

CLUSTAL W (1.83) multiple sequence alignment

G.max	MVFIDIEEGTKTRAEKICKYMEERGILVMQESSSRMRVVLHHQISASDVQYALSCFQQAL	363
A.thaliana(THA1)	MIFMDMEDGSRLTAEKLRKNLLEENGILLIRGNSSRIRIVIHHQITTSVDVHTLSCFQQAM	349
A.thaliana(THA2)	IIYVDIPEDPKFGAAEACKSLEDVGVLVIPQATFRIRIVLHQISDSDVQYALTCVEKIF	353
O.sativa	MVFFDIVD-SRISPDKLCQVLEQRNVLAMPAGSKSMRLVIHYQISDSDVQYALTCVEKAA	392
T.aestivum	MVFFDIAD-PRITPDKLCQVLEQRNVLAMPASSKSVRVLTTHYQISDSDVQYTLTCIEKAV	403
Z.mays	-----	
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S.tuberosum	AGVAEENGDK-----	359
S.esculentum	-----	
M.truncatula	QIENGN-----	370
G.max	AVKGVQNEMG-----	373
A.thaliana(THA1)	LTMQEPEPSRT-----	358
A.thaliana(THA2)	HS-----	355
O.sativa	EEILTGSKKFEXSDKRYYQEFIRAL-EITPFVPTDASVQRPACLSSH-----	439
T.aestivum	EEILSGNAKFEXPDKRHYHEFIWALGHFLSRHLWSAVQYPACLWPWPLQ	453
Z.mays	-----	

Medicago truncatula (TC95044), *Glycine max* (TC205585), *Solanum tuberosum* (TC76119), *Oryza sativa* (TC275073), *Triticum aestivum* (TC265508), *Zea mays* (TC309851), *Solanum esculentum* (TC166175)

Supplemental Figure 12. TC (Tentative Consensus) sequences of the species were derived from EST consensus sequences found in the TIGR database (<http://www.tigr.org/tdb>) using a BLAST search. The sequences were aligned using Clustal W (version 1.81). Stars represent identity at that position in all sequences. Colons represent similarity at that position. The conserved Gly residue that is changed to Arg in the *tha1-1* mutant is indicated by an arrow.