

S_cerevisiae	1	MDTLE-----EPECPPHKNRIFVSS
S_paradoxus	1	MDTLE-----EPECPPHKERIFVKS
S_mikata	1	MRDTDAMVSKIIILNDILSLVYVGSICIRMDTLEEPECPEHEDRVFVKS
S_bayanus	1	MDTLE-----EPEFPPHKPRVFVES
A_gossypii	1	MQGE-----YQYISR
S_castellii	1	MSES-----CVFITIS
K_waltii	1	MSASPV-----NDIRYIHD
K_Lactis	1	MEKYP-----YEYIPG
S_kluyveri	1	MQANA-----TEYKYIDS
V_polyspora_I	1	MDHI-----TKFVTS
V_polyspora_II	1	MTT-----
L_thermotolerans	1	MNSNLP-----SGLKYICD
Z_rouxii_XP	1	MSSS-----CLYVDS
C_glabrata	1	M-----

S_cerevisiae	21	SKDFEGYP---SKAIVPVQFVAALTSIHLTE-TKCLLIGFSNFFERRGDQS
S_paradoxus	21	SKDFEGYP---SIAIVPVQFVALLTSIHLTE-TKCLLIGFSNFFGRDDQV
S_mikata	51	SKDFEGYA---SKAIVPVHFVALLTSIYLTE-TKGLLIVFSNFFEEGESQV
S_bayanus	21	AKEFESFP---DDAIVPVQFVSVLTSIRLITE-TKCLLIGFSNFFGGRDRM
A_gossypii	11	PAELLRFFS-SDDIVAQKVEFVAVLTRIVETPSTSCVLMQLQNFEGHRDD-
S_castellii	11	PSQFQRF---DSKQISLRFVSLLTGIKYNG-KNFIELELSDFDNINV--
K_waltii	15	AVELESFVS-DDQVVKQCIQEFVSVLTSIDFNPTQTRCLFQFKNFKNQDGG-
K_Lactis	12	PECLNKYYQ-HGSIVSKPVHFISILSKVAYTKNDKCLFHEDNFTNGKAG-
S_kluyveri	14	PRDLEAYYS-NDEIVTHNIRFISVLTSLFIPNKKCLFIFQNFEGHRPD-
V_polyspora_I	11	SSQLIDLIENESEKANVYVEFVSLFTSLQYDSKTCFTLKEDESNSTLN-
V_polyspora_II	4	-----RQFYGLLTCIKVEE-NKFRLLTLHDG-----
L_thermotolerans	15	PLELKGFFS-EGEVLQRDIEFVSVLTSIDENPKSRCLFQFSNFRPGESV-
Z_rouxii_XP	11	PAQIGEIFV---N-CGCVRFVSLTSESRN-EFYCLEMNFAMGTPT-
C_glabrata	2	-----SIEITAVLTSISKDD-NGFHLALDDIAGEVRV-

S_cerevisiae	66	QEDQYLIKLFKDRGSERLARITISLLCQYFDIELP-DLSDSGASPTVI
S_paradoxus	66	EEDQYLIKVKFKDRSSERLARMTISLLCQYFEIELP-DLSDSGSSSTVV
S_mikata	96	EKDQYIILKFKDRSSERLARMTISLLCQYFDIELP-DLSDG----STLI
S_bayanus	66	-GQRYTVKLFKFKDSAERLARMTISLVCRYFDIELP-DSDLGTESCPAEL
A_gossypii	59	-RIPYVVKLPCRTWEQSQLVAIVLKLMLHGFGLDTE-KVGDE----SGFD
S_castellii	54	-ISPYRVKLRCSDENAKRLAQMISLLCQFFDFEIP-ELRTL---SDEFF
K_waltii	63	-DFDYTCIKSCNSAETLNLTKLTLSLFAQQFDLELT-DLDNP---EGFC
K_Lactis	60	-LNTYCGKIKNKSFECDVLLRMVLSLFEKLGMQIA-GLDYS---SDFV
S_kluyveri	62	-ECPYTAKIRCDAETSTLTRMMLSLIAQQFDLDLP-DLDDP---SGFH
V_polyspora_I	60	-SSPFVVFQEP--FSS-DTRTKVLRLCDKEDIDLPIDFNSE---SPSFS
V_polyspora_II	28	-DHLYSIFI--SDDPKNYQVAKICASLICRFYNIETIE-FEK-----QFYQ
L_thermotolerans	63	-SPDYTCIKTCNNVETLNLTKLTLSLVSOQFDLDFP-DLINDA---EGFY
Z_rouxii_XP	54	-SIPYRPIPKRHADSARSAKMVIELICNWNLDIP-ELQN---GITFI
C_glabrata	33	-L-----D-----IDEAQAREVVNECDLEVS---D---TNAEN

