```
glu1            ------------------------------------------------------------
schco           ------------------------------------------------------------
LACBI           ------------------------------------------------------------
COPCI           ------------------------------------------------------------
PENMQ           ------------------------------------------------------------
NEOFI           ------------------------------------------------------------
BOTFB           ------------------------------------------------------------
MAIZE           ------------------------------------------------------------
SCHPO           MRTTFATVALAFLSTVGALPYAPNHRHHRRDDDGVLTVYETILETVYVTAVPGANSSSSY


glu1            ------------------------------------------------------------
schco           ------------------------------------------------------------
LACBI           ------------------------------------------------------------
COPCI           ------------------------------------------------------------
PENMQ           ------------------------------------------------------------
NEOFI           ------------------------------------------------------------
BOTFB           ------------------------------------------------------------
MAIZE           ------------------------------------------------------------
SCHPO           TSYSTGLASVTESSDDGASTALPTTSTESVVVTTSAPAASSSATSYPATFVSTPLYTMDN


glu1            ------------------------------------------------------------
schco           ------------------------------------------------------------
LACBI           ------------------------------------------------------------
COPCI           ------------------------------------------------------------
PENMQ           ------------------------------------------------------------
NEOFI           ------------------------------------------------------------
BOTFB           --MRSFEIKSLAILASSLLVKETFAAPIYETEIHVVTEEVTVTRELDGSYATGHAHAVGT
MAIZE           -------------------------MIASKLTILTATAALLEPALALGHRHAHHQHAQKR
SCHPO           VTAPVWSNTSVPVSTPETSATSSSEFFTSYPATSSESSSSYPASSTEVASSYSASSTEVT


glu1            ------------------------------------------------------------
schco           ------------------------------------------------------------
LACBI           ------------------------------------------------------------
COPCI           ----MFPSSPSLAIWILALFTASAVNARPENWGKTKTEPAWTRPHEVSSSLAPADPSVQP
PENMQ           ------------------------------------------------------------
NEOFI           ------------------------------------------------------------
BOTFB           YTQHHSAAASSVVVVASTPAPAAVTSAVVVPTSSTTSHVAVESSSAKASSSSSSSVAVVK
MAIZE           GDWVVATIDGQVVSWENNYFGPGGSAPAATQPAAASQPEAYSAPAPAPAAARPTTIIKVA
SCHPO           SSYPASSEVATSTSSYVAPVSSSVASSSEISAGSATSYVPTSSSSIALSSVVASASVSAA


glu1            ----------------------------------MHSQSALLLFALCLASSVHAGKRGLA
schco           ------------------------------------MFQALAFVALC-ASAVSAGKRGLA
LACBI           -----------------------------------------------------NPKRGLA
COPCI           PVETPVLPPSGSSPLPPAESPVQPPASPSIPVSAGSSSSFAPPRPTNLTPGVKNPKRGLA
PENMQ           --------------------MRASTQAFLTALVLTCTEVALAQDVSGTTKFQSSNKRGLV
NEOFI           ----------------------------------MTFKTTFSILYALGPALALAQGKRGLA
BOTFB           ASTEAAAAAVLVQSSAKSSYKPAATSTKAAATTLATSAKASSAAAASSSSSSYSSSSGGK
MAIZE           KPSQAAKSAYEPASQPKKQETAAKAPQKAAIKEKTQSKAKSSSTQSKSSGSSSGGSAGFS
SCHPO           NKGVSTPAVSSAAASSSAVVSSVVSSATSVAASSTISSATSSSASASPTSSSVSGKRGLA
                                                                       . *

glu1            WPWYNSPLDPGVLNNGD---GEVVAIYDWETYAPPT-STGGTGGLGFIGMQGTMDSDSSP
schco           WPWYNGQLDPGVLNNGQ---GQVVAIYDWETYAPP--STNGNGGLGFIGMQGCWDCSSSP
LACBI           FAAGDTPGDLNNANQSA---SVISWQYNWADSPPD---YLVESNIKYIPMQWGGAGLDSF
COPCI           FAASKSPMDIHNANQTA---SLISWQYNWANIPPA---YLATSNIPFVPMQWGSGAIDNF
PENMQ           YIPSDHPSDDQIWVADN---SDLTWYYDYKDIPAAAYSNRTQQEFEFVPMLWGSANSSGF
NEOFI           YNDG----ALANLFSEH---SQVTWGYTWGYDRNG-----LSASLDFNPMLWGLPSSLNP
BOTFB           RGVAYNTADYVKQFTGS---SKVAWAYNWGSSSDG----LSASGIEFVPLLWGLKSTFTG
