CLUSTAL X (1.83) MULTIPLE SEQUENCE ALIGNMENT

File: C:sequences.ps **Date: Tue May 20 17:52:40 2008**

Page 1 of 4

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                                                                                                                                                                              *..
gae.Chlamydomonas.reinhardti --------------------------------------------------------MCVRASAYKTAPPQLGVLSKEQVDKFHRDGFLVLEKFASPEECAALQKRMDQLLQDFDP--QTVSIFS-----TKNQ---AATTDNYFLRSASD     84
                        Moss --------------------------------------------------------MGVEQG-----------LSQAQKDFYESEGYLVIPDYASPSECTTLIKRMDELLRDFDP--TTFSIFS-----TTNQ---KANMDSYFYNSANN     73
                       Grape --------------------------------------------------------MGISGK-----------PSPEQLHSFHSQGFLVIESFSSPEEIDDMRRRMDQLLDGFDCS-TAASIFS-----TKNQ---QKLTDDYFYESAEK     74
            Black.Cottonwood --------------------------------------------------------MGITGT-----------LSSDQFDSFNSQGYLVIESFANPEDIESMMKRMDKLLDDFDY--TNVSVFS-----TKNQ---RKVTDDYFYQSAEN     73
                 Arabidopsis --------------------------------------------------------MGITGS-----------LTPDQLDFFHSQGYLVIESFASEDEIRGLRKRMDELLNQFDC--SVSSIFS-----TKNQ---KHTTDNYFFESAEK     73
                        RIce --------------------------------------------------------MPPAGS-----------LTDEQLRFFDANGYLVLGSFSSAEEVRAMRDRMAELVDGFDG---AGDVFS-----TKDH---RQVKNDFFFKSAEN     72
Rice.Japonica.cultivar-group --------------------------------------------------------MLPAGS-----------LTDKQLHFFDANGYLVLGSFSSAEEVKAMRDRMAVLIDGFDG---AGDVFS-----TKDH---RQVKNDFFFKSAEN     72
    Ostreococcus.lucimarinus --------------------------------------------------------MRAKTSWSKCSTSG--SLAPEDVSAFETHGYLVLTDFASPTEISAMRARAAEIVDKFDANANRESIFS-----TVNQSGQKRATDEYFLGSADK     87
                       Human --------------------------------------------------------MACLSP--------------SQLQKFQQDGFLVLEGFLSAEECVAMQQRIGEIVAEMDVPLHCRTEFS----TQEEEQLRAQGSTDYFLSSGDK     76
               Horseshoe.Bat ----------------------------------------------------------------------------------------------------------------MDVPVHCRTEFS----TQEEEQLRAQGSTDYFLSSGDK     34
                    Marmoset --------------------------------------------------------MACLSP--------------SQLQKFQEDGFLVLEGFLSAEECVAMQQRIGKIVAEMDVPPHCRTEFS----THEEEQLQAQGSTDYFLSSGDK     76
                      Mouse1 ------------------------------------MKENSPGAIELSQLSPAVFPMACLSP--------------SQLKKFQEDGFLLLEGFFTADECVAMQQRIGEIVAEMDVPLHCRTEFS----TQEDEQLQTQGKTDYFLSSGDK     96
                      Mouse2 --------------------------------------------------------MACLSP--------------SQLKKFQEDGFLLLEGFFTADECVAMQQRIGEIVAEMDVPLHCRTEFS----TQEDEQLQTQGKTDYFLSSGDK     76
                      Mouse3 --------------------------------------------------------MACLSP--------------SQLKKFQEDGFLLLEGFFTADECVAMQQRIGEIVAEMDVPLHCRTEFS----TQEDEQLQTQGKTDYFLSSGDK     76
                       Horse --------------------------------------------------------MTGLSP--------------SQLQKFQEDGFLVLEGFLSAEECVALQQRIGQIVAEMDVPPHCCAEFPPRILNKAEEQQKTQDNTEYFLSSGDK     80
                    Platypus --------------------------------------------------------MAGLSP--------------EQVRKFQEDGFLVLEGVFSPEECEGLKARIAEIVAGMEVPLHCRTEFS----TDKEETLRAQGNSEYFLTSGDK     76
                     Chicken --------------------------------------------------------MASVTQ--------------HQMQKFREDGFLVLEHFFSPEECDSMRSSIQRILDGMEVPPHCRTEFS----TKEEEQLQAQGSSDYFLTSGDK     76
                        Frog --------------------------------------------------------MAPVTD--------------EQVQRYHRDGYLVLEGVFSPQECELMKQEIEKILEGMDVPSHCRTEFI----TQQEDQLRAQGSADYFMTSGDK     76
