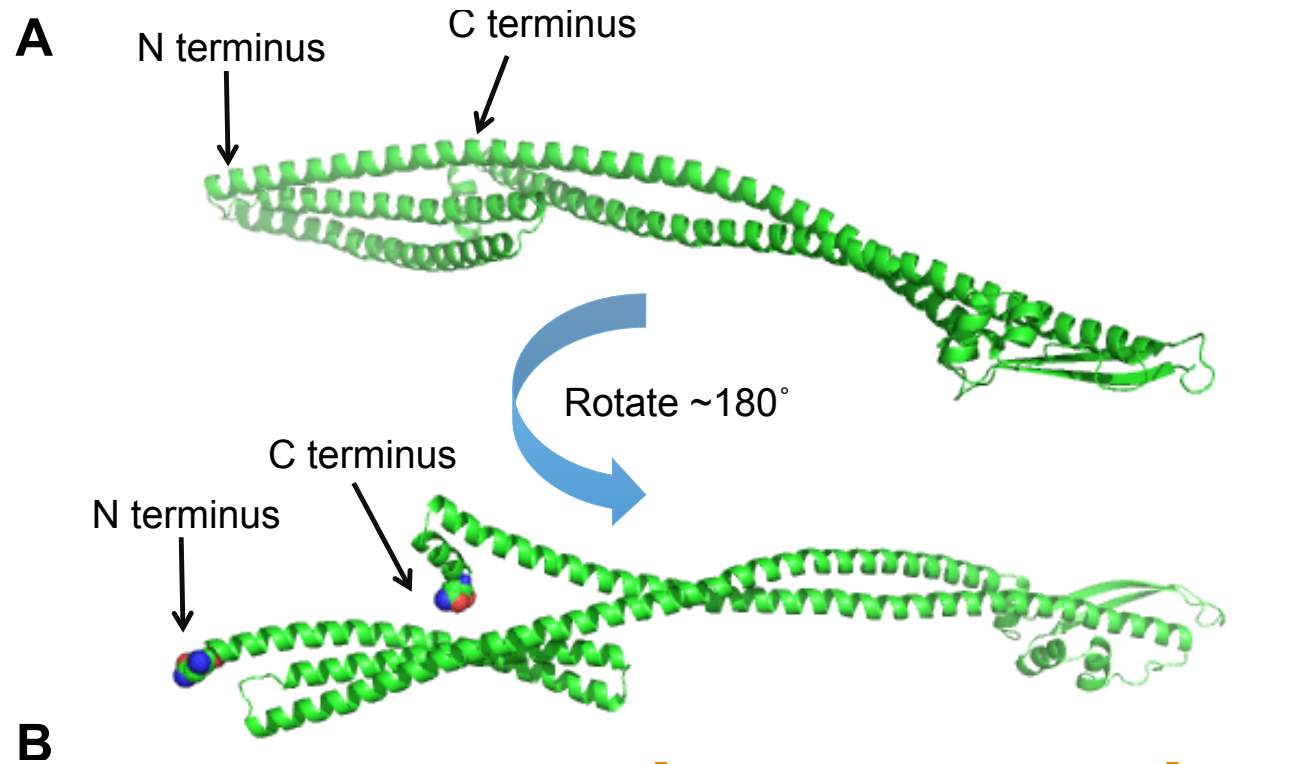

B

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Sc_Bni5 (1)      MGLDQDKIKKRLSQIEIDINQMNQMIDENDQLVEPAEDEAVEDNVKDTGVVDAVKVAETALFSGNDGADSN----PGDSAQVEEHKTAQVHIPTENEANKSTDDPSQLS (105)
Cg_Bni5 (1)      M-LDQEDVKKRMSQIELDINQMNKMIDENDQLGENDGHDSGTEGVEG-AVGEGVDGQAGPVEPVVTTAAEE----TSETKDIEHEQVTNEGMAKE------VEDASESS (97)
Vp_Bni5 (1)      MSLDQEKIQKRLSQIEIDINQMNQMIDDNDLVNEEQQQEQQQEVEESTAEDDGGDLKNEEKTGVDESIPNE(29)VDENEDSIEVTTQEADIKEDHVEHEKEIENEQGS (134)
Kl_Bni5 (1)      M--DSEQVKKRMSQIELEISEMNEMIDKNDSIHETTVKTKQDVSSD-------------------------------------------------------------DQDEDY (50)
Zr_Bni5 (1)      MGLDKASIEKRVSRIELDIDHMNQMIDENDKLNEAGDRLEQDSRGQHAEDNQHLGSAATHQGELSREDSVQ(28)SEAVYDSQEAPVARSEASNDEYYGWSEDQQEQDE (133)
Lt_Bni5 (1)      M--DQETLRKRMSQIELEIDEMNQVIDENDQLAEPHGDEPPEHEKKKRWDSGT----------------------SKDPETGPEEPETQQVIEAELFLRSATRPVPPSI (85)
Ag_Bni5 (1)      M-MVQEKLSVKIARLEKELEALHRGVSADLRPAEDAEESESSAG-------------------------------------------------------------ERYSTDKSS (52)

