

Legionella pneumophila prevents proliferation of its natural host *Acanthamoeba castellanii*

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Supplementary Data 1

***Homo sapiens* Cyclin-Dependent Kinase (CDK) protein sequences**

>CDK1

MEDYTKIEKIGEGTYGVVYKGRHKTTGQVVAMKKIRLESEEEGVPSTAIREISLLKEL
RHPNIVSLQDVLMOQDSRLYLIFEFLSMDLKKYLDLSDIPPGQYMDSSLVKSYLEYQILQGI
VFCHSRRVLHRDLKPQNLLIDDKGTIKLADDFGLARAFGIPIRVYTHEVVTLWYRSPEV
LLGSARYSTPVDIWSIGTIFAELATKKPLFHGDSEIDQLFRIFRALGTPNNEVWPEVESL
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DNQIKKM

>CDK2

MENFQKVEKIGEGTYGVVYKARNKLTGEVVALKKIRLDTEGVPSTAIREISLLKEL
NHPNIVKLLDVIHTENKLYLVF
EFLHQDLKKFMDASALTGIPLPLIKSYLFQLLQGLAFCHSHRVLHRDLKPQNLLINTE
GAIKLADDFGLARAFGVPVRTYTHEVVTLWYRAPEILLGCKYYSTAVDIWSLGCIFAE
MVTRRALFPGDSEIDQLFRIFRTLGTPEVVWPGVTSMPDYKPSFPKWARQDFSKVV
PPLDEDGRSLLSQMLHYDPNKRISAKAALAHPPFQDVTKPVPHLRL

>CDK3

MDMFQKVEKIGEGTYGVVYKAKNRETGQLVALKKIRLDLEMEGVPSTAIRESLLKE
LKHPNIVRLLDVVHNERKLYLVFEFLSQDLKKYMDSTPGSELPLHLIKSYLFQLLQGV
SFCHSHRVIHRDLKPQNLLINELGAIKLADFGGLARAFGVPLRTYTHEVVTLWYRAPEI
LLGSKFYTTAVDIWSIGCIFAEMVTRKALFPGDSEIDQLFRIFRMLGTPSEDTPWPGVTQ
LPDYKGSFPKWTRKGLEEIVPNLEPEGRDLLMQLLQYDPSQRITAKTALAHYPYSSPE
PSPAARQYVLQFRH

>CDK4

MATSRYPVAEIGVGAYGTVYKARDPHSGHFVALKSVRVPNGGGGGGLPISTVRE
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AETIKDLMRQFLRGLDFLHANCIVHRDLKPENILVTSGGTVKLADFGGLARIYSYQMA
LTPVVVTLWYRAPEVLLQSTYATPVDMWSVGCIFAEMFRRKPLFCGNSEADQLGKIF
DLIGLPPEDDWPRDVSLPRGAFPPRGPRPVQSVPEMEESGAQLLLEMLTFNPHKRIS
AFRALQHSYLHKDEGNPE

> CDK5

MQKYEKLEKIGEGTYGTVFKAKNRETHEIVALKRVRLLDDDDDEGVPSSALREICLLKE
LKHKNIVRLHDVLHSDKKLTLVFEFCDQDLKKYFDSCNGDLDPEIVKSFLFQLLKGL
GFCHSRNVLHRDLKPQNLLINRNGELKLADFGGLARAFGIPVRCYSAEVVTLWYRPPD
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MTKLPDYKPYMPYPATTSLVNVVVKLNATGRDLLQNLLKCNPVQRISAEELQHPYF
SDFCPP

>CDK6

MEKDGLCRADQQYECVAEIGEGAYGKVFKARDLKNNGGRFVALKRVRVQTGEEGMP
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EPGVPTETIKDMMFQLLRGLDFLHSHR VVHRDLKPQNILVTSSGQIKLADFGGLARIYS
FQMALTSVVVTLWYRAPEVLLQSSYATPVDLWSVGCIFAEMFRRKPLFRGSSDQDL
GKILDVIGLPGEEDWPRDVALPRQAFHSKSAQPIEFVTDIDELGKDLLLKCLTFNPA
KRISAYSALSHPYFQDLERCKENLDSHLPPSQNTSELNTA

>CDK7

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RTALREIKLLQELSHPNIIIGLLDAFGHKSNISLVDFMETDLEVIKDNSLVLTPSHIKA
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LGTPTTEEQWPDMCSPDYVTFKSFPGIPLHHIFSAAGDDLDDLIQGLFLFNPCARITAT
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>CDK9

