

Figure S1. Amino-acid alignment of cluster A GH18 catalytic domains.

	10	20	30	40	50	60
NP_979924_B._cereus	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....					
YP_077302_B._licheni	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....					
YP_091539_B._licheni	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....					
YP_079121_B._licheni	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....					
YP_074366_S._thermop	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....					
YP_075811_S._thermop	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....					
YP_075619_S._thermop	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....					
ZP_01354047_C._phyto	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....					
ZP_01354926_C._phyto	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....					
NP_902406_C._violace	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....					
ZP_01136704_A._cellu	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....					
ZP_00526542_S._usita	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....					
AAF46212.1_D._melano	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....					
AAF46534.1_D._melano	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....					
AAF46544.1_D._melano	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....					
At4g19720_A._thalian	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....					
At4g19750_A._thalian	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....					
EAA67655_G._zeae	.KRNMLYFTNWG.TYE...G....FN..PEN..LPVK...EITHVLYSFAK..VN...					
EAA73155_G._zeae	.SVNAVYFVNWG.IYG...RN....YQ..PMN..LPAS...QLTHVLYAFLN..VR...					
EAA74986_G._zeae	.PVNAVYFTNWG.IYG...RN....FQ..PQD..LPAS...EITQVLF AFLN..VK...					
EAA74223_G._zeae	.FRTVAYFVNWA.IYA...RK....HR..PQD..LPVE...NLTHILYSFAN..IR...					
MGG_05533_M._grisea	.YRSVAYVTNWS.IYG...AK....FL..PEQ..IAVD...SISHVQYAFAD..IL...					
MGG_01247_M._grisea	.YRSVLYFTNWG.IYG...AN....YQ..PQD..LPVD...TVTHILYSFAN..IA...					
MGG_00086_M._grisea	.LQNVAYFVNWG.IYG...RN....FH..VQN..VSAD...KVTHLLYAFAN..LR...					
MGG_07927_M._grisea	.QRTVAYFVNWA.IYG...RK....HR..PQE..LPAD...KLTHVLYAFAN..VK...					
Chi18_6_H._jecorina	.KKNVVYYADWS.IYD...AA....FL..PQQ..LP AE...DITHLLYAFAG..IE...					
Chi18_5_H._jecorina	.FANAVYFTNWG.IYG...RN....FQ..PAD..LVA S...DITHVIYSFMN..LQ...					
Chi18_7_H._jecorina	.YRSVAYFVNWA.IYA...RK....HR..PQD..LPVE...KLTHVLYAFAN..VR...					
04883_N._crassa	.YKNVVYFTNWG.IYG...RN....YQ..AAD..LPAD...KITHVLYSFAN..LK...					
04554_N._crassa	.YRTVAYFVNWA.IYG...RK....HR..PQD..LP AE...KLTHILYAFAN..VR...					
11407_B._fuckeliana	.YHNAA YFVNWA.IYG...RN....YQ..PQQ..LPAT...KLTHVLYAFAN..LQ...					
05350_B._fuckeliana	.YRAVAYFVNWA.IYG...RK....HF..PQE..LP AE...KLTHILYAFAN..VR...					
11700_S._sclerotioru	.YHNTAYFVNWA.IYG...RN....YQ..PQQ..LPAS...KLTHIYAFAN..LK...					
11304_S._sclerotioru	.YRAVAYFVNWA.IYG...RK....HF..PQE..LP AE...KLTHVLYAFAN..VR...					
08020_S._sclerotioru	.....A.IYG...RQ....FF..PQE..LPVA...NLTHVLYAFAN..ID...					
01250_A._capsulatum	.FKTVGYFTNWG.IYG...RN....YQ..PLD..IPGN...HLTHILYSFAN..VK...					
05886_A._capsulatum	.FKSVVYFVNWA.IYG...RN....YQ..PQD..LPAA...KLTHVLYAFAN..VH...					
06565_A._capsulatum	.YKSIVYYVNWA.IYA...RN....YN..PQD..LPVK...KLTHVLYAFAN..VR...					
05250_C._immitis	.YKTVAYFTNWG.IYG...RN....YQ..PNN..IPAS...HITHILYSFAN..IR...					
02795_C._immitis	.FRSVVYFVNWA.IYG...RG....HN..PQD..LKAD...QFTHILYAFAN..IR...					
03822_C._immitis	.YKSIVYYVNWA.IYD...RQ....YN..PQD..MPVD...KITHVLYAFAN..IR...					
AN5454_E._nidulans	.YRSMAYFVNWA.IYA...RH....HN..PQD..LPVS...HLTHILYAFAN..VR...					
AN4871_E._nidulans	.YKTVGYFVNWA.IYG...RN....YN..PQD..LP AE...KLTHILYAFAN..VR...					
00269_P._nodorum	.YKNVAYFVNWA.IYG...RN....FN..PQD..LPQ G...ELTHVLYAFAN..VR...					
04870.1_C._cinereus	.KKS VGYFVNWG.IYG...RK....Y..MPTY..IPAN...DLTHILYAFAN..IN...					
09921.1_C._cinereus	.KANFAYFTNWG.IYG...AN....FQ..PTD..IVPD...YITHILYSFAD..TD...					
124149_P._chrysospor	.....G.IYG...RK....F..PPHK..IPAQ...DLTHILYAFAN..IR...					
134311_P._chrysospor	.KANMAYFTNWG.IYG...AN....FQ..PTD..INPG...PLTHILYAFAD..VS...					
03412_F._neoformans	.KRTVGYFVNWG.IYG...RK....F..FPQN..IPGQ...HLTHINYAFGN..VK...					
13635_R._oryzae	.PVVAGYFANWG.IYD...RK....YNVVDLA..LQAD...KLTHILYAFAN..LQ...					
UM04261_U._maydis	.RVNLAYFTNWG.IYG...RK....Y..SPLD..VPYC...NLTHVLYAFAD..VN...					
EAA69503_G._zeae	.FTNAVYFPNYR.IYQ...GD.....TPGM..LNYS...CINHVYYAYAS..VS...					
EAA70860_G._zeae	.YINAVYYP SWR.CYK...ER.....PPSC..LDIS...SITHIFYAFV GQVSS...					
Chi18_3_H._jecorina	.YTNAVYFPSSR.IYQ...GD.....SPGM..LNYS...CINHVYYAYAS..VT...					
Chi18_2_H._jecorina	..MNGVYYP SWL.VYK...GK.....TPAT..LDID...NITHLT.....					
03026_N._crassa	.YNNAVYWP N HS.VYR...GD.....TPGS..LNYG...CINRVYYAFAN..IM...					
01594_B._fuckeliana	.YKNAVYYPNYR.VYR...GE.....TPGS..LNFG...CISHVFYAFAH..VG...					
05897_S._sclerotioru	.YKNAVYYPNYR.VYR...GE.....TPAS..LNFS...CISHVFYAFAH..VG...					

04742_A._capsulatum	...MIYKGKGGK.PRR...KY.....PQSS...GSPR...HFNFLGYNYSF...NQ...
04750_C._immitis	.YFNNAVYPSWR.IYK...KQ.....PPSS...LRLG...CVSHVFYAFAW..VN...
04719_P._nodorum	.YWNNAVYPNWR.IYR...DQ.....PPVS...LNYD...VISHVFYAFAW..VK...
MGG_08458_M._grisea	.YINNAVYPNWR.IYK...QL.....PPSK...LQVN...NITHVFYAFIG..VN...
CHT4_C._albicans	.FKTCVYFSNWS.VYQ...KK...HF..PQD..IPIE...YFTHIFYAFIL..ID...
01119_L._elongisporu	.FKSCVYFTNWA.VYE...KK...HF..PCD..IPYE...YYSHIFYAFIA..VD...
XP_454053_K._lactis	.FSVATYYSNWS.PYN...ARN...HK..PAD..IPTS...QLTHVYYAFFV..VD...
CTS2_S._cerevisiae	.FISGVYYSNWS.PYK...PRF...HF..PHD..INLK...QVSHIYYAFFK..IN...
246746_L._bicolor	.KYSVGYFVNWG.IYG...RK...F..PPSL..IPVQ...DLTHILYAFAN..VR...
03209_N._crassa	.YRNAVYFTNWG.IYG...AN...FQ..PQQ..LPAS...QITHALTPSR.....
14474_P._nodorum	.YQSQVFYTNWA.MYG...RK...HF..VTD..LPAD...HLTKINYGFAN..VN...
CE06282_C._elegans	.KRIIGYYSGSG.TSN.....ITS..TQLS...NLTHTVFAFVYMTDPG..
CE03547_C._elegans	.KRIIGYFATQ.TSV.....ITR..DQVS...KLTHAVFAFVNMTSDG..
CE03542_C._elegans	.KRIIGYYSENE.TTD.....ITK..RQLS...KLTHAIFAFIKLQPDG..
CE15845_B_C._elegans	.KRTVGFFTGNS.TTS.....ITQ..DQMR...KLTHATFCRIFLNST...
CE02997_C._elegans	.KRIVGYFAEFE.NSP.....LSK..KQLQ...MLTHIYLFaip.KNG..
CE36953_C._elegans	.RRRVGYITSWG.KHP.....FRD..DQAE...KLTHLVFAFFVVDSDG..
YP_432439_H._chejuen	.RRIIGYFTSWR.TGKNGAPS...YL..ASD..IPWE...KLTHINYAFAHVDGNN..
YP_529449.1_S._degra	.RRVIGYFTSWR.TGGNG.PA...YL..AHQ..IPWD...KLTHINYAFAHVDGNN..
YP_077582_B._licheni	.RRIIGYFTSWR.TGKGNQDR...YL..VSD..IPWK...YLSHINYAFAHIGEDH..
ChiI_S._coelicolor	.RRVIGYFTSWR.TGKDGPKA...YL..ASD..IPWD...KITHINYAFAHVDGNN..
NP_902986_C._violace	.RRIIGYFTSWR.TGKDGPSP...YL..ASD..IPWS...KLTHINYAFAHVDGSN..
ZP_01159608_Photobac	.RRVIGYFTSWR.AGDDPQSS...YL..VND..IPWE...QLTHINYAFVSIADG..
ZP_01234708_V._angus	.RRVIGYFTSWR.AGDDPQSS...YL..VND..IPWE...QLTHINYAFVSIADG..
NP_233087_V._cholera	.RRVIGYFTSWR.SGDDPQAA...YL..VKD..IPWE...QLTHINYAFVSIADG..
NP_230718_V._cholera	.RRIIGYFTSWR.TGKNGLPA...YL..AGD..LPWE...KLTHINYAFASINKSD..
AAO07185_V._vulnific	.RRVIGYFTSWR.SGDDPQAA...YL..VKD..IPWE...QLTHINYAFVSIADG..
ZP_01354150_C._phyto	.....DVPGD.....LLTDVNLAFGEIAP.....
ZP_01246933_F._johns	..IIAYYTGDSQ.LI.....DQ..YEVs...KLNQIIFSFCHLK.....
YP_012734_L._monocyt	.YRNVMYYGDWS.IWGG.EGN...FY..PKD..IPAD...QLTHLNFAFLDFNSN...
YP_529337.1_A_S._deg	.YRVIGYYMPSLDGS.....FPPSAIGEQQ..AQMLTHINYAFIGINSQ...
ChiA_A_P._kodakarae	.YRVIVYISWG.RY...ARK...FY..VSD..IPWE...KVTHVNYAFLDLKE...
AAG19274_Halobacteri	.GRVVGYYMQWA.QW...DRD...YF..PGD..IPLD...KVTHVNYAFLTVRE...
AAG19275_Halobacteri	.FKVVGYYPSWKGTD...DYD...FY..PAD..VPFD...QVTDVLYAFLDVQP...
CE03543_C._elegans	.KRIVGYYRNG.NDS.....IMM..GQLA...KLTHAVFAFLELHPDG..
CE34961_C._elegans	.KRIVGYYSEWE.GTE.....ITR..SQLG...KLTHAVFAFIHMDSEG..
CE20043_C._elegans	.SRIVGFYADWE.RTD.....ITS..HQVA...KLTHAVFAYVQMKFDG..
CE15845_A_C._elegans	.KRIIGLYSEFE.TMP.....ISK..KQLA...KLTHAVFRFVSMTDDG..
CE32863_A_C._elegans	.KRIIGLYSEFE.TMP.....ISK..KQLA...KLTHAVFRFVSMTDDG..
CE03544_C._elegans	.RRIVGYYSEYD.STD.....ISK..NQLA...KLTHAVFAFVDIKYDG..
CE08731_C._elegans	.....
CE28638_C._elegans	.KRIVGFFTDITQ.STE.....ITV..DQLS...KLTHAVFAFAKMDYLRL..
CE32863_B_C._elegans	.KRTVGFFTGNS.TTS.....ITQ..DQMR...KLTHATFCRIFLNSSG..
CE01673_C._elegans	.....IFAFAQLNTNG..
CE02993_C._elegans	.KRIVGYFAEFE.NSG.....LTR..RHLQ...MVTHIYLFARP.TNG..
CE02996_C._elegans	.KRIVGYFAEFE.NAG.....LSR..KQLH...MLTHIYLFARP.TNG..
CE02995_C._elegans	.KRIVGYFAEFE.NTA.....LTR..KQLQ...MLTHIYLFaip.KNG..
CE02992_C._elegans	.KRIVVAYSACE.....LSN..HQLK...KLTHFIFTSISIFPNG..
CE02999_C._elegans	.KRIIGYVSSDE.GSE.....ITI..KQLE...KLTHVIFAFILVHKDG..
CE02998_C._elegans	.KRIVGYTDEW.PRK.....ISA..KQLQ...KLTHLIFTNVPNMSSG..
CE09229_C._elegans	.KRIVGYTGWG.DRE.....ITE..NQLK...KLTHVIFAFVAMYEDG..
CE12928_C._elegans	.KRIVGYTGWG.ERE.....ITE..NQLK...KLTHVIFAFVAMYADG..
CE23907_C._elegans	.KRIVGYYSATE.TSE.....ITS..SQIF...KLTHAVFAFVYMTSEG..
CE32917_C._elegans	.KKVIGYFSESH.TSE.....ITI..NHIS...KLTHAVFAFVIMKSDG..
CE34579_C._elegans	.KRIIGYYSGTS.DSE.....ITI..NQVS...KLTHAIFAFVQLTFDG..
CE25073_C._elegans	.KRIIGYFATQ.TSV.....ITR..DQVS...KLTHAVFAFVNMTSDG..
CE03548_C._elegans	.NRVVGYFSSNQ.NST.....ITE..DQVS...KLTHAVFAFVNMTQGG..
NP_469498_L._innocua	.YRNVMYYGDWS.IWGG.EGN...FY..PKD..IPAD...QLTHLNFAFLDFNSN...
CE08730_C._elegans	.KRIIGYIYQKE.SSE.....IST..VGLS...RLTHAVFGSLRVQLNG..
Q8U1H4_P._furiosus	.FRVVVYISWG.IY...ARK...FF..PED..IPFE...KVTHVNYAFLNPKE...
CE12474_C._elegans	.KRRIVGYFSEIE.STE.....ISK..SQID...KLTHAVFAFVRIKYDG..
CE02990_C._elegans	.KRIVGYFAEFE.NSG.....LTR..KQLQ...MLTHIYLFaip.RNG..

CE40270\_C.\_elegans .KRVVGYYSRSE.TSK.....ITS..VQVS...KLTHAVFAFVYMNSDG..  
 CE40296\_C.\_elegans .KRIVGYFAEFE.NTA.....LTR..KQLR...MLTHIVFLFAFP.KNG..  
 ChiB\_S.\_marcescens .KAVIGYFIPTNQINNYTETDTSVVP.FPVSNIITPAK..AKQLTHINFSFLDINSN...  
 O10363\_O.\_pseudotsug .KTVAAYFVEWG.VYG...RG...FP..VDK..VPLP...NLSHLLYGFIPICGGDGL  
 AAP29899\_C.\_fumifera .KTVAAYFVEWG.VYG...RN...FP..VDK..VPLP...NLSHLLYGFIPICGGDGL  
 AAV73807\_B.\_mori\_NPV .KIVAAYFVEWG.VYG...RS...FP..VDK..VPLP...NLSHLLYGFIPICGGDGI  
 AAL56186\_H.\_zea\_SNPV .HTVAAYFVEWG.VYG...RS...FP..VDK..VPTP...NLSHILYGFIPICGGDGI  
 AAF33549\_S.\_exigua\_N .KIVAAYFVEWG.VYL...RQ...FP..VDK..VPAP...NLSHILYGFVPICGGDGI  
 AAZ38189\_A.\_segetum .KIVAAYFVEWG.VYP...RQ...FP..VDK..VPVP...NLSHLLYGFVPICGGEGI  
 AAS82706\_A.\_segetum .HVVAGYFVEWG.VYD...RQ...YP..ADL..VPVP...NLTHLLYGFVPLCGGDGI  
 ZP\_01159013\_Photobac .VVMGTYFVEWG.IYG...RE...YT..VDN..IPAD...NLTHILYGFIPVCGP...  
 ZP\_01161077\_Photobac .KVVGSYFVEWG.VYG...RK...FT..VDD..IPAQ...NLTHILYGFTPICGGDGI  
 ZP\_01159325\_Photobac .PVVAGYFADWQ.YNNE.ANP...YT..VKD..IPAD...KLTHVIYAFLSMCGP..H  
 ZP\_01160869\_Photobac .PVIAAAYPDWK.VYTP.KTP...YS..ANM..LPVN...DLTHIIYAFILAVCGP..I  
 ZP\_01233025\_V.\_angus .VVMGTYFVEWG.IYG...RE...YT..VDN..IPAD...NLTHILYGFIPICGP...  
 ZP\_01236284\_V.\_angus .KVVGSYFVEWG.VYG...RK...FT..VDD..IPAQ...NLTHILYGFTPICGGDGI  
 ZP\_01235109\_V.\_angus .PVVAGYFADWQ.YNNE.SNP...YT..VKD..IPAD...KLTHVIYAFLSMCGP..H  
 ZP\_01235465\_V.\_angus .PVIAAAYPDWK.VYTP.KTP...YS..ANM..LPVN...DLTHVIYAFILAVCGP..V  
 AAO08114\_V.\_vulnific .LVVGTYFVEWG.IYG...RN...YT..VDN..IPAQ...NLTHILYGFIPICGP...  
 AAO07498\_V.\_vulnific .KVVAGYFADWQ.YANA.SNP...YT..VKD..IPAE...KLTHVIYAFLSMCGP..H  
 NP\_232428\_V.\_cholera .TVIGTYFVEWS.IYD...RK...FT..VDN..IPGQ...NLTHILYGFIPICGP...  
 YP\_432951\_H.\_chejuen .TEIVTYIGDWV.IYG...RR...YD..FTK..LPVK...NLHRIVYGFSGICYPDAS  
 YP\_529337.1\_B\_S.\_deg .KIIVTYFVEWG.IYG...RD...YH..VNN..IPAS...NLTHVLFGFIAMCG....  
 YP\_435912\_H.\_chejuen .SVVGTYFVEWG.VYG...RN...FP..VEK..IPAQ...NLTHLLYAFIACVCGP...  
 ZP\_01137509\_A.\_cellu ...KVAYYDQWS.IY...LNA...FY..PKN..LDTSGIAGKLDFLIYDFENINP...  
 ChiE\_S.\_coelicolor ...KVGYFVQWG.IY...GRQ...YF..VKN..LDTSGAAKQLDVVNYAFENLDP...  
 ChiC\_S.\_coelicolor ...VKMGYFTNWG.VY...GRN...YH..VKN..LVTSGSADKITHINYAFGNVQG....  
 ChiD\_S.\_coelicolor ...KVVGYFTEWG.VY...DRN...YH..VKN..IESSGSADKLTHINYSFGNVTG....  
 NP\_903910\_C.\_violace .RHVGSYFAQWG.IY...DRN...YK..VFN..LVKSGGDKQLTFLNYAFGNVYA....  
 YP\_529072.1\_S.\_degra .DKIIGYFAEWG.VY...GRN...YH..VKN..IHTSGSADKLTHIVYAFGNVQN....  
 ZP\_01431615\_S.\_tropi .HKVVGYFAQWG.VY...ARN...YH..VKN..IHTSGSAAKLTHIMYAFGTTSG....  
 ZP\_01136287\_A.\_cellu ...VRAAAYTQWS.VY...S.G...FT..VAG..VVANGDAGRLNQINYAFINVAP....  
 01315.1\_C.\_cinereus .....AWYAG.W.HAT...TG...YP..LSR..VSWK...KYTHLTAYFAETSPDV..  
 03252.1\_C.\_cinereus .....AWYTG.W.HSR...D...FP..LSR..VSWK...KYTHMTYAFGITTPSP..  
 05285.1\_C.\_cinereus .....GWYPS.W.YKN...V...MP..PSE..IPWE...KYTELTFAFALTTPDT..  
 05291.1\_C.\_cinereus .....AWYPS.W.QAA...A...HP..PES..LSWD...KYNAMTFAFATTTSDP..  
 01586.1\_C.\_cinereus .....AAYPA.W.SAG...T...HP..PEK..LDFS...KFDILFYAFATPNSSS..  
 128098\_P.\_chrysospor .TWYTG.W.NAD...Q...LP..VDQ..VSWD...KYTSVTYAFALTQAD..  
 39872\_P.\_chrysospori .....AAYAG.W.HGV...GNSYNNFT..LDD..VAWT...KYTHLIYAFAVTDPAA..  
 138098\_P.\_chrysospor .TWYTG.W.HAQ...H...LS..LED..ISWE...KWSSISYAFAYTTPDP..  
 129436\_P.\_chrysospor .....AAYPS.Y.TAA...S...FP..PER..VDFT...RYDDWVDFAFVPAQAGG..  
 EAA71245\_G.\_zeae .....TYFAG.F.HAN...RG...FP..VSA..MPWD...KYTDKAYSFAETTEDG..  
 MGG\_04732\_M.\_grisea .....GYFAG.Y.HAK...RKG.V.TFG..VDQ..IPWD...KYDDVKYAFAEATTADG..  
 UM06190\_U.\_maydis .....GYWAD.W.TAS...T...LP..ATS..IDFS...KFDDIVNYAFALPTAEF..  
 04245\_F.\_neoformans .....GYYPD.W.SAY...Y...LS..PES..VDWD...RFDILDFAFaipnsdg..  
 16170\_R.\_oryzae .....AYVLD.W.D.....IP...KN..IKWD...KLDHIAYAFaepnang..  
 01334\_R.\_oryzae .....AYVLD.W.D.....IP...KN..IQWS...KLDHIAYAFaepdakg..  
 13934\_R.\_oryzae .....AYIVD.W.D.....LP...RT..IYWD...KLDHVSAYAFavpnkeg..  
 07611\_R.\_oryzae .....GYFPN.W.LYG...R...YT..PSK..IDFS...KYTHIYYAFaiqn.TA..  
 10252\_R.\_oryzae .....GYFPN.W.LYA...N...YP..VEN..IPYT...KYTHINYAFailnnpd..  
 14659\_R.\_oryzae .....GYYPQ.....S...FSK..IDFD...RYTHINYAFavmi.KG..  
 231399\_L.\_bicolor .....GWYEG.Y.QVN...DG...LP..LSQ..ISWY...KYTHLIYSFAETTPDV..  
 180319\_L.\_bicolor .....SWYPS.W.LGT...K...VP..PES..LSWD...KYTSVTFAFALTTSdp..  
 191848\_L.\_bicolor .....AWYPG.W.LGG...T...YA..PDT..ISWG...KYNALTFAFATTTSDA..  
 317003\_L.\_bicolor .....AAYPS.W.SAG...T...TP..PEK..LDFS...KFDILFYAFATPNSSS..  
 246840\_L.\_bicolor .....AAYTG.W.HAE...D...YP..LSD..VSWK...KYTHVIYSVASTTPNA..  
 144643\_L.\_bicolor .....GYYPD.W.AGP...R...FP..PEK..IDFD...RFDWIDFAFavpdeTF..  
 310136\_L.\_bicolor .....GWYPG.W.LGA...T...YA..PSN..ISWS...KYNALTFAFavTTNDP..  
 629882\_M.\_xanthus .....GYTGT.W.NAD...M...YP..PEK..VDFS...ALTHILVGRVTPNPd..  
 630509\_A\_M.\_xanthus .....GYFVG.Y.QLW...M...QP..VDA..VDLA...GITHLVVGRVKPNPN..  
 YP\_592598\_Acidobacte .....AAYPD.W.AKD...QTP..AYD..ASK..IPYT...KLTHILHAFLLLDPSG..  
 YP\_446903\_S.\_ruber .....GY.....VH...G.....T..VD...VSAEDARRLTHINYAFANVTE....

ZP\_00739282\_B.\_thuri .....GYFPSWG.VY...GRN...YQ..VAD..IDAS...KLTHLNIAFADICW....  
 ZP\_01245639\_F.\_johns .....GYFAQWS.IY...ARD...FN..VPK..IDGS...KLTHLNYSFYGTTY....  
 NP\_976824\_B.\_cereus .....GYFPSWG.IY...GRN...YQ..VAD..IDAS...KLTHLNIAFADICW....  
 YP\_077581\_B.\_licheni .....GYFPSWG.AY...GRD...FQ..VWD..MDVS...KVSHINYAFADICW....  
 631138\_M.\_xanthus .....GYFTAWG.IY...ARN...YH..VSN..VQPS...KLTHINYAFSNISG....  
 ZP\_01247029\_F.\_johns .....AYIPN.W.IDL..N....AF..SST..IQYS...KLTHINIAFENPDAN...  
 ZP\_01234549\_V.\_angus .....SYMKS...AND..Q....WF..DNP..HSN.....EISDLNIAFMNPSANM..  
 ZP\_01160697\_Photobac .....SYMKD...AND..Q....WF..DNP..HSN.....EISDLNIAFMNPSANM..  
 ZP\_01158584\_Photobac .....SYNKT.E.QNK...P....WV..DND..DNFG...EITDLNIAFMNPSANR..  
 AN0549\_E.\_nidulans .....GYEGWS.M.N...RP.CNAFY..PEQIPIGV.....YTHLNIAFASIDP....  
 AN8481\_E.\_nidulans .....GYEGWS.M.R...RY.CHSFY..PEQIPRGI.....YTHLNIAFASIDP....  
 AN9390\_E.\_nidulans .....GYEGWS.TSK..K..CNGLN..PEDLLMGA.....YTHLNIAFAFIDP....  
 AN0517\_E.\_nidulans .....GYEELFN.Y.Y..KG.CNVIE..PESLIIEP.....FTHLNIAFVNFGD....  
 AN0541\_E.\_nidulans .....AYYETWA.D.T...RE.CDAFR..PEDIPVKA.....LTHLNIAFAGIED....  
 AN5077\_E.\_nidulans .....GYWEGWS.T.Q...RS.CGTMS..AGEIPVNL.....LTHLNIAFGYIN....  
 AN0509\_E.\_nidulans .....AYYEGYL.FT...RE.CLYQD..ALQIDTSK.....YTHLHFGFASIT....  
 AN7613\_E.\_nidulans .....GYYESFN.LD...RP.CLNLH..AAHIKVND.....YSHIHWFVFSIN....  
 07035\_N.\_crassa .....GYEAWWS.TTN...RP.CYAML..PEQIPYGY.....YTDIIFSFATIDP....  
 07484\_N.\_crassa .....GYEAYS.LGG...RS.CLYQD..VRQIDTNK.....YSHIHFAFGDIT....  
 05317\_N.\_crassa .....AYFEAYN.LG...RD.CLFQD..ASQIDTSQ.....HTHIHFAFGTILT....  
 EAA74768\_G.\_zeae .....GYFEGWA.K.N...RA.CEVFM..PEQIPIGL.....YTHINFAFGTINP....  
 EAA78168\_G.\_zeae .....GYYGSGG.A.T...HK.CNPMI..PDAFPQGI.....YTHIYFAFGSIDP....  
 EAA75711\_G.\_zeae .....GYQSWN.VRT...RK.CDTKT..PKQLDTTG.....FTHLFYSFAFIDP....  
 EAA68447\_G.\_zeae .....GYFQGYG.MG...RP.CLYQD..ASQIDTSK.....YTHLHFAFGTILT....  
 EAA77156\_G.\_zeae .....GYFQSWN.LG...RP.CLNMD..VTKLPLT...AYTHIHFAFAGLT....  
 12510\_S.\_sclerotioru .....GYYESWA.S.S...RP.CNVFW..PEQIPIGL.....YTHINFAFGTINP....  
 00773\_S.\_sclerotioru .....GYASGG.A.T...RA.CDAML..PESFPQGI.....YSHIYFAFGSINP....  
 05454\_S.\_sclerotioru .....GYEAWN.Y.K...KK.CIGMG..IQNIPVGS.....LTHLYSFGYITP....  
 00677\_S.\_sclerotioru .....AYWQINS.AT...RS.CNALP..IPLINTQG.....LTHLIFAFMSISP....  
 02128\_S.\_sclerotioru .....GYWEGYN.FD...RP.CLNKP..ITSINTTAG...YTHVHLAFATIT....  
 MGG\_04534\_M.\_grisea .....GYEGWN.MAQ...RS.CNTMK..PSEIPLGY.....YTHIFYSFALIDP....  
 MGG\_01336\_M.\_grisea .....GYQAVA.AR...RP.CDRV...PLQINTAG.....YTHLYFSFVLIDR....  
 14527\_P.\_nodorum .....GYESWS.NTR...K..CSSVA..PEDLNLNG.....FTHINFAFAFFDP....  
 15411\_P.\_nodorum .....GYQGW.TRE...RK.CDKVA..PRQINTRG.....LTHLFYSFAFFHP....  
 02214\_P.\_nodorum .....AYQSWN.SRS...RG.CDKVM..PNQLNLSG.....ITHLVLAFAFIDP....  
 04761\_C.\_immitis .....GYEAWR.H.D...SN.CQGMG..LKDIPVNS.....LTHLFFSFGYITP....  
 04323\_A.\_capsulatum .....GYFESWV.Y.D...RP.CDVLH..PSKINTKP.....WTHLNYGFAQINP....  
 00533\_B.\_fuckeliana .....SYWQIGS.AT...RP.CNALP..VSLIPTQN.....ITHLIFAFMSISP....  
 Chi18\_1\_H.\_jecorina .....AYFEAFD.QK...RT.CLKMP..VTAVDTSA.....YTHIHFSFITLN....  
 Chi18\_8\_H.\_jecorina .....GYEAFS.YD...RD.CLAMH..PRSIPKNN.....FTHVHFAFATVT....  
 Chi18\_9\_H.\_jecorina .....GYEAFN.WE...RP.CLHME..SKLSNTDK.....YTHMHWFAGDIK....  
 Chi18\_10\_H.\_jecorina .....TYYESWN.LD...RS.CMHMD..VRTVGD LGQ...GYTHLHFAFVNIT....  
 02650\_A.\_capsulatum .....MYLTGQH.PHP...P....S...DS...SLIN...PITHVALAFMNSAL....  
 AN0221\_E.\_nidulans .....MYLTGVR.QHN...V....VP..EP...SLVS...DVTHVALAFMQSSI....  
 06020\_N.\_crassa .....MYLTG...QHP...V....AP..QI...DQLD...HVTHVALAFMSPSI....  
 EAA76014\_G.\_zeae .....MYLTG...QHD...V....VP..AK...HQFK...GVSHVVIAFMRSEF....  
 Chi18\_4\_H.\_jecorina .....MYLTG...QHV...V....MP..SED..HLID...PITHVILAFMRSDV....  
 09277\_P.\_nodorum .....MYLTG...QHN...V....VP..EYPMETMLR...GVTHVTLAFMRSDI....  
 05838\_A.\_capsulatum .....AYLDQ.W.HST...I....LP..GK...EITT...GVDCAIMAFANSSL....  
 EAA69039\_G.\_zeae .....IYYDQ.W.HTK...D....LP..SK...DITS...GVTHVMMSFANSSL....  
 MGG\_06594\_M.\_grisea .....VYYDQ.Y.HIT...P....PP..NK...TLTA...GITHVITAFQSDL....  
 Chi18\_11\_H.\_jecorina .....S....LP..DH...SVTA...GVTHVTTAFADSVI....  
 02644\_A\_P.\_nodorum .....MYADE.W.HPT...R....PT..NP...KDRS...GIDHVVI AFAMAN....  
 AN9447\_E.\_nidulans .....ANGDR.W.HVN...G....LP..GS...DQTQ...GITHAIMGFAKSTD....

.....70.....80.....90.....100.....110.....120  
 .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
 NP\_979924\_B.\_cereus .....  
 YP\_077302\_B.\_licheni .....  
 YP\_091539\_B.\_licheni .....  
 YP\_079121\_B.\_licheni .....  
 YP\_074366\_S.\_thermop .....



YP_075811_S._thermop	.....	
YP_075619_S._thermop	.....	
ZP_01354047_C._phyto	.....	
ZP_01354926_C._phyto	.....	
NP_902406_C._violace	.....	
ZP_01136704_A._cellu	.....	
ZP_00526542_S._usita	.....	
AAF46212.1_D._melano	.....	
AAF46534.1_D._melano	.....	
AAF46544.1_D._melano	.....	
At4g19720_A._thalian	.....	
At4g19750_A._thalian	.....	
EAA67655_G._zeae	AKD.....G.....	TVESSDPWA...DVQRTY..
EAA73155_G._zeae	AD.....G.....	TVYTGDSYA...DLEKHY..
EAA74986_G._zeae	PD.....G.....	TVYTGDAYA...DLEKHY..
EAA74223_G._zeae	SDS.....G.....	EVHLTDSWA...DTDIIHW..
MGG_05533_M._grisea	A.N.....G.....	TVVSSDAWA...DTQKQF..
MGG_01247_M._grisea	TD.....G.....	EVISSDTYS...DIDKHY..
MGG_00086_M._grisea	DD.....G.....	TVVGGDIEA...DVSKHY..
MGG_07927_M._grisea	PDS.....G.....	EVFLTDTWA...DTDIIHW..
Chi18_6_H._jecorina	D.D.....G.....	SVVSMDPWA...DEEKML..
Chi18_5_H._jecorina	SD.....G.....	TVVASDTYA...DVEKHY..
Chi18_7_H._jecorina	QDT.....G.....	EVHMTDGWA...DTDIIHW..
04883_N._crassa	ED.....G.....	TVFSSDTWS...DTDKRY..
04554_N._crassa	PDS.....G.....	EVYLTQWA...DTDIIHW..
11407_B._fuckeliana	TD.....G.....	TVYLSDTYS...DLQKHY..
05350_B._fuckeliana	PDS.....G.....	EVYMTDGWA...DTDIIHF..
11700_S._sclerotioru	TD.....G.....	TVYLSDTYS...DLEKHY..
11304_S._sclerotioru	PES.....G.....	EVYMTDGWA...DTDIIHF..
08020_S._sclerotioru	PES.....G.....	
01250_A._capsulatum	PDS.....G.....	EVYLSDTYS...DLEKHY..
05886_A._capsulatum	GDT.....G.....	EVYLTDNYA...DTDKHY..
06565_A._capsulatum	AES.....G.....	EVFLTDTWA...DTDKHF..
05250_C._immitis	GDT.....G.....	EVHLTDTYA...DLEKHY..
02795_C._immitis	PS.....G.....	EVYLSDTWA...DTDKHY..
03822_C._immitis	PTT.....G.....	EVYLSDEQA...DIKKRF..
AN5454_E._nidulans	PET.....G.....	EVYLSDTYS...DIEKHY..
AN4871_E._nidulans	PET.....G.....	EVYLSDTWS...DIEKHY..
00269_P._nodorum	PET.....G.....	EVYLTDTWS...DTDKHY..
04870.1_C._cinereus	PSS.....G.....	TVSLSDVWA...DKDIHY..
09921.1_C._cinereus	AST.....G.....	AIKLTDPYS...DEQKRF..
124149_P._chrysospor	PDS.....G.....	EVFLSDTWA...DQEIHY..
134311_P._chrysospor	PDT.....G.....	VISLTDSYA...DEQKHF..
03412_F._neoformans	ADS.....G.....	EVVLSDTWA...DVEIHY..
13635_R._oryzae	PD.....G.....	QVVLGDTYA...DLEKHF..
UM04261_U._maydis	PDT.....G.....	ECFLTDLWA...DEQIHY..
EAA69503_G._zeae	AD.....G.....	GVFLSDEWA...DAGAPV..
EAA70860_G._zeae	FK.....Q.....	HFQAIDWA...DNEKMPV..
Chi18_3_H._jecorina	AD.....G.....	NVLLGDEWA...DARAPV..
Chi18_2_H._jecorina	.....	LVQWIDEHA...DVVKDI..
03026_N._crassa	AD.....G.....	GVFLSDEWA...DVTAPC..
01594_B._fuckeliana	PD.....G.....	GVFLSDEWA...DMQMPV..
05897_S._sclerotioru	PD.....G.....	GVFLSDDWA...DMQMPV..
04742_A._capsulatum	AR.....	ELSNEWV...DECQPV..
04750_C._immitis	PD.....G.....	TVRLSDEWA...DDQMPV..
04719_P._nodorum	DD.....G.....	TVYLSDEWA...DAQIDV..
MGG_08458_M._grisea	KD.....G.....	TLKHFDEYA...DLQIEA..
CHT4_C._albicans	EQT.....G.....	KLKFSDEWC...DLQMPQ..
01119_L._elongisporu	PLT.....G.....	KLKFTDEWC...DLQMPL..
XP_454053_K._lactis	AKS.....G.....	AVKSSDSWS...DFELPL..
CTS2_S._cerevisiae	SRT.....G.....	GIENTDSWS...DLEMNL..
246746_L._bicolor	PDT.....G.....	EVFLSDVWA...DKDIHY..

03209_N._crassa	.....VSSDTYA.....DLEKRY..
14474_P._nodorum	NKT.....G.....EVFLSDEWS.....DVQFPY..
CE06282_C._elegans	.....TLLFN.....NQIE..
CE03547_C._elegans	.....HLQID.....GDLA..
CE03542_C._elegans	.....TLQFQ.....SGSA..
CE15845_B_C._elegans	.....SLTFR.....DESS..
CE02997_C._elegans	.....SVKLE.....GDAA..
CE36953_C._elegans	.....KISVGNVNNPENAAATGL
YP_432439_H._chejuen	.....HVSIG.ANTPTNAATGM
YP_529449.1_S._degra	.....RISVGEEADENNPSIGM
YP_077582_B._licheni	.....RLSVG.SDGEKNAATGM
ChiI_S._coelicolor	.....KLSVN.ETAPGNPATDM
NP_902986_C._violace	.....KVNIGDISDPNSNAAVGM
ZP_01159608_Photobac	.....KVNIGDTSDPNNAAVGM
ZP_01234708_V._angus	.....KVNVGDVNDPNNAAVKG
NP_233087_V._cholera	.....FSMQ.....VDDSATKM
NP_230718_V._cholera	.....KVNVGDVNDPTNAATGK
AAO07185_V._vulnific	.....DSTI.....QVNP....
ZP_01354150_C._phyto	.....DGKL.....SVDS..
ZP_01246933_F._johns	.....G.....DLV.....F.TDKDA.....AVGAPVG.
YP_012734_L._monocyt	.....LECDFI.....DVEKAD..
YP_529337.1_A_S._deg	DG.....TVAFY.....DTYADPL.
ChiA_A_P._kodakarae	DG.....AVDYI.....QENAMR..
AAG19274_Halobacteri	DG.....TVVLP.....DSDVDHES
AAG19275_Halobacteri	.....TIHFE.....SRKA..
CE03543_C._elegans	.....KLQFK.....TN.Q...
CE34961_C._elegans	.....SLGFK.....NDAA..
CE20043_C._elegans	.....QLEMS.....ER.A...
CE15845_A_C._elegans	.....QLEMS.....ER.A...
CE32863_A_C._elegans	.....TLQFK.....NLIT..
CE03544_C._elegans	.....SLILR.....KS.....
CE08731_C._elegans	.....ILDFE.....RSKY..
CE28638_C._elegans	.....SLQFE.....SAIS..
CE32863_B_C._elegans	.....VMTLD.....GERT..
CE01673_C._elegans	.....VITLD.....GEQT..
CE02993_C._elegans	.....NMTFG.....GERS..
CE02996_C._elegans	.....TIKWP.....N.....
CE02995_C._elegans	.....TIKFK.....YG.T...
CE02992_C._elegans	.....HVFFE.....NLA...
CE02999_C._elegans	.....SVKFG.....AVSEDDS
CE09229_C._elegans	.....SVKFG.....PVSADDP
CE12928_C._elegans	.....ILTFI.....DQYE..
CE23907_C._elegans	.....TVMFR.....DKLA..
CE32917_C._elegans	.....TLVFR.....NK.....
CE34579_C._elegans	.....HLQID.....GDLA..
CE25073_C._elegans	.....NLNI.....IN.....
CE03548_C._elegans	.....G.....DLV.....F.TDKDA.....AVGAPVG.
NP_469498_L._innocua	.....TFEIG.....NAFS..
CE08730_C._elegans	DG.....TVDFY.....DTWADPQ.
Q8U1H4_P._furiosus	.....TLQFD.....NSKA..
CE12474_C._elegans	.....VITIV.....DDRS..
CE02990_C._elegans	.....TLKFE.....KQDE..
CE40270_C._elegans	.....TITFG.....GESS..
CE40296_C._elegans	.....LECAWD.....PATNDA..
ChiB_S._marcescens	NDALKTIPG.....SFEALQRSCK.....GRADFKVAIHDPWA.....AIQKP...
O10363_O._pseudotsug	NDALKTIPG.....SFEALQRSCK.....GRSDFKVAIHDPWA.....AIQKP...
AAP29899_C._fumifera	NDALKTIPG.....SFEALQRSCK.....GREDFKVAIHDPWA.....AVQKP...
AAV73807_B._mori_NPV	NDALKTIPG.....SFEALQRSCK.....GRDNFKVSIHDPWA.....ALQKP...
AAL56186_H._zea_SNPV	NDALKTIPG.....SFEALQRSCK.....GRDNFKVSIHDPWA.....ALQKP...
AAF33549_S._exigua_N	NDALKTIPG.....SFEALQRSCK.....GRADFKVAIHDPWA.....AIQKP...
AAZ38189_A._segetum	NDALKTIPG.....SFEALQRSCK.....GRADFKVSIHDPWA.....ALQKP...

AAS82706\_A.\_segetum NDSLKQVPG...SFEALQKSCA...GREDFKVTIHDIWG...ALQKP...  
 ZP\_01159013\_Photobac NESVKS VGGN...SFNALQTACK...GVDDYEVVIHDPWA...AFQKSF...  
 ZP\_01161077\_Photobac NDSLKSIAG...SFNALQKACA...GQKDFEVS IHDPWA...AISKP...  
 ZP\_01159325\_Photobac QGAIDAVQK...QIKEACE...GKAPFS AVIVDQVS...ALQKD...  
 ZP\_01160869\_Photobac NASPDNIKK...IMKTQCK...NKPIGTAI VLDDYA...ALQMK...  
 ZP\_01233025\_V.\_angus NESVKS VGGN...SFNALQTACK...GVDDYEVVIHDPWA...AFQKSF...  
 ZP\_01236284\_V.\_angus NDSLKSIAG...SFNALQKACV...GQKDFEVS IHDPWA...AISKP...  
 ZP\_01235109\_V.\_angus QGASDAVQK...QIEAACQ...GKEPFS AVIVDQVS...ALQKD...  
 ZP\_01235465\_V.\_angus DASPDNIKK...IMKTQCK...NKPIGTAI VLDDYA...ALQIK...  
 AAO08114\_V.\_vulnific NESVKS VGGN...SFNALQTACQ...GVPDYE VVIHDPWA...AYQKSF...  
 AAO07498\_V.\_vulnific TGASET VQK...LVAKQCE...GKEPFS AI VVDTEA...ALEKD...  
 NP\_232428\_V.\_cholera NESLKS VGGN...SFNALQTACK...GVPDFE VVIHDPWA...AYQKSF...  
 YP\_432951\_H.\_chejue DTQDPGFPTS...APAAVNRTC NQ...SNLPDGA MAIADFEA...AFVRNVGV...  
 YP\_529337.1\_B.S.\_deg .DNPHASGG...AQAAIAS ECA...DKQDFE VTLVDRFA...NLEKT...  
 YP\_435912\_H.\_chejue NESLRQANPQ...GHSVLMNECS...DQADYTV TIHDRFA...ALEKS...  
 ZP\_01137509\_A.\_cellu TTL...QC FE.ATKAADQ NESNP NAGDGAGDQYA...DMDKMY...  
 ChiE.S.\_coelicolor TSL...TCQAGVT KGTSGNPQDPDEGTGAGDADA...DYARPM...  
 ChiC.S.\_coelicolor GK...CTI...GDSYA...DYDKAY...  
 ChiD.S.\_coelicolor GK...CAM...GDAYA...ATDRAY...  
 NP\_903910\_C.\_violace DG...KCGM.VTRAENGN...GDG.GDAWA...DYQRSF...  
 YP\_529072.1\_S.\_degra GE...CKI...GDSYA...AYDKAY...  
 ZP\_01431615\_S.\_tropi GR...CGI...GDSYA...DYEKAY...  
 ZP\_01136287\_A.\_cellu NPA...VSGSPIECLS...GDPWA...DYQMPF GG...  
 01315.1\_C.\_cinereus HKLSFEEAT...WTNPQ...LLP...  
 03252.1\_C.\_cinereus ...  
 05285.1\_C.\_cinereus S...ALTLE...GEEET...LR...  
 05291.1\_C.\_cinereus AN...PLALD...AESQA...LLP...  
 01586.1\_C.\_cinereus G...ITWDG...G.DKD...ILR...  
 128098\_P.\_chrysospor ...GTILLQ...DSDVA...LLP...  
 39872\_P.\_chrysospori P...ENATLA...DSDVE...LLT...  
 138098\_P.\_chrysospor ...AVVALQ...DSDAD...ILK...  
 129436\_P.\_chrysospor G...LGWDGA...DGSAGD...VLR...  
 EAA71245\_G.\_zeae G...LDLS...KSQPE...ELS...  
 MGG\_04732\_M.\_grisea S...LDLS...KSAPE...ELP...  
 UM06190\_U.\_maydis D...LWIPT...DP SGN...LLR...  
 04245\_F.\_neoformans S...LYFT...DDSST D...SLQ...  
 16170\_R.\_oryzae V...LK...GFDGN...NLK...  
 01334\_R.\_oryzae N...LK...GFESG...NLK...  
 13934\_R.\_oryzae D...LN...GFNKT...QLN...  
 07611\_R.\_oryzae S...SPTWSDSG...VFDSYVAY...GFP...  
 10252\_R.\_oryzae N...LPSFTD...DWAVES...SFP...  
 14659\_R.\_oryzae N...TPVWSD...PES IET...QLP...  
 231399\_L.\_bicolor NVLSLEKSN...PEG...LP...  
 180319\_L.\_bicolor G...AVSID...SDGLV...LLP...  
 191848\_L.\_bicolor S...VIALD...SESAS...LLP...  
 317003\_L.\_bicolor G...LSWDS...G.SQA...VLK...  
 246840\_L.\_bicolor SVVEVDVPD...DT...LLK...  
 144643\_L.\_bicolor N...LTWDNP...EESP.S...ILD...  
 310136\_L.\_bicolor S...VISLD...AQSVT...LLP...  
 629882\_M.\_xanthus .GTVNTQFDN...SNGP...AIAR...  
 630509\_A.M.\_xanthus .GTLNANFDANI...DDSHGR...AMAK...  
 YP\_592598\_Acidobacte N...GALQ...IDPEL...IEP...  
 YP\_446903\_S.\_ruber E...GRVVL...EQERDS...  
 ZP\_00739282\_B.\_thuri KGKHGN.PSTHPDNPNKQTWNCKE...SGVPLQNKEVPNGT LVLGEPWA...DVT KSY...  
 ZP\_01245639\_F.\_johns DPAH...PE...NTKLKCLDTYA...DFEHMEG...  
 NP\_976824\_B.\_cereus NGKHGN.PSTHPDNPNKQTWDCKE...SGVPLQNKEVPNGT LVLGEPWA...DVT KSY...  
 YP\_077581\_B.\_licheni EGRHGN.P...DPTGPNPQTWSCQD...ENG V...IDAPNGTIVMGDPWI...DAQSN...  
 631138\_M.\_xanthus DGR...CILGDPFA...DIDKSG...  
 ZP\_01247029\_F.\_johns ...GYLSFNS...GSN...AI...  
 ZP\_01234549\_V.\_angus DKEGIYHPDG...HVA...ALSTDK...  
 ZP\_01160697\_Photobac DEDGIYHPDG...HVA...ALSTDR...  
 ZP\_01158584\_Photobac DSEGISHPDG...IVP...SLDHEH...

