```
L. braziliensis    MAHKKQAWAKRVKKERFKKKYLTRMQATRLLQMESIQFRRLCILKGVYPRALTRSKQKQSGNEKQYYLAREIKWLVRDHIAEKMMTYRAWEKKVKRAEAMGRADDLKALQSSRVKPRHSL 120
L. mexicana        MAHKKQAWAKRVKKERFKKKFLTRMQATRLLQMESVQFRRLCILKGIYPRALQRSKQKQSGNEKQYYLAREIKWLVRDQIAEKMMAYRAWEKKVKRAEAMGRAEDLKVLQSSRVKPRHSL 120
L. major           MVHKKQAWAKRVKKERFKKKFLTRMQATRLLQMESVQFRRLCILKGIYPRALNRSKQKQSGNEKQYYLAREIKWLVRDQIAEKMMAYRAWEKKVKRAEAMGRSEDLKVLQTSRVKPRHSL 120
L. infantum        MAHKKQAWAKRVKKERFKKKFLTRMQATRLLQMESVQFRRLCILKGIYPRALNRSKQKQSGHEKQYYLAREIKWLVRDQIAEKMMAYRAWEKKVKRAEAMGRSEDLKVLQSSRVKPRHSL 120
L. donovani        MAHKKQAWAKRVKKERFKKKFLTRMQATRLLQMESVQFRRLCILKGIYPRALNRSKQKQSGHEKQYYLAREIKWLVRDQIAEKMMAYRAWEKKVKRAEAMGRSEDLKVLQSSRVKPRHSL 120
T. cruzi           -MHRKQVWAKRVKKERLKKKFLTRMQATRLLQVDSVHFRRLCILKGIYPRALARSKQKQSGNDKQYYLAREIKWLVRDHVAERMMAYRAWEKKVRRAEAMGLADELKVLRSKKAKPQYSL 119
T. brucei brucei   -MHRKQAWSKRVKKERQKKKYLTRMQATRLLQVDSIHFRRLCILKGIYPRALNRSKQKQSGNDKQYYLAREIKWLVRDHLADRMMAFRAWEKKVRRAEAMRLTEDLKVLHSNKVKPKYSL 119
                    *:**.*:******* ***:***********::*:::*********:***** ********:*:***************::*::**:::*******:***** :::**.*:::.:**:.*:**

L. braziliensis    VATIKERYPYFIDAIRDVDDAMSMIHMYAFLSPEIKSESTIEIHHSLTSGLSEKAKEMCHRWNRYIARAHVLTKGFISIKGYYYEAIIKGERVRWLCPHEYAHRFPPGIQQYVMLSFLEF 240
L. mexicana        VATIKERYPYFIDAIRDVDDAMSMIHLYAFLSPEIKSDTTIEIHHSLTSGMSEKAKEMCERWDRYVARARVLTKGFISIKGYYYEAIVKGERVRWLCPHEYAHRFPPGIQQYVMLSFLEF 240
L. major           VATIKERYPYFIDAIRDVDDAMSMIHLYAFLSPEIKSDTTIEIHHSLTSGLSERAKEVCERWDRYVARARVLTKGFISIKGYYYEAIVKGERVRWLCPHEYAHRFPPGIQQYVMLSFLEF 240
L. infantum        VATIKERYPYFIDAIRDVDDAMSMIHLYAFLSPEIKSDTTIEIHHSLTSGMSEKAKEVCERWDRYVARARVLTKGFISIKGYYYEAIVKGERVRWLCPHEYAHRFPPGIQQYVMLSFLEF 240
L. donovani        VATIKERYPYFIDAIRDVDDAMSMIHLYAFLSPEIKSDTTIEIHHSLTSGMSEKAKEVCERWDRYVARARVLTKGFISIKGYYYEAIVKGERVRWLCPHEYAHRFPPGIQQYVMLSFLEF 240
T. cruzi           VATIKERYPFFIDAVRDIDDAMSMIALYAFLSPEVMSETTIETHHALTSGLHERARGIIARWNRYVARAQVLSKGFISIKGYYFEAIVRGERVRWLCPHEYAHKFPPGIQQYITLSFLEF 239
T. brucei brucei   VATIKERYPYFADAVRDIDDAMSMIALYAFLSPEVASESTIETHHTLTSGLHRRARETCERWNSYVERAQALSKGFISIKGYYFEAIVRGERVRWLCPHEYAHKFPAGVQQYIMISFLEF 239
                    *********:* **:**:******* :*******: *::*** **:****: ..*:    **: *: **:.*:***********:***:*****************:** *:***: :*****

