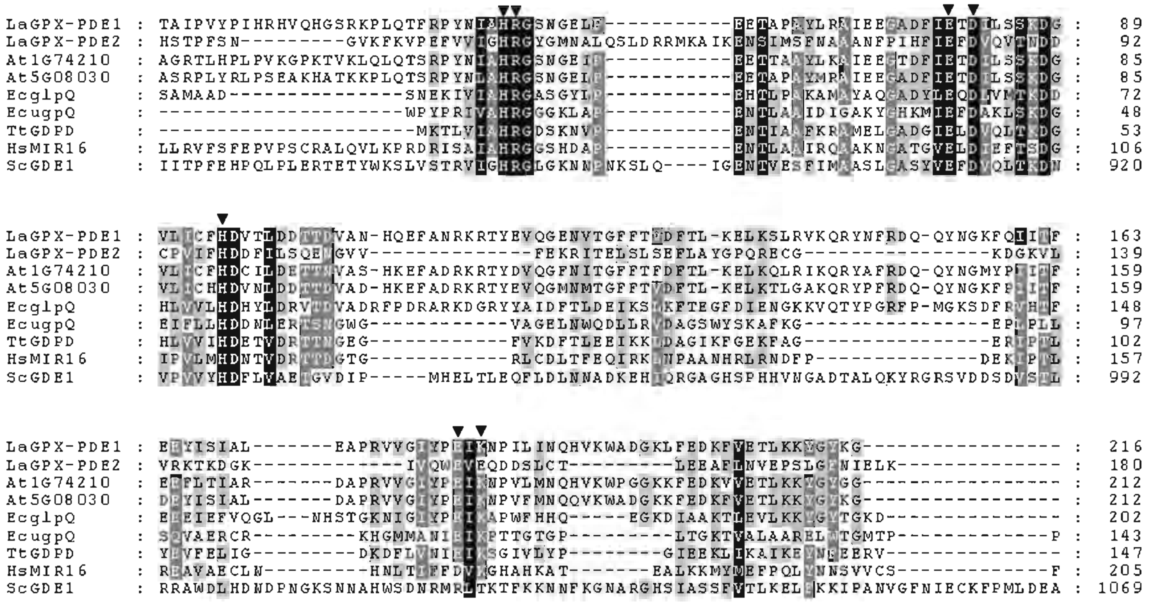
Figure S1

A



B

% identity	LaGPX-PDE1
LaGPX-PDE2	16
Gm17g08680	79
At1g74210	70
Os03g40670	68
Sb03g035370	68

% identity	LaGPX-PDE2
LaGPX-PDE1	16
Gm19g27060	75
At3g02040	64
Os02g31030	61
Sb04g021010	57

Supplemental Figure S1. Alignment of the Conserved Catalytic Domain of White Lupin Glycerophosphodiester Phosphodiesterases (GPX-PDEs) with the Orthologs of Various Species and the Amino Acid Identity of the Corresponding Plant Orthologs.

(A) Alignment of the deduced amino acids residing throughout the catalytic domain of GPX-PDEs from plants, animals, bacteria and yeast. La, *Lupinus albus* ; At, *Arabidopsis thaliana*; Ec, *Escherichia coli*; Tt, *Thermoanaerobacter tengcongensis*; Hs, *Homo sapiens*; Sc, *Saccharomyces cerevisiae*. ▼Represents conserved active site residues.

(B) The deduced amino acid identity of white lupin GPX-PDEs compared to those of other plant orthologs. La, *Lupinus alba*; Gm, *Glycine max*; At, *Arabidopsis thaliana*; Os, *Oryza sativa*; Sb, *Sorghum bicolor*.

Figure S2

A

```
>GPX-PDE1

MSVSMASSTSFASLVFMLLIIGCTAIPVYPIHRHVQHGSRKPLQTFRPYN  50
                                            *
IAHRGSNGELPEETAPAYLRAIEEGADFIETDILSSKDGVLICFHDVTLD  100
     *                            *            *
DTTDVANHQEFANRKRTYEVQGENVTGFFTVDFTLKELKSLRVKQRYNFR  150
 *               *               *
DQQYNGKFQIITFEEYISIALEAPRVVGIYPEIKNPILINQHVKWADGKL  200
               *
FEDKFVETLKKYGYKGSYLSKDWLKQPAFIQSFAPTSLVYTSNQTDLPKI  250
             *  *
LLIDDITIPTQDTNQSYWEITSDSYFEYIKDYVVGIGPWKETVVTVVNNY  300
                *   **
LQTPSDLVKRAHAHNLQVHTYTYRNENKFLCFNFNQDPYQEYDYWVKKIG  350
                     *                *    *
VDGLFTDFTGSLHKYQEWTSSNRHNESDDKTASRLLHKIASLVTSY  396
                          *
```

B

```
>GPX-PDE2

MALKAFHVSDIPSIDIVPETHLSLHSTPFSNGVKFKVPEFVVIGHRGYGM  50
                      *
NALQSLDRRMKAIKENSIMSFNAAANFPIHFIEFDVQVTNDDCPVIFHDD  100

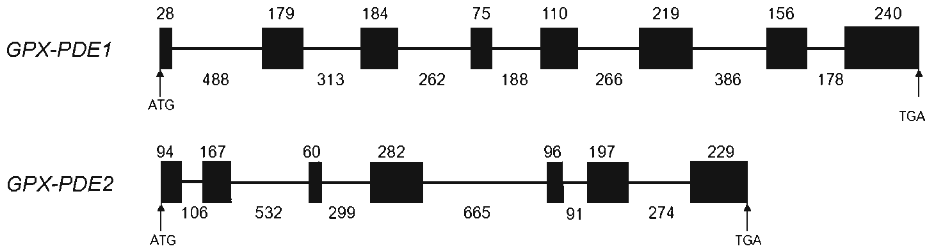
FILSQENGVVFEKRITELSLSEFLAYGPQRECGKDGKVLVRKTKDGKIVQ  150
   *              *                       *
WEVEQDDSLCTLEEAFLNVEPSLGFNIELKFDDHIVYHQDYLSHVLQAIL  200
          *
KVVFDNAKNRPIIFSTFQPDAASLVKKLQSTYPVFFLTNGGCEIYEDKRR  250
                                            *
NSLEEALKLCLENGLQGIVSEIKGVFRNPAIVTKIKESELSLLTYGSLNN  300
 *                                   *
VPEAVYMQHLMGIDGVIVDLVQEITEAVTNLITSAKVVVDEEGLNEKLKL  350
     *                           *
HSKPKFSQLELSFLLKLIPQLIQI  374
      *
```

Supplemental Figure S2. Analysis of Deduced Amino Acid Sequences of *GPX-PDE1* and *GPX-PDE2*.

(A) Predicted post-translational modification of *GPX-PDE1* and (B) *GPX-PDE2* deduced amino acid sequence. Predicted signal peptide is underlined, the putative N-glycosylation sites are boxed and the putative phosphorylation sites are indicated by asterisks. Numbers at the right indicate the position of amino acids.

Figure S3

A



B

```
>GPX-PDE1 promoter sequence
-1751 AACAAACTTTTTTCTACATAAAGAACTACGTAACTTTGATTCTCAGTTAG
-1701 CTATAGGGATACGTAAGAGACCTTACATTGTCAAGCACAATAACAAAAAT
-1651 TTGTCATTTTAATAATCAAATAACTTTAAAGTATAAATTAAGTCATGCAA
-1601 TTTAGTGATGAGTATTAGGGGTGAACGTGGGTCGGGTTGGGACGGGTTAA
-1551 GGTTTGTCCTTACCCGACCCTAAATGTTGGTCGGGTCATTTTTTTTAACC
-1501 TAGACCAGACCTTAGACTTGAAGTTAACGCGATCCTAAATATTCAAATGG
-1451 TCAACCTTTAAAACTCGGACTCGACCCTAGACCCGATTAAATATAATGTA
-1401 TCTCATTTTAGATAAAGTCTTCTAAATATTATTTATTATTGTGAATATGT
-1351 AATTTGACATATAAAATAATATATGTATATATATTATTAAACATTTACGT
-1301 ATGATGAAAAAATAGAAAATCATTTGTATTTTCAACAAAAAAGTATCATT
-1251 ACTTTATACACATTTGAATAGAGACACATACAATGATACACACATCAAGA
-1201 GTGAGTGATCATGGGACGAGTCATGTTTGGTTCGTACCCGACCCTAAATA
-1151 TTGATTGTGTCTAATTTTTGAACTCGAACTCGACCCTAAACCCAATGACA
-1101 CCCAATCCTATTCAGACCCGATCATGATCGGGCCATGCCGGATGAGCGGG
-1051 TTGGGTCTGGTCCTACTCACCCCTAAGGGGTACCATTTAAAATGGGTGGA
      G-box like                  W-box
-1001 CACTTGTGGGAGTAAACTTTTTAAGAAATTGACCTATTATAATATATGCC
                                             W-box
-951  TATTTAATGGAGTCTTACACCACAAATCATGTGTGAATATTGACCAATTA
-901  TAAAATTAATTAAATAATAATAAAATATAATATAATAATTAAGAACAATA
-851  AAATATATTTAAAATGTGTGTATACGATATAATAAGATATAAAAGTTTAT
-801  CTATTTTTCAATATAAATCATTATATTATCATTGGATAATTAATTAAGTA
-751  CTAATTTCATTTAGTAATTCATAATTAAATTGGAGAAAGAAATCTAGGGG
-701  AAAATAAATGGGTTCAACTTCTGAAATTGTTTCTCTACTCAAGAATCAAA
-651  AGTCCAATGTAATTGAACTAGAAGATTTTCTATATTTTTTACTATAAAAT
-601  ATAATGGTGACTTTAACAAAATCGTGTATCCGAAGATTAGGGTTAAACAA
-551  GAGCTTAAAAAGTCAAGTGGAATTAAGGATAAGCTAAAGAAATGGCATAG
-501  AACTTAACATTCAACATAGATTCCTTTCCTACTAATTCACACAACCACTT
-451  TGAAAGAAAGAAGAAAAAAAAAGGCATGATAGCTCATCTTTTTGTGCTATG
-401  TATATGTGTATATTAGAAACAACGGATTTAGAATATTGAAGTTTAGTATT
-351  TCTAAAAAAGAAAATAAAAAATATAGAAATTTTGTTGTATATTTTATGCCC
-301  CCACATACAACTCCCTTTGTCTTAAAATAAACACTTTATCTTTAAATATG
-251  ATACCATATGATGGGATAATTAATGAATAGTAGTTCCAGATATTGGGTT
-201  TCTATAAGAGGGTCGTGTCTATATTGGTATTGGTTTGAAGAGTGAAGACT
                                           P1BS
-151  CTTCTAAAGTCAATGGAATCAGAAAACAATACGGGGTATATTCTTAGACC
-101  CGATACACTATTTAAATCATATCAATTATCTATATATATGTACAAATAAG
-51   TTATAGCTTTCCAAAAACTACACTTTACAATCACAATTGGAGACAGGGGC
-1    CATG
```

Figure S3 (continued)