S_cerevisiae	115	LRDIHLERLCFSSCKALYVSK---HGNY-----TLFLEDIKPLDL
S_paradoxus	115	LRDIHLERLCFSSCKALYVSK---HGNY-----TLFLEDIKPLDL
S_mikata	141	LKDIHLERLCFSSCKALYVSR---SGNY-----TLFLEDIKPLDI
S_bayanus	114	LEDIHFERLCFSSCKTLYVSR---HGNY-----TLFLEDIKPLDL
A_gossypii	103	LADIHIKHLCFARCRGKFITN---DKNG-----SILLDEILGIDI
S_castellii	99	IDFIQLDRLCFINCKVIYIGK---DDKY-----SLFLDDIKPIDL
K_waltii	107	INEMHLDKLCFVCKGTFVSC---NNKG-----GIFVQRLRVIDL
K_Lactis	104	LEFLEKRYMCMISVKGLFITA---YDKA-----SLQIHEIKLLDL
S_kluyveri	106	LRGIYFERLCFVKCQGRFVST---KNKG-----SIFLQDIRCIDL
V_polyspora_I	103	IENIYLEKLCFVNCIGRYAYN---GIHP-----VVFAEKIRPISL
V_polyspora_II	69	FAAIHLTKICILQLQV-YNSK---N-----SIDDIKPLNL
L_thermotolerans	107	MKDIHLEKLCFVCKGTFVTC---DNKG-----GIFLQGLRIIDI
Z_rouxii_XP	98	KNRIHTQCLCFLECKVLYMAT---PSESSQNQPFEDPYLGYLESVKELSF
C_glabrata	59	ITKIQLKLCFVVAKCTSSGLQLVNGDMT-----FKLQPVVQVLDI

OB1

S_cerevisiae	152	VSVVISTISTKSTNSSK-HSSSELI	SECDLNNSLVDFNNLIEMNRDEKNR
S_paradoxus	152	VNVIRTISTKSKKGSSEHLLEPTSKCNL	KRSLVDFNNLIEMNRDEKNS
S_mikata	178	VNVINSISTKSKSGTEFLPSGPIIESNL	REPLLDIFNNLIKMNIDERNS
S_bayanus	151	AYVINTISKGPKISSNGVCLAPNAGPEL	KKSLAAIFDNLIAMNRDQKNS
A_gossypii	140	DKELRNEAAGSQRLS-----	NEDWGVVNKITDNLIRLDRDSSHR
S_castellii	136	NNAIRIARQLQST-----	LEQRTILKIFDNLIKLNNSRNG
K_waltii	144	HSTLFDDEKSKQK-----	DNIMGTLQATFDNLMKLNDSKAQ
K_Lactis	141	KSYFDQSTAD--EY-----	KLKPSIEKLFNNLLKREK--RNAD
S_kluyveri	143	NGTLYTARTF--KES-----	N-EITTLNRIFDNLIIRLNNDPKND
V_polyspora_I	140	PSVMKLLTNKTVN-----	ETAFSLSSIFDNLINLNSNSNRS
V_polyspora_II	100	ETVTRFVKSG-----	NEEVNIIKYLIDLDQDSTES
L_thermotolerans	144	HSSLFDPTKRDER-----	SSISSETVRVIFDNLVKLNDSKAQ
Z_rouxii_XP	145	TQAQELALE-AST-----	DVGKTIKRSILQNLQQLMHQNGSIG
C_glabrata	101	NYIQENWNTLDK-----	KKKDKISKILLALKKLDSDIKSE

$\alpha$ D

$\alpha$ E

S_cerevisiae	201	FKFVKLIHYDIE-LKKFVQIQ-----	QKVLISQKSKAA-----
S_paradoxus	202	FKFVKLIHYDIE-LKRFIQEQ-----	QNILSQKLIKAK-----
S_mikata	228	FKFVRLIHYNTE-LKRFIQEQ-----	QSLLSQKSKTK-----
S_bayanus	201	FKFVKLTHYDIE-FKEFIQER-----	QRLLSQKAKPS-----
A_gossypii	179	FNFNLAHSTRQ-FIDYLYKYR-----	TERLTQVD--L-----
S_castellii	172	FKFVKLDNYNNE-FAQFIQEK-----	QTMVNSRKKTT-----
K_waltii	181	FKFVKLQNYDLE-MRRYVQCR-----	QEALLKL-K-----
K_Lactis	176	FQFKSLTSYCTE-MQSYLDSLVLQEA	PTRLIPKENTA-----
S_kluyveri	179	FKFVKLLNYDHD-MKKFIQNR-----	QENLALTN--F-----
V_polyspora_I	176	FKFVLELENYEPK-FGEFIQGR-----	QQNLAVQLK-----
V_polyspora_II	131	FSFDEIPFALPEDFVLVIDSL-----	KS-----
L_thermotolerans	181	FKFVKLQNYDTA-MRKYIQSR-----	QESMLSL-K-----
Z_rouxii_XP	180	FNSNLIQQQQQQ-QQQQQQQQ-----	QQLLLLQEQSEPKQVSQSTQQSS
C_glabrata	136	FNFKVLLNRYKNT-LVHFLSGI-----	KM--TKQTK-----

$\alpha$ F

$\alpha$ G

S_cerevisiae	232	-----	AINPFFVFNRL
S_paradoxus	233	-----	AINPFFAPNRL
S_mikata	259	-----	LINPFFAPNRL
S_bayanus	232	-----	AVDFFVFNRL
A_gossypii	208	-----	RMNPMFGANQL
S_castellii	203	-----	IINNPLFRSHIT
K_waltii	209	-----	EKNPLFGLSRI
K_Lactis	213	-----	IVNPLFQLGLQ
S_kluyveri	208	-----	RKNPIFGVNRY
V_polyspora_I	205	-----	LKNPLFSASRG
V_polyspora_II	154	-----	NEL
L_thermotolerans	209	-----	EKNPLFGLLKP
Z_rouxii_XP	223	ISSQSENHNSRTSTSNQSHYQNSFRS	INSGSNNTPTTLASTNPIIFGNRL
C_glabrata	163	-----	ITSFETKO--