L. braziliensis    YLEMMKFVLFKLESDLARDEADRLAIEDEEGLTRANAEDFASGAALAVLDVGANQAQAK-VKEAESKRSLMEEELLKVRELFRGLTFYISREVPAKHFALIINACGGRVATDYVASNITH 359
L. mexicana        YLEMMKFVLFKLESDLARDEADRLAAEDEEGVARANAEDFANGAALAVLDVGANQAQAKEVKEAESKRSLMEEELQKVRELFRGLTFFISREVPAKHFALVIKACGGRVATDYVPSNITH 360
L. major           YLEMMKFVLFKLESDLARDEADRLAAEDEEGVTRANAEDFANGAALAVLDVGANQAQAKAVKEAESKRSLMEEELHKVRELFRGLTFFISREVPAKHFALVINACGGRVATDYVPSNITH 360
L. infantum        YLEMMKFVLFKLESDLARDEADRLAAEDEEGVTRANAEDFANGGALAVLDVGANQAQAKEVKEAESKRSLMGEELHKVRELFRGLTFFISREVPSKRFALVINACGGRVATDYVPSNITH 360
L. donovani        YLEMMKFVLFKLESDLARDEADRLAAEDEEGVTRANAEDFANGGALAVLDVGANQAQAKEVKEAESKRSLMGEELHKVRELFRGLTFFISREVPSKRFALVINACGGRVATDYVPSNITH 360
T. cruzi           YVELMQFVLYKLEHELQRDVAEQQEAEDEENNTH--AEDFRLPDKEMT------QSISDVKKDTLKKGELMQEELRKARRVFDGLTFYISREVPHKHATLIIEACGGRVATAYAADNITH 351
T. brucei brucei   YLELMRFVLFKLER----DLAEKQKAEEEEPNLN--AENFDTTNKETV------QGLGGTVGQVAKRVELMDEELRKVRRVFEGLSFYISREVPHKHAALVIKACGGRVATGYVAENITH 347
                    *:*:*:***:***      * *::  *:**   . **:*        .       ..  :..: .** *** *.*.:* **:*:***** *: :*:*:******* *. .****

L. braziliensis    VVVDRPALPPGWQQHDQMEYVQPQYIFDCLNARQMLPVTGYRIGEDLPPHVSPFSVSITNSAEDNAAVEQVKKDHPRIVGYVPARVHEIRKLINPSYSPVDPEGKVAQLEDEYSDEEMHV 479
L. mexicana        VVVDRPSLPPGMKRYDPLEYVQPQYIFDCLNARLMLPVTGYRMGEELPPHVSPFSVSITNSAEDNAAVEQVKKDHPKIVGYVPARVHEVRKLINPSYSAVDPEGKVAHLEDEYSDEECHV 480
L. major           VVVDRPSLPPGMKKHDQLEYVQPQYIFDCLNARLVLPVTGYRIGEELPPHVSPFSVSITNSAEDNAAVQVKKDHPRIVGYVPARVHEIRKLINPSYSAVDPEGKVAHLEDEYSDEESHV 480
L. infantum        VVVDRPALPPGMKKHDQLEYVQPQYIFDCLNARLMLPVTGYRIGEELPPHVSPFSVSITNSAEDNAAVEQVKKDHPRIVGYVPARVHEIRKLINPSYSAVDPEGKVAHLEGEYSDEESHV 480
L. donovani        VVVDRPALPPGMKKHDQLEYVQPQYIFDCLNARLMLPVTGYRIGEELPPHVSPFSVSITNSAEDNAAVEQVKKDHPRIVGYVPARVHEIRKLINPSYSAVDPEGKVAHLEGEYSDEESHV 480
T. cruzi           FVVDRPALPPGFERVDRIEYVQPQYLFDCLNARMLLPPNGYRIGEELPPHVSPFTVAITNSPEDIAAVEEAKKNHPKIVSYVPKRVHEIRALVNPQYTPLDPEGKASDLLLHDESDEDHA 471
T. brucei brucei   FVVDRPALPPGFEKDDRIEYVQPQYLFDCLNARLLLPPNGYRIGEELPPHVSPFTVAITNSTEDIAAVEEARRDHPKIVSYVPKRVHEIRKLINPQYTPTDPDGKAAELLLEEESDEENV 461
                    .****:**** :: * :*******:******* :** .***:**:*********:*:*** *** *** :.:::**:**.*** ****:* *:**.*:  **:**..:*  . ...* :.

