

Supplemental Figure

A

```

      10          20          30          40          50
      . . . . . | . . . . . | . . . . . | . . . . . | . . . . . |
TaGlu1a  MALLAAATLNPTTHLSLRSRAGRNSENLWLRSAASSQKSKGRFCNLITIRAGTPSK...
TaGlu1b  MALLAAATLNPTTHLSLRSRAGRNSENLWLRSTASSQKSKGRFCNLITIRAGTPSK...
TaGlu1c  MALLAAATLNPTTHLSLRSRAGRNSENLWLRSAASSQKSKGRFCNLITVRAGTPSK...
  
```

B

```

      10          20          30          40          50          60          70          80          90          100
      . . . . . | . . . . . | . . . . . | . . . . . | . . . . . | . . . . . | . . . . . | . . . . . | . . . . . |
TaGlu1a  1  AGTPSKPAEPIGPVFTKLPWQIPKRDWFDKDFLFGASTSAYQIEGAWNEDGKGPSTWDHFCHTYPERISDRRTNGDVAANSYHLYEEDVKALKDMGMKVY 100
TaGlu1b  1  AGTPSKPAEPIGPVFTKLPWQIPKRDWFDKDFLFGASTSAYQIEGAWNEDGKGPSTWDHFCHTYPERISDRRTNGDVAANSYHLYEEDVKALKDMGMKVY 100
TaGlu1c  1  AGTPSKPAEPIGPVFTKLPWQIPKRDWFDKDFLFGASTSAYQIEGAWNEDGKGPSTWDHFCHTYPERISDRRTNGDVAANSYHLYEEDVKALKDMGMKVY 100
ScGlu    1  AGTPSKPAEPIGPVFTKLPWQIPKRDWFDKDFLFGASTSAYQIEGAWNEDGKGPSTWDHFCHTYPERISDRRTNGDVAANSYHMYEEDVKALKDMGMKVY 100
ZmGlu1   1  ----SARVGSQ-NGVOMLSPEIIPKRDWFDKDFLFGAATSAYQIEGAWNEDGKGPSTWDHFCHNHPERILDGNSNDIGANSYHMYKTDVRLLEKMGMDAY 95
SbDhr1   1  ----AQTISSESAGIHRLSPWEIPKRDWFPSPFLFGAATSAYQIEGAWNEDGKGPSTWDHFCHNFPWIVDRSNGDVAADSYHYMAEDVRLLEKMGMDAY 96
AsP60b   1  -----ALBSG-----KLPWQIPKRDWFPPEFTFGAASAYQIEGAWNEDGKGPSTWDHFCHNYPERIMDGSNDVAANSYHYMYKEDVRLLEKMGMDAY 89

      110          120          130          140          150          160          170          180          190          200
      . . . . . | . . . . . | . . . . . | . . . . . | . . . . . | . . . . . | . . . . . | . . . . . | . . . . . |
TaGlu1a  101 RFSIAWSRILPDGT--GKVNQAGIDYNNKLNLSLIDNDIVPVYTIWHWDTPQALDKYGGFLNRKTI---VDDYKQFAEVCFKNFGRVKNWFTFNEPHTY 195
TaGlu1b  101 RFSISWSRILPDGT--GKVNQAGIDYNNKLNLSLIDNDIVPVYTIWHWDTPQALDKYGGFLNRKTI---VDDYKQFAEVCFKNFGRVKNWFTFNEPHTY 195
TaGlu1c  101 RFSISWSRILPDGT--GKPNQKIDYNNKLNLSLIRHGI VPVYTIWHWDTPQALDKYGGFLNRKTI---VNDYKHFQAKVCFESFGRVKNWFTFNEPHTY 195
ScGlu    101 RFSISWSRILPDGT--GKPNQKIDYNNKLNLSLIRHGI VPVYTIWHWDTPQALDKYGGFLDKQTI---VNDYKVFQAEVCFQSFGRVKNWFTFNEPHTY 195
ZmGlu1   96 RFSISWPRILPKGTLEGGINPDGIRYRNLLNLLLENGIEPYVTFHWDTPQALDKYGGFLDKSHKSIIVEDYTYFAKVCDFNFGDKVKNWFTFNEPHTY 195
SbDhr1   97 RFSISWPRILPKGTLAGGINEKGVYNNKLLDLLLENGIEPYITIFHWDTPQALVDAYGGFLDEED---YKDYTDFAKVCFEKFGKTVKNWFTFNEPHTY 193
