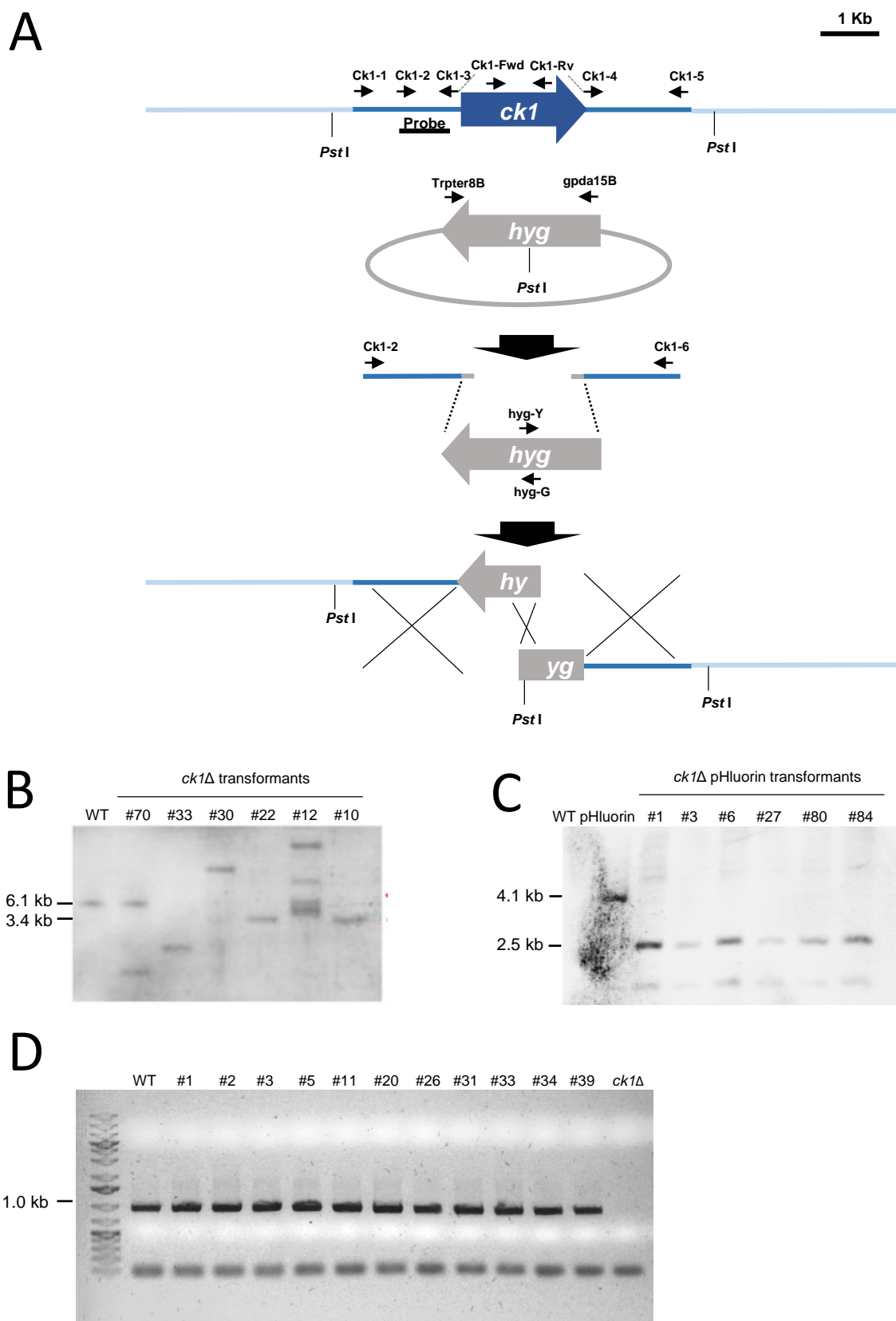


Supplementary Table S1. List of primers used in this study. Lowercase nucleotides do not belong to the original sequence and were introduced to generate overlapping ends for fusion PCR reactions

Gene	Name	[Tm]_Sequence 5'→3'
<i>hyg</i>	HygG	[62]_CGTTGCAAGACCTGCCTGAA
	HygY	[62]_GGATGCCTCCGCTCGAAGTA
<i>phleo</i>	Leo	[62]_GCCACGAAGTGCACGCAGTT
	Phe-5	[62]_CGGAGCGGTTCGAGTTCTGG
Casete <i>hyg/phleo</i>	gpdA15B	[62]_GGATCCCGAGACCTAATACAGCCCCCT
	trpC8B	[62]_GGATCCAAACAAGTGTACCTGTGCATTC
<i>ck1</i>	Ck1-1	[62]_GAGGTAGGATTGGGTGCGAC
	Ck1-2	[62]_CACGGGAAGGGTTGAGAGAG
	Ck1-3	[62]_tttaccagaatgcacaggtacacttggtATTTAGGCGGCG AAGGCGGT
	Ck1-4	[62]_tggtcgtttaggggctgtattaggtctcgTCATTGCTGCGG CGTTGTGC
	Ck1-5	[62]_TCATCGTGTCTGTTTCTCAGCG
	Ck1-6	[62]_TCTGTTTCACCCCTTCGTCCA
	Ck1-Fwd	[62]_GGCAAGAAGATTGGAGAGGG
	Ck1-Rv	[62]_CTCGCCATCCTCAACCTCG

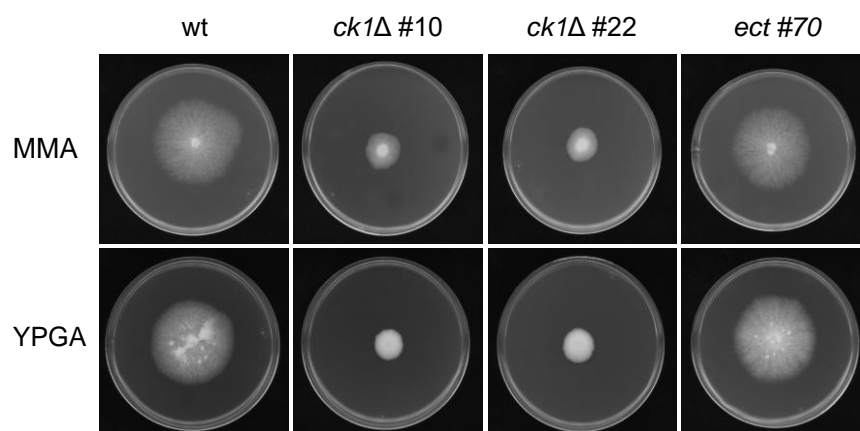
YCK1	---MSMPIAS---TTLAVNNL-----TNINGNANFNVOAKQLHHQAVDSPARS	43
YCK2	MSQVQSPLTATNSGLAVNNNTMNSQMPNRSNVRLVNGTLPPSLHVSSNLN-----	50
Cnck1	-----MATTHVIG-----	S
MoCk1	-----	0
FoCk1	-----	0
VdCk1	-----	0
YCK1	SMTATTAAANSNSNRDDSTIVGLHYHGIKGIKIGEGSGFVLFGFTGNMINGVPVAIKFEPRK	103
YCK2	HNTGNSASYSQGSRRDSTIVGLHYHGIKGIKIGEGSGFVLFGFTGNMINGLPAIKFEPRK	110
Cnck1	SN-PGGHLTASGHSSSSSNIYGVHYKVGKIKIGEGSGFVIFEGTNLNSQTVAIKFEPRK	68
MoCk1	-----MASSSSNVGVHYRVGKIKIGEGSGFVIFEGTNLNSQTVAIKFEPRK	47
FoCk1	-----MASSSSNVGVHYRVGKIKIGEGSGFVIFEGTNLNNQVVAIKFEPRK	47
VdCk1	-----MASSSSNVGVHYRVGKIKIGEGSGFVIFEGTNLNNQVVAIKFEPRK	47
	:.****.***:*****:*****:****.***:*****:	
YCK1	TEAPQLRDEYTKYKILNGTNPINPYYFQGEGLHNILVIDLLGPSLEDLFDWCGRRKFSVK	163
YCK2	TEAPQLRDEYRTYKILAGTPGIPQEEYFQGEGLHNILVIDLLGPSLEDLFDWCGRRKFSVK	170
Cnck1	SDAPQLRDEYRSYKILSGCLGIPQVYFQGEGLHNILVIDLLGPSLEDLFDWCGRRKFSVK	128
