PLANT PHYTOCHROME SIGNALING IN AN EVOLUTIONARY CONTEXT

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Fir de Claude

Villmools merci dass du do bass!

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SUMMARY

Although plants grow in highly diverse habitats, they all equally depend on monitoring and integrating the environmental factor light. Their genomes therefore encode a range of photoreceptors, among which phytochromes (PHY) perceive the red (R) and far-red (FR) regions of the light spectrum. Phytochromes are found across the whole plant kingdom; they have, however, diversified independently in seed plants (e.g. *Arabidopsis*) and cryptogams (e.g. ferns or mosses).

The present work addressed the functional evolution of phytochromes. The applied strategy comprised the investigation and comparison of phytochrome signaling systems in cryptogams and seed plants. Localization studies in the moss *Physcomitrella patens* and the fern *Adiantum capillus-veneris* revealed that cryptogam phytochromes accumulated in the nucleus upon activation by light, analogous to seed plant phytochromes. *P. patens* FAR-RED ELONGATED HYPOCOTYL1 (FHY1) was shown to be functionally equivalent to *Arabidopsis* FHY1, putatively acting as phytochrome nuclear transporter. Cryptogams do not contain homologs of seed plant PHYA. Nevertheless, physiological analyses revealed responses of *P. patens* to FR light, which were reminiscent of PHYA-mediated effects in seed plants. Moreover, one clade of *P. patens* phytochromes exhibited the molecular properties of PHYA that are required for FR light signaling in *Arabidopsis*. In conclusion, responses to FR light do not specifically depend on PHYA and are not limited to seed plants. A transcriptome analysis revealed strong effects of R light on gene expression in *P. patens* and, thereby, identified potential target genes of phytochrome signaling. The characterization of putative PHYTOCHROME INTERACTING FACTOR (PIF) homologs from *P. patens* revealed similar functional mechanisms for cryptogam and seed plant PIFs, suggesting the evolutionary conservation of phytochrome signaling mechanisms.

The present work contributed to the understanding of the sub-functionalization of phytochrome signaling in an evolutionary context. It raised the hypothesis that phytochrome-induced signaling as well as phytochrome-mediated responses to FR light had already evolved before the split of seed plants from cryptogams.

ZUSAMMENFASSUNG

Pflanzen sind in der Lage ausgesprochen diverse Lebensräume zu besiedeln. Sie sind dabei jedoch immer auf die Detektion und Verarbeitung der umgebenden Lichtinformation angewiesen. Hierzu besitzen Pflanzen verschiedene Photorezeptoren, wobei die Phytochrome Licht im roten und dunkelroten Bereich des Spektrums wahrnehmen. Phytochrome sind im gesamten Pflanzenreich zu finden; die Diversifizierung der Phytochrome aus Samenpflanzen (z.B. *Arabidopsis*) und aus Kryptogamen (z.B. Farne oder Moose) erfolgte jedoch erst nach der Auftrennung beider Klassen und somit unabhängig voneinander.

Die vorliegende Arbeit beschäftigt sich mit der funktionalen Evolution der Phytochrome. Hierzu wurden Phytochrom-Signalsysteme in Kryptogamen und Samenpflanzen untersucht und miteinander verglichen. Die Visualisierung von Phytochromen in dem Moos *Physcomitrella patens* sowie dem Farn *Adiantum capillus-veneris* zeigte, dass Kryptogam-Phytochrome nach ihrer Aktivierung durch Licht im Zellkern akkumulieren und sich somit ähnlich verhalten wie Phytochrome aus Samenpflanzen. Die anschließende Analyse des FAR-RED ELONGATED HYPOCOTYL1 (FHY1) Homologs in *P. patens* ließ auf eine Funktion als Mediator des Phytochrom Kerntransports schließen, vergleichbar mit dem für *Arabidopsis* beschriebenen Mechanismus der PHYA-Lokalisierung. Obwohl Kryptogame kein PHYA Homolog besitzen, zeigte *P. patens* spezifische Reaktionen auf Dunkelrotlicht, in Analogie zu PHYA-abhängigen Antworten in Samenpflanzen. Darüber hinaus wurden für eine Gruppe von *P. patens* Phytochromen molekulare Eigenschaften beobachtet, die typisch sind für PHYA, und in Samenpflanzen eine Dunkelrotlicht Perzeption ermöglichen. Somit wurde gezeigt, dass die Entwicklung von PHYA in Samenpflanzen nicht bestimmend war für die Perzeption und Integration von Dunkelrotlicht. Antworten auf Dunkelrotlich können auch von Phytochrom-Systemen in Kryptogamen vermittelt werden. Im weiteren Verlauf der Arbeit wurden in einer Transkriptomanalyse potentielle Zielgene der Phytochrom Signaltransduktion in *P. patens* bestimmt. Im Genom von *P. patens* konnten Homologe von bekannten Komponenten der Phytochrom Signaltransduktion, den PHYTOCHROME INTERACTING FACTORs (PIFs), identifiziert werden. Ihre Charakterisierung ließ

ebenfalls auf eine Konservierung der Proteinfunktion in Kryptogamen und Samenpflanzen schließen.

Die Ergebnisse dieser Arbeit ermöglichen somit ein besseres Verständnis der funktionalen Diversität von Phytochromen und ihrer Entstehung im Laufe der Evolution. Sie unterstützen die Hypothese, dass spezifische Phytochrom-Signalwege und Antworten bereits vor der Trennung von Kryptogamen und Samenpflanzen existierten.

CHAPTER 1

INTRODUCTION TO PHYTOCHROMES IN SEED PLANTS AND CRYPTOGAMS

Anja Possart

This chapter contains excerpts from:

Possart, A., Fleck, C. and Hiltbrunner, A. Mechanism and Evolution of Far-Red Light Perception. **Plant Science.** Invited review. In preparation.

1. PHYTOCHROMES FUNCTION AS RED/FAR-RED LIGHT RECEPTORS

Plants as sessile organisms have intriguing capacities to optimize their growth and development in response to a fluctuating natural environment. Using a wide range of sensory systems they integrate ambient factors like light, temperature or humidity in order to ensure survival and successful reproduction. Light, besides being the exclusive source of energy, controls a multitude of adaptive and developmental processes, collectively designated plant photomorphogenesis (Kami et al., 2010). Thus, light influences reversible responses like shoot bending or the opening and closing of stomata and flowers, as well as irreversible processes such as seed germination, seedling development, directional growth or the transition to flowering (Kami et al., 2010; Li et al., 2011). Plants monitor all kinds of light parameters, such as intensity, spectral composition, direction and duration, and thereby collect circadian, seasonal and positional information (Kami et al., 2010; Leivar and Quail, 2011).

Higher plants, like *Arabidopsis thaliana*, have evolved at least five major classes of photoreceptors that corporately monitor light ranging from UV-B to the near infrared (Figure 1). The receptor specifically sensing UV-B light (280-315 nm) was discovered only two years ago as UV RESISTANCE LOCUS 8 (UVR8) (Rizzini et al., 2011; Heijde and Ulm, 2012). Three distinct types of light sensors, cryptochromes, phototropins and members of the ZEITLUPE (ZTL) family perceive the ultraviolet-A (UV-A)/blue (B) part of the light spectrum (320-500 nm) (Kami et al., 2010). Finally, phytochromes (PHYs), which have absorption maxima in red (R) and far-red (FR) light (600-750 nm), sense and integrate the long-wave range of the visible light spectrum; they were the first pigments for plant photomorphogenesis to be described (Borthwick et al., 1952; Butler et al., 1959; Kami et al., 2010; Li et al., 2011).

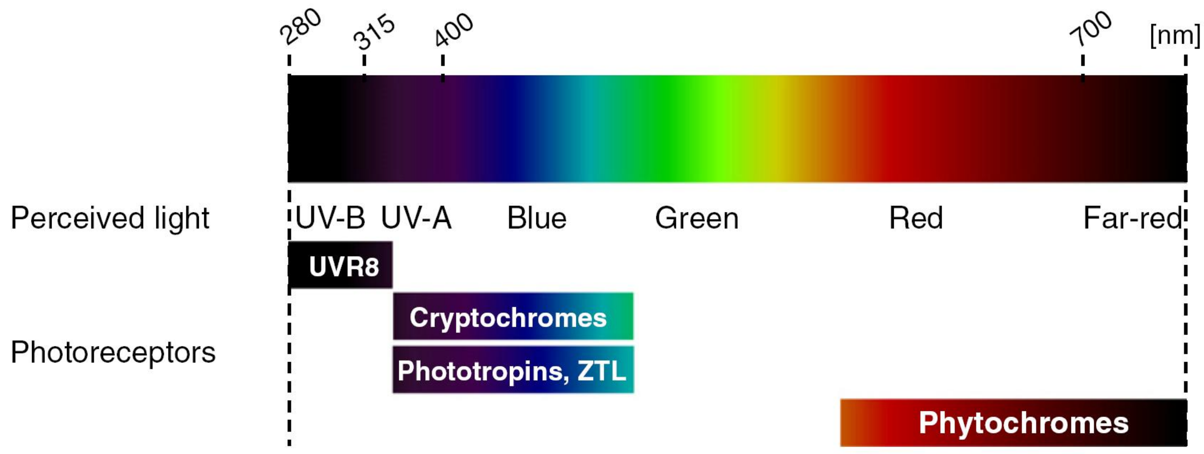

Figure 1. Photoreceptors in seed plants perceive different parts of the light spectrum. UVR8 specifically senses UV-B light; cryptochromes, phototropins and ZTL proteins perceive UV-A and B light; phytochromes have absorption maxima in R and FR light. (Adapted and reprinted from *Trends in Plant Science*, Vol. 17, No. 4, Heijde and Ulm, UV-B photoreceptor-mediated signalling in plants, pp 230-237, Copyright 2012, with permission from Elsevier)

Phytochromes translate the external R and FR light conditions into cellular signals based on their ability to exist in two distinct but photoreversible forms: the inactive Pr form with maximal absorption in R light (~660 nm), and the active Pfr form, with its absorption peak in FR light (~730 nm) (Mancinelli, 1994; Quail, 1997) (Figure 2A). The photoreceptors are soluble homo- and heterodimeric proteins covalently linked with a linear tetrapyrrole chromophore, phytochromobillin (PΦB) that allows absorption of light (Mancinelli, 1994; Sharrock and Clack, 2004; Li et al., 2011). It was assumed that the absorption of R light induces a reversible *Z* to *E* isomerization of the C15-C16 double bond and thus a rotation of the D pyrrole ring of the chromophore (Andel et al., 1996). This was supported by a study on the effects of locked *15 Z* and *15 E* phycocyanobilin derivates on phytochrome responses in moss and *Arabidopsis* (Yang et al., 2012). In contrast, NMR analyses of a phytochrome from the cyanobacterium *Synechococcus* OSB' indicated a rotation of the A pyrrole ring at the C4-C5 double bond (Ulijasz et al., 2010). This discrepancy may reflect differences between plants and cyanobacteria and is still to be resolved. The R light-induced motions in the chromophore lead to conformational rearrangements within the phytochrome protein and thus to the generation of the active Pfr form (Ulijasz et al., 2010). Similarly, Pfr converts to the inactive Pr form upon absorption of FR light. This results in a continuous dynamic equilibrium of phytochrome Pfr/Ptot ratio (Ptot = Pfr + Pr), which is a measure of the respective amounts of R and FR light in the plants' environment (Mancinelli, 1994).

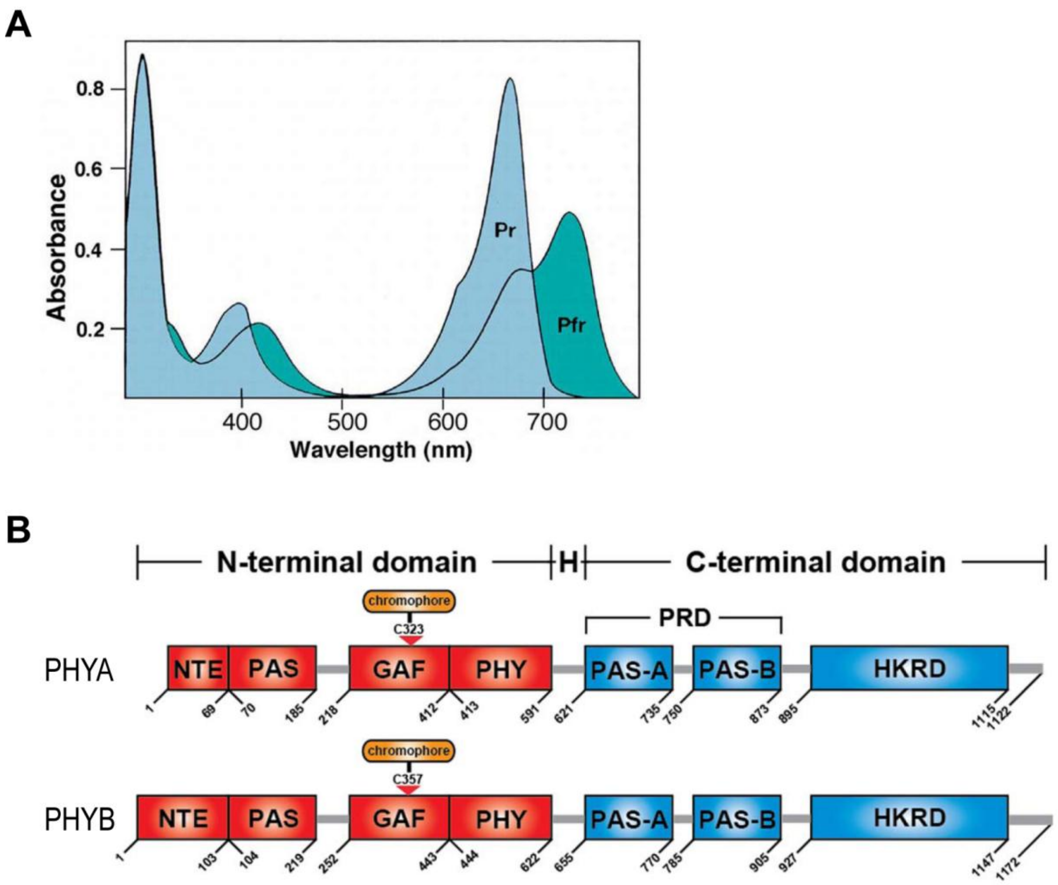

Figure 2. Absorption spectrum and structure of phytochromes. (Adapted and reprinted from *The Arabidopsis Book*, e0148, Li et al., Phytochrome Signaling Mechanisms, Copyright 2011 by the American Society of Plant Biologists, with permission of the American Society of Plant Biologists [previously adapted from the *Annual Review of Plant Biology*, 59, Bae and Choi, Decoding of Light Signals by Plant Phytochromes and Their Interacting Proteins, Copyright 2008 by Annual Reviews, republished with permission of Annual Reviews, Permission conveyed through Copyright Clearance Center, Inc])

(A) Absorption spectra of the inactive Pr and the active Pfr phytochrome forms. Pr has its absorption maximum at 660 nm, Pfr maximally absorbs at 730 nm.

(B) Domain structure of phytochromes, exemplarily shown for *Arabidopsis* PHYA and PHYB. N-terminal extension (NTE), Per-Arnt-Sim (PAS), cGMP phosphodiesterase-adenyl cyclase-FhlA (GAF), phytochrome-associated (PHY) and histidine kinase-related domains (HKRD).

All plant phytochromes consist of an N-terminal photosensory/signaling domain and a C-terminal regulatory domain (Li et al., 2011). The N-terminal domain has four subdomains, which are the N-terminal extension (NTE), Per-Arnt-Sim (PAS), cGMP phosphodiesterase-adenyl cyclase-FhlA (GAF) and phytochrome-associated (PHY) domains. The C-terminal domain consists of two subdomains, namely the PAS-related domain, which contains two PAS repeats, and the histidine kinase-related domain (HKRD) (Li et al., 2011) (Figure 2B). The N-terminal PAS and GAF domains are conserved in most phytochromes (Bae and Choi, 2008; Li et al., 2011). They constitute the core photosensory domain, with the chromophore bound to a conserved cysteine residue in the GAF domain of plant phytochromes (Bae and Choi, 2008; Li et al., 2011). Moreover, the N-terminal phytochrome domains confer specific properties to different phytochromes and are essential for specific signal transduction, which was indicated by phytochrome mutant analyses and domain swapping experiments (Matsushita et al., 2003; Mateos et al., 2006; Su and Lagarias, 2007; Bae and Choi, 2008; Li et al., 2011; Oka et al., 2012). Lacking a critical histidine residue the HRKD is presumably not an active histidine kinase and is considered to be an evolutionary remnant (Boylan, 1996). Nevertheless, the C-terminal domain plays a role in the attenuation of phytochrome activity and its PAS repeats are putative dimerization motifs (Matsushita et al., 2003; Bae and Choi, 2008; Li et al., 2011).

The phytochrome photosensory function of detecting the ratio of R and FR light in the environment has been conserved through millions of years of evolution (Mathews, 2006). Although originally described in seed plants (Butler et al., 1959) phytochromes are ubiquitous among the plant kingdom, including ferns, mosses and algae, and they are even represented in bacteria and fungi (Karniol and Vierstra, 2003; Kanegae and Wada, 2006; Lamparter, 2006).

2. LAND PLANT PHYTOCHROME FAMILIES AND TYPES

2.1 SEED PLANTS

Plant phytochromes are encoded by small gene families, which for instance consist of five PHY genes in *Arabidopsis* (*PHYA to PHYE*), three PHY genes in rice (*PHYA to PHYC*) and four PHY genes (*PHYP1/P2/N/O*) in *Pinus* (Sharrock and Quail, 1989; Clack et al., 1994; Mathews and Sharrock, 1997; Bae and Choi, 2008). It has been assumed that gene duplication and divergence were the basis for the development of antagonistic and complementary phytochrome functions (Mathews, 2006). In line with this, phylogenetic analyses have revealed that soon after the origin of seed plants the phytochrome lineage split into two gene lineages (Mathews, 2010) (Figure 3). Thus, phytochromes from modern seed plants like *Arabidopsis* belong either to the PHYA branch, including PHYA/C or to the PHYB branch, including PHYB/D/E (Mathews, 2006, 2010).

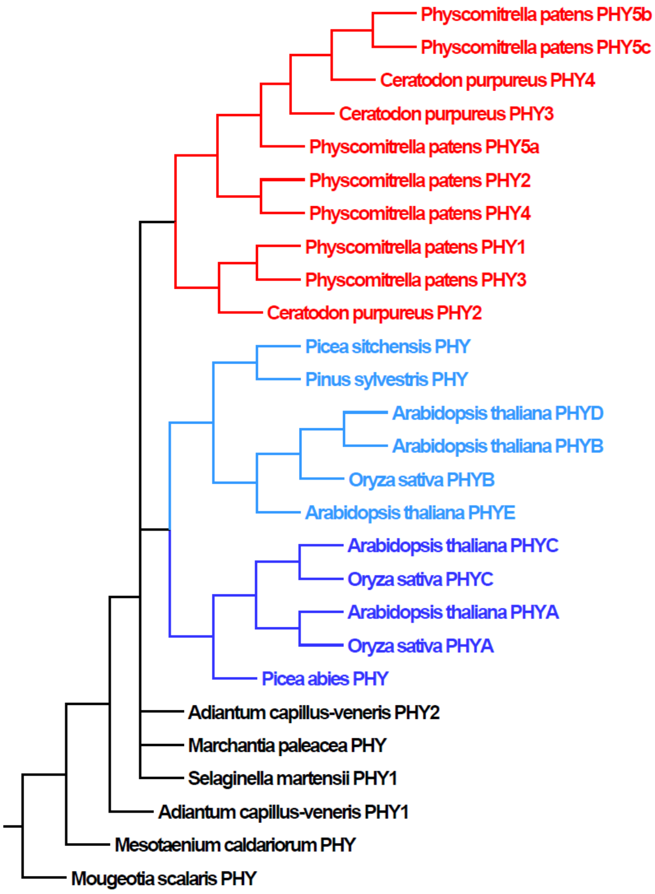

Figure 3. Phylogeny of phytochromes from seed plants and cryptogams. Seed plants: *A. thaliana* and *O. sativa* (angiosperms); *P. sitchensis*, *P. sylvestris* and *P. abies* (gymnosperms). Cryptogams: *A. capillus-veneris* (fern), *S. martensii* (spikemoss), *M. paleacea* (liverwort), *P. patens* (moss), *M. caldariorum* (green alga) and *M. scalaris* (green alga). (Generated as described by Harrison and Langdale, 2006 and Baldauf, 2003; kindly provided by Andreas Hiltbrunner)

Moreover, phytochromes can be grouped into type I and type II phytochromes based on their molecular properties, like protein stability in light (Sharrock and Quail, 1989). The only type I phytochrome - PHYA - is the most prevalent phytochrome in dark-grown etiolated seedlings, but is rapidly degraded in light (Sharrock and Clack, 2002). Due to this and other properties, which are discussed in chapter 4.2.2.2, PHYA represents the principle mediator of responses to low Pfr/Ptot ratios, like germination or seedling de-etiolation in deep shade (Casal et al., 2003; Li et al., 2011) (Chapter 4). PHYB to PHYE represent the light-stable type II phytochromes, among which PHYB is the most abundant phytochrome in light-grown seedlings and plants (Sharrock and Clack, 2002). PHYB translates a wide range of ambient R/FR light ratios into corresponding Pfr/Ptot ratios and is important during the shade avoidance response as well as during germination, de-etiolation and induction of flowering in red or white light (Casal et al., 2003; Li et al., 2011) (Chapter 4). The type II phytochromes PHYC, PHYD and PHYE are less abundant and of smaller importance for photomorphogenic responses (Sharrock and Clack, 2002; Casal et al., 2003; Li et al., 2011).

The diversification and subfunctionalization of seed plant phytochromes have been considered important for the gene family's evolution (Mathews, 2006). As the appearance of different phytochrome types probably coincided with an increasing complexity in the light environment it may have been a prerequisite for a successful radiation of seed plants (Mathews, 2006).

2.2 CRYPTOGAMS

Cryptogams i.e. plants that reproduce by spores, such as ferns, mosses and green algae, also contain small phytochrome gene families (Figure 3). The genome of the moss *Physcomitrella patens* (Pp) encodes seven PHYs (PHY1 to PHY4, PHY5a to PHY5c), which belong to two distinct lineages and have orthologs in the moss *Ceratodon purpureus* (Cp) (Lamparter, 2006; Mathews, 2006; Mittmann et al., 2009). The fern *Adiantum capillus-veneris* (Ac) has two phytochrome lineages represented by PHY1 and PHY2; the genome of the fern *Ceratopteris richardii* (Cr) contains homologs of both *Adiantum* phytochromes (Mathews, 2006). Similar to their origin in seed plants, cryptogam phytochrome families arose from gene duplication and subsequent diversification (Lamparter, 2006; Mathews, 2006). The amino acid identity between phytochromes from seed plants and cryptogams is about 50 % to 60 %, which is in the same range as the identity between different types of seed plant phytochromes (i. e. PHYA- and PHYB-like phytochromes) (Sharrock and Mathews, 2006). However, in phylogenetic analyses none of the cryptogam phytochromes associated with branches of the seed plant clade (Mathews, 2010). Thus, cryptogam phytochrome clades have evolved independently from seed plant phytochromes; one can therefore not assign them to the PHYA or PHYB group.

Cryptogam phytochromes have the same domain structure and photosensory properties as seed plant phytochromes (Oyama et al., 1990; Lamparter et al., 1995; Zeidler et al., 1998; Sineshchekov et al., 2000). To date, only one ferredoxin-dependent biliverdin reductase, LONG HYPOCOTYL 2 (HY2), was identified in flowering plants, which is why land plants have been assumed to exclusively utilize PΦB as phytochrome chromophore. However, Chen *et al.* could recently show that phytochrome signaling in the moss *P. patens* not only depends on PΦB but also requires the structurally different chromophore phycourobilin (PUB) (Chen et al., 2012).

Besides conventional phytochromes there exist non-canonical phytochromes in some cryptogam species, e. g. PHY3 in *Adiantum capillus-veneris* and PHY1 in *Ceratodon purpureus* (Kanegae and Wada, 2006; Lamparter, 2006). Cp-PHY1 is homologous to other plant phytochromes in the N-terminal half, but has an unusual serine/threonine kinase domain in the C-terminal region (Lamparter, 2006). Ac-PHY3 (neochrome, Ac-NEO1) is a chimeric protein that consists of a chromophore-binding domain of phytochromes at the N-terminus and a full-length phototropin at the C-terminus (Kawai et al., 2003). Interestingly, in the green algae *Mougeotia scalaris* (Ms) two neochrome homologs (Ms-NEO1, Ms-NEO2) have arisen independently from Ac-NEO1 which is an example of convergent evolution that resulted in similarly dramatic changes in the light perception of the fern and green algae (Suetsugu et al., 2005).

3. PHYTOCHROME CELLULAR LOCALIZATION AND SIGNALING

3.1 SEED PLANTS

The synthesis of the biologically inactive Pr form of phytochromes takes place in the cytosol. However, after conversion into the active Pfr form by light, phytochromes from seed plants like *A. thaliana* translocate into the nucleus and form so-called nuclear bodies (Kami et al., 2010; Li et al., 2011; Van Buskirk et al., 2012). In this process, type I and type II phytochromes respond differentially to different light qualities. While PHYB nuclear translocation is induced in an R/FR light-reversible manner and proceeds rather slowly (~2 hours), PHYA moves in response to all light qualities (R, B and FR light), with continuous FR light being most effective, and can be detected in the nucleus within minutes (Kircher et al., 1999; Kim et al., 2000; Kircher et al., 2002; Li et al., 2011). Interestingly, only PHYA translocates to the nucleus under light conditions that induce low Pfr/Ptot ratios (Kami et al., 2010) (see also chapter 4.2.2).

In line with these diverse translocation patterns, PHYA and PHYB are translocated into the nucleus by different mechanisms. Analyses of the N- and C-terminal domains of PHYB suggested that the C-terminal domain contains a putative nuclear localization signal (NLS) (Matsushita et al., 2003). It has been shown that the N-terminal and the C-terminal PHYB domains interact in a light-dependent manner, indicating an unmasking of the putative NLS during light activation (Chen et al., 2005). PHYB nuclear transport would thus be intrinsic to PHYB, a mechanism that, however, does not provide an explanation for the rather slow PHYB nuclear accumulation.

PHYA does not contain a NLS and its nuclear transport relies on two other components: far-red elongated hypocotyl 1 (FHY1) and its homolog FHY1-like (FHL) (Kami et al., 2010; Li et al., 2011). FHY1 and FHL contain a NLS and nuclear export signal (NES) at the N-terminus and a septin-related domain at the C-terminus, which is, together with the NLS, functionally essential and sufficient (Desnos et al., 2001; Zeidler et al., 2004; Genoud et al., 2008). The function of FHY1 and FHL firstly became evident when both proteins were demonstrated to light-reversibly interact with PHYA through the C-terminal septin-related domain and to co-localize with PHYA in nuclear bodies. Moreover, the analysis of *fhy1 fhl* double knockdowns revealed that FHY1 and FHL are required for PHYA nuclear translocation and PHYA function (Hiltbrunner et al., 2005; Zhou et al., 2005; Hiltbrunner et al., 2006; Rösler et al., 2010). Thus, according to the current assumption, PHYA makes use of the FHY1- and FHL-NLS for its nuclear import (Li et al., 2011).

Mutant phenotypes and the effects of phytochrome-NLS/NES fusions have strongly suggested that the major site of phytochrome action is in the nucleus (Kami et al., 2010; Li et al., 2011). There is some evidence of a cytosolic or plasma membrane-associated localization of phytochromes in seed plants, which, however, is mainly based on functional analyses rather than localization studies (Rösler et al., 2010; Hughes, 2013) (see also chapter 4.1).

Light-induced phytochrome translocation from the cytosol into the nucleus only constitutes one of the initial steps in phytochrome signaling in seed plants. In the nucleus, phytochromes bind to downstream signaling factors and regulate their activity, ultimately leading to differential gene expression and the modulation of biological responses (Kami et al., 2010; Li et al., 2011) (Figure 4).

One nuclear downstream signaling factor regulated by phytochromes is CONSTITUTIVE PHOTOMORPHOGENIC 1 (COP1), a master suppressor of photomorphogenesis (Deng et al., 1991; Deng et al., 1992). COP1 is a highly conserved RING finger E3 ubiquitin ligase that, in conjunction with members of the suppressor of PHYA (SPA) family, controls the abundance of several photomorphogenesis-promoting proteins (Kami et al., 2010; Li et al., 2011). Such proteins are for instance LONG HYPOCOTYL 5 (HY5), a bZIP transcription factor, LONG HYPOCOTYL IN FAR-RED 1 (HFR1), an atypical bHLH protein, or LONG AFTER FAR-RED LIGHT (LAF1), a MYB transcription factor (Li et al., 2011). In the dark, COP1 ubiquitinates HY5, HFR1 and LAF1 and targets them for proteasome-mediated degradation (Holm et al., 2002; Seo et al., 2003; Jang et al., 2005; Yang et al., 2005). Light-activated phytochromes, however, inactivate COP1 thereby inducing the accumulation of HY5, HFR1 and LAF1 which then promote photomorphogenesis. The mechanism of phytochrome-mediated COP1-inhibition is largely unknown; protein interaction between phytochromes and the COP/SPA complex as well as the depletion of COP1 from the nucleus have been proposed to play a role during this pathway of phytochrome signaling (von Arnim and Deng, 1994; Osterlund and Deng, 1998; Li et al., 2011).

A small subset of bHLH transcription factors, designated phytochrome interacting factors (PIFs), also interacts with phytochromes in the nucleus and has been demonstrated to play a central role in phytochrome signaling (Leivar and Quail, 2011). All PIFs contain a bHLH domain that mediates protein dimerization and DNA binding, as well as an active phytochrome-binding (APB) domain essential and sufficient for their interaction with the Pfr form of PHYB (Khanna et al., 2004; Leivar and Quail, 2011). Moreover, two PIFs, namely PIF1 and PIF3, contain an active PHYA-binding (APA) motif. Although this motif is not well conserved between the two PIFs, it is necessary for their binding to light-activated PHYA (Al-Sady et al., 2006; Shen et al., 2008). The role of PIFs had been investigated for quite some time, but due to their functional redundancy only the generation of multiple PIF mutants has revealed that PIFs suppress photomorphogenesis and promote skotomorphogenesis in the dark: e.g. seedlings of the PIF quadruple mutant *pif1 pif3 pif4 pif5* (*pifq*) show a *constitutively photomorphogenic* (*cop*)-like phenotype (Leivar et al., 2008a; Leivar et al., 2008b; Leivar et al., 2009; Shin et al., 2009). Several PIFs have been shown to act as transcription factors (Leivar and Quail, 2011); in line with this, genome-wide expression profiling of the *pifq* mutant revealed an important role of PIFs during light-dependent regulation of gene expression and identified potential direct PIF target genes (Leivar et al., 2009; Shin et al., 2009). Phytochromes promote photomorphogenesis by inducing the rapid degradation of PIFs and inhibiting their binding to target promotors (Kami et al., 2010; Leivar and Quail, 2011; Park et al., 2012). As already described above, light-activated PHYA and PHYB bind to PIFs; this binding induces the rapid phosphorylation of PIFs, upon which they are ubiquitinated and degraded via the ubiquitin-proteasome system (Kami et al., 2010; Leivar and Quail, 2011).

In summary, light-activated nuclear-localized phytochromes modulate the abundance of multiple positive and negative transcription factors and thereby regulate, for instance during the process of de-etiolation, the differential expression of about 20 % of the genes in *A. thaliana* (Tepperman et al., 2001; Tepperman et al., 2004; Tepperman et al., 2006; Li et al., 2011). While many of the early phytochrome-responsive genes encode transcription factors, indicating a network effect, later responding genes are related to phytohormone signaling or photosynthetic and metabolic changes that occur during light-induced transition to autotrophic growth (Leivar and Quail, 2011; Li et al., 2011).

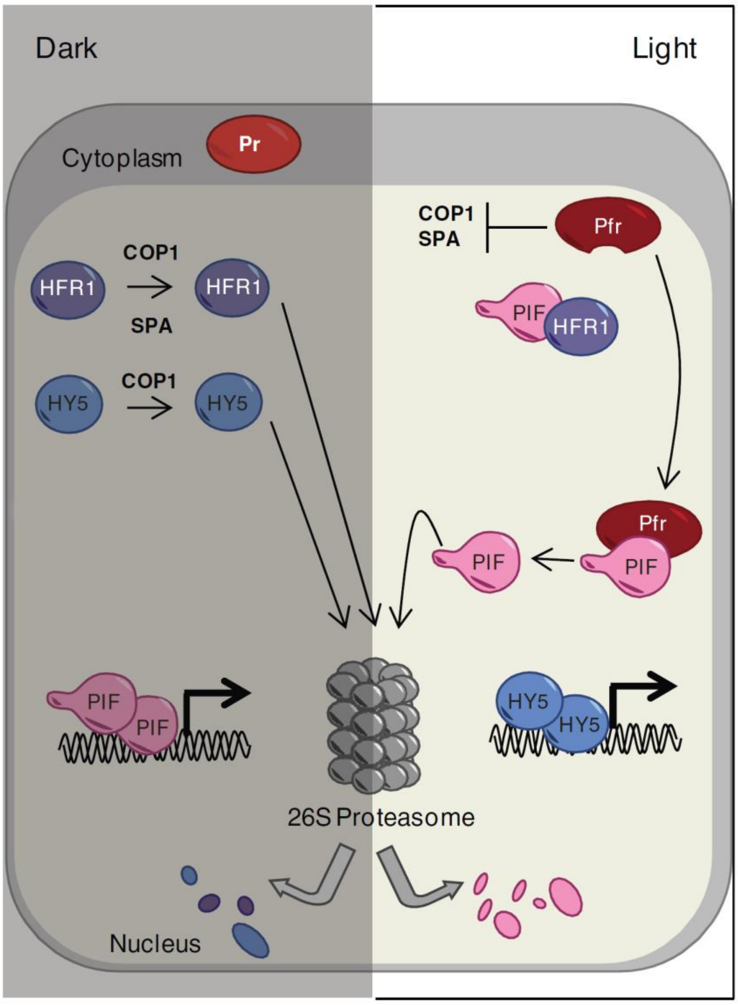

Figure 4. Phytochrome signaling in seed plants. In the dark, the inactive Pr form of phytochromes is located in the cytosol. Upon activation by light the Pfr form translocates to the nucleus, where it modulates the activity of transcription factors like PIF, HFR1 and HY5. (Adapted and reprinted from *Current Topics in Developmental Biology*, Vol. 91, Kami et al., Light-regulated plant growth and development, pp 29-66, Copyright 2010, with permission from Elsevier)

3.2 Cryptogams

In contrast to seed plants, phytochromes from cryptogams have been suggested to mainly localize to the cytosol or to associate with the plasmamembrane, as indicated by spectroscopic analyses and the transient expression of GFP-tagged moss phytochromes (Bose et al., 2004; Uenaka and Kadota, 2007). Moreover, Jaedicke et al. have recently shown that phytochromes interact with phototropins at the plasmamembrane in the moss *P. patens* (Jaedicke et al., 2012). However, most evidence for cryptogam phytochrome localization is based on indirect conclusions from physiological analyses (see also chapter 4.1). Phytochromes from ferns and mosses regulate phototropic and polarotropic growth as well as chloroplast positioning (Kagawa and Wada, 1994; Mittmann et al., 2004; Kanegae and Wada, 2006; Lamparter, 2006; Mittmann et al., 2009). The integration of directional and vectorial information during these responses indicates a fixed orientation of the responsible photoreceptor as would be facilitated by its binding or association to the plasmamembrane (Kraml, 1994; Rösler et al., 2010).

A potential nuclear localization of cryptogam phytochromes has been suggested based on experiments using microbeam irradiation: the locally selective activation of phytochromes in proximity to the nuclear region induced side branch formation of *P. patens* (Uenaka et al., 2005). Moreover, recent data on transiently transformed *A. capillus-veneris* gametophytes have indicated a nuclear localization of Ac-PHY2 (Tsuboi et al., 2012).

While phytochrome-signaling in seed plants relies on a complex nuclear signaling cascade that leads to massive changes in gene expression (see also chapter 3.1), so far there have been only few reports on a similar function of phytochromes in cryptogams. Some publications have suggested that cryptogam phytochromes regulate the transcript levels of individual genes, like those of phytochromes themselves in liverwort and green algae (Winands and Wagner, 1996; Christensen et al., 1998; Suzuki et al., 2001). Moreover, in a very recent approach Chen *et al.* performed transcriptome profiling by mRNA sequencing and identified R light-regulated genes in the moss *P. patens* that were misregulated in phytochrome-chromophore mutants (Chen et al., 2012).

Despite these hints on a nuclear phytochrome function, to date there is only little data available on the components of nuclear phytochrome signaling in cryptogams. Interestingly, several COP1/SPA-related genes have been reported for the genome of *P. patens* (Richardt et al., 2007). Homologs of the bZIP transcription factor HY5 have also been found in the moss genome (Richardt et al., 2007; Rensing et al., 2008), altogether indicating the presence of a signaling pathway similar to the COP1/SPA pathway in seed plants (see also chapter 3.1). Although the class of bHLH transcription factors is represented in the moss *P. patens*, PIFs, however, have not been described so far (Carretero-Paulet et al., 2010; Richardt et al., 2010; Rösler et al., 2010). Thus, there has been no indication on a light signaling pathway in cryptogams analogous to seed plant phytochrome-mediated regulation of PIFs and their target genes.

As phytochromes from seed plants and cryptogams differ in their subcellular localization they might induce different signaling mechanisms and thereby different physiological responses (see also chapter 4). However, testing this hypothesis requires a more comprehensive analysis of cryptogam phytochrome signaling.

4. PHYTOCHROME-MEDIATED RESPONSES AND THEIR EVOLUTIONARY CONSERVATION

4.1 TROPISMS AND CHLOROPLAST MOVEMENT

Phytochrome-mediated responses appear to be diverse between plant species. Seed plant phytochromes mainly regulate developmental responses, such as germination, de-etiolation, induction of flowering or the shade avoidance syndrome (see chapter 4.2.), but only play a minor role in phototropic growth, which primarily depends on phototropins. In contrast, phytochromes from cryptogams are important for developmental responses as well as for tropisms and chloroplast movement. It has been shown that, in contrast to seed plants, not only B light but also R light induces phototropic growth and chloroplast movement in mosses and ferns (Kanegae and Wada, 2006; Lamparter, 2006). These responses are induced by intermediate fluences (1-1000 µmol m^{-2} s^{-1}) and are R/FR light reversible, which defines them as typical phytochrome low fluence responses (LFR; chapter 4.2.1). In the moss *P. patens*, Mittmann *et al.* have directly demonstrated the phytochrome dependency of phototropism, polarotropism and chloroplast movement by disrupting Pp-*PHY1* to *Pp-PHY4* genes via gene targeting (Mittmann et al., 2004). Red light-induced phototropism in caulonema tip cells was impaired in all *Pp-phy* knockouts, with *Pp-phy4* showing the strongest phenotype (Mittmann et al., 2004). Also in the moss *C. purpureus* the analysis of aphototropic mutants (*ptr*) that are impaired in phytochrome chromophore biosynthesis (Esch and Lamparter, 1998; Suetsugu and Wada, 2007) as well as the direct knockout of *PHY* genes (Mittmann et al., 2009) has highlighted the importance of phytochromes for photo- and polarotropic growth. Moreover, although many mosses show a typical B light dependency of chloroplast movement, in *P. patens* this response is also triggered by R light and phytochromes (Kadota et al., 2000; Sato et al., 2003; Lamparter, 2006).

In ferns, like *A. capillus-veneris*, R light also affects phototropic growth and chloroplast movement (Wada, 2007). Interestingly, *Adiantum* and other polypod ferns like *Dryopteris filix-mas* or *Onoclea sensibilis* have a special photoreceptor, so called neochrome (e.g. Ac-PHY3), which consists of an N-terminus similar to phytochromes and a C-terminus containing complete phototropin domains (Kawai et al., 2003; Kanegae and Wada, 2006). The analysis of numerous red light-aphototropic (*rap*) mutants from *Adiantum* has provided strong evidence that neochrome is the R light-receptor for phototropic growth and chloroplast movement in ferns (Kawai et al., 2003; Suetsugu and Wada, 2007). As already described in chapter 3.2, the observed dichroic effects of polarized light on phototropic growth and chloroplast positioning in cryptogams indicates a fixed orientation of the corresponding photoreceptors. Thus, cryptogam phytochromes have been suggested to act associated with the plasma membrane and via direct cytosolic signals (Kraml, 1994; Rösler et al., 2010).

In contrast to cryptogams, in seed plants like *Arabidopsis* phytochromes mainly control morphogenic responses through gene regulation in the nucleus (see also chapter 3.1). Tropisms and chloroplast movement mainly depend on blue light and are regulated by phototropins (Banas et al., 2012; Sakai and Haga, 2012). Interestingly though, using the *fhy1 fhl* double mutant Rösler *et al.* have suggested a cytosolic function of PHYA during R light-induced sensitization of B light-dependent phototropism (Parks et al., 1996; Rösler et al., 2007). This function, however, may be based on a low residual level of nuclear PHYA in the *fhy1 fhl* double mutant (Kami et al., 2012). PHYA influences phototropin signaling in *A. thaliana*, and *P. patens* PHYs and PHYA seem to interact with phototropins at the plasmamembrane in moss (Han et al., 2008; Jaedicke et al., 2012). Although phytochromes appear to play a minor role during phototropic responses in higher plants, these results might provide a link between cryptogam phytochromes that act as light direction sensors and seed plant phytochromes that only modulate the directional responses (Rösler et al., 2010; Hughes, 2013).

