(a) Metaxin amino-acid alignment (p. 1-2)

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                        *        20         *        40         *        60         *        80         *       100         *       120         *       140
Physcomitr : -----MMDMVSSTSSAWAESSSGSADLVLVTRPP---AFGL----------PTA--------------CPACLPAYLYLRLAGARFDVHVTAVEPDSE------DLPSVEYGENVGFASENGGVVEFLREEKIVDLDAGLNE
Oryza_sati : -----MASAAAAAAAEWEEAERKVLVARKA-------AFGL----------PTA--------------CPTCLPVLLYLRMCNVPFDIHVDSSFPDAD------HIPYVEFGECVAFNNEKGGVIEYLKEEKIVDLNSKHPS
Sorghum_bi : ----MASAAAAAAAAEWEAAARKVLVARKP-------CFGL----------PTA--------------CPTCLPVFLYLRMAQVPFDIHVDTNFPDAD------HIPYVEFGDCVAFNNEKGGVIEYLKDEKIVDLNSNFPS
Populus_tr : -------MQESQERAEYTLVARKP-------------SFGL----------PTG--------------CPICLPVYIHLKFASFPFRLDFNNTFPDSD------QIPYIESGTYVAFNDENGGLIERLREDGIVDLDAAFCS
Arabidopsi : -------MEGDQETNVYTLVARKP-------------SFDL----------PTA--------------CPNCLPAYIYLKLAQLPFELAFNSTFPDSD------ELPYFESDTYVAYNNEDGGVIEKLKKDGIVNLDSQLQS
Ectocarpus : -MASEEHGDAVPVRTSWNPLRALR------------SWGRIEEQPDLEQPGPVITHGSALDVMVVTQFRPAWETQAHLRFVRLPYRVE-NSSYMGSAATG---LYPALTDGQF-VL--RSEDAAGHIASR-RSDVDVGLTE
Phytophtho : MFPEDRFHPLGPDADRLHDDLIEATELESTPKTSR--ELGS----------ALVLHQ-----------FLPAWDVQAYLRVAGIQLHVH-NSKYPTYEATG---ELPQLSDGNF-LL-PK-EEIIMHLQTF-HKDIDEFLTD
Albugo_lai : MFPTNRFTSLLPSAPSLKQILRKENDEDLEFVPKTSKDYGS----------RIVVHQ-----------FWPAYNVIAYMRMANLNFHVH-NSRYPRYEVSG---ELPQLHDGNY-LL-SK-SDINLHLQTF-HTDIDVHLTA
Canis_fami : --------------MMWSGNRRVRVQKAAE-------PWPE----------NATLYQQLKGEQILLSDNAASLAVQAFLQMCNLPIKVVCRANAEYMSPSG---KVPFIHVGNQ-VV-SELGPIVQFVKAK-GHSLSDGLDE
Ictalurus_ : -------MSLAAEAFVSQIAAAE--------------PWPE----------NATLYQPLREDQILLSDCASSLAVQAYLRMLGLPVRVRCRANAEYMSPSG---KVPFIHVGNQ-VV-SELGPIMQFTRAK-GHSLSDSLDD
Takifugu_r : -------MSLAAEAFVSQIAAAE--------------PWPE----------SATLYQPLKEDQVLLSDCASSLAVQTYLRMCGLPVEVMYRANAEYMSPSG---KIPFIHVGNQ-VV-SELGPIVQFTKAK-GHSLSDGLDD
Nasonia_vi : -------MQNSTLLDPWNVELGASILLVAAQE-----PWPQ----------PIHLYQPYEVEQILLPDNANCLAVQAYLKMCNLDFTIEPRWNAEYMSPSA---KVPFIKCGAF-VI-PDYDNIVSFISSK-GASLSEGLSE
Solenopsis : -------MPHVLLGDSIAVELEAQE------------PWPQ----------PITLYQPYEVEQILLPDNANCLAVQAFLKMCQLDFQIEPRKNAEFMSPSG---RVPFIKCGTK-LI-SEFDGIVAHIGSK-GISLSDHLDP
Brugia_mal : -------MTGSYFMTDLVADSLSSEIDV---------DWS-----------GAVLYTPYYT-QALLYEYADCVAVQTLLKMANLPVRLEERPNAEFMSPTG---KVPFLKLQSF-LV-SEFLPVVDFLAKR-NVKLSAGLTD
Drosophila : -------MKSQYLNQLHTAEKLVAE------------PWPE----------DATLYQPYEAEQILLPENASCLAVKAYLKMCNLPFGIRSCANAEHMSPGGRMTKLPFIRAGAF-IF-AEFEPIVNFVEQK-HLAIGNWQDE
Aedes_aegy : -------MSAITSEYLKNETIASQ------------PWPQ----------QAHLYQPYEEEQILLAEHASCLAVRTYLTMLNLPFVVDQRANAEFMSPGGKRTKLPVLRVENY-TY-AEFEHILSFVELK-GLSLTKQLTP
Anopheles_ : -------MASTIDNFYQKTATAAMK------------DWPR----------DAVLYQPYEEEQILLAENASCLAVRTYLKMLNLPVALEQRANAEFMSPGGKRTKLPVLRVENF-IY-AEFDHIVTFLEKNFNKSLSAPLTP
Ciona_inte : MSSPKKSTDGKMEVKCWGE------------------GWGL----------PSL--------------DPDCLSVIAYANLAKAPIEV--VPALPKDIITG---SLPELQIDEF-IY-PRAFTIIGIFRRE-GYNADYSLSQ
Acyrthosip : -----MFKPHQLEVESWKG-----------------DWGL----------PSI--------------DYKCLEVLAFARFTNAPINIY-HSNNPYRSVTG---HLPVVSYNKR-LL-MDRDSLIDCLEKQ-NLTPDFGLTS
Pediculus_ : -----------MELEVWGG-----------------DWGL----------PSI--------------DLDCLQILVYCKLSGAPVQLK-VKNNPLTI-------SLPTFRHGQV-VL-YKLQDVVSYLQSK-NFYADHILSS
Camponotus : -----MDNAEILQLDIWKG-----------------DWGL----------PSV--------------DIDCLQVLAYAKFSGIPLKVN-LTSNPFKIPNG---RLPLLRAGLN-TL-DTVKDILPFFRAK-HYNSDYTLTD
Apis_melli : --------MDMFELSIWKG-----------------DWGL----------PSV--------------DTECLQVLVYAKFNGIPLKIN-SAGNPFTIPNG---SLPVLKTRNG-TF-NAVKDIIEFFRKE-RYNTEYELSR
Strongyloc : -------MAAMMEMDCWKG-----------------DWGL----------PSV--------------DRDCLKVMAYAQFAGAPIKVH-RDRRLWRNISA---HYPVFYSDGR-TL-KSADSIIEHLKQN-QFDADSELND
Ixodes_sca : -----------MELNIWKG-----------------DWGL----------PSI--------------DTACLEALAYAKFSGAPLIIN-EVRRPWFA------TLPIMRHGPSTRI-TKFEDMVAHFRKQ-NYSADIQLTA
Nematostel : -------MADVLELFSWPG-----------------DFGL----------PSV--------------DIPCLAVLSYVKFAGCPLKVN-RSNKFWKSPTW---EFPVMKSGEE-VL-TSPYKINDHLRQK-NFNADYQLTA
Mus_muscul : -------MAAPMELSCWGG-----------------GWGL----------PSV--------------HSESLVVLAYAKFSGAPLKIN-IIDNTWRGSRG---DVPILTTEDS-IV-SKPAKILNFLRKQ-KYNADCELSA
Salmo_sala : --------MATSELYCWEG-----------------DWGL----------PSV--------------DTECLIILAYAKFAGAPLKLH-KIGNPWRSPTG---SLPALKTSENGSL-SRPSDIIIHLRKQ-KYNADFDLSA
Monodelphi : -------MAAPMELYCWAG-----------------GWGL----------PSV--------------DLESLIVLTYARFTGAPLKVH-KITNPWKSPSG---TLPALRTPDASVI-SQPHKIITHLRKQ-KYNADYDLSA

                        *       160         *       180         *       200         *       220         *       240         *       260         *       280
Physcomitr : RERAELETCKAMMQSWVADASAYEVWM---RDNSRQCKTVYFSELPWGLVQALDWKQRLAVMQRLEITPEN-----TMTRTEELYKKASNAYSALSILLSDQ--K---YFFNDRPTSLDALVLGHLLFHLRVP-LEVS-TLK
Oryza_sati : VSYSDVLSTKAMVMTWLSDALQYELWL---ASDGSIPHDIYFSDLSWPIGKILYWKKTREVKQQLGITKLN-----AAEKEEEIYQKANAAYDALSTRLGDQ--I---FLFDNSPTDVDALFLGHALFVLNV--LPDTSVLR
Sorghum_bi : VSSTTVQETKAMVSTWLADALLYELWV---ASDGSIANDIYFSDLAWPIGKILHWKKTRHVKQQLGITKLN-----AAEKEEEIYRKASAAYDSLSIRLGDE--V---FLFDNSPTDVDALFLGHALFVLSV--LPDTSVLR
Populus_tr : L--PEWISMKAMVCTWLAEAVMYELWV---GSDGTSARAIYYSDLPWLIGKALFMKQVYVVKQRFGITKEN-----AERKEEEIYKRAKIAYGALSTTLGDQ--T---FLF-ERPSSLDAYLLGHVLFTLQA--LPESSVLR
Arabidopsi : L--SDYLSLKALIVSWLEEALTYEIWV---GTEGISISKIYYSDLPWVISKVLFYKQTYLAKNRLGITKEN-----AEQREKQIYKRASEAYEALSTRLGEQ--K---FLFEDRPSSLDAFLLSHILFIIQA--LPVTSVLR
Ectocarpus : AEKVEAQALAMLVREGLQPLLRVMRYMGDEGEVRQTVHPPMKKALSWPLSWWSPAAEGRRSKRESAVR-GL-----DRLSKAELIGRAKEMYAALDLRLGNSKEA---FFFGSRPTSVDAVVFGHLAEAWTIA------VLL
Phytophtho : QQRSESYAYRSMLSEKLQRVMLYCRWV-DSATYREVTRPHMKRHIPFPLSLFLPKKMHLDTMEQLRLY--------GISTKEQAYVIARDCYTALNAKLESAGTP---YFFGDQPSALDVAVFGHIVD----A-MGNT-QLV
Albugo_lai : EEKADLFAFRSIVTEKLAYVLLYCRWV-DDVEYTEVTLPQLRNVIPFPLNRILPKMMRNAALREAQAH--------GICSREKAYMLARDCYASLNAKVSENSSR---YSFGYHPTSLDAEIVGHVID----G-LANT-QLR
Canis_fami : VQKAEMKAYMELVNNMLLTAELYLQWC-DEATVGEITHARYGSPYPWPLNHILAYQKQWEVKRKMKAI-GW-----GNKTLDQVLEDVDQCCQALSQRLGTQ--P---YFFNKQPTELDALVFGHLYTILTTQ-LTND-ELS
Ictalurus_ : VQRAEMKAYMELVNNMLLTAELYIQWC-YQNTAAEITRPRYSSPYSWPLNHILAYQKQWEVRRKMNAI-GW-----AGKSLEQVYEDVSQCCQALSQRLGTQ--P---FFFNKQPTELDALVFGHLFTILTTR-LTTD-ELS
Takifugu_r : VQRAEMKAYMELVNNMLLTAELYIQWC-DDATATGITRPRYSSPYSWPLSSFLAYQKQWEVRRKMNAI-GW-----GGKTLEQVYEDVNQCCQALSQRLGTQ--P---FFFNKQPTELDALVFGHLFTILTTR-LTST-ELA
Nasonia_vi : EDKVNLRAYQSLVNNVLHNAELYVCWC-HEDTYNSITKNRHGSVYPWPLNHLLNWQKRNQITKRLNVL-GY-----ATKTLKEIFDDVEKCCEALSERLEDK--M---YFFGDRPNELDALVFGHIFSIITTP-LTKDNTLA
Solenopsis : AGKVDMRAYQSLVNNVFVNAELYICWV-DPAILDGVTKQRHGSVYPWPLNYYLNWQKRREVIKKLSVL-GW-----YNKSLDEVFDDVKKCCIALSERLADE--E---FFFGKDPTEVDALMYGHVHTLIAFP-FSSNRDVA
Brugia_mal : LERGDMHAHMALFDDILKNVEMYVMWM-DKRNYSQVTKCRYGSVYLFPLNLILPRVKWREVNNYLTAV-DW-----KSKSQECVMDLADRCFKSMSSKLDHN--E---YFFGDSPTELDALAFGHFYTILTTE-LPNM-ELK
Drosophila : DEKADMRTYVSLVENIFTMAELYISFK-NERVYKEVTAPRNGVVFPWPLNHMQNYGKRRNALRLLKVY-QW-----DDLDIDSVIDNVAKCCETLEYKLKES--PETPFFYGDQPCELDAIAFGHLFSILTTN-LPNM-ALA
Aedes_aegy : DQKDDMRAHLCLVEQIFTNAEQYISWV-DPEVLHKVTRQRNGCVYPFPLNHIQNWRKQMAVRRQLGVA-DF-----LNITLDEVVEKVEKLCTSLSMQLGDK--K---YFYGDEPTELDALVFGHLFSIFTMT-LPNN-VLA
Anopheles_ : EEKDQMRSTNCLVEHLFTTAEQYVSWI-DPEVRNTVTKKRNGCVFPFPLNHVQNWRKESAVRRQLRMA-DY-----LHEGIDTIMGEVDHLCQDLSSRLGDK--R---YFFGDSPTELDALVFGHLYSIFTMK-LPNN-VLA
Ciona_inte : SENADTLAFLSYIEQKLKPAILYSLWI-DVRNFNKVTRPAYGKACGFPWSLWYPSRLVKSYTNQLWLSKGGESFTCIKEVEKVIYKDAHDCLNVLESRMSST--D---YFFGDFPTTIDAVLYGHLAVLLHAP-LVST-ELQ
Acyrthosip : LQLAEEHAAISMIDAQLEPALLFAWWM-DESNCLNFTKPWYRNALKFPFNWYYPNVYEREAKHKIYTLYNHLDS--DNDIMMEIYAEAIKCMNVLESRLGNN--F---YFFGSHPTLLDAVAYSYLGPLLKAP-LTGN-RLQ
Pediculus_ : RNISEIQAYIELLKEKLYPGLQFVWWV-DNKNCVNLTKSWFAKKLMFPLNFYYPGHYEAQAKNLITALYGSLEEN-LAAIETQVYSDAEKCLTLLSNRLGES--K---YFFGNQATSLDAIIYSYLAPLLRAP-FPNP-TLQ
Camponotus : KQCADVLAYDALLKEKLYPALQFIWWI-DKKNLDELIRPWYCKALPFPFKFYYPGKFERQAQALMQSLYSMEDN--IDVIENEVYSEAQKCLTLLSMRLGDG--D---FFFGQQPSTIDAIVYSYLALLLKAP-LPNP-VLQ
Apis_melli : KQCAKVMAYGTMLKEKLFPALQFIWWI-DEKNVNELIRPWYCKALPFPFNFYYPGKFERQAHTMFVTLYPLEDN--ITAIENKVYSEAQKCLTLLSTSLGDS--Q---YFLGQKPTILDAIVYSYLAPLLKAP-LPNP-ALQ
Strongyloc : QQRADILAYSSLLEEKLLPALQYTWWV-DAKNYTEFSRPWFAKTMHFPFNYFIPGQLQRTAESSLEVRRGGLHLL-DGELSQNVMKDARYCLNMLSERLGEK--E---FFFGESPTSLDALVFSYLAPLVRVP-FPSN-TLQ
Ixodes_sca : QQSSDVRAYTAMLRQKLKPALLYLWWV-DAKNYVELTRPWYARALAFPLNYVLPGQMQRDAMAALQCKLELLDLE-GKQAETALLKEAQECLTTLSQRLGKD--T---FFFGKRPTSLDAVVFAHLAPLLKAP-FPNA-ALQ
Nematostel : KQGADTLAFIALIEDKLLPAMHYTLWV-DSKNYVEFTRPMYARKLPLPLNFFVPGRIANQKKLRIGHKLDPEEEEANGELENMLFKEAIECLTHLSVLLGDK--D---FFFGESPTTLDAVAFAHLALIWRAPSLPNN-KLA
Mus_muscul : KQGADTLAYIALLEEKLLPAVLHTFWV-ENENYFTVTKQPWFASRIPFPLSLILPGRMSRGALNRILLTRGEPPLYHVQEVEAQIYRDARECLNLLSNRLGTS--Q---FFFGDTPSTLDAYVFGFLAPLYKVS-FPKV-HLQ
Salmo_sala : KEGADTLAFISLLEEKLMPALVYTRWI-DPKNYVEVTRRWHAEHAPFPLNFFLPGSIQRQQLQRLRLVRGDEELTAGEEVEKELYRDAMECMNLISQRLGSN--K---FFFGDSPSSLDAFVFGYLVPILKMK-LPNG-RLQ
Monodelphi : RQGADTLAFMSLLEEKLLPVLIHTFWV-DAKNYVELTRKWYAEAMPFPLNLFLPGRMQRKHLERLQLLCGERRPEEEEEVEKELYREARECLTLLSQRLGSQ--K---FFFGDSPASLDAFVFSYVALLLQAK-LPNG-KLQ
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                    *       300         *       320         *       340         *       360         *       380         *       400         *       420
Physcomitr : EAILKY-QNLVDYAEHWSKYLLG-----EEGNSIDSSFRPKTPHSSHASPPRQGPKERDNP-------------EKERREKDIFFKKRAKYF--------------------VIAQVTAVLMYVVFAGYGVDDDGE-----
Oryza_sati : SCLQKY-DNLVNFTKHLKVQLLE-----------------ADSDSSATGLGSTDPSSSSTP-------------RKRASSGRMQ----------------------------PVRGACSFAQHADGLGPQIFSASD-----
Sorghum_bi : GTLQKH-DNLVNFAEHHKVQLLE--TSSSSSSGLGSSPSPSSSTPRRRPSADQGYKPKPRA-------------KKERTEEEKKFRRRAKYF--------------------LATQLVAVLVFLSLMGGVDSSELDD----
Populus_tr : LALSEH-GNLIRYAEKLKSEYLE----------GGSSSSVPQFHSEASSTSTRRSKTKKQP-------------KREKTEEEKTFRRRAKYF--------------------LVTQLVAVLVFLSVMGGYDFSEVEVDD--
Arabidopsi : CKLLEH-SNLVRYAEKLKSEFLE----------ASSSSPSPPLHSFPSSFPRKSSKPKSKP-------------KVEKTEEEKKFKKRARFF--------------------LAAQFLAVVIYVSVMGGGSSD--------
Ectocarpus : DLLPAF-DNLSRLFRHVCDNYFR--------------PGSFPPPSSGGEGVAESKKSGSED-------------RLRDAMLRADYVNSHNAFNQLAGCALCSEVPYIEDPYPPRPIANAGIPPPVLAGDLPGVEGAQGTAAA
Phytophtho : STVHQHAPLLITLAERIRDAYFGAPGEQPSSLSEAAMYSENQPNYFTTSLDSAFMKKVSPPLQVAFLKPYRSLDWSRRELASEVAQKKRAKEAEERTQDEEHEEVFQKGSRNVVIGAIAALVLYGVATLPITVVDGDESDED
Albugo_lai : DVLFEFAPSLIDVAKTVRAQYFS--RDPEDYVGCLKAYTENEDNYFVKQTPRHFLDPVSFPVDKALLTPYQSIDWRKREMIEEIVEEKIKSSSDRLKDPSQDSVGIEGKRNL-VIGAVVTFALYAISCLPIEFASNDSPE--
Canis_fami : EKVKNY-SNLLAFCRRIEQHYFE-----------------------DRGKGSSSIRSS-------------------------------------------------------------------------
Ictalurus_ : EKIKSF-SNLLSFCRRIEQAYFE-----------------------SQDRDSQSGALD-------------YSKGPSLM-----------------------------------------------------
Takifugu_r : ERIKSH-SNLLSFCRRIEQTYFE-------------------------------------------------DKSS-----------------------------------------------------------
Nasonia_vi : NIVRNH-PTLIKHCRNIEDRYFR-------------------------------------------------RDEE-----------------------------------------------------------
Solenopsis : AIIRQF-PKLIEHMFRVKLYYIS----------------SGTRNEIAEEFEIIESSSKATL-------------WDDFRS--------------------------------HPESLPPLSEHSFTLSIN-----------
Brugia_mal : NCLRRY-SNLTEFCQRIDKKYFV-----------------------------------P-------------GTEAKK-----------------------------------------------------------
Drosophila : QTVQKY-KHLVEFCRFVDEKYFQ--------------------------------TRCLP-------------N-------------------------------------------------------------
Aedes_aegy : VTINQF-KNLTKFCKNIEEKYFK-----------------------------------------------KVAGGR-----------------------------------------------------------
Anopheles_ : LTIHKY-SNLNQFCKNIDETYFS-------------------------------------------------VKGK-----------------------------------------------------------
Ciona_inte : NHLNSC-DKLRAFCARMS--LFC--------------------PSSSSLPTQVKSNSEDQ-------------IINRDKIIS----------------------------IAVAVTAMLVYALTSGVLTARRSKLATK-
Acyrthosip : SHLKTC-KNLCIWIDRITREYFK-------------IDWQAHKCNEKKKLEETKQQMNVTP-------------WYKRDETKNVLI---------------------------GIVTVITMVVYSFKIGLISVS--------
Pediculus_ : NHLKAC-NNLVSFVIRISQKYFP--------------AISEEFEKTQKENIQKQQTNEEFP-------------NKKRNQFIA----------------------------GVIAVLAMATYALSLGIVQTSKYVDTIE-
Camponotus : NHLRNC-TNLVKYVSRISQRYFE------------YEYQTYEKDKAEKNAEKLGEDECEFP-------------NKRRNQIFA----------------------------AFVAAMAMAGYALSTGIVEVSAKDDETSD
Apis_melli : NHLKAC-TNLVTFISRISEKYFA--------------NECCEYKAKENAQNIRKYSQNEFP-------------NKRRNQLLA----------------------------GLFTTLIMATYIFSTGILEM---------
Strongyloc : VHCKAC-ENLVMFCSRILQRYFP--------------QDPQEPQTAPKESQATSEEVFDDP-------------HKTRNQILS----------------------------VLFAATAMVGYALFSGMVQFEIVDDDEMD
Ixodes_sca : NHLKAC-ENLAAFVGRILQQYFP-----------PASADSEKGDRPGGGSPGSSDTDFNFS-------------WLNTTLS----------------------------VAFAAGAMLIYAVTSGLIQIEFQEA----
Nematostel : NYLKGY-DNLYNFCGRILQRYFP----------------PDPEDPQQYKPSPTHPSLDEDP-------------YQKRKMWLS----------------------------VGIAVVAMVTYAVLSGLVQIEYKKDEKQE
Mus_muscul : KHLKQL-CNLCRFCDDILDSYFR--------------PGPGGVSPAGQEMVDANLQKLTQL-------------VNKESNLIEKMDGNLR----------------------QSPQLLPRKLPTLKLTPAEEESNSLQLLS
Salmo_sala : QHLKSL-DNLSHFCSNILALYFP--------------SEGREGISRKVSSQPEGGDADNEP-------------GKRRKQLLS----------------------------VLVALGAMLSYAFLTGIVAIQHVQQEALD
Monodelphi : AHVRGL-GNLCAYCTHILSLYFP----------------WDGAEAPPPRPALSASETDEEP-------------YRRRGQILS----------------------------VLAGLAAMVGYALLSGIVSIQRAAPARPS

                    *       440         *       460         *
Physcomitr : ----------------DDGGDDDD----------------------
Oryza_sati : ----------------------------------------------
Sorghum_bi : ----------------DDGLDYED----------------------
Populus_tr : ----------------DEGFSYD-----------------------
Arabidopsi : ----------------ELEYEDEDD---------------------
Ectocarpus : GSTTAAAAAAEAAAGKATAANESLPVKYTVISIAAFMVLSNILSRG
Phytophtho : ----------------EDEYDEDDE----------------------
Albugo_lai : ----------------DPSLSRSAD----------------------
Canis_fami : ----------------------------------------------
Ictalurus_ : ----------------------------------------------
Takifugu_r : ----------------------------------------------
Nasonia_vi : ----------------------------------------------
Solenopsis : ----------------------------------------------
Brugia_mal : ----------------------------------------------
Drosophila : ----------------------------------------------
Aedes_aegy : ----------------------------------------------
Anopheles_ : ----------------------------------------------
Ciona_inte : ----------------LKQLNEFDEFEQMD----------------
Acyrthosip : ----------------DTSDEEDED---------------------
Pediculus_ : ----------------DEGIDDDDD---------------------
Camponotus : MST-------------EYILDDEDAE---------------------
Apis_melli : ----------------------------------------------
Strongyloc : ----------------DHGMMDDEGDDYQAQE--------------
Ixodes_sca : ----------------EKEAQDED---------------------
Nematostel : TGDDELLPDVTSFQYQDERDDE-----------------------
Mus_muscul : P---------------------------------------------
Salmo_sala : HRSPGLRSL-------SSHGEEEDGEEEG-----------------
Monodelphi : GNR-------------ALGIAEEEEEE-------------------
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(b) Tim21 amino-acid alignment (p. 3-5)

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                     *        20         *        40         *        60         *        80         *       100         *       120         *       140
Phytophtho : ------------------------------------------------------------------------MLRFLSAPAIR------------------------------------------------------
Esil_TIM21 : ------------------------------------------------------------------------------------------------------------------------------------------
Thalassios : ------------------------------------------------------------------------------------MSIRSAFI-----------------------RPVVSFTKKGASNASSSRGGGIPLLAMMSTYSK
Phaeodacty : ------------------------------------------------------------------MIRCAANRLLLHQGRL-----------------------GLLQHS---------------------------
Physcomitr : ----------------------------------------MEERSSGSVPCYRAVAGAALVLPPSRQENREAMAGVLVRKARMRFASGAARTWDAALRQQKPRLLADQADLEVTGYCYFSSSGVSSSQGFLKRIMRPRS
Zea_mays_g : ------------------------------------------------------------------------MASRVTRLLLHRRLT-----------------------TAAEASARRAP----------------QAPCAR
Ricinus_co : ------------------------------------------------MEHFRRSAMSLRSRCSDLFECQNGLSSVLERKLIK-----------------------RVTDVGLATFSSSATSERAAVNNSTKKLPRDFK
Ostreococc : ------------------------------------------------------------------------------------------------------------------------------------------
Micromonas : ------------------------------------------------------------------------------------------------------------------------------------------
Schistosom : ------------------------------------------------------------------------MAILSAKLNVVKI------------------------------------------------------
Strongyloc : MVDTGMSAQRKRRAQRMANRCQRLALGPVSDHGNEILQAIEIVKAILVKAKQEAQAYPGGDFPEESKDQQIDSSAISTFIPKQSYTLEPEKSAHQNKSVDEEVIQMLQ-PKVSCQTLKLDDLLTFDMGWTVKSINTLQEIGR
Macaca_mul : ------------------------------------------------------------------------MICTFLRAIQYT-----------------------EKLHRSSAKRLL---------------LPHIVL
Pan_troglo : ------------------------------------------------------------------------MICTFLRAVQYT-----------------------EKLHRSSAKRLL---------------LPYIVL
Xenopus_Si : ------------------------------------------------------------------------MMLPRCLRRAVL-----------------------CSSRALGSPRSL---------------TVPCYR
Danio_reri : ------------------------------------------------------------------------MSSLVLRIGRT-----------------------TNCVQHILKRVHVR-------------LQQPRS
Anoplopoma : ------------------------------------------------------------------------MAYTHILRALLH-----------------------RNLQQTCKLTQVS--------------LLIHTH
Osmerus_mo : ------------------------------------------------------------------------MIYSFVLKSMHR-----------------------NLQQAVWIYSP---------------LQICKR
Vanderwalt : ------------------------------------------------------------------------MINLVLKRSPKF------------------------------------------------------
Kluyveromy : ------------------------------------------------------------------------MFCQFISRPAQS------------------------------------------------------
Saccharomy : ------------------------------------------------------------------MSSSLPRSLLRLGHR------------------------------------------------------
Candida_gl : ------------------------------------------------------------------------------------------------------------------------------------------
Podospora  : ------------------------------------------------------------------------------MMIKSHLT-----------------------PVLRLR---------------------TLPSTS
Magnaporth : ------------------------------------------------------------------------------------------------------------MKLQTAAAANII---------------IPRALA
Aspergillu : ------------------------------------------------------------------------MSAYLLPRPSLH------------------------------------------------------R
Microsporu : ------------------------------------------------------------------MNSSIQLHSLRSGPL------------------------------------------------FVRLVR

                     *       160         *       180         *       200         *       220         *       240         *       260         *       280
Phytophtho : --------------------------------AAQKSTLQQRSRAVQV---------------VARR-------------------------------------------------------------------
Esil_TIM21 : ------------------------------------------------------------------MMSK-------------------------------------------------------------------
Thalassios : QSTDVAYRLAT----------------------PLKARSLAAQLFIRGGTSAMRSPINHAHRSNTLRA-------------------------------------------------------------------
Phaeodacty : --------------------------------KASTSLLRWNQLRWQP-------------------------------------------------------------------------------------
Physcomitr : QIVPLNYRTGGVDSIQQVDVNFIGYRNVLLNKMSRFSTCTTSQMLHQLPKKEHVASLLPYSTRGIASQ-------------------------------------------------------------------
Zea_mays_g : AAVSKDVVKAE----------------------ASSLKNSRWYITRSNTSGPLTTRYECRKVFPCSVR-------------------------------------------------------------------
Ricinus_co : LGYVRRPVGEANHGPKDI---------------LCANGNYDKQCIAGLGSQFQLVKLLGGSTTNSWFA-------------------------------------------------------------------
Ostreococc : ------------------------------------MSRDRAYATRR---------------GTKS-------------------------------------------------------------------
Micromonas : ------------------------------------------RASARAA-------------------------------------------------------------------------------------
Schistosom : --------------------------------PISAGILRLQFYPSIK----------SSVSSISQQ-------------------------------------------------------------------
Strongyloc : GSYGRVVIARHRSTGVPLAIKEPSWSDDFASPGEMVEELKATRTRATKEAMIQQLLSGSPYFPKFWGTLDLGNELCQAVEFVGCKKTGTGYPLHEPPSLSMCNVVKIAEDIVKGMMEFHDHGLLHNDLKNDNVLLEKRGKRY
Macaca_mul : NKACLKTEPSLRWGL------------------QYQKKTVRPRCILGVT------------QKTIWTQ-------------------------------------------------------------------
Pan_troglo : NKACLKTEPSLRCGL------------------QYQKKTVRPRCILGVT------------QKTIWTQ-------------------------------------------------------------------
Xenopus_Si : NLSCL-------------------------------LLSQQRALAVPT-------------SRFCAE-------------------------------------------------------------------