L. braziliensis    AVPEMDMEDDVSLSGDELAEARKKPGWQEEEVTEEVQRPKLSAFKVKKQREMNLMNAPTNEVVARRRQALRKAQENLRQSETPEARLQRKMSEVKRQEAVTRKMQLQVARKKAARFYKMV 599
L. mexicana        AVPEMDMEDDVSLSGDELAEARRKPAWQEEEVTEEVQRPKLSAFKVKKQREMSLMNAPTNEIVARRRQALRKSQEKSRQAETSEARLQRRMSEVKRQEAATRKMQLQVARKKAARFYKMV 600
L. major           AVPEMDMEDDVSLSGDELAEARRKPAWQEEEVTEEVQRPKLSAFKVKKQREMNLMNAPTNEVVARRRQALRKAQEKSRQTETSEARLQRKMSEVKRQEAATRKMQLQVARKKAARFYKMV 600
L. infantum        AVPEMDMEDDVSLSGDELAEARRKPAWQEEEVTEEVQRPKLSAFKVKKQREMNLMNAPTNEVVARRRQALRKAQEKSRQTETSEARLQRKMSEVKRQEAATRKMQLQVARKKAARFYKMI 600
L. donovani        AVPEMDMEDDVSLSGDELAEARRKPAWQEEEVTEEVQRPKLSAFKVKKQREMNLMNAPTNEVVARRRQALRKAQEKSRQTETSEARLQRKMSEVKRQEAATRKMQLQVARKKAARFYKMI 600
T. cruzi           LVPELGADDDVSLSGDELLEASHRPKWEEEEVTENVQRSKLSALKVAKQRKMNLMNAPTDEVVARRRLAQLKSRESRQQQEPSGQRLKRKLAEMKRQEAATRKMQLQVARKKAARYYKMV 591
T. brucei brucei   AAQELDRDDDVQLSGDELQEARRRPKWEDEQVTESVERTKLSALKVRQQRELNLMNAPTNEAVARRRLAQQKAKEARKQQETDEHRLRRKLADVKRQEVATRKMQLQVARKKAARYYKMV 587
                    . *:. :***.****** ** ::* *:*:*:***.*:* ****:** :**::.*******: * ***** *  *::* :* *    **:*::::***..***************:***:

L. braziliensis    SGVVQGTAKKAATLEAKAKHIAEGKLHKTEDGKGLVNARLAARRQRAEAKGKKLKEKKADNPYKKLPKWVQ 670
L. mexicana        SGVVQGTAKKAATLEAKAKHIAEGKLHKTEDGKGLVNTRLEARRQRAEAKGKKLKEKKADNPYKKLPKWVQ 671
L. major           SGVVQGTAKKVATLEAKAKHIAEGKLRKTEDGKGLVNKRLEARRQRAEAKGKKLKERKAGNPYKKLPKWVQ 671
L. infantum        SGVVQGTAKKAATLEAKAKHIAEGKLHKTEDGKGLVNTRLEARRQRAEAKSKKLKERKAGNPYKKLPKWVQ 671
L. donovani        SGVVQGTAKKAATLEAKAKHIAEGKLHKTEDGKGLVNTRLEARRQRAEAKGKKLKERKAGNPYKKLPKWVQ 671
T. cruzi           NSVVQGSQRREKMLEAKAKQVADGRIAKKEDGRELVNVRVEAKRARAAASGKPLREKKAANPYKKLPKWVR 662
T. brucei brucei   NGVVQGNERREKMLTAKAKQLSEGRISAAKDGSGLVNNKLEARRAKAEAAGKKLKEKKPSNPYSKLPKWVR 658
                    ..****. ::   * ****:::*::   :**  *** :: *:* :* *  .* *:*:* ***.******: 
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S1

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LmjF.04.0810      ATGGTCCATAAGAAGCAGGCATGGGCGAAGCGGGTGAAGAAGGAGCGCTTCAAGAAGAAATTTCTGACGCGCATGCAGGCGACGCGGCTACTGCAGATGGAGTCCGTTCAGTTCCGCCGC 120
LmjPES_sequenced  ATGGTCCATAAGAAGCAGGCATGGGCGAAGCGGGTGAAGAAGGAGCGCTTCAAGAAGAAATTTCTGACGCGCATGCAGGCGACGCGGCTACTGCAGATGGAGTCCGTTCAGTTCCGCCGC 120
