NCU04423

DIM-10 protein alignment (Clustal Omega)

Homologs of DIM-10 to align:

>XP\_957500.2 Neurospora crassa OR74A

>XP\_009849614.1 Neurospora tetrasperma FGSC 2508 (e-value = 0.0)

>KAA8628490.1 Sordaria macrospora (e-value = 0.0)

>VBB84122.1 Podospora comate (e-value = 3.0e-155)

>XP\_003709568.1 Magnaporthe oryzae 70-15 (e-value = 3.0e-116)

>SCB64159.1 Fusarium graminearum (e-value = 1.0e-51)

>NP\_594986.3 uncharacterized protein SPAC29B12.08/Clr5 [Schizosaccharomyces pombe] (e-value = 8e-5)

>XP\_662201.1 Aspergillus nidulans FGSC A4 (e-value = 0.071)

>XP\_011391713.1 Ustilago maydis (e-value = 0.11)

CLUSTAL O(1.2.4) multiple sequence alignment

A\_nidulans ------------------------------------------------------------ 0

U\_maydis ------------------------------------------------------------ 0

S\_pombe-Clr5 ------------------------------------------------------------ 0

F\_graminearum ------------------------------------------------------------ 0

S\_macrospora ----MTQDVPHWRLQEQVPESAAPPAPLSTPTSNPHQNS--------------------- 35

N\_crassa MTTSPASDVPHWRLQEQLPESAAPLSPHHEPQAPPTRPTAPAAPDTPPQPDAPRIPLPSS 60

N\_tetrasperma MTTSTAPDVPHWRLQEQLPESAAPLSPHHEPQAPPRRPTAPVAPDTPPQPDAPRIPLPA- 59

P\_comata ----MKEHFGCFRLATQLHESHLQQPQNQEATAKQTVKSMEAHGQEP------SAAAAAA 50

M\_oryzae ------------------------------------------------------------ 0

A\_nidulans ------------------------------------------------------------ 0

U\_maydis ------------------------------------------------------------ 0

S\_pombe-Clr5 ------------------------------------------------------------ 0

F\_graminearum ------------------------------------------------------------ 0

S\_macrospora ----------------------QAPSPTAKDDHRHLLAAPRGITTTTTTTAIPTATSTSA 73

N\_crassa TAAAPTTGSSTSATAIEPPTSNAAPSPTAKADHQH--LPSCT------GPTTATATPRSS 112

N\_tetrasperma ----PTTGSSTSATAIEPPTSNAAPSPTAKADHQHLGLPSCT------GPTTSTATSSSS 109

P\_comata VSSSPSTGQHE-----NPPA-----------------------------------ESSPV 70

M\_oryzae ------------------------------------------------------------ 0

A\_nidulans -----------MTSIARGRPSRRSA----------------A------------ARKSYV 21

U\_maydis ------------------------------------------------------------ 0

S\_pombe-Clr5 ------------------------------------------------------------ 0

F\_graminearum ------------------------------------------------------------ 0

S\_macrospora VPNSDLFAPSATTNIEQGHDINGTVPDSAPTGGVE---TAKAPSGSIQTGSSTATGASSE 130

N\_crassa VSNSNISASSVTANIPQD-PKNGTVP-----GGVD---TA-APGGSF---------HSSE 153

N\_tetrasperma VSNSSLSTSSVTANIPQY-PKNGTVP-----GGVD---TA-APGGSF---------HSSE 150

P\_comata VPSIQQQTPSR--TTENAVPVVGAQPASSETRSENPFSHPREPGT-V-------NG---- 116

M\_oryzae ------------------------------------------------------------ 0