4.2 GROWTH AND DEVELOPMENT

4.2.1 LFRS / PHYB-DEPENDENT RESPONSES

The role of phytochromes during light-dependent regulation of growth and development is equally important in all clades of land plants. However, the spectral specificities of various phytochromes differ enormously and it is mainly the phytochrome action mode of low fluence responses (LFR) that is present in seed plants as well as in ferns, mosses and even in green algae (Mathews, 2006). LFRs are saturated at medium fluences of 1-1000 µmol m^{-2} (Li et al., 2011). Moreover, they show repeated reversibility, i.e. R light induces the response and FR light reverses it, which is at any one time translated into corresponding phytochrome Pfr/Ptot ratios (Li et al., 2011). One of the first phytochrome responses described was the LFR of lettuce seed germination, which is promoted and inhibited, respectively, after alternating exposure to R and FR light (Borthwick et al., 1952; Schaefer and Nagy, 2006). In *Arabidopsis*, type II phytochromes are the main regulators of LFRs, with PHYB being the major response mediator. PHYB regulates R light-induced seed germination and seedling de-etiolation (Reed et al., 1994; Shinomura et al., 1996); PHYC and PHYD also contribute to the latter (Aukerman et al., 1997; Franklin et al., 2003a; Franklin et al., 2003b; Monte et al., 2003).

LFRs of R/FR light reversible germination and de-etiolation seem to be one of the most basic and indispensable phytochrome functions (Mathews, 2006). They have not only been described for seed plants but are also observed in ferns, in the nonvascular plants (liverworts and mosses) and even in non-land plants (green algae) (Mathews, 2006). The germination of spores from, for instance, the mosses *C. purpureus* and *P. patens* has an action peak in R light and can be reversed by subsequent exposure to FR light (Cove et al., 1978; Hartmann and Jenkins, 1984). Fern spores germinate under light conditions typical for phytochrome-regulated LFRs (Miller, 1968; Furuya et al., 1997). Moreover, cryptogams seem to etiolate in the dark; similar to seed plants, mosses have been described to show elongated, strongly negatively gravitropic growth, reduced leave scale and down-regulation of chlorophyll-synthesis (Cove et al., 1978). When irradiated with light, etiolated mosses like *P. patens* and ferns like *C. richardii* de-etiolate in an R/FR light-reversible and thus phytochrome-dependent manner (Cove et al., 1978; Murata and Sugai, 2000).

Another response that is based on the translation of changing ambient R/FR light ratios into phytochrome Pfr/Ptot ratios is the shade avoidance syndrome (SAS). The SAS has been most extensively studied in *Arabidopsis* and it can be considered as a default output of the LFR. In *Arabidopsis*, PHYB is the predominant suppressor of shade avoidance responses under light conditions that lead to high Pfr/Ptot ratios; PHYD and PHYE are also involved in this response regulation (Nagatani et al., 1991; Somers et al., 1991; Devlin et al., 1998; Devlin et al., 1999). Because pigments in stems and leaves particularly absorb the R and B portion of the light spectrum, whereas FR light is mostly transmitted and reflected, plants growing under canopy shade detect a reduced R/FR light ratio (Franklin and Whitelam, 2005). The resulting low fraction of active phytochrome (Pfr) is no longer able to repress the SAS. The SAS includes elongation of stems and petioles, reduction of chlorophyll content and leaf size, increase of apical dominance and acceleration of flowering (Smith and Whitelam, 1997; Franklin and Whitelam, 2005). Thus plants respond to the presence of competitors for light by overtopping them or alternatively by completing their life cycle.

Although only little data is available, shade avoidance-like responses have been found in other groups of land plants, too (Mathews, 2006). When grown in FR light, mosses show elongated protonemata, lack of fully developed chloroplasts and reduced side branching. Moreover, the leaf size depends on the R/FR light ratio (Hartmann and Jenkins, 1984). Some ferns, too, show shade avoidance-like responses to changes in the R/FR light ratio (Mathews, 2006). It has been speculated that, although elements of the shade avoidance response have been observed in all groups of land plants, its significance increased during the evolution of vascular plants due to the accompanying expansion of shade conditions (Devlin et al., 1998; Mathews, 2006).

4.2.2 VLFRs and HIRs / PHYA-Dependent Responses

As described in chapter 4.2.1, LFRs of seed plants like *Arabidopsis* mainly depend on type II phytochromes, among which PHYB constitutes the major LFR-mediator. Type I phytochromes, namely PHYA, differ in their spectral specificity and mediate response modes that are induced by distinct light conditions and do not show photoreversibility.

One such PHYA-dependent response mode is the so-called very low fluence response (VLFR). VLFRs are induced by extremely low light intensities (0.1 – 1 µmol m^{-2}) of different wavelengths, like R, FR and B light (Li et al., 2011). An R/FR light photoreversibility of VLFRs is not possible because FR light cannot establish a sufficiently low level of inactive Pr and thus induces VLFRs rather than antagonizing them (Smith and Whitelam, 1990). During VLFRs, brief light pulses can induce seed germination, for instance, and even few seconds of starlight can be effective (Schaefer and Nagy, 2006). This indicates an importance of VLFRs for the initial development of seeds and seedlings that are buried in soil and rely on brief exposure to light. VLFRs have been considered to constitute the first phase during germination and de-etiolation followed by a second phase accomplished in the LFR or in the high irradiance response (HIR; see also chapter 4.2.2.2) mode (Casal et al., 1997; Casal et al., 2003). The analysis of *A. thaliana* mutants has revealed that VLFRs exclusively depend on PHYA (Botto et al., 1996; Shinomura et al., 1996).

There is only little evidence for VLFRs and their regulation by phytochromes in cryptogams. Spores of the fern *C. richardii* have been shown to germinate after brief light pulses, indicating a VLFR mode (Cooke et al., 1993). However, *C. richardii* has no PHYA homolog and so far the photoreceptor for this response has not been identified.

High irradiance responses (HIR) constitute another PHYA-specific response mode. In contrast to LFRs and VLFRs, which can be induced by transient exposure to light, HIRs require continuous, long-term irradiation with relatively high light intensities (>1000 µmol m^{-2}) (Smith and Whitelam, 1990; Li et al., 2011). HIRs do not obey the reciprocity law, which has become obvious during light pulse experiments: irradiation with continuous light or with light pulses, both of equal total fluence, did not have the same effect (Smith and Whitelam, 1990; Casal et al., 1998). This is in contrast to LFRs which can be equally induced by continuous light or hourly light pulses of the same total fluence (Mazzella et al., 1997). According to this, HIRs have been defined as responses that are induced more effectively by continuous light than by pulsed light and this reciprocity failure is used as criterion to separate HIRs from LFRs (Casal et al., 1998). Moreover, HIRs depend on the light quality; their maximum action is normally induced by light wavelengths that maintain a low phytochrome Pfr/Ptot ratio for a long time period, as is the case during *Arabidopsis* seed germination or seedling de-etiolation in continuous FR light (Smith and Whitelam, 1990; Li et al., 2011).

In *Arabidopsis*, the photoreceptor for FR-HIRs is PHYA. FR light-induced germination depends on PHYA, and to a lesser extent on PHYE (Botto et al., 1996; Shinomura et al., 1996; Hennig et al., 2002). Also the FR-HIRs of hypocotyl growth inhibition and opening of cotyledons are absent in *Arabidopsis phyA* mutants (Dehesh et al., 1993; Nagatani et al., 1993; Parks and Quail, 1993; Whitelam et al., 1993); seedlings of *phyA* mutants even die prematurely in continuous FR light (Yanovsky et al., 1995). Moreover, PHYA can substitute for reduced PHYB activity in low R/FR light conditions. Thus, FR-HIRs act antagonistically to the shade avoidance response, which is critical for seedling establishment under shade (Johnson et al., 1994; Yanovsky et al., 1995; Franklin and Whitelam, 2005). On the other hand, the analysis of *A. thaliana* seedlings overexpressing PHYB has indicated a suppressive effect of PHYB in FR light signaling (Zheng et al., 2013). From an ecological point of view it has been speculated that PHYB-mediated LFRs are most important in open habitats, and that PHYA-mediated FR-HIRs are especially relevant in shaded habitats, naturally enriched in FR light (Mathews, 2006).

While PHYB-dependent LFRs can be explained with a “classical” model in which phytochromes are switched on and off by R and FR light, the nature of FR-HIRs had remained an open question for a long time (Casal et al., 2003). One prerequisite for understanding FR-HIRs has been the observation that the absorbance spectra of phytochrome Pr and Pfr conformers overlap: consistent with the “switch model” Pr and Pfr show maximal absorption in R and FR light, respectively. However, both conformers also absorb FR and R light, respectively, to a certain extent (Mancinelli, 1994) (Figure 2A). R as well as FR light thus promote a continuous cycling between Pr and Pfr, establishing a wavelength-dependent equilibrium of both phytochrome conformers (Mancinelli, 1994). The PHYA and PHYB absorption spectra are very similar, with highest Pfr/Ptot ratios induced by R light (Eichenberg et al., 2000). The action spectrum of PHYA, however, has a peak in FR light rather than in R light, which becomes manifest in PHYA-dependent FR-HIRs (Shinomura et al., 2000; Dieterle et al., 2001) (see above).

This spectral shift of PHYA activity to FR light as well as the reciprocity failure of PHYA-dependent HIRs has been explained by several models (Casal et al., 2003). Based on experiments with alternating R and FR light pulses one model suggested that not PHYA Pr or Pfr, but a short-lived intermediate signal that is transmitted during PHYA photoconversion induces HIRs (Shinomura et al., 2000). Another model included the process of PHYA Pfr degradation, differentiating between the two steps of Pfr tagging and subsequent Pfr degradation (Hennig et al., 2000). The analysis of steady-state levels and wavelength dependencies of both steps indicated that the process of molecular PHYA tagging is pivotal for the action spectrum of HIRs (Hennig et al., 2000). However, the molecular nature and mechanism of PHYA tagging remained elusive.

A more recent publication was eventually able to demonstrate the shift of the HIR action peak towards FR light being intrinsic to the PHYA signaling network (Rausenberger et al., 2011). Combining mathematical and experimental approaches, Rausenberger *et al.* showed that HIRs can be explained in molecular terms: FHY1/FHL-dependent PHYA nuclear transport, constant photocycling between Pr and Pfr and the degradation of PHYA Pfr are essential to shift the PHYA action peak from R to FR light (Rausenberger et al., 2011). It had been demonstrated before that the formation of PHYA nuclear bodies is a HIR itself, because it requires continuous irradiation with FR light (Casal et al., 2002). Using PHYA mutants, which are constitutively in Pr- or Pfr-like states, Rausenberger *et al.* found that continuous cycling between Pr and Pfr and the resulting binding and dissociation of PHYA and FHY1/FHL are essential and causal for PHYA nuclear accumulation and signaling in FR light (Rausenberger et al., 2011). Moreover, the authors demonstrated that a reduced stability of the Pfr form is crucial for the shift of the action peak from R to FR light (Rausenberger et al., 2011).

In angiosperms HIRs are ubiquitous; rudimentary HIRs have also been found in gymnosperms (Burgin et al., 1999). However, similar to VLFRs, there has neither been substantial evidence for HIRs in cryptogams nor has it been possible to assign a corresponding phytochrome type. A high germination rate in FR light has been demonstrated for spores from the fern *C. richardii* (Cooke et al., 1993) and FR light effected the germination of spores from the moss *Funaria hygrometrica* (Hartmann and Jenkins, 1984). However, similar irradiances with FR light did not induce germination of spores from *P. patens* and the action spectrum revealed a germination response to R but not to FR light (Cove et al., 1978; Hartmann and Jenkins, 1984).

Phytochrome protein stability is a decisive factor in the different response modes of phytochromes in seed plants. In some cryptogams, phytochrome abundance is regulated in a light-dependent manner (Winands and Wagner, 1996; Mittmann et al., 2004), which suggests the possibility of different phytochrome functions in cryptogams, comparable to LFRs and HIRs in seed plants (Mathews, 2006).

However, PHYA, which is essential for HIRs in seed plants, has not been found in cryptogams. Phylogenetic analyses revealed that cryptogam phytochrome clades evolved independently of seed plant phytochromes and can be assigned neither to the PHYA nor the PHYB group (Mathews, 2005, 2010) (chapter 2.2). Thus, to date, PHYA and HIRs have been considered unique to seed plants, providing them with an adaptive advantage during the colonization of shaded habitats (Mathews, 2005, 2006). The physiological and ecological relevance of FR light responses in cryptogams has so far remained elusive.

OBJECTIVES OF THIS WORK

This work addresses the sub-functionalization of seed plant and cryptogam phytochromes in the course of land plant evolution.

I investigate the subcellular localization of phytochromes from mosses and ferns in order to provide a better comprehension of the site of phytochrome activity in cryptogams. My work aims at unraveling the underlying mechanisms and their implications for the diversification of phytochrome response modes. I use the moss *P. patens* to study the perception and integration of specific light information in cryptogams, with a particular focus on FR light responses.

Another important topic of my work is the analysis of phytochrome-induced signaling cascades in *P. patens*. Besides the detection of signaling targets on the gene expression level, I especially concentrate on the identification and characterization of potential components of phytochrome signaling pathways, such as PIF homologs.

The comparison of phytochrome-mediated effects on the molecular and physiological levels in cryptogams and seed plants contributes to understanding the diversification of phytochromes in an evolutionary context.

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CHAPTER 2

AN EVOLUTIONARILY CONSERVED SIGNALING MECHANISM MEDIATES FAR-RED LIGHT RESPONSES IN LAND PLANTS

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ABSTRACT

Phytochromes are plant photoreceptors important for development and adaptation to the environment. Phytochrome A (PHYA) is essential for the far-red (FR) high-irradiance responses (HIRs), which are of particular ecological relevance as they enable plants to establish under shade conditions. PHYA and HIRs have been considered unique to seed plants because the divergence of seed plants and cryptogams (e.g., ferns and mosses) preceded the evolution of PHYA. Seed plant phytochromes translocate into the nucleus and regulate gene expression. By contrast, there has been little evidence of a nuclear localization and function of cryptogam phytochromes. Here, we identified responses to FR light in cryptogams, which are highly reminiscent of PHYA-signaling in seed plants. In the moss *Physcomitrella patens* and the fern *Adiantum capillus-veneris*, phytochromes accumulate in the nucleus in response to light. Although *P. patens* phytochromes evolved independently of PHYA, we have found that one clade of *P. patens* phytochromes exhibits the molecular properties of PHYA. We suggest that HIR-like

responses had evolved in the last common ancestor of modern seed plants and cryptogams and that HIR-signaling is more ancient than PHYA. Thus, other phytochromes in seed plants may have lost the capacity to mediate HIRs during evolution, rather than that PHYA acquired it.

INTRODUCTION

Plants do not only gain energy from light, they also use light as a source of information in order to adapt growth and development to environmental conditions. They have a range of photoreceptors to detect different aspects of their light environment, such as the light intensity and spectral composition, the direction of the light gradient, or temporal light patterns (Kami et al., 2010). Cryptochromes, phototropins, members of the ZEITLUPE (ZTL) family, and UV RESISTANCE LOCUS 8 UVR8 monitor the blue (B) and UV-B range of the light spectrum, whereas phytochromes (PHYs) are essential for the perception of red (R) and far-red (FR) light (Kami et al., 2010; Heijde and Ulm, 2012). Phytochromes can exist in two different states, the inactive Pr form with maximal absorption in R light, and the active or Pfr form of phytochromes, which has an absorption peak in FR light. By absorption of light, these forms reversibly convert into each other, resulting in an equilibrium with a wavelength-specific Pfr/Ptot ratio (Ptot = Pfr+Pr [inactive form of phytochromes]) (Mancinelli, 1994).

Phytochromes have been most intensively studied in seed plants, but they are also present in ferns, mosses, and green algae (i.e., in cryptogams) (Mathews, 2006). They are encoded by small gene families, which are the result of independent gene duplication events in the different lineages (Mathews, 2006; Mittmann et al., 2009). In seed plants, the phytochrome gene lineage split into type I and type II phytochromes that are represented in *Arabidopsis thaliana* by PHYTOCHROME A (PHYA) and PHYTOCHROME B-E (PHYB-E), respectively. PHYB is the most abundant phytochrome in light-grown seedlings and adult plants. It translates the R/FR light ratio in the environment into a corresponding Pfr/Ptot ratio, which is the molecular basis of the shade avoidance response. Under light conditions resulting in high Pfr/Ptot levels, such as in strong R or white (W) light, PHYB also plays an important role in seed germination, de-etiolation, and induction of flowering (Li et al., 2011; Kami et al., 2012). PHYA is the only type I phytochrome. It is rapidly degraded in light but highly abundant in dark-grown (i.e., etiolated) seedlings. In contrast with type II phytochromes, PHYA mediates germination or de-etiolation in response to low levels of Pfr/Ptot, which are typically achieved by light pulses of any wavelength (very low fluence responses) or by continuous irradiation with FR light (high-irradiance responses [HIRs]) (Li et al., 2011).

Cryptogam phytochromes evolved independently of seed plant phytochromes and cannot be assigned to either the type I or type II clade of seed plant phytochromes (Mathews, 2006). Fern (*Pteridophyta*), moss (*Bryophyta*), and liverwort (*Marchantiophyta*) phytochromes are involved in R/FR light-reversible spore germination and deetiolation, but there are hardly any reports of HIR-like responses in cryptogams, perhaps none outside of vascular plants (i.e., seed plants and ferns) (Mathews, 2006). A number of studies have shown that cryptogam phytochromes also regulate phototropic growth of protonema filaments and light-induced chloroplast movement (Mittmann et al., 2004; Kanegae and Wada, 2006; Lamparter, 2006). As these responses are rapidly induced and depend on the orientation of the E vector in polarized light, it has been concluded that cryptogam phytochromes localize to the cytosol or associate with the plasma membrane by interacting with phototropins (Wada et al., 1983; Jaedicke et al., 2012). Indeed, in contrast with seed plants, there is only very limited evidence for a function of cryptogam phytochromes in the nucleus (Rösler et al., 2010). Experiments based on microbeam irradiation suggested that nuclear-localized phytochromes play a role in branch formation in the moss *Physcomitrella patens* or in spore germination in the fern *Adiantum capillus-veneris*, and a recent report indicated the presence of Ac-PHY2 in nuclei of transiently transformed *A. capillus-veneris* gametophytes (Uenaka et al., 2005; Tsuboi et al., 2012). However, spectroscopic methods and transient expression assays do not support the existence of nuclear-localized phytochromes in mosses but rather point to a localization and function at the plasma membrane or in the cytosol (Bose et al., 2004; Uenaka and Kadota, 2007).

By contrast, the vast majority of phytochrome-mediated responses in seed plants depend on nuclear-localized phytochromes and only a few examples of cytosolic phytochrome functions have been reported (Rösler et al., 2010). In seed plants, light-activated phytochromes translocate from the cytosol into the nucleus (Kami et al., 2010). They interact with PHYTOCHROME INTERACTING FACTORS

(PIFs), which are a subgroup of the basic helix-loop-helix transcription factors important for the regulation of elongation growth and photomorphogenesis (Leivar and Quail, 2011). In total, several hundred genes in *Arabidopsis* are regulated by phytochromes at the transcriptional level (Li et al., 2011).

Interestingly, type I and type II phytochromes from seed plants employ different mechanisms for translocation into the nucleus. The main type II phytochrome, PHYB, possibly does not rely on a specific transport protein and may enter the nucleus bound to transcription factors, such as PIFs, or using a nuclear localization signal (NLS) of its own (Chen et al., 2005; Pfeiffer et al., 2012). By contrast, light-regulated nuclear accumulation of PHYA depends on the two functional homologs FAR-RED ELONGATED HYPOCOTYL 1 (FHY1) and FHY1-LIKE (FHL), which contain a NLS and physically interact with PHYA (Hiltbrunner et al., 2006; Rösler et al., 2007).

Based on the different subcellular localization and site of action of seed plant and cryptogam phytochromes, it has been assumed that in the two plant lineages phytochrome signaling relies on fundamentally different molecular mechanisms and mediates different response modes (Rösler et al., 2010). Type I and type II phytochromes have virtually identical photophysical properties, based on which they are expected to have an action peak in R light, where the Pfr/Ptot ratio is maximal (Mancinelli, 1994; Eichenberg et al., 2000). While R light indeed is the most efficient trigger for responses depending on PHYB and other type II phytochromes, we have recently shown that PHYA-specific properties, such as the rapid degradation of the Pfr form and the interaction with the nuclear transport proteins FHY1 and FHL, shift the action peak of PHYA from R to FR light (Rausenberger et al., 2011). This shift is typical of HIRs, which exclusively depend on PHYA and have been considered unique to seed plants. Under FR light conditions, seed plants depend on PHYA for germination and deetiolation (Yanovsky et al., 1995; Botto et al., 1996). Thus, HIRs have been hypothesized to be essential for survival in light environments dominated by FR light, such as in canopy shade (Yanovsky et al., 1995). HIRs are ubiquitous among angiosperms, and rudimentary HIRs have also been described in some gymnosperms (Burgin et al., 1999). By contrast, there has been little evidence for HIR-like responses in cryptogams, and the emergence of HIRs has been associated with the evolution of seed plant PHYA and PHYA orthologs (Mathews, 2006).

However, data presented in this report support the idea that HIR-like responses to FR light are not restricted to seed plants and do not specifically require PHYA. We describe the light-dependent nuclear accumulation of phytochromes in the moss *P. patens*. Furthermore, we show that *P. patens* FHY1 (Pp-FHY1) is functionally equivalent to *Arabidopsis* FHY1 and plays a key role in phytochrome nuclear transport and HIR signaling in *P. patens*.

RESULTS

Light induces rapid nuclear accumulation of cryptogam phytochromes

We have chosen the moss *P. patens* as a model system to investigate the subcellular localization of PHYs in cryptogams. By homologous recombination, we generated independent transgenic *P. patens* lines expressing endogenous Pp-PHY1, Pp-PHY2, Pp-PHY3, Pp-PHY4, Pp-PHY5a, or Pp-PHY5b with a C-terminal yellow fluorescent protein (YFP) tag. In dark-adapted gametophore leaves and protonema filaments exposed to microscope light, we observed a clear nuclear localization of Pp-PHY1:YFP (Figures 1A and 1B). Pp-PHY3:YFP and Pp-PHY4:YFP showed a similar localization, and after chlorophyll bleaching using the herbicide norflurazone, we also found a nuclear accumulation of Pp-PHY2:YFP and Pp-PHY5a:YFP, which were only weakly expressed (Supplemental Figures 1A to 1D). In an immunoblot analysis, full-length phytochrome YFP fusions were detected (Supplemental Figure 1E). We could not detect Pp-PHY5b:YFP by microscopy or immunoblot.

Time series experiments confirmed the light dependency of *P. patens* phytochrome nuclear accumulation (Figure 1C). Pp-PHY1:YFP did not accumulate to detectable levels in nuclei of dark-adapted protonema filaments, whereas 1 min of irradiation with microscope light was sufficient to induce nuclear translocation. Although we detected Pp-PHY1:YFP in the nucleus after both R and FR light treatments, the nuclear signal was stronger in R light than in FR light (Figure 1D). We also observed Pp-PHY3:YFP in the nucleus after R light treatment but possibly due to the weaker YFP signal it was hardly detectable in the nucleus after irradiation with FR light (Supplemental Figure 2B). All nuclear-localized *P. patens* phytochromes formed nuclear bodies, which are also observed for seed plant phytochromes and which have been implicated in signal transduction (Figure 1 and Supplemental Figure 1) (Van Buskirk et al., 2012).

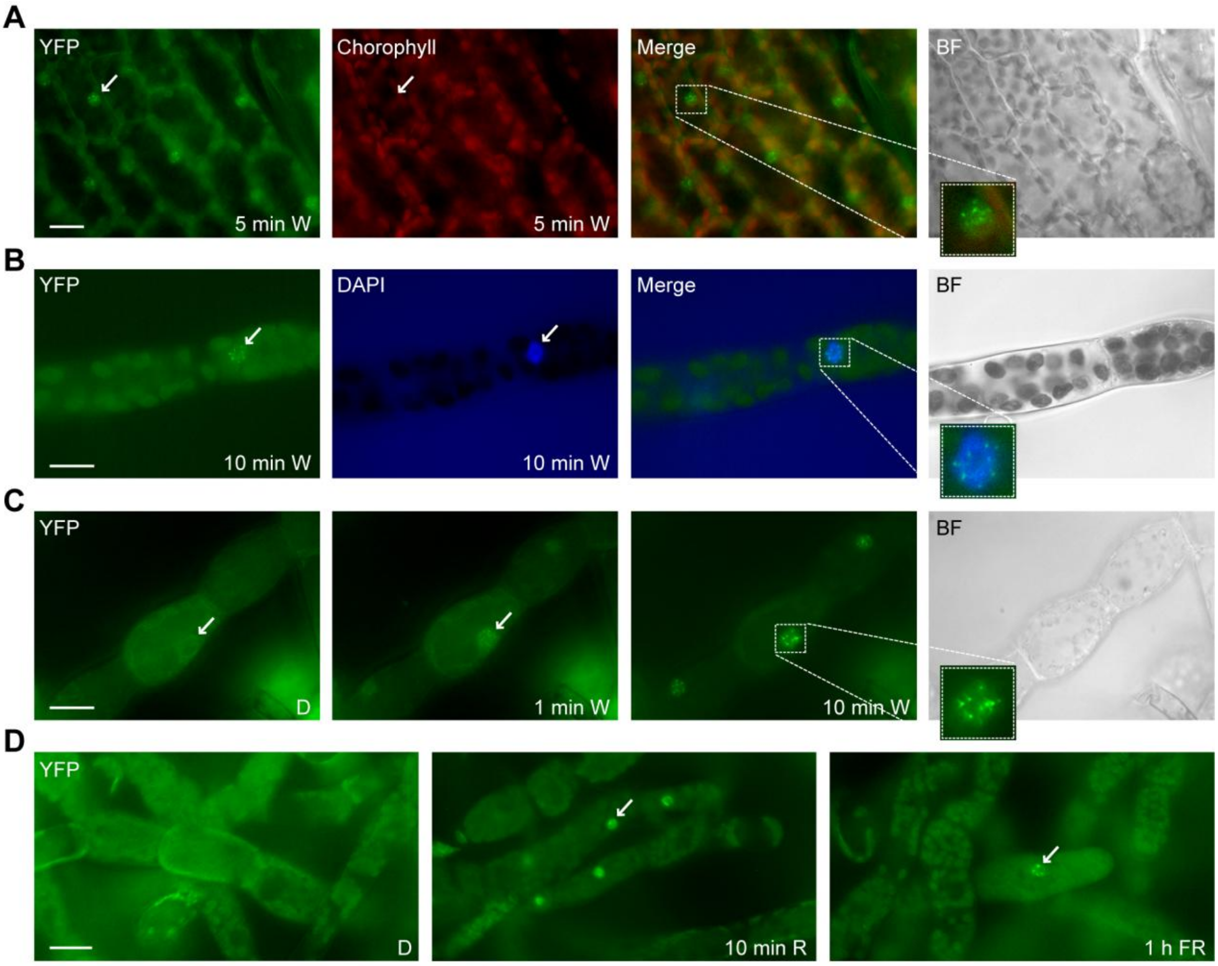

Figure 1. Rapid light-induced nuclear transport of *P. patens* PHY1.

(A) Light-regulated nuclear accumulation of Pp-PHY1 in gametophores. Dark-adapted gametophores of transgenic *P. patens* plants expressing Pp-PHY1:YFP were exposed to W light for 5 min and used for fluorescence microscopy.

(B) DAPI staining. Dark-adapted protonema filaments of Pp-PHY1:YFP expressing *P. patens* plants were exposed to W light for 10 min, fixed with formaldehyde, stained with DAPI and analyzed by fluorescence microscopy.

(C) Rapid light-induced nuclear transport of Pp-PHY1 in protonema filaments. Dark-adapted protonema filaments of *P. patens* plants expressing YFP-tagged Pp-PHY1 were used for time series fluorescence microscopy. Images were acquired before (dark control [D]) and 1 and 10 min after the onset of irradiation with W light.

(D) Nuclear accumulation of *P. patens* PHY1 is induced by R and FR light. Protonema filaments of *P. patens* plants expressing Pp-PHY1:YFP were dark-adapted and used for fluorescence microscopy. Images were acquired before and after irradiation with R light (10 min, 22 μmol m^{-2} s^{-1}) or FR light (1 h, 18 μmol m^{-2} s^{-1}). The samples were fixed with formaldehyde before microscopic analysis.
Arrows indicate nuclei; insets show enlargements of nuclei. Merge, merge of YFP and chlorophyll/DAPI channels; BF, bright field. Bars = 20µm.

Using particle bombardment, we also found that PHY2 from the moss *Ceratodon purpureus* (Cp-PHY2) accumulated in the nucleus of *P. patens* protonema cells (Supplemental Figure 3A). Moreover, phytochromes from the fern *A. capillus-veneris* (Ac-PHY1, Ac-PHY2, Ac-PHY3) localized in the nucleus of *A. capillus-veneris* gametophore cells, although a fraction may remain in the cytosol (Supplemental Figure 3B). In summary, our findings in cryptogams support the hypothesis that nuclear accumulation of phytochromes is not restricted to seed plants.

To investigate if nuclear transport of cryptogam phytochromes depends on a mechanism similar to seed plants, we expressed YFP-tagged Cp-PHY2 and Ac-PHY1 in *Arabidopsis* plants. In etiolated seedlings irradiated for 6 h with either R or FR light, Cp-PHY2:YFP and Ac-PHY1:YFP accumulated in the nucleus (Supplemental Figure 4A). Moreover, transiently expressed *Arabidopsis* PHYA:YFP localized to the nucleus in *P. patens* protonema cells (Supplemental Figure 4B), confirming recent results by Jaedicke et al. (2012). This suggests that phytochrome nuclear transport is mediated by a similar mechanism in seed plants and cryptogams. However, despite light-dependent nuclear accumulation, cryptogam phytochromes are not functional in *Arabidopsis* but interfere with proper light perception (Supplemental Figure 4C and 4D).

P. patens FHY1 is essential for light-regulated phytochrome nuclear transport and gene expression

FHY1-like proteins consist of an NLS and a PHYA binding motif, linked by a spacer of roughly 150 amino acid residues (Genoud et al., 2008). Using the consensus sequence of the PHYA binding motif to search protein, genome, and EST databases we found potential FHY1-like proteins from different cryptogam species. In EST databases for *P. patens*, *Selaginella moellendorffii* (spikemoss) and *Ceratopteris richardii* (fern), we identified clones that code for proteins, which contain an NLS, a spacer, and a C-terminal PHYA binding motif (Figure 2A). For *A. capillus-veneris* (fern) and *Closterium* sp. (green alga) our search identified partial cDNA clones coding for the PHYA binding motif and part of the spacer, but lacking the 5' end of the coding sequence (Figure 2A). Using RT-PCR, we amplified the Pp-*FHY1* coding sequence predicted in the database (Phypa_446283). Pp-*FHY1* contains two introns, similar to *FHY1* from *Arabidopsis*, and codes for a protein of 402 amino acids.

In *Arabidopsis*, FHY1 (At-FHY1) is essential for PHYA nuclear translocation and signaling. To test cryptogam FHY1-like proteins for a function in phytochrome nuclear transport, we knocked out *P. patens FHY1* in Pp-PHY1:YFP lines using gene targeting (Figure 2B). Nuclear accumulation of Pp-PHY1:YFP was strongly reduced in two independent Pp-*FHY1* KO lines (Figure 2C and Supplemental Figure 5), suggesting that Pp-FHY1 functions as a nuclear transport factor for phytochromes, similar to seed plant FHY1.

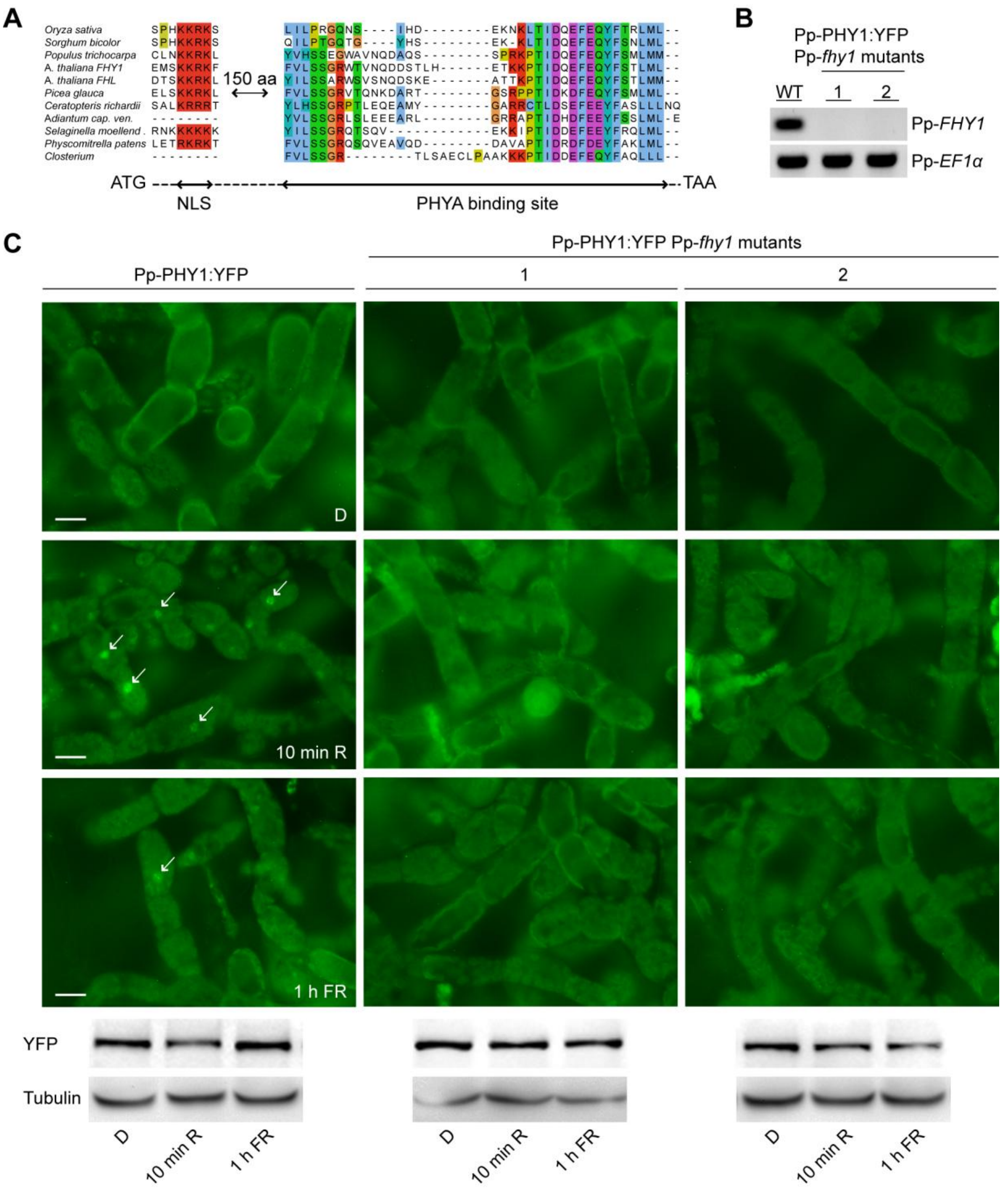

Figure 2. Pp-FHY1 is essential for Pp-PHY1 nuclear transport in *P. patens*.

(A) Cryptogams contain FHY1-like proteins. Sequence alignment of FHY1-like proteins from monocots, dicots, gymnosperms and cryptogams. Only regions of high sequence similarity are shown. The dashed line indicates nonaligned regions. aa, amino acids.

Using yeast two-hybrid assays, we found that FHY1-like proteins from ferns, mosses, and algae interact with *Arabidopsis* PHYA in a Pfr-dependent manner, similar to FHY1-like proteins from gymnosperms, monocots, and dicots (Figure 3A). Moreover, Pp-FHY1 interacted predominantly with the Pfr form of Pp-PHY1, Pp-PHY2, Pp-PHY3, and Pp-PHY4 fragments corresponding to the minimal At-PHYA fragment (PHYA 1-406), which binds to At-FHY1 (Figure 3B). Testing further cryptogam FHY1-like proteins and phytochromes, we also found Pfr-specific interactions between Cr-FHY1 and both Ac-PHY1 and Ac-PHY2 as well as between Pp-FHY1 and Cp-PHY2 (Supplemental Figure 6A and 6B). Furthermore, the expression of Pp-FHY1 and Cr-FHY1 in the *Arabidopsis fhy1-1* mutant restored hypocotyl growth inhibition in FR light (Figure 3C), suggesting that FHY1-like proteins from cryptogams and seed plants are functionally equivalent. In line with this notion, we found that Pp-FHY1 colocalizes with At-PHYA in light-induced nuclear bodies in mustard (*Sinapis alba*; Figure 3D), similar to seed plant FHY1 (Hiltbrunner et al., 2005; Hiltbrunner et al., 2006). Moreover, transiently expressed Pro35S:Pp-FHY1:YFP was detected in the nucleus of *P. patens* protonema cells (Supplemental Figure 6C).

Considering a potential nuclear function of cryptogam phytochromes, we analyzed the transcriptional activity of *P. patens* genes that are homologous to different R and FR light-regulated *Arabidopsis* genes (Tepperman et al., 2001; Hare et al., 2003; Jang et al., 2007). Quantitative RT-PCR analyses showed that in wild-type *P. patens* protonemata, the expression of *CONSTANS-LIKE 2* (*COL2*) (Phypa_441024), *Asparagine Synthetase* (*ASN*) (Phypa_458363), and *Ferredoxin NADP+ Reductase-like Protein* (*FNR*) (Phypa_444678) is induced by R and FR light (Figure 4A and Supplemental Figure 7). Interestingly, in Pp-*fhy1* knockout mutants, FR-dependent transcription of *COL2*, *ASN,* and *FNR* is strongly impaired, whereas the transcript levels in R light were only slightly changed (Figure 4A and B and Supplemental Figure 7).

Figure 2. (continued)

(B) RT-PCR analysis of Pp-*fhy1* mutants. Pp-*FHY1* was deleted in Pp-PHY1:YFP-expressing lines. Two independent Pp-*fhy1* mutants were used for RT-PCR analysis and Pp-*EF1*α was used as a control. WT, the wild type.

(C) Light-induced nuclear transport of Pp-PHY1 depends on Pp-FHY1. Dark-adapted protonema filaments of *P. patens* wild type or Pp-*fhy1* mutants expressing Pp-PHY1:YFP were fixed before microscopy analysis. Images were acquired before (dark control [D]) and after irradiation with either R light (10 min, 22 μmol m^{-2} s^{-1}) or FR light (1 h, 18 μmol m^{-2} s^{-1}). Arrows indicate nuclei. Immunoblot analysis shows Pp-PHY1:YFP levels in the different light conditions. Bars = 20µm.

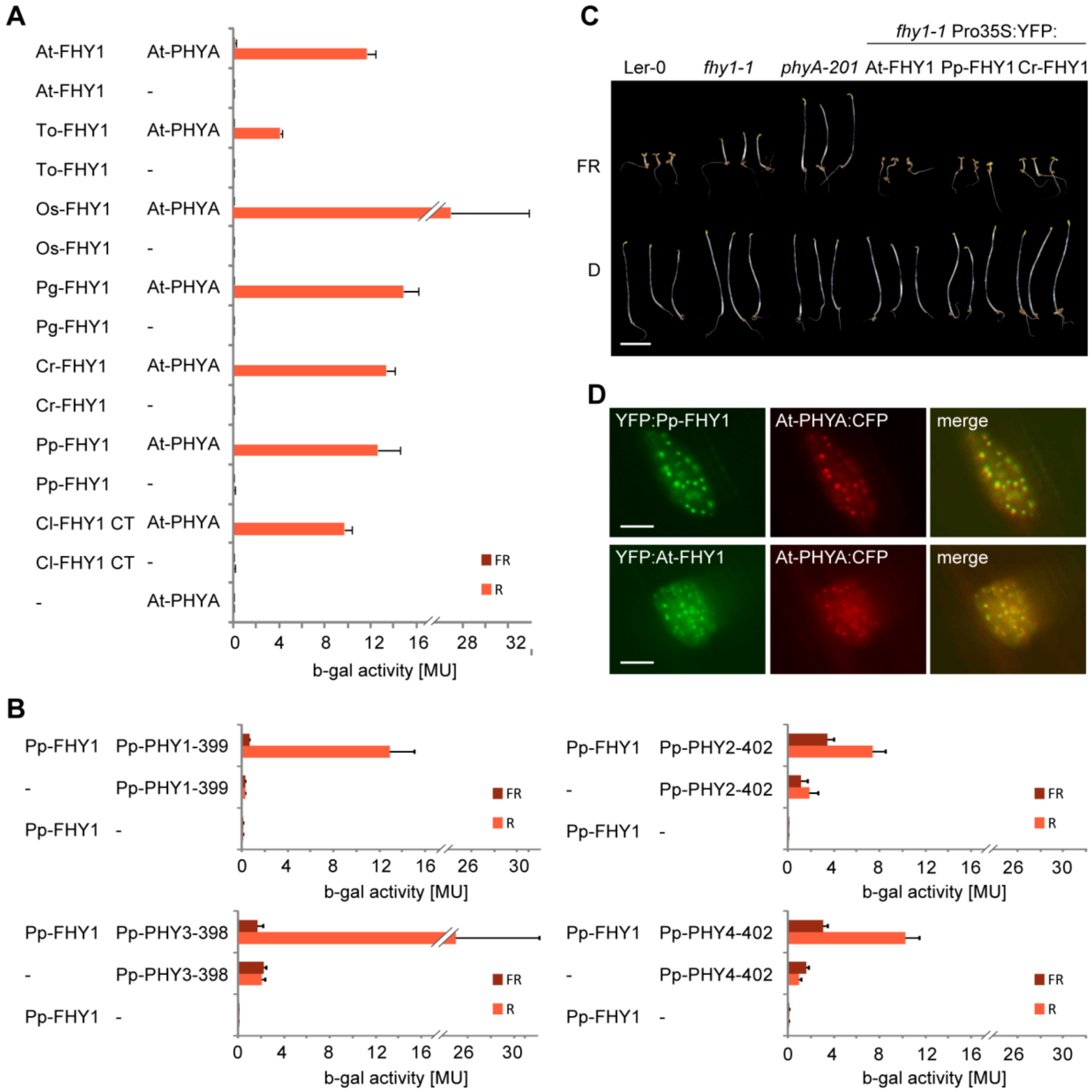

Figure 3. Cryptogam and seed plant FHY1 are functional homologues.