MAIZE           HKRGVCYNNVELANTFAGDCKNCGWGYNWDSSSDG-----LTKGLNFIPTLWNDQPLHTD
SCHPO           WIPGTDLGYSDNFVNKG-----INWYYNWGSYSSG-----LSSSFEYVLNQHDANSLSSA
                                          * :               : :

glu1            VAQLATR-QAQQGWATVFSLNEPDING------ITPAEAASWYIEWVNPLAIK--KALPA
schco           VGELAAR-QKAQGWATVFSLNEPDLNG------ISAASAADWYKQHINPLAIK--KAFPA
LACBI           ADQVKAQ-RADTILVLPKTFNEPDFVSES---NMDPVYAAKLWMTSIQPMKAA--GVRLG
COPCI           VDAVRAQ-GAEVVLG----FNEPDYDREA---NMDPEQAASLWMSYIEPLKQH--GVRLG
PENMQ           ASEIKSQIATGRNITHILTFNEPDGTSSTGGSEISPADAASIWIDDIEPLRNE--NVKIG
NEOFI           QWTAAVR---ATGVEAILGFNEPDLGSQS---NISPADAAAGYLVSMEPFAG---QVRIS
BOTFB           AWSAAASSAISSGSTHLMSFNEPDLSTQAN---IGASDAAAGYKTYMQPFAG---KAKLG
MAIZE           RFADNCAQALSDGAKAIFSFNEPDNAGQAD---MTPAYAATAHVKWLNPYAG---KALIG
SCHPO           SSVFTGG-------ATVIGFNEPDLSAAGN--PIDAATAASYYLQYLTPLRESGAIGYLG
                                   :****         : .  **      : *          .

glu1            VTSSTT---SGQGLSWLSEMISACAG---ACYFDYINLHWYGTS--FAEFQAYIEQAHNQ
schco           VTSSTN---SGMGLDWLQNFLNSCGG---GCYGDYINLHWYGND--FSGFQSHVTNAHNR
LACBI           GPAVTA---SDNGQQWLQAFLAACS----GCTIDFLPLHWYVYGPGVEGFYSYIWQMHNT
COPCI           GPAVTS---AGTGRPWLRRFFRECSRL--QCTIDFLPVHWYGFG--ITGFYDYLWSIHNE
PENMQ           APSVTG---SQSGLTWLSEFFSNCTSLKTNCTVDFIPLHWYGNF---QGLASYLGQVVAT
NEOFI           TPAVTNGPPPNMGTGWMDQFFEHCTT----CTIDFVAIHWYANN-DPEGFKAHVQQFYDK
BOTFB           APAVTNG-ASPMGLTWLKSFLSSCSD----CTIDFVCIHWYDSASNVAYFKQYVQDAYTA
MAIZE           APSISNSGLPGEGVEWLKSWVSECEKLDEQCHYDFCNVHWYSEVEYGSTLFDHLKASHEA
SCHPO           SPAISN-----VGEDWLSEFMSACSD----CKIDFIACHWYGID--FSNLQDYINSLANY
                 .: :       *  *:   .  *      *  *:   ***        :  ::
```

```
glu1            FPSYTIVISEFALTN------GG--NQVAFFESAFPFLDGLSYVLLYFPFVATSP-----
schco           FPNYKVVISEFALANPS----GGQTAQVNFFKQAFAWLDSQSWVELYFPFVATSP-----
LACBI           YPQYPIWITEYASTS------TDSSVVADFLNQTITYMDTLDWIERYSWFGYF-------
COPCI           FPEYPIWVTEYADIS------SNDAEVYNFMNASIHYLDELEWVERYAWFGFFRPEPDVH
PENMQ           YPNTSIWITEYALAH------ADLKDTQAFFQTSAEYFDRLDYVERYSYFGSFRSSISNV
NEOFI           Y-HLPIWITEFAASG-------SEAEQIQFLQAVLPWLDAQPYVERYAYFGVFPG-----
BOTFB           GGNRPLWITEFQASG-------STDEQNAFMKEVLPWLDASTMVDRYAWFMADTAAG---
MAIZE           CGGKPIWLTEFAPTG-------SDEAIASWLKDAIPQLEDLSYLDAYSYFKVETG-----
SCHPO           G--LPIWLTEFACTNWDDSNLPSLDEVKTLMTSALGFLDGHGSVERYSWFAPATELG---
                     : ::*:           .       :      ::    :  *  *

glu1            -ALLQAND------------PGAVTTVGTGSCLYTNAGGPSSVGNLMY------------
schco           -ALLQAND------------GGAVTNVGTGSCLYTNSGGPSAVGNLMLSNTGNVIRDLWK
LACBI           ------------------------------------------------------------
COPCI           YNMLRADGGLNALGELYIGAETVHTHVIDPFAGYKTFDGADYAGQPIITTFPALYGAAHC
PENMQ           GPNATMLTQ-----------NGQLTDIGSWYLGGAATGNAPNSSSSSSSPTSSGSTGVGY
NEOFI           ------------------------------FLVNEGGDGLSQLGQVYATYSG--------
BOTFB           -------------------------------GLMSSTSALSTLGNTFKTA----------
MAIZE           -------------------------------MLMTSETELSSYGSVYASA----------
SCHPO           ------------------------AGVGNNNALISSSGGLSEVGEIYIS-----------

glu1            --------------------------------
schco           LSRPHEATSSVYRADIP---------------
LACBI           --------------------------------
COPCI           RRAVFGQGGLTLLAVLVTILSGSLAGVFGMLW
PENMQ           KVDSYQAMLQALVVFLVILAFV----------
NEOFI           --------------------------------
BOTFB           --------------------------------
MAIZE           --------------------------------
SCHPO           --------------------------------
```

Fig. S1 Alignment of proteins that had similarity to GLU1.

glu1:*Lentinula edodes*
schco: *Schizophyllum commune*
LACBI: *Laccaria bicolor*
COPCI: *Coprinopsis cinerea*
PENMQ: *Penicillium marneffei*
NEOFI: *Neosartorya fischeri*
BOTFB: *Botryotinia fuckeliana*
MAIZE: *Zea mays*
SCHPO: *Schizosaccharomyces pombe*

Underline indicates signal peptide of GLU1
Red type indicates N-terminal amino acid sequence of GLU1
Yellow maker indicates conserved domain among these putative glucanases