

In silico characterization of putative gene homologues involved in somatic embryogenesis suggests that some conifer species may lack *LEC2*, one of the key regulators of initiation of the process

Sonali Sachin Ranade, Ulrika Egertsdotter

Department of Forest Genetics and Plant Physiology, Umeå Plant Science Center (UPSC), Swedish University of Agricultural Science (SLU), 901 83 Umeå, Sweden

Alignments of EMK gene

Table S1 List of protein sequences included in the CLUSTAL multiple sequence alignment by MUSCLE (3.8)

Species	Sequence ID
<i>Arabidopsis</i>	AT5G57390
<i>Picea abies</i>	PAB00031051
<i>Pinus taeda</i>	PTA00002401
<i>Pinus sylvestris</i>	PSY00016492
<i>Pinus pinaster</i>	PPI00042898
<i>Pseudotsuga menziesii</i>	PME00112031

Figure S1 Alignment of PAB00031051 and AT5G57390

```
AT5G57390      MKNNNNKSSSSSYDSSLSPSSSSSSHQNWLSFSLNNNNNFNSSSNPNLTSSTSDHHHP
PAB00031051    -----MAVTSSFAQQSVGYNNTDAHRELPNSIP-----
                  : : ** * : : : : : : : : * * *

AT5G57390      HPSHLSLFQAFSTSPVERQDGGSPGVSPSDATAVLSVYPGGPKLENFLGGGASTTTTRPMQ
PAB00031051    ---LTL-----ERSD-----
                  * : *      * * : *

AT5G57390      QVQSLGGVVFSSDLQPPLHPPSAAEIYDSELKSIAASFLGNYSGGHSSEVSSVHKQQPNP
PAB00031051    -----ISALRHNAGP-----
                  * . : : : . *

AT5G57390      LAVSEASPTPKKNVESFGQRTSIYRGVTRHRWTGRYEAHLWDNSCRREGQSRKGRQVYLG
PAB00031051    LSFMEALNEPNNG-----G
                  * : . * * * : : .

AT5G57390      GYDKEDKAARAYDLAALKYWGPTTTTNFPISNYESELEEMKHMTRQEFVASLRRKSSGFS
PAB00031051    GYDQEEKAARAYDMAALKYWGPKTTTNFPISQYRDALNEMQHLTRQAYVASIR-----
                  *** : * : * * * * * : * * * * * * * : * * * : * * * : * * * : *

AT5G57390      RGASMYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFFSTQEEAAEAYDIAAIKFRGLNAV
PAB00031051    -----RHHQHGRWQARIGRVAGNKDLYLGTFSSEKEAAEAYDVAAIKFRGPNAV
                  * * * * * * * * * * * * * * * * : : * * * * * * * * * *

AT5G57390      NFDISRYDVKSIASCNLPVGGLMPKPSATAAADKTVDLSPSDSPSLTTPSLTFNVATPV
PAB00031051    NFEMSKYDLKTIENCILPIGAARKLKAKAESAVEGSVNNGRSTDEECTLSSQT-----
                  * * : * : * : * : * : * : * : * : * : * : * : * : *

AT5G57390      NDHGGTFYHTGIPIKPDPAHYWSNIFGFQANPKA----EMRPLANFGSDLHNPSPGYA
PAB00031051    ---DTSYIGNAARTE----WLPLISLQQQSHPMQAAYELQKVQLYNQDLHMLHNVN
                  . : : * . . : * : : : * : : . * : : : . * * * .

AT5G57390      IMPVMQEGENNFG-----GSFVGS DGYNHSAASNP-----VSAIPLS
PAB00031051    QQKYIQASGSTHELHNLSLESAVNNNNNNNNNASNSTPGIYTNISNGLAINGLLANPSYH
                  : * . . . . * * . . . . * * : : * * : : : .

AT5G57390      STTTMSNGNEGYG-----GNI-----NWINNNI-----SSSY
PAB00031051    SAVIFGENSEGYAAAKSLTFGNMLMPPQHFAMNNLYYLPQQKQHQQSPGLAKDTS DNLEY
                  * : . : : . * * . * * : : * * : : * * : : . . *

AT5G57390      QT---AKSNLSVLHTPVFGLE
PAB00031051    NNGMETRPNLKAGHAPIF---
                  : . : . * * . . * * : *
```

