

**A**

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AAx81451GmosAAP1      MASTPP-TDYKAEAVLDVSETRDVETGEVKNNG---LKQDLKNRHMQMIAIGGAIGAGLF
XP_385750G.zeae      MASTPPQADYKAEAVLDVSENQDVETGEVKNNG---LQRDLKNRHMQMIAIGGAIGAGLF
BAE66406A.oryzae     MAS-FDQEAKEGNDAKNPTNTPDALAGDVEEANGNTLKRALEGRHIQMIAMGGAIGAGLF
***                   : . : :. . * . :*:*:*. . . * : : * . :*:*:*:*:*:*:*:*:*:

AAx81451GmosAAP1      VSGGALQKGGGPAALLIGYLIIGIMLLCTCLALAEMAVLYPVNGAFFTYIVRFVDPSWGF
XP_385750G.zeae      VSGGALQKGGGPAALLIGYLIIGIMLLCTCLALAEMAVLYPVNGAFFTYICRFVDPSPWGF
BAE66406A.oryzae     VSGSEALANGGPASVLIIGYLVIVGVLLLCTIMSLGELAIMYPINGAFYQYSTRFIDPCWGF
**** * :*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:

AAx81451GmosAAP1      AMGQYALAWLTVLPFELIAASITIRFWREDINMAVWVSVFLVLLMGIQIFGVRGYGEVE
XP_385750G.zeae      AMGQYALAWLTVLPFELIAASITIKFWREDINMAVWVSVFLVTLIGIQFFGVRGYGEVE
BAE66406A.oryzae     AIGWAYSLSGLWLVTLPEITASLTIEYWNNDLNPAIFVSIFLIVLVIQVFGVRGYGEVE
*:** * :*:*. . :*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:

AAx81451GmosAAP1      FVLSIIKICACVGFIIIGIVINCGGVGD--QGYIGVKYWRDPGAFTS-FKGFCAVFNVA
XP_385750G.zeae      FVLSIIKICACVGFIIIGIVINCGGVGD--QGYIGVKYWQDPGAFTS-FKGFCAVFNVA
BAE66406A.oryzae     FVLSIIKVIACIGLIIIGIIINTGGVPGSPQGYIGKYYWRDPGAFANGFKGFCAVFNVA
*****: * :*:*:*:*:*:*:* * * . * * * * * :*:*:*:*:*:*:*:

AAx81451GmosAAP1      FSFGGTEMVGLAAAESANPRKSIIPMASKQVFWRIAFYIILNLFIVGLILPANDPRLMG--
XP_385750G.zeae      FSFGGTEMVGLAAAESADPRRSIIPMASKQVFWRIAFYIILNLFIVGLILPANDPRLMG--
BAE66406A.oryzae     VAFSGTELVLGAAAEETKNPQKTLPTATKQVLRVTFYIVNLLIVGLNVPNHPNQLLGG
.:*.***:*****: :*:*:*: * :*:*:*:*:*:*:*:*:*:*: * * :*:*:

AAx81451GmosAAP1      ----ASGANTKASPFVLAIQDAGIKVLPsimNAVITVAVLSVANSTFGSTRTIQAMAER
XP_385750G.zeae      ----ASGANTKASPFVLAIQDAGIKVLPsimNAVITVAVLSVANSTFGSTRTIQAMAER
BAE66406A.oryzae     DAASSAGVSANASPFVLAIQDAGIHVLPsiINAVLIISSLSVANSTFASTRTLQALAAD
.:* . . :*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:

