISAFNIRTFGDKKMSNVTIANIIVHLIERNDIILIQEVRDADLSAVKILMNKLQSSS.AQTYSYIVSDPLGHSSYKPRYLFIYRNSAVS
  2 Xlae1L5     ............MRFLVLVAMTACFLQAGFAFKIASFNIQRFSMTKVDDPVVLELLIRILSRYEIIAIEEVMNADNTAIISLVKELSLAT.KLNYNVLISDHLGRSSYREKYAYVYREDIVK
    Rtem1L5     ............MKSLVLVALAACFLQAGVALKIAAFNIERFSATKVDDPVVLNLLIQILRRYELIAVQEVMNRDDTAITRLVQELNNDT.GLSYNLLISDHLGRSTYRBKYVVVYREDILK
    Lcha1L5     ............MRVAVLLALIGCLLQGSSAFKIASFNIQRFSWHKVDNPEIRNILTRILRYDLIVIEEIMDEDNTPITELVMALNDVS.GVHYNFIISDHLGRSSYKEKYGFVFNEAVLK
    Ecal1L5     ............MNIFILLVLLGTSLKESQALKIASFNIQRFDESKSNNAEIMNVLTTILQRYQLVAVQEIMDSDNAAVKHLVHQLNQES.GCHYNFILSDHLGRSSYREKYAFVYNEELLQ
    Scan1L5     MRISDNPSGFPGFTTMAFLLLMVLIGCFMQGSQGLKIASFNIQRFDQTKVNDPVTLDILIQRYDLITIEEVMDSDNSAMTELVKELNRST.KLHYNYIISDHLGRSSYREKYAFVYNENILK
    Arad1L5     ............MELRVMFIVLGCLLQWSQGLKIASFNIQRFSQRKVDDHVTLDILIRILKRYDLITIEEVMDSDSSAVTDLVRELNYAT.KLNYNYIISDYLGHSTYREKYAFIFKENILK
                                              ▼   ●●  ●●●                              ▼         ★         ★              ★★★ ★    ●●     ▲

           100       110       120       130       140       150       160       170       180       190       200       210
  1 Hsap1_4AWN  AVDSYYYDDGCEPCGNDTFNREPAIVRFFSRFTEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDVMLMGDFNAGCSYVRPSQWSSIRLWTSPTFQWLIPDSADTTA.TPTHCAYDRI
    Hsap1       AVDSYYYDDGCEPCGNDTFNREPAIVRFFSRFTEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDVMLMGDFNAGCSYVRPSQWSSIRLWTSPTFQWLIPDSADTTA.TPTHCAYDRI
    Xlae1       VQDSYHYHDHCMYTGEDTFSREPFVVKFNAQGTVIEDFVLIPLHSAPKDAVREIDALYDVYEDVWNKWQTDSMIFLGDFNAGCSYVTKSDWDNIRLRTNEEFAWLIPDSTDTTV.GNTCCAYDRI
    Rtem1       AENSYHYHDHNLYTGEDTFSREPFVVHFNCPNTAIQDFVLVPLHSAPKDAVREIDALYDVYRDVLDKWQTDNIIFLGDFNAGCNYVKESDWDSIRLYTCEDFLWLIPHDMDTTA.GRTHCAYDRI
    Lcha1       VIDSYQYDDGCESCGTDTFSREPFVVKFSPFSDVREFVIVPQHTSPDEAVEEIDGLYDVFLDVQSKWRNDNILFMGDFNADCDYVRPDEWHKIRLRTDTQFLWLISNSSDTTV.STTHCAYDRI
    Ecal1       AVSSFQYDDGCESCGTDTFNREPFVVKFASPFSAISEFAIIPQHTSPDEAVKEIDALYDVCTETTAQWKSDNILLMGDFNADCSYVRPSDWSKIRLRSNLQFEWLISDSIDTTV.TDTNCAYDRI
    Scan1       VVNSYLYNDASKNTGQDSFNREPFLVKFYSRYSVIHEFVIMPMHTSPSAAVKEIDALYDVFLDAKKKLGTDNMLIMGDLNADCSYVKPTDWPHIRIRKDTQFQWLIPDTADTTTTISTKCAYDRI
  2 Xlae1L5     PTEWYHFDDGCENCGTDSFIREPFVARFTSLTTVVKDFALISIHTSPDYAIMEVDALYDAWVDAKQRLKMENILILGDYNAACSYVASRHWPIIRLRHVEELVWLIGDKEDTTVSTNTNCAYDRM