A\_nidulans EETSESEDPGNV------TPTPSYPDGDDDGEEEFTPVPQKK---APARASRRRMTSETP 72

U\_maydis ------------------------------------------------------------ 0

S\_pombe-Clr5 ------------------------------------------------------------ 0

F\_graminearum ------------------------------------------------------------ 0

S\_macrospora QPTTVTQVPGSSTPTTDGPPPTSTLNGQPPQPQRPPQVPAPSPTSIPDATNSA-ATST-- 187

N\_crassa QPTTVTTGAA-RGVTVDG--PPSALNGQPQQSQNPSQVPAPSPIPAPDATNSA-ATST-- 207

N\_tetrasperma QPTTATTG-A-RGVTVDG--PPSALNGQPQQSQNPSQVPAPSPIPTPDATNSA-ATST-- 203

P\_comata LVASISEAIGRPGSSVNEP-PVVKPDGEEVQTSTTTPAPAPAPAPAPAPAPAP------- 168

M\_oryzae ------------------------------------------------------------ 0

A\_nidulans KAQAPRRSRRSRTAEPTDTSSVADPSEDGESIASAQDESESASPNTSVKRKSMGHEEPES 132

U\_maydis ------------------------------------------------------------ 0

S\_pombe-Clr5 ------------------------------------------------------------ 0

F\_graminearum ------------------------------------------------------------ 0

S\_macrospora STTTPANATLSATDPAT--TTIPSTTTTASARSSFRDPIRWRDPLTVHYDSNSGHAHPAR 245

N\_crassa STSTPANATVSATDPAT--TTIPSTTITASARSNFRDPIRWRDPITVHYDSDSGHAHPAR 265

N\_tetrasperma STSTPANATLSATDPAT--TTIPSTTITASARSNFRDPIRWRDPITIHYDSDSGHAHPAR 261

P\_comata -APAPAPPVLSSAPPPA--APAPAP---------------APAPASVSV----------- 199

M\_oryzae ------------------------------------------------------------ 0

A\_nidulans PSRTATMKRKSMARKSRVSSTPNPEKSSLPTPEP----------------SLSPEPHPLP 176

U\_maydis ------------------------------------------------------------ 0

S\_pombe-Clr5 ------------------------------------------------------------ 0

F\_graminearum ------------------------------------------------------------ 0

S\_macrospora LH----------AQPAHPSSA----SSQLPPPAQLKYEPSRQHQEHPAPQPPS-QSQPPA 290

N\_crassa LH----------AQSAHPASASSSSSSQLPPPSQLKYELFRQHIEHHPPSQPATESQLPA 315

N\_tetrasperma LH----------AQSAHPASAS--SSSQLPPPSQLKYELSRQHIEHHPASQPATQSQLPA 309

P\_comata -P----------AQ----GPAPTGPAPQLPPPQQPSQ---QQHSQPPPPQQPLPLPRPTP 241

M\_oryzae ----------------------------------------------------------MA 2

A\_nidulans QRDNVPPLADI--------TDSAVNQTPAKPTE-DTKSQFSIVKPNTTILE-KPMDIMLK 226

U\_maydis ------------------------------------------------------------ 0

S\_pombe-Clr5 ------------------------------------------------------------ 0

F\_graminearum MAANAV--------PVAHMENGING----------TKSPAQAAHPYTHSQT-------PV 35

S\_macrospora HD----------------------PP--ARPHH--YNQPSYQFHPQPYHT-QPPLQPAPA 323

N\_crassa QAQ----LQSL----------GQPAPAQARSHHEPNRCPPSRSHPQTYHTQQPPLQPAPV 361

N\_tetrasperma QAQ----SQSS----------AQPAPAQARSHHEPNRCPPSRSHPQTYHT-QPPLQPAPA 354

P\_comata AAQNHHPAPSLPSQPLAHPGQAQPPSHQAHPVH------PPQFHPSVRVVS-------PQ 288

M\_oryzae STATQHPTGHLGGQPTPIITSDL--PHSYAPST------TATMHPDNVRRF-------TQ 47