AN0549_E._nidulans	.....	ETFE	..	VLVPSV	..
AN8481_E._nidulans	.....	ETFE	..	ILAPDA	..
AN9390_E._nidulans	.....	ESYK	..	IANMQD	..
AN0517_E._nidulans	.....	DYTL	..	IDEY	..
AN0541_E._nidulans	.....	SEIT	..	IDSS	..
AN5077_E._nidulans	.....	SAFQ	..	ITNMDG	..
AN0509_E._nidulans	.....	ENYE	..	VSIGD	..
AN7613_E._nidulans	.....	SDFQ	..	ISVND	..
07035_N._crassa	.....	NSFE	..	IKPGDS	..
07484_N._crassa	.....	PDFK	..	VSAGD	..
05317_N._crassa	.....	PDYE	..	VEVGD	..
EAA74768_G._zeae	.....	FTYV	..	VEANDE	..
EAA78168_G._zeae	.....	KSEK	..	VQANA	..
EAA75711_G._zeae	.....	TSFK	..	ITPAHD	..
EAA68447_G._zeae	.....	KDFD	..	VEVGD	..
EAA77156_G._zeae	.....	SDFS	..	VLIEP	..
12510_S._sclerotioru	.....	TTFK	..	VEPDSE	..
00773_S._sclerotioru	.....	DTFE	..	VIPGAD	..
05454_S._sclerotioru	.....	DDFD	..	IIPMDDGN	..
00677_S._sclerotioru	.....	NTFH	..	VVPFDT	..
02128_S._sclerotioru	.....	TDFE	..	VDVSS	..
MGG_04534_M._grisea	.....	KTFH	..	VADMDA	..
MGG_01336_M._grisea	.....	TSFA	..	ITPADA	..
14527_P._nodorum	.....	SSFQ	..	IAPMDG	..
15411_P._nodorum	.....	TTFE	..	IMPMND	..
02214_P._nodorum	.....	VTYK	..	IGLRDT	..
04761_C._immitis	.....	GDFK	..	IAGMDG	..
04323_A._capsulatum	.....	KDNT	..	LTSMH	..
00533_B._fuckeliana	.....	NSFH	..	VVPFDT	..
Chi18_1_H._jecorina	.....	EDYS	..	VNIDG	..
Chi18_8_H._jecorina	.....	DKFD	..	VDISN	..
Chi18_9_H._jecorina	.....	SDFS	..	VYIND	..
Chi18_10_H._jecorina	.....	KDLK	..	VSVQ	..
02650_A._capsulatum	.....	FNKVL	..	TDPPTT	..
AN0221_E._nidulans	.....	FNR	..	NSTSS	..
06020_N._crassa	.....	FN	..	DPLNQ	..
EAA76014_G._zeae	.....	FN	..	VDEQPD	..
Chi18_4_H._jecorina	.....	FN	..	VDETPT	..
09277_P._nodorum	.....	FN	..	DANRT	..
05838_A._capsulatum	.....	FV	..	ESPSG	..
EAA69039_G._zeae	.....	FT	..	TQPGG	..
MGG_06594_M._grisea	.....	FL	..	NSSG	..
Chi18_11_H._jecorina	.....	FN	..	SGT	..
02644_A_P._nodorum	.....	FT	..	ATA	..
AN9447_E._nidulans	.....	FT	..	GDAPA	..

	130	140	150	160	170	180
NP_979924_B._cereus	....	....	....	....	....	....
YP_077302_B._licheni	.....	.....	.....	.....	.....	.....
YP_091539_B._licheni	.....	.....	.....	.....	.....	.....
YP_079121_B._licheni	.....	.....	.....	.....	.....	.....
YP_074366_S._thermop	.....	.....	.....	.....	.....	.....
YP_075811_S._thermop	.....	.....	.....	.....	.....	.....
YP_075619_S._thermop	.....	.....	.....	.....	.....	.....
ZP_01354047_C._phyto	.....	.....	.....	.....	.....	.....
ZP_01354926_C._phyto	.....	.....	.....	.....	.....	.....
NP_902406_C._violace	.....	.....	.....	.....	.....	.....
ZP_01136704_A._cellu	.....	.....	.....	.....	.....	.....
ZP_00526542_S._usita	.....	.....	.....	.....	.....	.....
AAF46212.1_D._melano	.....	.....	.....	.....	.....	.....
AAF46534.1_D._melano	.....	.....	.....	.....	.....	.....



[illegible]

YP_529449.1_S._degra	.....EWPD.....VAGAEMD.....PSFSYKG..HFNLLNKYKK
YP_077582_B._licheni	.....TWPE.....HPDVKMD.....QTLPLYKG..HFNLLHQYKD
ChiI_S._coelicolor	.....TWPG.....VEGAEMD.....PGLPLYKG..HFNLLNKFKK
NP_902986_C._violace	.....SWPG.....VAGAEMD.....ASLPLYKG..HFNLLTQYKR
ZP_01159608_Photobac	.....EWD.....G.VEID.....PALGFKG..HFGALATAKA
ZP_01234708_V._angus	.....EWD.....G.VEID.....PALGFKG..HFGALATAKE
NP_233087_V._cholera	.....EWP.....G.VEID.....PTLGFKG..HFGALATYKQ
NP_230718_V._cholera	.....TWEN.....VPGAEMD.....PSLPYQG..HFNLLSKFKK
AAO07185_V._vulnific	.....EWP.....G.VEID.....PTLGFKG..HFGALATYKE
ZP_01354150_C._phyto	.....IKE.....LD..LPKELEILKQ
ZP_01246933_F._johns	.....AKD.....SL..TIKHLVSLKA
YP_012734_L._monocyt	.....QEG.....VQWGGAN.....AG..VLNAIQDLRA
YP_529337.1_A_S._deg	.....AETQIIAELQALKN
ChiA_A_P._kodakarae	.....NLEAMKEYKR
AAG19274_Halobacteri	.....VLEPKSWHHDH
AAG19275_Halobacteri	.....LLASFASLKQ
CE03543_C._elegans	.....KE..SFLYLRLKLAS
CE34961_C._elegans	.....KE..RFEKLTAVK
CE20043_C._elegans	.....RI..RFSNLRDKVR
CE15845_A_C._elegans	.....KE..RFKDLKSKVK
CE32863_A_C._elegans	.....KE..RFKDLKSKVK
CE03544_C._elegans	.....EQ..KFFSLKSKAR
CE08731_C._elegans	.....P..RFEELKRVAA
CE28638_C._elegans	.....KT..RFLAFRDAAK
CE32863_B_C._elegans	.....KQ..KFLNLRKSK
CE01673_C._elegans	.....RR..KFQEMRSKAR
CE02993_C._elegans	.....RR..KFEEMKSKAR
CE02996_C._elegans	.....RR..KFEEMKNEAR
CE02995_C._elegans	.....CE..NFESYARKAK
CE02992_C._elegans	.....KD..GFFDMKRKSM
CE02999_C._elegans	.....Q..R..R..RFLNLRKAQ
CE02998_C._elegans	.....GPQ.....AAKKAER..RFLNMKKKAR
CE09229_C._elegans	.....GPQ.....AGKKAER..RFVDMKKKAR
CE12928_C._elegans	.....MD..RFSKLKEVVR
CE23907_C._elegans	.....QE..RFLKIRDIAN
CE32917_C._elegans	.....N..RFMALRNIK
CE34579_C._elegans	.....KN..RFTNLIETIAK
CE25073_C._elegans	.....RQ..RFLSLTKIAK
CE03548_C._elegans	.....AG..VLNAIQDLRA
NP_469498_L._innocua	.....KR..KFKNWQRAVK
CE08730_C._elegans	.....NLEKFKELKK
Q8U1H4_P._furiosus	.....DL..RFSILKDKTR
CE12474_C._elegans	.....LR..KFEEMKSNAR
CE02990_C._elegans	.....ED..RFMQLKDIVN
CE40270_C._elegans	.....SQ..KFEEMRRNVR
CE40296_C._elegans	.....KARDVVNRLTALKA
ChiB_S._marcescens	.....QKG.....VSAWNEP.....YKG..NFGQLMAAKL
O10363_O._pseudotsug	.....QKG.....VSAWNEP.....YKG..NFGQLMAAKL
AAP29899_C._fumifera	.....QKG.....VSAWNEP.....YKG..NFGQLMAAKL
AAV73807_B._mori_NPV	.....QTG.....VSAWNEP.....YKG..NFGQLMAAKL
AAL56186_H._zea_SNPV	.....QKG.....VSSWNEP.....YKG..NFGQLMAMKR
AAF33549_S._exigua_N	.....QKG.....VSAWNEP.....YRG..NFGQLMATKL
AAZ38189_A._segetum_	.....QKG.....VGAWDDP.....YKG..NFGQLMAIKR
AAS82706_A._segetum_	.....KQA.....GHEYSTP.....IKG..NYAMLMAIKQ
ZP_01159013_Photobac	.....QQG.....VSEHSDP.....YRG..NFGQLMALKK
ZP_01161077_Photobac	.....F.G.....PTKAKVA.....YKG..HFAQLKDLKN
ZP_01159325_Photobac	.....LNG.....KTSNKVS.....YHG..NFGQLKLLSY
ZP_01160869_Photobac	.....KQA.....GHEYSTP.....IKG..NYAMLMAIKQ
ZP_01233025_V._angus	.....QQG.....VSEHSDP.....YRG..NFGQLMALKK
ZP_01236284_V._angus	.....F.G.....PTKAKVA.....YKG..HFAQLKDLKN
ZP_01235109_V._angus	.....LKG.....KTSSKVG.....YHG..NFGQLKLLSD
ZP_01235465_V._angus	

AAO08114_V._vulnific	.....PQA.....GHQYSTP.....IKG..NYAMMMALKQ
AAO07498_V._vulnific	.....F.G.....KVSVKVP.....FKG..HFAQLAELKK
NP_232428_V._cholera	.....PQA.....GHQYSSP.....IKG..NYAMLMALKK
YP_432951_H._chejuen	...PGGVTG.....TESMYELEPAS.....VGG..VFGVLYKLRLK
YP_529337.1_B.S._deg	.....YPG.....DTWYDDTTGQD.....YNG..NFGQLRKLKA
YP_435912_H._chejuen	.....YP.....GDKWDDP.....MRG..NFGQLRRLKK
ZP_01137509_A._cellu	.SADISVNGQ.....ADVWNQ.PVA.....G..NFHQQLLLKA
ChiE_S._coelicolor	.SAAQSVDBGV.....ADDGWG.KLR.....G..NLNQLKKLKA
ChiC_S._coelicolor	.TADQSVDBGV.....ADTWDQ.PLR.....G..NFNQLRKLKA
ChiD_S._coelicolor	.TAADSVDBGV.....ADTWDQ.PLR.....G..NFNQLLKLKQ
NP_903910_C._violace	.AANESVDGK.....ADSWND.PLR.....G..NFNQLRKLKL
YP_529072.1_S._degra	.SAADSVDBGV.....ADTWDDGVLRL.....G..NFGQLRRLKA
ZP_01431615_S._tropi	.TAADSVDBGV.....ADTWDQ.PLR.....G..SFNQLRKLKA
ZP_01136287_A._cellu	ATGRPSVDGT.....ADDWSG..LQ.....G..NFKQLRELKT
01315.1_C._cinereus	.....QFVSEAH.
03252.1_C._cinereus	.....AFVQEAH.
05285.1_C._cinereus	.....KFVEQAH.
05291.1_C._cinereus	.....RLVAAAR.
01586.1_C._cinereus	.....QFVEAAH.
128098_P._chrysospor	.....EFVAKAK.
39872_P._chrysospori	.....RLVDMAH.
138098_P._chrysospor	.....RLVARAH.
129436_P._chrysospor	.....CFVNAAK.
EAA71245_G._zeae	.....KFVDAAH.
MGG_04732_M._grisea	.....GFVKAAK.
UM06190_U._maydis	.....RLVSSGH.
04245_F._neoformans	.....SVVTQAH.
16170_R._oryzae	.....SVVTQAH.
01334_R._oryzae	.....QVVKEAH.
13934_R._oryzae	.....KLISLAH.
07611_R._oryzae	.....KLIVQMAH.
10252_R._oryzae	.....QLVSAAH.
14659_R._oryzae	.....QFVAEAR.
231399_L._bicolor	.....KFVAQAK.
180319_L._bicolor	.....TFVSAAK.
191848_L._bicolor	.....RLADSAR.
317003_L._bicolor	.....QFVTLAH.
246840_L._bicolor	.....RLVAAAH.
144643_L._bicolor	.....EFVTEAG.
310136_L._bicolor	.....TLSTRAH.
629882_M._xanthus	.....ALATRAH.
630509_A_M._xanthus	.....ALTRNAH.
YP_592598_Acidobacte	.....L..NLARLRDLKS
YP_446903_S._ruber	...PGS..GT.....TWEDCDKYA.....RCG..NFGELKRLKA
ZP_00739282_B._thuri	...GIP.....WDA.PVK.....G..NFYDLMKLKQ
ZP_01245639_F._johns	...PGS..GT.....TWEDCDKYA.....RCG..NFGELKRLKA
NP_976824_B._cereus	...PGD.....VWDEPIR.....G..NFKQLLKLKK
YP_077581_B._licheni	...GWQ..G.....EWDPGQLR.....G..NFRAFKEMKR
631138_M._xanthus	.....INAAHAQ.
ZP_01247029_F._johns	.....INKLTSTIQKFRDQ.
ZP_01234549_V._angus	.....INKLTSTIRKFKDQ.
ZP_01160697_Photobac	.....EKLIVKTIQTFRDK.
ZP_01158584_Photobac	.....YEKDLMQRLTLLK.
AN0549_E._nidulans	.....YEAKMMKRLTSLK.
AN8481_E._nidulans	.....SDEEYMPRLTALK.
AN9390_E._nidulans	.....DIVDRVSFLK.
AN0517_E._nidulans	.....EMISRIVKLK.
AN0541_E._nidulans	.....LSADVYKQVGNLK.
AN5077_E._nidulans	.....ELISYEFNNFKYLT.
AN0509_E._nidulans	.....TYN..QWEDFISLK.
AN7613_E._nidulans	.....KTADYMQRISAIK.
07035_N._crassa	

07484_N._crassa	.....	VISTYEF	EAF	RSMT	.
05317_N._crassa	.....	VLSSYQ	FQEF	KRVR	.
EAA74768_G._zeae	.....	EGKLMY	ERL	IALK	.
EAA78168_G._zeae	.....	GDEQLY	SQ	LSALK	.
EAA75711_G._zeae	.....	DDVKQM	REFT	DL	S.
EAA68447_G._zeae	.....	KLSQYQ	FKNF	ARLT	.
EAA77156_G._zeae	.....	ATRE	QFIK	FKEV	K.
12510_S._sclerotioru	.....	NDVGIY	KRL	MLLK	.
00773_S._sclerotioru	.....	GDEALY	TK	LSALQ	.
05454_S._sclerotioru	.....	PPPEST	LAEL	AGMK	.
00677_S._sclerotioru	.....	TAVPLM	HPFT	LLA	.
02128_S._sclerotioru	.....	IQE	AFSD	FLSMS	.
MGG_04534_M._grisea	.....	EVGSHY	DAVA	ALK	.
MGG_01336_M._grisea	.....	ADQALY	SQ	FTALK	.
14527_P._nodorum	.....	KTGALY	NRFT	GLK	.
15411_P._nodorum	.....	GDIPIY	GEFT	SLK	.
02214_P._nodorum	.....	ADDDVY	REFL	SLP	.
04761_C._immitis	.....	LPDKLF	SDFT	SLK	.
04323_A._capsulatum	.....	YDEKFY	RVFT	DLK	.
00533_B._fuckeliana	.....	TAVPLM	YPFT	ALA	.
Chi18_1_H._jecorina	.....	VES	QLRLL	SGMA	.
Chi18_8_H._jecorina	.....	YDI	EFNAWK	EG	.
Chi18_9_H._jecorina	.....	THH	QWDG	FMLK	.
Chi18_10_H._jecorina	.....	DPRG	QFEH	FKGLS	.
02650_A._capsulatum	.....	KLFTTV	VDKVR	.	.
AN0221_E._nidulans	.....	LFTTV	DAVR	.	.
06020_N._crassa	.....	LFTTV	VHVR	.	.
EAA76014_G._zeae	.....	MFTSV	SDVR	.	.
Chi18_4_H._jecorina	.....	LFATV	SEVR	.	.
09277_P._nodorum	.....	LFTTV	DEV	R.	.
05838_A._capsulatum	.....	PFPP	ISEIR	.	.
EAA69039_G._zeae	.....	PFQPL	EKVR	.	.
MGG_06594_M._grisea	.....	PFKPI	SEIR	.	.
Chi18_11_H._jecorina	.....	PFMAP	DQVR	.	.
02644_A_P._nodorum	.....	PKVP	ISTIR	.	.
AN9447_E._nidulans	.....	PFEP	VSTFR	.	.

	190	200	210	220	230	240
NP_979924_B._cereus	.... .... .... .... .... .... .... .... .... .... .... ....	LRDA	.....			
YP_077302_B._licheni	.....	LT	DQ	.....		
YP_091539_B._licheni	.....	LN	QP	.....		
YP_079121_B._licheni	.....	LN	QP	.....		
YP_074366_S._thermop	.....	LN	DQ	.....		
YP_075811_S._thermop	.....	LN	NP	.....		
YP_075619_S._thermop	.....	LS	DP	.....		
ZP_01354047_C._phyto	.....	AQ	NV	.....		
ZP_01354926_C._phyto	.....	LS	KT	.....		
NP_902406_C._violace	.....	ST	.....			
ZP_01136704_A._cellu	.....	LS	NP	.....		
ZP_00526542_S._usita	.....	MA	NA	.....		
AAF46212.1_D._melano	.....	VA	NH	.....		
AAF46534.1_D._melano	.....	LE	SS	.....		
AAF46544.1_D._melano	.....	VA	SN	.....		
At4g19720_A._thalian	.....	AS	NP	.....		
At4g19750_A._thalian	.....	AS	NS	.....		
EAA67655_G._zeae	.....	KQN	..RNLKVLISIGGFD	.....	GSP	ALASGVST
EAA73155_G._zeae	.....	KAN	..RKLKVMLSIGGWT	.....	WSTN	FPAAAST
EAA74986_G._zeae	.....	KAH	..RHLKVILSIGGWT	.....	WSTN	FPSAAGT
EAA74223_G._zeae	.....	RRN	..RNLKVLLSIGGWT	.....	FSSN	FKGPAST
MGG_05533_M._grisea	.....	QAN	..RNVKMLLSIGGYT	.....	WSP	KFVPVAAD
MGG_01247_M._grisea	.....	KKN	..RHLKVLLSIGGWT	.....	WSPK	FAPIAAT



MGG_00086_M._grisea	.....KAN..RHVKVLLSIGGWT.....WSTN.....FPSAASS.....
MGG_07927_M._grisea	.....KAN..RNLKVLLSIGGWT.....YSSN.....FRAPAST.....
Chi18_6_H._jecorina	.....KRH..RHKMTLLSIGGWN.....MSQSG.....KFAPVLNT.....
Chi18_5_H._jecorina	.....KAN..RNLKVMSISIGGWT.....YSTN.....FASAAST.....
Chi18_7_H._jecorina	.....KRN..RNLKVLLSIGGWT.....YSGN.....FKGPAST.....
04883_N._crassa	.....KAN..RNVRVLLSIGGWT.....YSQTSPTS.....RFALTAST.....
04554_N._crassa	.....RRN..RNLKVLLSIGGWT.....YSSN.....FKEPASK.....
11407_B._fuckeliana	.....KNN..RQMKTLLSIGGWT.....YSTN.....FAAAAST.....
05350_B._fuckeliana	.....SRN..RSLKILLSIGGWT.....YSSN.....FAQPAST.....
11700_S._sclerotioru	.....KHN..RQMKTLLSIGGWT.....YSAN.....FAAAAST.....
11304_S._sclerotioru	.....SRN..RSLKILLSIGGWT.....YSSN.....FAQPAST.....
08020_S._sclerotioru	.....KQN..RNLKVLLSIGGWT.....YSSN.....FPAAAST.....
01250_A._capsulatum	.....KHY..RHLKTLISIGGWT.....YSAN.....FPAPAST.....
05886_A._capsulatum	.....KQN..RNLKILLSIGGWT.....YSSN.....FPGAASST.....
06565_A._capsulatum	.....KQN..RHLKVLLSIGGWT.....YSPH.....FGAAVST.....
05250_C._immitis	.....KKN..RHLKILLSIGGWT.....YSSN.....FRA.AAT.....
02795_C._immitis	.....KNN..RNLKTLISIGGWT.....YSPN.....FKTPAST.....
03822_C._immitis	.....KRN..RNLKVLLSIGGWT.....YSEN.....FAPAAST.....
AN5454_E._nidulans	.....QQN..RHLKVLLSVGGWT.....YSKN.....FARMAAT.....
AN4871_E._nidulans	.....RQH..RQLKVLLSIGGWT.....YSPN.....FTNGAGT.....
00269_P._nodorum	.....KKN..RKLVLLSIGGWT.....YSAN.....FAQPAST.....
04870.1_C._cinereus	.....KKH..RHLKLLLSIGGWT.....YSPS.....IHPVULD.....
09921.1_C._cinereus	.....MKK..RDLKVLLSIGGWT.....YSQAG.....HFNFTVN.....
124149_P._chrysospor	.....KQH..RHLKVLLSIGGWT.....YSPS.....FHPVVVN.....
134311_P._chrysospor	.....MAH..RNLKVSLSVGGWT.....YSQDG.....HFSFVTD.....
03412_F._neoformans	.....KQN..RNLKVLLSIGGWS.....FSPN.....FAG.IVH.....
13635_R._oryzae	.....QRH..RHLKVSLSIGGWT.....WSTH.....FGAVTRD.....
UM04261_U._maydis	.....KKN..RALKMLSVGGWT.....FGPH.....FAPMAAD.....
EAA69503_G._zeae	.....QKH..PHLRVLLSIGGG.....NSSEI.....FPVVASS.....
EAA70860_G._zeae	.....SQH..PHIKTLVSIIGGG.....SSSKE.....FPALAAAN.....
Chi18_3_H._jecorina	.....QRH..PHLQVLLSIGGS.....TASEV.....FPIVASN.....
Chi18_2_H._jecorina	.....RNH..PRLKTIVSIIGGG.....TASKE.....FPALAAAN.....
03026_N._crassa	.....QKY..PHLQVLLSIIGGG.....ASSET.....FALVASS.....
01594_B._fuckeliana	.....QQH..PHLQLIISIGGG.....AASQH.....FPQVAAS.....
05897_S._sclerotioru	.....QQH..EHLQLVISIGGG.....AASQN.....FAHVAAS.....
04742_A._capsulatum	.....RD..SKVKVLLSVGGGDNGGDIVGSRN.....FAAVAAS.....
04750_C._immitis	.....EQY..TGMKVILSIIGGG.....TGSQH.....FATVAKD.....
04719_P._nodorum	.....RKY..TKLRVLLSVGGGG.....KGSEP.....FKGVAAD.....
MGG_08458_M._grisea	.....HQN..PHLKTIVSLIGGG.....SGSAE.....FPALATN.....
CHT4_C._albicans	.....KKN..RHLKLIMSIGGWT.....ICHL.....FESVVSAN.....
01119_L._elongisporu	.....KLN..RQLKVCMSIGGWT.....THTQ.....FEAVVQD.....
XP_454053_K._lactis	L.....ESK..HEFKTILCLGGWS.....NREA.....YKKIAKS.....
CTS2_S._cerevisiae	T.....CSD..KKFKVIMSIGGWS.....DSEN.....FKIIIKD.....
246746_L._bicolor	.....KAN..RQLKVLLSIGGWT.....YSPS.....FHPVVVN.....
03209_N._crassa	.....KRN..RNMKVLLSIGGWT.....YSPK.....FPPVAAT.....
14474_P._nodorum	.....QKN..RNLKVILSVGGWT.....WRGN.....FKPALAT.....
CE06282_C._elegans	N.....GN..SKIKLMFSIGG.K.....DNSKY.....FSSVIPS.....
CE03547_C._elegans	Q.....QT..PQVKVMISIGG.N.....DNSNN.....FKPGLSS.....
CE03542_C._elegans	S.....S...TLKVMISIGG.M.....DINSN.....FSLVISD.....
CE15845_B_C._elegans	S.....ANTKTLVSIIS.....ID.....WHTMAF.....
CE02997_C._elegans	K.....ES..STLKVMSISIGG.Q.....YSSGE.....FSGLVSK.....
CE36953_C._elegans	R.....H..PDLKLLYAVGG.W.....ENSQY.....FSLTAD.....
YP_432439_H._chejuen	Q.....Y..PNVKTLISVGGWA.....ETGGYFDEDGKRV.DSGGFYTMTTN.ADNSI
YP_529449.1_S._degra	Q.....Y..PHVKTLISIGGWA.....ETGGYFDSNGDRV.NSGGFYTMTTN.ADGSV
YP_077582_B._licheni	R.....Y..PDVKVLAAGVGGWA.....ETGGYVDKDGKRI.PSGGFYSMTTN.GDGSV
ChiI_S._coelicolor	Q.....H..PDVKTMSIVGGWA.....ETGGYFADDGSRV.DSGGFYSMATK.ADGSV
NP_902986_C._violace	K.....Y..PGVKTLSIVGGWA.....ETGGYFDANGKRV.ASGGFYSMTVN.ADGTV
ZP_01159608_Photobac	K.....H...DVKTLISIGGWA.....ETGGHFGTDGGRA.PDGGFYTMTTN.ADGSV
ZP_01234708_V._angus	K.....H...DVKTLISIGGWA.....ETGGHFGTDGGRA.ADGGFYTMTTN.ADGSV
NP_233087_V._cholera	K.....Y...GVKTLISIGGWA.....ETGGHFDANGNRV.ADGGFYTMTTN.ADGSV
NP_230718_V._cholera	Q.....Y..PDVKTLISVGGWA.....ETG.....GFYPMTTDLASCSTV
AAO07185_V._vulnific	K.....Y...GVKTLISIGGWA.....ETGGHFGADGKRV.ADGGFYTMTTN.ADGSV

ZP\_01354150\_C\_phyto N.....Y..PNLRINLAIGGWG.....ADG.....FSDMAFT.....  
 ZP\_01246933\_F\_johns K.....N..PQLKIIVSLGGWG.....GCEP.....CSDAFST.....  
 YP\_012734\_L\_monocyt Q.....N..PNLKIGVSVGGWS.....KSGD.....FSTVAAD.....  
 YP\_529337.1\_A\_S\_deg .....WN..ADLKILFSVGGWAESNDAAETVSR.....YRDAF.A.....  
 ChiA\_A\_P\_kodakarae K.....Y..PAVKVLISVGGWT.....LSKY.....FSVVAAD.....  
 AAG19274\_Halobacteri TGFDDLVD..PETSFLFSIGGWN.....DSTY.....FSNAAQS.....  
 AAG19275\_Halobacteri DR.....A..ADTRLKLSIGGWG.....LSPG.....FEDAAAD.....  
 CE03543\_C\_elegans I.....LK..FDAKIMFSIGG.P.....ANTQF.....FSPIIQN.....  
 CE34961\_C\_elegans N.....AN..SDTKVMISIGG.D.....HNSEN.....FGSVLSD.....  
 CE20043\_C\_elegans RN.....ED..SNVKMMISIGG.F.....ENSQH.....FYPVLSN.....  
 CE15845\_A\_C\_elegans .....N..SMTMLMISIGG.F.....ENSNY.....FSSVLED.....  
 CE32863\_A\_C\_elegans .....N..SMTMLMISIGG.F.....ENSNY.....FSSVLED.....  
 CE03544\_C\_elegans S.....LH..SNLKMFSIGG.D.....ENSFD.....FSSALAN.....  
 CE08731\_C\_elegans .....VKKMISIGG.C.....DYSTN.....FTSVVSN.....  
 CE28638\_C\_elegans T.....SN..SGVKIMISIGG.D.....ENSQY.....FSSVLSN.....  
 CE32863\_B\_C\_elegans S.....ANTKTLVSI.....ID.....WHTMAF.....  
 CE01673\_C\_elegans H.....IN..NNVNRILSIGG.T.....NYSEK.....LSIMLQD.....  
 CE02993\_C\_elegans E.....VS..STVKVMISVGG.H.....DHSGA.....FSAIMSN.....  
 CE02996\_C\_elegans E.....AS..STLKVMISVGG.H.....DYYKE.....YSRLVSN.....  
 CE02995\_C\_elegans K.....AN..STLKVMISIGG.Q.....SNSRS.....FSRLVSN.....  
 CE02992\_C\_elegans M.....DN..PNLKIMVEING.....K.....FFSVLAE.....  
 CE02999\_C\_elegans E.....LN..RGLKVMVSIIGG.Y.....ESSPL.....FSDVLVK.....  
 CE02998\_C\_elegans L.....MN..VKVMFSIGG.H.....KNAEH.....YSTVVD.....  
 CE09229\_C\_elegans A.....AN..SGVRVLFVAVGG.W.....DNSQY.....FSSVAAD.....  
 CE12928\_C\_elegans A.....VN..SGVRVLFVAVGG.W.....DNSQY.....FSSVAAD.....  
 CE23907\_C\_elegans N.....GK..YKVKLLFSIGG.K.....DNSRN.....FSTVISS.....  
 CE32917\_C\_elegans Q.....AS..PKLKMLISIGG.P.....ANSN.....FLPVISS.....  
 CE34579\_C\_elegans T.....EN..STVKFMFSIGG.P.....GHSQN.....FSPVVRN.....  
 CE25073\_C\_elegans Q.....QT..PQVKVMISIGG.N.....DNSNN.....FKPVLSS.....  
 CE03548\_C\_elegans Q.....QT..PPVKVMISIGG.D.....DNSNN.....FYKVLNS.....  
 NP\_469498\_L\_innocua Q.....N..PNLKIGVSVGGWS.....KSGD.....FSTVAAD.....  
 CE08730\_C\_elegans N.....SS..SNVKSMISIGR.W.....DSVTQ.....LSSVLLN.....  
 Q8U1H4\_P\_furiosus K.....Y..PQVKILISVGGWT.....LSKY.....FSVIAAD.....  
 CE12474\_C\_elegans .....G..SNVEMMVSIGGGY.....ENAHY.....FASALSD.....  
 CE02990\_C\_elegans E.....AS..STLKIMISIGG.H.....YNSRS.....FSGLVFN.....  
 CE40270\_C\_elegans M.....GT..SPVKIMISIGG.K.....ENSON.....FSPVIES.....  
 CE04296\_C\_elegans K.....AS..STLKIMISIGG.Q.....YNSGE.....FSGLVSN.....  
 ChiB\_S\_marcescens .....HN..PSLRIMFSIGGWYYSNDLGVSAN.....YVNAVKT.....  
 O10363\_O\_pseudotsug A.....N..PHLKILPSIGGWT.....LSDP.....FYFMH.D.....  
 AAP29899\_C\_fumifera A.....N..PHLKILPSIGGWT.....LSDP.....FYFMH.D.....  
 AAV73807\_B\_mori\_NPV A.....N..PHLKILPSIGGWT.....LSDP.....FYFMH.D.....  
 AAL56186\_H\_zea\_SNPV A.....N..PNLKVLASIGGWT.....LSDP.....FYHMH.D.....  
 AAF33549\_S\_exigua\_N A.....N..PHIKVFASIGGWT.....LSDP.....FYHMH.D.....  
 AAZ38189\_A\_segetum\_ A.....Y..PHLKVLPSIGGWT.....LSDP.....FYHMH.E.....  
 AAS82706\_A\_segetum\_ H.....N..PDLTILPSIGGWT.....LSDP.....FFKLS.S.....  
 ZP\_01159013\_Photobac R.....N..PDLKIIPSIGGWT.....LSDP.....FFDFV.D.....  
 ZP\_01161077\_Photobac A.....H..PDLKILPSVGGWT.....LSDP.....FFFLD.D.....  
 ZP\_01159325\_Photobac E.....K..PELKILPSFGGWT.....MSEP.....FHAMAKD.....  
 ZP\_01160869\_Photobac D.....N..PNLSILPSFGGWT.....LSEP.....FHTVALN.....  
 ZP\_01233025\_V\_angus R.....N..PDLKIIPSIGGWT.....LSDP.....FFDFV.D.....  
 ZP\_01236284\_V\_angus A.....H..PDLKILPSVGGWT.....LSDP.....FFFLD.D.....  
 ZP\_01235109\_V\_angus E.....K..PELKILPSFGGWT.....MSEP.....FHAMAKD.....  
 ZP\_01235465\_V\_angus E.....N..PNLSILPSFGGWT.....LSEP.....FHTVALN.....  
 AAO08114\_V\_vulnific R.....Y..PDLKIIPSIGGWT.....LSDP.....FFDFV.D.....  
 AAO07498\_V\_vulnific Q.....H..PDLKILPSFGGWT.....MSEP.....FHAMAKD.....  
 NP\_232428\_V\_cholera T.....Y..PDLKIIPSIGGWT.....LSDP.....FFSET.D.....  
 YP\_432951\_H\_chejue E.....N..PHKLKDLVGGWT.....LSEG.....FGWMSRD.....  
 YP\_529337.1\_B\_S\_deg Q.....H..PHLKILPSIGGWT.....MSTP.....FYEMAKN.....  
 YP\_435912\_H\_chejue T.....N..PDLTILPSIGGWT.....LSDP.....FFYFAND.....  
 ZP\_01137509\_A\_cellu K.....Y..PNLKILLSIGGWT.....YSKY.....FSDAAAT.....  
 ChiE\_S\_coelicolor K.....Y..PHLKVVVSLGGWT.....YSKF.....FSDAAAT.....  
 ChiC\_S\_coelicolor K.....Y..PNIKILYSFGGWT.....WSGG.....FPDAVKN.....

ChiD_S._coelicolor	K.....H..PDLKILWSFGGWT.....WSGG.....FAQAAQN.....
NP_903910_C._violace	A.....N..PQLKVLISLGGWT.....WSKN.....FGKFAAT.....
YP_529072.1_S._degra	M.....H..PQIKIVWSFGGWT.....WSGG.....FGEAAAN.....
ZP_01431615_S._tropi	M.....Y..PHLKIVWSFGGWT.....WSGG.....FTQAAQN.....
ZP_01136287_A._cellu	R.....Y..PNLRITIASLGGYS.....WSGY.....FSDAALT.....
01315.1_C._cinereus	.....KH...GVKALISIGGWT.....GSRF.....FSTAVGS.....
03252.1_C._cinereus	.....D...NVTASLSIGGWT.....GSRF.....FSPAVGS.....
05285.1_C._cinereus	.....AN...NVKALLSIGGWT.....GSQY.....FSPAVAS.....
05291.1_C._cinereus	.....QH...NVKALLSLGGWT.....GSIY.....FSDHVST.....
01586.1_C._cinereus	.....KSG.YGTKIVLSVGGWG.....GCYW.....FSQACST.....
128098_P._chrysospor	.....SH...NTRAMLTIGGWT.....GSMY.....FSPMVAT.....
39872_P._chrysospori	.....NN...SVKAMLSIGGWT.....GGRA.....FSTNVGS.....
138098_P._chrysospor	.....QN...HVDVLLTVGGWT.....GSRY.....FSTAVGS.....
129436_P._chrysospor	.....AA...GKHVKVSVGGWT.....GSAR.....FSGAVAG.....
EAA71245_G._zeae	.....KN...GVKALVSIGGWT.....GARY.....FSTNFGN.....
MGG_04732_M._grisea	.....AH...GKKAQVALGGWA.....GSIH.....FSSNVGS.....
UM06190_U._maydis	.....AG...NAKPMLSLGGWG.....GSTY.....FSPAVRT.....
04245_F._neoformans	.....AA...GKRVKLSIGGWT.....GSAY.....FSTIVAN.....
16170_R._oryzae	.....KN...KVGVSISIAGWS.....GSIH.....MSTLVGS.....
01334_R._oryzae	.....KN...NVGVVISVAGWS.....GSIH.....MSTLLND.....
13934_R._oryzae	.....HH...GKGVSLAIGGWT.....GSIY.....FSSLVRT.....
07611_R._oryzae	.....AA...GTKVLVSIGGWS.....GSTQ.....FSTMAAS.....
10252_R._oryzae	.....QS...KTKVLLSVGGWT.....GSKR.....FSPMVAS.....
14659_R._oryzae	.....KK...NVKVLTSIGGWT.....GSLT.....F.....
231399_L._bicolor	.....RH...GVKAMASVGGWT.....GSRW.....WSSNVGS.....
180319_L._bicolor	.....SH...NVNALITIGGWT.....GSQF.....FSSNVAT.....
191848_L._bicolor	.....SH...NVKALLSIGGWT.....GSQY.....YSSNVAT.....
317003_L._bicolor	.....SSG.YGTKVVLISIGGWG.....GCYW.....FSQACST.....
246840_L._bicolor	.....QN...NVKASLSIGGWT.....ASRW.....YSSNVGS.....
144643_L._bicolor	.....AK...KSKIKLSIGGWS.....GSKY.....FSPAVRT.....
310136_L._bicolor	.....NN...GVSALLSIGGWT.....GSLY.....FSTAVGN.....
629882_M._xanthus	.....AA...GRKALIMVGGAG.....EHDG.....WVGAAS.....
630509_A_M._xanthus	.....QQ...GRKALLMLGGFG.....EHEH.....FVHAAS.....
YP_592598_Acidobacte	.....KA...GVKVMISIGGAD.....AEQAT.....AFATIAAS.....
YP_446903_S._ruber	A.....N..PDLKIVLSIGGWA.....WSDY.....FSDAART.....
ZP_00739282_B._thuri	K.....Y..PHLKTIISVGGWT.....WSNR.....FSDMAAD.....
ZP_01245639_F._johns	K.....Y..PHLKILISVGGWT.....KGQD.....LSPIAAS.....
NP_976824_B._cereus	K.....Y..PHLKTIISVGGWT.....WSNR.....FSDMAAD.....
YP_077581_B._licheni	S.....H..PHLKTFISVGGWT.....WSNR.....FSDVAAD.....
631138_M._xanthus	Q.....N..PHLKLLISVGGWS.....WSTH.....FSTVASS.....
ZP_01247029_F._johns	.....N....IKVFVSLGGGS.....VSEGGAIRD.....NYFNLLIT.....
ZP_01234549_V._angus	.....NP...DGRVFISFGGWR.....DSEKNESDDNIIGRDIVYEKIAAS.....
ZP_01160697_Photobac	.....NP...DGRVFISFGGWR.....DSEKNESDDNIIGRDIVYEKVAAS.....
ZP_01158584_Photobac	.....SA...NGRVFLSFGGWR.....DNESGENDDGMTGRDIVYEKIAAS.....
AN0549_E._nidulans	.....KSDP.DLKVFVAVGGWS.....FN..DPG.P...TATVFSDIAGS.....
AN8481_E._nidulans	.....NLDP.DLKVFIAVGGWT.....FN..DPG.P...TATVFSDIASS.....
AN9390_E._nidulans	.....NYNP.SLEVWIAIGGWS.....MN..DPDQP...TRRTFSELAAS.....
AN0517_E._nidulans	.....FSNP.GLRVNIIVGGWA.....FS..D.A.P...TQHLWTQMARS.....
AN0541_E._nidulans	.....RRNR.SLKVFIAVGGWA.....FS..DPG.P...TRTAWSDMAST.....
AN5077_E._nidulans	.....SRNP.SLKIMIALGGWT.....FS..DPGP...WQAIFPTLAST.....
AN0509_E._nidulans	.....GP....KKVLSFGGWD.....FS...TNPR...TYNIFRQGTQP.....
AN7613_E._nidulans	.....GV....KRIASFSGGWG.....YS...INSA...SYDVLREAMFP.....
07035_N._crassa	.....LIQP.DIRIWIIVGGWA.....FN..DPG.P...TQTTFS DIAAS.....
07484_N._crassa	.....NV....HRVISFGGWA.....FS...TDAA...TYNIFRTGVTA.....
05317_N._crassa	.....GA....KRVVSFGGWD.....FS...TMPA...TYSIFRNGVTS.....
EAA74768_G._zeae	.....RRDR.NLKIFLAIGGWT.....FN..DPG.R...THKVFSNLVNS.....
EAA78168_G._zeae	.....TRDS.GQELWLSIGGWA.....FS..DKGSP...TATTFSDLVNAD.....
EAA75711_G._zeae	.....KGGK..LQTWIAIGGFD.....MS..DEDKP...THTTWSDMVST.....
EAA68447_G._zeae	.....GV....KRILSFGGWD.....FS...ALPA...TYSIFREGVKP.....
EAA77156_G._zeae	.....GS....WKKIISFGGWA.....GS...TDAS...SFQIYRDAIKP.....
12510_S._sclerotioru	.....KKDP.GLKVFVAIGGWT.....FN..DPG.P...TATTFSDIAAS.....
00773_S._sclerotioru	.....TRDA.TQKFWSLIGGWT.....FT..DSDQA...TATTFSDLAAAD.....

05454\_S.\_sclerotioru .....RKNP.GLKVLIALGGWT.....FN..DNGTI....WQPVFSNVVST.....  
 00677\_S.\_sclerotioru .....STT...LATYMAIGGGG.....SS....GLS.....QVWSQMVKS.....  
 02128\_S.\_sclerotioru .....GLG...FKRILSFGGWD.....FS....TDVA....TYQIFRDAMAP.....  
 MGG\_04534\_M.\_grisea .....NKQP.GLQVWIAIGGWA.....MN..DPG.P....WRTAFSDMARS.....  
 MGG\_01336\_M.\_grisea .....SKG...VQTWVAIGGGE.....FNTLDPNDPE..RYKIWSRMAAS.....  
 14527\_P.\_nodorum .....STNQ.GLKYISVGGWS.....FT..DPG.P....TRTAFSTMAGS.....  
 15411\_P.\_nodorum .....RNG...LQTWIAIGGWS.....FN..DPGTK....TYNAYSDMVST.....  
 02214\_P.\_nodorum .....DS....VSKWIGIGGFQ.....FT..DSDQP....THQTFSKMSSS.....  
 04761\_C.\_immitis .....KKNP.GLKTVIALGGWT.....FN..DP.....  
 04323\_A.\_capsulatum .....KQKP.SLKCFISIGGWD.....AG..G.....KVFSDMAKS.....  
 00533\_B.\_fuckeliana .....SAS...LATYMAIGGGG.....SS....VLP....LIWSQMVSN.....  
 Chi18\_1\_H.\_jecorina .....GV.....KRIVSVGGWD.....FS....TSPS....TYQIFRKAVSSE.....  
 Chi18\_8\_H.\_jecorina .....DY.....KKIVSFGGWD.....FS....TGSD....TFQFRQATTS.....  
 Chi18\_9\_H.\_jecorina .....NV.....KRIVSFGGWS.....FS....TGVA....SYDVLRKAMTP.....  
 Chi18\_10\_H.\_jecorina .....G.....IKRIAAFSGGWS.....FS....VGVD....TYATLRQAIPK.....  
 02650\_A.\_capsulatum .....KQFAPGTKVMIAIGGWS.....DTKG.....FSDAART.....  
 AN0221\_E.\_nidulans .....TEFSNGTSILISIGGWS.....DTQG.....FSTAART.....  
 06020\_N.\_crassa .....PRFPNHTKVLIAGGWS.....DTIG.....FSVAALN.....  
 EAA76014\_G.\_zeae .....ARVPQHTKVMVAIGGWS.....DTQG.....FEEAAKT.....  
 Chi18\_4\_H.\_jecorina .....KQFKPATKIMVAIGGWS.....DSQG.....FEAAARD.....  
 09277\_P.\_nodorum .....PKFNGTRVQVAIGGWS.....DTAG.....FEKGAKT.....  
 05838\_A.\_capsulatum .....GRFANGTKLLIAIGGWS.....DTAG.....FSACSKE.....  
 EAA69039\_G.\_zeae .....SLFDHDIKVCLAVGGWS.....DNAG.....FDEGVKT.....  
 MGG\_06594\_M.\_grisea .....GMFNNGTKVCMAIGGWS.....DNVG.....FSKAALT.....  
 Chi18\_11\_H.\_jecorina .....SLFDGTGKLCLAVGGWS.....QSAG.....FDAAAKT.....  
 02644\_A\_P.\_nodorum .....SEF.PGAKLMIAVGGWS.....DDVG.....FLQASKT.....  
 AN9447\_E.\_nidulans .....NRFSPDTKVMIAIGGWS.....DSAG.....FSAGAKD.....

	250	260	270	280	290	300
NP_979924_B._cereus	..TIQNKFITNIIQTA	..E	..KY	..GMRDIH	..FDFESVAP	
YP_077302_B._licheni	..NVKNRLLDNIVAAAR	..	..RY	..GFKDIH	..FDFEYLRLP	
YP_091539_B._licheni	..AVRNRLIDNIVQTIS	..	..RK	..GYAGVN	..IDFEQILE	
YP_079121_B._licheni	..AVRNRLIDNIVQTIS	..	..RK	..GYAGVN	..IDFEQILE	
YP_074366_S._thermop	..AVQDRLLGEIQRLIR	..	..EM	..GFRDVH	..FDFEFLRP	
YP_075811_S._thermop	..AAVQRAIDELVILR	..	..VQ	..GYAGLN	..VDFEYVYP	
YP_075619_S._thermop	..ARRSRAVADMLAIAR	..	..EH	..GLAGID	..IDIENVPVG	
ZP_01354047_C._phyto	..EVRDHLIDELLAVVK	..	..EK	..QYVGVN	..VDFEYIKA	
ZP_01354926_C._phyto	..SSRERLINELIAQAI	..	..KY	..NLDGIN	..IDFESLSV	
NP_902406_C._violace	..SAQSQAVANLVKFAQ	..	..DK	..RFSGIN	..VDFEAVAQ	
ZP_01136704_A._cellu	..TTRTQHEQALLALAT	..	..RY	..GASGID	..LDYENMAV	
ZP_00526542_S._usita	..EARRRMNATLLAECR	..	..KY	..GYYGIQ	..FDFENINY	
AAF46212.1_D._melano	..AMRKLFRLSLREILR	..	..TYP	..SLDGID	..LDWEFPSA	
AAF46534.1_D._melano	..NARIPFINSASLSVK	..	..TY	..GFDGLD	..LGWQFPKN	
AAF46544.1_D._melano	..ERRQQFIKNILKFLR	..	..QN	..HFDGID	..LDWEYPAH	
At4g19720_A._thalian	..TSRKSFISWAISSAR	..	..YY	..RFDGLD	..LVWKYPKD	
At4g19750_A._thalian	..KNRKAFIDSSIDIAR	..	..KK	..DFYGLD	..LAWEYPSN	
EAA67655_G._zeae	..QNGRKRFISTAIKLIT	..	..DWG	..FDGID	..VDWEYP..	
EAA73155_G._zeae	..AATRAATFAQSSVALMK	..	..DWG	..FDGID	..VDWEYP..	
EAA74986_G._zeae	..RENRIREFSKSAVTLMK	..	..DWG	..FDGID	..VDWEYP..	
EAA74223_G._zeae	..PQGRATFAKSCVDLIK	..	..NLG	..FDGID	..IDWEYP..	
MGG_05533_M._grisea	..AGKRAAFVSSAVALMG	..	..DWG	..MDGLD	..VDWEYP..	
MGG_01247_M._grisea	..AAGRNRFATSAVKLLA	..	..DWG	..LDGLD	..IDWEYP..	
MGG_00086_M._grisea	..EANRNRFASTAVGLMK	..	..DWG	..FDGLD	..IDWEYP..	
MGG_07927_M._grisea	..PEGRSHPARTAVELVR	..	..QLG	..FDGID	..IDWEYP..	
Chi18_6_H._jecorina	..NEGRIRFAKTAVNLLA	..	..NWG	..LDGID	..IDYEYP..	
Chi18_5_H._jecorina	..DANRKRFASTAITYMK	..	..DWG	..FDGID	..IDWEYP..	
Chi18_7_H._jecorina	..QQGRETFAKSSLELLK	..	..NMG	..FDGLD	..IDWEYP..	
04883_N._crassa	..AESRTKFATSALALVK	..	..DWG	..FDGID	..IDWEYP..	
04554_N._crassa	..EEGRRRFAESAVELVK	..	..NLG	..FDGLD	..IDWEYP..	
11407_B._fuckeliana	..NATRTKFAATAVQFVQ	..	..DLG	..FDGID	..IDWEYP..	
05350_B._fuckeliana	..ESGRRKFAESAVDLIR	..	..NLG	..FDGID	..IDWEYP..	



