

CLUSTAL 2.1 MULTIPLE SEQUENCE ALIGNMENT

File: /media/morpheus/disk1/fst/pep_msa/CEPD20cps Tue Feb 1 11:40:54 2022

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* : :: *::*:**** *::*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:
Pavo_muticus      MVSRSADRLILIVSVLEGRCFPKRPKYMLLIVEAKFDGEQLATDPVEHTDQPEFATELAW 60
Pavo_cristatus    MVSRSADRLILIVSVLEGRCFPKRPKYMLLIVEAKFDGEQLATDPVEHTDQPEFATELAW 60
Gallus_gallus     MVSRAADRLILIVSVILEGRCFPKRPKYMLLIVEAKFDGEQLATDPVEHTDQPEFATELAW 60
Chelonia_mydas    MVSRS-SDQLLIVSVILEGRHFPKRAKHLVVEAKFDGEQLATDPVDHSDQPEFATELAW 59
Mus_musculus      MVPK-SDQLLIVSVILEGRHFPKRPKHLVVEAKFDGEQLATDPVDHTDQPEFATELAW 59
Rattus_norvegicus MVPK-SDQLLIVSVILEGRHFPKRPKHLVVEAKFDGEQLATDPVDHTDQPEFATELAW 59
Homo_sapiens      MVSX-SDQLLIVSVILEGRHFPKRPKHLVVEAKFDGEQLATDPVDHTDQPEFATELAW 59
Pan_troglodytes   MVSX-SDQLLIVSVILEGRHFPKRPKHLVVEAKFDGEQLATDPVDHTDQPEFATELAW 59
Macaca_mulatta    MVSX-SDQLLIVSVILEGRHFPKRPKHLVVEAKFDGEQLATDPVDHTDQPEFATELAW 59
Callithrix_jacchus MVSX-SDQLLIVSVILEGRYFPKRPKHLVVEAKFDGEQLATDPVDHTDQPEFATELAW 59
Canis_lupus_familiaris MVSX-SDQLLIVSVILEGRHFPKRPKHLVVEAKFDGEQLATDPVDHTDQPEFATELAW 59
Equus_caballus    MVSX-SDQLLIVSVILEGRHFPKRPKHLVVEAKFDGEQLATDPVDHTDQPEFATELAW 59
Bos_taurus        MVSX-SDQLLIVSVILEGRHFPKRPKHLVVEAKFDGEQLATDPVDHTDQPEFATELAW 59
Heterocephalus_glaber MVSX-SDQLLVVSVILEGRHFPKRPKHLVVEAKFDGEQLATDPVDHTDQPEFATELAW 59
Xenopus_tropicalis MGYK-SDQ-LIVSVILEGRHFPKRSRHLVVDKFDGEQLSDPVPHPLEQPFATELAW 58
Rhinatrema_bivittatum MGGK-AEQLLIVSVILEGRHFPKRPKHLVVEAKFDGEQLATDPVDHSDQPEFATELAW 59
1.....10.....20.....30.....40.....50.....60

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:***.*****:*. :*.:*.:*:*:*:*:*. ** *:***: ***.***
Pavo_muticus      LDRKALHQHRLQRTPIKLCFALDPLSSVKENIGYVVLDLRAVQEKQTPKWYSLLSNKY 120
Pavo_cristatus    LDRKALHQHRLQRTPIKLCFALDPLSSVKENIGYVVLDLRAVQEKQTPKWYSLLSNKY 120
Gallus_gallus     LDRKALHQHRLQRTPIKLCFALDPLSSVKENIGYVVLDLRAVQEKQTPKWYSLLSNKY 120
Chelonia_mydas    LDRKALHQHRLQRTPIKLCFALDPVSSTKENIGYIVDLRAAQEKQAPKWPPLLSNKY 119
Mus_musculus      IDRKVLHQHRLQRTPIKLCFALDPQTSAKETVGIVLDRTAQETKQAPKWPPLLSNKY 119
Rattus_norvegicus IDRKVLHQHRLQRTPIKLCFALDPQTSAKETVGIVLDRTAQETKQAPKWPPLLSNKY 119
Homo_sapiens      IDRKALHQHRLQRTPIKLCFALDPVTSAKETIGYIVLDRTAQETKQAPKWPPLLSNKY 119
Pan_troglodytes   IDRKALHQHRLQRTPIKLCFALDPVTSAKETIGYIVLDRTAQETKQAPKWPPLLSNKY 119
Macaca_mulatta    IDRKALHQHRLQRTPIKLCFALDPITSAKETIGYIVLDRTAQETKQAPKWPPLLSNKY 119
Callithrix_jacchus IDRKALHQHRLQRTPIKLCFALDSITSAKETIGYIILDRTAQETKQAPKWPPLLSNKY 119
Canis_lupus_familiaris IDRKALHQHRLQRTPIKLCFALDPVSSAKETIGYIVLDRTAQETKQAPKWPPLLSNKY 119
Equus_caballus    IDRKALHQHRLQRTPIKLCFALDPLSSAKETIGYIVLDRTAQETKQAPKWPPLLSNKY 119
Bos_taurus        IDRKALHQHRLQRTPIKLCFALDPSTARETIGYIVLDRTAQETKQAPKWPPLLSNKY 119
Heterocephalus_glaber IDRKALHQHRLQRTPIKLCFALDPVSSAKETVGIVLDRTAQETKQAPKWPPLLSNKY 119
Xenopus_tropicalis LDRKTLHQHRLQRTPIKLCFALDTLTSAKESVGIVLDRRAAQEKQAPKWPPLLSNKY 118
Rhinatrema_bivittatum LDRKALHQHRLQRTPIKLCFALDSLTSAKESLGIVLDRTAQEQKQAPKWPPLLSNKY 119
.....70.....80.....90.....100.....110.....120