A\_nidulans S-RTL-GPPKPEEPQGPKSRLMITTLVLNNFKSYAGKQVVGPFHASFSSVVGPN-GSGKS 283

U\_maydis ----------------------------------------------------MAVAHRH- 7

S\_pombe-Clr5 ------------------------------------------------------------ 0

F\_graminearum ----------PLPTYAA-------------PQ--GQ-----APNASPAQSS--------- 56

S\_macrospora PVPSTQL-PPP--APSQ-------------PQSYQH-----HLQASQHQHQAPPPAHPQQ 362

N\_crassa PVTAIQP-PPP--AHSP-------------RQSYQH-----HLQASPYQYQAPPPAHPQH 400

N\_tetrasperma PVTATQL-PPP--AHSP-------------RQSYQY-----HLQASPYQYQAPPPAHPQH 393

P\_comata TREQIPPPPPPQPPQSQ-------------PQSQPQ-----HWHRWTAPSHPPPSAHHPP 330

M\_oryzae P-ASV-EPPPPRVISAQ-------------PS--GG-----AFHRSPASTAPVTSTYSP- 84

A\_nidulans NVIDALLFVFGFRASKMRQGKISALIHNSAN--HPNLPFCEVEVYFQ-EIIDLPGGEH-- 338

U\_maydis DGVGQY--GFGQHHLGMAPPPSS-NS----------------FGYDRRPKMENPAE---- 44

S\_pombe-Clr5 ------------------------------------------------------------ 0

F\_graminearum -----PLISSQQHHSP--PVQPGTLYQ---GH-------------SQPPAMQN------- 86

S\_macrospora HYQHSYLLGDPRHHPP--PPPSQQQYHPH----EPRYTSRNDGLISKPIIMDPPRSRPVS 416

N\_crassa HYQHSYPVGAPQHHPP--PPPSQQQHHPY----EYQYPSRNDGLISRPIIMDPPRSRPVS 454

N\_tetrasperma HYQHSYPVGAPLHHPP--PPPSQQQHHPY----EHPYSSRNDGLISRPIIMDPPRSRPVS 447

P\_comata AVHHA--HQQPQHHHQ-------PQPHHYPQHTLPSQPLPRRSMTDRPVIMDPPARRTSH 381

M\_oryzae -----------------------AQSQP-----SPSAGLPG-RPRNRPSIMDPPGNKIS- 114

A\_nidulans ------EVV-------PDSQL------------------------IISRKAFKNNTS--- 358

U\_maydis -----------PVWPVPRIQHQPQQGNAIDRTRDSGGFANSFSQPELTRQ---------- 83

S\_pombe-Clr5 ---------------------------------------------------MTKEWECRR 9

F\_graminearum ---GNVAPIPLRGHLSPSAQGNPQQTESAGTYQTL-VALIDRAPASVVRHVIRDKWEKSL 142

S\_macrospora QPPPQAEPVPSSGFPSPVTTHAHLNKKFADDCTRL-TYAIQQSTPDAVRRVFRDNWEKCM 475

N\_crassa QLPPPAEPISSSGFPSPATTHAHLNKKFADDCTRL-TYAIQQSTPEAVRRVVRDNWEKCM 513

N\_tetrasperma QLPPPAEPISSSGFPSPATTHAHLNKKFADDCTRL-TYAIQQSTPEAVRRVVRDNWEKCM 506

P\_comata M-----PAQTSGGFPSPTLDHASANPKFVDDCTRM-TYAIQQSLPEAVRRIVRDQWEKCL 435

M\_oryzae N-----PTMRGGGYPSPTMDHATINPKFVDDVARI-TYAIQQSLGDAVRRAIRDNWEKCL 168

A\_nidulans -----------------------KYYMNGKETN----FTAVTTLLRDRGIDLDHKRFLIL 391

U\_maydis ----------------Q--GHTANYTYDGSSSALRNPVVYSQPAQAPWGMAAHSSADYAE 125

S\_pombe-Clr5 EQIIELSKINGMTIRELQARMSKMYKFDAS-------IRSYKRVLARWGIRVHRQRFVSP 62

F\_graminearum ----------------MGSQYHIAFLLNAT-------MHQASPETVGNAVKEFGADFVQK 179

S\_macrospora ----------------LGTEFHQAFILNAS-------IHHAVPSITRRAVRDFGQKMVLE 512

N\_crassa ----------------LGTEFHQAFILNAA-------IHHAVPSITRRAVRDFGQKMVLE 550

N\_tetrasperma ----------------LGTEFHQAFILNAS-------IHHAVPSITRRAVRDFGQKMVLE 543

P\_comata ----------------LGTEFHQAFILNAS-------IHHAVPSITQRAVRDFGAKMVAD 472

M\_oryzae ----------------LGTDFHQAFVLNAS-------IHHATVPMTKRAIRDFGSKMVKA 205

: :. . .:

A\_nidulans QGEVESIAQMKPKAANEHEDGLLEYLEDIIGTSKYKQPIEEAATELEALNDVCVEKNNRV 451

U\_maydis YPTASFMAPMGQRAQP-------------------------------------------- 141

S\_pombe-Clr5 -RTEEAAART---ASG-------------------------------------------- 74

F\_graminearum -AKHELVGHL---SST-------------------------------------------- 191

S\_macrospora -SKHELISHF---STA-------------------------------------------- 524

N\_crassa -SKHELISHF---STA-------------------------------------------- 562

N\_tetrasperma -SKHELISHF---STA-------------------------------------------- 555

P\_comata -SIVDIMNHF---TTA-------------------------------------------- 484

M\_oryzae -GKADLLEHF---SQA-------------------------------------------- 217

. :

A\_nidulans QHVEKEKNALVDKKDKALAYLRDENELAQKQSALYQIYIDECADNLRVTEEAILQMQELL 511

U\_maydis ---------PMH------------S-PAPYVGSANGAYGDSAFA---------------- 163

S\_pombe-Clr5 ---------DVS------------KALDELVTQLFHA---RQSDKDS------------- 97

F\_graminearum ---------DID------------ELADSLISRASPDFLDRVL-ARR------------- 216

S\_macrospora ---------DLD------------DVSDAIINKASDAFLDKCL-NAR------------- 549

N\_crassa ---------DLD------------DIADAIINKASEAFLDKCL-NAR------------- 587

N\_tetrasperma ---------DLD------------DIADAIINKASEAFLDKCL-NAR------------- 580

P\_comata ---------DID------------KVADMIIDKASDNFLDKCL-EKR------------- 509

M\_oryzae ---------DLD------------VVSDTILAKASHSFLDKAL-ELR------------- 242

:

A\_nidulans NLELEKHEGNESGIKELEKAYKRAMKEYERMEKETQELAKGMAKYDKETVKFEEKKKFLV 571

U\_maydis ------------------------------------------------------------ 163

S\_pombe-Clr5 ------------------------------------------------------------ 97

F\_graminearum ------------------------------------------------------------ 216

S\_macrospora ------------------------------------------------------------ 549

N\_crassa ------------------------------------------------------------ 587

N\_tetrasperma ------------------------------------------------------------ 580

P\_comata ------------------------------------------------------------ 509

M\_oryzae ------------------------------------------------------------ 242

A\_nidulans GKQKKLEKAMTSARLAASECQSLVKRHSEAIENKSKETADYENEV--EHEE---QELTKI 626

U\_maydis -----------------SGSDPYS-----------KV-MG-------------GGSAPSM 181

S\_pombe-Clr5 --------------LAQIEANFGLKLSKRALHYRRKR-LALKRPPPDSHDSPN-NSIPLM 141

F\_graminearum --------------LETISARQLVNAL-----ARAER-LGYN--VRDIVREHDEQVIPSM 254

S\_macrospora --------------LLTIEAKPLITAL-----ARAER-LGYN--PADVVEEQHERVMPTT 587

N\_crassa --------------LLTIEAKPLITAL-----AKAER-LGYN--PADIVEEQHERVTPTS 625

N\_tetrasperma --------------LLTIEAKPLITAL-----AKAER-LGYN--PADIVEEQHERVTPTS 618

P\_comata --------------LLTIEAAPLTNAL-----AKAER-LGYE--LGDVIPEQQQGQAHP- 546

M\_oryzae --------------LRTIEAKPLVDAL-----SRAER-LGYE--SNDVVEQDNNHQERVI 280

. :