                   Zebrafish --------------------------------------------------------MDVLTD--------------QDVQKFRDEGYLVLEGLLSPEECDALRRRMSEIIESMDVPEHCRTQFS----TDHDEQLKTQGNADYFITSGDK     76
                  Sea.Urchin ------------------------------------------------------------------------------------------------------------------------------------------------MTSGDK      6
           Purple.Sea.Urchin ---------------------------------------------------------------------------------FEKDGFLVVENFLTKEEVESLKIECHDIVQNMDPKQHARCTFD--------TSENTQARNEYFMTSGDK     61
       Yellow.Fever.Mosquito --------------------------------------------------------MRNQL----------------ISQILEDG-YTVIDDFLTPEEVTELLEAGKNLHK--DAPKEERKVFS-----TIN-SSATQSRDRYFIESGDK     69
              Culex.Mosquito --------------------------------------------------------MPVDLGGRHYVQCG-----IGLGRMLYARTVRVVDDFLSPDEVQELLEAGKNCTK--MPP---RRNAS-----TIN-SKTSQSRDRYFIESGDK     78
            Malaria.Mosquito -----------------------------------------------------FLYLSP-----------------FLPVQIREDGFAVIDDFLTPDEVQELLQVGQNLHK--DAPKEERKVFS-----AKADSKSAQSREQYFLESADK     73
     Drosophila.Melanogaster --------------------------------------------------------MHS-----------------KLLDELNENGYIVIEDFLTAEEVDSLYQAGRALCL--DAPQNNRKIFS-----TIK-QEDAQGKELYFMESGDK     69
            Red.Flour.Beetle --------------------------------------------------------MWN------------------IKQQFEKDGYVVLEDFLSETEINELRAECDNLVE--NMPEESKRAVF-----SSADSNILQDKDKYFLDSADK     69
                   C.Elegans ------------------------------------------------------------MWD--------------LREKFERDGFVVVENVFNDQEIDEMKKSISKIVNDMDLAEHPKSVFSTY--DEDK-----HAADSYFLNSSDK     69
                 Sea.Anemone --------------------------------------------------------MVDTNKD--------------LHSKFASDGYVVIENFLSLDEVQELREAMRNIVDDLDLSQNPLSVFKTG--DD-------QVGDDYFLTSGDK     71
        Monosiga.brevicollis -----------------------------------------------------------------------------------------------------MRTAIEGEIARYDPAKEHTTIFSSN--AET------QNSNDYFLESGDK     41
           Rice.Blast.Fungus -------------------------------------------------MSSSTP-APGLSPT--------------QLDFFHQNGYLIVPDALPPSTVSSLLAETSRLLESLDLSTHPMTKFRTG--GE---DGKDHVGDDYFLGSGDK     81
           Neurospora.crassa -------------------------------------------------MASEPPTSDGLTPT--------------QLAFFHQNGYLIIPRALPPTTVSRLLSETQKLLSDFDLTTHPLTRFRTG--GS---SGHDHVGDDYFLSSGDK     82
      Fungus.Gibberella.zeae --------------------------------------------------MADTP---GLSPE--------------QLEAFSRDGYLILPGALSSSTVKSLLDETHNLLENFSLDDHPLTRFSTG-------EKRDHVGDDYFLTSGDK     76
   Podospora.anserina.Fungus -------------------------------------------------MSTSSEPKPGLTPE--------------QLSFFHTNGYLIIPSALPPTTVTNLLNETHSLLSSLDITTHPLTKFSTG--GQ---DGTDHVGDDYFLSSGDK     82
lerotinia.sclerotiorum.Fungu --------------------------------------------MS-SPTPLGPAASKGLTKE--------------QLDTFNKDGYSIIPGALSPETVSSLLSETHSMLNNFSLEDHPMTKFSTG--EG---EEVEHVGDSYFLESGDK     86
otryotinia.fuckeliana.Fungus --------------------------------------------MSPSRTSPPPAASKGLTKE--------------QLDTFNKDGYLIIPGALSQETVSSLLSETHSMLNNFSLEDHPMTKFSTG--EG---DDVEHVGDSYFLESGDK     87
   Yarrowia.lipolytica.Yeast MYCMCCTCTYHTRLYVVLSTLSPPQLDHPTNLNTVLYFLCSACKVLRDFTSSSTRTSIMLTPN--------------QIEKFQKDGCIVVPNELSPETISSLLQESHRLLSEFSLEGHPMTKFSTG--DSLGSGDAKHIGDAYFLESSDK    134
      Candida.albicans.Yeast --------------------------------------------------------MVGLTKE--------------QLSTFEREGMLCIPDFLTPEQTAKLLAESKTLLSNCDLSTHPKTTFKT--------ADDDHIGDKYFFESSDK     72
ast-like.Fungus.Cryptococcus --------------------------------------------------------MPYLTEE--------------QKQRWKEDGYLVLPSFFTDEETKDMLNEAKRLCGEFDIEGHPMTTFKTA--ADD-----AHIGDEYFLNSGDK     73