                  ************************************************************************************************************************

LmjF.04.0810      CTCTGCATCCTCAAGGGCATCTACCCCCGCGCCCTCAACCGCAGCAAGCAGAAACAAAGTGGGAACGAGAAGCAGTACTATCTCGCCCGTGAGATCAAGTGGCTGGTGCGCGACCAGATA 240
LmjPES_sequenced  CTCTGCATCCTCAAGGGCATCTACCCCCGCGCCCTCAACCGCAGCAAGCAGAAACAAGGTGGGAACGAGAAGCAGTACTATCTCGCCCGTGAGATCAAGTGGCTGGTGCGCGACCAGATA 240
                  ********************************************************** **************************************************************

LmjF.04.0810      GCGGAGAAGATGATGGCATATCGGGCATGGGAGAAGAAGGTGAAGCGGGCAGAGGCGATGGGCCGCTCCGAGGACCTCAAGGTGCTGCAGACCTCACGCGTGAAGCCGCGCCACAGCCTG 360
LmjPES_sequenced  GCGGAGAAGATGATGGCATATCGGGCATGGGAGAAGAAGGTGAAGCGGGCAGAGGCGATGGGCCGCTCCGAGGACCTCAAGGTGCTGCAGACCTCACGCGTGAAGCCGCGCCACAGCCTG 360
                  ************************************************************************************************************************

LmjF.04.0810      GTGGCGACGATCAAGGAGCGCTACCCATACTTCATCGACGCCATCCGTGACGTGGATGACGCCATGTCGATGATCCACCTTTACGCCTTCCTTAGCCCGGAGATCAAGTCCGATACCACC 480
LmjPES_sequenced  GTGGCGACGATCAAGGAGCGCTACCCATACTTCATCGACGCCATCCGTGACGTGGATGACGCCATGTCGATGATCCACCTTTACGCCTTCCTTAGCCCGGAGATCAAGTCCGATACCACC 480
                  ************************************************************************************************************************

LmjF.04.0810      ATCGAGATACATCACTCCCTCACCTCCGGCCTGAGCGAGAGGGCCAAGGAGGTGTGCGAACGCTGGGACCGCTACGTCGCACGCGCGCGTGTACTGACGAAGGGCTTCATCTCCATCAAG 600
LmjPES_sequenced  ATCGAGATACATCACTCCCTCACCTCCGGCCTGAGCGAGAGGGCCAAGGAGGTGTGCGAACGCTGGGACCACTACGTCGCACGCGCGCGTGTACTGACGAAGGGCTTCATCTCCATCAAG 600
                  ********************************************************************** *************************************************

LmjF.04.0810      GGCTACTACTACGAGGCGATTGTCAAGGGCGAGCGGGTGCGGTGGCTGTGCCCGCACGAGTACGCTCACCGCTTCCCCCCGGGCATCCAGCAATACGTGATGCTCAGCTTCCTCGAATTC 720
LmjPES_sequenced  GGCTACTACTACGAGGCGATTGTCAAGGGCGAGCGGGTGCGGTGGCTGTGCCCGCACGAGTACGCTCACCGCTTCCCCCCGGGCATCCAGCAATACGTGATGCTCAGCTTCCTCGAATTC 720
                  ************************************************************************************************************************

LmjF.04.0810      TACCTGGAGATGATGAAGTTCGTCCTGTTCAAGCTCGAGTCGGACCTCGCGCGCGATGAGGCGGACCGCCTGGCGGCCGAGGATGAGGAAGGTGTGACCCGCGCGAACGCCGAGGACTTC 840