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:***.***:*. :*.:*.:*:*:*:*. ** *:***: ***.***
Pavo_muticus      AKFKSEIKVGIVLETDKAPVDDLKAKEAPPREGRVSALLSRLDPKSIVPVLNEEGGYHQ 180
Pavo_cristatus    AKFKSEIKVGIVLETDKAPVDDLKAKEAPPREGRVSALLSRLDPKSIVPVLNEEGGYHQ 180
Gallus_gallus     AKFKSEIKVGIVLETDKAPVDDLKAKEAPPREGRVSALLSRLDPKSIVPVLNEEGGYHQ 180
Chelonia_mydas    TKFKSEIQISLVLETDKAPVDGFKAKEAPPREGKVPALLSGLDPKSILAVLNEEGGYHQ 179
Mus_musculus      TKFKAQVQISLTLETDKAPVDSYKAKAAPPRDGKVLASLAGVDPKDIVAVLNEEGGYHQ 179
Rattus_norvegicus TKFKSEVQISITLETDKAPVDSFKAKGAPPRDGKVPAILAGLDPRDIVAVLNEEGGYHQ 179
Homo_sapiens      TKFKSEIQISIALETDKAPVDSFKAKGAPPRDGKVPAILAGLDPRDIVAVLNEEGGYHQ 179
Pan_troglodytes   TKFKSEIQISIALETDKAPVDSFKAKGAPPRDGKVPAILAGLDPRDIVAVLNEEGGYHQ 179
Macaca_mulatta    TKFKSEIQISIALETDKAPVDSFKAKGAPPRDGKVPAILAGLDPRDIVAVLNEEGGYHQ 179
Callithrix_jacchus TKFKSEIQISIALETDKAPVDSFKAKGAPPRDGKVPAILAGLDPRDIVAVLNEEGGYHQ 179
Canis_lupus_familiaris TKFKAQISIALETDKAPVDSFKAKGAPPRDGKVPANLSGLDPKDIVAVLNEEGGYHQ 179
Equus_caballus    SKFKSEIQISIALETDKAPVDSFKAKGAPPRDGKVPASLSGLDPKDVAVLNEEGGYHQ 179
Bos_taurus        TKFKSEIQISIALETDKAPVDSFKAKGAPPRDGKVPASLSGLDPKDIVAVLNEEGGYHQ 179
Heterocephalus_glaber TKFKSEIQISITLETDKAPVDSFKAKGAPPRDGKVPASLPGLDPKDIVAVLNEEGGYHQ 179
Xenopus_tropicalis TKFKPEIQISITLETDKAPVDSFKAKGAPPRDGKVPASLPGLDPKDIVAVLNEEGGYHQ 178
Rhinatrema_bivittatum TKFKPEIQISITLETDKAPVDSFKAKGAPPRDGKVPASLPGLDPKDIVAVLNEEGGYHQ 179
.....130.....140.....150.....160.....170.....180

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CLUSTAL 2.1 MULTIPLE SEQUENCE ALIGNMENT