    Rtem1L5     PTEWFHYDDGCENCGTDVFMREPFVARFSSLTTEVKDFALATIHTSPDYAVREVDALFDVWEDAKQRLLMEDIIILGDYNAGCSYVKSTHWPMIRLRQEASLHWLIGDNADTTVSTNTNCYYDRI
    Lcha1L5     PTDWYYYNDGCENCGTDTFIREPFVRFSSLPTVLKDFALISIHTSPDYAVREVDALYDVWEDAKHRFKTENIMILGDFNADCNYIKTKDWPNIRLRQSPSLHWLIGDDEDTTVSGNTNCAYDRI
    Ecal1L5     PLDWYHYDDGCEECGTDSFIREPFIVKFSSPSTVLKELVLVVIHTSPDYAVQEVDSLFDVWTDAKQHFNTEDVIILGDNADCSFLPANKWPLVRLRQSKALSWLIVDSEDTTVSVNTHCAYDRI
    Scan1L5     PMAWYHFDDGCEKCGTDTFIREPFIVHFHSLTTIVKDFVLVAIHTSPSYAVREVDALYDVWADARNHFNTENILILGDYNAACRYVTDNDWPHIRLRQHKNFHWLIDDAIDTTVSKYTHCAYDRF
    Arad1L5     PVGWYHFDDGCEQCGTDTFMREPFIVHFHSLTTIVKDFVLAAIHTSPSYAVREVDALYDVWADARKHFNTENILILGDYNAACRYVTDKDWPSIRLRQYNNFHWLIGDEVDTTVSINTHCAYDRI
                ▶              ▶    ● ▶ ★                                       ▲                            ▲  ▲                    ◀◀  ●      ▲

           220       230       240       250       260
  1 Hsap1_4AWN  VVAGMLLRGAVVPDSALPFNFQAAYGLSDQLAQAISDHYPVEVMLK.............
    Hsap1       VVAGMLLRGAVVPDSALPFNFQAAYGLSDQLAQAISDHYPVEVMLK.............
    Xlae1       VVSGADLQEAIVQDSVQVFDFQKKYKLTQEEALAVSDHFPVELELMSD..........
    Rtem1       VVSGAELQNAIVEDSAQIFNFHKQYKLTLEQALAVSDHFPVELELMLA..........
    Lcha1       VASGEAMKNALVPGSAVVYNYQAAFNLKYDDAYAVSDHFPVEVTLL............
    Ecal1       VAHGLAMQNAVVPGSANIYNFQSALQLSSATALAVSDHFPVEVELRNP.........
    Scan1       IAVGSQLKNAVIDGSAAIYNFTRVLNLSNKMTLAVSDHYPVEVELRAA.........
  2 Xlae1L5     VAGGEELQRGIVPDTAKAFNYHVAYDLTYEMAKAVSDHYPVELYDDVLYSGQSFEPSASTGISGGLSLNGPCTCEGVDFSSCRGRCGASGKTYPCNCNASCT...NCCVDYTSSCKL
    Rtem1L5     VVGGSSLQNSVVPGSAKAFNYQEAYGLTYEETKAASDHYPVVELRNDPFYNGQKFGVSAGIGISGGLAQNGVCDCVGVDFSSCVGRCGANSSSYPCNCNATCSSSQKCCADYAAVCKM
    Lcha1L5     VVSGSELIHALIPGTAKTFNFQDIYDLSYYQTKDVSDHYPVEVELRLDSGYFGKGFQLSSSIGIPTS.NPSAPCDCIGINFSSCRGRCSAYSQSFPCNCNAACSKYDSCCSDYQQFCSN
    Ecal1L5     VASGT.VPDTIIPGSASAFNYQKALGLLYDKARDVSDHYPIEVVKDSATWDGMMFEPSSSLGIEGG.QSGMPCDCVGVDFTTCKGRCGAYNPSLPCHCNASCSKYNSCCADYKEFCQD
    Scan1L5     VVTTKGLLKTIVPGSVKTFNFQEAYGLPYYTVKEVSDHYPIELELEKDPNTIGAKYGTESSIGINGG.ISGGPCSCEGVDFTSCAGRCGAYSPTMPCTCTASCSKYNDCCADYGNYC..
    Arad1L5     VMTGESLIDTVVPGSVKVFYFQKAFDLPYETVKDVSDHYPIBLELKRDPQAPDSYYKTGGIIGINGG.TSGGPCSCQGVDMSSCAGRCGAYSDRFPCSCTSSCSKHNDCCADYKNYC..
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