A\_nidulans RESLKGKTQGLSDQIAAKQKSLEPWDEKINK-----KQSELAVAQSELDIL-KEKSNAGA 680

U\_maydis GGAYE---------HTT----ETLWPLGPTS---LDAFAGMPAPNARLTLTSTA------ 219

S\_pombe-Clr5 AN---SCLL-SADNSSS-STTSNPNV--------APPISTLPDPVATISSSSSSHLDMGA 188

F\_graminearum HSVLTSSTI-PPGNDTMRVKHYQPRPIPSQQLQQPQPQPPVPQPFAR------------- 300

S\_macrospora QA--------------A-------RP---------PP----------------------- 594

N\_crassa QA--------------A-------RP---------PP----------------------- 632

N\_tetrasperma QA--------------A-------RP---------PP----------------------- 625

P\_comata -AAAA------PNGHQA-------HP---------TQ------PAAG------------- 564

M\_oryzae PSDSP------PATHSA-------------------A------RPAS------------- 296

A\_nidulans VLLEEAQSKITSIEETIARKEEDLQECKTQRSTLEDEVEQLQHDLKKYSMK-----EPDV 735

U\_maydis ----DK----NRFKARSSLPPPKQFKCSACDAIFSR-----NHDLKRHARI--------- 257

S\_pombe-Clr5 IHPPHH----SSLPPHMGVDPSTMADAHNAHSSLTP----PQSG--YSSMPSLPYLQQPF 238

F\_graminearum -APPLK----ASSLDDVPMGPPE-IVSCNCGWPCA-----SEEALNYHKKKNACYKVLPT 349

S\_macrospora -------------PPPSQSTHAGRLQCMGCYRIFT-----HQAPYEYHMSRQLCAVPPPT 636

N\_crassa -------------PP--QSTYPGRLQCMGCYRVFT-----HQVPYEYHTSRRLCTVRPPA 672

N\_tetrasperma -------------PP--QSTYPGRLQCMGCYRVFT-----HQVPYEYHTSRRLCTVRPPA 665

P\_comata -YPPA--------PSAPPSSQHPMLQCARCFRTFA-----QTSAFEYHTAYSICTILPPT 610

M\_oryzae -YVPTG----GSATRASGTDPKAPWQCTVCYRTFT-----QQSAYDHHMRKQVCTRAPAL 346

.

A\_nidulans R-AHVSNARQKAEEAR-ATVASTQNRGSVLTGLMRLKE--SGRIEGFHGRLGNLGTIDEK 791

U\_maydis HLAVKPFPCGFCD-------------------------------KAFSRKDALKRH---- 282

S\_pombe-Clr5 QIPSQRFSRQQQSHPFPAAQHAVNGQPQALYPFIYQSRNVPMGSTMFASSNQSAAH---- 294

F\_graminearum DQAG-RDICVFCG-------------------------------CRFGSNGGILYH---- 373

S\_macrospora SVKGFEFSCQHCG-------------------------------EGFTRSDEHQSH---- 661

N\_crassa SAKGFEFSCQYCG-------------------------------EGFTRSDEHQTH---- 697

N\_tetrasperma SVKGFEFSCQYCG-------------------------------EGFTRSDEHQSH---- 690

P\_comata -SAGFKHSCPYCG-------------------------------QGFTELVDLNGH---- 634

M\_oryzae -PEGFRYSCAHCG-------------------------------QGFTTTVGLQYH---- 370

\*

A\_nidulans YDVAISTACPALENMVVDTVEVGQQCIDYLRKNNLGRANFILLDRL-----------PKR 840

U\_maydis ---VLVKGCGIGNKKPSDNR-KRAATLSKLENTKSGSSNRAPYDDS-----------PSR 327

S\_pombe-Clr5 ---PDGNNALPMDNTHA--------NISYMQSSQSMPVNSYSYDRYTPNQPSYLESKPGN 343

F\_graminearum ---EKSEVCGPRTAD-------------------------------------TCQKMMD- 392

S\_macrospora ---ERAQTCFHAGP--------------------------------------ASHRGPG- 679

N\_crassa ---ERARTCFHPGP--------------------------------------PLARGPG- 715

N\_tetrasperma ---ERARTCFHTGP--------------------------------------PLARGPG- 708

P\_comata ---LNGRVCGHFDTV-------------------------------------KLPRGPG- 653

M\_oryzae ---LNNKVCGDFGLT-------------------------------------PAEQGMN- 389

.