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***. * : * : ***:*****:*. *: *** *****:*****:.*:
IGPAEYCRDYFVLSVTIAFATQLEQLVPSTIVKLPPEHQPPEFFFFYSSLGNDVTNEPFTDLI
IGPAEYCRDYFVLSVTIAFATQLEQLVPSTIVKLPPEHQPPEFFFFYSSLGNDVTNEPFTDLI
IGPAEYCRDYFVLSVTIAFATQLEQLVPSTMKLPEHQPPEFFFFYSSLGNDVTNEPFTDLI
IGPPEYCREYFVLSVTIAFATQLEQLIPSTMKLPERQPEFFFFYSSLGNDVTNEPFTDLI
IGPAEHCCTDFILSVTIAFATQLEQLIPCTMKLPERQPEFFFFYSSLGNDVTNEPFSDLI
IGPAECCTDSFTLSVTIAFATQLEQLIPCTMKLPERQPEFFFFYSSLGNDVTNEPFSDLI
IGPAEYCTDSFIMSVTIAFATQLEQLIPCTMKLPERQPEFFFFYSSLGNDVTNEPFNDLI
IGPAEYCTDSFIMSVTIAFATQLEQLIPCTMKLPERQPEFFFFYSSLGNDVTNEPFNDLI
IGPAEYCTDSFIMSVTIAFATQLEQLIPCTMKLPERQPEFFFFYSSLGNDVTNEPFNDLI
IGPAEYCTDSFIMSVTIAFATQLEQLIPCTMKLPERQPEFFFFYSSLGNDVTNEPFNDLI
IGPAEYCTDSFIMSVTIAFATQLEQLIPCTMKLPERQPEFFFFYSSLGNDVTNEPFNDLI
IGPAEYCTDYFIMSVTIAFATQLEQLIPCTMKLPERQPEFFFFYSSLGNDVTNEPFNDLI
IGPAGYCTDFEIMSVTIAFATQLEQLIPCTMKLPERQPEFFFFYSSLGNDVTNEPFSDLI
IGPAEYCTDAFIMSVTIAFATQLEQLIPCTMKLPERQPEFFFFYSSLGNDVTNEPFNDLI
IGPAEYCKDYFVLSVTIAFATQLEQLIPSTLRLPEPQPEFFFFYSSLGNDVTNEPFTDLI
IGPTDYCRDFVLSVTIAFATQLEQLIPSTMKLPERQPEFFFFYSSLGNDVTNEPFTNLM
.....190.....200.....210.....220.....230.....240

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[illegible][illegible]

CLUSTAL 2.1 MULTIPLE SEQUENCE ALIGNMENT

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      :      ..      *      . : . : * : * : * : * : * :
Pavo_muticus      KQPKKKVLSPIGGEAKGLQERSQDVPS---QTHSSAIEDEATESEAESLK--FEKGTTEL 413
Pavo_cristatus    KQPKKKVLSPIGGEAKGLQERSQDVPS---QTDHSSAIEDEATESEAESLK--FEKGTTEL 413
Gallus_gallus     KQPKKKVLSPTGGEAKGLQERSQDVPS---QIDHSSPIEDEATESEAESLK--SEKGTTEL 413
Chelonia_mydas    EHSQKRVLSPTTRDKTKSPEQRSQSAPSPAPLONHSPPTKDEATESEVESLQ--YDRGTKL 415
Mus_musculus      EHSQKRVLTPIKEKTLTGPKSPRESAPPPPPNPPTPTKDDATESEVESLQ--YDKDPKP 417
Rattus_norvegicus EHSQKRVLTPIKEKTLTGPKSPRVSPAPPQ--NQTPPTKDDATESEVESLQ--YDKDPKP 415
Homo_sapiens      EHSKKKVLTPIKEKTLTGPKSPTVSPVPSH--NQSPPTKDDATESEVESLQ--YDKDTKP 415
Pan_troglodytes   EHSKKKVLTPIKEKTLTGPKSPRVSPVPSH--NQSPPTKDDATESEVESLQ--YDKDTKP 415
Macaca_mulatta    EHSKKKVLTPIKEKTLTGPKSPRVSPVPSH--NQSPPTKDDATESEVESLQ--YDRDTKP 415
Callithrix_jacchus EHSKKKVLTPVKEKTLTGPKSPRVSPVPSH--NQSPPTKDDATESEVESLQ--YDKDTKP 415
Canis_lupus_familiaris QHSKKRVLTPIKEKTLTGPKSPMSPPVPPQ--NLSPPTKDDATGSEVESLQ--YDKDTKP 415
Equus_caballus    QHSKKKVLTPIKEKTLTGPKSPSVSPVPPH--NQSPPTKDDATESEVESLQ--YDKDMKP 415
Bos_taurus        HHSKKRVLTPIKENTHTGPQSPSESPVPPH--NQSPPTKDDATESEVESLQ--YDKDTKL 415
Heterocephalus_glaber ELSKKRVLSPVKEKTLTGPKSPSISPAAPP--NQTPPAKDDATESEVESLQ--YDKDLKT 415
Xenopus_tropicalis VAAEEVPTTPLKKSANLKEGARSPPPKPLMFSDSPPTKDEATESEAESIKSDFQAEPPPL 415
Rhinatrema_bivittatum PKKKTVLSPTLKKRSRSPKPRPRSASPTLP--HYSNSPPTKDESTEGEIESLQ---ENDAPI 415
.....370.....380.....390.....400.....410.....420