C

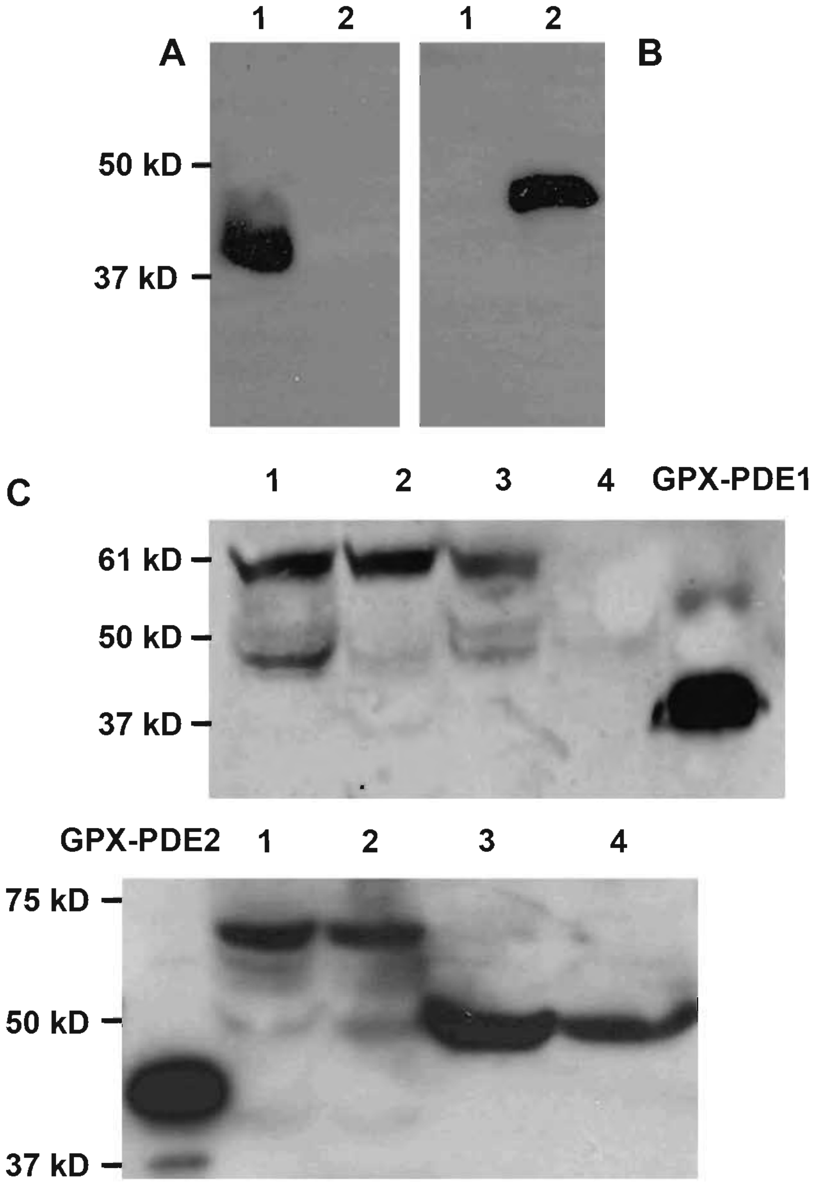
```
>GPX-PDE2 promoter sequence
-1772 CTGCTCAGTCATAGCTTTCCACTTCATAAGTGCTTCGTTCCTCTGCTGCC
-1722 AATAAAATTAAACATAAATGTTTGGAAAGTGCTATTAGAGACAGTAAACC
-1672 ATTGAATTGTTGAAATGCTCGCGAATTGTTTAACATTTACCTCCATCAAA
-1622 CTAATTTCACCTTTCTCTTGTTGCTTTGCAATTAGGTGTTCCATATCTCT
-1572 GCTATGCAGATGAGCTTGTTAAAGATTAACATATAGTAATCATACAAAAT
                               P1BS
-1522 TCTTTATTAAATTTGAGTTTTCAAGGTATATACTTCTTCATTTGGGCCAT
-1472 TTCTATTTTAAGAATTTCCAGTTCACCAATAGTATCAGCATTCTGAGACG
-1422 GAACATTGTCTGCCCTAAATGTAGATGGCAGTATCCAGTAAGGGTCGTTC
-1372 ACCCCAGCCTCCTGGCGGACCTTATCCAAGTTTGCACTCTCCAACCAATA
-1322 CTCCATTATTCCGCTGGTGTTGAACCTTCGTCTGAATAGCTCAGTTCCTC
-1272 CAGGAGCCACTTTACCGTCAATGTGCTTCAGTAAGTGGTCTAACAGTCCA
-1222 GTATCACCAATGTGCTTACGGGTGGCCATCCTTAGTGAAGGTTGGGTTAT
-1172 GGGATTTCCAGAAGTTGCACCTTCATCTTTTAAGACCTCCCACAAGTTTT
-1122 GCTCGGACAACTTATACCTGCATCTCACAGTTGTCTCAACTTAATATATA
-1072 TTACTAATAAAAATGACCAAAAACAGAAAGAATATCACACTATTATTTAC
                 G-box like                W-box
-1022 CTCTCATCTGACCACTTGTCCCTGCTTTCTTGCTTATTTGACTTCAGCTT
-972  GCTACCACTTTGGCTCTCACATAATCCTGCTTTTATCTCTCTAAGACGAT
-922  TACGACTAAGGCGCTTTCTTTTCTTAAATTTTGGCATGAAGATAGGTTTA
-872  GGTTTAATGTGTTTTTCTTCATCTTGTGGCTCCTCTTCCTCAGAGGCACT
-822  GGAAGTAAGCCTACTTCCATACTCTTTATGCTTACAGATGAACATGGCTT
-772  GATGACAAACACCCCAACGGTCCATCCTTTCAGCCTTCAGTTAAACATGG
-722  ATCATTTTAGAAATTTGATTCATTAATTTAGAAATATATTTAATTTAAAA
-672  AAGAAGAAGATAAATAGATAATAGTCGAGTCTTTTCATATTTAGAAATAC
-622  ATTAATATATTAATATATATTTAATATGTGAGAGATTCACTTACTCTAAG
-572  AGTAAATGTTTTAAACTTACTTCACATCTTAGTCACAAATTCTAGTGGAT
-522  CCAATTGTTTATATTAGTGAGTATATCTAAACCATTGATTTTCCCTAAAA
-472  TTAATGGATAAGATGTGGAGCAAGTTTAAAAAATTTACTCCTATAGTAGA
-422  TGGATTCCTCCTCATTTAATATTGTATCATATATAATAATAGTTTAATCT
-372  TAAATAAAAGTAATAAAAATAAATAACAATGTATATAAATTTGTACACTA
-322  AAATTATATAAATATTAATCTCTTAATTATCCATAATATTAAGCATCAAT
-272  AAATAAATAATAAATAAAATAAAATGTGAATAGATAAGAATTAAGAATAG
                          W-box
-222  TGGATTGATAAGTGTCATAATTGACTAAGAGGTGGACGTTGACAAAACAT
                  P1BS                         P1BS
-172  AGCAAGAATTGGAATATCCAGAGCATATAACTTAACACCAAGAATATTCA
           P1BS
-122  ATGCGAATATCCCTTTCTACATAACCTTTCTCTTTTTTCATATAAATACT
-72   CAAACCCATTTCATTTTTTCTCAACAACAATAACAATTTCTTGTTTATAC
-22   CCAATTTCTCTTCTTTCTTACTATG
```

Figure S3 (continued)

Supplemental Figure S3. Gene Structure and the 5' upstream Cis-element Analysis of *GPX-PDE1* and *GPX-PDE2*.

(A) Gene structure of *GPX-PDE1* and *GPX-PDE2*. Exons are indicated by the boxed regions and introns are represented by lines. Numbers indicate the length of the corresponding exon and intron region.
(B) Sequence of the 1681 bp 5' upstream region of *GPX-PDE1*. The following cis elements are highlighted: the P1BS element (PHR1 transcription factor binding site), two W-box elements (WRKY transcription factor binding site) and a G-box like element.
(C) Sequence of the 1743 bp 5' upstream region of *GPX-PDE2*. The following cis elements are highlighted: four P1BS elements, two W-box elements, one G-box like element and four TATCCA elements.
Element sequence: P1BS element, GNATATNC; W-box sequence, TTGACT/C; G-box element, CACGTG. Numbers to the left indicate the position from the translation start site (underlined and bold).

Figure S4

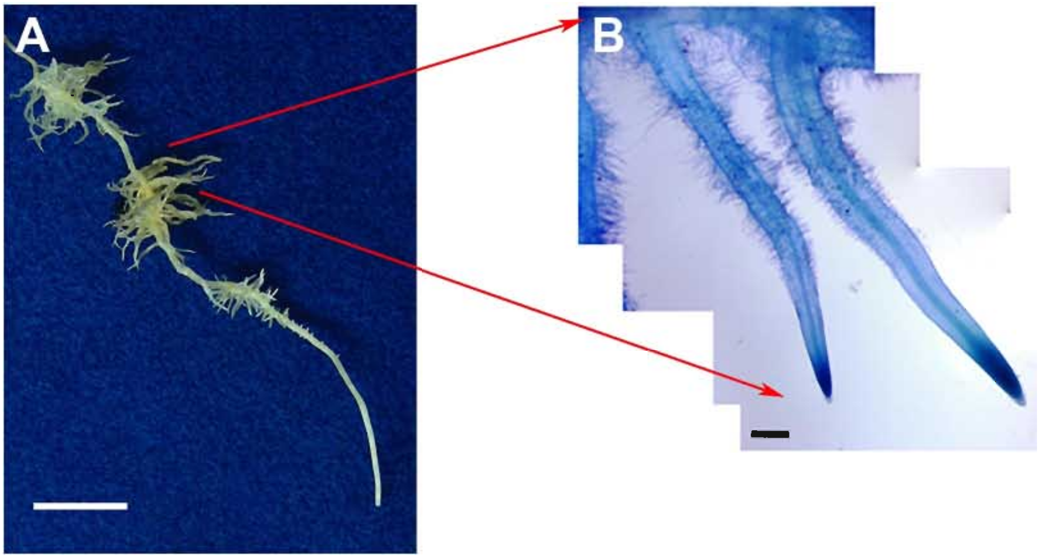


Supplemental Figure S4. Immunological detection of the GPX-PDE1 and GPX-PDE2 in Cluster Roots of White Lupin Grown Under Pi-sufficient and Pi-deficient Conditions.

(A) and (B) Immunological detection of GPX-PDE1 and GPX-PDE2. Recombinant LaGPX-PDE proteins were cleaved from GST with thrombin, electrophoresed on an SDS-PAGE gel, immunoblotted and the blots probed with (A) GPX-PDE1 antisera or (B) GPX-PDE2 antisera. Lanes 1 and 2 contain GPX-PDE1 and GPX-PDE2 proteins, respectively. Note the lack of cross reactivity between GPX-PDE1 and GPX-PDE2.

(C) SDS-PAGE gel immunoblot using GPX-PDE1 or GPX-PDE2 antiserum raised against recombinant GPX-PDE1 or GPX-PDE2 protein, following enhanced chemiluminescence detection showing expression of GPX-PDE proteins in a 25-75% $(NH_4)_2SO_4$ precipitated soluble protein and cell wall associated protein extracted from cluster roots of 14 d white lupin plants supplied with –Pi (0 mM) and +Pi (1 mM). Lanes labeled as GPX-PDE1 and GPX-PDE2 are GST cleaved purified recombinant protein; lane 1, -Pi cluster root protein precipitated by 25-75% $(NH_4)_2SO_4$; lane 2, +Pi cluster root protein precipitated by 25-75% $(NH_4)_2SO_4$; lane 3, -Pi cell wall associated protein; lane 4, +Pi cell wall associated protein. Lanes 1-4 were loaded with 40 µg of protein.

Figure S5



Supplemental Figure S5. Cluster Root Development in White Lupin Grown under Pi-Deficient Conditions.

(A) Phosphorus stress induced white lupin cluster roots appear as waves along secondary roots. Cluster roots from Pi-deficient white lupin 14 days after emergence can comprise greater than 60% of the root mass (Johnson et al., 1994; Keerthisinghe et al., 1998). Note that cluster roots also form on Pi-sufficient roots but comprise 10% or less of the total root mass. Bar = 1 cm.

(B) Rootlets in the most mature zone of cluster roots are densely covered with root hairs. Rootlets and root hairs stained with methylene blue. Bar = 1 mm.