(A) Cryptogam FHY1 proteins contain a PHYA binding motif. AD-plasmids containing the coding sequence for the C-terminal phytochrome binding motif of FHY1 from *Closterium sp.* (Cl; green algae) or full-length FHY1 from *Arabidopsis* (At), dandelion (Taraxacum officinale; To), rice (Oryza sativa; Os), white spruce (*Picea glauca*; Pg), *Ceratopteris richardii* (Cr; fern) or *P. patens* (Pp) fused to the GAL4 activation domain were used for yeast two-hybrid analysis with *Arabidopsis* PHYA fused to the GAL4 DNA-binding domain. To convert PHYA to the Pfr or Pr form, yeast cultures were irradiated for 5 min with R (12 μmol m^{-2} s^{-1}) or FR light (12 μmol m^{-2} s^{-1}) and incubated for 4 h in the dark before measuring the β-galactosidase activity. MU, Miller Units. Error bars represent SE; n=3.

(B) *P. patens* phytochromes interact with Pp-FHY1 in a light regulated fashion. N-terminal fragments of *P. patens* phytochromes fused to the binding domain were used for yeast two-hybrid assays with AD:Pp-FHY1 as described in (A). MU, Miller Units. Error bars represent SE; n=3.

(C) *P. patens* and *Ceratopteris* FHY1 are functional in *Arabidopsis*. Landsberg *erecta*-0 (Ler-0), *fhy1-1* and *phyA-201* as well as *fhy1-1* seedlings expressing 35S promoter-driven YFP:At-FHY1, YFP:Pp-FHY1, or YFP:Cr-FHY1 were grown for 5 d in darkness (D) or FR (12 μmol m^{-2} s^{-1}). Bar = 5 mm.

(D) Pp-FHY1 and At-PHYA colocalize in light-induced nuclear bodies. Etiolated mustard seedlings were transformed by particle bombardment with constructs coding for Pro35S:PHYA:CFP and either Pro35S:YFP:At-FHY1 or Pro35S:YFP:Pp-FHY1. After transformation, the seedlings were incubated for 2 d in darkness and used for microscopy. The images were acquired after 5 min irradiation with W light. Bars = 10 μm.

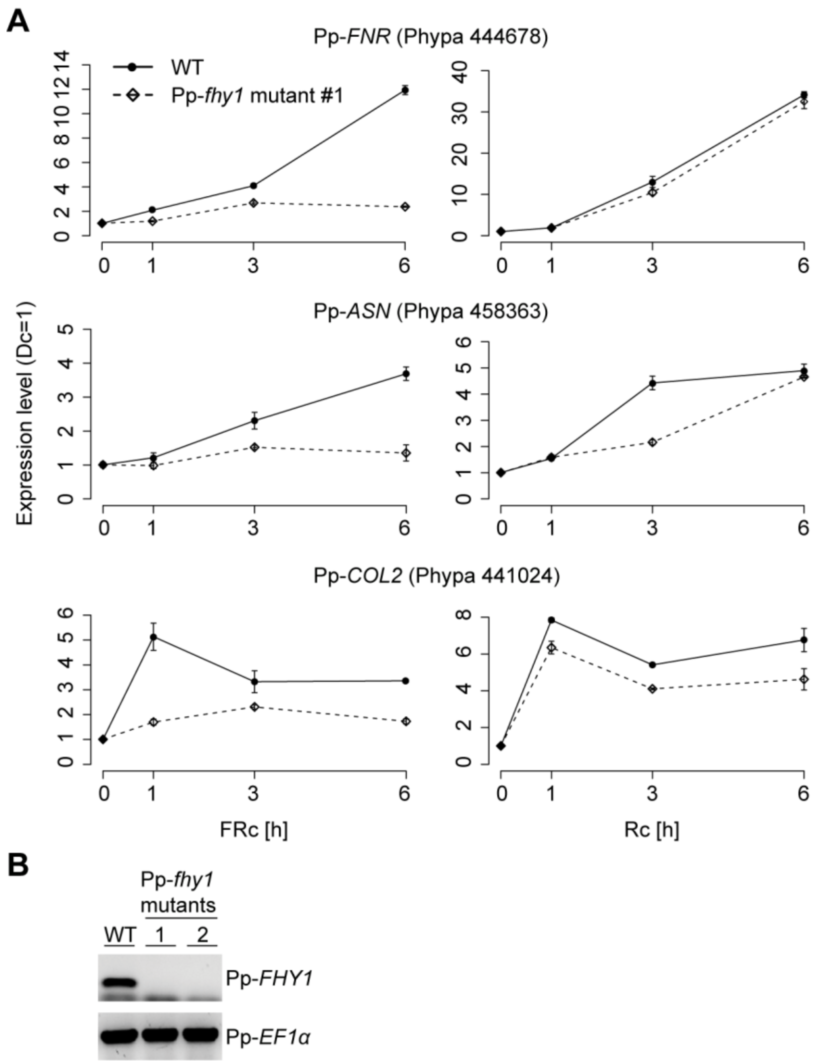

Figure 4. Pp-FHY1 is essential for FR light-induced gene expression.

(A) Protonemata cultures of *P. patens* wild type (WT) and Pp-*fhy1* mutant lines were dark adapted and exposed to either R light (28 μmol m^{-2} s^{-1}) or FR light (16 μmol m^{-2} s^{-1}). Samples for quantitative RT-PCR analyses were harvested after 1, 3, and 6 h of light treatment or darkness. The expression levels of *FNR*, *ASN*, and *COL2* were normalized to the levels of *26S rRNA*. Expression levels in darkness were set to 1. Error bars represent SE of technical replicates, n=3. An independent biological replicate is shown in Supplemental Figure 7.

(B) RT-PCR analysis of Pp-*fhy1* mutants. Pp-*fhy1* knockout lines were generated using gene targeting. Two independent Pp-*fhy1* mutant lines were used for RT-PCR analysis with primers specific for either Pp-*FHY1* or Pp-*EF1α*.

P. patens shows HIR-like responses

Next, we investigated whether FR light-dependent regulatory processes affected adaptive and developmental responses. *P. patens* spore germination as well as protonemata and gametophore growth were induced in continuous FR light (Figures 5A to 5C), whereas no growth was observed in darkness (see Supplemental Figure 8). This response mode was reminiscent of HIRs in seed plants. A distinctive feature of HIRs in seed plants is that they do not follow the reciprocity law (i.e., FR light pulses with the same total fluence cannot substitute for continuous FR irradiation) (Li et al., 2011). Indeed, in *P. patens,* FR light-induced spore germination as well as growth of protonemata and gametophores depended on continuous irradiation (Figures 5A to 5C) and therefore may be classified as HIR-like responses.

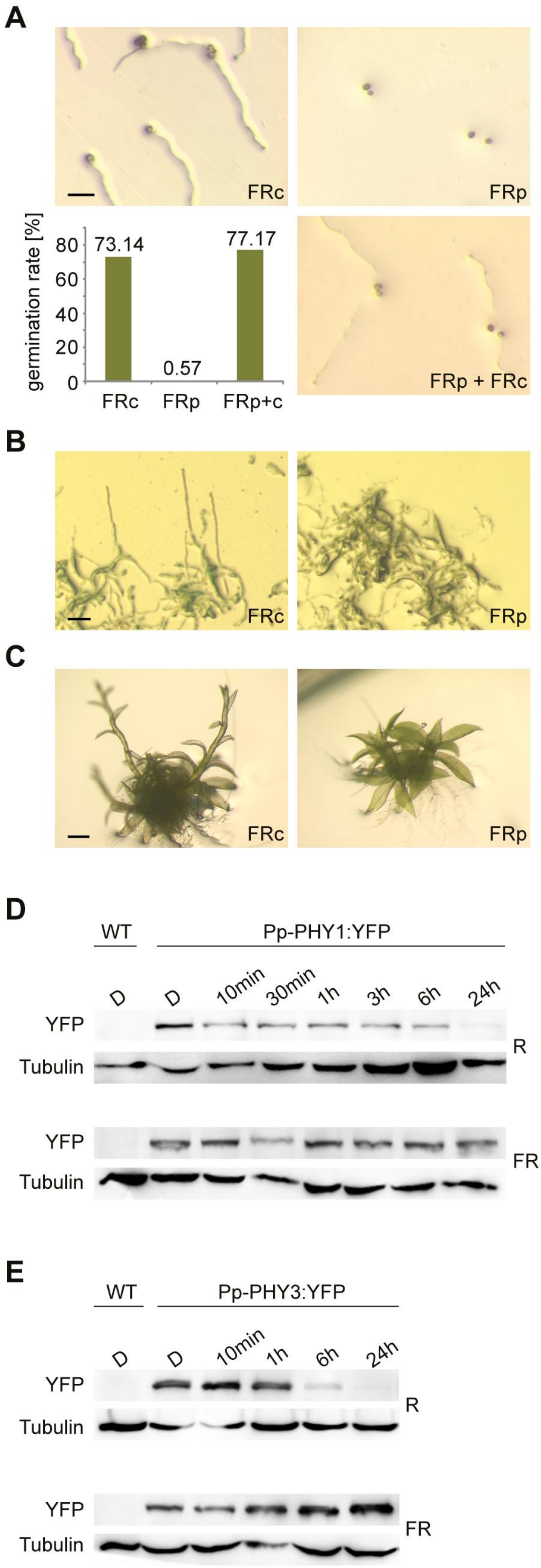

Figure 5. HIR-like responses to high fluence rate FR light in *P. patens*.

(A) Spore germination in FR light requires continuous irradiation. *P. patens* spores were irradiated for 3 d with continuous FR light (FRc; 3.5 μmol m^{-2} s^{-1}) or with 3 min FR light pulses (FRp; 70 μmol m^{-2} s^{-1}) of the same total fluence, interrupted by 57 min dark periods. To ensure that spores irradiated with FR pulses were viable, they were irradiated for an additional 3 d with continuous FR light (FRp + FRc). The bar plot shows significantly reduced germination rate in FRp (Fisher's exact test $P < 2.2e-16$). Bar = 100 μm.

(B) Protonemata growth in FR light depends on continuous irradiation. *P. patens* cultures were grown for 20 d in continuous FR light (3.5 μmol m^{-2} s^{-1}) or irradiated with 3 min FR light pulses (70 μmol m^{-2} s^{-1}) of the same total fluence, interrupted by 57 min dark periods. For dark controls, see Supplemental Figure 8B. Bar = 100 μm.

(C) Continuous irradiation is essential for FR light-induced gametophore growth. *P. patens* gametophores were grown for 9 d in continuous FR light (3.5 μmol m^{-2} s^{-1}) or irradiated with 3 min FR light pulses (70 μmol m^{-2} s^{-1}) of the same total fluence, interrupted by 57 min dark periods. For dark controls, see Supplemental Figure 8C. Bar = 500 μm.

(D) Pfr-dependent degradation of Pp-PHY1. Dark-adapted protonemata cultures of *P. patens* lines expressing YFP tagged Pp-PHY1 were irradiated with R light (22 μmol m^{-2} s^{-1}) or FR light (18 μmol m^{-2} s^{-1}) for different time periods. Total protein was isolated and analyzed by SDS-PAGE and immunoblotting with anti-YFP antibody. Protein extracts from dark-adapted wild-type *P. patens* cultures were used as negative controls. Tubulin is shown as a loading control. D, darkness. WT, the wild type.

(E) Pfr-dependent degradation of Pp-PHY3. Dark-adapted protonemata cultures of *P. patens* lines expressing Pp-PHY3:YFP were irradiated with either R or FR light and used for SDS-PAGE and immunoblot analysis as described in (D).

Pp-FHY1 is required for HIR-like responses of P. patens

Rapid degradation of PHYA after its conversion into the light-activated Pfr form is essential for HIRs in seed plants (Rausenberger et al., 2011). We analyzed the stability of *P. patens* phytochromes in lines expressing endogenous phytochromes tagged with YFP. Immunoblot analyses with YFP-specific antibodies and microscopy analyses demonstrated that Pp-PHY1:YFP and Pp-PHY3:YFP were degraded in the Pfr form (R light) but were stable in Pr (FR light) (Figures 5D and 5E, Supplemental Figure 2A and 2B). Pp-PHY1 and Pp-PHY3 are therefore potential photoreceptors for the HIR-like responses in *P. patens*.

Another essential determinant for *Arabidopsis* HIRs is continuous photocycling and nuclear accumulation of PHYA, which depends on the nuclear transport proteins At-FHY1 and At-FHL (Rausenberger et al., 2011). Pp-*fhy1* knockout interfered with the nuclear accumulation of Pp-PHY1:YFP (Figure 2C and Supplemental Figure 5), which is in line with the idea that Pp-PHY1 and its closest homolog, Pp-PHY3, are receptors for HIR-like responses in *P. patens*. Analogous to At-FHY1 in *Arabidopsis*, Pp-FHY1 would then constitute an upstream prerequisite for phytochrome-mediated HIR-like responses in *P. patens*. Indeed, FR light-dependent spore germination as well as protonemata and gametophore growth were severely inhibited in two independent Pp-*fhy1* mutant lines (Figures 6A to 6C). Furthermore, protonemata side branching was reduced in light with a low R:FR ratio (Supplemental Figure 9). These effects of Pp-*fhy1* knockout were specific for FR light and low Pfr/Ptot ratios, as we did not observe any differences in other light qualities or in darkness (Supplemental Figure 8A to 8C). Thus, Pp-FHY1 is essential for HIR-like responses in *P. patens*.

DISCUSSION

Localization and function of cryptogam phytochromes in the nucleus

Using stable transgenic *P. patens* lines, we visualized the dynamics of the subcellular localization of cryptogam phytochromes. We found that *P. patens* phytochromes accumulated in the nucleus upon light-dependent conversion to the active Pfr form, which is reminiscent of the first steps in phytochrome signaling in seed plants.

Moreover, we showed that cryptogam phytochromes translocated into the nucleus in *Arabidopsis* seedlings and that, in agreement with Jaedicke et al. (2012), *Arabidopsis* PHYA accumulated in the nucleus of *P. patens* protonema cells. Thus, it seems that seed plant and cryptogam phytochrome nuclear transport rely on an evolutionarily conserved mechanism. Interestingly, previous studies have described cryptogam phytochromes as mainly localizing and acting in the cytosol and/or at the plasma membrane and there has been only limited evidence for a function in the nucleus (Rösler et al., 2010; Tsuboi et al., 2012). In contrast with this, phytochromes from *Arabidopsis* and other seed plants were shown to translocate to the nucleus after activation by light, where they mediate changes in gene expression (Li et al., 2011).

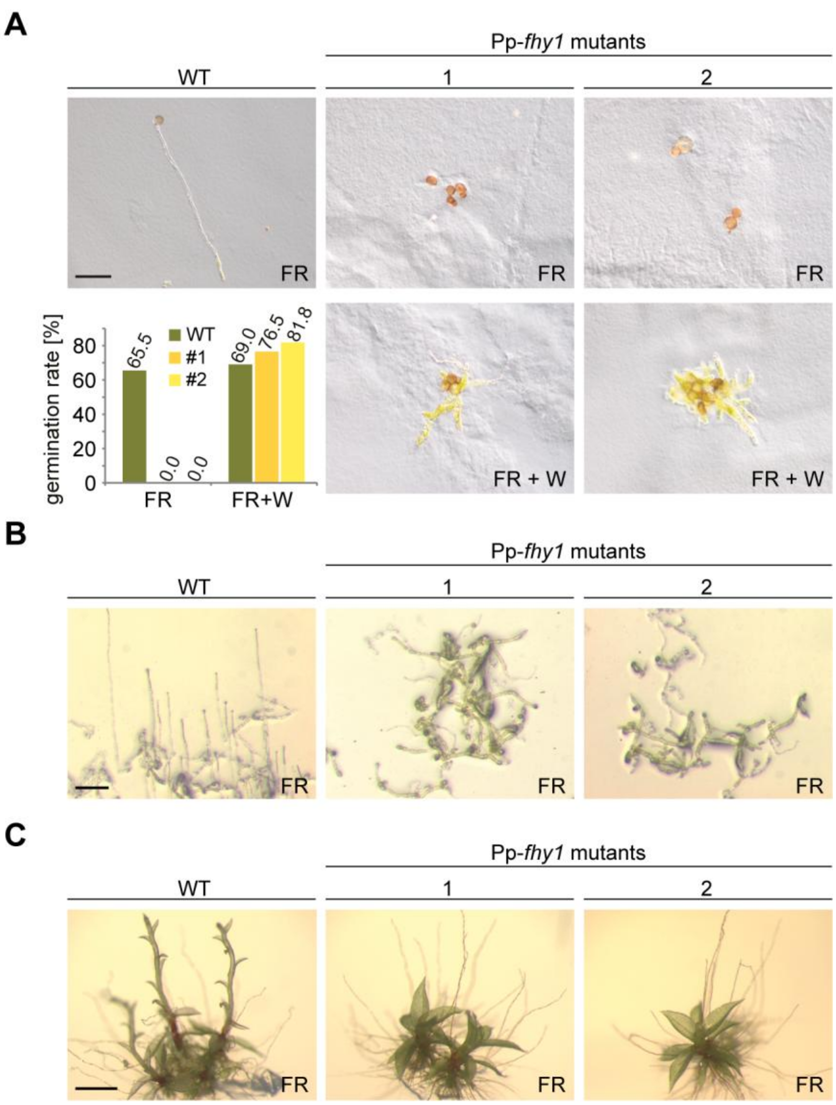

Figure 6. Pp-FHY1 is essential for HIR-like responses to high fluence rate FR light.

(A) Spore germination in FR light depends on Pp-FHY1. Spores from wild type (WT) *P. patens* plants and two independent Pp-*fhy1* mutant lines were irradiated for 8 d with continuous FR light (18 μmol m^{-2} s^{-1}). To ensure that Pp-*fhy1* mutant spores irradiated with FR light were viable, they were irradiated for an additional 5 d with W light after the FR light treatment. The bar plot shows significantly reduced germination rate in Pp-fhy1 mutants (Fisher's exact test $P < 3.4e\text{-}05$) Bar = 100 μm.

(B) Pp-FHY1 is essential for protonemata growth in FR light. Wild type and Pp-*fhy1* mutant *P. patens* cultures were grown for 13 d in FR light (18 μmol m^{-2} s^{-1}). Bar = 100 μm.

(C) FR light-induced gametophore growth requires Pp-FHY1. Wild type and Pp-*fhy1* mutant *P. patens* gametophores were grown for 11 d in FR (18 μmol m^{-2} s^{-1}). Bar = 500 μm.

Consistent with our observations of a light-dependent nuclear localization of *P. patens* phytochromes, R and FR light also induced changes in gene expression in *P. patens*. However, Moss and fern phytochromes interfered with phytochrome signaling in *Arabidopsis*, which might reflect differences between seed plants and cryptogams regarding downstream signal transduction. Considering these novel aspects of phytochrome localization and signaling in cryptogams, one can assume a dual localization and spatial function of *P. patens* phytochromes, with one phytochrome pool in the cytosol and/or at the plasma membrane and one pool translocating to the nucleus. In summary, our data show that nuclear localization and function of phytochromes are not exclusive to seed plants but are common to all land plants.

FHY1 proteins from seed plants and cryptogams are functional homologues

The split of the phytochrome gene lineage into PHYA- and PHYB-like phytochromes only occurred in seed plants. Nevertheless, even though cryptogams do not have PHYA-like phytochromes, we identified FHY1-like proteins in several cryptogams. In *Arabidopsis*, the nuclear translocation of light-activated At-PHYA depends on At-FHY1 and its homolog At-FHL and is about ten-fold faster than At-PHYB nuclear transport (Kircher et al., 2005; Hiltbrunner et al., 2006; Rösler et al., 2007). The rapid nuclear accumulation we observed for *P. patens* phytochromes is reminiscent of At-PHYA nuclear transport, suggesting a similar transport mechanism for cryptogams. Indeed, in the *P. patens fhy1* KO mutant, the nuclear accumulation of Pp-PHY1:YFP was strongly reduced in R and FR light and FR-induced gene expression was inhibited. Furthermore, FHY1-like proteins from cryptogams were functional in *Arabidopsis*. We therefore postulate the existence of an FHY1-dependent phytochrome nuclear transport system in cryptogams, similar to the transport system essential for PHYA signaling in seed plants. Interestingly, recent studies have shown that growth of *P. patens* mutants deficient in phytochrome chromophore biosynthesis is strongly reduced in R light (Chen et al., 2012), whereas the phenotype of Pp-*fhy1* knockout mutants is mostly FR light-specific. Thus, we assume the existence of alternative nuclear transport systems for phytochromes in *P. patens* as present in seed plants (Chen et al., 2005; Pfeiffer et al., 2012).

HIR-like responses are not restricted to seed plants

According to the current assumption, seed plants acquired the ability to respond to FR light along with the evolution of PHYA. It has been shown that PHYA is essential for germination and seedling establishment in environments enriched in FR light, such as in canopy shade (Yanovsky et al., 1995; Botto et al., 1996). In contrast with seed plants, cryptogams do not contain PHYA-like phytochromes, and there has been little evidence that FR light has major effects on growth and development of cryptogams (Mathews, 2006). Thus, it has been suggested that PHYA-like FR light signaling is restricted to seed plants.

However, we observed that FR light triggered several adaptive and developmental responses in the moss *P. patens*. Importantly, these responses failed to obey the reciprocity law (i.e., FR light pulses with the same total fluence could not substitute for continuous FR irradiation). This is a hallmark of the HIRs in seed plants, which strictly depend on PHYA (Mathews, 2006; Li et al., 2011). We have recently shown that rapid degradation of the Pfr form and FHY1-dependent nuclear transport are key features of PHYA that are required for the HIRs (Rausenberger et al., 2011). Interestingly, in *P. patens*, nuclear transport of Pp-PHY1 depends on Pp-FHY1, and Pp-PHY1 as well as Pp-PHY3 are rapidly degraded after conversion to the Pfr form. Thus, our data suggest that Pp-PHY1 and Pp-PHY3 are potential receptors for HIRs in *P. patens* and that HIR-like responses do not require PHYA. In general, any phytochrome that meets the requirements defined by Rausenberger et al. (2011) (i.e., rapid degradation of the Pfr form and FHY1-dependent nuclear transport) may work as a sensor for HIRs. We conclude that FR light signaling and HIR-like responses are not restricted to seed plants but had already evolved in the last common ancestor of modern seed plants and cryptogams. The capacity to mediate HIRs might have been intrinsic to all phytochromes and could have been lost in the course of evolution by PHYB and other type II phytochromes from seed plants. In seed plants, PHYB works as sensor for the R/FR light ratio, which is important to detect potential competitors at an early stage. As a function in HIR signaling is likely to interfere with the perception of R/FR light ratios, plants may have been under ecological pressure driving the sub-functionalization of phytochromes specialized for either detecting the R/FR light ratio or mediating HIRs. Although the mechanistic similarity of FR light sensing in seed plants and cryptogams strongly suggests a common evolutionary origin, we cannot rule out that they are the result of convergent evolution, leading to similar FR light signaling and response mechanisms.

Interestingly, FR light-induced protonemata and gametophore growth in *P. patens* were reminiscent of etiolation and shade avoidance growth in seed plants. In *Arabidopsis*, these responses can be considered as default development at low levels of activated phytochromes, which are thus positive regulators of deetiolation and photomorphogenesis. Under FR light, PHYA antagonizes the shade avoidance response by promoting deetiolation. In contrast with this, we found that *P. patens* etiolation- and shade avoidance-like growth were impaired in Pp-*fhy1* knockout lines. They therefore do not constitute a default response but rather depend on phytochromes acting as positive regulators. This indicates that in seed plants and cryptogams the adaptation to shade conditions relies on phytochrome-dependent FR light sensing but follows different strategies.

In terms of physiological relevance, it is conceivable that FR light signaling is advantageous not only to seed plants, which had to adapt to increased shade conditions, but also to cryptogams. Grassland habitats of *P. patens* might equally require adaptation of growth and development to micro environments enriched in FR light. Due to its short height, *P. patens* has to cope with shade conditions induced by neighboring plants typical for grasslands and could thus rely on the ability to perceive and integrate this information. Moreover, other cryptogams typically grow in forest habitats, where the ability to sense FR light might be equally important as for seed plants. As we also identified a potential FHY1 homolog in the green algae *Closterium sp* (Figure 2A), one could even assume a more general role of FR light signaling, which would not only be important for land plants but also for green algae and which might already have been relevant in their last common ancestor.

Similar to seed plants, the phytochrome gene lineage in *P. patens* split into two branches, with Pp-PHY1 and Pp-PHY3 on one branch, and Pp-PHY2, Pp-PHY4, and Pp-PHY5a/b/c on the other branch (Mittmann et al., 2009). Thus, it is tempting to speculate that Pp-PHY1 and Pp-PHY3 have PHYA-like functions, whereas Pp-PHY2, Pp-PHY4, and Pp-PHY5a/b/c may have functions similar to PHYB. Future work will have to resolve the sub-functionalization of phytochromes from cryptogams and even more ancient branches of the plant kingdom in order to increase our knowledge on the evolution of phytochrome signaling.

METHODS

Cloning of constructs

A detailed description of DNA constructs and a list including all primers used in this work can be found in the Supplemental Methods (see enclosed disc). A schematic representation of targeting constructs and genomic loci is given in Supplemental Figure 10.

Plant material and growth conditions

The *Arabidopsis thaliana* wild type used was either the Columbia-0 or Landsberg *erecta*-0 ecotype. The *fhy1-1* and *phyA-201* mutants as well as a transgenic line expressing YFP:At-FHY1 (*fhy1-1* Pro35S:YFP:FHY1) have been described previously (Whitelam et al., 1993; Quail et al., 1994; Hiltbrunner et al., 2005). *Arabidopsis* seeds were stratified for at least 2 d at 4 °C and grown on 0.5x Murashige and Skoog medium (Duchefa)/0.7% (w/v) agar at 22 °C in continuous R (12 μmol m^{-2} s^{-1}, 656 nm, 24 nm full width at half maximum [FWHM]) or FR light (15 μmol m^{-2} s^{-1}, 730 nm, 128 nm FWHM).

Cultivation of *Physcomitrella patens* on solid Knop medium or in liquid KNOP culture was performed according to Frank et al. (2005). To induce sporophyte development, gametophores were grown at 16 °C and 8/16h light/dark photoperiod (20 μmol m^{-2} s^{-1} PAR). After 4 to 6 weeks, gametophores were flooded with autoclaved tap water and cultivated for another 6 weeks. The sporophytes were opened by mechanical disruption, distributed on solid Knop medium, and incubated in R (670 nm), FR (740 nm), and B light (473 nm) or in darkness. For analysis of protonemata growth, protonemata liquid culture was spotted on solid Knop medium and vertically incubated in R, FR and B light or darkness. For testing gametophore growth, *P. patens* gametophores were pregrown in white light and then incubated in R, FR, or B light or darkness.

Adiantum capillus-veneris gametophyte cultures (provided by M. Wada, Kyushu University, Fukuoka, Japan) were grown on White's Basal Salt Mixtures (Sigma-Aldrich)/0.8% (w/v) agar at 25 °C and 16/8h light/dark photoperiod (50 to 70 μmol m^{-2} s^{-1} PAR). Fragmentation of the culture was performed every 2 weeks using a T18 Ultra Turrax disperser (IKA).

Transformation of Arabidopsis and P. patens

Arabidopsis lines expressing Pro35S:Ac-PHY1:YFP:TerRbcS, Pro35S:Cp-PHY2:YFP:TerRbcS, Pro35S:YFP:Pp-FHY1:TerRbcS or Pro35S:YFP:Cr-FHY1:TerRbcS were obtained by *Agrobacterium tumefaciens*-mediated transformation (Clough and Bent, 1998). The selection for transgenic plants using the herbicides BASTA (Hoechst Schering

AgrEvo) and Butafenacil/Inspire (Syngenta Agro) was performed as previously described (Block et al., 1987; Rausenberger et al., 2011).

P. patens transformation was performed according to Frank et al. (2005) using liquid cell culture for protoplast preparation. The selection was done on 12.5 mg/mL G418 or hygromycin. Positively selected gametophores were tested with PCR using primers derived from the sequence of the gene of interest and the integrated YFP (p050/p051 for Pp-PHY1:YFP, p028/ah070 for Pp-PHY2:YFP, p062/ah070 for Pp-PHY3:YFP, p023/ah070 for Pp-PHY4:YFP, p030/ah070 for Pp-PHY5a:YFP, and p026/ah070 for Pp-PHY5b:YFP) or with primers p046/p047 and p223/p225 for Pp-FHY1:HPT (see Supplemental Table 1 for primer sequences). PCR products were ligated blunt-end into pJET1.2 (Fermentas) and sequenced to verify sequences and borders. The molecular characterization of Pp-*fhy1* mutant lines is shown in Supplemental Figure 11.

Fluorescence microscopy

Arabidopsis seedlings used for microscopy were grown for 4 d on 0.5x Murashige and Skoog medium/0.7% (w/v) agar as described above and irradiated with either R light (12 μmol m^{-2} s^{-1}, 656 nm, 24 nm FWHM) or FR light (15 μmol m^{-2} s^{-1}, 730 nm, 128 nm FWHM) prior to microscopy analyses. A Zeiss Axioscope 2 equipped with YFP-, cyan fluorescent protein (CFP-), and mCherry-specific filter sets (AHF Analysentechnik) was used for image acquisition and ImageJ (version 1.44k; National Institute of Health) and Photoshop (version 10.0.0.1; Adobe) software for image processing.

P. patens protonema liquid culture was transferred to Knop plates with or without 5 μM norflurazone and grown for 2 to 6 d at 25 °C and 16/8h light/dark photoperiod (50 to 70 μmol m^{-2} s^{-1} PAR). The cultures were then adapted to darkness for 3 to 6 d. The preparation of samples was done in safety green-light (526 nm); for preparation of fixed probes, the protonemata samples were transferred to 1.2% formaldehyde/MTSB (7.5 g PIPES, 0.95 g EGTA, 0.66 g $MgSO_4 \cdot 7\ H_2O$, and 2.5 g KOH in 500 mL, pH 7.0) directly after light treatment and incubated in darkness for 10 to 15 min. For 4’,6-diamidino-2-phenylindole (DAPI) staining, *P. patens* samples were exposed to white light for 3 to 10 min, and then imbibed in 0.1 mg/L DAPI in 3% p-formaldehyde/MTSB and incubated in darkness for 15 min. Image acquisition of *P. patens* and *A. capillus-veneris* cultures was done on an Axiovert 200M MAT system (Zeiss) or an Axioscope 2 equipped with YFP-, CFP-, chlorophyll-, and mCherry-specific filter sets. All images were acquired using Metamorph (version 6.2r4). ImageJ (version 1.44k) and Photoshop (version 10.0.0.1) software was used for image processing.

Transient expression in mustard, P. patens, and A. capillus-veneris

The transient transformation of mustard (*Sinapis alba*) seedlings has been described previously (Stolpe et al., 2005). After cotransformation with pUC1940:At-PHYA and either pCHF70:At-FHY1 or pCHF70:Pp-FHY1, the mustard seedlings were grown overnight in darkness and used for microscopy analysis as described for *Arabidopsis* seedlings.

P. patens and *A. capillus-veneris* cultures were inoculated onto cellophane sheets placed on solid medium, covered with another sheet of cellophane to prevent upright growth, and incubated under standard growth conditions for 4 to 6 d. pCHF70:Pp-FHY1, pPPO30:Ac-PHY1, pUC1930:Ac-PHY2, pUC1930:Ac-PHY3, pPPO30:Cp-PHY2, and pUC1930:At-PHYA, either with or without pCHF150myc or pUC1942, were transiently transformed into *P. patens* or *A. capillus-veneris* cultures by particle bombardment with the Biolistic Particle Delivery System (Bio-Rad). Gold particle diameter was 1 µm, helium pressure 7 bar. chamber vacuum pressure 0.8 bar, and target distance 5 cm. After bombardment, the samples were kept in darkness for 1 to 5 d before microscopy analysis.

RNA extraction and RT-PCR analyses

P. patens protonemata liquid cultures were inoculated onto cellophane sheets placed on solid Knop medium and incubated for 7 d under standard conditions. At the end of the light period on the 7th day, the samples were transferred to darkness for 5 d. After incubation in R or FR light or continuing darkness, the cultures were harvested and RNA was extracted using the RNeasy Plant Mini Kit (Qiagen). Total RNA (0.5 to 1 µg) was treated with DNaseI (Fermentas) and reverse transcribed using the First-Strand cDNA Synthesis Kit (Fermentas). One to two microliters of the resulting cDNA solution was used for PCR or quantitative PCR (Maxima SYBR Green qPCR Master Mix, Fermentas; Bio-Rad CFX384 real-time-system) using standard protocols and primers as follows: p065/p066 for Pp-*EF1α*, p069/p070 for Pp-*FHY1*, p158/p159 for *26S rRNA*, p118/p119 for Pp-*COL2*, p186/p187 for Pp-*ASN*, and p188/p189 for Pp-*FNR* (see Supplemental Table 1 for primer sequences).

Immunoblot analyses

P. patens protonemata liquid cultures were inoculated onto cellophane sheets placed on solid Knop medium and incubated in darkness for 5 d. After light treatment, the plant material was harvested, ground in liquid nitrogen, and resuspended in protein extraction buffer (50 mM Tris, pH 7.5, 150 mM NaCl, 1 mM EDTA, 10% [v/v] glycerol, 1 mM DTT, and complete Protease Inhibitor [Roche]). After centrifugation at 4°C, the cleared protein samples were used for SDS-PAGE and immunoblot transfer according to standard protocols. Immunodetection was performed using protein specific antibodies (GFP, Abcam; tubulin, Sigma-Aldrich).

Yeast two-hybrid analyses

Yeast two-hybrid analyses and o-Nitrophenyl-β-D-galactopyranoside (ONPG) assays were performed according to previously published protocols (Hiltbrunner et al., 2005). For all yeast two-hybrid, assays the yeast strain Y187 (Clontech) was used. The growth medium was supplemented with phycocyanobilin purified from *Spirulina* (final concentration 10 μM) (Kunkel et al., 1993).

Database searches

We searched the databases available at http://www.ncbi.nlm.nih.gov/ and http://www.cosmoss.org/ for proteins from cryptogams containing the consensus PHYA binding motif of FHY1/FHY1-like proteins from seed plants (YVLSSGRWXVNQDKPTIDQEFEQYFSMLML). As suggested by the National Center for Biotechnology Information BLAST program selection guide (http://www.ncbi.nlm.nih.gov/blast/producttable.shtml), we used settings optimized to identify short, nearly exact matches for this search. Sequences were aligned using MAFFT v6.717b and Jalview 2.7 (Waterhouse et al., 2009).

Accession numbers

Sequence data from this article can be found in the The Arabidopsis Information Resource, GenBank, or Cosmoss (www.cosmoss.org) databases under the following accession numbers: DK958635 (Ac-*FHY1*), AB016168 (Ac-*PHY1*), AB016232 (Ac-*PHY2*), AB012082 (Ac-*PHY3*), AT5G02200 (At-*FHL*), AT2G37678 (At-*FHY1*), AT1G09570 (At-*PHYA*), BW647715 (Cl-*FHY1*), U56698 (Cp-*PHY2*), BE640872 (Cr-*FHY1*), AK070454 (Os-*FHY1*), BT111284 (Pg-*FHY1*), Phypa_458363 (Pp-*ASN*), Phypa_441024 (Pp-*COL2*), Phypa_424011 (Pp-*EF1*□), Phypa_446283 (Pp-*FHY1*), Phypa_444678 (Pp-*FNR*), AB275304 (Pp-*PHY1*), AB275305 (Pp-*PHY2*), XM_001765983 (Pp-*PHY3*), AB275307 (Pp-*PHY4*), XM_001761093 (Pp-*PHY5a*), XM_001767172 (Pp-*PHY5b*), HM751653 (Pp-*26S rRNA*), XM_002309031 (Pt-*FHY1*), XM_002468063 (Sb-*FHY1*), XM_002992728 (Sm-*FHY1*), and DY831102 (To-*FHY1*).

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AUTHOR CONTRIBUTIONS

A.P. and A.H. designed the research, did the experimental work, analyzed the data, and wrote the article.

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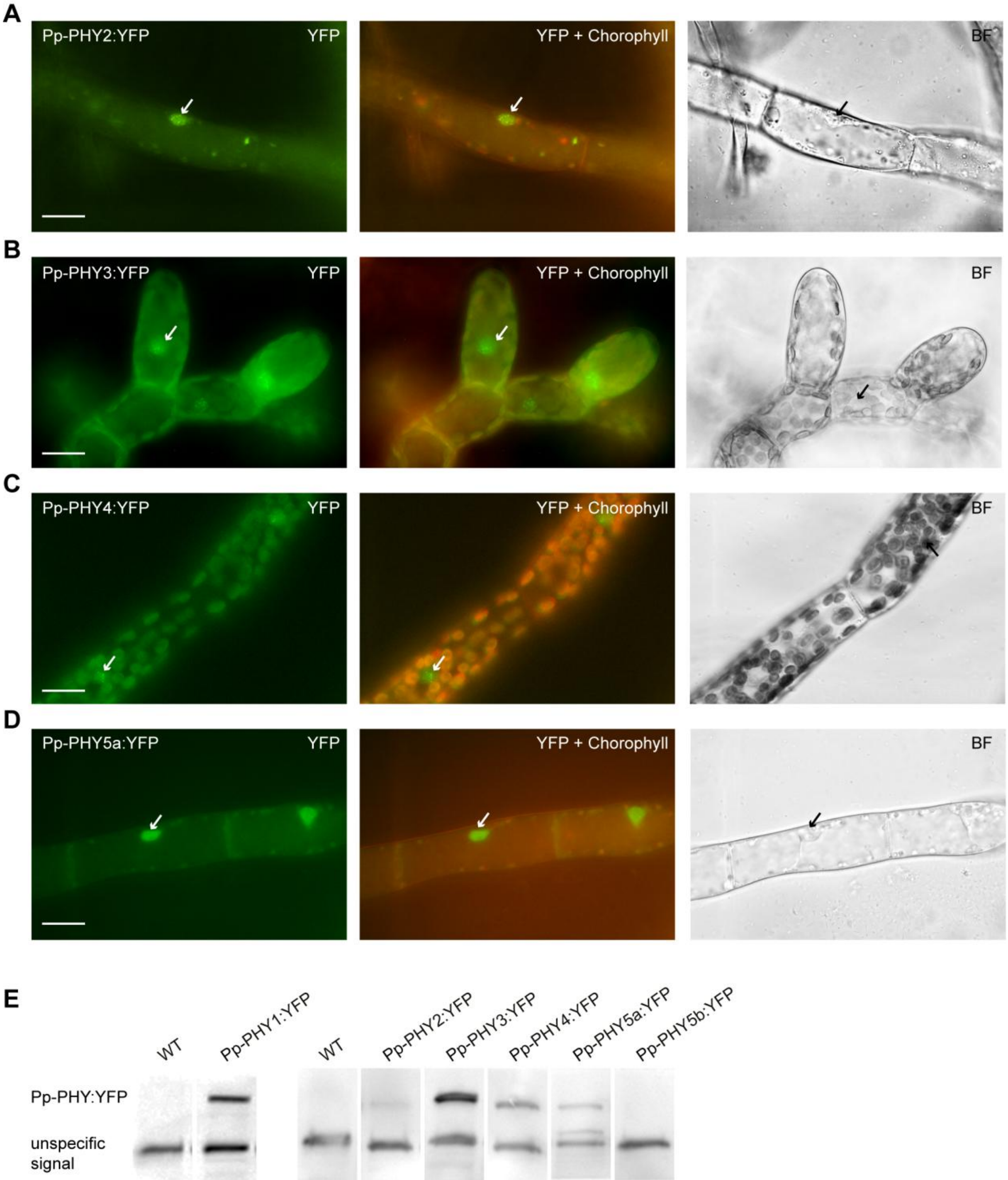
SUPPLEMENTAL DATA

Supplemental Figures

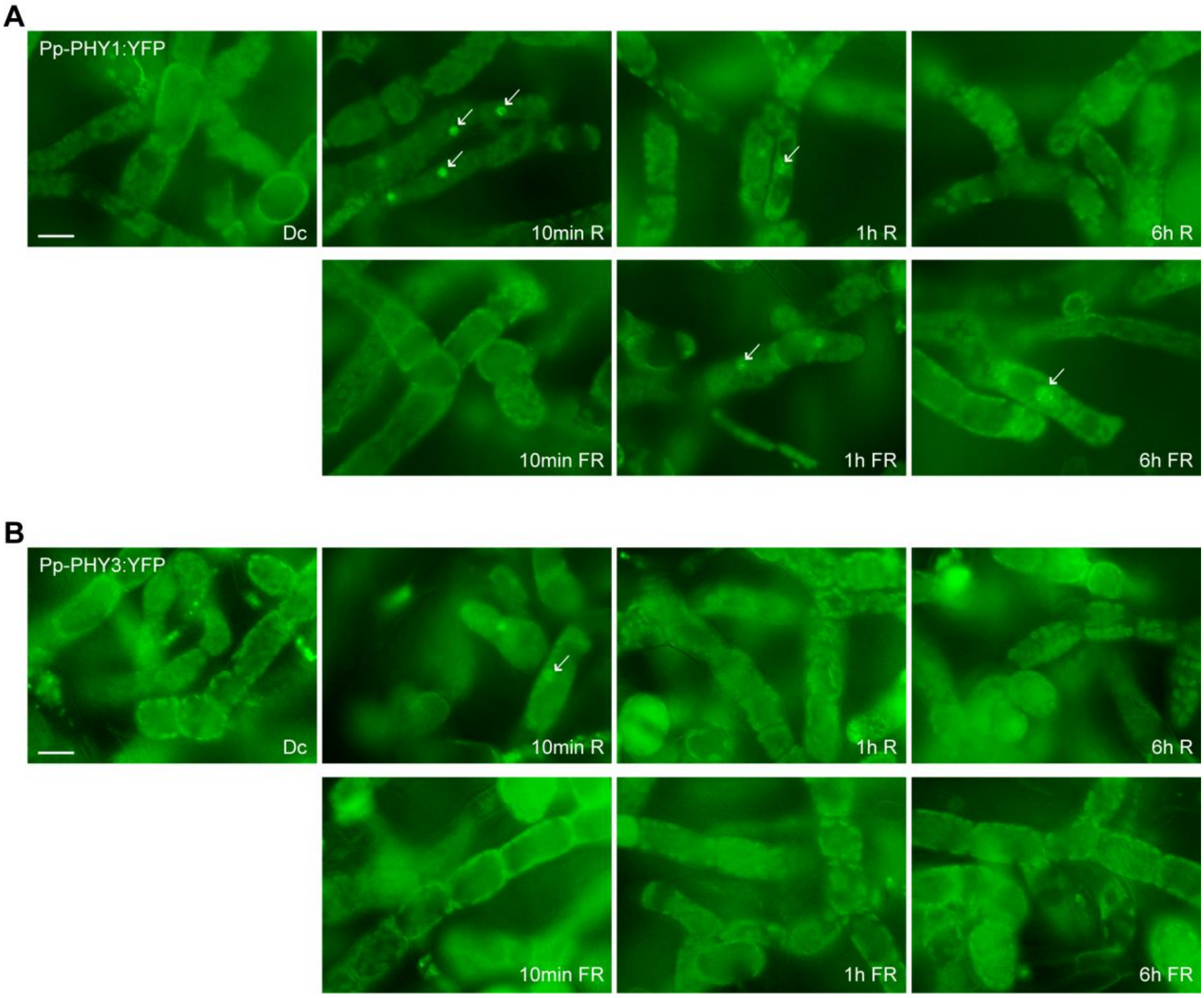


Supplemental Figure 1. Nuclear localization of *Physcomitrella* phytochromes.