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Pavo_muticus      KEAGLVGESCRDVKQYTEELPVFKSQSSAKSLLLSADDAPAAAPQPS----- 461
Pavo_cristatus    KEAGLVGESCRDVKQYTEELPVFKSQSSAKSLLLSVDDAPAAAPQPS----- 461
Gallus_gallus     KEAGLVDESCRDVSEQYTEELPVFKSQNSTKSLLSADDAPAVAPQPN----- 461
Chelonia_mydas    NKKALN-----ALAPVQS----- 430
Mus_musculus      TVKGIG-----SVPASLAQ----- 431
Rattus_norvegicus VVKGTG-----SIPASLAQ----- 429
Homo_sapiens      NPKASS-----SVPASLAQ----- 429
Pan_troglodytes   NPKASS-----SVPASLAQ----- 429
Macaca_mulatta    NPKASS-----SVPASLAQ----- 429
Callithrix_jacchus NPKAGS-----SVPVSLAQ----- 429
Canis_lupus_familiaris NPKAITSVP-----ASVAQAVGO----- 433
Equus_caballus    NPKAVR-----SSVPASLAQ----- 430
Bos_taurus        NPKAIS-----SSVPALLAK----- 430
Heterocephalus_glaber HVKGTS-----SSVPASLAQ----- 430
Xenopus_tropicalis SKPLTR-----SKSPPLSEPPPLSGSHCPTPIQ 442
Rhinatrema_bivittatum TQKDSN-----DPAPALEVD----- 430
.....430.....440.....450.....460.....470.....480

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Pavo_muticus      --SVSASGCSETAS-AQKVLIPAAASHHFCFSIDLRSVRGLEVGFPINCILRYSYPFFGSA 518
Pavo_cristatus    --SVSASGCSETAS-AQKVLIPAAASHHFCFSIDLRSVRGLEVGFPINCILRYSYPFFGSA 518
Gallus_gallus     --SVGASGCSETAS-AQKVLIPAAASHHFCFSIDLRSVRGLEVGFPINCILRYSYPFFGSA 518
Chelonia_mydas    --PGAASNASESAS-GQKIAVPAASHHFCFSIDLQSIHNLEVGFPVNCILRYSYPFFGSA 487
Mus_musculus      --PEATCGASEVVTSGQKIAVPAASHHFCFSVDLRSVHDLELSFPVNCILRYSYPFFGSA 489
Rattus_norvegicus --PEATGNPSEVVTSGQKIAVPATSHHFCFSIDLRSIHGLEISFPVNCILRYSYPFFGSA 487
Homo_sapiens      --LVTTSNASEVAS-GQKIAVPATSHHFCFSIDLRSIHGLEISFPVNCILRYSYPFFGSA 486
Pan_troglodytes   --LVTTSNASVVAS-GQKIAVPATSHHFCFSIDLRSIHGLEISFPVNCILRYSYPFFGSA 486
Macaca_mulatta    --PVTTSNASEVAS-GQKIAVPATSHHFCFSIDLRSIHGLEISFPVNCILRYSYPFFGSA 486
Callithrix_jacchus --PVTTSNASEVAS-GQKIAVPATSHHFCFSIDLRSIHGLEISFPVNCILRYSYPFFGSA 486
Canis_lupus_familiaris --AVTASHASETAS-GQKIAVPATSHHFCFSIDLRSIHGLEISFPVNCILRYSYPFFGSA 490
Equus_caballus    --PVTITNVSETAS-GQKIAVPATSHHFCFSIDLRSVHDLEVGFPINCILRYSYPFFGSA 487
Bos_taurus        --PVTTSIASEAAS-GQKIAVPATSHHFCFSIDLRSIHGLEISFPVNCILRYSYPFFGSA 487
Heterocephalus_glaber --PVAASKASETAS-AQKIAVPATSHHFCFSIDLRSIHGLEISFPVNCILRYSYPFFGSA 487
Xenopus_tropicalis GVSIAIAKNTSESSS-AQKITVPPAAHHFCFTIDLRSIRNVDVGFPVNCILRYSYPFFGSA 501
Rhinatrema_bivittatum --SAAICSSSDSVS-RQKIAIPPAHHFCFSIDLRSVHDLEVGFPVNCILRYSYPFFGSA 487
.....490.....500.....510.....520.....530.....540

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CLUSTAL 2.1 MULTIPLE SEQUENCE ALIGNMENT