Figure S6

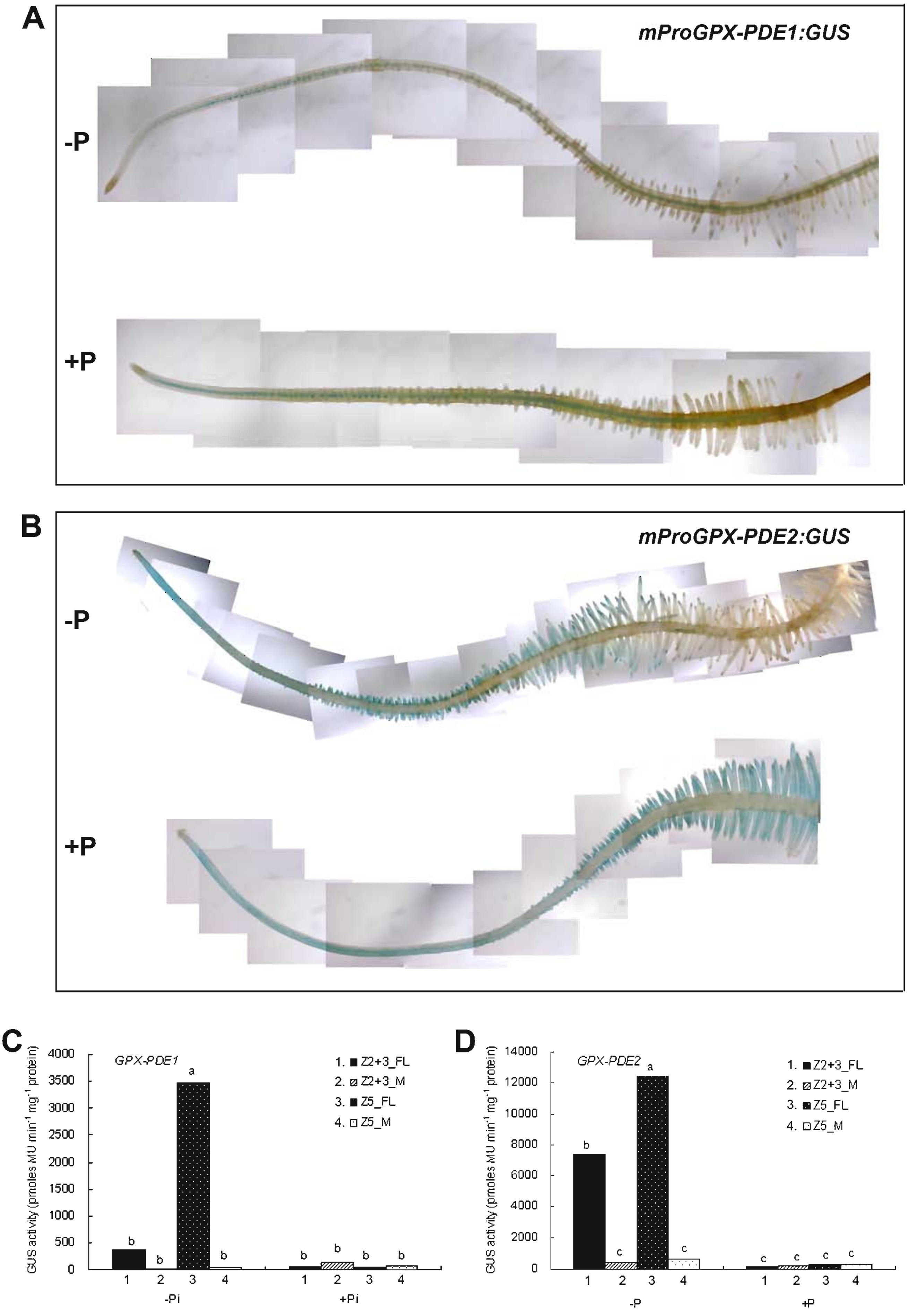

A
mProGPX-PDE1:GUS
-P
+P
B
mProGPX-PDE2:GUS
-P
+P
C
GPX-PDE1
GUS activity (pmoles MU min⁻¹ mg⁻¹ protein)
4000
3500
3000
2500
2000
1500
1000
500
0
b
b
a
b
b
b
b
b
1 2 3 4
-Pi
1 2 3 4
+Pi
1. ■ Z2+3_FL
2. ▨ Z2+3_M
3. ■ Z5_FL
4. □ Z5_M
D
GPX-PDE2
GUS activity (pmoles MU min⁻¹ mg⁻¹ protein)
14000
12000
10000
8000
6000
4000
2000
0
b
c
a
c
c
c
c
c
1 2 3 4
-P
1 2 3 4
+P
1. ■ Z2+3_FL
2. ▨ Z2+3_M
3. ■ Z5_FL
4. □ Z5_M

Figure S6 (continued)

Supplemental Figure S6. GUS Reporter Gene Activity Driven by the P1BS Mutated Promoter of *GPX-PDE1* or *GPX-PDE2* in Pi-deficient and Pi-sufficient Cluster Roots of White Lupin.

Histochemical localization of GUS activity directed by the P1BS mutated *GPX-PDE1 and GPX-PDE2* promoter (*mProGPX-PDE1:GUS* and *mProGPX-PDE2:GUS*) was evaluated using *A. rhizogenes* mediated white lupin transformation system. Transgenic plants were grown under Pi-deficient (0 Pi) and Pi-sufficient (1 mM Pi) conditions for 4 weeks. Transgenic hairy roots were harvested and stained with GUS solution and incubated at 37°C for 1 h.

(A) GUS staining in hairy roots containing the *mProGPX-PDE1:GUS* construct was abolished in both Pi-sufficient and Pi- deficient plants.
(B) GUS staining in hairy roots containing the *mProGPX-PDE2:GUS* construct was strongly reduced in both Pi-sufficient and Pi- deficient plants.
(C) and (D) MUG assays confirmed the negative effect of P1BS mutagenesis on the response of lupin *GPX-PDE1* (C) and *GPX-PDE2* (D) to Pi starvation. The reduction of MUG activity in the P1BS mutated tissue (M) is compared to the MUG activity of the full length promoter (FL). Z2+3, cluster root zone 2 and 3 tissue pooled; Z5, cluster root zone 5 tissue. Lower case letters denote significant differences between treatments ($P < 0.05$). Statistical significance based on four biological replicates.

Supplemental Table 1. In vitro enzyme activity for recombinant produced GPX-PDE1 and GPX-PDE2. Activity represents the average of two assays with protein derived from at least two independent transformants selected for each construct.

	GPX-PDE1	GPX-PDE2
	nmol/min/mg protein[a]	
GPC-PDE, Ca^{2+} [b]	68	0
GPC-PDE, Mg^{2+}	0	207
GPI-PDE, Ca^{2+} [c]	0	0
GPI-PDE- Mg^{2+}	0	714

[a] No detectable activity in the absence of Ca^{2+} or Mg^{2+}

[b] Ca^{2+} or Mg^{2+} dependent glycerophosphocholine activity

[c] Ca^{2+} or Mg^{2+} dependent glycerophosphoinositol activity

Supplemental Table 2. Oligonucleotides Used in this Study.

Primer name	Sequences (5' - 3')	Description
GPX-PDE1sF	ATCATTGGCTGCACTGCAATC	Quantitative PCR for cluster root zones, Pi/Phi resupply, dark/light treatment and RNAi
GPX-PDE1sR	CGCGATGTGCAATGTTATATGG	
GPX-PDE2sF	ACAAAGATCAAGGAATCTGAAC	Quantitative PCR for cluster root zones, Pi/Phi resupply, dark/light treatment
GPX-PDE2sR	TAATTCTAAAGCCTATCAGTGTG	
GPX-PDE2qF	CAGCCAGATGCTGCATGACTAG	Quantitative PCR for RNAi
GPX-PDE2qR	CCTTGCAACCCATTCTCCAA	
SAP1qF	AACACCACACGGCAGTTTTGG	Quantitative PCR for RNAi
SAP1qR	TCTGTAAACCTTCCCCAGGTG	
PT1qF	TGGGCCGAATTTACTACCACG	Quantitative PCR for RNAi
PT1qR	CATCAGGGTCATGCCATACAC	
GPX-PDE1RTF	GTTGCTCATCATTGGCTGCACTG	RT PCR for RNAi
GPX-PDE1RTR	CCAGTGACATTCTCTCCTTGGAC	
GPX-PDE2RTF	CGCGGATCCATGGCTCTTAAAGCTTTTC	RT PCR for RNAi
GPX-PDE2RTR	GCAGCATCTGGCTGGAAAGTTG	
SAP1RTF	GGAACGGCCCTACTGTATGTTG	RT PCR for RNAi
SAP1RTR	CCAAGGTGCATGCATGAGAACG	
PT1RTF	GGGAAGCCTGGTACATTGCCTC	RT PCR for RNAi
PT1RTR	GTGGAACAGTTGAACCAACTGG	
GSTGPX-PDE1F	CGCGGATCCTCTGTTTCCATGGCTTC	Construction of plasmids for whole and truncated coding region expression in E.coli
GSTtGPX-PDE1F	CGCGGATCCCCTCTACAAACATTTC	
GSTGPX-PDE1R	CCGGAATTCCTTGTCAACTTCTCAATAAGA	

Supplemental Table 2 (continued from previous page).

Primer name	Sequences (5' - 3')	Description
GSTGPX-PDE2F	CGCGGATCCGCTCTTAAAGCTTTTC	Contruction of the plasmid for expression in E.coli
GSTGPX-PDE2R	CCGGAATTCTGGCTTTTACTTTCAAATCTG	
ProGPX-PDE1GUSF	CCCAAGCTTCCTTACATTGTCAAGCAC	Construction of the plasmids for GPX-PDE1 promoter:GUS and P1BS mutated promoter:GUS
ProGPX-PDE1GUSR	TGCTCTAGAGCCATGGAAACAGACATG	
mProGPX-PDE1GUSF	AAACAATACGGGGTCCATTCTTAGACCCG	
mProGPX-PDE1GUSR	GGTCTAAGAATGGACCCCGTATTGTTTTC	
ProGPX-PDE2GUSF	CCCAAGCTTGTGCTTCGTTCCTCTGCTGC	Construction of the plasmids for GPX-PDE2 promoter:GUS and P1BS mutated promoter:GUS
ProGPX-PDE2GUSR	TGCTCTAGAGCTTTAAGAGCCATAGTAAG	
m12ProGPX-PDE2GUSF	CTTAACACCAAGACCATTCAATGCGACCATCCCTTTCTACAT	
m12ProGPX-PDE2GUSR	GTAGAAAGGGATGGTCGCATTGAATGGTCTTGGTGTTAAGTT	
m3ProGPX-PDE2GUSF	TAGCAAGAATTGGACCATCCAGAGCATATAAC	
m3ProGPX-PDE2GUSR	TATATGCTCTGGATGGTCCAATTCTTGCTATG	
m4ProGPX-PDE2GUSF	GAGTTTTCAAGGTCCATACTTCTTCATTTGG	
m4ProGPX-PDE2GUSR	AAATGAAGAAGTATGGACCTTGAAAACTCAA	

Supplemental Table 2 (continued from previous page).

Primer name	Sequences (5' - 3')	Description
GPX-PDE1GFPF1	GCTCTAGAGAGACCTTACATTGTCAAGCAC	Construction of the plasmid for GPX-PDE1:EGFP
GPX-PDE1GFPF2	CAGGGGCCATGTCTGTTTCCATGGCTTCC	
GPX-PDE1GFPR1	AAGCCATGGAAACAGACATGGCCCCTGTC	
GPX-PDE1GFPR2	CGCGGATCCGACCAAGGAAGCAATTTTATGC	
RNAiGPX-PDE1F	CACCAAATATGGATACAAGGGTTC	Construction of the plasmids for GPX-PDE1 and GPX-PDE2 RNAi
RNAiGPX-PDE1R	AAGACCCTGGCATACAAAATGAGC	
RNAiGPX-PDE2F	CACCGAAATTGCAAAGCACATACC	
RNAiGPX-PDE2R	GCCTATTCTATTAGTGTGAAGGAC	
pCu416GPX-PDE1F	CGCGGATCCATGTCTGTTTCCATGGC	Construction of plasmid for whole coding region and truncated GPX-PDE1 yeast complementation
pCu416tGPX-PDE1F	CGCGGATCCATGCCTCTACAAACATTTC	
pCu416GPX-PDE1R	CCGGAATTCCTTGTCAACTTCTCAATAAGA	
pCu416GPX-PDE2F	CGCGGATCCATGGCTCTTAAAGCTTTTC	Construction of plasmid for GPX-PDE2 yeast complementation
pCu416GPX-PDE2R	CCGGAATTCTGGCTTTTACTTTCAAATCTG	
α-TubulinF	GCCTGATGGACAAATGCC	RT PCR for RNAi
α-TubulinR	GCCTGCAAATGTCATAGATAGC	
LysoPLase 1F	CCTGACCAACTCAAAGCCACCG	Quanitative PCR for cluster roots
LysoPLase 1R	GGAAGAAGTGGAGCGAGGTAGC	
LysoPLase 2F	CACTGCGGACGAGTTCTACGC	Quanitative PCR for cluster roots
LysoPLase 2R	GGTGATCGATGGCGCAGGTGGC	

Supplemental Table 3. Yeast Strains Used in This Study.