Danio_reri : SLLTLDPVFQ-----------------------TNHCPCSKWAFYHTRS--------------LYTGV-------------------------------------------------------------------
Anoplopoma : SVSTFLRRVE-----------------------APSWGLPVLSCFIQAQ-----------SQRGFSLD-------------------------------------------------------------------
Osmerus_mo : TQSNFILQRR-----------------------GNFASTSTPFFHGIEGHPSILGSVLCTQKRNIYFH-------------------------------------------------------------------
Vanderwalt : --------------------------------GTSLKVIAKPIYSTALQRSLI-------------------------------------------------------------------------------
Kluyveromy : --------------------------------LSGKFSSKTLCLPLIA-------------------------------------------------------------------------------------
Saccharomy : ----------------------------------KPLFPRYNTFVNSS---------------VITH-------------------------------------------------------------------
Candida_gl : -------------------------------------MVLRSRPLASI-------------------------------------------------------------------------------------
Podospora  : PVVNL-------------------------------RALQPRHYATHH------------------Q-------------------------------------------------------------------
Magnaporth : SQ-----------------------------QIRPLIASRRCYATN-------------------------------------------------------------------------------------
Aspergillu : ASSALLLRP-----------------------GFPRTVELTRCYATHSDL-------------------------------------------------------------------------------
Microsporu : NSGR---------------------------PVSLSLTRYNHYATQS-------------------------------------------------------------------------------
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                    *       300         *       320         *       340         *       360         *       380         *       400         *       420
Phytophtho : ------------------------------------------------------------------------------------PAASTRSFTSTRSRLNADKAT-----PEGQKAPDALV----------------------
Esil_TIM21 : ------------------------------------------------------------------------------------ASRKGDDSKGEQQQQQKQQGEE----QQYEDADYEPE----------------------
Thalassios : ------------------------------------------------------------------------------------TSSSTNSSGGQKDKASSEKTTGT---EGEEPMSQEIV----------------------
Phaeodacty : ------------------------------------------------------------------------------------SMLRTLSSDASQKGGNEKKK------SEGEDTTSEIV----------------------
Physcomitr : ------------------------------------------------------------------------------------SSPLLRQAQNESKGLSKQPEE-----DPFDSITDKIP----------------------
Zea_mays_g : ------------------------------------------------------------------------------------PSASYSTQASDQKGKQEGKDLSNVE-HPFDDITYNIP----------------------
Ricinus_co : ------------------------------------------------------------------------------------RSFASKASKKTGEATSETRKEVSTVEDPFDAPTYNIP----------------------
Ostreococc : ------------------------------------------------------------------------------------SSSADEAASGTRGDLASTPESG----RYDEITDKWIP----------------------
Micromonas : ------------------------------------------------------------------------------------AAASSESAKSARADVATTRGG-----TYDEITDKWIP----------------------
Schistosom : ------------------------------------------------------------------------------------WPVCSRRSFSSSSNSSVTPSE-----GRGNLPSTSVT----------------------
Strongyloc : NAVIIDYGMASSITAPPKMVGVTKEVKMAYVHGGEADYITPEVVLDEQPTSIASDVFSVGRIFSDMGEIFGGHRFPVVRELSKLGAQCMADNPDHRPSLDTIKSQITRLQRPSRWRRVKRWVAKKLHLRRKLSVIEGYLDSK
Macaca_mul : ------------------------------------------------------------------------------------GPSPRKAKEGSSKQVSVHR-------SQREGTAVPTS----------------------
Pan_troglo : ------------------------------------------------------------------------------------GPSPRKAKEDSSKQVSVHR-------SQRGGTAVPTS----------------------
Xenopus_Si : ------------------------------------------------------------------------------------RPISTGSALLQVKDKRVSVQS-----RGDGASPQTAS----------------------
Danio_reri : ------------------------------------------------------------------------------------YLCSRKDEQKDTDQLSVSR-------SPHTPSRGSAT----------------------
Anoplopoma : ------------------------------------------------------------------------------------SQARNQSSPEERKSVSR---------YQSGAPKPSAA----------------------
Osmerus_mo : ------------------------------------------------------------------------------------TSLRNKIKPEDTESGQLSTS------RLGTAPNLSAA----------------------
Vanderwalt : ------------------------------------------------------------------------------------LSTTNKTYYSTFHSNANSK-------KGNQDKKIPLW----------------------
Kluyveromy : ------------------------------------------------------------------------------------SPVRIKHTVQGYSTFNAQQNAG----NKQQKKKIPLW----------------------
Saccharomy : ------------------------------------------------------------------------------------TSLLRTRLYSNGTGATSGKKD-----DKTRNKPKPLW----------------------
Candida_gl : ------------------------------------------------------------------------------------PRVQFYSSKGKSKGKTSGE-------KKPEHKKIPVW----------------------
Podospora  : ------------------------------------------------------------------------------------TSSSKSEPEIKRRSVTPFNDTG-----SVPWSSLSIL----------------------
Magnaporth : ------------------------------------------------------------------------------------TSANDSNATQRRRAVTPFNDD-----GRVPWTELSGG----------------------
Aspergillu : ------------------------------------------------------------------------------------GGGSGPSSTSKRRNVTVLSDD-----GRYEWGELTGR----------------------
Microsporu : ------------------------------------------------------------------------------------SLNSSKSAQPTRKSITVTSDD-----GTIKWGQLSRG----------------------

                    *       440         *       460         *       480         *       500         *       520         *       540         *       560
Phytophtho : -------------------------------LTPYEKVTATATGGFWLGLIGLGAVGVYFVARELLPNRMSPNGLFSESLDFLSENT------DVTSRLGLP--IHGYGYDHGGHREGRRNRIEHVNLQA-KDGTPRLRIK
Esil_TIM21 : -------------------------------PEEKISIVKTVAGVCVL---GLVVAALSATITELWPSHMAPQSIMSHAHDVFQADP------DTANHFGTP--LKGYGRDNNRHREGRRNFVEHVDHEDPIDKSKRTRVR
Thalassios : -------------------------------LTPGEKVVVGTRLFFWAGAFAFASVCAYYIGKELIPTKMSPNNVFDKATSIIRENA------EVKRRFGEA--FKTYGRDHGGHREGRRNFIEHTEYVSPDDGTKRTRVR
Phaeodacty : -------------------------------LTPGQKVVEASRLTMWGGIAVFAACCAYYIGRELFPTKMSPNRVFDRSFAAIRADS------EVQRRYGDN--LKAYGRDHGGHREGRRNFIEHTEYTDAEDGSKRTRVR
Physcomitr : -------------------------------QKPVTAVEGASYSVVILAGLAVFGFAAYAVLKQLIFEP-KEYKIFGISLARVQNDH------QVMVRIGSP--ITGYGQ-ESRNRAARQR-ISNRIHVD-EDGVEHVEVM
Zea_mays_g : -------------------------------EKPVTFTEGASYSLVILAGLGIAGLAGYAVFKELIFEP-KEYKIFGKALARIQSDS------QVTSRIGHP--ITGYGQ-ETRNRAARQR-IPNKIWTD-EDGVEHVEVN
Ricinus_co : -------------------------------EKPVTFTEGASYSIIILAGLGVAAAAGYAVFKELIFEP-KEYKIFNKALKRIQDDA------QVRVRIGSP--ITGYGQ-ESRNRAARQR-IPNKIYTD-EDGVEHVLVN
Ostreococc : -------------------------------EKPVSVVEGASYGAVGLIGLGIAAGAVMYGASELLVTP-REQKVFNAAMDKLHDDV------RVTVALGSP--MTGYGS-ESRSRSARHR-IAHRVVID-ERGRERLRVQ
Micromonas : -------------------------------EKPVTAVESVSYGAVALVGVGVAVGALMYGIGELLFAP-PAQAAFDEALLLERDP------RIAVRVGTP--MTSYGN-EGRSRRGRQQ-LAHATEVD-GHGNEWIIAQ
Schistosom : -------------------------------KTVKQVTKDVGYFAIVLGGIVLTGSTLYTIIQELFSKK-SPNGVFDDAFKICKTDN------RVLDVFGSA--IKAHGD---PNSRGRRRHVAHDSWYD-DKGRLHMAMK
Strongyloc : MLNELSCRGAYYVFSSLSSKLLQRCTTCSTRSSAVAQTSKDASYAGIIVLGVGITGLMFFTLGKELFSSD-SPNSIYTKAYKVCKKNV------EIQDALGTP--IKGYGE---MTRRKRRRHVSHLEYS--QDGVSFVRMK
Macaca_mul : -------------------------------QKVKEAGRDFTYLIVVLFGISITGGLFYTIFKELFSSS-SPSKIYGRALEKCRSHP------EVIAVFGEP--VKGYGE---VTRRGRRQHVSFTEYV--KDELKHTRVK
Pan_troglo : -------------------------------QKVKEAGRDFTYLIVVLFGISITGGLFYTIFKELFSSS-SPSKIYGRALEKCRSHP------EVIGVFGES--VKGYGE---VTRRGRRQHVRFTEYV--KDGLKHTCVK
Xenopus_Si : -------------------------------HKVKEAGRDFTYFIVVLIGIGVTGGLFYVVFEELFSSS-SPSKIYGEALEKCRSHP------EVIGAFGEP--IKGYGE---TTRRGRRQHVSHMEYV--KDGIKCVRLK
Danio_reri : -------------------------------QKVKQAGKDFTYLIVVLIGLGVTGGLLYVVFQELFSSS-SPSKIYGKAFERCRSHP------EVIGAFGEP--IKGFGE---TSRRGRRQQVSHLEYM--KDGLKYVRLK
Anoplopoma : -------------------------------QKVKEAGRDFTYLIVVLIGLGVTGGLLYVVFQELFSSS-SPNKVYGKAFNKVKLDP------EVIGAFGEP--IKCYGE---TTRRGRRQQVSHQEYL--KDGLKHMRLK
Osmerus_mo : -------------------------------QKVKEAGKDFTYLIVVLIGLGVTGGLLYVVFQELFSTS-SPSKIYGKAFDKTRLNP------EVIGAFGEP--IKCYGE---TTRRGRRQQVSHAEFM--KDGLKHMRLK
Vanderwalt : -------------------------------TRIKSFSTFTASGALVIGATGISTVVIYLILTELFSPS-GDTQLFNRAVTLVEKDEIVRTLLQCDDTDNKKERLKAYGELYADDKWTRNRPIASNKRID-KNGKEHYLMR
Kluyveromy : -------------------------------PRIRAFTTFTFSGILVIGATGLAGVVIYLIGAELFSPS-GDTQIFNRAVSKVENDEVARRLLKCNDTETSTERLKAYGEILTDDRWTRNRPISSTRRID-KEGKEHYLMR
Saccharomy : -------------------------------PQVKSASTFTFSGILVIGAVGISAIVIYLILSELFSPS-GDTQLFNRAVSMVEKNKDIRSLLQCDDGITGKERLKAYGELITNDKWTRNRPIVSTKKLD-KEGRTHHYMR
Candida_gl : -------------------------------HKLKALTSFTASSLLVVGGVGVSGVVLYLILSELFSPS-GDTMLFNRAVTLVEDNEEVRKLLQCNDSSFKKERLKAYGELVTNDRWTRNRPIVSTQKID-KYGKCHHFMR
Podospora  : -------------------------------EKGARASQQTFNFGLVILGLTLTSGVLYVLYTEVFSPS-SRTAYFNRAVDRIKADP------RLIGLLGDGKKIEAFGE-ETGNKWRRARPIASSEVTD-RNGVQHMYIN
Magnaporth : -------------------------------EKTSRAVQQTFNFGMVLVGMALT----------VFSPD-SKVAYYNRAVDRIRKDP------RCLELLGESKSITAFGE-ETSNKWRRARPIASTLRKD-SQGNEHMMIH
Aspergillu : -------------------------------EKVARATQQSFNFVIILAGAALTGGVFYLLYSEVFSPN-SRTWQYEKAVERILDDS------RCTDILGDRREIKAYGE-STSNKWARNRPIAATIEKD-RLGREHLRMN
Microsporu : -------------------------------EKAARATQQSVNFLVILAGAVMTCGVFTFLYLDVFAPD-SKTNQFNRAVSRVKDSE------ECIALLGDSNKIRAYGE-TSWNKWTRNRPIATTIEKD-RKGNEHMRMN
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                 *       580         *       600         *       620         *       640         *
Phytophtho : YNIKG--PSGHAYVFAEVNKGMKKNEY--VYLIVQVT----KT--GELLKIIDNRQI-----LSAETKEEQDALRQLLGK----
Esil_TIM21 : FNVEG--PHGHGMAYAEVSNKMESGEW--VYLCVQDL----QT--GHVITLHDNRAL-LMAQAQAGSDEEKNAFRKMLGQ----
Thalassios : FNLEG--QYGNAFVFAEVSKDMPSGEF--VYLLVQDK----RN--GQVITVVDNRSALLAKRMAGGSQEGADVFANLLGGGKK-
Phaeodacty : YNLEG--RFGTAFVFAEVSASMPSGEF--VYILVQDK----SN--GRVHTVVDNRAALTAARLASGSKEAQSAMSQLLGGGGQK
Physcomitr : FYIRG--PQGACKVYSKMFKDKEDKQWKYTDLIVETT----SP--TPTRLTLESYMPAVPLPMRAS------------------
Zea_mays_g : FLIRG--PHGACKVYSEMFKDTDR-TWKFTYLVVDIV----SPPHAKTQLMLESYLPA--------------------------
Ricinus_co : FYIRG--PHGACKVSAEMFKDKVDKEWKYTYLIVQFL----QP--NQSQLILESYMPAPAPVAA--------------------
Ostreococc : FHARG--ARGSAVVHAEAGLDESTGKWEFQYIIVDVQGA--NP--TRIHVVSPQAQPRRLVAL--------------------
Micromonas : GAVRG--PQGRCAVHLKARKDKESGEWVFAYVAVDV-----------------------------------------------
Schistosom : FYIKG--NLASCIVHLEVVEN-ESKEFDYRYLIVETE----GGFSKKQVVLRPLSEAVNAN----------------------
Strongyloc : FYLEG--PERKATVHLEMKKN-ESGRYEYRYLFVELD-G--YP--KRTIVLEDNR---------------------------
Macaca_mul : FYIEGSEPGKQCTVYAEVKENRESGEYDFRYIFVEIE-S--YP--RRTIIEDNRSQDD------------------------
Pan_troglo : FYIEGSEPGKQCTVYAQVKEVWES--WDVGSEVLSAVLFKFWK--GK-----------------------------------
Xenopus_Si : FYIEGLEPRKQCTVHTEVKENPESGKYEFQYIFVEID-T--YP--RRTIVIEDNRRQS-------------------------
Danio_reri : FYIEGSEPGLRCTVHSESKENPETGKYEFRYIFVEID-T--YP--RRTIVIEDNR----------------------------
Anoplopoma : FYIEGSEPGRKCTVHSESKENPETGKYEFRYIFVEVD-T--YP--RRTIIVEDNR----------------------------
Osmerus_mo : FYIEGEEPGRKCTVHSESKENPETGKYEFRYIFVEVD-T--YP--RRTIVVEDNR----------------------------
Vanderwalt : FHVES--KQKMCLVHIEAVESEKRYQPDFVSVYIDIP----GE--KRYYLIKPKINR---------IVRPKGFLGINWGPRKQ-
Kluyveromy : FHVES--KQKMCIVHVEAKESDVNYQPDFVSMYLDIP----GE--KRHYLIKPKLSI----------VKPKGFLGVNWGPKRD-
Saccharomy : FHVES--KKKIALVHLEAKESKQNYQPDFINMYVDVP----GE--KRYYLIKPKLHP---------VSNSKGFLGIRWGPRKD-
Candida_gl : FHLES--KKKLCLVHVEAVDSEQNYKPNFVSMYIDIP----GE--KRFYIIRPKLRQ---------VVRPKSIFGFPWGSRKE-
Podospora  : FNLKG--PKGTCTAFVHLFKPVGGKQWEYRYFYVDVK----GQ--QRIYLENAEAAATLAAKERSKTD-GIKFLGIRW------
Magnaporth : FNLEG--SKGRCMANMHLIKRVGAEDFEYRYFYLDVV----GH--QRIYLENSEATG------RDGSG-KKTIFGIRFS-----
Aspergillu : FHVEG--PRNQCVVHVHWIKPLDKNEWEYQLLALDVK----GH--SRVILEQAREKP--------GVGQALKIFGIQWR-----
Microsporu : FHVSG--PLNDCVVLVHLVKLAGQHDFEYHLLALDVK----GH--RRIYLENADAAK------KAAAKAGSTIFGIQWR-----
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(c) Tim50 amino-acid alignment (p. 5-8)

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                    *        20         *        40         *        60         *        80         *       100         *       120         *       140
Saccharomy : ------------------------------------------------------------------MLSILRNSVRLNSRALRVVPSAANTLTSVQASRRLLTSYSSFLQKE------------------------
Cyanidiosc : ------------------------------------------------------------------------------------------MLVDRYAGLRALR-----------------------------------------
Esil_TIM50 : ------------------------------------MLLGRVGTLLPSCSGRVATRRFLAKKAAGGGGGGKKGSGTPKKGPAAIKARGAMPVSKAGKQGSKTGKTGGAAAREAAATTTSTAKAAAAEAAASVKPPPVG-----
Arabidopsi : ------------------------------------------------------------------------------------------MASIVLRSRLLPRLAKLRSRNLRCFSA----------------------------
Zea_mays_g : ------------------------------------------------------------------------------------------------------------------------------------------------------
Phaeodacty : ------------------------------------------------------------------------------------------------------------------------------------------------------
Phytophtho : ------------------------------------------------------------------------------------------MMLKLVLRAQRGMRAFAGIGATRK---------------------------------
Phytophtho : ------------------------------------------------------------------------------------------MMLRPVLRNAQR-----------------------------------------
Magnaporth : ------------------------------------MLSRLAIRTLRAPALQGLGRTTAARQTTSLLAARTWTRG--------------MAKNNKPAPTPSQQTSK-SNAPSEEQASSPAPKQSENATK--------------
Aspergillu : ------------------------------------MLRRAILPLTRPSGLVSAPRLSALPVSHS----RCYAKGSKPKTPYKLPESVKSSKPEQP-AKPSQQEQYAAEQAEFETTSDPQANTANTTSQASSS----------
Penicilliu : ------------------------------------MLSRSVLPLARARPVPSALRSPLTASPYP----RWYAQGNKPRTPYVLPN--QKAKPAQSKATPSQKNTS-TKSQPTQQKSKPTVVGTTSKAKAAASASSGASTNAS
Talaromyce : ------------------------------------MLSRSVLPLARARPVPSTLRS------YP----RWYAQNNKPRTPYVLPN--QKPKPAQPNPARSQSNTSTTNNQSTQPKTKPTVVGASSGAKATESVPPDAASSKT
Ostreococc : ------------------------------------------------------------------------------------XXTW-----------------------------------------------
Micromonas : ------------------------------------------------------------------------------------------MFTRVAARALA-----------------------------------------
Chlamydomo : MVLPVRAKKIVLASVVVVTVLTLVNYHQIVHFAETALPHRLPEPFTHNHIFYEPSGGWLVGPAAPCPQRWIPGIWVSKSQRQHTGGVLPLTEDAQQEVFQAMNPPGCGGAKFLVHRVEPQGFAAAIHELGVALQLALDSGRV
Ixodes_sca : ------------------------------------------------------------------------------------------MAAVGRGGMCVWHGLRPKICS--------------------------------
Xenopus_(S : ------------------------------------------------------------------------------------------MAASLVPVCGRSVRLLRVL-----------------------------------
Pan_troglo : MASALSLGNKCDPFLRCVLCRGGGALQGPRGRGPDDFESQLSPPGPARRLVRGKRACGNPPDAFGLSRASVHQPLPRVSIGCSSGPGRAKRERVGGAAWRQRKMA-----------------------------------
Homo_sapie : ------------------------------------------------------------------------------------AWRQRKMA-----------------------------------
Bos_taurus : ------------------------------------------------------------------------------------WRQRKMA-----------------------------------
Mus_muscul : ------------------------------------------------------------------------------------------------------------------------------------------------------
Nematostel : ------------------------------------------------------------------------------------------------------------------------------------------------------
Strongyloc : ------------------------------------------------------------------------------------------------------------------------------------------------------
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                    *       160         *       180         *       200         *       220         *       240         *       260         *       280
Saccharomy : ------------------------------------TKDDKPKSILTDDMLFKAGVDVDEKGQ--------------------GKNEETSGEGGE--------------------------------------------
Cyanidiosc : ------------------------------------PIGSALLRPGRVLRCLTSGNGGRAAGE--------------------AGSKPTSGPIHP--------------------------------------------
Esil_TIM50 : ------------------------------------GGGGFTKSEMLAARKARKASVTAKTAA--------------------AAATAKAAAPAA--------------------------------------------
Arabidopsi : ------------------------------------EASSTNSTSRYSGVTSTQSMFSDFPPP--------------------NQPPPPPPPQVE--------------------------------------------
Zea_mays_g : --------------------------------------MSRVAGSRLLPRISALSFCTASPAT--------------------AAASSSSSTAAV--------------------------------------------
Phaeodacty : ------------------------------------------------------------------------------------------------------------------------------------------
Phytophtho : ------------------------------------LMLAAEASAPSSVAEASSIFAKVGRDI--------------------PLKVVPRAERRA--------------------------------------------
Phytophtho : ------------------------------------GAALGTTRRLMLQAEASSVLAKVGRDI--------------------PLKVVPRAERRA--------------------------------------------
Magnaporth : --------PEASDAQPEQ--------VPFNLPDLTKGLPSTFEYEASGADKASKMALEGVASA--------------------GG---------R--------------------------------------------
Aspergillu : --------PESSPSQSEQDA------PQRPLPDLTQGIPSTLAAELEARSKKSGSGTLNLTED--------------------PSRFEEDYSD-D--------------------------------------------
Penicilliu : E--TPKSEPDVSPEQPEFETVAQAEKTPQPLPDLTQGIPSTLGAELDAARKGRKTTSLNLTED--------------------PS--QDDYEDEG--------------------------------------------
Talaromyce : EPKKPLSEPDVAPEQPEFDTAAQPEKPQKPLPDLTQGIPSTLGAELEAARKGRKTTALNLTED--------------------PS--QHDYEEED--------------------------------------------
Ostreococc : ------------------------------------IPTRALASEAEGEAAKTGTLSDRLGTV--------------------ALVVGTLAGSVV--------------------------------------------
Micromonas : ------------------------------------GTLLGSGARVAQLSRGTSMGGETAPAT--------------------AAAIARRSLQRR--------------------------------------------
Chlamydomo : LVEAPGSPHAEGVPECGALRNTLDSCYLLPFSSCRPSEADIIAALNTTQSQASGSAPQGVTVPREPRIIFTNTAMVEAARHRAPKRFEERLQQTAVDHQKHRYWWRAQAAAYLLRPNMGTLANLGKRRMQELRGPEPSPGCI
Ixodes_sca : ------------------------------------AGVPRLGPVRFTSTSGGGG--------------------------------AAAPTG--------------------------------------------
Xenopus_(S : ------------------------------------GQRTELRYRAFSSEQGAEGGLT------------------------GAVLQEKLQRRE--------------------------------------------
Pan_troglo : ------------------------------------ASAAVFSRLRSGLRLGSRGLCTRLATP--------------------PRRAPDQAAEIG--------------------------------------------
Homo_sapie : ------------------------------------ASAAVFSRLRSGLRLGSRGLCTRLATP--------------------PRRAPDQAAEIG--------------------------------------------
Bos_taurus : ------------------------------------ASAAVFLRLRSGLRQGARGLCARLATP--------------------PPRAPDQAAEIG--------------------------------------------
Mus_muscul : ------------------------------------------------------------------------------------------------------------------------------------------
Nematostel : ------------------------------------------------------------------------------------------------------------------------------------------
Strongyloc : ------------------------------------------------------------------------------MPFPSGCDGE--------------------------------------------

                    *       300         *       320         *       340         *       360         *       380         *       400         *       420
Saccharomy : ---------DKNEPSSKSEKSRRKRQTS-------------------------------------------------------------------------------------------------------------
Cyanidiosc : ---------EEGAAAASDGAAESKRPQH-------------------------------------------------------------------------------------------------------------
Esil_TIM50 : ---------GAGAGRTGGAGAAASAAGA-------------------------------------------------------------------------------------------------------------
Arabidopsi : ---------AAAAAATG-------KERK-------------------------------------------------------------------------------------------------------------
Zea_mays_g : ---------AAAAATAGDPSSQPPQTAR-------------------------------------------------------------------------------------------------------------
Phaeodacty : ------------------------------------------------------------------------------------------------------------------------------------------
Phytophtho : ---------ARKAAKHSADAATGHKVVR-------------------------------------------------------------------------------------------------------------
Phytophtho : ---------ARKAAKHSADAAEHKVVRT------------------------------------------------------------------------------------------------------------
Magnaporth : ---------GKGELPASAYVSSSDRRRQ-------------------------------------------------------------------------------------------------------------
Aspergillu : ---------GRGDIPKGGYESSLDRKRA-------------------------------------------------------------------------------------------------------------