      Ustilago.maydis.Fungus ----------------------------------------------MVTNAETCGSDGTLTSA--------------QIAQFHRDGYLLLPSFF---DPTALLAHSKHLISSFSLENHPLTAFTTS--SEEE-GEEAHVGDRYFLESGDR     84
     Laccaria.bicolor.Fungus ---------------------------------------------------------------------------------FHRNGYLIIPGFLSAQEAEELLSRSKQLLDDFDINDHPLVRFHTK--FTT--GEDNHVGDDYFLTSGDK     65
           Oikopleura.dioica ---------------------------------------------------------MDLKQ---------------VADDFKENGLAVVKGFASAEECEAMRDEMRKICADLKADEIHCFETE-------------SGRNDYFTQSGDK     65
      Stigmatella.aurantiaca ---------------------------------------------------------MSRAR------------------DFEQQGFLILPGFVSGNSCDALKHRAEELVTGFQPET-RSIFTTHE---------QTRTSDAYFLSSGDQ     65
       Alpha.proteobacterium --------------------------------------------------MNAVPRFAATATGAP---------TPAMLAAWDRDGVLVIEDAVSHADCDSLIERSRAIVDDWDPTSGAAVFSTTA---------PRHAADRYFRESGDA     82
      Legionella.pneumophila -----------------------------------------------------MILIFEEHRMQL---------SSEQCDFFFTNGYLVINNFFSESVCDLLKQRIETLLENNQAEIPKTIFSTQT---------NEHAKKQYFLDSGDK     79
                 Marinomonas --------------------------------------------------------MLNEGQIK----------------QYQDQGFLVLDEVFPLDELEQVKQQAAKIVNDWHDDDRSHTFGTKD---------NDRSGNDFFLDSAET     69
eudoalteromonas.atlantica.Ba --------------------------------------------------------MLSVDQKN----------------EFRAQGYIVLNQLFSTAEMASLKSEAESIVELFDPNSTRAVFSTQD---------QSKSRDDYFLQSGDK     69
trahymena.thermophila.Protaz -----------------------------------MILKKFLNCNKYICNLQLQRFSFKPLNQIF---------TEEHLNQFQENGATIVHNVVTEEMIEELINQCKKIMKSNNFKEKRVCFSKGE---------LEVAQS--FIDSGDQ     95
                       ruler 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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CLUSTAL X (1.83) MULTIPLE SEQUENCE ALIGNMENT


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gae.Chlamydomonas.reinhardti IGFFFEDK----AFDEA-GQLRQAKELSINKVGHALHDLDPVFRQFSRSA-------------AVCNVMRSLGYAR-PLPVQSMYIFKQPSIG-------GEVVPHQDSSFIHTSPLS-CVGLWWALEDCTKDNGCLWAMPGIHKDGLKR   207
                        Moss IGFFFEER----AFDEN-RNLKQPKELSINKVGHAMHDLDPEFRKFSRSA-------------KVSAIAASLGYRR-PAPIQSMYIFKQPGIG-------GEVVPHQDNTFMCTDPPS-VLGYWWALEDATKENGCLWVVPKSHKQGLKR   196
                       Grape ISFFFEEK----AFGED-GNLKQAKQLSINKVGHALHEIDPVFKTFSCSE-------------KLSSLMLSLGYKG-PVIIQSMYIFKQPGIG-------GEVVPHQDNSFLYTEPPT-CTGLWLALEDATILNGCLWAIPGSHKNGLVR   197
              Black.Cottonwood ISFFFEEK----AFGDD-GSLKQPKQLSINKVGHALHELDPVFKGFSSSE-------------KCSGLLSSLGYKK-PVIIQSMYIFKQPGIG-------GEVVPHQDNSFLYTEPTT-CTGMWLALEDATLLNGCLWAIPGSHKNGLVR   196
                   Arabidopsis ISFFFEEK----AFGDD-GKLKQPKQLSINKVGHALHELDPLYKDFTYSS-------------KFSSLASSLGYKR-PVVMQSMYIFKQPGIG-------GEVVPHQDNSFVYTDPQS-CTGLWIALEDSTLVNGCLWAIPGSHKNGLVR   196
                       RIce ISFFFEEK----AFGDD-GCLKQAKELSINKVGHALHELDPVFKKFSFGA-------------NVSSLFSSLRYKR-PAVIQSMYIFKQPGIG-------GEVVPHQDNTFLYTDPPS-CTGLWLALEDATKTNGCLWAIPGSHKNGLKR   195
Rice.Japonica.cultivar-group ISFFFEEK----AFGDD-GCLKQAKELSINKVGHALHELDPVFKKFSFGE-------------NVSSLFSSLRYKR-PAVIQSMYIFKQPGIG-------GEVVPHQDNTFLYTNPPS-CTGLWLALEDATKTNGCLWAIPGSHKNGLKR   195
    Ostreococcus.lucimarinus VCCFFEEG----AFDER-GELRVPKHLSINKIGHALHDLDPVFRAWSRSE-------------KVKNLFKTLGSPRNPQPVQSMYIFKQPSIG-------GEVVPHQDSTFLNTDPPT-CVGIWLALEDCTLENGCLHALSG--TPDVAR   209
                       Human IRFFFEKG----VFDEK-GNFLVPPEKSINKIGHALHAHDPVFKSITHSF-------------KVQTLARSLGLQM-PVVVQSMYIFKQPHFG-------GEVSPHQDASFLYTEPLGRVLGVWIAVEDATLENGCLWFIPGSHTSGVSR   200