Strain	Relevant Genotype	Genotype	Source
JPV125	*gde1Δ*	*his3Δ1, leu2Δ0, met15Δ0, ura3Δ0, YPL110c::KanMX, MATa*	Research Genetics
JPV203	wild type	*his3Δ1, leu2Δ0, met15Δ0, ura3Δ0, MATa*	Research Genetics

```
#MEGA
!Title alignment;
!Format
  DataType=Protein
  NSeqs=30 NSites=1347
  Identical=. Missing=? Indel=-;


!Domain=Data;
#La_GPX-PDE2   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#Gm19g27060    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#Sc_GDE1       MKFGKTFANH RIPEWSSQYV GYKSLKKMIK EITRLQEDIY RAHNKNSYDE GRPPTKMRDS SNSAQNYLDS PKIQKLLASF  [  80]
#Ec_glpQ       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#Ec_ugpQ       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#Sc_PGC1       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#At1g66980     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#At3g20520     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#At5g58050     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#At5g43300     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#At5g58170     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#Gg_GDE2       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#Mm_GDE3       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#Gm17g08680    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#Os03g40670    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#Stc_glpQ1     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#Stc_glpQ2     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#At5g41080     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#At3g02040     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#At1g71340     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#Hs_GDE1/Mir16 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#Os02g31030    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#At1g74210     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#At5g55480     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#Sb03g035370   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#At4g26690     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#At5g08030     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#Sb04g021010   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#La_GPX-PDE1   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]
#At1g66970     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [  80]

#La_GPX-PDE2   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 160]
#Gm19g27060    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 160]
#Sc_GDE1       FFAVDRDIEK VDTFYNSQYA EYKKRFERLL SSNQFNEIKS TLVVDANKED AVAQTLLTKD TREMNMLLKG TSQASRLSYH  [ 160]
#Ec_glpQ       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 160]
#Ec_ugpQ       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 160]
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#Sc_PGC1      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 160]
#At1g66980    ---------- ---------- ---------- ---------- ---------- ---------- -------MNS QQSTRTKQML  [ 160]
#At3g20520    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 160]
#At5g58050    ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----MLRFF  [ 160]
#At5g43300    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 160]
#At5g58170    ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----MLRFI  [ 160]
#Gg_GDE2      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 160]
#Mm_GDE3      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 160]
#Gm17g08680   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 160]
#Os03g40670   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 160]
#Stc_glpQ1    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 160]
#Stc_glpQ2    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 160]
#At5g41080    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 160]
#At3g02040    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 160]
#At1g71340    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 160]
#Hs_GDE1/Mir16 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 160]
#Os02g31030   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 160]
#At1g74210    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 160]
#At5g55480    ---------- ---------- ---------- ---------- ---------- ---------- -------MIN MRDNPTMHVL  [ 160]
#Sb03g035370  ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 160]
#At4g26690    ---------- ---------- ---------- ---------- ---------- ---------- ---------- MRG-----LL  [ 160]
#At5g08030    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 160]
#Sb04g021010  ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 160]
#La_GPX-PDE1  ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 160]
#At1g66970    ---------- ---------- ---------- ---------- ---------- ---------- -------MNS RPSNPTKLVI  [ 160]

#La_GPX-PDE2  ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 240]
#Gm19g27060   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 240]
#Sc_GDE1      KDDLIEIQSI LAELRKQFRN LKWYAELNKR AFGKILKKLD KKVGTNQQMS TMKTRILPLQ FANDSLITKD LSLLKTIWEQ  [ 240]
#Ec_glpQ      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 240]
#Ec_ugpQ      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 240]
#Sc_PGC1      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 240]
#At1g66980    QQSSTHLLCG VVLLQLFAAQ VDAQ--RSTS PWQTLSGDAP LVIARGGFSG LFPDSSLAAY QFAMVVSVAD VVLWCDVQLT  [ 240]
#At3g20520    --MACPRVIF LILITFFILQ TAFS-----S SWQTLSGKPP AVIARGGFSG MFPDSSIQAY QLVNITTSPD VMLWCDLQLT  [ 240]
#At5g58050    ILFSLFLHSS VAAPKTPAAA AAVP----AK KWLTLNGQEP AVVARGGFSG LFPESSISAN DLAIGTSSPG FTMLCNLQMT  [ 240]
#At5g43300    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 240]
#At5g58170    IFFSLFIHLC VAAPQTPAAA AAVP----AK KWLTLNGQEP AVVARGGFSG LFPESSASAN DLAIGTSSPG LTMLCNLQMT  [ 240]
#Gg_GDE2      ---------- ---------- ---------- ---------- ---------- ---------- ---------- --MVKHQPLQ  [ 240]
#Mm_GDE3      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---MADSPGC  [ 240]
#Gm17g08680   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 240]
#Os03g40670   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 240]
#Stc_glpQ1    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 240]
#Stc_glpQ2    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 240]
#At5g41080    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 240]
#At3g02040    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 240]
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#At1g71340     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 240]
#Hs_GDE1/Mir16 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 240]
#Os02g31030    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 240]
#At1g74210     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 240]
#At5g55480     Q-ASKFLFLA LILIQLLSTQ LFAQ--RSKS PWQTLTGDAP LVIARGGFSG LLPDSSLDAY SFVSQTSVPG AVLWCDVQLT  [ 240]
#Sb03g035370   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 240]
#At4g26690     R-ASSLLLCG VILIQLLAAQ IHAQSKKPKS PWPTLTGDPP LVIARGGFSG LFPDSSYDAY NFAILTSVPD AVLWCDVQLT  [ 240]
#At5g08030     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 240]
#Sb04g021010   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 240]
#La_GPX-PDE1   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 240]
#At1g66970     R-SSTLLFCG VVLIHLFAAQ IDAQ--RSTS RWQTLNGDAP LVIARGGFSG LYPDSSIAAY QLATLTSVAD VVLWCDLQLT  [ 240]

#La_GPX-PDE2   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 320]
#Gm19g27060    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 320]
#Sc_GDE1       VTFRINSYER VMRSTSPNAN ANDNTEFFKI ICVFIEEDDS KGLIRELTNL YSELSLIPTR IMISVLNKAA LSKSLACIDA  [ 320]
#Ec_glpQ       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 320]
#Ec_ugpQ       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 320]
#Sc_PGC1       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 320]
#At1g66980     KDGHGICFPD LNLANASNSE EVYPNRQKSY PVNGVTTKGW FPIDFSLTEL QKVLFSLIRG ILSRSGKFDE NGYSISTVQN  [ 320]
#At3g20520     KDGVGICFPN LKLDNGSNVI RIDPHYKER- ---------- FSVDFTWKEL SD--VKLAQG VVSRPYIFDD VS-SILAIEE  [ 320]
#At5g58050     KDGVGLCLSD IRLDNATTIS SVFPKAQKTY KVNGQDLKGW FVIDYDADTI FN-KVTLVQN IFSRPSIFDG QM-SVSAVED  [ 320]
#At5g43300     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 320]
#At5g58170     KDGVGLCLSD IILDNATTIS SVFPKAQKTY KVNGQDLKGW FVLDYDADTI FN-NVTLVQN IFSRPSIFDG QM-SVSAVED  [ 320]
#Gg_GDE2       YYEPQLCLSC LTGIYGCRWK RYQRSH---- ---------- ---------- ---------- -------DDT TKWERLWFLI  [ 320]
#Mm_GDE3       CSIWARCLHC L---YSCHWR KYPKQK---- ---------- ---------- ---------- -------MQT SKCDCIWFGL  [ 320]
#Gm17g08680    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 320]
#Os03g40670    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 320]
#Stc_glpQ1     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 320]
#Stc_glpQ2     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 320]
#At5g41080     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 320]
#At3g02040     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 320]
#At1g71340     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 320]
#Hs_GDE1/Mir16 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 320]
#Os02g31030    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 320]
#At1g74210     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 320]
#At5g55480     KDAIGLCFPD VKMMNASNIQ DVYPKRKTSY LLNGVPTQDW FTIDFNFKDL TK--VILKQG ILSRSAAFDG NSYGISTVKD  [ 320]
#Sb03g035370   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 320]