LmjPES_sequenced  TACCTGGAGATGATGAAGTTCGTCCTGTTCAAGCTCGAGTCGGACCTCGCGCGCGATGAGGCGGACCGCCTGGCGGCCGAGGATGAGGAAGGTGTGACCCGCGCGAACGCCGAGGACTTC 840
                  ************************************************************************************************************************

LmjF.04.0810      GCGAACGGTGCGGCGCTGGCCGTGCTGGATGTAGGCGCGAACCAGGCGCAGGCCAAGGCGGTGAAGGAGGCGGAGTCGAAGCGCTCTTTGATGGAGGAAGAGCTGCACAAGGTGCGCGAG 960
LmjPES_sequenced  GCGAACGGTGCGGCGCTGGCCGTGCTGGATGTAGGCGCGAACCAGGCGCAGGCCAAGGCGGTGAAGGAGGCGGAGTCGAAGCGCTCTTTGATGGAGGAAGAGCTGCACAAGGTGCGCGAG 960
                  ************************************************************************************************************************

LmjF.04.0810      CTGTTCCGCGGGCTAACCTTCTTCATATCGCGTGAGGTGCCCGCGAAGCACTTCGCCCTCGTCATCAACGCCTGCGGCGGCCGTGTGGCGACCGACTACGTGCCGTCGAACATCACTCAC 1080
LmjPES_sequenced  CTGTTCCGCGGGCTAACCTTCTTCATATCGCGTGAGGTGCCCGCGAAGCACTTCGCCCTCGTCATCAACGCCTGCGGCGGCCGTGTGGCGACCGACTACGTGCCGTCGAACATCACTCAC 1080
                  ************************************************************************************************************************

LmjF.04.0810      GTCGTTGTTGACCGCCCCGCGCTGCCGCCAGGGATGAAAAAGCATGACCAGCTGGAGTACGTGCAGCCGCAGTACATCTTCGACTGCCTGAACGCGCGGCTGGTGCTCCCGGTGACGGGC 1200
LmjPES_sequenced  GTCGTTGTTGACCGCCCCGCGCTGCCGCCAGGGATGAAAAAGCATGACCAGCTGGAGTACGTGCAGCCGCAGTACATCTTCGACTGCCTGAACGCGCGGCTGGTGCTCCCGGTGACGGGC 1200
                  ************************************************************************************************************************

LmjF.04.0810      TACCGCATTGGTGAGGAGCTGCCGCCGCACGTGTCGCCCTTCTCTGTCTCCATCACGAACTCCGCCGAGGACAACGCGGCGGTGGTGCAGGTGAAGAAGGACCACCCGAGGATTGTGGGC 1320
LmjPES_sequenced  TACCGCATTGGTGAGGAGCTGCCGCCGCACGTGTCGCCCTTCTCTGTCTCCATCACGAACTCCGCCGAGGACAACGCGGCGGTGGTGCAGGTGAAGAAGGACCACCCGAGGATTGTGGGC 1320
                  ************************************************************************************************************************

LmjF.04.0810      TACGTGCCGGCGCGCGTGCATGAGATCCGCAAGCTGATCAACCCCTCTTACTCTGCGGTCGACCCAGAGGGGAAGGTGGCGCATCTGGAGGACGAGTACAGCGACGAAGAGTCTCACGTG 1440
LmjPES_sequenced  TACGTGCCGGCGCGCGTGCATGAGATCCGCAAGCTGATCAACCCCTCTTACTCTGCGGTCGACCCAGAGGGGAAGGTGGCGCATCTGGAGGACGAGTACAGCGACGAAGAGTCTCACGTG 1440
                  ************************************************************************************************************************

