

S. cerevisiae 1095 INIFTILESGPDEEERYMQMILSLKSCPETQKVNFFILDQPFISDTRLKSCSEYINSSDEMGRNVIFLNYEWPQWLRPQR
C. albicans 1137 INIFTIAGG--QLYEKLTSMIASVRKHNPSSTIKFWILED-FVTPQFKHLVELISIKYNVE--YEFISYKWPNFLRQKQ
Y. lipolytica 1164 INIFTVASG--HLYERFLS IMTASVMAH-TDHTVKFWLIEN-FLSASFKAFLPHLAAHYGFE--YELVITYQWPHWLRGQT
S. pombe 1157 INIFSVASG--HLYERFLYIMTKSVIEH-TDKKVKFWFIEN-FLSPSFKSSIPAIAKKYNFE--YEYITYNWPHWLRKQE
N. crassa 1192 INIFSVASG--HLYERMLSIMILSVMEH-TDHSVVKFWFIEQ-FLSPSFKSFLPHLAAEYGFK--YEMVAYKWPHWLRHQS
G. zeae 1167 INIFSVASG--HLYERMLNIMMVSVMRN-TKHSVVKFWFIEQ-FLSPSFKFIPHMAAEYGFK--YEMVTYKWPHWLRQKQ
A. niger 1188 INIFSVASG--HLYERMLNIMMVSVMRN-TNHSVVKFWFIEQ-FLSPSFKSFLPHLAKEYNFS--YEMVTYKWPHWLRAQ
H. sapiens 1 1256 INIFSVASG--HLYERFLRIMMLSVLKN-TKTPVKFWFLKN-YLSPTFKEFIPYMANEYNFQ--YELVQYKWPWRWLHQQT
H. sapiens 2 1231 LNIFSVASG--HLYERFLRIMMLSVLRN-TKTPVKFWLLKN-YLSPTFKEVIPHMAKEYGFR--YELVQYRWPWRWLHQQT

S. cerevisiae 1175 FSSRRRDVSRFLFLDVLLPQNISKVLVYMSPTTEVPLDPPDIFQFQG LKRAPLGLFRMS-.GDGYWKEGEGYWEKMLRE
C. albicans 1212 TKERM I WGYKILFLDVLFPQDLNKIIFIDADQICRADLTELVNMDLEGAPYGFTPMCDSTR EMEGFRFWKEGEGYWSVDVLKD
Y. lipolytica 1238 EKQRQ I WGYKILFLDVLFPQDLERVIFIDSDQIVRTDLYELVEMDLEGAPYGFTPMCDSTRKEMDGF FRFWKQGYWDTFLGD
S. pombe 1231 EKQRE I WGYKILFLDVLFPLELHKVIVVDADQIVRADLQELMDMDLHGAPYGYTPMCDSTR EMEGFRFWKKGYYWKKFLRG
N. crassa 1266 EKQRE I WGYKILFLDVLFP LSLDKVIVVDADQVVRTDMYDLVSLDLEGAPYGFTPMCDSTR EMEGFRFWKTGYWANYLRG
G. zeae 1241 EKQRE I WGYKILFLDVLFP LSLDKVIVVDADQIVRTDMYDLVSLDLEGAPYGFTPMCDSTR EMEGFRFWKQGYWANYLRG
A. niger 1262 EKQRE I WGYKILFLDVLFP LSLDKVIVVDADQIVRTDMYDLVSLDLEGAPYGFTPMCDSTR EMEGFRFWKQGYWKNFLRG
H. sapiens 1 1330 EKQRI I WGYKILFLDVLFP L VVDKFLFVDADQIVRTDLKELRDFNLDGAPYGYTPFCDSRREMDGYRFWKSGYWASHLAG
H. sapiens 2 1305 ERQRI I WGYKILFLDVLFP L AVDKIIFVDADQIVRHDLKELRDFDLGAPYGYTPFCDSRREMDGYRFWKTGYWASHLLR