S_cerevisiae	243	GIP---YIESQNEFNSQLM	TLNVDEPTT-----D		
S_paradoxus	244	GIP---YLESQNEFNSQLM	TLNVDEPIT-----E		
S_mikata	270	GIP---YVETQNEFNSQLM	TLNSEQPIT-----D		
S_bayanus	243	GAP---SLESQNEFNSQLM	TLNADEEVP-----N		
A_gossypii	219	-LC---MKESQDDFN	SQQDDPYFNS-----		
S_castellii	216	DTRE-NEMTSQDFDN	SQYLNTENSNDST-----		
K_waltii	220	H-A---DHDSQNDFDSQ	IPDTSNIGFTLHDSEKHS	A-----EI	
K_Lactis	224	REV---NNSDFNEFDSQ	TQQHNIPT-----LPL	-----QS	
S_kluyveri	219	-LS---AQESQDDFDSQ	RMETQSTLFGFTALGH	DNPTDIQQTHSKHSP	PG
V_polyspora_I	216	YQDSCKDFDSMREFESQ	CNDSSVKEEPT-----		
V_polyspora_II	157	SFL---SRE-SSGFNGQ	VKSEI-DDEYF-----D		
L_thermotolerans	220	R-A---DHDSQNDFDSQ	LPDPSNLDNAIFYGHR	IPS-----ES	
Z_rouxii_XP	273	I-----TVESQLDFNS	I--NTQNDELYE-----		
C_glabrata	171	-TT---MVESQNDFNSQ	AMNTQQFTSQA-----		

OB1

RD

S\_cerevisiae 269 IISNMGEEEMHDSADPI-----EDSDSSTT-SSTGKY-----  
 S\_paradoxus 270 IGDKGDNMHDSADPI-----EDSDSSTT-SSTGKY-----  
 S\_mikata 296 ISSNGDDMRYSADPI-----EEDSSTI-SSTGKF-----  
 S\_bayanus 269 TSGRKDDPDASSDPI-----EDSDASSSSSSTGTF-----  
 A\_gossypii 240 -AEQLHTGFSLPNPL-----EETAAVSS-GYPQ-----GV  
 S\_castellii 243 -----SPSHDSIDPI-----EESDANSSS-----IH-----  
 K\_waltii 255 LISTT-DS-LAFDRI-----EDSENSRLTTSTT-----SY  
 K\_Lactis 251 ISSNPDG--E-ADQVAKESTKTAIESDTPOF-SLE-----QN  
 S\_kluyveri 265 LSGTLHDT-STEDLI-----EESDSSTT-S-EFMA-----TP  
 V\_polyspora\_I 244 -----TSL-----FNNES-----GY-----  
 V\_polyspora\_II 181 T-----AQSS-VS-----  
 L\_thermotolerans 255 LDSQT-PNLVSSSEII-----EEGQSPSVAGAAGTPAALSGSNKPSSY  
 Z\_rouxii\_XP 294 -----VELEPTPEPK-----RKEIIRTVS-----SP  
 C\_glabrata 195 -----SIPGISDDEL-----IDSDDDLNDNISEGSY-----PT----

S\_cerevisiae 298 FSSKS-----Y-----  
 S\_paradoxus 299 FSSRS-----Y-----  
 S\_mikata 325 VSPGS-----C-----  
 S\_bayanus 299 LSSRS-----Y-----  
 A\_gossypii 268 --V-T-----EPKADSPVELP--STEHGRSYTRDERPVLMSQPISR---  
 S\_castellii 264 LSRNT-----S-----  
 K\_waltii 283 GSS--A-----V-----  
 K\_Lactis 285 PCNDSI-----  
 S\_kluyveri 293 VSFRSCRNNTKNTADPPKVVRPDLTTSNSRHLQSSSEESGLPLNPGESNLL  
 V\_polyspora\_I 254 KSREA-----S-----  
 V\_polyspora\_II 188 -----  
 L\_thermotolerans 296 QGSGSL-----S-----  
 Z\_rouxii\_XP 315 MGKSS-----S-----  
 C\_glabrata 195 -----SIPGISDDEL-----IDSDDDLNDNISEGSY-----PT----

S\_cerevisiae 304 -----IQSQTPERKTS-----VPNNWHD--  
 S\_paradoxus 305 -----IQSQTPERKTS-----VPNNWHD--  
 S\_mikata 331 -----IQSHTPERKTS-----VPNNWLD--  
 S\_bayanus 305 -----IQSQTPERKTK-----VPNNWLD--  
 A\_gossypii 305 -----IMQLT--NSSKRK-Q-----MPHS---P-  
 S\_castellii 270 -----R-----Q-----  
 K\_waltii 288 -----IRA-TPTSQNTDDTLASDSTMGTFPGGRANVPQKRG--  
 K\_Lactis 291 -----IQSAKEQKRPI-----GSNKGMS  
 S\_kluyveri 343 FQRNVYTRITAMIAEHSKERESA-----IARR---AS  
 V\_polyspora\_I 260 -----D-----EE-----FD--  
 V\_polyspora\_II 188 -----QIQRPAT-SS-----AFETFRN--  
 L\_thermotolerans 303 -----ISQISPPRETE-----YVRLSRD--  
 Z\_rouxii\_XP 321 -----F-----LE-----SG--  
 C\_glabrata 228 -----T-----KHD-----IPTNHNG-