(A)-(D) Nuclear localization of Pp-PHY2, Pp-PHY3, Pp-PHY4 and Pp-PHY5a in protonema filaments. Dark-adapted protonema filaments of *Physcomitrella* plants expressing YFP-tagged Pp-PHY2 **(A)**, Pp-PHY3 **(B)**, Pp-PHY4 **(C)** or Pp-PHY5a **(D)**, of which Pp-PHY2:YFP and Pp-PHY5a:YFP lines had been bleached with Norflurazone, were used for fluorescence microscopy. Images were acquired after 10-30 min irradiation with W light. Bars = 20 μm. Arrows indicate nuclei BF, bright field.

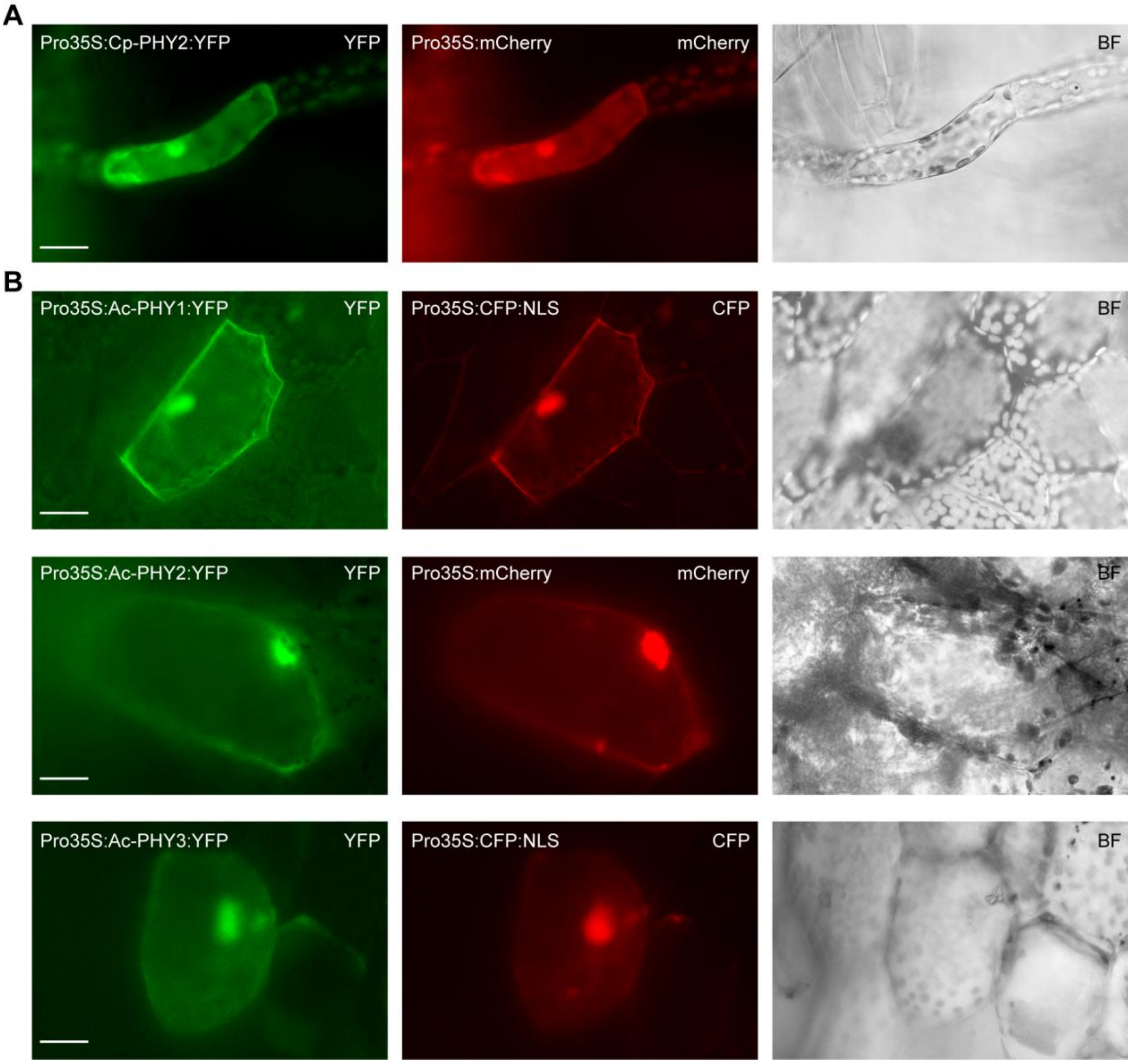
Supplemental Figure 1. (continued)

(E) (Duplicates images in Figure 5E) Immunoblot analyses for Pp-PHY:YFP expressing lines. Dark-adapted protonema cultures of *Physcomitrella* lines expressing YFP-tagged Pp-PHY1, Pp-PHY2, Pp-PHY3, Pp-PHY4 or Pp-PHY5a were used for protein extraction. Total protein was analyzed by SDS-PAGE and immunoblotting with anti YFP antibody. Protein extracts from dark-adapted wild-type *Physcomitrella* cultures were used as negative controls. An unspecific signal was used as loading control.



Supplemental Figure 2. (Duplicates images in Figure 1D) Pfr-dependent degradation of PHY1 and PHY3 in *Physcomitrella*.

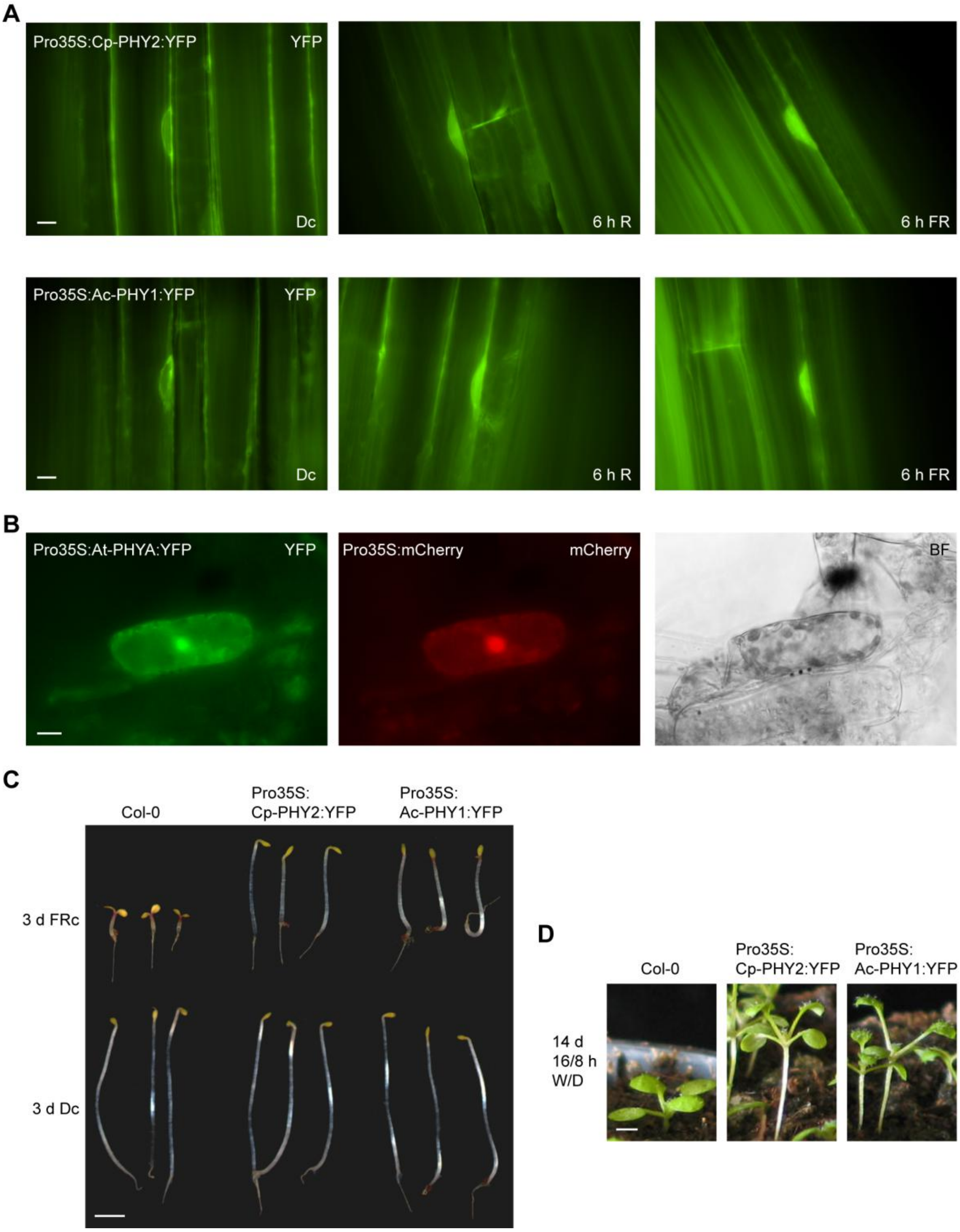
Dark-adapted protonema filaments of Pp-PHY1:YFP **(A)** or Pp-PHY3:YFP **(B)** expressing *Physcomitrella* lines were used for fluorescence microscopy. Images were acquired before (dark control, D) and after irradiation with either R light (22 μmol m^{-2} s^{-1}; Pfr) or FR light (18 μmol m^{-2} s^{-1}; Pr). The duration of irradiation is indicated in the figure. Before microscopic analysis, the samples were fixed with formaldehyde. Bar = 20 μm. Arrows indicate nuclei.



Supplemental Figure 3. Nuclear localization of *Ceratodon* and *Adiantum* phytochromes.

(A) Nuclear localization of *Ceratodon purpureus* PHY2 in protonema filaments. Protonema filaments of *Physcomitrella* were transiently transformed with Pro35S:Cp-PHY2:YFP and Pro35S:mCherry using particle bombardment. After transformation, the protonema filaments were grown in the dark (D) for 1 day and used for epifluorescence microscopy with filter sets specific for YFP and mCherry. The images were acquired after 15-30 min irradiation with microscope light. Bar = 20 μm. BF, bright field.

(B) Nuclear localization of phytochromes in fern gametophytes. *Adiantum capillus-veneris* gametophytes were transiently transformed by particle bombardment with Pro35S:Ac-PHY1:YFP, Pro35S:Ac-PHY2:YFP or Pro35S:Ac-PHY3:YFP. Pro35S:CFP:NLS or Pro35S:mCherry were co-transformed as a control. The gametophytes were grown for 2-5 days in D after transformation and used for microscopy with YFP, CFP and mCherry-specific filters. The images were acquired after 15-30 min irradiation with microscope light. Bar = 20 μm. BF, bright field.



Supplemental Figure 4. Conserved nuclear transport mechanisms for cryptogam and seed plant phytochromes.

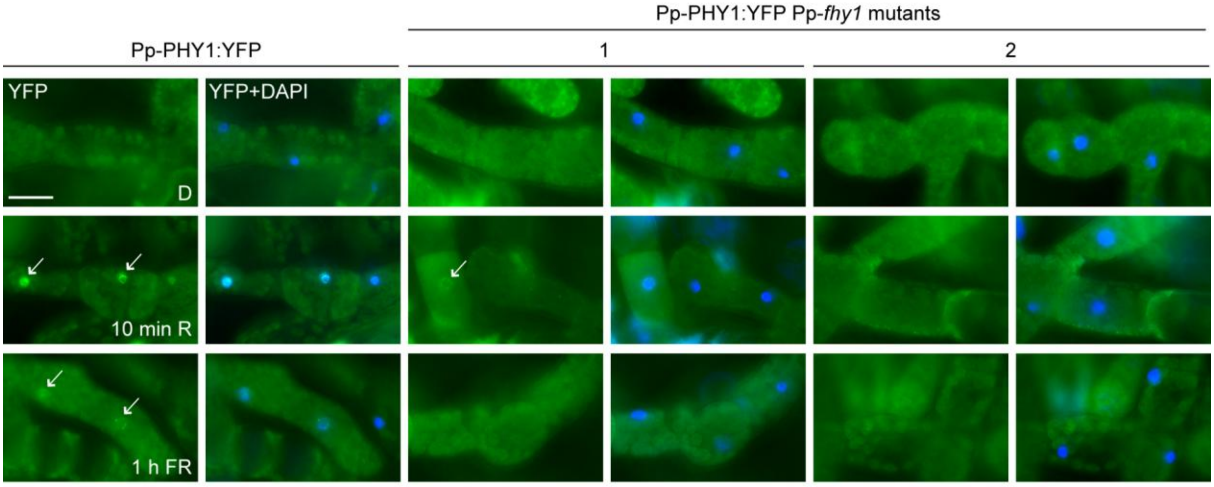
(A) Light enhanced nuclear accumulation of moss and fern phytochromes in *Arabidopsis*. Four-day-old etiolated *Arabidopsis* seedlings expressing 35S promoter driven Cp-PHY2:YFP or Ac-PHY1:YFP were used for fluorescence microscopy. Images were acquired before (dark control, D) or after a six-hour irradiation with R light (15 μmol m^{-2} s^{-1}) or FR light (15 μmol m^{-2} s^{-1}). The scale bar represents 10 μm.

(B) Nuclear localization of At-PHYA in *Physcomitrella*. *Physcomitrella* protonema filaments were transiently transformed with a Pro35S:At-PHYA:YFP construct using particle bombardment. After transformation, the protonema filaments were incubated in D for 1 day and used for microscopy. The images were acquired after 15-30 min irradiation with microscope light. Bar = 10 μm. BF, bright field.

Supplemental Figure 4. (continued)

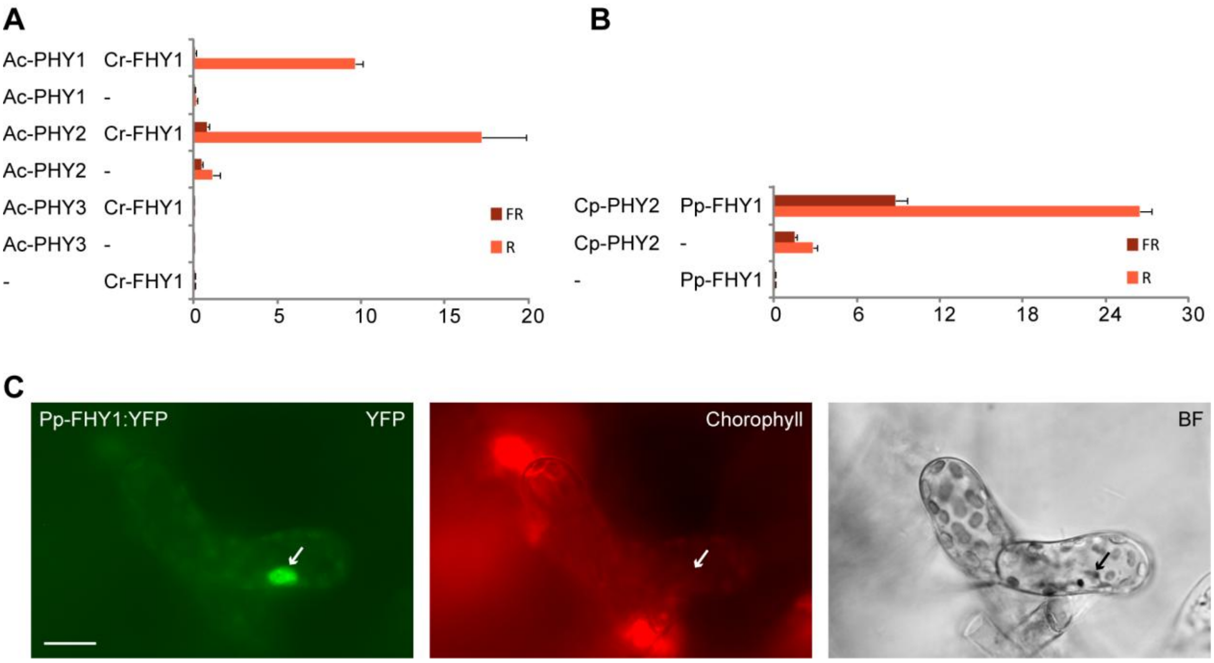
(C) Wild-type (Col-0) seedlings as well as transgenic lines expressing 35S promoter driven Cp-PHY2:YFP or Ac-PHY1:YFP in the Col-0 background were grown for 3 days in D or FR (15 µmol m^{-2} s^{-1}). Bar = 2 mm.

(D) Wild-type (Col-0) as well as Col-0 plants expressing Pro35S:Cp-PHY2:YFP or Pro35S:Ac-PHY1:YFP were grown for 14 days in the green house (16 h/8 h L/D cycles). Bar = 2 mm.



Supplemental Figure 5. Light-induced nuclear transport of Pp-PHY1 depends on Pp-FHY1.

Dark-adapted protonema filaments of *Physcomitrella* wild type or Pp-*fhy1* mutants expressing Pp-PHY1:YFP were used for microscopy. Images were acquired before (dark control, D) and after irradiation with either R light (10 min, 22 µmol m^{-2} s^{-1}) or FR light (1 h, 18 µmol m^{-2} s^{-1}). The samples were fixed and stained with DAPI before microscopic analysis. Arrows indicate nuclei. Bar = 20 µm.



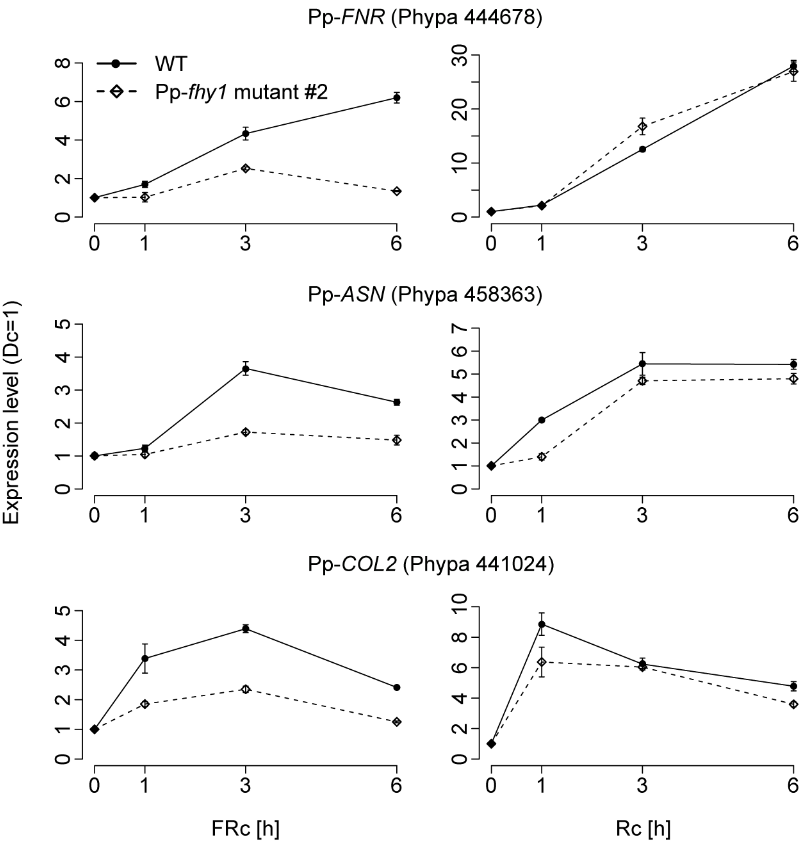
Supplemental Figure 6. Light regulated interaction of FHY1 and phytochromes from mosses and ferns.

Supplemental Figure 6. (continued)

(A) *Adiantum* phytochromes interact with Cr-FHY1. FHY1:AD and BD:PHY constructs were transformed into yeast strain Y187 and used for yeast two-hybrid assays. To convert PHYs to the Pfr or Pr form, yeast cultures were irradiated for 5 min with R light (12 μmol m^{-2} s^{-1}), either followed by a 5 min FR light pulse (12 μmol m^{-2} s^{-1}) or not. After 4 hours incubation in the dark the β-galactosidase activity was measured using the ONPG assay. Error bars represent SE; n=3. AD, GAL4 activation domain; BD, GAL4 DNA binding domain; Ac, *Adiantum capillus veneris* (fern); Cr, *Ceratopteris richardii* (fern).

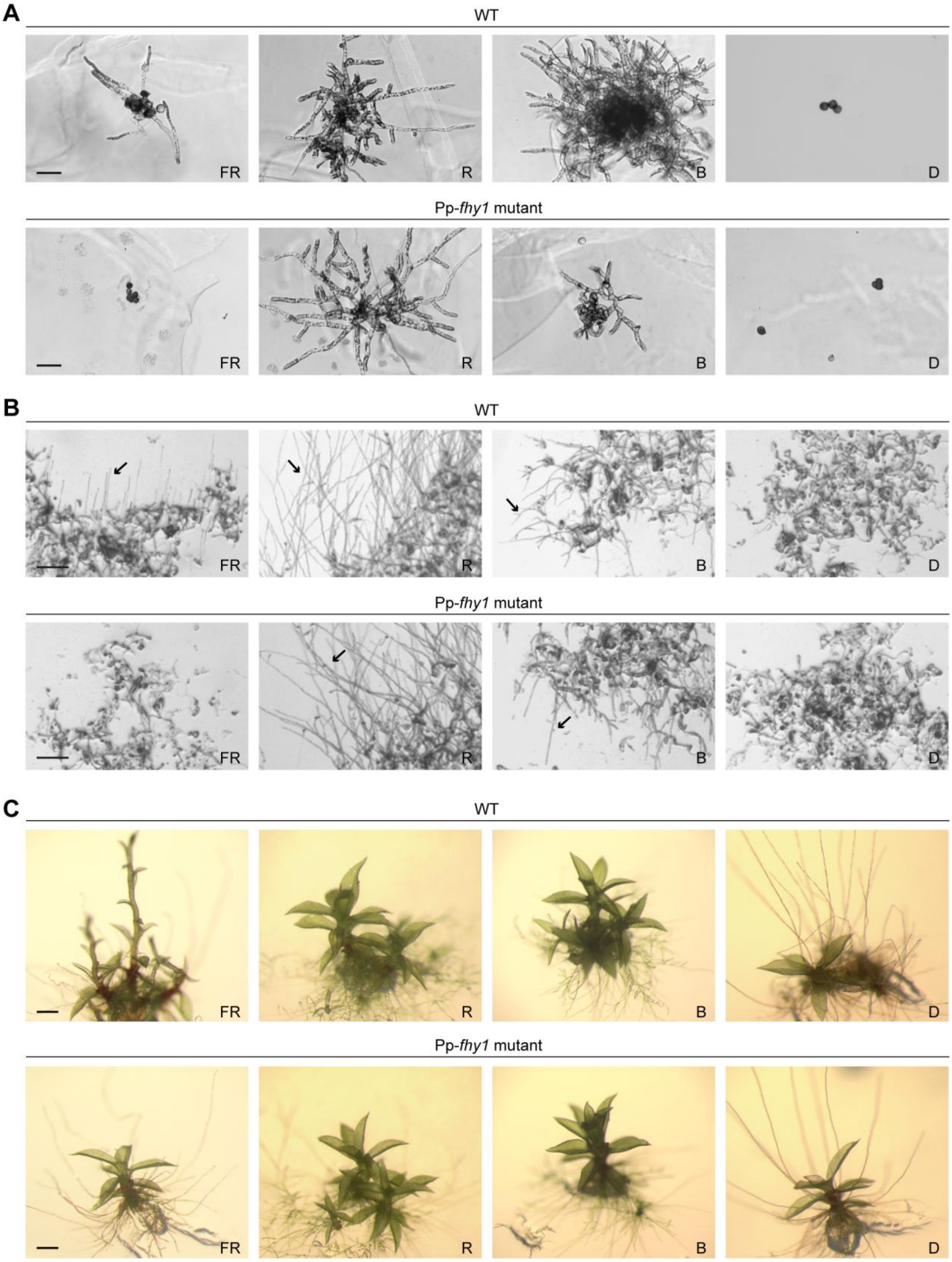
(B) Pfr dependent interaction of Pp-FHY1 and PHY2 from *Ceratodon purpureus*. Constructs coding for AD:FHY1 and PHY:BD were used for yeast two hybrid analysis as described in (C). SE; n=3. AD, GAL4 activation domain; BD, GAL4 DNA binding domain; Cp, *Ceratodon purpureus* (moss); Pp, *Physcomitrella patens* (moss).

(C) Pp-FHY1 localizes to the nucleus in *Physcomitrella* and forms nuclear bodies. *Physcomitrella* protonema filaments were transiently transformed with Pro35S:YFP:Pp-FHY1 using particle bombardment. Transformed protonema filaments were grown for 3 days in D and used for microscopy. The images were acquired after 15 min irradiation with microscope light. Arrows indicate nuclei. Bar = 20 μm.



Supplemental Figure 7. Pp-FHY1 is essential for FR light-induced gene expression.

Protonemata cultures of *Physcomitrella* wild type and Pp-*fhy1* mutant lines were dark adapted and exposed to either R light (28 μmol m^{-2} s^{-1}) or FR light (16 μmol m^{-2} s^{-1}). Samples for qRT-PCR analyses were harvested after 1, 3 and 6 hours of light treatment or darkness. The expression levels of *FNR*, *ASN*, and *COL2* were normalized to the levels of *26S rRNA*. Expression levels in D were set to 1. Error bars represent SE of technical replicates, n=3. An independent biological replicate is shown in Figure 4A.



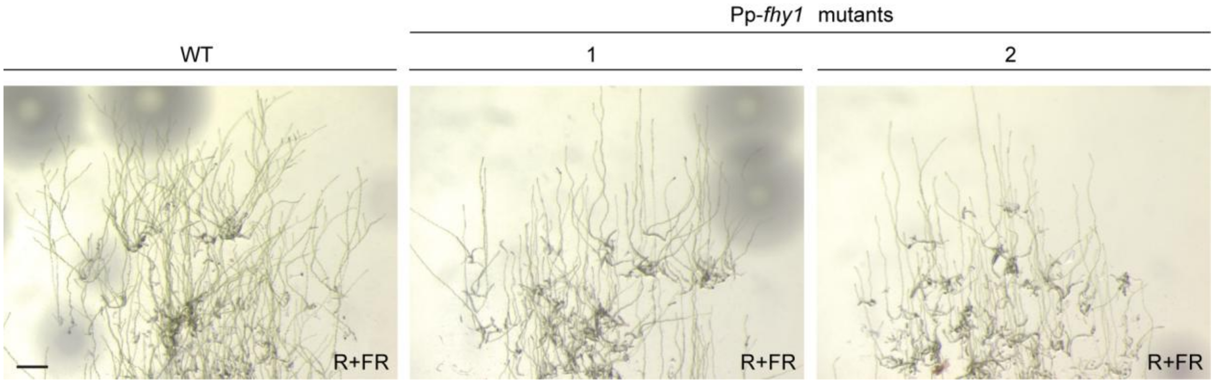
Supplemental Figure 8. Phenotype of the Pp-*fhy1* mutant under different light conditions.

(A) Spore germination depends on Pp-FHY1 in FR but not in R and B light. Spores from the wild type and Pp-*fhy1* mutant were kept in darkness, D, or irradiated for 6 days with continuous FR light (18 μmol m^{-2} s^{-1}), R light (22 μmol m^{-2} s^{-1}) or B light (7 μmol m^{-2} s^{-1}). Bar = 100 μm.

Supplemental Figure 8. (continued)

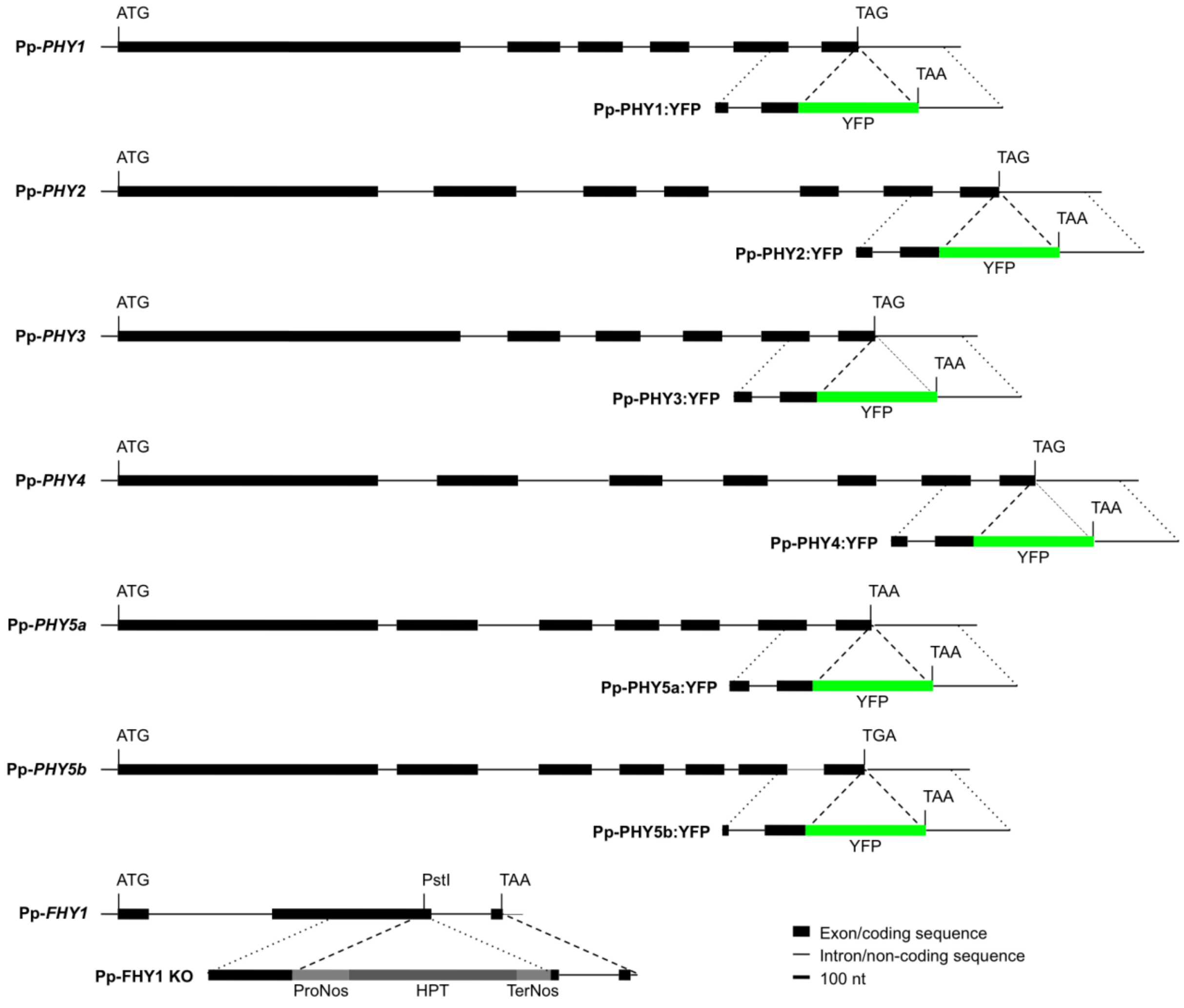
(B) Protonemata growth depends on Pp-FHY1 in FR but not in R and B light. Wild-type and Pp-*fhy1* mutant *Physcomitrella* cultures were grown on vertical plates for 10 days in continuous FR light (18 μmol m^{-2} s^{-1}), R light (28 μmol m^{-2} s^{-1}) or B light (7 μmol m^{-2} s^{-1}) or in D. Bar = 200 μm.

(C) Pp-FHY1 is essential for gametophore growth in FR but not in R or B light. Wild-type and Pp-*fhy1* mutant *Physcomitrella* gametophores were grown for 11 days in FR light (18 μmol m^{-2} s^{-1}), R light (22 μmol m^{-2} s^{-1}), B light (7 μmol m^{-2} s^{-1}) or D. Bar = 500 μm.

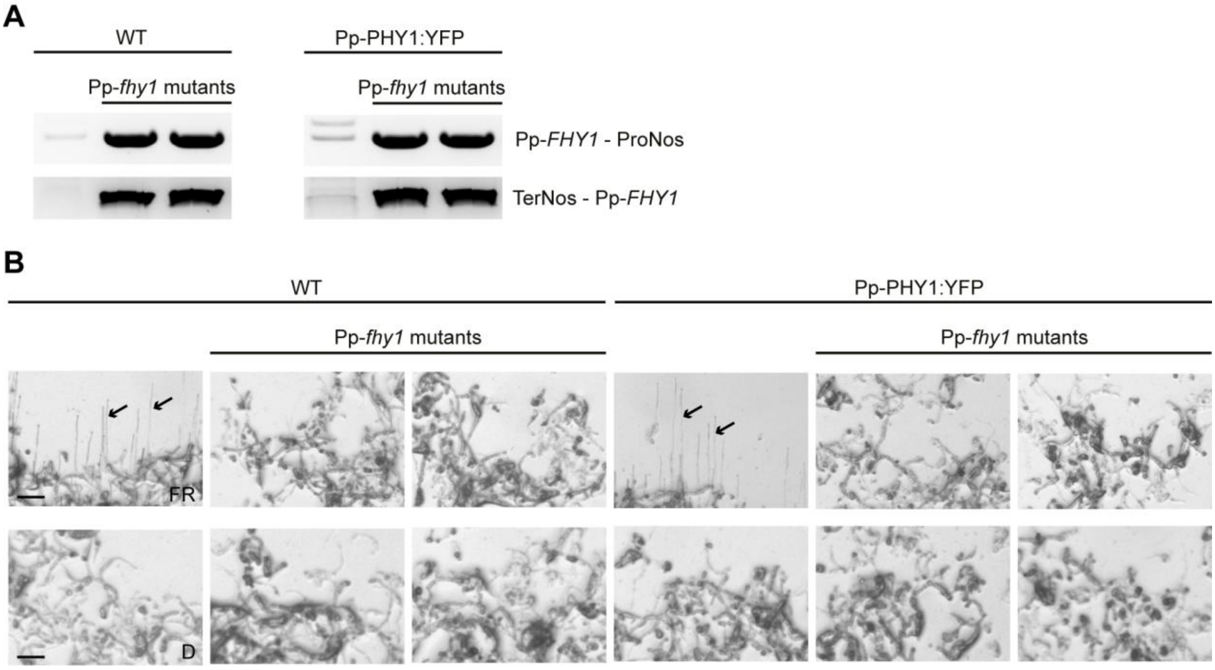


Supplemental Figure 9. Pp-FHY1 is required for branching of protonema filaments in a R-FR light mixture.

Wild type and Pp-*fhy1* mutant protonema filaments were grown for 10 days in continuous R light (22 μmol m^{-2} s^{-1}) supplemented with FR light (16 μmol m^{-2} s^{-1}). The scale bar represents 500 μm.



Supplemental Figure 10. Schematic representation of genomic loci (Pp-*PHY1-5b*, Pp-*FHY1*) and targeting cassettes (Pp-PHY1-5b:YFP, Pp-FHY1 KO). The targeting cassettes were cut from pBS II KS vectors using NotI.



Supplemental Figure 11. Molecular and phenotypical characterization of independent Pp-*fhy1* mutant lines.

(A) Pp-*fhy1* mutants and Pp-*fhy1* mutants expressing Pp-PHY1:YFP were analysed in PCR experiments using primers specific for the targeting cassette and genomic Pp-*FHY1*. The correct insertion of the targeting construct was verified by sequencing the PCR products.

(B) (Duplicates images in Supplemental Figure 8B) Pp-*fhy1* mutants and Pp-*fhy1* mutants expressing Pp-PHY1:YFP were tested for the protonemata growth phenotype in FR light. *Physcomitrella* protonemata were grown on vertical plates for 10 days in continuous FR light (18 μmol m^{-2} s^{-1}) or in D. Arrows indicate new-grown protonema filaments. Bar = 200 μm.

Supplemental Methods and Tables

For detailed information on the cloning of DNA constructs as well as on used primers please refer to the enclosed disc.

- Supplemental Data > Chapter 2 > Supplemental Methods. Cloning of Constructs.
- Supplemental Data > Chapter 2 > Supplemental Methods. Supplemental Table 1. Primer List.

CHAPTER 3

IDENTIFICATION OF PIFS AND THEIR POTENTIAL ROLE IN LIGHT SIGNALING IN THE MOSS *PHYSCOMITRELLA PATENS*

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ABSTRACT

Across the whole plant kingdom phytochrome photoreceptors play an important role during adaptive and developmental responses to light. Extensive studies have shown that in seed plants light-activated phytochromes accumulate in the nucleus, where they regulate several downstream signaling components, such as the phytochrome interacting factors (PIFs). PIFs are bHLH transcription factors that repress photomorphogenesis through the regulation of gene expression. In *Arabidopsis*, light-activated nuclear phytochromes bind to PIFs and induce their rapid degradation, thus suppressing PIF activity and altering the expression of several hundred genes. In cryptogams (e.g., ferns and mosses) PHYs equally accumulate in the nucleus after activation by light. Their nuclear function, however, has so far remained elusive. Here we have analyzed the effect of red (R) light on gene expression in the moss *Physcomitrella patens* (Pp), thereby identifying putative target genes of phytochrome signaling. Among the differentially expressed genes we found homologs of genes that are regulated by PIFs in *Arabidopsis*. We identified putative PIF homologs in the genome of *P. patens*, which resemble *Arabidopsis* PIFs in their molecular properties and physiological effects. Our results suggest that Pp-PIFs are involved in phytochrome signaling in *P. patens*, similar to the function of PIFs in seed plants. Thus, although phytochrome clades from cryptogams have evolved

independently of seed plant phytochromes, the function of PIFs during phytochrome signaling may have been conserved during the course of evolution.

INTRODUCTION

Upon changing light conditions plants, as photoautotrophic organisms that use light as energy source, have to adapt their growth and development. To detect different aspects of their light environment, e.g. spectral composition or light intensity, seed plants such as *Arabidopsis thaliana* are equipped with different types of photoreceptors. Blue (B) light and UV-B light are monitored through cryptochromes, phototropins, members of the ZEITLUPE (ZTL) family and UV RESISTANCE LOCUS 8 (UVR8), respectively, whereas red (R) and far-red (FR) light are perceived and integrated by the different members of the phytochrome (PHY) family (Kami et al., 2010; Li et al., 2011; Heijde and Ulm, 2012). Phytochromes function as R/FR light receptors, as they exist in two different states that reversibly convert into each other by the absorption of light: the inactive Pr form, which has an absorption peak in R light, and the active Pfr form with maximal absorption in FR light. The external R/FR light conditions are thus translated into an equilibrium of a wavelength-specific phytochrome Pfr/Ptot ratio (Ptot = Pfr + Pr) (Mancinelli, 1994).

The *Arabidopsis* genome contains five phytochromes that can be divided into type I and type II phytochromes, represented by PHYTOCHROME A (PHYA) and PHYTOCHROME B-E (PHYB-E), respectively. PHYB is the most abundant phytochrome under light conditions that result in a high Pfr/Ptot ratio and regulates seed germination, seedling de-etiolation and induction of flowering. The only type I phytochrome, PHYA, is most abundant in dark-grown seedlings and mediates germination and de-etiolation under light conditions that induce a low Pfr/Ptot ratio (Kami et al., 2010; Li et al., 2011).

Phytochromes are not restricted to higher plants but are also found in cryptogams, such as ferns and mosses. Phytochromes from cryptogams and seed plants have undergone independent evolution, therefore cryptogam phytochromes cannot be assigned to any of the seed plant phytochrome clades (Mathews, 2010). They have been described as photoreceptors of phototropic and polarotropic growth, but also regulate response modes that are similar to seed plant PHYA- or PHYB-dependent responses, such as R/FR light-reversible spore germination or FR light-induced protonemata growth (Mathews, 2006; Hughes, 2013; Possart and Hiltbrunner, 2013).

As a first step in phytochrome signaling, activated phytochromes translocate from the cytosol into the nucleus. In seed plants, it has been shown that PHYB possibly enters the nucleus bound to transcription factors or using its own NLS, whereas PHYA is transported into the nucleus by the functional homologs FAR-RED ELONGATED HYPOCOTYL1 (FHY1) and FHY1-LIKE (FHL) (Chen et al., 2005; Kami et al., 2010; Li et al., 2011; Pfeiffer et al., 2012). There is only little data available on phytochrome nuclear localization in cryptogams. However, we and others have recently shown that phytochromes from the moss *Physcomitrella patens* (Pp) and the fern *Adiantum capillus-veneris* (Ac) also accumulate in the nucleus in a light-dependent manner (Tsuboi et al., 2012; Possart and Hiltbrunner, 2013). Moreover, the nuclear import of Pp-PHY1 depends on Pp-FHY1, which is analogous to PHYA nuclear transport in *Arabidopsis* (Possart and Hiltbrunner, 2013).

The subsequent effects and signaling steps of phytochromes in the nucleus have been most intensively studied in seed plants. In *Arabidopsis*, one branch of phytochrome signal transduction involves the phytochrome-mediated inhibition of the E3 ubiquitin ligase CONSTITUTIVE PHOTOMORPHOGENIC 1 (COP1). In the dark, COP1, in conjunction with SUPPRESSOR OF PHYA-105 (SPA1) or SPA1-related proteins, ubiquitinates light-signaling transcription factors and targets them for proteasome-mediated degradation. Thus, COP1 controls the abundance of several photomorphogenesis-promoting proteins, such as the bZIP transcription factor LONG HYPOCOTYL 5 (HY5), the atypical bHLH protein LONG HYPOCOTYL IN FARRED 1 (HFR1) or the MYB transcription factor LONG AFTER FAR-RED LIGHT (LAF1) (Kami et al., 2010; Li et al., 2011). Light-activated phytochromes inhibit COP1/SPA function and induce an accumulation of HY5 and LAF1 (Kami et al., 2010; Li et al., 2011).

