

An	1	MAAQPAL-AIAPSAAPLAPALVAK-----PTVSPSPGP--GTPGSVTSKEWIIIPPRPKPGRKPATD	58
Nc	113	PPIAPRP-SVAPKPAPIRAASVSSQGAMSPVDCPTPGG--GGPLSMTTKEWVIPP RP KPGRKPATD	175
Ca	20	AGSPSSSASTPRSAASPPVSVNTKSSLNNTNSNTIMPR--QVMSIQTSKEWVLP RP KPGRKPSVD	83
Cn	70	ATNIPTSARSPAPRANSSSSTSTAVAATPIMGKDTSSSAGKIFAKPSKEWVLP ER AK PGRKVSND	135
An	59	TPPTKRKAQNRAAQRAFRRERRAARVSELE EQIKCIEDDHEIHVATFKEQIANLSREVEQCRTE MGW	124
Nc	176	TPPTKRKAQNRAAQRAFRRERRAARVGELE DQLEEQKEEHERVSELQGRISHFEVQVQTLQSR CRW	241
Ca	84	TPASKRKAQNRAAQRAFRRERRATRVOELE QKLMEVEKERDIKEMALVNTINKLKVENQFLVKN LEQ	149
Cn	136	EPDNKRQSQNRLSQR AHRARRTDYIQTLE ERLRQYEAD E IHSNVRLQEVARALKADNERL KAEVNE	201
An	125	WRDRCHALEKEVS-----VERAARETLVKELRSSLP----EKN-----TSGTD	163
Nc	242	LEDMLEKEKQARN-----TLKNSWDNNNNMSQSFLSQ--QSNGYTLQQQQOQTQOTQLAPKVD	299
Ca	150	LKGEMNQMKQSF SRSQQQLISKSSPAASTASAQQIKPTFSFASNSAPSSHPSPHHNSISPTGSSY	215
Cn	202	LKNKCM EYNGEKD-----VWEMERRTLKEAVRDMRIEIEALRAGSG-----METIVRMDIDQS	254
An	164	AVPLP-PR-SSR-----SSRMELEKSSPVDR----RS-----ELG--EEVPLGCNR	201
Nc	300	SVPIAEPRPTAQF----FSISQIISPPEEAPQSF LDVTCGNCQSSGSCACAEELMQSSNVL MGCGG	361
Ca	216	SVQQISPAPSTDSPPNSYNLSNDSYRQFHSTLTPISNN--NTPD-----KPLSAADV AN FDCGV	272
Cn	255	TIDSLVPGPSIP-----RRQSAHRLSPRSAS---RP-----G--NVTLQDCPI	292
An	202	CSTS--HCQCIEDAFGMPP IEMNRAPEPKIP----EPEE-----MEIDFTTRF	244
Nc	362	CTPEG--RCACLEESIRVLAADLKRPLPSSPSL---GPDEKRQRS---DAGVEDMQLETDFTALF	420
Ca	273	CPKE--ECLCESVGLKEPTKDKTENAKKLQDQVNSFKPMPAVSLSRKRKIKSTDEEQEIDFTKQF	336
Cn	293	CPNPDPDCPCQRPHARQEQYPPEHLTLAPSAA-----EDHAVACG-----LCHSTDECLCR	343
An	245	AA---PHHEEDTAASPVASP----PVD-----PCGFCQDGTPCICAEMAAQEEE-----	286
Nc	421	SS---KKPETMTMPLPAPAQQSQPITSVEMH---ESCGFCCKDGTVCVCAESMALSAASMTVASVV	421
Ca	337	SVKAKPMPDLKLLKKTTF SQPQTETASTFNEDSPVDNCGFCSDDTPCVCREAAKEAAKLNEYLNNP	402
Cn	344	AV-----DEDVKPDISSPSHD-LKTLDD-----DRCGLCTGGDFCACREAAAAASVRTSVTSDT	396
An	287	-RRR-----NSTFE--SNRLAPIQNI SQFTP----PPSDSDVRS DN-----VTLPPIS----	327
Nc	422	QQVQ-----MHTPPPSSENDVVPMPLEVTATGAVKLPSFGSLNRASN-----TNQDMQSK---	470
Ca	403	HQSSIMEEEISEEAKTLPP-LQTNNPNHNF SKSALPVMHPGPTVEIREFTNINAVPNVLPASKNEN	467
Cn	397	KTTV-----ATTTA--VSGIVTASSSSAALPLRLRTKNGS AKAS IWS---LNAAPAV----	444
An	328	-----QATAANPCANG-PGTCAACLSDPRRTLFC KTLAASR-----SASGTPSGCCGGK	376
Nc	471	-----RPVKTGGCGPGGPGTCAOCLADPKSGLFCRSLAANFERNRQQTDNSSSAAPPSGCCGGG	529
Ca	468	EKEESTKDTSSDGGCTGN-PGTCRQCQMDPMS TLFC TTVASRSTKSDSVSS TRQISIR TNSKTSIS	532
Cn	445	-----S-REAICTGD-PSNCDACRDSFGREFCQHLFEAAE-----SSSSVKPCSSCPGN	492
An	377	GRDGGCCQSQS-----RTSAPRRSN-----TDRSATPLTLSCAD	410
Nc	530	GPGGGCCKTEKPDNDVVPINLNRYKTANQLPAPTSPNPISSSSSSSNVAASN FALSLSCAE	593
Ca	533	IDSLNPNQSP I P P P L L A N N K T G ---G S N A P T P T P A P S T P S H S S ---S V S S N S G I F I P C A D	586
Cn	493	CMNVKAGLSPSPGITQASSSSS-----NQIRTPPTPPVNQPS-----AVEDDTPLAPLQMVCCG	546

Supplementary Figure 4 Alignment of *A. nidulans* HapX (An) with putative orthologs of *Neurospora crassa* (Nc), *Candida albicans* (Ca), and *Cryptococcus neoformans* (Cn). Amino acid residues identical in all four proteins are shaded, the bZip region is boxed and conserved cysteine-rich motifs are marked by bars.