S\_cerevisiae 322 -D-----  
 S\_paradoxus 323 -D-----  
 S\_mikata 349 -N-----  
 S\_bayanus 323 -R-----  
 A\_gossypii 322 --LST-----  
 S\_castellii 272 -----  
 K\_waltii 323 -F--SSH--EKAQLLELISSDEDDDKLSSGDEAISELRLRAQSGSDSHF  
 K\_Lactis 311 DFIS-----  
 S\_kluyveri 372 NVVMS-----  
 V\_polyspora\_I 265 -----  
 V\_polyspora\_II 204 -V-----  
 L\_thermotolerans 321 -F--ETSAIESNKRSVVTSQEIIRDDSSLLDDDDILEFSLSTHS-VDKNEL  
 Z\_rouxii\_XP 326 -----  
 C\_glabrata 239 -----

RD

S_cerevisiae	323	----D-----	SGSKR--	KRKLS	-----
S_paradoxus	324	----D-----	SGRNK--	KRKLS	-----
S_mikata	350	----D-----	SEGKN--	KRRLS	-----
S_bayanus	324	----T-----	S-ERK--	KRKLS	-----
A_gossypii	325	----HS----	APCDGNTKR		-----PT
S_castellii	272	----S-----	ITTER--	SPKLR	-----
K_waltii	368	NYM-NS-----	SSPNI--	KRARS	-----
K_Lactis	315	-----	SGTVK--	KIKLTDL	GALTHHRQVTRQDLDISYQLP
S_kluyveri	377	----QSIPDITPKNGTNTQDDRALHR			-----SNFQPE
V_polyspora_I	265	----P-----	NPPKR--	QKSV	-----
V_polyspora_II	205	----E-----	RNLSK--	KRKLS	-----
L_thermotolerans	367	SQTSRG-----	SQPTS--	KRQRI	-----
Z_rouxii_XP	326	----P-----	SPPKR--		-----L
C_glabrata	239	----S-----	SANKH--	SKKDS	-----

RD

S_cerevisiae	334	-----	FHS-PNAS	SIRKATSYEQ--	LSLASVGSVE-RLEG
S_paradoxus	335	-----	FQG-PSAPLSQKATSYER--	LSLANVGSVE-RLEG	
S_mikata	361	-----	FQC-TSAPSSQQVIDYER--	LSLAKVGSVE-RLKG	
S_bayanus	334	-----	FTD-RTAPSSQLGIDYER--	LSLASLGSME-TFEG	
A_gossypii	338	-LPLVPDDA-TGKRKRTS-TTAGVVETALTIDT--	LENSEEGKLV-STTG		
S_castellii	283	-----	KLN-KNSKPVA--NKPEY--	YRCVDIGTIC-EIQG	
K_waltii	383	-----	AFSEKPPP-SD--VGF-C--	IPNISSGECV-ILRG	
K_Lactis	349	YDPIISSQS-QFEQPTI-QEEGSDPFDLKPD--	SISKAITDRLYHISDG		
S_kluyveri	405	PSTVTSTDTNEQLKKRQK-LDIPTLHIAVFPEILS	L VHASPNTF-RLQG		
V_polyspora_I	275	-----	VN-ETSDDVKKWGSNDI--	MNSSRIGERY-TVEG	
V_polyspora_II	216	-----	EIVTSPAPIVAK--SSV--	FIDAPLGEVH-SITG	
L_thermotolerans	383	-----	QMLGNISQ-KD--PNS-Y--	MFHASLDEPL-IISG	
Z_rouxii_XP	333	-----	KRS-----RTRIDPAI--	LNAEESDIF-ELKG	
C_glabrata	250	-----	CLYVNFMDPHRNQLWTYNG--DNS----	SVI-ISHC	

S_cerevisiae	365	KIVGMNPPQFASINEFK-YC-TLKLYFTQL-LPN----	V-PDKVLVPGV
S_paradoxus	366	KFVGMYPPTQFASINEFK-YC-TLKLYYTHLPLSN----	I-PDKVLLPGT
S_mikata	392	KFVGMYPSPHFSGITEFR-YC-TLKLYFTHLSVSK----	I-PDKLILPGT
S_bayanus	365	KFVGMYPPEFHSVDDFK-HC-SLKLYFTPLPLSG----	P-LDRVLVPSV
A_gossypii	382	FIAGLYPNVYEECV-R-GS-SFILYFPLTT-----	AD-TCEVQDPAK
S_castellii	312	KLVGSIPLNLIE-SNLN-AS-PARFFFIPNEWTEGKEGNDEAMIKLLPNY	
K_waltii	411	LVLGLRIND-----ASY-TP-SVVLFFRPESLLD----	KNDRGPLFIHD
K_Lactis	395	KILGFIPNQYLDPESSLIEDDFLLIYVYTYE-----	LPLLSAVFVPEY
S_kluyveri	453	KFVGMPLPNELQKKVPQK-IS-TLKLYFQPASWDE----	KVLSSKYLNASK
V_polyspora_I	306	KFLNIFPIRFDSLNLK-YW-SLRLYFQPTIEWYD-----	RNADIIIPNK
V_polyspora_II	245	TIAGTYPSDFKDLSDLK-DT-ILRLYIIPREWET-----	EAERQILIPNS
L_thermotolerans	411	VVFGLRIND-----AAS-SP-SIALYIHAGSLQN-----	ESVSANLYPYK
Z_rouxii_XP	357	RFAVHPLE-----NLTYFLPEGI-----	ETPSHLSPGI
C_glabrata	279	SLQSMSPVGFKSLDDLD-KF-TLRLVFKQKTM-----	VDELLIPNN