A\_nidulans DLNKILTPDNVPRLFDLVKPKDPKFAPAF----YSVMQNTLVARDLDQANRIAYGARRWR 896

U\_maydis DFTN-FRD-------------DLHYQGQQQPQGFQGEASS-----------SRSFPGRM- 361

S\_pombe-Clr5 HQPSYTSE-------------QPMYSTASVPQQISNGPTAVNGLPMN-----SYTPHSN- 384

F\_graminearum -LIEHF--------------------------------RTHGRSAHYRAAHSLMTPR-G- 417

S\_macrospora -RPPRAVP-------------QPQPVPSS------VVPLTQ----------VQATPAVT- 708

N\_crassa -RPPRAAP-------------VP---------------SSI----------VQATPAVA- 735

N\_tetrasperma -RPPRAAP-------------VP---------------SSI----------AQATPAVT- 728

P\_comata -RPPRAAP-------------VQHASPVP------IASSAPNGTPN---A-SLSTPARS- 688

M\_oryzae -STAVAAA-------------GAMAAVAP------AHTTAPLRTEFYQYP-AASTPQRT- 427

:

A\_nidulans VVTLDGQLIDTSGTMSGGGTR--V-A----RGAMSSKQVGDITKEQLVQMESDLEEMERK 949

U\_maydis ------DTSWP---------S----TLADGSNPGLNADYAANRG----GTNEERTQSS-- 396

S\_pombe-Clr5 ------HLHSP-SPNSNSGPTDSLSAPNSTSSPSMAHANGASFASQYPSLNKSIFPASYS 437

F\_graminearum ------RTKAP-STEHHATLA--TPTSSQPSSTPQRDPYAHLTPDKYREFNAIMKTAEE- 467

S\_macrospora ------RTVDL--TSAGSTPS--AETPAVSKTPNPADPYGHLTQEQLAMMDADLKEAEK- 757

N\_crassa ------RTIDL--TSAGSTPS--AETPAGTKTPNAADPYGHLTEEQLAAMDADLKEAEA- 784

N\_tetrasperma ------RTIDL--TSAGSTPS--AETPAGTKTPNAADPYGHLTEEQLAAMDADLKEAEA- 777

P\_comata ------QLVN---RALAGTPT---------ASPIPGDPYAHLTPEQFQAMNEELHEAEI- 729

M\_oryzae ------ATYGSATPRTAGTPE--TPVDGMGKTIGGSDPYAHLTQSQRESLQEELRQAEI- 478

. : .

A\_nidulans YQHFQEKQRRVESALREKTEEIPRAETKIQKIMIEIDSAKRSLADAERRVQELSAAHKPS 1009

U\_maydis ------HG-----------TQLPSQ-AGL-ITSYGSQQ-QT---------QP-------- 419

S\_pombe-Clr5 SS--AEDG---------QNMQAPAH-AYMQSSIYGVNQEQK---------SE-------- 468

F\_graminearum ---------------------------------------------------K-------- 468

S\_macrospora ---------------------------------------------------K-------- 758

N\_crassa ---------------------------------------------------K-------- 785

N\_tetrasperma ---------------------------------------------------K-------- 778

P\_comata ---------------------------------------------------K-------- 730

M\_oryzae ---------------------------------------------------A-------- 479

A\_nidulans KTDASRVKVLEEQIVGLEEQIED----LRSQKGGIEEEIQALQNKIMEVGGVRLRSQKAK 1065

U\_maydis --Y-PNFGM------GGEDAFQQ--QQRPQLAGGLVNAFNSPEATS-------------- 454

S\_pombe-Clr5 --YPSNLSM------QSSMSIKDPSQLQRIHLYPQHSQYDPNGMTMRDHYSERIEPEA-- 518

F\_graminearum --YGGL--M------REA-ALLDE-PERSKRLAGLKNSYNTKQSTTRKKFGIRLRERRTR 516

S\_macrospora --FAPR--F------AEAYAIPDE-NERRIKIEGLRNSFGTKQSMIRKKYGVRLRQRRTK 807

N\_crassa --FAPR--F------AEAYAIPDE-NERRIKIEGLRNSFGTKQSMIRKKYGVRLRQRRTK 834

N\_tetrasperma --FAPR--F------AEAYAIPDE-NERRIKIEGLRNSFGTKQSMIRKKYGVRLRQRRTK 827

P\_comata --YRPR--F------AEAEAIPDE-NERRQRVEGLRNSFGTKQSMIRKKYGVRLRERRTK 779

M\_oryzae --FADR--F------KAAESIADL-NERRIRIDSLRNGFGTKQSMIRKNYGVRLRERRTK 528

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A\_nidulans VD--GLKEQISLLSEEISNAEVARSKNEK----------------------LIKKHENAR 1101