MoCk1	SDAPQLRDEYRTYKILVCGCPINPYYFQGEGLHNILVIDLLGPSLEDLFDHCNRRFTIK	107
FoCk1	SDAPQLRDEYRTYKILVCGCPINPYYFQGEGLHNILVIDLLGPSLEDLFDHCNRRFTIK	107
VdCk1	SDAPQLRDEYRTYKILVCGCPINPYYFQGEGLHNILVIDLLGPSLEDLFDHCNRRFTIK	107
	:.****.***:****.*** *****:*****:*****.*.***:	
YCK1	TVVQVAVQMITLIEDLHAHLDIYRDIKPNDFLIGRPGQPDANNIHLIDFGMAKYRDPKT	223
YCK2	TVVQVAVQMITLIEDLHAHLDIYRDIKPNDFLIGRPGQPDANKVHLIDFGMAKYRDPKT	230
Cnck1	TCMTAKQMLSRVQTHEKNLIYRDIKPNDFLIGRPSKNAHLIHVDFGMAKYRDPKT	188
MoCk1	TVVMVAKQMLSRVQTHEKNLIYRDIKPNDFLIGRPGTKAANVIHVDFGMAKYRDPKS	167
FoCk1	TVVMVAKQMLSRVQTHEKNLIYRDIKPNDFLIGRPGTKASSVIHVDFGMAKYRDPKT	167
VdCk1	TVVMVAKQMLSRVQTHEKNLIYRDIKPNDFLIGRPGTKAANVIHVDFGMAKYRDPKT	167
	*.***:.*:*****:*****.***:*****:*****:	
YCK1	KQHIPYREKKSLSGTARYMSINTHLGREQSRDDMEALGHVFFYFLRGHLPWQGLKAPNN	293
YCK2	KQHIPYREKKSLSGTARYMSINTHLGREQSRDDMEAMGHVFFYFLRGHLPWQGLKAPNN	280
Cnck1	KQHIPYREKKSLSGTARYMSINTHLGREQSRRDDLEALGHVFFYFLRGHLPWQGLKAATN	248
MoCk1	KQHIPYREKKSLSGTARYMSINTHLGREQSRRDDLEALGHVFFYFLRGHLPWQGLKAATN	227
FoCk1	KQHIPYREKKSLSGTARYMSINTHLGREQSRRDDLEALGHVFFYFLRGHLPWQGLKAATN	227
VdCk1	KQHIPYREKKSLSGTARYMSINTHLGREQSRRDDLEALGHVFFYFLRGHLPWQGLKAATN	227
	*****:*****:*****:*****.***:*****:*****.*	
YCK1	KQKYEKGKRRSTNVYDLAQGLPQFGRYLEIVRSLFEECPDYEYGRKLLSVLDDLGL	343
YCK2	KQKYEKGKRRSTNVYDLAQGLPQFGRYLEIVRSLFEECPDYEYGRMLLSVLDDLGL	350
Cnck1	KQKYEKGKQKQTPTAELVEGYNPFESIYLNYYRKLTFDETPDYVFLRGLFDLALSNSG	388
MoCk1	KQKYEKGKQKQTAKELCEGFPQFEKYLTYVRNLGFEDTPDYVFLRGLFDTQALKESSG	287
FoCk1	KQKYEKGKQKQTAKDLCEGFPESKYLTYVRNLGFEDTPDYVFLRGLFDTQALKNTG	287
VdCk1	KQKYEKGKQKQTARDLCEGFPDELNKYLTIVRNLGFEDTPDYVFLRGLFDTQALKNTG	287
	*****:.*:.*:***:.* ** ***:***:***:***:.*:.*:*	
YCK1	ETADGQYDWMKLND--GRGDWLINKNKPNLHG--GHPNPPEKSRKHNRKLQMQQLQM	399