#At4g26690     KDALGICFPD LTMRNSSSIE AVYPTRQKSY PVNGVPTSGW FTIDFSLKDL KD--VNLIRG ILSRSKKFDG NSNPIMTVQS  [ 320]
#At5g08030     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 320]
#Sb04g021010   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 320]
#La_GPX-PDE1   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 320]
#At1g66970     KDGLGICFPD LNLANASTID RVYPNREKSY SVNGVTTKGW FPNDFSLTEL QN--FLLIRG ILSRTDRFDG NGYLISTIED  [ 320]

#La_GPX-PDE2   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 400]
#Gm19g27060    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 400]
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#Sc_GDE1      ILKVIPSLND SEDINRRNFF HHHIIAIGKL IRKQEILSRK KKSQPSKYTN SEGEIVTDLR TLHTTLSAPA ESDSITEEEK  [ 400]
#Ec_glpQ      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 400]
#Ec_ugpQ      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 400]
#Sc_PGC1      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 400]
#At1g66980    VATQMKPALF WLNVQHDEFY EQHNLSMSSF LLSTSRTVSI DFISSPEVNF FRKIAGGFGN NGPSFVFQFM GKEDFEPTTN  [ 400]
#At3g20520    VA-KLTASGL WLNIQDSAFY AKHNLSMRNS VVSLSRRLKV NFISSPGISF LKSMKNSVKP TVTKLIFRFL KQEHIEPFTN  [ 400]
#At5g58050    VLGTKPPK-F WLSVQYDAFY MEHKLSPAEY LRSLRFRG-I NVISSPEIGF LKSIGMDAGR AKTKLIFEFK DPEAVEPTTN  [ 400]
#At5g43300    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 400]
#At5g58170    VLGTKPPK-F WLSVQYDAFY MEHKLSPAEY LRSLQFRG-I NVISSPEIGF LKSIGMDAGR AKTKLIFEFK DPEAVEPTTN  [ 400]
#Gg_GDE2      LTSSFFLTLV WFYFWWEVHN DYNEINWFLY NRMG------ -YWSDWSIPI LVTTAAGFTY ITVLLILALC HIAVGQQMNL  [ 400]
#Mm_GDE3      LFLTFLLSLG WLYIGLILLN DLHNFNEFLF RHWG------ -HWMDWSLIV LLVVSLLVTY ASLLLLLGLL LQLCGQPLHL  [ 400]
#Gm17g08680   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 400]
#Os03g40670   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 400]
#Stc_glpQ1    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 400]
#Stc_glpQ2    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 400]
#At5g41080    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 400]
#At3g02040    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 400]
#At1g71340    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 400]
#Hs_GDE1/Mir16 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 400]
#Os02g31030   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 400]
#At1g74210    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 400]
#At5g55480    ISTQLKPEGF WLNVQHDAFY AQHNLSMSSF LLSISKTVII DYLSSPEVNF FRNIGRRFGR NGPKFVFRFL EKDDVEVSTN  [ 400]
#Sb03g035370  ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 400]
#At4g26690    VSTQMKPSFF WLNVQHDAFY AQHNLSMSSF LVAASKTVLI DFISSPEVNF FKKIAGRFGR NGPSLVFRFL GQDEFEPTTN  [ 400]
#At5g08030    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 400]
#Sb04g021010  ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 400]
#La_GPX-PDE1  ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 400]
#At1g66970    VVTTLNREGF WLNVQHDAFY EQQNLSMSSF LLSVSRTVSI DFISSPEVNF FKKITGSFGR NGPTFVFQFL GKEDFEPTTN  [ 400]

#La_GPX-PDE2  ---------- ---------- ---------- ---------- --------MA LK------AF HVSDIPSIDI VP--ETH-LS  [ 480]
#Gm19g27060   ---------- ---------- ---------- ---------- --------.. ..------.V ..T.V..L.L ..--.NAS.A  [ 480]
#Sc_GDE1      SSACTLSYIL EELPIHLRPC LFQHDNYKRT PLHYSCQYGL SEVTKLIIKL M.EWNIWNEI PID.VSAFGD AESLTPLH.C  [ 480]
#Ec_glpQ      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------M  [ 480]
#Ec_ugpQ      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 480]
#Sc_PGC1      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 480]
#At1g66980    RTYGSILSNL SFVKTFASGI LVPKSYILPL DDKQYLLPHT SLVQDAHKAG ..LYASGF.N D.DIAYNYSW D.--VSEY..  [ 480]
#At3g20520    QSYGSLAKNL SYIRTFSSGI LVPKSYIWPV DSALYLQPHT SLVTDAHKEG .QVFASEF.N DFVIAYNYSY D.--TAEY..  [ 480]
#At5g58050    KKYSEIQQNL AAIKAFASGV LVPKDYIWPI DSAKYLKPAT TFVADAHKAG .EVYASGF.N DLRTSFNYSY D.--SAEY.Q  [ 480]
#At5g43300    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 480]
#At5g58170    KKYSEIQQNL AAIKAFASGV LVPKDYIWPI DSAKYLKPAT TFVADAHKAG .EVYASGF.N DLRTSFNYSY D.--SAEY.Q  [ 480]
#Gg_GDE2      HWLHKIGLMT TLITTVVT-- -MSSIAQLWD DEWEMVFISL QATAPFLHIG ALAAVTALSW LIAGQFARME KA--TSQM.M  [ 480]
#Mm_GDE3      HSLHKVLLLL IVLLVAAG-- -LVGLDIQWR QEWHSLRLSL QATAPFLHIG AVAGITLL.W P.A.TFYRIH PR--GPKV.L  [ 480]
#Gm17g08680   ---------- ---------- ---------- ---------- ---------- ---------- ---MASLPSF A.--FVFL.L  [ 480]
#Os03g40670   ---------- ---------- ---------- ---------- ---------- ---------- ---MAAFWL. SI--IVLV.L  [ 480]
#Stc_glpQ1    ---------- ---------- ---------- ---------- ---------- ------MGTQ ESDERAGGGT GR--RALLGA  [ 480]
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#Stc_glpQ2     ---------- ---------- ---------- ---------- ---------- ---------- ---------- --------MH  [ 480]
#At5g41080     ---------- ---------- ---------- ---------- --------.. .R------TV L...V..LPD SV--YGLSEG  [ 480]
#At3g02040     ---------- ---------- ---------- ---------- --------.S ..------.I ...EV..L.H F.--.NPS.I  [ 480]
#At1g71340     ---------- ---------- ---------- --------MA IFEWRHRRRP FDGGGTRRRR FF.PLY.RNF KR---.ILFA  [ 480]
#Hs_GDE1/Mir16 ---------- ---------- ---------- ---------- --------.W .WEDQGGLLG PF.FLLLVLL LVTRSPVNAC  [ 480]
#Os02g31030    ---------- ---------- ---------- ---------- --------.. .-------DV LAAGA.ATSA IL--AEVDAA  [ 480]
#At1g74210     ---------- ---------- ---------- ---------- ---------- ---------- ---M.LTRCL PL--IWLS.L  [ 480]
#At5g55480     QTYGSLAGNL TFLKTFASGV LVPKSYIWPI ES-QYLLPRT SFVQDAHKAG .EVYASGFGN DFDLAYNYSF D.--LAEY..  [ 480]
#Sb03g035370   ---------- ---------- ---------- ---------- ---------- ---------- ---MR..LYC A.--LFLL.L  [ 480]
#At4g26690     RTYGSILSNL TFVKTFASGI LVPKSYILPL DDQQYLLPHT SLVQDAHKAG .EVFVSGF.N DIDIAHDYSF D.--VSEY..  [ 480]
#At5g08030     ---------- ---------- ---------- ---------- ---------- ---------- ---MAFKYLL PL--LLLS.L  [ 480]
#Sb04g021010   ---------- ---------- ---------- ---------- --------.. .LKAARVADV PTL.VVAPGL .V--.AGTA.  [ 480]
#La_GPX-PDE1   ---------- ---------- ---------- ---------- ---------- ---------M S..MAS.TSF AS--LVFM.L  [ 480]
#At1g66970     RTYGSILSNL TFVKTFASGI LVPKSYILPL DDEQYLVPHT SLVQDAHKAG .QVYVSGF.N D.DIAYNYSS D.--VSEY..  [ 480]


#La_GPX-PDE2   LHSTPFSNGV K-----FKVP EFVVIGHRGY G--------M NALQSLDRRM KAIKENSIMS FNAAANFPIH FIEF-DVQVT  [ 560]
#Gm19g27060    .C.SR.P..L EMCRSGLEI. K........N .--------. .V...S.... R.....T... .....T..LD ....-.....  [ 560]
#Sc_GDE1       VLGAHPKTTE VLLQSLDPNV KLKSSSLLHL ATEWNNYPLL HV.L.SK.FD INYQD.ELHE TPLYLACRLN .F.AAVCLLY  [ 560]
#Ec_glpQ       KLTLKNLSMA IMMSTIVMGS SAMAADSN-- ---------E KIVIAHRGAS GYLP.HTLPA KAM.YAQGAD YL.Q-.LVM.  [ 560]
#Ec_ugpQ       ---------- ---------- ---MSNWP-- ---------Y PRIVAHRGGG .LAP..TLAA IDIG.KYGHK M...-.AKLS  [ 560]
#Sc_PGC1       ---------- ---------- ---------- ---------. VEIVGHRAFK ARYP..TLLA .EK.YAAGAD V..T-.L.M.  [ 560]
#At1g66980     FVDNGNFSVD GMLSDFPLTA SAS.DCFSHI .-RNATKQVD FLVI.KNGAS GEYPGCTKLA YEK.IKDGSD V.DC-P..MS  [ 560]
#At3g20520     FIDNGNFSVD GFLSDFPVT. YRAINCFSHV DPKRAKEQAK ITII.KNGAS GDFPGCTDLA YQR..SDGAD ILDC-N..MS  [ 560]
#At5g58050     FVDNGQFSVD GVITDFPPTA SQSITCFSHQ N-GNLPKAGH ALVITHNGAS GDYPGCTDLA YQK.IDDGAD I.DC-S..MS  [ 560]
#At5g43300     ---------- ---------- ----M....F .--------. .M...P.EK. .F.....LL. ..V..D...D ....-.....  [ 560]
#At5g58170     FVDNGQFSVD GVITDFPPTA SQSITCFSHQ N-GNLPKAGH ALVITHNGAS GDYPGCTDLA YQK.VDDGAD V.DC-S..MS  [ 560]
#Gg_GDE2       VTAYLAVVVA LYLVP-LTIS SPCIMEKKAL .-------PK P.IIGHRGAP MLAP..TL.. .QK.VEQK.Y GVQA-..ILS  [ 560]
#Mm_GDE3       .LLFFGVTL. IYLMPLLFIS SPCIMKL.DL P-------PK PG.VGHRGAP MLAP..TL.. LRKT.ECGAA VF.T-..M.S  [ 560]
#Gm17g08680    VIGSNARTLY PLPSKGGNGS RKPLQTF.-- ---------- PYNIAHRGSN GELP.ETRPA YLR.IEEGAD ...T-..LSS  [ 560]
#Os03g40670    SGESNANPAA SQQSQLDVNH RKPLQTF.-- ---------- PYNIAHRGSN GE.P.ETTAA YLR.IEEGAD ...S-.ILA.  [ 560]
#Stc_glpQ1     AVLGAGGAVL GLPGTARAAG TRHGG..G.G V----GSLPV PTVIGHRGAS GYRP.HTFG. YEL.LDLGAD IV.AG.LVP.  [ 560]
#Stc_glpQ2     VRAVAVTTTA LLGVALTAPL SHARADEA.D D--------G PTVVAHRGAS GYAP..TLAA VDR..ELG.R WV.N-...R.  [ 560]
#At5g41080     .ELSKPTS-- ------.RL. G.S......I .--------. .V...S...A RGV.....L. ..S..KY..D ....-.....  [ 560]
#At3g02040     CS.RKAN.-- ---------- K...V....H .--------. .MS..P.L.F S.L.....L. ....SK..LD ....-.....  [ 560]
#At1g71340     VIFLAIFPPL YFHFKLRRIR QI.AQKCDWL H-------HP PLVCAHGGDS TLAFP.TMDA YSF.IRSRVD C..V-..SRS  [ 560]
#Hs_GDE1/Mir16 .LTGSLFVLL RVFSFEPVPS CRALQVLKPR D--------R ISAIAHRGGS HDAP..TLAA IRQ..KNGAT GV.L-.IEF.  [ 560]
#Os02g31030    GARSAAAG.G G----GGGGQ R.A......K .--------. ...A.P.... QEV....LR. ..E..R..VD YV..-.....  [ 560]
#At1g74210     TVCAAGRTLH PLPVKGP.TV KLQLQTS.-- ---------- PYNIAHRGSN GE.P.ETTAA YLK.IEEGTD ...T-.ILSS  [ 560]
#At5g55480     FMDNGDFSVD GLLSDFPLTA SSA.DCFSHL .-SNASSQVD FLVI.KNGAS GDYPGCTDLA YTK.IKDGAD V.DC-SL.MS  [ 560]
#Sb03g035370   ..LAFARPLF PLPSKTKYEE KKPIQTF.-- ---------- PYNIAHRGSN GE.P.ETAAA YLR.IEEGAD ...S-.ILAS  [ 560]
#At4g26690     FVDNGNFSVD GVLSDFPITA SASLDCFSHV .-RNATKQVD FLVITK.GAS GDYPGCTDLA YKK.IKDGAD V.DC-S..LS  [ 560]
#At5g08030     VANCASRPLY RLPSEAKHAT KKPLQTS.-- ---------- PYNLAHRGSN GELP.ETAPA YMR.IEEGAD ...T-.ILSS  [ 560]
#Sb04g021010   VATMVK.G.G G----GGGGG R.S......K .--------. ...A.A.P.. QEVR..TVR. ..D..R..VD YV..-.....  [ 560]
#La_GPX-PDE1   IIGCTAIPVY PIHRHVQHGS RKPLQTF.-- ---------- PYNIAHRGSN GELP.ETAPA YLR.IEEGAD ...T-.ILSS  [ 560]
#At1g66970     FVDNGDFSVD GVLSDFPITA SAA.DCFSHI .-RNATKQVD FLVI.K.GAS GDYPGCTDLA YEK.IKDGAD V.DC-S..MS  [ 560]