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*****.*:.*:*****.*.*****:****.*:*****:*****:****.*
APIMTSPPIEIRKNMEVFFLPQSYCVFHFATTPHQLODTFFRLPLLVELWHKDKTTTKDLLL
APIMTSPPIEIRKNMEVFFLPQSYCVFHFATTPHQLODTFFRLPLLVELWHKDKTTTKDLLL
APIMTSPPIEIRKNMEVFFLPQSYCVFHFATTPHQLODTFFRLPLLVELWHKDKTTTKDLLL
APIMTNPPVEVRKNMEVFFLPQSYCAFD FATMPHQLODTFFRLPLLVELWHKDKMTKDILL
APIMTNPPVEVRKNMEVFFLPQSYCAFD FATMPHQLODTFLRIPLLVELWHKDKMSKDLLL
APIMTNPPVEVRKNMEVFFLPQSYCAFD FATMPHQLODTFLRIPLLVELWHKDKMSKDLLL
APIMTNPPVEVRKNMEVFFLPQSYCAFD FATMPHQLODTFLRIPLLVELWHKDKMSKDLLL
APIMTNPPVEVRKNMEVFFLPQSYCAFD FATMPHQLODTFLRIPLLVELWHKDKMSKDLLL
APIMTNPPVEVRKNMEVFFLPQSYCAFD FATMPHQLODTFLRIPLLVELWHKDKMSKDLLL
APIMTNPPVEVRKNMEVFFLPQSYCAFD FATMPHQLODTFLRIPLLVELWHKDKMSKDLLL
APIMTNPPVEVRKNMEVFFLPQSYCAFD FATMPHQLODTFLRIPLLVELWHKDKMSKDLLL
APIMTNPPVEVRKNMEVFFLPQSYCAFD FATMPHQLODTFLRIPLLVELWHKDKMSKDLLL
APIMTNPPVEVRKNMEVFFLPQSYCAFD FATMPHQLODTFLRIPLLVELWHKDKMSKDLLL
APIMTNPPVEVRKNMEVFFLPQSYCAFD FATMPHQLODTFLRIPLLVELWHKDKMSKDLLL
APIMTNPPVEVRKNMEVFFLPQSYCAFD FATMPHQLODTFLRIPLLVELWHKDKMSKDLLL
APIMTNPPVEVRKNMEVFFLPQSYCAFD FATMPHQLODTFLRIPLLVELWHKDKMSKDLLL
APIMTNPPVEVRKNMEVFFLPQSYCAFD FATMPHQLODTFFRLPLLVEVWHKDKMAKDLLL
.....550.....560.....570.....580.....590.....600

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*:::***:* * *:*****: : : . *::*: : : * : *****

GIARQLSNVLTSEKTRFLGGNGEQCWRQTYNETVSVTAAQGS DTRIAELLYAITLEDYG
GIARQLSNVLTSEKTRFLGGNGEQCWRQTYNETVSVTAAQGS DTRIAELLYAITLEDYG
GIARQLSNVLTSEKTRFLGGNGEQCWRQAYSETVSVTAAQGS DTRIAELLYAITLEDYG
GVARQLSNVLGLEKTRFLGTNGEQCWRQTCSETVGVMAAQ GANNRIAELLYAITLEDYG
GVARIQLSNILSSEKTRFLGANGEQCWRQTYSESVPIAAQGS SNNRILDLSYMTLEDYG
GIARIQLSNILSSEKTRFLGANGEQCWRQTYSEKVPVIAAQGS SNNRIVDLSTMTLEDYG
GIARIQLSNILSSEKTRFLGSGNGEQCWRQTYSESVPIAAQGS SNNRIADLSYTVTLEDYG
GIARIQLSNILSSEKTRFLGSGNGEQCWRQTYSESVPIAAQGS SNNRIADLSYTVTLEDYG
GIARIQLSNVLSSSEKTRFLGSGNGEQCWRQTYSETVPIIAAQGS SNNRIADLSYTVTLEDYG
GIARIQLSNILSSEKTRFLGSGNGEQCWRQTYSESVPIAAQGS SNNRIADLSYTVTLEDYG
GIARIQLSNVLSSSEKTRFLGSSGEGCWRQTYSESVPIAAQGS SNNRIIDLSTYTVTLEDYG
GIARIQLSNILSSEKTRFLGSGNGEQCWRQTYSESVPIAAQGS SNNRIIDLSTYTVTLEDYG
GIARIQLSNILSSEKTRFLGSGNGEQCWRQTFSESVPIVATQGS SNNRIVDLSTYTVTLEDYG
GISRIQLSNILSSEKTRFLGSGNGEQCWRQTYSESVPIAAQGS SNNRIVDLSTYTVTLEDYG
GVTKIQLSNVLSSSEKTRFLGPHGDQWRQTFSERITVTAVEGSKNKVAELSYIITLEDYG
GVARQLSHVLTAAKTRFLGPQDQCWRQTYSDRISITAVOGTSNQIAELSYMTLEDYG