OB2

S_cerevisiae	406	NCIEIIVPTIRERICELFGVLNCQSDK- <b>ISDILLLE</b> --	KPDRI	SVEVERIL
S_paradoxus	408	NCIEIIPTRERICELFGVLNCQSSK- <b>ISDILLLK</b> --	TPGPI	SVEIERIM
S_mikata	434	NCIEIIPTRERICELFGVLNCQNSM- <b>ISNILLLD</b> --	KPDIS	SVEIERVM
S_bayanus	407	NCIEIIPTRERICELFGVLNCQSDK- <b>ISAILLMD</b> --	KPDIS	SVEIERIL
A_gossypii	421	NCIEIYSSDIDYVLQYQYDIDHNMDRK-EALILLNSRLDKLEVRISITKAK		
S_castellii	359	NCIEVLVSKFSELKGFISKFTTDFTK-LNHFLI-N--N--	KVQVRIVRSK	
K_waltii	449	NCIEILVHITDNVKNSEVIRTESLLELLDIMRYN- <b>VEDKAVTVEVRKTP</b>		
K_Lactis	438	NCYEIAITNVAKFFSKIGVRSYPHSIKNSLLELKEIDNNRYDITTYKKE		
S_kluyveri	497	NCLEVVTNCIDQLLDIFSLSKQPDNR-SLLGDI <b>STVLLYRTFEVKIQKRR</b>		
V_polyspora_I	348	NCIEIMVFNLDEFKNLFGTLVNNSES-LSLILF-S--Y--	EVSLEIKRSK	
V_polyspora_II	288	NCIEVLILDASEIHKFFGRLVNDSSQ-S-FREVIS-S--T--	EFFIRLERAK	
L_thermotolerans	449	NCTEVLAYASDSIELNSKLFPAENSAEMLEALRWY- <b>VEDKKVELKVKKSS</b>		
Z_rouxii_XP	386	NCIEISSEA-----MPL-E--K-EYTIEIERVE		
C_glabrata	318	NCCEVVIKNKLEYMETFGRLADTSSK- <b>LRKYL</b> --	N--G--	DLNITVKKWK



S_cerevisiae	453	WDND---KTA-----SPGMAVW <b>SLKNI</b> STDTQAQAQV-Q--VPA----
S_paradoxus	455	WDND---ETI-----SPGI <b>AVW</b> SLKNI <b>STDT</b> QAQA-----PV----
S_mikata	481	WNN <b>D</b> ---ETI-----SPGLTVW <b>SLKNI</b> SVK <b>TQAQ</b> ASA-Q--SPA----
S_bayanus	454	WDND---ETV-----SPGLAVW <b>SLKNI</b> CADTHVQPPA-----PR----
A_gossypii	470	LFFS-----DSTY <b>SFCWELKALQVNAETLTQF</b> -T--SIK----
S_castellii	403	F <b>PFKLLKNDTFHAYNKEHAF</b> APIWTL <b>QDIDLLPSKIPKK</b> -K--AVP----
K_waltii	498	YLLT-----DQY <b>FTFSWTLR</b> DV <b>RT</b> EQGLPPKL-A--VIS----
K_Lactis	488	ETIG-----AAK <b>SSK</b> WAL <b>KDV</b> VLSALPTPK-E--VTF----
S_kluyveri	546	V <b>SMA</b> -----GIFYS <b>FCSW</b> SLTD <b>ISTDS</b> PKKIEE-K--RSQ----
V_polyspora_I	392	<b>WSFD</b> -----KTIF <b>TSVW</b> TLSNM <b>KILR</b> KLEIDN-E--TNQ----
V_polyspora_II	332	LQLE---NSF-----HTFY <b>WTFQ</b> TVNISG <b>QSQNTS</b> IQNLDPSS <b>SSFM</b>
L_thermotolerans	498	ILLA-----DGY <b>FTFAW</b> TLVSV <b>KTAGDAPKLS</b> -T--SQT----
Z_rouxii_XP	410	KPLF-----DDK <b>FTLQW</b> IL <b>K</b> SP <b>EP</b> ESE-----
C_glabrata	361	Y <b>EI</b> -----RGYDS <b>FKW</b> T <b>IEK</b> LDFNPEMPVKE----KV----

OB2

S_cerevisiae	486	-----QSSA-----S---I--DPSRTRMSK <b>MARKDPTIEFCOL</b>
S_paradoxus	484	-----QSLP-----P---T--NPPRTRMRE <b>MARKDPTIEFCOL</b>
S_mikata	514	-----KSLP-----P---V--NAPRTKMR <b>KMAEKDPTIEFCHL</b>
S_bayanus	485	-----ASS-----P---S--NPPRLKMRELAK <b>KDPTIEFREL</b>
A_gossypii	501	-----MPNPLP-----E--RG--N-----ALSID <b>Q</b>
S_castellii	446	-----RLLPST--IANNQDEDLNKILNQ <b>QFERTKND</b> SVIK <b>FEEL</b>
K_waltii	529	-----DAGSQS-----S--QV-ITSSQ <b>ESSQRMPDPLKTFSEL</b>
K_Lactis	518	-----TEN <b>KFPL</b> RV <b>SNI</b>
S_kluyveri	577	-----SSFPVA-----K--GV--T-PLQHR <b>TYRVDPVKTVGEL</b>
V_polyspora_I	423	-----RLTPTTEDIKNN <b>NGKYKSKIKDDMAW</b> ND <b>KDELIKFEDL</b>
V_polyspora_II	370	PSR <b>NLLSSSTESIP</b> PTS <b>F--KPQQ-S--TPN</b> KND <b>RKNPSRIDPLIQEKDL</b>
L_thermotolerans	529	-----SHTPRS-----S--QI-VGSSQ <b>EASQDSLDPKTFGEI</b>
Z_rouxii_XP	432	-----PPS-----GRTRD <b>QLIWFKDL</b>
C_glabrata	389	-----PEQG--KCSNRYDFN--SIN <b>FIDESTRDQVIQFKDM</b>