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#La_GPX-PDE2   NDDCPVIFHD DFILSQENGV VFEKRITELS -LSEFLAYGP QRECGKDGKV -LVRKTKDGK IVQWE----- ----------  [ 640]

#Gm19g27060    R......... .L..TE...T ..G....... -.....S... ...DE.E.N. -.L..-.... .M..D----- ----------  [ 640]

#Sc_GDE1       .GADLE.REK L.GWTAIFVA AA.GFTDIVK -.LIANNANF DI.DEGGWTP -MEHAVLR.H LHIADMVQIR DELVTHPHSQ  [ 640]

#Ec_glpQ       K..HL.VL.. HYLDRVTDVA DRFPDRARKD GRYYAIDFTL DEIKSLKFTE GFDIENGKKV QTYPG----- --RFPMG---  [ 640]

#Ec_ugpQ       K.GEIFLL.. .NLERTS..W GVAGELNWQD ---------L L.VDAGSWYS ----.AFK.- ---------- ----------  [ 640]

#Sc_PGC1       S.GMV.VN.. SDTGRMWDKN LVIGES.WEE -VKRLRCKED GSLAMMTL.E I.TWAVCHPG AKLMLD---- ----------  [ 640]

#At1g66980     S.GI.FCSSS IDLVNSTTVG QTH-LRNRSI -IVPEIS-SV AGIFTFSLTW -HEIQSLTPA .SNPF-RENG MSRNPN----  [ 640]

#At3g20520     K.KI.FCMSS FDLINST.VI ETS-FRNLS. -VVSEINPRR SGIYTFSLTM -SQIQ.LKPT .SNL.-KDSG LFRNPR----  [ 640]

#At5g58050     K.GIAFCHDA ADLSAST-TA RTT-FMSRAT -SVPEIQ-PT NGIFSF.LTW -AEIQSVKPQ .ENPF-TATG FQRNPA----  [ 640]

#At5g43300     R.G....... I.MFT..Q.. II...V..MD -.H...S... ..D-.TNV.P -MW......R .FE.K----- ----------  [ 640]

#At5g58170     K.GIAFCHDA ADLTAST-TA MTI-FMSRAT -SVPEIQ-PT NGIFSF.LTW -AEIQSVKPQ .ENPF-TATG FQRNPA----  [ 640]

#Gg_GDE2       Y.GV.FLM.. KTLRRTT.VE EVFPGRAYEH -S.M.NWTDL EMLNAGEWFL -RNDPFWTAG SLSRS----- ---DYL----  [ 640]

#Mm_GDE3       S.GV.FLM.. ERLSRTT.VA SVFPERISAH -S.D.SWAEL ..LNAGTWFL -ERQPFWGA. KLSGS----- ---DRK----  [ 640]

#Gm17g08680    K.GVLIC... VTLDDTTDIA NHTGFANRKR -TY.VQGINM TGFFPV.FTL -KEL.SLRV. QRYSF----- --RDQQ----  [ 640]

#Os03g40670    K.GHLIC... VILDATTDIA NRTEFANRKR -TY.VERQNV TGWFVV.FTL -EEL.SLRV. QRYNF----- --RDQQ----  [ 640]

#Stc_glpQ1     K.GHL.CR.E PE.GGTTDVA DHREFADRKR -TKLLDGVST TGWFTE.FTL -AEL..LRAT ERIPA----- --NRPHNT--  [ 640]

#Stc_glpQ2     R.GEL.VL.. ESLARTTDVE EVFPDRSPWK -VKD.T.AEI A.LDAGSWFG -SEYAG---- ---------- ----------  [ 640]

#At5g41080     K......... ...Y.E...I .N.S.V.D.. -.....L... .K.TE.I..T -.M..S.E.. VLK.D----- ----------  [ 640]

#At3g02040     R.G..I.... ...Y.E.Q.. .Y...V..VC -....MS... ..DT..T..P -.L..S.E.. .HK.S----- ----------  [ 640]

#At1g71340     S.GVLFAL.N RDLQRIARNS SVQVGDLSMK QIK.LDVSEI VKGTLGS--- ---------- ---------- ----------  [ 640]

#Hs_GDE1/Mir16 S.GI..LM.. NTVDRTTD.T GRLCDL.FEQ --IRK.NPAA NHRLRN.FPD ---------- ---------- ----------  [ 640]

#Os02g31030    K.G....... N..FTK.D.K ILD..V.D.Q -.ED..L... .N.Q..G..P -.L..L...R ..N.N----- ----------  [ 640]

#At1g74210     K.GVLIC... CILDETT.VA SHKEFADRKR -TYDVQGFNI TGFFTF.FTL -KEL.QLRI. QRYAF----- --RDQQ----  [ 640]

#At5g55480     S.GI.FCLSS INLGEST.V. QSP-FRNRST -TVPEIG-SL PGIYSFSLAW -SEIQ.LRPA .ENPYSREFT MFRNPR----  [ 640]

#Sb03g035370   K.GTLIC... VTLDDTTDVA RRKEFANRRR -TY.VEWFNV SGWFVV.FTL -EEL..LKV. QRYSF----- --RDQK----  [ 640]

#At4g26690     S.GT.FCLSS IDLGNSTTVS LTA-FRNRST -TVPE.G-SL GAIYTFSLTW -AEIQ.LTPA .SNPY-RVTS LFRNPK----  [ 640]

#At5g08030     K.GVLICH.. VNLDDTTDVA DHKEFADRKR -TY.VQGMNM TGFFTV.FTL -KEL..LGA. QRYPF----- --RDQQ----  [ 640]

#Sb04g021010   K.G..I.... N..FT..D.K ISQ..V.DIH -.ED..Q... .N.Q..V..P -.L.RL...R M.N.N----- ----------  [ 640]

#La_GPX-PDE1   K.GVLIC... VTLDDTTDVA NHQEFANRKR -TY.VQGENV TGFFTV.FTL -KEL.SLRV. QRYNF----- --RDQQ----  [ 640]

#At1g66970     S.GV.FCLRS IDLRNSIAAL QNT-FSNRST -SVPEIS-SV PGIFTFSLTW -PEIQSLTPA .SNPF-RVYR IFRNPR----  [ 640]


#La_GPX-PDE2   ----VEQDDS LCTLEEAFLN VE-PSLGFN- ---------- ---------- -----IELKF DDHIVYHQ-- --DYLSHVLQ  [ 720]

#Gm19g27060    ----.....P ....Q...VK ..-.T....- ---------- ---------- -----..... ......E.-- --...V....  [ 720]

#Sc_GDE1       LNSGS.EKEP .NEISAGE.. ERNENGNGGN KGSLGKLAGP IKSYGHRFLD NNESL.LITL GSNDTRNKSP SISLS.EA.A  [ 720]

#Ec_glpQ       -----KS.FR VH.F..EIEF .QGLNHSTGK NIG------- ---------- -----.YPEI KAPWFH..-- ---EGKDIAA  [ 720]

#Ec_ugpQ       --------EP .PL.SQVAER CRKHGMMA.- ---------- ---------- ---------- ---------- ----------  [ 720]

#Sc_PGC1       ---IKFTNEK IIMIKTFVIM L.VKNDLKFW QER------- ---------- -----.TWGL WLLDW.DFGI ETGV.KDFKV  [ 720]

#At1g66980     ----ERNSGN .IS.Y.FLNL AKNSTSLSG- ---------- ---------- -----.LISL ENVVYLRE-- --KKGLD.VK  [ 720]

#At3g20520     ----NNKAGK FL..S.FLFL PNRY.SLLG- ---------- ---------- -----LLIEV ENAAYLVE-- --HQGIS.VD  [ 720]

#At5g58050     ----NKNAGK FT..ADFLEL GK-AKAVTG- ---------- ---------- -----VLINI QNAAYLAS-- --KKGLG.VD  [ 720]

#At5g43300     ----..K..P .....D.... .K-H.....- ---------- ---------- -----..... ..NT..GE-- --GE.RQT.D  [ 720]

#At5g58170     ----NKNAGK FI..ADFLDF SK-AKAVTG- ---------- ---------- -----VMINI ENAAYLAS-- --KKGLG.VD  [ 720]

#Gg_GDE2       ----EAANQ. V.K.ADML-E .IKDNTSLIL N--------- ---------- -----FQDLP P..PY.TS-- -------YIN  [ 720]

#Mm_GDE3       ----EAENQT IPA...LLKE AAALN.SIMF D--------- ---------- -----LRRPP RN.TY.DT-- -------FVN  [ 720]
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#Gm17g08680    ----FNGKFQ II.F..FITI AQDAPRVVG- ---------- ---------- -----.YPEI KNPVFIN.QV KWSHGKRFED  [ 720]
#Os03g40670    ----YNGKYQ II.FD.YI.I ALYADRVVG- ---------- ---------- -----.YPEL KNP.FINEHV KWSDGKKFED  [ 720]
#Stc_glpQ1     ---LYDGRWE IP.F..VLRW QNEQTRRRGK QV-------- ---------- ----W.YPEL KHPTYFRKLG LG-----TEE  [ 720]
#Stc_glpQ2     --------AR VP...QYVHR ..HNHQKLL- ---------- ---------- -------.EL KSPGL.PG-- -------IE.  [ 720]
#At5g41080     ----.DL... ....Q...EQ ..-QT....- ---------- ---------- -----..... ..QT..ER-- --EF.V.I.R  [ 720]
#At3g02040     ----.AT... F...Q...EK ..N.N....- ---------- ---------- -----....L ..NVF.SS-- --.H..RL.L  [ 720]
#At1g71340     --------SR IP.....LAL ISNSVRKVI- ---------- ---------- -----LDA.V GPPMYEKG-- -------LA.  [ 720]
#Hs_GDE1/Mir16 --------EK IP..R..VAE CLNHN.TIF- ---------- ---------- -------FDV KG.AHKAT-- ---------E  [ 720]
#Os02g31030    ----.QS..P ....Q...EK .N-.R....- ---------- ---------- -----..... ..NLE.QE-- --EE.TCI..  [ 720]
#At1g74210     ----YNGMYP II.F..FLTI ARDAPRVVG- ---------- ---------- -----.YPEI KNPVLMN.HV KWPGGKKFED  [ 720]
#At5g55480     ----ERSSGK FVS.SDFLNL AKNS.SLTG- ---------- ---------- -----VLISV ENATYLRE-- --KQGLDAVK  [ 720]
#Sb03g035370   ----YNGMF. II.F..FISI ALDADRTVG- ---------- ---------- -----.YPEI K.PVFINKHV KWADGKKFED  [ 720]
#At4g26690     ----QKNAGK .FS.SDFLSL AKNSTSLSG- ---------- ---------- -----VLISV ENAAYLRE-- --EQGLD.VK  [ 720]
#At5g08030     ----YNGKFP II.FD.YISI ALDAPRVVG- ---------- ---------- -----.YPEI KNPVFMN.QV KWADGKKFED  [ 720]
#Sb04g021010   ----.QSE.A ........EK .N-TR....- ---------- ---------- -----V.... ..SLE.QE-- --EE.TRI..  [ 720]
#La_GPX-PDE1   ----YNGKFQ II.F..YISI ALEAPRVVG- ---------- ---------- -----.YPEI KNP.LIN.HV KWADGKLFED  [ 720]
#At1g66970     ----EKNSGK .IS.SQFLDL AKTYTSLSG- ---------- ---------- -----VLISV ENAAYLRE-- --KQGLD.V.  [ 720]


#La_GPX-PDE2   AILKVVFDNA ---------- KNRPIIFSTF QPDAASLVKK LQSTYPVFFL TNGGCEIYED KRR------- ----------  [ 800]
#Gm19g27060    T.......Y. ---------- .D........ .....M.IR. ..TN...... .......... V..------- ----------  [ 800]
#Sc_GDE1       KVIGLET.C. LSLVISCNDS IDKSSVILDL PL.DNVDAVD FKVPFK.DYS HTLYFD.VPT YGTR------ ----SLETHN  [ 800]
#Ec_glpQ       KT.E.LKKYG -------YTG .DDKVYLQC. DA.ELKRI.N VLEPKMGMD. NLVQLIA.T. WNETQQKQPD GSWVNYNYDW  [ 800]
#Ec_ugpQ       --IEIKPTTG ---------- -TG.LTGK.V ALA.RE.WTG MTPP----L. SSFEIDAL.A AQQ------- ----------  [ 800]
#Sc_PGC1       IVISLSL.I. SQFVKRSLTL NDPHYKLFGI SVHFV.SWTS QFRLRLLPV. MKNDIKV.LW TVN------- ----------  [ 800]
#At1g66980     VV.NRLTETG -----YIVG- -TLKVMIQST TRLVLVDF.N QSTY---KTV YKIKET.GNI TDS------- ----------  [ 800]
#At3g20520     .V.DELKRAT T----QQNKT SA.T.LIQST DKSVLMKF.E KNKMNHDELV YRVDDN.RDV ADS------- ----------  [ 800]
#At5g58050     VVKSALTNST ------LDKQ STQKVLIQSD DSSVL.SFEA VPPY---TRV LSIDK..GDA PKT------- ----------  [ 800]
#At5g43300     N..T..NEHS ---------- ........S. H....R.IRN M.RC...... ........K. V..------- ----------  [ 800]
#At5g58170     .VKSALAKST ------LDKQ STQKVLIQSD DSSVLASFEA VPPY---TRV LSIDK..GGA PKP------- ----------  [ 800]
#Gg_GDE2       IT..TILASG IQQQAVMWLP DTERQLVRQI A.AFQQTSGL KLDAERLREK GIVKLNLRYT .VT------- ----------  [ 800]
#Mm_GDE3       QT.EA.LSAN VSQAMVLWLP DEDRANVQQR A.RMRQIYGH QGGNWTERPQ ---FLNLPYQ DLP------- ----------  [ 800]
#Gm17g08680    KFVETLQKYG YKGSYLSKDW LRQ.VFIQS. A.TSLVYISN KTDLPKI.LI DDVIVPTQDT NQS------- -------FWE  [ 800]
#Os03g40670    KFVQTLLKYG YKGEYMSEDW LKQ.LFIQS. A.SSLIYMSN MTNSPKI.LI DDTTVRTQDT NQS------- -------YYE  [ 800]
#Stc_glpQ1     RLARLLRKYG -------KDR ..S.V.IQS. E.TSIQRMN. .VGNPLAVL. SGANSRPWDF VETGD----- ----PRTTAD  [ 800]
#Stc_glpQ2     QT...LANEG ----WLDRRH VAGRLVVQS. DA.SIRT.HD .KPAVKTG.. GTPAVSELP- ---------- ----------  [ 800]
#At5g41080     SV.Q..SNY. ---------- .D..V...S. .....K..RE .......... .DA.N..HN. E..------- ----------  [ 800]
#At3g02040     P..Q..S.IG ---------- ND.T....S. H....L..R. ..T....... ....T.M.H. T..------- ----------  [ 800]
#At1g71340     D..SIIERAQ ---------- C.NC.VWAKS DTL.RDIIRR APD.MVGYIV MVDPLTGARN ---------- ----------  [ 800]
#Hs_GDE1/Mir16 .LK.MYMEFP ---------Q LYNNSVVCS. L.EVIYKMRQ TDRDVITALT HRPWSLSHTG DGK------- ----------  [ 800]
#Os02g31030    .......EY. ---------- .D......S. .....QVMR. .......Y.. ....T...A. V..------- ----------  [ 800]
#At1g74210     KVVETLKKYG YGGSYLSKKW LKK.LFIQS. A.TSLVYISN .TDSPK.LLI DDVTMPTQDT NQT------- -------YAE  [ 800]
#At5g55480     .V.DTLTEAG -----YSNKT TTTRVMIQST NSSVLIDF.. QSRY---ETV YKVEET.RDI LDT------- ----------  [ 800]
#Sb03g035370   KFVDTLLKYG YKGQYMSENW LKQ.LFIQS. A.TSIVH.SD .IDSPK..LI DDITVRTQDT NQS------- -------YWE  [ 800]
