

clustalw.aln

CLUSTAL 2.1 multiple sequence alignment

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BAU98542.1      -----MADVSPANDSTASQDVANRFARKGALRQKNVHEVKDHFIARFFKQPTFCSHCTD
KAI4054112.1    -----MADFAAGPPPSSEGEESTVRFARKGALRQKNVHEVKNHFTARFFKQPTFCSHCTD
XP_809943.1      -----
XP_845346.1      -----
PWV04907.1      -----MDTVDPRTGQGESENNNNNNNGNGNGKEGGGGSQAKATSEKKNVETVRRV
ESS64742.1      MISKFLRLDPQRREKHEINPHDIKALRGMAATHNITSVAVPQYRVRENVEYVIECSKRS
AAK64304.1      MSLKFLFRYDTLQKGQELSTADHRSLELSMTDNITSVEIPQYRVRGTFVENVIECTKRN

BAU98542.1      FIWFGKGQGFQCVCCFVHKRCHEFVTFSCPG-----ADKGPDTDDPSKHKFK
KAI4054112.1    FIWFGKGQGFQCVCCFVHKRCHEFVTFSCPG-----ADKGPASDDPSKHKFK
XP_809943.1      -----
XP_845346.1      -----
PWV04907.1      FTPKCLKCGVTFPSPRRTIPPKRWCPCPTKGGCG-----KLWQPDASQVCDVCGA
ESS64742.1      VKWHVFRRYQQFALDQKLQKFCSMGSGYHCEYGVLPVLTGSHWAEVTNQSIDLVEKRRR
AAK64304.1      MTWQVFRRYQQFALDQSLQKLCGRSGSRHCDYGVIPVLCGSHWTEVTNQSIDLVEKRRR

BAU98542.1      IHTYGSPTFCDHCG-----SLLYGLIHQGMKCDTCMDNVHKQCVINVPSCMGMDHTEKR
KAI4054112.1    IHTYSSPTFCDHCG-----SLLYGLIHQGMKCDTCMDNVHKRCVMNVPSCGTDHTERR
XP_809943.1      -----
XP_845346.1      -----
PWV04907.1      MVARFTRHHCRRCGLYKCSKCLFKFTILTEWSLTKQRVCRCAVPAVPAISGWLKLGL
ESS64742.1      YLEIYLEQLLVPKNFLVYVAKTALYKFLHEGEVFPVRCGTNVLRLLIGFAAVE---PSRRPE
AAK64304.1      HLEIYLRLQVLPNGVYVAKTVIYDFLHDGAVPAHQRRAIRLIGATPDSDLHLLEN

BAU98542.1      GRIYLKAEVADEKLHVTVRDAKNLIMPDPNGLSDPYVKLKLIPDPKNESKQKTKTIRSTL
KAI4054112.1    GRIYIQAHIHDRDLVILVRDAKNLVPMDPNGLSDPYVKLKLIPDPKSESKQKTKTKCSL
XP_809943.1      G---KFYKKNQTRYFELRGPMCLCWKRRPSSGPHVS-----
XP_845346.1      G---ASSEVTASRYFERGSLIYCWTKYPENPGDK-----
PWV04907.1      QRATFFGKLMHRYFELRGVTLVYGRAKSNGADEGLTSVSLPKDARNGRGTSIGSTSD
ESS64742.1      ESEDDATTVEESPNLDISAAGNLKLVTTTTCCTTPERGVSN----SVESFSTRSSGME
AAK64304.1      RNEGGSASRLGAASTLNDKSIISMLGPSAVGESDRVDGVEEPECKSPPGTVEESGEE

BAU98542.1      NPQWN-----ESFTFKLKPSDKDRRLSVEINDWRDT
KAI4054112.1    NPENW-----ETFRFQLKESDKDRRLSVEINDWLDT
XP_809943.1      -----
XP_845346.1      -----
PWV04907.1      GANSSSSNSHNSKNNNNNNNGCSSSSNAQPTNSILTGQIDISGAKVMQDAIHPHAF
ESS64742.1      YDDVPSSRED-----TDNEIDHMPASPFLCQCAEFSSMLYPHRCFL
AAK64304.1      CEDLPSADN-----SEADVVRVPPPSGLRCQCAEFSSVLYPHRCFF

BAU98542.1      RNDFMGSLSPFGVSELMKMPASGWYKLLNQEAGEYYNVPIPEGDEEGNMELRQKFKAELG
KAI4054112.1    RNDFMGSLSPFGISELQKASVDGWKLLSQEAGEYFNVPVPEEGSEANEELRQKFERAKIS
XP_809943.1      IEGDHLKSTFTLTADTTEQREAWREMSKVKNPENRQPSSTAVQSGDVHATVLTGGR--
XP_845346.1      VQGGKLRKPHMFTAENEEREYKEMKAHPNANTEILRTLQTSDDGDDTAPLCSGGS--
PWV04907.1      IVGFFLPGRGYLSASSQAQKTQWVEAIREQVRKAHQQRGDEEEDDLSETEKVLVYAGSGA
ESS64742.1      CKQRFRCNCLRNVELEE-EVVRVLCQCYENHERHSKKQTAKDATPETPFQSFQGVTTAP
AAK64304.1      CRQQFCRDCLHPVELEGEVARSVCQCYENFARKTCKPQYPTFMASTPIQLCAAGGAL