.....610.....620.....630.....640.....650.....660

::*::*:: : . . :*****::***:*

LVKIHEVLVSESSQCVGAGQQRHATHTQ--LHCASEKQPEPRETLEYKAALELELWKEMQ
LVKIHEVLVSESSQCVGAGQQRHATHTQ--LHCASEKQPEPRETLEYKAALELELWKEMQ
LVKIHEVLVSDSSQCVGAGQQRHATHTQ--LHCASEKQTEPRETLEYKAALELELWKEMQ
LVKMHEVLVSDSSQCLGAGQ-QIPPPQ--PHHPVETETEPRETLEYKAALELEMWKEMQ
LVKMREIFVSESSQGVPAVDQKPPSPPP--APCPSEIQMEPRETLEYKAALELEMWKEMQ
LVKMREIFVSESSQGMSAVGQRASPPPPPPAPCPSEIQVEPRETLEYKAALELEMWKEMQ
LVKMREIFISDSSQGVSAVQKPPSSLPP--APCPSEIQTEPRETLEYKAALELEMWKEMQ
LVKMREIFISDSSQGVSAVQKPPSSLPP--APCPSEIQTEPRETLEYKAALELEMWKEMQ
LVKMREIFVSDSSQGVSAIQKPPSSLPP--APCPSEIQTEPRETLEYKAALELEMWKEMQ
LVKMREIFVSDSSQGLSAVHQKPPSSLPP--APCPSEIQTEPRETLEYKAALELEMWKEMQ
LVKMREILVSDSSQGLSAAQKPPSIIPP--APCPSEVQTEPRETLEYKAALELEMWKEMQ
LVKMREIFVSDSSQGVSAIEQKPPSSLPP--APCPSEIQTEPRETLEYKAALELEMWKEMQ
LVKMREIFVSDSSQGLSAVQKPPSVPP--APCPSEIQTEPRETLEYKAALELEMWKEMQ
LVKMREIFVSDSSQGLPAVQKPPSSLPP--APCPSEIQTEPRETLEYKAALELEMWKEMQ
LVKVREVVVSESSQSTGQ-EKGSIP-AQ--TLQSTAPLPEPRETLEYKAALELEMWKEMQ
LVKVQEVVSESSQSLGAGQKIAFSPSP--SSQVKESQPEPRETLEYKAALELEMWKEVQ

670 680 690 700 710 720

CLUSTAL 2.1 MULTIPLE SEQUENCE ALIGNMENT

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Pavo_muticus      EDIFENQLKKKEMARMQALAEFWKKRDEEREALVKKKVAEYTALEEQLKTLRDLDKRER 756
Pavo_cristatus    EDIFENQLKKKEMARMQALAEFWKKRDEEREALVKKKVAEYTALEEQLKTLRDLDKRER 756
Gallus_gallus     EDIFENQLKKKEMARMQALAEFWKKRDEEREALVKKKVAEYTALEEQLKTLRDLDKRER 756
Chelonia_mydas    EDIFENQLKKKELAHMQALAEFWKKRDKEREALVKKKVAEYTNLEEQLKTLTDLEKRE 724
Mus_musculus      EDIFESQLKQKELAHMQALAEFWKKRDRERESLVKKKVAEYSILEGKLOKALTELETRE 727
Rattus_norvegicus EDIFESQLKQKELAHMQALAEFWKKRDRERESLVKKKVAEYSILEGKLOKALTELESRE 727
Homo_sapiens      EDIFENQLKQKELAHMQALAEFWKKRDRERESLVKKKVAEYTILEGKLOKTLIDLEKRE 724
Pan_troglodytes   EDIFENQLKQKELAHMQALAEFWKKRDRERESLVKKKVAEYTILEGKLOKTLIDLEKRE 724
Macaca_mulatta    EDIFENQLKQKELAHMQALAEFWKKRDRERESLVKKKVAEYTILEGKLOKTLIDLEKRE 724
Callithrix_jacchus EDIFENQLKQKELAHMQALAEFWKKRDRERESLVKKKVAEYTILEGKLOKTLIDLEKRE 724
Canis_lupus_familiaris EDIFENQLRQKELAHMQALAEFWKKRDRERESLVKKKVAEYTVLEGKLOKTLIDLEKRE 728
Equus_caballus    EDIFENQLKQKELAHMQALAEFWKKRDRERESLVKKKVAEYTILEGKLOKTLIDLEKRE 725
Bos_taurus        EDIFENQLKQKELAHMQALAEFWKKRDRERESLVKKKVAEYNILEGKLOKTLIDLEKRE 725
Heterocephalus_glaber EDIFENQLKQKELAHMQALAEFWKKRDRERESLVKKKVAEYNILEGKLOKTLIDLEKRE 725
Xenopus_tropicalis EDLFFVNLKKKELVHMQALAEFWKKRDKEREALVKKKVAEYTVLEEQLKALADLEKRE 737
Rhinatrema_bivittatum EDLFFENQLKRKELAHMQALAEFWKKRDREREALVKKKVAEYSILEEQLKTLADLEKRE 725
.....730.....740.....750.....760.....770.....780