YCK2	ETADGQYDWMKLND--GRGDWLINKNKPNLHG--GHPNPPEKSKRHNRKHWQYSSPDH	406
Cnck1	EMDDGVYDWMMLNN--GGGWEASGRQSAQAE-----TARHN-----TRGR	347
MoCk1	GVDEGEYDWMKVSKDKKNDWDRQ-----AMHNPSQVRGASNLMLHGAS-----RGAH	334
FoCk1	EVEDGEYDWMKISKDSGKGWDS--KSHSGAYLHNPNRPGPSQMLHSGH-----RPGN	339
VdCk1	EVEDGEYDWMKISKDSGKGWDSKGHNNAHLHNPNRPGPSQMLHSGQ-----RGGA	340
	** ****.***:	
YCK1	QQ-----LQQQQQQQYVA-QKTEADMRNSQYKPKL	428
YCK2	HHHYNQOQQOQOQAQAQAQAQVQQOQLQQAQAQQOQANRYQLQPDSDHYDEEREASKL	466
Cnck1	DREYRDRVDKLR-----NG-----SAAN-----QPSPGKPRK-----SGSA	378
MoCk1	ATSLDRPPRARLT-----VDR-----LNAA-----QPPPPSPITKAN-QGKD	368
FoCk1	TTD-HQQAQNLTL-----VGR-----LNAA-----QPPPPSPITKMGKQRD	373
VdCk1	SAA-HAQAQNLTL-----VSR-----LNAA-----QPPPPSPITKMQNK--G	372
	:	
YCK1	DPTS YEAYQHQTQKYQLQEQQKRQQQQQLQEQQLEQQQLQQOQQQQQQQLRATGQPPSPQ	488
YCK2	DPTS YEAYQQQTQKYQAQQQKQMQKSKQF-----ANTGAGQNTN-----	507
Cnck1	LPNVSN-----QAM-----VGVS-----PSPLPQSRRSQ	394
MoCk1	LRNAPGAIMASRG-----T-AGG-----LRDMATPTGSTQ	407
FoCk1	RPSAPGALSAQRG-----SGVG-----LRDMATPTGSTQ	403
VdCk1	RPNAPGALGAQRS-----SGVG-----LRDMATPAGSTQ	402
YCK1	AQTQSQQFGARYQPQQQPSA-----ALRTEQHPNDNSSLAAHSKGGFFQKLGGC----	538
YCK2	-----KYPYNAQPTA-----NDEQN-AKNAQDRNKSXGKFFSLKGLCC-----	546
Cnck1	QAVQSQ-----AGLQPISPMNVNSRGGTANASQ-QLGEGDYHNSKNGGFRITTCGFR	459
MoCk1	AQFQNS-----TQNLQPRPMH-----QQSNMTQPQL--NNGRPAEPEPTGFQKFMKVLCCG--	446
FoCk1	AQFQNS-----AQNLPPQPT--SQQQAQPAQ--ASQQAQNPQSGQKFMKVLCCG--	453
VdCk1	AQFQNS-----ARNLQPTAT--SQQQAQPAQ--PSRGSPEPQPSGQKFMKVLCC--	448

Supplementary Figure S1. Amino acid sequence alignment of the *Yck1* (YHR135C) and *Yck2* (YNL154C) proteins from *S. cerevisiae* with Ck1 proteins from *C. neoformans* (CNA05390), *M. oryzae* (MGG_08097), *F. oxysporum* Ck1 (FOXG_05428) and *V. dahliae* (VDAG_08537).