U\_maydis -----------VSSPNDPHAKSALSGNAGL------LTGEGLDSKVE--PKAISRPGSAN 495

S\_pombe-Clr5 ---KPSDETLTVRSSRD-----LSVHNVG---TLPVLSAAAATQAAMPHTMGPSAHDSAS 567

F\_graminearum EEIEAEENRLFNSRGD-----------AGTP------TN------GTPVPDHEFRP---- 549

S\_macrospora AEIQAEEERMGLEKLKK-RQKAEKAAAQQ---------A------AAPASASTG------ 845

N\_crassa AEIQAEEERMGLEKLRK-KQKAAAQQAAAAAA-----SA------SV--SAATG------ 874

N\_tetrasperma AEIQAEEERMGLEKLRK-KQKAAAQQAAAAAA-----SA------SVSASASTG------ 869

P\_comata AEIQAERERLGIKQAEK-DQARASMGPAGKTEDRPVVIS------DVPVPVVPP------ 826

M\_oryzae KEIEAERERMGRQHEER-YDRNAL-DDARR--SLTAIHG------GVPRPVGPGRP---- 574

A\_nidulans AEAEKELANVAEELQKLNEDVANQANDASGWKEKVDEAQDALESKKAELKTMKAELDEKV 1161

U\_maydis LPASAPYNAQQLPVAGSYSLAPMLSPLL------GGPDQ--------------------G 529

S\_pombe-Clr5 APSPHMQSQQALPYQYYNPLPAMADP------AQNVPQQLPP--------PIHSHLS--- 610

F\_graminearum ------------------------------------------------------------ 549

S\_macrospora --------------------AAPPRPTGSGWVAANAPRANA------------------- 866

N\_crassa --------------------TALPRPAGSGWVAANAPRANA------------------- 895

N\_tetrasperma --------------------TAPPRPAGSGWVAANAPRANA------------------- 890

P\_comata -------------------MP--VGPPAAGWVAANTPRPKPG---------AA------- 849

M\_oryzae ----------PKAYA-TTPVPVPKPAASNTWSTPNTANDNVP---------VKRELDSDA 614

A\_nidulans AELNETRATEIEMRNKLEENQKALAENEKRSRYWQEKLSKLTLQNISDLGEDQQPSEFQT 1221

U\_maydis --------LGN-------------FHALKRQQQQ--Q-------------------PFGP 547

S\_pombe-Clr5 --------------------------------DD--QHIQYSYPN--T------------ 622

F\_graminearum ---------------------------NKRPRTD--DMEASASGVNGNLEP-PQKRVFRA 579

S\_macrospora --------VWE-------------EHKAKRRRMD--ASGTYQTPTKSTLSVSEI------ 897

N\_crassa --------VWE-------------EHEAKRRRMD--ASGTYQTPTKSTLSVSEI------ 926

N\_tetrasperma --------VWE-------------EHEAKRRRMD--ASGTYQTPTKSTLSVSEI------ 921

P\_comata --------EEE-------------EHHAKRRRTD--TNGGYQTPYRTGVEDTPTRKVSAS 886

M\_oryzae --------SPI-------------EGDLKRRRVD--GEGTNSINNLGSVQQSRTEEVS-P 650

A\_nidulans FTKDELAEMNKD-------SL------------KAAIAALE------------EKTQNSS 1250

U\_maydis YFGNSAAS---------------------------------------------------- 555

S\_pombe-Clr5 FVNRFPQNIHHPSANLLDASA--------------------------------------- 643

F\_graminearum EMGGGLSGSQAT-AELTDPTAHLNPPQPRYTPQKPSATK--------------PAWSSKR 624

S\_macrospora --GGGLAGA-AATAEVHDPTRP--PPALNYLSANSNGQSDEEDEDESGSGSGSPSTANDE 952

N\_crassa --GGGLAGV-AATAETHDPTRP--SPISGHQTASSNGQSEDE--EDSASGSGRSSTANDE 979

N\_tetrasperma --GGGLAGV-AATAETHDPTRP--SPISGHQTASSDGQSEDE--EDSGSGSGRSSTANDE 974

P\_comata FDGAGGSG-------VQNTGNP--YPALGKTPNHADLAA-------------QAAAATAA 924

M\_oryzae FVSSGSKSPQSQDSESQSSGTP--ERQL---------AA-------------ESVAAQQS 686

A\_nidulans IDL-----------SVIEEYR--------RRAAEHESRSADLATALAARDSAKSRLDGLR 1291

U\_maydis ------------------------------------------------------------ 555