Penicilliu : ---------AGGGRSSDAYESSLDRRRA-------------------------------------------------------------------------------------------------------------
Talaromyce : ---------GGGGRSSDAYESSLDRRRA-------------------------------------------------------------------------------------------------------------
Ostreococc : ---------GASTYASTTEELRREVEAN-------------------------------------------------------------------------------------------------------------
Micromonas : ---------GLSTESASKAGAEEQGVMA-------------------------------------------------------------------------------------------------------------
Chlamydomo : TVIARSGKSGDGAAASDFKDADYDERAAKLRALDPTRFNDHIFLSASSGHTLSYFANGTGATADAGAHRWHTGYVAGLKHFGGGMSLRLRKAGGGHDLDAVPKDAVYESMLNTLLELDLALECSGFVGSIDSHWVRLVDEMR
Ixodes_sca : ---------ASGSTSGGSSGRAADDFSQ-------------------------------------------------------------------------------------------------------------
Xenopus_(S : ---------NEASSDSSGSEEKQKKQKE-------------------------------------------------------------------------------------------------------------
Pan_troglo : ---------SRGSTK--TQGPQQQPGSE-------------------------------------------------------------------------------------------------------------
Homo_sapie : ---------SRGSTK--AQGPQQQPGSE-------------------------------------------------------------------------------------------------------------
Bos_taurus : ---------SRAGTKAQTQGPQQQRSSE-------------------------------------------------------------------------------------------------------------
Mus_muscul : ------------------------------------------------------------------------------------------------------------------------------------------
Nematostel : ------------------------------------------------------------------------------------------------------------------------------------------
Strongyloc : ---------KQGTNITGTCQPQLDEHGK-------------------------------------------------------------------------------------------------------------
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                 *       440         *       460         *       480         *       500         *       520         *       540         *       560
Saccharomy : ------------------------------------------------------TDIKREKYANWFYIFSLSALTGTA-IYMARDWEPQESEELKKDI----DNGYTLSLMYKRFKAR-----------------------
Cyanidiosc : ------------------------------------------------------SRWRALFRPGRLLGFV---ALGSA-ATVLTFWVVDPEGTVARLE---------------RLRHE-----------------------
Esil_TIM50 : ------------------------------------------------------GGAKGQGKWGWGTKLV-AGTSVGL-AALGIAWQLKP-DEMRKLL-----DDSPIDHFFI---------------------------
Arabidopsi : ------------------------------------------------------GLKYLGYALLWALTGA----TAAT-GYASFAYTIDEVNEKTKAFRESATKTPVIKSSGIDVIDKYQTKLYSAAMTGSARAIDKYLEL
Zea_mays_g : ------------------------------------------------------NPWGALKFAAFAAVSA---AVGGT-GYVSYAYSLEEVDQMTRELRKKSKQPIPEDASGFERFQA---MAYSAAMKVPVAAIEVYLDV
Phaeodacty : ------------------------------------------------------------------------------------------------------------------------------------------------
Phytophtho : ------------------------------------------------------TSSLPARISFALLAGSI-----SGS-IVWNFVLDDGIKSRVKETL-----GATFLGDIYAIIAKK-----------------------
Phytophtho : ------------------------------------------------------SSLPARISFALLAGSI-----SGS-ILWHFVLDDGIKTRITETL-----GATVLGDVYAFLAKK-----------------------
Magnaporth : ------------------------------------------------------KVAQWVFYGFVAGGLF------GV-VFLGRNWEDEEERAKHADV----PDGWTPVLWWKRAMAR-----------------------
Aspergillu : ------------------------------------------------------RMAK-LMYALFLLGSV-----GGM-AYLGRNWDTVEEENAHPDV----PSGWSFGLWYNRIKAR-----------------------
Penicilliu : ------------------------------------------------------RLAN-VMYGILLGGIL-----GGT-VYMGRNWDSEEEARLHKDA----PSGWGIRLFYDRIKAR-----------------------
Talaromyce : ------------------------------------------------------RVAN-VMYGILLGGLI-----GGT-VYMGRNWDSEEEAQAHKDA----PSGWGLGLFYNRIKAR-----------------------
Ostreococc : ------------------------------------------------------EHVPKALRETPLGGVY-----GGA-IERLLALRE-------------------------------------------------
Micromonas : ------------------------------------------------------TVVDTVSTMGTAVGCL----VGAT-IGVSYYTHSTKQLEEALEKGEHVPGALKDTPLKQALDYA---------------FGHLLEF
Chlamydomo : SVVRCSADAPYIDVGHDDPRQMNLHCVLDEVAQARLKRIKSQLEATGELPVEPPSGGVWGAIRMLWRGALLGATGLGATAAYYTYAYDTKELVSIVKQTRAELKAEEKPNPLRKLWCDG---------------MQRYLVF
Ixodes_sca : ------------------------------------------------------RA---MKYTFVAFGAI---FTGVA-GYLVVSWGAPSVDETGKEM-----------------------------------------
Xenopus_(S : ------------------------------------------------------NAANAKRFLLRAAGLL---GVAGS-GSLVYIFGSNSVDEQGNKI----PDEFDSDPPVVQQIRR----------------------T
Pan_troglo : ------------------------------------------------------GPSYAKKVALWLAGLL---GAGGT-VSVVYIFGNNPVDENGAKM-----------------------------------------
Homo_sapie : ------------------------------------------------------GPSYAKKVALWLAGLL---GAGGT-VSVVYIFGNNPVDENGAKI----PDEFDNDPILVQQLRR----------------------T
Bos_taurus : ------------------------------------------------------GPSYAKKVALWLAGLL---GAGGT-VSVIYIFGNNAVDENGAKI----PDEFDNDPILVQQLRR----------------------T
Mus_muscul : ------------------------------------------------------------------------------------------------------------------------------------------------
Nematostel : ------------------------------------------------------------------------------------------------------------------------------------------------
Strongyloc : ------------------------------------------------------VIVDEFEDDFIVFGYL---------------------KRAYREMNTYRTVSFKQKIIRIRHF-------------------------

                *       580         *       600         *       620         *       640         *       660         *       680         *       700         *
Saccharomy : ---FNSMFTYFQEPPFPDLLPPPP-PPPY-----QRPLTLVITLEDFLVHSE---------WSQKHGWRTAKRPGADYFLGYLS-QYYEIVLFSSNYMMYSDKIAEKLDPIHAF-VSYNLFKEHCVYKDGVHIKDLSKLNRD
Cyanidiosc : ---LESRIRYYVEPSREKLLPDPVAPFPGS----LPPRTLVLDLDETLVHSD---------WTRSTGWRTSKRPGVDAFLAYMA-QFYEIVVFTSALPGYADPILDRMDP-NGY-ITHRLYRHETKYRDGLHMKDLAKLNRD
Esil_TIM50 : --WFMGKWALYSSPVKDKLLLDCP-LPPGA----LPPPTLVLDLEGTLLGTI---------YTRKKGWRVAKRPGLDAFLKEMS-QLYEIVVFTDSMGGLADEWITQMDP-QGT-ISQRVYRDGTRYIDGKYVKDLSALNRP
Arabidopsi : REIVEEQVKGFTEPLSEKLLPD---LHPAE----QHVFTLVLDLNETLLYTD---------WKRERGWRTFKRPGVDAFLEHLG-KFYEIVVYSDQMEMYVLPVCEKLDP-NGY-IRYKLARGATKYENGKHYRDLSKLNRD
Zea_mays_g : RSQIEDQIRGFSEPVSDKLLPD---LAPQE----QHVLTLVLDLNETLVYSD---------WKRERGWRTFKRPGVDAFLEHLG-RFYEIVVYSDQLSMYVDPVVDRLDP-KGN-IRHRLSRVATKYENGKHYRDLSKLNRN
Phaeodacty : ---------PLAKPAHEKLLPDWS-QLPNVPQDIPVPHTLVLDLENTLVSST---------WDRRYGWRHAKRPGVDKFLRELA-QYYEIVLYSPSIDGIADPVVTSLDK-DGC-IMHRLYREATYYTGGVHVKDLNRLNRP
Phytophtho : ---VEETVKPFTDPSRQKLLPDW--PIPQVPADTPPVPVLVLDLEDTLVHSE---------WSRKHGWRHAKRPGVDEFLETLC-QYYEIVIFSQNYG--AEEIVQKLDP-KQC-ALHILSRDATRYLNGAHVKDLSNLNRD
Phytophtho : ---VEETVKPFTDPSRQKLLPDW--PIPQVPADTPPVPVLVLDLEDTLVHSESLMVYRFIILQRKHGWRHAKRPGVDEFLETLC-QYYEIVIFSQNYG--AEEIVQKLDP-KQC-ALHVLSRDATRYLNGAHVKDLSNLNRD
Magnaporth : ---MGDTVSYYQEPAFEKLLPD---PDPVN----SPPYTLCISLEDLLVHSE---------WTRDHGWRVAKRPGVDYFIRYLS-QYYELVLFTSVPYGIAEPLWRKMDP-FRF-VQWPLFREATKYVDGKIVKDLSYLNRD
Aspergillu : ---MGDFTSYYKDPAFPKLLPD---EDPNL----RQPYTLVLSLEDLLVHSE---------WSREHGWRVAKRPGVDYFLRYLN-QYYELVLFTSVPSMMADQVLRKLDP-YRI-IRWPLFREATRYKDGEYIKDLSYLNRD
Penicilliu : ---MDSFTSYYRDPAFDKLLPE---EDPSL----RQPYTLVLSLEDLLVHSE---------WTREHGWRVAKRPGVDYFLRYLN-QYYELVLFTSVPSMMADQVLRKLDP-FRI-IRWPLFREATKYKDGEYVKDLSYLNRD
Talaromyce : ---LDNLTSYYRDPAFEKLLPD---EDPSL----RQPYTLVLSLEDLLVHSE---------WTREHGWRVAKRPGVDYFLRYLN-QYYELVLFTSVPSMMADQVLRKLDP-FRI-IRWPLFREATKYKDGEYVKDLSYLNRD
Ostreococc : --WMDDQSHNYLDPISDKLLPDHP-PQAEY----I-PHTLVLDLDDTLINSN---------WKRERGWRVFKRPGVDGFLAHMA-QFYEMVIFTDQLMTYGDPIIERLDP-TRY-VTHRLYRESAQYKNGEYIRDLSKLNRD
Micromonas : RQWADGLRHQYLDPVSDKLLPDHP-PNAVY----I-PHTLVLDLDECLIKSD---------WRRERGWRTFKRPGAGDFIKHMA-QFYEVIVFSDQTSMYVDPILERLDP-QRF-LAGRLAREANQYVDGEYLRDLTKLNRD
Chlamydomo : RHDMESRIKDFTDPATDKLLPD---QHPAM----KGAITLVLDLDEVLVWKE---------WTRQRGWSIYKRPGVQEFLLEMA-QYFEIVVYTDEPYTYADPILNKFDP-QRVAVMHRLYRTDTQYLDGKHVRDLSKINRD
Ixodes_sca : ----------IQEPSRDKLLPDPL-TEPYF----QPPYTLVLEMTGVLVHPD---------WTYQTGWRFKKRPGVNLFLQQVGPPLFEVVVYTSEQGFTAYPILDSLDP-QGF-IMYRLFRDATRYTKGHHVKDLSCLNRD
Xenopus_(S : YKYFIDYRQMIIEPTSPKLLPDPL-KEPYY----QPPYTLVLELTDVLLHPE---------WSLSTGWRFKKRAGIDNLFQQLA-PLYEIVIFTSETGLTAFPLIDNVDP-HGF-VSYRLFRDATRYTDGHHVKDISCLNRD
Pan_troglo : ----------IIEPTSPCLLPDPL-QEPYY----QPPYTLVLELTGVLLHPE---------WSLATGWRFKKRPGIETLFQQLA-PLYEIVIFTSETGMTAFPLIDSVDP-HGF-ISYRLFRDATRYMDGHHVKDISCLNRD
Homo_sapie : YKYFKDYRQMIIEPTSPCLLPDPL-QEPYY----QPPYTLVLELTGVLLHPE---------WSLATGWRFKKRPGIETLFQQLA-PLYEIVIFTSETGMTAFPLIDSVDP-HGF-ISYRLFRDATRYMDGHHVKDISCLNRD
Bos_taurus : YKYFKDYRQMIIEPTSPCLLPDPL-REPYY----QPPYTLVLELTGVLLHPE---------WSLATGWRFKKRPGIETLFQQLA-PLYEIVIFTSETGMTAFPLIDSVDP-HGF-ISYRLFRDATRYMDGHHVKDISCLNRD
Mus_muscul : ---------MIIEPTSPCLLPDPL-REPYY----QPPYTLVLELTGVLLHPE---------WSLATGWRFKKRPGIETLFQQLA-PLYEIVIFTSETGMTAFPLIDSVDP-HGF-ISYRLFRDATRYMEGHHVKDISCLNRD
Nematostel : ---------MFVEPSSTKLLPDPL-PEPYI----QPPYTLILEMTDVLVHPE---------YDRKSGWRFKRPGVEFFLNQLA-PLFEIVVFTHEVGFSASPVIDGIDP-HQM-IMYRLFRDATKYIKGTHVKDLSGINRD
Strongyloc : ---ISHFVQMIAEPSAEKLLPDPL-VEPYY----QPPYTLVLEMKDILVHPE---------WTYANGWRFKKRPGVEYFLQQAGPPLFEIVIYTSEQGFTAFPILDSLDP-KGC-IMYRLFRDATKYVNGHHVKDLSSLNRD
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                    720         *       740         *       760         *       780         *       800         *       820         *       840         *
Saccharomy : LSKVIIIDTDPNSYKLQPENAIPVEPW---NG-EAD---------DK-LVRLIPFLEYLATQQTKDVRPILNSFEDK-----KNLAEEFDHRVKKL--KDKFYGDHKSGGNWAMTAL-------------------------
Cyanidiosc : LRRTIIIDNDPRVFALQSENGIEIAPW---NGTDPD---------DKELLRLTAFLEWVVRNDVADVRPIIATVRNCD----RTTSRSFAERFEAC--RQQVESVLASQKLAAVAGA-------------------------
Esil_TIM50 : LEQTLIIDDNADCISMQPENAIKVKAFSLEDGSDPTA--------DTALYDLAPFLRALATQGVADFRDVLRPHVGEDS---NAVVADFRSKVNAVRQKEDAEKSKGLGGLVRQIAPVVGAGGPAAGMGGMLTSKDIVGDAP
Arabidopsi : PKKILFVSANAFESTLQPENSVPIKPY---KL-EAD---------DTALVDLIPFLEYVARNSPADIRPVLASFER------KDIAKEFIDRSIEY--QKRKQGQLGQGRFWRR---------------------------
Zea_mays_g : PAQVLYISAHAKESSLQPENSVEIKPW---KL-END---------DTQLLDLIPFLEYVAMARPSDIRAVLASYQS------GDIAAEFIER------SKEHQRRMQEQKK-----------------------------
Phaeodacty : LNRMVVIDDDPSEVQFNPENLIRVKPY---AD-PTDRT-------DNTLERILPFLVEIAREGYNDVPGLLRQYEGMDA---DQIADEQDRRIHELRTHRERRSQQGLGALARG---------------------------
Phytophtho : LRQVVILDDDPAAYQLQPENAIPVTPFT--NGRDRD---------DHELKDLIPFLKALASERVPDFRQVIGEFRDEDGVV-RDLATKYGARVHQLEMQKEQKKKKGFGGFVRGRLS-------------------------
Phytophtho : LRQVVILDDDPAAYQLQPENAIPVKPFT--NGRDRD---------DHELKDLIPFLKALASERVPDFRQVIGEFRDDDGVV-RDLATKYGARVHQLEMEKEQKKKKGFGGFVRGRMS-------------------------
Magnaporth : LSKVIIIDTNPEHVSAQPENAIILPKW---TG-DAQ---------DKDLVALIPFLEYIHTMQYPDVRKVLKSFEG------KNISEEFARREAIA--RKKFQEQLEQNRKKHPNKPGAGVFGALGNAFGLKPSKMSMMVPV
Aspergillu : LSKVILIDTKEEHARLQPENAIILDKW---NG-NPK---------DKTLVALIPFLEYLAGMGVDDVRTVLKSFEG------QSIPIEFAKREKAM--RERFEKELAEEQKKRPRSG----MGSLASALGLKSSART----L
Penicilliu : LSKVILIDTVPGHAREQPENAIILPKW---KG-DTK---------DKSLVALIPFLEYVAGMNVEDVRPVIKSFEG------TYIPAEFAAREKVM--REKFQKQLEEEQKSRPRRG----VGSLAALLGLKPQS-S----I
Talaromyce : LSKVILIDTVPAHAREQPENAIILPKW---KG-DPK---------DKSLVALIPFLEYVAGMNVEDVRPVIKSFEG------TYIPAEFAVREKVM--REKFQKQMEEEQKSRPRRG----VGNLAALLGLKPQS-S----I
Ostreococc : MGQILYISSKPRSAELHPANVIPIKPWTYEDG--SK---------DTALLDLMPFLESIVRLNVQDVRVVLDSYKKEMSATGKDIPTIFRERQLAL--QRRRRDKLANQTKMSR---------------------------
Micromonas : VGMVLYITARPKT-SMQQENVVQISPY---IV-DSEGRTAGGDGPDTTLLDLMPFLESIVRLNVKDVREVLASYKQEQEATGKSVPEIFRSRQYRF--QKQQRQKTVTKPA-----------------------------
Chlamydomo : LNHVLMISAKPEAWALQPENTLKLKPW---KG-QPG---------DTGLIDLIPFLQFLAMRRVKD-------------------------------------------------------------------------
Ixodes_sca : LSKVILVDWSEEACSLQPRNALKLRKW---DG-GDE---------DRTLLDLAQFLRTIGTSEVEDVRTVLDYYRQF-----EDPLVAFKENQKRL----QEEKQLASIEAVPSQ---------------------------
Xenopus_(S : PSHVVIVDCKREAFKLQPYNGLAIKKW---DG-SSE---------DRALYDLTAFLKTIAVSGVSDVRSVLENYALE-----EDPLEAFKRRQTQL--EQEEQQRLADMSQLSKRQ---------------------------
Pan_troglo : PARVVVVDCKKEAFRLQPYNGVALRPW---DG-NSD---------DRVLLDLSAFLKTIALNGVEDVRTVLEHYALE-----DDPLAAFKQRQSRL--EQEEQQRLAELSKSNKQ---------------------------
Homo_sapie : PARVVVVDCKKEAFRLQPYNGVALRPW---DG-NSD---------DRVLLDLSAFLKTIALNGVEDVRTVLEHYALE-----DDPLAAFKQRQSRL--EQEEQQRLAELSKSNKQ---------------------------
Bos_taurus : PARVVVVDCKKEAFRLQPYNGVALRPW---DG-NSD---------DRVLLDLSAFLKTIALNGVEDVRTVLEHYALE-----EDPLEAFKQRQSRL--EQEEQQRLAELSKSSKQ---------------------------
Mus_muscul : PARVVVVDCKKEAFRLQPFNGVALRPW---DG-NSD---------DRVLLDLSAFLKTIALNQVEDVRTVLEHYALE-----DDPLEAFKQRQSRL--EQEEQQRLAELSKSNRQ---------------------------
Nematostel : LKKVIVIDCNKAATELNERNAIILKKW---EG-NPA---------DTTLVDLLPLLQTIATSGVDDVRAVLDFYRQE-----DDIVAAFKRNQARL--REAEQARLQKLEQQNKQ---------------------------
Strongyloc : LSKVIIVDCNAKSYQLQFKNALGLKKW---EG-NDD---------DRTLFELAAFLRTVAASGVEDVRTVLEFYQQF-----EDPMEAFRINQARLQVRSEQEEEAKRIAEAKEKGG-------------------------

                    860         *       880         *       900         *       920         *       940         *       960
Saccharomy : ---GLGNSLGGSTKFPLDLIHEEGQKNYLMFMKMIEEEKEKI---------RIQQEQMGGQTFTLKDYVEGNL---PSPEEQMKIQLEKQKEVDALFEEEKKKKKIAESK
Cyanidiosc : ----------------------------ATASSSSADGHLSGNGVRAPVRGLGIFAIPRRDPAEQSATTTSE---ASSPAAPAQPVPDQSIWTRLRR------------
Esil_TIM50 : ETLSPGMAAAAAATAGGKGGGKGGGGSKPLAEKQKGGLWKSLQEGNKEREEDFMRRNEAFQRVMEKRMAREKA---KRDEQAQQQ-------------------------
Arabidopsi : ------------------------------------------------------------------------------------------------------------
Zea_mays_g : ------------------------------------------------------------------------SGRIW---RR--------------------------------
Phaeodacty : ------------------------------------------------------------------------------------------------------------
Phytophtho : ------------------------------------------------------HHPASPTGGVAASGFSSGPHV-------------------------------------
Phytophtho : ------------------------------------------------------HHPAPPNGGVAASGFGGGH---------------------------------------
Magnaporth : EGEESVADALAQGKMLQDIARERGQRQYERIDKMVRENGEKWLKEEAEMMEKMQAEAMANMKTGFMGWFGSSEQKDGAKDEPKKA-------------------------
Aspergillu : DGEQLPSAGLQEGKMLWDQIRERGQKNYELIEKEIRENGEKWLAEMAAEEEKLRQEQMESMKGSLTGFFGG-----GKKE-------------------------------
Penicilliu : DGQ----GA-SEEKMLWDQIRERGQKNYEMMEQEIRENGETWLKMMAEEEEKARQEQMKNMKGSLTGFFGASG--EGEKK-------------------------------
Talaromyce : DGQ----AAGSEEKMLWDQIRERGQKNYEMMEQEIRENGETWLKMMAEEEEKARQEQMKNMKGSFTSFFGATG---GEKK-------------------------------
Ostreococc : ------------------------------------------------------------GYDVGKRAQREA---RAAA-------------------------------
Micromonas : ------------------------------------------------------------------------FSRGW-----------------------------------
Chlamydomo : ------------------------------------------------------------------------------------------------------------
Ixodes_sca : ------------------------------------------------------------------RSWTKGLW---KRN--------------------------------
Xenopus_(S : ------------------------------------------------------------TLSLGSFTGRLW---PRSKQQ-----------------------------
Pan_troglo : ------------------------------------------------------------NLFLGSLTSRLW---PRSKQP-----------------------------
Homo_sapie : ------------------------------------------------------------NLFLGSLTSRLW---PRSKQP-----------------------------
Bos_taurus : ------------------------------------------------------------NLFFSSLTSRLW---PRSKQP-----------------------------
Mus_muscul : ------------------------------------------------------------GLSFGSLASRLW---PRSKQP-----------------------------
Nematostel : ------------------------------------------------------------GRSWGGMFGR-----------------------------------------
Strongyloc : ------------------------------------------------------------SSLVGGWTRGLI---GRR--------------------------------
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(d) Sam50 amino-acid alignment (p. 9-16)

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                        *        20         *        40         *        60         *        80         *       100         *       120         *       140
Neorickett : ----------------------MRKKLFLVWLLFLSRFCFADEVVEIRISGNKRVAETTIHGLLHVEVGQDVTSDELNAVFKRLTASRLFSSVELDLTAG-ILEVKLQENPILRNVVVKGNKLLSRAAIDKILVYKKDAIFD
Rhizobium_ : --MKAGSRFLNAVSAFALSASMVATGTGAAL-VASTSVAQAAVISRVEVRGATRVSPETVRANITIVPGKSFSNADIDASVKRLYATGYFSDVSISISGG-TLVVNVSENQLVNQVVFNGNRKIKDDKLQGVVRTQPLGPYS
Rickettsia : ----------------MKIISISKLTILLLTIFYYHISFADYVIRKITIEGNHRVERSTIESYLKLNVGETYNNSKEDEAIKRLYATSLFRNINMYITNDGNLIVNVTETPFISSVVFSGNSKIKTNILAKEIYTMSGESLS
Rickettsia : ----------------MKIISISKLTILLLTVFYYHISFADDVIRKITIKGNHRIERSTIESYLKFNVGETYNNSKEDEAIKRLYATSLFKNINMYITNDGNLIVNVTETPFISSVVFSGNSKIKTNILAKEIYTMSGESLS
Magnetospi : MSRFQGNGFTNLRGAWMRFVLWTAVLLGILVGVMPASAQEGGRIRSISILGTQRIEVETVKSYMTVAEGDLYDTDRVNRSLKALFNTGLFQDVAIRREGD-QLLVRVVENPIINRIAYEGNNRIKEEQLNTEVQLRPRTVYT
Gluconacet : MPTKRSTLLASVCLIPLFFAGAAEARQGVATRGPVAHTPTGGVIESIDISGNDRIETNTVLSYMVVQPGDPFNQDQLDRSLKTLYATGLFRDVTLHRAGN-VLQVHLVENPIVNRIVFEGNHAAKDEDLRKVIALRPRAVFS
Chlamydomo : ----------------------------------------------MTSSEAEPAPATAASASPAAADASGSSAG----ASGAAAT---------------------PAAGGPHGVVD--------------YE--------
Phaeodacty : ----------------------------------------------------MNQAQLQQKQERLRQLQEEERQLRLQLQVQEHAATY-------------------------------------------------------
Thalassios : ----------------------------------------------MNNNHQQRRQGGDASSASSAISHQQRLQRHRQQQQQQMME---------------------KLNQLKAQYVSDYSLPLNYPANVTSLL--------
Saccharomy : ----------------------------------------------------MTSSSGVDNEISLDSPMPIFNESST-------------------------------------------------------------------
Ectocarpus : ------------------------------------------------------------MVIPLD-------------------------------------------------------------------------------
Phytophtho : ----------------------------------------------------MASTNSEAPEPTAE-PPHPW-------------------------------------------------------------------------
Phytophtho : ----------------------------------------------------MASTRSEAPKAAAE-PPHPW-------------------------------------------------------------------------
Phytophtho : ----------------------------------------------------MASTNSSETPKPAAEDPPHPW-------------------------------------------------------------------------
Physcomitr : ----------------------------------------------------MNIMSEKLV----------------------------------------------------------------------------------
Zea_mays_A : ----------------------------------------------MAIAADSAADQDPNPIPNEAAGESVELPAYTDHGEPNAD---------------LADVDYEDEEELDGVTAEAAARDK-------VE--------
Sorghum_bi : ------------------------------------------MAAAADSAAGQNPKDDERHVLTADSDARFSEEEYEEDGEEEYE-------------------EEEEEEELDGPAAEAAERERVQSVFRRLS--------
Oryza_sati : ----------------------------------------------------MATAADQNPNDAEHREAAAGANAAAEEYEEEDEEE---------------------EEVELDGPAAVAAEREK--------VQ--------
Arabidopsi : ----------------------------------------------------MENPAEKPDPNPSKPKIESEDEREELGDINGDEEEE--------------------EEYEEEDDGKPRTREDAIADRI---KA--------
Vitis_vini : ------------------------------------------MALKENQEETPISENPNGDEEGGEESQADGVGDFEDEDEDEA--------------------EEEDEEEEARSEKSRESRLAEDGSKLE--------
Ricinus_co : ------------------------------------------------------------MEKPDPIAENPDNGEEEEEDDLDDDEDDLE--------------------PEPEPLNPRARESQARVEREKVENLIR--------
Populus_tr : ------------------------------------------------------------MAEPESDISDPVVQNPNNEDEEDLYEQSDDVE--------------------DEDEDEDEDLESQKAKLRNR-FQNFFR--------
Ostreococc : ----------------------------------------------MATTTTTDARDDDASFTARGERRDATSDAADAAESSAS---------------------AESSASADAGATTSTPPVNEF--------------
Micromonas : ----------------------------------------------------MADQAGQKKPYDYQERYRHVR-----------------------------------------------------------------------
Micromonas : ------------------------------------MTIENDVATSDATPSSSSSATEEPPPPPPPPPPPPPPQQQGGPPPGYDHQA-----------------------------------------------------------------
Pichia_sti : ----------------------------------------------MSLDHDDMLDRLASSPTGGHQDLSKSEK----ELQSLMQ---------------------EKQELMMKQSKDF------------ME--------
Hydra_magn : ----------------------------------------------------MGGSFVKPIYAADASQFVIQAEETDIDENDIPL-----------------------------------------------------------
Ciona_inte : ------------------------------------------------------------------------------------------------------MAGSSKEIV----------------LD--------
Trichoplax : ------------------------------MVTMVNLKLKLNLHIKYKNAFDFFLGKMPNQVLVSYPSPVYKNLQYFYLVPLSTRLKNTHVDTIVDTLQETTGKGSSMQGAENEKRGATRLTKLTDCIMYFLS--------
Salmo_sala : ----------------------------------------------------MGTVHARSMDPLPMHGRDMGVHPD----DMIEVQE---------------------AEQETKQEV----------------LE--------
Danio_reri : ----------------------------------------------------MGTVHARSLDPLPMQGPELGVQAD----DM-DLGE---------------------PEREEKQEV----------------LE--------
Xenopus_la : ----------------------------------------------------MGTVHARSLDPLPMNGPDFGS-PD----DA-DLVE---------------------VEPEKKQEI----------------LE--------
Monodelphi : ----------------------------------------------------MGTVHARSLEPLPVSGPDFGGLGE----EA-EFVE---------------------AEPEIKQEV----------------LE--------