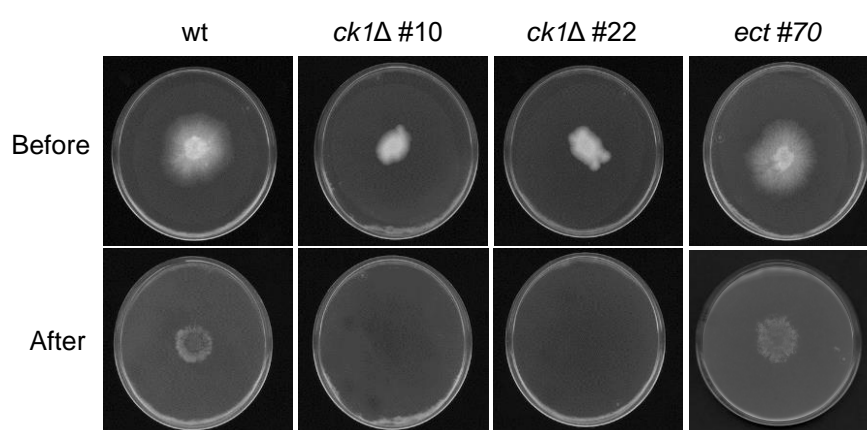


Supplementary Figure S2. Targeted replacement of the *ck1* gene in the *F. oxysporum* wild type and pHluorin-expressing strain (**A**) Physical maps of the *F. oxysporum ck1* locus and of the split-marker gene replacement constructs obtained by fusion PCR. Relative positions of restriction sites and PCR primers are indicated. *hyg*, hygromycin resistance gene. (**B**) Southern blot analysis of genomic DNA of the wild type strain (WT) and six independent transformants, treated with *Pst* I, separated on a 0.7% agarose gel, transferred to a nylon membrane and hybridized with the DNA probe indicated in (A). (**C**) Southern blot analysis of genomic DNA of the pHluorin-expressing background strain (pHluorin) and six independent transformants, treated with *Nsi* I, separated on a 0.7% agarose gel, transferred to a nylon membrane and hybridized with the DNA probe indicated in (A). (**D**) PCR amplification of genomic DNA of the WT, the *ck1Δ* and eleven independent complemented transformants, using primers Ck1-Fwd and Ck1-Rv indicated in (A).

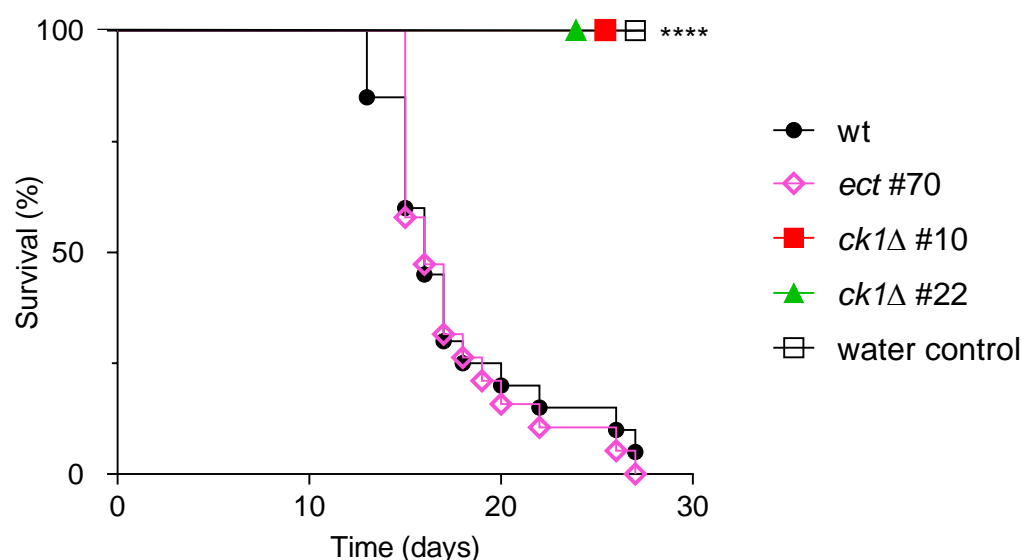
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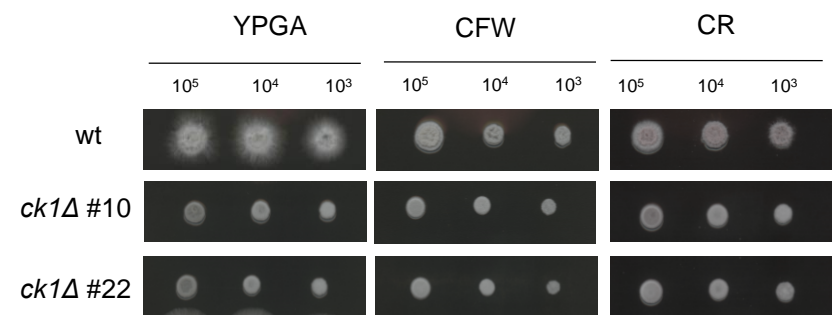
B



C



Supplementary Figure S3. Ck1 is required for growth, invasion and pathogenicity of *F. oxysporum*. **(A)** Aliquots of 5×10^4 fresh microconidia of the indicated strains were spot-inoculated on MMA or YPGA plates. Colonies were imaged 3 days after inoculation. **(B)** Aliquots of 5×10^4 fresh microconidia of the indicated strains were spot-inoculated on the top cellophane membranes placed on unbuffered MMA plates. Colonies were imaged 3 days after inoculation (before), then the cellophane membrane with the fungal colony was removed and plates were incubated for an additional day to visualize the presence on the plate, indicative of penetration through the cellophane (after). **(C)** Kaplan-Meier plots showing survival of tomato plants (cv. Moneymaker) inoculated by dipping roots into a suspension of 5×10^6 fresh microconidia/mL of the indicated fungal strains. Survival of tomato plants was recorded for 27 days. Twenty plants were used per treatment. $p < 0.0001$ (****) versus wt according to log-rank test. All data shown are from one representative experiment. Experiments were performed twice with similar results.