In a concomitant signaling pathway, light-activated nuclear phytochromes bind to several members of the subfamily 15 of *Arabidopsis* basic helix–loop–helix (bHLH) transcription factors, designated as phytochrome interacting factors (PIFs) (Leivar and Quail, 2011). All PIFs share a conserved active phytochrome B-binding (APB) motif, which is necessary and sufficient for specific interaction with PHYB (Khanna et al., 2004; Leivar and Quail, 2011). Besides, PIF1 and PIF3 have an active phytochrome A-binding (APA) domain, necessary for binding to PHYA (Al-Sady et al., 2006; Shen et al., 2008). The interaction of PIFs with light-activated nuclear phytochromes initiates the rapid phosphorylation and subsequent degradation of the PIFs via the ubiquitin-proteasome system (Al-Sady et al., 2006; Kami et al., 2010; Leivar and Quail, 2011). PIF-degradation is associated with a rapid co-localization of PIFs and phytochromes and the formation of nuclear bodies (NBs) (Bauer et al., 2004; Chen, 2008). In the dark, PIFs function as repressors of seed germination, promote skotomorphogenesis and inhibit photomorphogenesis of etiolated seedlings (Leivar and Quail, 2011). Moreover, PIFs have been reported to promote the shade avoidance syndrome (SAS) in de-etiolated seedlings and to regulate flowering time (Leivar and Quail, 2011). In line with this, *Arabidopsis* higher order *pif* mutants exhibit constitutive photomorphogenic and light-hypersensitive seedling phenotypes as well as reduced SAS, whereas light-grown *PIF* overexpressors (OX) show constitutively long hypocotyls and petioles, pale green leaves and early flowering (Fujimori et al., 2004; Khanna et al., 2007; Leivar et al., 2008a; Leivar et al., 2008b; Shin et al., 2009; Leivar and Quail, 2011; Kumar et al., 2012). Several PIFs have been shown to have transcriptional activity (Leivar and Quail, 2011). Genome-wide expression profiling of the *pif1 pif3 pif4 pif5* (*pifq*) mutant revealed an important role of PIFs during light-dependent regulation of gene expression and identified potential direct PIF target genes (Leivar et al., 2009; Shin et al., 2009). Light-activated phytochromes induce the rapid degradation of PIF proteins and inhibit their binding to target promoters, thereby reversing PIF activities and changing the expression of PIF-regulated genes (Leivar and Quail, 2011; Park et al., 2012).

Seed plant phytochromes regulate the expression of numerous genes related to phytohormone signaling or photosynthetic and metabolic changes that occur during light-induced transition from hetero- to photoautotrophic growth (Leivar and Quail, 2011). There have been only few reports on a similar function of phytochromes in cryptogams. Phytochromes from moss, liverwort and green algae have been shown to regulate the transcript levels of individual genes (Winands and Wagner, 1996; Christensen et al., 1998; Suzuki et al., 2001; Possart and Hiltbrunner, 2013). Moreover, a very recent approach identified R light-regulated genes in the moss *P. patens* that were misregulated in phytochrome-chromophore mutants (Chen et al., 2012).

Only some homologs of signaling components, besides PHYs themselves, have been described in cryptogams: The genome of the moss *P. patens* contains homologous sequences of *COP1*, *SPA1* and the gene encoding for the bZIP transcription factor HY5, indicating an analogy to the PHY-COP1-pathway of seed plants (Richardt et al., 2007; Rensing et al., 2008). However, although the class of bHLH transcription factors is represented in the moss *P. patens*, there have been no reports on PIFs in cryptogams (Carretero-Paulet et al., 2010; Richardt et al., 2010; Rösler et al., 2010; Feller et al., 2011). Thus, there has been no indication on a light signaling pathway in cryptogams that would be analogous to seed plant phytochrome-mediated regulation of PIFs and their target genes.

Here, we present evidence of a PIF-dependent phytochrome signaling pathway in the moss *P. patens* that is analogous to *Arabidopsis*. Our microarray analysis revealed global effects of R light on gene expression in *P. patens* and, by comparison with expression data from *Arabidopsis*, homologs of PIF-dependent genes. We identified potential PIF homologs in *P. patens*, whose functional characterization revealed PIF-specific molecular properties. Our data strongly suggest an important role of these proteins during light signaling in *P. patens*.

RESULTS

Early and late R light-responsive genes in P. patens

Phytochrome-mediated light signaling in seed plants involves dramatic changes in gene expression. In order to compare phytochrome systems in seed plants and cryptogams, we analyzed the effects of R light on the genome-wide gene expression in the moss *P. patens*. We performed microarray analysis on 6-weeks old, dark-adapted *P. patens* plants that were either harvested directly in darkness or after subjection to R light treatment for 30 min and 4 h (Supplemental Figure 1A and 1B); several differentially expressed genes (DEGs) were validated by quantitative real-time PCR (Supplemental Figure 1C). Compared to the dark control the expression of 278 genes changed significantly (unpaired cyber-t test with Benjamini-Hochberg fdr, $q<0.05$) after 30 min R light treatment; 313 differentially expressed genes (DEGs) were detected upon 4 h in R light (Supplemental Dataset 1). After 30 min R, the majority of DEGs (96%) was down-regulated, whereas after 4 h R most DEGs (92%)

showed an up-regulation (Figure 1A). Consequently, the majority of detected genes were differentially regulated between 30 min and 4 h of R light. Based on k-means clustering we identified three major profiles: 295 DEGs were repressed in darkness and after 30 min R and became activated after 4 h R (cluster 1 - late/R activation); 65 genes were active during darkness and were repressed upon 30 min and 4 h R (cluster 2 - dark active); 157 genes were active during darkness, repressed at 30 min R, and de-repressed at 4 h R (cluster 3 - temporarily repressed in R).

The DEGs of each expression cluster were grouped into functional categories according to Gene Ontology terms. Cluster 2 (dark-active) was enhanced for genes related to amino acid metabolism and mitochondrion, but not for protein metabolism. Genes in cluster 3 (temporarily-repressed) were mainly related to translation and other biosynthetic activity. Cluster 1 genes (late-active) could be mainly assigned to photosynthesis, namely light harvesting and light reaction, carbon fixation and plastid terms. According to a potential direct effect of R light signaling on transcription, we identified 26 transcription factors and transcriptional regulators. Among these, we assigned 11 to cluster 2 (dark-active), 10 to cluster 3 (temporarily-repressed) and 5 to cluster 1 (late-active).

In order to further integrate these expression patterns, we compared our data with the transcriptome profiling recently published by Chen *et al.* (Chen et al., 2012). These authors performed next-generation sequencing to analyze the effects of 1 h R light on the transcriptome of *P. patens* protonemata and found a total number of 2,202 DEGs, of which approximately half were up-regulated and half were down-regulated (Chen et al., 2012). We found an overlap of only 22% for up-regulated DEGs and 11% for down-regulated DEGs (Supplemental Dataset 2). In contrast to the equal distribution of up- and down-regulated genes described by Chen *et al.*, we observed either mainly repressed (30 min R) or mainly induced (4 h R) DEGs for the different time-points of R light treatment (see also above).

Putative PIF genes are encoded in the genome of P. patens

In seed plants, phytochrome-mediated changes in gene expression depend on transcription factors like PIFs. Former works have identified PIF target genes using *Arabidopsis* higher order *pif* mutants (Monte et al., 2004; Leivar et al., 2009; Shin et al., 2009). By comparing our microarray analysis with data from *Arabidopsis* we identified potential homologs of PIF-regulated genes in the moss *P. patens*. Among those *P. patens* DEGs for which we could determine potential *Arabidopsis* homologs (259), 30 % overlapped with DEGs described as R light-induced by Leivar *et al.* (Leivar et al., 2009) (Supplemental Dataset 3). 56 DEGs were homologous to *Arabidopsis* genes that were regulated in a PIF-dependent manner (Leivar et al., 2009). Moreover, 11 DEGs were homologous to *Arabidopsis* genes that had been described as direct PIF target genes (Leivar et al., 2009). We found almost no overlap for R light-repressed genes, which are, however, underrepresented for early time points in *Arabidopsis* (Leivar et al., 2009). We also compared the *P. patens* transcriptome data from Chen *et al.* with the *Arabidopsis* data and found an overlap of 12 % for R light-induced and, similar to our expression analysis, almost no overlap for R light-repressed genes. In contrast to the comparison with our microarray data, we observed a considerable cross-overlap between down-regulated genes from Chen *et al.* and up-regulated genes from Leivar *et al.* (Leivar et al., 2009; Chen et al., 2012) (Supplemental Dataset 3). Altogether, the presence of putative PIF-dependent genes among R light-affected DEGs in *P. patens* suggests a similar role of bHLH transcription factors during phytochrome signaling in seed plants and mosses.

Using the sequence of the bHLH and APA domains, respectively, of *Arabidopsis* PIFs to search the *P. patens* genome we found 4 potential *PIF* homologs (Phypa_437018, Phypa_437040, Phypa_439387 and Phypa_446229). The sequence similarity of all 4 genes compared to Arabidopsis PIF proteins was restricted to the bHLH domain, an APB-like domain, an APA-like domain and a motif of unknown function, which is similar to the degree of homology among seed plant *PIF*s (Figure 1B). A phylogenetic analysis of full-length protein sequences equally revealed a similar degree of relatedness between *P. patens* and *A. thaliana* bHLH-containing proteins on the one side and among Arabidopsis bHLH proteins on the other side (Supplemental Figure 2). When we restricted the analysis to the sequences of the predicted bHLH domains, all potential Pp-PIFs appeared to be most closely related to *Arabidopsis* PIF3 (Figure 1C). In general, other bHLH proteins from the *Arabidopsis* subfamily 15 that were not annotated as PIFs showed a lesser degree of similarity to Pp-PIFs (Figure 1C).

We cloned the *Phypa_437018* and *Phypa_437040* coding sequences, here designated *Pp-PIF68* and *Pp-PIF69*, respectively, predicted in the database by RT-PCR. Moreover, we amplified a splicing variant of *Pp-PIF69* that lacks the APB-like domain. In contrast to PIFs from *Arabidopsis*, which consist of about 450 amino acids, *Pp-PIF68*, *Pp-PIF69* and *Pp-PIF69ΔAPB* encode proteins of 702, 728 and 688 amino acids, respectively. The exon-intron structure of *Pp-PIF68* and *Pp-PIF69* genes is most similar to the ones of *At-PIF1* and *At-PIF3*.

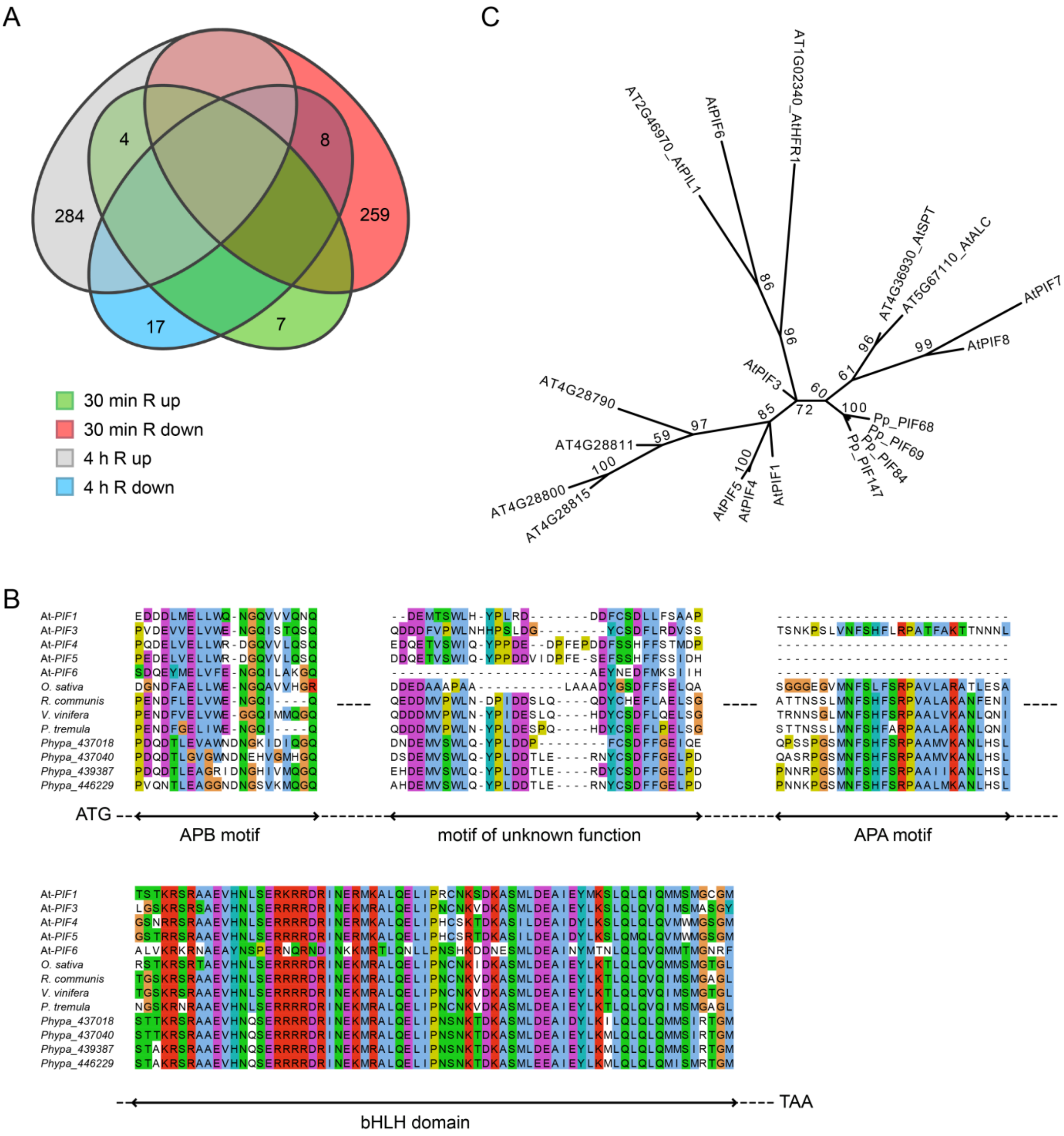

Figure 1. R light effects on gene expression and PIF homologs in *P. patens*.

(A) Venn diagram of DEG directionality upon R light treatment. Microarray analysis was performed on dark-adapted *P. patens* gametophores that were subjected to R light treatment for 30 min and 4 h, respectively and harvested immediately. Controls were harvested directly from darkness.

(B) The moss *P. patens* contains PIF homologs. Sequence alignment of PIF proteins from *P. patens* and seed plants. Only regions of high sequence similarity are shown. The dashed line indicates non-aligned regions.

(C) PIFs from *P. patens* are closely related to At-PIF3. Phylogeny of bHLH domains from *P. patens* and *Arabidopsis* bHLH proteins based on Bayesian inference (BI). Node labels represent BI posterior probabilities (in %).

P. patens PIFs interact with phytochromes and localize to the nucleus

One important step in seed plant phytochrome signaling is the interaction of light-activated phytochromes with PIFs. In a Yeast-Two-Hybrid assay we found that *P. patens* PIF68 and its truncated version, which lacks the bHLH domain (PpPIF68ΔbHLH), interact with different phytochromes in a light-dependent manner (Figure 2A and Supplemental Figure 3A). R light-activated Pp-PHY1 to 4 from *P. patens* and PHYA from *Arabidopsis* bound to Pp-PIF68 and Pp-PIF68ΔbHLH. These interactions were strongly reduced when the phytochromes had been inactivated by FR light. While yeast transformed with full-length Pp-PIF69 did not grow, we were able to assay a version of the corresponding coding sequence that lacked the bHLH domain. In contrast to Pp-PIF68ΔbHLH, Pp-PIF69ΔbHLH did not interact with phytochromes (Supplemental Figures 3B). We are aware, however, that this may be due to an insufficient expression level of these proteins in yeast. In summary, based on its light-specific interaction with the photoreceptors, Pp-PIF68 can be considered as potential modulator of phytochrome signaling output.

In *Arabidopsis*, PIFs localize in the nucleus, where they regulate gene expression. Their interaction with activated phytochromes is accompanied by the formation of nuclear bodies, a process that has been implicated in PIF-degradation and signal transduction (Van Buskirk et al., 2012). In order to analyze the localization pattern of cryptogam PIFs we expressed YFP-fusions of Pp-PIF68, Pp-PIF69 and Pp-PIF69ΔAPB in *Nicotiana benthamiana*. Similarly to *Arabidopsis* PIFs, all three Pp-PIFs localized to the nucleus and formed nuclear bodies (Figure 2B to 2D; Supplemental Figure 4A). In line with our observations on Pp-PIF-phytochrome-interaction in yeast, we moreover found that Pp-PIF68 co-localized with *Arabidopsis* PHYA and PHYA-NLS in the nuclear bodies (Figure 2B; Supplemental Figure 4B). Besides, Pp-PIF68 co-localized with At-PIF3 (Figure 2B). Although we did not detect an interaction of Pp-PIF69 with phytochromes in yeast, in *N. benthamiana* Pp-PIF69 and its splicing variant Pp-PIF69ΔAPB co-localized with At-PHYA and At-PHYA-NLS as well as with At-PIF3 in the nucleus (Figure 2C and 2D; Supplemental Figure 4C and 4D). Using particle bombardment we transiently transformed *P. patens* protonema cells and also observed a nuclear accumulation of Pp-PIF68, Pp-PIF69 and Pp-PIF69ΔAPB, similar to PIFs in seed plants (Figure 2E). We conclude that

PIFs from *P. patens* and *Arabidopsis* may act analogously as nuclear regulators of gene expression.

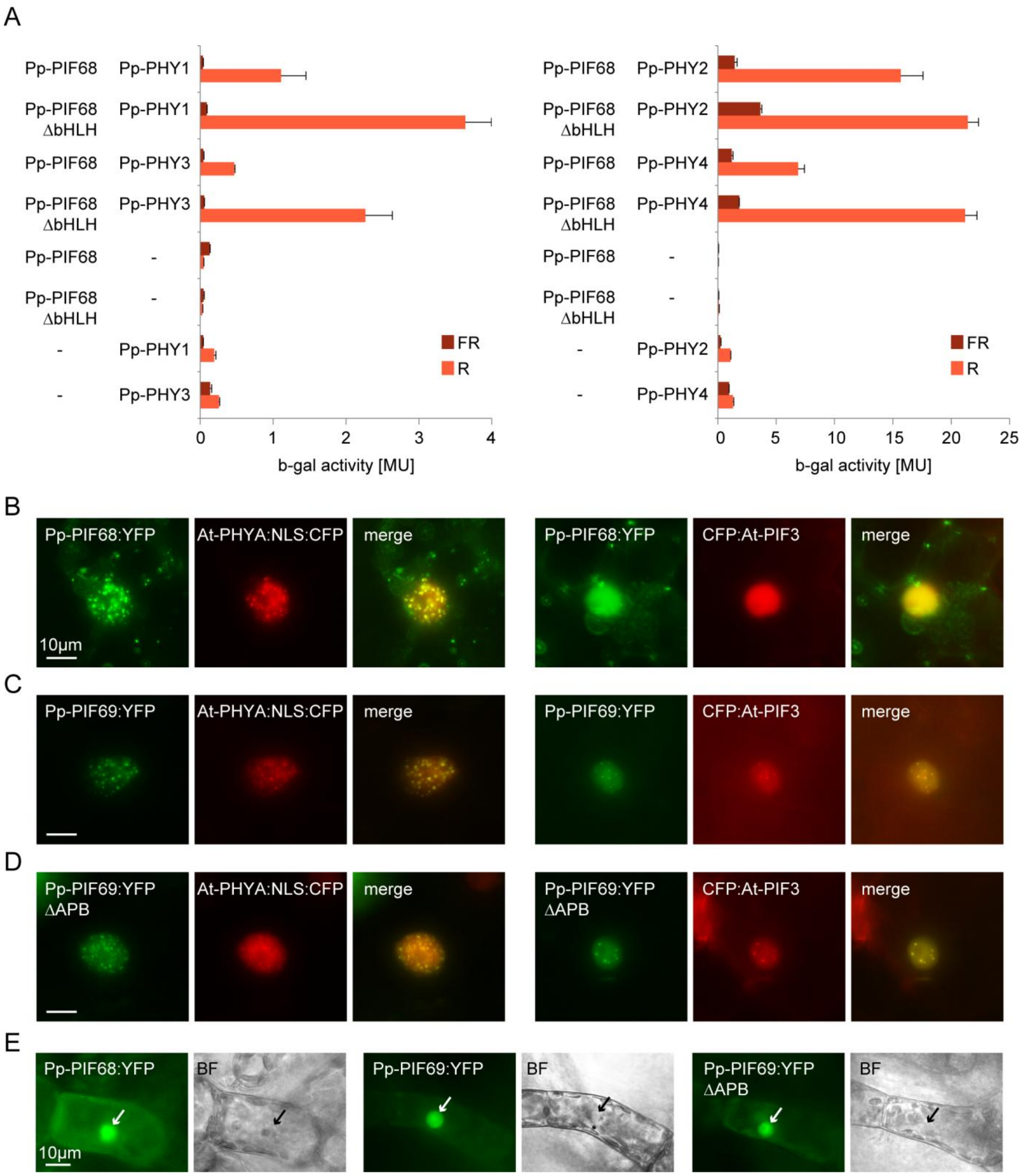

Figure 2. *P. patens* PIFs interact with phytochromes and localize to the nucleus.

(A) Pp-PIF68 and Pp-PIF68ΔbHLH interact with *P. patens* phytochromes in a light-dependent manner. AD plasmids containing the coding sequence for Pp-PIF68 or Pp-PIF68ΔbHLH fused to the GAL4 activation domain were used in yeast-two-hybrid assays with BD plasmids containing the coding sequence for Pp-PHY1, 2, 3 or 4 fused to the GAL4 DNA binding domain. Phytochromes were converted into the Pfr or Pr form by irradiating yeast cultures for 5 min with R (12 µmol $m^{-2} s^{-1}$) or FR (12 µmol $m^{-2} s^{-1}$) light. The β–galactosidase activity was measured after an additional incubation in the dark for 4 h. MU, Miller Units, Error bars represent SE; n=3

P. patens PIFs affect phytochrome-mediated responses in Arabidopsis

To further investigate the functional homology of *P. patens* and seed plant PIFs, we expressed YFP-fusions of Pp-PIF68, Pp-PIF69 and Pp-PIF69ΔAPB under control of the constitutive *35S* promotor in *Arabidopsis* Columbia-0 background. In order to examine whether Pp-PIFs influence photomorphogenic responses we analyzed seedling deetiolation in these overexpressor lines under different light conditions. The expression of all three Pp-PIFs led to a clear hyposensitive response in R and B light and we observed a similar but weaker phenotype under FR light (Figure 3A). Under R, B and FR light Pp-PIF-seedlings showed longer hypocotyls than the wild type; they partially failed to open their cotyledons in R and B light. Dark-grown Pp-PIF-seedlings were etiolated showing an apical hook and closed cotyledons, but they had much shorter hypocotyls and partially exaggerated apical hooks in comparison to the wild type control (Figure 3A). These effects resembled the phenotype of *Arabidopsis* PIF5 overexpressors, suggesting an interference of Pp-PIFs with the endogenous PIF function (Khanna et al., 2007). In adult plants, the expression of all three Pp-PIFs resulted in reduced chlorophyll accumulation and early flowering (Figure 3B). Pp-PIF69 and Pp-PIF69ΔAPB showed stronger effects than observed in Pp-PIF68-expressing plants. The phenotypes were reminiscent of *Arabidopsis* PIF4 or PIF5 overexpressor plants, again indicating an interference of Pp-PIFs with the endogenous signaling system (Fujimori et al., 2004; Khanna et al., 2007; Kumar et al., 2012). Despite weak fluorescence signals, we detected a nuclear localization for all Pp-PIF YFP-fusions in etiolated seedlings (Figure 3C).

Figure 2. (continued)

(B) Pp-PIF68 co-localizes with At-PHYA:NLS and At-PIF3 in the nucleus. Leaves of *N. benthamiana* were transformed by infiltration with *A. tumefaciens* containing a Pro*:35S:Pp-PIF68:YFP* construct and either a *Pro:35S:At-PHYA:NLS:CFP* or a *Pro:35S:CFP:At-PIF3* construct. One day after transformation plants were transferred into darkness for another two days before microscopic analysis of epidermal leaf cells. Bar = 10 µm.

(C) Pp-PIF69 co-localizes with At-PHYA:NLS and At-PIF3 in the nucleus. Leaves of *N. benthamiana* were transformed with *Pro:35S:Pp-PIF69:YFP* and either *Pro:35S:At-PHYA:NLS:CFP* or *Pro:35S:CFP:At-PIF3* and analyzed as described in (B).

(D) Pp-PIF69deltaAPB co-localizes with At-PHYA:NLS and At-PIF3 in the nucleus. Leaves of *N. benthamiana* were transformed with *Pro:35S:Pp-PIF69ΔAPB:YFP* and either *Pro:35S:At-PHYA:NLS:CFP* or *Pro:35S:CFP:At-PIF3* and analyzed as described in (B).

(E) Pp-PIF68, Pp-PIF69 and Pp-PIF69ΔAPB localize to the nucleus in *P. patens*. *P. patens* protonema filaments were transiently transformed with either *Pro:35S:Pp-PIF68:YFP*, *Pro:35S:Pp-PIF69:YFP* or *Pro:35S:Pp-PIF69ΔAPB:YFP* using particle bombardment, and incubated in darkness for 2 to 4 days before microscopic analysis. Bar = 10 µm. Arrows indicate nuclei.

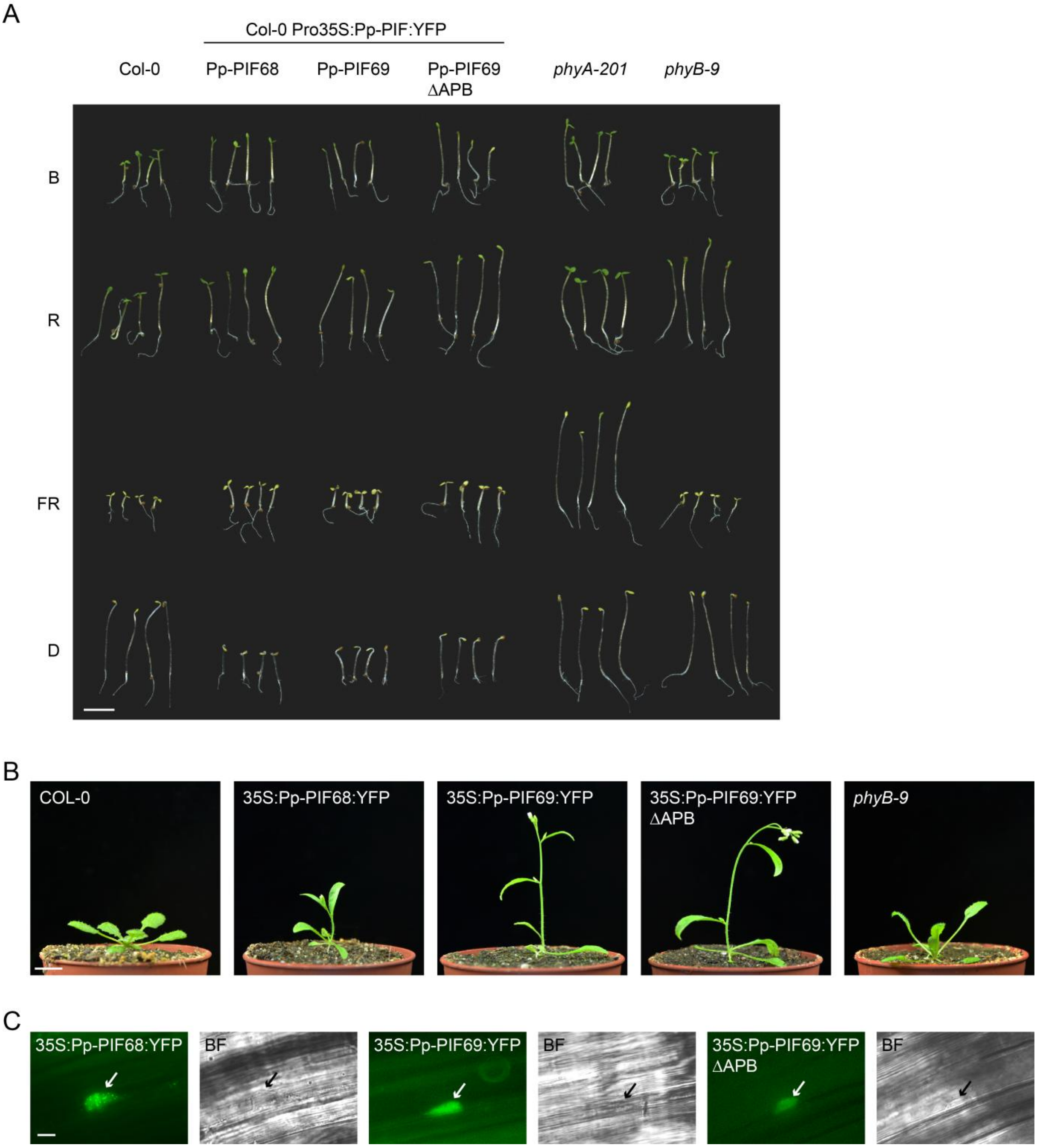

Figure 3. Effects of PIFs from *P. patens* on light signaling in *Arabidopsis*.

(A) Seedling development is impaired by Pp-PIF overexpression. Columbia-0 (Col-0), *phyB-9, phyA211* as well as Col-0 seedlings expressing 35S-promotor-driven *Pp-PIF68:YFP*, *Pp-PIF69:YFP* or *Pp-PIF69ΔAPB:YFP* were grown for 4 d in blue (B) (4 µmol m^{-2} s^{-1}), red (R) (10 µmol m^{-2} s^{-1}) or far-red (FR) (12 µmol m^{-2} s^{-1}) light or in darkness (D). Bar = 5 mm.

(B) *P. patens* PIF overexpression results in early flowering in *Arabidopsis*. Columbia-0 (Col-0), *phyB-9* and plants expressing 35S-promotor-driven *Pp-PIF68:YFP*, *Pp-PIF69:YFP* or *Pp-PIF69ΔAPB:YFP* were grown for 23 d under standard greenhouse conditions. Bar = 1 cm

(C) Pp-PIF68, Pp-PIF69 and Pp-PIF69ΔAPB localize to the nucleus in *Arabidopsis*. Col-0 seedlings expressing 35S promotor-driven *Pp-PIF68:YFP*, *Pp-PIF69:YFP* or *Pp-PIF69ΔAPB:YFP* were grown for 4 d in darkness before microscopic analysis. Bar = 10 µm. Arrows indicate nuclei.

DISCUSSION

R light broadly affects gene expression in P. patens

Phytochromes from cryptogams, e.g. ferns and mosses, mediate light-dependent transient and developmental responses (Mathews, 2006; Hughes, 2013). In contrast to seed plants, however, little is known about the down-stream components of phytochrome signaling in cryptogams. We and others have previously demonstrated that phytochromes from ferns and mosses accumulate in the nucleus upon activation by light, indicating an analogy to the first steps of seed plant phytochrome signaling (Tsuboi et al., 2012; Possart and Hiltbrunner, 2013). The data presented here suggest that also the subsequent steps of phytochrome signaling in the moss *P. patens* resemble those in seed plants. We analyzed the R light-induced changes in gene expression in the moss *P. patens*, thereby determining potential target genes of phytochrome signaling. Moreover, we identified putative PIF homologs in *P. patens* and demonstrated that these proteins are similar to seed plant PIFs in their molecular properties and physiological effects.

R light-induced DEGs in *P. patens* clustered into dark-active, temporarily-repressed and late-active genes. This, together with the functional DEG classification, reveals the molecular processes that are induced by the transition from darkness to (R) light. In dark-adapted plants, the high proportion of DEGs that were involved in amino acid metabolism indicates the use of non-photosynthetic energy sources through the metabolization of amino acids in the mitochondria. After 30 min R this kind of energy production seems to be repressed. Photosynthesis is probably induced, which was, however, not yet detectable on the transcriptional level. After 4 h R light, biosynthesis is reactivated and photosynthetic functions are activated also on the transcriptional level.

Our expression analysis differed in several aspects from a recently published work on *P. patens* (Chen et al., 2012). We detected a four-fold smaller total number of DEGs after 30 min and 4 h R light compared to the 1 h R light treatment described by Chen *et al.*, and the overlap of identified DEGs was below expectation. While we mostly observed down-regulated DEGs after 30 min R and up-regulated DEGs after 4 h R, Chen *et al.* reported similar numbers of up- and down-regulated genes after 1 h of R light treatment (Chen et al., 2012). This discrepancy may mostly result from the respective developmental stages of *P. patens* that were used for the different analyses (gametophores versus protonemata) as well as from the differing expression profiling techniques. Some differences, however, may also be attributed to the duration of R light treatments (30 min and 4 h, respectively, versus 1 h). The relatively small overlap as well as the respective DEG profiles could reflect the time course of R light induced changes in gene expression.

The comparison of our results to transcriptome analyses from *Arabidopsis* suggests similar effects of R light on cryptogams and seed plants. As described by Leivar *et al.*, late (2 d) R light-repressed *Arabidopsis* genes are dominated by genes involved in cellular metabolism, which is consistent with cluster 2 DEGs (dark active) in this study (Leivar et al., 2009). Moreover, photosynthesis- and chloroplast-related genes are the most abundant among R light-induced genes in *Arabidopsis*, resembling the function of cluster 1 DEGs (late active) (Leivar et al., 2009). In contrast to seed plants, however, we found that R light affects the expression of only a few transcription factors in *P. patens*, corresponding to the results from Chen *et al.* (Chen et al., 2012). This could be partially attributed to the different proportions of transcription factor genes in the genomes of cryptogams and seed pants (e.g. 3.5% in *P. patens* versus 7% in *Arabidopsis*) (Richardt et al., 2007). It may also indicate differences in the early light-induced gene network of cryptogams and seed plants.

PIFs from P. patens show molecular functionality

Although the direct effects of R light on gene expression in *P. patens* do not seem to involve a transcription factor cascade, we gained evidence for an important role of PIF transcription factors. 30 % of DEGs for which we could determine potential *Arabidopsis* homologs overlapped with PIF-dependent genes from *Arabidopsis* (Class 4 and 7) (Leivar et al., 2009). These genes had been described by Leivar *et al.* as indirect (Class 4) and direct (Class 7) targets of PIF-regulated seedling deetiolation (Leivar et al., 2009). The comparison of a recently published transcriptional analysis from *P. patens* with data from *Arabidopsis* also revealed an overlap, although not as conspicuous, of PIF-dependent genes (Leivar et al., 2009; Chen et al., 2012). Thus, considering the independent evolution of moss and seed plant phytochrome systems, we have revealed a substantial overlap of effects on gene expression in *P. patens* and *Arabidopsis*.

In line with this, we have identified 4 putative PIF homologs in the genome of *P. patens*. The sequence homology of these genes was mainly restricted to 4 regions, namely the APB and APA motifs, the bHLH domain and a motif of unknown function, i.e. the regions that are also conserved among PIF proteins from seed plants. Despite the small overall homology, this was consistent with the importance of these domains for PIF function in *Arabidopsis* and suggested a functional conservation for PIFs in mosses and seed plants (Leivar and Quail, 2011). Indeed, we found that *P. patens* PIFs resemble *Arabidopsis* PIFs in their molecular properties. Pp-PIF68 interacted with phytochromes from *P. patens* as well as with PHYA from *Arabidopsis* in a light-dependent manner. This interaction did not require the bHLH domain, which has also been described for At-PIFs (Khanna et al., 2004). Moreover, *P. patens* PIFs localized to the nucleus. They co-localized with At-PHYA and At-PIF3 and showed the typical formation of nuclear bodies (NBs) formerly described for *Arabidopsis* PIFs (Bauer et al., 2004; Chen, 2008). NBs have been associated with PIF-phytochrome interaction and subsequent phytochrome-induced PIF degradation (Bauer et al., 2004; Chen, 2008). In a recent work we have shown that light-activated phytochromes from *P. patens* also form NBs (Possart and Hiltbrunner, 2013). Thus, our observations suggest a phytochrome-mediated regulation of PIF activity in *P. patens* that is analogous to that in seed plants, e.g. through protein degradation, inhibition of binding to target promotors or other mechanisms (Park et al., 2012). We conclude that, according to their molecular properties, *P. patens* PIFs could act as modulators of phytochrome signaling output.

Moss PIFs resemble seed plant PIFs in their physiological effects on Arabidopsis growth and development

We gained further insight into *P. patens* PIF functionality through the overexpression of Pp-PIF68, Pp-PIF69 and Pp-PIF69ΔAPB in *Arabidopsis*. All three Pp-PIFs induced a phenotype that resembled the overexpression of *Arabidopsis* PIFs. The hyposensitive response of Pp-PIF-OX seedlings towards R and FR light had been formerly described for At-PIF5-OX seedlings (Fujimori et al., 2004; Khanna et al., 2007). At-PIF5 acts as a negative factor during PHYB-mediated photomorphogenesis (Fujimori et al., 2004; Khanna et al., 2007). Khanna *et al.* correlated the effect of At-PIF5 overexpression with reduced PHYB levels, indicating a regulation of PHYB abundance by endogenous At-PIF5 (Khanna et al., 2007). The phenotype of Pp-PIF-OX seedlings suggested that PIFs from *P. patens* might interfere with the endogenous phytochrome signaling in a similar way. Also dark-grown Pp-PIF-OX seedlings resembled the phenotype of At-PIF5-OX seedlings, showing a shorter hypocotyl and an exaggerated apical hook. These effects are attributed to elevated ethylene levels and the overexpression of At-PIF5 increases the ethylene production in dark-grown seedlings, which is not observed for At-PIF1, At-PIF3 or At-PIF4 OX-lines (Khanna et al., 2007). The effects of *P. patens* PIFs on seedling etiolation suggest a high similarity to At-PIF5.

The analysis of later developmental stages further supports an interference of *P. patens* PIFs with light signaling in *Arabidopsis*. Pp-PIF-OX plants had reduced chlorophyll content and showed very early flowering, again resembling the phenotype of At-PIF5 as well as of At-PIF4 overexpressor plants (Fujimori et al., 2004; Kumar et al., 2012). In addition, this phenotype was reminiscent of the *phyB* and higher order *phy Arabidopsis* mutants, which flower very early and produce only a couple of siliques (Reed et al., 1993; Strasser et al., 2010). At-PIF5 indirectly affects the flowering time through the At-PHYB signaling pathway (Fujimori et al., 2004). *P. patens* PIFs might have a similar effect when they are expressed in *Arabidopsis*, based on their ability to mimic endogenous At-PIFs. It is, however, also possible that Pp-PIFs form heterodimers with endogenous At-PIFs, thereby interfering with phytochrome-signaling. For example, the light-induced regulation of PIF levels through ubiquitination and degradation might be disturbed by Pp-PIFs. Although we cannot define the physiological function of Pp-PIFs in *P. patens*, our data support the notion that Pp-PIFs are highly similar to seed plant PIFs.

Interestingly, we observed similar phenotypes for the expression of Pp-PIF69 and its splicing variant Pp-PIF69ΔAPB even though Pp-PIF69ΔAPB presumably does not interfere with At-PHYB signaling because the APB motif is necessary for the interaction of At-PIFs and At-PHYB (Khanna et al., 2004; Leivar and Quail, 2011). The Pp-PIF69ΔAPB-OX phenotype may result from the formation of AtPIF-PpPIF heterodimers, as already described above. Alternatively, it suggests a prominent role of the APA motif that is present in all Pp-PIFs we have identified. In *Arabidopsis*, this motif is important for the interaction of At-PIF1 and At-PIF3 with At-PHYA, but the actual binding sequence seems to differ between both PIF proteins (Al-Sady et al., 2006; Shen et al., 2008). The APA motif of PIFs from *P. patens* might be sufficient for an interaction with phytochromes. Moreover, the combination of APB and APA motifs in Pp-PIF splicing variants could constitute an additional regulatory level during PIF-dependent responses in *P. patens*, which is not present in seed plants like *Arabidopsis*.

In summary, our data strongly suggest that Pp-PIFs play a role during light-induced adaptation and development in *P. patens*, similar to the function of PIFs in *Arabidopsis*. Thus, also in cryptogams, nuclear phytochromes might regulate gene expression through the interaction with PIF proteins. The PIF-branch of phytochrome signaling may have been functionally conserved during the course of evolution, further emphasizing its importance during light-dependent plant development.

METHODS

Cloning of Constructs

A description of DNA constructs can be found in the Supplemental Methods (please refer to the enclosed disc). A list including all primers used for the generation of DNA constructs can also be found in the Supplemental Methods, Supplemental Table 1.

Microarray Analysis

P. patens strain Gransden 2004 (Rensing et al., 2008) was cultivated on Knop agar plates under standard conditions (16/8 h light/dark photoperiod, 70 µmol m^{-2} s^{-1} PAR). Four week old cultures were subjected to constant darkness (D) for 2 weeks before R light treatment (656 nm, 24 nm full width at half-maximum; 12 µmol m^{-2} s^{-1}). All samples, including the control (D), were harvested and immediately frozen in liquid nitrogen. An additional control experiment was setup using three weeks of darkness. All experiments were conducted in triplicates. RNA was isolated using the Qiagen RNeasy Plant Mini Kit. Amplification and labeling was carried out using the Kreatech ampULSe kit, QC was done using Nanodrop and Bioanalyzer. Hybridization and data processing was carried out as described previously (Wolf et al., 2010). The Hierarchical Clustering was generated with Genedata Analyst 7.5.7 (distance: positive correlation (1-r); linkage: Average). The principal component analysis (PCA) was performed with Genedata Analyst 7.5.7 (use: covariance matrix, imputation: row mean). One of the three two week control samples behaved aberrant on the second component; numbers of genes detected as differentially expressed varied largely depending on the control group chosen. Since using all three two week control samples might have led to the detection of false positives, a control group consisting of five experiments (3x three weeks darkness, 2x two weeks darkness - devoid of the outlier) was used for the following analyses.