Bos_taurus : ----------------------------------------------------MGTVHARSLEPLPASGPDFGALGE----EA-EFVE---------------------VEPEAKQEI----------------LE--------
Mus_muscul : ----------------------------------------------------MGTVHARSLEPLPSSGTDFGALGE----EA-EFVE---------------------VEPEAKQEI----------------LE--------
Homo_sapie : ----------------------------------------------------MGTVHARSLEPLPSSGPDFGGLGE----EA-EFVE---------------------VEPEAKQEI----------------LE--------
Macaca_mul : ----------------------------------------------------MGTVHARSLEPLPSSGPDFGGLGE----EA-EFVE---------------------VEPEAKQEI----------------LE--------
Pediculus_ : ------------------------------------------------------------------------------MKLEKK-----------------------------------------------------LI--------
Apis_melli : ----------------------------------------------------MGTVYAKEKMNL------------------FEKRK---------------------EEPID--------------------LH--------
Tribolium_ : ----------------------------------------------------MGTVHAKSEENAPI-------LPT----IPQEHIK---------------------SEPAQHQDQREIF------------LD--------
Laccaria_b : ------------------------------------------MDGEFELSATPLRPPLQNSSAPRDKEPDDLQKLIKWQEERLAR---------------------RLRGEYESAVLH-------------LS--------
Coprinopsi : ------------------------------------------MSEELSHPPLKPPLQNSSAPRDKEPKEIEKLLKWQQQRIER---------------------RLRGEYESAVMH-------------LQ--------
Schizosacc : ----------------------------------------------------MSVSPTDTMENTPA-----GIDTEQLKLSMEDLAQ-----------------------------------------------------
Neurospora : ----------------------------------------------------MASSPSAPGNPVEAATAKIDKAAAIVHQKAAAVV---------------------TEPKEPQPYQ---------------VP--------
Nectria_ha : ----------------------------------------------MAAIPSSSGGLSGDPLNKLHTDTGSLLHEAESKPEFQRE---------------------QEEAKQRRM--------------------------
Phaeosphae : ------------------------------------------MAAP---HEDDVFERLKN----KT-DQAEWQR----KQDELNT---------------------RLYAQQHKSQER-------------LG--------
Aspergillu : ----------------------------------------MASFSPPGASRGQPKRTVRGLLAIAAAEMSSPLSAEDEDIFERLQ-------------------QRADPKVLEEQQQAINERVHAIYQKAQMR--------
Ajellomyce : ----------------------------------------------MVSPLESDENIFERLKQKSTDPKVLEEQQQAVNERINA---------------------IYQKAQSRL--------------------------
Coccidioid : ----------------------------------------------MASPLQDDDGIFERLRKQNEDPKVLEERQQAVNERIHA---------------------IYQKAQTRL--------------------------
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                    *       160         *       180         *       200         *       220         *       240         *       260         *       280
Neorickett : VHEFENSITALKTYYRDSVVEKTAISYRVVPIDENNVNVEVTVKEAKPTV--IRAI--EFEGNI----RYSDRVLKHVIRSREKSILRLFGTAHYYSREKLEFDKDLLADFYQGKGYFDYSLEGLEERENEDGVVL--VFKL
Rhizobium_ : EATVETDIQAIKDAYAAIGRSDVTVTTQVVPIAEGRVNLAFVINEGERTK--ITQI--NFVGNE----AYSDGRLQSVIATKESGIFSFLTRKDVYNPDKLRADEELLRQFYYNRGYADFNIISSEATLNEATNEYTVTITV
Rickettsia : QAKIELDVKKILEIYKRSGRFSTKVTPKIKSLENNRVKVIFDIAEGPKTV--IKSI--YFSGNE----HYSDSELKSIVLTKESRWFRFLESNDTYDPDRVEYDKELLREFYQSVGFADFRVISASVALNDTKEYFTITYSI
Rickettsia : QAKIELDVKKILEIYKRSGRFSTKVIPKIKNLENNRVKVIFDIAEGPKTG--IKSI--YFSGNE----HYSDSELKSIVLTKESRWFRFLENNDTYDPDRVEYDKELLREFYQSVGFADFRVISASVELNDTKEYFTLTYSI
Magnetospi : RSKVQADVKRILELYRRSGRFAATVEPKIIQLEQNRVDLVYEISEGQPTY--VRRI--AFVGNK----RYDQDKLREVLQTKEERWYRFLTTDDTYDPDRVTYDRELLRRYYLKQGFADFRVSSAIAELTPSREGFFITYTI
Gluconacet : TQTTAADRQKILGVYAEKARYAATVTPQIIRLSHNRVDVVFQINEATQTL--IKKI--SFVGNR----AFSEARLAQVVSSKETAWYRFFASSDEYNPERLRYDGELLRRFYLRNGFVDFQVKNATGELSPDRKSFYVTFTV
Chlamydomo : ------------------------------------A-LYEQIKDKPCH--VVQINQRKDGFNGGTFRTRASLIEREIE-P-------------------------------------------------------IYKA
Phaeodacty : ---------------------------------------------QVELAWPARIV--DSNGNAP---RTNNELIQHRLLESGV-------------------------------------------------------LYEV
Thalassios : ---------------------------------------DASDDNTSDAS--------KSKQNEPSLLRTDQDFINARLLEA-------------------------------------------------------GVPL
Saccharomy : ----------------------------------------------LKPIR--VAGV--VTTGTD----HIDPSVLQAYLDDT-------------------------------------------------------IMKS
Ectocarpus : ----------------------------------------------ELPLR--VRTV--KIVGNN----RTKPYVVEDQLQ-D-------------------------------------------------------AYEA
Phytophtho : ----------------------------------------------GPQIH--IGKV--FLKGNE----RTKPEVFENELQ-E-------------------------------------------------------AYSA
Phytophtho : ----------------------------------------------GPHMR--IGKV--FLKGND----RTKPEVFENELQ-E-------------------------------------------------------AYGA
Phytophtho : ----------------------------------------------GPRMR--IGKV--FLKGND----RTKPEVFENELQ-A-------------------------------------------------------AYSA
Physcomitr : ----------------------------------------------KEPVKVRVHDI--EIRGNV----KTKDSVIEAQLK-E-------------------------------------------------------LREV
Zea_mays_A : -------------------------------------A-VFQRLSEAPVGIRVHDI--IIKGNT----KTRDALIEAEVVGL-------------------------------------------------------IRSA
Sorghum_bi : ----------------------------------------------SNPVGIRVHDV--LIKGNT----KTRDELIEAEVA-D-------------------------------------------------------LLRA
Oryza_sati : -------------------------------------A-VFKRLSSDPVGIRVHDV--IIKGNA----KTKEELIEAEVAEL------------------------------------------------------LRAA
Arabidopsi : -------------------------------------ESLFRRMRATPVAVRVHDV--IVKGNE----KTKDHVIEAEVD-V-------------------------------------------------------VRQA
Vitis_vini : -------------------------------------S-MFRRLASEKVKLRVHDV--LIKGNT----KTKDSLIEAELE-A-------------------------------------------------------IKNA
Ricinus_co : ----------------------------------------RMQTETVPLR--VHDV--IIKGNV----KTKDSILESETA-L-------------------------------------------------------LKDV
Populus_tr : ----------------------------------------RIQHESVPIR--VHDV--VIKGNT----KTKDTLIEAETA-S-------------------------------------------------------LKDA
Ostreococc : -------------------------------------RARYDRVRDDACA--VSSI--EIRGNE----RTRASVIEREIA-R-------------------------------------------------------AYEA
Micromonas : ----------------------------------------------QKPLS--VYSV--EVKGDE----RTRPGLFARVLD-P-------------------------------------------------------VYRA
Micromonas : ----------------------------------------RYQALKDKPIA--VESV--EIQGIE----RTRRGILEAALE-P-------------------------------------------------------LYRA
Pichia_sti : -------------------------------------E-LFKQNSTQPIK--VKNV--QITNGH----SFRDNFLQAQFS-P-------------------------------------------------------LLNS
Hydra_magn : ----------------------------------------------KVPAV--IKNI--FIDGLC----KTKNVLIANQLS-D-------------------------------------------------------LFKA
Ciona_inte : ----------------------------------------------NKDIE--IVKV--HISGLV----KTKSDYVLDDIK-P-------------------------------------------------------VFGS
Trichoplax : -----------------------SISSALLYFGVIIIKSAEQQLKNKKIK--VHNI--NIDGLR----VTRTDLVQPKIH-N-------------------------------------------------------VFEA
Salmo_sala : ----------------------------------------------NKDVV--VQHV--NIEGLG----RTKEDLLGYEIS-E-------------------------------------------------------VFHA
Danio_reri : ----------------------------------------------NKDVV--VQHV--HIDGLG----RTKEDILTYEIA-D-------------------------------------------------------VFHA
Xenopus_la : ----------------------------------------------NKDVV--VQRV--HFEGLG----RTKDDLIAHEIG-Q-------------------------------------------------------VFKA
Monodelphi : ----------------------------------------------NKDVV--VQHV--HFEGLG----RTKDDIIMYEIG-D-------------------------------------------------------VFKA
Bos_taurus : ----------------------------------------------NKDVV--VQHV--HFDGLG----RTKDDIIMYEIR-D-------------------------------------------------------VFKA
Mus_muscul : ----------------------------------------------NKDVV--VQHV--HFDGLG----RTKDDIIICEIG-E-------------------------------------------------------VFKA
Homo_sapie : ----------------------------------------------NKDVV--VQHV--HFDGLG----RTKDDIIICEIG-D-------------------------------------------------------VFKA
Macaca_mul : ----------------------------------------------NKDVV--VQHV--HFDGLG----RTKDDIIICEIG-D-------------------------------------------------------VFKA
Pediculus_ : ----------------------------------------------YLESE--VDKI--NIEGLQ----RTKDDVVVETVQ-D-------------------------------------------------------LFKA
Apis_melli : ----------------------------------------------SVKAR--VDRI--HVDGLI----RTKDDIIKAQVI-E-------------------------------------------------------LFKA
Tribolium_ : ----------------------------------------------GVKAR--VDKI--HVDGLA----RTKDDIIEDCIR-D-------------------------------------------------------LFKA
Laccaria_b : -------------------------------------E-VVSCNRQTPVT--ISSV--RVEGAI----HTRKSFLGFIID-P-------------------------------------------------------ALKA
Coprinopsi : -------------------------------------E-TVNNNLKTPVN--IASV--RVEGAH----GTRTSFLGSIID-P-------------------------------------------------------ILAA
Schizosacc : ----------------------------------------ILNDNSTLPLG--IASI--RVVGAT----RTRPSFLEKAVSYK-------------------------------------------------------LAQK
Neurospora : -------------------------------------NPIIEDHLLTPAT--VNSI--EIHGAN----NTRRGLLDHVFK-P-------------------------------------------------------VVEE
Nectria_ha : -------------------------------------AQIVADQNLAPMT--VNEI--RVHGAV----NTRTDFLDPLFQ-P-------------------------------------------------------LVRD
Phaeosphae : -------------------------------------E-LVGEQLGTEEL--VLMS--NRSKTT----PRFPSFLERVVN-P-------------------------------------------------------ILSA
Aspergillu : ------------------------------------LGELIDQNSTLPCA--ISSV--QVLNAT----HTRRSFLQSIFD-P-------------------------------------------------------LLSV
Ajellomyce : -------------------------------------AELIDQNSTLPCT--ISSV--QVLNAN----NTRRGFLEKVIS-P-------------------------------------------------------LLSA
Coccidioid : -------------------------------------AELIDQNSTLPCT--ISSV--QVLNAS----HTRKDFLEKVLS-P-------------------------------------------------------LLSS
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                    *       300         *       320         *       340         *       360         *       380         *       400         *       420
Neorickett : KEGARYSFGRVNVVSEKSEIEISDLKEKVRIREGAVFNIGAVRENALTLLSVLNERGHMFVNVVPQYQPD-ADGRVDVT--YYYVSTKKYRIRKINISGNIRTRDTVIRREMLLSENDLYQPSKVADSRRRILNLGFFDEVY
Rhizobium_ : EEGPRYDFGAINVESTVEGVNAEELKGLVQSREGSVYKAKDIQDTMSEISKRVASAGYPFARVTPRGNRDLANHTIAVD--YLVDQGERAYVERIEIRGNTRTRDYVIRREFDVGEGDAFNQEMIARAKRRLEALGYFSSVN
Rickettsia : EEGEKYRFGNVTIDNKLTNINIKQLNKIVNIKQGKIFNMKTVDDIAEKIGEYFTANGYPAVNVYPDIKKN-DNHTADIK--FIIEKADKVYINKINIINNLKTEDHVIRRAFKIEEGDVMNRSYIEKGERNLRNLDYFE---
Rickettsia : EEGEKYRFGNVTIDNKLTNINMKYLNKIVNIKQGKIFNMKKVDDIAEKIGEYFTANGYSAVNVYPEIKKN-DNHTADIK--FIIEKGDKVYINKINIINNLKTEDHVIRRAFKIEEGDVINRSYIEKGERNLRNLDYFEKVS
Magnetospi : DEGERYKFGSSVINAELRDLKPEDLQPLLISETGGWYNADQVEDIVQRLTDAVGTKGYAFVDVKPQVQRNRETHTIDIT--YEIKEGPRVFVERIDISGNVRTLDQVIRREFRLVEGDAFNSAKLRRSRQRLKDLNFFEKAE
Gluconacet : DEGLRYRLGRVNIRSSLKHVPAASLRKYIELFANQWYDGSAVQHNATDMEEILQGQGHPFAMVRPEIARNPEKRTVDLL--FDVSEGPRVYVERIDINGNTITEDKVIRRNLPMAEGDPYTPSERKYAKAMLQDLGYFSSVS
Chlamydomo : --------------ETLAEVHEEMEAAGKRLRQLGVFT--GV--------SVLAHE-------EPLDDPT----ACTVE--LAVEE-SNWF----------------------------------------------
Phaeodacty : -------------PVRVGATVESTNAFIQDLEKTGCFN--SV--------RVEVGQ-------GVSDEDASTRVQKQLK--ITLDE-KRWY----------------------------------------------
Thalassios : GGGVPDLTPTSQSKMTITDHNASIARFIHDLEGTGCYD--AV--------QVYLGNNNEVSTSGNQDDGATSTDSFDVT--VRLKE-KKWY----------------------------------------------
Saccharomy : --------------ITLGQLVKNADVLNKRLCQHHIAL--NAKQSFHFQGNTYISDE----KETHDVVPL-----MEVVSQLDILP-PKTF----------------------------------------------
Ectocarpus : --------------TTVGDVYGGLVEGAQRLDGLGLFE--SV--------QVSVDAV------DDGSLDQ-----TDVT--VTVKE-KNWY----------------------------------------------
Phytophtho : --------------KRIGRLVRNLEEATEELKALDIFE--SI--------DIKLDKA------SSGERDE-----TDIT--ITVKE-KGWR----------------------------------------------
Phytophtho : --------------ERIGHLVRKLEEATEEFKALDIFE--SI--------NIELDKA------SSGKHDE-----TDVT--ITVKE-KGWR----------------------------------------------
Phytophtho : --------------ERIGQLVHKLEEATEEFRALDIFE--SI--------NIELDKA------SSGQLDE-----TDLT--ITVKE-KGWR----------------------------------------------
Physcomitr : --------------DTVQELLQECVRANSRIRALGIFD--KC--------VITLDA-------GPQELPG-T---ANVI--LEVEEVKRLF----------------------------------------------
Zea_mays_A : --------------VTVQDLVRTANIAAVRLRLLDVFD--SV--------HVLLDA-------GPPELPG-T---TNVI--IQVVEAANPI----------------------------------------------
Sorghum_bi : -------------APTVQDLLRAASVATARLHSLDVFD--TV--------KITLDA-------GPPELPG-T---TNVV--IEVVEAANPL----------------------------------------------
Oryza_sati : --------------PTVQDLLRNASIASARLRQLDVFD--SV--------NITLDA-------GPPELPG-T---TNVV--VEVVEAANPI----------------------------------------------
Arabidopsi : --------------TTVQELLKASKVANFNLQALDIFD--SV--------KITLDS-------GPPELPG-T---TNVV--IDVVESKSPI----------------------------------------------
Vitis_vini : --------------TTVQELLKAAGIANHRFHSFGIFD--SV--------GITLDC-------GPPELPG-T---VNVI--VDVVETKNPL----------------------------------------------
Ricinus_co : --------------SSVQELLEASKVVNFRLQALEVFD--SV--------RITLDS-------GPSELAG-T---ANVV--VEVVESKSPV----------------------------------------------
Populus_tr : --------------STFKELFAASSDVNFRLQALEIFD--SV--------KITIDS-------GPPELPG-T---ANVI--VDVVETKSPL----------------------------------------------
Ostreococc : --------------RTLDGIKDALFAANARLYEYGIFK--DV--------AIVIDADHEGGRLDGGDVPG-----AKVV--VSVEE-KDAF----------------------------------------------
Micromonas : --------------STLDELRVRCVEANAVLNSYDIFD--RV--------DIEVDA-------GPREHPD-S---AKVT--VEVSE-KKKL----------------------------------------------
Micromonas : --------------SSLDDLRDKCVDANGALNAYDVFE--SI--------DIVCDA-------GASSRPD-T---ASVI--VRVEE-KKRL----------------------------------------------
Pichia_sti : -----KQP------VSLQEFLKQLSVVENLM--VGIHP--VV--------GTITTQS---IF-GRRTVPD-NGACISVVPIFNTLP-VKKF----------------------------------------------
Hydra_magn : --------------KTFSDIMTEAHLGKLKLERLGIFS--TI--------DVLVDV-------SEDSHGD----AFDVH--YIVKE-KRRF----------------------------------------------
Ciona_inte : --------------KTFLDAYQQSLFCREKLMSRGIFK--DV--------DVVIDTT----D-GYDNAPDNG---VQVV--FNVKE-RNGV----------------------------------------------
Trichoplax : --------------ATFEELVKEMYLSKNYLEDLDIFH--PV--------NVFIDAA------SDKKADPIE---LDVT--FRVRE-LSRF----------------------------------------------
Salmo_sala : --------------KNLIDVMKKSHIARQKLLRLGIFK--EV--------EVVIDTS----D-GADALPN-G---LDVT--FEVTE-MKRL----------------------------------------------
Danio_reri : --------------KNLIDVMKKSHEARQKLLRLGIFR--HV--------EVVIDTA----E-GADALPN-G---LDVT--FEVRE-LRRM----------------------------------------------
Xenopus_la : --------------KNLIEVMRKSHEAREKLLRLGVFR--NV--------EVLIDTS----E-GEDAVPN-G---LDVT--FEVTE-LRRL----------------------------------------------
Monodelphi : --------------KNLIDVMRKSHETREKLLRLGIFR--QV--------DVLIDTC----Q-GDDALPN-G---LDVT--FEVTE-LRRL----------------------------------------------
Bos_taurus : --------------KNLIEVMRKSHEAREKLLRLGIFR--QV--------DVLIDTC----Q-GDDALPN-G---LDVT--FEVTE-LRRL----------------------------------------------
Mus_muscul : --------------KNLIEVMRRSHEAREKLLRLGIFR--QV--------DVLIDTC----H-GEDALPN-G---LDVT--FEVTE-LRRL----------------------------------------------
Homo_sapie : --------------KNLIEVMRKSHEAREKLLRLGIFR--QV--------DVLIDTC----Q-GDDALPN-G---LDVT--FEVTE-LRRL----------------------------------------------
Macaca_mul : --------------KNLIEVMRKSHEAREKLLRLGIFR--QV--------DVLIDTC----Q-GDDALPN-G---LDVT--FEVTE-LRRL----------------------------------------------
Pediculus_ : --------------KDFQEVIINAHKVRGKLEKLGCFQ--NI--------GIFIDTS----T-GAEATLD-G---LEVT--FFVKE-LKRM----------------------------------------------
Apis_melli : --------------QDFYDVVLRAYKVREKLQGLGCFG--NI--------GIYIDTS----Q-GPRATPE-G---VEVT--FMVRE-IRRL----------------------------------------------
Tribolium_ : --------------ADFQDVLLRAHRARLKLDELGCFK--NI--------AVFIDTS----K-GQGASPD-G---LEVT--FNVTE-HKRV----------------------------------------------
Laccaria_b : -----STVSPLDSQTNLESVLHTTRRIYHMLNKSDLFA--TI--------EAKVERA----R-DPLASSE-G---VDLV--FKTRE-RGRY----------------------------------------------
Coprinopsi : -----SNKDSPEGQSDLESVLHTTRKIGAVLTKSDLFS--TV--------EAKIERA----K-NSSAANT-D---VDII--FKTKE-RGRW----------------------------------------------
Schizosacc : ---------GNIKSIPLGESLETAQQIAERLMEFGIYE--DA--------KLLIDRAS-----GPIAGEN-D---IDIT--ILVKE-KSRL----------------------------------------------
Neurospora : ---------TASPTTTLGEALARISTATQKLTRFGIFKEDGF--------GVFIDSDARQQQQ-EQFQSPT-DRTELDVS--IRVKE-QSRL----------------------------------------------
Nectria_ha : ---------DQNATSTVGEVINKLRIASNKLDALQIFQPQP---------ELFLTSA---QQTDPSTSPT-D---VNVD--IRVKE-LSRF----------------------------------------------
Phaeosphae : -----NRAEP----YTLEEALKEVGEATEKLNRFGIFK-SPI--------SVYLDRP--NQS-IASSSPS-D---VDVY--ITAYE-RGNY----------------------------------------------
Aspergillu : ---------NQSRPYTLSEALREISSRADKLGKFDIFQ-QPI--------SVYIDQSQDAK--SQNGIPN-----IDVF--FSVKE-KSRV----------------------------------------------
Ajellomyce : ---------NNDRPYTLSEALSEISICTDKLSRFDIFE-HPI--------SVFLDKP---SQTDPSTTPT-D---LEVY--LSVKE-KSRI----------------------------------------------
Coccidioid : ---------NKDHPYTLAEALQEVGACTDKLHKFDIFQ-QPI--------SVYLDKP---SQTDPSTTPT-D---LDVY--LSVKE-RSRF----------------------------------------------
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                 *       440         *       460         *       480         *       500         *       520         *       540         *       560
Neorickett : IEER---KVDDQNLILEVRVKERPTGTLNLSGGYG--------SDVGFFGNFSFVENNLFGTSDRLVVELQRASLG---------SNYSVEFQRKRIFDTF-ITAGAS------------------------------VFY
Rhizobium_ : ITTAPG-SAADRVIV-VVDVQDQSTGSFGIGAGYAAGSGGGFLVEASI------EEKNFLGRGQYIRLAAGKGEDS---------QTYNVSFTEPYFLGYR-LAAGFD------------------------------LFK
Rickettsia : -------KVSISLAQTKAKDKYDVNVEVDEKSTSSIGFDLGYNTAGGLFGRFSFLERNLVGTGKLLNAGVQVSKNST--------SYYG-CITDPHFLDRD-LSLSVN------------------------------AFR
Rickettsia : ISLA---KTKAKDKY-DVNVEIDEKSTSSIGFDLGYNTAGGLFGRFSF------LERNLVGTGKLLNAGVQVSKNS---------TSYYGCITDPHFLDRD-LSLSVN------------------------------AFR
Magnetospi : VTNIPSDTAPDRTII-KVDVQEKSTGELMFGVGWA--SSAGPIIEASL------RERNLLGRGQDLRLGAGLGTKR---------SSLDLSFTEPYFMDRE-VAAGFD------------------------------AFV
Gluconacet : IDQSPG-SAPDKINV-AANLVEKPTGEFSLGGGYS--TDVGILGNIGL------KQHNLLGSGVDAGISGTMAYYQ---------RQADISVSDPYFLNRN-MVAGVD------------------------------IFA
Chlamydomo : -------KLRAATYV-QGGES-----T----------------FELGA------GLTNASGRAEALSANVEYGMENS--------HTASVAFKQPRVGGLP-ATLELR------------------------------GSQ
Phaeodacty : -------RVNAGAGV-------------------------------------------------------------------KTDGWLRPETAVND-----------------------------------GF-
Thalassios : -------KLYIGGGV-NSEDLSSFGGTSGMGNTLGGPGGAALGILPKLQFETSASLLNLTGFADVSTALYSVDQTGA--------SSFKFTHDRPLCSWLP-KHSSIREWLMPPDPRLIDPEERNASNGQSADSVDENQVFV
Saccharomy : -------TAKTGTNF--GNDNDAEAYL----------------QFEKL------IDKKYLKLPTRVNLEILRGTKIH--------SSFLFNSYSSLSPQSI---LNLK------------------------------VFS
Ectocarpus : -------LLQSGATT-TGTAKGNLDAS----------------EFSNLRYSVAGALRNPLGHGEMLDVGYNSPIKGQEGHTVSAKLHLPHLFRTPVSGTLE-AIMDTV------------------------------VFE
Phytophtho : -------SLHVGATT-DGSDE-----A----------------GESTL------TLSNALGEAEKITLSATYARSGS--------NTQRATFKKPRFLGLP-LYLSAI------------------------------GTN
Phytophtho : -------SLHVGATT-DGNDE-----A----------------GESSL------TLSNALGEAEKITLSATYARSGS--------NTQRATFKKPRFLGMP-LYLSAV------------------------------GTN
Phytophtho : -------SLHVGATT-DGNDE-----A----------------GESSL------TLSNALGEAEKITLSATYARSGS--------NTQRATFKKPRFFGLP-LYLSAV------------------------------GTN
Physcomitr : -------SGDLGMFSKPETKA----WT----------------LEGTV------KYKNLAGLAETLDATGCYGLDTT--------SELSAGVTYPRFKGLP-ASLATR------------------------------LTL
Zea_mays_A : -------DGSVGCFSKPEARS----WT----------------VEGSV------RWRNIFGYGDIWDASGAYGWDQS--------SEISIGVSLPRFRSIP-TPSTAR------------------------------ASL
Sorghum_bi : -------TGTAGVYSKPEARS----WS----------------LEGSL------KLKNLFGYGDIWDASGSFGWDQT--------TEVGVGVYLPRFKSIP-TPLMAR------------------------------ASL
Oryza_sati : -------TGSAGVYSKPEARS----WS----------------LEGSV------KLKNLFGYGDIWDASGAYSWDQT--------SEVGIGVSLPRFKSIS-TPLMAR------------------------------ASL
Arabidopsi : -------TGQIGTFTKAEARS----SS----------------LEGSL------KYKNIFGYGDIWDGSLAYGCDHS--------AEVGLGMYLPRFRGRP-TPFTSR------------------------------VYL
Vitis_vini : -------TGDLGIFTKPEART----WS----------------LEGSL------KLKNLFGYGDLWDGSLVYGWDQS--------SEISAGVSLPRFKGMV-TPMLAR------------------------------VSL
Ricinus_co : -------SCEVGAYTKGEARS----ST----------------VEGTL------KYKNLFGYGDLWDSSVAYGGDHM--------TEVSAGVYVPRFKGRV-TPLTAR------------------------------LFL
Populus_tr : -------LGEIGVFNKGEASS----ST----------------LEGTL------KYKNIFGYGDLWDGSLAYDCDHK--------AEVSAGVFLPRFKGLV-NPVTAR------------------------------LFL