Supplementary Figure S4. Ck1 is not required for the response of *F. oxysporum* to cell wall stress. Aliquots of 10⁵, 10⁴ and 10³ fresh microconidia of the indicated strains were spot-inoculated on YPGA plates in the absence or presence of 50μg/ml Calcofluor White (CFW) or 100μg/ml Congo Red (CR). The plates were imaged after two days of incubation at 28°C. Images are from one representative experiment. Experiments were performed twice, each with three independent plates per growth condition.

S.cerevisiae	MTDTSSSSSSSSASSV--S-----AHQPTQEKPAK--TYDDAASESSDDDDIDALIE-	48
V.dahliae	MA--ESNSAAAPALNTPIESHRFEKDRPLDTGVDAP--VKPKVEEEDEDEDIDALIE-	55
M.oryzae	MADSTQPTGAGPAINTPIESGKFDEKEGLAHNPAAKP--K---VADEEEDEDEDIDALIE-	54
N.crassa	MA--DHSASGAPALSTNIESGKFDEKAAEAAAYQPKP--K----VEDDEDEDIDALIE-	50
T.reesei	MA--DDKAVGAPALDTNIESGNFDEKRAQAPAGVPP--K-KAPAEEEDEDEDIDALIE-	53
F.graminearum	MA--EEKAVGAPALDTNIETGGFDEKRGQAP-ATHNP--K-APVAEDEEPDEDMDALIE-	53
F.oxysporum	MA--EEKAAGAPALDTNIETGGFDEKRGQAPPPTHAP--K-APVAEDEEPDEDMDALIE-	54
F.verticillioides	MA--EEKATGAPALDTNIETGGFDEKRGQAAPPTHAP--K-APVAEDEEPDEDMDALIE-	54
C.neoformans	MGLTNR-----KNHKKDPEAGDPETEAKRQ-EEDKKKKYSGEEDVLLKY	44
A.nidulans	MAERKI-----SYA-ADVENDHS-----RPTDVNDSAGLDEYGALNRY	38
Z.triciti	MAAPRV-----SFSDKDLENEGGPERSRKWSQAPGNIEDLDEYALQKY	45
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S.cerevisiae	--ELQSNH--GVDD-----EDSDNDGPVAAAGEARVPPEEYLQTDPSYG	87
V.dahliae	--DLESQD--GHE-----E-DE-EETAVGGARVIPEDQLATDTRLG	92
M.oryzae	--DLESVD--GHGD-----LEEE-EEEAGPGAARVIPEDLLQTSTRTG	92
N.crassa	--DLESHD--GHD-----AEEE-EEATPGGGRRVPEDMLQTDTRVG	87
T.reesei	--DLESED--GHA-----FDDE-EETNPATGRVVPEDMLQTD SRLG	90
F.graminearum	--DLESED--GHE-----IDDD-E-EATPGGGRRVPEDQLQTD SRVG	89
F.oxysporum	--DLESED--GHA-----FDDE-E-ETQPGGGRRVPEDQLQTD SRVG	90
F.verticillioides	--DLESED--GHA-----FDDE-E-ETQPGGGRRVPEDQLQTD SRVG	90
C.neoformans	VADQQEIKKGGGDDKEDEENVKYIRKWYTPWKTKV---ETGGKKVPPDWLGTDRQKG	101
A.nidulans	ISTARDNRR-GSTSSA-GALSMKQKKKPWYKFwak-AGGENGEEGFVAPEDWLETDL-NG	94
Z.triciti	ISTYRDPKL-AQQQDEVANAHAESQKKKPWQ-FWKAPKAEDDGDAMVVPEDWLNADIRQG	103
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S.cerevisiae	LTSDEVLRKKKYGLNQMADEKESLVVKFVMFFVGPIQFVMEAAAILAAGLSDWVDFGVI	147
V.dahliae	LTEAEVLNRRRKYGANQMKEEKENLILKFFVME-----SRCPSSAAGLEDWVDFGVI	144
M.oryzae	LTEQEVQARRRKYGLNQMKEEKENLIMKFLGYFIGVPQFVMEAAVILAAGLQHWVDFAVI	152
N.crassa	LTSEEVVQRRRKYGLNQMKEEKENHFLKFLGFFVGPIQFVMEGAAVLAAGLEDWVDFGVI	147
T.reesei	LTEAEVLARRRKYGLNQMKEEKENLVKFLGFFIGPIQFVMEAAAVLAAGLQDWVDFGVI	150
F.graminearum	LTEAEVIARRKKWGLNAMKEEQENMILKFLMFFVGPIQFVMEAAAVLAAGLEDWIDFGVI	149
F.oxysporum	LTEAEVINRRRKWGLNQMKEERENMILKFLMFFVGPIQFVMEAAAVLAAGLEDWIDFGVI	150
F.verticillioides	LTEAEVINRRRKWGLNQMKEERENMILKFLMFFVGPIQFVMEAAAVLAAGLEDWIDFGVI	150
C.neoformans	LSSSEIEERRKHSGWNELESPNENQFLKISYFRGPILYVME LAVILAAGLRDWIDFGVI	161