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DPYALDLIDKLLVLDPAQRIDSDDALNHDFFWSDPMPSDLKGMLSTHLTSMFEYLAP
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>CDK10

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>CDK11a

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LERKRERERKMREQQKEQREQKERERRAEERRKEREARREVSAAHRTMREDYSDKV
KASHWSRSPRPPRERFELGDGRKPVKEEKMEERDLLSDLQDISDSERKTSSAESSA
ESGSGSEEEEEEEEEEEEEEGSTSEEEEEEEEEEEEEEEEEETGSNSEEASEQSAAEVSEEEM
SEDEERENENHLLVVPESRFDRDSGESEEAEEEEVGEVTPQSSALTEGDYVPDSPALLPI
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QPFLPGEVKTLMIQLLRGVKHLHDNWILHRDLKTSNLLLSHAGILKVGDFGLAREYG
SPLKAYTPVVVTQWYRAPELLLGAKEYSTAVDMWSVGCIFGELLTQKPLPFGNSEID
QINKVFKELGTPSEKIWPGYSELPVVKKMTFSEHPYNNLRKRFGALLSDQGFDMNK

FLTYFPGRRISAEDGLKHEYFRETPLPIDPSMFPTWPAKSEQQRVKRGTSPPPEGGLG
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>CDK11b

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HSAEGGKHARVKEKEREHERRKRHREEQDKARREWQKRREMAREHSRRERDRL
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SAESGSGSEEEEEEEEEEEEEEGSTSESEEEEEEEEEEEEEETGSNSEEASEQSAAEVSEEE
MSEDEERENENHLLVVPESRFDRDSGESEEAEEEVGEFTPQSSALTEGDYVPDSPALS
PIELKQELPKYLPALQGCRSVEEFQCLNRIEGTYGVVYRAKDKKTDEIVALKRLKM
EKEKEGFPITSLREINTILKAQHPNIVTVREIVVGSNMDKIYVMNYVEHDLKSLMETM
KQPFLPGEVKTLMIQLLRGVKHLHDNWILHRDLKTSNLLSHAGILKVGDFGLAREY
GSPLKAYTPVVVTLWYRAPELLLGAKEYSTAVDMWSVGCIFGELLTQKPLFPGKSEI
DQINKVFKDLGTPSEKIWPGYSELPAVKKMTFSEHPYNNLRKRFGALLSDQGFDMN
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GYSQLGDDDLKETGFHLTTTNQGASAAGPGFSLKF

>CDK12

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EKETPPPPLTIASPPPPLPTTTPPPQTPPLPPLPIPALPQQPPLPPSQAFAFSQVPASSTSTL
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LDNEKEGFPITAIKILRQLIHRVVMKEIVTDKQDALDFKKDKGAFYLVFEYMD
HDLMGLLESGLVHFSEDHKSFMKQLMEGLECHKKNFLHRDIKCSNILLNNSGQIKL
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ALDLLDHMLTLDPSKRCTAEQTLQSDFLKDVESKMAPDLPHWQDCHELWSKKRR
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QDLRFARVPLALHPVVGQPFLKAEGSSNSVVHAETKLQNYGELGPGTTGASSGAGL
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>CDK13

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EKRRVFSLPQPQDGGGGASSGGVTPLEVEDVSSQSEQLLLGGASAATAATAA
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SKSRSRSHSHSGEERAEVAKSGSSSSSGRRKSASATSSSSSRKDRDSKAHRSRTKSSK
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SGKSRSRSPYSSRHSRSRSRHLSRSRSRHSSISPSTLTLKSSLAAELNKNKKARAAEA
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EIKILRQLTHQSIINMKEIVTDKEDALDFKKDKGAFYLVFEYMDHDLMGLLESGLVHF
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GGIQPSSQTIQPKVETDAAQAAVQSAFAVLLTQLIKAQQSKQKDVILLEERENGSGHE
ASLQLRPPPEPSTPVSGQDDLIQHQDMRILELTPEPDRPRILPPDQRPEPEPEPPVTEED
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PQPFAFSESFSSVAGYGDIYLNAGPMLFSGDKDHRFEYSHGPIAVLANSSDPSTGPES
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RGRGLPY