$\alpha$ A

S_cerevisiae	514	GLDT-FET <b>KYITMFGMLV</b> SCSFD-KP- <b>AFISFVFS</b> DFTKNDI-V <b>QNYLYD</b>
S_paradoxus	512	ELNN-FET <b>KYVTFMFGMLV</b> SCSFD-KP-S <b>FISFVFT</b> DFTKNDI-V <b>QNYLYD</b>
S_mikata	542	ELNT-FET <b>KYVTFMFGMLV</b> SCSFD-KP-A <b>FVSFVFT</b> DFTTNDI-V <b>QNYLYD</b>
S_bayanus	512	GLGA-FDT <b>KFVTFMFGMLV</b> SCSFD-KP-A <b>FSSFVFT</b> DFTKNDI-T <b>QNYLYD</b>
A_gossypii	518	---SA-TT <b>SSATIFAM</b> LICARVD-PGSKV <b>HHSFTDFTENLL</b> -IS-CKLD
S_castellii	483	RLSP-HE <b>VKFTMFGLLV</b> SVTFE-NS-Q <b>YVSLVFTDFTTNSI</b> D <b>QKYLEG</b>
K_waltii	559	SLAG-NQ <b>VEFIRAYALLV</b> AKPF-TS-K <b>MYKFVMTDFTSHPL</b> -NKLSAFD
K_Lactis	531	-VPS-ASS <b>RYT</b> VI <b>GLAV</b> IVKYT-GG-K <b>TLVLSFTDFTANPK</b> -V-NYGYD
S_kluyveri	605	SVKKE <b>GEVEFVTIFAL</b> MVA <b>AKIN</b> -DP-Y <b>KRFVFTDFTANPL</b> -TGSYTFD
V_polyspora_I	462	RVPI-NE <b>KIFFKT</b> VG <b>MLISCS</b> FT-HP-S <b>FVSLVFTDFTYNSI</b> -P <b>QKYLEF</b>
V_polyspora_II	415	VLNE-SE <b>IKYVTMMGL</b> L <b>VSCS</b> FE-HK-S <b>EAKLIFTDFTKNNV</b> -T <b>QNELED</b>
L_thermotolerans	559	SISG-NE <b>VEFIRTFALL</b> VSA <b>KTF</b> -GS-K <b>MHKFVFTDFTSHPK</b> -NKLSAFD
Z_rouxii_XP	448	K--K-Q <b>DEHYVRMIAL</b> L <b>VSSDPKQ</b> KG-K <b>FASVIFTDFTKNSV</b> -R <b>QYPLEF</b>
C_glabrata	421	IIEENT <b>AKFYIVFGYLL</b> AC <b>STD</b> -NS-N <b>YANFVFTDFTTNR</b> KY <b>EQYTFD</b>

OB3

$\beta$ 1

$\beta$ 2

S_cerevisiae	560	R <b>YLIDYENKLELN</b> EG <b>FKA</b> IM <b>YKNQ</b> FET <b>FDSKLR</b> KIF <b>NNGLRDLQ</b> NGR---
S_paradoxus	558	R <b>YLIDYESKLELN</b> EG <b>FKA</b> IM <b>YKNQ</b> FET <b>FDTKIRQ</b> IF <b>NKGLSDLR</b> NGR---
S_mikata	588	R <b>YLDVYEAKLELN</b> EG <b>FKA</b> IM <b>YRNQ</b> FET <b>FDSKILNI</b> FN <b>KRLNELQ</b> NGR---
S_bayanus	558	R <b>YLDVYEAKL</b> DL <b>NEG</b> FKA <b>IMYKNQ</b> FE <b>VFD</b> SH <b>IEKI</b> FG <b>KRLKDLQ</b> NGN---
A_gossypii	561	P <b>YLNDYCNRL</b> KATE <b>CIYV</b> KS <b>YPEY</b> I <b>HNL</b> DAY <b>TLRH</b> Y <b>NRRLV</b> D <b>CH</b> NGR---
S_castellii	529	N <b>YLIDPIVR</b> M <b>NGDQ</b> G <b>FRVIM</b> Y <b>PEH</b> FE <b>IF</b> NR <b>NVAKV</b> FG <b>STLKD</b> IL <b>NGR</b> ---
K_waltii	605	S <b>FLGSYVHRLRQ</b> E <b>MAFP</b> VI <b>YNDH</b> Y <b>FEF</b> KS <b>LKRAI</b> G <b>REMS</b> E <b>LF</b> SGN---
K_Lactis	575	S <b>FLGSFQERIP</b> ENE <b>HVHALI</b> Y <b>LN</b> RV <b>ESL</b> NE <b>KLQSI</b> IK <b>MGLME</b> CAD <b>KG</b> ---
S_kluyveri	652	P <b>FICSYHN</b> RIS <b>STET</b> L <b>HSVM</b> Y <b>DDEY</b> G <b>KFLNR</b> IT <b>QCMR</b> CK <b>FEDL</b> FN <b>VK</b> ---
V_polyspora_I	508	R <b>FLIDYDNKLEL</b> DE <b>GYR</b> VI <b>YHNQ</b> FE <b>FDEE</b> V <b>KVY</b> G <b>YSTRE</b> MI <b>KHG</b> ---
V_polyspora_II	461	R <b>FLIDYNNKID</b> IDE <b>GFRV</b> VI <b>YLNQ</b> FE <b>KFEKS</b> IE <b>EAYG</b> YE <b>IKK</b> MF <b>IND</b> ---
L_thermotolerans	605	S <b>FLGSYTNRLPQ</b> D <b>MAFP</b> VI <b>YNDH</b> F <b>REFT</b> TR <b>LQ</b> R <b>H</b> T <b>GYN</b> FN <b>QLY</b> SGN---
Z_rouxii_XP	493	K <b>FVVHYE</b> KK <b>LDE</b> DE <b>GIR</b> TL <b>MYLDRY</b> REF <b>GK</b> K <b>IQNV</b> Y <b>NK</b> TL <b>DQ</b> TY <b>APD</b> ---
C_glabrata	469	R <b>YINDYNTK</b> L <b>DH</b> D <b>Q</b> S <b>FRV</b> IS <b>SYNH</b> FE <b>EN</b> FM <b>KV</b> K <b>AKY</b> G <b>KDL</b> NAM <b>VN</b> ENS <b>QI</b>