A.nidulans	LPSSQIEPRRKRGGWNELTTEKTNFFVQFIGYFRGPILYVME LAVLLAAGLRDWIDLGVI	154
Z.triciti	ITNADVESRRKKFGWNEISTDKENLFKFLTFTGPILYVME LAVLLAAGLRDWIDFGVI	163
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S.cerevisiae	CGLLMLNAGVGFVQEFQAGSIVDELKKT LANTAVVIRDGQLVEIPANEVVPGDILQLEDG	207
V.dahliae	IALLLLNAVVGfyQEFQAGSIVDELKKT LALKAVVLRDGLKEVEAHEVVPGDILQVEDG	204
M.oryzae	CALLLLNACVGFQEFQAGSIVDELKKT LALKAVVLRDGLKEVEAHEVVPGDILQVEEG	212
N.crassa	CGLLLLNAVVGfyQEFQAGSIVDELKKT LALKAVVLRDGLTKEIEAHEVVPGDILQVEEG	207
T.reesei	CGLLMLNACVGFQEFQAGSIVDELKKT LALKAVVLRDGLTKEIEAHEVVPGDILQVEEG	210
F.graminearum	CALLLLNACVGFQEFQAGSIVDELKKT LALKAVVLRDGLTKEIEAHEVVPGDILQVEEG	209
F.oxysporum	CALLLLNACVGFQEFQAGSIVDELKKT LALKAVVLRDGLTKEVEAHEVVPGDILQVEEG	210
F.verticillioides	CALLLLNACVGFQEFQAGSIVDELKKT LALKAVVLRDGLTKEVEAHEVVPGDILQVEEG	210
C.neoformans	IGILFLNAGVGWYQEKQAGDIVAQLKAGIALKADVIRDGKEQEIEARELVPGDILVLEEG	221
A.nidulans	IGILMLNAVVGWYQEKQADVVASLKGDIAMKAVVKRDGQEQEILARELVTGDIVVIEEG	214
Z.triciti	IAILLNAAVVGWYQEKQADVVASLKGDIAMKATVVRDGGQEQDIKARELVPGDIVVIEEG	223
	. : * : *** ** : ** ** . : * . ** : * . * * * * : : * * : * * : * : *	
S.cerevisiae	TVIPTDGRIVTED-----CFL	223
V.dahliae	TIIPADGRIVTDD-----AFL	220
M.oryzae	TIIPADGRIVTDD-----AYL	228
N.crassa	TIIPADGRIVTDD-----AFL	223
T.reesei	TIIPADGRIVTEG-----AFL	226
F.graminearum	TIIPADGRFVTEG-----CFC	225
F.oxysporum	TIIPADGRFVTEG-----CFV	226
F.verticillioides	TIIPADGRFVTEG-----CFV	226
C.neoformans	KTIAADAKIIGDYEDKDGSKSDIL-DRV--EKSKHSGKGDDDD-----EDDGPDKGPSLC	274
A.nidulans	TIVPADVRLICDYDKPETYETYKEYLATANDDTLKE----NDDDDDDHGI EARLGVS LV	269
Z.triciti	QSVPADSRLICDYEPEDFEKYKELREQHALNPEEDPAGSEDAEGEGEGE- IQHQGHSII	282
	: : * : : :	

T.reesei	ARKRGE GAW E ILGIMPCSDPPRHDTARTINEAKQLGLSIKMLTGD AVGIARETSRQLGLG	578
F.graminearum	ARKRGE GAW E ILGIMPCSDPPRHDTARTINEAKRLGLSIKMLTGD AVGIARETSRQLGLG	577
F.oxysporum	ARKRGE GAW E ILGIMPCSDPPRHDTARTINEAKRLGLSIKMLTGD AVGIARETSRQLGLG	578
F.verticilliioides	ARKRGE GAW E ILGIMPCSDPPRHDTARTINEAKRLGLSIKMLTGD AVGIARETSRQLGLG	578
C.neoformans	AVKEEGKDWE LLGMLCMFDP RPVD TAKTIGE AHD LGIQVKMLTGD AVAI AKETCKQLGLK	626
A.nidulans	AVQKEGEPWQL LGMPYMFDP RPRED TAHTIAEAQH LGLSVKMLTGD ALAI AKETCKMLALS	623
Z.triciti	AYQKNNDPWVLLGMLS MFDPPREDTAQTII EAQQLGVPVKMLTGD ALAI AKETCKMLALG	636
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S.cerevisiae	TNIYNAERLGLGGGGDMPGSELADFVENADGFAEVFPQH KYRVVEILQNRGYLVAMTGDG	635
V.dahliae	TNIFNADRLGLGGGGDMPGSEVYDFVEAADGFAEVFPQH KYNVVEILQQRGYLVAMTGDG	632
M.oryzae	TNVYNAERLGLGGGGDMPGSEVYDFVEAADGFAEVFPQH KYNVVEILQQRGYLVAMTGDG	640
N.crassa	TNIYNAERLGLGGGGDMPGSEVYDFVEAADGFAEVFPQH KYNVVEILQQRGYLVAMTGDG	635
T.reesei	TNVYNAERLGLGGGGDMPGSEVYDFVEAADGFAEVFPQH KYSVVEILQQRGYLVAMTGDG	638
F.graminearum	TNVYNAERLGLGGGGDMPGSEVYDFVEAADGFAEVFPQH KYNVVEILQQRGYLVAMTGDG	637