For comparison between DEGs identified in our microarray study and genes identified as differentially expressed upon R light treatment in *Arabidopsis* (Leivar et al., 2009) we proceeded as follows. We used the *P. patens* genome annotation V1.6 from the Phytozome repository (ftp://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Ppatens_v1.6/annotation/Ppatens_152_protein.fa.gz) and extracted the best hit homolog from *A. thaliana* indicated in the *P. patens* annotation for each DEG. We then counted the number of *A. thaliana* genes with the same locus identifier in the data of Leivar *et al.* for each of their seven classes for up- and down-regulated genes, respectively. We did this analysis separately for the DEGs identified in the four treatments of our microarray study. For comparison of our data with the RNA-sequencing dataset from Chen *et al.* (Chen et al., 2012) we counted the number of identical *P. patens* gene locus identifiers between DEGs of any of the four conditions of our microarray studies and genes identified as either up- or down-regulated by *Chen et al*.

Quantitative Realtime PCR

P. patens cultivation, light treatments and sampling were carried out as described for the microarray analysis. RNA isolation was performed with the Qiagen RNeasy Plant Mini Kit. Contained DNA was eliminated via on-column DNase treatment. First-strand cDNA was obtained by reverse-transcription of the RNA using Superscript III (Invitrogen) and random hexamer primers (Fermentas). Gene-specific oligonucleotides (Supplemental Methods, Supplemental Table 2 (see enclosed disc)) were designed utilizing Primer3 (Steve Rozen and Helen J. Skaletsky, 2000) with standardized melting temperature of 60 °C and GC content of 50 to 60%. Quantitative Realtime PCR was conducted using SensiMix SYBR Kit (Bioline) on a LightCycler480 (Roche). For each 25 µL reaction 50 ng of RNA equivalent were used. Expression values (Cp, crossing point) were normalized against the respective reference gene, employing the comparative Ct method. All values were converted into fold changes to time point zero. Thioredoxin (Phypa_461491) showed Cp values suitable for all genes except for Lhc SR1 (Phypa_169593), for which Phypa_4364 (pectinesterase family protein) was chosen. One-tailed, heteroscedastic T-test was applied to test for significance. All analyses were performed with Expressionist Analyst v7.0.5a (Genedata).

Database Searches and Phylogenetic Analysis

The protein sequences of *A. thaliana* PIFs were aligned using MAFFT in order to define the APA consensus motif (Katoh et al., 2009). The APA motif was used to search the databases available at http://www.ncbi.nlm.nih.gov/ and http://www.cosmoss.org/ for proteins from *P. patens*.

For *A. thaliana PIF* genes TAIR10 gene identifiers are as follows: AT2G20180=At-PIF1, AT1G09530=At-PIF3, AT2G43010=At-PIF4, AT3G59060=At-PIF5, AT3G62090=At-PIF6, AT5G61270=At-PIF7 and AT4G00050=At-PIF8. For *P. patens*, CGI v.1.6 gene identifiers are: Phypa_437018=Pp-PIF68, Phypa_437040=Pp-PIF69, Phypa_439387=Pp-PIF84 and Phypa_446229=Pp-PIF147.

For phylogenetic analyses basic Helix-Loop-Helix (bHLH) motives were selected from the full-length protein sequences according to pfam predictions (www.arabidopsis.org). Alignments of PIF full-length proteins and of bHLH domains were generated using MAFFT (Katoh et al., 2009). Phylogenetic analysis by Bayesian inference was performed using MrBayes v.3.2.1 (Huelsenbeck and Ronquist, 2001) with eight gamma-distributed rate categories. We ran 200,000 generations with a burn-in of 25 %. Graphical displays of radial trees were generated using FigTree v.1.3.1.

Yeast Two Hybrid Analysis

Yeast two hybrid analyses and ONPG assays were carried out according to previously published protocols (Hiltbrunner et al., 2005). Yeast two hybrid assays were performed with the yeast strain Y187 (Clontech, Mountain View). As chromophore phycocyanobilin (PCB) from *Spirulina* was added to the growth medium (final concentration 10 µM) (Kunkel et al., 1993).

Transient Expression in N. benthamiana and P. patens

The transient transformation of *N. benthamiana* was carried out as described previously (Grefen et al., 2008). Leaves from 4 to 6 weeks old *N. benthamiana* plants were infiltrated with *Agrobacterium tumefaciens* strain C58 at the adaxial sides. In order to suppress transgene silencing the p19 protein from tomato bushy stunt virus was co-expressed with proteins of interest (Voinnet et al., 2000). After co-transformation with pPPO30:Pp-PIF68, pPPO30:Pp-PIF69 or pPPO30:Pp-PIF69ΔAPB and either pphyA40:At-PHYA, pCHF40:At-PHYA-NLS or pCHF83myc:At-PIF3 the tobacco plants were incubated in D for 2 days prior to microscopic analysis.

In order to prevent upright growth *P. patens* cultures were inoculated between two cellophane sheets placed on solid medium, and incubated under standard growth conditions (16/8 h light/dark photoperiod, 50-70 µmol m^{-2} s^{-1} PAR) for 4 to 6 days. The transient transformation of *P. patens* with pUC1930:Pp-PIF68, pUC1930:Pp-PIF69 or pUC1930:Pp-PIF69ΔAPB was carried out by particle bombardment with a Biolistic Particle Delivery System. Gold particle diameter was 1 µm, helium pressure 7 bar; chamber vacuum pressure 0.8 bar and target distance 5 cm. After bombardment the samples were incubated in darkness for 1 to 5 days prior to microscopic analysis.

Transformation of Arabidopsis

Arabidopsis lines expressing Pro35S:Pp-PIF68:YFP:TerRbcS, Pro35S:Pp-PIF69:YFP:TerRbcS or Pro35S:Pp-PIF69ΔAPB:YFP:TerRbcS were obtained by *Agrobacterium*-mediated transformation (Clough and Bent, 1998; Davis et al., 2009). Transgenic plants were selected using the herbicide Butafenacil/Inspire (Syngenta Agro) as previously described (Block et al., 1987; Rausenberger et al., 2011).

Phenotypic Analysis

Arabidopsis seedlings were grown on 0.5x Murashige and Skoog medium (Duchefa) / 0.7% (w/v) agar. After a stratification for at least 2 d at 4°C, the germination of seeds was induced with 4 to 6 hours white light, followed by an incubation for 4 days at 22°C in darkness (D), continuous R (peakwave: 670 nm, 10 µmol m^{-2} s^{-1}), FR (peakwave: 740 nm, 12 µmol m^{-2} s^{-1}) or B light (peakwave: 473 nm, 4 µmol m^{-2} s^{-1}) before phenotypic analysis of seedlings.

For the analysis of later developmental stages *Arabidopsis* seeds were incubated in 0.1% Agarose solution for at least 2 d at 4°C before sowing on soil. The positions of controls and Pp-PIF-overexpressor lines were randomized and plants were grown under standard conditions in the greenhouse.

Microscopic analysis

A Zeiss Axioscope 2 (Zeiss) equipped with YFP, CFP and mCherry specific filter sets (AHF Analysentechnik) was used for image acquisition. Image processing was done with the ImageJ (version 1.44k; National Institute of Health) and Photoshop (version 10.0.0.1; Adobe) softwares.

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AUTHOR CONTRIBUTIONS

AP and AH conceived the study. AP, SK, HH and SH did the experimental work. SR and CB analyzed the microarray data. CB performed the phylogenetic analysis. AP and AH wrote the paper with contributions from CB, SR and SH.

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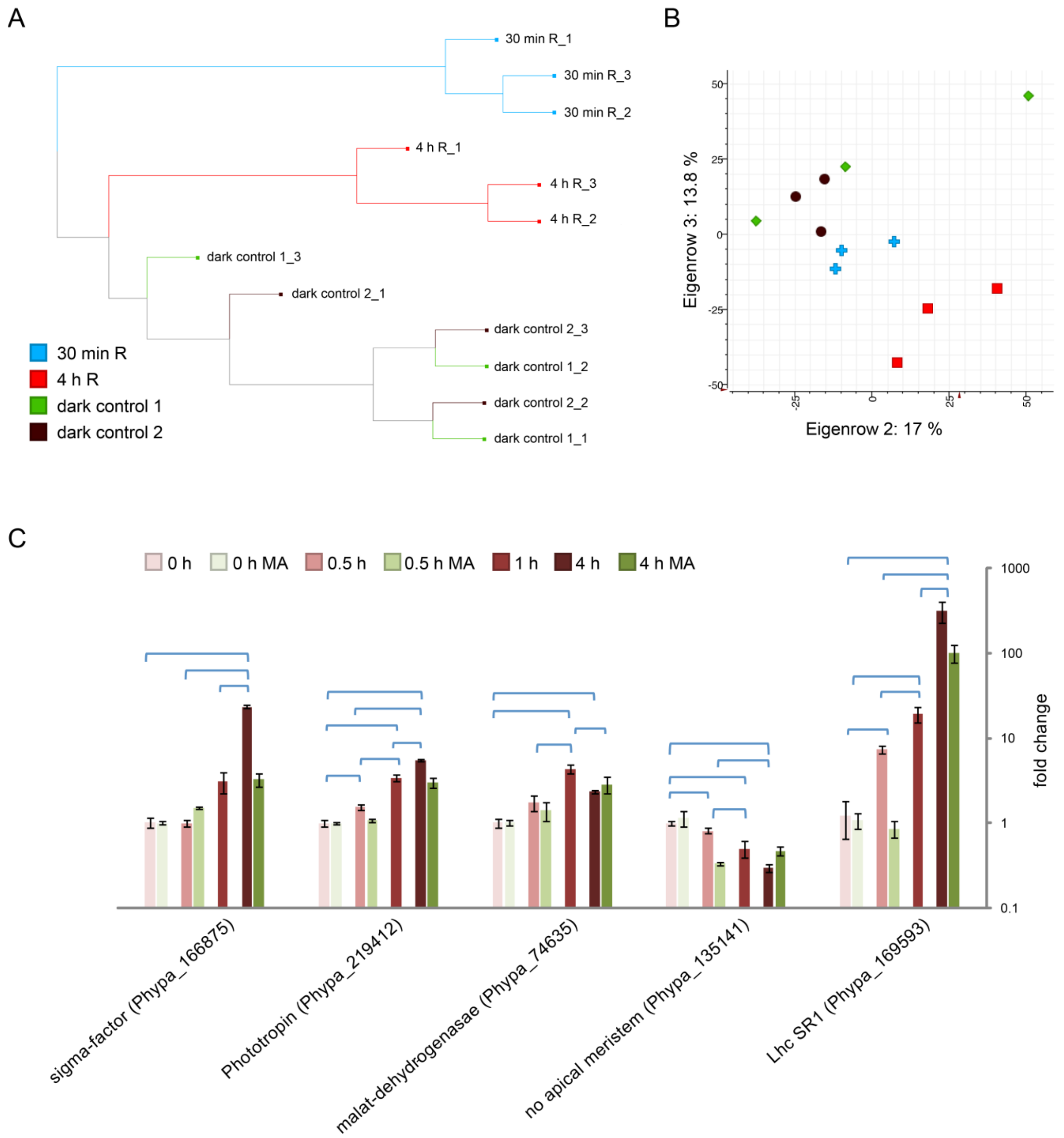
SUPPLEMENTAL DATA

Supplemental Figures

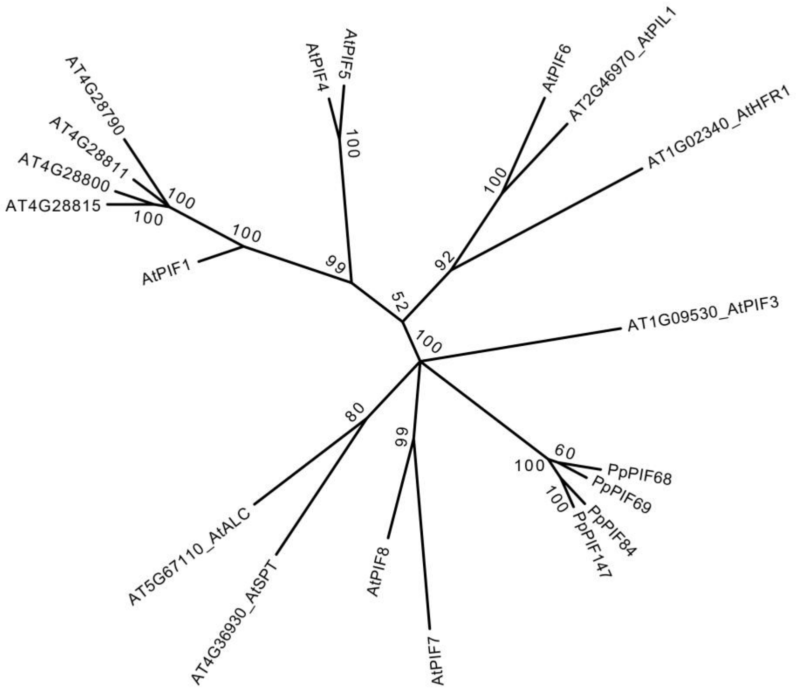


Supplemental Figure 1. Global review and validation of microarray data.

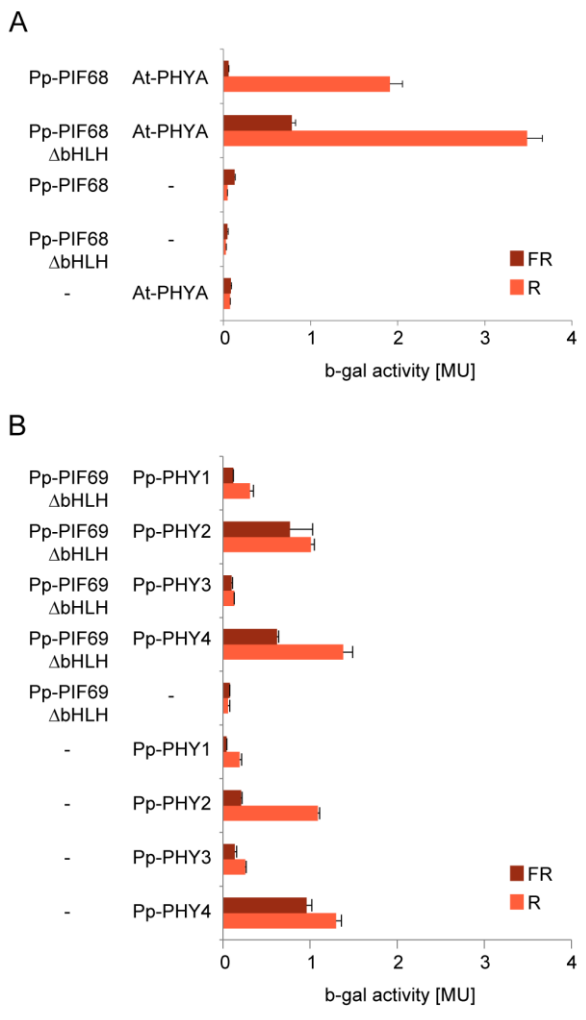
(A) Hierarchical Clustering of microarray experiments (biological triplicates are indicated as 1-3). Prior to light treatment plants were adapted to darkness for 2 weeks (dark control 1, 2 weeks). Also shown is an additional dark control (dark control 2, 3 weeks).

(B) Principal Component Analysis of microarray experiments. Color legend same as in (A).

(C) Validation of fold changes of selected genes by qPCR. Cp-values of genes of interest (GOI) were normalized to Phypa_461491 (Thioredoxin) except for Phypa_169593 (Lhc SR1), that was normalized with Phypa_4364 (pectinesterase family protein), by applying the DDCt method. Reference genes were selected by their constant expression in this treatment as well as for their little variation over a wide range of treatments. Final fold changes were calculated in comparison to 0h. Error bars represent standard error of biological triplicates. qPCR results are shown in red and microarray (MA) results in green graduation from 0h up to 4h, respectively. Significant (student's t-test: one-tailed, heteroscedastic) differences between time points in qPCR are shown as brackets above the respective bars.



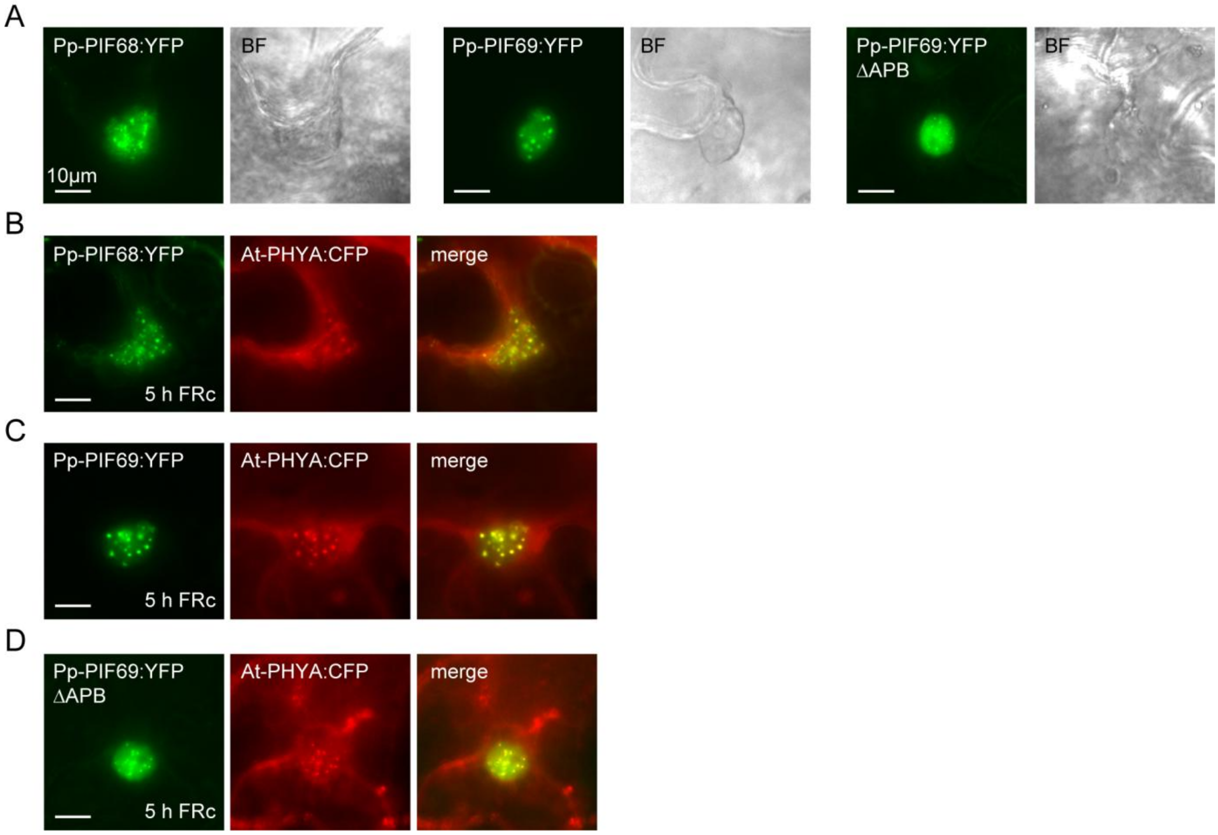
Supplemental Figure 2. Phylogeny of *P. patens* and *A. thaliana* full-length bHLH proteins based on Bayesian inference (BI). Node labels represent BI posterior probabilities (in %).



Supplemental Figure 3. Interaction of *P. patens* PIFs and phytochromes.

(A) Pp-PIF68 and Pp-PIF68ΔbHLH interact with At-PHYA in a light-dependent manner. Constructs coding for AD-Pp-PIF68 or AD-Pp-PIF68ΔbHLH and At-PHYA-BD were used for yeast-two-hybrid assays. To convert At-PHYA to the Pfr or Pr form, yeast cultures were irradiated for 5 min with R light (12 µmol $m^{-2} s^{-1}$) or FR (12 µmol $m^{-2} s^{-1}$) light. The β–galactosidase activity was measured after an additional incubation in the dark for 4 h. MU, Miller Units, Error bars represent SE; n=3. AD, GAL4 activation domain; BD, GAL4 DNA binding domain.

(B) Pp-PIF69ΔbHLH does not interact with *P. patens* phytochromes in yeast.
Constructs coding for AD-Pp-PIF69ΔbHLH and Pp-PHY1/2/3/4-BD were used for yeast-two-hybrid analysis as described in (A). MU, Miller Units, Error bars represent SE; n=3. AD, GAL4 activation domain; BD, GAL4 DNA binding domain.



Supplemental Figure 4.

(A) Pp-PIFs localize to the nucleus and form nuclear bodies. Constructs that code for Pp-PIF68:YFP, Pp-PIF69:YFP or Pp-PIF69ΔAPB:YFP under control of the *35S* promotor were transformed into leaves of *Nicotiana benthamiana* by *Agrobacterium tumefaciens* infiltration. One day after transformation plants were transferred into darkness for another two days before microscopic analysis of epidermal leaf cells. Bar = 10 µm.

(B) – (D) Pp-PIF68, Pp-PIF69 and Pp-PIF69ΔAPB co-localize with At-PHYA in the nucleus. Constructs that code for either Pp-PIF68:YFP **(B)** Pp-PIF69:YFP **(C)** or Pp-PIF69ΔAPB:YFP **(D)** and At-PHYA:CFP under control of the *35S* promotor were transformed into *N. benthamiana* and analyzed as described in (A).

Supplemental Datasets, Methods and Tables

For supplemental data on the microarray analysis as well as on the cloning of DNA constructs and used primers please refer to the enclosed disc.

- Supplemental Data > Chapter 3 > Supplemental Dataset 1. DEGs from Microarray Analysis in *P. patens* after R light treatments.
- Supplemental Data > Chapter 3 > Supplemental Dataset 2. Comparison of present study with transcriptome profiling by Chen et al., 2012.
- Supplemental Data > Chapter 3 > Supplemental Dataset 3. Comparison of Transcriptome Analyses from *P. patens* and *Arabidopsis* (Leivar et al., 2009).
- Supplemental Data > Chapter 3 > Supplemental Methods. Cloning of Constructs.
- Supplemental Data > Chapter 3 > Supplemental Methods. Supplemental Table 1. Primer List (cloning).
- Supplemental Data > Chapter 3 > Supplemental Methods. Supplemental Table 1. Primer List (qRT-PCR).

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“The most exciting phrase to hear in science, the one that heralds new discoveries, is not ‘Eureka!’ but ‘That’s funny …’.”

Isaac Asimow

CHAPTER 2 - SUPPLEMENTAL METHODS

Cloning of constructs

A list including all primers used in this work can be found in Supplemental Table 1. Schematic representations of targeting constructs and genomic loci can be found in Supplemental Figure 10.

The gene targeting cassettes used to generate transgenic *Physcomitrella* lines containing a YFP tag fused to the endogenous phytochromes were obtained as follows. First, pBS II KS:YFP was generated by PCR amplifying EYFP from pEYFP (Clontech, Mountain View, CA, USA) using the primers ah042 and ah043 and ligating the resulting fragment into the BamHI/KpnI site of pBS II KS (Stratagene, La Jolla, CA, USA). In the next step, the region of the *Physcomitrella* phytochrome genes between the stop codon and approximately 500 bp upstream of it were PCR amplified from genomic *Physcomitrella* DNA using the primers ah406/ah407 for Pp-*PHY1*, ah410/ah411 for Pp-*PHY2*, ah414/ah415 for Pp-*PHY3*, ah418/ah419 for Pp-*PHY4*, ah430/ah431 for Pp-*PHY5a* and ah426/ah427 for Pp-*PHY5b*. These fragments were cut with SpeI/XbaI and ligated in sense orientation into the XbaI site of pBS II KS:YFP. Finally, the region of the *Physcomitrella* phytochrome genes between the stop codon and approximately 500 bp downstream of it were amplified by PCR from genomic *Physcomitrella* DNA using the primers ah408/ah409 for Pp-*PHY1*, ah412/ah413 for Pp-*PHY2*, ah416/ah417 for Pp-*PHY3*, ah420/ah421 for Pp-*PHY4*, ah432/ah433 for Pp-*PHY5a* and ah428/ah429 for Pp-*PHY5b*. These fragments were digested with XbaI/KpnI and ligated into the NheI/KpnI site of the pBS II KS:YFP vectors already containing the first fragment of the respective phytochrome gene, resulting in gene-targeting cassettes for each of the seven *Physcomitrella* phytochromes. These gene-targeting cassettes were flanked by NotI sites, which were used to cut the cassettes for transformation of *Physcomitrella*.

pRT101neo (provided by R. Reski, University of Freiburg, Germany and W. Frank, University of Munich, Germany), which confers resistance to G418 in *Physcomitrella*, was used for co-transformation with the YFP constructs described above.

The gene-targeting cassette used to generate the transgenic Pp-*fhy1* knock out *Physcomitrella* lines was obtained as follows. First, part of Pp-*FHY1* gene sequence of about 1000 bp (500 bp upstream and 500 bp downstream of the PstI restriction site) was PCR-amplified from genomic *Physcomitrella* DNA using the primers ah434/ah435. This fragment was cut with SpeI/KpnI and ligated into the XbaI/KpnI site of pBS II KS:YFP to replace YFP. A hygromycin resistance cassette, ProNOS:HPT:TerNOS (hygromycin phosphotransferase), was PCR amplified from pGAP:Hyg (GenBank Acc. EU933993; provided by R. Reski, University of Freiburg, Germany and W. Frank, University of Munich, Germany) using the primers ah483/ah484. The fragment was cut with BamHI/SpeI and ligated in pBS II KS cut with BamHI/SpeI. The HPT-cassette was cut from the resulting plasmid with SbfI and ligated into the PstI site of pBS II KS containing the 1000 bp fragment of Pp-FHY1. The gene-targeting cassette was flanked by NotI sites, which were used to cut the cassettes for transformation of *Physcomitrella*.

D153ah:At-PHYA and D153ah:At-PHYA 1-406, which have been described previously (Hiltbrunner et al., 2006), are yeast two-hybrid vectors coding for At-PHYA:GAL4 BD and At-PHYA 1-406:GAL4 BD, respectively. D153ah containing fragments of the *Physcomitrella* phytochromes corresponding to At-PHYA 1-406 were obtained as follows. These fragments were PCR amplified from genomic *Physcomitrella* DNA using the primers ah441/ah442 for Pp-PHY1 399, ah443/ah444 for Pp-PHY2 402, ah442/ah445 for Pp-PHY3 398 and ah447/ah448 for Pp-PHY4 402. The fragments for Pp-PHY1 399 and Pp-PHY3 398 were cut with BamHI/SpeI, and those for Pp-PHY2 402, and Pp-PHY4 402 with BglII/SpeI. Finally, the fragments were ligated into D153ah:At-PHYA digested with BamHI/SpeI to replace At-PHYA.

D153ah:At-FHY1 is a yeast two-hybrid vector, which contains At-FHY1:GAL BD. To generate it we cut At-FHY1 from pGADT7:At-FHY1 (Hiltbrunner et al., 2005) using BamHI/SpeI and ligated it into D153ah:At-PHYA digested with BamHI/SpeI to replace At-PHYA. D153ah:Ac-PHY1, D153ah:Ac-PHY2 and D153ah:Ac-PHY3 are yeast two-hybrid vectors containing Ac-PHY1:GAL4 BD, Ac-PHY2:GAL4 BD and Ac-PHY3:GAL4 BD (=*Adiantum capillus-veneris* PHY). Ac-PHY1, Ac-PHY2 and Ac-PHY3 were PCR-amplified using the primers ah471/ah472 for Ac-PHY1, ah474/ah475 for Ac-PHY2 and ah477/ah478 for Ac-PHY3. As templates for the PCR, we used vectors containing the cDNA fragments for Ac-PHY1, Ac-PHY2 and Ac-PHY3, respectively, which were provided by M. Wada (Kyushu University, Fukuoka, Japan). The Ac-PHY1 fragment was digested with BamHI/SpeI and the Ac-PHY2 and Ac-PHY3 fragments with SpeI and ligated into D153ah:At-FHY1 cut with either BamHI/SpeI or XbaI/SpeI to replace At-FHY1.

pPPO30:Ac-PHY1 is a T-DNA vector containing a Pro35S:Ac-PHY1:YFP:TerRbcS cassette and a mutated version of *PPO* as a marker for selection using Butafenacil (Rausenberger et al., 2011). To generate it, Ac-PHY1 was cut from D153ah:Ac-PHY1 using BamHI/SpeI and ligated into the BamHI/XbaI site of pPPO30 (Rausenberger et al, 2011).

pUC1930:Ac-PHY2 and pUC1930:Ac-PHY3 are vectors containing Pro35S:Ac-PHY2:YFP:TerRbcS and Pro35S:Ac-PHY3:YFP:TerRbcS, respectively. Ac-PHY2 and Ac-PHY3 were cut from D153ah:Ac-PHY2 and D153ah:Ac-PHY3 with Xba/SpeI and ligated in sense orientation into pUC1930 cut with XbaI.

D153ah:Cp-PHY2 is a yeast two-hybrid vector containing Cp-PHY2:GAL4 BD (=*Ceratodon pupureus* PHY2), which we generated as follows. First, a C-terminal fragment of Cp-PHY2 was PCR amplified from plasmid p781_a2 (provided by T. Lamparter, Karlsruhe Institute of Technology, Karlsruhe, Germany) using the primers ah312/ah456. This PCR fragment was cut with BglII/SpeI and ligated into the BglII/SpeI site of pBS II KS:At-PHYA (Hiltbrunner et al., 2005) to replace part of At-PHYA. To obtain the full-length cDNA of Cp-PHY2, the N-terminal fragment was amplified by PCR from plasmid p781_a2 using the primers ah455/ah457. This PCR fragment was cut with BamHI and ligated in sense orientation into the BamHI/BglII site of the pBS II KS vector already containing the C-terminal part of Cp-PHY2. Finally, full-length Cp-PHY2 was cut from pBS II KS:Cp-PHY2 using BamHI/SpeI and this fragment was ligated into the BamHI/SpeI site of D153ah:At-PHYA to replace At-PHYA.

pPPO30:Cp-PHY2 is a T-DNA vector containing a Pro35S:Cp-PHY2:YFP:TerRbcS cassette and was obtained as follows. Cp-PHY2 was cut from pBS II KS:Cp-PHY2 using BamHI/SpeI and ligated into the BamHI/XbaI site of pPPO30 (Rausenberger et al, 2011).

pGADT7ah:Pp-FHY1 is a yeast two hybrid vector coding for GAL4 AD:Pp-FHY1 (=*Physcomitrella patens* FHY1) and pCHF70:Pp-FHY1 is a T-DNA vector containing a Pro35S:YFP:Pp-FHY1:TerRbcS cassette and a Basta resistance gene as selection marker. Pp-FHY1 was PCR amplified from *Physcomitrella* total cDNA using the primers ah357/ah404. This PCR fragment was cut with BglII/SpeI and ligated into the BamHI/SpeI site of pGADT7:At-FHY1 to replace At-FHY1 as well as into the BamHI/XbaI site of pCHF70 (Hiltbrunner et al., 2005).

pPPO70 contains a mutant version of *PPO*, which confers resistance to Butafenacil (Hanin et al., 2001; Li et al., 2003). A PvuII-PstI fragment containing *PPO* was cut from pWCO35 (Hanin et al., 2001) (provided by J. Paszkowski, University of Geneva, Switzerland) and ligated into pCHF70 cut with PmlI/SbfI to replace the Basta resistance gene as selectable marker.

pGADT7ah:Cr-FHY1 is a yeast two-hybrid vector, which codes for GAL4 AD:Cr-FHY1 (=*Ceratopteris richardii* FHY1) and pPPO70:Cr-FHY1 is a T-DNA vector containing a Pro35S:YFP:Cr-FHY1:TerRbcS cassette. Cr-FHY1 was PCR amplified from cDNA clone Cri2_1_J13_SP6 (GenBank Acc. BE640872; provided by S. J. Roux, University of Texas, Austin, TX, USA) using the primers ah349/ah350, cut with BamHI/SpeI and ligated into the BamHI/SpeI site of pGADT7:At-FHY1 to replace At-FHY1 as well as into pPPO70 cut with BamHI/XbaI.

pGADT7ah:Os-FHY1 is a yeast two-hybrid vector, which contains GAL4 AD:Os-FHY1

(=*Oryza sativa* FHY1) and was obtained as follows. Os-FHY1 was PCR amplified from cDNA clone J023050K07 (GenBank Acc. AK070454; provided by the Rice Genome Resource Center, Tsukuba, Japan) using the primers ah309/ah310, cut with BamHI/XbaI and ligated into the BamHI/SpeI site of pGADT7:At-FHY1 to replace At-FHY1.

pGADT7ah:To-FHY1 is a yeast two-hybrid vector containing GAL4 AD-To-FHY1 (=*Taraxacum officinale* FHY1) and was generated as follows. Total RNA was extracted from a dandelion (*Taraxacum offinicale*) leaf collected in front of the Institute of Biology II, University of Freiburg, Germany, using the RNeasy Plant Mini Kit (Qiagen, Hilden, Germany). This RNA was reverse transcribed using the ProtoScript First Strand cDNA Synthesis Kit (New England Biolabs, Beverly, MA, USA). To-FHY1 was PCR amplified from the resulting total cDNA using the primers ah351/ah352, cut with BamHI/SpeI and ligated in sense orientation into the BamHI/SpeI site of pGADT7:At-FHY1 to replace At-FHY1.

pGADT7ah:Cl-FHY1 CT is a yeast two-hybrid vector coding for GAL4 AD:Cl-FHY1 CT (=*Closterium* sp. FHY1 CT), which was obtained as follows. Cl-FHY1 CT was PCR amplified from cDNA clone CL20_G09 (GenBank Acc. BW647715; provided by H. Sekimoto, Japan Women's University, Tokyo, Japan) using the primers ah383/ah384, cut with XbaI/SpeI and ligated in sense orientation into the XbaI/SpeI site of pGADT7:At-FHY1 to replace At-FHY1.

pGADT7ah:Pg-FHY1 is a yeast two-hybrid vector coding for GAL4 AD:Pg-FHY1 (=*Picea glauca* FHY1), which was obtained as follows. Pg-FHY1 was PCR amplified from cDNA clone GQ03235_G10 (GenBank Acc. BT111284; provided by the Center for Forest Research, Université Laval, Canada) using the primers ah527/ah528, cut with XbaI/SpeI and ligated in sense orientation into the XbaI/SpeI site of pGADT7:At-FHY1 to replace At-FHY1.

pGADT7:At-FHY1 is a yeast two-hybrid vector containing GAL4 AD-At-FHY1 and has been described previously (Hiltbrunner et al., 2006).

pUC1940:At-PHYA, which was used for transient transformation of mustard seedlings, contains a Pro35S:At-PHYA:CFP:TerRbcS cassette and has been described (Hiltbrunner et al., 2005).

pUC1930 contains a Pro35S:BamHI:XbaI:YFP:TerRbcS cassette and has been obtained as follows. The DNA fragment containing the Pro35S:BamHI:XbaI:YFP:TerRbcS cassette was cut from pCHF30 (Hiltbrunner et al., 2006) with EcoRI/HindIII and ligated into the EcoRI/HindIII site of pUC19 (Fermentas, St. Leon-Rot, Germany).

pUC1930:At-PHYA contains a Pro35S:At-PHYA:YFP:TerRbcS cassette and was used for transient transformation assays. At-PHYA was cut from pBS II KS:At-PHYA with BamHI/SpeI and ligated into the BamHI/XbaI site of pUC1930.

pCHF70:At-FHY1 is a T-DNA vector, which contains a Pro35:YFP:At-FHY1:TerRbcS cassette (Hiltbrunner et al., 2005) and was used for transient expression in mustard seedlings.

pCHF150myc is a T-DNA vector containing a Pro35S:myc:mCherry:BamHI:AvrII:XbaI:TerRbcS cassette and *bar* as selection marker and was obtained as follows. First, mCherry was PCR amplified from pBinAR-DCP2:mCherry (provided by A. Wachter, University of Tübingen, Germany) using the primers ah094/ah791. To add the myc tag to mCherry, this fragment was purified and used as template for a second PCR with the primer pair ah094/ah792. This PCR fragment was digested with BglII/SpeI and ligated into the BamHI/XbaI site of pCHF5 (Hiltbrunner et al., 2005).

pUC1942 is a vector containing a Pro35S:CFP:NLS:TerRbcS cassette and was obtained as follows. CFP:NLS was PCR amplified from pUC1940:At-PHYA (Hiltbrunner et al., 2005) using the primers ah042 and ah-nls, which included the NLS described by Matsushita et al. (2003). The PCR fragment was digested with BamHI/SpeI and ligated into pCHF5 (Hiltbrunner et al., 2005) cut with BamHI/XbaI to obtain pCHF42. The EcoRI/HindIII fragment of pCHF42 containing the Pro35S:CFP:NLS:TerRbcS cassette was then ligated into the EcoRI/HindIII site of pUC19 (Fermentas, St. Leon-Rot, Germany), resulting in pUC1942.

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Supplemental Table 1. Primer List (restriction sites are underlined).

Name	Sequence (5' → 3')	Restriction Sites
ah042	CGC GGA TCC CGC TCT AGA ATG GTG AGC AAG GGC GAG G	BamHI, XbaI
ah043	CGG GGT ACC GCT AGC TTA ACT AGT CTT GTA CAG CTC GTC CAT G	KpnI, NheI, SpeI
ah070	AGA AGT CGT GCT GCT TCA TG	-
ah094	GGA CTA GTT ATC TAG AGC CCT AGG ATC CGC CTT GTA CAG CTC GTC CAT G	SpeI, XbaI, AvrII, BamHI
ah309	CGC GGA TCC AAA AAT GGA TCA CAG CGG CAG CG	BamHI
ah310	GCT CTA GAA AGC ATG AGC CTT GTA AA	XbaI
ah312	GGA CTA GTC CTA GGC ATT TGG CTT GCA GCG TCA	SpeI, AvrII
ah349	CGC GGA TCC AAA AAT GGG GTT GCG TCG TCT G	BamHI
ah350	GGA CTA GTT TGA TTC AAC AAC AGT GA	SpeI
ah351	CGC GGA TCC AAA AAT GTT ACA GTT ATA TTC A	BamHI
ah352	GGA CTA GTT AGC ATA AGC GTT GAA AA	SpeI
ah357	GGA CTA GTG AGC ATA AGC TTG GCG AAG	SpeI
ah383	GCT CTA GAA AAA TGT TTG TCC TGT CCT CTG GCC G	XbaI
ah384	GGA CTA GTC AAG AGC AGC TGC GCA AAG	SpeI
ah404	GAA GAT CTA AAA ATG ACG ACG GGG AAG GTG	BglII
ah406	GGA CTA GTC ACC TGA AGG TTG GGT CA	SpeI
ah407	GCT CTA GAC ATT TGA CTT GAA GCA TCA	XbaI
ah408	GCT CTA GAG AGT TTA TAC TCC TAT TTG	XbaI
ah409	CGG GGT ACC GCG GCC GCT AAG TAT ATA ACC TAA AG	KpnI, NotI
ah410	GGA CTA GTA ATG CTG TGC GAT TCA CCC CA	SpeI
ah411	GCT CTA GAG ACA ACA GTA GAT CTC ACA	XbaI
ah412	GCT CTA GAT TTA TTA GAG TAA CAA TCT A	XbaI
ah413	CGG GGT ACC GCG GCC GCT GAA TCT CAT GTA AAA ACC A	KpnI, NotI
ah414	GGA CTA GTT TCT TAT TAA ACG CAG TG	SpeI
ah415	GCT CTA GAC ATT TGA CTC GCA GCA TCA	XbaI
ah416	GCT CTA GAG AGC TCA TAT ACC CTT TT	XbaI
ah417	CGG GGT ACC GCG GCC GCA ATG AGT TAT CAG TAT ATA	KpnI, NotI
ah418	GGA CTA GTA TTC ACC CCA TCC TCT GG	SpeI
ah419	GCT CTA GAT CTC ACA CTG CCT GCA TCA	XbaI
ah420	GCT CTA GAA GCT TTA TGA TAG TGG GCA	XbaI
ah421	CGG GGT ACC GCG GCC GCG ATC GTC ACA AAG ATC TA	KpnI, NotI
ah426	GGA CTA GTG GAA ACG CCT TGG TGG TG	SpeI
ah427	GCT CTA GAG CAA TTC AAA GGG CCC GA	XbaI
ah428	GCT CTA GAT GAT CCT GTT TTT GAA GA	XbaI
ah429	CGG GGT ACC GCG GCC GCA CAA GAC CTG CAG AAC ACG	KpnI, NotI
ah430	GGA CTA GTT TTA CTC CCT CTT CCG AG	SpeI
ah431	GCT CTA GAC CGC ATA GTA CCG GTA TCA TCT CGT ACA GCC A	XbaI
ah432	GCT CTA GAA TGG CCA CTA GAA TGC CAA TGA ACC TTG TTT G	XbaI
ah433	CGG GGT ACC GCG GCC GCA GCT GTT CAT CTA CAG CTT A	KpnI, NotI
ah434	GGA CTA GTA CCG GAG GCA GCA ACC TA	SpeI
ah435	CGG GGT ACC GCG GCC GCC CAG GAG CGC TGG GGA GG	KpnI
ah483	CGC GGA TCC TGC AGG GCC GCC AAG GAT CTG ATG GC	BamHI, SbfI
ah484	GGA CTA GTC CTG CAG GCG ATC TAG TAA CAT AGA TGA	SpeI, SbfI
ah441	CGC GGA TCC AAA AAT GTC GAC TCC CAA GAA G	BamHI
ah442	GGA CTA GTA GCG GCT AAC TCG ACC TCC A	SpeI
ah443	GAA GAT CTA AAA ATG TCG ACC CCC AAG TTG	BglII
ah444	GGA CTA GTA GCT GCA AGC TCA ACC TCC A	SpeI
ah445	CGC GGT ACC AAA AAT GTC GGC TCC GAA GAA G	BamHI
ah447	GAA GAT CTA AAA ATG TCG ACC ACC AAG TTG	BglII
ah448	GGA CTA GTA GCT GCA AGT TCA ACT TCC A	SpeI
ah455	CGC GGA TCC ACG GAG AAT GAG CTG AAG GG	BamHI
ah456	GAA GAT CTT TTC AGG ATA TTG ATG ACA G	BglII
ah457	CGC GGA TCC AAA AAT GTC GGC TCC CAA GAA G	BamHI
ah471	CGC GGA TCC AAA AAT GTC GAG TAC AAG ACA CAG	BamHI
ah472	GGA CTA GTT CTT ACG CTA GTA GCA TCA TCT CTG	SpeI
ah474	GGA CTA GTC AAA AAA TGT CCT CCA AAA CCA TG	SpeI
ah475	GGA CTA GTG TCA TCT TCT TGA ACA AG	SpeI
ah477	GGA CTA GTC AAA AAA TGG CGA CTC CAG GGG GG	SpeI
ah478	GGA CTA GTG AAT GTA TCT TGA AAG GA	SpeI
ah527	GCT CTA GAA AAA TGG GGC GAA CAA GAG GA	XbaI
ah528	GGA CTA GTG AGC ATT AAC ATG GAA AA	SpeI
ah791	AGC TGA TCT CAG AGG AGG ACC TGG CTA GCA TGG TGA GCA AGG GCG AG	-
ah792	GAA GAT CTA AAA ATG GCC GAG GAG CAG AAG CTG ATC TCA GAG GAG G	BglII
p023	AAG GTC TGC AAT TGA TAC GGG A	-

Supplemental Table 1 (continued)

Name	Sequence (5' → 3')	Restriction Sites
p026	CAA GTT CGT TTA CAA CAG GTC CT	-
p028	CAA TTA ATC CGG GAG ACT CCC A	-
p030	GTG AAA CGC CTC GGG AA	-
p046	GCG GTT CTG TCA GTT CCA A	-
p047	GGT TGT AGT GAG CAA AAC CTC CA	-
p050	GTG ATG CTC AAC GGA CTC GCT T	-
p051	GAG GTG AAG TTC GAG GGC GA	-
p062	CGC CGT TAT CAG TCA AGG TAT GA	-
p065	AGC GTG GTA TCA CAA TTG AC	-
p066	GAT CGC TCG ATC ATG TTA TC	-
p069	CCG AAG AGC GAC TTT ATT CAC T	-
p070	GGC GAA GTA TTC ATC GAA GTC T	-
p158	GTG CTT CGC ACC TCG AAT TG	-
p159	TTG TTC GCT ATC GGT CTC TTG	-
p118	ACA GGA ATT CAA CCC GAC AG	-
p119	GAG CAC CTT GAG AAT CCA GTG	-
p186	GGC AAT TAT CGA TCC CAC GTC	-
p187	ATC GCG AGC AGC AAT GAA TG	-
p188	GCG CGC ACA TCT ACT TCT G	-
p189	TTG ACA GCC TCA CAC ACC TG	-
p223	GAT AAA TTA TCG CGC GCG GTG	-
p225	GAT TCC ACC AGG TTC GGA C	-

CHAPTER 3 - SUPPLEMENTAL METHODS

Cloning of constructs

A list including all primers used for the generation of DNA constructs can be found in Supplemental Table 1.