LmjF.04.0810      GCGGTGCCGGAGATGGACATGGAGGACGATGTCTCGCTCTCCGGTGACGAGCTTGCGGAGGCACGCAGGAAGCCGGCGTGGCAGGAAGAGGAGGTCACGGAGGAGGTGCAGCGGCCGAAG 1560
LmjPES_sequenced  GCGGTGCCGGAGATGGACATGGAGGACGATGTCTCGCTCTCCGGTGACGAGCTTGCGGAGGCACGCAGGAAGCCGGCGTGGCAGGAAGAGGAGGTCACGGAGGAGGTGCAGCGGCCGAAG 1560
                  ************************************************************************************************************************

LmjF.04.0810      CTGTCGGCGTTCAAGGTGAAGAAGCAGCGCGAGATGAACCTGATGAACGCGCCGACGAACGAAGTGGTGGCGCGGCGGCGGCAGGCACTGCGCAAGGCGCAGGAGAAGTCACGTCAGACG 1680
LmjPES_sequenced  CTGTCGGCGTTCAAGGTGAAGAAGCAGCGCGAGATGAACCTGATGAACGCGCCGACGAACGAAGTGGTGGCGCGGCGGCGGCAGGCACTGCGCAAGGCGCAGGAGAAGTCACGTCAGACG 1680
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S2 (1/2)

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LmjF.04.0810      GAGACGTCCGAGGCACGTCTGCAGCGCAAGATGAGCGAGGTGAAGCGCCAGGAGGCGGCGACGCGCAAGATGCAGCTGCAGGTCGCCCGCAAGAAGGCAGCACGTTTTTACAAGATGGTC 1800
LmjPES_sequenced  GAGACGTCCGAGGCACGTCTGCAGCGCAAGATGAGCGAGGTGAAGCGCCAGGAGGCGGCGACGCGCAAGATGCAGCTGCAGGTCGCCCGCAAGAAGGCAGCACGTTTTTACAAGATGGTC 1800
                  ************************************************************************************************************************

LmjF.04.0810      AGCGGTGTGGTGCAGGGCACGGCGAAGAAGGTGGCGACGCTGGAGGCAAAGGCAAAGCACATCGCCGAAGGGAAGCTGCGTAAGACCGAGGATGGCAAGGGACTTGTCAACAAGCGGCTG 1920
LmjPES_sequenced  AGCGGTGTGGTGCAGGGCACGGCGAAGAAGGTGGCGACGCTGGAGGCAAAGGCAAAGCACATCGCCGAAGGGAAGCTGCGTAAGACCGAGGATGGCAAGGGACTTGTCAACAAGCGGCTG 1920
                  ************************************************************************************************************************

LmjF.04.0810      ATCGCCGAAGGGAAGCTGCGTAAGACCGAGGATGGCAAGGGACTTGTCAACAAGCGGCTGGAGGCGCGACGGCAGCGAGCTGAGGCGAAGGGCAAGAAGCTCAAGGAGAGGAAGGCTGGC 1980
LmjPES_sequenced  ATCGCCGAAGGGAAGCTGCGTAAGACCGAGGATGGCAAGGGACTTGTCAACAAGCGGCTGGAGGCGCGACGGCAGCGAGCTGAGGCGAAGGGCAAGAAGCTCAAGGAGAGGAAGGCTGGC 1980
                  ************************************************************************************************************************

LmjF.04.0810      AACCCGTACAAGAAACTGCCCAAGTGGGTGCAGTAA 2016
LmjPES_sequenced  AACCCGTACAAGAAACTGCCCAAGTGGGTGCAGTAA 2016
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S2 (2/2)