S. cerevisiae 1248 NNLEFYSTEPAF L VNLERFRELDAGDKYRIHYQRISTDAMSLVNI GQDLVNNLQLEVP I RFLKGSYKKKLVINDECVSEW
C. albicans 1292 D--LKYHISALFVVDLQKFRS I KAGDRLRAHYQKLS SDPNLSNL DQDLPNMQR SIKIFSLPQNWLWC E MWCS DKSLED
Y. lipolytica 1318 D--LVYHISALFVVDLKV FRAQQIGDRLRVHYHQLSADPASLSNL DQDLPNNLQRQVP I FSLPQDWLWCETWCSDES LKT
S. pombe 1311 ---LKYHISALYVVDLDRFRKMGAGD L LRRQYQLSADPNLSNL DQDLPNHLQHL IPIYSLPQDWLWCETWCSDES LKT
N. crassa 1346 ---QPYHISALYVVDLRRFR ELAAGDRLRQQYHTLSADPNSLANLDQDLPNHMQFQ IPIKSLPQEWLWCETWCSDET LTK
G. zeae 1321 ---LPYHISALYVVDLNRFRQLAAGDRLRQQYHTLSADPNLSNL DQDLPNM MQFA IPIHSLPQEWLWCETWCSDDSLTK
A. niger 1342 ---QPYHISALYVVDLNRFR AIAAGDRLRGQYQMLSADPESLSNL DQDLPNHMQHH IPIKSLPQEWLWCETWCSDESQSQ
H. sapiens 1 1410 ---RKYHISALYVVDLKKFRK I AAGDRLRGQYQGLS QDPNLSNL DQDLPNM I HQVP I KSLPQEWLWCETWCD DASKKR
H. sapiens 2 1385 ---RKYHISALYVVDLKKFR R I GAGDRLRSQYQALS QDPNLSNL DQDLPNM I YQVA I KSLPQDWLWCETWCD DESKQR

S. cerevisiae 1328 IKKKIINKFASSPGDE--DVPGESVSSKYQDSDNAAPLHDEL-.
C. albicans 1370 AKMIDL CNPLTRENKLDAAKRLIPEWIEYEQAIEPLVLSLVQNN TAKEVVQEIEIDTDGEEQE EQESNDDDFI HDEL-
Y. lipolytica 1396 AKTIDMCNNPLTKEPKLDRARRQVPEWTKYDDEIRKLRKEAEGIE---GKKKEEERAGPVEVEVEIDEPEADLHDEL
S. pombe 1388 AKTIDLCQNPLTKEKKLDRARRQVSEWTSYDNEIASVLQTASSQ-.SDKEFE EKDNSSPDEL-.
N. crassa 1423 ARTIDLCNNPMTKEPKLERARRQVPEWTVYDEEVAALAKRVREQE EKKAGEVLEGGKVEEQVIVEEKHEEKE-HVIDEL
G. zeae 1398 ARTIDLCNNPQTKEPKLDRARRQVPEWTIYDNEIAALDQRRK-.GVAGKNENTRSRESEDKA-HTKDEL
A. niger 1419 ARTIDLCNNPMTKEPKLDRARRQVPEWTEYDDEIAALSKRVAE-. KQQGQVEEERAGESYPDEDEEGETSSGWDKDEL
H. sapiens 1 1487 AKTIDLCNNPMTKEPKLEAAVR I VPEWQDYDQEI KQLQIRFQKE-.KETGALYKEKTKEPSREGPQKREEL
H. sapiens 2 1462 AKTIDLCNNPKTKESK LKAAAR I VPEWVEYDAEIRQLLDHLENK-.KQDTILTHDEL-.

FIGURE S1. Sequence similarity comparison of the C-terminal portion of homologues of UDP-glucose:glycoprotein glucosyltransferase (UGGT). *S. cerevisiae*: *Saccharomyces cerevisiae*; *C. albicans*: *Candida albicans*; *Y. lipolytica*: *Yarrowia lipolytica*; *S. pombe*: *Schizosaccharomyces pombe*; *N. crassa*: *Neurospora crassa*; *G. zeae*: *Giberella zeae*; *A. niger*: *Aspergillus niger*; *H. sapiens 1*: *Homo sapiens* UGGT1; *H. sapiens 2*: *Homo sapiens* UGGT2.