AsP60b   90 RFSISWPRILPEGLTEGGINHEGIIQYNDLLDCLLENGIEPYITIFHWDTPQALADKYNDFLDRRTI---VKDYTDYATVCFEHEFGDKVKNWFTFNEPHTY 186

      210          220          230          240          250          260          270          280          290          300
      . . . . . | . . . . . | . . . . . | . . . . . | . . . . . | . . . . . | . . . . . | . . . . . | . . . . . |
TaGlu1a  196 CCFSYGEIHAPGRCSPGMDCAVPFGDSLREPYTAGHHILLAHAEAVELFKACYNKHGDSKIGMAFDVMGYEPEYQDSFLDDQARERSIDYNLGFLEPVV 295
TaGlu1b  196 CCFSYGEIHAPGRCSPGMDCAVPEGDSLREPYTAGHHILLAHAEAVELFKARYNMHGDSKIGMAFDVMGYEPEYQDSFLDDQARERSIDYNLGFLEPVV 295
TaGlu1c  196 CCFSYGEIHAPGRCSPGMDCAVPEGDSLREPYTAGHHILLAHAEAVELFKAHYNEHGDSKIGMAFDVMGYEPEYQDSFLDDQARERSIDYNLGFLEPVV 295
ScGlu    196 CCFSYGEIHAPGRCSPGMDCAVPEGDSLREPYTAGHHILLAHAEAVELFKAHYNNKHGDSKIGMAFDVMGYEPEYQDSFLDDQARERSIDYNLGFLEPVV 295
ZmGlu1   196 TSFSYGTGVFAPGRCSPGMDCAVPTGNSLVEPYTAGHILLAHAEAVDLVYNKHVKRD-DTRIGLAFDVMGRVPYGTSLFDKQAEERSWDLNGLWFLEPVV 294
SbDhr1   194 CSVSYGTGVFAPGRCSPGVSCAVPTGNSLSEPYIVAHNLLRAHAETVDIYNKYHKA-DGRIGLALNFGRVPTNTFLDQQAQERSMDKCLGFLEPVV 292
AsP60b   187 CGLAYGTGLHAPGLCSPGMDCALPQGDALRQPYIVGHNLLAHAEAVDVIYVYKFFYKGD-DGQIGMVDVMAYEPEYGNFVDDQQAQERSIDFHIWGFLEPVV 285

      310          320          330          340          350          360          370          380          390          400
      . . . . . | . . . . . | . . . . . | . . . . . | . . . . . | . . . . . | . . . . . | . . . . . | . . . . . |
TaGlu1a  296 RGDYPFMSRSLIGDRLPKFTKEEQEKLASSCDIMGLNYYTSRFSKHIDISSDFTPKLNTDDAYASSETKGS DGNIDIGPITGTYWIYMPKGLTDLLLIMK 395
TaGlu1b  296 RGDYPFMSRSLIGDRLPKFTKEEQEKLASSCDIMGLNYYTSRFSKHVDISSDFTPKLNTDDAYASSETKGS DGNIDIGPITGTYWIYMPKGLTDLLLIMK 395
TaGlu1c  296 RGDYPFMSRSLIGDRLPKFTKEEQEKLASSCDIMGLNYYTSRFSKHVDISSDFTPKLNTDDAYASSETKGS DGNIDIGPITGTYWIYMPKGLTDLLLIMK 395
ScGlu    296 RGDYPFMSRSLIGDRLPKFTKEEQEKLASSCDIMGLNYYTSRFSKHVDISSDFTPKLNTDDAYASSETKGS DGNIDIGPITGTYWIYMPKGLTDLLLIMK 395
ZmGlu1   295 RGDYPFMSRSLARERLPFFKDEQEKLAGSYNNMLGLNYYTSRFSKHIDISSDFTPKLNTDDAYASQEVNPGDPKPIGPPMGNPWIYMPKGLTDLLLIMK 394
SbDhr1   293 RGDYPFMSRVSARDRVPYFKEQEKLVGSYDMDIGINYYTSRFSKHIDISSDFTPKLNTDDAYASQETKGFDPGNATGPPFGNWINMYPKGLTDLLLIMK 392
AsP60b   286 RGDYPFMSRSLVGDRLPFFKSEQEKLVSSYDFVGVGINYYTARFSEHIDISSEIIPKLNNTDDAYASTPEFNDSNGIPIGPDLMGYWELSYPKGLTDLLLIMK 385

      410          420          430          440          450          460          470          480          490          500