BAU98542.1      P---AGNKVISPSEDRQPSNNLDRVKLTDFNFMVLGKGIGFGKMLSHKKGTKEYAIK
KAI4054112.1    QGTKVPEEKTNTVSKFDNNGNRDRMKLTDFNFMVLGKGSFGKVMLSERKGTDELYAVK
XP_809943.1      -----
XP_845346.1      -----
PWV04907.1      -----
ESS64742.1      -----
AAK64304.1      -----

BAU98542.1      ILKKDVUIQDDDVECTMVEKRVALLDKPPFLTQLHSCFQTVDRLYFVMEYVNGDLMYH
KAI4054112.1    ILKKDVUIQDDDVECTMVEKRVALLDKPPFLTQLHSCFQTVMDRLYFVMEYVNGDLMYH
XP_809943.1      EMGKELIQHNMLSNIAAEKHILQITISHP-FIVSLHYAFETKCKLYLVLDLPGGELFFH
XP_845346.1      KMEKEVIERYNMIDNISAEKLLIQKIDHP-FIVSLHYAFQTKGSLYLVMDFLGGELFFH
PWV04907.1      ILDKDQVQVHHLVPHNTAEKILISEISHP-FVVKLYAFQTKRHLILVLEFLCGGELFFH
ESS64742.1      ILNKCIHKRRMVEYIEEKDILASLPFHPYVVTCHFAFQTDYHLFFVLDFLPGGELYS
AAK64304.1      VLNKCVIHKRRMIEYIEEKDILASLPFHPYVVTCHFAFQTDYHLFFVLDFLPGGDMHSR
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BAU98542.1      IQQVGKFKEPQAVFYAAEISIGLFFLHKRGIYRDLKLDNVMLDSEGHKIAADFGMCKEH
KAI4054112.1    IQQVGKFKEPHAFVYAAEIAIGLFFLQSKGIYRDLKLDNVMLDSEGHKIAADFGMCKEN
XP_809943.1      LAKEKVFDEYRAKFYCGEIALAIGLYHSLDIIFRDLKPENIVLDEHGACLTDFGLAKMN
XP_845346.1      LESVSFVDEWRAKFYCGEIALALGILYHAQDIYRDLKPENAVLADAGHVLCTDFGLAKMD
PWV04907.1      LQRCRFDENRAKFYTAETIGMAVEYHSHSVLYRDLKPENIVLADREGHVLTDFGLAKRD
ESS64742.1      IYPKCTLSPVDVRLIIAEVVLALALEHLHRYDIVHRDLKPENIVFADAGHLKLTDFGLARMN
AAK64304.1      VYPKLKLTESDVRLYIAELVLALQHLHRHDIHRDVKLENIVLGEDGHLKLTDFGLARMN
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BAU98542.1      MMDGVTRTFCGTPDYIAPEIIAYQPYGKSVDDWVAGVLLYEMLAGQPPFDGEDEDELQ
KAI4054112.1    IWDGVTTKTCGTPDYIAPEIIAYQPYGKSVDDWVAFVLLYEMLAGQAPFGEDEDELQ
XP_809943.1      VSNASN-FTFCGTEYIAPEFLGQPHGRAVDWVWALGILLYEMIEGIPPFNNENSMEME
XP_845346.1      VRDACN-FTFCGTEYIAPEFLGQPHGKAVDWNWSLGAFLYEMIEGIPPFYSENVSAMYD
PWV04907.1      VAEDVRTHTCGTEYMAPELVKKSCHTTAVDWNWSLGAFLYEMVDMGMPFFYSPNVAEMEY
ESS64742.1      FSRHRR-YSFVGSPEYLAPEITIRGECQSRALDWNWSVGMVYEMLVGSTPFFAANNNDVCN
AAK64304.1      FSRQRR-RSFVGSPEYLPETIQGYQTKAVDWNWSAGVMLYEMLSKGTFFYSAYNCIYN
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Figure S1: Alignment of PKC amino acid sequences. Multiple sequence alignment using the ClustalW algorithm (<https://www.genome.jp/tools-bin/clustalw>) was performed using the following sequences: BAU98542.1 protein kinase C alpha [Homo sapiens]; KAI4054112.1 protein kinase C beta [Homo sapiens]; ESS64742.1 protein kinase [Trypanosoma cruzi Dm28c (TcPKC1)]; PWV04907.1 putative serine-threonine kinase [Trypanosoma cruzi TcPKC2]; XP_809943.1 serine-threonine kinase [Trypanosoma cruzi strain CL Brener TcPKC3]; AAK64304.1 zinc finger protein kinase

[Trypanosoma brucei brucei]; XP_845346.1 putative serine-threonine kinase
[Trypanosoma brucei brucei TREU927].