Sc_Bni5 (106)    VTQPFIAKEQITHTAIAIGDSYNSFVANSAGNEKA----------------KDSCTENKEDGTVNIDQNRGE-ADVEIIENNDDE---WEDEKSDVEEGRVDKGTEENS (194)
Cg_Bni5 (98)     VQATEQAQDQQAGTNEET-NTFKTESMPEPETQAP----------------EVNDLEMKEPEMKEPEMKEPETVEPETVEPEMKE---PETVEPEMKEPVIKETDALEP (186)
Vp_Bni5 (135)    IVEAEIASETNNLKSIKEKTAMETTIEPQVLVISPNEEQKLTQRFD(38)GEVDSTEHEEPSKEEIEIEIKESIKEEIVVKEVEANTIEDEVSSPRHEEPIVKNETEEV (277)
Kl_Bni5 (51)     LELQKLTANQVDQFVQNAIKSDGEDEVPETLSSGR----------------ETALQAEEREDIKEEKP----------------GTQLEAAVVAEVVAEVQ (119)
Zr_Bni5 (134)    QAYTTGQSEADTEYDNEEEDPEETFQAPEERESQEHVNGGMQLHKR(79)PPESQSETHSETQSDIKQNEQELPTTHPYPQEIHNHQHTHETDAQELDHKEYSHETETQ (317)
Lt_Bni5 (86)     PAATELGKEQRTKPALENEPTHSEHMNQPPAERVP----------------LEQTPSDGGVSLAPSQYVDAPEAVPAQSSSKSEAAPADIGLRETQPLNGISSRQAGSVG (179)
Ag_Bni5 (53)     YASSVQAVLRARTASAASADTAMSSSTAASDSAGG----------------AKMDAADADDATRSLELR----------------LAALATQDPAVDSADTASG (124)

Sc_Bni5 (195)    E-----IESFKSPMPQNNTLGGENKLDAELVLDKFSSANKDLDIQPQT------IVVGGDNEYNHESSRLADQTPHD-----DNSENCPNRSGGSTPLDSQTKIFIPKK (287)
Cg_Bni5 (187)    E-----MKHAEIP-PQATTE--EQPTRHDEWEDVEEEEFNEIDTSTES------NNVIGDTKQVEGSSVLAAGDLRG-----NVADNG-NLTPVTDIDDAESTIFIPKK (275)
Vp_Bni5 (278)    Q-----VPEFDNEIKPGTVEEQSIDVEDLADEEILKTALEDNPIDTQIGTLESPENIESEKSTGNSMDMSNDSNIDN-----EVSDDTSSSIDTAKLEQTVLKGEIDRT (376)
Kl_Bni5 (120)    T-----EPTAEKAIPAVSVTSVPAKRIPSEKIEVSTSTEEDEAAAAAT-------IVPNTDKSSTYPAPAAIGHTQN-----GTVPRAPN--TDSSNIPTSPRILTPK- (208)
Zr_Bni5 (318)    E(23)TEQYKEVPNPPRGMEFVETREDESLDYSYEPAHQDSPETHKRTIGATQNHNSNGNSLPDTTQSVMGQGTSGEK(69)NTSQDSNGSTDNPFTSDKVYERSTSGS (510)
Lt_Bni5 (180)    S----AGSPRESQPSTETAETPSSEVDREQPDEHLQPPSEEFTTTASR-------GFKAASREDARKEMPQQSTLGNN----EPQEASAGMSFDENSPSTQSSAGSKQP (273)
Ag_Bni5 (125)    ------ASPASPAAPPSPPPSAATEGSDEAAAPLEVPKQRGDAGTAAG-------GEPVRRRPTNPFRVISVGGS-------STFKRAAGADGQASRTSSAGDKAAP-- (211)