>CDK14

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SYEKLEKLGEGSYATVYK GKSKVNGKLVALKVIRLQEEEGTPFTAIREASLLKGLKH
ANIVLLHDIHTKETLTLVFEYVHTDLCQYMDKHPGGLHPDNVKLFLFQLLRGLSYIH
QRYILHRDLKPQNLLISDTGELKLADFGLARAKSVPSHTYSNEVVTLWYRPPDVLLGS
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>CDK15

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LGEYSYATVYKGISRINGQLVALKVISMNAEEGVPFTAIREASLLKGLKHANIVLLHDI
IHTKETLTFVFEYMHTDLAQYMSQHPGGLHPHNVRLFMFQLLRGLAYIHHQHVLHR
DLKPQNLLISHLGELKLADFGLARAKSIPSQTYSSSEVVTLWYRPPDALLGATEYSSEL
DIWGAGCIFIEMFQQGPLFPGVSNILEQLEKIWEVLGVPTEDTWPGVSKLPNYPNPEWF
PLPTPRSLHV VWNRLGRVPEAEDLASQMLKGFPRDRVSAQEALVHDYFSALPSQLYQ
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>CDK16

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KRLSLPADIRLPEGYLEKLTLSPIFDKPLSRRLRRVSLSEIGFGKLETYIKLDKLGEGT
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KSLTLVFEYLDKDLKQYLDDCGNIINMHNVKLFLFQLLRGLAYCHRQKVLHRDLKP
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VGCIFYEMATGRPLFPGSTVEEQ LHFIFRILGTPTEETWPGILSNEEFKTYNYPKYRAE
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>CDK17

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SDEVQSPTGVCLRNRIHRRISMEDLNKRLSLPADIRIPDGYLEKLQINSPPFDQPMSRRS
RRASLSEIGFGKMETYIKLEKLGE GTYATVYKGRSKLTENLVALKEIRLEHEEGAPCT
AIREV SLLKDLKHANIVTLHDIVHTDKSLTLVFEYLDKDLKQYMDDCGNIMSMHNV
KLFLYQILRGLAYCHRRKVLHRDLKPQNLLINEKGELKLADFGLARAKSVPTKTYSN
EVVTLWYRPPDVLLGSSEYSTQIDMWGVGCIFFEMASGRPLFPGSTVEDELHLIFRLL
GTPSQETWPGISSNEEFKNYNFPKYKPQPLINHAPRLDSEGIELITKFLQYESKKRVSA
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>CDK18

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ALQPFDVSKRLSLPMDIRLPQEFLQKLQMESPDLPKPLSRMSRRASLSDIGFGKLET
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NIVTLHDLIHTDRSLTLVFEYLDSDLKQYLDHCGNLMSMHNVKIFMFQLLRGLAYCH
HRKILHRDLKPQNLLINERGELKLADFGLARAKSVPTKTY SNEVVTLWYRPPDVLLG
STEYSTPIDMWGVGCIIHYEMATGRPLFPGSTVKEELHLIFRLLGTPTEETWPGVTAFS

EFRTYSFPCYLPQPLINHAPRLD TDGIHLLSSLLLYESKSRMSAE AALSHSYFRSLGER
VHQLEDTASIFSLKEIQLQKDPGYRGLAFQQPGRGKNRRQSIF

>CDK19

MDYDFKAKLAAERERVEDLFEYEGCKVGRGTYGHVYKARRKD GKDEKEYALKQIE
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KIADMGFARLFNSPLKPLADLDPVVVTFWYRAPELLLGARHYTKAIDIWAIGCIFAEL
LTSEPIFHCRQEDIKTSNPFHHDQLDRIFSVMGFPADKDWEDIRKMPEYPTLQKDFRR
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>CDK20

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KGVAFCHANNIVHRDLK PANLLISASGQLKIADFG LARVFSPDGSRLYTHQVATR WY
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VWPELTEL PDYNKISFKEQVPMPLEEVLPDVSPQALDLLGQFLLYPPHQRIAASKALL
HQYFFTAPLPAHPSELPIPQRLGGPAPKAHPGPPHIHDFHVDRPLEESLLNPELIRPFILE
G

***Homo sapiens* outgroup protein sequences used to built the phylogenetic tree**

>CDKL1

MMEKYEKIGKIGEGSYGVVFKCRNRDTGQIVAIKKFLESEDDPVIKKIALREIRMLKQ
LKHPNLVNLLEVFRRKRRLHLVFEYCDHTVLHELDRYQRGVPEHLVKSITWQTLQA
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FSTNQYFSGVKIPDPEDMEPELELKFPNISYPALGLLKGCLHMDPTQRLTCEQLLHHPY
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DTKKLNYRFPNI