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** * *: : : :*: : :. :* :*:**:*:* :*:*:*: * :** *:
Pavo_muticus      QLLTAESEI-----QRVKRELQAEHEONKQELQDSVRRTREECACHQIELERSKIKOLGED 811
Pavo_cristatus    QLLTAESEI-----QRVKRELQAEHEONKQELQDSVRRTREECACHQIELERSKIKOLGED 811
Gallus_gallus     QLLTAESEI-----QRVKRELQAEHEONKQELQDSVRRTREECACHQIELERSKIKOLGED 811
Chelonia_mydas    QLVNAESEL-----QRVKRELQAEHEONKQELQDSVRRVKEECACHQIELERSKIKOLEED 779
Mus_musculus      QLASAESEL-----QREKRELQERERNLQELQDSVRRARDDCVQVVELERLKLKOLEED 782
Rattus_norvegicus QLVTAETEL-----QREKRELQERERNLQELQDSVRRARDDCVHQVVELERLKLKOLEED 782
Homo_sapiens      QLASVESEL-----QREKRELQERERNLQELQDSIRRAKEDCIHQVVELERLKLKOLEED 779
Pan_troglodytes   QLASVESEL-----QREKRELQERERNLQELQDSIRRAKEDCIHQVVELERLKLKOLEED 779
Macaca_mulatta    QLASAESEL-----QREKRELQERERNLQELQDSIRRAKEDCIHQVVELERLKLKOLEED 779
Callithrix_jacchus QLASAESEL-----QREKRELQERERNLQELQDSIRRAKEDCIHQVVELERLKLKOLEED 779
Canis_lupus_familiaris QLVLAESV-----QREKRELKSERERNLQELQDSIRRAKEDCVHQVVELERLKMROLEED 783
Equus_caballus    QLVIAESEL-----QREKRELKSERERNLQELQDSIRRAKEDCVHQVVELERLKLKOLEED 780
Bos_taurus        QLAIAESEMFLKLRERRELKSERERNLQELQDSIRRAKEDCVHQVVELERLKMROLEED 785
Heterocephalus_glaber QLASTESEL-----QREKRELQERERNLQELQDSVRRVREDCVHQVVELERLKLKOLEED 780
Xenopus_tropicalis QLANDEMEL-----KKLKAQLQDCERSIQERQDSIRRVREDCMHQVVELERSKAKOLEED 792
Rhinatrema_bivittatum QLTSAESEL-----RKVKSELQADHERGLOELHDSMRRVRDDCVHQVEMEKSNIKOLEED 780
.....790.....800.....810.....820.....830.....840

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Pavo_muticus      KLRMQQQLYEANKYKILEKEFOQYKEQQSSKPEIQLOSEINLLTLEKAELEKLESATK 871
Pavo_cristatus    KLRMQQQLYEANKYKILEKEFOQYKEQQSSKPEIQLOSEINLLTLEKAELEKLESATK 871
Gallus_gallus     RLRIQQQLYEANKYKILEKEFOQYKEQQSSKPEIQLOSEINLLTLEKAELEKLESATK 871
Chelonia_mydas    KVRLOQHFFYEANKYKILEKEFOQYKEQQSSKPEIRLOSEINLLTLEKAELEKLESATK 839
Mus_musculus      KQRLQQQLNDAGNKYKILEKEFOQFKDQONNKPEIRLOSEINLLTLEKAELEKLESATK 842
Rattus_norvegicus KHRLQQQLNDAENKYKILEKEFOQFKDQONNKPEIRLOSEINLLTLEKAELEKLESATK 842
Homo_sapiens      KHRLQQQLNDAENKYKILEKEFOQFKDQONNKPEIRLOSEINLLTLEKAELEKLESATK 839
Pan_troglodytes   KHRLQQQLNDAENKYKILEKEFOQFKDQONNKPEIRLOSEINLLTLEKAELEKLESATK 839
Macaca_mulatta    KHRLQQQLNDAENKYKILEKEFOQFKDQONNKPEIRLOSEINLLTLEKAELEKLESATK 839
Callithrix_jacchus KHRLQQQLNDAETKYKILEKEFOQFKDQONNKPEIRLOSEINLLTLEKAELEKLESATK 839
Canis_lupus_familiaris KHRLQQQLNDAENKYKILEKEFHQFKDQONNKPEIRLOSEINLLTLEKAELEKLESATK 843
Equus_caballus    KHRLHQQLNDAENKYKILEKEFHQFKDQONNKPEIRLOSEINLLTLEKAELEKLESATK 840
Bos_taurus        KHRLQQQLNDAENKYKTLEKEFHQFKDQONNKPEIRLOSEINLLTLEKAELEKLESATK 845
Heterocephalus_glaber KHRLQKQLLDAENKNKTLEKEFHQFKDQONNKPEIRLOSEINLLTLEKAELEKLESATK 840
Xenopus_tropicalis KLRLQQQLQEAHKKVLMKEFEFQYKEQQSSKPEIRLOSDINLLTLEKAELEKLELTK 852
Rhinatrema_bivittatum KLRLQQQLHDAEHKFKLLEKEFHQYKEQQSSKPEIRLOSEINFLTLEKAELEKLESSTK 840
.....850.....860.....870.....880.....890.....900

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CLUSTAL 2.1 MULTIPLE SEQUENCE ALIGNMENT