Ostreococc : -------HFKVGTYV-SKRGE----GE----------------AEATF------GLRNPLGYGEKFEVELIKGQNSS--------STYSAAWEQPKLYGSD-VNLDAR------------------------------AFQ
Micromonas : -------NLKGGAYV-SQQGE----GS----------------MEVSV------GLNNALGYAEKLDVEFIKGHERS--------NSCTLAWNQPRVGNVD-VDVVTR------------------------------AFQ
Micromonas : -------NLKGGAFV-SQARS----------------------MELSA------GVNNALGYAEKVDVEIARGHERS--------STYTLSWHQPRVRNED-VDVVTR------------------------------AFQ
Pichia_sti : -------YAKTGTNI--GNGE----GD----------------GYIQF------QLKNIFGGAENISFDAVTGTKTS--------SSYLLNYNQPVFNNAD--YISEN------------------------------SFS
Hydra_magn : -------SMNIGTSI--GANE----GG----------------MTMNA------NINNIRGYGETLKSGLSFGTRVS--------SAYEFAYIKPFSNDSD-KKFTIR------------------------------LIK
Ciona_inte : -------VGSISTEM--SNTE---RPR----------------WVARL------LSPNLFGRGETLSTDIAHQLNSTTGNHLYQPTDFSATFMKPMRG----SSVKLR------------------------------LLQ
Trichoplax : -------SAQFKTEV--GNQD----SR----------------LVIGG------KLRNLFGRAEELMGSIAYGAKKS-------------------------TTLQII-----------------------------------
Salmo_sala : -------TGSYNTMV--GNNE----GS----------------MVLGV------KLPNVFGRAEKLTFQFSYGTKET--------S-YGLSFFKPQPGNFE-RNLTLN------------------------------LYK
Danio_reri : -------TGSYNTMV--GNNE----GS----------------MVLGI------KLPNVLGRAEKLTFQFSYGTKET--------S-YGLSFFKPQPGHFE-RNFSLN------------------------------LYK
Xenopus_la : -------TGSYNTMV--GNNE----GS----------------MVLGL------KFPNLFGRAEKMTFQFSYGTKET--------S-YGLSFFKPQVGNFE-RNFSVN------------------------------LYK
Monodelphi : -------TGSYNTMV--GNNE----GS----------------MVLGL------KLPNIFGRAEKVTFQFSYGTKET--------S-YGLSFFKPQPGNFD-RNFSVN------------------------------LYK
Bos_taurus : -------TGSYNTMV--GNNE----GS----------------MVLGL------KLPNLLGRAEKVTFQFSYGTKET--------S-YGLSFFKPQPGNFD-RNFSVN------------------------------LYK
Mus_muscul : -------TGSYNTMV--GNNE----GS----------------MVLGL------KLPNLLGRAEKVTFQFSYGTKET--------S-YGLSFFKPQPGNFE-RNFSVN------------------------------LYK
Homo_sapie : -------TGSYNTMV--GNNE----GS----------------MVLGL------KLPNLLGRAEKVTFQFSYGTKET--------S-YGLSFFKPRPGNFE-RNFSVN------------------------------LYK
Macaca_mul : -------TGSYNTMV--GNNE----GS----------------MVLGL------KLPNLLGRAEKVTFQFSYGTKET--------S-YGLSFFKPRPGNFE-RNFSVN------------------------------LYK
Pediculus_ : -------IGGANTMV--GNNE----GS----------------LVVSL------RAPNMFGRGEKLQAEYSYGSRRT--------NNLSLSFVKPLRTKYD-AMFTSS------------------------------IFQ
Apis_melli : -------TGGISTMV--GNNE----GS----------------VIVHA------KAPNLFGRGERLQMEYSYGSKSS--------TNISISAVKPFIDNWRHTVLTGS------------------------------VFN
Tribolium_ : -------TGGVTTQV--GNNE----GA----------------LLIGL------RAPNLFGRGERVQLEYSHGSKRT--------TNFNVAFIKPMRGKYR-PMFTTS------------------------------VFQ
Laccaria_b : -------YVSSSTEL--GNNE----GS----------------ASASA------RVRNVFGGAETFTANLSLGTKTK--------RAFRASLVTPLTSDLD-TFGEVN------------------------------VYG
Coprinopsi : -------YLSSATEL--GNNE----GS----------------ASASA------RVRNVFGGAETFTANLSLGTKTR--------RSFTASLSAPLTPDLN-TFGEFS------------------------------VYG
Schizosacc : -------LAKTGTDI--GNVE----GN----------------VYANI------LARNAFGGAEFIEGNLSYGTRNR--------MLASLTFDTPINADPY-THFRVN------------------------------AIN
Neurospora : -------VFKAGTDF--GNAE----GS----------------AYTNA------VLRNIFGGAETLSVNAAAGTRTR--------SAYNAVFSTPVNGNPD-IRLALE------------------------------ALR
Nectria_ha : -------KLQTGTDV--GNGE----GS----------------AYGSL------LWRNMFGGAEMLTLNAKAGTRTR--------SAYSANLSMPVASNPD-LRISLE------------------------------GVA
Phaeosphae : -------TIKTGTEA--GASE----AD----------------AYVHA------ELRNLLGGAETLNAHGSLGTRTR--------SAYSLAFDSPILSNPD-LKFQVN------------------------------GFA
Aspergillu : -------LLKTGTDL--GNTE----GS----------------AYGNL------LWRNVFGGAETLNLNAAMGTRTR--------SAYQAAFETPILSDPD-FRFELG------------------------------GIA
Ajellomyce : -------LLKTGTDL--GNAE----GS----------------AYANF------MWRNIFGGAESLNVNASLGTRTR--------SAYQAAFDTPILSNPD-FRCEIG------------------------------GIG
Coccidioid : -------LLKTGTDL--GNAE----GS----------------AYANA------LWRNIFGGAETLNLNASLGTRTR--------SAYQATFETPILSDPD-FRFEIG------------------------------ALA
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                 *       580         *       600         *       620         *       640         *       660         *       680         *       700         *
Neorickett : KNRNE------KANGLYKFSSVGGDGSV---------SYSLRDD------------------------------------LRLHLGYSLSFDRI------FDVDGDAPE-----SVK-RSAGTKILSAVSYSLFLNK--LD
Rhizobium_ : NEHDF-------DDDNYSYNDQGFSLRVTAPI-----TENLSTT------------------------------------LRYNYT---ELEYF------GDQDELSSP-----YDRVVEDSPWTRSSVSQSVTYNT--LD
Rickettsia : NYTGRGASVLNTTDQSYKLHSIGVKISL---------GYDMKED------------------------------------LSHEIDYLIKRDIL------SAPSPSNSI-----FLN-EQMGKLITSAIGHTITYDQ--TD
Rickettsia : NYTGRGASVLNTTDQSYKLHSIGVKISLGYDM-----KEDLSHE------------------------------------IDYLI----KRDIL------SAPSPSNSI-----FLN-EQMGKLITSAIGHTITYDQ--TD
Magnetospi : IDRKL------QKESSYDASSIGGDLRAGYRL-----SESLRQD------------------------------------VIYTL----KQDT-------VKGISSTSP-----YVL-EQIGSKVSSVIGQSLMYDR--RD
Gluconacet : IQNNY------QTYQNYSEGRYGISFRMGYSY-----NNHLSQS------------------------------------FSYSLT---DRDI-------DNAYSDASW-----YVL-KQTGWSLLSQLSTTLTYDT--RD
Chlamydomo : LFRNN------Q-------------------------NMDGSQG------------------------------------LEYELG---WRRL-------LDPSRSASR-----AVMGQGVGPT-----DLMFQLPH--PA
Phaeodacty : -----------LPTAEIDHSLASPEY-----------TPDLYYG------------------------------------VEYSLL---SRDLVPRRQSKMPYAMDASP-----EVV-SQAGPSLKHSILAEFRSNGELLD
Thalassios : ADDAQ------YSLGGGSHTSLGIHAMVHDLDFE---STRSSKEFVRSIGVRLANHCRGAAGGSNKPGVSPPEAMAGPYLFLDVNAS---LRDTMPRRNAEFPFALDCSK-----EVA-SQAGTVFKHSLTGGMYLNGCFTD
Saccharomy : QFYNW------NTNKGLDIGQRGARLSLRYEPLFLHKLLHNPHS-----------------------------NESPTLFHEVFLETC-WRST------KICSQGTSAPYMYSGTML-SQAGDQLRTILGHTFVLDK--RD
Ectocarpus : DENTR-----QEHWTLTVERHASS-------------DVETRQA------------------------------------KRIT-------AIRTALSTA-----SCY-DQTLLLLLLLLLLLLLLLLLL--LL
Phytophtho : ELHNQ------EWLSSYSEKIRAGSISIS--------DYEGVHD------------------------------------LSLNVG---WRDLLPRRDAKVPTAYRASP-----SIL-AEAMPSTKTSVKYVFTDDN--RN
Phytophtho : ELHNQ------EWLSSYNEKIRAGSISIS--------DYEGVHD------------------------------------LSLNVG---WRDLLPRRDPKIPTAYRASP-----SIL-AEAMPSTKTSVKYIFTDDN--RN
Phytophtho : ELHNQ------EWLSSYNEKIRAGSISIS--------DYEGVHD------------------------------------LSLNVG---WRDLLPRRDSKIPTAYRASP-----SIL-AEAMPSTKTSVKYVFTDDK--RN
Physcomitr : LTQDW------QRYSSYRERLTGFSVGL---------VGDNQHD------------------------------------ISYNLT---WRDL-------KDPSRSASK-----SVR-RQLGHSLLSAVKYTYRRDT--RD
Zea_mays_A : LSHDW------LKFSSYKERLLGLSFGL---------LSDMHHD------------------------------------LSYNLT---WRTL-------TDPSQAASK-----SIT-RQLGHNLLSALRYTYTIDQ--RD
Sorghum_bi : SSQDW------LKFSSYKERLLGLSFGL---------LSTRNHD------------------------------------LSYNLT---WRTL-------TDPSHVSSK-----AIR-RQLGHNLLSALKYIYKIDK--RD
Oryza_sati : SSQDW------LKFSSYKERLLGLSFGL---------ISTMQHD------------------------------------LSYNLT---WRTL-------TDPSQVSSK-----SIR-RQLGHNLLSALKYTYKIDQ--RN
Arabidopsi : STQDW------LKFSSYKERALGLSLGL---------IASKYHE------------------------------------LAYNIA---WRNL-------IDPSQMASR-----SIR-RQLGHNLVSALKYTFKFDQ--RN
Vitis_vini : LSQDW------LKFSSYKERSLGLNLGL---------ISTKRHD------------------------------------LTYNLL---WRTL-------TDPSQMSSR-----AVR-RQLGHGLLSSLKYTFRIDN--RN
Ricinus_co : LSQDW------LRFSSYKERSLGLSLGL---------VSSRNHD------------------------------------LVYNLA---WRTL-------TDPSQMASR-----SIR-RQLGHGLLSSLKYTFKVDQ--RN
Populus_tr : QSQDC------LKFSSFKERSLGLSLGL---------FSTRNHD------------------------------------VVYNLA---WRTL-------TDPSRTASS-----SVR-GQLGHGLLSSLKYTFKIDR--RN
Ostreococc : SVECF------KKLSSFDVTSRGIRVGV---------AGDGPGT------------------------------------VDYEIA---WRDV-------QDPTRMASR-----EVR-RQLGHSLKSAVTHTYVSDR--LD
Micromonas : QVSCS------KRLSSFDETARGISVTA---------VGGGPAT------------------------------------VDYSLV---WREI-------ADPTRLASK-----SIR-QQLGHSLKSSVSYTYQVDE--RD
Micromonas : SVTCE------KRLSSFDETDRGVSVQV---------LGGGPAT------------------------------------LEYALV---LREI-------ADPTRLASR-----AVR-NQLGHSLKSSLSYSIGGDA--RD
Pichia_sti : TNTRK------WDWIQSNVKTFGFSNKIY---TQF--DGPVNHE------------------------------------FTVENY---WKVL-------ENLN-SKSI-----DVY-TQSGSHFKNSLIYNVSYDT--RN
Hydra_magn : SMEDK-------SQSLYNENTKGAGFDFQ---IP---SALGVHV------------------------------------FGLDFM---CRE--------NLINLEAPF-----SVR-ENAGHSLKSSIKHTLTSDG--RD
Ciona_inte : E-KQD------CYWSSYGMTIRGEVGVE---GS---VKGNTHR------------------------------------LSYVGH---WREL-------LCLNRNTAF-----DVR-EQMGHSLKSSIIHSMTMDR--VD
Trichoplax : ----------------------------------TEFGAHS------------------------------------LHFDSV---WREI-------QCLSDRSSW-----AVR-EESGHSLKCSIKHAFMRDT--RD
Salmo_sala : V-TGQ------FPWSSLKETDRGVSTELN---FP---LWRTNHT------------------------------------LKMEGV---WREL-------GCLARSASF-----AVR-EESGHTLKSALSHTMSIDT--RN
Danio_reri : V-TGQ------FPWSSLRETDRGVSAEIS---FP---IWRTSHT------------------------------------LKMEGV---WREL-------GCLARTASF-----AVR-EESGHSLKSSLAHAMVIDT--RN
Xenopus_la : V-TGQ------FPWSSLRETDRGVSAEIN---FP---IWKTSHT------------------------------------LKMEGV---WREL-------GCLARTASF-----AIR-EESGHTLKSSLSHTMVIDS--RN
Monodelphi : V-TGQ------FPWSSLRETDRGVSAEYS---FP---IWKTSHT------------------------------------VKMEGV---WREL-------GCLARTASF-----AVR-KESGHSLKSSLSHAMVIDS--RN
Bos_taurus : V-TGQ------FPWSSLRETDRGVSAEYS---FP---TWKTSHT------------------------------------VKMEGV---WREL-------GCLSRVASF-----AVR-KESGHSLKSSLSHSMVIDS--RN
Mus_muscul : V-TGQ------FPWSSLRETDRGVSAEYS---FP---LWKTSHT------------------------------------VKMEGV---WREL-------GCLSRTASF-----AVR-KESGHSLKSSLSHAMVIDS--RN
Homo_sapie : V-TGQ------FPWSSLRETDRGMSAEYS---FP---IWKTSHT------------------------------------VKMEGV---WREL-------GCLSRTASF-----AVR-KESGHSLKSSLSHAMVIDS--RN
Macaca_mul : V-TGQ------FPWSSLRETDRGMSAEYS---FP---IWKTSHT------------------------------------VKMEGV---WREL-------GCLSRTASF-----AVR-KESGHSLKSSLSHAMVIDS--RN
Pediculus_ : H-GSD------WPWSGYRVIERGVLFDLV---IK---ILQLRHN------------------------------------IQYEGA---WREM-------GTSSRSSAF-----DVR-QESGHKIKSALRHILTFDK--RD
Apis_melli : T-SNR------FPWSGFSQCDKGFLLDIG---LNPDGAGTLKHN------------------------------------LQYEAT---YREI--------ISSKQVSF-----RVR-EQCGPNLKSALRHICSIDK--RD
Tribolium_ : S-NAE------WPVSGYKQLDRGLLFDFG---FHS--TALIKHN------------------------------------IQMEAA---IRDL-------AVLSRNTSF-----EVR-EQAGLSLKSALRHIISIDL--RD
Laccaria_b : LERDQ------SSYASCSEGLRGVKAVVRNGT-----PETGTHE------------------------------------LGYEAV---VRHI-------SDLAPTASI-----SMR-EAAGESLKSSISHTYLFDT--RD
Coprinopsi : LERDQ------TSYASCFEGLRGLKAVVKGGT-----LEKGLHE------------------------------------MGYEAV---HRHV-------RDLLPTASI-----SMR-QAAGESIKSSIFHSYTLDT--RN
Schizosacc : VLRDN------KLIASHDILTRDVNASITHKD-----AWNGFHE------------------------------------LKQSLT---WRQV-------TNLVDTASP-----SIR-LAAGDSLKQAFSYSYTLDK--RD
Neurospora : -SSTH------KPWASHDEHLTGGNLRLAWST-----DNGDDHA------------------------------------LTYSGV---WRQL-------TGLSASASP-----TVR-ADAGDSLKSSITHTFTRDR--RD
Nectria_ha : SAAEK-------PWASHEEVLKGGTVRFSWLN-----SERDTQS------------------------------------VEYSHV---WRQI-------TGLGEGASP-----TVR-ADAGDSIKASIKHSFYRER--RD
Phaeosphae : S-STL------KSWASHEEVLRGGTSKLLWRS-----KTGHQHE------------------------------------LGYSGV---WRQV-------TSLAENASP-----TVR-ADAGDSFKSSITHAWTNDK--RD
Aspergillu : SSTQK-------SWANHEEVLKGGWSKLRWLS-----QSGHRHE------------------------------------IGYNGF---WRQV-------TGLAENASP-----TVR-ADAGDSVKSSIFHSWVADR--RD
Ajellomyce : SSTEK-------SWASHEEVVKGAWTKLRWLS-----PSGHRHE------------------------------------LGYNGF---WRQV-------TGLSTDASP-----TVR-GDAGDSVKSSISHTWVNDR--RD
Coccidioid : SDTQK-------SWASHEEVVKGAWSRLRWMS-----AAGHRHE------------------------------------LGLNGF---WRQV-------TGLAGSASP-----SVR-ENAGDSVKTSISHTWTKDQ--RD
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                    720         *       740         *       760         *       780         *       800         *       820         *       840         *
Neorickett : NYFVPRY--GYGVRFGNKFAGIG-----GDVKFLRSDFKAGGFVSIFD------------------------QSAVLSLVVRAGNIFGYSGQ---------GVDVA-NRFFL-------------NEMRGFDSLGIGPRDV
Rhizobium_ : DAQLPHE--GILASVTQEFAGLG-----GTSDFYKLTGKAKWYYTVND------------------------EADIIASLAGSAGHLFKTSGS----------MEVF-DQFQLGS-----------NDIRGFERNGIGPRVN
Rickettsia : NKIVPKN--GYLVSGTQEFAGVG-----GDNKYIKHEIECKFYKSFIN------------------------NKVTLKLSAAGGDMAGLGGK---------MVRIS-DRFNLGD-----------YSLRGFASGGVGPREK
Rickettsia : NKIVPKN--GYLVSGTQEFAGIG-----GDNKYIKHEIECKYYKSFIH------------------------NKVTLKLSAAGGDMAGLGGK---------IVRIS-DRFNLGD-----------YSLRGFASGGVGPREK
Magnetospi : SRLDPTE--GYFIKLGTDGAGLG-----GDIRYLRGTLTGGQYFTL-T------------------------DKVILGVSSSVGYIYGLDQR----------VRIT-DRFFVGG-----------DNLRGFANGGVSPRDK
Gluconacet : NRMNPHS--GYVVRLAGDFAGIG-----GNERYLRGKLDAAYYIPLDDLMGN---------------------HDWTVALTAGAGDIVNWGGG---------RSDII-DNFYLGG-----------STLRGFMDGGAGPRTM
Chlamydomo : LKLLRLH--GHAFVNGGNVIQLA-----GTGRSPSELLSE--------------------------------FGSSWRWSCGTGLVLPTPFGRFEANYCVLLSSQEHDRNSL------------VLSLLGLALI-------
Phaeodacty : HPYSPTG--GVEMHGSAEVAVPP-----GSVGFVRCNGGFGIHMPL-L------------------------QSLSVHSIFNAGYLKALSFG-----GLCRPPTLS-DRYYVGG----------PLRFRGFVPAGIGPRTK
Thalassios : DRYDPTM--GYDAHVLGEVAG--P---PGDVGFWKLKGGGSWHLPL-ELIGMMAFGVNEEEYTSKEEDESPVVIGATLHSSFNAGLIRPLSFSGLCNSGSIGGVPSS-DKFYVGG----------PGQLRGFLPSGIGPRSA
Saccharomy : HIMCPTK--GSMLKWSNEL---------SPGKHLKTQLELNSVKSW-MND-----------------------DFITFSTTIKTGYLKNLSSQ------QSLPVHIC-DKFQSGG----------PSDIRGFQTFGLGPRDL
Ectocarpus : LLLLPSPPVGDTHTFGMRI-GLM-----GDTSFAKGMLEMQRHIPL-FGVELGPET----------------YSPVTLSLCASGGAIRPFGPS--------KRTFFS-DRFNLGG----------PMTLRGFPFYGAGPRSP
Phytophtho : NVVYPTA--GGLFKYTTEIAGLV-----GDVKFVKAEVEGQKHVAV-GPNVFG------------------FPILNFSLSCHLGTVKSYGNE------QHRPARIS-DRFFLGG----------PMNVRGFNHKGIGPRAS
Phytophtho : NAVYPTA--GGLFKYTTEIAGLV-----GDVKFVKAEVEGQKHVAL-GPVVFG------------------FPILNFSLSYHVGTVKSYGSE------QHRPARIS-DRFFLGG----------PMNVRGFNHKGIGPRAS
Phytophtho : NVVYPTA--GGLFKYTTEIAGLV-----GDVKFVKAEVEGQKHVAL-GPVLNG------------------FPILNFSLSYHLGTVKSYGSE------QNRPARIS-DRFFLGG----------PMNVRGFNHKGIGPRAS
Physcomitr : SVFRPRR--GIAFISTTQIAGLGP--DAKLLRFARQEVELRLAIPLGL------------------------ANAALNLGVAGGIILPWGPG-----YKTKATPIG-DRFYVGGHSSLLGELKGPSALLGFRTRGVGPNEL
Zea_mays_A : SHLRPTK--GYAFVSTSQVSGLWG---SKGLRFFRQEFDIRGAVPLGF------------------------YNAALNAGISAGVILPLGRG-----FMESPSSVP-DRFFLGGHSSPVISLCSLTSLLGFKTRGVGPTEL
Sorghum_bi : SHLRPTK--GYAFQSTSQVGGLW---NSKGLRYFRQEFDVRGAVPLGF------------------------YNAALNVGVGAGVILPLGGG-----FMNSTSPVP-ERFYLGGNSSPVCSLGGLSSLLGFRLRGVGPTEA
Oryza_sati : SHLRPTK--GYAFLSTSQVGGLW---DSKGLRFFRQEFDVRGAVPLGF------------------------YNSALNVGLGVGAILPLGRG-----FMNLSSSVP-DRFYLGGHSSPVCSLSGLSSLLGFRTRGIGPTEP
Arabidopsi : SSLRPTR--GYSFISTSQIGGLAP--DSRTLRFLRQEIDLRYAVPLGF------------------------YRAALNFGIAGGITFPWGSG-----YKSRASCVP-ERFFLGGNISPVCSLGGPSALWGFKTRGLGPNEP
Vitis_vini : SVLRPTQ--GYAFISTSQIGGLVP--DYRSLRFLRQEIDLRCAIPLGF------------------------YRTALNLGISGGVIFPWGNG-----ALSMPSSLP-ERFFLGGNSSPVCTLGGPTTLLGFKSRGLGPTER
Ricinus_co : SPLRPTH--GYAFVSTTQVGGLAP--DSRSLRFLRQELDLRCAIPLGF------------------------LRSALNLGISVGVVFPWGTG-----FSNMPSPLP-ERFFVGGNLSPVCTLGGPMAFYGFRTRGLGPTEP
Populus_tr : SPLRPTR--GFAFVSTTQIGGLAP--DSRSLRFLRQELDLRCAIPLGF------------------------YHSALNLGISAGVVFPWGSG-----FSSMPSPLP-ERFFLGGNLSPVCTLGGPTSLWGFRTKGLGPTEP
Ostreococc : RQVRPTS--GYLWKIRSELAGIGFMDNALAAKFVKSEVSAHVVETL-DAS------------------------RGITASASGRFGVLFPWGKS---GNDGDSRTCIA-DRFFLGG----------VGCLRQFENNGVGPSDA
Micromonas : RPVRPGA--GYLARVRSELAGVGW--DPQMTRFLKHEAEVQAAHTP-A------------------------EGVTFFASAKLGAMMPLGQN---AKDPEKGTCIA-DRFFLGG----------VGSLRGFEPHGAGPSDE
Micromonas : RAVRPTT--GALWRLRSELAGIGF--DRNATRFFKQEAEVKAFKRL-A------------------------EGVTWHLGGKLGALVPLGAA---AREDQRGTCIA-DRFFLGG----------VGSLRGFEPRGVGPSDV
Pichia_sti : NKHLPTQ--GKFLRFGVEYNGLF---KFTTSPFIKSVFESQFVYAF-PKN------------------------WYTSVILTGKSGFLFPLNKT----------TSVL-DRFYIGG----------PNDVRSFTLNGLGPKDY
Hydra_magn : DWIFPSS--GHLVKHSVEYSGIG-----GNVKSIKSDLELQINKEI-I------------------------PNVVVSCSFQGGVVRSLTSD---------LLLIN-DRLFLGG----------PVSIRGFAMRGIGRHDG
Ciona_inte : DVILPMR--GGLVKMEEEVAGVG-----GDVSFIKETMEAKVAATI-F------------------------DKITFVASMHCGVMVGW----------RGVSVC-DKFFIGG----------PLTLRGFELNSVGARSG
Trichoplax : HSVSPTT--GHFIRFEQEHAGLG---SLGDTKFHRFFLECQYNKTL-P------------------------YNIVFSSSLNLGLLASDGQS----------KIS-DRFFLGG----------PLSIRGFQMRGIGPHSE
Salmo_sala : SAIFPKK--GALLRINQELAGYTG----GDASFLKEDFELQVNRRL-V------------------------WDSVLSASLWGGCLLPIGGR---------PSSIA-DRFYLGG----------PTSVRGFGMYSIGPQSE
Danio_reri : STILPRK--GALLKINQELAGYTG----GDVSFLKEDFEIQLNKTL-F------------------------WDSVLSTSLWGGMLLPLGEK---------ASSIA-DRFYLGG----------PTSVRGFSMYSIGPQSE
Xenopus_la : ASILPKR--GALLKINQELAGYTG----GDVSFLKEDFELQLNKQL-A------------------------WDSVLSTSLWGGMLVPVGDR---------PSSIA-DRFYLGG----------PTSVRGFSMYSIGPQSE
Monodelphi : SSILPRK--GTLLKVNQELAGYTG----GDVSFLKEDFELQLNKQL-F------------------------FDTVLSGSLWGGMLVPIGEK---------PSCIA-DRFYLGG----------PTSVRGFSMYSIGPQSE
Bos_taurus : SSILPKR--GALLKVNQELAGYTG----GDVSFLKEDFELQLNKQL-I------------------------LDTVFSASLWGGMLVPMGDK---------PSSIA-DRFYLGG----------PTSVRGFSMHSVGPQSE
Mus_muscul : SSILPRR--GALFKVNQELAGYTG----GDVSFIKEDFELQLNKPL-A------------------------LDSVFSTSLWGGMLVPIGDK---------PSSIA-DRFYLGG----------PTSVRGFSMHSIGPQSE
Homo_sapie : SSILPRR--GALLKVNQELAGYTG----GDVSFIKEDFELQLNKQL-I------------------------FDSVFSASFWGGMLVPIGDK---------PSSIA-DRFYLGG----------PTSIRGFSMHSIGPQSE
Macaca_mul : SSILPRR--GALLKVNQELAGYTG----GDVSFIKEDFELQLNKQL-I------------------------FDSVFSASLWGGMLVPIGDK---------PSSIA-DRFYLGG----------PTSVRGFSMHSIGPQSE
Pediculus_ : AQIFPSS--GTLFRFTTELAGLG-----GDIKFLKNDFFAQYNFPL-I------------------------ADMVLQATLQAGYLQPLGDG--------EAVGLP-DKFYVGG----------PMSVRGFETRGVGPRSD
Apis_melli : SLIFPTM--GSLVQFSTEVAGLG-----GDIGFVKNELTMQTNWSP-Y------------------------ECLTFQLGFQSGLLRGISND--------MKINIA-DHFFLGG----------PLNLRGFDMRGCGPRHD
Tribolium_ : DLIFPTS--GSLLQLTSEVAGLG-----GDVGFLKNEFFIQGNYSL-V------------------------EDFVLQGTLSGGFMRGLSND--------MKIGMS-DMYYLGG----------PLTLRGFQMRGVGPHSE
Laccaria_b : DRMMAKK--GVYAKLYHEFAGLG-----GDASFYKAEAEGQVSRPV-S------------------------NGVSISLAARAGLLSSLKGS----------TLFS-DRFQLGG----------PTSIRSFKANSMGPRDG
Coprinopsi : DRIAATR--GGYVKFYHEFSGLG-----GDASFYKTEAEGQVSRPL-I------------------------PGLSFSLAGRTGLL--WGLN--------KPLLFS-DRFQLGG----------PTSVRSFKANGLGPHDG
Schizosacc : NPALPTK--GGLLKYMLELAGMGP--IIGDAKFVKNEIWSQLSIPL-NVS------------------------HSSCATVGLRAGAIHDLDNE---------TIGIC-DRFYLGG----------PTSLRGFTEGRIGPKDG
Neurospora : NPMLPQA--GYLVRTAAELAGWGP--LKGDVSFAKSEVELSAAQALPL------------------------PGVSVGAGFRAGLLYPLPMGYSLSSTSVAPSRIN-DRFQLGG----------PTDVRGFSMGGLGPHDG
Nectria_ha : NPQLPQD--GYMVRTGLEVAGFGP--LVGDVAFSKGEVEVGGAIPV-PLPGIKD------------------RTGISIGGGLRLGLLCPLPLG-YDFGGKLGLSRIN-DRFQLGG----------PTDVRGFKLGGLGPRD-
Phaeosphae : YPLLPSS--GYLMKTVSELAGFGG--LSGDVAFFKSEAESQVALPFGN------------------------TGITLTAGLRGGLIYPLALP---GQNQPQGSRIN-DRFILGG----------PNNVRGFRLAGLGPHDG
Aspergillu : NPLLPSR--GYYAKAFNELAGWGP--LKGDVSFWKSEVEAQGAIPI-PIPGIKG------------------DSGISFTTGFRAGLLYPLGLD---SDSRPQLSRIN-DRFVLGG----------PTDVRGFRLCGLGPHDG
Ajellomyce : NPLLPSR--GFYTRTFNEVAGLGP--LKGDVSFWKSELEAQGAVPI-PIPGVKG------------------DSGISLTTGFRAGILYPLGLD---ATQKPQLSRIN-DRFQLGG----------PTDVRGFRLAGIGPREG
Coccidioid : NPILPTK--GFYAKTLNELAGWGP--LKGDVSFWKSEIETQAAVPV-PIPGLKG------------------DSGISFTAGFRAGLIYPLGMD---SNSKPQLSRIN-DRFQLGG----------PTDVRGFRISGLGPRE-
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                 860         *       880         *       900         *       920         *       940         *       960         *       980         *
Neorickett : DT---------------------------GDALGGNSFILGTAEVQVPMR---L--PVELD-------LKAAFFYEVGTLAGVDV-----------------------TAEKVYD----SHA-LRSSIGAGLVWNSP-FGV
Rhizobium_ : N----------------------------GDALGGTTYFTASAEASFPLP---G---IPRDSG-----FRGALFVDAGTLYGNDV-----------------------ALTGAGEFAEGTDASLRVSVGVSLIWASP-FGP
Rickettsia : NT---------------------------NEGLGGERYYTFSTELNFPTP---V----PEEFN-----FTGAVFIDLGSV--WGV--GLN------------------KKQYKTPNGFYNDQSLRASVGFGFIWVTR-FAP
Rickettsia : NT---------------------------NEGLGGEKYYTFSTELNFPTP---T----PEEFN-----LTGAVFIDLGSV--WGV--GLN------------------KKQYKTPNGFYNDKSLRASVGFGFIWVTR-FAP
Magnetospi : NT---------------------------GDALGGIWQAVGSAQVKFPLG---L----PEEFG-----VSGQAFTDIGAVGETDT-----------------------ADTAAVQQ---SSS-VRVSPGVGISWKSP-MGP
Gluconacet : GIPAYTWQGVTYPMHSQ------------EDFLGGRFMYTGSATVNFPMP---L----AADMG-----IKGRYFVDMGLDGLRI--PRR------------YTAYPQDMPYYTPVYSDTIK-PRVSTGVGFSWKSP-FGL
Chlamydomo : ----------------------------SSYSLDIDTICNFLDLDLDPA---I--RIARSNH-----VDSSSEEAVEDLVLWRK-----------------------PKEAGAIF---GGA--TAAYLADIMHTRSAAPG
Phaeodacty : HG------------GSSTPG----------GDAVGGDFFYTATAMASI-------------------------------------------------------------------------------TP-TSG
Thalassios : KG------------GSSVPG----------GDSLGGDVYYTTTLAGSIPFP---SYFATLRQNG-----ARVFGFTNVGTCVSTGG--SVL------------------GMPAFSQI---LQS-SRVAVGGGVSVGSP-MGR
Saccharomy : ------------------------------YDAVGGDAFVSYGLSVFSRLP---W--KKVEKSN-----FRLHWFFNGGKLVNHDN---------------------TSLGNCIGQL---SKE-HSTSTGIGLVLRHP-MAR
Ectocarpus : KE------------EGGCEG----------GDALGGDIRYTASASLGFPFP---V--PAMATAG-----WRGYLFTNLGNLTTWDT--------------------------PLKQY---GRD-TRVSVGVAAAWNFLGVGR