11700_S._sclerotioru	.EATRAREFASTAVQFVQ.....	DLG.....	FDGLD..	IDWEYP..
11304_S._sclerotioru	.ESGRRRFAESAVDLIR.....	NLG.....	FDGID..	IDWEYP..
08020_S._sclerotioru	.ISKRATFASSVVSIVQ.....	NLG.....	LDGID..	VDWEYP..
01250_A._capsulatum	.PTGRQTFARTAVKLLA.....	DLG.....	FDGID..	IDWEYP..
05886_A._capsulatum	.AANRAHFADTATKMLL.....	DMG.....	FDGLD..	IDWEYP..
06565_A._capsulatum	.PAARTKFAESATQLLL.....	NLG.....	FDGLD..	VDWEYP..
05250_C._immitis	.HEGRQTFARSADVLLA.....	DCG.....	FDGID..	IDWEYP..
02795_C._immitis	.EEGRKKFADTSLKLMK.....	DLG.....	FDGID..	IDWEYP..
03822_C._immitis	.EAGRSMFAESAVKMLL.....	DMG.....	MDGLD..	VDWEYP..
AN5454_E._nidulans	.EEGRRLEFAKSAVELMG.....	DLG.....	MDGVD..	VDWEYP..
AN4871_E._nidulans	.PENRARFAQTATKLIT.....	DLG.....	FDGID..	IDWEYP..
00269_P._nodorum	.EAGRAKFASSAVALLQ.....	DLG.....	FDGLD..	IDWEYP..
04870.1_C._cinereus	.PAKRAEFVKSSVALLD.....	DYG.....	LDGLD..	VDYEYP..
09921.1_C._cinereus	.PTARAKFISDAVQLIE.....	DYG.....	FDGID..	IDYEYP..
124149_P._chrysospor	.PALRAKFVASSIRLME.....	DHG.....	LDGLD..	VDYEYP..
134311_P._chrysospor	.SGKRQAFVNSALQLIE.....	DYG.....	FDGLD..	LDFEYP..
03412_F._neoformans	.PKWRSTFVQSAVKLVE.....	DVG.....	LDGLD..	IDYEYP..
13635_R._oryzae	.PLKRQRFVNSSMKLLT.....	DLA.....	LDGLD..	IDWEYP..
UM04261_U._maydis	.AKKRAKFVSTAITILE.....	NDG.....	LDGID..	IDWEYP..
EAA69503_G._zeae	.TLLRDNFARSARGLVE.....	ASG.....	LDGID..	IAWEYP..
EAA70860_G._zeae	.KTARQTFARRISEFCV.....	THQ.....	FDGVD..	IDWEHP..
Chi18_3_H._jecorina	.TLLRDNFARSALGLVE.....	ASG.....	LDGID..	IAWEFP..
Chi18_2_H._jecorina	.SHARETFAKQAREFCD.....	RHV.....	LDGID..	IDWEHP..
03026_N._crassa	.AILRNNFAQSARGLVE.....	ASG.....	LDGIDTPVVDYDYP..	
01594_B._fuckeliana	.AATRDHFGKSVRGLVD.....	ATG.....	FNGID..	IDWEHP..
05897_S._sclerotioru	.AATRDHFGKSVRGLVD.....	ATG.....	FNGID..	IDWEHP..
04742_A._capsulatum	.PAAVERFLSSAADLMN.....	KFL.....	LDGLD..	INWEHP..
04750_C._immitis	.PIALQNFISAKNMVD.....	RFG.....	LDGLD..	IDWEHP..
04719_P._nodorum	.PAKRQQFAQSALGLVQ.....	QFG.....	IDGID..	IDWEHP..
MGG_08458_M._grisea	.PRARDTLARATRFQVD.....	QHG.....	FDGVD..	IDWEQP..
CHT4_C._albicans	.DTKFDFNVNSTIEFVE.....	KYG.....	FDGVD..	IDWEYP..
01119_L._elongisporu	.PEKQHSFVKSVVEFVE.....	KYH.....	FDGVD..	IDWEYP..
XP_454053_K._lactis	.EKKVKKFIETAVDCMF.....	RYG.....	FDGID..	LDWEFPE..
CTS2_S._cerevisiae	.DKLLQNFVDSSVETMF.....	RLG.....	FDGID..	LDWEFPG..
246746_L._bicolor	.PILRSKFVESSVQLLE.....	DYG.....	LDGLD..	VDYEYP..
03209_N._crassa	.EEGRRRFASSAVKLIVQ.....	DWG.....	FDGLD..	IDWEYP..
14474_P._nodorum	.EAGRQKFCDSQLLIA.....	DLG.....	LDGFD..	IDWEYA..
CE06282_C._elegans	.EERIQTFIESILEFLE.....	AYD.....	LDGVD..	LFWKWPEE..
CE03547_C._elegans	.PDRKKLFINSTVSFLQ.....	TYD.....	IDGVD..	LYWKWPGK..
CE03542_C._elegans	.EKKRRSLIESIVSFLT.....	EHQ.....	IDGVD..	IFWKWSSS..
CE15845_B_C._elegans	.KKRIRLLAGNITSFLK.....	EYK.....	LDGVD..	IQCNNWLE..
CE02997_C._elegans	.ETSRNLFTNSIVSFVQ.....	NYD.....	IDGVD..	IFWTWPKY..
CE36953_C._elegans	.HSRRSILISNFVKVIK.....	EYG.....	FDGVD..	IDWEYPTV..
YP_432439_H._chejuen	NQQGINTFADSVVAFILR.....	SYG.....	FDGVD..	IDYEYPTS..
YP_529449.1_S._degra	NTAGINTFADSVVEFLR.....	TYS.....	FDGAD..	IDYEYPTS..
YP_077582_B._licheni	NHKGIIHTFAESVVAFLR.....	KYE.....	IDGID..	IDYEYPTS..
Chi1_S._coelicolor	NQAGIDTFADSAVDVFR.....	KYG.....	FNGVD..	IDYEYPTT..
NP_902986_C._violace	NQAGINAFSDSAVAFILR.....	KYG.....	FDGVD..	IDFEYPTS..
ZP_01159608_Photobac	NHAGIEKFATSAVEMILR.....	KYK.....	FDGLD..	IDYEYPTS..
ZP_01234708_V._angus	NHAGIEKFATSAVEMILR.....	KYK.....	FDGLD..	IDYEYPTS..
NP_233087_V._cholera	NHAAIEKFAASAVEMIR.....	KYK.....	FDGVD..	IDYEYPTS..
NP_230718_V._cholera	NMEGIKAFNKSVDLIR.....	QYD.....	FDGVD..	IDYEYPTSS..
AAO07185_V._vulnific	NHAGIEKFATSAVEMIR.....	KYK.....	FDGVD..	IDYEYPTS..
ZP_01354150_C._phyto	.KETRSVFINSIVSYLE.....	AYD.....	LDGVD..	IDWEYPT..
ZP_01246933_F._johns	.AEGRLKFAKSVKEVSD.....	YFK.....	VDGLD..	LDWEYPS..
YP_012734_L._monocyt	.PTKRANFVKVMKFKVK.....	YTN.....	MDFVD..	LDWEYPAS..
YP_529337.1_A_S._deg	.PANREHFVSSCVAFMQ.....	QHG.....	FDGID..	IDWEYP..
ChiA_A_P._kodakarae	.PAKRQRFATTAIEILR.....	KYN.....	LDGID..	IDWEYPPG..
AAG19274_Halobacteri	.QASRERFADTAIEIMR.....	THN.....	FDGLD..	IDWEYPPG..
AAG19275_Halobacteri	.QASRERFATTAVDLMR.....	TYD.....	FDGID..	VDWEHPGP..
CE03543_C._elegans	.EEMKRKFIDSIYFLK.....	QYK.....	LDGVD..	LFWKWSSS..
CE34961_C._elegans	.SEKKSMFIDSIARFIR.....	QHK.....	LDGVD..	IYWKWLGN..

CE20043_C._elegans	.VEMKKAFLNSISSFLA.....	YHE.....	LHGVD..	IFWKWPSP
CE15845_A_C._elegans	.EQKKSIFIKSILSFLI.....	EHK.....	IDGVD..	IFWKWPKL
CE32863_A_C._elegans	.EQKKSIFIKSILSFLI.....	EHK.....	IDGVD..	IFWKWPKL
CE03544_C._elegans	.TQMKSTLITSIIAFIH.....	SHM.....	IDGVD..	LHWKWPTS
CE08731_C._elegans	.QTIRRVFIESIIALLI.....	EHN.....	LDGVD..	LFWRWVPA
CE28638_C._elegans	.ITMCKLFIESIIAFIH.....	TNS.....	IDGMD..	IHWKWVPE
CE32863_B_C._elegans	.KKRIRLLAGNITSFLK.....	EYK.....	LDGVD..	IQCNWVLE
CE01673_C._elegans	.LKKTRRFIMSIIIRFLK.....	DNE.....	LDGVE..	LLWNRNT.
CE02993_C._elegans	.EASRSVFIKSIVSFVK.....	NED.....	IDGIE..	IFWMPKH
CE02996_C._elegans	.ETSRNVFVKSIVSFFQ.....	KND.....	IDGIE..	IFWTRPKY
CE02995_C._elegans	.ETSRNVFVNSIVSFVQ.....	KYD.....	IDGIE..	IFWTWPKY
CE02992_C._elegans	.DEKKNSFIKSISFFV.....	DHK.....	FDGVD..	IFWSWP..
CE02999_C._elegans	.KKKK..LIASIALLVK.....	KFD.....	LDGVD..	IFWNWPSI
CE02998_C._elegans	.STKRSVFIDSIVSFIK.....	SNN.....	ASGVD..	LFWEWPNI
CE09229_C._elegans	.SGKRKKFVDSIASFVE.....	DQK.....	IDGVD..	LDWEYPDS
CE12928_C._elegans	.SGKRRNFVDSVASFIE.....	HHK.....	IDGVD..	LDWEYPEM
CE23907_C._elegans	.EKRIQTFIKSILDFLK.....	DHN.....	LNGVD..	LFWKWPEE
CE32917_C._elegans	.PDRKKIFINSIVSFLK.....	KYD.....	IDGVD..	LFWKWPRL
CE34579_C._elegans	.QEKRRFIKSIFSFLA.....	EHK.....	LDGVD..	IFWKWPHL
CE25073_C._elegans	.PDRKKLFINSTVSFLQ.....	TYD.....	IDGVD..	LYWKWPGK
CE03548_C._elegans	.PNRRKVFLNATTSFLQ.....	IYG.....	IDGID..	LFWKWPGG
NP_469498_L._innocua	.PTKRANFVKVMKFVK.....	YTN.....	MDFVD..	LDWEYPAS
CE08730_C._elegans	.VKSRRMFIESIVDFLK.....	EHQ.....	LDGID..	LFWRWVPL
Q8U1H4_P._furiosus	.PAKRERFARTALEIIR.....	KYN.....	LDGLD..	IDWEYPGG
CE12474_C._elegans	.SQKKKNFIDSILAFIV.....	EHR.....	IDGVD..	FFCNG...
CE02990_C._elegans	.ETSRNVFVNSIVSFVE.....	KYD.....	IDGIE..	MFWMWERY
CE40270_C._elegans	.EYRRQIFINSILTFLK.....	END.....	LDGID..	LFWEWPCS
CE40296_C._elegans	.ETSRNLVFNISIAFVR.....	DYD.....	IDGVD..	IFWTWPKH
ChiB_S._marcescens	.PAARTKFAQSCVRIMK.....	DYG.....	FDGVD..	IDWEYP..
O10363_O._pseudotsug	.ADKRRVFVESVKEFLQ.....	VWKF.....	FDGVD..	IDWEFPGG
AAP29899_C._fumifera	.AEKRRVFVDSVKEFLQ.....	VWKF.....	FDGVD..	IDWEFPGG
AAV73807_B._mori_NPV	.VEKRRNVFVESVKEFLQ.....	VWKF.....	FDGVD..	VDWEFPGG
AAL56186_H._zea_SNPV	.ARTRQIFVESVREFVL.....	TWKF.....	FDGID..	IDWEFPGG
AAF33549_S._exigua_N	.ADVRRVFIDSVEEFLI.....	TWKF.....	YDGVH..	IDWEFPGG
AAZ38189_A._segetum	.PSVRRVFIDSVEEFLI.....	TWKF.....	FDGVD..	IDWEFPGG
AAS82706_A._segetum	.AENRAVFVESAREYLR.....	TWKF.....	FDGLD..	IDWEFPGG
ZP_01159013_Photobac	.KANRDTFVASVEKFLK.....	TWKF.....	YDGVH..	IDWEFPGG
ZP_01161077_Photobac	.PAKRKVFDVSVKEFLQ.....	TWKF.....	FDGVD..	IDWEFPGG
ZP_01159325_Photobac	.KESIEHFSKSAVELIA.....	EYDF.....	FDGID..	LDWEYPGG
ZP_01160869_Photobac	.DEYRKTFVDSAIIKLIQ.....	KYDF.....	FDGIQ..	IDWEYPGG
ZP_01233025_V._angus	.KANRDTFVASVEKFLK.....	TWKF.....	YDGVH..	IDWEFPGG
ZP_01236284_V._angus	.PAKRKVFDVSVKEFLQ.....	TWKF.....	FDGVD..	IDWEFPGG
ZP_01235109_V._angus	.KASIEHFSKSAVELIA.....	QYDF.....	FDGID..	LDWEYPGG
ZP_01235465_V._angus	.DKYRKTFVDSAIIKLI.....	KYDF.....	FDGIQ..	IDWEYPGG
AAO08114_V._vulnific	.KKNRDTFVASVKRFLT.....	TWKF.....	YDGVH..	IDWEFPGG
AAO07498_V._vulnific	.PKAMAQFSKTAVELIK.....	QYDF.....	FDGID..	LDWEYPGG
NP_232428_V._cholera	.KAKRDVVFVASVKRFLK.....	TWKF.....	YDGVH..	IDWEYPGG
YP_432951_H._chejuen	.DARRKAFVDSLIIHFLQ.....	RFD.....	FDGVD..	IDWEYPAS
YP_529337.1_B_S._deg	.EANRAVFVESAVNFIK.....	KYDF.....	FDGVD..	IDWEYPVY
YP_435912_H._chejuen	.AQKRAVFVDSVDFLK.....	TYKF.....	FDGVD..	IDWEYPGG
ZP_01137509_A._cellu	.DASRKSFVSSCIDMFIKGNLPKDSAGFGGPGVIA.....		GLFDGID..	IDWEYPAS
ChiE_S._coelicolor	.PESRKKFVESCIDVWIKGNLPVY.NGAGGPGTAA.....		GIFDGID..	IDWEWPGS
ChiC_S._coelicolor	.PA...AFAKSCHDLVED.....	PRWA.....	DVFDGID..	LDWEYPNA
ChiD_S._coelicolor	.PE...AFAQSCYDLVEN.....	SKWA.....	DVFDGID..	IDWEYPNA
NP_903910_C._violace	.DAGRKAMVSSCIDLYIKGNLPVG.ENAGGQAAAL.....		GVFDGFD..	IDWEYPGG
YP_529072.1_S._degra	.AD...HFANSYDLVFD.....	ARWA.....	DVFDGID..	IDWEYPND
ZP_01431615_S._tropi	.PA...AFAESCYNLVED.....	SRWA.....	DVFDGID..	IDWEYPNA
ZP_01136287_A._cellu	.AESRAHLVASCIDLLINGNLPG.....	LPPGAAK.....	GIFDGID..	VDWEYPGA
01315.1_C._cinereus	.ASNRTAFVKTIVNFAQ.....	KY.....	HLDGVD..	FDWEYPGN
03252.1_C._cinereus	.ASNRTTFVNTLLDVVR.....	RY.....	NLDGLD..	FDWEYPNM
05285.1_C._cinereus	.AENRTTFVKTITDMAT.....	EF.....	GLDGID..	FDWEYPNA
05291.1_C._cinereus	.PERRTAFVKAVIDLAT.....	QY.....	NLDGID..	FDWEFPNK

01586.1_C._cinereus	.ANNRTKFCNALMEVVN.....	QY.....	GLDGID..	LDWEYPNS
128098_P._chrysospor	.ADNRTSFVNAAMQLVS.....	QY.....	NLDGLD..	FDWEYPGA
39872_P._chrysospori	.AENRTAFVKTVVGLKN.....	QF.....	QLDGID..	FDWEYPND
138098_P._chrysospor	.AENRTAFANALLGLVQ.....	QY.....	NLDGLD..	IDWEYPNK
129436_P._chrysospor	.ADGRGALVDAIVRLYG.....	AY.....	ALDGID..	IDWEYPGQ
EAA71245_G._zeae	.EKNRTAFVKTCVDFAK.....	EH.....	SLDGLD..	FDWEYPNR
MGG_04732_M._grisea	.AENRTAFVKTCLDLVQ.....	KY.....	NLDGLD..	FDWEYPNK
UM06190_U._maydis	.AASRATFISNIVKTYN.....	QY.....	GLDGID..	LDWEYPGQ
04245_F._neoformans	.DALRATFVSNIYDIYN.....	QY.....	NLDGLD..	IDWEYPGT
16170_R._oryzae	.VSKRNTFVRNIVNMVQ.....	KY.....	KLDGVN..	IDWEFPNS
01334_R._oryzae	.VQSRETFVKNVVMVQ.....	KY.....	SLDGVN..	LDWEFPNS
13934_R._oryzae	.EASRKSFATNLINAVE.....	EY.....	DLNGLN..	IDWEYPND
07611_R._oryzae	.QANRQAWIDWNINFIK.....	QY.....	NTDGVD..	IDWEYPTS
10252_R._oryzae	.KESRRNFINWNVFEME.....	KY.....	NTDGVD..	IDWEYPCK
14659_R._oryzae	....R.....	F.....	KLDGID..	IDWEYPGR
231399_L._bicolor	.AENRTAFVRTLSSFFVK.....	RH.....	NLDGLD..	FDWEYPGR
180319_L._bicolor	.AANRTIFVKTLTQLVT.....	KY.....	QLDGLD..	FEWEYPNQ
191848_L._bicolor	.ADSRTTFVKAVADLAT.....	KY.....	NLDGLD..	FDWEYPNH
317003_L._bicolor	.AANRTTFCNALVSAVN.....	TY.....	GLEGID..	LDWEYPNS
246840_L._bicolor	.AINRTTFVNTVTTLAK.....	KY.....	DLDGLD..	FDWEYPM
144643_L._bicolor	.LESRRVFAENILAAYN.....	TF.....	NLDGLD..	LDWEYPGH
310136_L._bicolor	.AANRSFVKAVTGAT.....	KY.....	NLDGLD..	FDWEYPNR
629882_M._xanthus	.NANRAQFVQNLLNAMD.....	TF.....	GYDGLD..	IDWEYPVEQ
630509_A_M._xanthus	.EAQRAHFIRNIQLMD.....	EL.....	GYDGLD..	VDWE....
YP_592598_Acidobacte	.AHLRNTFAKNLHAFIV.....	AH.....	DYDGLD..	IDWEVPNA
YP_446903_S._ruber	.DSSRARFARTAVDLLAK.....	.....	HLDGLD..	LDWEYPGQ
ZP_00739282_B._thuri	.EKTRKVFESTVAFIR.....	AYG.....	FDGVD..	LDWEYPGV
ZP_01245639_F._johns	.PVARAALAADMANFIV.....	TYP.....	FIDGFD..	IDWEYP.L
NP_976824_B._cereus	.EKTRKVFESTVDFIR.....	EYG.....	FDGVD..	LDWEYPGV
YP_077581_B._licheni	.PAARENFAASAVEFIR.....	KYG.....	FDGVD..	LDWEYPVS
631138_M._xanthus	.PASRAAFVKSCVDLYIR.....	GQYPGVDPVNGEGVFDGID..	IDWEYPVG	
ZP_01247029_F._johns	.PANRTAFIQKIYDYVV.....	AH.....	NFDGVD..	VDLEGPAI
ZP_01234549_V._angus	.PEYRENLINDMMDVVN.....	TY.....	GFDGVD..	LDWEYPQV
ZP_01160697_Photobac	.PEYRENLINDMMDVVN.....	TY.....	GFDGVD..	LDWEYPQI
ZP_01158584_Photobac	.PEARENFIESIMRVVN.....	RY.....	DLDGLD..	LDWEYPRT
AN0549_E._nidulans	.EANQKKFFRSLVSFLS.....	TY.....	DFDGLD..	LDWEYPVA
AN8481_E._nidulans	.LKNQRAFFKSLISFMS.....	TY.....	NFDGLD..	LDWEYPVA
AN9390_E._nidulans	.KSHQDVFFESLLSFMD.....	KY.....	GFDGVD..	IDWEYPVA
AN0517_E._nidulans	.HENRQTFINSVVKYLQ.....	DY.....	HLDGLD..	IDWEYPSA
AN0541_E._nidulans	.SDNRQKFINSMLDLFE.....	TH.....	GLDGVD..	LDWEYPVA
AN5077_E._nidulans	.AANRATFIQNLLGFMS.....	EY.....	GYDGLD..	FDWEYPGA
AN0509_E._nidulans	..ANRLKLATNIAKFVK.....	DH.....	GLDGVD..	IDWEYPGA
AN7613_E._nidulans	..ENVDTFIVSIMEFVA.....	DN.....	NLDGVD..	FDWEYPGA
07035_N._crassa	.SANTKFIIDSLVKLMN.....	KY.....	GFDGID..	IDWEYPVA
07484_N._crassa	..ANRLTLATNIAFVK.....	EK.....	GLDGVD..	IDWEYPGE
05317_N._crassa	..ANRLKMATNIAFIK.....	EH.....	DLDGVD..	IDWEYPGA
EAA74768_G._zeae	.EGNQOKFLVSLMSFMA.....	LH.....	KFDGLD..	LDWEYPVD
EAA78168_G._zeae	.KIRQTYFFATLTLEFMQ.....	TW.....	GFTGLD..	IDWEYPVD
EAA75711_G._zeae	.KANRAAFIESVRDYM.....	EY.....	GFQGV.....	LDWEYPGE
EAA68447_G._zeae	..ANRLNMAKKIAAFIV.....	KH.....	KLDGVD..	IDWEYPGA
EAA77156_G._zeae	..ANRNKFAYNVMTVLN.....	NH.....	KLDGVD..	FDWEYPGS
12510_S._sclerotioru	.VPRQKTFIESLISFMS.....	TY.....	EFDGVD..	LDWEYPAA
00773_S._sclerotioru	.ITHQNVFFSSLTLEMT.....	TW.....	GFSGVD..	IDWEYPAA
05454_S._sclerotioru	.KANRAKFISNVKSFLT.....	RY.....	GFDGVD..	LDWEYPGA
00677_S._sclerotioru	.VGSRAVFIGSVEGWSL.....	SF.....	GFQGV.....	LDWEFPGS
02128_S._sclerotioru	..ANSKKFAANVAAFVK.....	KY.....	DLDGVD..	FDWEYPGE
MGG_04534_M._grisea	.TASQDAFFQSLVSFLA.....	LH.....	DFDGLD..	LDWEYPVA
MGG_01336_M._grisea	.ATSRAQFIRSLVSFMA.....	QY.....	GFQGV.....	LDWEWPTD
14527_P._nodorum	.SQNRGKFISGLMSFMN.....	EY.....	GFDGVD..	LDWEYPQA
15411_P._nodorum	.QGNRAAFVSSLIHFMD.....	TY.....	GFQGV.....	IDWEYPAE
02214_P._nodorum	.KENRKAFIDSLQQFSL.....	TY.....	KFSGVD..	IDWEYPGN
04761_C._immitis	.....DNLFSEFMR.....	QY.....	AFDGLD..	FDWEYPGA

04323_A._capsulatum	.EDSRKSFIFSVIDFMK.....	KY.....	GFDGVD..IDWEYPVA
00533_B._fuckeliana	.QGNRAAFIGSVEGWLS.....	TF.....	NFQGVLD..LDWEFPSS
Chi18_1_H._jecorina	..ENRQTLVNNIVDFLA.....	EY.....	DLDGVD..WDWEYPDE
Chi18_8_H._jecorina	..AYRGTFVNNLVNFMK.....	RE.....	NIDGFD..FDWEYPGA
Chi18_9_H._jecorina	..ENRGHFVSNVVAFAK.....	KM.....	GIDGID..LDWEYPGA
Chi18_10_H._jecorina	..EHREFFATQVVDFLK.....	QH.....	KLDGVD..FDWEYPGA
02650_A._capsulatum	.VEGRKNWAANVAAMVK.....	EM.....	GADGID..VDWEYPGG
AN0221_E._nidulans	.DESRLKFAENIRRMVD.....	DT.....	GADGVD..IDWEYPGG
06020_N._crassa	.DETRTLFAANVAKMVE.....	AT.....	GADGVD..VDWEYPGG
EAA76014_G._zeae	.YFSRKRWTRQVAAAMVK.....	AT.....	EADGID..VDWEYPGG
Chi18_4_H._jecorina	.ATSRRRWAGQVKAMVD.....	LT.....	GADGVD..IDWEYPGG
09277_P._nodorum	.EKSRLKFASNVKAMLE.....	AT.....	GADGID..MDWEYPGG
05838_A._capsulatum	.DASRKQYAKNVAEMVN.....	KH.....	GFDGVD..IDWEYPGG
EAA69039_G._zeae	.DRSRERFARNVASTLD.....	RL.....	GFDGVD..IDWEYPGG
MGG_06594_M._grisea	.DESRLKEFAKNVAATVD.....	RL.....	GYDCVD..MDWEFPGG
Chi18_11_H._jecorina	.DETRQLYAKNVADTIK.....	NL.....	GYDCVD..IDWEYPGG
02644_A_P._nodorum	.DAAIAQFAADVGTMLT.....	NT.....	GADGVD..IDWEYPGG
AN9447_E._nidulans	.EASRERYAKNVAAMLE.....	ST.....	GFDGVD..IDWEYPGG

	310	320	330	340	350	360
NP_979924_B._cereus	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	EDR	EA	YNRFLRN	VK	TR..
YP_077302_B._licheni	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	EDR	EA	YNQFLRD	AR	AR..
YP_091539_B._licheni	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	EDR	DL	FSGFLRL	LLK	ER..
YP_079121_B._licheni	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	EDR	DL	FSGFLRL	LLK	ER..
YP_074366_S._thermop	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	QDR	EA	YNRFLRR	AA	DL..
YP_075811_S._thermop	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	SDR	EA	YNNFLRQ	LR	PR..
YP_075619_S._thermop	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	DLR	AG	YTALAAE	AA	AV..
ZP_01354047_C._phyto	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	EDR	IG	FAEFVAE	LT	RR..
ZP_01354926_C._phyto	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	ETG	PH	YIQFLRE	LS	VK..
NP_902406_C._violace	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	GDR	NN	FSHFIQV	LG	RA..
ZP_01136704_A._cellu	YANSN..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	PALVQ	PTR	TG	FDALVQ	ELS..TL..
ZP_00526542_S._usita	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	LDR	DL	LASMVK	ETS	AA..
AAF46212.1_D._melano	YD..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	RER	MH	LSQLLYE	IR	TE..
AAF46534.1_D._melano	KPKKVH...GSIGKF..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	WKG	FKK	IF	SGDHVV	DEK..AE..
AAF46544.1_D._melano	REG..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	GKS	RDR	DN	YAQFVQ	ELR..AE..
At4g19720_A._thalian	D..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	VEM	RN	FGQLLEQ	WR	EA..
At4g19750_A._thalian	D..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	VEM	AN	FGKLVKE	WR	AA..
EAA67655_G._zeae	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	VNAQ	EA	RN	YVLILN	GLR..KA..
EAA73155_G._zeae	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	ANDT	DA	NN	MVLLLQ	AVR..KE..
EAA74986_G._zeae	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	NDEN	EA	TN	FDLLLQ	AVR..DE..
EAA74223_G._zeae	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	QNAD	EA	RN	YVELLG	AVR..YE..
MGG_05533_M._grisea	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	DTAE	TN	KN	CVLLLQ	ELR..RG..
MGG_01247_M._grisea	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	TNKN	EA	DN	YVLLLK	ACR..EA..
MGG_00086_M._grisea	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	ADAT	QG	QN	MVLLLQ	AVR..DA..
MGG_07927_M._grisea	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	QNPQ	EA	AD	LVALLO	QACR..HE..
Chi18_6_H._jecorina	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	INER	EA	VG	FVDLLR	ECR..KA..
Chi18_5_H._jecorina	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	ADST	QA	SN	MILLLE	QACR..SQ..
Chi18_7_H._jecorina	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	QNAD	EA	RN	FVELLAT	VR..RE..
04883_N._crassa	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	ASET	EA	QN	FLLLLK	KEIR..SQ..
04554_N._crassa	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	QNAQ	EA	SD	FVSLLS	ACR..SA..
11407_B._fuckeliana	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	ANDV	EA	GN	FVLLLQ	AVR..SA..
05350_B._fuckeliana	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	KNAE	EA	RD	YVLLLR	ECR..EA..
11700_S._sclerotioru	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	ANDV	EA	AN	FVLLLK	AIR..SA..
11304_S._sclerotioru	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	KNTD	EA	RD	YVLLLR	ECR..EA..
08020_S._sclerotioru	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	SDDT	EA	ND	FVLLLQ	QACR..DA..
01250_A._capsulatum	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	QDDA	QA	HN	FVLLLQ	ETR..LA..
05886_A._capsulatum	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	NDDE	EA	KN	FVELLK	VTR..EK..
06565_A._capsulatum	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	KDDE	EA	KN	LVELLK	TTR..EV..
05250_C._immitis	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	QNDT	EA	LN	FVYLLY	ETR..MA..
02795_C._immitis	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	EDEK	QA	ND	FVLLLK	ACR..EA..
03822_C._immitis	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	KDDK	EA	QD	FAALLK	AVR..QK..



AN5454_E._nidulans	.....	ENDD	QA	SD	.....	FVELLRETR	EE	..	
AN4871_E._nidulans	.....	QNDQ	QA	QN	.....	YVDLLRRCR	EA	..	
00269_P._nodorum	.....	ANEA	QA	ND	.....	MVSLLAATR	KA	..	
04870.1_C._cinereus	.....	QNAE	QA	RG	.....	YVDLLRELR	EA	..	
09921.1_C._cinereus	.....	STPE	QG	QG	.....	LADLVTS LR	TA	..	
124149_P._chrysospor	.....	SNEA	QA	RG	.....	YVELLREMR	LA	..	
134311_P._chrysospor	.....	SSTA	QG	QG	.....	FADLITS LR	SA	..	
03412_F._neoformans	.....	KTPR	DA	EA	.....	YVDLLRELR	QG	..	
13635_R._oryzae	.....	KDDE	EA	FY	.....	YVHLLYELR	LA	..	
UM04261_U._maydis	.....	SDST	QA	AN	.....	FVLLLKELR	AG	..	
EAA69503_G._zeae	.....	CDAQ	QG	YD	.....	FLALLAAVR	IH	..	
EAA70860_G._zeae	.....	QTPE	AG	RN	.....	YVFLQDIR	NV	..	
Chi18_3_H._jecorina	.....	SEAR	HG	QD	.....	FLALLAAVR	IH	..	
Chi18_2_H._jecorina	.....	SNAE	QG	RD	.....	YVKLLKECR	RA	..	
03026_N._crassa	.....	CSPQ	QG	SD	.....	FVSLAAVR	VH	..	
01594_B._fuckeliana	.....	SDPE	QG	RN	.....	FLALLAIR	IH	..	
05897_S._sclerotioru	.....	SDPE	QG	RN	.....	FLALLAIR	LH	..	
04742_A._capsulatum	.....	ETLE	QG	YD	.....	YNTLLYRLR	EQ	..	
04750_C._immitis	.....	SDSQ	QG	ED	.....	YVNLLRLLR	EG	..	
04719_P._nodorum	.....	SDSK	QG	QD	.....	FIALLADLR	QF	..	
MGG_08458_M._grisea	.....	SNTN	EG	EA	.....	YVALLTALR	QA	..	
CHT4_C._albicans	.....	KNST	QA	AK	.....	LVELLARLR	NK	..	
01119_L._elongisporu	.....	KNLS	QG	KA	.....	LANLLKVL R	HA	..	
XP_454053_K._lactis	.....	EDSN	EP	IV	.....	YLEMMRGIR	EG	..	
CTS2_S._cerevisiae	.....	NNES	EP	RG	.....	YKLVRMLR	LK	..	
246746_L._bicolor	.....	SNDA	QA	LG	.....	YVELLKEMR	AA	..	
03209_N._crassa	.....	TNAR	EA	QD	.....	FVLLLRCR	QA	..	
14474_P._nodorum	.....	EDAT	DA	AN	.....	FLDTVMRCRKL TNQA	..		
CE06282_C._elegans	.....	E	YRD		.....	AYFAFINQLR	KT	..	
CE03547_C._elegans	.....	T	SKD		.....	IYSQFINDLR	YS	..	
CE03542_C._elegans	.....	R	DKF		.....	NFSVFMRDLR	EK	..	
CE15845_B_C._elegans	.....	S	NQH		.....	MVSEFLSEL R	QA	..	
CE02997_C._elegans	.....	S	DEN		.....	NYLMFIRELR	YAFT	..	
CE36953_C._elegans	GGAVE	GTPA	DRR		.....	NYVNL MREL R	NELR	..	
YP_432439_H._chejuen	MNDA	GNPD	DFAIANARRAGLMASYVELMKT LR		.....		EK	..	
YP_529449.1_S._degra	MNDA	GNPS	DFAIANARRKGLNASYNVLMKT LR		.....		QK	..	
YP_077582_B._licheni	MQDA	GNPA	DWNIANPRRGNLKSFEALMKT LR		.....		EK	..	
ChiI_S._coelicolor	MKDA	GNPL	DWSFANGRRAGLVKGAAALMKT LR		.....		EK	..	
NP_902986_C._violace	MNNA	GNPL	DWTFSNARLGSLNKGYVALLQT LR		.....		DR	..	
ZP_01159608_Photobac	MAGA	GNPY	DKEFMETRRPYLWASYQELMKVL R		.....		EK	..	
ZP_01234708_V._angus	MAGA	GNPY	DKEFMETRRPYLWASYQELMKVL R		.....		EK	..	
NP_233087_V._cholera	MAGA	GNPD	DKGFMEPRRAYLWASYQELMRVL R		.....		EK	..	
NP_230718_V._cholera	MKDS	GNPV	DFEQSNKCRGQLWDNYMVMMT ELR		.....		KA	..	
AAO07185_V._vulnific	MAGA	GNPD	DKAFMEPRRAYLWASYQELMRVL R		.....		EK	..	
ZP_01354150_C._phyto		RDHS	GLIKARPEDT	EN	.....	FILLMKEIR	SK	..	
ZP_01246933_F._johns		IEGL	PGHLYQAADK	PN	.....	FTELVKILR	S	..	
YP_012734_L._monocyt	VRDADLV DNKNDE	GTPNAKPADK		QN	.....	FITLLQDLR	TA	..	
YP_529337.1_A_S._deg			RAED	VDN	.....	FIAGLAAMR	NQ	..	
ChiA_A_P._kodakarae		GGMAGNY	ESPD	DG	KN	.....	FVLLKDLR	EA	..
AAG19274_Halobacteri		GGNSGNV	VRDG	DK	QR	.....	YTELLQTVR	EK	..
AAG19275_Halobacteri		RRGKCEC	GSAQ	GP	AN	.....	HVALLETVR	DR	..
CE03543_C._elegans			G	DKF		.....	TYSSFLQELK	HK	..
CE34961_C._elegans			SET	EHH		.....	DFPSFLKDLK	EK	..
CE20043_C._elegans			E	DKA		.....	HYSRFLADLR	QH	..
CE15845_A_C._elegans			G	NRA		.....	SYSKFLREL N	QK	..
CE32863_A_C._elegans			G	NRA		.....	SYSKFLREL N	QK	..
CE03544_C._elegans			R	DKS		.....	NYATLIREIR	EK	..
CE08731_C._elegans			A	LQS		.....	EFCSFLKELK	NE	..
CE28638_C._elegans			T	KED		.....	VYVSFLRN LH	KA	..
CE32863_B_C._elegans			S	NQH		.....	MVSEFLSEL R	QA	..
CE01673_C._elegans				EET		.....	LYCELLQHLK	MG	..
CE02993_C._elegans			R	DVN		.....	NYSIFIQDLR	NEFT	..

CE02996_C._elegans	.....E.....DIK.....SYSSFIQELR.....SAFT
CE02995_C._elegans	.....E.....DAN.....NYLIFIQELR.....YAFI
CE02992_C._elegans	.....E.....DED.....TFHLFIKEFR.....E
CE02999_C._elegans	.....T.....DQS.....NYLIFIRELR.....KKLT
CE02998_C._elegans	.....S.....EMN.....DFITTIKELR.....KKLA
CE09229_C._elegans	.....NGK.....DAK.....NHVQLIKEIR.....EKFS
CE12928_C._elegans	.....KGG.....DKQ.....NHVTLIRELR.....ERFN
CE23907_C._elegans	.....K.....EKM.....KYSKFIQRLK.....K...
CE32917_C._elegans	.....E.....DKY.....YYSRFISMLK.....ER..
CE34579_C._elegans	.....A.....DKH.....AYSQFLLLELN.....EI..
CE25073_C._elegans	.....T.....SKD.....IYSQFINDLR.....YS..
CE03548_C._elegans	.....A.....SKT.....LYTKFISDLR.....HN..
NP_469498_L._innocua	VRDADLVDNKNDE.....GTPNAKPADK.....QN.....FITLLQDLR.....TA..
CE08730_C._elegans	.....A.....VQS.....EFCFLFEEVK.....IE..
Q8U1H4_P._furiosus	.....GGMEGNY.....VSPD.....DG.....KN.....FVLLVKTVR.....EI..
CE12474_C._elegans	.....Q.....QFKTLS.....
CE02990_C._elegans	.....R.....DKN.....NYLMFIQELR.....YAFT
CE40270_C._elegans	.....T.....YKS.....VYLHFICELK.....QQ..
CE40296_C._elegans	.....S.....DEN.....NYLMFIRELR.....YAFT
ChiB_S._marcescens	.....QAAE.....VDG.....FIAALQEIR.....TL..
O10363_O._pseudotsug	.....KGANPA.....LGNGE.....RDA.....DT.....YLVLLKELR.....AM..
AAP29899_C._fumifera	.....KGANPT.....LGNGE.....RDA.....DT.....YNILLKELR.....AM..
AAV73807_B._mori_NPV	.....KGANPS.....LGDAE.....RDA.....KT.....YILLDELRL.....EM..
AAL56186_H._zea_SNPV	.....KGANPN.....VG DVE.....RDN.....NT.....YIALLGELR.....AM..
AAF33549_S._exigua_N	.....KGANPD.....VGDAE.....RDR.....ET.....YTLLQELR.....LR..
AAZ38189_A._segetum	.....KGANPN.....VGDAE.....RDR.....AT.....YTALLSELRL.....VR..
AAS82706_A._segetum	.....KGANPE.....LG DPE.....KDG.....VT.....YVQLLKELR.....EM..
ZP_01159013_Photobac	.....GGAAAD.....RGDAV.....KDG.....PA.....YIALMRELRL.....AM..
ZP_01161077_Photobac	.....DGANPA.....LGNPE.....KDG.....QT.....YVTLMKELR.....AM..
ZP_01159325_Photobac	.....GGLTTSPWNPDTKLSDEQKASEK.....EA.....YTHLVKTLH.....AE..
ZP_01160869_Photobac	.....HGLSG.....LGNDNIESER.....LA.....YTKLIHELRL.....TQ..
ZP_01233025_V._angus	.....GGAAAD.....RGDAV.....KDG.....PA.....YIALMRELRL.....AM..
ZP_01236284_V._angus	.....DGANPA.....LGNPE.....KDG.....QT.....YVTLMKELR.....AM..
ZP_01235109_V._angus	.....GGLTTSPWNPDTKLSDEQKASEK.....EA.....YTYLVKTLR.....AE..
ZP_01235465_V._angus	.....HGLSG.....LGIDNV DNER.....LA.....YTKLIHELRL.....TQ..
AAO08114_V._vulnific	.....DGAAPN.....LGDPA.....RDG.....QA.....YVDLMRELRL.....TM..
AAO07498_V._vulnific	.....GGLTTSPWNPATKLSDEQKAAER.....DA.....FTYLVKTLR.....AD..
NP_232428_V._cholera	.....GGQAAD.....LGDPV.....KDG.....PA.....YVALMAELRL.....AM..
YP_432951_H._chejuen	.....DGAVPD.....ADRP.....EDA.....AN.....YVRLLEIR.....AG..
YP_529337.1_B_S._deg	.....GGTAPE.....LSTA.....ADR.....DA.....YTALMRDLR.....AA..
YP_435912_H._chejuen	.....GGANTG.....LGSP.....QDR.....DG.....YAEMLRDLR.....AA..
ZP_01137509_A._cellu	P.....DGHVGNH.....YSPA.....DT.....AN.....FTALLAEFR.....SE..
ChiE_S._coelicolor	.....EGHPGNH.....YGAQ.....DK.....DN.....LTALLAEFR.....TR..
ChiC_S._coelicolor	.....CGLSCDE.....TSAP.....N.....AFS.....SM..
ChiD_S._coelicolor	.....CGLSCD.....TSGR.....D.....AFP.....KL..
NP_903910_C._violace	.....GGLPTNT.....VDPN.....DK.....QN.....YTLLMAEFR.....NQ..
YP_529072.1_S._degra	.....CGLSCD.....NSGY.....D.....GYR.....VL..
ZP_01431615_S._tropi	.....CGLTCD.....SSGP.....A.....AFK.....NV..
ZP_01136287_A._cellu	AGATLT.NGNGNPT.....ARPE.....DT.....RN.....FTLLLAEFR.....RQ..
01315.1_C._cinereus	Q.GI.....GCN.....TINP.....QDT.....SN.....FLLFLQELR.....RD..
03252.1_C._cinereus	Q.GL.....GCN.....IVHE.....DDT.....AN.....FLTFLRELRL.....NT..
05285.1_C._cinereus	E.GI.....GCN.....LRTP.....EDT.....EN.....FLTFLRELRL.....EH..
05291.1_C._cinereus	Q.GI.....GCN.....HISN.....ADS.....AN.....FLAFLQELR.....QD..
01586.1_C._cinereus	P.GA.....GN.....PYSA.....NDT.....AN.....YLSLMKLLR.....NA..
128098_P._chrysospor	S.G.....DCN.....VNTP.....QDT.....QN.....FLLFLQELR.....SQ..
39872_P._chrysospori	A.GI.....GCN.....AVSP.....NDT.....AN.....FLTFLQELR.....AD..
138098_P._chrysospor	Q.GL.....GCN.....VISP.....QDT.....PN.....FLALLQELR.....AS..
129436_P._chrysospor	P.GA.....DGN.....AYAP.....QDT.....AN.....FLAFLRLRL.....QR..
EAA71245_G._zeae	Q.GL.....GCN.....TINE.....NDT.....AN.....FLEFLKELR.....KD..
MGG_04732_M._grisea	Q.GL.....GCN.....AISP.....NDT.....AN.....FISFLTELRL.....KA..
UM06190_U._maydis	A.GS.....GN.....LLDA.....SDT.....RN.....YQTFLETELRL.....AA..
04245_F._neoformans	A.GA.....DGN.....AVSS.....DDS.....AN.....FLIFLQDLR.....AA..

16170_R._oryzae	PDSI.....ANA.....ARNP..NDT.....AN.....LLFIKILLR....QK..
01334_R._oryzae	RDSI.....ACA.....SRNP..NDT.....AN.....LLTFIQILLR....KS..
13934_R._oryzae	PRGI.....FCN.....RRNL..QDT.....SN.....FLALIQLLR....ET..
07611_R._oryzae	K.GA.....GCN.....AVND..NDV.....QN.....LNTLVKELR....SA..
10252_R._oryzae	Q.AA.....GCN.....EVAD..DDA.....DN.....FLLLLKELR....LA..
14659_R._oryzae	Q.GA.....GCN.....TFDEK..NDV.....KN.....FLTLLKELR....QA..
231399_L._bicolor	Q.GA.....GFN.....VVS..HDA.....AN.....FLSFLLEELR....RD..
180319_L._bicolor	S.GI.....GCN.....VMSP..SDS.....AN.....FLLFLQELR....LD..
191848_L._bicolor	Q.GI.....GCN.....LISS..SDS.....AN.....FLSFLQELR....QD..
317003_L._bicolor	P.GA.....GN.....PYSA..ADA.....AN.....LLSLITLLR....TA..
246840_L._bicolor	Q.GI.....GCN.....TVNP..KDT.....AN.....FLSFLQQLR....TT..
144643_L._bicolor	Q.GA.....GGN.....LVDP..HDT.....AN.....FLLFLQYLR....TV..
310136_L._bicolor	Q.GL.....GCN.....AIS..SDS.....AN.....FLAFLQQLK....QD..
629882_M._xanthus	V.....DKP.....A.....LLALIQALR....AA..
630509_A_M._xanthus	.....
YP_592598_Acidobacte	P.....DDT.....TH.....CTQIMEALR....HE..
YP_446903_S._ruber	.....PGQD..NV.....YRPE..DK.....EN.....FTRLRLTVR....RH..
ZP_00739282_B._thuri	.....ETIPGGS.....YRPE..DK.....QN.....FTLLLQDVR....NA..
ZP_01245639_F._johns	SGGTDG.TEIVNGMPV.PPQKYS..DN.....KN.....LVLLLKAMR....QA..
NP_976824_B._cereus	.....ETIPGGS.....YRPE..DK.....QN.....FTLLLQEV..NA..
YP_077581_B._licheni	.....GGLPGNS.....TRPE..DK.....RN.....YTLLLQEV..KK..
631138_M._xanthus	.....GGLPGNS.....NSPA..DK.....QN.....YTLLMQEFR....SQ..
ZP_01247029_F._johns	N.....GD.....YGGFVIALA....NK..
ZP_01234549_V._angus	G.....NG.....ANQ.....YADFNRLA....DR..
ZP_01160697_Photobac	G.....DG.....ANQ.....YADFNRLA....DR..
ZP_01158584_Photobac	D.....DTV.....AYN.....YTEFVNMLA....DR..
AN0549_E._nidulans	DDRS.....G.....RE..EDY.....KN.....FPSFIANLK....KA..
AN8481_E._nidulans	DDRS.....G.....RP..ADY.....EN.....FPRFIANLK....KA..
AN9390_E._nidulans	EERS.....G.....AP..EDF.....EN.....YVSFLKNLR....AV..
AN0517_E._nidulans	SDRG.....G.....AP..QDA.....AN.....FN.....
AN0541_E._nidulans	GDRG.....G.....KD..EDY.....EN.....YVSLVREM..EA..
AN5077_E._nidulans	DDRG.....G.....SDSM.VDG.....EN.....YTLLKELQ....EA..
AN0509_E._nidulans	PDIP.....GI.....PAGSE.DEG.....DN.....YLFKFLVVLK....NL..
AN7613_E._nidulans	ADVL.....NI.....SPGLE.SDG.....PN.....YIAFIKKLR....KI..
07035_N._crassa	EDRS.....G.....RG..ADY.....KN.....FVTFQKALY....DR..
07484_N._crassa	PDIP.....GP.....PPGAD.DEG.....TN.....YLAFLVLK....NL..
05317_N._crassa	PDIP.....GI.....PAASL.DDG.....PN.....YLAFLVLK....NL..
EAA74768_G._zeae	KDRG.....G.....ME..SDY.....EN.....FPKFMSNLK....DL..
EAA78168_G._zeae	TDRN.....G.....RE..SDF.....KA.....YPRFLKRLK....SA..
EAA75711_G._zeae	PKRG.....G.....RKL..ADT.....RN.....FSMLLREMR....AA..
EAA68447_G._zeae	PDIP.....GI.....PPADK.DEG.....KN.....YLAFLVLK....NL..
EAA77156_G._zeae	ASS.....DGSS.TDT.....AN.....YVEFLKIMR....SK..
12510_S._sclerotioru	DDRS.....G.....RE..VDF.....SN.....FPKFMDRLK....SS..
00773_S._sclerotioru	SDRS.....G.....RT..EDY.....AN.....YPKFLANLK....SA..
05454_S._sclerotioru	GDRG.....G.....KP..EDG.....IN.....FTKLLKEMR....TA..
00677_S._sclerotioru	LD.....DR.....DG.....FVALVREM..ES..
02128_S._sclerotioru	PDIP.....GI.....PAGSL.DDG.....VN.....YVRFDELA....AV..
MGG_04534_M._grisea	EDRG.....G.....VP..EDF.....EN.....YVTMISRLR....MA..
MGG_01336_M._grisea	PNRG.....G.....SP..VDT.....AN.....YVSLVREL..VA..
14527_P._nodorum	DDRG.....G.....AE..VDR.....DN.....YVALVKQMR....SA..
15411_P._nodorum	PKRG.....G.....RK..EDT.....DN.....LVLLMKEMH....AA..
02214_P._nodorum	SDRG.....G.....DS..GDK.....AN.....QVELLQDMR....QA..
04761_C._immitis	DDRG.....G.....IP..GDG.....KN.....FVKFLKELN....DV..
04323_A._capsulatum	DDRG.....A.....SK..EDF.....KN.....YVRLKELK....TA..
00533_B._fuckeliana	DN.....DR.....DG.....FVALVREM..ES..
Chi18_1_H._jecorina	PDIP.....GI.....PEGTE.DET.....TG.....YFLLLDLELK....LK..
Chi18_8_H._jecorina	PDIP.....DV.....PPGSA.SEG.....DN.....YLDLFLSLR....SR..
Chi18_9_H._jecorina	PDIP.....GI.....PKGLP.SDG.....PN.....YLETFLRALR....KA..
Chi18_10_H._jecorina	TDLP.....I.....PAGSP.EDP.....AN.....YLRFLQLLR....KK..
02650_A._capsulatum	N.GA.....DYK.....QIPNS.EKKWE..IDA.....YPCLLAEIR....SA..
AN0221_E._nidulans	N.GE.....DYK.....RIPNS.EKFWE..TAA.....YPQLLAEIR....AA..
06020_N._crassa	N.GE.....DYK.....QIPNS.DKRWE..IAA.....YPLLLQELR....SA..