      . . . . . | . . . . . | . . . . . | . . . . . | . . . . . | . . . . . | . . . . . | . . . . . | . . . . . |
TaGlu1a  396 EKYGNPPIFITENGIADV--SDPTMTDP--LDDWKRLDYLQRHISAVKDAIDQGADVGRHFTWGLIDNFWSLGYSSRFGLVYIDKKGDNKRKLLKKSAR 491
TaGlu1b  396 EKYGNPPIFITENGIADV--GDESMPDP--LDDWKRLDYLQRHISAVKDAIDQGADVGRHFTWGLIDNFWSLGYSSRFGLVYIDKKGDNKRKLLKKSAR 491
TaGlu1c  396 EKYGNPPIFITENGIADV--SDPTMTDP--LDDWKRLDYLQRHISAVKDAIDQGADVGRHFTWGLIDNFWSLGYSSRFGLVYIDKKGDNKRKLLKKSAR 491
ScGlu    396 EKYGNPPIFITENGIADV--GDEMPDP--LDDWKRLDYLQRHISAVKDAIDQGADVGRHFTWGLIDNFWSLGYSSRFGLVYIDKKGDNKRKLLKKSAR 491
ZmGlu1   395 NKYGNPPIYITENGIADV--TKETPLPMEALNDYKRLDYIQRHIALTKESIDLGSNVQYFAWSLLDNFEWFAQFTERYGIVYVDRNNNCTRYMKESAR 493
SbDhr1   393 NKYGNPPIYITENGIADV--KGD--LPPKVALEDHTRLDYIQRHLSVLKQSIDLGADVGRYFAWSLLDNFEWSSGYTERFGIVYVDRNCGCERTMKRSAR 489
AsP60b   386 EKYGNPPIYITENGIADVMDGWCNPPMTDP--LDDPLRIEYLOQHMATAIKBAIDLGADVGRHFTWGLIDNFWSLGYSSRFGLVYIDRNDGFKRIMKKSAR 483

      510          520          530
      . . . . . | . . . . . | . . . . . |
TaGlu1a  492 WFAKFN----SVPKRLKTTN--NNATVTVTSVSV---- 520
TaGlu1b  492 WFSKFN----SVPKRLKTTN--NNATMTAASVSV---- 520
TaGlu1c  492 WFAKFN----SVPKALLKTTN--NNKPAVTASVSL---- 521
ScGlu    492 WFAKFN----SVPKRLKTTN--NNATVT--ASVSV---- 519
ZmGlu1   494 WLKEFN-----TAKKP-SKKILTPA----- 512
SbDhr1   490 WLQEFNG-----AAKKVENKILTPAQQLN--- 514
AsP60b   484 WLKEFN--GATKEV--NNKILGASSCCSGELMWFV--QNPYGK 521
  
```

Amino acid sequences of monocot β -D-glucosidases.

A, the amino acid sequences of the N-terminal region of TaGlu1 – TaGlu1c precursors. The possible cleavage sites of the signal peptides are indicated by downward arrowheads (see Supplemental Text). B, sequence alignment of mature glucosidases from monocotyledonous plants. The amino acid sequences were aligned by ClustalW. Identical residues are shaded. The residues that constitute the substrate binding pocket are indicated by downward open and closed triangles. The open

triangles indicate the residues to which mutations were introduced in this study. The N-terminal sequences replaced with the corresponding part of ZmGlu1 were underlined. The DDBJ/EMBL/GenBank accession numbers of ZmGlu1, SbDhr1 and AsP60b are U25157, U33817 and AF082991, respectively. ScGlu is the sequence obtained in the present study. Residues A324 and S326 are substituted by G and L, respectively, in the sequence in data base (accession number AF293849).