#At4g26690     .V.DTLTQTG -----YSN-S TATKVMIQST NSSVLVDF.. QSQY---ETV YKVEEN.RDI LDS------- ----------  [ 800]
#At5g08030     KFVETLKKYG YKGSYLSEDW LKQ..FIQS. AATSLVYISN MTDSPKL.LI DDVTILTEDT NKT------- -------YAE  [ 800]
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#Sb04g021010   .....I.EH. ---------- .D...L..S. .....Q.MR. ..G....Y.. ....T.L.T. V..------- ----------  [ 800]
#La_GPX-PDE1   KFVETLKKYG YKGSYLSKDW LKQ.AFIQS. A.TSLVYTSN QTDLPKILLI DDITIPTQDT NQS------- -------YWE  [ 800]
#At1g66970     .V.DTLTEAG -----YSNGT TTTKVMIQST NSSVLVDF.. QSKY---ETV YKIEET.GNI RDS------- ----------  [ 800]

#La_GPX-PDE2   ----NSLEEA LKLCLENGLQ G-IVSEI--- KGVFRNPAIV TKIKESELSL LTYGSLNNVP EAVYMQHLMG IDGVIVDLVQ  [ 880]
#Gm19g27060    ----...... M........E .-.....--- ..I....GA. .Q....K... .S..K..... .......... .N........  [ 880]
#Sc_GDE1       RIDCQKNNNN YVMARGVSML NKSY.SVGVN RSILNGSVT. PI.ANHT.EI .GTLKFEYII ITPFEHPQLP LERTETYWKS  [ 880]
#Ec_glpQ       MFKPGAMKQV AEYADGI.PD YHMLI.E--- TSQPG.IKLT GMVQDAQQNK .VVHPYTVRS DK---LPEYT T.VNQLYDAL  [ 880]
#Ec_ugpQ       --------A. PE.PRGLL.D EWRDDWR--- ----ELT.RL GCVSIHLNHK .LDKARVMQL KDAGLRI.VY TVNKPQRAAE  [ 880]
#Sc_PGC1       --KPIDFKYL CE.PIHGAIT DDPIKAR--- ----KLCDGH .VA.KPTAEK KFVAPSLASV DGLRFHAFIK VYNILCT.LY  [ 880]
#At1g66980     -----AI.DI K.FANAVVIN KAS.FPN--- SDS.LTGQTT NVLERLQKFQ .PVYVELFQN .F.SQPFDFF A.ETVEINAY  [ 880]
#At3g20520     -----AIKDI KNFAGSIVIS KKS.FPY--- ..FIILEKET NIASKLKSNG .RVYVERFSN .C.THAFDFY D.PTLEIDSF  [ 880]
#At5g58050     -----.I..I K.HADAVN.L RTSLITV--- SQS.ATGKT- NVVE.MHKAN ISVYVSVLRN .YIAIAFDYF S.PT.ELATF  [ 880]
#At5g43300     ----...D.. I...K.S... .-L...V--- .AIL.T.NAI .RV.D.K... .S..Q....V .VI.L.Y... VE.....M.K  [ 880]
#At5g58170     -----.VD.I K.YAEAVN.L RTSLVTV--- SQS.TTGKT- NVVE.MHKGN ISVYVSVLRN .YISVAFDYF S.PT.ELATF  [ 880]
#Gg_GDE2       ---NEDVRDY MAAN.SVN.Y TVNEPWL--- YSILWCTGVP SVTSD.SHV. RKVPFPIWLM PPDEYRLIWI TSDL.SFIII  [ 880]
#Mm_GDE3       ---ALDIKAL HQDNISVN.F VVNKPWL--- FSLLWCAGVD SVTTNACQL. QQMQNPLWLL PPQKYLMIWV .TDCASI.LL  [ 880]
#Gm17g08680    ITSDEY.DYI KQYVVGI.PW KDT.VPV--- VEN-YMTNPT NLVARAHAHN .QVHPYTYRN .FPFLHFNFS Q.PYMEYDYW  [ 880]
#Os03g40670    ITSDAY.AFI R.YIVGI.PW KDTIVPP--- INN-YLGPPT DLVARAHALN .QVHPYTFRN .NMFLHFDFH Q.PYLEYEYW  [ 880]
#Stc_glpQ1     LVTPEG.K.I ASYAQGI.PT LDLIVPK--- DSAG.LTEPT .LVRDAHRAG .ILHPYTMRN .NPFLPAEFR QG--------  [ 880]
#Stc_glpQ2     --------AY AEFADQINPS YGSL.MS--- ----YVS.VH AFTGPHGRP. EVLTWTV.DA DTARRVAGYD V..I.TNKPD  [ 880]
#At5g41080     ----...... IQV...G... .-....V--- ........AI S.....N... ....K....G ......YV.. .......F.E  [ 880]
#At3g02040     ----...... I.V...G... .-....V--- ........L. N.....K... M...K....A .......... .E.....H.E  [ 880]
#At1g71340     ---------- -S.LRMK.AR VVG.YHP--- -----LIDEE LVRVVRRRNK EV.AWTVDDA DPMKRMLHL. V.A.VTSDPS  [ 880]
#Hs_GDE1/Mir16 -------PRY DTFWKHFIFV MMDILLDWSM HNILWYLCGI SAFLMQKDFV SPAYLKKWSA KG-IQVVGWT VNTFDEKSYY  [ 880]
#Os02g31030    ----...... I....AS.M. .-....A--- R.I..H..A. P....AN... ....T..... .......... VN........  [ 880]
#At1g74210     ITSDAYF.YI KQYVVGI.PW KDTIVPV--- NNN-YVL.PT DLV.RAHAHN .QVHPYTYRN .HEFLHYNFS Q.PYKEYDYW  [ 880]
#At5g55480     -----AI.DI K.FADAVVIS KKS.FPT--- SES.TTGQT- KLVERLQKFQ .PVYVEVFRN .F.SQPWDFF A.ATVEINSH  [ 880]
#Sb03g035370   ITSDDY.AYI G.YVVGL.PW KDTIVPA--- S.N-YLMPPS DLVARAHAHN .QVHPYTYRN .NQFLHFNFH Q.PYTEYDFW  [ 880]
#At4g26690     -----AI.DI K.FADAVVI. KLS.FPV--- AQS.ITTQT- NVVEKLQK.Q .PVYVELFQN .FLSQPYDFF A.ATVEINSY  [ 880]
#At5g08030     ITSDAY.DYI KPYVIGI.PW KDTIVPV--- NNN-.LMTPT DLVARAHSRN .QVHPYTYRN .NQFLHLEFN Q.PYLEYDYW  [ 880]
#Sb04g021010   ----...... V....AS.M. .-....A--- R.I..H..A. P....AN... ....T..... .......... VN.......P  [ 880]
#La_GPX-PDE1   ITSDSYF.YI KDYVVGI.PW KET.VTV--- VNN-YLQTPS DLV.RAHAHN .QVHTYTYRN .NKFLCFNFN Q.PYQEYDYW  [ 880]
#At1g66970     -----AI.DI K.FANAVVIN KDS.FPN--- SDS.LTGQT- NVVERLQK.Q .PVYVELFRN .F.SQAYDFF S.ATVEINAY  [ 880]

#La_GPX-PDE2   EITEAVTNLI TSAKVVVDEE GLNE------ ---------- ---------- ---------- ----KLKLHS KPKFSQLELS  [ 960]
#Gm19g27060    ......ADM. KPT.GGEG.- ..A.GCG--- ---------- ---------- ---------- ----.VQGN. ..Q...Q...  [ 960]
#Sc_GDE1       LVSTR.IGHR GLG.NNPNKS LQIGENTVES FIMAASLGAS YVEFDVQLTK DNVPVVYHDF LVAETGVDIP MHELTLEQFL  [ 960]
#Ec_glpQ       YNKAG.NG.F .DFPDKAVKF LNK.------ ---------- ---------- ---------- ---------- ----------  [ 960]
#Ec_ugpQ       LLRWG.DCIC .D.ID.IGPN FTAQ------ ---------- ---------- ---------- ---------- ----------  [ 960]
#Sc_PGC1       SKWVHIKLCG W.IAY.IFLF LRTIHFL--- ---------- ---------- ---------- ---------- ----------  [ 960]
#At1g66980     IFGAGINGT. .EFPYTAARY KR.RCLGR-- -----EEVPP YMLPVNPGGV LTLISTSSLP PAQDPNPIFT HDDVTEPP.P  [ 960]
#At3g20520     VRDVQIDGI. .DFPATTARY RK.KCYG--- ---------- EFGLTTTGEL ITFANPMLLP PAEAPYPALL DSDVTEPP.P  [ 960]
#At5g58050     IAGRG.DGV. .EFPATATRY LRSPCSDLN- -----KDQPY AILPADAGAL LTVADKEAQL PAIPPNPPLD AKDVIDPP.P  [ 960]
#At5g43300     D.S..IA.IE VTNEDDCEG. DERKCLIR-- ---------- ---------- ---------- ----FGEERK .VEITKDMIT  [ 960]
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#At5g58170     ISGSG.DGV. .EFPATATRY LKSPCSDLN- -----KEQPY AILPAEAGGL VVVADKEAQP PASAPNPPLE AKDVIDPP.P  [ 960]
#Gg_GDE2       VGVFIFQ.YH NDQWRLGSIR TY.PEQIM-- ---------- ---------- ---------L SAAVRRSSRD VKIMKEKLIF  [ 960]
#Mm_GDE3       LSIFLLRGGC AKRNRTG--- ---------- ---------- ---------- ---------- ---------- ---LETAV.L  [ 960]
#Gm17g08680    INKIG.DG.F .DFTGSLHRY QEWTSN---- ---------- ---------- ---------- -------HKD DDDK---N.L  [ 960]
#Os03g40670    LGEIG.DG.F .DFTGTLHRF QECTTP---- ---------- ---------- ---------- --------YP .NEKNAEA.L  [ 960]
#Stc_glpQ1     ----SDPDAY GDVFGAFRTY FATGIDG--- ---------- ---------- ---------- ---------V FTDNPDTGVL  [ 960]
#Stc_glpQ2     VVRD..D--- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [ 960]
#At5g41080     ..I.ST.RMM IRPPPSSSPL PSPSK-D--- ---------- ---------- ---------- ----DDVAIT R.E...K.I.  [ 960]
#At3g02040     ......REMM KPSNRDA.G- ---------- ---------- ---------- ---------- -------TKP ..N..DR...  [ 960]
#At1g71340     MFQGLMED.R .ECLEEGFSI RT-------- ---------- ---------- ---------- ---------- ----------  [ 960]
#Hs_GDE1/Mir16 .SHLGSSYIT D.MVEDCEPH F--------- ---------- ---------- ---------- ---------- ----------  [ 960]
#Os02g31030    ......SE.. .VPEPDLNAD N.SNG----- ---------- ---------- ---------- ----AA.DAA T.H...C.I.  [ 960]
#At1g74210     INEIG.DG.F .DFTGSLHNF QEWTSP---- ---------- ---------- ---------- --------LP DTSK.PRQ.L  [ 960]
#At5g55480     VTGAGINGT. .EFPLTAARY KR.SCLTR-- -----KDVPP YMIPVQPAGL LTIVSPASLP PAEAPSPVFT DADVTEPP.P  [ 960]
#Sb03g035370   IN.VG.DG.F .DFTGTLHRY QELTSP---- ---------- ---------- ---------- --------.P .DE-TANS.L  [ 960]
#At4g26690     ITGAGINGT. .EFPFTAARY KR.LCLGR-- -----KETIP YMAPAQPGAL LTLVSPTAFP PAEAPNPVFT DADVTEPP.P  [ 960]
#At5g08030     LNKIG.DG.F .DFTGSLHNY QELKSP---- ---------- ---------- ---------- --------LP QQQ-------  [ 960]
#Sb04g021010   ...D..SE.. ALPEPDLEVD N.SNQ----- ---------- ---------- ---------- ----AARGAT T.N...R.I.  [ 960]
#La_GPX-PDE1   VKKIG.DG.F .DFTGSLHKY QEWTSSNR-- ---------- ---------- ---------- -------HNE SDDKTASR.L  [ 960]
#At1g66970     IYGAGINGT. .EFPFTAARY KR.RCLGR-- -----EEVPP YMLPVNPGGL LNVMSPLSLP PAQAPNQDFI EADVTEPP..  [ 960]


#La_GPX-PDE2   FLLKLIPQLI QI-------- ---------- ---------- ---------- ---------- ---------- ----------  [1040]
#Gm19g27060    ..F......L ..-------- ---------- ---------- ---------- ---------- ---------- ----------  [1040]
#Sc_GDE1       D.NNADKEH. .RGAGHSPHH VNGADTALQK YRGRSVDDSD VSTLRRAWDL HDNDPNGKSN NAHWSDNRMR LTKTFKKNNF  [1040]
#Ec_glpQ       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1040]
#Ec_ugpQ       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1040]
#Sc_PGC1       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1040]
#At1g66980     PVIAKS.TST LGTPSTIAKP LISWSVAGVV LFLVLLTLVF CFHRKRETRL RQQKLKALIP LEHYTYAQVK RITKSFAEVV  [1040]
#At3g20520     EARSQP.ASS PSKAEEKAIE VP-----FAF IAMAILVCFF ISV------- ---------- ---------- ----------  [1040]
#At5g58050     PVA..AS-NG TEGGPPQTPP RSGTVAIAAN LSLSLLAMMA LGLLYTA--- ---------- ---------- ----------  [1040]
#At5g43300     L.N.FV.K.L ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1040]
#At5g58170     PVAN.AASNA TGGAQSHPPP ASGTVANAAN LGLSLLAMLA LGV------- ---------- ---------- ----------  [1040]
#Gg_GDE2       SEINNGVETT DELSLCSENG YANEMVTPTD HRDTRLRMN- ---------- ---------- ---------- ----------  [1040]
#Mm_GDE3       TKINN----- ---------- FASE------ ---------- ---------- ---------- ---------- ----------  [1040]
#Gm17g08680    HKIA.LVSSY E--------- ---------- ---------- ---------- ---------- ---------- ----------  [1040]
#Os03g40670    QKINYMLKD- SGY------- ---------- ---------- ---------- ---------- ---------- ----------  [1040]
#Stc_glpQ1     AREDFVNG-- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1040]
#Stc_glpQ2     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1040]
#At5g41080     .....LS... .H-------- ---------- ---------- ---------- ---------- ---------- ----------  [1040]
#At3g02040     .......E.. .H-------- ---------- ---------- ---------- ---------- ---------- ----------  [1040]
#At1g71340     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1040]
#Hs_GDE1/Mir16 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1040]
#Os02g31030    ...R...E.V .--------- ---------- ---------- ---------- ---------- ---------- ----------  [1040]
#At1g74210     SQIASLVLPY AKA------- ---------- ---------- ---------- ---------- ---------- ----------  [1040]