EAA76014_G._zeae	N.RD....DYK.....EIPNS.EREWE...IEA.....FVSLLELR...AA..
Chi18_4_H._jecorina	N.RD....DYK.....LIPNS.QRKWE...IEA.....FPLLVAELR...SA..
09277_P._nodorum	N.GE....DYK.....VNPNS.SKVWE...ITA.....FPPELLAAVR...AA..
05838_A._capsulatum	N.GL....DYK.....ETSNS.AKKSE...IDN.....FPLFLKEIR...NA..
EAA69039_G._zeae	N.GQ....DYK.....QVPNS.KKTYE...IKA.....FPKLLKEIK...KF..
MGG_06594_M._grisea	N.GQ....DYK.....QNPNS.GRVSE...IET.....FPLLLQDIK...AA..
Chi18_11_H._jecorina	N.GE....DYK.....VVPNS.EKAWE...IEA.....YPLFLEAVR...KA..
02644_A_P._nodorum	N.GG....DYK.....EVLNS.DKAYQ...IEA.....YPKFLAAIR...AA..
AN9447_E._nidulans	N.GE....DYK.....KVPND.QKVDE...IET.....FPLLLQALR...TA..

	370	380	390	400	410	420
NP_979924_B._cereus	.... .... .... .... .... .... .... .... .... ....	.LPN....GYT.....LSTTLVPKTSSNQK.....GKFFEAH				
YP_077302_B._licheni	.FRQ....EGWL.....ISTALAPKTRADQP.....GQWYEAH					
YP_091539_B._licheni	.LKP....SGYV.....LTIIVPPKTEN.....IAWLKGYD					
YP_079121_B._licheni	.LKP....SGYV.....LTIIVPPKTEN.....IAWLKGYD					
YP_074366_S._thermop	.IHG....EGAL.....ISTALAPKVSAGQT.....GQWYEAH					
YP_075811_S._thermop	.LHA....EGRS.....LSTAIAPKVRADQP.....GLLYEAH					
YP_075619_S._thermop	.LKP....GGIR.....LTLSPAKTWDDTT.....SNWGGAF					
ZP_01354047_C._phyto	.MNE....EDFF.....VSVALAPKTSENQP.....GLLYEGM					
ZP_01354926_C._phyto	.CRS....NQIV.....LSSDTYVPASYS.....KFYD					
NP_902406_C._violace	.LHA....KGLK.....LIVSVPAFSAKDEN.....HPANYGYD					
ZP_01136704_A._cellu	.LHQ....HGMT.....LAVDVMSKTSEPGA.....TPAGQVYD					
ZP_00526542_S._usita	.LGR....GGFK.....LSIATVPNEGDEPGKSDYTRWVFQNRGAF					
AAF46212.1_D._melano	.WRR....EKRTN.....DILSLAVAPEGIAFY.....AYD					
AAF46534.1_D._melano	.EHK....EAF TALVRELKNAFRP.DGYILGLSVLPNVNSS.....LFFD					
AAF46544.1_D._melano	.FER....EAEKTGR.....TRL L L TMAVPAGIEYID.....KGYD					
At4g19720_A._thalian	.IED....DAERTER.....MPL L L TAAVYYSVPYDS.....VSYP					
At4g19750_A._thalian	.VVE....ESDRTNQ.....LP L L L TAAVYYSPTYG.....EEYP					
EAA67655_G._zeae	.LDK....YSQDY....K..LNY...RFL L TVASPA..GSSHY.....NTMD					
EAA73155_G._zeae	.LDT....YSKQY....AS..GY...HFQLSIAAPA..GPENY.....GKLK					
EAA74986_G._zeae	.LDS....YASQN....AP..GH...HFL L SIAAPA..GPEKY.....KKLH					
EAA74223_G._zeae	.MDA....YAQTL....S..RPY...HFELTVACPA..GATNF.....QKLD					
MGG_05533_M._grisea	.LDD....YSQQH....TG..SQY...KFSL S MPAPA..GP THY.....AAFD					
MGG_01247_M._grisea	.LDA....YSAKN....AQ..GY...KFL L TVATPA..GPENY.....GNMN					
MGG_00086_M._grisea	.LDA....YAAQH....AP..GY...HFL L TIASPA..GP THY.....QKMQ					
MGG_07927_M._grisea	.LDA....YASHV....DGENPY...HFELTVACPA..GASNY.....EKMD					
Chi18_6_H._jecorina	.LDE....YASLH....N..QRY...HYLLTAAVSA..AQQHY.....KWL D					
Chi18_5_H._jecorina	.LDA....YAAQH....AP..GY...HFL L SIAAPA..GEVNY.....SLLR					
Chi18_7_H._jecorina	.LDA....YSATL....P..NYS...HFELTVACPA..GP THF.....QKLD					
04883_N._crassa	.MDK....YAAAH....AD..GY...HFL L TMAASA..GPSKY.....GVLE					
04554_N._crassa	.LDA....YASTV....PG..NP...HFEMSVACPA..GPQNY.....EKMD					
11407_B._fuckeliana	.LDA....YAAQH....AP..GY...HFLITVASPA..GPEKY.....NVLH					
05350_B._fuckeliana	.MDR....YSNTL....P..TPH...HFELTVACPA..GPQNY.....NNMD					
11700_S._sclerotioru	.LDA....YAARY....AP..GY...HFLITAATPA..GPDHY.....NVLH					
11304_S._sclerotioru	.MDR....YSSTL....S..NFH...HFELTVACPA..GPQNY.....NNMD					
08020_S._sclerotioru	.LDR....FGDSL....Q..SPY...HFL L TVASPA..SPAVC.....QNWK					
01250_A._capsulatum	.LDS....YAAQH....A..QPK...RLL L TVAVPC..GPSNY.....KKLR					
05886_A._capsulatum	.LD....ALSK.......NR...KFYLTVACPA..GPKHF.....KKLR					
06565_A._capsulatum	.LDR....AGGK.......DR...RFL L TVACPA..GRQNF.....EKLR					
05250_C._immitis	.LEN....YAAQY....A..QGR...HFL L TIAAPC..GPKNY.....SQLR					
02795_C._immitis	.LDA....YSAKH....P..NGK...KFL L TIASPA..GPQNY.....NKLK					
03822_C._immitis	.LN....SVAG.......GR...KFL L TIAASA..GAEHY.....EKLH					
AN5454_E._nidulans	.LDR....YAADN....D..SDK...PFL L SVASPAEPGPSKY.....TTLH					
AN4871_E._nidulans	.LN....AAQG.......QR...RFQLTVAVPA..GPDNY.....NKL R					
00269_P._nodorum	.LDA....YSAAH....A..PNQ...HLL L TVASPA..GAKNY.....NIMK					
04870.1_C._cinereus	.LDQ....REREN....GE..GC...KFL L TIAAPC..GPDNY.....KKLL					
09921.1_C._cinereus	.LTQ....LASRK....GE..SN...PYLITAAVGA..GPAGY.....SNLK					
124149_P._chrysospor	.LDQ....HAAKK....GA..NY...RFL L TIAAPC..GPDNY.....KKLF					
134311_P._chrysospor	.FDT....YQAQK....GD..TT...PYLLTSAVSA..GSANY.....EYLV					
03412_F._neoformans	.LEQ....LAQSK....GKP.QG...QYQLTVAAPC..GWEQM.....QVLR					
13635_R._oryzae	.MDK....YQQQC....GQLNQP...RLL L TVAVPC..GPDHY.....RKLR					



UM04261_U._maydis	.LTA...HQAKK....NE..TN..PYLLSIAAPC..GPDHY.....KVLQ
EAA69503_G._zeae	.LP.....EE...HYVLTAALPA..AKAVL.....QFLD
EAA70860_G._zeae	.MT.....HS...QFLLTALPT..GEYCL.....KHIN
Chi18_3_H._jecorina	.LP.....DD...RFILTAVLPA..AKEVL.....QLID
Chi18_2_H._jecorina	.LP.....EP...NYLITTALPV..GQYIL.....RHID
03026_N._crassa	.LP.....ED...RYLLTAALPG..AKSIL.....QNIN
01594_B._fuckeliana	.LP.....DE...RYLLTAALPA..GRWAL.....QNID
05897_S._sclerotioru	.LP.....DE...RYLLTAALPA..GRWAL.....QNID
04742_A._capsulatum	.FP.....SP...AYLLTTALSA..GEWVL.....NKIN
04750_C._immitis	.LP.....WP...QYTLTTALPA..GEWAL.....RHIN
04719_P._nodorum	.LP.....GP...QYTLSTALPA..GEWAL.....QHIN
MGG_08458_M._grisea	.LP.....AP...RYLLTTALPC..GEWAL.....QHIP
CHT4_C._albicans	.LN.....S...KYIITVAAPG..GSDNI.....EILK
01119_L._elongisporu	.LP.....P...QRLLTIAAPG..GHEHI.....KQLP
XP_454053_K._lactis	.MDQ...LERQIFGSPAEEKDHP...HFQLSVATPA..FAEKL.....NILP
CTS2_S._cerevisiae	.LNS...LESQIFGKRTED...HFQLSIAAPA..FKDKL.....FYLP
246746_L._bicolor	.LDQ...HASVK....GA..GC...KFLLTIAAPC..GPDNY.....KKLR
03209_N._crassa	.LDD...YARQY....AP..GY...HFLITIAAPA..GPQHY.....GVMD
14474_P._nodorum	.YDE...YAAAN....AH..GY...HFDLGISAPA..GPSRY.....SVLR
CE06282_C._elegans	.FEAK...KK.....YYILSIVIPPTLDG.W.....G.KKR.
CE03547_C._elegans	.LQRQ...KR.....NYIMSIVLPPPDGMANY.....E.AGID
CE03542_C._elegans	.LDKQ...LK.....SYIVSILLPPAGVDI.W.....E.MGYD
CE15845_B_C._elegans	.LQT.....QYLLISIQVP.AFMQN.....YN
CE02997_C._elegans	.ELQKKL.NRK.....ETFVISLVISR...NV.....N.HLSN
CE36953_C._elegans	.DLESET.GKS.....YLISFAGAAG..HWVL.....K.PGYD
YP_432439_H._chejuen	.LDAAS..AEDG.....KHYMLTIASPS...SGYL.....L.RGME
YP_529449.1_S._degra	.LDIAG..EQDG.....KHYMLTIASPS...SGYL.....L.RGME
YP_077582_B._licheni	.LDQAS..AEDG.....KYYMLTIAAPS...SAYL.....L.RGME
ChiI_S._coelicolor	.LDRAG..AADG.....RHYLLSVAAPS...SGYL.....L.RGME
NP_902986_C._violace	.LDRAA..AQDG.....RYYQITAAPVPA..SGYL.....L.RGME
ZP_01159608_Photobac	.LDVAS..AEDD.....IHYMLTIAAPS...SGYL.....L.RGME
ZP_01234708_V._angus	.LDVAS..AEDG.....IHYMLTIAAPS...SGYL.....L.RGME
NP_233087_V._cholera	.LDQAS..AQDG.....HHYMLTIAAPS...SGYL.....L.RGME
NP_230718_V._cholera	.LDKAG..EEDG.....RRYMLTIASPS...SAYL.....L.RGMQ
AAO07185_V._vulnific	.LDQAS..AQDG.....VHYMLTIAAPS...SGYL.....L.RGME
ZP_01354150_C._phyto	.FN....ELSKT.....SDK..KYTLSFAAP..AGD.....WAV
ZP_01246933_F._johns	.....T.....LGK..KYELSFAAGG..FQK.....CLD
YP_012734_L._monocyt	.LD....KQGVVD...INK..KYELSVALPA..AKS.....TLE
YP_529337.1_A_S._deg	.LDARGNGE.....LVTIAGAGGAFFLS.....RYYS
ChiA_A_P._kodakarae	.LD....KAAKE.....DHK..DYLLTAATPA..DPV.....KAG
AAG19274_Halobacteri	.LD....VAEDE.....DGK..RYQLTTALSA..DPE.....KNT
AAG19275_Halobacteri	.LN....DAEVE.....DGR..TYDLSVANGG..SDW.....NAA
CE03543_C._elegans	.LRSH...RQ.....NYIISIVLPPAGVDT.W.....E.LGYD
CE34961_C._elegans	.LKTV...RD.....DSIISIVAPQAKMDR.R.....H.DGYK
CE20043_C._elegans	.LG.....Y.....EFIISVAVPQAEVSN.L.....E.LGYD
CE15845_A_C._elegans	.LKNQ...EK.....RYILSVVPPVDVDN.F.....E.MGFD
CE32863_A_C._elegans	.LKNQ...EK.....RYILSVVPPVDVDN.F.....E.MGFD
CE03544_C._elegans	.VDEL...DA.....KIIISITIPPVGVS.D.W.....E.SGFD
CE08731_C._elegans	.LMNQ...EK.....QYILSVGAPPAGIEN.L.....E.DGYD
CE28638_C._elegans	.LQRE...LEGL.....RDPLTILSVVVP.HYINH.R.....E.AGYS
CE32863_B_C._elegans	.LQT.....QYLLISIQVP.AFMQN.....YN
CE01673_C._elegans	.LEKQ...EK.....QYSISLRVPQTGIG.KW.....H.IGCE
CE02993_C._elegans	.ELQKRT.NRK.....NEYIISLLVPK...KS.....Y.WSFD
CE02996_C._elegans	.ELQKRW.NRK.....NEYIISLIVPK...EK.....H.WSFD
CE02995_C._elegans	.ELQKKL.NRK.....EDYVISIIVNC...YD.....N.QLSN
CE02992_C._elegans	.KLEK...H.....MIISIAIPR...LAQQ.....L.EGFN
CE02999_C._elegans	.NLKDEN.GRS.....NEYVISVIAPSS..SSHS.....E.YPYK
CE02998_C._elegans	.ALTKAQ.PKG.....TRYLLSIIVPSS..PSDL.....E.YYLR
CE09229_C._elegans	.EMAKKK.KRK.....DPYVITLASAAG..EWNL.....R.KGYD
CE12928_C._elegans	.GMASRN.NRK.....DPYLITLASAAG..EWNL.....R.EGYD
CE23907_C._elegans	.....E.....EG.W.....E.RAYD
CE32917_C._elegans	.FQME...EK.....NYILSIIIPP CGFGG.W.....N.NKFD

CE34579_C._elegans	.LKTR.....K.....	DYILSILVPPQGIG..F.....	A.SGFK
CE25073_C._elegans	.LQRQ.....KR.....	NYIMSIIVLPPDGMANY.....	E.AGID
CE03548_C._elegans	.LQQK.....NK.....	NYILSIIVLPPPDLEGNY.....	E.AGIN
NP_469498_L._innocua	.LD.....KQGV.....	INK.....KYELSVALPA..AKS.....	TLE
CE08730_C._elegans	.FLNQ.....EK.....	QYILSITAPPVGIEN.Y.....	E.DGYD
Q8U1H4_P._furiosus	.FD.....QAELE.....	DKK.....RVSPNCSSSS.....	
CE12474_C._elegans	.....	IMLHL.....SN.....	
CE02990_C._elegans	ELQNK.....NRK.....	EDFVISLVASS.....NL.....	N.LLFN
CE40270_C._elegans	.LQTK.....DK.....	DYILSIVVPPPEVGG.W.....	I.DGFD
CE40296_C._elegans	ELQKKL.....NRK.....	ETFVISLVISR.....NV.....	N.HLSK
ChiB_S._marcescens	.LNQQTIA...DGRQ.....	AL.....PYQLTIAGAGGAFFLS.....	RYYS
O10363_O._pseudotsug	.LD.....ELQLQ.....	TNK.....TYELTS...AIS...GYD.....	KIA
AAP29899_C._fumifera	.LD.....QLQLQ.....	TGK.....TYELTS...AIS...GYD.....	KIA
AAV73807_B._mori_NPV	.LD.....DLEVQ.....	TGR.....VYELTS...AIS...GYD.....	KIA
AAL56186_H._zea_SNPV	.LD.....QVQIQ.....	TNR.....TLELT...AIS...GYD.....	KIA
AAF33549_S._exigua_N	.LN.....ALGAR.....	TNR.....YYALT...SAV...SA...GND.....	KIA
AAZ38189_A._segetum	.LD.....ALGVR.....	TNR.....YYALT...SAV...SA...GND.....	KIA
AAS82706_A._segetum	.LN.....DLSKE.....	TGK.....KYQLT...SAV...SA...GYD.....	KIS
ZP_01159013_Photobac	.LD.....KLEAD.....	TGR.....TYELT...SAV...SA...GYD.....	KIE
ZP_01161077_Photobac	.LD.....ELSAE.....	TGR.....QYELT...SAV...SA...SEK.....	GIN
ZP_01159325_Photobac	.LD.....NLEKK.....	TGR.....QYELT...SAV...SA...GSK.....	AES
ZP_01160869_Photobac	.LN.....TLGIE.....	NQR.....TYQLT...SAV...SA...APK.....	TLP
ZP_01233025_V._angus	.LD.....KLEAD.....	TGR.....TYELT...SAV...SA...GYD.....	KIE
ZP_01236284_V._angus	.LD.....ELSAE.....	TGR.....QYELT...SAV...SA...SEK.....	GIN
ZP_01235109_V._angus	.LD.....NLEKK.....	TGR.....EYELT...SAV...SA...GSK.....	AES
ZP_01235465_V._angus	.LN.....TLGIK.....	NKR.....TYQLT...SAV...SA...APK.....	TLP
AAO08114_V._vulnific	.LN.....ELEAE.....	TGR.....TYELT...SAV...SA...GHD.....	KIE
AAO07498_V._vulnific	.LD.....ALEKK.....	TNR.....EYELT...SAV...SA...GAK.....	AAQ
NP_232428_V._cholera	.LD.....ELEAE.....	TGR.....KYELT...SAV...SA...GHD.....	KIE
YP_432951_H._chejuen	.MD.....WLGRK.....	TGK.....QYRLT...SAV...SA...GTG.....	RLD
YP_529337.1_B_S._deg	.LD.....ELAEE.....	TGR.....EYELT...SAV...SA...APE.....	KIA
YP_435912_H._chejuen	.LD.....TLEAE.....	TGR.....EYQLT...SAV...SA...APS.....	KID
ZP_01137509_A._cellu	.LD.....AYGAS.....	VGR.....KMYLT...AAL...PS...GQD.....	KIR
ChiE_S._coelicolor	.LD.....ALGGE.....	HR.....LLTAF...TPA...DPA.....	KIE
ChiC_S._coelicolor	.MK.....AMRAE.....	FGQ.....DYLIT...AAV...TA...DGS...DG.....	GKID
ChiD_S._coelicolor	.MG.....ALRAK.....	FGQ.....DYLVT...AAI...TA...DATAG.....	GKID
NP_903910_C._violace	.LN.....ALSTA.....	NKR.....RYLLT...AAI...GS...GVD.....	KIR
YP_529072.1_S._degra	.MQ.....ALRNR.....	FG.....NKLVT...AAI...GA...GES.....	KQN
ZP_01431615_S._tropi	.VD.....ALRSR.....	FGP.....SALVT...AAI...TG...DASNG.....	GRID
ZP_01136287_A._cellu	.LDS.....AARAN.....	HHR.....RYLLT...AAL...SA...NPT.....	KIA
01315.1_C._cinereus	.PVG.....SKLL.....	.....VTAAA...ATVPFYGSN.....	GRPSSD
03252.1_C._cinereus	.TTG.....RDLV.....	.....LSAAV...YVKPFNDAS.....	GSPSTD
05285.1_C._cinereus	.PVG.....VNLK.....	.....LTAAH...HITPLMDAT.....	GTPGSD
05291.1_C._cinereus	.PTG.....GKLM.....	.....LTAAG...VLLPFVGSN.....	GQPMSSD
01586.1_C._cinereus	.MG.....PCKI.....	.....LSSAV...AHL...PWLGSN.....	GRPLTN
128098_P._chrysospor	.AP.....NIT.....	.....LSAAV...ALT...PFDVTS.....	GSPATD
39872_P._chrysospori	.PDG.....KDLI.....	.....LSAAT...PVL...PWKDET.....	GSPSTD
138098_P._chrysospor	.PAG.....QNMT.....	.....ISTAT...SIV...PFTSPD.....	GTPTAD
129436_P._chrysospor	.LP.....PQAK.....	.....ISAAAM...TV...PWADAH.....	GAPLAD
EAA71245_G._zeae	.PVG.....KDLY.....	.....LTAAG...SLL...PWNDKD.....	GAPSKD
MGG_04732_M._grisea	.QP.....KPLL.....	.....LTAAG...VSL...PYNDAA.....	GQQSAN
UM06190_U._maydis	.LP.....KGAL.....	.....ITGAV...AHT...PVMASN.....	GQPVAS
04245_F._neoformans	.LP.....SEAI.....	.....ITTAT...QV...WPFADS.....	GNPMTD
16170_R._oryzae	.LDITTFPKAHKV.....	.....ITVAAS...VGPFLDER.....	GRSIRH
01334_R._oryzae	.LDAKYPKVHKV.....	.....ITVAAS...VGPFLDSN.....	GHAVRH
13934_R._oryzae	.LDKKYPKEHKI.....	.....ITAAG...VSTYTFKDDK.....	QNSIKT
07611_R._oryzae	.LDNSFPNDHKE.....	.....LTMAV...HIT...PFG..G.....	ATPVTD
10252_R._oryzae	.LDTKFPQKHKE.....	.....ISMAV...HV...QPFVRS.....	GTPMSD
14659_R._oryzae	.IRREFK.EKKE.....	.....ITIAAF...VNPLA.....	AD
231399_L._bicolor	.PVG.....SSLV.....	.....LSACAS...VVPFAGED.....	GKPSGD
180319_L._bicolor	.PVG.....SKLI.....	.....ISAAAG...IT...PFTGSD.....	GKPMSSD
191848_L._bicolor	.PMG.....STLI.....	.....LSSAV...GLTPYAGSD.....	GTPMAD

317003_L_bicolor	.LG.....PCKI.....ISAAVAHLPWLGSN.....GKPLTD
246840_L_bicolor	.TTG.....SKLI.....ISVPV.AAPFADAS.....GSPSTN
144643_L_bicolor	.LP.....PCAR.....ISAAAQTLPFVDAQ.....EQPLQD
310136_L_bicolor	.PVG.....SKLI.....LSAAVGETPFMGAN.....GTPMTD
629882_M_xanthus	.RPQ.....MLLT.....MPIGWVNSNFPEDA.....DP.....
630509_A_M_xanthus	.....
YP_592598_Acidobacte	.LPS.....PRWL.....ISMAIPSDPRGYGT.....G.....FD
YP_446903_S_ruber	.LEK.....QGRAD.....GHTGDERYLLTIAAGA..DAD.....YL.
ZP_00739282_B_thuri	.LN.....KAGAE.....DGK...QYLLTIASGA..SQR.....YAD
ZP_01245639_F_johns	.MP.....N.....KLVTTAAGN..NVR.....NVS
NP_976824_B_cereus	.LT.....KAGAE.....DGK...QYLLTIASGA..SQR.....YAD
YP_077581_B_licheni	.LD.....AAEAK.....DGK...EYLLTIASGA..SPD.....YVS
631138_M_xanthus	.LN.....AVTTQ.....TGK...PYLLTIATGA..SPD.....LLE
ZP_01247029_F_johns	.LHA.....NGKL.....ISAALS EGYGGANV.....P.....
ZP_01234549_V_angus	.LHA.....EGKY.....FTAAIIGSKDKPND.....DGKGAG
ZP_01160697_Photobac	.LHA.....EGKY.....FTAAIIGSKDKPND.....DGKGAG
ZP_01158584_Photobac	.LHE.....EGLY.....FTAALINGRGTQTK.....DKSECG
AN0549_E_nidulans	.LK.....ASGGRD.....GLSITLPASYWYL.....QHFD
AN8481_E_nidulans	.LK.....GSGGRD.....GLSITLPASYWYL.....QHFD
AN9390_E_nidulans	.LG.....NRG.....LTITLPASFWYL.....QHFD
AN0517_E_nidulans	.....PGW.....EISATLPTS YWYL.....RGFD
AN0541_E_nidulans	.FQ.....KRNP SW.....DISMAIPASYWYL.....QHFD
AN5077_E_nidulans	.IT.....ASGRNY.....LVTFTAPT SYWYL.....RHFD
AN0509_E_nidulans	.LK.....DKS.....VSIAAPASYWYL.....RGFP
AN7613_E_nidulans	.FP.....SDKT.....ISVAAPATY WHL.....KSFP
07035_N_crassa	.MK.....GGGLKK.....QVSLTLPASYWYL.....QHFD
07484_N_crassa	.LP.....GKT.....VSIAAPASYWYL.....KQFP
05317_N_crassa	.LP.....GKS.....ISIAAPSSYWYL.....KQYP
EAA74768_G_zeae	.ME.....DGD..R.....GLTITLPASYWYL.....QYFD
EAA78168_G_zeae	.LN.....NYK..Y.....GLSVTLTTSYWYL.....QHFD
EAA75711_G_zeae	.YG.....DKY.....GISLTLAPDYWYL.....RWFD
EAA68447_G_zeae	.LK.....GKS.....VSIAAPSSYWYL.....KQYP
EAA77156_G_zeae	.IGK.....SGKT.....MSVALPAAYWYL.....KPFP
12510_S_sclerotioru	.MD.....SAS..K.....GVSITLPASYWYL.....QHFD
00773_S_sclerotioru	.LD.....EYS..Y.....GLSITLPTS YWYL.....QHFD
05454_S_sclerotioru	.FD.....GMSGRYK.....EISFTAPT SYWYL.....RHFD
00677_S_sclerotioru	.FN.....ENFP EKNW.....GISVVLPPDISAL.....QFFD
02128_S_sclerotioru	.LP.....AGTT.....QSVTAPT SYWYL.....APFL
MGG_04534_M_grisea	.LN.....ASGKRY.....GLSITLPASYWYL.....RGFD
MGG_01336_M_grisea	.FG.....TQY.....GLSMAIPADWGSM.....LYFD
14527_P_nodorum	.FG.....SKYG.....ITVTLP TS YWYL.....QHFD
15411_P_nodorum	.FA.....GRY.....GSSLTIAPDYWYL.....R...
02214_P_nodorum	.LG.....NNI.....GLGVAIPAQYTYL.....QNID
04761_C_immitis	.NK.....KQPMHY.....SVSFTAPSSYWYL.....RHFD
04323_A_capsulatum	.IA.....DKYG.....LTVALPAS YWYL.....RGFD
00533_B_fuckeliana	.FS.....ANYPGKNW.....GISVVLPPDIYSL.....QFFD
Chi18_1_H_jecorina	.LP.....SNRT.....VSITAPASFWYL.....QYFP
Chi18_8_H_jecorina	.LS.....KDKS.....ISIAIPASFWYL.....QSYF
Chi18_9_H_jecorina	.LP.....SKYS.....LSIAVPA.....SYC
Chi18_10_H_jecorina	.LP.....AEMS.....LSIAAPASFWYL.....KAFF
02650_A_capsulatum	.LGS.....DKT.....ISAAVPGLPRDMLA.....FTP.ET
AN0221_E_nidulans	.IP.....DKL.....ITAAMPGLPRDMLA.....FTK.ET
06020_N_crassa	.LGP.....DKV.....ISAAVPGLHRDMLA.....FTR.ET
EAA76014_G_zeae	.LGP.....EKI.....LSAAVPGKEGDLMA.....FTT.DT
Chi18_4_H_jecorina	.LGD.....DKL.....LSVAVPALERDLMA.....FTN.ST
09277_P_nodorum	.VGP.....LMT.....ISAAVPGLERDMLA.....FTP.AT
05838_A_capsulatum	.IGT.....EKQ.....LSIAVPGRKSDMIA.....YTP.EN
EAA69039_G_zeae	.IGE.....KE.....LSIAVPGLERDMIA.....YLP.TE
MGG_06594_M_grisea	.IGT.....KE.....LSIAVPGKEVDMIA.....YTA.EQ
Chi18_11_H_jecorina	.LPE.....NIE.....LSIAVPPARVEDMMA.....FTA.EN
02644_A_P_nodorum	.IGN.....KL.....LSIAVPGKKGDMIA.....YTK.ET
AN9447_E_nidulans	.VGD.....KKI.....ISIATPGKREDMIA.....YTT.EQ

	430	440	450	460	470	480
NP_979924_B._cereus	.....YKAQGQI.....	.....VDFVV.....	.....IMTYDWGW.....			
YP_077302_B._licheni	.....YRAHGEI.....	.....VDFVV.....	.....LMTYEWGY.....			
YP_091539_B._licheni	.....YGGIGAV.....	.....SDLIF.....	.....IMAYDWHH.....			
YP_079121_B._licheni	.....YGGIGAV.....	.....SDLIF.....	.....IMAYDWHH.....			
YP_074366_S._thermop	.....YAAHGQT.....	.....VDFVV.....	.....LMTYEWGY.....			
YP_075811_S._thermop	.....YPVHGEV.....	.....CDFVV.....	.....IMTYEWGY.....			
YP_075619_S._thermop	.....YAAIGEI.....	.....ADEIA.....	.....IMAYDEHT.....			
ZP_01354047_C._phyto	.....YRLLEGA.....	.....ANSVL.....	.....LMTYEWGY.....			
ZP_01354926_C._phyto	.....RQEQGAV.....	.....LDYVI.....	.....IMAYDEHH.....			
NP_902406_C._violace	.....LRALGAA.....	.....ADYLQ.....	.....IMSYDEAI.....			
ZP_01136704_A._cellu	.....YPTIGRW.....	.....ADRVV.....	.....IMTYDQHS.....			
ZP_00526542_S._usita	.....LRQLAPY.....	.....VDFIS.....	.....LMTYDQHT.....			
AAF46212.1_D._melano	.....IREINLY.....	.....ADYVN.....	.....LMSYDFHF.....			
AAF46534.1_D._melano	.....VPAIINN.....	.....LDYVN.....	.....LHTYDFQT.....			
AAF46544.1_D._melano	.....VPKLNKY.....	.....LDWFN.....	.....VLTDFHS.....			
At4g19720_A._thalian	.....IREIKKK.....	.....LDWVN.....	.....LIAYDFYS.....			
At4g19750_A._thalian	.....VQAADN.....	.....LDFVN.....	.....IMAYDFYG.....			
EAA67655_G._zeae	.....LKKMDPW.....	.....VDAWH.....	.....LMAYDYAG.....			
EAA73155_G._zeae	.....MKEIGSV.....	.....LDHIN.....	.....LMAYDYAG.....			
EAA74986_G._zeae	.....LDKISNI.....	.....VDQIN.....	.....IMAYDYSG.....			
EAA74223_G._zeae	.....IRGMDRY.....	.....LDFWN.....	.....LMAYDYAG.....			
MGG_05533_M._grisea	.....FKAMDAS.....	.....LDFWS.....	.....IMAFDFAG.....			
MGG_01247_M._grisea	.....LEGMDKF.....	.....VDFWN.....	.....LMAYDYAG.....			
MGG_00086_M._grisea	.....LGQLAGV.....	.....VDKMY.....	.....LMAYDYAG.....			
MGG_07927_M._grisea	.....IAGMDPL.....	.....LDFWN.....	.....LMAYDYAG.....			
Chi18_6_H._jecorina	.....MPAIDRY.....	.....LDAWH.....	.....LMAYDYAG.....			
Chi18_5_H._jecorina	.....MADLGQV.....	.....LDYVN.....	.....LMXYDYAG.....			
Chi18_7_H._jecorina	.....VAGMDQY.....	.....LDFWN.....	.....LMAYDYAG.....			
04883_N._crassa	SS...MKEIGET.....	.....LDFMN.....	.....LMAYDYAG.....			
04554_N._crassa	.....LPGMDRY.....	.....LDFWN.....	.....LMAYDYAG.....			
11407_B._fuckeliana	.....LADMDKY.....	.....LDSWH.....	.....LMAYDYAG.....			
05350_B._fuckeliana	.....IYGMNQY.....	.....LDFWN.....	.....LMAYDYAG.....			
11700_S._sclerotioru	.....MADMDKY.....	.....LDSWH.....	.....LMAYDYSG.....			
11304_S._sclerotioru	.....VRSMNEY.....	.....LDFWN.....	.....LMAYDYAG.....			
08020_S._sclerotioru	.....LSEMDQY.....	.....VDFWN.....	.....FMAYDYSG.....			
01250_A._capsulatum	.....MAEMDVH.....	.....LDFWN.....	.....MMCXYDFAG.....			
05886_A._capsulatum	.....LEEMTPY.....	.....LDFYN.....	.....LMAYDYAG.....			
06565_A._capsulatum	.....LAEMTPY.....	.....LDFYN.....	.....LMAYDYSG.....			
05250_C._immitis	.....MAEMDPY.....	.....LDFWN.....	.....LMCYDFAG.....			
02795_C._immitis	.....LAEMDKY.....	.....LDFWN.....	.....LMAYDFSAG.....			
03822_C._immitis	.....LKEMGQD.....	.....LDFIN.....	.....IMAYDYAG.....			
AN5454_E._nidulans	.....LSSMDRY.....	.....LDFWN.....	.....LMAYDYSAG.....			
AN4871_E._nidulans	.....LQEMTPY.....	.....LDFYN.....	.....LMAYDYAG.....			
00269_P._nodorum	.....LGAMDKY.....	.....LDFWN.....	.....LMAYDYAG.....			
04870.1_C._cinereus	.....VAEMDQY.....	.....LDFWN.....	.....LMAYDYSAG.....			
09921.1_C._cinereus	.....VAQMDRA.....	.....MDYWN.....	.....LMAYDYAG.....			
124149_P._chrysospor	.....VREMDAV.....	.....LDFWN.....	.....MMAYDFSAG.....			
134311_P._chrysospor	.....VPQMDKA.....	.....LSYWN.....	.....LMAYDYAG.....			
03412_F._neoformans	.....VREMDQV.....	.....LDFWN.....	.....LMAYDFAG.....			
13635_R._oryzae	.....LREMOPY.....	.....VDLFY.....	.....LMAYDYAG.....			
UM04261_U._maydis	.....VAKMDQY.....	.....LDFWN.....	.....LMAYDFAG.....			
EAA69503_G._zeae	.....LMEIAEY.....	.....LDFIN.....	.....LMAYDFFG.....			
EAA70860_G._zeae	.....LPVVAHL.....	.....LDFLN.....	.....LMGYDFTG.....			
Chi18_3_H._jecorina	.....LARAAEY.....	.....LDYIN.....	.....LVAYDFFG.....			
Chi18_2_H._jecorina	.....LDAVSRI.....	.....IDYLN.....	.....LMAYDFTG.....			
03026_N._crassa	.....VRQAAEY.....	.....LDSIN.....	.....LMAYDYFG.....			
01594_B._fuckeliana	.....LYKAQDY.....	.....LDLIN.....	.....LMAYDFHG.....			
05897_S._sclerotioru	.....LYKAQDY.....	.....LDLIN.....	.....LMAYDFSAG.....			
04742_A._capsulatum	.....LVEAHLY.....	.....VDLIN.....	.....LMTYDFSAG.....			



04750_C._immitis	.....LIHAQCY.....	VDLIN.....	LMTYDFSG.....
04719_P._nodorum	.....LGHAAPHY.....	LDMIN.....	LMAYDYSG.....
MGG_08458_M._grisea	.....LGRAAAL.....	LDMLN.....	LMSYDFSG.....
CHT4_C._albicans	.....IQEMDKY.....	LTFWN.....	LMCYDFAGE.....
01119_L._elongisporu	.....IKVMDQY.....	LSFWN.....	LMAYDFSGL.....
XP_454053_K._lactis	.....ISEMSKY.....	VDIWN.....	MMCYDFHGE.....
CTS2_S._cerevisiae	.....ITEIDQY.....	VDYWN.....	MMTYDYYGS.....
246746_L._bicolor	.....VADMDSK.....	LDFTN.....	MMSYDFSG.....
03209_N._crassa	.....LPGMNPY.....	IDSWH.....	LMAYDYAG.....
14474_P._nodorum	.....MKEMDQY.....	VDNWN.....	LMAFDYQGG.....
CE06282_C._elegans	.....LNKIIES.....	VDFIN.....	AYSTDYYT.....
CE03547_C._elegans	.....IENIFDN.....	VDFLN.....	IFTMGYFG.....
CE03542_C._elegans	.....LDEIIDH.....	IDFMN.....	VYSMDYSG.....
CE15845_B_C._elegans	.....LDDIPEH.....	VDYIN.....	VYSMEKFS.....
CE02997_C._elegans	.....LVEFSNF.....	VDFLN.....	IYLFNSF.....
CE36953_C._elegans	.....LQQLMKY.....	CDFVN.....	VMSYDYFG.....
YP_432439_H._chejue	.....VMQITPY.....	LDYVN.....	IMTYDLHG.....
YP_529449.1_S._degra	.....AFEATQY.....	LDYVN.....	IMSYDLHG.....
YP_077582_B._licheni	.....TFKPLRY.....	VDYVN.....	IMSYDLHG.....
ChiI_S._coelicolor	.....TFQVQKY.....	LDYVN.....	IMSYDLHG.....
NP_902986_C._violace	.....TFQGLKY.....	LDFTN.....	VMSYDLHG.....
ZP_01159608_Photobac	.....TFDVTKY.....	LDYVN.....	IMSYDLHG.....
ZP_01234708_V._angus	.....TFDVTKY.....	LDYVN.....	IMSYDLHG.....
NP_233087_V._cholera	.....TFDVTKY.....	LDYVN.....	IMSYDLHG.....
NP_230718_V._cholera	.....DFAMQDV.....	LDYVN.....	IMSYDLHG.....
AAO07185_V._vulnific	.....TFDVTKY.....	LDYVN.....	IMSYDLHG.....
ZP_01354150_C._phyto	ET.FGIKEVSNT.....	VDYIN.....	LMAYDYVG.....
ZP_01246933_F._johns	ES.IDWKAVAPF.....	VNRIN.....	IMSYDLVN.....
YP_012734_L._monocyt	NG.IDVANLFKV.....	VDFAN.....	VMTYDLNG.....
YP_529337.1_A_S._deg	....KLAAIVEQ.....	LDFTN.....	LMTYDLNG.....
ChiA_A_P._kodakarae	R..IDWVEASKY.....	LDSIN.....	IMTYDYHG.....
AAG19274_Halobacteri	G..LDHAANAFA.....	LDFTN.....	VMTYDYHG.....
AAG19275_Halobacteri	L..INHREVAHV.....	VDDIY.....	MMAYDFTG.....
CE03543_C._elegans	.....LEEIMEH.....	VDFMN.....	VYSMDYSG.....
CE34961_C._elegans	.....FDDFMEY.....	IDFTN.....	VFSMDYYG.....
CE20043_C._elegans	.....LRTISSH.....	VDFFN.....	VHSMYYG.....
CE15845_A_C._elegans	.....LDEIIEH.....	VDFLN.....	VHSMDFAG.....
CE32863_A_C._elegans	.....LDEIIEH.....	VDFLN.....	VHSMDFAG.....
CE03544_C._elegans	.....LDAIQKH.....	VDFIN.....	VHSMYAK.....
CE08731_C._elegans	.....IEEIIIRH.....	VDFVN.....	VYSMDYAG.....
CE28638_C._elegans	.....IPDILKY.....	VDFVN.....	VFTMDYYG.....
CE32863_B_C._elegans	.....LDDIPEH.....	VDYIN.....	VYSMEKFS.....
CE01673_C._elegans	.....LED.QEN.....	ADSIN.....	LISMAEYE.....
CE02993_C._elegans	.....FEDFLKF.....	VDFFN.....	IYSTQFR.....
CE02996_C._elegans	.....LKDFSKE.....	VDFFN.....	IYSTQFR.....
CE02995_C._elegans	.....LMGFSKE.....	VDFFN.....	IYSIHYQ.....
CE02992_C._elegans	.....LKLLMNH.....	IDFTN.....	VLSINYFE.....
CE02999_C._elegans	.....WTEILEN.....	VDFIN.....	VITFEYFY.....
CE02998_C._elegans	.....MDGLLHY.....	VDFLN.....	VLTYGYAA.....
CE09229_C._elegans	.....LKGILKY.....	ADFTN.....	VMTYDYYG.....
CE12928_C._elegans	.....LKGILNY.....	ADFTN.....	VMTYDYYG.....
CE23907_C._elegans	.....FKQLVQD.....	VDFVN.....	IYSMDYYG.....
CE32917_C._elegans	.....IENIVAV.....	ADFTN.....	IYSMDYYG.....
CE34579_C._elegans	.....MNEIVEN.....	VDFIN.....	IFAMDYYG.....
CE25073_C._elegans	.....IENIFDN.....	VDFLN.....	IFTMGYFG.....
CE03548_C._elegans	.....ITSIVNN.....	VDFLN.....	IFTMGYFG.....
NP_469498_L._innocua	NG.VDVANLFKV.....	VDFAN.....	VMTYDLNG.....
CE08730_C._elegans	.....IEEIIER.....	VDFVN.....	VYSMNYYA.....
Q8U1H4_P._furiosus	.....H.....	VDFFN.....	VYSMDYAG.....
CE12474_C._elegans	.....LVEFLNS.....	VDFFG.....	IYLFNSY.....
CE02990_C._elegans	.....MNNIVQI.....	VDFIN.....	VFSLDYYG.....

CE40296_C._elegans	.....LV <del>E</del> FSNF.....	VDFIN.....	IYSFNSY.....
ChiB_S._marcescens	....KLAQIVAP.....	LDYIN.....	LMTYDLAG.....
O10363_O._pseudotsug	V..VKYDAAQRF.....	LDKIF.....	LMSYDFKG.....
AAP29899_C._fumifera	V..VQYDVAQKL.....	LDKIF.....	LMSYDFKG.....
AAV73807_B._mori_NPV	V..VNYAEAQKS.....	LDKIF.....	LMTYDFKG.....
AAL56186_H._zea_SNPV	A..VNYDRAQQY.....	LDKIF.....	VMSYDFKG.....
AAF33549_S._exigua_N	V..VNYTEAQKY.....	LDTIF.....	LMTYDFKG.....
AAZ38189_A._segetum_	V..VNYTEAQKY.....	LDTIF.....	LMTYDFKG.....
AAS82706_A._segetum_	I..VNYENAEY.....	LDHIF.....	VMTYDFKG.....
ZP_01159013_Photobac	D..VDYGEAIQY.....	MDYIF.....	AMTYDFYF.....
ZP_01161077_Photobac	R..VDYNQAQQY.....	MDHIF.....	LMSYDMFG.....
ZP_01159325_Photobac	...IDWVAVAPH.....	LTNMF.....	AMTYDYL.....
ZP_01160869_Photobac	G..IDWKKVSQD.....	LDQIF.....	LMSFDLFG.....
ZP_01233025_V._angus	D..VDYGEAIQY.....	MDYIF.....	AMTYDFYF.....
ZP_01236284_V._angus	R..VDYNQAQQY.....	MDHIF.....	LMSYDMFG.....
ZP_01235109_V._angus	...IDWAAVAPH.....	LTNMF.....	AMTYDYL.....
ZP_01235465_V._angus	G..IDWKKVSQD.....	LDQIF.....	LMSFDLFG.....
AAO08114_V._vulnific	D..VNYADAIQY.....	MDYIF.....	AMTYDFYF.....
AAO07498_V._vulnific	...IDWKAAPY.....	LTNMF.....	AMTYDFLFG.....
NP_232428_V._cholera	D..VNYGQAVQY.....	MDYIF.....	AMTYDFYF.....
YP_432951_H._chejuen	L..IDWPAAPHY.....	MDRLY.....	VMTYDLTG.....
YP_529337.1_B_S._deg	A..VDYASATTY.....	MDYIF.....	LMSYDYM.....
YP_435912_H._chejuen	S..VNYSTAVQY.....	MDYVF.....	AMTYDYY.....
ZP_01137509_A._cellu	L..IQTDKIGQY.....	LDFA.....	VMTYDMHG.....
ChiE_S._coelicolor	AG.WDLTRIFDS.....	LDYAN.....	VQGYDFHSGSD
ChiC_S._coelicolor	A..ADYGEASKY.....	IDWYN.....	VMTYDFFG.....
ChiD_S._coelicolor	A..ADYAGAAQY.....	VDWYN.....	PMTYDFFG.....
NP_903910_C._violace	N..TEPAAAYSSY.....	LDWIN.....	VMTYDFHG.....
YP_529072.1_S._degra	A..ADYGGAAQY.....	LD FYM.....	LMTYDFFG.....
ZP_01431615_S._tropi	A..ADYAGAAPN.....	LDWIM.....	AMTYDYF.....
ZP_01136287_A._cellu	L..LEVPOISRL.....	LDQMD.....	VMDYDFHG.....
01315.1_C._cinereus	....VAAFAKL.....	LDYIA.....	IMNYDLWG.....
03252.1_C._cinereus	....VSGFAEV.....	LDYIA.....	VMNYDVPV.....
05285.1_C._cinereus	....MSGFAEV.....	LDHLA.....	IMAYDIHG.....
05291.1_C._cinereus	....VSGFAEV.....	FD FIA.....	IMAYDVWG.....
01586.1_C._cinereus	....VSEFAAI.....	MNYIC.....	IMNYDVWG.....
128098_P._chrysospor	....VSGFAKV.....	LDYIA.....	IMDYDVFGP.....
39872_P._chrysospori	....VSGFSKV.....	LD FIT.....	IMNYDVWG.....
138098_P._chrysospor	....VSPFAAV.....	LDYVT.....	LM DYDVWG.....
129436_P._chrysospor	....ASAFAQV.....	LDWIL.....	IMNYDTWG.....
EAA71245_G._zeae	....LGGFADV.....	LDYLM.....	IMNYDLYG.....
MGG_04732_M._grisea	G..ALKPMGDL.....	LDYSI.....	IMGYDVFG.....
UM06190_U._maydis	....VARAAAA.....	MDYIM.....	IMNYDVWG.....
04245_F._neoformans	....VSEFAKV.....	LDWIL.....	IMNYDVWG.....
16170_R._oryzae	....FEPDWVTN.....	VDYFY.....	LMSY EYNG.....
01334_R._oryzae	....FESGWVSD.....	VDYFY.....	LMSY EYNG.....
13934_R._oryzae	....LDDGWSKY.....	MDAFY.....	IMAYDLNG.....
07611_R._oryzae	....ASGFVPY.....	VDRFH.....	VMTFDVNG.....
10252_R._oryzae	....VKEFVPY.....	FDHVN.....	IMTYDMNG.....
14659_R._oryzae	....VSGFAKV.....	LD RVN.....	VMTYDING.....
231399_L._bicolor	....MSGFSVV.....	LN FIS.....	VMNYDVWG.....
180319_L._bicolor	....VSAFADS.....	LDWIS.....	LMVYDVWG.....
191848_L._bicolor	....VSAFAEY.....	LDWIA.....	IMAYDVWG.....
317003_L._bicolor	....VSAYAAQ.....	MNFVN.....	IMNYDVWG.....
246840_L._bicolor	....VSAFGDV.....	LDYIT.....	VMNYDTGS.....
144643_L._bicolor	....VSDFADS.....	LDWVL.....	IMNYDVWG.....
310136_L._bicolor	....VSAFADV.....	LDHIA.....	IMNYDVWG.....
629882_M._xanthus	....WFTNLVPY.....	LDQMN.....	VMTYEMTGP.....
630509_A_M._xanthus	.....	.....	.....
YP_592598_Acidobacte	....VPALAPL.....	LD FIN.....	VMTYDFTG.....
YP_446903_S._ruber	AH.TNMAAAHTP.....	LDYVN.....	LMTYDFHG.....
ZP_00739282_B._thuri	H..TELKKISQI.....	LDWIN.....	IMTYDFHG.....