The coding sequences of Pp-PIFs were amplified by PCR on *P. patens* cDNA using the primers ah839/ah708 for Pp-PIF68 and ah840/ah841 for Pp-PIF69 and Pp-PIF69ΔAPB; the PCR products were introduced into pJET1.2 (Thermo Fischer Scientific/Fermentas) via blunt end ligation.

The coding sequences of Pp-PHYs were amplified by PCR on *P. patens* cDNA using the primers p079/p080 for Pp-PHY1, p086/p087 for Pp-PHY2, p084/p085 for Pp-PHY3 and p081/p083 for Pp-PHY4; the PCR products for Pp-PHY1, Pp-PHY2 and Pp-PHY3 were introduced into pJET1.2 and the PCR product for Pp-PHY4 into TOPO (life technologies/Invitrogen) via blunt end ligation.

D153ah:At-PHYA is a yeast two hybrid vector coding for At-PHYA:GAL4 BD, which has been described previously (Hiltbrunner et al., 2006). To generate yeast two hybrid vectors coding for Pp-PHY:GAL4 BD we cut Pp-PHY1 and Pp-PHY3 from the corresponding pJET constructs using AvrII and ligated them into D153ah:At-FHY1 (Possart and Hiltbrunner, 2013) digested with XbaI/SpeI. Pp-PHY2 and Pp-PHY4 were cut from the corresponding pJET and TOPO constructs, respectively, using NheI and ligated into D153ah:At-FHY1 digested with XbaI/SpeI, thereby replacing At-FHY1.

Yeast two hybrid vectors coding for Pp-PIF:GAL4 AD were generated as follows. Pp-PIF68 was cut from pJET:PpPIF68 using BamHI/SpeI and ligated into pGADT7:At-FHY1 (Hiltbrunner et al., 2005) digested with BamHI/SpeI. Pp-PIF69 and Pp-PIF69ΔAPB, respectively, were cut from the corresponding pJET constructs with SpeI and ligated into pGADT7:At-FHY1 digested with XbaI/SpeI, thereby replacing At-FHY1. To obtain truncated versions of Pp-PIFs that do not code for the bHLH domain, we amplified fragments of each Pp-PIF using the primers ah849/ah994 for Pp-PIF68, ah852/ah995 for Pp-PIF69 and ah852/ah995 for Pp-PIF69ΔAPB, and the corresponding pGADT7:Pp-PIF constructs as templates. The PCR fragments were digested with XbaI/SpeI and ligated into the corresponding pGADT7:Pp-PIF constructs digested with XbaI/SpeI, thereby removing the bHLH domains.

For transformation of tobacco and *Arabidopsis*, respectively, we cloned Pp-PIF coding sequences into the Pro35S:YFP:TerRbcS cassette of the T-DNA vector pPPO30

(Rausenberger et al., 2011). Pp-PIF68 was cut from pJET:Pp-PIF68 using BamHI/SpeI and ligated into the BamHI/XbaI site of pPPO30. Pp-PIF69 and Pp-PIF69ΔAPB, respectively, were cut from the corresponding pJET constructs using SpeI and ligated into pPPO30 digested with AvrII/XbaI. A T-DNA vector containing a Pro35S:myc:CFP:At-PIF3:TerRbcS cassette was obtained as follows: pCHF83myc is a T-DNA vector containing a Pro35S:myc:mCerulean:TerRbcS cassette. First, a fragment coding for mCerulean and part of the myc tag was amplified from mCerulean cDNA (Rizzo et al., 2004) using the primers ah791/ah094. This fragment was then used as template for a second PCR with primers ah792/ah094 to add the remaining part of the myc tag. Finally, the PCR fragment was cut with BglII/SpeI and ligated into BamHI/XbaI site of pCHF5 (Hiltbrunner et al., 2005). At-PIF3 was PCR amplified from an At-PIF3 cDNA clone using the primers ah127/ah867.2 and blunt-end ligated into pJET. At-PIF3 was cut from pJET:At-PIF3 with BamHI/AvrII and ligated into the BamHI/XbaI site of pCHF83myc. D153ah:At-PHYA:NLS is a Y2H BD vector containing At-PHYA-NLS-BD. A PHYA fragment containing the NLS was PCR-amplified from ProPHYA:PHYA:NLS:GFP5 (Genoud et al., 2008) using the primers ah010/ah385, cut with XbaI/SpeI and ligated into D153ah:At-PHYA (Hiltbrunner et al., 2006) digested with XbaI/SpeI. To obtain a T-DNA vector containing a Pro35S:At-PHYA:NLS:CFP:TerRbcS cassette, At-PHYA:NLS was cut from D153ah:phyA:NLS using BamHI/SpeI and ligated into the BamHI/XbaI site of pCHF40 (Hiltbrunner et al., 2005). pphyA40:At-PHYA is a T-DNA vector coding for At-PHYA:CFP under the control of the PHYA promoter (Genoud et al., 2008).

pUC1930 contains a Pro35S:BamHI:XbaI:YFP:TerRbcS cassette and has been described previously (Possart and Hiltbrunner, 2013). To generate constructs coding for Pro35S:Pp-PIF:YFP:TerRbcS that were used for particle bombardment we cut Pp-PIF68 with BamHI/SpeI, Pp-PIF69 and Pp-PIF69ΔAPB, respectively, with SpeI from the pJET:Pp-PIF constructs. The obtained fragments were ligated into pUC1930 digested with BamHI/XbaI and XbaI, respectively.

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Supplemental Table 1. Primer List (cloning) (restriction sites are underlined).

Name	Sequence (5' → 3')	Restriction Sites
ah010	TTA CAC CAT CCG GAG GTC AG	-
ah094	GGA CTA GTT ATC TAG AGC CCT AGG ATC CGC CTT GTA CAG CTC GTC CAT G	SpeI
ah127	CGC GGA TCC AAA AAT GCC TCT GTT TGA GCT TTT CA	BamHI
ah385	GGA CTA GTT GCG GCC GCT CCT CCA ACC T	SpeI
ah708	GGA CTA GTT TGA AGT GGA CCT CCA CCC A	SpeI
ah791	AGC TGA TCT CAG AGG AGG ACC TGG CTA GCA TGG TGA GCA AGG GCG AG	-
ah792	GAA GAT CTA AAA ATG GCC GAG GAG CAG AAG CTG ATC TCA GAG GAG G	BglII
ah839	CGC GGA TCC AAA AAT GAG TCT CTA TGT GCC A	BamHI
ah840	GGA CTA GTG AAA AAA TGA GTC TCT GTG TGC CAG	SpeI
ah841	GGA CTA GTA TGA GGT GGG ACC CCA CTC	SpeI
ah849	GTG GTT CAA GTT TAT TAG CG	-
ah852	GGA CTA GTT GGA AGT AAC AGA GGG ACC AC	SpeI
ah867.2	CGC GGA TCC TAG GCG ACG ATC CAC AAA ACT GAT CA	BamHI, AvrII
ah994	GGA CTA GTT GTA ATA GGT TTA TGT TTT GTG TCT ACC	SpeI
ah995	GGA CTA GTT GTT GCA GGT TTT TGT TTG GTG	SpeI
p079	GGT TTC CTA GGG CTA GCA AAA ATG TCG ACT CCC AAG AAG A	AvrII, NheI
p080	GGT TTC CTA GGG CTA GCC ATT TGA CTT GAA GCA TCA TCC C	AvrII, NheI
p081	GGT TTC CTA GGG CTA GCA AAA ATG TCG ACC ACC AAG TTG G	AvrII, NheI
p083	GGT TTC CTA GGG CTA GCT CTC ACA CTG CCT GCA TCA	AvrII, NheI
p084	GGT TTC CTA GGG CTA GCA AAA ATG TCG GCT CCG AAG AAG A	AvrII, NheI
p085	GGT TTC CTA GGG CTA GCC ATT TGA CTT GCA GCA TCA TCC T	AvrII, NheI
p086	GGT TTC CTA GGG CTA GCA AAA ATG TCG ACC CCC AAG TTG	AvrII, NheI
p087	GGT TTC CTA GGG CTA GCG ACA ACA GTA GAT CTC ACA CTA CCT	SpeI

Supplemental Table 2. Primer List (qRT-PCR).

Name/ Phypa_ID	Sequence (5' → 3')	Gene description
Phypa_461491	TGC CCT CTT TTC AAT TCC AC	Thioredoxin
Phypa_461491	ACA AAG TGC CGG TTT ACG TC	Thioredoxin
Phypa_219412	TGA GTG GGT ACA GTG CGA AG	Phototropin
Phypa_219412	TCA GCA AAC GAC CAC AGA AG	Phototropin
Phypa_169593	CCT TGA GGG ACG ACT ACG AG	Lhc SR1
Phypa_169593	GAT CTC TTC ACC CGA GAC CA	Lhc SR1
Phypa_166875	CAC AGA GCG AAA GGT CAC AA	sigma factor
Phypa_166875	CTT CGT CAG CTT CCC TTC AC	sigma factor
Phypa_135141	CCT GTC ATT GCT GAG GTG AA	no apical meristem
Phypa_135141	TGT GGA TGG GTT TGT CTG TG	no apical meristem
Phypa_74635	GAG GAG GTT TTT GCT GAT GC	malat-dehydrogenase
Phypa_74635	CGA TCA GAG CAT TCG TGT TG	malat-dehydrogenase
Phypa_4364	ACG AGT GAA CTG GTC CAA GG	pectinesterase family
Phypa_4364	CGG TAG TGG CTC AGT GCA TA	pectinesterase family

<u>Supplemental Dataset 1.</u> DEGs from Microarray Analysis in *P. patens* after R light treatments

A	Phypa ID (*P. patens* genome v.1.2)
B	Functional description of BLAST best hit (*P. patens* genome v.1.2; COSMOSS database)
C	V1.6 CGI (*P. patens* genome v.1.6)
D	At homolog (Phytozome; TAIR10 best hit)
E	Gene Ontology accession
F	Gene Ontology name
G	Red light 4h (Shifted using Median) vs dark combined - outlier
H	Red light 30 min (Shifted using Median) vs dark combined - outlier

Phypa_ID	Funct. descr. BLAST BH	V1.6 CGI	At homolog	GO accession	GO name	Red light 4h (Shifted using Median) vs dark combined - outlier	Red light 30 min (Shifted using Median) vs dark combined - outlier
Phypa_194318	MMB12.18; pathogenesis-related protein, putative [Arabidopsis thaliana] : "MMB12.18; pathogenesis-related protein, putative [Arabidopsis thaliana]"	Pp1s215_2V6.1	AT3G19690.1	GO:0005576	extracellular region	0,096789151	0,118830025
Phypa_140125	Bcat1; branched chain aminotransferase 1, cytosolic [EC:2.6.1.42] [KO:K00826] [Mus musculus] : "Bcat1; branched chain aminotransferase 1, cytosolic [EC:2.6.1.42] [KO:K00826] [Mus musculus]"	Pp1s163_127V6.1	AT5G65780.1	GO:0003824 : GO:0004084 : GO:0005524 : GO:0008152 : GO:0009081 : GO:0015986 : GO:0016469 : GO:0046933 : GO:0046961	ATP binding : ATP synthesis coupled proton transport : branched chain family amino acid metabolism : branched-chain-amino-acid transaminase activity : catalytic activity : hydrogen-transporting ATP synthase activity, rotational mechanism : hydrogen-transporting ATPase activity, rotational mechanism : metabolism : proton-transporting two-sector ATPase complex	0,114057675	0,131770775

Phypa_201470	F1N19.23; Cys/Met metabolism pyridoxal-phosphate-dependent enzyme family protein [Arabidopsis thaliana] : "F1N19.23; Cys/Met metabolism pyridoxal-phosphate-dependent enzyme family protein [Arabidopsis thaliana]"	Pp1s2_113V6.1;Pp1s2_113V6.2 : "Pp1s2_113V6.1;Pp1s2_113V6.2" : "Pp1s2_113V6.1;Pp1s2_113V6.2 : ""Pp1s2_113V6.1;Pp1s2_113V6.2"""	AT1G64660.1	GO:0003962 : GO:0006520	amino acid metabolism : cystathionine gamma-synthase activity	0,132681727	0,383303523
Phypa_127238		Pp1s64_60V6.1	AT5G60250.1	GO:0008766 : GO:0016881 : GO:0018169	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate-D-alanyl-D-alanine ligase activity : acid-amino acid ligase activity : ribosomal S6-glutamic acid ligase activity	0,136593819	0,663212538
Phypa_147280	F5N5.2; expressed protein [Arabidopsis thaliana] : "F5N5.2; expressed protein [Arabidopsis thaliana]"	Pp1s257_73V6.1;Pp1s257_73V6.2;Pp1s257_73V6.3;Pp1s257_73V6.4;Pp1s257_73V6.5 : "Pp1s257_73V6.1;Pp1s257_73V6.2;Pp1s257_73V6.3;Pp1s257_73V6.4;Pp1s257_73V6.5" : "Pp1s257_73V6.1;Pp1s257_73V6.2;Pp1s257_73V6.3;Pp1s257_73V6.4;Pp1s257_73V6.5 : ""Pp1s257_73V6.1;Pp1s257_73V6.2;Pp1s257_73V6.3;Pp1s257_73V6.4;Pp1s257_73V6.5"""	AT3G22850.1			0,136921167	0,611669719

Phypa_86312	MJP23.6; homogentisate 1,2-dioxygenase [EC:1.13.11.5] [KO:K00451] [Arabidopsis thaliana] : "MJP23.6; homogentisate 1,2-dioxygenase [EC:1.13.11.5] [KO:K00451] [Arabidopsis thaliana]"	Pp1s144_86V6.1	AT5G54080.1	GO:0004411 : GO:0006559 : GO:0006570	L-phenylalanine catabolism : homogentisate 1,2-dioxygenase activity : tyrosine metabolism	0,151854366	0,256557852
Phypa_144156	Ribose-phosphate pyrophosphokinase 1 (Phosphoribosyl pyrophosphate synthetase 1) [Spinacia oleracea]	Pp1s212_43V6.2;Pp1s212_43V6.1 : "Pp1s212_43V6.2;Pp1s212_43V6.1" : "Pp1s212_43V6.2;Pp1s212_43V6.1 : ""Pp1s212_43V6.2;Pp1s212_43V6.1"""	AT2G44530.1	GO:0004749 : GO:0009116 : GO:0009165 : GO:0016740	nucleoside metabolism : nucleotide biosynthesis : ribose-phosphate diphosphokinase activity : transferase activity	0,152254298	0,246926278

Phypa_221150	F24J8.4; 2-oxoisovalerate dehydrogenase, putative / 3-methyl-2-oxobutanoate dehydrogenase, putative / branched-chain alpha-keto acid dehydrogenase E1 alpha subunit, putative [EC:1.2.4.4] [KO:K00166] [Arabidopsis thaliana] : "F24J8.4; 2-oxoisovalerate dehydrogenase, putative / 3-methyl-2-oxobutanoate dehydrogenase, putative / branched-chain alpha-keto acid dehydrogenase E1 alpha subunit, putative [EC:1.2.4.4] [KO:K00166] [Arabidopsis thaliana]"	Pp1s207_68V6.1	AT1G21400.1	GO:0003863 : GO:0008152 : GO:0016624 : GO:0017086	3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring) activity : 3-methyl-2-oxobutanoate dehydrogenase (lipoamide) complex : metabolism : oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor	0,156903371	0,292422086
Phypa_72790		Pp1s38_338V6.1	AT4G27670.1			0,169191703	0,681571424
Phypa_140836	T4C15.1; expressed protein [Arabidopsis thaliana] : "T4C15.1; expressed protein [Arabidopsis thaliana]"	Pp1s171_5V6.1;Pp1s171_5V6.2;Pp1s171_5V6.3 : "Pp1s171_5V6.1;Pp1s171_5V6.2;Pp1s171_5V6.3" : "Pp1s171_5V6.1;Pp1s171_5V6.2;Pp1s171_5V6.3 : ""Pp1s171_5V6.1;Pp1s171_5V6.2;Pp1s171_5V6.3"""	AT2G35320.1	GO:0007275	development	0,178035915	0,421088994

Phypa_170328	F18O14.29; expressed protein [Arabidopsis thaliana] : "F18O14.29; expressed protein [Arabidopsis thaliana]"	Pp1s241_42V6.1	AT1G19530.1			0,178636104	0,148956716
Phypa_138954	MRP15.9; 2-oxoisovalerate dehydrogenase / 3-methyl-2-oxobutanoate dehydrogenase / branched-chain alpha-keto acid dehydrogenase E1 beta subunit (DIN4) [EC:1.2.4.4] [KO:K00167] [Arabidopsis thaliana] : "MRP15.9; 2-oxoisovalerate dehydrogenase / 3-methyl-2-oxobutanoate dehydrogenase / branched-chain alpha-keto acid dehydrogenase E1 beta subunit (DIN4) [EC:1.2.4.4] [KO:K00167] [Arabidopsis thaliana]"	Pp1s152_53V6.1	AT3G13450.1	GO:0003863 : GO:0017086	3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring) activity : 3-methyl-2-oxobutanoate dehydrogenase (lipoamide) complex	0,180547997	0,175413847
Phypa_170614	F3F9.15; VQ motif-containing protein [Arabidopsis thaliana] : "F3F9.15; VQ motif-containing protein [Arabidopsis thaliana]"	Pp1s252_83V6.1				0,183856502	0,248237416

Phypa_9490	F16B22.16; senescence-associated protein-related [Arabidopsis thaliana] : "F16B22.16; senescence-associated protein-related [Arabidopsis thaliana]"	Pp1s194_166V6.1	AT1G78020.1				0,184449226	0,213457555
Phypa_215944	Tat; tyrosine aminotransferase [EC:2.6.1.5] [KO:K00815] [Mus musculus] : "Tat; tyrosine aminotransferase [EC:2.6.1.5] [KO:K00815] [Mus musculus]"	Pp1s121_161V6.1	AT5G36160.1	GO:0003824 : GO:0004838 : GO:0006519 : GO:0008483 : GO:0009058 : GO:0016769 : GO:0016847	1-aminocyclopropane-1-carboxylate synthase activity : amino acid and derivative metabolism : biosynthesis : catalytic activity : transaminase activity : transferase activity, transferring nitrogenous groups : tyrosine transaminase activity		0,19196026	0,281802148
Phypa_232568		Pp1s106_48V6.1;Pp1s106_48V6.2 : "Pp1s106_48V6.1;Pp1s106_48V6.2" : "Pp1s106_48V6.1;Pp1s106_48V6.2 : ""Pp1s106_48V6.1;Pp1s106_48V6.2"""	AT3G10740.1				0,200583532	0,399326682
Phypa_159781	hypothetical protein [Dictyostelium discoideum]	Pp1s15_300V6.1	AT1G28070.1				0,201041818	0,118116081
Phypa_166310	contains EST C28646(C61919) similar to Arabidopsis thaliana chromosome1,At1g27340 unknown protein [Oryza sativa (japonica cultivar-group)]	Pp1s111_44V6.2;Pp1s111_44V6.1;Pp1s111_44V6.3 : "Pp1s111_44V6.2;Pp1s111_44V6.1;Pp1s111_44V6.3" : "Pp1s111_44V6.2;Pp1s111_44V6.1;Pp1s111_44V6.3 : ""Pp1s111_44V6.2;Pp1s111_44V6.1;Pp1s111_44V6.3"""	AT1G27340.1				0,204498544	0,189308524

Phypa_203561		Pp1s15_268V6.1	AT5G43430.1	GO:0005489 : GO:0006118	electron transport : electron transporter activity	0,213229284	0,201970205
Phypa_116273	T28A8.80; transporter-related [Arabidopsis thaliana] : "T28A8.80; transporter-related [Arabidopsis thaliana]"	Pp1s15_89V6.2;Pp1s15_89V6.1;Pp1s15_89V6.3 : "Pp1s15_89V6.2;Pp1s15_89V6.1;Pp1s15_89V6.3" : "Pp1s15_89V6.2;Pp1s15_89V6.1;Pp1s15_89V6.3 : ""Pp1s15_89V6.2;Pp1s15_89V6.1;Pp1s15_89V6.3"""	AT3G43790.1	GO:0005215 : GO:0006810 : GO:0015520 : GO:0015904 : GO:0016021	integral to membrane : tetracycline transport : tetracycline:hydrogen antiporter activity : transport : transporter activity	0,215700373	0,384992421
Phypa_88255		Pp1s167_89V6.1				0,219760314	0,410347909
Phypa_89931	F4P9.39; DNA-binding family protein / AT-hook protein 1 (AHP1) [Arabidopsis thaliana] : "F4P9.39; DNA-binding family protein / AT-hook protein 1 (AHP1) [Arabidopsis thaliana]"	Pp1s190_33V6.1	AT2G33620.2			0,225308016	0,421804011
Phypa_231396		Pp1s130_124V6.1				0,227704018	0,332573652
Phypa_171030	T6G21.26; expressed protein [Arabidopsis thaliana] : "T6G21.26; expressed protein [Arabidopsis thaliana]"	Pp1s271_68V6.1	AT5G21940.1			0,240576088	0,238900676
Phypa_6580		Pp1s77_184V6.1	AT1G69780.1	GO:0003677 : GO:0003700 : GO:0005634 : GO:0006355	DNA binding : nucleus : regulation of transcription, DNA-dependent : transcription factor activity	0,246063799	0,166493505

Phypa_142560	T19F6.30; glycosyl hydrolase family protein 37 / trehalase, putative [EC:3.2.1.28] [KO:K01194] [Arabidopsis thaliana] : "T19F6.30; glycosyl hydrolase family protein 37 / trehalase, putative [EC:3.2.1.28] [KO:K01194] [Arabidopsis thaliana]"	Pp1s194_104V6.3;Pp1s194_104V6.2;Pp1s194_104V6.1 : "Pp1s194_104V6.3;Pp1s194_104V6.2;Pp1s194_104V6.1" : "Pp1s194_104V6.3;Pp1s194_104V6.2;Pp1s194_104V6.1 : ""Pp1s194_104V6.3;Pp1s194_104V6.2;Pp1s194_104V6.1"""	AT4G24040.1	GO:0004555 : GO:0005991	alpha,alpha-trehalase activity : trehalose metabolism	0,248179898	0,18968749
Phypa_67109	T6B20.10; lipase class 3 family protein [Arabidopsis thaliana] : "T6B20.10; lipase class 3 family protein [Arabidopsis thaliana]"	Pp1s13_266V6.1	AT1G51440.1	GO:0003824 : GO:0004806 : GO:0006629	catalytic activity : lipid metabolism : triacylglycerol lipase activity	0,259246826	0,162308514
Phypa_136723	IMP-specific 5'-nucleotidase 1 [no tax name]	Pp1s131_67V6.1				0,261101544	0,155414581
Phypa_19427	F9H16.14; RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] : "F9H16.14; RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana]"	Pp1s126_15V6.2;Pp1s126_15V6.1 : "Pp1s126_15V6.2;Pp1s126_15V6.1" : "Pp1s126_15V6.2;Pp1s126_15V6.1 : ""Pp1s126_15V6.2;Pp1s126_15V6.1"""	AT1G76460.1	GO:0003676	nucleic acid binding	0,272717386	0,187899098
Phypa_19797	Glycine-rich RNA-binding protein 2 [Sorghum bicolor]	Pp1s136_70V6.1	AT4G39260.3	GO:0003676	nucleic acid binding	0,273535252	0,146159947

Phypa_68875	hypothetical protein [Dictyostelium discoideum]	Pp1s20_367V6.2;Pp1s20_367V6.1 : "Pp1s20_367V6.2;Pp1s20_367V6.1" : "Pp1s20_367V6.2;Pp1s20_367V6.1 : ""Pp1s20_367V6.2;Pp1s20_367V6.1"""	Pp1s20_367V6	GO:0001584 : GO:0007186 : GO:0016021	G-protein coupled receptor protein signaling pathway : integral to membrane : rhodopsin-like receptor activity	0,295511216	0,429158002
Phypa_65350		Pp1s6_72V6.1				0,309841394	0,265095204
[Phypa_182736;Phypa_182738]						0,311539173	0,101547599
Phypa_169977	T14P4.6; lipase class 3 family protein [Arabidopsis thaliana] : "T14P4.6; lipase class 3 family protein [Arabidopsis thaliana]"	Pp1s226_43V6.1	AT3G61680.1	GO:0003824 : GO:0004806 : GO:0006629	catalytic activity : lipid metabolism : triacylglycerol lipase activity	0,314513654	0,209570616
Phypa_102704		Pp1s698_1V6.1	AT1G63440.1	GO:0004008 : GO:0005524 : GO:0006825 : GO:0016020 : GO:0030001 : GO:0046872	ATP binding : copper ion transport : copper-exporting ATPase activity : membrane : metal ion binding : metal ion transport	0,316046476	0,191597581
Phypa_152834	MQM1.6; serine C-palmitoyltransferase, putative [EC:2.3.1.50] [KO:K00654] [Arabidopsis thaliana] : "MQM1.6; serine C-palmitoyltransferase, putative [EC:2.3.1.50] [KO:K00654] [Arabidopsis thaliana]"	Pp1s377_35V6.1	AT5G23670.1	GO:0004758 : GO:0008152 : GO:0009058 : GO:0016740 : GO:0016769 : GO:0017059	biosynthesis : metabolism : serine C-palmitoyltransferase activity : serine C-palmitoyltransferase complex : transferase activity : transferase activity, transferring nitrogenous groups	0,323173106	0,207481936

Phypa_194709	T28K15.1; no apical meristem (NAM) family protein [Arabidopsis thaliana] : "T28K15.1; no apical meristem (NAM) family protein [Arabidopsis thaliana]"	Pp1s223_12V6.1;Pp1s223_12V6.2 : "Pp1s223_12V6.1;Pp1s223_12V6.2" : "Pp1s223_12V6.1;Pp1s223_12V6.2 : ""Pp1s223_12V6.1;Pp1s223_12V6.2"""	AT1G12260.1			0,324899018	0,297114611
Phypa_64122		Pp1s1_863V6.1				0,327404141	0,237342849
Phypa_152231	T17M13.16; ribonuclease 1 (RNS1) [EC:3.1.27.1] [Arabidopsis thaliana] : "T17M13.16; ribonuclease 1 (RNS1) [EC:3.1.27.1] [Arabidopsis thaliana]"	Pp1s358_60V6.1;Pp1s358_60V6.2 : "Pp1s358_60V6.1;Pp1s358_60V6.2" : "Pp1s358_60V6.1;Pp1s358_60V6.2 : ""Pp1s358_60V6.1;Pp1s358_60V6.2"""	AT2G02990.1	GO:0003723 : GO:0004521	RNA binding : endoribonuclease activity	0,345334768	0,122478336
Phypa_22569	MXC17.9; expressed protein [Arabidopsis thaliana] : "MXC17.9; expressed protein [Arabidopsis thaliana]"	Pp1s4_62V6.1;Pp1s4_62V6.2 : "Pp1s4_62V6.1;Pp1s4_62V6.2" : "Pp1s4_62V6.1;Pp1s4_62V6.2 : ""Pp1s4_62V6.1;Pp1s4_62V6.2"""	AT5G24690.1			0,352403224	0,228243411
Phypa_144846	F5N5.17; expressed protein [Arabidopsis thaliana] : "F5N5.17; expressed protein [Arabidopsis thaliana]"	Pp1s220_112V6.1	AT3G22970.1			0,354538053	0,329436511
Phypa_172857	F13H10.2; dehydration-induced protein (ERD15) [Arabidopsis thaliana] : "F13H10.2; dehydration-induced protein (ERD15) [Arabidopsis thaliana]"	Pp1s387_21V6.1	AT2G41430.5	GO:0004497 : GO:0005507	copper ion binding : monooxygenase activity	0,358750075	0,205835104

Phypa_92771	F17I23.270; expressed protein [Arabidopsis thaliana] : "F17I23.270; expressed protein [Arabidopsis thaliana]"	Pp1s230_66V6.2;Pp1s230_66V6.1 : "Pp1s230_66V6.2;Pp1s230_66V6.1" : "Pp1s230_66V6.2;Pp1s230_66V6.1 : ""Pp1s230_66V6.2;Pp1s230_66V6.1"""	AT4G30390.1			0,370066732	0,16195567
Phypa_120509	F6I18.170; cytosol aminopeptidase family protein [EC:3.4.11.1 3.4.11.5] [KO:K01259] [Arabidopsis thaliana] : "F6I18.170; cytosol aminopeptidase family protein [EC:3.4.11.1 3.4.11.5] [KO:K01259] [Arabidopsis thaliana]"	Pp1s33_172V6.1	AT2G24200.1	GO:0004177 : GO:0004178 : GO:0005622 : GO:0005737 : GO:0006508 : GO:0019538 : GO:0030145	aminopeptidase activity : cytoplasm : intracellular : leucyl aminopeptidase activity : manganese ion binding : protein metabolism : proteolysis and peptidolysis	0,370426893	0,142946362
Phypa_135141	F27G19.10; no apical meristem (NAM) family protein (RD26) [Arabidopsis thaliana] : "F27G19.10; no apical meristem (NAM) family protein (RD26) [Arabidopsis thaliana]"	Pp1s117_16V6.1	AT4G27410.2			0,374271512	0,267820805
Phypa_217194	T6H22.13; elongation factor 2, putative / EF-2, putative [EC:3.6.5.3] [KO:K03234] [Arabidopsis thaliana] : "T6H22.13; elongation factor 2, putative / EF-2, putative [EC:3.6.5.3] [KO:K03234] [Arabidopsis thaliana]"	Pp1s138_85V6.1	AT1G56070.1	GO:0003924 : GO:0005525 : GO:0006412 : GO:0008547	GTP binding : GTPase activity : protein biosynthesis : protein-synthesizing GTPase activity	0,375573367	0,057615653

Phypa_122793	F26K9.200; transport protein-related [Arabidopsis thaliana] : "F26K9.200; transport protein-related [Arabidopsis thaliana]"	Pp1s41_98V6.1	AT3G62770.1			0,376133978	0,230104417
Phypa_23467		Pp1s31_291V6.1	AT4G16110.1	GO:0000156 : GO:0000160 : GO:0003677 : GO:0005634 : GO:0006355	DNA binding : nucleus : regulation of transcription, DNA-dependent : two-component response regulator activity : two-component signal transduction system (phosphorelay)	0,380984604	0,214307725
Phypa_148104	F15D2.30; RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] : "F15D2.30; RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana]"	Pp1s271_57V6.2;Pp1s271_57V6.1 : "Pp1s271_57V6.2;Pp1s271_57V6.1" : "Pp1s271_57V6.2;Pp1s271_57V6.1 : ""Pp1s271_57V6.2;Pp1s271_57V6.1"""	AT1G29400.1	GO:0003676	nucleic acid binding	0,387953848	0,097114339
Phypa_56066	MIO24.3; fructokinase, putative [EC:2.7.1.4] [KO:K00847] [Arabidopsis thaliana] : "MIO24.3; fructokinase, putative [EC:2.7.1.4] [KO:K00847] [Arabidopsis thaliana]"	Pp1s27_234V6.2;Pp1s27_234V6.1 : "Pp1s27_234V6.2;Pp1s27_234V6.1" : "Pp1s27_234V6.2;Pp1s27_234V6.1 : ""Pp1s27_234V6.2;Pp1s27_234V6.1"""	AT5G51830.1	GO:0004747 : GO:0006014 : GO:0008865	D-ribose metabolism : fructokinase activity : ribokinase activity	0,390992135	0,156448096

Phypa_169905	grl-25; Hypothetical protein ZK643.8 [Caenorhabditis elegans] : "grl-25; Hypothetical protein ZK643.8 [Caenorhabditis elegans]"	Pp1s224_13V6.1				0,39762345	0,179525718
Phypa_132416	putative pumilio/Mpt5 family RNA-binding protein [Oryza sativa (japonica cultivar-group)]	Pp1s96_110V6.1	AT2G29200.1	GO:0003723 : GO:0016071	RNA binding : mRNA metabolism	0,398833454	0,202344209
Phypa_61245	Auxin response factor 16 [Arabidopsis thaliana]	Pp1s339_42V6.1	AT2G28350.1			0,402942151	0,14515397
Phypa_135187	T32M21.100; glycosyltransferase family 47 [Arabidopsis thaliana] : "T32M21.100; glycosyltransferase family 47 [Arabidopsis thaliana]"	Pp1s117_57V6.1	AT5G04500.1			0,40556258	0,174940556
Phypa_116683	F20C19.19; GDSL-motif lipase/hydrolase family protein [Arabidopsis thaliana] : "F20C19.19; GDSL-motif lipase/hydrolase family protein [Arabidopsis thaliana]"	Pp1s17_356V6.1	AT1G54790.2	GO:0003824	catalytic activity	0,405568361	0,05078559
Phypa_159854						0,411191702	0,199471027
[Phypa_152430;Phypa_98737]						0,414247602	0,048952408
Phypa_64463	proteophosphoglycan ppg1 [Leishmania major]	Pp1s2_651V6.1		GO:0031177	phosphopantetheine binding	0,415999442	0,354295015

Phypa_27706	contains ESTs D22340(C10768),D15812(C1318),C98241(C1318) [Oryza sativa (japonica cultivar-group)]	Pp1s1_349V6.1	AT1G49950.2	GO:0003677 : GO:0005634	DNA binding : nucleus	0,416662484	0,242362857
Phypa_169504	Immune inhibitor A precursor [Bacillus thuringiensis serovar alesti]	Pp1s211_85V6.2;Pp1s211_85V6.1;Pp1s211_85V6.3;Pp1s211_85V6.4 : "Pp1s211_85V6.2;Pp1s211_85V6.1;Pp1s211_85V6.3;Pp1s211_85V6.4" : "Pp1s211_85V6.2;Pp1s211_85V6.1;Pp1s211_85V6.3;Pp1s211_85V6.4 : ""Pp1s211_85V6.2;Pp1s211_85V6.1;Pp1s211_85V6.3;Pp1s211_85V6.4"""	Pp1s211_85V6			0,417472303	0,091382161
Phypa_76520	Elongation factor 1-alpha (EF-1-alpha) [Glycine max]	Pp1s59_188V6.1;Pp1s59_188V6.2;Pp1s59_188V6.3 : "Pp1s59_188V6.1;Pp1s59_188V6.2;Pp1s59_188V6.3" : "Pp1s59_188V6.1;Pp1s59_188V6.2;Pp1s59_188V6.3 : ""Pp1s59_188V6.1;Pp1s59_188V6.2;Pp1s59_188V6.3"""	AT1G07920.1	GO:0003746 : GO:0003924 : GO:0005525 : GO:0005737 : GO:0006412 : GO:0006414 : GO:0008547	GTP binding : GTPase activity : cytoplasm : protein biosynthesis : protein-synthesizing GTPase activity : translation elongation factor activity : translational elongation	0,417644739	0,106779329

Phypa_141291	F8B4.220; glycine hydroxymethyltransferase, putative / serine hydroxymethyltransferase, putative / serine/threonine aldolase, putative [EC:2.1.2.1] [KO:K00600] [Arabidopsis thaliana] : "F8B4.220; glycine hydroxymethyltransferase, putative / serine hydroxymethyltransferase, putative / serine/threonine aldolase, putative [EC:2.1.2.1] [KO:K00600] [Arabidopsis thaliana]"	Pp1s176_89V6.3	Pp1s176_89V6	GO:0004372 : GO:0006544 : GO:0006563	L-serine metabolism : glycine hydroxymethyltransferase activity : glycine metabolism	0,422598034	0,190376878
Phypa_74339		Pp1s47_2V6.1				0,425832093	0,10563641
Phypa_80245	F6E13.10; La domain-containing protein [Arabidopsis thaliana] : "F6E13.10; La domain-containing protein [Arabidopsis thaliana]"	Pp1s84_286V6.1	AT5G46250.1	GO:0003723 : GO:0005634 : GO:0005737 : GO:0006396 : GO:0006405 : GO:0030529	RNA binding : RNA processing : RNA-nucleus export : cytoplasm : nucleus : ribonucleoprotein complex	0,426421344	0,110749088
Phypa_172497	T6C23.11; TCP family transcription factor, putative [Arabidopsis thaliana] : "T6C23.11; TCP family transcription factor, putative [Arabidopsis thaliana]"	Pp1s356_40V6.1	AT3G47620.1	GO:0004402	histone acetyltransferase activity	0,428136051	0,214480698
[Phypa_105021;Phypa_177288]						0,440628409	0,085498117
Phypa_168549		Pp1s180_137V6.1	AT1G06330.1	GO:0030001 : GO:0046872	metal ion binding : metal ion transport	0,442340314	0,101943001

Phypa_36231	FCAALL.129; DNA-binding protein-related [Arabidopsis thaliana] : "FCAALL.129; DNA-binding protein-related [Arabidopsis thaliana]"	Pp1s485_11V6.1	AT2G35270.1			0,444371521	0,215661496
Phypa_226674	contains ESTs AU093161(C63864),AU078381(S21490) [Oryza sativa (japonica cultivar-group)]	Pp1s373_11V6.1	AT5G12330.4			0,45257929	0,220228598
Phypa_38810						0,453237116	0,057985749
Phypa_5536	F15J1.20; ankyrin repeat family protein / AFT protein (AFT) [Arabidopsis thaliana] : "F15J1.20; ankyrin repeat family protein / AFT protein (AFT) [Arabidopsis thaliana]"	Pp1s411_31V6.1	AT4G35450.2			0,455024034	0,106464922
Phypa_213630	Ubiquitin-conjugating enzyme E2-17 kDa (Ubiquitin-protein ligase) (Ubiquitin carrier protein) [Medicago sativa]	Pp1s91_88V6.1	AT2G02760.1	GO:0004840 : GO:0004842 : GO:0006464 : GO:0006512	protein modification : ubiquitin conjugating enzyme activity : ubiquitin cycle : ubiquitin-protein ligase activity	0,457350701	0,25421679
Phypa_38771	hypothetical protein [Oryza sativa (japonica cultivar-group)]	Pp1s91_206V6.1;Pp1s91_206V6.2 : "Pp1s91_206V6.1;Pp1s91_206V6.2" : "Pp1s91_206V6.1;Pp1s91_206V6.2 : ""Pp1s91_206V6.1;Pp1s91_206V6.2"""	AT4G13830.2	GO:0006457 : GO:0031072 : GO:0051082	heat shock protein binding : protein folding : unfolded protein binding	0,458711386	0,143441662

Phypa_72129	T29H11.150; protein-L-isoaspartate O-methyltransferase / PIMT (PCM) [Arabidopsis thaliana] : "T29H11.150; protein-L-isoaspartate O-methyltransferase / PIMT (PCM) [Arabidopsis thaliana]"	Pp1s35_262V6.1;Pp1s35_262V6.2;Pp1s35_262V6.3;Pp1s35_262V6.4 : "Pp1s35_262V6.1;Pp1s35_262V6.2;Pp1s35_262V6.3;Pp1s35_262V6.4" : "Pp1s35_262V6.1;Pp1s35_262V6.2;Pp1s35_262V6.3;Pp1s35_262V6.4 : ""Pp1s35_262V6.1;Pp1s35_262V6.2;Pp1s35_262V6.3;Pp1s35_262V6.4"""	AT5G50240.1	GO:0004719 : GO:0006464 : GO:0008757	S-adenosylmethionine-dependent methyltransferase activity : protein modification : protein-L-isoaspartate (D-aspartate) O-methyltransferase activity	0,45931986	0,179387778
Phypa_234454		Pp1s136_127V6.1	AT3G48050.2			0,464630038	0,206902787
Phypa_172732		Pp1s376_9V6.1				0,467223644	0,194206357
Phypa_130931	T9L6.10; trihelix DNA-binding protein, putative [Arabidopsis thaliana] : "T9L6.10; trihelix DNA-binding protein, putative [Arabidopsis thaliana]"	Pp1s85_58V6.1	AT1G76890.2	GO:0003677 : GO:0005634	DNA binding : nucleus	0,470208734	0,380021155
Phypa_211705	K7P8.3; expressed protein [Arabidopsis thaliana] : "K7P8.3; expressed protein [Arabidopsis thaliana]"	Pp1s72_271V6.2;Pp1s72_271V6.1 : "Pp1s72_271V6.2;Pp1s72_271V6.1" : "Pp1s72_271V6.2;Pp1s72_271V6.1 : ""Pp1s72_271V6.2;Pp1s72_271V6.1"""	AT1G68140.3			0,472169727	0,30242905
[Phypa_228450;Phypa_227610;Phypa_109208]						0,472248554	0,046503007
[Phypa_73588;Phypa_123042]						0,47298187	0,108228274
Phypa_168035		Pp1s164_49V6.1				0,475311965	0,104166321