Sc_Bni5 (288)    NSKEDGTNINHFNSDGDGQKKMANFETRRPTNPFRVISVSSNSNSRN--GSRKSSLNKYDSPV-SSPITSASELGSIAKLEKRHDYLSMKCIKLQKEIDYLNKMNAQGS (393)
Cg_Bni5 (276)    QNQ---------NSELTEQMKETLRNTRRTTNPFRVISVSSSNSSTN--SSRKSSGHDMG------LEQTPSEQ--LKRYEQRHYYLTTKCGKLQKEIDYLNKMNSQGT (365)
Vp_Bni5 (377)    ISPIEPPSQIFVAKSNMKGSVNDKQGTRRSTNPFRVVSVSGSSSPRSNPSSRHASGSSNNEPRRIPSTESTSSVNSIEKLQSRQDYLIMKCSKLQKEINYLKNMNTQGM (485)
Kl_Bni5 (209)    ----------------------------SNPFRVVHVGSQPSSRN--ASRNSSRVS--------STSSDISDINFEQLQQNYNSLSVKCTKLQKEIDYLHKFKNEST (277)
Zr_Bni5 (511)    TDTDDFIHIPKNSAQRPATTSNTPVTSRRPTNPFRVVSVGVVGPDGR--TSRKTSAGTFS-------SYKDSNVDGPAILQKKLDHLVKKCTKLQREIDYLTKMNTASS (610)
Lt_Bni5 (274)    VSPDSTQSSPQLNLPKTRNPAFPGKRATSNPNPFRVVSVTS----------------------KQTEDVSPAQKLQTRHDYLARKCIKLQREHQYLSDLRDRGA (355)
Ag_Bni5 (212)    ------------------------------------------------------------VSADEQSMLKLQRKHDYLTMKCVKLSKEIKYLPNLKKTGS (251)

Sc_Bni5 (394)    LSMEDGKRLHRAVVKLQEYLDKKTKEKYEVGVLLSRHLRKQIDRGENGQFWIGTK. (448)
Cg_Bni5 (366)    LSIDDSRKLTRAIAKLQEYLDKKNKERYEVGVLLSRQLRRDINRGENGEFWIGTK. (420)
Vp_Bni5 (486)    LSIEDSRKLNSAIQKLQDYLDRKTKEKYEVGLSLSRQLRKGVDRGENAQFWVSNK. (540)
Kl_Bni5 (278)    LTLEDRRKLITAIEKLQEYLDKKNKQRYDTGVILSRQIRKNVDMGANGQFWVGRS. (332)
Zr_Bni5 (611)    LPIEDSRKLSRAVDKLQEYLDKKNKEKYDVGVLLSRQLRREIDRGENGQFWVGTK. (665)
Lt_Bni5 (356)    VAPEDARKINSALEKLQEYLDLKTKERYEIGVLLSRQLRREIDRGENGQFWVGH.  (409)
Ag_Bni5 (252)    LSVEDTRKMNDALDKLQEYLDRKSKEKYEIGVLLSRRIRKHINNGSNGQFWLSGK. (306)
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Figure S2. Structure prediction and sequence alignment of *S. cerevisiae* Bni5 with apparent orthologs in other fungal species. (A) Phyre[2] (KELLEY AND STERNBERG 2009) was used to model the predicted structure of *S. cerevisiae* Bni5. (B) Proteins homologous to *S. cerevisiae* Bni5 were identified using a recent version of the BLAST algorithm (NEUMANN *et al.* 2014) and aligned using CLUSTAL-W (THOMPSON *et al.* 1994). Residue numbers are given for each species: Cg, *Candida glabrata*; Vp, *Vanderwaltozyma polyspora*; Kl, *Kluyveromyces lactis*; Zr, *Zygosaccharo-myces rouxii*; Lt, *Lachancea thermotolerans*; and, Ag, *Ashbya gossypii*. Invariant residues, white letters in a black box; highly conserved residues, blue. An orange triangle marks the extent of each of the N-terminal truncations and a green triangle marks the extent of each of the C-terminal truncations generated in this study. Purple asterisks indicate Ser and Thr residues that were also analyzed.