ZP_01245639_F._johns	KQYLGPNNRAQYGMTEDISTYCDYIT.....	YFGYDFGG.....
NP_976824_B._cereus	H...TELKKISQI.....LDWIN.....	IMTYDFHG.....
YP_077581_B._licheni	N...TELDKIAQT.....VDWIN.....	IMTYDFNG.....
631138_M._xanthus	NK.QETKKLSDV.....LDWIN.....	VMSYDYHG.....
ZP_01247029_F._johns	.....SSTFAA.....YDWIN.....	IMAYDATGP.....
ZP_01234549_V._angus	.....YLDVALNA.....FDTVH.....	LMTYDMQN.....
ZP_01160697_Photobac	.....YLDVALNA.....FDTVH.....	LMTYDMQN.....
ZP_01158584_Photobac	DF..YMDEALDV.....FDTVN.....	LMTYDMRN.....
AN0549_E._nidulans	.....IVKLQKS.....VDFFN.....	IMSYDLHG.....
AN8481_E._nidulans	.....IINLQDH.....VDFFN.....	IMSYDLHG.....
AN9390_E._nidulans	.....IKNMEPI.....LDWFN.....	IMSYDLHG.....
AN0517_E._nidulans	.....VDRMQKY.....VDYFN.....	LMSYDLHG.....
AN0541_E._nidulans	.....VSAMEKE.....VSWFN.....	LMSYDMRG.....
AN5077_E._nidulans	.....LKAMMEY.....VDWVN.....	LMSYDLHG.....
AN0509_E._nidulans	.....INSISKV.....VDYIV.....	FMTYDLHG.....
AN7613_E._nidulans	.....IEMWQH.....VDYLI.....	YMTYDFHG.....
07035_N._crassa	.....IVNLEKY.....VDWFN.....	VMSYDMHG.....
07484_N._crassa	.....IAQISKV.....VDYIV.....	LMCYDLHG.....
05317_N._crassa	.....LKQIGAV.....VDYIV.....	YMSYDGHG.....
EAA74768_G._zeae	.....IKKLERT.....VDFFN.....	IMSYDLHG.....
EAA78168_G._zeae	.....LDNIEPS.....VDWFN.....	VMSYDLHG.....
EAA75711_G._zeae	.....AKAMEPY.....VDFFG.....	FMAYDLHG.....
EAA68447_G._zeae	.....IKDIGKV.....VDYIV.....	YMTYDLHG.....
EAA77156_G._zeae	.....VTQIAPL.....VDYIV.....	YMTYDLHG.....
12510_S._sclerotioru	.....LKALAKS.....VSWFN.....	VMSYDLHG.....
00773_S._sclerotioru	.....LISIEPS.....VDWFN.....	YMAYDLHG.....
05454_S._sclerotioru	.....IKASAEA.....ADFN.....	IMAYDLHG.....
00677_S._sclerotioru	.....PINLEPY.....TTFFN.....	FMSYDLHG.....
02128_S._sclerotioru	.....ILELSLI.....VDYVI.....	YMTYDLHG.....
MGG_04534_M._grisea	.....LQKIEPH.....LDFFN.....	VMTYDIHG.....
MGG_01336_M._grisea	.....MQAMHPY.....LDTIG.....	LMSYDLRS.....
14527_P._nodorum	.....LAGLQPN.....VDWFN.....	LMSYDLHG.....
15411_P._nodorum	.....LKGLEAQ.....VDWLS.....	ILTYDLHG.....
02214_P._nodorum	.....LKA.VDY.....VDFVN.....	MMTYDLHG.....
04761_C._immitis	.....LKGMEY.....VDWFN.....	VMTYDIHG.....
04323_A._capsulatum	.....PINLEPY.....INFFN.....	FMSYDLHG.....
00533_B._fuckeliana	.....ILALSFV.....VDYIV.....	YMTYDLHG.....
Chi18_1_H._jecorina	.....VKDMAKY.....VDYFI.....	YMTYDLHG.....
Chi18_8_H._jecorina	.....EKASRSS.....S.....	LG.....
Chi18_10_H._jecorina	.....IADIKT.....VDYIV.....	YMTYDLHG.....
02650_A._capsulatum	.....LPSILES.....VDFFN.....	IMTYDLMN.....
AN0221_E._nidulans	.....IPSIAS.....VDFLN.....	VMTYDLMN.....
06020_N._crassa	.....VPRIMRH.....VDFLN.....	VMTYDMMN.....
EAA76014_G._zeae	.....VPRIMKE.....VNFLN.....	IMSYDLMN.....
Chi18_4_H._jecorina	.....VPSIVEH.....VDFIN.....	LMTYDMMN.....
09277_P._nodorum	.....IPRIMES.....IDFLN.....	VMTYDMMN.....
05838_A._capsulatum	.....GPAIWES.....VDFVNVLFNSNKPSTLTTFERMLTVLFKIMTYDLIN.....	
EAA69039_G._zeae	.....APLINKY.....VDFVN.....	VMTYDLMN.....
MGG_06594_M._grisea	.....VPKINAA.....VDFIN.....	VMAYDLMN.....
Chi18_11_H._jecorina	.....VAKINGI.....VNYVN.....	IMTYDLMN.....
02644_A_P._nodorum	.....GPKIWRS.....VDFIN.....	VMSYDLMN.....
AN9447_E._nidulans	.....GPKIWPS.....VDMIN.....	IMSYDLMN.....

	490	500	510	520	530	540
NP_979924_B._cereus	.... .... .... .... .... .... .... .... .... .... .... ....	QGG.....	PPMAISPIG.....			
YP_077302_B._licheni	.... .... .... .... .... .... .... .... .... .... .... ....	SGG.....	PPMAVSPIG.....			
YP_091539_B._licheni	.... .... .... .... .... .... .... .... .... .... .... ....	GTS.....	EPGPIAPIN.....			
YP_079121_B._licheni	.... .... .... .... .... .... .... .... .... .... .... ....	GTS.....	EPGPIAPIN.....			
YP_074366_S._thermop	.... .... .... .... .... .... .... .... .... .... .... ....	SGG.....	PPMAVSPID.....			
YP_075811_S._thermop	.... .... .... .... .... .... .... .... .... .... .... ....	VTG.....	PPMAIAPLR.....			

YP_075619_S._thermop	.WG.....	LPHGVPASLP.....		
ZP_01354047_C._phyto	.TYS.....	EPMAVAPIN.....		
ZP_01354926_C._phyto	.SKS.....	EEAGSVASIG.....		
NP_902406_C._violace	.PA.....	WDPGPVAGSD.....		
ZP_01136704_A._cellu	.AGSA.....	YPGGPISSIS.....		
ZP_00526542_S._usita	.RNT.....	PPGPVAGMT.....		
AAF46212.1_D._melano	.YRE.DTPFTG.....	LNAPLYARSQ.....	ER.....	S
AAF46534.1_D._melano	.PER.NNEVAD.....	FPAPIYELNE.....		
AAF46544.1_D._melano	.SHE.PS..VN.....	HHAPLYSLEEDSEY.....		N
At4g19720_A._thalian	.S...ST.TIG.....	PPAALFDPSN.....		
At4g19750_A._thalian	.PGW.SP.VTG.....	PPAALFDPSN.....		
EAA67655_G._zeae	.PWDST.....	TGHQANVFAS.....	RKSP.....	LAT
EAA73155_G._zeae	.AWSAF.....	SGHQANKYAN.....	AKIP.....	NAT
EAA74986_G._zeae	.SWDSA.....	SGHNANLFPY.....	KAST.....	N
EAA74223_G._zeae	.SWDQT.....	AGHQANLYPS.....	HDNP.....	VST
MGG_05533_M._grisea	.SWDNT.....	TGHQANVYPG.....	PD.....	LTT
MGG_01247_M._grisea	.SWDTT.....	TGHQSNLYLD.....	DQNK.....	VAT
MGG_00086_M._grisea	.AWDAT.....	SGHQANLFPS.....	GSNP.....	TST
MGG_07927_M._grisea	.SWDQT.....	AGHQANLFPS.....	HGNP.....	TST
Chi18_6_H._jecorina	.SWDDL.....	SGDQSNVFHD.....	ATNP.....	HRT
Chi18_5_H._jecorina	.SWSNA.....	SGHDANLYHN.....	PQNP.....	NAT
Chi18_7_H._jecorina	.SWDQT.....	SGHQANLHPS.....	YDNP.....	AST
04883_N._crassa	.AWDKK.....	AGHQANLYPD.....	EKNP.....	DTT
04554_N._crassa	.SWDQV.....	AGHQANLFHC.....	NSNP.....	AAT
11407_B._fuckeliana	.SWDNV.....	TGHMANLNPS.....	VNNN.....	SST
05350_B._fuckeliana	.SWDGV.....	AGHQANVLAS.....	HNNP.....	SST
11700_S._sclerotioru	.SWDNT.....	TAHNANLYPS.....	VLNP.....	KST
11304_S._sclerotioru	.SWDSV.....	AGHQANLHPS.....	ESNP.....	DST
08020_S._sclerotioru	.PWSTV.....	SAHQANLSPS.....	GNG.....	ST
01250_A._capsulatum	.SWDSK.....	AGHMANVFPS.....	KSVP.....	EST
05886_A._capsulatum	.SWDTV.....	AGHQANLEVS.....	KSDP.....	KST
06565_A._capsulatum	.SWDTI.....	AGHQSNIEPS.....	KSNP.....	KST
05250_C._immitis	.SWDST.....	AGHMANVFPS.....	QSSP.....	EST
02795_C._immitis	.SWDKV.....	SGHMSNVFPS.....	TTKP.....	EST
03822_C._immitis	.SWSTM.....	AGHQANLRPS.....	MSNP.....	QST
AN5454_E._nidulans	.SWDTI.....	TGHMANLFAS.....	RQNP.....	AST
AN4871_E._nidulans	.SWDQT.....	AGHQANLYPS.....	TSNP.....	TST
00269_P._nodorum	.SWDAN.....	AGHQANFNPS.....	GNNA.....	IST
04870.1_C._cinereus	.SWDRT.....	ANHQANLLG.....	P.....	
09921.1_C._cinereus	.SWLTW.....	ADNQANFYGG.....	AR.....	T
124149_P._chrysospor	.SWDSI.....	ANHQANLFG.....	G.....	
134311_P._chrysospor	.SWLTY.....	ADNQANLYGG.....	AR.....	T
03412_F._neoformans	.SWDSV.....	AGHQANLYSD.....	KP.D.....	
13635_R._oryzae	.SWDRV.....	AGHQAAVFG.....	G.....	
UM04261_U._maydis	.SWSAL.....	TGHQANLWNI.....	KG.A.....	
EAA69503_G._zeae	.SWTPK.....	AGHHAQLYAM.....	DK.....	EET
EAA70860_G._zeae	.GWTDV.....	CGHHAQLLPP.....	S.QNLN.....	EVYPTL
Chi18_3_H._jecorina	.TWTSK.....	SGHHAQLYTL.....	NK.....	DEP
Chi18_2_H._jecorina	.SWTKV.....	CGNHAQLCSP.....	G.TRLQ.....	STHPCL
03026_N._crassa	.SWSHR.....	SGHHSQLYAM.....	NK.....	EEA
01594_B._fuckeliana	.SWSQK.....	SGHHAQLYPG.....	NM.....	PDA
05897_S._sclerotioru	.SWSHK.....	SGHHAQLYPG.....	NL.....	QDA
04742_A._capsulatum	.PWMPL.....	SGHHAQLYAP.....	PDPQKAAL	EATATTTST
04750_C._immitis	.PWTPH.....	SGHQSQLFSP.....	HTPH.....	SEAA
04719_P._nodorum	.PWTSK.....	CGHQAQLFTP.....	QIPH.....	SPEA
MGG_08458_M._grisea	.PWAKV.....	SAHHAQLRHP.....	QPARLPP.....	QADGCL
CHT4_C._albicans	.GWSSK.....	TAFHSNLFNG.....	N.....	GDN
01119_L._elongisporu	.GWSEK.....	VGYHSNLFNG.....	N.....	GDN
XP_454053_K._lactis	.WSDV.....	TGYHSNLYLQ.....	GHSRRSLSN.....	RISNS
CTS2_S._cerevisiae	.WSET.....	TGYHSNLF.....		SET
246746_L._bicolor	.SWDSI.....	ANHQANIYG.....	G.....	
03209_N._crassa	.SWDST.....	TGHQANLLPS.....	PKNL.....	LTT



14474_P._nodorum	.GFSNF.....TGHQSNVYAS.....KTNP.....KTTDGWDSVLG
CE06282_C._elegans	.PLADNLSLSD.....DIAGPSAPIYFGAQ.....
CE03547_C._elegans	.PWQNDAG.....MITGAASQLFNGVNGVP.....
CE03542_C._elegans	.PWDNKWG.....TPTGPSAPMNYNIG.....
CE15845_B_C._elegans	....S.....LIGP.LPLYSGHEP.....
CE02997_C._elegans	.....L.....NQIGPDSPLYGGGSR.....
CE36953_C._elegans	.AWASKWG.....AYTGPPAPLQFAMPKKF.....
YP_432439_H._chejuen	.AWN.....QFVGPNAALYDTGEDV.....
YP_529449.1_S._degra	.AWN.....QFVGPNAALFDNGQDA.....
YP_077582_B._licheni	.AWN.....EFVGPNASLFDNGEDA.....
ChiI_S._coelicolor	.AWN.....EYVGPNASLFDGGRDA.....
NP_902986_C._violace	.AWN.....RFVGPNAALYDDGKDA.....
ZP_01159608_Photobac	.AWN.....DHVGHNAALFDTGKDS.....
ZP_01234708_V._angus	.AWN.....DHVGHNAALFDTGKDS.....
NP_233087_V._cholera	.AWN.....DHVGHNAALYDTGKDS.....
NP_230718_V._cholera	.TWN.....EFVGPQAALFDGKDA.....
AAO07185_V._vulnific	.AWN.....DHVGHNAALYDTGDS.....
ZP_01354150_C._phyto	.PWSR.....VTGHHSNLMCE.....KEAPN.....
ZP_01246933_F._johns	.GYSK.....VTGHTPLYST.....N.....PK.....
YP_012734_L._monocyt	.AWTP.....NSAHTTALYGN.....PKDPN.....
YP_529337.1_A_S._deg	.PWNGVTK.....TNFHAHLYGNQEPFRFYNALREADLG.....LTWEEIVERFP
ChiA_A_P._kodakarae	.AWETI.....TGH LAPLYC.....D.....PNAPYTDENV.....
AAG19274_Halobacteri	.AFNDY.....TNHQAPLYG.....T.....EADPSPNAD.....
AAG19275_Halobacteri	.VWHGT.....AGLNAPIYG.....T.....PPDYPPSGD.....
CE03543_C._elegans	.PWDNQWG.....TPTGPSAPLAFNIG.....
CE34961_C._elegans	.PWPNQWG.....TPTGPSAPLYGGIG.....
CE20043_C._elegans	.PWPNEWG.....KPTGPISPLY.....G.....
CE15845_A_C._elegans	.PWANQYG.....VPTGPSAPMC.....
CE32863_A_C._elegans	.PWANQYG.....VPTGPSAPMCGGFG.....
CE03544_C._elegans	.PLPNQWG.....TPTGPSASMNFNIG.....
CE08731_C._elegans	.PWDNQWG.....TPTGPSAPLYGGLD.....
CE28638_C._elegans	.PSD...G.....STGPLSPLYSG.....
CE32863_B_C._elegans	....S.....LIGP.LPLYSGHEP.....
CE01673_C._elegans	.N.....QLFGSGGVIRISEA.....
CE02993_C._elegans	.....E.....KQVGPDSPLYGGEGR.....
CE02996_C._elegans	.....E.....KQVGPDSPLYGGEGR.....
CE02995_C._elegans	.....S.....RQVGPPSSPLYGGGSR.....
CE02992_C._elegans	.PLP.GN.G.....ANIGPISPLYGGQRG.....
CE02999_C._elegans	.....E.A.....NKIGPISPLYGGSFG.....
CE02998_C._elegans	.PWSGVN.G.....KFVGPNAPLYGGNRE.....
CE09229_C._elegans	.AWESKW.G.....AYTGTAPPLYFGSLKG.....
CE12928_C._elegans	.AWESKW.G.....AYTGTAPPLYFGSLKG.....
CE23907_C._elegans	.PWPDDLAG.....DTTGPSAPIFGCPW.....
CE32917_C._elegans	.PWKNPYG.....NPTGPISPIYNGAQ.....
CE34579_C._elegans	.PWASGWG.....NPTGPISPIYGGSE.....
CE25073_C._elegans	.PWQNDAG.....MITGAASQLFNGVNGVP.....
CE03548_C._elegans	.PWPNPKG.....MITGATSQLFYGVNGVL.....
NP_469498_L._innocua	.AWTP.....NSAHTTALYGN.....PKDPN.....
CE08730_C._elegans	.PWSNQWG.....TPTGPSAPLYGGLD.....
Q8U1H4_P._furius	.....
CE12474_C._elegans	.PWPNQWG.....VPTGPSSPMFYNIG.....
CE02990_C._elegans	.....S.....YQVGPDSPLYGGGSR.....
CE40270_C._elegans	.PTQNDFG.....KITGPTAPMFNGVP.....
CE40296_C._elegans	.....L.....YQVGPDSPLYGGGSR.....
ChiB_S._marcescens	.PWEKIT.....NHQAALFGDAAGPTFYNALREANLG.....WSWEELETRAFF
O10363_O._pseudotsug	.AWSNT.....DLGYQTTLTYAP.....SWNA.....
AAP29899_C._fumifera	.AWSNT.....DLGYQTTLTYAP.....SWNP.....
AAV73807_B._mori_NPV	.AWSNT.....DLGYQTTVYAP.....SWNS.....
AAL56186_H._zea_SNPV	.AWSNT.....DLGHQTALYGS.....AWKP.....
AAF33549_S._exigua_N	.AWSNT.....ELGHQTALFAP.....TWRP.....
AAZ38189_A._segetum	.AWSNT.....DLGHQTALFAP.....AWRP.....
AAS82706_A._segetum	.AWSNT.....DLGYHTTLYSP.....SWNA.....

ZP_01159013_Photobac	.GWN	VPGHQTALYCG	NFMRPGQCDGTGLDENGEP
ZP_01161077_Photobac	.AWNND	NLGHQSGLYNG	SHQP
ZP_01159325_Photobac	.GWGT	QTGHLTNLHAT	DNGW
ZP_01160869_Photobac	.SWGP	TVGHHSNLYST	PLTP
ZP_01233025_V._angus	.GWN	VPGHQTALYCG	NFMRPGQCDGTGLDENGEPY
ZP_01236284_V._angus	.AWNND	NLGHQSGLYNG	SHQP
ZP_01235109_V._angus	.GWGT	QTGHLTNLHAT	DNGW
ZP_01235465_V._angus	.SWGP	TVGHHSNLYST	PLTP
AAO08114_V._vulnific	.GWN	VPGHQTALYCG	NFMRPGQCDGTGVDENGVPY
AAO07498_V._vulnific	.GWGQ	QTGHTTNLHAT	ERSW
NP_232428_V._cholera	.GWN	VLGHQTALYCG	SFMRPGQCDGKGVDENGEPY
YP_432951_H._chejuen	.AWER	ELSNHTPMQVN	PSAQ
YP_529337.1_B.S._deg	.AWAN	TTGHHTPLYNN	NEER
YP_435912_H._chejuen	.GWN	QLGHQTGLYAG	DHEI
ZP_01137509_A._cellu	.AWDATG	PTNFQDPLFESPND	PSTPVPPGS
ChiE_S._coelicolor	NSWEPD	RTGHASNLHT	D.AEDPYP
ChiC_S._coelicolor	.AWAKNG	PTAPHSPLTA	Y.DGIPQQG
ChiD_S._coelicolor	.AWDATG	PTAPHSPLTS	Y.SGIPKED
NP_903910_C._violace	.GWDAKG	PTNFQSNLYR	D.PAAPVTGDQ
YP_529072.1_S._degra	.AFNPQG	PTAPHSPLYN	Y.PGMPIEG
ZP_01431615_S._tropi	.AFSPQG	PTAPHSPLYS	Y.AGIPQQG
ZP_01136287_A._cellu	.PWEAHG	PTDFQSELYP	SA.AEVAVIGSA
01315.1_C._cinereus	.PWSPTVGPNA	PLDDACAPANS	
03252.1_C._cinereus	.NPSVGAGSRS	PLDDTCAPAGA	
05285.1_C._cinereus	.NWLQVGPNA	PLRGSCPAS	
05291.1_C._cinereus	.AWSPTVGPNA	PLQDSCAAN	
01586.1_C._cinereus	.ASGTPGPNA	PYGNLCGTSKQ	
128098_P._chrysospor	.GWSKVAGPNA	PLNDTCAPSGQ	
39872_P._chrysospori	.SWSSAVGPNS	PLNDTCAAAAN	
138098_P._chrysospor	.AWSPAVGPNA	PLADACAAPEH	
129436_P._chrysospor	.SASPPGPNA	PLSNACHNSTQ	
EAA71245_G._zeae	.GWSNVAGPNA	ALYSSCDERN	
MGG_04732_M._grisea	.AWAPTGGPNA	PLEQACDPRN	
UM06190_U._maydis	.SSSNPGPNA	PLANLCGNSTQ	
04245_F._neoformans	.SSSTPGPNA	PLSDGCGNSTQ	
16170_R._oryzae	.NWNVAGPNA	ALWGSSHWG	
01334_R._oryzae	.NWNVAGPNA	ALRGSSRGWG	
13934_R._oryzae	.IFSQNSSANA	PLEISNMTNP	
07611_R._oryzae	.AWNSTSGPNA	PFHNTPGWG	
10252_R._oryzae	.AWASTTGPNA	PFKYLEGKG	
14659_R._oryzae	.AWNATGPNA	PLNAPQGQ	
231399_L._bicolor	.HWSNSVGPNA	PLDDTCAAPEY	
180319_L._bicolor	.SWSDVVGPNA	PLADSCAAANL	
191848_L._bicolor	.SWSTAVGPNA	PLGDSCAPS	
317003_L._bicolor	.ASSTPGPNA	PLGNLCGTSKQ	
246840_L._bicolor	.NPSFVGVPNS	PLDDLCAVSG	
144643_L._bicolor	.SSSPPGPNS	PLHDGCGNSTQ	
310136_L._bicolor	.SFSPTVGPNS	PLDDSCAPT	
629882_M._xanthus	.WGGWLSWYTS	ALTGEAGNH	
630509_A.M._xanthus			
YP_592598_Acidobacte	.PWMDEAGLNS	PLYQDPNDPE	
YP_446903_S._ruber	.GWSDH	TGHLANLYP	PAAPDT
ZP_00739282_B._thuri	.GWEAT	SNHNAALYK	D.PNDPAANTN
ZP_01245639_F._johns	.NWYDK	TCYNAPLYASGN	PNDPLYG.A
NP_976824_B._cereus	.GWEAT	SNHNAALYK	D.PNDPAADTK
YP_077581_B._licheni	.GWQSI	SAHNAPLFY	D.PKAKEAGVPN
631138_M._xanthus	.AFEST	VNFHSALHR	V.TGDPGAATG
ZP_01247029_F._johns	.W	PGNPGQHSP	
ZP_01234549_V._angus		EDHSS	
ZP_01160697_Photobac		EDHSS	
ZP_01158584_Photobac		EDHSS	
AN0549_E._nidulans	.AWDSNSKWL	EPQLNAHTN	

AN8481_E._nidulans	.AWDQNNKWL.....EPQLNSHTN.....
AN9390_E._nidulans	.TWDGTNPYL.....GPYINSHTN.....
AN0517_E._nidulans	.MWDQDSKWT.....GPYLQGHSTN.....
AN0541_E._nidulans	.KWDQFNEWT.....GPYVFGHTN.....
AN5077_E._nidulans	.TWDSEN.PI.....GNQILAHSTN.....
AN0509_E._nidulans	.QWDAANPNSQDQCP.....SGNCLRSQVN.....
AN7613_E._nidulans	.QWEYETSFIQDWCN.....GGNCLRSHV.....
07035_N._crassa	.SWDIDNKWT.....GPYANSHSN.....
07484_N._crassa	.QWDYGNKWSQEGCA.....NGNCLRSHVN.....
05317_N._crassa	.QWDAGNRFSQEGCD.....TGNCLRSQVN.....
EAA74768_G._zeae	.VWDQHAWT.....KPYLNAHTN.....
EAA78168_G._zeae	.AWDVGNKWT.....GAFVGAHTN.....
EAA75711_G._zeae	.FWDEDVRTL.....GKIIRGQAD.....
EAA68447_G._zeae	.QWDTENSHSQEGCV.....FGNCLRSQVN.....
EAA77156_G._zeae	.QWDYGNPTINSQCP.....DGNCLRSHVN.....
12510_S._sclerotioru	.TWDKGNKWT.....GAFLNTHSTN.....
00773_S._sclerotioru	.TWDIGNEWT.....GAILDAHTN.....
05454_S._sclerotioru	.IWDANN.PI.....GSTVLAHSN.....
00677_S._sclerotioru	.PWESTNPSL.....GAYIRPQTS.....
02128_S._sclerotioru	.QWDYGSASFSDASCP.....AGNCLRSGAN.....
MGG_04534_M._grisea	.VWDKTVNSI.....GPYAFAHSTN.....
MGG_01336_M._grisea	.FEYSTDG.....LIRAQTD.....
14527_P._nodorum	.IWDAQSKAI.....GPYIAPHSTN.....
15411_P._nodorum	.....GKPF.....
02214_P._nodorum	.AWDATTPL.....GPKIRPHTD.....
04761_C._immitis	.VWDRDN.PI.....GSHIYGHSN.....
04323_A._capsulatum	.TWDGNSKWT.....QSVVNPHSTN.....
00533_B._fuckeliana	.PWEASNPA.....GAFVRPQTS.....
Chi18_1_H._jecorina	.QWDYINKYASPGCPSYDQGLGNCLRSHVN.....
Chi18_8_H._jecorina	.QWDVENKWAIPSC.....GGNCLRSHVN.....
Chi18_9_H._jecorina	.QWDVGNTWAMSECP.....SGNCLRSHVN.....
Chi18_10_H._jecorina	..EAYLHLNLQ.G.....KG.....IVN.....
02650_A._capsulatum	.....LR.....DTVTKHHTG.....
AN0221_E._nidulans	.....RR.....DTVTKHHTG.....
06020_N._crassa	.....RR.....DTVTKHHTG.....
EAA76014_G._zeae	.....RR.....DNTTVHHS.....
Chi18_4_H._jecorina	.....RR.....DSYVKHHS.....
09277_P._nodorum	.....RR.....DNVTKHAG.....
05838_A._capsulatum	.....RR.....DNVTAHHTS.....
EAA69039_G._zeae	.....RR.....DHYTTHVS.....
MGG_06594_M._grisea	.....RR.....DNVTLPHTD.....
Chi18_11_H._jecorina	.....RR.....MNETTHHTS.....
02644_A_P._nodorum	.....RR.....DNVTKHHS.....
AN9447_E._nidulans	.....RR.....NNETKHHTG.....

	550	560	570	580	590	600
NP_979924_B._cereus	.... .... .... .... .... .... ....	PVKEVLQ.....YA.....	KSQMPPQ.....			
YP_077302_B._licheni	.... .... .... .... .... .... ....	PVRDVIE.....YA.....	LTEMPAS.....			
YP_091539_B._licheni	.... .... .... .... .... .... ....	EVROTIQ.....FA.....	LRHVPKE.....			
YP_079121_B._licheni	.... .... .... .... .... .... ....	EVROTIQ.....FA.....	LRHVPKE.....			
YP_074366_S._thermop	.... .... .... .... .... .... ....	QVRRVLE.....FA.....	VTQIPRE.....			
YP_075811_S._thermop	.... .... .... .... .... .... ....	QVRQVLD.....YA.....	VSAIPPE.....			
YP_075619_S._thermop	.... .... .... .... .... .... ....	WVERVVA.....YA.....	VTQIPPE.....			
ZP_01354047_C._phyto	.... .... .... .... .... .... ....	KVREVLD.....FA.....	VTQIPVD.....			
ZP_01354926_C._phyto	.... .... .... .... .... .... ....	FLQKAIE.....DT.....	LLQVPKE.....			
NP_902406_C._violace	.... .... .... .... .... .... ....	WMEDDL.....YA.....	VERVPAA.....			
ZP_01136704_A._cellu	.... .... .... .... .... .... ....	WVQTILN.....FA.....	VTVIPPR.....			
ZP_00526542_S._usita	.... .... .... .... .... .... ....	WVEKLAA.....YA.....	ESQMPKA.....			
AAF46212.1_D._melano	LMATFNINYTVQW.....WL.....	KSGLEPQ.....				
AAF46534.1_D._melano	RNPEFNVNYQVKY.....WT.....	GNRAPAA.....				
AAF46544.1_D._melano	YDAELNIDYSIKY.....YL.....	KAGADRD.....				

At4g19720_A._thalian	.PKGPCGDYGLKE...	WI.....	KAGLPAK.....
At4g19750_A._thalian	.PAGRSGDSGLSK...	WL.....	EAKLPAK.....
EAA67655_G._zeae	...KLSTDATIND...	YIAA.....	G.VSPN.....
EAA73155_G._zeae	...PFNTDQAVSA...	YVGG.....	G.VPSG.....
EAA74986_G._zeae	...PYNSDKAIND...	YIDA.....	G.VPAE.....
EAA74223_G._zeae	...PFSTSAAIDF...	YVRS.....	G.VSPS.....
MGG_05533_M._grisea	...KASIDVAVSD...	YVKA.....	G.VAPG.....
MGG_01247_M._grisea	...KFSTEKAVQD...	YFAR.....	G.IDAA.....
MGG_00086_M._grisea	...PFSTDRAVAD...	YMAA.....	G.VPPS.....
MGG_07927_M._grisea	...PFSTDAIAAH...	YASQ.....	G.VALD.....
Chi18_6_H._jecorina	...RANSDDQAVND...	YVAA.....	G.VNPE.....
Chi18_5_H._jecorina	...PFNTDDAVKA...	YING.....	G.VPAS.....
Chi18_7_H._jecorina	...PFSTDAAIDY...	YTRS.....	G.VAPS.....
04883_N._crassa	...PFSTDRAVTD...	YIKF.....	G.IPSN.....
04554_N._crassa	...PFSTQRAVEY...	YLST.....	G.VAAD.....
11407_B._fuckeliana	...PYSTQRAITD...	YIAK.....	G.VSVS.....
05350_B._fuckeliana	...PYNTEHAVRA...	YEAK.....	G.VRSH.....
11700_S._sclerotioru	...PFSTQRAIVD...	YVAK.....	G.VPIS.....
11304_S._sclerotioru	...PFNTEHAVRA...	YEAR.....	G.VQGH.....
08020_S._sclerotioru	...PFNTQTGISY...	YIAH.....	G.ITSa.....
01250_A._capsulatum	...PFNADEAVTA...	YIAG.....	G.VHPK.....
05886_A._capsulatum	...PYSTEAAALDF...	YIGV.....	GKVPAS.....
06565_A._capsulatum	...PFSTKEAVDY...	YLGv.....	GNVPPS.....
05250_C._immitis	...PFSADIAVSA...	YISA.....	G.IHPG.....
02795_C._immitis	...PFSSDKAVKD...	YIKA.....	G.VPAN.....
03822_C._immitis	...SFSTEALDY...	YINT.....	GGIPAS.....
AN5454_E._nidulans	...PFNTHTAVTA...	YLAA.....	G.IPAS.....
AN4871_E._nidulans	...PFNTVQAVNH...	YIDA.....	GGVPSN.....
00269_P._nodorum	...PFNTQQALKD...	YAAA.....	G.VPLN.....
04870.1_C._cinereus	...PINTHEALEF...	YVSG.....	G.VASH.....
09921.1_C._cinereus	...GYSTDAAALKW...	YISQ.....	G.ATKS.....
124149_P._chrysospor	...PISASQAINW...	YIEQ.....	G.VPRH.....
134311_P._chrysospor	...GVSTDAAVKW...	YLSQ.....	G.ASAG.....
03412_F._neoformans	...GQSVDRSVRF...	YLEA.....	G.VHPT.....
13635_R._oryzae	...PLHTDQAVSH...	YLAA.....	G.IPAH.....
UM04261_U._maydis	...PPSADDSINY...	YIGQ.....	G.VVSH.....
EAA69503_G._zeae	...S..ASSGVSy...	LMSK.....	G.FPPK.....
EAA70860_G._zeae	...RKSCQRGVDF...	LIAN.....	G.FPRH.....
Chi18_3_H._jecorina	...S..ASSGVAY...	LMAQ.....	G.FPAK.....
Chi18_2_H._jecorina	...QACATDGVdY...	ILSR.....	G.FPSR.....
03026_N._crassa	...S..GASSVQY...	LMAS.....	A.VPGK.....
01594_B._fuckeliana	...AN.GSAAVDY...	VVST.....	G.FPAS.....
05897_S._sclerotioru	...AN.GSAAVDY...	VIST.....	G.FPAS.....
04742_A._capsulatum	...TASGSSGVAY...	LLSW.....	G.VPAG.....
04750_C._immitis	...GISCHSGISY...	VLAQ.....	G.VPSS.....
04719_P._nodorum	...AISGHSAVSY...	LVRQ.....	G.VPTH.....
MGG_08458_M._grisea	...RLSAMQAVSY...	MIVH.....	G.VHPG.....
CHT4_C._albicans	...SLNASDVVQT...	YIN.....	KGVHPT.....
01119_L._elongisporu	...DMCADSIVKA...	YTK.....	HGVSPQ.....
XP_454053_K._lactis	...SLSSDTAVKL...	MTDR.....	HNISSR.....
CTS2_S._cerevisiae	...ELNGNFAMHY...	MIDR.....	FGVNSR.....
246746_L._bicolor	...AISAHEALTW...	YIGQ.....	G.VARN.....
03209_N._crassa	...RFNTDQAVRD...	FVRR.....	G.IPAN.....
14474_P._nodorum	KFMFPNTKEAIDY...	YKAN.....	V.ASPC.....
CE06282_C._elegans	GKSERNVHHTARN...	YS.....	CLT.KQAS.....
CE03547_C._elegans	GRKTYNIHSTER...	YV.....	CKT.GQSD.....
CE03542_C._elegans	PRKHFTVDWTMKY...	YA.....	CKT.RQPN.....
CE15845_B_C._elegans	.QINFNVARIMDG...	YT.....	SNNEKHAK.....
CE02997_C._elegans	....IVDENMKY...	YI.....	CKS.GQPS.....
CE36953_C._elegans	SG.RMNVHATMKD...	YS.....	CQI.KATD.....
YP_432439_H._chejuen	ELKAWNYYNTSQYQRIGYLNTDWAYKY...		FRGTMQAG.....
YP_529449.1_S._degra	ELIQWNAYG.GQYKNIGYLNTDWAYHY...		FRGAMPAG.....



YP_077582_B._licheni	ELKQSNIIYTTPEYEGIGYLNTDWAYHY.....	FRGAVESG.....
ChiI_s._coelicolor	ELAAANVYGSAQYGGIGYLNTDWAYHY.....	FRGSMPAG.....
NP_902986_C._violace	ELAFWNVYSTPQYGNIGYLNTDWAYHY.....	YRGGLPAS.....
ZP_01159608_Photobac	ELAQWNVYGTAAAYGGIGYLNTDWAYHY.....	FRGSMPAG.....
ZP_01234708_V._angus	ELAQWNVYGTAAAYGGIGYLNTDWAYHY.....	FRGSMPAG.....
NP_233087_V._cholera	ELAQWNVYGTAAQYGGIGYLNTDWAYHY.....	FRGSMPAG.....
NP_230718_V._cholera	ELAKWGVYTTAEYQGGIGYLNQAWTHHF.....	FRGAFKPS.....
AAO07185_V._vulnific	ELAQWNVYGTAAQYGGIGYLNTDWAYHY.....	FRGSMPAG.....
ZP_01354150_C._phyto	HIS...TYQVIQN...YLK.....	VC.NP.E.....
ZP_01246933_F._johns	EES...TDRAVEF...LLK.....	QG.VPAE.....
YP_012734_L._monocyt	YDSGFSVDQTVKY...LKE.....	KG.AVSN.....
YP_529337.1_A.S._deg	SPFELTVDAAIKQ...HLMMD.....	IPRE.....
ChiA_A.P._kodakarae	.KYHFCVNYTVQW...YIQH.....	V.PDKT.....
AAG19274_Halobacteri	...EFYVDASMSF...WLDT.....	A.FDPA.....
AAG19275_Halobacteri	.AQQYTLLETTLTI...WKEQGYWVDWMEWEDHGPV.DDPG.....	
CE03543_C._elegans	PRKNFNVDTMKY...YS.....	CKT.QQPG.....
CE34961_C._elegans	VKKHFNVDSTMKY...YT.....	CMT.EDPS.....
CE20043_C._elegans	PTRH.NVDWTLRY...YA.....	EKT.GEPG.....
CE15845_A.C._elegans	.....	DPS.....
CE32863_A.C._elegans	ARKNFNVHHTMKY...YV.....	EKI.EDPS.....
CE03544_C._elegans	LRQHYNVDWTMKH...YT.....	CEL.KKPS.....
CE08731_C._elegans	ARRNFNVDTIKS...YI.....	RNI.RRPE.....
CE28638_C._elegans	.....	
CE32863_B.C._elegans	.QINFNVARIMDG...YT.....	SNNEKHAK.....
CE01673_C._elegans	....FNTAWEMKY...HA.....	CNS.NQSS.....
CE02993_C._elegans	....NIDETMKY...YT.....	CKT.GQPS.....
CE02996_C._elegans	....NIDETMKY...YI.....	CKT.GQPS.....
CE02995_C._elegans	....NIDETMKY...YI.....	CRT.GQPS.....
CE02992_C._elegans	....NVDDTLKY...LT.....	CIT.KRPS.....
CE02999_C._elegans	....NVDDTLKY...LI.....	CRT.RTPN.....
CE02998_C._elegans	....NVDETMQY...LI.....	CKT.RTPS.....
CE09229_C._elegans	FSGKLNADFSMKF...YA.....	CKT.EKPS.....
CE12928_C._elegans	FSGKLNADFSMKF...YA.....	CNT.KKPS.....
CE23907_C._elegans	KKGAYNVHHSKI...YS.....	CRT.KKSS.....
CE32917_C._elegans	GREAYNVHSSALT...YS.....	CKV.KQSK.....
CE34579_C._elegans	RREQWNVDTAAI...YS.....	CET.MRSS.....
CE25073_C._elegans	GRKTYNIHHSER...YV.....	CKT.GQSD.....
CE03548_C._elegans	GRRNYNIHHSVQS...YV.....	CKT.DQSN.....
NP_469498_L._innocua	YNSGFSVDQTVKY...LKE.....	KG.AVSN.....
CE08730_C._elegans	ARRKFSVDYTMKY...YI.....	RYT.RKPE.....
Q8U1H4_P._furiosus	.....	
CE12474_C._elegans	ARKNFYVDWTMKH...YT.....	CKL.KQPS.....
CE02990_C._elegans	....NVDEIMKY...YI.....	CKT.GQPS.....
CE40270_C._elegans	GRETFNVDDTSKV...LS.....	CET.MQSN.....
CE40296_C._elegans	....NVDEIMKY...YI.....	CKT.GQPS.....
ChiB_s._marcescens	SPFSLTVDAAVQQ...HLMMEG.....	VPSA.....
O10363_O._pseudotsug	.NELYTTDHAVKL...LTG.....	QG.VAAH.....
AAP29899_C._fumifera	.NELYNTDHAVKL...LTN.....	QG.VDPR.....
AAV73807_B._mori_NPV	.EELYTTHYAVDA...LLE.....	QG.VDPN.....
AAL56186_H._zea_SNPV	.NEPYTANVAVDA...LLA.....	QR.VNPK.....
AAF33549_S._exigua_N	.DEPYCADRAVEL...LLG.....	QH.VPAG.....
AAZ38189_A._segetum	.DEPYCADRAVEA...LLK.....	QN.VPAS.....
AAS82706_A._segetum	.EEKYTAEYATKE...LLK.....	QN.VNSK.....
ZP_01159013_Photobac	KGPAYTSDIGIQL...LLD.....	QG.VPAN.....
ZP_01161077_Photobac	.EIKHTVDLAVKT...LLN.....	QG.VEPK.....
ZP_01159325_Photobac	..WGMGTDVFNK...MIS.....	LG.IPAD.....
ZP_01160869_Photobac	..DDMSVDSQVNA...LLK.....	QG.VDRK.....
ZP_01233025_V._angus	KGPAYTSDIGIQL...LLD.....	QG.VPAN.....
ZP_01236284_V._angus	.EIKHTVDLAVKT...LLN.....	QG.VEPK.....
ZP_01235109_V._angus	..WGMGTDVFNK...MIS.....	LG.IPAD.....
ZP_01235465_V._angus	..DDMSVDSQVNS...LLK.....	HG.VDRK.....
AAO08114_V._vulnific	KGPAYTSDHGIQL...LLA.....	QG.VPAN.....

AAO07498_V._vulnific	..WGMGADVFINQ...	MIE	..LG	IPSE
NP_232428_V._cholera	KGPAYTTDNGIQL...	LLA	..QG	VPPS
YP_432951_H._chejuen	..SANTSVTTAMSY...	LQS	..KG	VPNN
YP_529337.1_B_S._deg	..EGFNTHASVQN...	LLT	..AG	VPSS
YP_435912_H._chejuen	..HEGFSSDATINN...	LMS	..AG	VPAN
ZP_01137509_A._cellu	..EHYaidNAIRA...	YTGGDAAYGIP	..GG	FPAa
ChiE_S._coelicolor	..FHFSVENAIQT...	YLD	..AG	VNPR
ChiC_S._coelicolor	....FNTADAMAK...	FKS	..KG	VPAD
ChiD_S._coelicolor	....FHTSATIAK...	LKG	..LG	VPSS
NP_903910_C._violace	..VYYTVDDAVKT...	LVN	..AG	VPRA
YP_529072.1_S._degra	....FSSDHGIQV...	LKS	..KG	VPaE
ZP_01431615_S._tropi	....FWSDAAIQK...	LKS	..KG	VAAD
ZP_01136287_A._cellu	..QQFSVDQSIDA...	FLR	..AG	ADRH
01315.1_C._cinereus	..RYGSATSAVRQ...	WS	..AAGIPHN	
03252.1_C._cinereus	..KWGSaVSSIEE...	WT	..KAGIPLE	
05285.1_C._cinereus	..PLGSVEGSVEA...	WT	..AAGFPaE	
05291.1_C._cinereus	..GVGSVASSVAA...	WT	..GAGFPAN	
01586.1_C._cinereus	..PHASAQAALaQ...	WK	..AAGFPAN	
128098_P._chrysospor	..QDGSaVSAVQa...	WT	..SAGFPAN	
39872_P._chrysospori	..QMGSaVSAVKA...	WT	..AAGMPaH	
138098_P._chrysospor	..QQGSATSaVAA...	WT	..RAGLPAS	
129436_P._chrysospor	..ASASaVAGIAA...	WT	..AAGFPAS	
EAA71245_G._zeae	..NMGSgNQAVTK...	WN	..DAGIPLS	
MGG_04732_M._grisea	..NQGGIKEGVaK...	WV	..AAGVPaE	
UM06190_U._maydis	..PRANAAGVKA...	WS	..AAGMPRD	
04245_F._neoformans	..PLANAyAAVAS...	WT	..SAGMPAN	
16170_R._oryzae	...VDT...TVNL...	WY	..NAGIPKN	
01334_R._oryzae	...VET...TVNL...	WY	..NAGIPKN	
13934_R._oryzae	...TTSgAAAVQS...	WI	..SAGIPSN	
07611_R._oryzae	..YgAGFVEGIQS...	WN	..AAGVPYK	
10252_R._oryzae	..APFSFTDSIKQ...	WK	..LAGVPSE	
14659_R._oryzae	....ISFSSSIES...	WI	..QAGMPaH	
231399_L._bicolor	..QIASAISaVRL...	WT	..NAGMPRK	
180319_L._bicolor	..QQGSaESaVAA...	WT	..AAKFPID	
191848_L._bicolor	..QAGSaESaVNA...	WT	..AAKFPAN	
317003_L._bicolor	..PQASaQAALaQ...	WK	..AAKFPAS	
246840_L._bicolor	..QRSSaARLVDA...	WS	..AAGMHLd	
144643_L._bicolor	..ADANAyAAyNA...	WT	..SAGFPAS	
310136_L._bicolor	..KAGSaVAaVKA...	WT	..GAKFPANQVKERCISLEPAYQTFLF	
629882_M._xanthus	...PTSvSSSLSa...	WA	..NAGIPKN	
630509_A_M._xanthus				
YP_592598_Acidobacte	..QAGSLKTSMDL...	FHG	..IYGVPRa	
YP_446903_S._ruber	..LQRSaATAVNM...	FVK	..AG	VPPQ
ZP_00739282_B._thuri	....FYVDGaIDV...	YTN	..EG	VPVD
ZP_01245639_F._johns	..TQSESLDELtNQ...	YLN	..VIG	FPAN
NP_976824_B._cereus	....FYVDGaIDI...	YTN	..EG	VPAD
YP_077581_B._licheni	..aETYNIENTVKR...	YKE	..AG	VKGD
631138_M._xanthus	....FYTDGSVSK...	MLa	..LG	VGPa
ZP_01247029_F._johns	....YSMAVNQFNy...	WT	..GRGLPAS	
ZP_01234549_V._angus	...YKDSVNALNy...	WLI	..ERHLDPQ	
ZP_01160697_Photobac	...YKDSVNALNy...	WLI	..ERHLDPQ	
ZP_01158584_Photobac	...YKDTKTALDY...	WIH	..KRHLDPH	
AN0549_E._nidulans	...LTeITNALDL...	LW	..RNDISPD	
AN8481_E._nidulans	...LTeITNALDL...	LW	..RNNIKPG	
AN9390_E._nidulans	...LTeIDLAMEL...	LW	..RNDIDPK	
AN0517_E._nidulans	...ITQIElGLDL...	LW	..RNNIDPa	
AN0541_E._nidulans	...VTEIEIGVDL...	LR	..RNNINLy	
AN5077_E._nidulans	...LTeIDLALDL...	FW	..RVDVDPS	
AN0509_E._nidulans	...LTETMTSLAM...	IT	..KAGVPSD	
AN7613_E._nidulans	.....T		..KAGVPRS	
07035_N._crassa	...MTEIQQALDL...	LW	..RNNIKPa	
07484_N._crassa	...LTETKTALAM...	IT	..KAGVDSG	

05317_N._crassa	...LTETKQSLAM...	IT	...	KAGVPGR	.....
EAA74768_G._zeae	...LTEIDSDLDL...	FW	.....	RNDIDPD	.....
EAA78168_G._zeae	...LTEIKSSIDL...	LW	.....	RNKVSPS	.....
EAA75711_G._zeae	...IREIGNNTIP...	LW	.....	FDGLDPK	.....
EAA68447_G._zeae	...LTETQYSLAM...	IT	.....	KAGVPSN	.....
EAA77156_G._zeae	...KTETLDSLAM...	IT	.....	KAGVDPA	.....
12510_S._sclerotioru	...LTEIDLAMD...	IW	.....	RNDINPN	.....
00773_S._sclerotioru	...LTEIESSMNL...	LW	.....	WNNITSS	.....
05454_S._sclerotioru	...ITEINLALNL...	FW	.....	RNDVPAP	.....
00677_S._sclerotioru	...LLDINSVLSP...	LW	.....	FAGVDPS	.....
02128_S._sclerotioru	...LTETLESLSM...	IT	.....	KAGVASN	.....
MGG_04534_M._grisea	...LTEIQIGLEL...	LW	.....	RNNINPA	.....
MGG_01336_M._grisea	...IRDITEFIKP...	LW	.....	YSSVPAA	.....
14527_P._nodorum	...ITEIDLGLDL...	LW	.....	RAGVDPK	.....
15411_P._nodorum	...YRKL	.....	.....	FDGVDP	.....
02214_P._nodorum	...LQEVDTALNL...	LW	.....	GTQIDSR	.....
04761_C._immitis	...ITEMRLALDL...	LW	.....	RNDVPAH	.....
04323_A._capsulatum	...LTEISAALDL...	LW	.....	RNSVPPE	.....
00533_B._fuckeliana	...LPDITNAISP...	LW	.....	FAGVDPM	.....
Chi18_1_H._jecorina	...LTETLNALSM...	IT	.....	KAGVPSN	.....
Chi18_8_H._jecorina	...KTETYNALAM...	IT	.....	KAGVKST	.....
Chi18_9_H._jecorina	...QTEVVLALSM...	IT	.....	KAGVSAS	.....
Chi18_10_H._jecorina	...MTETLNALAM...	IT	.....	KAGVEAR	.....
02650_A._capsulatum	...LALSLESIDA...	YM	.....	AAGLPSS	.....
AN0221_E._nidulans	...VQLSLESIDA...	YI	.....	EAGMPPE	.....
06020_N._crassa	...VELSLQAVDA...	YV	.....	AAGAAPQ	.....
EAA76014_G._zeae	...VENSQEAQOR...	YI	.....	DRGASPS	.....
Chi18_4_H._jecorina	...IDESEAAIRR...	YM	.....	DRGAPPH	.....
09277_P._nodorum	...TQQSLAAIKA...	YR	.....	KRGVPAD	.....
05838_A._capsulatum	...EKGCLQTVQN...	YL	.....	DIKLPPE	.....
EAA69039_G._zeae	...IAGAARAIK...	YI	.....	SLGFPPS	.....
MGG_06594_M._grisea	...VKGSAAVVDR...	YI	.....	ALGCEPK	.....
Chi18_11_H._jecorina	...VNGSLNSVNT...	YL	.....	ERGLSPD	.....
02644_A_P._nodorum	...VVDSAATIER...	YL	.....	AIGAPPE	.....
AN9447_E._nidulans	...IADSHDTIKA...	YL	.....	EIGAPPE	.....