                 Horseshoe.Bat IRFFFEKG----VFDKK-GNFLVPPEKSINKIGHALHAHDPVFKHVTHSP-------------KVQALARSLGLQM-PMVVQSMYIFKQPRFG-------GEVSPHQDASFLYTEPLGRVLGLWIAVEDATLENGCLWFIPGSHTSGVSR   158
                     Marmoset IRFFFEKG----VFDEK-GNFLVPPEKSINKIGHALHAHDPIFRSITHSP-------------KVQALARSLGLQM-PVVVQSMYIFKVSSLGP------AVVFPHQDASFLYTEPLGRVLGVWIALEDATVENGCLWFIPGSHTSGVSR   201
                      Mouse1 IRFFFEKG----VFDEK-GNFLVPPEKSINKIGHALHAHDPVFRSITHSP-------------KVQALVRSLGLQM-PVVVQSMYIFKQPHFG-------GEVSPHQDATFLYTEPLGRVLGLWIAMEDAMLENGCLWFIPGSHTRGVSR   220
                      Mouse2 IRFFFEKG----VFDEK-GNFLVPPEKSINKIGHALHAHDPVFRSITHSP-------------KVQ---------------------QPHFG-------GEVSPHQDATFLYTEPLGRVLGLWIAMEDAMLENGCLWFIPGSHTRGVSR   179
                      Mouse3 IRFFFEKG----VFDEK-GNFLVPPEKSINKIGHALHAHDPVFRSITHSP-------------KVQALVRSLGLQM-PVVVQSMYIFKQPHFG-------GEVSPHQDATFLYTEPLGRVLGLWIAMEDAMLENGCLWFIPGSHTRGVSR   200
                       Horse IRFFFEKG----VFDEK-GNFLVPPEKSINKIGHALHAHDPVFKGATHSS-------------KVQVSRGGARAGAGPDVTGPSSLLQQPRIG-------GKVPAHQDATFLYTEPLGRLLGLWIALEDTTVENGCLWFIPGSHTSGVSR   205
                    Platypus IRFFFEKD----VFDKE-GNFKVPKEMSINKIGHGLHARDPVFKKITHSP-------------IVQAITRNLGYEE-PVVVQSMYIFKQPHIG-------GEVLAHQDSTFLYTEPLGSLLGFWIAVEDATLENGCLFFIPGSHKGGISQ   200
                     Chicken IRFFFEKG----VLDER-GNFLIAKEKSVSKIGHALHAHDPVFKQITHSS-------------KVQELGRKLGLER-PVVVQSMYIFKQPGIG-------GEVTPHQDATFLHTEPLGRVLGFWIALEDATQENGCLWFIPGSHTSGITR   200
                        Frog IRFFFEKG----VFDEK-GHFLVPREKSVNKIGHALHAHSLVFKEVTHKA-------------QVQETGRRLGLMK-PVIVQSMYIFKQPGIG-------GEVTPHQDATFLHTEPLGRIIGFWIAVQDATEENGCLWFIPGSHRAGISR   200
                    Zebrafish IRFFFEKG----VFDDK-GEFVVPKEQSLNKIGHALHAYEPLFKRVTHSP-------------KVQNICKKLELIN-PVILQSMYIFKQPGIG-------GEVTPHQDATFLYTQPLGRVMGVWVALEDAMQENGCLWFIPGSHNDGITR   200
                   Sea.Urchin IRFFFEKE----ALDKE-GNLLVDKHSSLNKVGHALHELSPPFKKVSCSK-------------KVQDIARNLDFKK-PVIAQSMYIFKPPHFG-------GEVGAHQDAIFMYNTPL-KLIGYWIALEDAEIDNSCLHFIPGSHSRDITT   129
              Purple.Sea.Urchin IRFFFEKE----ALDKE-GNLLVDKHCSLNKVGHALHELSPPFKTISCSK-------------KVQDIARNLDFKK-PVIVQSMYIFKPPHFG-------GEG-----------------------------------------DITT   142
           Yellow.Fever.Mosquito VRYFFEEG----AVAEN-GELLVDPSVALNKVGHALHTDHAVFNKVTFSN-------------RVKEVCWQLGFQK-PAVAQSMYIFKNPGIG-------GEVKPHQDATYLYTEPS-STIGFWIPLEDATLQNGCLYFIKGSHKSGVHR   192
                  Culex.Mosquito VRYFFEEG----SVGEN-GELLVDPSVALNKVGHALHSEHPVFTKVTMSN-------------RVKEVCWQLGFQT-PAVAQSMYIFKNPGIG-------GEVKSHQDATYLYTEPS-TTIGFWIPLEDATLQNGCLHFIKGSHKSGVHR   201
                Malaria.Mosquito VRYFFEEG----AVGEN-GELLVDPAIALNKVGHALHTEHPAFEEVTFSN-------------RVKEVCWQLGFRR-PAVAQSMYIFKNPGIG-------GEVKSHQDATYLYTEPS-TTIGFWIPLEDAMLQNGCLHFIKGSHKSGVHR   196
          Drosophila.Melanogaster VRYFFEKG----AVGDE-GQLLVDPMIALNKVGHALHVEHPAFNAITFSN-------------RVREICWQLNYNK-PAVCQSMYIYKNPGVG-------GEVTPHQDSWFLHTDPN-SAVGFWLALEDCTLQNGCLQFIKGSHKSGVHR   192
                 Red.Flour.Beetle ISYFYEAD----ALGPN-GELKVKPELSLNKIGHALHELNPVFRRITLDE-------------RVKECCFQLGFED-PVVVQSMYIFKNPGLG-------SEVIAHQDASYLHTEPV-KVVGFWIALEDATLENGCLWFSKGSHKSGVHR   192
                       C.Elegans IRFFFEEG----AVDKD-GELTVPKDKALNKIGHGLHFLDPTFEKMTFNSK-------------IQNIFKEIG-YQEPGVVQSMYIFKQPKIG-------GAVTDHVDSTFLRVDPIDHLTGVWIAIDEASVENGCLSFIPGSHKDTSSA   193
                   Sea.Anemone IRPFMEEG----AFDKQ-GNLVKDKHVAINKIGHALHAFNPVFKKATFSKK-------------IQEIAKSVAGMKNPVVPQSMYIFKQPGIG-------GEVNPHRDSTYLYTEPIS-AIGFWIPLEDCTTENGCLWFIPGSHK-VDKI   194
             Monosiga.brevicollis IRYFFEPG----AIDDQ-GRIVVPTESAFNKIGHALHSLNPTFRKYTFDPR-------------IVDIAADLG-LNEPVVPQSMYIFKQPGIG-------GEVTSHQDSTFLYTTPLS-TTGFWIPLQDCDRENGCLQMVPGSHHQGLLG   164