Figure S2 Alignment of PTA00002401 and AT5G57390

AT5G57390	MKNNNNKSSSSSYDSSLSPSSSSSSHQNLFSLSNNNNNFSSSNPNLTSSTDHHP
PTA00002401	-----MVHYCMSTINME-----
	: : .: *::
AT5G57390	HPSHLSLFQAFSTSPVERQDQSPGVSPDATAVLSVYPGGPKLENFLGGGASTTTTRPMQ
PTA00002401	-----
AT5G57390	QVQSLGGVVFSSDLQPPLHPPSAAEIYDSELKSIAASFLGNYSGGHSSEVSSVHKQQPNP
PTA00002401	-----GGKLVLEEL-----
	** :. :.*
AT5G57390	LAVSEASPTPKKNVESFGQRTSIYRGVTRHRWTGRYEAHLWDNSCRREGQSRKGRQVYLG
PTA00002401	-----QETKIF-----IWEHLV-----
	* *.*: :*::
AT5G57390	GYDKEDKAARAYDLAALKYWGPTTTTNFPISNYESELEEMKHMTRQEFVASLRRKSSGFS
PTA00002401	--SSEKEAAEAYDIAAIKFRGRNAVTFNFDMSRY--DVKAIESVTLPIGAARKLKSEAESA
	.*. ** ***:**:* .: ***:*. * : : : : * .*. . . : :
AT5G57390	RGASMYRGVTRHHQHGRWQARIGRVAGNKDL--YLGTFSTQEEAAE--AYDIAAIKF
PTA00002401	VDGPVNNGLSNDEECTLSSQTEATSYTGNAALRNEWLPLISLQKSNPLQVQYQLQKVPL
	. . : . *: : : * : ** * : * : * * : : * : : : :
AT5G57390	RGLN-AVTNFDISRYDVKSIASCNLPVGGLMPKPSPATAAADKTVDLSPSDSPSLTTPSL
PTA00002401	YNQDLQMGMHNVNQKYLQASGSTHELSNLISLGSVN-----NNSNNASSSTPGI
	. : : . : . . . : . : . : . : * * . . . * : * : :
AT5G57390	TFNVATPVNDHGGTFYHTGIPIKPDADHYWSNIFGFQANPKAEMRPLANFGSDLHNPSP
PTA00002401	YSNIPNALAING-----LMGPNPSDRS-AVIFGETSELSAAAKPLT-YGNMLMSPE-
	* : . . : : * : * : * : * : * : * : * : * : * : *
AT5G57390	GYAIMPVMQEGENNFGGSFVGSDDGYNNHSAASNPVSAIPLSSTTTMSNGNEGYYGGINWI
PTA00002401	-----QLARNNL-----YYLYQQQSPGLFKAASDNMAYNNGME-----
	* . ** : * : . . * . * . : . ** *
AT5G57390	NNNISSSYQTAKSNLSVLHTPVFGL-----
PTA00002401	-----ASSNLKVGHGPMFSVFDDSQG
	* . ** . * * * : * : :