>GSK3alpha

MSGGGPSGGGPGGSGRARTSSFAEPGGGGGGGGGGPGGSASGPGGTGGGKASVGA
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HCNIVRLRYFFYSSGEKKDELYLNLVLEYVPETVYRVARHFTKAKLTIPILYVKVYM
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YYRAPELIFGATDYTSSIDVWSAGCVLAELLLGQPIFPGDSGVDQLVEIHKVLGTPTRE
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FDEL RCLGTQLPNNRPLPPLFNFSAGELSIQPSLNAILIPHLRSPAGTTTTLTPSSQALTE
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>MAK

MNRYTTMRQLGDGTYGSVLMGKSNESGELVAIKRMKRKFYSWDECMNLREVKSLK
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LLRSSVYSSPIDVWAVGSIMAELYMLRPLFPGTSEVDEIFKICQVLGTPKKS DWPEGY
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VGQVLGPSSNHLESKQSLNKQLQPLESKPSLVEVEPKPLPDIIDQVVGQPQPKTSQQPL
QPIQPPQNLSVQQPPKQQSQEKPPQTLFPSIVKNMPTKPNGTLSHKSGRRRWGQTIFKS
GDSWEELEDYDFGASHKKPSMGVFKEKRKKDSPFRLPEPVPSGSNHSTGENKSLPA
VTSLKSDSELSTAPTSKQYYLKQSRYLPGVNPKKVSLIASGKEINPHTWSNQLFPKSL
GPVGAELAFKRSNAGNLGSYATYNQSGYIPSFLKKEVQSAGQRIHLAPLNATASEYT
WNTKTGRGQFSGRTYNPTAKNLNIVNRAQPIPSVHGRTDWVAKYGGHR

Putative *A. castellanii* CDK resulting from the blast of all human CDKs

>XP_004353710.1 Cdc2b

MQAKPSPLQRYDIKEKLGEGTYGEVYKAIDTENQRFIALKKMRLLEAEDEGVPATAL
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YLYQILKGIAYCHSHRILHRDLKLANLLIDRKGVLKLADFGLARAFGVPIRTYTHEVV
TLWYRAPEILLGQARYSTPVDMWSVGCIFAELVTKRPLFPGDCEIDELFRIFRTLGTPN
EEVWPGVTTLPDYKSTFGQWKPQSLASVVPGLDPLGLDLLSKMLRYAPQERISAKEA
LKHPYFDDLDKTKYP

>XP_004336625.1 cdk10/11

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VLVAAMRSCRSVDHYERLNRIQEGAYGVVHRAKDKETGEVVALKKFKIKGDESPV
TALRELAVLMEMDHPNVVRAKEIVIGKDPNSFYLVMEFLEHDLKDLMTAMRDPFLQ
SEIKCLLQQLLEAIAIYIHDNWYLHRDLKTSNLLLSSKGILKVADFGLARHYGDPLRPY
TQPVVTLWYLAKRPIDPYRAPELLLGAKEYSWEIDMWA VGCIFAEMLCKEPLMKAQ
TELQ MIDQIFKMLGTPNDDVWPGFSELPFVKMKFKTYPSAIRQRMFSATTDAGFDL
LMSFLAYDPKKRITAREALSHRYFTEPPLPREPGMIQTFPSLHEGTRPRPNSPGVEGGL
FGAHLSDSTDAHAALGIDPYGHQPTGFKLR

>XP_004367653.1 protein kinase domain containing protein

MKRSREEMPTTLHRRTQSHGSILPTNASSSSSSARASTFLPPAAPSLGSSSSSSSSSVARP
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MGTCRRIQQYETLEQVGEVYGVVYRARDMRSNRIVALKKVRMEKEKDGIPITCLRE

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KRRF

>XP_004335644.1 Cyclindependent kinase

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>XP_004342572.1 protein kinase domain containing protein

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FSTNVVTLWYRAPELLGVNAYGPKVDIWSAGCLFIELLTRQSPFPGREEKHQLELIV
RTC GTPDERNWPGVTKLEGYKQLQGLMGHKNRLREVFGKFDPRALD LLSRMLSLNP

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