Phytophtho : PL------------DGGVAQ----------GDALGGDVSYNGTASVGFPVP---L--PLLAALG-----LRGQLFANAGNLTTWDR--LLD------------------EKKWMKNL---ADD-TRVSIGLGLVWGTR-IGR
Phytophtho : PL------------DGGVAQ----------GDALGGDVSYNGTAALGFPVP---L--PLFAALG-----LRGQLFANAGNLTTWDR--LLD------------------EKKWMKNL---ADD-TRVSVGLGLVWGTR-IGR
Phytophtho : PL------------DGGVAQ----------GDALGGDVSYNGTASLGFPVP---L--PLFVALG-----LRGQFFANAGNLTTWDR--LLD------------------EKKWLKNL---TDD-TRVSVGMGLVWGTR-IGR
Physcomitr : RRTTASQTDKVDSEVETSLK----------RDTLGGDLAVSGFADISFDLP---M--QFLKSYG-----IHAHTFACAGNLVPLTG--NNT------------------TQWSLRNF---LSG-FRVSSGAGIVIPTK-LFR
Zea_mays_A : RRIVPSESVTNE--STASPG----------WDYLGGDFAVSAFADLSFDLP---L--KLFQDAG-----IHGHAFLSAGNLAKLSE--GEF------------------RNFSFSKF---GRT-FRSSAGVGIILPTK-LLR
Sorghum_bi : RRHVLDKPES----GSGDPG----------RDYLGGDLAVSAFADLSFDLP---L--KIFRDAG-----IHGHAFLTAGNLAKLSE--GEY------------------KNFTASEF---QRT-FRSSAGVGIILPTK-LFR
Oryza_sati : RRLVPSESEDG---SAASPG----------RDYLGGDLAVSAFADLSFDLP---L--KIFRDAG-----IHGHAFLTAGNLAKLSE--GEY------------------KKFSLSEF---GRT-FRSSVGAGIVVPTS-LFR
Arabidopsi : RREVQDDE------SGDTYE----------RDFVGGDVAVTAFADLSFDFP---L--KWFRDRG-----IHGHVFACAGNMAELSE--NKY------------------RNFTAPKL---LET-FRSSVGAGIVVPTS-LFR
Vitis_vini : RRLIRDKSNGE---NSETSG----------RDVIGGDLAVTAFADLSFDLP---L--KLFRDAG-----IHGHVFACAGNLTKLTE--NEF------------------RKFSFQKF---LDS-FRSSAGFGIIVPTK-LFR
Ricinus_co : RRQLQSNSTD----DSADPG----------RDYLGGDLAVTAFADLSFDFP---S--KWCQAKG-----IHGHVFASAGNVDKLTE--NAY------------------RNFSLQKF---VES-SRSTVGVGIVVPTN-LFR
Populus_tr : RRQLQNNPADENADSG--------------RDYLGGDLAVAAFADFSFDFP---S--KWLSAKG-----IHGHLFASAGNVDKLTE--NSY------------------RNFSLQKF---TQS-FRSSVGVGVVIPTN-LFR
Ostreococc : RRGTKKTAAAEESPGAKTPSSAEDGEPSLTRDALGGDFVWSATAALQMDIPGEKF--EAMREAG-----IHFHAFATAGTLLPLAALSGA------------------PKDAIKVV---RDA-TRASLGVGIVWPLP-IGQ
Micromonas : RRPPPTKAAAS---GENLIT----------RDALGGDVLAQLFASYQLEPE---W--SKLRDIG-----VYGHFFVNAGTLMPWIT--GER------------------KRVSGREL---ADS-FRASVGVGLVFPLP-VGN
Micromonas : RRPPKDPAAAAAAGMSS------------RDALGGDLLAQAFTAVQATPT---W--SKLSDIG-----VYAHAFANVGTLARVNTPGVAA-----AAAAAAGEGGDGDRPSSAREF---LEG-FRGSLGVGLVFPLP-VGN
Pichia_sti : ----------------------------NSSIGGDMFINGGLSFISKIP---R---VSSESN-----FKLHNFVNFGKLVPMDK--SAG------------------FVRNFKSV---VGD-FSLSYGFGILYNHP-MAR
Hydra_magn : ----------------------------QASLGGEKYWASGLHLYTPLP---F-RPGQGGFG---DLFRLHLFFNAGSLSDFNT--------------------------CFRDF---ISK-PRYSYGLGVMIMLGAVAR
Ciona_inte : ----------------------------GDYLGSGAFWLSGLHIYTPLP---F-YWSRFGGGSWLDNFRTHAFVNGGNSFDVNI--TES------------------AGANFNAA---TNN-VRLSCGIGLVYKFMNSAR
Trichoplax : ----------------------------GDSIGGNALWASGLHLISPLP---F-KPLQGGFG---ERLRTHLFVNAGNLGHIRS--SA-------------------IRDSTEEL---IRG-YRWSYGIGLLVKLG-VAQ
Salmo_sala : ----------------------------GDYLGGEAYWAGGLHLYTPLP---F-RPGRGGFG---DLFRTHFFLNAGNLCNLNY--GEG------------------PRAHLQKL---AEC-IRWSYGAGIVLRLANIAR
Danio_reri : ----------------------------GDYLGGEAYWAGGVHLYTPLP---F-RPGRGGFG---DLFRTHFFLNAGNLCNLNY--GEG------------------PRAHLSKL---AEC-IRWSYGAGIVLRLGNIAR
Xenopus_la : ----------------------------GDYLGGEAYWAGGVHLYTPLP---F-RPGRGGFG---DLFRTHFFLNAGNLCNLNY--GEG------------------PRAHLQRL---AEC-IRWSYGAGLVLRLGNIAR
Monodelphi : ----------------------------GDYLGGEAYWAGGLHLYTPLP---F-RPGQGGFG---DLFRTHFFLNAGNLCNLNY--GEG------------------PRAHLRKL---AEC-IRWSYGAGIVLRLGNIAR
Bos_taurus : ----------------------------GDYLGGEAYWAGGLHLYTPLP---F-RPGQGGFG---ELFRTHFFLNAGNLCNLNY--GEG------------------PKAHIRKL---AEC-IRWSYGAGIVLRLGNIAR
Mus_muscul : ----------------------------GDYLGGEAYWAGGLHLYTPLP---F-RPGQGGFG---ELFRTHFFLNAGNLCNLNY--GEG------------------PKAHIRKL---AEC-IRWSYGAGVVLRLGNIAR
Homo_sapie : ----------------------------GDYLGGEAYWAGGLHLYTPLP---F-RPGQGGFG---ELFRTHFFLNAGNLCNLNY--GEG------------------PKAHIRKL---AEC-IRWSYGAGIVLRLGNIAR
Macaca_mul : ----------------------------GDYLGGEAYWAGGLHLYTPLP---F-RPGQGGFG---ELFRTHFFLNAGNLCNLNY--GEG------------------PKAHIRKL---AEC-IRWSYGAGIVLRLGNIAR
Pediculus_ : ----------------------------GNATGSNVALAGGLHLYTPLP---F-RPGKGGFG---DLFRVHFFLNMGQCKEYEF--GNG------------------VTEDVKNI---LDG-YRLSYGCGLALRLGQLAR
Apis_melli : ----------------------------GNSIGGDAYWALALHLYTPLP---F-RPGRNGFG---DLFKLHGFINGGNVSNFTFKFAND------------------YKENMKIF---KEN-VRCAVGGGIAMKLGNIAR
Tribolium_ : ----------------------------GDALGSMAYWASGLHLFSPLP---F-RPGRGGFG---DLFKTHLFITAGNVGDFSL----S------------------DKNLIDSL---TAS-VRISYGVGIALRLGNMAR
Laccaria_b : ----------------------------PDYIGGDIYYSAGASLISNIP-------KKPHWP-----VKAHLWVNAGRLDALDK-----------------------SRPLLESIQNTLSR-PSISAGVGLIYRFD-PIR
Coprinopsi : ----------------------------QDSIGGDIYYSVGASLIGDIP---N----KAHWP-----LKGHLWVNAGRLEQVDR--ARP------------------LTDNVKDM---LAR-PSISAGLGLIYRFD-PVR
Schizosacc : ----------------------------KDCLGGTAYLAASASLTSPVP---G---VNPSKP-----FRMQFFINAGGLRMLDQ---RQ-----------------PLRTFRDI---IQK-PCVISGIGLIYATG-VAR
Neurospora : ----------------------------ADSVGGDVFAAGSVNMLLPLP------RAGPTSP-----LRFQLFANGGRLVALQGKKTAE-----GSVSLDSGAVASGMKSAVAEL---ANGLPSIAAGFGLVYAHP-VAR
Nectria_ha : -------------------G----------ADSVGGDVFAAGSVNMLLPVP---Y---KGPDSG-----LRFQLFANGGRLVALKN--PNKSSSGAATQTLRPSAVRDGMLNAVGEL---FNGVPSLAAGVGLVYAHP-VAR
Phaeosphae : ----------------------------SDAVGGDVYAAGGASLLLPVP------RVGKDTP-----LRLQAFINGGRLLSLKGQKGQQ---------------TSLSQTFASL---TDELPSVAAGIGLVYAHP-IAR
Aspergillu : ----------------------------ADAVGGDVYAAGSANLFLPLP------RVGADKP-----LRLQAFVNGGRLLPLRTLQKEA--------PTNSTEVKDAMTATISEL---GNGLPSVAAGIGLVYAHP-VAR
Ajellomyce : ----------------------------PDALGGDVFAAGSANLLFPLP------RVGAEKP-----LRLQAFVNAGRLLPLKTQDRKL--------PSTQGEVRDSMVATVSEL---GNGLPSMAAGLGLVYAHP-AAR
Coccidioid : -------------------G----------PDALGGDVYAAGSANLLCPLP---R---VGADKP-----FRLQAFVNAGRLLALKT--PQGAS------PTSPQEVRESVASTLSEL---ANGLPSTAAGVGLVFAHP-VAR
```

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                1000         *      1020
Neorickett : LRVDVAKALIEGKGDKVK--TVKF---GIVSPF--
Rhizobium_ : LRVDYAVPVAKEDFDEIQ-N-FKF---GINSSF--
Rickettsia : IRMDWGFPIKKKQYDDTQ--NFHL---RFSTHL--
Rickettsia : IRMDWGFPIKKKQYDDTQ--NFHL---RFSTHL--
Magnetospi : VSVDLGYPLVKEKFD-KK-EFFRF---NFGTKF--
Gluconacet : INIDLGIPVLKEKHDRTR-L-FRF---GFGQQF--
Chlamydomo : TPASIHTELAQLPGPTVS-PRLDLFHPSLGPTHS-
Phaeodacty : IQSVDSLRLRVVLG--------------------
Thalassios : FEATYAVPMRYGPRDATK--AVQF---GFGFSFG-
Saccharomy : FELNFTLPITAHENDLIR-KGFQF---GLGLAFL-
Ectocarpus : LEINYAHVLRRSPRDLHRERPLQF---GFGVSFE-
Phytophtho : LEANYSWILKAHDHDNIK-R-AQL---GLGMTFC-
Phytophtho : LEANYSWILKAHDHDNIK-R-AQL---GLGMTFS-
Phytophtho : LEANYSWILKAHAHDNIK-R-AQL---GLGMTFC-
Physcomitr : LEVNYCYLLRYQENDRIK-RGVQI---SLNSPQ--
Zea_mays_A : AEINYCYILKQFEHDRGK-TGIQF---SFSSPM--
Sorghum_bi : VEVNYCHILKQAEHDSSK-TGIQF---SFSSPM--
Oryza_sati : VEVNYCYILKQAEHDSGR-TGIQF---SFSSPL--
Arabidopsi : MELNYCHILKKQEHDRAK-SGFFM---TFSTSS--
Vitis_vini : MEVNYCYILKQFEHDHGR-TGVQF---SFSAT---
Ricinus_co : LELNYCFILKKFEYERGK-SGFRV---SFSTPS--
Populus_tr : MELNYCNILKKFGEDRGK-SGFRV---SFSSPS--
Ostreococc : IEMNYGKVVRAGTNDRVS-DGFQV---GIAAHVSM
Micromonas : IEVNYCHTLRSRPGDRVK-NGLQI---GLATALA-
Micromonas : IEVNYVKTVRAGANDRVK-DGLQV---GLATQMSI
Pichia_sti : FELNFVLPLVVHDRDYVR-KGLQY---GIGVSFL-
Hydra_magn : LEINYCIPKNAQAGDVIN-NGLQV---GVGMSFL-
Ciona_inte : IELNFCVPLRNVPTDKVV-NGLQF---GIGVTSV-
Trichoplax : LELNYCVPCRAHATDRIS-PGFQF---GVGLSFL-
Salmo_sala : LELNYCIPMGVQSGDRIC-DGVQF---GAGIRFL-
Danio_reri : LELNYCIPMGVQSGDRIC-DGVQF---GAGIRFL-
Xenopus_la : LELNYCIPMGVQSGDRIC-DGVQF---GAGIRFL-
Monodelphi : LELNYCIPMGVQRGDRIC-DGVQF---GAGIRFL-
Bos_taurus : LELNYCVPMGVQRGDRIC-DGVQF---GAGIRFL-
Mus_muscul : LELNYCIPMGVQGGDRIC-DGVQF---GAGIRFL-
Homo_sapie : LELNYCVPMGVQTGDRIC-DGVQF---GAGIRFL-
Macaca_mul : LELNYCIPMGVQTGDRIC-DGVQF---GAGIRFL-
Pediculus_ : VEFNYVIPLKAQDADVTA-EGFQF---GVGLQFL-
Apis_melli : VELNLVMPLLFVRSDVLQ-Q-FQF---GIGLQYL-
Tribolium_ : VEVNYCFPHTFEKGDQIH-PGIQF---GIGVQFV-
Laccaria_b : VEVNFGVPLVASKSDGSR-RGIQV---GMGLEFL-
Coprinopsi : VEVNLGVPLVASKSDGTR-KGIQV---GVGLEFL-
Schizosacc : FELNFTLPLMTTVKDLGR-RGFQL---GAGLEFL-
Neurospora : FELNFSLPLVVRRGEEAR-KGLQV---GVGINFL-
Nectria_ha : FELNFSLPLALRRGEVST-KGLQV---GVGINFL-
Phaeosphae : FEINFSLPLVVRAREESR-KGLSF---GVGIEFL-
Aspergillu : FELNFSLPLVLRKGEEGR-KGLQL---GIGINFL-
Ajellomyce : FELNFSLPLILRRGEEGR-KGLQF---GIGINFL-
Coccidioid : FELNFSLPLVLRKGEEGR-KGLQL---GIGISFL-
```

(e) YidC, Oxa1, Cox18/Oxa2, Alb3 amino-acid alignment (p. 17-22)

```
                        *        20         *        40         *        60         *        80         *       100         *       120         *       140
Cme_Alb3   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Ptr_Alb32  : ------------------------------------------------------------------------------------------------------------------------------------------------------M
Tps_Alb32  : ------------------------------------------------------------------------------------------------------------------------------------------------------
Ota_Alb3_1 : ------------------------------------------------------------------------------------------------------------------------------------------------------
Olu_Alb3_1 : ------------------------------------------------------------------------------------------------------------------------------------------------------
Ptr_Alb31  : ------------------------------------------------------------------------------------------------------------------------------------------------------
Tps_Alb31  : ------------------------------------------------------------------------------------------------------------------------------------------------------
Cme_Oxa1   : ------------------------------------------------------------------------------------------------------------------------------------------------MGVDPA
CreAlb3_1  : ------------------------------------------------------------------------------------------------------------------------------------------------MSPSDLGD
CreAlb3_2  : ------------------------------------------------------------------------------------------------------------------------------------------------MAVSRRPA
OtaAlb3_2  : ------------------------------------------------------------------------------------------------------------------------------------------------MFNAHA
OluAlb3_2  : ------------------------------------------------------------------------------------------------------------------------------------------------------
OsaAlb3_a  : ------------------------------------------------------------------------------------------------------------------------------------------------MAGLDLHA
AthAlb3_a  : ------------------------------------------------------------------------------------------------------------------------------------------------MASVDIGA
PAlb3_a1   : ------------------------------------------------------------------------------------------------------------------------------------------------MASVDFNT
PAlb3_a2   : ------------------------------------------------------------------------------------------------------------------------------------------------MASIDFNS
OsaAlb3_b  : ------------------------------------------------------------------------------------------------------------------------------------------------MDFAEVGE
AthAlb3_b  : ------------------------------------------------------------------------------------------------------------------------------------------------MSPDSFD
PAlb3_b2   : ------------------------------------------------------------------------------------------------------------------------------------------------------
PAlb3_b1   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Syn_YidC   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Pma1_YidC  : ------------------------------------------------------------------------------------------------------------------------------------------------------
Pma2_YidC  : ------------------------------------------------------------------------------------------------------------------------------------------------------
Tps_Oxa2   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Ptr_Oxa2   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Esi0025_01 : MLTGARLSRQSRRLVGRVHGNGASLTAPAIAENRLTHHDGSDNSKRTCRGYLRPPQHLLQAQTLHVPALQQRGHRSSSVTRLGGDGSAIGAAALGGGRGLDLSAAWRGAAAAGGTVGARRSFWGRSGGDGSQAGSSGSGSDS
Mbr_Oxa2   : ------------------------------------------------------------------------------------------------------------------------------------------------MAA
Ptr_Oxa1   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Tps_Oxa1   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Yli_Oxa1   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Cal_Oxa1   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Sce_Oxa1   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Mbr_Oxa1   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Hsa_Oxa1   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Cfa_Oxa1   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Mmu_Oxa1   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Aga_Oxa1   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Dme_Oxa1   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Pin_Oxa1   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Pra_Oxa1   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Pso_Oxa1   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Ota_Oxa1   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Olu_Oxa1   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Osa_Oxa1   : ------------------------------------------------------------------------------------------------------------------------------------------------MALALSH
AthOxa12   : ------------------------------------------------------------------------------------------------------------------------------------------------------
AthOxa11   : ------------------------------------------------------------------------------------------------------------------------------------------------------
POxa11     : ------------------------------------------------------------------------------------------------------------------------------------------------------
POxa12     : ------------------------------------------------------------------------------------------------------------------------------------------------------
Cme_Oxa2   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Esi0028_00 : ------------------------------------------------------------------------------------------------------------------------------MSTAAGTGHSGDVATTADLGPDAMAGGADA
Mmu_Oxa2   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Hsa_Oxa2   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Cfa_Oxa2   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Aga_Oxa2   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Dme_Oxa2   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Yli_Oxa2   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Cal_Oxa2   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Sce_Oxa2   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Olu_Oxa2   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Ota_Oxa2   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Esi0170_00 : ------------------------------------------------------------------------------------------------------------------------------------------------------
Pra_Oxa2   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Pin_Oxa2   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Pso_Oxa2   : ------------------------------------------------------------------------------------------------------------------------------------------------------
Osa_Oxa2   : ------------------------------------------------------------------------------------------------------------------------------------------------------
AthOxa21   : ------------------------------------------------------------------------------------------------------------------------------------------------------
AthOxa22   : ------------------------------------------------------------------------------------------------------------------------------------------------------
POxa2      : ------------------------------------------------------------------------------------------------------------------------------------------------------
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                    *       160         *       180         *       200         *       220         *       240         *       260         *       280
Cme_Alb3   : ----------------------------MTAG-------------------------------------------------------------------------HEQTKR-SGGL-----TLW--LTGSAIALRLIT-LPLE
Ptr_Alb32  : ASVDGLVQQSAAATAPSDDGWWGAYIQLFKT-------------------------------------------------------------------------TLNAVHSTIQGPLQNVGI-EQSWGVSIATFTTIVRTLL-VPLS
Tps_Alb32  : ------MMQHQVTLDAKDENSWWESYIQIYKN-------------------------------------------------------------------------GLAFVHDNVDEPLRKLGF-DQTWGVSIFLFTAGVRALL-VPFS
Ota_Alb3_1 : --------------QPQRMEGLLA----PVSN-------------------------------------------------------------------------ALEDLLFTIKGQLLDLGV-PYPTGNAIIIVTILVKMVT-YPLT
Olu_Alb3_1 : --------------APQRMEGLLA----PVSD-------------------------------------------------------------------------ALEDLLFAIQGQLQGLGV-PYSTGNAIIIVTILVKFVT-YPLT
Ptr_Alb31  : --MRDLPQQSLLQDVAESDSGWFG----FLTI-------------------------------------------------------------------------PIKLLLQAIHSLLLTVGLNTNSWGVAIVLLTILIKVVT-FPLT
Tps_Alb31  : --------------APNAQNGWFG----FLTL-------------------------------------------------------------------------PIEGLLKLIHGGLDSMGMSSNAWGISIIAMTVVIKALT-FPLT
Cme_Oxa1   : ALQDSWHTTFALASAGAQAGLWNG----FVHL-------------------------------------------------------------------------IE-TIITGTGDTLAALGV-PGSYGFAIIFLTIIVKAIT-FPLN
CreAlb3_1  : ALHRL-GAIYVLADAPQRAGGWVA----PVAD-------------------------------------------------------------------------ALEQVLYAIQEGLDKLHV-PYSYGYSIILLTLIVKLLT-YPLT
CreAlb3_2  : VVVKASLLDAASAALTLAEGGPID----VLAQ-------------------------------------------------------------------------FFEFVLQTIDEGLESAKI-PYSYGFAIIALTVLVKVAT-FPLT
OtaAlb3_2  : ALVSSPLFDLAARLAGIQKGGWLG----PITD-------------------------------------------------------------------------ALEGALRGIDGVLDGK--VPYSYGYSILLLTVLVKLAT-FPLS
OluAlb3_2  : --------------AGLQKGGWLG----PITD-------------------------------------------------------------------------GLESALEGIDSVLDGR--VPYSYGFSIVLTVLVKLAT-FPLS
OsaAlb3_a  : ALERAEAALYTLADSAQKNGGWFG----FISE-------------------------------------------------------------------------ALEVVLKVLKDGLSAVHV-PYSYGFAIILLTVIVKAAT-LPLT
AthAlb3_a  : IFTRAESLLYTI-ADVQKSGGWFG----FISD-------------------------------------------------------------------------AMELVLKILKDGLSAVHV-PYAYGFAIILLTIIVKAAT-YPLT
PAlb3_a1   : IISRAEGFLYTL-ADAQKNGGWFG----FISD-------------------------------------------------------------------------GMEFVLKVLKDGLSSVHV-PYAYGFAIILLTIAVKVAT-LPLT
PAlb3_a2   : IISRAEGFLYTL-ADAQKSGGWFG----FISD-------------------------------------------------------------------------GMEFVLKVLKDGLSAVHV-PYAYGFAIILLTVFVKVAT-LPLT
OsaAlb3_b  : LFGRVEAFLYTV-ADKEAAGDWLS----GITN-------------------------------------------------------------------------SMETVLKVLKDGLSALHV-PYPYGFAIILLTVLVKAAT-FPLT
AthAlb3_b  : FIKDHAENLLYTIADTTQSNDWFS----GIAN-------------------------------------------------------------------------YMETILKVLKDGLSTVHV-PYSYGFAIILLTVLVKAAT-FPLT
PAlb3_b2   : -LFGRAESIVYTIADTTQNSDWLS----GITY-------------------------------------------------------------------------GLESTLKVLKDGLSAVHL-PYAYGFAIILLTVLVKAAT-FPLS
PAlb3_b1   : LFGRAESIIYTI-ADTKQNSDWLS----GITS-------------------------------------------------------------------------CLESTLKVLKDGLSALHV-PYAYGFAIILLTVLVKAAT-FPLS
Syn_YidC   : -------------------MDF------GVGF-------------------------------------------------------------------------LSNNVMLPILDFFYGI---VPSYGLAIIFLTLVIRFAL-YPLN
Pma1_YidC  : ----------------------------MIGY-------------------------------------------------------------------------ISDNILLPILDFFYGL---VPSYGLAIVALTVVIRLAL-FPLS
Pma2_YidC  : ----------------------------MIGY-------------------------------------------------------------------------ISDNILLPILDFFYGL---VPSYGLAIVALTVVIRLAL-FPLS
Tps_Oxa2   : ------------------------------------------------------------------------------------------------------MSLTNICIRTSL-LPIA
Ptr_Oxa2   : ----------MWPEVLQNVSVW------GGSG-------------------------------------------------------------------------YLLKAIHA-DGVV-----PYWACFAAINMMVRIGL-FPLV
Esi0025_01 : GSGSEDSAGFPETGGAADADGLSA----PPDAWAPDEVPPEIPQDASVPGFDVGEGFSVDSAAAALDAVAGAAPDASAVGTAMTATGLSAADLGMYPHHLFMHVIEYVQA-TAGV-----PYWEAIVMVSVAARIAV-LPAV
Mbr_Oxa2   : AAVQPALSVGGTRLSLEALTLT-G----IVDG-------------------------------------------------------------------------TE-AALVGLQA-QTQA-----PWPVAVLLTAGLVRTVVGAPAA
Ptr_Oxa1   : --------------MQPWDPTYYN----LADQ-------------------------------------------------------------------------AI-LAVKSLHE-FSGL-----EYGWSIVGVTVILRLCL-FPVM
Tps_Oxa1   : --------------MSPFEPTWW------PSDQ-------------------------------------------------------------------------LL-LLLNHVHDVLPAY-----PYAVTIGVTTLAARLLL-FPIY
Yli_Oxa1   : ------------MDTGSLWSLW------PSDI-------------------------------------------------------------------------YL-NLLEHVHV-YTGL-----PWWAAIASTTVIVRVLL-FPLF
Cal_Oxa1   : --------------MQIGLAQGW-G----PTSL-------------------------------------------------------------------------IE-RLLEVTHV-YTGL-----PWWGTIVVATIAVRLVL-FPLY
Sce_Oxa1   : --------------MFGLAQTYYW----PSDI-------------------------------------------------------------------------IQ-HVLEAVHV-YSGL-----PWWGTIAATILIRCLM-FPLY