Figure S3 Alignment of PSY00016492 and AT5G57390

```
AT5G57390      MKNNNNKSSSSSYDSSLSPSSSSSSHQNWLSFSLNNNNNFNSSSNPNL--TSSTSDHH
PSY00016492    MASANNWLDVSLSNLTVDMQSGGGQGGHDQNSASRNNMLVTSNFPHLGIGYNNDDAH
* . ** . . * * : ::. .*. .: . . . :..** : :*. *: * ..: * *

AT5G57390      HPHPSH---LSLFQA-----FSTSPVERQDQSPGVSPSDATAV
PSY00016492    QELPSKSIPLTLERTDGSTLRHNAGYMETLSAPDNGGFQSDQPDETQGYNNLEQTQTSAN
: ** : *:* .: *.. : :* .. :*: *

AT5G57390      LSVYPPGGPKLENFLGGGASTTTTRPMQQVQSLGGVVFSSDLQPPLHPPSAAEI-----Y
PSY00016492    -NVYGPSSDVMRFMANNCQAGSDE-MNQMSNAANSFLSSAITAPNVTTTAKVQPGPRAM
.*. . .: .*: . . .: : *:* . . .*: : . * ..: *:

AT5G57390      DSELKSIAASFLG-----NYSGGHSSEVSSVHKQPNNPL-----
PSY00016492    HDDVNYMSVNWFGMNQAAEDRSKNNNTNTGEEGAIALRPNIMQNLSNNHNQANANDS
.: : :*: * .. :*: . . .*: :

AT5G57390      -----AVSEASPTPKK
PSY00016492    NILSGYGLQIPQGPVNDVYGIPNVNVVRNQASEEANMNNTTNFPAHITAVTATTSTAKE
* : :*: * :

AT5G57390      NV-----ESFGQRTSIYRGVTRHRWTGRYE
PSY00016492    TSTNGDSPSAGGSKKRALEDAITPFESAVPIQSRPADQSLGHRTSIYRGVTRHRWTGRYE
. :*: *:*****

AT5G57390      AHLWDNSCRREGQSRKGRQVYLGGYDKEDKAARAYDLAALKYWGPTTTTNFPISNYESEL
PSY00016492    AHLWDNTRSRENQTRKGRQVYLGGYDQEEKAARAYDMAALKYWGPRTTTTNFPISQYREAL
*****: * :*: *****: *:***** *****: * . *

AT5G57390      EEMKHMTRQEFVASLRRKSSGFSRGASMYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFS
PSY00016492    EEMQNLTRQEFVSSLRRKSSGFSRGASKYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFG
***: :*****:***** *****:*****

AT5G57390      TQEEAAEAYDIAAIKFRGLNAVTFNFDISRYDVKSIASCNLPVGGLMPKPSATAAADKTV
PSY00016492    SEKEAAEAYDIAAIKFRGRNAVTFNFDMSKYDVKTIESCTLPIGAARKLSEAESAVDGPV
: :*****:*****:*.***: * * :*: *

AT5G57390      DLSPSDSPSLTTPSLT-----FNVATPVNDHGGTFYHTGIPIKPDPA
PSY00016492    NNGLSNDEECTLSSQTEATSYTGDAALRNEWLPLISLQKSNPLQVQYQLQKVPLYNQDL
: . *: . * . * : : * : :*: :

AT5G57390      DHYWSNIFG---FQAN-PKAEMRPLANFGSDLHN-----PSPG-YAIMPVMQEGENNF
PSY00016492    QMQMHNVNQKYLQANGSTHELSNLISLGSVNNNCNNASSSTPGIYTNIPNALAMNGLM
: * : :*** .: * :*: * :*: * :*: * : :

AT5G57390      GGSFVGSDGYNNHSAASNVPVSAIPLSSTTTMSNGNEGYGGNINWI-----
PSY00016492    GANPSDRSAVIFGETSELSASAKPLTYGNMLMSPEQFARNNLYLYQQQQQQQSPGLFKA
* . . . . : : . * *: . : . : :*: :

AT5G57390      --NNNISSSYQTAKSNLSVLHTPVFGL-----
PSY00016492    AGDNMAYNNGMEARSNLKVGHGPMFSVFDDSQG
: * . . * .*: * * *: :
```