F.oxysporum	TNVYNAERLGLGGGGDMPGSEVYDFVEAADGFAEVFPQH KYNVVEILQQRGYLVAMTGDG	638
F.verticilliioides	TNVYNAERLGLGGGGDMPGSEVYDFVEAADGFAEVFPQH KYNVVEILQQRGYLVAMTGDG	638
C.neoformans	TNVYDSEK LIG --- GGMAGSDI RHD FVEAADGFAEVFPEHKYQVVNLLQERGH LTAMTGDG	683
A.nidulans	TKVYDSERLIH --- GGLAGSAQI RDLVEKADGFAEVFPEHKYQVVEM LQQRGH LTAMTGDG	680
Z.triciti	TKVYNSQK LIH --- GGLSGT TQHD LVERADGFAEVFPEHKYQVVEM LQQRGH LTAMTGDG	693
	* : : : : : * * : * : * : * : * : * : * : * : * : * : * : * : * : * : *	
S.cerevisiae	VNDAPSLKKADTGIAVEGATDAARSAADIVFLAPGLSAIIDALKTSRQIFHRMYSYVVYR	695
V.dahliae	VNDAPSLKKADTGIGMFDVPRSST -----VSILP	661
M.oryzae	VNDAPSLKKADTGIAVEGASDAARSAADIVFLAPGLGAIIDALKTSRQIFHRMAYVVYR	700
N.crassa	VNDAPSLKKADTGIAVEGSSDAARSAADIVFLAPGLGAIIDALKTSRQIFHRMAYVVYR	695
T.reesei	VNDAPSLKKADTGIAVEGASDAARSAADIVFLAPGLGAIIDALKTSRQIFHRMAYVVYR	698
F.graminearum	VNDAPSLKKADTGIAVEGASDAARSASDIVFLAPGLGAIIDALKTSRQIFHRMAYVVYR	697
F.oxysporum	VNDAPSLKKADTGIAVEGASDAARSASDIVFLAPGLGAIIDALKTSRQIFHRMAYVVYR	698
F.verticilliioides	VNDAPSLKKADTGIAVEGASDAARSADIVFLAPGLGAIIDALKTSRQIFHRMAYVVYR	698
C.neoformans	VNDAPSLKKADCGIAVEGASDAARTAADVVFLDEGLSTIITAIKVARQIFHRMKAYIIYR	743
A.nidulans	VNDAPSLKKADCGIAVEGSTEAQAADIVFLAPGLSTIVDAIKLARQIFQRMKAYIQYR	740
Z.triciti	VNDAPSLKKADCGIAVEGSSEAQAADIVFLAPGLSTIVFAIKTARQIFQRMKAYIQYR	753
	***** * : . :	
S.cerevisiae	IALSLHLEIFLGLWIAI LDNSLDIDLIVFIAIFADVATLAIAYDNAPYSPKPVKWNLPRL	755
V.dahliae	LTRSQLSKLYLGLWIAI LNRS LNIELVVFIAIFADIATLAIAYDNAPYSKAPVKWNLPKL	721
M.oryzae	IALSIHLEIYLGILIAALNQSLNINLVAFIAIFADIATLAIAYDNAPYSKSPVKWNLPKL	760
N.crassa	IALSIHLEIFLGLWIAI LNRS LNIELVVFIAIFADVATLAIAYDNAPYSQTPVKWNLPKL	755
T.reesei	IALSLHMEIFLGLWIAI LNRS LNIELVVFIAIFADIATLAIAYDNAPYSQTPVKWNLPKL	758
F.graminearum	IALSLHMEIFLGLWIAI LNRS LNIELVVFIAIFADIATLAIAYDNAPFSQTPVKWNLPKL	757
F.oxysporum	IALSLHMEIFLGLWIAI LNRS LNIELVVFIAIFADIATLAIAYDNAPFSQTPVKWNLPKL	758
F.verticilliioides	IALSLHMEFFLGLWIAI LNKS LNIELVVFIAIFADIATLAIAYDNAPFSQTPVKWNLPKL	758
C.neoformans	IALCVHLEVYLMLSILIN ETIRVDLVVFLAIFADVATIAIAYDRAPYAHQPVEWQLPKV	803
A.nidulans	IALCIHLELYLVTSMIIN ETIKADLIVFIALFADLATIAYAYDNAHFARPVEWQLPKI	800
Z.triciti	IALCLHLEIYLVTSIII IREVIASELIVFIALFADLATVAIAYDNAHSEQRVVEWQLPKI	813
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S.cerevisiae	WGMSIILGIVLAIGSWITLTTMFL -- PKGGIIQNFGAMNGIMFLQISLTENWLFITRAA	813
V.dahliae	WGISVILGIVLAIGTWITVTTMYAHGPNGGIVQNFGNLDEVVFLQVSLTENWLFITRAN	781
M.oryzae	WGMSVLLGVVLAIGTFITITTMFVHGEGGIVQNNQIDAVVFL EISLTENWLFITRAN	820
N.crassa	WGMSVLLGVVLAVGTWITVTTMYAQGENGGIVQNFNMDEVFLQISLTENWLFITRAN	815
T.reesei	WGMSVLLGTVLAIGTWIATLTTMYAGGQNGGIVQNFGNIDEVVFL EISLTENWLFITRAN	818
F.graminearum	WGMSVLLGVVLAVGTWIALTTMLANSEGGIVQNF GK IDEVLFLEISLTENWLFITRAN	817
F.oxysporum	WGMSVLLGVVLAVGTWIALTTMYANSEGGIVQNF GK IDEVLFLEISLTENWLFITRAN	818