	610	620	630	640	650	660
NP_979924_B._cereus	...KIMMGQNLGYFD	...	WKL	...	FK	...
YP_077302_B._licheni	...KIVMGQNLGYD	...	WTL	...	YT	...
YP_091539_B._licheni	...KIVLGFPLYGYN	...	WTL	...	YQ	...
YP_079121_B._licheni	...KIVLGFPLYGYN	...	WTL	...	YQ	...
YP_074366_S._thermop	...KIMMGQNLGYD	...	WTL	...	YR	...
YP_075811_S._thermop	...KILMGIPTYGRD	...	WRL	...	YQ	...
YP_075619_S._thermop	...KILLGIPAYGYD	...	WIAG	...	T	...
ZP_01354047_C._phyto	...RIDMGIPNYGYD	...	WALP	...	YV	...
ZP_01354926_C._phyto	...KLIMGIPFYARL	...	WKEY	...	TE	...
NP_902406_C._violace	...KILNGIPAYGYD	...	WKR	...		...
ZP_01136704_A._cellu	...KIFMGVPLYGYD	...	WAS	...	T	...
ZP_00526542_S._usita	...KISLGVALYGRR	...	WSAG	...	MR	...
AAF46212.1_D._melano	...RLVVGLPTYGHS	...	FTLVN	...	PLNHR	...
AAF46534.1_D._melano	...KINVGIATYGRA	...	WKLTK	...	D.SGL	...
AAF46544.1_D._melano	...KLVLGIPTYGRS	...	YTLIN	...	EESTE	...
At4g19720_A._thalian	...KAVLGFPPYVGT	...	WSLG	...	SG	...
At4g19750_A._thalian	...KAVLGFPSYCGWA	...	WTLED	...	AENNG	...
EAA67655_G._zeae	...KIHLGMPYGRS	...	FAN	...	TA	...
EAA73155_G._zeae	...KMLGMPYIGRA	...	FQN	...	TG	...
EAA74986_G._zeae	...KIVLGMPYIGRS	...	FEG	...	NL	...
EAA74223_G._zeae	...KIVLGMPYIGRA	...	FQN	...	TD	...
MGG_05533_M._grisea	...KINLGLPLYGRS	...	FDK	...	TT	...
MGG_01247_M._grisea	...KITLGLPLYGRS	...	FAS	...	TG	...
MGG_00086_M._grisea	...KIVLGMPYIGRT	...	FQN	...	TD	...

MGG_07927_M._grisea	...KIVMGMPYIGRA.....FEN.....TD.....
Chi18_6_H._jecorina	...KIILGIPLYGRS.....FMN.....TD.....
Chi18_5_H._jecorina	...KIVLGMPYIGRS.....FES.....TS.....
Chi18_7_H._jecorina	...KIVLGMPYIGRA.....FEN.....TD.....
04883_N._crassa	...KIVLGMPYIGRA.....FAS.....TD.....
04554_N._crassa	...KIVLGMPYIGRA.....FQG.....TE.....
11407_B._fuckeliana	...KIIMGLPLYGRA.....FES.....TI.....
05350_B._fuckeliana	...KIVLGMPYIGRA.....FQG.....TE.....
11700_S._sclerotioru	...KIILGLPINKGS.....FLN.....TT.....
11304_S._sclerotioru	...KIVLGMPYIGRA.....FQG.....TE.....
08020_S._sclerotioru	...KIVLGMPYIGRS.....FEQ.....TN.....
01250_A._capsulatum	...KLVFGLPLYGRA.....FEN.....TD.....
05886_A._capsulatum	...KMILGMPYIGRE.....FAD.....TD.....
06565_A._capsulatum	...KLILGMPYIGRT.....FAD.....TD.....
05250_C._immitis	...KIIFGLPLYGRG.....FEN.....TQ.....
02795_C._immitis	...KIVLGMPYIGRA.....FAS.....TD.....
03822_C._immitis	...KLVLGMPYIGRA.....FAN.....TE.....
AN5454_E._nidulans	...KINLGMPYIGRS.....FTH.....TD.....
AN4871_E._nidulans	...KIILGMPYIGRA.....FQN.....TD.....
00269_P._nodorum	...KIVLGMPYIGRA.....FAN.....TD.....
04870.1_C._cinereus	...KLVMGIPLYGRS.....FTQ.....TD.....
09921.1_C._cinereus	...KINVGMPLYGRA.....FQN.....TD.....
124149_P._chrysospor	...KLILGIPLYGRS.....FMN.....TD.....
134311_P._chrysospor	...KIVMGIPLYGRA.....FED.....TT.....
03412_F._neoformans	...KLVIGLPVYGRA.....FAN.....TK.....
13635_R._oryzae	...KLVIGLPVYGRG.....FSN.....TA.....
UM04261_U._maydis	...KLVIGIPLYGRG.....FEN.....TD.....
EAA69503_G._zeae	...KILLGIPTFGRS.....FLH.....CT.....
EAA70860_G._zeae	...KIILGIPVYARY.....FGQ.....AR.....
Chi18_3_H._jecorina	...NILLGIPTYGRS.....FLK.....SN.....
Chi18_2_H._jecorina	...KIVLGIPAYARY.....FPR.....AE.....
03026_N._crassa	...KILFGIPLEGRS.....FLH.....AS.....
01594_B._fuckeliana	...KILLGVPVYGRS.....FLN.....SR.....
05897_S._sclerotioru	...KILLGVPVYGRS.....FLN.....SR.....
04742_A._capsulatum	...KILLGIPVYGRA.....FPG.....AN.....
04750_C._immitis	...KILLGISVYGRA.....FPG.....TT.....
04719_P._nodorum	...KIVLGVPAYGRS.....FTG.....TK.....
MGG_08458_M._grisea	...QIVLGVPAYARF.....FRG.....AR.....
CHT4_C._albicans	...KLILGMPMYGRI.....FHG.....VDRP.....
01119_L._elongisporu	...KLVLGMPMYARI.....FSG.....VQEG.....
XP_454053_K._lactis	...RIALGMAAYGRG.....FTN.....V.....ETNDDN.....
CTS2_S._cerevisiae	...KLVLGMAAYGRS.....FHIKDNKF.....EPFNQNTV.....
246746_L._bicolor	...KIVLGIPLYGRS.....FMN.....TQ.....
03209_N._crassa	...KIVLGIPLYGRS.....FEG.....TD.....
14474_P._nodorum	...KIVLGMPYIGRS.....FGN.....VVDLSKDQ..R.....
CE06282_C._elegans	...KFNIVIPFYATL.....WENVY.....ETVLD.....
CE03547_C._elegans	...KYNIAIPFYTML.....WKHVK.....GPVNP.....
CE03542_C._elegans	...KFNIVIPFYARI.....WRSVG.....EAIT.....
CE15845_B_C._elegans	...KFNLGILFSAKL.....WKNVE.....EPAE.....
CE02997_C._elegans	...KFNIIVSEFHATY.....WNGAE.....LPLRD.....
CE36953_C._elegans	...KINMGVPFYGRF.....WKNVG.....DAVD.....
YP_432439_H._chejuen	...RINIGVPYYSRG.....WQGVNGGDNMGWGTASAPDQN.....
YP_529449.1_S._degra	...RINIGVPYYTRG.....WQGVTTGGTNGLWGQASLPNQS.....
YP_077582_B._licheni	...RINIGVPYYTRG.....WKNVTGGANGLWGRAKSA.....
ChiI_S._coelicolor	...RINIGLPYYTRG.....HKNVQGGTDGLWGRASAS.....
NP_902986_C._violace	...RVNMGVPYYTRG.....WKNVSGGSNGLWGSSVGS.....
ZP_01159608_Photobac	...RINIGVPYYTRG.....WQDVKGVNDNGLWGRAALPNQS.....
ZP_01234708_V._angus	...RINIGVPYYTRG.....WQDVKGGDNGLWGRAALPNQS.....
NP_233087_V._cholera	...RINIGVPYYTRG.....WQGVTTGGENGLWGRAALPNQN.....
NP_230718_V._cholera	...QINMGIPYYTRG.....WQGVSGGDKGLWGRAVEPNQS.....
AAO07185_V._vulnific	...RINIGVPYYTRG.....WQGVTTGGTNGLWGRAALPNQA.....
ZP_01354150_C._phyto	...KLVLGIPAYGYG.....WRGVASE.....NH.....



ZP_01246933_F._johns	...KLVI <b>GGAFY</b> TRQ.....	WKN <b>VENI</b> .....	NN.....
YP_012734_L._monocyt	...KIV <b>VGA</b> AFYTRG.....	WNK <b>VAA</b> G.....	TD <b>TAL</b> .....
YP_529337.1_A.S._deg	...KIV <b>MGV</b> PFYGRA.....	FFNT <b>GSSN</b> ..	TGLY <b>QTFN</b> .....
ChiA_A.P._kodakarae	...KIT <b>VGL</b> PFYSR.....	SFAN <b>VPP</b> .....	EN.N.....
AAG19274_Halobacteri	...QLS <b>LGL</b> PFYGR.....	SFG <b>NVASS</b> .....	DN.N.....
AAG19275_Halobacteri	...TLVL <b>GMP</b> FYGRGCNV <b>ENGIWD</b> ..	TFSL <b>SEWQ</b> .....	QG.D.....
CE03543_C._elegans	...KFN <b>MVIP</b> FYARY.....	WNN <b>VQ</b> .....	EA <b>VD</b> .....
CE34961_C._elegans	...KFN <b>MVIP</b> FYVRL.....	WKN <b>VK</b> .....	EP <b>IS</b> .....
CE20043_C._elegans	...KLN <b>MVIP</b> FFVRL.....	WKN <b>V</b> P.....	EP <b>VE</b> .....
CE15845_A.C._elegans	...KLN <b>LVIP</b> FFYARR.....	WEH <b>VK</b> .....	ES <b>LD</b> .....
CE32863_A.C._elegans	...KLN <b>LVIP</b> FFYARR.....	WEH <b>VK</b> .....	ES <b>LD</b> .....
CE03544_C._elegans	...MIN <b>LVIP</b> FFYVRM.....	WKN <b>VQ</b> .....	KA <b>ID</b> .....
CE08731_C._elegans	...KFN <b>LAIP</b> FSVRL.....	WRN <b>VE</b> .....	DA <b>IQ</b> .....
CE28638_C._elegans	.....	H <b>LD</b> .....	KK <b>LN</b> .....
CE32863_B.C._elegans	...KFN <b>L</b> GILEFS <b>AKL</b> .....	WKN <b>VE</b> .....	EP <b>AE</b> .....
CE01673_C._elegans	...KFN <b>L</b> VIP.....	.....	.....
CE02993_C._elegans	...KFN <b>I</b> VSF <b>HGT</b> F.....	WK <b>DAE</b> .....	LP <b>LRN</b> .....
CE02996_C._elegans	...KFN <b>I</b> VSF <b>HGT</b> F.....	WE <b>GAE</b> .....	LP <b>LRD</b> .....
CE02995_C._elegans	...KFN <b>MMV</b> L <b>FHGT</b> F.....	WK <b>GAE</b> .....	LP <b>LRN</b> .....
CE02992_C._elegans	...ILN <b>MGV</b> T <b>FTG</b> IF.....	WNG <b>VK</b> .....	DG <b>LNE</b> .....
CE02999_C._elegans	...KLN <b>MV</b> VS <b>FNGIY</b> .....	WG <b>NTT</b> .....	LP <b>FDD</b> .....
CE02998_C._elegans	...KLN <b>MAL</b> S <b>FGY</b> RY.....	WEN <b>VN</b> .....	DN <b>VP</b> .....
CE09229_C._elegans	...QLN <b>MGV</b> PFY <b>GRY</b> .....	WKN <b>V</b> L.....	GP <b>IDK</b> .....
CE12928_C._elegans	...QLT <b>MGV</b> PFY <b>GRY</b> .....	WKN <b>V</b> L.....	EP <b>IDA</b> .....
CE23907_C._elegans	...KFN <b>IAIP</b> FYATL.....	WEN <b>VY</b> .....	EP <b>FPS</b> .....
CE32917_C._elegans	...KFN <b>I</b> VIPFFARL.....	WKN <b>VE</b> .....	KP <b>IQH</b> .....
CE34579_C._elegans	...KFN <b>I</b> VIPFFARL.....	WNN <b>VG</b> .....	KP <b>IDF</b> .....
CE25073_C._elegans	...KYN <b>IAIP</b> FYTML.....	WKH <b>VK</b> .....	GP <b>VNP</b> .....
CE03548_C._elegans	...KYN <b>IAIP</b> FYTML.....	WKH <b>VQ</b> .....	GP <b>INP</b> .....
NP_469498_L._innocua	...KIV <b>VGA</b> AFYTRG.....	WNK <b>VAA</b> G.....	TD <b>TAL</b> .....
CE08730_C._elegans	...KFN <b>LIIP</b> FYVRH.....	WRN <b>VE</b> .....	NA <b>IK</b> .....
Q8U1H4_P._furiosus	.....	.....	.....
CE12474_C._elegans	...MLN <b>MVIP</b> FSARI.....	WNN <b>VQ</b> .....	EA <b>ID</b> .....
CE02990_C._elegans	...KFN <b>IIIS</b> F <b>HATY</b> .....	WE <b>GTD</b> .....	LP <b>LRD</b> .....
CE40270_C._elegans	...KFN <b>IAIP</b> FYTTL.....	WEN <b>VQ</b> .....	GP <b>ID</b> .....
CE40296_C._elegans	...KFN <b>IIVS</b> F <b>HATY</b> .....	WE <b>GAE</b> .....	LP <b>LRD</b> .....
ChiB_S._marcescens	...KIV <b>MGV</b> PFYGRA.....	FKG <b>VSGGN</b> ..	GGQY <b>SSHS</b> .....
O10363_O._pseudotsug	...KLIV <b>GVAM</b> YGRG.....	WTG <b>VSGY</b> .....	AG.....
AAP29899_C._fumifera	...KIIV <b>GVAM</b> YGRG.....	WTG <b>VAGY</b> .....	DG.....
AAV73807_B._mori_NPV	...KIIV <b>GVAM</b> YGRG.....	WTG <b>V</b> TNY.....	TN.....
AAL56186_H._zea_SNPV	...KLVL <b>GVAM</b> YGRG.....	WTG <b>VHNY</b> .....	DS.....
AAF33549_S._exigua_N	...KIAL <b>GVAM</b> YGRG.....	WSG <b>VVSD</b> .....	DT.....
AAZ38189_A._segetum_	...KIAL <b>GVAM</b> YGRG.....	WTG <b>VSSD</b> .....	G.....
AAS82706_A._segetum_	...KIVL <b>AVAM</b> YGRG.....	WTG <b>VHDI</b> .....	KN.....
ZP_01159013_Photobac	...KLVL <b>GAA</b> MYGRG.....	WTG <b>VTPD</b> .....	TL <b>TD</b> .....
ZP_01161077_Photobac	...KIIV <b>GTP</b> FYGRG.....	WKG <b>VHDV</b> .....	QG.....
ZP_01159325_Photobac	...KL <b>VVGA</b> AFYGRG.....	WE <b>G</b> TKGF.....	DG <b>KAI</b> .....
ZP_01160869_Photobac	...KVI <b>IGSP</b> FYGRG.....	WKG <b>VDNA</b> .....	STD <b>KL</b> .....
ZP_01233025_V._angus	...KLVL <b>GAA</b> MYGRG.....	WTG <b>VTPD</b> .....	TL <b>TD</b> .....
ZP_01236284_V._angus	...KIIV <b>GTP</b> FYGRG.....	WKG <b>VHDV</b> .....	QG.....
ZP_01235109_V._angus	...KL <b>VVGA</b> AFYGRG.....	WE <b>G</b> TKGF.....	DG <b>KAI</b> .....
ZP_01235465_V._angus	...KII <b>IGSP</b> FYGRG.....	WKG <b>VDNA</b> .....	SAD <b>KL</b> .....
AAO08114_V._vulnific	...KLVL <b>G</b> TAM <b>YGRG</b> .....	WE <b>G</b> VMPS.....	TL <b>RD</b> .....
AAO07498_V._vulnific	...KL <b>VIGA</b> AFYGRG.....	WQ <b>G</b> TKDY.....	DGQ <b>AP</b> .....
NP_232428_V._cholera	...KL <b>VVGA</b> AM <b>YGRG</b> .....	WE <b>G</b> VTPA.....	SL <b>KD</b> .....
YP_432951_H._chejuen	...KLM <b>GV</b> ANY <b>HRAKRLNSAADITEYS</b> DGIAGA.....	.....	TAH <b>Q</b> P.....
YP_529337.1_B.S._deg	...KL <b>VVGA</b> AFYGRG.....	WV <b>G</b> TQNT.....	NA <b>AKS</b> .....
YP_435912_H._chejuen	...KLVL <b>GAA</b> MYGRG.....	WKG <b>V</b> TGG.....	TE.....
ZP_01137509_A._cellu	...KIN <b>IGV</b> PFY <b>RR</b> .....	GWT <b>GVSAG</b> .....	SN.H.....
ChiE_S._coelicolor	...KL <b>T</b> VG <b>FP</b> FYGR.....	GWQ <b>G</b> VGE <b>G</b> .....	GA.A.....
ChiC_S._coelicolor	...KLL <b>IGIG</b> FYGR.....	GWT <b>G</b> VTQS.....	AP.....
ChiD_S._coelicolor	...KLL <b>LGLG</b> FYGR.....	GWT <b>G</b> VTQA.....	DP.....

NP_903910_C_violace	...KINVGLPFYGR.....	GWAGVAAG.....	PKGD.....	
YP_529072.1_S_degra	...KILLGIGFYGR.....	GWNTVTQD.....	AP.....	
ZP_01431615_S_tropi	...KLLLGIGFYGR.....	GWTVGTQA.....	AP.....	
ZP_01136287_A_cellu	...KLLVGVVPFYGH.....	GWVGVDPG.....	GT.H.....	
01315.1_C_cinereus	...QLVLGVAAAYGHG.....	FRVRR.....	ANAFAA.....	GSN.....
03252.1_C_cinereus	...KLVLGVPAHGHS.....	YDVSP.....	VVALSR.....	SNS.....
05285.1_C_cinereus	...KLLGLPAYARS.....	FTVAK.....	DDVLDA.....	DG.....
05291.1_C_cinereus	...KLVLGVPAYGRS.....	YYVDP.....	ANALSA.....	AG.....
01586.1_C_cinereus	...KQLLGLALYGWV.....	SKSTK.....	NVLTGAFMPTDDMVLLTKSETSS	
128098_P_chrysospor	...QIVLALAAAYGHG.....	FVVDS.....	TAAFDT.....	SNS.....
39872_P_chrysospori	...QIVLGVASYGHS.....	FTVPP.....	SAAFTS.....	GDD.....
138098_P_chrysospor	...KIVLGVAAAYGHS.....	YHVAP.....	ADAFGG.....	ASSAGEA
129436_P_chrysospor	...KIVLGVPSYGYI.....	SHSSA.....	DGLQT.....	R.....
EAA71245_G_zeae	...QIVLGMPPNYGHG.....	FKVNA.....	TSAYN.....	
MGG_04732_M_grisea	...KLILGIGAYGHG.....	FTVSQ.....	ADAFVP.....	TTDG.....
UM06190_U_maydis	...KILLGIPAYGYI.....	NTSKK.....	QTLR.....	T.....RS.....
04245_F_neoformans	...QITLGVPAYGYI.....	QVSSA.....	SSLIQ.....	RRS.LP.....
16170_R_oryzae	...KMHVGVTFYGVK.....	LKTAQ.....	PITSTS.....	
01334_R_oryzae	...KMHVGITFYGVK.....	LKTAQ.....	PITATS.....	
13934_R_oryzae	...KIYLGVPFYGYT.....	HKTTA.....	EINLET.....	
07611_R_oryzae	...KLAGGIPFYGRA.....	QTLSTV.....	D.....SAP.....	
10252_R_oryzae	...KITAGLAFYGRA.....	MKANV.....	NMITDP.....	
14659_R_oryzae	...QLTGGGLAFYGRS.....	TTAKV.....	N.MLKK.....	
231399_L_bicolor	...QIVLGVAGYGRQ.....	YRVRR.....	SDAFMS.....	GS.....
180319_L_bicolor	...KLVLGVAAAYGHS.....	FSVSK.....	NIAVVN.....	S.....
191848_L_bicolor	...KIALGVAAAYGHS.....	FSVAN.....	SAAVVN.....	N.....
317003_L_bicolor	...QLLLGLPLYGYV.....	SQSTK.....	TALTGSLMPSDDMVLLQNIERP	G.....
246840_L_bicolor	...QIVLGVPAYGYG.....	YSVSK.....	KLAFTS.....	G.....
144643_L_bicolor	...KLVLGIPSYGYV.....	ITSNS.....	TRLKT.....	R.....
310136_L_bicolor	FFCKIALGVAAAYGHS.....	FHVTT.....	SAALGS.....	SG.....
629882_M_xanthus	...KLGMPFYGYMA.....	WRNIT.....	GPYQPY.....	TDW.....
630509_A_M_xanthus	...	...	...	...
YP_592598_Acidobacte	...KLNIGTAFYGYE.....	FDNVR.....	R.LWN.....	
YP_446903_S_ruber	...KLVLGVVPFYGR.....	GWSGAGAR.....	DD.....	
ZP_00739282_B_thuri	...KLVLGVVPFYGR.....	GWKSCGKE.....	NN.....	
ZP_01245639_F_johns	...KLIMGLPFYGK.....	KFDNVAAN.....	STN.....	
NP_976824_B_cereus	...KLVLGVVPFYGR.....	GWKSCGKE.....	NN.....	
YP_077581_B_licheni	...KLVLGTFPYGR.....	GWSGCEPG.....	GH.....	
631138_M_xanthus	...KIVVGVVPFYGR.....	GWGSVPNV.....	NN.....	
ZP_01247029_F_johns	...KAIIGLPFYGYG.....	FG.....		
ZP_01234549_V_angus	...RITLGLPAYPR.....			
ZP_01160697_Photobac	...RITLGLPAYPR.....			
ZP_01158584_Photobac	...RVTLGLPSYSH.....			
AN0549_E_nidulans	...KVVVLGVAFYARV.....	FSASN.....	PGCME.....	
AN8481_E_nidulans	...KVVVLGMFAFYARV.....	FAAAS.....	PSCME.....	
AN9390_E_nidulans	...KVVVMGMGFYGRS.....	FTLSD.....	PACNT.....	
AN0517_E_nidulans	...NVVFGIAFYGRS.....	FTLTD.....	SNCYQ.....	
AN0541_E_nidulans	...KVSIGMGFYGRT.....	FTLSD.....	PGCSE.....	
AN5077_E_nidulans	...SIVLGIGFYGRT.....	FQLSS.....	GSCWK.....	
AN0509_E_nidulans	...RVVVGVASYGRS.....	FAMAE.....	VGCYG.....	
AN7613_E_nidulans	...AITIGVASYGRA.....	FGMAE.....	ADCIR.....	
07035_N_crassa	...KVTFGMAFYRSR.....	FALTS.....	PSCNT.....	
07484_N_crassa	...KVVVGVSYSYGRS.....	FNMAAD.....	AGCYS.....	
05317_N_crassa	...KIIIVGVTSYGRS.....	FEMAQ.....	PGCWG.....	
EAA74768_G_zeae	...KIVMGLGFYGRA.....	FMAKI.....	ASCVE.....	
EAA78168_G_zeae	...KVVVLGLAFYGRS.....	VTLAS.....	SSCSE.....	
EAA75711_G_zeae	...KINFGGLAMYGRG.....	YTVAD.....	KSCNG.....	
EAA68447_G_zeae	...KVIVGVTSYGRS.....	FKMAS.....	AGCYG.....	
EAA77156_G_zeae	...KVVVGISSYGRS.....	FRMKD.....	PKCTG.....	
12510_S_sclerotioru	...QVVLGLGFYGRS.....	FSVSS.....	PSCIE.....	
00773_S_sclerotioru	...KVNGLGLAFYGRS.....	FTIAS.....	SNCDT.....	
05454_S_sclerotioru	...KLNMLGLGFYGRS.....	FQLAD.....	PSCSK.....	

00677_S._sclerotioru	...KLNLGLAAYGRG.....	YTLSN.....	PGCHE.....
02128_S._sclerotioru	...KVIIVGVTSYGRS.....	FQMAT.....	PGCYL.....
MGG_04534_M._grisea	...RVNLGLGFYGRS.....	FTMKD.....	PNCMS.....
MGG_01336_M._grisea	...KINLGLASYGRG.....	YTLRS.....	SSCAS.....
14527_P._nodorum	...NVVLGQGWWYGRS.....	FTLKD.....	SSCNL.....
15411_P._nodorum	...KVNFGIAYYGRT.....	YQLVD.....	PSCDK.....
02214_P._nodorum	...KINMGIAN YGRG.....	YTVEK.....	KECAY.....
04761_C._immitis	...KVNMLGLGFYGRS.....	FQLQD.....	PACDK.....
04323_A._capsulatum	...KVSILGLAFYGRS.....	FTLAD.....	PSCST.....
00533_B._fuckeliana	...KVNGLGLAAYGRG.....	YTLAN.....	PGCAE.....
Chi18_1_H._jecorina	...MITVGVSSYGRS.....	FQMSS.....	AGCWT.....
Chi18_8_H._jecorina	...KIAVGVTSYGRS.....	FRMAD.....	QNCSE.....
Chi18_9_H._jecorina	...KVVVGESSYGRS.....	FKMAK.....	AGCTG.....
Chi18_10_H._jecorina	...QVVVGVAS YGRS.....	FEMND.....	PKCKG.....
02650_A._capsulatum	...RANLGF AFYVKW.....	FRTE DPTK.....	GSGCDK.....
AN0221_E._nidulans	...KLNLGLAAYYVKW.....	FKTVP.....	GEQCAK.....
06020_N._crassa	...KLNLGF AFYLYK.....	FKTEQ.....	DACAQ.....
EAA76014_G._zeae	...SVNLGLGY YVKW.....	FMTEK.....	CDP.....
Chi18_4_H._jecorina	...KLNLGLGY YAKW.....	FMTEK.....	CDA.....
09277_P._nodorum	...RLNVGTAFYVKW.....	FKTAN.....	GKDCSA.....
05838_A._capsulatum	...KINLGF AFYAKY.....	FTLDP.....	KANCTS.....
EAA69039_G._zeae	...KLVLGIPFYAKY.....	FMTKK.....	GYTC.....
MGG_06594_M._grisea	...KLNLGF AFYAKW.....	FTTAK.....	GVEC.....
Chi18_11_H._jecorina	...KINLGF AFYAKW.....	FSTEA.....	GYQC.....
02644_A_P._nodorum	...KLNLGF AYYAKY.....	FTTKP.....	GCTS.....
AN9447_E._nidulans	...KINLGF AYYAKW.....	FTTQS.....	DVDCG.....

	670	680	690	700	710	720
NP_979924_B._cereus	.... .... .... .... .... .... .... .... .... .... .... ....		QG			
YP_077302_B._licheni			PG			
YP_091539_B._licheni			PG			
YP_079121_B._licheni			PG			
YP_074366_S._thermop			PA			
YP_075811_S._thermop			RG			
YP_075619_S._thermop						
ZP_01354047_C._phyto			KG			
ZP_01354926_C._phyto			LGN			P
NP_902406_C._violace						
ZP_01136704_A._cellu						
ZP_00526542_S._usita			DKD			P
AAF46212.1_D._melano			IG			AP
AAF46534.1_D._melano			TG			LPPVAE
AAF46544.1_D._melano			LG			AP
At4g19720_A._thalian			ND			AA
At4g19750_A._thalian			YD			AA
EAA67655_G._zeae			GLG			KPYDG
EAA73155_G._zeae			GLG			QGYSG
EAA74986_G._zeae			GIG			KSFSD
EAA74223_G._zeae			GPG			RPYQG
MGG_05533_M._grisea			GLG			KGYTA
MGG_01247_M._grisea			GLG			KPFSG
MGG_00086_M._grisea			GPG			GAYSG
MGG_07927_M._grisea			GPG			APFQG
Chi18_6_H._jecorina			GPG			KPYEG
Chi18_5_H._jecorina			GIG			QFPTG
Chi18_7_H._jecorina			GPG			KPYSG
04883_N._crassa			GPG			TAYSG
04554_N._crassa			GLG			QPYSG
11407_B._fuckeliana			GMG			LTENG
05350_B._fuckeliana			GLG			RPFNG
11700_S._sclerotioru			GLG			MQATG

11304_S._sclerotioru	.....GLG.....	KPFNG.....
08020_S._sclerotioru	.....GLD.....	QSFQG.....
01250_A._capsulatum	.....GPG.....	KPFQG.....
05886_A._capsulatum	.....GPG.....	TPFTG.....
06565_A._capsulatum	.....GPG.....	TPFHG.....
05250_C._immitis	.....GPG.....	SPFQG.....
02795_C._immitis	.....GIG.....	TSFNG.....
03822_C._immitis	.....GPG.....	KPYQG.....
AN5454_E._nidulans	.....GPG.....	TEFEG.....
AN4871_E._nidulans	.....GPG.....	RPYSG.....
00269_P._nodorum	.....GPG.....	KPFSG.....
04870.1_C._cinereus	.....GPG.....	HAFVG.....
09921.1_C._cinereus	.....GLG.....	APYSG.....
124149_P._chrysospor	.....GPG.....	TPFQG.....
134311_P._chrysospor	.....GIG.....	APYNG.....
03412_F._neoformans	.....GIG.....	SPFSG.....
13635_R._oryzae	.....GPE.....	QAFQG.....
UM04261_U._maydis	.....GPQ.....	QPYRG.....
EAA69503_G._zeae	.....GAG.....	HKYKG.....
EAA70860_G._zeae	.....GPG.....	HPFKG.....
Chi18_3_H._jecorina	.....GPG.....	QEFNG.....
Chi18_2_H._jecorina	.....GPG.....	CSTEK.....
03026_N._crassa	.....GSG.....	HKFQG.....
01594_B._fuckeliana	.....GPG.....	HPYQG.....
05897_S._sclerotioru	.....GPG.....	HPYHG.....
04742_A._capsulatum	.....GIN.....	QPYER.....
04750_C._immitis	.....GVGQT.....	HCISN.....
04719_P._nodorum	.....GVG.....	HGFSG.....
MGG_08458_M._grisea	.....ALG.....	AGFSE.....
CHT4_C._albicans	.....EIG.....	VPFTK.....
01119_L._elongisporu	.....HVG.....	SKFAK.....
XP_454053_K._lactis	.....YLG.....	KKYHG.....
CTS2_S._cerevisiae	.....LIN.....	KIFKG.....
246746_L._bicolor	.....GPG.....	SVFSG.....
03209_N._crassa	.....GLG.....	KPYSG.....
14474_P._nodorum	.....GLG.....	QKFNG.....
CE06282_C._elegans	.....SK.....	RGVYRH.....
CE03547_C._elegans	.....PN.....	IEIYRN.....
CE03542_C._elegans	.....LK.....	TEVFRN.....
CE15845_B_C._elegans	.....NG.....	RDLFIH.....
CE02997_C._elegans	.....DS.....	DDIWKD.....
CE36953_C._elegans	.....ST.....	DDMWRT.....
YP_432439_H._chejuen	.....NCPPGTGTGDKNDCGHGAVGIDNIWHD.....	
YP_529449.1_S._degra	.....ECPVGTGGSATSKCGNGAVGIDNLWHD.....	
YP_077582_B._licheni	.....DCPQG.....LRQCGDGATGIDNIWHD.....	
ChiI_S._coelicolor	.....TCPAGSG.....LTKCGDGAVGIDNLWHD.....	
NP_902986_C._violace	.....NCPAG.....LTECGDGAVGIDNIWHD.....	
ZP_01159608_Photobac	.....ECQAGTGEGEKNNCGYGAIGIDNMWHD.....	
ZP_01234708_V._angus	.....ECQAGTGEGEKNNCGYGAIGIDNMWHD.....	
NP_233087_V._cholera	.....LCAPGTGEGEKNNCGHGATGIDNMWHD.....	
NP_230718_V._cholera	.....SCPEG.....TTVCGWGAEGTDNIWHD.....	
AAO07185_V._vulnific	.....ECAPGTGEGEKNNCGHGAMGIDNMWHD.....	
ZP_01354150_C._phyto	.....G.....	LFQAA.....
ZP_01246933_F._johns	.....G.....	LYQAG.....
YP_012734_L._monocyt	.....PG.....	LFQAA.....
YP_529337.1_A_S._deg	.....TPNG.....	DPYVG.....
ChiA_A_P._kodakarae	.....G.....	LYQPF.....
AAG19274_Halobacteri	.....G.....	LYQPF.....
AAG19275_Halobacteri	.....P.....	KYQN.....
CE03543_C._elegans	.....PR.....	TEVFRN.....
CE34961_C._elegans	.....SG.....	TEVFRR.....
CE20043_C._elegans	.....PG.....	RQVFRD.....



CE15845_A_C._elegans	.....SN.....	TEVFRN.....
CE32863_A_C._elegans	.....SN.....	TEVFRN.....
CE03544_C._elegans	.....NR.....	TEVFRN.....
CE08731_C._elegans	.....PG.....	IEVFRN.....
CE28638_C._elegans	.....	VADA.....
CE32863_B_C._elegans	.....NG.....	RDLFIH.....
CE01673_C._elegans	.....	.....
CE02993_C._elegans	.....DF.....	DDIFKD.....
CE02996_C._elegans	.....YS.....	DDIWKE.....
CE02995_C._elegans	.....DS.....	DDIFKD.....
CE02992_C._elegans	.....Q.....	DDIWKV.....
CE02999_C._elegans	.....	KGWVWP.....
CE02998_C._elegans	.....	DEMFKE.....
CE09229_C._elegans	.....S.....	DNMWRT.....
CE12928_C._elegans	.....S.....	DNMWRT.....
CE23907_C._elegans	.....PG.....	RDVFRY.....
CE32917_C._elegans	.....PG.....	REVYRN.....
CE34579_C._elegans	.....PG.....	KEVYRN.....
CE25073_C._elegans	.....PN.....	IEIYRN.....
CE03548_C._elegans	.....PN.....	IEIYRN.....
NP_469498_L._innocua	.....PG.....	LFQAA.....
CE08730_C._elegans	.....PG.....	IEVFRN.....
Q8U1H4_P._furiosus	.....	.....
CE12474_C._elegans	.....NR.....	TEVFRN.....
CE02990_C._elegans	.....DS.....	DNWKV.....
CE40270_C._elegans	.....K.....	IEIFRN.....
CE40296_C._elegans	.....DS.....	DDIFKD.....
ChiB_S._marcescens	.....TPGE.....	DPYPN.....
O10363_O._pseudotsug	.....D.....	KYFSG.....
AAP29899_C._fumifera	.....D.....	NYFTG.....
AAV73807_B._mori_NPV	.....G.....	NYFSG.....
AAL56186_H._zea_SNPV	.....D.....	NPFSG.....
AAF33549_S._exigua_N	.....D.....	NPFLG.....
AAZ38189_A._segetum	.....E.....	NPFLG.....
AAS82706_A._segetum	.....N.....	NPFTG.....
ZP_01159013_Photobac	.....PT.....	DPMTG.....
ZP_01161077_Photobac	.....N.....	NPMTG.....
ZP_01159325_Photobac	.....PK.....	ELSST.....
ZP_01160869_Photobac	.....EG.....	LSSK.....
ZP_01233025_V._angus	.....PT.....	DPMTG.....
ZP_01236284_V._angus	.....N.....	NPMTG.....
ZP_01235109_V._angus	.....PK.....	ELSST.....
ZP_01235465_V._angus	.....EG.....	LSSK.....
AAO08114_V._vulnific	.....PN.....	DPMTG.....
AAO07498_V._vulnific	.....KG.....	DLLSE.....
NP_232428_V._cholera	.....PN.....	DPMTG.....
YP_432951_H._chejuen	.....NQ.....	APGTT.....
YP_529337.1_B_S._deg	.....DL.....	FPLYG.....
YP_435912_H._chejuen	.....T.....	DPFAG.....
ZP_01137509_A._cellu	.....G.....	LYQPA.....
ChiE_S._coelicolor	.....G.....	EWQDA.....
ChiC_S._coelicolor	.....	GGTA.....
ChiD_S._coelicolor	.....	GGTA.....
NP_903910_C._violace	.....G.....	LYQVA.....
YP_529072.1_S._degra	.....	GGSA.....
ZP_01431615_S._tropi	.....	GGTA.....
ZP_01136287_A._cellu	.....G.....	LYQTA.....
01315.1_C._cinereus	.....SVLASV.PPFDG.....VDRPIG.....	DSWD.....
03252.1_C._cinereus	.....SQLNAY.PSYSP.....ADKRKG.....	DRWD.....
05285.1_C._cinereus	.....NIVTFNPAFDK.....ESYPLG.....	EGEVE.....
05291.1_C._cinereus	.....ELTPY.AQFDK.....SKQPLG.....	EGETG.....
01586.1_C._cinereus	LDGNGEITFLNGAHPRPKDGAIQSVAVENADG.....	EGSIA.....

128098_P._chrysospor	...GT..TLLAAY.PPVAN.....SSNPQG.....DPTDV.....
39872_P._chrysospori	.....NTLAAY.PAFNS.....TSFPLG.....DGWD.....
138098_P._chrysospor	QPPGT..TPVAPY.PPFD A.....AQQPMG.....DVWDE.....
129436_P._chrysospor	.....SG.....TDGAG.....SAGVP.....
EAA71245_G._zeae	...KN..HKLNLY.PAONS.....TDRFQG.....SSWD.....
MGG_04732_M._grisea	...KP..FPLSAY.PKNNG.....TRR.QG.....SSWD.....
UM06190_U._maydis	.....RSRS.....SSSQRR.....AAKLT.....
04245_F._neoformans	.....LL.....PHKR.....SKHAK.....KASHV.....
16170_R._oryzae	.....GMYVKLDG.....HT.QIKG.....DKYDE.....
01334_R._oryzae	.....GMYVKLDG.....HT.QIKG.....DKHDE.....
13934_R._oryzae	.....GIHVPFDR.....KIPQIKG.....DSYDD.....
07611_R._oryzae	.....K.TQYNPAVS.....PNPPLG.....DQLDG.....
10252_R._oryzae	.....T.NQYQPSQ.....LGAPKG.....DSDDA.....
14659_R._oryzae	.....K.SLYQDQVQ.....GKIPQG.....DQDDT.....
231399_L._bicolor	.....PFLASH.PPFVK.....TRE.....DPRP.....
180319_L._bicolor	.....QLAPY.PTFVK.....SPQTPG.....EGETA.....
191848_L._bicolor	.....QLAAY.PAFSK.....AAQPAG.....EGETS.....
317003_L._bicolor	DHGG...HFLNGAHPVSKK.....QPNQNN.....EAGLA.....
246840_L._bicolor	.....SILAPY.PAYNV.....SNTPPG.....DKWS.....
144643_L._bicolor	.....S.....RHQVR.....SASVK.....
310136_L._bicolor	.....NVNLY.PSF DK.....SQQPLG.....DS DTS.....
629882_M._xanthus	SD.....
630509_A.M._xanthus	.....
YP_592598_Acidobacte	.....YCPSG.....D.....
YP_446903_S._ruber	.....G.....LYQC.....
ZP_00739282_B._thuri	.....G.....QYQPC.....
ZP_01245639_F._johns	.....G.....LFVAA.....
NP_976824_B._cereus	.....G.....QYQPC.....
YP_077581_B._licheni	.....G.....EYQKC.....
631138_M._xanthus	.....G.....LFQSG.....
ZP_01247029_F._johns	.....
ZP_01234549_V._angus	.....
ZP_01160697_Photobac	.....
ZP_01158584_Photobac	.....
AN0549_E._nidulans	.....PG.....CTFV.....
AN8481_E._nidulans	.....PG.....CLFQ.....
AN9390_E._nidulans	.....PG.....CGFS.....
AN0517_E._nidulans	.....PNGE.....CEFS.....
AN0541_E._nidulans	.....PG.....CEFS.....
AN5077_E._nidulans	.....PG.....CPFD.....
AN0509_E._nidulans	.....PE.....CLYTGSRA.....A
AN7613_E._nidulans	.....PE.....CKFTGP.....
07035_N._crassa	.....PG.....CPIS.....
07484_N._crassa	.....KD.....CFFTGSA...T
05317_N._crassa	.....PS.....CTFTGDR...T
EAA74768_G._zeae	.....PG.....CQFN.....
EAA78168_G._zeae	.....PG.....CPYL.....
EAA75711_G._zeae	.....LG.....CSFV.....
EAA68447_G._zeae	.....PD.....CFYTGSK...I
EAA77156_G._zeae	.....VT.....CQFTGSF...S
12510_S._sclerotioru	.....PG.....CTYE.....
00773_S._sclerotioru	.....PG.....CAYL.....
05454_S._sclerotioru	.....PG.....CIFK.....
00677_S._sclerotioru	.....QG.....CAYT.....
02128_S._sclerotioru	.....DS.....CTYTGP.....
MGG_04534_M._grisea	.....AG.....CEFT.....
MGG_01336_M._grisea	.....LDAN.....CGFT.....
14527_P._nodorum	.....PNGV.....CQFS.....
15411_P._nodorum	.....MG.....CRFI.....
02214_P._nodorum	.....FG.....CTYT.....
04761_C._immitis	.....PG.....CVFK.....
04323_A._capsulatum	.....PG.....CPFKKVDNET.....

00533_B._fuckeliana	.....IG.....	CAYT.....
Chi18_1_H._jecorina	.....EQ.....	CTYTG.....
Chi18_8_H._jecorina	.....PM.....	CTFLGGK...L
Chi18_9_H._jecorina	.....PL.....	CKFTGAN...G
Chi18_10_H._jecorina	.....PM.....	CTFTG.....P
02650_A._capsulatum	.....N.PIG.....	CKTVL.....
AN0221_E._nidulans	.....Q.PIG.....	CPTVL.....
06020_N._crassa	.....TSPVG.....	CPTVE.....
EAA76014_G._zeae	.....AKPVG.....	CRTPI.....
Chi18_4_H._jecorina	.....QQPLG.....	CRTQL.....
09277_P._nodorum	.....Q.ATG.....	CPTL.....
05838_A._capsulatum	.....EKPVG.....	CPIVH.....
EAA69039_G._zeae	.....TEPIG.....	CPTL.....
MGG_06594_M._grisea	.....TTSTG.....	CETAL.....
Chi18_11_H._jecorina	.....TTPTG.....	CPTAL.....
02644_A_P._nodorum	.....NPPLG.....	CPIVL.....
AN9447_E._nidulans	.....TYPIG.....	CPTVA.....

	730	740	750	760	770	780
	.... .... .... .... .... .... .... .... .... .... .... ....					
NP_979924_B._cereus	NPPAK.....	AV.....	SSV.....			AAV.....
YP_077302_B._licheni	GPLAR.....	AI.....	SPQ.....			RAI.....
YP_091539_B._licheni	AVYP.....	GI.....	ANQ.....			DAV.....
YP_079121_B._licheni	AVYP.....	GI.....	ANQ.....			DAV.....
YP_074366_S._thermop	GEYAR.....	AI.....	SPQ.....			EAI.....
YP_075811_S._thermop	VTRAEE.....	TF.....	SPV.....			AAT.....
YP_075619_S._thermop	RQVVG.....	GL.....	STG.....			GAY.....
ZP_01354047_C._phyto	ETRAR.....	AI.....	GNI.....			EAV.....
ZP_01354926_C._phyto	ALASE.....	AV.....	SMT.....			SAE.....
NP_902406_C._violace	PGDGG.....	ML.....	YWK.....			DTQ.....
ZP_01136704_A._cellu	GGRAB.....	AV.....	TYP.....			QVV.....
ZP_00526542_S._usita	AVAAS.....	TI.....	YAA.....			DAV.....
AAF46212.1_D._melano	.ASGYGK.....	CG.....				QLG.....
AAF46534.1_D._melano	.ADGVAP.....	AGT.....	QTQ.....			IPG.....
AAF46544.1_D._melano	.AEGPGE.....	QGD.....	ATR.....			EKG.....
At4g19720_A._thalian	.TSRVAT.....	SA.....				EG.....
At4g19750_A._thalian	.TDGAAI.....	SS.....				DG.....
EAA67655_G._zeae	..VA.....	GS.....	PAN.....			LG.....
EAA73155_G._zeae	..VG.....	SG.....	SWE.....			NG.....
EAA74986_G._zeae	..VG.....	QG.....	SWE.....			RG.....
EAA74223_G._zeae	..VG.....	EG.....	TWE.....			QG.....
MGG_05533_M._grisea	..ST.....	AG.....	SLEGQ.....			AG.....
MGG_01247_M._grisea	..LG.....	DG.....	SIE.....			RG.....
MGG_00086_M._grisea	..TG.....	PG.....	SWE.....			NG.....
MGG_07927_M._grisea	..VG.....	QG.....	TWE.....			QG.....
Chi18_6_H._jecorina	..VG.....	KG.....	SIE.....			KG.....
Chi18_5_H._jecorina	..IG.....	SG.....	SWE.....			NG.....
Chi18_7_H._jecorina	..IG.....	EG.....	SWE.....			NG.....
04883_N._crassa	..VG.....	EG.....	SWE.....			KG.....
04554_N._crassa	..VG.....	EG.....	TWE.....			NG.....
11407_B._fuckeliana	..IG.....	TG.....	SWE.....			SG.....
05350_B._fuckeliana	..VG.....	EG.....	TWE.....			NG.....
11700_S._sclerotioru	..IG.....	PG.....	SWE.....			AG.....
11304_S._sclerotioru	..VG.....	EG.....	TWE.....			NG.....
08020_S._sclerotioru	..VG.....	QG.....	TWA.....			SG.....
01250_A._capsulatum	..VG.....	QG.....	SWE.....			NG.....
05886_A._capsulatum	..TGG.....	NG.....	SFE.....			PG.....
06565_A._capsulatum	..DGG.....	QG.....	SFE.....			KG.....
05250_C._immitis	..VG.....	EG.....	SWE.....			NG.....
02795_C._immitis	..VG.....	GG.....	SWE.....			NG.....
03822_C._immitis	..NGG.....	AG.....	SWE.....			PG.....
AN5454_E._nidulans	..VGY.....	EG.....	SFE.....			AG.....