$\beta$ 3

$\alpha$ B



S_cerevisiae	738	LLDSS-----ARLPRPQQTHKSN	TLYSCEGRITATE-----
S_paradoxus	738	LLNSF-----ARC--PQQTHKSN	TLYNCEGRIVATE-----
S_mikata	771	LLNSL-----SRCPHRQIHKTS	TLYSCRGRITATE-----
S_bayanus	640	-----	-----
A_gossypii	735	ELQSN-----PL-----	SSEGVLYLLKGIKILSTV-----
S_castellii	737	LLNVL-----Q-----	DDEPVI FRVSGKLIINVE-----
K_waltii	786	VLHKT-----RG-----	VDGRQIYHITGKVVAAV-----
K_Lactis	769	DIKNN-----VQ-----	MDHK-DIKVTAKILSIF-----
S_kluyveri	845	ALNTI-----EK-----	LTPKKVYHVQGVVDIT-----
V_polyspora_I	671	VLQSA-----TD-----	SENKNDYILRIKVL SVE-----
V_polyspora_II	656	ELNL-----	ANPKDNIVYEIDCQIMNIK-----
L_thermotolerans	787	VLYGL-----DA-----	TDSSHLELRAKVVAAI-----
Z_rouxii_XP	632	ELEKATDDFLETNSSSQISS-SLQFDQECFS	INAKILYFFTNDNPINHW-----
C_glabrata	622	QLNHL-----Q-----	HLTPKIYVLNVYIIDVE-----

**αA** ● ● ● ● ● **β1** ●

S_cerevisiae	769	-----YHASDLCFHITNELPLLQTRGI	-AP-ERVLIQIHITTSKNFAYFF
S_paradoxus	767	-----HHASGLCFHITNELPLSQTRIP	-AP-QRVLQIHITTSKNFAYFF
S_mikata	802	-----YTASDICFHITNEFSLSQGRSA	-DS-QKVLKLIHITTPKNFAYFF
S_bayanus	640	-----	-----
A_gossypii	759	-----VDSSKATIYITNDAKL--QEEV	-SV-RGFLRLQILCEANVSYFC
S_castellii	760	-----YHPSYLALTIITNDF-A-KDAI	-EW-TRILKIEVFSSENIRYFF
K_waltii	810	-----QTQQLLTFYITNDYV-S-QDML	-DP-ERVLRVEIPGAQNVEYFF
K_Lactis	792	-----DNGNVTIYLTRSGMVGTOCTI	ENPFEEELKVKQIWGRQNLTLFF
S_kluyveri	869	-----QDDDCLSFLITNDLIS--EGVL	-DP-TRILKVDIICQDNLDYFY
V_polyspora_I	695	-----NDKELIRLIVTDDL-D-E-QEFI	-NP-NNILNIDILNQT-LDTIN
V_polyspora_II	679	-----YNMSYLSILVTNDFVT--NNFI	-DP-TRMLRIDITNVDNLKQLL
L_thermotolerans	811	-----RTGELLAFYVTNDWI-S-QDML	-DP-TRVLRVEIPGRSNMDYFF
Z_rouxii_XP	680	SLLVAIEDNSTKTNVISG---D-HRFV	-DP-RSILRIEIFCKENLEYFT
C_glabrata	645	----IVYDQEIIRIKVVNELPMV-GKYV	-PP-VDILEVYIITCKEEVQNEL

**β1** ● ● ● ● ● **β2** ● ● ● ● ● **β3** ● ● ● ● ● **αB**

S_cerevisiae	811	NRSSAYL-----QRQPL-----	EKEYTQLAQFLGHSFKENITSSLT
S_paradoxus	809	NRSAYL-----QRQPL-----	EKEYAQLAQFLGHSFKENITSSLK
S_mikata	844	NRPNAYI-----QRQSL-----	EEICTQLTQFLGHSFQENITSSYK
S_bayanus	640	-----TQDL-----	DGRHTQLAQFLGHPKFNITSSRL
A_gossypii	799	GADEA-----	STDVLAQAINLRAFKFYLLFGEV
S_castellii	800	NAGVEPPLVEMSTQSQVLSTENAINIEDN	LNILKGFVKGFEFSFKITKGTL
K_waltii	850	GANAGRQ-----PYHGI-----	SARDPQLQPMIGEIFTFRIVAFSV
K_Lactis	836	GNPNYS-----	YKREELTACTGSIVDFTLIPRVL
S_kluyveri	909	NQRDYK-----	AFQNDLTLVKGILAFRLSRVLI
V_polyspora_I	734	ESLNF---M-----ES-----	INNIRLRKLIIDKTIELQITKCLK-
V_polyspora_II	719	DIQISET-----QLTDI IKDK---	SNPIIAKIDDLINESVVLRIKRKLV
L_thermotolerans	851	GTYASQE-----TRPDL-----	AARDAQLGTMIGETFTFRIVTEAV
Z_rouxii_XP	723	ASQLSK-----	TDSILQQLDQYRGRTCKLRVKRGI
C_glabrata	687	GDEALT-----	MDIFTPLINETSRLRVFQ---