S\_pombe-Clr5 -------ALNPVQNPLLMPQQ-NHEHSPLVRSDAALHDHGPLLPVYPDVD---SRFV--- 689

F\_graminearum IGV----HVGTQEDPM-----SIDEDDSDTDSDSDSDSDGDIPATLN------------- 662

S\_macrospora MDIDRQLGSEPASRPVQTNYNSNHNDDD---DDSDSSDDEDIPSTLPAHV---RQTLTTR 1006

N\_crassa MDVDEQPGSGPASRPLQNNHNSNHNDDDDDDDDSDSSDDEDIPSTLPAHV---RQTLATR 1036

N\_tetrasperma MDVDEQLGSGPASRPLQNNHNSNHNDDDD--DDSDSSDDEDIPSTLPAHV---RQTLATR 1029

P\_comata LNG---QNGNSSKQPI--AID-DGDDD-----SDSSGDDEDIPSTLPAHV---RNSLGAS 970

M\_oryzae ANATT-ETTAPAAQPVVNLVD-DDDDDEEESSDESEDDDEGIPAVLPQAV---RQGLSQT 741

A\_nidulans SARLNGFMEGFGIISLRLKEMYQMITMGGNAELELVDSLDPFSEGILFSVMPPKKSWKNI 1351

U\_maydis ------------------------------------------------------------ 555

S\_pombe-Clr5 ------------------------------------------------------------ 689

F\_graminearum ------------------------------------------------------------ 662

S\_macrospora NA---------------------------------------------------------- 1008

N\_crassa NA---------------------------------------------------------- 1038

N\_tetrasperma NA---------------------------------------------------------- 1031

P\_comata AAGKTGSRAGS---------TAS-MTPG-------------------------------- 988

M\_oryzae GRGVTNP----------------------------------------------------- 748

A\_nidulans GNLSGGEKTLSSLALVFALHHYKPTPLYVMDEIDAALDFRNVSIVASYIKERTKNAQFVV 1411

U\_maydis ------------------------------------------------------------ 555

S\_pombe-Clr5 ------------------------------------------------------------ 689

F\_graminearum ------------------------------------------------------------ 662

S\_macrospora ------------------------------------------------------------ 1008

N\_crassa ------------------------------------------------------------ 1038

N\_tetrasperma ------------------------------------------------------------ 1031

P\_comata ------------------------------------------------------------ 988

M\_oryzae ------------------------------------------------------------ 748

A\_nidulans ISLRNNMLSVEAPMVQVRQYYKNVVRKTTFIELRMTELQRPQQVREAFKESKQLIKLSMK 1471

U\_maydis ------------------------------------------------------------ 555

S\_pombe-Clr5 ------------------------------------------------------------ 689

F\_graminearum ------------------------------------------------------------ 662

S\_macrospora ------------------------------------------------------------ 1008

N\_crassa ------------------------------------------------------------ 1038

N\_tetrasperma ------------------------------------------------------------ 1031

P\_comata ------------------------------------------------------------ 988

M\_oryzae ------------------------------------------------------------ 748

A\_nidulans TRKNP 1476

U\_maydis ----- 555

S\_pombe-Clr5 ----- 689

F\_graminearum ----- 662

S\_macrospora ----- 1008

N\_crassa ----- 1038

N\_tetrasperma ----- 1031

P\_comata ----- 988

M\_oryzae ----- 748