Figure S4 Alignment of PPI00042898 and AT5G57390

```
AT5G57390      MKNNNN-----KSSSSSYDSSLSPS-----SSSSSH
PPI00042898    MASANNWLDVSLNNLTVDMQGGGGQGQHDQNLASARNMMLVPSNFPHLGIGYNNTDAH
* . **                .....:*.**.* . . . .:

AT5G57390      QNWLSFS-----
PPI00042898    QEIPSKIPLTLERTDGSALRHNAGYMETLSAPDNGGFQSDQPDQTQGYNNLEQTQKSAN
*: * *

AT5G57390      -----LSNNNNNFNSS--SNPNLTSSTS-DHHHPHPSH-
PPI00042898    NIYGPSSDVMRFMANNYQAGSDEMNMQMSNAANSFLSSAITAPAVTTTTAKDQPGPRAMHG
                :** *.**.* :*:**.*:*.**.*

AT5G57390      -----LSLFQAFSTSPVERQDGSPGVSPSDATAVLSVYP-----GGPKLENF
PPI00042898    DVNYMSVNWFGMNQTAEDRSEQNNNTNTGEEEGAIALRPNTMQNLSNNNNQANANDSNI
                :. * .*: :... ..: . . .: * . . .:.*:

AT5G57390      LGGGASTTTTRPMQQVQSLGGVVF----SSDLQPPLHPPSAAEIYDSELKSIAASFLGNY
PPI00042898    LSGYGLQIPQGPVNDVYGIPNVNWWVRNQASEEANMNNTTNFPAHITAVTATTSAAKETS
*.* . . *::*. :.* : .: .: .: .: .: .: .: .: .:

AT5G57390      SGGHSSEVS SVHKQQPNPLAVSEASPT--KKNVESFGQRTSIYRGVTRHRWTGRYEAH
PPI00042898    GNGDSPSSGGSKKRALEDAITPFESAVPIQSRADQSLGHRTSIYRGVTRHRWTGRYEAH
..* *.. .:*. : ..*.* . :*.*:*****

AT5G57390      LWDNSCRREGQSRKGRQVYLGGYDKEDKAARAYDLAALKYWGPTTTTNFPISNYESELEE
PPI00042898    LWDNTSRRENQTRKGRQVYLGGYDQEEKAAARAYDMAALKYWGPRTTTNFPISQYREAL
*****.*.*.*:*****.*:*****.*:*****.*:*****.*:*****.*:*****.*

AT5G57390      MKHMTREQEFVASLRRKSSGFSRGASMYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSQ
PPI00042898    MQNLTRQEFVSSLRRKSSGFSRGASKYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFGSE
*:*:*****.*:*****.*:*****.*:*****.*:*****.*:*****.*:*****.*:

AT5G57390      EEAAEAYDIAAIKFRGLNAVTFNFDISRYDVKSIASCNLPVGGMLPKPSPATAAADKTVDL
PPI00042898    KEAAEAYDIAAIKFRGRNAVTFNFDMSKYDVKTIESCTLPIGAARKLKSEAESAVDGPVNN
:*****.*:*****.*:*****.*:*****.*:*****.*:*****.*:*****.*:

AT5G57390      SPSPSPSLTTPSLT-----FNVATPVNDHGGTFYHTGIPIKPD PADH
PPI00042898    GLSNDEECTLSSQTEATSYTGNAALRNEWLPLISLQQKSNPLQVQYQLQKVPLYNQDLQM
. *: . * . * . . . .: .: * : :*: : :

AT5G57390      YWSNIFG---FQAN-PKAEMRPLANFGSDLHN-----PSPG-YAIMPVMQEGENNFGG
PPI00042898    QMHNVNQQKYLQANGSTHELNLISLGSVNNNSNNASSSTPGIYTNIPNALAINSLMGA
*: :*** ..*: * .:* :*: .:****: :* .:*.

AT5G57390      SFVGSDGYNNHSAASNPSAIPLSSTTTMSNGEGYGGNINWI-----
PPI00042898    NPSDRSAVIFGETSELSASAKPLTYGNMLMSPEQFARNNLYLYQQQQQQSPGLFKAAG
. . . . .:..** ***: .: .: .: .: .: .:

AT5G57390      NNNISSSYQTAKSNLSVLHTPVFGL--E
PPI00042898    DNMAYNNGMEARSNLKVGHGPMFSVFDD
:* ..*.*.*.**:.*: .:
```