**αC** **β4**

S_cerevisiae	847	LFPDTTVALQIWCPIECTFRELOQQ	LAHPKVAAAPDSGSL---DCAINAT
S_paradoxus	845	FLPGTTMTLQIWCPIECTFRELOQQ	LAHLKVAAAPDSGSL---GCAITAT
S_mikata	880	LLPETALALQIWCPIECTLRELOQQ	LAHLKAATTPDSGSL---GYAITAA
S_bayanus	668	RLXXXXXXXXLQIWCPIECTFQELQQ	QAYTAAGSAGSGSPRGIN
A_gossypii	826	QI-SPSKTARVWCPVECSIEELNSQL	QL-S-----
S_castellii	850	KL-FTNIGVSVWCPVEYTLLEEMKG	QMLLRHDRDAKDSK-----
K_waltii	886	PV-SPQRNLRIWCPIECTIQEMKCE	LAARTAQS-----
K_Lactis	865	RV-NEYLYIKIWCPIYATLESLLI	HSRLEY-----
S_kluyveri	938	AV-SSKKRLFAYWPVECTMEEMKS	QLQK-Q-----
V_polyspora_I	764	-I--KDSKLLLWTPANHSLKKILS	Q-----
V_polyspora_II	760	QL-SLNSKLAIWNPYTCTSNKHIV	DQYSENVQ-----
L_thermotolerans	887	PV-SPSRFLRTWCPVECTIQELSYE	LAARRGQA-----
Z_rouxii_XP	754	TL-RSQIALLVWCPIELTLEELE	VKLV-----
C_glabrata	711	RP-SKTDRIIRWSPICECTIQELRL	QRMFLRD-----

● ● **β5** **αD**

OB4

S_cerevisiae	894	VNPLRLLAAQNGVTVKKEEDNDDDDAG-----AVPTS
S_paradoxus	892	VNPLRLLAAQNGVTVKKEEDNDDDDAGAVSASLDMGAAKCGGAKLQ
S_mikata	927	VNPPRFLAAQDGVTVKKEEDNGDEAGTFSSASWDTIGAAQRGGAKFQ
S_bayanus	718	ADHPRLLAALDGVTVKREDTDDAVT-----AGFCPPRAT
A_gossypii	854	-----DN-LVKLEQH-----TCNN
S_castellii	888	-----PLTSSHG-MVKQETHSL-----VEIID
K_waltii	918	-----SSVVKRE-----DA
K_Lactis	894	-----DNDTLKYENL-----SDID
S_kluyveri	966	-----LTVSVKQEQID-----LTDM
V_polyspora_I	786	-----SS
V_polyspora_II	791	-----VSNVITVKK-----EQ
L_thermotolerans	919	-----AARVKLE-----DS
Z_rouxii_XP	779	-----EES
C_glabrata	742	-----TIKVEET-----LSLTQ

OB4

**Figure S1** Alignment of large Cdc13 homologues from *Saccharomyces* and *Kluyveromyces spp.* Multiple Cdc13 homologues are culled from the SGD and NCBI databases, aligned using the T-COFFEE server (<http://www.igs.cnrs-mrs.fr/Tcoffee/tcoffee.cgi/index.cgi>) and displayed using Boxshade ([http://www.ch.embnet.org/software/BOX\\_form.html](http://www.ch.embnet.org/software/BOX_form.html)). Structure based assignment of the  $\alpha$  helices and  $\beta$  strands within the first, the third, and the last OB folds are indicated by red and blue boxes, respectively, while the predicted  $\alpha$  helices and  $\beta$  strands of *ScCdc13* are indicated by pink and green boxes. In *ScCdc13*<sub>OB1</sub>, red dots denote the *S. cerevisiae* residues important for dimerization (Ile87, Leu91, and Tyr95) whereas the pink dot denotes the less important residue Leu84 as shown in the gel filtration, yeast two-hybrid and co-IP assays; yellow dots denote the residues important for dimerization indicated by the crystal structure; and blue dots denote the residues involved in the Cdc13<sub>OB1</sub>-Pol<sub>CBM</sub> interaction. In *CgCdc13*<sub>OB4</sub>, green dots denote the *C. glabrata* residues important for dimerization. The accession codes for the homologues are as follows: *S. cerevisiae* (NP\_010061.1); *S. paradoxus* (spar429-g20.1); *S. mikata* (smik194-g3.1); *S. bayanus* (sbayc535-g11.1); *A. gossypii* (NP\_982792.1); *C. glabrata* (XP\_446604.1); *S. castellii* (Scas677.11); *K. waltii* (Kwal23.4628); *K. lactis* (XP\_456019.1); *S. kluyveri* (SAKL0E13266g); *V. polyspora I* (XP\_001645836); *V. polyspora II* (XP\_001642283); *L. thermotolerans* (XP\_002552111); *Z. rouxii* (XP\_002496083).

## Supplementary Figure S1