F.verticilliioides	WGMSVLLGVVLAVGTWIALTTMYANSEGGIVQNF GK IDEVLFLEISLTENWLFITRAN	818
C.neoformans	WIISTIMGLLLAAGTWIIRATLWI -- DNGGIVQNF GSTQEILFLEVALTESWVIFITRLA	861
A.nidulans	WWISVVLGVLLAAGTWIMRASLFL -- ENGGIIQNFGSPQPMFLFVSLTENWLFIVTRGG	858
Z.triciti	WIISVILGIELAIATWIARGTFFM -- PGGGIIQNYGNFEEILFLEIALTENWLFITRGA	871
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S.cerevisiae	GP -- FWSSIPSWQLAGAVFAVDIIATMFTLFGWWE -----NW-TDI	852
V.dahliae	GP -- FWSSIPSWQLSGAIFIVDILATLFCIFGWFEH -----GQ-TSI	820
M.oryzae	GP -- FWSSIPSWQLTGAIFFVVDIIASCFAIWGWVFG -----NKMTHI	860
N.crassa	GP -- FWSSIPSWQLSGAIFLVDILATCFTIWGWFEH -----SD-TSI	854
T.reesei	GP -- FWSSIPSWQLSGAILVVDIIATLFCVFGWFIG -----ED-TSI	857
F.graminearum	GP -- FWSSIPSWQLSGAILIVDILATLFCIFGWVFG -----GQ-TSI	856
F.oxysporum	GP -- FWSSIPSWQLSGAILIVDILATLFCIFGWVFG -----GQ-TSI	857
F.verticilliioides	GP -- FWSSIPSWQLSGAILIVDILATLFCIFGWVFG -----GQ-TSI	857

C.neoformans	QEPGTPNVWPSFQLVAAVIGVDALATIFALFGWISGDAP-----HGGWTDV	907
A.nidulans	-----KTWPSWQLVGAI FVVDVLATLFCVFGWLAGDYVETSPPS---QATFSTNNDDTI	909
Z.triciti	-----QTLPSWQLVGAILGVDILATLFCIFGWLNSSIYQRPLPSPMSTFQQTANGHTDV	925
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S.cerevisiae	VTVVRVWIWSIGIFCVLGGFYEMSTSEAFDRLMNGKPMKEKKSTRSVEDFMAAMQRVST	912
V.dahliae	VAVVRIWIFSFGVFCVCAGVYYILQDNAGFDNMMHGKSPKGSQKQRSLEDFVVS LQRVST	880
M.oryzae	VAVVRIWVFSFGVFCIMGGLYYILQDSQGF DNLMHGKSPKGNQKQRSLEDFVVS LQRVST	920
N.crassa	VAVVRIWIFSFGIFCIMGVYYILQDSVGF DNLMHGKSPKGNQKQRSLEDFVVS LQRVST	914
T.reesei	VAVVRIWIFSFGIFAIMGGLYYFLQGSGTFDNLMHGKSPKQNKQRSLEDFVVS LQRVST	917
F.graminearum	VAVVRIWIFSFGVFCVMGGLYYFMQGSGTFDNLMHGKSPKQNKQRSLEDFVVS LQRVST	916
F.oxysporum	VAVVRIWIFSFGVFCVMGGLYYFMQGSGTFDNLMHGKSPKQNKQRSLEDFVVS LQRVST	917
F.verticillioides	VAVVRIWIFSFGVFCVMGGLYYFMQGSGTFDNLMHGKSPKQNKQRSLEDFVVS LQRVST	917
C.neoformans	VTVVKIWCFSFGVVIILLVYLM LNSIRWLDHIGRKS R---SKKNEKLENFLTDLQRLTI	964
A.nidulans	VTVVWIWAYSIGVTIIIAVVYYLLTIIPALDNLGRKNR---SVVDTKVENLLNHLSKLAI	966
Z.triciti	VTVVVVWMFSIGVMIVIAITYYLLNKIPGLADLGRQNR---SLHDTQMENIIGHLSKLAL	982
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S.cerevisiae	QHEKET*-----	918
V.dahliae	QHEKSQ-----	886
M.oryzae	QHEKSQ-----	926
N.crassa	QHEKSQ-----	920
T.reesei	QHEKSQ-----	923
F.graminearum	QHEKSQ-----	922
F.oxysporum	QHEKSQ-----	923
F.verticillioides	QHEKSQ-----	923
C.neoformans	VHETDHNGSY Y-RFASKKEEESGDN GKKDDKKDEAKSADTKKQESNAKKGDDEKKKDD	1023
A.nidulans	EHEVDANGKSRYTLGARAEPEDDE-----	990
Z.triciti	KHERDENG DARWTLATKATDDEDD-----	1007
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S.cerevisiae	-----	918
V.dahliae	-----	886
M.oryzae	-----	926
N.crassa	-----	920
T.reesei	-----	923
F.graminearum	-----	922
F.oxysporum	-----	923
F.verticillioides	-----	923
C.neoformans	GGKKGATGGDKGLSDQTGKGHEHAQAQGKGANEVQPDGTQPKPDDQSSEGT HVDPN	1079
A.nidulans	-----	990
Z.triciti	-----	1007