                 Rice.Blast.Fungus IRFFFEED----AVDDA-GNLTKDKSRAVNKIGHYLHALSPPFAKLLGND-----GAVA--KASPAAVARDLGFR-DPRCLQSMVICKQPEIG-------GAVPPHQDSTFLYTNPPS-AVGFWYALEDATLENGCLSFLPGSHRWAP--   208
                 Neurospora.crassa IRFFFEED----AFDDASGNLIKPKDKAINKIGHYLHGLNPAFASLLATSPDDERGWVQDLKARPAAVARDLGFK-DPRCLQSMVICKQPEIG-------GAVPPHQDSTFLYTNPPS-AVGFWYALEDATLENGCLSFLPGSHLWAP--   217
             Fungus.Gibberella.zeae VRFFFEED----AFDDE-GKLIKPKARAVNKIGHYLHALSPPFAHLLDHDTS---------KVSPPAVARSLGFK-DPRCLQSMVICKQPEIG-------GAVPPHQDSTFLYTNPPS-AVGFWYALEDATLENGCLSFLPGSHRWAP--   201
          Podospora.anserina.Fungus IRFFFEQD----AFGPD-GQLTKPKHLAVNKIGHFLHGLSPPFAELLKGVPGQ--------RALPKDVAKDLGFE-DPRCLQSMVICKQPEIG-------GAVPPHQDSTFLYTDPPS-AVGFWYALEDATRENGCLSFLPGSHLWSR--   208
lerotinia.sclerotiorum.Fungu IRFFFEED----ALSLK-GELLKPKHLSINKIGHALHTLSPPFAALLSPQS----------THSPSLIAKSLGFQ-QPQCLQSMIICKNPEIG-------GAVPAHQDSTFLYTDPPS-AVGFWYALEDATKENGCLSFWPGSHRWEG--   210
otryotinia.fuckeliana.Fungus IRFFFEED----ALSPT-GELLKPKHLSINKIGHALHSLSPPFAALLSPNA----------THSPSLIAQSLGFK-KPQCLQSMIICKNPEIG-------GAVPPHQDSTFLYTDPPS-AVGFWYALEDATRENGCLSFWPGSHKWEK--   211
   Yarrowia.lipolytica.Yeast IRFFFEEG----AVR-D-GKLTVAKEKAVNKIGHALHDLNPEFNKMSVTAR-------------NRDIATSLGLK-DPKILQSMLIFKQPEIG-------GKVPSHQDGTFLYTKPQS-AIGFWYALEDCTSHNGTLAFVPGSHKTHP--   254
       Candida.albicans.Yeast VSFFFDTD----AFDKD-GNLQVDLSKAINKIGHGLHIHNQLFQETTFDKK-------------VQDIARSLEFK-DPRVLQSMCIFKQPTTKTSNNSRDNAVPPHTDATFLYTDPQT-AIGFWYALEDCTLDNGCLAYIAGSHKKYP--   200
ast-like.Fungus.Cryptococcus IRYFLEPSSVTPATATTPAKLLVPPAQSINKIGHALAVLNPVFRKYTLETP------------KMSNLAKELGEQESPRVLQSMVICKQPRIG-------GAVPCHNDSTFLYTDPPS-AIGAWIALEECTPQNGCLSFLPGSHRLSR--   201
       Ustilago.maydis.Fungus IHYFFEQG----ALDATTKSLLVPKDRAINKCGHGLHMLDPVFREFSFSS-------------KLQNVARSLAVHKDPRVLQSMIICKQPSIG-------GAVPSHNDSTFLYTDPPS-AIGFWFALEDCTTSNGCLSFLPGSHRWPKNP   209
     Laccaria.bicolor.Fungus VRYFLEED-----AVDKHGKLIREKQKSVNKIGHALHELDPVFRKVTLENE------------SLRALARDLKFHRDPVALQSMVITKQTQIG-------GEVREHNDSTFLYTNPPS-ALGFWIALEQCTQHNGALSFLPGSHLTVP--   188
            Oikopleura.dioica IRFFFDTD-----AKASADDLVKTAFTSLNKVGHALHTHPGVFQDLVTAP-------------KTKEVLRAINLKK-VCVPQSMYIFKQAKFG-------SAVPPHQDSTFLHTSPTQTVVGLWLALEDATEDNGCLWFIPGSHKPYKDE   189
        Stigmatella.aurantiaca IRFFFEED----AFRPD-GSLRQPQALSINKIGHALHDLEPVFDRFSRTP-------------ELAALAAELGLTR-PLLLQSMYIFKQPHIG-------GEVTSHQDATFLFTEP-STCLGFWFALEDATLENGCLWVQPRGHRQGLKK   188
         Alpha.proteobacterium IRVFLEDG----AVDAD-GTLTRPKHAAVNKLGHAMHDLDPVFDRVSRRP-------------TLAALACGLGLAD-PRLVQSMVIWKPPSIG-------GAVTCHQDATFLITDP-PSVIGFWLALEDADAGNGCLFVIPGGHRGPLRQ   205
        Legionella.pneumophila IHYFFEPG----AFDEA-GDWLRPFNQSINKIGHALHELDPVFRQYSRDD-------------RIKKIAHQLGLKT-LGLVQSMYIFKQPGIG-------AEVLCHQDSTYIFGED-SDALGFWFAIEDATLENGCLEVIPSPCTTPLKQ   202
                   Marinomonas MSCFFEEE----AFDEK-GEFVQDRALCINKIGHALHELDPVFKRFSHQK-------------ILGDIAKDIGLQE-PQIRQSMYIYKQPNIG-------GEVNWHQDATFFFTTP-QSVVTYWFAMEDATLENGCLWVEPEGHKGPLRE   192
eudoalteromonas.atlantica.Ba IRCFFEEE----AFDEK-GDLKQAKAVSINKIGHALHTLNPVFKAFSHDP-------------RIRQLARDVGLFK-PQIHQSMYIFKQPKIG-------GVIRWHQDGTYFLSDP-LSVVTFWFAVEDATIENGCLQVKADGSDTPLRE   192
trahymena.thermophila.Protaz IGFFFEPN----VFDEH-NNLKVPEDQVLNKMGHALHDLDPVFEKFSYRP-------------LLQYILKQLGYQK-PQCIQSMYIFKNQKVG-------TPVAPHSDNTFLITVPQSSAVGFWFALHDATIENGCMWGIPGSHKNPTTH   219
                     ruler .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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CLUSTAL X (1.83) MULTIPLE SEQUENCE ALIGNMENT

File: C:sequences.ps **Date: Tue May 20 17:52:40 2008**