File: /media/morpheus/disk1/fst/pep_msa/CEPD200pep Tue Feb 1 11:40:54 2022

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*****.*****.:*****:***:*** *****.:*:*:*:
SKLHYKQQWARALKELARLKOREQENAMARLKKQOOELEHMRLCYLAEEKELGKTDROE
SKLHYKQQWARALKELARLKOREQENAMARLKKQOOELEHMRLCYLAEEKELGKTDROE
SKLHYKQQWARALKELARLKOREQESAMARLKKQOOELEHMRLCYLAEEKELGKTDROE
SKLHYKQQWARALKELARLKOREQENAMARLKKQOOELEHMRLRYLAAEEKEVGKTERKE
SKLHYKQQWGRALKELARLKOREQESQMARLKKQOOEELQMRLRYLAAEEKETVRTEQQE
SKLHYKQQWGRALKELARLKOREQESQMARLKKQOOEELQMRLRYLAAEEKD TVKTEQQE
SKLHYKQQWGRALKELARLKOREQESQMARLKKQOOEELQMRLRYLAAEEKD TVKTERQE
SKLHYKQQWGRALKELARLKOREQESQMARLKKQOOEELQMRLRYLAAEEKD TVKTERQE
SKLHYKQQWGRALKELARLKOREQESQMARLKKQOOEELQMRLRYLAAEEKD TVKTERQE
SKLHYKQQWGRALKELARLKOREQESQMARLKKQOOEELQMRLRYLAAEEKD TVKTERQE
SKLHYKQQWGRALKELARLKOREQESQMARLKKQOOEELQMRLRYLAAEEKD TVKTERQE
SKLHYKQQWGRALKELARLKOREQESQMARLKKQOOEELQMRLRYLAAEEKD TVKTERQE
SKLHYKQQWGRALKELARLKOREQESQMARLKKQOOEELQMRLRYLAAEEKD TVKTEQQE
SKLHYKQQWGRALKELARLKOREQENAMARLKKQOOELEHMRLRYLAAEEKD TVKTERQE
SKLHYKQQWGRALKELARLKOREQDNAMARLKKQOOELEHMRLRYLAAEEKEVVKTERQE
.....910.....920.....930.....940.....950.....960

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* :*****:***      .:  :      : :      .      .:..**::**:*::*****:
LEDIRNELNRLKQOEQERKQFQDAARDDSAKVDGLHTRKSSENIDDYLSRLMEERDTLL
LEDIRNELNRLKQOEQERKQFQDAARDDSAKVDGLHTRKSSENIDDYLSRLMEERDTLL
LEDIRNELNRLKQOEERKQFQDVR-DNSACKVDLSLHTRKSNENIDYVSRLMEERDTLL
LEDIRNELNRLKQOE-DKKQSQDSR-DISVEQAGSVHTRQNLNESLDDYLTRLIEERDTLL
LLDIRNELNRLRQOE--QNYQDCK-EIASGKLGSPRGSGLEEGLDYYLTRLIEERDTLM
LLDIRNELNRLRQOE--QKQYQDYK-EIASGKQGSPRGSGLEEGLDYYLTRLIEERDTLM
LLDIRNELNRLRQOE--QKQYQDST-EIASGKKDGPHGSVLEEGLDYYLTRLIEERDTLM
LLDIRNELNRLRQOE--QKQYQDST-EIASGKKDGPHGSVLEEGLDYYLTRLIEERDTLM
LLDIRNELNRLRQOE--QKQYQDSR-EIASGKKDGPHGSVLEEGLDYYLTRLIEERDTLM
LLDIRNELNRLRQOE--QKQYQDSR-EIASGKKDGPDGTVLEEGLDYYLTRLIEERDTLM
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LLDIRNELNRLRQOE--QKQYQDSR-EIASGKMDGLRGSALALEEGLDYYLTRLIEERDTLM
LEEIRNELNRLRQOE--DRK--QPP-DTSANAGSPGARLKDEGLDDYLSRLIEERDTLL
LEEIRNELNRLKQOE--EKKQDQSG-EITSGTKESPQARLLSDGLDDYYLTRLIEERDTLL
.....970.....980.....990.....1000.....1010.....1020

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*****.*.:*:*:**:*****.:*.*
RTGVYNHEDHIVSELDRQIREAIAKRNATK 1021
RTGVYNHEDHIVSELDRQIREAIAKRNATK 1021
RTGVYNHEDHIVSELDRQIREAIAKRNATK 1020
RTGVYNHEDHIVSELDRQIREALAKRSSNK 987
RTGVYNHEDRIISELDRQIREVLTKNSAS- 988
RTGVYNHEDRIISELDRQIREVLTKNSASN 989
RTGVYNHEDRIISELDRQIREILAKSNASN 986
RTGVYNHEDRIISELDRQIREILAKSNASN 986
RTGVYNHEDRIISELDRQIREILAKSNASN 986
RTGVYNHEDRIISELDRQIREILAKSNASN 986
RTGVYNHEDRIISELDRQIREVLAKNNASN 990
RTGVYNHEDRIISELDRQIREVLAKNSASN 987
RTGVYNHEDRIISELDRQIREVLAKNNASN 992
RTGVYNHEDRIISELDRQIREVLAKNNASN 987
RTGVYTHEDRIISELDRQIRETMAKRSNR- 996
RTGVYTHEDRIISELDRQIREAMTKRSSN- 986
.....1030.....1040.....1050

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