AN4871_E._nidulans	..IG.....	QG.....	TWE.....	QG	
00269_P._nodorum	..VG.....	QG.....	TWE.....	AG	
04870.1_C._cinereus	..IG.....	EG.....	TWE.....	RG	
09921.1_C._cinereus	..IG.....	PG.....	TIE.....	PG	
124149_P._chrysospor	..LG.....	PG.....	SWE.....	SG	
134311_P._chrysospor	..IG.....	PG.....	TTE.....	AG	
03412_F._neoformans	..TG.....	EG.....	SWE.....	AG	
13635_R._oryzae	..VP.....	KG.....	TWE.....	EG	
UM04261_U._maydis	..TG.....	QG.....	TWE.....	AG	
EAA69503_G._zeae	..IG.....	G.....	AED.....	G	
EAA70860_G._zeae	..AG.....				
Chi18_3_H._jecorina	..VG.....	G.....	QD.....	G	
Chi18_2_H._jecorina	..AG.....				
03026_N._crassa	..AG.....	G.....	GDD.....	G	
01594_B._fuckeliana	..CG.....	G.....	EE.....	G	
05897_S._sclerotioru	..CG.....	G.....	EE.....	G	
04742_A._capsulatum	..GT.....	A.....	GGE.....	K	
04750_C._immitis	..ET.....	P.....	EDK.....	I	
04719_P._nodorum	..QA.....	G.....	EE.....	G	
MGG_08458_M._grisea	..AG.....				
CHT4_C._albicans	..ERK.....	SG.....	CIEA.....	D	
01119_L._elongisporu	..TDK.....	ED.....	TLGYNKI.....	KD	
XP_454053_K._lactis	..VGG.....	G.....	SEGE.....	PG	
CTS2_S._cerevisiae	..VGKPTK.....	EIDK.....	ADGK.....	EG	
246746_L._bicolor	..VG.....	QG.....	TWE.....	AG	
03209_N._crassa	..IG.....	AG.....	TLE.....	PG	
14474_P._nodorum	..SG.....	EG.....	TWE.....	PG	
CE06282_C._elegans	..VAP.....	FYG.....	RTV.....	GK	
CE03547_C._elegans	..AT.....	FQG.....	GVV.....	GE	
CE03542_C._elegans	..AKL.....	ING.....	KAD.....	GD	
CE15845_B_C._elegans	..AD.....		K.....	GA	
CE02997_C._elegans	..NNS.....	GRL.....	P.I.....	A.	
CE36953_C._elegans	..ATA.....	TNSEG.....	TKFE.....	GG	
YP_432439_H._chejuen	..LDK.....	QGNEM.....	GAGS.....	NP	
YP_529449.1_S._degra	..KDE.....	NGNEM.....	GAGS.....	NP	
YP_077582_B._licheni	..KDE.....	QGNEL.....	GAGA.....	NP	
ChiI_S._coelicolor	..LDT.....	NGKES.....	PAGS.....	NP	
NP_902986_C._violace	..LDD.....	SGKEI.....	PAGS.....	NP	
ZP_01159608_Photobac	..LDP.....	DGKEM.....	GAGS.....	NP	
ZP_01234708_V._angus	..LDP.....	DGKEM.....	GAGS.....	NP	
NP_233087_V._cholera	..VNA.....	AGDEM.....	GAGS.....	NP	
NP_230718_V._cholera	..VDA.....	NGNEI.....	KAGV.....	VP	
AAO07185_V._vulnific	..TDP.....	KGNEI.....	GAGS.....	NP	
ZP_01354150_C._phyto	..EAA.....	ISHEES.....	DFTYN.....	NL	
ZP_01246933_F._johns	..EHF.....	QGV.....	FK.....	NY	
YP_012734_L._monocyt	..EKT.....	NKDADG.....	SLTYG.....	AN	
YP_529337.1_A_S._deg	..DAS.....	LLVGCEACEARG.....		EPR	
ChiA_A_P._kodakarae	..SG.....	TPAG.....	TW.....	GPA.....	YETYG
AAG19274_Halobacteri	..DG.....	TPDG.....	TW.....	G.....	QDNG
AAG19275_Halobacteri	..DV.....	IPPG.....	TWNDL.....	RGPD.....	DANTG
CE03543_C._elegans	..AEI.....	RNN.....	RAD.....		GV
CE34961_C._elegans	..ADL.....	KNG.....	AAV.....		GN
CE20043_C._elegans	..VEL.....	VDN.....	KPQ.....		GE
CE15845_A_C._elegans	..ADL.....	VNG.....	IAV.....		GE
CE32863_A_C._elegans	..ADL.....	VNG.....	IAV.....		GE
CE03544_C._elegans	..VEL.....	KDN.....	EVE.....		GR
CE08731_C._elegans	..VTL.....	QDD.....	RAI.....		GE
CE28638_C._elegans	..DE.....		NSE.....		ES
CE32863_B_C._elegans	..AD.....		K.....		GA
CE01673_C._elegans					
CE02993_C._elegans	..KNL.....	TKG.....	A.F.....		A.
CE02996_C._elegans	..KNV.....	ARG.....	P.F.....		A.



CE02995_C._elegans	..QNS.....	AKG.....	G.F.....	A.....
CE02992_C._elegans	..AQN.....	ENG.....	PGK.....	S.....
CE02999_C._elegans	..DDS.....	AQG.....	P.Y.....	S.....
CE02998_C._elegans	..ADL.....	ING.....	KAQ.....	GM.....
CE09229_C._elegans	..AAP.....	QNG.....	KYE.....	GG.....
CE12928_C._elegans	..AAP.....	QNG.....	KYE.....	GG.....
CE23907_C._elegans	..VAS.....	NNG.....	MTI.....	GQ.....
CE32917_C._elegans	..VHL.....	VHG.....	SAV.....	GE.....
CE34579_C._elegans	..VTL.....	IDG.....	KAV.....	GE.....
CE25073_C._elegans	..AT.....	FQG.....	GVV.....	GE.....
CE03548_C._elegans	..AT.....	FNG.....	TVF.....	GE.....
NP_469498_L._innocua	..EKT.....	NKDADG..	SLTYG.....	AN.....
CE08730_C._elegans	..VTL.....	QNN.....	GAI.....	GE.....
Q8U1H4_P._furius	.....	.....	.....	.....
CE12474_C._elegans	..AEL.....	KNN.....	MAE.....	GR.....
CE02990_C._elegans	..NES.....	GRL.....	A.V.....	A.....
CE40270_C._elegans	..VNK.....	VHG.....	KIV.....	GQ.....
CE40296_C._elegans	..QNS.....	AKG.....	G.F.....	A.....
ChiB_S._marcescens	..ADY.....	WLVGCD	ECVRDK..	DPR.....
O10363_O._pseudotsug	..TAD.....	GPVPG.....	TWE.....	NG.....
AAP29899_C._fumifera	..TAA.....	GPVTG.....	TWE.....	DG.....
AAV73807_B._mori NPV	..TGN.....	GPVSG.....	TWE.....	DG.....
AAL56186_H._zea SNPV	..VAV.....	GPITG.....	TWE.....	NG.....
AAF33549_S._exigua N	..VAD.....	GPVPG.....	TWE.....	AG.....
AAZ38189_A._segetum	..VAT.....	GPVPG.....	TWE.....	AG.....
AAS82706_A._segetum	..VAQ.....	GPIKG.....	TWE.....	SG.....
ZP_01159013_Photobac	..TGT.....	GKLTGSKA	QGVWE.....	DG.....
ZP_01161077_Photobac	..KGT.....	GPVKG.....	TWE.....	DG.....
ZP_01159325_Photobac	..QGA.....	SFGTS.....	AQE.....	PG.....
ZP_01160869_Photobac	..GTI.....	DKGSD.....	IAD.....	PG.....
ZP_01233025_V._angus	..TGT.....	GKLTGSKA	QGVWE.....	DG.....
ZP_01236284_V._angus	..KGT.....	GPVKG.....	TWE.....	DG.....
ZP_01235109_V._angus	..QGA.....	SFGTS.....	AQE.....	PG.....
ZP_01235465_V._angus	..GTM.....	DKGSD.....	IAD.....	PG.....
AAO08114_V._vulnific	..TAT.....	GKLTGSKA	QGVWE.....	DG.....
AAO07498_V._vulnific	..QGA.....	QFGTG.....	EN.....	G.....
NP_232428_V._cholera	..VGN.....	GKLTGSKA	QGVWE.....	AG.....
YP_432951_H._chejuen	..NFI.....	LAIAG.....	YGSWE.....	AG.....
YP_529337.1_B_S._deg	..QAS.....	GAAKG.....	TWE.....	AG.....
YP_435912_H._chejuen	..TGG.....	GKHAG.....	TWE.....	DG.....
ZP_01137509_A._cellu	..TG.....	PAPG.....	HQY.....	SGN.....
ChiE_S._coelicolor	..GG.....	AAPG.....	QFP.....	AEA.....
ChiC_S._coelicolor	..TG.....	PATG.....	TYE.....	AG.....
ChiD_S._coelicolor	..NG.....	PAKG.....	TYE.....	NG.....
NP_903910_C._violace	..TG.....	PAKG.....	TYE.....	QG.....
YP_529072.1_S._degra	..NG.....	AAPG.....	TYE.....	KG.....
ZP_01431615_S._tropi	..TG.....	AAPG.....	TYE.....	PG.....
ZP_01136287_A._cellu	..TG.....	PSWL.....	NGG.....	SP.....
01315.1_C._cinereus	..GPGGG.....	TDVCGS.....	PTL.....	PGG.....
03252.1_C._cinereus	..GEGG.....	MDVCGV.....	TWG.....	PGG.....
05285.1_C._cinereus	..GQV.L.....	TDKCGR.....	PEF.....	PAG.....
05291.1_C._cinereus	..EQT.....	VDQCGV.....	ASG.....	PSG.....
01586.1_C._cinereus	..AASKDGDEG	KKKADGLV	TVQAADLRR..	WWG.....
128098_P._chrysospor	..WSAGGA.....	VDECGR.....	VTQPG.....	WGG.....
39872_P._chrysospori	..GPQG.....	TDVCGV.....	TNNN.....	PGG.....
138098_P._chrysospor	..ASPAG.....	TDACGN.....	PVAGG.....	FSG.....
129436_P._chrysospor	..VVLN.....	EDGN.....	AAD.....	G.....
EAA71245_G._zeae	..NDPL.....	IDACGN.....	PNP.....	PGG.....
MGG_04732_M._grisea	..DDPA.....	VDACGA.....	AQP.....	AGG.....
UM06190_U._maydis	..SSD.....	GS.....	TSS.....	G.....
04245_F._neoformans	..TVQN.....	ESGG.....	TTD.....	G.....
16170_R._oryzae	..SDADP.....	CPN.....	CKPS.....	YTG.....

01334_R._oryzae	.LAADP.....	CPN.....	ATPG.....	YTG
13934_R._oryzae	.FAADP.....	CPG.....	ANRS.....	FSG
07611_R._oryzae	.PWQDA.....	YCSSL.....	DSQS.....	ASG
10252_R._oryzae	.YWQDP.....	YCNV.....	EPGG.....	LSG
14659_R._oryzae	.FSQDP.....	YCSK.....	DPGG.....	LSG
231399_L._bicolor	.CSEDR.....	IDECAL.....	APL.....	VQG
180319_L._bicolor	.DTK.T.....	TDSCGV.....	TSG.....	PTG
191848_L._bicolor	.TTS.T.....	TDQCGT.....	TSG.....	PTG
317003_L._bicolor	.PAN.....	LQS.....	WWG.....	Q
246840_L._bicolor	.GVGG.....	IDVCGI.....	SEG.....	PGG
144643_L._bicolor	.VVD.....	EDG.....	GSD.....	S
310136_L._bicolor	.TSASV.....	LDPCGQ.....	PEG.....	ISG
629882_M._xanthus	.....	YV.....	GSD.....	N
630509_A_M._xanthus	.....	.....	.....	.....
YP_592598_Acidobacte	.....	CSA.....	APS.....	.....
YP_446903_S._ruber	.YD.....	TSRG.....	SYS.....	YDT.....
ZP_00739282_B._thuri	.KPG.....	SDGKLASKG.....	TWD.....	DYS.....
ZP_01245639_F._johns	.PRYIVPG.....	CTNPQNPTG.....	TWDGSGACEKSGSIEICDLVGNPVTNSHA	TGDTG
NP_976824_B._cereus	.KPG.....	SDGKLASKG.....	TWD.....	DYS.....
YP_077581_B._licheni	.GP.....	AKEG.....	TWE.....	K.....
631138_M._xanthus	.VP.....	TRG.....	TWD.....	DGS.....
ZP_01247029_F._johns	.....	A.....	SAN.....	Q
ZP_01234549_V._angus	.....	.....	.....	H
ZP_01160697_Photobac	.....	.....	.....	H
ZP_01158584_Photobac	.....	.....	.....	H
AN0549_E._nidulans	.SGGN.....	AGN.....	CSN.....	EVG
AN8481_E._nidulans	.SGGN.....	AGP.....	CSN.....	EVG
AN9390_E._nidulans	.AGGN.....	PGK.....	CSA.....	SAG
AN0517_E._nidulans	.DGGK.....	PGS.....	CSD.....	TTG
AN0541_E._nidulans	.DAGL.....	RGE.....	CSG.....	ESG
AN5077_E._nidulans	.GPGA.....	GGR.....	CTA.....	TPG
AN0509_E._nidulans	NSDAT.....	KGP.....	CTG.....	TAG
AN7613_E._nidulans	RTAAI.....	PGM.....	CTR.....	TPG
07035_N._crassa	.SGGN.....	AGK.....	CSG.....	TTG
07484_N._crassa	ASDAS.....	KGP.....	CTD.....	TAG
05317_N._crassa	NSYAK.....	PGV.....	CTG.....	TAG
EAA74768_G._zeae	.GPAN.....	AGK.....	CSA.....	EKG
EAA78168_G._zeae	.SAGD.....	AG.....	CSG.....	EAG
EAA75711_G._zeae	.GPSE.....	KGE.....	CTD.....	SDG
EAA68447_G._zeae	HSDAK.....	EGK.....	CTG.....	QAG
EAA77156_G._zeae	VSEAE.....	PGV.....	CTG.....	EPG
12510_S._sclerotioru	.SGGM.....	KGK.....	CSR.....	EVG
00773_S._sclerotioru	.SAGD.....	EGV.....	CSA.....	SAG
05454_S._sclerotioru	.GGAS.....	PGP.....	CTA.....	NSG
00677_S._sclerotioru	.GPSI.....	PGP.....	CTT.....	QMG
02128_S._sclerotioru	TSGAY.....	AGA.....	CTQ.....	TP.
MGG_04534_M._grisea	.DGAK.....	GGE.....	CTG.....	TPG
MGG_01336_M._grisea	.GPSAG.....	GD.....	CQR.....	SPG
14527_P._nodorum	.GGAN.....	PGP.....	CSN.....	AAG
15411_P._nodorum	.GGSAGA.....	AGS.....	CTA.....	FPG
02214_P._nodorum	.GPSK.....	AGS.....	CTL.....	QEG
04761_C._immitis	.GGAA.....	KGA.....	CSG.....	ESG
04323_A._capsulatum	AGGAQ.....	PGL.....	CTL.....	NSG
00533_B._fuckeliana	.GLSE.....	PGP.....	CST.....	EAG
Chi18_1_H._jecorina	DSGAL.....	PGP.....	CTN.....	TSG
Chi18_8_H._jecorina	DSKAY.....	KGR.....	CTG.....	TAG
Chi18_9_H._jecorina	KSEAA.....	AGR.....	CTN.....	ARG
Chi18_10_H._jecorina	QSLAA.....	PGG.....	CTN.....	SSG
02650_A._capsulatum	.LEDP.....	NTGE.....	STG.....	QAG
AN0221_E._nidulans	.MEDP.....	DTGA.....	DLG.....	QAG
06020_N._crassa	.MEDP.....	VSGA.....	DLG.....	RSB
EAA76014_G._zeae	.LEDP.....	ETGA.....	DLG.....	KTG

Chi18_4_H._jecorina	.LEDP.....	TSGA....	DLG.....	RTG
09277_P._nodorum	.MEDP.....	KTGA....	DLG.....	KAG
05838_A._capsulatum	.GEF.....	ENGT....	DAG.....	TSG
EAA69039_G._zeae	.LENP.....	EDGS....	DTG.....	KSG
MGG_06594_M._grisea	.LEDA.....	E.GN....	DTG.....	LSG
Chi18_11_H._jecorina	.LENP.....	D.GS....	DPL.....	VSG
02644_A_P._nodorum	.AEDP.....	VTGK....	DTL.....	TSG
AN9447_E._nidulans	.MEA.....	ADGS....	DNG.....	KSG

	790	800	810	820	830	840
NP_979924_B._cereus	ALARKYNVP		IRYDFT			
YP_077302_B._licheni	ETASENNAA		IQYDET			
YP_091539_B._licheni	QLAMKHQAP		IQYDTN			
YP_079121_B._licheni	QLAMKHQAP		IQYDTN			
YP_074366_S._thermop	RQAARRGAA		IEFDTR			
YP_075811_S._thermop	NRAIDVGAW		IQYDED			
YP_075619_S._thermop	SLAARHGAE		VRWDDE			
ZP_01354047_C._phyto	QIAAANNVAV		IQFDEV			
ZP_01354926_C._phyto	KTLEANKAT		KSWDQT			
NP_902406_C._violace	ALIARYGAQ		PRYDAG			
ZP_01136704_A._cellu	NLVAQYHAT		PRWSAP			
ZP_00526542_S._usita	DLAKAIDAT		VQWDPL			
AAF46212.1_D._melano	FTTLTETCE		CVTKFF		KPNLSY.D	
AAF46534.1_D._melano	LLSWPEVCA		KLPNPA		NQHLKGADGPLRKVG	
AAF46544.1_D._melano	YLAYYEICQ		TLKDDP		EWTVVQPN	
At4g19720_A._thalian	SINYDQIKR		LIVDHK		ARPVFD	
At4g19750_A._thalian	SITYAKIRN		YIIDNG		AATFHD	
EAA67655_G._zeae	VYLLKDLPR		PG		AVTTYNAD	
EAA73155_G._zeae	IWDYKVLPK		PG		ASLVYDRD	
EAA74986_G._zeae	VWDYKALPK		PG		AEIKYDEE	
EAA74223_G._zeae	VYDYKALPL		EG		AQEYGDRG	
MGG_05533_M._grisea	IWIYKDLPR		AG		ATVLYDDV	
MGG_01247_M._grisea	VWLYKDLPR		PG		AIVAYDNV	
MGG_00086_M._grisea	IWDYKALPR		PG		ATELYDAA	
MGG_07927_M._grisea	VYDFKALPL		PG		AEERFDEE	
Chi18_6_H._jecorina	VWLYRDLPR		PG		SVVNLNRD	
Chi18_5_H._jecorina	VWDYKALPK		AG		ATVQYDDV	
Chi18_7_H._jecorina	IFDYKVLPL		PG		SQEFWDEA	
04883_N._crassa	IWDYKVLPK		SG		AKVFLDEK	
04554_N._crassa	VHDYKKLPL		EG		AEERVDYE	
11407_B._fuckeliana	VWDYKDLPR		AG		ATEYYASD	
05350_B._fuckeliana	VHDFKKLPQ		EG		AREFVDEE	
11700_S._sclerotioru	IYDYKVLPR		AG		ATEFYLPD	
11304_S._sclerotioru	VHDFKKLPQ		EG		AEIIVDEE	
08020_S._sclerotioru	VYDYKALPL		AG		ATEVYDKK	
01250_A._capsulatum	VWDYKVLPR		QG		SEEMNDHE	
05886_A._capsulatum	IWDYKVLPR		EG		AKEHMEGSGSKGG	
06565_A._capsulatum	IWDYKSLPK		VG		AVEYIDSLEKGG	
05250_C._immitis	VWDYKALPR		PD		SEEQNDDQ	
02795_C._immitis	VWDYKDMPQ		QG		AQVTELED	
03822_C._immitis	IWDYKTLPR		PG		AKEFMDPMVNGG	
AN5454_E._nidulans	VWDYKALPK		PG		AEVVEVEE	
AN4871_E._nidulans	VYDYKALPR		PG		ATEQLDTN	
00269_P._nodorum	VYDYKTLPR		AG		ASVTNLDL	
04870.1_C._cinereus	VYDYRTLPL		PLD.T		TFTYNDED	
09921.1_C._cinereus	IYSYKALPL		AG		GQVYENKT	
124149_P._chrysospor	VYDYRALPL		PG		SYVLQDDA	
134311_P._chrysospor	IYSYSALPL		AG		AQVFENLT	
03412_F._neoformans	MWDYKALPR		PG		AQETNDHR	
13635_R._oryzae	QFDYKCLPK		PG		ATEYHDFQ	
UM04261_U._maydis	NWDYKFLPV		KG		AKEMINTK	

EAA69503_G._zeae	TFEYNQLPR.....	KGC.....	KEVVDKR.....
EAA70860_G._zeae	EIDYCDLPD.....	EWVT.....	NAEVDQS.....
Chi18_3_H._jecorina	TFEYSELPR.....	KGC.....	KEIVDRR.....
Chi18_2_H._jecorina	EMDYCDIPD.....	EWVR.....	QAVVDEA.....
03026_N._crassa	SFEYCQLPR.....	RGT.....	KEQVDKR.....
01594_B._fuckeliana	TFEYKLLPR.....	PGT.....	QEVVDTT.....
05897_S._sclerotioru	TFEYKLLPR.....	PGT.....	QEVVDTA.....
04742_A._capsulatum	VFDYRELPL.....	PGT.....	EEVHDAV.....
04750_C._immitis	VFDYCDLPL.....	PGS.....	VEQHDDR.....
04719_P._nodorum	TFEYRDLPR.....	PGA.....	TEHVDER.....
MGG_08458_M._grisea	EVDYNDLPT.....	ADLD.....	RAMVDPE.....
CHT4_C._albicans	VVDYNKFGD.....	TF.....	DYEDFDP.....
01119_L._elongisporu	ILGNAKDQN.....	IL.....	EHG.FDVK.....
XP_454053_K._lactis	IWLYNQLPI.....	DG.....	SKEQFDSN.....
CTS2_S._cerevisiae	IWPYKNLPR.....	IG.....	TIEQYDPK.....
246746_L._bicolor	SYDYRALAL.....	PG.....	SFTYRDQD.....
03209_N._crassa	TWVYRDLPR.....	PG.....	AKEEYDNL.....
14474_P._nodorum	TLDYKFLPL.....	NG.....	SKVYQDKE.....
CE06282_C._elegans	TYLSRLAVK.....	Q.EGFQVE.....	SYSYDPA.....
CE03547_C._elegans	TSMSRKLVS.....	E.EGYDFS.....	NPTYNPE.....
CE03542_C._elegans	PYISRLSVK.....	Q.KGIELF.....	PYSWDNA.....
CE15845_B_C._elegans	T.MSRSIK.....	K.KGWRLT.....	SADWDET.....
CE02997_C._elegans	.LPRRQLR.....	QYNWNLT.....	DIKFHNL.....
CE36953_C._elegans	DVQWRDLH.....	EKFDTT.....	KTKFHS.....
YP_432439_H._chejue	LWHAKNLAE.....	GVAG.SYIADYGLDPA.....	NDPTDVLTSYSRHYDAT.....
YP_529449.1_S._degra	MWHAKNLEN.....	NILG.DYLTAYGLDPI.....	NNPDHQLSGNYQRYDDV.....
YP_077582_B._licheni	MWHAKNLEK.....	GIAG.SYLERYGLS.....	KADLTGVYKRHYDAG.....
ChiI_S._coelicolor	MWHAKNLEK.....	GIVG.DYVTDYGF.....	ADTKLTGTYARKYDST.....
NP_902986_C._violace	MWHAKNLEK.....	GLAG.SYLAAYGIDP.....	TLPINQLTGSYQRNYNGA.....
ZP_01159608_Photobac	MWHAKNLEQ.....	GIFG.SYTAAYGLDPV.....	NDPQDKLVGSYTRNYDDV.....
ZP_01234708_V._angus	MWHAKNLEQ.....	GIFG.SYTAAYGLDPV.....	NDPQDKLVGSYTRNYDDV.....
NP_233087_V._cholera	MWHAKNLEK.....	GIWG.SYAAAYKLDPT.....	TTP...LIGTYVRNYDSV.....
NP_230718_V._cholera	MWHAAMNLMHAEKLGIDGMP	SYGPAWMDP.....	NNPKHLIEGKYERVWSQE.....
AAO07185_V._vulnific	MWHAKNLEK.....	GIFG.SYASAYKLDPV.....	NDPQDKLVGSYVRNYDSV.....
ZP_01354150_C._phyto	KENYISK.N.....	G.....	YTRYWDDI.....
ZP_01246933_F._johns	ATTYTEA.N.....	G.....	WKYFWDDK.....
YP_012734_L._monocyt	NENPIKTGD.....	GGRAGGVWAYRSIDALKAKTPT	LKEYFDDT.....
YP_529337.1_A_S._deg	IATFNDIQ.....	LIEGN.....	YGYTRHFDDQ.....
ChiA_A_P._kodakarae	VMDYWDVAE.....	KN.....	QSSEYEYHWDPI.....
AAG19274_Halobacteri	IKEYWDITQ.....	N.LA.....	PSSDYETFWDDT.....
AAG19275_Halobacteri	AFDYGDIAA.....	N.YE.....	GADAWTKQRNEQ.....
CE03543_C._elegans	PYMDRSSAD.....	Y.K.....	MASWDNL.....
CE34961_C._elegans	SYMSRWTVD.....	H.EGWELT.....	PALWDDV.....
CE20043_C._elegans	AYMSRWSAQ.....	H.EELDLS.....	PADWDEE.....
CE15845_A_C._elegans	PYISRWSAE.....	KTHGLSLG.....	STNWDTE.....
CE32863_A_C._elegans	PYISRWSAE.....	KTHGLSLG.....	STNWDTE.....
CE03544_C._elegans	SQLSRYTVE.....	H.EDMELS.....	PESWDNA.....
CE08731_C._elegans	A.....		
CE28638_C._elegans	AYMSRKTVA.....	K.EKIRLT.....	LPSWDTL.....
CE32863_B_C._elegans	T.MSRSIK.....	K.KGWRLT.....	SADWDET.....
CE01673_C._elegans	.....		TIEQTEQ.....
CE02993_C._elegans	.VRWRELL.....	QQKWNLE.....	DIKFHNL.....
CE02996_C._elegans	.VRWRHLR.....	QRNWNLT.....	DIKFHNL.....
CE02995_C._elegans	.VRWRELL.....	QQKWDM.....	NIKFHNL.....
CE02992_C._elegans	.IGWRKFIF.....	DRRNTIP.....	QWHD.....
CE02999_C._elegans	.YGWKQFAR.....	MSHGFQDN.....	DFEWNEE.....
CE02998_C._elegans	FVAWKNLA.....	GRGWKDS.....	EALWHEE.....
CE09229_C._elegans	YVGWRNLA.....	KEGWKNG.....	SASWHEK.....
CE12928_C._elegans	YVGWRNLE.....	KEGWKNG.....	SATWHKK.....
CE23907_C._elegans	RYMNRSIVK.....	Q.QGFQLE.....	RYSYDEL.....
CE32917_C._elegans	SFMSRKSVL.....	E.KGYKLN.....	SYSYDEL.....
CE34579_C._elegans	VYMPRRSAL.....	Q.KGYNLS.....	SYNYDDL.....



CE25073_C._elegans	TSMSRKL <sup>V</sup> Q.....	E.EGYDFS.....	NPTYNPE.....
CE03548_C._elegans	ANMSRKL <sup>V</sup> Q.....	Q.EGYDLS.....	HP <sup>T</sup> FNSE.....
NP_469498_L._innocua	NENPIKT <sup>G</sup> ED.....	GGRAGGVWAYRSIDALKAKTPTLKE <sup>Y</sup> WDDT.....	
CE08730_C._elegans	VYMSRWTA <sup>E</sup> .....	S.DGIELS.....	NPSWDDT.....
Q8U1H4_P._furiosus			
CE12474_C._elegans	TQISRWTAE.....	H.EGLELS.....	PSSWDNL.....
CE02990_C._elegans	.LRWREL <sup>P</sup> .....	HHKWNLE.....	NIK <sup>F</sup> HNL.....
CE40270_C._elegans	SHMSRMIV <sup>Q</sup> .....	Q.KGFVLT.....	PYSFDNA.....
CE40296_C._elegans	.VRWRELL.....	QQKWDMS.....	NIK <sup>F</sup> HNL.....
ChiB_S._marcescens	IASYRQLE <sup>Q</sup> .....	MLQGN.....	YGYQRLW <sup>N</sup> DK.....
O10363_O._pseudotsug	VVDYRQINN.....		ELSKYIYRFDA <sup>A</sup> .....
AAP29899_C._fumifera	VVDYRQIEN.....		ELNKYIYKFDSV.....
AAV73807_B._mori_NPV	VVDYRQIQK.....		DLNNYVYTFDSA.....
AAL56186_H._zea_SNPV	VVDYRQIAK.....		NISRYEYAFDDV.....
AAF33549_S._exigua_N	VVDYRQIVH.....		NMSQYDYVYDEV.....
AAZ38189_A._segetum	VVDYRQIVH.....		NITQYNYDYDEV.....
AAS82706_A._segetum	VVDYKDLIQ.....		RYTDTYY..DSV.....
ZP_01159013_Photobac	VIDYKGIKS.....	YMLG.....	ANSQGINGFEYGYDEQ.....
ZP_01161077_Photobac	VVDYRDIVD.....		NRSTNGWESHYDAK.....
ZP_01159325_Photobac	YFMYWDLKR.....	NYT.....	KAQGYISGYDEK.....
ZP_01160869_Photobac	YFNYSDIVK.....	YLIN.....	N.KKMGYQYYYDEK.....
ZP_01233025_V._angus	VIDYKGIKS.....	YMLG.....	ANSQGINGFEYGYDEQ.....
ZP_01236284_V._angus	VVDYRDIVD.....		NRSTNGWESHYDAQ.....
ZP_01235109_V._angus	YFMYWDLKR.....	NYT.....	KAQGYISGYDEK.....
ZP_01235465_V._angus	YFNYSDIVK.....	YLIN.....	N.KKMGYQYYYDEK.....
AAO08114_V._vulnific	VIDYKGIKS.....	FMLG.....	PNSTGINGFEYGYDDQ.....
AAO07498_V._vulnific	YFMFWDLVK.....	NYG.....	EKQGYQYNYDEQ.....
NP_232428_V._cholera	VIDYKGVKN.....	FMLG.....	ANKTGVNGFEYGYDEQ.....
YP_432951_H._chejuen	VLEGYDMYQ.....	SFLDP.....	SLRPYNGYKLYTDKA.....
YP_529337.1_B_S._deg	VQDYRDLYD.....	NYIG.....	TNGTGINGFSAHYDEI.....
YP_435912_H._chejuen	VLDYRAIEQ.....	KFLGG.....	ANGQGIDGYKYFYDEK.....
ZP_01137509_A._cellu	IAMYKELTG.....	FVD.....	N..PAYTFWDPV.....
ChiE_S._coelicolor	VRGYSNLIG.....	SYPS.....	M..TVHHDEESV.....
ChiC_S._coelicolor	IEDYKVL.....		K..NSCPATGTI.....
ChiD_S._coelicolor	IEDYKVL.....		K..TSCPATGTV.....
NP_903910_C._violace	IEDYRIL.....	VK.....	R..SAKQFNSPV.....
YP_529072.1_S._degra	IEDYKVL.....		K..NTCPATGTI.....
ZP_01431615_S._tropi	FDDYKVL.....		K..NTCPVTGTV.....
ZP_01136287_A._cellu	WAQLEALG.....		YAPYRDPI.....
01315.1_C._cinereus	TFNFWGLIE.....	NG.....	FLNK.....
03252.1_C._cinereus	VYTYWGLFE.....	GG.....	FLNA.....
05285.1_C._cinereus	LFTFNGLIA.....	GG.....	LLGT.....
05291.1_C._cinereus	LFNFAGLVD.....	AG.....	YLN <sup>P</sup> .....
01586.1_C._cinereus	QIPFKTIVS.....	SGA.....	LVKK.....
128098_P._chrysospor	VWNFAGMIS.....	GG.....	YLDQ.....
39872_P._chrysospori	NWDYWGLVS.....	EG.....	WVWP.....
138098_P._chrysospor	IYNYRGLVE.....	KG.....	YLDA.....
129436_P._chrysospor	EVQFRDLVQ.....	QGV.....	LHTADTL <sup>S</sup> FAGH.....
EAA71245_G._zeae	TYPFWSLIK.....	EAK.....	FLDA.....
MGG_04732_M._grisea	TFTFWSMVT.....	EGQ.....	FLDE.....
UM06190_U._maydis	QINFSTLVS.....	QGA.....	LKLG.....
04245_F._neoformans	QVMWYGLLN.....	QGA.....	LTLS.....
16170_R._oryzae	EYQWRSIVA.....	NG.....	ILEN.....
01334_R._oryzae	EYQWRSIVA.....	NG.....	ILEN.....
13934_R._oryzae	EIQWRTIEQ.....	RG.....	IDRN.....
07611_R._oryzae	VWRWAYLRS.....	QGI.....	LTSP.....
10252_R._oryzae	IWKWTNLRK.....	EGI.....	LKDDF.....
14659_R._oryzae	TWQYSHLLS.....	QQV.....	LKTA.....
231399_L._bicolor	ILDFKRITQ.....	EG.....	YLDK.....
180319_L._bicolor	VFSFEG <sup>L</sup> VT.....	AG.....	YLTS.....
191848_L._bicolor	VFNFE <sup>G</sup> MVS.....	AG.....	YLTS.....
317003_L._bicolor	QIPFSAIVK.....	SGA.....	LVKK.....

246840_L._bicolor	EYTYWGLME.....EG.....FLNT.....
144643_L._bicolor	QVQFRDLLS.....QGA.....LVRX.....
310136_L._bicolor	VFNFNGMIA.....HG.....FLNS.....
629882_M._xanthus	SFTYSKILQ.....LSA.....
630509_A_M._xanthus	.....
YP_592598_Acidobacte	.WNYGTIYK.....QR.....
YP_446903_S._ruber	LANHVAT.....Q.....P.....GFERQWDAV.....
ZP_00739282_B._thuri	VYDYGDLTA.....NYVN.....K.NGFVRYWNDT.....
ZP_01245639_F._johns	YLDPNTMMV.....TPSA.....ASAGWVRYFDNT.....
NP_976824_B._cereus	VYDYGDLLAA.....NYVN.....K.NGFVRGWNDI.....
YP_077581_B._licheni	VFD FSDLER.....NYVN.....Q.NGYKRYWNDQ.....
631138_M._xanthus	VFD FDKDIKA.....NYER.....PGSGYTKFFHPE.....
ZP_01247029_F._johns	GISYANIVA.....QY.....
ZP_01234549_V._angus	APTYGVLVK.....DD.....
ZP_01160697_Photobac	APTYGALVK.....EN.....
ZP_01158584_Photobac	GPTYTKMVH.....DQ.....
AN0549_E._nidulans	ILLNSEITE.....VMADRK.....VKST.LN.K.....
AN8481_E._nidulans	ILLNSEIVD.....IMNEQQ.....VKPS.LD.K.....
AN9390_E._nidulans	SLMFSEIQE.....IIDAGG.....AKVT.ND.E.....
AN0517_E._nidulans	ILTYAEISS.....RNNSLD.....VHTF.YD.P.....
AN0541_E._nidulans	ILTFKEIMA.....RQKRLN.....QKVIKYD.E.....
AN5077_E._nidulans	ILSYMEIME.....LLENSG.....ATAH.LD.E.....
AN0509_E._nidulans	YLANAEINK.....ILSGSPSGLNTR.....DTASSRVTAH.YL.D.....
AN7613_E._nidulans	IIAIAEIEA.....LMIEG.....DINES.FH.D.....
07035_N._crassa	VLLHAEIQD.....EISARK.....LTPT.LH.R.....
07484_N._crassa	YISNAEIND.....IIVN..N.....ASRVNQ.N.FI.D.....
05317_N._crassa	YIADAEIAE.....IMAGTGS.....KRSGRVTAS.FV.D.....
EAA74768_G._zeae	ILLNSEIEG.....VIKDWD.....LTPK.LY.K.....
EAA78168_G._zeae	ILFNSEISD.....LIREKK.....LRPK.LY.K.....
EAA75711_G._zeae	VMSLGEIKN.....LIKNGK.....VKSIIYLE.....
EAA68447_G._zeae	YIADAEIAE.....ILKDKS.....RVVKH.FV.D.....
EAA77156_G._zeae	YLSDAEIRL.....IAYDAKK.....G.KAGVTAKTWY.D.....
12510_S._sclerotioru	ILLNSEIDD.....LVKANG.....VKPK.LY.E.....
00773_S._sclerotioru	ILLSSEIEQ.....IMSDND.....LTPV.FY.K.....
05454_S._sclerotioru	TLSYAEIVD.....IIDRNK.....LSPY.HD.K.....
00677_S._sclerotioru	ILSMREIEV.....LVLREG.....LGVSWVG.GEAAGQ.....
02128_S._sclerotioru	..ANAEIDS.....IISGNATVLGT.....DGSSVRVTGTPFV.YL.....
MGG_04534_M._grisea	VLSVAEINK.....IINKGG.....KVT.YD.A.....
MGG_01336_M._grisea	VLSLNEINR.....IAAARG.....LTPRYDS.....
14527_P._nodorum	ILD LQEIKD.....IVSKNN.....LNPT.WD.K.....
15411_P._nodorum	VLSNLEIRR.....LIKDEG.....ITPYFNT.....
02214_P._nodorum	ILSSCEIRR.....LISEKH.....LSWKVIQ.G.....
04761_C._immitis	ILTYREIMA.....MIKTDK.....LKPF.HD.K.....
04323_A._capsulatum	TLSNYEINR.....VLKEQS.....PEVI.YN.K.....
00533_B._fuckeliana	ILSMREIEV.....LVLREG.....LRATWAG..ASAAE.....
Chi18_1_H._jecorina	YISNYEINR.....IVAGNP.....SAEVHWD.....
Chi18_8_H._jecorina	YISNAEITE.....IINKHG.....NYSIVNS.YI.D.....
Chi18_9_H._jecorina	YLANAEINE.....IISKSK.....GH..PKT.WY.D.....
Chi18_10_H._jecorina	YISNAEILD.....IMEDRK.....SYPVQAWY.D.....
02650_A._capsulatum	AFSWNEPAP.....G.....
AN0221_E._nidulans	AFSWNDRVP.....Q.....
06020_N._crassa	AFSWHDDVP.....K.....
EAA76014_G._zeae	GFSWHDEV P.....K.....
Chi18_4_H._jecorina	AFSWHDEV P.....V.....
09277_P._nodorum	AFSWHDQVP.....S.....
05838_A._capsulatum	SVTFEVAEI.....S.PPRAP.....VGVSPNATCGPLNGFRC.....
EAA69039_G._zeae	SMTFEAANF.....A.AAPT.N.....LTTSTDATCGAGTFFKC.....
MGG_06594_M._grisea	AFTFEAANF.....A.TTPT.N.....LTLTTDASCGANTFNKC.....
Chi18_11_H._jecorina	AITFEASTY.....A.G.....
02644_A_P._nodorum	AWTFEP SHM.....KPV DASA.....LTVSYDGT CGPDKGTRC.....
AN9447_E._nidulans	AMTFEPQNM.....A.AQPSD.....LKVSTDMTCGLAKGTRC.....

	850	860	870	880	890	900
NP_979924_B._cereus	.....	.....	.....	AQAPHFNYFD	.....	.....
YP_077302_B._licheni	.....	.....	.....	AQAPNFRYTD	.....	.....
YP_091539_B._licheni	.....	.....	.....	SESPFFRYTD	.....	.....
YP_079121_B._licheni	.....	.....	.....	SESPFFRYTD	.....	.....
YP_074366_S._thermop	.....	.....	.....	AQAPFYRYVD	.....	.....
YP_075811_S._thermop	.....	.....	.....	AQSPFYRYWD	.....	.....
YP_075619_S._thermop	.....	.....	.....	AQVPWFRYV	.....	.....
ZP_01354047_C._phyto	.....	.....	.....	AQTPFFTYTR	.....	.....
ZP_01354926_C._phyto	.....	.....	.....	TGQYYAEYEK	.....	.....
NP_902406_C._violace	.....	.....	.....	THSLTFNYGA	.....	.....
ZP_01136704_A._cellu	.....	.....	.....	DGEPYVTTYD	.....	.....
ZP_00526542_S._usita	.....	.....	.....	EHAPWFFYFR	.....	.....
AAF46212.1_D._melano	.....	.....	.....	AESCSPYLSAL	.....	.....
AAF46534.1_D._melano	.....	.....	.....	DPTKRFGSYAYS	.....	.....
AAF46544.1_D._melano	.....	.....	.....	ANVMGPYAYRR	.....	.....
At4g19720_A._thalian	.....	.....	.....	STVVGDYCFAG	.....	.....
At4g19750_A._thalian	.....	.....	.....	PAVIGFYCYVG	.....	.....
EAA67655_G._zeae	.....	.....	.....	LMASYTYD	.....	.....
EAA73155_G._zeae	.....	.....	.....	AQASYSYD	.....	.....
EAA74986_G._zeae	.....	.....	.....	AQAYYSYD	.....	.....
EAA74223_G._zeae	.....	.....	.....	CCASYCYN	.....	.....
MGG_05533_M._grisea	.....	.....	.....	AKASYTMD	.....	.....
MGG_01247_M._grisea	.....	.....	.....	AKASYSYD	.....	.....
MGG_00086_M._grisea	.....	.....	.....	TGATWSYD	.....	.....
MGG_07927_M._grisea	.....	.....	.....	AGATYSYD	.....	.....
Chi18_6_H._jecorina	.....	.....	.....	IIAAYSYD	.....	.....
Chi18_5_H._jecorina	.....	.....	.....	AKASYSYD	.....	.....
Chi18_7_H._jecorina	.....	.....	.....	IGASYCYN	.....	.....
04883_N._crassa	.....	.....	.....	VGASWSYD	.....	.....
04554_N._crassa	.....	.....	.....	SGATYCYH	.....	.....
11407_B._fuckeliana	.....	.....	.....	VVGTYSYD	.....	.....
05350_B._fuckeliana	.....	.....	.....	TCASYSYN	.....	.....
11700_S._sclerotioru	.....	.....	.....	VVATYSYD	.....	.....
11304_S._sclerotioru	.....	.....	.....	TCASYSYN	.....	.....
08020_S._sclerotioru	.....	.....	.....	IGASYSWD	.....	.....
01250_A._capsulatum	.....	.....	.....	LFASWSYD	.....	.....
05886_A._capsulatum	.....	.....	.....	CGASWSYD	.....	.....
06565_A._capsulatum	.....	.....	.....	CGASWSYD	.....	.....
05250_C._immitis	.....	.....	.....	LLASWSYS	.....	.....
02795_C._immitis	.....	.....	.....	IAASYSYD	.....	.....
03822_C._immitis	.....	.....	.....	AGASWSYD	.....	.....
AN5454_E._nidulans	.....	.....	.....	IAASFSYD	.....	.....
AN4871_E._nidulans	.....	.....	.....	IGASWSYD	.....	.....
00269_P._nodorum	.....	.....	.....	LGASWSYD	.....	.....
04870.1_C._cinereus	.....	.....	.....	LGASWTTYD	.....	.....
09921.1_C._cinereus	.....	.....	.....	DMTSYSYD	.....	.....
124149_P._chrysospor	.....	.....	.....	AVASWTYN	.....	.....
134311_P._chrysospor	.....	.....	.....	DVTSYSYD	.....	.....
03412_F._neoformans	.....	.....	.....	LGASYSYD	.....	.....
13635_R._oryzae	.....	.....	.....	RLASWSYD	.....	.....
UM04261_U._maydis	.....	.....	.....	IAASWSYD	.....	.....
EAA69503_G._zeae	.....	.....	.....	HVAAQCM	.....	.....
EAA70860_G._zeae	.....	.....	.....	VAAASFVD	.....	.....
Chi18_3_H._jecorina	.....	.....	.....	YIAAQCV	.....	.....
Chi18_2_H._jecorina	.....	.....	.....	AVAAWYVD	.....	.....
03026_N._crassa	.....	.....	.....	AVAAQCV	.....	.....
01594_B._fuckeliana	.....	.....	.....	TISASCY	.....	.....
05897_S._sclerotioru	.....	.....	.....	TVSASCY	.....	.....
04742_A._capsulatum	.....	.....	.....	FCAAYCVD	FGGGS	.....
04750_C._immitis	.....	.....	.....	LCAAF	CV	.....

04719_P._nodorum	.....VGAAYCM.....
MGG_08458_M._grisea	.....LCAAWYLCE.....
CHT4_C._albicans	.....KVGALKYD.....
01119_L._elongisporu	.....KVAAFAYN.....
XP_454053_K._lactis	.....AVSAYCFD.....
CTS2_S._cerevisiae	.....YVSAYCFD.....
246746_L._bicolor	.....AIASWSYD.....
03209_N._crassa	.....AKATYSYD.....
14474_P._nodorum	.....TLSSWSWD.....
CE06282_C._elegans	.....PRAAFSYN.....
CE03547_C._elegans	.....IRAAFKYN.....
CE03542_C._elegans	.....TKSSYIWK.....
CE15845_B_C._elegans	.....TKTSYIWN.....
CE02997_C._elegans	.....TKTSYIWI.....
CE36953_C._elegans	.....SKTPFIWL.....
YP_432439_H._chejuen	.....AVAPWLWN.....
YP_529449.1_S._degra	.....LVAPWLWN.....
YP_077582_B._licheni	.....LAAPWLWN.....
ChiI_S._coelicolor	.....LVAPWLWN.....
NP_902986_C._violace	.....LAAPWLWN.....
ZP_01159608_Photobac	.....AVAPWLWN.....
ZP_01234708_V._angus	.....AVAPWLWN.....
NP_233087_V._cholera	.....AVAPWLWN.....
NP_230718_V._cholera	.....LQTAWLWN.....
AAO07185_V._vulnific	.....AVAPWLWN.....
ZP_01354150_C._phyto	.....SKAACLHN.....
ZP_01246933_F._johns	.....AKAPYWYN.....
YP_012734_L._monocyt	.....AKAPYLYS.....
YP_529337.1_A_S._deg	.....TKAPWLYH.....
ChiA_A_P._kodakarae	.....AQVAWLYS.....
AAG19274_Halobacteri	.....AKVPWLYS.....
AAG19275_Halobacteri	.....GGVPYLWN.....
CE03543_C._elegans	.....TSTPYIWK.....
CE34961_C._elegans	.....TKTPYVWN.....
CE20043_C._elegans	.....TRSSYTWN.....
CE15845_A_C._elegans	.....TKTSFLWD.....
CE32863_A_C._elegans	.....TKTSFLWD.....
CE03544_C._elegans	.....TQTPYVLD.....
CE08731_C._elegans	.....TETSSMYN.....
CE28638_C._elegans	.....TKTSYIWN.....
CE32863_B_C._elegans	.....IDMQYVWN.....
CE01673_C._elegans	.....TKTSYIWI.....
CE02993_C._elegans	.....TKTSYIWI.....
CE02996_C._elegans	.....TKTSYIWI.....
CE02995_C._elegans	.....TKTSYMWI.....
CE02992_C._elegans	.....SKSSYAWD.....
CE02999_C._elegans	.....TRTPYIWK.....
CE02998_C._elegans	.....TQIPYIWN.....
CE09229_C._elegans	.....TKTPYIMN.....
CE12928_C._elegans	.....TKTPYIMN.....
CE23907_C._elegans	.....TKGSFIYN.....
CE32917_C._elegans	.....SRSAFIYN.....
CE34579_C._elegans	.....SETAFIYN.....
CE25073_C._elegans	.....IRAAFKYN.....
CE03548_C._elegans	.....IRAAFKYN.....
NP_469498_L._innocua	.....AKAPYLYS.....
CE08730_C._elegans	.....TKTLYIWK.....
Q8U1H4_P._furiosus	.....TMTPYILD.....
CE12474_C._elegans	.....TKTSYIWI.....
CE02990_C._elegans	.....TRNAFIYN.....
CE40270_C._elegans	.....TKTSYMWI.....
CE40296_C._elegans	.....TKTSYMWI.....



