

Membrane domain

VIMAG domain

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Ta4  GSGSFWTKSPVLYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
In1  POSNTEWKSPLPVYFISGLAFLILVALIVLACSHFRRLSSGSG-
In4  PSRNALPVKSPVLYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
GDU6  RPTPKVEIWKSPVLYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Os4  SPAMAYPMSVPLVYFGHIAAMGLITLALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Sb4  AALAPASPVVPLVYFGHIAAMGLITLALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Sb1  TATHASAWQSPVPLVYFGHIAAMGLITLALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Os1  ASVAARSWQSPVPLVYFGHIAAMGLIALSLLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Os3  NGTAAHSPWQSPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Le2  PHSPPSPVPLVYFGHIAAMGLIACAVLIIICSYWKLISGKLELITVVALIVLACSHFRRLSS-
In2  PAAFPVSPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
In3  TSPVATSPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Sb3  GSAAASWMSVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Os2  GGAASWMSVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Le1  VESFQSPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
GDU1  HGVTBQSPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
GDU4  NHRPPIVSPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
GDU5  VESQTRSPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Bv1  STGQSPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
M2  SVOVHSPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Pc1  SOQPHSPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Lj1  SUIPHSPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
La1  SQQPHSPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
La2  SPQPHSPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Gm4  SPOPHSPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Pop1  LAQPRSPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Gm1  SPSQHSWMSVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Gm3  SPSQHSWMSVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
M1  ASMMHNSWSPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
GDU2  SMVVHSPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
GDU3  MGGPHSPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Cj1  YGESHAGWSPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Pin5  SYEETHRWSPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Pin3  ---HESPXXVLYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Pin2  NFWTHSETFAPVLYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Pin1  ---AVSAPKSPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Pin4  ---LGGVCMIALISFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Pin6  SHRFNTPVKTPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Hb1  GAGVGFHNSPMPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Pop2  GAHGGHNSPMPVAVPAGLALMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Gm2  VSGSGNINIKWSPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Pc2  ---TRVPIGFTLMMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Ta3  TOTNEIKIMOSPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Hv2  GHGAHPLWRPVPVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Hv3  GHGAFGFWRPVPVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Ta1  ATARFGGGR-RRRTSSASLMMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Os5  GGGHGPWRPVPVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Ta2  SPMIPPPFWSPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Hv1  PTMIPPPPFWSPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
Sb2  GRVQVPPPPFWSPVPLVYFGHIAAMGLIAFALLIIAACYWKLISGKLELITVVALIVLACSHFRRLSS-
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....

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Supplementary figure 1. Multiple sequence alignment of the GDU1-similar proteins from plants. Genbank EST database was searched with GDU1 protein sequence using tBLASTn. Only plant ESTs (104) displayed a significant score. Ninety-eight ESTs were successfully grouped into 44 contigs which were translated into proteins. Genbank genome database search identified GDU1-similar sequences in *Arabidopsis*, rice and Alfalfa. The EST- and genome-derived protein sequences were aligned using Clustal X (Thompson *et al.*, 1997). Similar residues are shaded (>60% conservation in dark gray, >40% conservation in bright gray). Only the sequences flanking the membrane domain and the VIMAG domain are shown.