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gae.Chlamydomonas.reinhardti ----------------------------RFTLGPGGK--VSFDAPQPAYDLS---------------------QFVPLECPAGTLVLLQGENVHYSAENTSPVSRHSYSMHLVESAP-GVTWSADNWAQRAPENP--WQPLY-------   295
                        Moss ----------------------------KF-LKEGDS--VRYDVPQPEYDMS---------------------TFIPVEMKAGSLILLHGDLVHQSYENKSSKQRPAYSIHVIETD--GTFYPETNWLQRRPDFP--LEPFYEKPGSLA   289
                       Grape ----------------------------RFIRGDEG---VYFDQPSPSYDDK---------------------DFVPVEVKAGSLVVLHGDLIHQSFENQSPKSRHAYSLHVVDTD--GCKWAQENWIRRKVDP----EPLYES-----   283
            Black.Cottonwood ----------------------------RFLRGENG---VYFDQPSPSYDQK---------------------DFVPIEVKAGSLVLIHGDLIHQSFENQSSKSRHAYSWHVVDTD--GCKWAPENWIRRKVEP----EPLYAS-----   282
                 Arabidopsis ----------------------------RFIRGDNG---ITFDQPSPSYEQK---------------------DFVSIEMKAGSLIAIHGDLIHQSFENLSSKSRHAYSLHVVESD--GCKWAKDNWIQRAKMP----EPLYVLP----   283
                        RIce ----------------------------RMIRDEID---THFDHPSPTYDLK---------------------EFVPLEVKSGDLVVIHGDLIHQSFENLSPVSRHALSLHVIDTE--GCEWSKQNWLQRKIPP----QPLYEN-----   281
Rice.Japonica.cultivar-group ----------------------------RMIRDEND---THFDHPSPTYDLK---------------------EFVPLEVKSGDLVVIHGDLVHQSFENLSLVSRHALSLHVIDTE--GCEWSKQNWLQRKIPP----QPLYEN-----   281
    Ostreococcus.lucimarinus ----------------------------RMVVDHDGTRAVEFIGDAPTHDLT---------------------VAEPLDVPAGTLVVLHGQNVHYSRPNLSPASRHAYSVHYVDAT---ATWRPTNWLRRSPDFP--FVPL--------   296
                       Human ----------------------------RMVRAPVGSAPGTSFLGSEP--ARDNS-------------------LFVPTPVQRGALVLIHGEVVHKSKQNLSDRSRQAYTFHLMEASG--TTWSPENWLQPTAELP--FPQLYT------   291
                 Horseshoe.Bat ----------------------------RMVRAPAGSAPGTCFLGSEP--ARDNS-------------------LFVPTPVQRGALVLIHGEVVHKSEQNLSNRSRQAYTFHLMEASG--TIWSPENWLQPTAELP--FPPLYT------   249
                      Marmoset ----------------------------RMVRAPAGSAPGTSFLGSEP--AWDSS-------------------LFVPTPVQKGALVLIHGEVVHKSKQNLSDCSRQAYTFHLMEASG--TTWSPENWLQPTAELP--FPPLYT------   292
                        Mouse1 ----------------------------RMIRAPSDSGPGTSFLGSDP--AWASN-------------------LFVPLPVRRGGLVLIHGEVVHKSEQNHSDHSRQAYTVHLMEAAG--TVWSPGNWLQPTPELP--FPPLYS------   311
                        Mouse2 ----------------------------RMIRAPSDSGPGTSFLGSDP--AWASN-------------------LFVPLPVRRGGLVLIHGEVVHKSEQNHSDHSRQAYTVHLMEAAG--TVWSPGNWLQPTPELP--FPPLYS------   270
                        Mouse3 ----------------------------RMIRAPSDSGPGTSFLGSDP-------------------------------------------------------------------------------------------------------   220
                         Horse ----------------------------RMVRTPAGSMTGISIRGSDP--AWDNS-------------------LYVPTEVGRGSLILIHGEVVHKSEQNLSDRSRHVYTFHLMEASG--TVWSPENWLQPTAELP--FPPLYT------   296
                      Platypus ----------------------------RLVRAPPDSVPATHFIGSEQ--VYDDS-------------------SFIAIPIQKGGLVLFHGEAVHKSEMNRSSCSRHAYTFHLMESKG--ILWSQDNWWQPTPEMP--FPALYS------   291
                       Chicken ----------------------------RMVRAAQGASTCVEFVGSEP--AYDDS-------------------KFIPVPISKGGLIVIHGEVVHKSAMNSSAFSRHVYTFHVMEAEG--TNWSKENWLQPTPELP--FPPLYT------   291
                          Frog ----------------------------RMVRTPPGTYPLTEFVGEEP--KYDED-------------------QFVAAPVPKGSLVLIHGEVVHKSELNSSPNSRHAYSFHVMESEE--SRWSPENWLQPTPELP--FPSLFT------   291
                      Zebrafish ----------------------------RMVRTPKGTFPLTDFIGREK--DYDDK-------------------LFVPAPVKKGGAVLIHGEVVHRSAANTSDASRHVYTFHIMESEN--TVWSPENWLQATEELP--FPSLYT------   291
                     Sea.Urchin ----------------------------RMVKDPDGT--ATFFTGDPHPMKIPDD-------------------DFIPVPVKAGSLILINKKVIHRSSQNTSDRSRHIYTFHVAESEN--TEWSKENWLQPTPEKP--FTQLYTQE----   222