Figure S5 Alignment of PME00112031 and AT5G57390

```
AT5G57390      MKNNNNKSSSSSYDSSLSPSSSSSSHQNWLSFSLNNNNNFNSSSNPNLTSSTSDHHHP
PME00112031    -----

AT5G57390      HPSHLSLFQAFSTSPVERQDGSPGVSPDATAVLSVYPGGPKLENFLGGGASTTTTRPMQ
PME00112031    -----

AT5G57390      QVQSLGGVVFSSDLQPPLHPPSAAEIYDSELKSIAASFLGNYSGGHSSEVSSVHKQQPNP
PME00112031    -----

AT5G57390      LAVSEASPTPKKNVESFGQRTSIYRGVTRHRWTGRYEAHLWDNSCRREGQSRKGRQVYLG
PME00112031    -----

AT5G57390      GYDKEDKAARAYDLAALKYWGPTTTTNFPISNYESELEEMKHMTRQEFVASLRRKSSGFS
PME00112031    -----AALKYWGATTTTNFPISQYKDALEEMQNMTTQEYIASIRRKSSGFS
                      *****.******.*:.  *****:.* *:*:*:*:*:*:*
                      *****.******.******.******.******.******.*

AT5G57390      RGASMYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTQEEAAEAYDIAAIKFRGLNAV
PME00112031    RGVSQYRGVTKHHQHGRWQARIGRVAGNKDLYLGTFSSEKEAAEAYDVAAIKFKGHNALT
                      **.* *****.******.******.******.******.******.*
                      *****.******.******.******.******.******.*

AT5G57390      NFDISRYDVKSIASCNLPVGGLMPKPSATAAADKTVDLSPSDSPSLTTPSLTFNVATPV
PME00112031    NFDMSKYELKKLESSILPIGAAKRPRLETESAVD----GPTNNGCSTNEERTLSSQTDA
                      ***.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*
                      *****.******.******.******.******.******.*

AT5G57390      NDHGGTFYHTGIPIKPDADHYWSNIFGFQANPKAEMRPLANFGSDLHNPSPGYAIMPVM
PME00112031    TSYINNAARHNNAARP-----KCLHLMALQQQAKPL-----QPAYQLQ---
                      ..: .. . . . . * : : : * : : .** .**.* :
                      *****.******.******.******.******.******.*

AT5G57390      QEGENNFGGSFVGSDGYNNHSAASNVPVSAIPLSSTTTMSNGEGYGGNINWINNNISSY
PME00112031    -----KVSLYNQDLHRQL
                      :.. *::: .

AT5G57390      QTAKSNLSVLHTPVFGLE
PME00112031    HSGNQQ-----
                      ::::.
```

Figure S6 Alignment of *EMK* sequences from all conifer species included in the study

```

AT5G57390      MKNNNNKSSSSSSYDSSLSPSSSSSSSHQNWLSFSLNNNNNFNSSSNPNLTSSTSDHHHP
PME00112031    -----
PAB00031051    -----MAVTSSFAQQSVGYNNTD--
PTA00002401    -----
PSY00016492    MASANNWLDVSLSNLTVDMQGGGGQGGHDQNSASARNMLVTSNFPHLGIGYNNTD--
PPI00042898    MASANNWLDVSLSNLTVDMQGGGGQGGHDQNLASARNMLVPSNFPHLGIGYNNTD--

```

```

AT5G57390      HPSHLSLFQAFSTSPVERQDQSPGVSPSDATAVLS-----
PME00112031    -----
PAB00031051    --AHRELPSNSIPLTLERSDISALRHNAGPLSFME-----
PTA00002401    -----
PSY00016492    --AHQELPSKSIPLTLERTDGSTLRHNAGYMETLSAPDNGGFQSDQPDETQGYNNLEQTQ
PPI00042898    --AHQEIPSKSIPLTLERTDGSALRHNAGYMETLSAPDNGGFQSDQPDETQGYNNLEQTQ