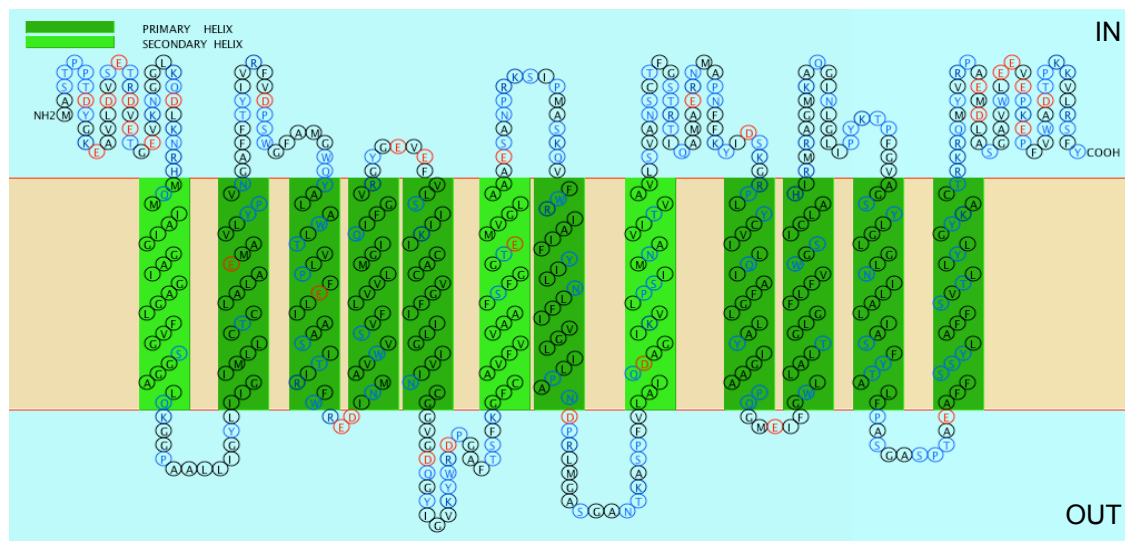
AAx81451GmosAAP1      NMAPNFFKYIDSKGRPLYCVILQIAFGLLAYIGAAPQGMIEFGWLLALTGLGFLFVWGS
XP_385750G.zeae      NMAPGFFKYIDSKGRPLYCVLLQIAFGLLAYIGAAPQGMIEFGWLLALTGLGFLFVWGS
BAE66406A.oryzae     GGAPSFYIDKAGRPLAIALQVLFGLAYLQFASGLTIFNLLSIAGVSTVMMNLSI
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AAx81451GmosAAP1      CLAHIRMragMKAQGINLGLIPYKTPFGVAGSYLGLGNILALIASFYTALFPASGASPT
XP_385750G.zeae      CLAHIRMragMKAQGVNGLGLIPYKTPFGVAGSYLGLGNILALIASFYTALYPASGASPA
BAE66406A.oryzae     NMAHIRFRLAKAQRSTDEIPWKSTLGTGVSSIGAFLSAIALVAMFYSALYAPGGDPPS
:****:* . :***. . . * :*:*. . :* * . :*:* * * :*:*. . . * :*

AAx81451GmosAAP1      AEAFSSYLAFFSVTLVLYGKACTRKRQMYVRPAEMDLASGAVWLEEEVEPKPEFWWADT
XP_385750G.zeae      AEAFSSYLAFFSVTLVYGVYKCTRKWQMYVRPSEMDLSTGAVFLEEEEPKPEFWWADA
BAE66406A.oryzae     AFNFFQYLAGFMGLVLMIFWKVWNRQWVLGVLPLRQIDLDTGRRFMEQVTPDETGESL
* * * . * * * * : * : * . . * : * : * * : * : * : * . . .

AAx81451GmosAAP1      PKKVLRSFY--
XP_385750G.zeae      PKRVLRSFF--
BAE66406A.oryzae     PWWKRAKQTIC
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**B****Supplemental data S1.**

A, ClustalW alignment of the GmosAAP1 amino acid sequence with *Gibberella zeae* (XP\_385750) and *Aspergillus oryzae* (BAE66406) amino acid permeases. The amino acid domains used to design the oligonucleotides are in bold and underlined.

(\* ) identical amino acid (: ) strongly similar amino acid (.) weakly similar amino acid.

B, The predicted hydrophobicity profile of GmosAAP1 as defined using the SOSUI programme.