                Purple.Sea.Urchin ----------------------------RMVRDPDGS--ATSFQGDPYPMQVPDE-------------------DFIPVPVKAGSLILIDAKVVHRSSQNTSDRSRHIYTFHVAESEK--TDWSEENWLQPTSEMP--FPQLYTQN----   235
          Yellow.Fever.Mosquito ----------------------------RYIRNPDKSSPELLIYDRPAP-LYPQS-------------------NFCANPVKAGSLVLIHSQVVHRSDANRSDRSRHAYTFHVIETEN--SAYSCENWLQPATDQP--FPVLYERD----   286
                   Culex.Mosquito ----------------------------RYIRNPDASSPELLIYDRPAP-LYPQS-------------------NFVAVPVKAGSLVLIHSQAVHRSDANRSDRSRHAYTFHVIETEG--CEYSAENWLQPAEDRP--FPVLYERDP---   296
                  Malaria.Mosquito ----------------------------RWIRNPDKGADELLVYDRPAP-LYPQS-------------------NFVAVPVKAGSCVLIHSQAVHRSDANKSDRSRHAYTFHVIETED--SEYSKENWLQPAEDHP--FPVLYERK----   290
            Drosophila.Melanogaster ----------------------------RYLRNPDKDASELMVYDRAAP-IYPQS-------------------SFTPMQVSKGTCILIHGNVVHKSEPNRSQKSRHAYTFHVIETENN-VKYSEDNWLQAPKDKP--FPVLFERKA---   288
                 Red.Flour.Beetle ----------------------------RYIRNPDKNSNDLLIYTSPPP-YYQKS-------------------GFTAVPVKKGTCVLIHGQVVHFSEPNKSEKSRHAYTFHVVEQKN--TKYSEDNWLQLPQDKQ--FLSLYKN-----   285
                        C.Elegans -------------------------NYRFVRTHDTSGGALLKFIGTRPTYDQS-------------------KFQHVPISKGSLILIHGLVVHKSEANTSEKSRHAYTIHVMERK--NTKWSEQNWLQETENYK--FPDLYKD-----   288
                     Sea.Anemone -------------------------ERRLIRTPGSKE-HVVLHIGPQEEYNEA-------------------QSVPALTKKGSLVVIHGSVLHRSFPNKSSKSRHAYTFHMVEQ---NAKWSEQNWYVL------------------   275
              Monosiga.brevicollis -------------------------DRRMVRSTNESGVLGTTFTGQYFAPPPE-------------------EFQACETPMGSLVIIHGSVVHRSDPNKSARSRHAYTFHAIESQ--DTVYASDNWLQYPEDKP--FPRLVPESG---   261
                 Rice.Blast.Fungus ------------------------VERRLVRSAGDAAGTEMADNDGPKFPVGE---QYGEDKKP---AGADADAYVPGEVKAGSLVLIHGNLLHKSEKNLSNKGRIIYTFHVIEGQ-D-AIYDERNWLQPPAEG---FTELYR------   316
                 Neurospora.crassa ------------------------IEKRLVRKEGAKEGTEMVDNDGPRFPPGE---QYGEDKKPEEVKGREEEAYVPGEVKAGDLVLIHGNILHRSERNLSQKGRIIYTFHVIEGE-EGREYDERNWLQPPQEG---FTRLYA------   329
            Fungus.Gibberella.zeae ------------------------VENRLVRKEGN-AGTEMVNNDGPRFPATD---GYGKDEPE------DKHDYIPGEVKAGDLVLIHGNLLHKSEKNTSQKGRIIYTFHIIEGQ-D-RDYDAKNWLQPPEEG---FTKLYA------   305
         Podospora.anserina.Fungus ------------------------IRQRLVR--GGRTGAEMVENEGRQFPRDTREMKYGEDKKV------EEEEYVMGEVKAGDLVLIHGNLLHKSERNLSKKGRIIYTFHVIEQG-EGYKYDERNWLQPPEGG---FTRLYQ------   315
lerotinia.sclerotiorum.Fungu ------------------------VGKRFVRKSGG-GGTEFVGNDGERFPRRLE--RREK-GDQ------EE-NYVLGEVKAGDLVLIHGNLLHKSERNTSQKGRIIYTFHVIEGE-A--VYDERNWLQPPEGG---FTRL--------   310
otryotinia.fuckeliana.Fungus ------------------------VGKRFVRRKDG-GGTEFVENEGEVFPRGLE--KKEKEGEE------KEGSYVMGEVKAGDLVLIHGNLLHKSERNTSGKGRIIYTFHVIEGE-N--VYDERNWLQPPEGG---FTRL--------   313
   Yarrowia.lipolytica.Yeast ------------------------VSKRFVR--DGAGGTTFEDVEDICAGPEP----------------SEEEFKVLDIPAGSLVLIHNSVLHKSEANVSQKSRFAYTFHAIDGE-C--EYDRRNWLQVPTTGGNNFTRL--------   349
       Candida.albicans.Yeast ------------------------VTKRFVRVEGGAKGCNFKYLNDKEQEPVI----------------EEEEYKYVPCKAGSLILIHNSVLHKSEKNASDKSRYAYAFHVIDGT-A--QYDQLNWLQVPYTGGTNFSKLYNKE----   301
ast-like.Fungus.Cryptococcus ------------------------TSTRFVR----APNGGTTFVDVPGVEPNT-------------ENWDEMEGWKEAACPPGTLVLIHGSVMHKSPPNPSDKSRLIYTFHMIEGG-KGVKYDERNWLQPTKEMP--FPALF-------   299
       Ustilago.maydis.Fungus PPPPPAFETARPLDVHNEHLGISRGVNKRFVRKIPSNPDAGTTFLPLSDTEE--------------SSWND-ESAQTAECTAGTLVLIHGSVLHKSEMNLSDKSRFIYTFHMIEGDTEIAKYDERNWLQPTPQHT--FPSLFEKQQP--   339