Mbr_Oxa1   : -----------------GLGSFAT----PVGL-------------------------------------------------------------------------IQ-NLVEFNTV-MLDA-----PWAVGICATTILMRTLM-LPLV
Hsa_Oxa1   : --------------MPELGLGSY-T----PVGL-------------------------------------------------------------------------IQ-NLLEFMHV-DLGL-----PWWGAIAACTVFARCLI-FPLI
Cfa_Oxa1   : --------------PELGLGSY-T----PVGL-------------------------------------------------------------------------IQ-NLLEFMHV-NLGL-----PWWGAIAACTVLARCLV-FPLI
Mmu_Oxa1   : --------------SELGLGSY-T----PVGL-------------------------------------------------------------------------IQ-NLLEYIHV-DLGL-----PWWGAIATCTVLARCLV-FPLI
Aga_Oxa1   : ---------------TLGLGGW-T----PVGI-------------------------------------------------------------------------VQ-NCMEFLHI-GLDL-----PWWGCIATGTVCVRTLL-FPLV
Dme_Oxa1   : --------------MSIGLGGW-S----PVGM-------------------------------------------------------------------------VQ-NCLEFLHC-TWDI-----PWWGTIAIGTLAVRTII-FPLV
Pin_Oxa1   : ---------------SVSDLGY------SLSD-------------------------------------------------------------------------MAIRSLDVIHS-TTGL-----PWWATIIATTVAVRTVF-FPVT
Pra_Oxa1   : --------------MVSVSDLGY------SLSD-------------------------------------------------------------------------IAIRSLDVIHA-TTGL-----PWWATIIATTVAVRTAF-FPIT
Pso_Oxa1   : ---------------SVSDLGF------SLSD-------------------------------------------------------------------------IAIRSLDVIHA-TTGL-----PWWATIIATTVAVRTVF-FPVT
Ota_Oxa1   : --------------MDPVAVQSW------PTTA-------------------------------------------------------------------------ALMYAMEYFHV-AHGL-----EWWLAIVGATVFMRTVT-FPLV
Olu_Oxa1   : ---------------PVASQSW------PTTA-------------------------------------------------------------------------ALMYAMEYFHV-AHGL-----EWWLAIVGATVFMRTIT-FPLI
Osa_Oxa1   : PATAPAAAAEAVAPVAAAADSF-F----PVAA-------------------------------------------------------------------------LQ-HVIDYIHT-FTGL-----NWWACIALATVLIRSAT-VPLL
AthOxa12   : --MARGIDCRHMAAIAAADSAF------PVAA-------------------------------------------------------------------------LQ-HLIDAVHS-FTGL-----NWWASIALTTVLIRGVT-IPIL
AthOxa11   : ---MAQTLSYRYMQTLAAADSFF----PIAA-------------------------------------------------------------------------LQ-QCIDMVHT-FTGF-----EWWASIVVATILIRSST-VPLL
POxa11     : --------------AIAAADSF-L----PVAV-------------------------------------------------------------------------LQ-HAIDAVHN-FTGF-----NWWASIVVTTLLIRSFT-LPLL
POxa12     : ---MARSLDCRDMQAIAAADSY-F----PVAA-------------------------------------------------------------------------LQ-HVIDAVHS-FTGF-----NWWASIIVTTLLIRGAT-VPLL
Cme_Oxa2   : -----------MTAALSAERNYYD----PVV--------------------------------------------------------------------------QGIIMFQE-YTDL-----PWWATVAAVTVLARILV-LPLT
Esi0028_00 : AMAAAGTADQAQAALEVAPETKMALYTPPQV-------------------------------------------------------------------------AM-MAVDYVHA-TTGM-----PYWMTIVAITVGIRTAI-LPIG
Mmu_Oxa2   : -------------MGYEALAAS-A----PVRT-------------------------------------------------------------------------AE-EVLLGAQE-ATGL-----PWWSNIILSTVALRGAVTLPLA
Hsa_Oxa2   : -------------MGYEALAAS-S----PVRV-------------------------------------------------------------------------AE-EVLLGVHA-ATGL-----PWWGSIILSTVALRGAVTLPLA
Cfa_Oxa2   : -------------MGYEALAAS-A----PVRG-------------------------------------------------------------------------AE-EMLLGLHA-AAGL-----PWWACIGLGTVALRGAVTLPLA
Aga_Oxa2   : --------------FWQTLSQS-A----PVAY-------------------------------------------------------------------------VQ-QGMINLHD-LTGL-----PWWATVILTTVGLRTLVTLPLA
Dme_Oxa2   : -------------MYWQTLSNS-T----PVAY-------------------------------------------------------------------------MQ-DVLIKIHD-YSGL-----PWWASIVLSTFLFRSVVTLPLT
Yli_Oxa2   : -------------MTVRQLSTV-D----IVRP-------------------------------------------------------------------------VE-TALNAIHD-FSGL-----PWWAVIPLVTLTLRSTVTLPIA
Cal_Oxa2   : -------------MRNFSIDHN-A----IINT-------------------------------------------------------------------------MT-SSFQTVHE-FSGL-----PWWALIPLTTFTLRSVWTLPLA
Sce_Oxa2   : -------------MTPSTKRSF-S----LFQS-------------------------------------------------------------------------VA-DTFLTVHE-ASHI-----PWIVLVPLTTMTLRTLVTLPFS
Olu_Oxa2   : ------------------------------------------------------------------------------------------------------MS-DSWTHLHA-ATGA-----PWFVAIAASAALVRAAT-APIS
Ota_Oxa2   : ------------------------------------------------------------------------------------------------------MSTLHH-ASGL-----PWCATIAVSALCARLVT-APVA
Esi0170_00 : ---------------------M-H----VWGG-------------------------------------------------------------------------VQ-SGVQAVHH-TTGL-----PWWATIAVATIGVKISL-LPVV
Pra_Oxa2   : -------------MSTTGHEPW-A----IVQG-------------------------------------------------------------------------VQ-SVLETVHT-TTGL-----PWWATLLLSGVTLRAAV-FPFY
Pin_Oxa2   : -------------MNGTGNEPW-A----IVQG-------------------------------------------------------------------------VQ-SVLETVHT-TTGL-----PWWATLLLSGVTVRAVI-FPFY
Pso_Oxa2   : -------------MSGTGGEPW-A----IVQG-------------------------------------------------------------------------VQ-SVLEAVHT-TTGL-----PWWATLMLSGVTVRAAI-FPFY
Osa_Oxa2   : ------------MADGGSASGF------AVSS-------------------------------------------------------------------------LI-DILDGFHN-LTGI-----PWWITISLSTVAMRLLI-LPVL
AthOxa21   : -------------MEIPTDDSS-L----PVLA-------------------------------------------------------------------------VV-DFLEGFHE-FTGL-----PWWMIIASSTVAVRLAL-LPLL
AthOxa22   : --------------MLQDLSNYDY----LTQP-------------------------------------------------------------------------VI-SLLDSYHD-ITGL-----PWWVVIATSTVAFRTAL-LPIL
POxa2      : --------------MTDGVVNGIL----PVDS-------------------------------------------------------------------------MI-WLLDSYHD-LTGL-----PWWIIIASSTLAMRLTL-FPLH
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                    *       300         *       320         *       340         *       360         *       380         *       400         *       420
Cme_Alb3   : AYQARQWLRLREAQR----LASAAYQLLTRSSQVQLASNDDLL--------SSLTCLQRKALQRY--GTSRWRALVWGRVVGLPAFVFAALRVRQL-----------------------------------------
Ptr_Alb32  : IEQSKSAEYIKSLKP----YVADIKAKYKNNQ------------------EAQNRATAKLYEDA--QQNPLAGCFV-ALIQLPVFLGLYRGVRLL-----------------------------------------
Tps_Alb32  : IQQSKSSEYVKALKP----YQQKIKEKYTDK-------------------NMQNRAISKLFEDA--QANPLAGCVT-SFAQIPIFLGLYRSVTRL-----------------------------------------
Ota_Alb3_1 : KDQVVSSLNVKNLQP----QIAAIREKYEDDQ------------------ERMNKEINRVYEEN--GVNPLAGCGP-ALLSFPVLAGLYRAFNNA-----------------------------------------
Olu_Alb3_1 : RDQVVSSLNVKNLQP----QIAAIREKYEDDQ------------------ERMNKEINRVYEEN--GVNPLAGCGP-ALLTFPVLAGLYRAFNNA-----------------------------------------
Ptr_Alb31  : KTQLESTNKMQAVQP----AIKELQAKYQSNP------------------EVMNQKIAEFYQTN--EINPLAGCIP-STVQIPVFIGLYRAVLEL-----------------------------------------
Tps_Alb31  : KSQLESTNKMQALQP----TIKSLQAKYQSNP------------------EVMNQKIAEVYQTN--EVNPLAGCIP-SLVQIPVFIGLYRAVLNL-----------------------------------------
Cme_Oxa1   : YKQMKSTMAMQALAP----KVRELQARYRDNP------------------QLLNLETARLYQEA--KVNPLTGCIP-VFVQLPVWIALYRALMNL-----------------------------------------
CreAlb3_1  : KQQVESAMAVQALKP----RIDLIKDRFGEDK------------------DKIQKETSVLYEQA--GVNPLAGCIP-TLATIPIFIGLFSSLTNV-----------------------------------------
CreAlb3_2  : QKQVESTLSLQALQP----RVKELQAKYADDP------------------ENLQLETARLYKEA--GVNPLAGCFP-TLATIPVFIGLYNALSNA-----------------------------------------
OtaAlb3_2  : KQQVESSIQMQAVQP----RIKELQAMYANDP------------------ERLQLEQARLYREA--GFNPLAGCIP-LFATLPVFIGLYRALSNA-----------------------------------------
OluAlb3_2  : KKQVESSMQMQAVQP----RIKELQAMYANDP------------------ERLQMEQARLYKEA--GFNPLAGCIP-VFATLPVFIGLYRALSNA-----------------------------------------
OsaAlb3_a  : KQQVESTLAMQNLQP----QIKAIQQRYAGNQ------------------ERIQLETARLYKQA--GVNPLAGCFP-TLATIPVWIGLYQALSNV-----------------------------------------
AthAlb3_a  : KQQVESTLAMQNLQP----KIKAIQQRYAGNQ------------------ERIQLETSRLYKQA--GVNPLAGCIP-TLATIPVWIGLYQALSNV-----------------------------------------
PAlb3_a1   : KKQVESTLAMQNLQP----KIKAIQQRYAGNQ------------------ERIQLETSRLYRQA--GVNPLAGCFP-TLATIPVWIGLYQALSNV-----------------------------------------
PAlb3_a2   : KKQVESTLAMQNLQP----KIKAIQQRYAGNQ------------------ERIQLETSRLYRQA--GVNPLAGCFP-TLATIPVWIGLYQALSNV-----------------------------------------
OsaAlb3_b  : KKQVESAIAMRSLQP----QVKAIQERYAGDQ------------------ERIQLETARLYKLS--DVDPLAGCIP-TLVTIPVWIGLYRALSNV-----------------------------------------
AthAlb3_b  : KKQVESAMAVKSLTP----QIKAIQERYAGDQ------------------EKIQLETARLYKLA--GINPLAGCIP-TLATIPVWIGLYRALSNV-----------------------------------------
PAlb3_b2   : KKQVESAMAMRSLQP----QIKAIQQRYAGDQ------------------ERIQLETARLYKLA--GINPLAGCIP-TLATIPVWIGLYRALSNV-----------------------------------------
PAlb3_b1   : KKQVESAMAMRSLQP----QIKAVQQLYAGDQ------------------ERIQLETARLYKLA--GINPLAGCIP-TLATIPVWIGLYRALSNV-----------------------------------------
Syn_YidC   : VGSIRNMRMKVINPLMQRRMREIQEKYRDDP------------------QKLREAQAKLYSEL--GVNPLGGCIP-LLIQMPVLFALFATLRGSPFAATYDLPAEVAAEVVPTPYVSPSKNIFVTDSVHKPVVLVAPKGT
Pma1_YidC  : AGSIRSARMRIAQPAMKKRQDEIKSRYAKDP------------------QKQQEELGKVMKEF--G-NPLSGCIP-LLVQMPILFALFATLRGSPFADPYLLPSDQIAAIEPKPFTSSKHSIFISETKHFPVIASLPSGT
Pma2_YidC  : AGSIRSARMRIAQPAMKKRQDEIKSRYAKDP------------------QKQQEELGKVMKEF--G-NPLSGCIP-LLVQMPILFALFATLRGSPFADPYLLPSDQIAAIEPKPFTSSKHSIFISETKHFPVIASLQSGT
Tps_Oxa2   : IQGAKTSVSFGKVAP----EVQYLISSFQRDFRLLREGMEAAQAQMSLL--KTTVATLRGIFRLH--KVNLLDIFKS-PLMQIPVFWYFAIDIRKI-----------------------------------------
Ptr_Oxa2   : LYGAQTSTRFAKVVP----EVQFLLSLFQADWQRLRQNPLRERLMLM----RTNLGTLGGIYKLH--GIHPMAVFIS-PLLQVPLFWYVSVDLRKI-----------------------------------------
Esi0025_01 : ATFLGMSKRLNMIKP----EMAVHQGKMQDIKNRMEANPEIKEAAMAEM--MLVSQEMGNILKQH--RIHFPKMMLS-MFAQFPVFISLFLATRDM-----------------------------------------
Mbr_Oxa2   : WYQAHWSSRVELQRR----RLMQWADAIGHQVMRRKANTDAEAENLIQ---EQVRAQQKVLMDEI--GWRRWKLVP-ALVQVPIFITVSLALRRL-----------------------------------------
Ptr_Oxa1   : VASQQTSSRMAHIQP----ELQQIKARYEALGTPSRQDQ-----------LQFSGQMKAIFAKY--KVKPFRAFAG-PVIQMPLFMGMFGLRKM-----------------------------------------
Tps_Oxa1   : AAGQRNSSRMAHVQP----EMKKIMDATPKQPDQATQ-------------QKVMAQTRALWRKY--DCNPMKGLVV-PIASFPFFMGMFGLKKA-----------------------------------------
Yli_Oxa1   : VQAANEQGKMSEVKP----ELNVIDEKLKSAANMTEM--------------QMVAHEKKKILKKY--GTSQMKLFYP--MAMFPLIIGIFLGIRRM-----------------------------------------
Cal_Oxa1   : VRASSNATKMSKIKP----QIDELLQQIKTGDTVDQ---------------MRAMEKRRLIMKEN--GVSTLATLFP--AVQLPLAYGFFQALRKM-----------------------------------------
Sce_Oxa1   : VKSSDTVARNSHIKP----ELDALNNKLMSTTDLQQG-------------QLVAMQRKKLLSSH--GIKN-RWLAA-PVLQIPIALGFFNALRHM-----------------------------------------
Mbr_Oxa1   : FGSMRNNTILMNIQP----QLQLHSQRIRECQTRNDHDGA-----------AQAAANLNGLFKEH--GVHPLKGLIP-LFVQAPVFISFFMALRQM-----------------------------------------
Hsa_Oxa1   : VTGQREAARIHNHLP----EIQKFSSRIREAKLAGDHIEY-----------YKASSEMALYQKKH--GIKLYKPLIL-PVTQAPIFISFFIALREM-----------------------------------------
Cfa_Oxa1   : VKGQREAAKIHNHLP----EIQKFSTRIREAKLAGDQAEF-----------YKASSEMTFYQKKH--DVKLFRPLIL-PLTQAPIFISFFIALREM-----------------------------------------
Mmu_Oxa1   : VKGQREAAKIHNHMP----EMQKFSARIREAKLAGDQAEF-----------YKATIEMTRYQKKH--DIKLLRPLIL-PLTQAPVFISFFIALREM-----------------------------------------
Aga_Oxa1   : IASQRNAAKMNNYMP----QLQVLQMKMTEARQAGNAIDS-----------ARYGQEMVLFMKEK--NLNPLKNMLV-PLAQAPIFISFFMGLREM-----------------------------------------
Dme_Oxa1   : ILAQRNSAKMNNNMP----QMQMLQLKMTEARQSGNAIES-----------ARYAQEMMLFMREK--GVNPLKNMVV-PLAQAPLFISFFMGLRQM-----------------------------------------
Pin_Oxa1   : VISMRNAAKMKLFQP----DMEKLKAQMDANPTQSPEST------------KEFQTKYKALMKKH--DVNPFKSVIT-PLSQIPVFLGFFWGLQDI-----------------------------------------
Pra_Oxa1   : VVSMRNAAKMKLFQP----DMEKLRDEMDANPTRDEKST------------REFQTKYKALMKKH--GVNPFKSMIT-PLAQIPVFLGFFWGLQDI-----------------------------------------
Pso_Oxa1   : VISMRNAAKMKLFQP----DMEKLRDEMDSNPTQTPETA------------QEFQKKYKALMKKH--DVNPFKSMIT-PMAQIPVFLGFFWGLQDI-----------------------------------------
Ota_Oxa1   : VMQMRNTARMQLCKP----ELEALQAKMKSNPSQDPELA------------TAYYAEMQKVWKKY--DVNPFKSFAP-VLINAPVFISFYFAISKM-----------------------------------------
Olu_Oxa1   : VMQMRNTAKMQLCKP----ELEALQAKMKSNPQQDPELA------------NAYYKEMQKVWKKY--DVNPVKSFAP-ILINAPVFISFFFAISKM-----------------------------------------
Osa_Oxa1   : VNQLKATQKLNAIRP----EMEAIKEEMNAMDPKSA--------------KEGKAKMTALFQKH--GVSPFTPLKG-LLIQGPIFMSFFFAIRNM-----------------------------------------
AthOxa12   : LNQLKATYKLNVLRP----QLEELRQEMSTKAQDPEAM------------AEGQRRMQLLFKEH--GVTPFTPLKG-LLIQGPIFISFFFAIRNM-----------------------------------------
AthOxa11   : IKQMKDTTKLALVRP----RLESIREEMQNKGMDSVTM------------AEGQKKMKNLFKEY--GVTPFTPMKG-MFIQGPLFICFFLAIRNM-----------------------------------------
POxa11     : INQLKATSKLSIVRP----HLEEVKQRVERQGMDPTAV------------SEGQKEMKKLFKEH--GVSPFTPLKG-LFIQAPVFISFFLAITNM-----------------------------------------
POxa12     : INQLKATTKLTLVRP----HLEEIRQQMSDKAMDPMAL------------AEGQKQMKKLFKEY--GVSPLTPLKG-LFIQGPIFVSFFLAISNM-----------------------------------------
Cme_Oxa2   : LNTFRNAARMQSIKP----DVDAIKERMQAAMHSGDQQRI-----------RALQQQVFRLLREN--QISPLRSLVN-PLVQMPLFISFFLGLRKI-----------------------------------------
Esi0028_00 : LLAARNGARTAAVKP----EMDELQAAIKGDQQSSQPRKA-----------DRYRQETKALFQKH--KASLVMNAAL-PIVQLPLFIGFFLGLRRM-----------------------------------------
Mmu_Oxa2   : AYQHYILAKVENLQP----EIKDIAKRLNQEVAVCARGWSKRVARLTYL--KNMRRLVSELYVRD--NCHPFKATVL-VWVQLPMWVFISVALRNL-----------------------------------------
Hsa_Oxa2   : AYQHYILAKVENLQP----EIKTIARHLNQEVAVRANGWSKRDARLTYL--KNMRRLISELYVRD--NCHPFKATVL-VWIQLPMWIFMSFALRNL-----------------------------------------
Cfa_Oxa2   : AYQHYILAKVENLQP----EIKNIARHLNQEVAVRANKWSKRVARLTYL--KNMRRLVSELYVRD--NCHPFKATIL-VWIQFPMWIFMSVALRNF-----------------------------------------
Aga_Oxa2   : VYQNKILARLEQISL----EMPELIKELKAETAYAKNWTEKEARIMYN---HSLKKQWNNLIVRE--NCHPAKTMVL-LWGQIPLWIVQSVAIRNL-----------------------------------------
Dme_Oxa2   : IYQHKITARIEKMAL----EMPAIVEELKKEAAM-AHKWSEKQTQIVYR--RSIKKQWQNLIVRD--NCHPMKTMIV-LWGQIPLWIFQSVALRNL-----------------------------------------
Yli_Oxa2   : ISTRLRAQKQHELRP----LISALGPILRAKLAFNANAPQIEMLAM-----KERRKRRVKLYKEH--GCEMWKSLFIGPLVQLPIWITMSLAVRAM-----------------------------------------
Cal_Oxa2   : ILQRKRIQKQSQLRP----LVSAMNPILKLNLARRQSTIQSKYEQILLLSAKEARKRQKELFAKN--GVQLWKNFIL-PAFQVPLWIMMSITMRDL-----------------------------------------
Sce_Oxa2   : IWQRRRILKQQELRK----LVQPITPIIKLRLAAVNSSNPLQPEQITLLAVKETRKRQKKLFKKY--NVPLWKNALL-PMVQIPLWVTVSMGIRTL-----------------------------------------
Olu_Oxa2   : ARTIKASATVSAASA-----LAKSRKRGNSEHVGVRDV------------LDAIGELRGKAPGT--GAHPAWLVAG-PLAQIPFFLCAVMAVRRL-----------------------------------------
Ota_Oxa2   : ARTTKASATVSAASA----LAKATKQGDAERVSI----------------KDVLEAMKELRERSGVGAHPAWLVAG-PLAQIPLFACAMMAVRRL-----------------------------------------
Esi0170_00 : VYQAGHMDRMRAAWP----EIQILRGYLATSLEEIPQERVLERWRKY----KVFFSGARGVLGLH--GTH-LRGMFATPLVNLPVFITFVWSIRGM-----------------------------------------
Pra_Oxa2   : VFQIQAMQRLMHARP----DFSKLYSAYKYARTFTPGSDHKGHLDAV----LLGRQGMKAVMKKY--NTRPVQTIVG-SLAYIPIFVLMAYSARDM-----------------------------------------
Pin_Oxa2   : VLQIQAMQRLIQARP----DFSKLHSAYKYARTFTPGSDHKGHLDAI----LLGRQGLKAVMKKY--NTRPIQTIVG-SVAYIPIFVLMAYSARDM-----------------------------------------
Pso_Oxa2   : VFQIQAMQRLVQAKP----DFSKLYSAYKYARTFTPGSDHKGHLDAI----LLGRKGVKAVTKKY--NTRPVQTVVG-SVAYIPIFVLMAYSARDM-----------------------------------------
Osa_Oxa2   : ITQIKKAAKIGKILP----ELPPPFPPPLSGRSFRDQF------------SLYQKKRREL------GCPSFLW----NWAYFSIQIAFHGTHTKH-----------------------------------------
AthOxa21   : ILQLKKLKTISELLP----KLPMPIPETPTLKGSIDQF------------SHFLKESRAI------GCPSFLWFFPYLSVQLPCFFLLMASIRKM-----------------------------------------
AthOxa22   : ILQRKQTKRISQFLP----KLPHFWPPQGSGRSVLDQL------------KLFRKERKDI------GCPSFLWVPAYFSIQISCFFLWITSIRRM-----------------------------------------
POxa2      : VLQMHKIKKISRSFS----KLPPLFPPPLSGRSYIEQI------------SLFRNERRAI------GCPSYLWFVAFLSVQIPCFLLWMTSIRRM-----------------------------------------
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                 *       440         *       460         *       480         *       500         *       520         *       540         *       560
Cme_Alb3   : ------------------------------------------------------------ALAGDLGGTLPG---LVLKDLS-------EPDPF--YLL--------------------PI---LCNMVLMLRNLEYSF
Ptr_Alb32  : ------------------------------------------------------------AMDGVLEE-PFLVIPSLEGPVAP---PNFQGLDWLVQGWVNGAPALGWETTLAFLIMP---VILVVLQSVTMQVLQ
Tps_Alb32  : ------------------------------------------------------------AQEGRLDE-PFLVIPSLQGPVTAETNYRGTE--WLTQGWVDGVPPLSWETTLAFCVMP---VLLVLGQSFTMNVLQ
Ota_Alb3_1 : ------------------------------------------------------------GIDGAFDE-PWFFLPSLAGP-----TDARDLSWLLPLDADLAPPIGWDDASLYLLFP---IMTTLSQFVSMEVLK
Olu_Alb3_1 : ------------------------------------------------------------GIDGAFDE-AWFFLPSLAGP-----TDARDLSWLLPLDSDYAPPIGWEEASLYLIFP---VLTTISQFVSMEVLK
Ptr_Alb31  : ------------------------------------------------------------AQANKLDE-SFLFLPNLEGPTYGA--EPGSAADWILKGWTDGVPSLGWPDTIAFLILP---VFLVISQYLSMELMQ
Tps_Alb31  : ------------------------------------------------------------AKENALDE-PFLFLPNLEGPTYGA--DPAHGSDWLFKNWVDGVPGLGWEDTIAFLSIP---VFLTISQVISMNMMQ
Cme_Oxa1   : ------------------------------------------------------------AADNRLDQ-GFFWLPSLEGPV-----RQGQGLSWLFPF-QNGAPPIGWHDAIAYLVLP---CLLVVSQSISQKILQ
CreAlb3_1  : ------------------------------------------------------------ANDGLLDQ-GFYFVPSLAGPTTMAMRQSGLGTSWLWPLGPDGAPPIGWEDAAAYLTLP---LLLVAVQYASSSVTS
CreAlb3_2  : ------------------------------------------------------------AKEGLLTE-GFFWIPSLGGPT-----TIGGGLEWLVPF-ENGAPPVGWANAAAYLVMP---VLLVASQYASQKIIS
OtaAlb3_2  : ------------------------------------------------------------AAEHLLDD-GFYWIPSLGGPTSIAARNDGNGFAWLWPF-VDGHPPLGWYETGCYLVLP---VLLVVSQFVSQTIIS
OluAlb3_2  : ------------------------------------------------------------ASEGLLTD-GFYWIPSLGGPTSIASRNAGSGFAWLWPF-VDGHPPLGWHDTTAYLVLP---VLLVASQYVSQQIVS
OsaAlb3_a  : ------------------------------------------------------------ANEGLLTE-GFFWIPSLGGPTTIAARQSGAGISWLLPF-VDGHPPLGWHDTICYLVLP---VLLVASQFVSMEIMK
AthAlb3_a  : ------------------------------------------------------------ANEGLFTE-GFFWIPSLGGPTSIAARQSGSGISWLFPF-VDGHPPLGWYDTVAYLVLP---VLLIASQYVSMEIMK
PAlb3_a1   : ------------------------------------------------------------ANEGVLTE-GFFWIPSLGGPTTIAARQSGSGISWLFPF-VDGHPPLGWHDTAAYLVLP---VLLIASQYVSMEIMK
PAlb3_a2   : ------------------------------------------------------------ANEGVLTE-GFFWIPSLGGPTTIAARQSGSGISWLFPF-VDGHPPLGWNDTAAYLVLP---VLLVVSQYVSMEIMK
OsaAlb3_b  : ------------------------------------------------------------ANEGLLTE-GFFWIPSLAGPTTIAARQSGQGISWLFPF-TDGHPPLGWSDTLAYLVLP---VLLVISQYVSSQVMQ
AthAlb3_b  : ------------------------------------------------------------ADEGLLTE-GFFWIPSLAGPTTVAARQNGSGISWLFPF-IEGHPPLGWPDTLAYLVLP---LLLVFSQYLSIQIMQ
PAlb3_b2   : ------------------------------------------------------------ANEGLLTE-GFFWIPSLAGPTAIASRQNGSGISWLFPF-VDGHPPLGWSDTVAYLVLP---VMLVVSQYISVQIMQ
PAlb3_b1   : ------------------------------------------------------------ANEGLLTE-GFFWIPSLAGPTTIAERQNGSGISWLFPF-VDGQPPLGWSDTVAYLVLP---AMLVVLQYMSVQIMQ
Syn_YidC   : KIAVGEQVQFRLQGPGGKPFEQLVAEAGGDPTLRPTWKITKGEERAQIQPDGTLLALQPGEVTVEVAIPGLASDTGFLFIDKLGRVG-----AFDPTIHWDI----------------------IGMIVLFGVSIYLNQSLTN
Pma1_YidC  : KLGVGDKAQIKLQTLTGESFTSRLSGVEGGTKFTPTWSVTKGDDLVKVSADGTVQALAEGDATVQGKIPGLAAQSGFLFIKALGQVGF----YVDGEINWDI----------------------A---ILVGGFGLTLLVSQI
Pma2_YidC  : KLGVGDKAQIKLQTLTGESFTSRLSGVEGGTKFTPTWSVTKGDDLVKVSADGTIQALSEGDATVQGKIPGLAAQSGFLFIKALGQVGF----YVDGEINWDI----------------------A---ILVGGFGLTLLVSQI
Tps_Oxa2   : ------------------------------------------------------------INGSDLAQQLVDS-SFLWITDLT-------EPDPW--YGL--------------------PI---IITGLLLYWNVETAV
Ptr_Oxa2   : ------------------------------------------------------------VNGLDLAQQLVES-SVAWVPDLT-------EADPW--FGL--------------------PI---VLAGLVMYANVEVAI
Esi0025_01 : ------------------------------------------------------------GTYFPGYMTG-GLDWMMNLN-------APDPT--WTL--------------------PI---ILTSGSMILLMELGS
Mbr_Oxa2   : ------------------------------------------------------------QDSDLYQADLASQ-GPLWTASLT-------EHDI---LLL--------------------PI---LVLGITNWFTLELST
Ptr_Oxa1   : ------------------------------------------------------------PSIFPEELSTG-GMYWFTDLT-------ASDPL--YIL--------------------PI---FTSALSFLALIELGK
Tps_Oxa1   : ------------------------------------------------------------PDYFPDLLSNGGLFWFTDLT-------QADPL--MIL--------------------PI---VLSAGTFLVMTELTK
Yli_Oxa1   : ------------------------------------------------------------CEIGGVQGLSTE-GVLWFQNLA-------APDPY--LGL--------------------QI---VITAAMYMASIRLGS
Cal_Oxa1   : ------------------------------------------------------------ANHNVEGFSDQ-GYAWFQNLI-------EVDPY--LGL--------------------QI---AISAAAIIAVVRVGG
Sce_Oxa1   : ------------------------------------------------------------ANY--PVDGFANQ-GVAWFTDLT-------QADPY--LGL--------------------QI---VITAAVFISFTRLGG
Mbr_Oxa1   : ------------------------------------------------------------ANLPIESMKTG-GLLWFTDLT-------AADPY--YVL--------------------PI---VIASATMLATIEFGS
Hsa_Oxa1   : ------------------------------------------------------------ANLPVPSLQTG-GLWWFQDLT-------VSDPI--YIL--------------------PI---LAVTATMWAVLELGA
Cfa_Oxa1   : ------------------------------------------------------------ANLPVPSLQTG-GLLWFQDLT-------LSDPT--YIL--------------------PI---LVVTATMWGVLELGA