```

```

AT5G57390      ----VYPGGPKLENFLGGGASTTTTRPMQQVQSLGGVVFSSDLQPPLHPPSAE----
PME00112031    -----
PAB00031051    -----ALNEPNNG-----
PTA00002401    -----
PSY00016492    TSANNVYGPSSDVMRFMANNCQAGSDEMNMQMSNAANSFLSSAITAPNVTTTTAKVQPGPR
PPI00042898    KSANNIYGPSSDVMRFMANNYQAGSDEMNMQMSNAANSFLSSAITAPAVTTTTAKDQPGPR

```

```

AT5G57390      IYDSELKSIAASFLGNYSYG-----
PME00112031    -----
PAB00031051    -----
PTA00002401    -----
PSY00016492    AMHDDVNYMSVNWFGMNQAAEDRSKQNNNNNTNTGEEGAIALRPNIMQNLNNHNQANAN
PPI00042898    AMHGDVNYMSVNWFGMNQTAEDRSEQNNNNNTNTGEEGAIALRPNTMQNLNNNNQANAN

```

```

AT5G57390      -----HSSEVSSVHKQQPNPLAVSEASPT----
PME00112031    -----
PAB00031051    -----
PTA00002401    -----
PSY00016492    DSNILSGYGLQIPQGPVNDVYGIPNVNVVVRNQASEEANMNNTTNFPAHITAVTATTSTA
PPI00042898    DSNILSGYGLQIPQGPVNDVYGIPNVNVVVRNQASEEANMNNTTNFPAHITAVTATTSA

```

```

AT5G57390      -----PKKNVESFGQRTSIYRGVTRHRWTGR
PME00112031    -----
PAB00031051    -----
PTA00002401    -----
PSY00016492    KETSTNGDSPSAGGSKKRALEDAITPFESAVPIQSRPADQSLGHRTSIYRGVTRHRWTGR
PPI00042898    KETSGNGDSPSSGGGSKKRALEDAITPFESAVPIQSRADQSLGHRTSIYRGVTRHRWTGR

```

AP2 domain1

```

AT5G57390      YEAHLWDNSCRREGQSRKGRQVYLGGYDKEDKAARAYDLAALKYWGPRTTTNFPISNYES
PME00112031    -----AALKYWGATTTNFPISQYKD
PAB00031051    -----GGYDQEEKAARAYDMAALKYWGRKTTNFPISQYRD
PTA00002401    -----MVHYCYMSDITIN--MEGGKL
PSY00016492    YEAHLWDNTSRRENQTRKGRQVYLGGYDQEEKAARAYDMAALKYWGRRTTTNFPISQYRE
PPI00042898    YEAHLWDNTSRRENQTRKGRQVYLGGYDQEEKAARAYDMAALKYWGRRTTTNFPISQYRE

```

::: * * :

AP2 domain1

```

AT5G57390      ELEEMKHMTRQEFVASLRRKSSGFSRGASM YRGVTRHHQHGRWQARIGRVAGNKDLYLGT
PME00112031    ALEEMQNMTTQEYIASIRRKSSGFSRGVSQ YRGVTKHHQHGRWQARIGRVAGNKDLYLGT
PAB00031051    ALNEMQHLTRQAYVASIRR-----HHQHGRWQARIGRVAGNKDLYLGT
PTA00002401    VLEELQE--TKIFI-----WEHLV-----
PSY00016492    ALEEMQNLTRQEFVSSLRRKSSGFSRGASK YRGVTRHHQHGRWQARIGRVAGNKDLYLGT
PPI00042898    ALEEMQNLTRQEFVSSLRRKSSGFSRGASK YRGVTRHHQHGRWQARIGRVAGNKDLYLGT

```

*::: :::

*: :