      Laccaria.bicolor.Fungus ------------------------LTKRFIR-LPECKGTGFELLVTPVEEQKI------------KNGIK-GDYVLEPCKPGDLVLIHGSVLHKSERNTSANTRFAYTFHMIESP-LFADYDEKNWLQPTQAMP--FSHILGEATHVD   295
          Oikopleura.dioica SKREK-------------------LDHAFMNRVPSSDGSVKTEYRLGTSKKYYES----------------CDYTWVPAQVRKGDLVLIHDMVHHKSLPNHSNKSRNIYAWHLFESSE--ASWDSDNWLQYPEGKT--FMEFETQ-----   295
      Stigmatella.aurantiaca ----------------------------RFVRAPEGGTVFRVLDATPLAEED----------------------MVPLEVKKGTLVVLHGMLPHRSGANTSSTSRHAYSLHLIDGS---ATYPEDNWLRRSPALP--PRGF--------   274
       Alpha.proteobacterium ----------------------------RFHEVG-GELVTEALDSTPFDESA----------------------TVPLPAPKGTLVVLHGTLPHGSAPNTSERSRMAYTLHAVDGA---ARWSAGNWLQRASDIP--FHGFERSA----   294
       Legionella.pneumophila ----------------------------RMFRRE-NEIYFENFDSSPWPEEN----------------------SVPLPVKKGALIILHGRVPHKSQANFSNQSRHAYTLHLVDIS---LPYPEKNWLQWPNGIP--CL----------   285
                   Marinomonas ----------------------------RFNRCGSD-TKMQPLSDKAWPIDT----------------------GVPVEVKAGSLVIFQGKLPHYSAPNRSNKSRQAYTLHVTDGR---TEYAVENWLH-ANTLP--LTGFDS------   278
eudoalteromonas.atlantica.Ba ----------------------------QFMRFTDDSTELKVLDDTPWPKDED----------------------AKPLEVKKGSLVVFDGLLPHFSAPNRSEKSRHAFTLHMTCAT---TKYDPLNWLQ-ASPSL--L-----------   275
trahymena.thermophila.Protaz ----------------------------FCYRSDIGNELIYVGQEKKYDLTK----------------------AVPIEVKRGSVFIFHGDYIHLSKHNQSNLPRHAYALHFIDSQG--HKWHEKNWLQRRPHLP--FRDYNQVISNLY   314
                       ruler .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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CLUSTAL X (1.83) MULTIPLE SEQUENCE ALIGNMENT


```
gae.Chlamydomonas.reinhardti -------   295
                        Moss SA-----   291
                       Grape -------   283
            Black.Cottonwood -------   282
                 Arabidopsis -------   283
                        RIce -------   281
Rice.Japonica.cultivar-group -------   281
    Ostreococcus.lucimarinus -------   296
                       Human -------   291
               Horseshoe.Bat -------   249
                    Marmoset -------   292
                      Mouse1 -------   311
                      Mouse2 -------   270
                      Mouse3 -------   220
                       Horse -------   296
                    Platypus -------   291
                     Chicken -------   291
                        Frog -------   291
                   Zebrafish -------   291
                  Sea.Urchin -------   222
          Purple.Sea.Urchin -------   235
       Yellow.Fever.Mosquito -------   286
              Culex.Mosquito -------   296
            Malaria.Mosquito -------   290
     Drosophila.Melanogaster -------   288
            Red.Flour.Beetle -------   285
                  C.Elegans -------   288
                 Sea.Anemone -------   275
        Monosiga.brevicollis -------   261
           Rice.Blast.Fungus -------   316
           Neurospora.crassa -------   329
      Fungus.Gibberella.zeae -------   305
   Podospora.anserina.Fungus -------   315
lerotinia.sclerotiorum.Fungu -------   310
otryotinia.fuckeliana.Fungus -------   313
   Yarrowia.lipolytica.Yeast -------   349
      Candida.albicans.Yeast -------   301
ast-like.Fungus.Cryptococcus -------   299
      Ustilago.maydis.Fungus -------   339
     Laccaria.bicolor.Fungus NNYGLQG   302
           Oikopleura.dioica -------   295
      Stigmatella.aurantiaca -------   274
       Alpha.proteobacterium -------   294
      Legionella.pneumophila -------   285
                Marinomonas -------   278
eudoalteromonas.atlantica.Ba -------   275
trahymena.thermophila.Protaz PV-----   316
                       ruler .......
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