Mmu_Oxa1   : ------------------------------------------------------------ANLPVPSLQTG-GLWWFQDLT-------VSDPI--YVL--------------------PI---LVVTATMWCVLELGA
Aga_Oxa1   : ------------------------------------------------------------ANTPVESMRDG-GLFWFTDLT-------ICDQF--YAL--------------------PI---IITSLTLFATIELGT
Dme_Oxa1   : ------------------------------------------------------------ANA--PVESMRDG-GLFWFTDLT-------MADPF--YLL--------------------PI---LITSATLYLTIEIGT
Pin_Oxa1   : ------------------------------------------------------------SKYFPEYAHE-GIGWVPDLS-------VADPT--LAL--------------------PI---VISSALMAASVELGG
Pra_Oxa1   : ------------------------------------------------------------SKYFPEYAHE-GIGWVTDLS-------ASDPT--MAL--------------------PI---IISSALMVASVELGG
Pso_Oxa1   : ------------------------------------------------------------SKYFPEYAHE-GIGWVTDLS-------AADPT--MAL--------------------PI---CISSALMVASVELGG
Ota_Oxa1   : ------------------------------------------------------------AAGVPSFETG-GPSMYPDLS-------IADPT--YSL--------------------PI---ILSSLTFLASVELGT
Olu_Oxa1   : ------------------------------------------------------------AQGVPSFESG-GPSMYPDLS-------MADPT--YSL--------------------PI---ILSSLTFLASVELGA
Osa_Oxa1   : ------------------------------------------------------------IDKVPSMKGG-GSLWFTDLT-------TPDPL--YIL--------------------PI---VLTALIFLVTVELNL
AthOxa12   : ------------------------------------------------------------AEKVPSFKTG-GTLWFTDLT-------TTDTT--YIL--------------------PI---LLTAVTFLIMVESNM
AthOxa11   : ------------------------------------------------------------AEKVPSFQTG-GALWFTDLT-------TPDSL--YIL--------------------PI---VITGLTFLITVECNA
POxa11     : ------------------------------------------------------------AEKVPSFKSG-GAFWFVDLT-------TADDL--YIF--------------------PI---VLTALTFLITVECNT
POxa12     : ------------------------------------------------------------TEKVPSFKSG-GAYWFLDLT-------TPDSL--YIL--------------------PI---ILTGLTFWITVECNM
Cme_Oxa2   : ------------------------------------------------------------AKIYPDELRNG-GLGWFRDLS-------LPDPF--YGL--------------------PI---ALTSATMLFMIQMGT
Esi0028_00 : ------------------------------------------------------------PDVVPEFATG-GVLWFQDLG-------APDPY--MIF--------------------PI---VMTGVMMMAMAELGG
Mmu_Oxa2   : ------------------------------------------------------STGATHVQEQLAAG-GTLWFPDLT-------AVDST--WIL--------------------PI---VSVGVVNLLIVEIFA
Hsa_Oxa2   : ------------------------------------------------------STGAAHVQEQLATG-GILWFPDLT-------APDST--WIL--------------------PI---ISVGVINLLIVEICA
Cfa_Oxa2   : ------------------------------------------------------STGAAHVQEQLATD-GILWFPDLT-------ALDST--WIL--------------------PI---ISVGVINLLIVEIFA
Aga_Oxa2   : ------------------------------------------------------VSMLDEAAYTELTLG-GFGWIPNLT-------ELDHS--LHF--------------------PI---VALGVINLSIIEIQA
Dme_Oxa2   : ------------------------------------------------------VYMLDQ-AVTTEMTIG-GFGWIPNLT-------VVDNS--YIL--------------------PI---VALGLINLAIIEVQA
Yli_Oxa2   : ------------------------------------------------------CGWTVVVKSMGTE-GALWFDLL-------MMDHS--GVL--------------------PI---AAVGIITLLNVELTT
Cal_Oxa2   : ------------------------------------------------------SGWSWNLDPSLYEE-GILWFQDLS-------IADPM--HVF--------------------PI---VILGITALCNIEWTL
Sce_Oxa2   : ------------------------------------------------------TETQLIESFYPSWFSALG-------LSSPLVPLLA--------------------PI---ILVGTLAVLNVELNG
Olu_Oxa2   : ------------------------------------------------------AADGANNGLVTG-GALWFQDLTVPAVDVAMTAPMGPGGIL--------------------PI---VLTAAALFANVNANF
Ota_Oxa2   : ------------------------------------------------------ASEGGSNGLISG-GVFWFSDLTLPAMDIATSAPMGPGAVL--------------------PI---IVTAGALFANVNANF
Esi0170_00 : ------------------------------------------------------LRDGTVPGLDTG----------------EADTVHSLML--------------------PI---IITGTLCTYTSLEIVK
Pra_Oxa2   : ------------------------------------------------------VRSGNFSGFDTG-GLLFWKNLV-------ETDST--FIL--------------------PI---ILAATSTYGSLELSM
Pin_Oxa2   : ------------------------------------------------------VRSGNFAGFDSG-GLLFWKNLM-------ETDST--YVL--------------------PI---ILAATSTYGNLELSV
Pso_Oxa2   : ------------------------------------------------------VRSGNFAGFDSG-GLLFWKNLM-------ETDST--YIL--------------------PI---IIAAASTYGNLELSI
Osa_Oxa2   : ------------------------------------------------------------------YPGIF--------------------------------------------G---VLAKYYR--------
AthOxa21   : ------------------------------------------------------SLDGHPGFDSG-GVLWFQNLS-------DLPGGSFPYF--------------------PI---ILIATFHYINIQISF
AthOxa22   : ------------------------------------------------------SLDHHPGFDSG-GALWFQNLT-------EIPNGLYPLF--------------------PI---FLIAGLHYTNTQVCT
POxa2      : ------------------------------------------------------CLDNHPGFDCG-GALWFQNLT-------ELPHGVLPIF--------------------PI---FLIAGLHGVNVHY--
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                 *       580         *       600         *       620         *       640         *       660         *       680         *       700         *
Cme_Alb3   : PLMPFPYWLQSQSLK--VLLQGAVLVI--TPGVYNLPSAVLLFWLTNSCIQTALTSAWWRQRWHRWI-QQT-----------------ALQREL--------------------------------------------
Ptr_Alb32  : PPVDEEERETLERSQ--TILKFLPLLI--GFFALQVPAGLTIYWFTSNIFILTQSLAVRAYFSANPP-QIE-----------------LPDYWD--------------------------------------------
Tps_Alb32  : QPDDDETKKQMESTK--TILKFLPLMI--GFFSLQVPAGLTIYWFTSNLFTVSQSLIIRGYYAA----NPP-----------------EVKLPD--------------------------------------------
Ota_Alb3_1 : PEEDEKTKEMQN-QS--VILKLLPFFI--GYISLTVPAGLALYWFWNNVFITGIQVYLRNGGA-------------------------------------------------------------------------
Olu_Alb3_1 : PEETEKTDEMKN-QS--VILKLLPLFI--GYISLTVPAGLALYWFWNNVFITGIQVFLRNGGAK----ATV-----------------E-------------------------------------------------
Ptr_Alb31  : PKTDDPAQQQSN-----AILKVLPIMI--GWFSLSVPAALSVYWVINNIITTGTSLIIRNSMSVETV--------------------TPSGTA--------------------------------------------
Tps_Alb31  : PKTDDPQQQQAN-----VILKVLPFMI--GWFALNVPAALGVYWVVNNIVITATTLYVR-----------------------------------------------------------------------------
Cme_Oxa1   : PPVQDPQQQQAN-----AILRFLPFMV--GWFSLNVPSGLGLYWVTNNIVSTIQTIGIKRYLASKQP--------------------ERVGAP--------------------------------------------
CreAlb3_1  : PPIDPKDENANT-QR--ALLVFLPLMV--GWFSLNVPAGLSLYYLANTVLSSAIQIYLKKLGGANVV-MNE----------------LGPVTK--------------------------------------------
CreAlb3_2  : SQNNQDPSQQQ--AQ--AILKFLPLMI--GWFSLNVPSGLTLYWFVNNLLSTGQQLYLK---ATVKV-NIP----------------EAIKAP--------------------------------------------
OtaAlb3_2  : PQPKTDDPAQQQ-SQ--AILKFLPFMI--GFFSLNVPAGLTLYWFFNNIITTAQTVVLR--KITKPI-EVP----------------TGAGAG--------------------------------------------
OluAlb3_2  : PQPKTDDPAQQQ-SQ--AILKFLPLMI--GFFSLNVPAGLTLYWFANNIITTAQTIILRK-------------------------TTTAPE--------------------------------------------
OsaAlb3_a  : PPQTDDPSQKNTL----LVLKFLPFMI--GWFSLSVPSGLSIYWFTNNILSTAQQVWLRKLGGAKPV-VNQ----------------GGSGII--------------------------------------------
AthAlb3_a  : PPQTDDPAQKNTL----LVFKFLPIMI--GYFALSVPSGLSIYWLTNNVLSTAQQVYLRKLGGAKPN-MDE----------------NASKII--------------------------------------------
PAlb3_a1   : PPQTDDPTQKNTL----LVFKFLPIMI--GYFSLSVPSGLSIYWFTNNVLSTAQQVWLRKLGGAKPV-VNE----------------NASGII--------------------------------------------
PAlb3_a2   : PPQTDDPTQKNTL----LVFKFLPLMI--GYFSLSVPSGLSIYWFTNNVLSTAQQVWLRQLGGAKPV-VNE----------------NASGII--------------------------------------------
OsaAlb3_b  : PPQNNDPSQQGAQ----AVVKFLPLLI--GYFALSVPSGLSLYWLTNNILSTAQQVWLQKLGGAKNP-VKE----------------YIDKLA--------------------------------------------
AthAlb3_b  : SSQSNDPAMKSSQ----AVTKLLPLMI--GYFALSVPSGLSLYWLTNNILSTAQQVWLQKYGGAKNPVEKF----------------TNLVTK--------------------------------------------
PAlb3_b2   : SSQSDDPNVKNSQ----AITKFLPLMI--GYFSLSVPSGLSLYWLTNNILSTAQQVWLQKSGGAKNP-MVK----------------SSDDIV--------------------------------------------
PAlb3_b1   : SSQSDDPNVKNSQ----AIMKFLPLMI--GYFSLSVPSGLSLYWLTNNILSTTQQVWLQKLGGAK-----------------------------------------------------------------------
Syn_YidC   : AGQEDPSQS-------SVARITPVLFSAMFLFFPLPAGVLLYTLVSNIFQTVQTFLLSREPLPENIQQLV----------------EEERRR--------------------------------------------
Pma1_YidC  : LSGRGPANPQQS-----TANKITPVMITGMFLFFPLPAGVLLYMVIANIFQAGQTFLLSREALPENLQKIL----------------NDQLSK--------------------------------------------
Pma2_YidC  : LSGRGPANPQQS-----TANKITPVMITGMFLFFPLPAGVLLYMVIANIFQAGQTFLLSREALPENLQKIL----------------NEQQSK--------------------------------------------
Tps_Oxa2   : GKKALSQSRMALFLK--DAFQSLAVFM--PCFMAQQPSGVQIYLTTSMLFSLLQSYAMRDDAVREYI-GLP----------------ALNAKP--------------------------------------------
Ptr_Oxa2   : GRRSLSKADTGVLLK--DVFQSLAVFM--PCFTSQMPAGVQIYLVTSFLFTMGQSAALRTEAFRAAV-GLP----------------SLATAP--------------------------------------------
Esi0025_01 : DMPAAHGPDKPN-FNPKVLFRVMSVVF--VPVAFSMPAGVLVYWTTTNVFGMLQRGLFEMRPVQQAL-GWPLPEDMPAP---------AAPADK--------------------------------------------
Mbr_Oxa2   : IKRPVSPESREDRLG--TALRYLAHAY--IPVAAAVPSGLSLYWASSSVLTLTQNLMLRHPSVRQRV-GLP----------------AVPSEL--------------------------------------------
Ptr_Oxa1   : EQMVAQNAQSGHLMV--NFFRVMSIGY--VPVCVNFEAAMLCYWTSNNFMTLTQTAILKAPAARSYF-GIW----------------DAPKPV--------------------------------------------
Tps_Oxa1   : DQMMSSDPVRGRNMV--NAMRALAIVY--VPLTAYFNSAVLCYWVTNNSFIMGQSLFFKLEPVKKMF-GIW----------------DPPKPV--------------------------------------------
Yli_Oxa1   : ETGTNNLSPGMK-----KILQWAPWIS--VPFLYKMPAALLLHFFVNGILMLIQGVALRNPFFRKKL-GIH----------------EIVPLP--------------------------------------------
Cal_Oxa1   : ETGQHAMAAGMK-----KVMTVVPIAS--IFITKGFASAILYFAVNSIFSLIQSSLFKSSWFRKIA-GVP----------------PKLSLA--------------------------------------------
Sce_Oxa1   : ETGAQQFSSPMK-----RIFTILPITS--IPATVNLSSAVVLYFAFNGAFSVLQTVILRNKWVRSKL-KIT----------------EVAKPR--------------------------------------------
Mbr_Oxa1   : EGVKQNNVMMK------NVFRGLSIVL--LPVTINLPTAIFVYWCTANVFSLSQMLMLKIPGLKKSL-GIP----------------EQIQH---------------------------------------------
Hsa_Oxa1   : ETGVQSSDLQW--MR--NVIRMMPLIT--LPITIHFPTAVFMYWLSSNLFSLVQVSCLRIPAVRTVL-KIP----------------QRVVHD--------------------------------------------
Cfa_Oxa1   : ETGMQSSDLQW--MR--NIIRVMPLAV--LPITIHFPTAVFMYWLSSNVFSLCQVACLRIPAVRTIL-KIP----------------QRVVHD--------------------------------------------
Mmu_Oxa1   : ETGVQSNDLQF--MR--NIIRVMPLVV--LPVTIHFPSAVFMYWLSSNVFSLCQVACLRIPAVRTVL-KIP----------------QRVVHD--------------------------------------------
Aga_Oxa1   : DSARMSAANMQT-AK--YILRALPLFI--FPFTINFPGAILCYWACSNFFSLVQVGFLRIPKVRDFF-KID----------------RIVTHK--------------------------------------------
Dme_Oxa1   : DSARLSAANMNT-MK--YVLRALPIVI--FPFTVNFPAAILTYWACSNFISLGQVAVLRIPSVREYF-KIE----------------KMLTHA--------------------------------------------
Pin_Oxa1   : DAMGGDMQRNLK-----FGMRCFALMM--VPLTVNFQSGIFVYWVTSNMFTLTQTALMRLNVVKRAL-NIP----------------VTEVQR--------------------------------------------
Pra_Oxa1   : EAMGDEMKGKMK-----FGMRCFALMM--IPLTVNFQSGIFVYWVSSNMYTLVQTALMRLNFVKRAL-KIP----------------VSEVQR--------------------------------------------
Pso_Oxa1   : EAMTGEMKDKMK-----FGMRCFALMM--VPLTVNFQSGIFVYWVTSNMYTLTQTALLRVNFIKRAL-KIP----------------VTEVQR--------------------------------------------
Ota_Oxa1   : VEGMQTSQSAQ--MK--WFLRALAVAM--VPLTASFPQGVFVYWITSNMFSGVQTSITRTKGFKAAM-GIP----------------DVSAVA--------------------------------------------
Olu_Oxa1   : VEGMQTSQSAQ--MK--WFLRALAVAM--VPLTASFPQGVFVYWITSNIFSGFQTSITRTKAFKSTM-GIP----------------DVSAVA--------------------------------------------
Osa_Oxa1   : QEGMEGNPMARK-MK--NFSRGMAVLT--VPFTVSFAKGIFCYWITSNLFTLTYGFVIRRPAVRKFC-NLP----------------ALEAQS--------------------------------------------
AthOxa12   : QEGLEGNPVAGT-MK--KFSRIIAFLS--IPVLIGIEKALFCYWLTSNLFILVYGLTLRRPDVRKLI-NLP----------------DVVNSS--------------------------------------------
AthOxa11   : QEGMEGNPMAGT-VK--TVCRVFALLT--VPMTVSFPQAIFCYWITSNLFSLMYGLVIKRPQVKKML-RIP----------------DLPPPP--------------------------------------------
POxa11     : QEGMEGNPAAGT-MK--NVSRALAAAS--VPLTVSFPKAIFCYWITSNLFSLTYGLVLKAPGVKEFL-GVP----------------KVPVAP--------------------------------------------
POxa12     : QEGLEGNPIAAT-MK--KVSRVFAVAS--VPLTVGFPNAIFCYWVTSNLFSLFYGLTLKAPGVKKFL-GLP----------------EIPVAP--------------------------------------------
Cme_Oxa2   : ETGGAQLPPFAL-----NLMRIFALIL--LPLTAQFPAILFCYWLPNNLFSMLQAFALRHQRVRRWL-GCP----------------PLGARS--------------------------------------------
Esi0028_00 : EGGALAGSSVK--MK--AGMRGMALLV--TPLTMYVSTGVFVYWTTSNFYSILQTIAFKSSGIKKFF-DFP----------------DLPPNKLKSNTAEKEIGWLDVLGGDHPIKEYRKMQDQREVQAWFVEGEGGWTRK
Mmu_Oxa2   : LQKIGTSRFQMH-VT--NFVRAVSVLM--IPVAATVPSALVLYWLCSSLMGLAQNLLLRSPGFRQLC-RIP----------------PSKSDS--------------------------------------------
Hsa_Oxa2   : LQKIGMSRFQTY-IT--YFVRAMSVLM--IPIAATVPSSIVLYWLCSSFVGLSQNLLLRSPGFRQLC-RIP----------------STKSDS--------------------------------------------
Cfa_Oxa2   : LQKIGMSRFQTY-IT--YFVRAVSVLM--IPVAATVPSSIVLYWLCSSLMGLSQNLLLRSPRFRQLC-RIP----------------LTKSDS--------------------------------------------
Aga_Oxa2   : ASRTKLPSKLQTIFT--NIFRGLSILM--VPIAASVPSCLCLYWVTSSAYGLGQNLLLLSPRVRRTV-GIP----------------AVPSEL--------------------------------------------
Dme_Oxa2   : MSRTRPSTRLQNIAN--NVFRGLSVVM--VPVACTVPSALCVYWVASSSFGLAQNLLILSPEVRRSV-GIP----------------KTQTEL--------------------------------------------
Yli_Oxa2   : KAQAQAGPKLPKMMA--NFARVGAIAL--FSIAAQTPTAVCLYWISSSGFSLIQNVLLNKYMPLR---EEP----------------PMFTAA--------------------------------------------
Cal_Oxa2   : KTLELRPTLTDA-FG--NITKMSIVFM--MAISLHAPAALTIYWISSQLYSLLQNVMMDL--------MLP-------------------IS--------------------------------------------
Sce_Oxa2   : RLMFSNSTRVQEAMSILNVSRLGCVVM--LAMSSQAPFLLSLYWISSQLFSLVQNIILNWIYPYQR-------------------------------------------------------------------
Olu_Oxa2   : ASAAAQSRGMTI-VK--LVLEWMTLPM--LVIGMQLPQAVHCYWLTSSAWALAQNRALSTTFAREAL-GIN----------------ALAKVT--------------------------------------------
Ota_Oxa2   : AAAAQQSRGMTI-VK--LCLEWMTLPM--LLIGLQLPQAVHCYWITSSAYAYAQNRALSTAYAREAL-GLN----------------ELAKTT--------------------------------------------
Esi0170_00 : MKGATGWMKFFQ-----DGMQTFIILM--LPWVSTFPQGVFMYWIPSAVFQMGQTYTMKNNKVRELL-GLKPLGLPPREAAGATPSLAPAPAPA-------------------------------------------
Pra_Oxa2   : RTKSGLWTDLL------QMGQYGSLLA--IPWLATLPQGIFFYWLGASWSSMAQIAAMDNNNFRRRI-GLK----------------PRITQT--------------------------------------------
Pin_Oxa2   : RNKSGFWTTLL------QGGQYTTIFA--VPVLVNLPQGVFFYWLGASCSSMAQTIAMNNNNFRRRI-GLK----------------PRITET--------------------------------------------
Pso_Oxa2   : RKKSSFWTQVL------QFGQYGTIFA--IPLMANLPQGVFFYWLGASWSSMAQTIAMDNNNFRRRI-GLK----------------PRIAHT--------------------------------------------
Osa_Oxa2   : ----------------VYLEILTIPL--FLIGYVIPQGSLVYWTTNGLITVAQQLSLKNDAVKKVL-GLP----------------DTRAHQ--------------------------------------------
AthOxa21   : DTSTITGLLMRY-YK--LYLEILSVPL--FFVGYAIPQGSLVYWVTNSSVNIFQQLSLKHPTVGAKL-GLL----------------SQGATP--------------------------------------------
AthOxa22   : ----------------------------VWFFVGS-----------------------------------------------------------------------------------------------------
POxa2      : -------------YR--KYLNFVMIPL--FFIGYCIPQGSLVYWVTNSSLTAIQQVSLKLPVVRAKL-GLL----------------DKDFPK--------------------------------------------
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                    720         *       740         *       760         *       780
Cme_Alb3   : -------DKFDQALDQASKH-------------------------------------------------------
Ptr_Alb32  : -------TALKNQAVSA----------------------------------------------------------
Tps_Alb32  : -------YWGASKT-------------------------------------------------------------
Ota_Alb3_1 : ----------------------------------------------------------------------------
Olu_Alb3_1 : ----------------------------------------------------------------------------
Ptr_Alb31  : -------TASAPPRAN-----------------------------------------------------------
Tps_Alb31  : ----------------------------------------------------------------------------
Cme_Oxa1   : -------RTLDGAVDDR----------------------------------------------------------
CreAlb3_1  : -------PGSGRRNGAAGGA-------------------------------------------------------
CreAlb3_2  : -------ATAGSSTPIKKA-------------------------------------------------------
OtaAlb3_2  : -------SSPASAEPISSG-------------------------------------------------------
OluAlb3_2  : -------PPVAKSGAAG----------------------------------------------------------
OsaAlb3_a  : -------TAGRAKRTAS----------------------------------------------------------
AthAlb3_a  : -------SAGRAKRSAE----------------------------------------------------------
PAlb3_a1   : -------TAGRAKRSSG----------------------------------------------------------
PAlb3_a2   : -------TAGRAKRSAG----------------------------------------------------------
OsaAlb3_b  : -------KEESTNLGPCNK--------------------------------------------------------
AthAlb3_b  : -------EDKTQQISSTTR--------------------------------------------------------
PAlb3_b2   : ----------------------------------------------------------------------------
PAlb3_b1   : ----------------------------------------------------------------------------
Syn_YidC   : -------AAQASTGEAKEVFEP-----------------------------------------------------
Pma1_YidC  : -------PALATEAIGGSDRSK-----------------------------------------------------
Pma2_YidC  : -------PALATEAIGGSDRK------------------------------------------------------
Tps_Oxa2   : -------VDMGDSVQEFPKK-------------------------------------------------------
Ptr_Oxa2   : -------PPEAKYQFIAKKG-------------------------------------------------------
Esi0025_01 : -------KEPAEADFASKEDLERWGGGGEGASGEASRAAAEAAERAREAVAKASKVRHEELKRQHGERSGEDGPK
Mbr_Oxa2   : -------PRPLTSLRRHGNP------------------------------------------------------
Ptr_Oxa1   : -------PGQEPETKAA----------------------------------------------------------
Tps_Oxa1   : -------PGQETGLEK----------------------------------------------------------
Yli_Oxa1   : -------AAAPGAGVRK----------------------------------------------------------
Cal_Oxa1   : ---EMQANNPKANQSIQRH--------------------------------------------------------
Sce_Oxa1   : -------TPIAGATENM----------------------------------------------------------
Mbr_Oxa1   : ----------------------------------------------------------------------------
Hsa_Oxa1   : -------LDKLPPGFLEPLG-------------------------------------------------------
Cfa_Oxa1   : -------SNKLLPGFLKPLG-------------------------------------------------------
Mmu_Oxa1   : -------PDKLPPGFLKPLG-------------------------------------------------------
Aga_Oxa1   : -------PETLPKGFTD----------------------------------------------------------
Dme_Oxa1   : -------PSALPPGFVGEQG-------------------------------------------------------
Pin_Oxa1   : -------LEASTITTSP----------------------------------------------------------
Pra_Oxa1   : -------LEASSITQTP----------------------------------------------------------
Pso_Oxa1   : -------LEAASITTSP----------------------------------------------------------
Ota_Oxa1   : -------DAPADAALSR----------------------------------------------------------
Olu_Oxa1   : -------EAPAEAALGR----------------------------------------------------------
Osa_Oxa1   : -------ASAKKQMFNLMRP------------------------------------------------------
AthOxa12   : ------TRQPSPPLKKK----------------------------------------------------------
AthOxa11   : -------PGQQPSFDLSKK-------------------------------------------------------
POxa11     : -------PTTAAKSFDLK-------------------------------------------------------
POxa12     : -------ASTTPSFDLNKR------------------------------------------------------
Cme_Oxa2   : -------AAATAGHTNR----------------------------------------------------------
Esi0028_00 : AHNAEQGEGGNVAREGAPFHAPPSMAGPVSGKAKTPSFASSAAAGTPKVVLRSVRPKPAGDRGKTAARGPRKNRG
Mmu_Oxa2   : -------ETPYRDLSAA---------------------------------------------------------
Hsa_Oxa2   : -------ETPYKDIFAA---------------------------------------------------------
Cfa_Oxa2   : -------DSPYKDLFAA---------------------------------------------------------
Aga_Oxa2   : -------THPYQHIRS----------------------------------------------------------
Dme_Oxa2   : -------SEPYDLLWLA----------------------------------------------------------
Yli_Oxa2   : -------NEALPKEH-----------------------------------------------------------
Cal_Oxa2   : -------FTPKKRININ---------------------------------------------------------
Sce_Oxa2   : ----------------------------------------------------------------------------
Olu_Oxa2   : -------REIAASLGGE----------------------------------------------------------
Ota_Oxa2   : -------REIVRELHSD----------------------------------------------------------
Esi0170_00 : -------PIPAPKAIGG----------------------------------------------------------
Pra_Oxa2   : -------ESPAAAAAEM----------------------------------------------------------
Pin_Oxa2   : -------KPPAAAVAEM----------------------------------------------------------
Pso_Oxa2   : -------ESPAAAAAEM----------------------------------------------------------
Osa_Oxa2   : -------KFPRVGMMQEKEH-------------------------------------------------------
AthOxa21   : -------GGHSMEISESSHF-------------------------------------------------------
AthOxa22   : ----------------------------------------------------------------------------
POxa2      : -------APALSALSSS---------------------------------------------------------
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