AP2 domain2

AT5G57390
PME00112031
PAB00031051
PTA00002401
PSY00016492
PPI00042898

FSTQEEAAEAYDIAAIKFRGLNAVTFNFDISRYDVKSIASCNLPVGGMLMPKPSPATAAADK
FSSEKEAAEAYDVAAIKFKGHNALTNFDMISKYELKKLESSILPIGAAKRPRLETESAVD-
FSSEKEAAEAYDVAAIKFRGPNAVTNFEMSKYDLKTIENCILPIGAAKRLKAKAESAVE-
-SSEKEAAEAYDIAAIKFRGRNAVTFNFDMSRYDVKAIESVTLPIGAAKRLKSEAESAVD-
FGSEKEAAEAYDIAAIKFRGRNAVTFNFDMSKYDVKTIESCTLPIGAAKRLKSEAESAVD-
FGSEKEAAEAYDIAAIKFRGRNAVTFNFDMSKYDVKTIESCTLPIGAAKRLKSEAESAVD-
.:.:*****:*****.* ***:***:*.***:* : . ***:*. : :*.:

AP2 domain2

AT5G57390
PME00112031
PAB00031051
PTA00002401
PSY00016492
PPI00042898

TVDLSPSDSPSLTTPSLTFNVATPVNDHGGTFYHTGPIKPD PADHYWSNIFGF---QAN
----GPTNNGCSTNEERTLSSQTDATSYINNAARHNNAARPK-----CLHLMALQQQQAK
---GSVNNGRSTDEECTLSSQTDSTSYIGN-----AARTE----WLPLISL-QQQSH
----GPVNNGLSNDEECTLSSQTEATSYTGNA-----ALRNE----WLPLISL-QQKSN
----GPVNNGLSNDEECTLSSQTEATSYTGDA-----ALRNE----WLPLISL-QQKSN
----GPVNNGLSNDEECTLSSQTEATSYTGNA-----ALRNE----WLPLISL-QQKSN
.. :. . . *:. * .. : . . . :.: :.:

AT5G57390
PME00112031
PAB00031051
PTA00002401
PSY00016492
PPI00042898

P---KAEMRPLANFGSDLHNPSPGYAIMPVMQEGENNFG-----GSFVGS DGYN NHSA
PLQPAYQLQKVS LYNQDLHRQLHSGNQ-----
PMQAAYELQKVQLYNQDLHMQ LHN VNQQKYIQASGSTHELHNLISLES AVNNNNNNNNNAS
PLQVQYQLQKVPLYNQDLQM QMHN VNQQKYLQASGSTHELSNLISLGS AVNNN--SNNAS
PLQVQYQLQKVPLYNQDLQM QMHN VNQQKYLQANGSTHELSNLISLGS AVNNN--CNNAS
PLQVQYQLQKVPLYNQDLQM QMHN VNQQKYLQANGSTHELSNLISLGS AVNNN--SNNAS
* :. : :. **: .

AT5G57390
PME00112031
PAB00031051
PTA00002401
PSY00016492
PPI00042898

ASN P-----VSAIPLSSTTTMSNGNEG--YGGNI---NWINN

NSTPGIYTNISNGLAINGLL-ANPSYHSAVIFGENSEG YAAKSLTFGNMLMPPQH FAMN
SSTPGIYSNIPNALAINGLMGPNPSDRSAVIFGETSELSAAKPLTYGNMLMSPEQLARN
SSTPGIYTNIPNALAMNGLMGANPSDRSAVIFGETSELSASAKPLTYGNMLMSPEQFARN
SSTPGIYTNIPNALAINSLMGANPSDRSAVIFGETSELSASAKPLTYGNMLMSPEQFARN

AT5G57390
PME00112031
PAB00031051
PTA00002401
PSY00016492
PPI00042898

NISSSYQ-----TAKSNLSVLHTPVFGLE-----

NLYYLPQQKQHQQSPGLAKDTS DNLEYNNGMETRPNLKAGHAPIF-----
NLYYLYQ---QQQSPGLFKAASDNMAYNNGMEASSNLKVGHGPMFSVFDDSQG
NLYYLYQQQQQQQSPGLFKAAGDNMAYNNGMEARSNLKVGHGPMFSVFDDSQG
NLYYLYQQQQQQQSPGLFKAAGDNMAYNNGMEARSNLKVGHGPMFSVFDD---