#At5g55480     PVSARA.TTT PGPQSTGEKS PN----GQTR VALSLLLSAF ATVFAS---- -------LLL L--------- ----------  [1040]
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#Sb03g035370    VKISQMISAY EGL------- ---------- ---------- ---------- ---------- ---------- ----------  [1040]

#At4g26690      PVTAKA.TSS PGTPSTNAQA PS----GQTR ITLSLLLSVF AMVLAS---- -------LLL L--------- ----------  [1040]

#At5g08030      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1040]

#Sb04g021010    ...R...E.V .--------- ---------- ---------- ---------- ---------- ---------- ----------  [1040]

#La_GPX-PDE1    HKIASLVTSY ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1040]

#At1g66970      PVIAKA.TST PGTPSTIAQA PS----GQTR LKLSLLLSVF FLS------- -------LLL L--------- ----------  [1040]


#La_GPX-PDE2    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#Gm19g27060     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#Sc_GDE1        KGNARGHSIA SSFVTLKELF KKIPANVGFN IECKFPMLDE AEEEELGQIM MEMNHWVDTV LKVVFDNANG RDIIFSSFHP  [1120]

#Ec_glpQ        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#Ec_ugpQ        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#Sc_PGC1        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#At1g66980      GRGGFGIVYK GTLSDGRVVA VKVLKDTKGN GEDFINEVAT MSRTSHLNIV SLLGFCSEGS KRAIIYEFLE NGSLDKFILG  [1120]

#At3g20520      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#At5g58050      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#At5g43300      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#At5g58170      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#Gg_GDE2        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#Mm_GDE3        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#Gm17g08680     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#Os03g40670     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#Stc_glpQ1      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#Stc_glpQ2      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#At5g41080      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#At3g02040      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#At1g71340      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#Hs_GDE1/Mir16  ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#Os02g31030     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#At1g74210      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#At5g55480      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#Sb03g035370    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#At4g26690      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#At5g08030      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#Sb04g021010    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#La_GPX-PDE1    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]

#At1g66970      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1120]


#La_GPX-PDE2    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]

#Gm19g27060     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]

#Sc_GDE1        DICIMLSLKQ PVIPILFLTE GGSEQMADLR ASSLQNGIRF AKKWNLLGIV SAAAPILKAP RLVQVVKSNG LVCVTYGVDN  [1200]

#Ec_glpQ        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]

#Ec_ugpQ        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]

#Sc_PGC1        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]

#At1g66980      KTSVNMDWTA LYRIALGVAH GLEYLHHSCK TRIVHFDIKP QNVLLDDSFC PKVSDFGLAK LCEKKESILS MLDTRGTIGY  [1200]
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#At3g20520      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]
#At5g58050      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]
#At5g43300      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]
#At5g58170      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]
#Gg_GDE2        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]
#Mm_GDE3        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]
#Gm17g08680     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]
#Os03g40670     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]
#Stc_glpQ1      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]
#Stc_glpQ2      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]
#At5g41080      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]
#At3g02040      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]
#At1g71340      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]
#Hs_GDE1/Mir16  ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]
#Os02g31030     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]
#At1g74210      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]
#At5g55480      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]
#Sb03g035370    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]
#At4g26690      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]
#At5g08030      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]
#Sb04g021010    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]
#La_GPX-PDE1    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]
#At1g66970      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1200]

#La_GPX-PDE2    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]
#Gm19g27060     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]
#Sc_GDE1        NDPENASIQI EAGVDAVIVD SVLAIRRGLT KKNEK----- ---------- ---------- ---------- ----------  [1280]
#Ec_glpQ        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]
#Ec_ugpQ        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]
#Sc_PGC1        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]
#At1g66980      IAPEMISRVY GNVSHKSDVY SYGMLVLEII GARNKEKANQ ACASNTSSMY FPEWVYRDLE SCKSGRHIED GINSEEDELA  [1280]
#At3g20520      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]
#At5g58050      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]
#At5g43300      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]
#At5g58170      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]
#Gg_GDE2        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]
#Mm_GDE3        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]
#Gm17g08680     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]
#Os03g40670     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]
#Stc_glpQ1      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]
#Stc_glpQ2      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]
#At5g41080      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]
#At3g02040      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]
#At1g71340      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]
#Hs_GDE1/Mir16  ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]
```

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#Os02g31030    ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]

#At1g74210     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]

#At5g55480     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]

#Sb03g035370   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]

#At4g26690     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]

#At5g08030     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]

#Sb04g021010   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]

#La_GPX-PDE1   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]

#At1g66970     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------  [1280]


#La_GPX-PDE2   ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#Gm19g27060    ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#Sc_GDE1       ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#Ec_glpQ       ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#Ec_ugpQ       ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#Sc_PGC1       ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#At1g66980     KKMTLVGLWC IQPSPVDRPA MNRVVEMMEG SLEALEVPPR PVLQQIPISN LHESSILSED VSVYTEG [1347]

#At3g20520     ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#At5g58050     ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#At5g43300     ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#At5g58170     ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#Gg_GDE2       ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#Mm_GDE3       ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#Gm17g08680    ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#Os03g40670    ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#Stc_glpQ1     ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#Stc_glpQ2     ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#At5g41080     ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#At3g02040     ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#At1g71340     ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#Hs_GDE1/Mir16 ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#Os02g31030    ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#At1g74210     ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#At5g55480     ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#Sb03g035370   ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#At4g26690     ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#At5g08030     ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#Sb04g021010   ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#La_GPX-PDE1   ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]

#At1g66970     ---------- ---------- ---------- ---------- ---------- ---------- ------- [1347]
```