ChiB_S._marcescens	TKTPYLYH
O10363_O._pseudotsug	AKAAYVFN
AAP29899_C._fumifera	AKAAYVFN
AAV73807_B._mori_NPV	AQASYVFD
AAL56186_H._zea_SNPV	AKAAYVFD
AAF33549_S._exigua_N	VKGAYVYN
AAZ38189_A._segetum	AKGAYVYD
AAS82706_A._segetum	AQAAYAFa
ZP_01159013_Photobac	AEAPYVWN
ZP_01161077_Photobac	AEASYQWN
ZP_01159325_Photobac	AEAPYLWN
ZP_01160869_Photobac	AEAAVLFS
ZP_01233025_V._angus	AEAPYVWN
ZP_01236284_V._angus	AEASYQWN
ZP_01235109_V._angus	AEAPYLWN
ZP_01235465_V._angus	AEAAVLFS
AAO08114_V._vulnific	AEAPYVWN
AAO07498_V._vulnific	SQAPYLWN
NP_232428_V._cholera	AEAPWVWN
YP_432951_H._chejuen	SNADYLVQ
YP_529337.1_B_S._deg	AEAAYLWN
YP_435912_H._chejuen	AQAPFLWN
ZP_01137509_A._cellu	TQ_AAWF
ChiE_S._coelicolor	ST_FGYT
ChiC_S._coelicolor	AG_TAYA
ChiD_S._coelicolor	GG_TAYA
NP_903910_C._violace	AK_QLWT
YP_529072.1_S._degra	AG_TAYA
ZP_01431615_S._tropi	GG_TAYA
ZP_01136287_A._cellu	TGGYWLYD
01315.1_C._cinereus	DGSP_TQGIHRYDTCsq
03252.1_C._cinereus	DGSV_AEGIVSRYDDCSq
05285.1_C._cinereus	DGEA_APGVVYGFNDCTE
05291.1_C._cinereus	DGTA_AEGMVYLCDDCSq
01586.1_C._cinereus	SDGTYGQGGGFTMGWDNCSN
128098_P._chrysospor	NGTA_VAGLGYRFDTCsq
39872_P._chrysospori	NGTA_RPGIESRFDDCSq
138098_P._chrysospor	NGTA_VSGMGFRYDTCSE
129436_P._chrysospor	TIANVFTGLRGFERRDACSs
EAA71245_G._zeae	SGNP_APGIAYTWDKCSK
MGG_04732_M._grisea	SGKP_RAGIAYGYDDCSq
UM06190_U._maydis	ADGLFDGAGGFTRYWDCCSD
04245_F._neoformans	DGQYVGAGGFTRYWDCCSS
16170_R._oryzae	KNGWTTYWDEQSQ
01334_R._oryzae	KNGWTTYWDEQSQ
13934_R._oryzae	ASGWATFWDSTSQ
07611_R._oryzae	TTA_ASPWIRNFDDHTQ
10252_R._oryzae	ITP_GEGWVRHWDDVTQ
14659_R._oryzae	QKA_RKPWVRTWDKATS
231399_L._bicolor	NGAP_RLGIAYRYDDCSq
180319_L._bicolor	TGSP_AFNMLSRFDNCSq
191848_L._bicolor	NGTA_APNMVYRFDDCSK
317003_L._bicolor	SDGTYGEGGGFTMGWDNCSd
246840_L._bicolor	DGTT_KTGIAYRYDNCSq
144643_L._bicolor	STSPTFAASGGFERNDCCSC
310136_L._bicolor	NGTA_ANGIDYAFDNCSq
629882_M._xanthus	TGVYHWDEAAK
630509_A_M._xanthus	
YP_592598_Acidobacte	VN_AKGWKRYWDGSAQ
YP_446903_S._ruber	ARASTLWA
ZP_00739282_B._thuri	AKVPYLYN
ZP_01245639_F._johns	TKVPYLYN

NP_976824_B._cereus	.....AKVPYLYN.....
YP_077581_B._licheni	.....AKVPFLYN.....
631138_M._xanthus	.....AKEAYVYN.....
ZP_01247029_F._johns	.....PGAENLDQVG.....
ZP_01234549_V._angus	.....KHYACRDTVT.....
ZP_01160697_Photobac	.....KHYACRDTVT.....
ZP_01158584_Photobac	.....HQMCRDTIEG.....
AN0549_E._nidulans	.....EAAVKIVKFDI.....
AN8481_E._nidulans	.....EAAVKILKFDI.....
AN9390_E._nidulans	.....KAGVQMTWDT.....
AN0517_E._nidulans	.....ETTVKYNVYEG.....
AN0541_E._nidulans	.....DSGVKYMVYDE.....
AN5077_E._nidulans	.....EAAVQYLVYAD.....
AN0509_E._nidulans	.....EDSDSNILVYD.....
AN7613_E._nidulans	.....PASDSNILVYN.....
07035_N._crassa	.....EAAVKSWSWG.....
07484_N._crassa	.....SSSNSRIVVYD.....
05317_N._crassa	.....ASSNSDILVYD.....
EAA74768_G._zeae	.....EEAVKLITWG.....
EAA78168_G._zeae	.....DAAIKTIQWNN.....
EAA75711_G._zeae	.....EAMMKQISWD.....
EAA68447_G._zeae	.....STSHSDILVYD.....
EAA77156_G._zeae	.....KASDSDIMTYGTQKG.....
12510_S._sclerotioru	.....KDASKVASWG.....
00773_S._sclerotioru	.....DAAVKAITWDN.....
05454_S._sclerotioru	.....EAAVKWITWGG.....
00677_S._sclerotioru	.....EGDEAVKQIVFGGG.....
02128_S._sclerotioru	.....DDSYSNIVVYN.....
MGG_04534_M._grisea	.....AAAVKIVTWDT.....
MGG_01336_M._grisea	.....KAMVKQLSWD.....
14527_P._nodorum	.....VAGVKWITWDS.....
15411_P._nodorum	.....TAMVKYFKYAG.....
02214_P._nodorum	.....GAEVNEVTWD.....
04761_C._immitis	.....TAGVKYITYSG.....
04323_A._capsulatum	.....ASGVNWSWDK.....
00533_B._fuckeliana	.....EGGTAVKQIVFAGG.....
Chi18_1_H._jecorina	.....QDSYSNIVVYN.....
Chi18_8_H._jecorina	.....GDSASNILEYGNG.....
Chi18_9_H._jecorina	.....KDTASDYLVIN.....
Chi18_10_H._jecorina	.....EKTDSDYLIYN.....
02650_A._capsulatum	.....EVASSFERALAGGRYDDYVPIHYGGV.....
AN0221_E._nidulans	.....ELAASFEEKAKISGEYDPF.....
06020_N._crassa	.....HLRASVDRLAQGVYDHD.....
EAA76014_G._zeae	.....DVAQSFSRARYDGKYDVD.....
Chi18_4_H._jecorina	.....ELNESFTRAQAHGFYDYD.....
09277_P._nodorum	.....ELSNSFDKALKHGVCDRE.....
05838_A._capsulatum	EDGFCCSSAG.....
EAA69039_G._zeae	PAGSCCAASGWCSTPAHCGTGCSAFG.KCDGVDINNSFHKALKDGRDITV.....
MGG_06594_M._grisea	AEGDCCSQYGF CGNTAAHCGTGCFGYG.KCDGFSTKDSFQKAIANGKTDEA.....
Chi18_11_H._jecorina	.K.....LEHAVANGIADEE.....
02644_A_P._nodorum	SSG.CCSQYGNCGNSPEHC SGACQHAFGTGCTDPDVAGSWQSALAGGMTDNR.....
AN9447_E._nidulans	PAGTCCSIYGNCGTGDDFCLAACDSNFG.ECKGVPIQDSWRRARAEGQTDEE.....

	910	920	930	940	950	960
NP_979924_B._cereus	.... ... ... ... ... ... ... ... ... ... ... ...					
YP_077302_B._licheni	....E..NGVQ.H.....	....EVWFE.....		....DARSIQSKFNLMEQ.GI		
YP_091539_B._licheni	....N..AGKQ.H.....	....EVWFE.....		....DARSIQAKFDLIREL.NL		
YP_079121_B._licheni	....E..QGRR.H.....	....VWFE.....		....DARSIGKKLQLITEY.GL		
YP_074366_S._thermop	....E..QGRR.H.....	....VWFE.....		....DARSIGKKLQLITEY.GL		
YP_074366_S._thermop	....E..QGR.T.H.....	....EVWFE.....		....DARSIQAKFNLLKEL.GL		
YP_075811_S._thermop	....A..QGENE.H.....	....IVWFE.....		....DARSLQAKFDITVKEY.GL		
YP_075619_S._thermop	....A..DGAE.H.....	....IVYFE.....		....NSRSAAAKLRLVGRY.GL		

ZP_01354047_C._phyto	.....EGVD.H.....	EVWFE.....	DVRSIKAKLDLVKEY.DF
ZP_01354926_C._phyto	.....DGAK.Y.....	KIWLE.....	EEESI EAKLKLISEA.DL
NP_902406_C._violace	....A..DGSR.H.....	TVWTE.....	NARSVALKASLVNAY.GL
ZP_01136704_A._cellu	....A..SGVQ.H.....	SVWYN.....	DANALQARLPLVGKY.GL
ZP_00526542_S._usita	.....DGIR.E.....	YVFYN.....	DARSFEDRYAMARER.GL
AAF46212.1_D._melano	...QE.....	WISYE.....	NQTSIACKANYVKS.L.NL
AAF46534.1_D._melano	...ADDSGENG.V.....	WVGYE.....	DPDTAAIKAEYVKRE.GL
AAF46544.1_D._melano	...NQ.....	WVGYD.....	DEAIVRKKAEYVVAQ.GL
At4g19720_A._thalian	...TS.....	LIGYD.....	DHQSVVAKVKYAKQK.GL
At4g19750_A._thalian	...TT.....	WIGYD.....	DNQSI VSKVRYAKLK.GL
EAA67655_G._zeae	.....RKK.R.....	ELVTMD.....	DLKSAQAKAGYINER.NL
EAA73155_G._zeae	.....ANT.K.....	ELISFD.....	TPGMVENKVLVYVKNK.SL
EAA74986_G._zeae	.....SIM.H.....	ELISYD.....	TPEEVEKKVDYVLKH.GL
EAA74223_G._zeae	.....PQT.R.....	TMVTYD.....	TPRVAVDKAEYVRKW.KL
MGG_05533_M._grisea	.....NST.G.....	QLISYD.....	DLKSVQFKSDYVQKQ.QI
MGG_01247_M._grisea	.....AAK.R.....	EFVTYD.....	TVDSAREKTRYMKQK.GL
MGG_00086_M._grisea	.....AAR.R.....	EMVTYD.....	TADNVRKVDWARAR.GL
MGG_07927_M._grisea	.....PAT.R.....	HMVTYD.....	TVPLARRKAEFIRER.GL
Chi18_6_H._jecorina	.....NAT.R.....	ELVTYD.....	NMETTTTLKAEYLGKK.GL
Chi18_5_H._jecorina	.....PST.K.....	ELISFD.....	TPDVVNTKVSYLKSL.GL
Chi18_7_H._jecorina	.....PQT.R.....	KLVSYD.....	TPYAARAKARYVKEW.GL
04883_N._crassa	.....ETN.K.....	VMVSYD.....	TPEMVKQKVSYIKEK.GL
04554_N._crassa	.....PGT.K.....	TLVSYD.....	TPGMARMKAEYIRER.GL
11407_B._fuckeliana	.....NST.K.....	ELVSYD.....	NVKAIQTKTEYIMSS.GL
05350_B._fuckeliana	.....ENT.K.....	TLISYD.....	TVEVGRRKAHYIKQR.GL
11700_S._sclerotioru	.....NVT.K.....	ELISYD.....	NVKSVMKTKYIMTS.GL
11304_S._sclerotioru	.....EDT.K.....	TLITYD.....	TV EIARRKAYYIKER.GL
08020_S._sclerotioru	.....TSK.R.....	EIISYD.....	NPMVAIQKAQWIQSM.NL
01250_A._capsulatum	.....KTA.R.....	KMISYD.....	TPTIAAAKVDHIRRR.GM
05886_A._capsulatum	.....KSS.R.....	SMISYD.....	TVPMVEKKTKYIINK.GL
06565_A._capsulatum	.....SSS.R.....	TMISYD.....	NVAMVEEKKTKYIIQK.GL
05250_C._immitis	.....PSA.K.....	KMISYD.....	TPHMAQRKAEYIRNR.GL
02795_C._immitis	.....KNK.R.....	YLISYD.....	TVKIAGKKA EYITKN.GM
03822_C._immitis	.....PSK.K.....	LMISYD.....	TVPMVEAKTKYIVDK.GL
AN5454_E._nidulans	.....EDK.K.....	EVISYD.....	NVGVRHKG VLYMRL.GM
AN4871_E._nidulans	.....PSS.R.....	EMVSYD.....	TVAADLKAAYIQSR.RL
00269_P._nodorum	.....QGQ.R.....	LMISYD.....	TPQVIQKKS ELVKSM.GL
04870.1_C._cinereus	.....KTT.R.....	EMISFD.....	TP E IARLKGQFIRDN.GL
09921.1_C._cinereus	.....PVK.R.....	ELVSYD.....	TPNIVRMKAIYVEKN.GL
124149_P._chrysospor	.....YQT.R.....	EMVSFD.....	SEKVGAAKGAWIARE.GL
134311_P._chrysospor	.....SAK.K.....	ELVSYD.....	TPHIASLKAQYVNSN.NL
03412_F._neoformans	.....PAK.R.....	LLITYD.....	TQAI AHQKASYIAYH.GL
13635_R._oryzae	.....PNA.R.....	ELITYD.....	TPQIVSAKCSYLLQR.KL
UM04261_U._maydis	.....SAK.R.....	EFISYD.....	TPQNVLLKCCQYIRNK.RL
EAA69503_G._zeae	.....GAD.G.....	GFVTYD.....	NPDTVKMKAGFCKQK.GL
EAA70860_G._zeae	.....NKSD.K.....	GFVSFD.....	VPSTVSIKAGYAKAL.GL
Chi18_3_H._jecorina	.....GGD.G.....	GFVTYD.....	NHETVKVKA EFCQK.GL
Chi18_2_H._jecorina	.....ANGD.K.....	GYLTFD.....	VPRTVHMKARFAMQR.GL
03026_N._crassa	.....GGD.G.....	GFVTYD.....	NPDTVKAKATFCKQK.GL
01594_B._fuckeliana	.....GGD.G.....	GWVSYD.....	NPQ TGLFYWTGTAD....
05897_S._sclerotioru	.....GGD.G.....	GWVSYD.....	NPQTVKMKAEYCRQR.RL
04742_A._capsulatum	....SGSGGE.GPAA.....	GFISYD.....	SPRTVMQKAQFVSEY.EL
04750_C._immitis	.....DRN.M.....	GFVSYD.....	STRTVVQKAKFVREM.AL
04719_P._nodorum	.....GGD.G.....	GFVTYD.....	TPQTVRMKADYVRQN.AL
MGG_08458_M._grisea	.....GEGG.K.....	GFVSLD.....	TPATVRLKAGYVRAN.GL
CHT4_C._albicans	.....SHS.K.....	QLITFD.....	NPQCARIKASFVQSR.QL
01119_L._elongisporu	.....LKT.K.....	QFITYD.....	NVQS AKIKGSYVKLH.EL
XP_454053_K._lactis	.....PKS.R.....	TFVGYD.....	NVQSM DIKGK YIKKK.NL
CTS2_S._cerevisiae	.....EKN.S.....	IFISYD.....	NTKSVKTKAEYVTHN.NL
246746_L._bicolor	.....PQK.R.....	EMVSFD.....	NEDVADWKGQYIKNQ.GL
03209_N._crassa	.....ALS.R.....	ELITYD.....	NVLSALVKTKYIFLR.GL
14474_P._nodorum	.....PVK.K.....	EVVSFD.....	TPKTAVVKTDFLKSE.GL

CE06282_C._elegans	.....RTI.G.....IYLTFE.....TKESIRAKIDYVKDR.IL
CE03547_C._elegans	.....ATT.E.....TFLTFE.....TNDTIAAKIDYVKDR.IL
CE03542_C._elegans	.....PKE.K.....TFLTFE.....NERSIEKKLQYVNM.NL
CE15845_B_C._elegans	.....PET.K.....ELLTFE.....TDRSINEKTKYIKRV.NI
CE02997_C._elegans	.....PGPPT.....RFMTLE.....EERSLREKNRYVADH.NI
CE36953_C._elegans	.....SEQ.K.....TFVGYE.....NAESLKHKVDYIVEN.NI
YP_432439_H._chejuen	.....AEK.R.....VFLSIE.....DEESIGVKANYVVDN.GI
YP_529449.1_S._degra	.....AAK.Q.....VFISTE.....DEQSINRKADYVVEN.GI
YP_077582_B._licheni	.....PEK.K.....VFLSTE.....DEESIKTKADYVIDK.GI
ChiI_S._coelicolor	.....AEK.K.....VFLSTE.....DEQSVGAKADYVADR.GI
NP_902986_C._violace	.....AGK.K.....VFLSTE.....DEQSIAQKAAWIDAN.NV
ZP_01159608_Photobac	.....AEK.S.....VFISTE.....DKASVGVKADYVIDK.EI
ZP_01234708_V._angus	.....AEK.S.....VFISTE.....DKASVSVKADYVIDK.EI
NP_233087_V._cholera	.....AEK.K.....VFLSTE.....DKQSIDVKADYVIDK.EI
NP_230718_V._cholera	.....DTK.K.....VFLSIE.....DKDSLKPCLDYIVDN.GL
AAO07185_V._vulnific	.....AEK.A.....VFLSTE.....DKASVSVKADYVIDK.EI
ZP_01354150_C._phyto	.....G...D.....ILITYE.....DLEAIRYKVDTVKKL.RL
ZP_01246933_F._johns	.....AQT.K.....TFATSD.....DLKSIKAKTEYVKEK.KL
YP_012734_L._monocyt	.....KET.G.....EFYTYD.....NTRSIGYKAQYVKDN.NL
YP_529337.1_A_S._deg	.....AE.NN.....IFVTYD.....DAQSLVYKTDYIKQQ.GL
ChiA_A_P._kodakarae	.....PSK.R.....IFITFD.....DPRAIGIKVDYMLKN.GL
AAG19274_Halobacteri	.....PSK.N.....VLVSVD.....SPRSVEAKTAYAAQH.DI
AAG19275_Halobacteri	.....DSE.G.....VFISYD.....DPTSLAAKVELAVAE.DL
CE03543_C._elegans	.....PDE.R.....RFFTFE.....NQKSIAIKTRYAIDM.NL
CE34961_C._elegans	.....QET.G.....NFLTFE.....NKKSLIAKLAYAIH.NL
CE20043_C._elegans	.....PDT.R.....NFVTFE.....TDKSIQEKMKYVKEK.NL
CE15845_A_C._elegans	.....KNK.N.....TFVTLE.....SDRSIREKKKYVCDM.KL
CE32863_A_C._elegans	.....KNK.N.....TFVTLE.....SDRSIREKKKYVCDM.KL
CE03544_C._elegans	.....LKT.R.....TFFTYE.....NEKSIKVKLDYVNMK.DL
CE08731_C._elegans	.....SKANYVSK.NL
CE28638_C._elegans	.....NST.K.....TFLAFE.....TEKSIHAKIEYVMNK.NL
CE32863_B_C._elegans	.....PET.K.....ELLTFE.....TDRSINEKTKYIKRV.NI
CE01673_C._elegans	.....PEK.K.....EIQRFN.....S....STKTEYTK.L.QM
CE02993_C._elegans	.....PGPPT.....WFMTLE.....DKRSLREKTKYVADY.NI
CE02996_C._elegans	.....PGPPT.....WFLTLE.....DEKSLREKNRYVADH.NI
CE02995_C._elegans	.....PGS.S.....LFLTLE.....DEQSLRVKNRYVADH.NI
CE02992_C._elegans	.....PKS.K.....IFLAFE.....NEKSLSEKVIYVRNK.NI
CE02999_C._elegans	.....ADT.Q.....QFLTFE.....NEKSLTEKMNYAVAH.NI
CE02998_C._elegans	.....SEE.R.....KFFVFE.....NERSLQAKMDYAADH.NI
CE09229_C._elegans	.....NGA.K.....KFLGFE.....NERSLKEKMKYATDR.NL
CE12928_C._elegans	.....NGA.R.....MFLGFE.....NERSLKEKMDYATNR.NL
CE23907_C._elegans	.....STT.V.....RYLTFE.....TERSIREKTGYVKDG.VM
CE32917_C._elegans	.....STT.K.....EYLTFE.....TEKSLIAKVNYVKDR.AL
CE34579_C._elegans	.....STT.K.....EYLTFE.....VKRSIAAKLDYVQNM.NL
CE25073_C._elegans	.....ATT.E.....TFLTFE.....TNDTIAAKIDYVKDR.IL
CE03548_C._elegans	.....ATT.E.....TFLTFE.....TNDTIAAKIDYVKDR.IL
NP_469498_L._innocua	.....KET.G.....EFYTYD.....NTRSIGYKAQYVKDN.NL
CE08730_C._elegans	.....PET.K.....TFITFE.....TEKSLIAKANYVKSM.NL
Q8U1H4_P._furiosus	.....LKA.K.....TFLTFE.....DKRSIKIKTDYAKKM.DL
CE12474_C._elegans	.....PGPPT.....RFLTLE.....DEQSLREKNRYVADH.NI
CE02990_C._elegans	.....SST.K.....IYLTFE.....TDQSIVAKIEYVSEH.LL
CE40270_C._elegans	.....PGPPT.....RFMTLE.....DEKSLREKNRYVADH.NI
ChiB_S._marcescens	.....AQ.NG.....LFVTYD.....DAESFKYKAKYIKQQ.QL
O10363_O._pseudotsug	.....KER.G.....DLISFD.....SVDSVLAKNVYVQQN.GL
AAP29899_C._fumifera	.....KDK.G.....DLISFD.....SVDSVLAKNSYVDQN.GL
AAV73807_B._mori_NPV	.....KSK.G.....DLISFD.....SVDSVLGKVKYVDRN.KL
AAL56186_H._zea_SNPV	.....RAS.G.....DLISYD.....SERSVLAKGEYVLKR.RL
AAF33549_S._exigua_N	.....REN.G.....NLITYD.....DPKSVADKTKYVLDH.EL
AAZ38189_A._segetum	.....RES.G.....NLISYD.....DPKSVADKTKYVIDH.EL
AAS82706_A._segetum	.....ENV.G.....DLLTYD.....NPTSVQAKGKFVIDN.NL
ZP_01159013_Photobac	.....RST.G.....DLITFD.....DDRSVKAKGNYVKS.L.GL



ZP_01161077_Photobac	.....	PTT.G.....	ELITYD.....	TPRAVKAKAQYVLQH.NL
ZP_01159325_Photobac	.....	EEK.Q.....	VFISYD.....	DSHSVKAKADWVKKN.KL
ZP_01160869_Photobac	.....	RKK.N.....	EYISFE.....	DKRSLQAKADYVKKH.KL
ZP_01233025_V._angus	.....	RST.G.....	DLITFD.....	DERSVKAKGNVYKSL.GL
ZP_01236284_V._angus	.....	PTT.G.....	ELITYD.....	TPRAVKAKAQYVLQH.NL
ZP_01235109_V._angus	.....	EEK.Q.....	VFISYD.....	DSRSVKAKADWVKKN.KL
ZP_01235465_V._angus	.....	QKK.N.....	EYISFE.....	DKRSLQAKVDYVKKH.QL
AAO08114_V._vulnific	.....	RTT.G.....	ELITFD.....	DHRSVLAKGAYAKSL.GL
AAO07498_V._vulnific	.....	PEK.K.....	VFISFE.....	DQRSIKAKAQWAKQS.NL
NP_232428_V._cholera	.....	RTT.G.....	QLVTFD.....	DDRSVKAKGAYVRNL.GL
YP_432951_H._chejuen	.....	PAI.G.....	SFITIE.....	SPRTAALKAQYAKDN.GF
YP_529337.1_B.S._deg	.....	SST.G.....	EFISYD.....	SPRSIAAKADYVKQY.NL
YP_435912_H._chejuen	.....	FSN.G.....	SLITYD.....	NARSVKAKGEYVRDK.GL
ZP_01137509_A._cellu	.....	YDG.T.....	TFYTGE.....	SAQSIRARTDYVHCK.GL
ChiE_S._coelicolor	.....	GPG.G.....	QWWSFD.....	DTWSIGKKTWVWVSK.GL
ChiC_S._coelicolor	.....	HCG.S.....	NWWSYD.....	TPATIKSKMDWAEQQ.GL
ChiD_S._coelicolor	.....	KCG.S.....	DWWSYD.....	TPQTIATKMAYKNEQ.GL
NP_903910_C._violace	.....	YDG.N.....	EFWSYD.....	DPATIRGKLDYVRSQ.QL
YP_529072.1_S._degra	.....	KCG.S.....	NWWSYD.....	TPATIDSKMDYAKQQ.GL
ZP_01431615_S._tropi	.....	KCG.N.....	NWWSYD.....	TPSTINGKMTYAKNE.GL
ZP_01136287_A._cellu	.....	QAS.E.....	TLYVVD.....	DPVEIGQKMHYILRR.DL
01315.1_C._cinereus	....	TPYVYNR.TTEI.....	MVAFD.....	NAQSFAAKGNFIKSN.GL
03252.1_C._cinereus	....	TPFVYNP.ETQV.....	YVSYE.....	NPRSYYAAGDFIYST.GL
05285.1_C._cinereus	....	TPFLYRE.SDSR.....	MVSFD.....	DARSFAAKGRFINEK.GL
05291.1_C._cinereus	....	TPFVYQK.DTGT.....	MITYD.....	DAESTAAGNFIKAEQ.GL
01586.1_C._cinereus	....	TPYLENT.AQQT.....	VISYD.....	DTWSLNDKAKLARDS.GM
128098_P._chrysospor	....	TPYIYLE.DRQT.....	MVAYD.....	DPTSIAAKGKFIAEQ.GL
39872_P._chrysospori	....	TPYVYNK.TSQI.....	MVSFD.....	DPAAFKAKEGFIKSA.GL
138098_P._chrysospor	....	TPFLYDP.NTST.....	MISYD.....	DPQSFAAKGRFIHES.RL
129436_P._chrysospor	....	TPFLRSA.RAGQ.....	VVAYD.....	DPQSLELKAALARYA.GL
EAA71245_G._zeae	....	TPFLYDE.EKQI.....	YVSYD.....	NARSFTEKGKFKVAK.GL
MGG_04732_M._grisea	....	TPFVYNN.ATSW.....	WVSYD.....	DSKSLGVKGKYITDN.KL
UM06190_U._maydis	....	TPYLSDA.SR.....	VITYD.....	DTSSIFDKGAFASAA.GI
04245_F._neoformans	....	TPWLKSS.ESGQ.....	IVTYD.....	DTESMNLKAQFAAQA.GL
16170_R._oryzae	....	TPYAYHA.GKHT.....	FLSYD.....	NTKSFEAKLNYVKSE.GL
01334_R._oryzae	....	TPYAYHA.GNST.....	FLTYD.....	NPKSFEAKLDYVKSQ.GL
13934_R._oryzae	....	TPFAYKQ.DNQO.....	FVTFD.....	NPTSIRIKSNYVNE.NL
07611_R._oryzae	....	TPWLYNP.TNKQ.....	YISYD.....	DPVSLKVKVQYAIHQ.GL
10252_R._oryzae	....	TPWLFNP.TTQH.....	YITYD.....	DPQSLNIKVQHALCE.DL
14659_R._oryzae	....	TPWLFNP.KTNI.....	FISYD.....	DPKSISKKACYAHNK.HL
231399_L._bicolor	....	TPYVYNK.ETQS.....	MVSYD.....	DTRSFAAKGQFIKTA.GL
180319_L._bicolor	....	TPYVYNP.STSV.....	EISYD.....	DAKSFAAKGSFIKEK.AL
191848_L._bicolor	....	TPYVYNP.STNV.....	EISYD.....	DATSFAADKGSFINEK.GL
317003_L._bicolor	....	TPYLENV.AQKT.....	VVTYD.....	DTWSLTDKAKFAKQS.GM
246840_L._bicolor	....	TPYMYNA.TSQV.....	YVSFD.....	NAQSFAAKGDFIHSK.GL
144643_L._bicolor	....	TPFLRSS.SSGQ.....	VVTYD.....	DLVSVRMKAAPVKEL.GM
310136_L._bicolor	....	TPFVYNP.TAQT.....	MLS YD.....	DARSFAAKGNYISSN.GL
629882_M._xanthus	....	ASYVTFD.VPVEDGTVRWISYD.....		SPQTIAAKGAFAH.DNGY
630509_A_M._xanthus	.....			
YP_592598_Acidobacte	....	SPYLLYQ.GTGGK.....	DGLISYD.....	DPISTALKTYVVLKTRDF
YP_446903_S._ruber	.....	PDS.S.....	VLITHE.....	TPRSLRAKAHYVQSR.GL
ZP_00739282_B._thuri	.....	ATT.G.....	TFISYD.....	DNESMKYKTDYIKTK.GL
ZP_01245639_F._johns	.....	STL.K.....	QFISYE.....	DKQSMDLKVQYIKSR.NL
NP_976824_B._cereus	.....	ATT.G.....	TFISYD.....	DNESMKYKTDYIKTK.GL
YP_077581_B._licheni	.....	AEN.G.....	NFITYD.....	DEQSFHGKTDFIKAN.GL
631138_M._xanthus	.....	PAT.G.....	IWIGYD.....	DVQSINAKADYILNK.NL
ZP_01247029_F._johns	.....		NTIYYN.....	GIPTIKQKTTFA..VQNA
ZP_01234549_V._angus	....	K.....	NNTTHYYN.....	GLPTIRSKVHLAKDDYHL
ZP_01160697_Photobac	....	K.....	NNTTHYYN.....	GLPTIRSKVHLAKDDYHL
ZP_01158584_Photobac	....	K.....	DGVTHYYN.....	GLPTIRSKVHLA..EDYHL
AN0549_E._nidulans	....	N.....	Q.....	DAETFKMKQAQFAAGQ.CL
AN8481_E._nidulans	....	N.....	Q.....	DAETFKLKAQFASSQ.CL

AN9390_E._nidulans	....N.....Q.....	WVSyd	.....	DDETLKAKMEYANEL	.CL
AN0517_E._nidulans	....T.....Q.....	WISyd	.....	DEQSFFDKKKYVSE	.CL
AN0541_E._nidulans	....N.....Q.....	WITYD	.....	DEESFEKKREMLDNE	.CF
AN5077_E._nidulans	....N.....S.....	WVSyd	.....	DATTFAAKIDYAKRI	.GL
AN0509_E._nidulans	...DN.....Q.....	WVAYMS	.....	PEVRESRVSRYSKL	.NM
AN7613_E._nidulans	...DT.....Q.....	WVGfMS	.....	KSTMRRRVEREKEM	.KF
07035_N._crassa	....D.....Q.....	WVTFD	.....	DAATWRLKANIIRGQ	.CI
07484_N._crassa	...NN.....Q.....	WVAFMD	.....	DSIRAARTAIYKGL	.GM
05317_N._crassa	...NT.....Q.....	WVGyMS	.....	AATKKSRAALYTAW	.GM
EAA74768_G._zeae	....R.....E.....	WASyd	.....	DAETLKLKVNRAEER	.CL
EAA78168_G._zeae	....D.....Q.....	WVSyd	.....	DRDTWKLKAKFLKSQ	.CL
EAA75711_G._zeae	....D.....Q.....	WIGYD	.....	DEETFAAKKAWADGY	.CF
EAA68447_G._zeae	...NT.....E.....	WVSyMS	.....	PSTKMARETVYKAF	.GM
EAA77156_G._zeae	...MT.....D.....	WVAYMG	.....	PTTKLKRTQWVQGL	.NF
12510_S._sclerotioru	....N.....Q.....	WVAYD	.....	DEETFKLKSEYAQSS	.CL
00773_S._sclerotioru	....D.....Q.....	WVSFD	.....	DQETFKIKSDFAKSQ	.CL
05454_S._sclerotioru	....D.....Q.....	WVSyd	.....	DFDTIQQKIEFANSL	.GL
00677_S._sclerotioru	....R.....Q.....	WMGFD	.....	DFETWGLKRRFADGL	.CM
02128_S._sclerotioru	...DD.....Q.....	WISyMN	.....	DANKIVRTALYKH	.NF
MGG_04534_M._grisea	....D.....Q.....	WVSFD	.....	DVETLKIQQDYANRR	.CL
MGG_01336_M._grisea	....N.....Q.....	WVGyD	.....	DAQTWAACKTWADSV	.CI
14527_P._nodorum	....N.....Q.....	WVSyd	.....	DDDTFQKKRDFSNKR	.CL
15411_P._nodorum	....D.....S.....	WVGyD	.....	DAETYAMKEAFANDR	.CL
02214_P._nodorum	....D.....Q.....	WIAWD	.....	DTNTLGKKLELANDR	.CL
04761_C._immitis	....D.....Q.....	WVSyDHTVSL	LGLEGANCSQDDAETFKQKKE	LADEL	.GL
04323_A._capsulatum	....D.....Q.....	WVSyd	.....	DGRTLKQKADFGNKL	.CL
00533_B._fuckeliana	....R.....Q.....	WMGFD	.....	DEESWGLKRRYADQL	.CI
Chi18_1_H._jecorina	...GT.....Q.....	WVAFMN	.....	DSNKATRTALYPSI	.NF
Chi18_8_H._jecorina	...AV.....D.....	WVAYMD	.....	GGLKAERIKWIQLL	.NF
Chi18_9_H._jecorina	...DV.....E.....	WVAYMS	.....	DKTKQSRREKWKGL	.NF
Chi18_10_H._jecorina	...QT.....Q.....	WVAYMS	.....	KSVKEARIKKYQAL	.NF
02650_A._capsulatum	GGGGHYFWDK.KENI	...WWTWD	.....	TGEAIKKKMQPIMVARGL	
AN0221_E._nidulans	..GGGYFWDS.NENI	...FWSWD	.....	TANAIKRKFPAILEKRKL	
06020_N._crassa	..QGGYYWDP.TEAL	...WVTFD	.....	TPDAIKQKFPKVMKRRL	
EAA76014_G._zeae	...GSYYYWDE.QELR	...WVSFD	.....	TTRSIIQTKEFIVPQLKL	
Chi18_4_H._jecorina	...GSYGYWDA.EEKR	...WVSyd	.....	TPDTIGARIAWLVGQLEL	
09277_P._nodorum	..SGGCTYWDA.DERL	...FWSWE	.....	SKDTIYRKLRVVIGEMKL	
05838_A._capsulatum		YW	.....		
EAA69039_G._zeae	..NGGQYWDS.ETRI	...FWTWD	.....	TAELIAQKIAFMAQTRGV	
MGG_06594_M._grisea	..LGAQYWDS.TASL	...YWSWD	.....	TPALMKQKINDIVFAKGL	
Chi18_11_H._jecorina	..EGGQWWDA.AEEV	...YWTWD	.....	TADLVARKFSEIVVPKKL	
02644_A_P._nodorum	..AGGQYFDDT.ENNL	...FWTWD	.....	TPALISRKFDDIVRKYKL	
AN9447_E._nidulans	..GGGQYYMDT.QNHL	...FWTWD	.....	TPTLMTRKFTETVDVEKL	

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NP_979924_B._cereus	.... .... ..	GGISYWKIGLP	
YP_077302_B._licheni		RGISYWKLGLS	
YP_091539_B._licheni		DGGGVWQLTSL	
YP_079121_B._licheni		DGGGVWQLTSL	
YP_074366_S._thermop		RGISYWKLGLD	
YP_075811_S._thermop		RGVSYWVLGNP	
YP_075619_S._thermop		GGIAIWRLGLN	
ZP_01354047_C._phyto		RGVGYWQLMRL	
ZP_01354926_C._phyto		AGVASWRLGFE	
NP_902406_C._violace		GGTSLYALGME	
ZP_01136704_A._cellu		GGVAFWSFGDE	
ZP_00526542_S._usita		HGISAWILGSE	
AAF46212.1_D._melano		GGVMVFSLNTD	
AAF46534.1_D._melano		GGIAVVDLSFD	
AAF46544.1_D._melano		GGIMFWAIDND	
At4g19720_A._thalian		LGYFSWVHGAD	

At4g19750_A._thalian	LG YFSW HVGAD.
EAA67655_G._zeae	GGAFYWEARGD.
EAA73155_G._zeae	GGSMFW EASAD.
EAA74986_G._zeae	GGSMFW EASGD.
EAA74223_G._zeae	GGAMWWESSAD.
MGG_05533_M._grisea	GGVMFW ESSQD.
MGG_01247_M._grisea	GGAVFW EASGD.
MGG_00086_M._grisea	GGSMFW ELSGD.
MGG_07927_M._grisea	GGAMWWESSAD.
Chi18_6_H._jecorina	GGAVFW EASGD.
Chi18_5_H._jecorina	GGSMFW EASAD.
Chi18_7_H._jecorina	GGGMWWESSAD.
04883_N._crassa	GGAMYWEASGD.
04554_N._crassa	GGAMWWESSAD.
11407_B._fuckeliana	GGAMFW ESSGD.
05350_B._fuckeliana	GGAMV.....
11700_S._sclerotioru	GGAMFW ETSAD.
11304_S._sclerotioru	GGAMWWESSAD.
08020_S._sclerotioru	GGAMWWESSAD.
01250_A._capsulatum	GGGMWWE LSGD.
05886_A._capsulatum	GGGMWWEASGD.
06565_A._capsulatum	GGGMWWESSGD.
05250_C._immitis	GGAMWWE LSGD.
02795_C._immitis	GGGMWWESSSD.
03822_C._immitis	GGAMWWEASGD.
AN5454_E._nidulans	GGGMWWESSGD.
AN4871_E._nidulans	GGAMWWE TSAD.
00269_P._nodorum	GGGMWWESSSD.
04870.1_C._cinereus	GGSMFW ELSGD.
09921.1_C._cinereus	GGTMFW ELSTD.
124149_P._chrysospor	GGSMFW ELSGD.
134311_P._chrysospor	GGNMFW DLSTD.
03412_F._neoformans	GGAMWWE LDDSD.
13635_R._oryzae	GGAMFW EL SAD.
UM04261_U._maydis	RGAMFW ELSGD.
EAA69503_G._zeae	GGLFYWNAPAD.
EAA70860_G._zeae	GGLFYWTGAGD.
Chi18_3_H._jecorina	GGLFYWNGPAD.
Chi18_2_H._jecorina	GGLFYWTGTGD.
03026_N._crassa	GGLFYSSAPSD.
01594_B._fuckeliana	.....
05897_S._sclerotioru	G.....
04742_A._capsulatum	GGLFYWH LAAD.
04750_C._immitis	GGLFYWHVAAD.
04719_P._nodorum	GGLFYWTGTGD.
MGG_08458_M._grisea	AGLFYWQGVGD.
CHT4_C._albicans	GGGMWWD SAGD.
01119_L._elongisporu	GGGMWWD SSGD.
XP_454053_K._lactis	NGGFWWE SCGD.
CTS2_S._cerevisiae	GGGFWWE SCGE.
246746_L._bicolor	GGSMFW ELSGD.
03209_N._crassa	GGAVFW EASGD.
14474_P._nodorum	GGAWWWD SSSD.
CE06282_C._elegans	GGVWIFSV DMD.
CE03547_C._elegans	GGVWIWAV DMD.
CE03542_C._elegans	GGVWIWSV DMD.
CE15845_B_C._elegans	GGVCLWAV DMD.
CE02997_C._elegans	GGITMTID QD.
CE36953_C._elegans	GGVMIWAID FD.
YP_432439_H._chejuen	GGVMFW ELAGD.
YP_529449.1_S._degra	GGIMFW ELAGD.
YP_077582_B._licheni	GGVMFW DLSGD.

ChiI_S._coelicolor	GGAMIWELAGD.
NP_902986_C._violace	GGVMFWELAGD.
ZP_01159608_Photobac	GGIMFWELAGD.
ZP_01234708_V._angus	GGIMFWELAGD.
NP_233087_V._cholera	GGIMFWELAGD.
NP_230718_V._cholera	GGMMIWEMAGD.
AAO07185_V._vulnific	GGIMFWELAGD.
ZP_01354150_C._phyto	GGMMYWEQTQD.
ZP_01246933_F._johns	GGIMFWELTLD.
YP_012734_L._monocyt	GGMISWMQSQD.
YP_529337.1_A_S._deg	GGAMFWHLGQD.
ChiA_A_P._kodakarae	GGVMIWEITAD.
AAG19274_Halobacteri	GGMMFWTFSGD.
AAG19275_Halobacteri	GGVMIWELSQD.
CE03543_C._elegans	GGVWIWSVDMG.
CE34961_C._elegans	GGVWIHLVDKD.
CE20043_C._elegans	GGVWIWHVDAN.
CE15845_A_C._elegans	GGVWIWTVDMG.
CE32863_A_C._elegans	GGVWIWTVDMG.
CE03544_C._elegans	GGVWIWSVDMG.
CE08731_C._elegans	GGVWIWTEHED.
CE28638_C._elegans	GGVWIWSVDMG.
CE32863_B_C._elegans	GGVCLWAVDMG.
CE01673_C._elegans	GGVSIWSRDMG.
CE02993_C._elegans	GGITMWTIDQD.
CE02996_C._elegans	GGITMWTIDQD.
CE02995_C._elegans	GGITMWTIDQD.
CE02992_C._elegans	GGVLIWNVDQD.
CE02999_C._elegans	GGVAMYTIDDD.
CE02998_C._elegans	GGVYIWAIGAD.
CE09229_C._elegans	GGVMIWALDLD.
CE12928_C._elegans	GGVMIWALDLD.
CE23907_C._elegans	GGVWIWSVDMG.
CE32917_C._elegans	AGVWIWFVDLD.
CE34579_C._elegans	GGVWIWQMDMG.
CE25073_C._elegans	GGVWIWAVDMG.
CE03548_C._elegans	GGVWIWGVDMG.
NP_469498_L._innocua	GGMISWMQSQD.
CE08730_C._elegans	GGVWIWLMEND.
Q8U1H4_P._furiosus	.....
CE12474_C._elegans	GGVWLWSVDMG.
CE02990_C._elegans	GGITMWTIDQD.
CE40270_C._elegans	GGICIWTVDKD.
CE40296_C._elegans	GGITMWTIDQD.
ChiB_S._marcescens	GGVMFWHLGQD.
O10363_O._pseudotsug	GGVFAWEIDAD.
AAP29899_C._fumifera	GGVFAWEIDAD.
AAV73807_B._mori_NPV	GGVFAWEIDAD.
AAL56186_H._zea_SNPV	GGVFAWEIDAD.
AAF33549_S._exigua_N	AGVFAWEIDAD.
AAZ38189_A._segetum	AGVFAWEIDAD.
AAS82706_A._segetum	GGVFAWEIDAD.
ZP_01159013_Photobac	AGVFSWEIDAD.
ZP_01161077_Photobac	GGVFSWEIDSD.
ZP_01159325_Photobac	AGVFWDLSDG.
ZP_01160869_Photobac	GGVFGWEATSD.
ZP_01233025_V._angus	AGVFSWEIDAD.
ZP_01236284_V._angus	GGVFSWEIDSD.
ZP_01235109_V._angus	AGVFWDLSDG.
ZP_01235465_V._angus	GGVFGWEATSD.
AAO08114_V._vulnific	AGVFSWEIDAD.
AAO07498_V._vulnific	GGVFWELSDG.



NP_232428_V._cholera	AGLFSWEIDAD.
YP_432951_H._chejuen	AGVFFWMAEQD.
YP_529337.1_B.S._deg	AGMLTWEIDGD.
YP_435912_H._chejuen	AGIFTWEVDAD.
ZP_01137509_A._cellu	GGVMMFSLYDL
ChiE_S._coelicolor	LGGFVWEMSGD.
ChiC_S._coelicolor	GGAFFWEFSGD.
ChiD_S._coelicolor	GGTFFWELSGD.
NP_903910_C._violace	GGVFSWSLDGD.
YP_529072.1_S._degra	GGAFFWEELSGD.
ZP_01431615_S._tropi	GGAFFWEELSGD.
ZP_01136287_A._cellu	GGTAAWSLDGD.
01315.1_C._cinereus	RGFATWEAGGD.
03252.1_C._cinereus	GGFAMWEAGGD.
05285.1_C._cinereus	AGFAVWHISGD.
05291.1_C._cinereus	KGFaiWHIGD.
01586.1_C._cinereus	AGCFSWSLDQD.
128098_P._chrysospor	RGFAIWEAAGD.
39872_P._chrysospori	RGFNIWEAGGD.
138098_P._chrysospor	LGfAMWEAAGD.
129436_P._chrysospor	RGVNMFDahGD.
EAA71245_G._zeae	GGFATYEAGGD.
MGG_04732_M._grisea	AGFSVWEELGGD.
UM06190_U._maydis	AGISMWSLDGD.
04245_F._neoformans	RGcNVFSVDGD.
16170_R._oryzae	AGFMIWSLEMD.
01334_R._oryzae	AGFMIWSLEMD.
13934_R._oryzae	GGVMLWSLEMD.
07611_R._oryzae	AGLFAWSVDED.
10252_R._oryzae	AGVMGYPSR...
14659_R._oryzae	AGVMVWAINQD.
231399_L._bicolor	RGFAMWEVGSD.
180319_L._bicolor	KGFAMWHAAGD.
191848_L._bicolor	LGfAMWHVVGd.
317003_L._bicolor	AGCFTWSLDQD.
246840_L._bicolor	RGFSMWEAGGD.
144643_L._bicolor	LGtNMFDICGD.
310136_L._bicolor	LGFAVWPVTGD.
629882_M._xanthus	GGTIIWTINQG.
630509_A_M._xanthus	.....
YP_592598_Acidobacte	GGMFMWDLSDG.
YP_446903_S._ruber	GGVMYWEHSAD.
ZP_00739282_B._thuri	SGAMFWELSGD.
ZP_01245639_F._johns	AGGMIWEELSQD.
NP_976824_B._cereus	SGAMFWELSGD.
YP_077581_B._licheni	SGAMFWDFSGD.
631138_M._xanthus	GGAMFWELSGD.
ZP_01247029_F._johns	GGVMIWEELSQD.
ZP_01234549_V._angus	GGVMLWEELPCD.
ZP_01160697_Photobac	GGVMLWEELPCD.
ZP_01158584_Photobac	GGVMLWEELPCD.
AN0549_E._nidulans	GGVMVWAVSHD.
AN8481_E._nidulans	GGVMVWAVSHD.
AN9390_E._nidulans	GGVMVWAASD.
AN0517_E._nidulans	SGWMVWAIDQD.
AN0541_E._nidulans	GGVMIWAIDQD.
AN5077_E._nidulans	SGLMIWAIDL.
AN0509_E._nidulans	GGSVNWATDLE.
AN7613_E._nidulans	AGFANWAVDLT.
07035_N._crassa	PGVMVWAMSQD.
07484_N._crassa	GGTSNWATDLE.
05317_N._crassa	GGTTDWASDLQ.

EAA74768_G._zeae	GGVMVWAITHD.
EAA78168_G._zeae	SGVLVWAVDYD.
EAA75711_G._zeae	GGTMVWSIDFQ.
EAA68447_G._zeae	GGTTDWAVDLQ.
EAA77156_G._zeae	GGVVDWAVDLE.
12510_S._sclerotioru	GGLMVWAISHD.
00773_S._sclerotioru	GGVLVWSVDYD.
05454_S._sclerotioru	GGLLIWAVDLQ.
00677_S._sclerotioru	GGTVVWSIDLQ.
02128_S._sclerotioru	GGTADWAVDLQ.
MGG_04534_M._grisea	GGTMVWAIDLQ.
MGG_01336_M._grisea	GGTMVWATDFT.
14527_P._nodorum	GGTMVWAMDQV.
15411_P._nodorum	GGIMIWSIDFD.
02214_P._nodorum	GGTALWAIDYD.
04761_C._immitis	GGYLIWAIDQD.
04323_A._capsulatum	GGTFAWAIDLQ.
00533_B._fuckeliana	GGTVVWSIDLQ.
Chi18_1_H._jecorina	LGIADWAVDLL.
Chi18_8_H._jecorina	AGSSDWAILDE.
Chi18_9_H._jecorina	LGTVDWAVDLQ.
Chi18_10_H._jecorina	GGISNWAIDLE.
02650_A._capsulatum	GGAFAWGLGED.
AN0221_E._nidulans	GGVFAWGLGED.
06020_N._crassa	GGVFAWGLGED.
EAA76014_G._zeae	GGVFAWGLGED.
Chi18_4_H._jecorina	GGVFAWGLGED.
09277_P._nodorum	EGAFAWGLGED.
05838_A._capsulatum	.....
EAA69039_G._zeae	KSVMAWALALD.
MGG_06594_M._grisea	GGGYAWTLGED.
Chi18_11_H._jecorina	GGVFAWSLAQD.
02644_A_P._nodorum	GGVMAWSLGED.
AN9447_E._nidulans	GGVMAWSLGED.