Phypa_148936	F16B3.17; ubiquitin family protein [Arabidopsis thaliana] : "F16B3.17; ubiquitin family protein [Arabidopsis thaliana]"	Pp1s286_52V6.1	AT3G02540.3	GO:0005634 : GO:0006289 : GO:0006464	nucleotide-excision repair : nucleus : protein modification	0,47583124	0,121078096
Phypa_162432	F28P22.31; mitochondrial substrate carrier family protein [Arabidopsis thaliana] : "F28P22.31; mitochondrial substrate carrier family protein [Arabidopsis thaliana]"	Pp1s43_27V6.1	AT1G72820.1	GO:0005488 : GO:0005743 : GO:0006810 : GO:0016020	binding : membrane : mitochondrial inner membrane : transport	0,480834991	0,210287541
Phypa_66696	F25I18.8; expressed protein [Arabidopsis thaliana] : "F25I18.8; expressed protein [Arabidopsis thaliana]"	Pp1s11_386V6.1;Pp1s11_386V6.2 : "Pp1s11_386V6.1;Pp1s11_386V6.2" : "Pp1s11_386V6.1;Pp1s11_386V6.2 : ""Pp1s11_386V6.1;Pp1s11_386V6.2"""	AT2G33180.1			0,484127671	0,278585464
Phypa_17256	FCAALL.129; DNA-binding protein-related [Arabidopsis thaliana] : "FCAALL.129; DNA-binding protein-related [Arabidopsis thaliana]"	Pp1s58_127V6.2;Pp1s58_127V6.1 : "Pp1s58_127V6.2;Pp1s58_127V6.1" : "Pp1s58_127V6.2;Pp1s58_127V6.1 : ""Pp1s58_127V6.2;Pp1s58_127V6.1"""	AT2G35270.1			0,49132359	0,16037488
[Phypa_117402;Phypa_176895]						0,493042439	0,275963128
Phypa_88890	MDC8.9; jacalin lectin family protein [Arabidopsis thaliana] : "MDC8.9; jacalin lectin family protein [Arabidopsis thaliana]"	H/ACA small nucleolar RNP component GAR1		KOG3262		0,497340381	0,071924299

Phypa_48243		Pp1s108_36V6.1	AT2G37820.1	GO:0005554 : GO:0007242	intracellular signaling cascade : molecular function unknown	0,498899966	0,325610906
Phypa_98215		Pp1s347_9V6.1	AT1G63440.1	GO:0004008 : GO:0005524 : GO:0006825 : GO:0016020 : GO:0030001 : GO:0046872	ATP binding : copper ion transport : copper-exporting ATPase activity : membrane : metal ion binding : metal ion transport	0,499338835	0,381324112
Phypa_129458	Chalcone synthase (Naringenin-chalcone synthase) [Arabis alpina] : CHS			GO:0008415 : GO:0009058	acyltransferase activity : biosynthesis	0,507325649	0,070344061
Phypa_234354		Pp1s132_73V6.1;Pp1s132_74V6.1 : "Pp1s132_73V6.1;Pp1s132_74V6.1" : "Pp1s132_73V6.1;Pp1s132_74V6.1 : ""Pp1s132_73V6.1;Pp1s132_74V6.1"""				0,510151744	0,181330204
Phypa_71337	Loricrin [Mus musculus]	Pp1s32_94V6.2;Pp1s32_94V6.1 : "Pp1s32_94V6.2;Pp1s32_94V6.1" : "Pp1s32_94V6.2;Pp1s32_94V6.1 : ""Pp1s32_94V6.2;Pp1s32_94V6.1"""		GO:0004402	histone acetyltransferase activity	0,516984522	0,256750971
Phypa_144932	F6D8.37; formamidopyrimidine-DNA glycolase family protein / mutM, putative (MMH-1) [Arabidopsis thaliana] : "F6D8.37; formamidopyrimidine-DNA glycolase family protein / mutM, putative (MMH-1) [Arabidopsis thaliana]"	Pp1s221_62V6.1	AT1G52500.2	GO:0003723 : GO:0003735 : GO:0005622 : GO:0005840 : GO:0006281 : GO:0006412	DNA repair : RNA binding : intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	0,517555296	0,251464337

Phypa_56898	K24M7.20; MATE efflux protein - related [Arabidopsis thaliana] : "K24M7.20; MATE efflux protein - related [Arabidopsis thaliana]"	Pp1s48_46V6.2;Pp1s48_46V6.1 : "Pp1s48_46V6.2;Pp1s48_46V6.1" : "Pp1s48_46V6.2;Pp1s48_46V6.1 : ""Pp1s48_46V6.2;Pp1s48_46V6.1"""	AT5G52450.1	GO:0006855 : GO:0015238 : GO:0015297 : GO:0016020	antiporter activity : drug transporter activity : membrane : multidrug transport	0,520631492	0,153957978
Phypa_216076	F7C8.160; ring-box protein - like [KO:K03868] [Arabidopsis thaliana] : "F7C8.160; ring-box protein - like [KO:K03868] [Arabidopsis thaliana]"	Pp1s123_104V6.1	AT5G20570.1	GO:0000151 : GO:0004842 : GO:0008270 : GO:0016567	protein ubiquitination : ubiquitin ligase complex : ubiquitin-protein ligase activity : zinc ion binding	0,527962983	0,177933723
Phypa_89036	Epstein-Barr nuclear antigen 1 (EBV nuclear antigen 1) (EBNA-1) [Human herpesvirus 4 (strain B95-8)]	Pp1s177_101V6.1;Pp1s177_102V6.1 : "Pp1s177_101V6.1;Pp1s177_102V6.1" : "Pp1s177_101V6.1;Pp1s177_102V6.1 : ""Pp1s177_101V6.1;Pp1s177_102V6.1"""	AT2G19810.1	GO:0004402	histone acetyltransferase activity	0,531080306	0,106441781
Phypa_99968	F1O17.3; esterase/lipase/thioesterase family protein [Arabidopsis thaliana] : "F1O17.3; esterase/lipase/thioesterase family protein [Arabidopsis thaliana]"	Pp1s405_1V6.1	AT2G36290.1	GO:0003824	catalytic activity	0,537661374	0,197317347

Phypa_151194	F3L17.4; splicing factor RSZp22 (RSZP22) / 9G8-like SR protein (SRZ22) [Arabidopsis thaliana] : "F3L17.4; splicing factor RSZp22 (RSZP22) / 9G8-like SR protein (SRZ22) [Arabidopsis thaliana]"	Pp1s332_29V6.1;Pp1s332_29V6.2 : "Pp1s332_29V6.1;Pp1s332_29V6.2" : "Pp1s332_29V6.1;Pp1s332_29V6.2 : ""Pp1s332_29V6.1;Pp1s332_29V6.2"""	AT4G31580.2	GO:0003676	nucleic acid binding	0,538656533	0,158369869
Phypa_27940		Pp1s3_98V6.1	AT1G79650.4	GO:0006464	protein modification	0,543376446	0,128752068
Phypa_124814	MKD15.6; expressed protein [Arabidopsis thaliana] : "MKD15.6; expressed protein [Arabidopsis thaliana]"	Pp1s51_16V6.1;Pp1s51_16V6.2;Pp1s51_16V6.3 : "Pp1s51_16V6.1;Pp1s51_16V6.2;Pp1s51_16V6.3" : "Pp1s51_16V6.1;Pp1s51_16V6.2;Pp1s51_16V6.3 : ""Pp1s51_16V6.1;Pp1s51_16V6.2;Pp1s51_16V6.3"""	AT5G23200.1			0,543508589	0,209889635
Phypa_132376	putative pumilio/Mpt5 family RNA-binding protein [Oryza sativa (japonica cultivar-group)]	Pp1s96_109V6.1	AT2G29200.1	GO:0003723 : GO:0016071	RNA binding : mRNA metabolism	0,54717046	0,193075806
Phypa_16354	Glycine-rich RNA-binding protein 2 [Sorghum bicolor]	Pp1s123_58V6.1	AT4G39260.3	GO:0003676	nucleic acid binding	0,548510551	0,08181303
[Phypa_232463;Phypa_234904]						0,548551381	0,005946427
Phypa_127785	contains ESTs AU093946(E1391),C72298(E1391) [Oryza sativa (japonica cultivar-group)]	Pp1s67_121V6.1	AT3G07880.1	GO:0005094 : GO:0005737	Rho GDP-dissociation inhibitor activity : cytoplasm	0,5489465	0,160569549

Phypa_150088	MXH1.11; auxin-induced protein family [Arabidopsis thaliana] : "MXH1.11; auxin-induced protein family [Arabidopsis thaliana]"	Pp1s310_2V6.1	AT5G35735.1	GO:0004500 : GO:0006584	catecholamine metabolism : dopamine beta-monooxygenase activity	0,555240929	0,134066865
Phypa_1326	F10B6.24; expressed protein [Arabidopsis thaliana] : "F10B6.24; expressed protein [Arabidopsis thaliana]"	Pp1s228_73V6.1	AT2G01750.1			0,559633076	0,162675768
Phypa_113830	F15J1.30; thioredoxin reductase 1 / NADPH-dependent thioredoxin reductase 1 (NTR1) [EC:1.8.1.9] [KO:K00384] [Arabidopsis thaliana] : "F15J1.30; thioredoxin reductase 1 / NADPH-dependent thioredoxin reductase 1 (NTR1) [EC:1.8.1.9] [KO:K00384] [Arabidopsis thaliana]"	Pp1s8_297V6.1	AT2G17420.1	GO:0004791 : GO:0005737 : GO:0006118 : GO:0015036 : GO:0016491 : GO:0019430	cytoplasm : disulfide oxidoreductase activity : electron transport : oxidoreductase activity : removal of superoxide radicals : thioredoxin-disulfide reductase activity	0,559795916	0,205409765

Phypa_192815	MUK11.19; calcium-dependent protein kinase (CDPK)(AK1) [EC:2.7.1.-] [Arabidopsis thaliana] : "MUK11.19; calcium-dependent protein kinase (CDPK)(AK1) [EC:2.7.1.-] [Arabidopsis thaliana]"	Pp1s187_88V6.1;Pp1s187_88V6.2 : "Pp1s187_88V6.1;Pp1s187_88V6.2" : "Pp1s187_88V6.1;Pp1s187_88V6.2 : ""Pp1s187_88V6.1;Pp1s187_88V6.2"""	AT3G10660.1	GO:0004675 : GO:0004676 : GO:0004677 : GO:0004679 : GO:0004680 : GO:0004681 : GO:0004683 : GO:0004686 : GO:0004688 : GO:0004689 : GO:0004690 : GO:0004692 : GO:0004693 : GO:0004694 : GO:0004695 : GO:0004696 : GO:0004697 : GO:0004698 : GO:0004700 : GO:0004701 : GO:0004702 : GO:0004703 : GO:0004704 : GO:0004705 : GO:0004706 : GO:0004707 : GO:0004708 : GO:0004709 : GO:0004710 : GO:0004711 : GO:0004712 : GO:0004713 : GO:0004714 : GO:0004715 : GO:0004716 : GO:0004718 : GO:0005509 : GO:0005524 : GO:0006468 : GO:0008338 : GO:0008339 : GO:0008349 : GO:0008384 : GO:0008443 : GO:0008545 : GO:0008607 : GO:0008819 : GO:0016307 : GO:0016538 : GO:0016773 : GO:0016908 : GO:0016909 : GO:0018720 : GO:0019199 :	dependent protein kinase activity : AMP-activated protein kinase activity : ATP binding : DNA-dependent protein kinase activity : G-protein coupled receptor kinase activity : IkappaB kinase activity : JUN kinase activity : JUN kinase kinase activity : JUN kinase kinase kinase activity : Janus kinase activity : MAP kinase 1 activity : MAP kinase 2 activity : MAP kinase activity : MAP kinase kinase activity : MAP kinase kinase kinase activity : MAP kinase kinase kinase activity : MAP/ERK kinase kinase activity : MP kinase activity : NF-kappaB-inducing kinase activity : SAP kinase activity : atypical protein kinase C activity : cGMP-dependent	0,56172967	0,135296702
Phypa_71211	MPH15.6; homeobox-leucine zipper protein HAT14 (HD-Zip protein 14) [Arabidopsis thaliana] : "MPH15.6; homeobox-leucine zipper protein HAT14 (HD-Zip protein 14) [Arabidopsis thaliana]"	Pp1s31_272V6.1	AT5G06710.1	GO:0003677 : GO:0003700 : GO:0005634 : GO:0006355	DNA binding : nucleus : regulation of transcription, DNA-dependent : transcription factor activity	0,562984645	0,152967602

Phypa_182704	T6D22.2; elongation factor 1-alpha / EF-1-alpha [EC:3.6.5.3] [KO:K03231] [Arabidopsis thaliana] : "T6D22.2; elongation factor 1-alpha / EF-1-alpha [EC:3.6.5.3] [KO:K03231] [Arabidopsis thaliana]"	Pp1s59_181V6.1	AT1G07920.1	GO:0003924 : GO:0005525 : GO:0006412 : GO:0008547	GTP binding : GTPase activity : protein biosynthesis : protein-synthesizing GTPase activity	0,56436938	0,095892705
Phypa_231575		Pp1s134_155V6.2;Pp1s134_155V6.1;Pp1s134_155V6.3 : "Pp1s134_155V6.2;Pp1s134_155V6.1;Pp1s134_155V6.3" : "Pp1s134_155V6.2;Pp1s134_155V6.1;Pp1s134_155V6.3 : ""Pp1s134_155V6.2;Pp1s134_155V6.1;Pp1s134_155V6.3"""	AT5G65170.1			0,564515293	0,122510344
Phypa_200899	F19K6.12; 60S ribosomal protein L37 (RPL37B) [KO:K02922] [Arabidopsis thaliana] : "F19K6.12; 60S ribosomal protein L37 (RPL37B) [KO:K02922] [Arabidopsis thaliana]"	Pp1s475_18V6.1	AT1G52300.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	0,567241132	0,151771113
Phypa_8347	K3G17.6; myb family transcription factor [Arabidopsis thaliana] : "K3G17.6; myb family transcription factor [Arabidopsis thaliana]"	Pp1s10_267V6.1	AT3G50060.1	GO:0003677 : GO:0005634	DNA binding : nucleus	0,574779868	0,338170946
Phypa_128382	putative PSTVd RNA-biding protein [Oryza sativa (japonica cultivar-group)]	Pp1s70_77V6.1				0,576279342	0,420424491

[Phypa_101257;Phypa_101260;Phypa_110814]						0,58395052	0,0805123
Phypa_142157	Sigma factor sigB regulation protein rsbQ [Bacillus subtilis]	Pp1s188_47V6.1	AT4G37470.1	GO:0003824 : GO:0006725 : GO:0016787	aromatic compound metabolism : catalytic activity : hydrolase activity	0,591057658	0,189785555
Phypa_140533	Trans-cinnamate 4-monooxygenase (Cinnamic acid 4-hydroxylase) (CA4H) (C4H) (P450C4H) (Cytochrome P450 73) [Populus kitakamiensis]	Pp1s168_84V6.1	AT2G30490.1	GO:0004497 : GO:0006118 : GO:0016710	electron transport : monooxygenase activity : trans-cinnamate 4-monooxygenase activity	0,592575908	0,184454501
Phypa_168895	contains EST AU033244(S5767) unknown protein [Oryza sativa (japonica cultivar-group)]	Pp1s193_54V6.1;Pp1s193_54V6.2 : "Pp1s193_54V6.1;Pp1s193_54V6.2" : "Pp1s193_54V6.1;Pp1s193_54V6.2 : ""Pp1s193_54V6.1;Pp1s193_54V6.2"""	AT1G80000.1			0,596568346	0,216451898
Phypa_119898	putative ribosomal protein L26 [Oryza sativa (japonica cultivar-group)]	Pp1s30_298V6.1	AT3G49910.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412 : GO:0015934	intracellular : large ribosomal subunit : protein biosynthesis : ribosome : structural constituent of ribosome	0,598854125	0,155753464
Phypa_66307	T7B11.33; expressed protein [Arabidopsis thaliana] : "T7B11.33; expressed protein [Arabidopsis thaliana]"	Pp1s10_122V6.1				0,599128306	0,3320539
Phypa_124611		Pp1s50_146V6.1	AT4G12040.2	GO:0003677 : GO:0005554 : GO:0008270	DNA binding : molecular function unknown : zinc ion binding	0,605029762	0,083572932

Phypa_123034	Two-component response regulator ARR2 (Receiver-like protein 5) [Arabidopsis thaliana]	Pp1s42_161V6.1	AT4G16110.1	GO:0000156 : GO:0000160 : GO:0003677 : GO:0005634 : GO:0006355	DNA binding : nucleus : regulation of transcription, DNA-dependent : two-component response regulator activity : two-component signal transduction system (phosphorelay)	0,615352809	0,29110986
Phypa_159009	F15J1.30; thioredoxin reductase 1 / NADPH-dependent thioredoxin reductase 1 (NTR1) [EC:1.8.1.9] [KO:K00384] [Arabidopsis thaliana] : "F15J1.30; thioredoxin reductase 1 / NADPH-dependent thioredoxin reductase 1 (NTR1) [EC:1.8.1.9] [KO:K00384] [Arabidopsis thaliana]"	Pp1s8_302V6.1	AT2G17420.1	GO:0004791 : GO:0005737 : GO:0006118 : GO:0015036 : GO:0016491 : GO:0019430	cytoplasm : disulfide oxidoreductase activity : electron transport : oxidoreductase activity : removal of superoxide radicals : thioredoxin-disulfide reductase activity	0,615364552	0,230036184
Phypa_165037	extremely serine rich protein [Candida albicans SC5314]	Pp1s81_168V6.1				0,617043495	0,230740815
Phypa_122357	Vacuolar sorting receptor 3 precursor (AtVSR3) (Epidermal growth factor receptor-like protein 2a) (AtELP2a) (BP80-like protein a') (AtBP80a') [Arabidopsis thaliana]	Pp1s39_354V6.2;Pp1s39_354V6.1 : "Pp1s39_354V6.2;Pp1s39_354V6.1" : "Pp1s39_354V6.2;Pp1s39_354V6.1 : ""Pp1s39_354V6.2;Pp1s39_354V6.1"""	AT2G14720.2	GO:0005509 : GO:0006508 : GO:0008233	calcium ion binding : peptidase activity : proteolysis and peptidolysis	0,623853981	0,189556926
[Phypa_53670;Phypa_53669;Phypa_225790]						0,62629807	0,313709348

Phypa_167013	T10I14.150; expressed protein [Arabidopsis thaliana] : "T10I14.150; expressed protein [Arabidopsis thaliana]"	Pp1s133_17V6.2;Pp1s133_17V6.1;Pp1s133_17V6.3 : "Pp1s133_17V6.2;Pp1s133_17V6.1;Pp1s133_17V6.3" : "Pp1s133_17V6.2;Pp1s133_17V6.1;Pp1s133_17V6.3 : ""Pp1s133_17V6.2;Pp1s133_17V6.1;Pp1s133_17V6.3"""	AT4G22320.1			0,626645207	0,198548645
Phypa_55884		Pp1s22_18V6.1	AT4G17520.1			0,631478727	0,11825528
Phypa_9740	MPF21.9; AP2 domain transcription factor, putative [Arabidopsis thaliana] : "MPF21.9; AP2 domain transcription factor, putative [Arabidopsis thaliana]"	Pp1s259_104V6.1	AT2G33710.2	GO:0003700 : GO:0005634 : GO:0006355	nucleus : regulation of transcription, DNA-dependent : transcription factor activity	0,632226527	0,304354578
Phypa_29816	AP22.21; G-box binding factor 1 (GBF1) [Arabidopsis thaliana] : "AP22.21; G-box binding factor 1 (GBF1) [Arabidopsis thaliana]"	Pp1s27_273V6.1	AT1G32150.1	GO:0003677 : GO:0005634 : GO:0006355	DNA binding : nucleus : regulation of transcription, DNA-dependent	0,633425713	0,105064034
Phypa_114453	F6F9.7; regulator of chromosome condensation (RCC1) family protein [Arabidopsis thaliana] : "F6F9.7; regulator of chromosome condensation (RCC1) family protein [Arabidopsis thaliana]"	Pp1s10_244V6.1	AT1G19880.1			0,634386301	0,317604065

Phypa_140886	Fructose-bisphosphate aldolase, chloroplast precursor (ALDP) [no tax name]	Pp1s171_150V6.1	AT2G01140.1	GO:0004332 : GO:0006096	fructose-bisphosphate aldolase activity : glycolysis	0,638651907	0,067240015
Phypa_42952	MGL6.2; protein phosphatase 2C-related / PP2C-related [Arabidopsis thaliana] : "MGL6.2; protein phosphatase 2C-related / PP2C-related [Arabidopsis thaliana]"	Pp1s66_193V6.2;Pp1s66_193V6.1 : "Pp1s66_193V6.2;Pp1s66_193V6.1" : "Pp1s66_193V6.2;Pp1s66_193V6.1 : ""Pp1s66_193V6.2;Pp1s66_193V6.1"""	AT3G16560.1	GO:0000158 : GO:0003824 : GO:0004721 : GO:0004723 : GO:0004724 : GO:0005963 : GO:0008420 : GO:0008597 : GO:0015071 : GO:0017018 : GO:0017020 : GO:0017023 : GO:0030357	CTD phosphatase activity : calcium-dependent protein serine/threonine phosphatase activity : calcium-dependent protein serine/threonine phosphatase regulator activity : catalytic activity : magnesium-dependent protein serine/threonine phosphatase activity : magnesium-dependent protein serine/threonine phosphatase complex : myosin phosphatase activity : myosin phosphatase complex : myosin phosphatase regulator activity : phosphoprotein phosphatase activity : protein phosphatase type 2A activity : protein phosphatase type 2B activity : protein phosphatase type 2C activity	0,640496373	0,21194534
Phypa_198924	Glutamine synthetase, cytosolic isozyme (Glutamate--ammonia ligase) (GS1) [Lotus corniculatus var. japonicus]	Pp1s345_10V6.1	AT5G16570.1	GO:0004356 : GO:0006542 : GO:0006807	glutamate-ammonia ligase activity : glutamine biosynthesis : nitrogen compound metabolism	0,641427338	0,101234213

Phypa_199029	contains EST AU093701(C63333) [Oryza sativa (japonica cultivar-group)]	Pp1s350_28V6.1	AT1G53540.1			0,650231659	0,154921353
Phypa_97737						0,65133822	0,148996785
Phypa_93647		Pp1s246_1V6.1				0,656110644	0,113783464
Phypa_219988	T1O24.43; chitinase, putative [Arabidopsis thaliana] : "T1O24.43; chitinase, putative [Arabidopsis thaliana]"	Pp1s184_140V6.1	AT3G54420.1	GO:0004568 : GO:0006032 : GO:0008061 : GO:0008843 : GO:0009613 : GO:0016998	cell wall catabolism : chitin binding : chitin catabolism : chitinase activity : endochitinase activity : response to pest, pathogen or parasite	0,659029186	0,171788409
Phypa_73809	F11O4.1; major intrinsic family protein / MIP family protein [Arabidopsis thaliana] : "F11O4.1; major intrinsic family protein / MIP family protein [Arabidopsis thaliana]"	Pp1s44_31V6.1	AT4G01470.1	GO:0005215 : GO:0006810 : GO:0016020	membrane : transport : transporter activity	0,659080744	0,097421654
Phypa_92860	F4F15.230; SWAP (Suppressor-of-White-APricot)/surp domain-containing protein / D111/G-patch domain-containing protein [Arabidopsis thaliana] : "F4F15.230; SWAP (Suppressor-of-White-APricot)/surp domain-containing protein / D111/G-patch domain-containing protein [Arabidopsis thaliana]"	Pp1s232_50V6.1	AT3G52120.2	GO:0003723 : GO:0006396	RNA binding : RNA processing	0,660121202	0,244570017

Phypa_77631	MJM18.1; hypothetical protein [Arabidopsis thaliana] : "MJM18.1; hypothetical protein [Arabidopsis thaliana]"	Pp1s66_143V6.1	AT5G66950.1	GO:0006508 : GO:0008237 : GO:0008270	metallopeptidase activity : proteolysis and peptidolysis : zinc ion binding	0,661254048	0,24130103
Phypa_219977	contains EST C98236(C1282) [Oryza sativa (japonica cultivar-group)]	Pp1s184_111V6.1	AT2G34480.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	0,666699052	0,189467102
[Phypa_160180;Phypa_109545]						0,701686144	0,118788898
Phypa_29541	MQK4.29; zinc finger protein 3 (gb|AAD27875.1) [Arabidopsis thaliana] : "MQK4.29; zinc finger protein 3 (gb|AAD27875.1) [Arabidopsis thaliana]"	Pp1s6_324V6.1	AT2G47850.3	GO:0003676	nucleic acid binding	0,704067826	0,321853638
[Phypa_117940;Phypa_118049]						0,721372843	0,232552081
Phypa_194737	F5O24.180; 40S ribosomal protein S8 (RPS8A) [KO:K02995] [Arabidopsis thaliana] : "F5O24.180; 40S ribosomal protein S8 (RPS8A) [KO:K02995] [Arabidopsis thaliana]"	Pp1s223_73V6.1	AT5G59240.1	GO:0005622	intracellular	0,723065853	0,112163298
Phypa_127844	contains ESTs AU093946(E1391),C72298(E1391) [Oryza sativa (japonica cultivar-group)]	Pp1s67_110V6.1	AT3G07880.1	GO:0005094 : GO:0005737	Rho GDP-dissociation inhibitor activity : cytoplasm	0,725540817	0,204524279
Phypa_170625						0,72685802	0,213547155
Phypa_71025	hypothetical protein [Dictyostelium discoideum]	Pp1s30_337V6.1		GO:0004553 : GO:0005975	carbohydrate metabolism : hydrolase activity, hydrolyzing O-glycosyl compounds	0,732338846	0,231627122

Phypa_97140	T7B11.33; expressed protein [Arabidopsis thaliana] : "T7B11.33; expressed protein [Arabidopsis thaliana]"	Pp1s319_48V6.1;Pp1s319_47V6.2;Pp1s319_47V6.1 : "Pp1s319_48V6.1;Pp1s319_47V6.2;Pp1s319_47V6.1" : "Pp1s319_48V6.1;Pp1s319_47V6.2;Pp1s319_47V6.1 : ""Pp1s319_48V6.1;Pp1s319_47V6.2;Pp1s319_47V6.1"""					0,732586801	0,266162694
Phypa_166622	T3F17.29; transmembrane protein-related [Arabidopsis thaliana] : "T3F17.29; transmembrane protein-related [Arabidopsis thaliana]"	Pp1s120_82V6.1	AT2G46060.1				0,733399808	0,222376227
Phypa_165920	F8A24.7; serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B' (B'beta) [Arabidopsis thaliana] : "F8A24.7; serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B' (B'beta) [Arabidopsis thaliana]"	Pp1s98_213V6.1;Pp1s98_214V6.2 : "Pp1s98_213V6.1;Pp1s98_214V6.2" : "Pp1s98_213V6.1;Pp1s98_214V6.2 : ""Pp1s98_213V6.1;Pp1s98_214V6.2"""	AT4G15415.1	GO:0000159 : GO:0007165 : GO:0008601 : GO:0047778	[citrate-(pro-3S)-lyase] thiolesterase activity : protein phosphatase type 2A complex : protein phosphatase type 2A regulator activity : signal transduction		0,737400889	0,30164212
[Phypa_154682;Phypa_200520;Phypa_154659]							0,740243196	0,085557252
Phypa_197211	contains EST C98230(C1257) [Oryza sativa (japonica cultivar-group)]	Pp1s287_20V6.1	AT5G02960.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412 : GO:0015935	intracellular : protein biosynthesis : ribosome : small ribosomal subunit : structural constituent of ribosome		0,742098629	0,194557458

Phypa_84171	T4C21.160; transketolase, putative [EC:2.2.1.1] [KO:K00615] [Arabidopsis thaliana] : "T4C21.160; transketolase, putative [EC:2.2.1.1] [KO:K00615] [Arabidopsis thaliana]"	Pp1s120_127V6.1	AT3G60750.1	GO:0001584 : GO:0004802 : GO:0007186 : GO:0016021	G-protein coupled receptor protein signaling pathway : integral to membrane : rhodopsin-like receptor activity : transketolase activity	0,74499321	0,16637145
Phypa_122336	Chalcone synthase 1B (Naringenin-chalcone synthase 1B) [Pisum sativum]	Pp1s39_349V6.1	AT5G13930.1	GO:0008415 : GO:0009058 : GO:0016747	acyltransferase activity : biosynthesis : transferase activity, transferring groups other than amino-acyl groups	0,745880425	0,167349294
Phypa_111068		Pp1s1_845V6.1	AT1G52380.1			0,747252405	0,058475826
Phypa_68756		Pp1s20_156V6.1	AT3G49180.1			0,752233148	0,26688534
Phypa_208348	60S ribosomal protein L23A [Fritillaria agrestis]	Pp1s46_72V6.1	AT3G55280.2	GO:0003723 : GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	RNA binding : intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	0,75369662	0,13576977
[Phypa_2572;Phypa_2573]						0,754574001	0,154844254
[Phypa_9662;Phypa_9653]						0,760293543	0,293537468

Phypa_174734	F1P15.5; amidophosphoribosyltransferase / glutamine phosphoribosylpyrophosphate amidotransferase / phosphoribosyldiphosphate 5-amidotransferase [EC:2.4.2.14] [KO:K00764] [Arabidopsis thaliana] : "F1P15.5; amidophosphoribosyltransferase / glutamine phosphoribosylpyrophosphate amidotransferase / phosphoribosyldiphosphate 5-amidotransferase [EC:2.4.2.14] [KO:K00764] [Arabidopsis thaliana]"	Pp1s8_239V6.1	AT2G16570.1	GO:0004044 : GO:0008152 : GO:0009113 : GO:0009116 : GO:0016740	amidophosphoribosyltransferase activity : metabolism : nucleoside metabolism : purine base biosynthesis : transferase activity	0,764638901	0,172985569
Phypa_19276		Pp1s161_109V6.1	AT3G56580.2	GO:0000151 : GO:0004842 : GO:0008270 : GO:0016567	protein ubiquitination : ubiquitin ligase complex : ubiquitin-protein ligase activity : zinc ion binding	0,767300069	0,293027043
Phypa_168983		Pp1s195_100V6.1				0,767765641	0,096723825
Phypa_192417	F2N1.17; acetylesterase, putative [Arabidopsis thaliana] : "F2N1.17; acetylesterase, putative [Arabidopsis thaliana]"	Pp1s179_68V6.1	AT4G01130.1	GO:0003824	catalytic activity	0,768680692	0,150505453
[Phypa_143434;Phypa_157535]						0,772110999	0,053465303

Phypa_168832	MMG4.16; expressed protein [Arabidopsis thaliana] : "MMG4.16; expressed protein [Arabidopsis thaliana]"	Pp1s190_90V6.1;Pp1s190_91V6.1;Pp1s190_89V6.1 : "Pp1s190_90V6.1;Pp1s190_91V6.1;Pp1s190_89V6.1" : "Pp1s190_90V6.1;Pp1s190_91V6.1;Pp1s190_89V6.1 : ""Pp1s190_90V6.1;Pp1s190_91V6.1;Pp1s190_89V6.1"""		GO:0004402 : GO:0005669 : GO:0006352 : GO:0016986	histone acetyltransferase activity : transcription factor TFIID complex : transcription initiation : transcription initiation factor activity	0,772661269	0,357897133
Phypa_19709	Protein At1g77540 [Arabidopsis thaliana]	Pp1s91_93V6.1;Pp1s91_93V6.2 : "Pp1s91_93V6.1;Pp1s91_93V6.2" : "Pp1s91_93V6.1;Pp1s91_93V6.2 : ""Pp1s91_93V6.1;Pp1s91_93V6.2"""	AT1G21770.1			0,774628222	0,228804603
Phypa_129054	60S ribosomal protein L44 [Gossypium hirsutum]	Pp1s74_73V6.1	AT4G14320.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	0,775292635	0,117170632
Phypa_169417	hypothetical protein [Oryza sativa (japonica cultivar-group)]	Pp1s208_161V6.1	AT5G13470.1			0,791498244	0,175396621
Phypa_169433		Pp1s209_54V6.2;Pp1s209_54V6.1 : "Pp1s209_54V6.2;Pp1s209_54V6.1" : "Pp1s209_54V6.2;Pp1s209_54V6.1 : ""Pp1s209_54V6.2;Pp1s209_54V6.1"""	Pp1s209_54V6			0,791922569	0,039040361

Phypa_106639		Pp1s88_212V6.2;Pp1s88_212V6.1;Pp1s88_212V6.3 : "Pp1s88_212V6.2;Pp1s88_212V6.1;Pp1s88_212V6.3" : "Pp1s88_212V6.2;Pp1s88_212V6.1;Pp1s88_212V6.3 : ""Pp1s88_212V6.2;Pp1s88_212V6.1;Pp1s88_212V6.3"""	AT3G51880.2	GO:0000785 : GO:0003677 : GO:0005634 : GO:0006355	DNA binding : chromatin : nucleus : regulation of transcription, DNA-dependent	0,792756081	0,311272472
[Phypa_201226;Phypa_228370]						0,794928849	0,020068619
Phypa_173974	F28O9.190; DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] : "F28O9.190; DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana]"	Pp1s2_417V6.1	AT3G57340.2	GO:0006457 : GO:0031072 : GO:0051082	heat shock protein binding : protein folding : unfolded protein binding	0,799828351	0,241305634
Phypa_231987		Pp1s148_7V6.1	AT5G58470.1			0,800969481	0,244506344

Phypa_182655	contains EST AU029985(E50436) [Oryza sativa (japonica cultivar-group)]	Pp1s59_81V6.1	AT1G55150.1	GO:0003676 : GO:0004003 : GO:0004004 : GO:0004386 : GO:0005524 : GO:0008026 : GO:0008094 : GO:0008186 : GO:0015462 : GO:0015616 : GO:0016887 : GO:0017116 : GO:0042623 : GO:0042624 : GO:0042625 : GO:0042626	ATP binding : ATP-dependent DNA helicase activity : ATP-dependent RNA helicase activity : ATP-dependent helicase activity : ATPase activity : ATPase activity, coupled : ATPase activity, coupled to transmembrane movement of ions : ATPase activity, coupled to transmembrane movement of substances : ATPase activity, uncoupled : DNA translocase activity : DNA-dependent ATPase activity : RNA-dependent ATPase activity : helicase activity : nucleic acid binding : protein-transporting ATPase activity : single-stranded DNA-dependent ATP-dependent DNA helicase activity	0,802012861	0,053963114
Phypa_143182	F7O18.23; expressed protein (SWP1) [Arabidopsis thaliana] : "F7O18.23; expressed protein (SWP1) [Arabidopsis thaliana]"	Pp1s199_104V6.2;Pp1s199_104V6.3;Pp1s199_104V6.1 : "Pp1s199_104V6.2;Pp1s199_104V6.3;Pp1s199_104V6.1" : "Pp1s199_104V6.2;Pp1s199_104V6.3;Pp1s199_104V6.1 : ""Pp1s199_104V6.2;Pp1s199_104V6.3;Pp1s199_104V6.1"""	AT3G04740.1			0,806212187	0,170076117

Phypa_203817		Pp1s16_334V6.1	AT1G73500.1	GO:0004672 : GO:0004674 : GO:0004713 : GO:0005524 : GO:0006468	ATP binding : protein amino acid phosphorylation : protein kinase activity : protein serine/threonine kinase activity : protein-tyrosine kinase activity	0,816588879	0,222672269
Phypa_213049	F3H11.5; organic cation transporter family protein [Arabidopsis thaliana] : "F3H11.5; organic cation transporter family protein [Arabidopsis thaliana]"	Pp1s85_39V6.1	AT3G20660.1	GO:0005215 : GO:0006810 : GO:0016020 : GO:0016021	integral to membrane : membrane : transport : transporter activity	0,829653919	0,303406924
Phypa_177219	Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplast precursor (Phospho-2-keto-3-deoxyheptonate aldolase 1) (DAHP synthetase 1) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 1) [Nicotiana tabacum]	Pp1s22_79V6.2;Pp1s22_79V6.1 : "Pp1s22_79V6.2;Pp1s22_79V6.1" : "Pp1s22_79V6.2;Pp1s22_79V6.1 : ""Pp1s22_79V6.2;Pp1s22_79V6.1"""	AT1G22410.1	GO:0003849 : GO:0009073	3-deoxy-7-phosphoheptulonate synthase activity : aromatic amino acid family biosynthesis	0,838056207	0,103027001
Phypa_114336	50S ribosomal protein L15, chloroplast precursor (CL15) [Pisum sativum]	Pp1s9_435V6.1	AT3G25920.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412 : GO:0015934	intracellular : large ribosomal subunit : protein biosynthesis : ribosome : structural constituent of ribosome	0,843063951	0,270281196
Phypa_37877	contains ESTs AU062952(C51837),AU100820(C51837) [Oryza sativa (japonica cultivar-group)]	Pp1s118_100V6.1	AT5G61030.1	GO:0003676	nucleic acid binding	0,843249679	0,080965132

Phypa_171592	F14F8.90; F-box protein family [Arabidopsis thaliana] : "F14F8.90; F-box protein family [Arabidopsis thaliana]"	Pp1s301_11V6.2;Pp1s301_11V6.1 : "Pp1s301_11V6.2;Pp1s301_11V6.1" : "Pp1s301_11V6.2;Pp1s301_11V6.1 : ""Pp1s301_11V6.2;Pp1s301_11V6.1"""	AT5G15710.1			0,844341695	0,214153677
Phypa_65365	MSL3.12; NTF2-containing RNA-binding protein, putative [Arabidopsis thaliana] : "MSL3.12; NTF2-containing RNA-binding protein, putative [Arabidopsis thaliana]"	Pp1s6_129V6.1	AT5G60980.1	GO:0003676 : GO:0004308 : GO:0005622 : GO:0005634 : GO:0006606 : GO:0008565	exo-alpha-sialidase activity : intracellular : nucleic acid binding : nucleus : protein transporter activity : protein-nucleus import	0,850712419	0,23524487
Phypa_171055		Pp1s272_60V6.1				0,850947678	3,110301971
Phypa_71336	Glycine-rich cell wall structural protein 1.0 precursor (GRP 1.0) [Phaseolus vulgaris]	Pp1s32_87V6.2;Pp1s32_87V6.1 : "Pp1s32_87V6.2;Pp1s32_87V6.1" : "Pp1s32_87V6.2;Pp1s32_87V6.1 : ""Pp1s32_87V6.2;Pp1s32_87V6.1"""	Pp1s32_87V6	GO:0004308	exo-alpha-sialidase activity	0,861103237	0,19533141
Phypa_73609	Glycine-rich RNA-binding protein 2 [Sorghum bicolor]	Pp1s42_251V6.2;Pp1s42_251V6.1 : "Pp1s42_251V6.2;Pp1s42_251V6.1" : "Pp1s42_251V6.2;Pp1s42_251V6.1 : ""Pp1s42_251V6.2;Pp1s42_251V6.1"""	AT4G39260.3	GO:0003676	nucleic acid binding	0,865923226	0,192914203

Phypa_159184	LOC499168; similar to protein tyrosine phosphatase, receptor type, F [Rattus norvegicus] : "LOC499168; similar to protein tyrosine phosphatase, receptor type, F [Rattus norvegicus]"	Pp1s10_115V6.1				0,868392587	0,202090234
Phypa_180041	contains EST AU064366(E30232) [Oryza sativa (japonica cultivar-group)]	Pp1s39_288V6.1;Pp1s39_288V6.2 : "Pp1s39_288V6.1;Pp1s39_288V6.2" : "Pp1s39_288V6.1;Pp1s39_288V6.2 : ""Pp1s39_288V6.1;Pp1s39_288V6.2"""	AT3G10950.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	0,879733145	0,24730359
Phypa_73571		Pp1s42_188V6.1				0,890588045	0,130379632
Phypa_46426	40S ribosomal protein SA (p40) [Daucus carota]	Pp1s173_16V6.1	AT1G72370.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412 : GO:0015935	intracellular : protein biosynthesis : ribosome : small ribosomal subunit : structural constituent of ribosome	0,892170012	0,023343721
Phypa_47533	Glycine-rich protein 2 [Nicotiana sylvestris]	Pp1s103_65V6.1	AT4G36020.1	GO:0003676 : GO:0003677 : GO:0006355	DNA binding : nucleic acid binding : regulation of transcription, DNA-dependent	0,896122396	0,129166648
Phypa_149624	F16M14.18; DNA-binding protein-related [Arabidopsis thaliana] : "F16M14.18; DNA-binding protein-related [Arabidopsis thaliana]"	Pp1s301_48V6.1	AT2G38250.1	GO:0003677 : GO:0005634	DNA binding : nucleus	0,901133239	0,25491184
Phypa_172235		Pp1s337_35V6.1				0,924979389	0,240913823

Phypa_18892	F5H14.27; expressed protein [Arabidopsis thaliana] : "F5H14.27; expressed protein [Arabidopsis thaliana]"	Pp1s87_57V6.1	AT2G40060.1			0,929344714	0,069294564
Phypa_183211	Glycine-rich protein 2 [Nicotiana sylvestris]	Pp1s64_4V6.2;Pp1s64_4V6.1 : "Pp1s64_4V6.2;Pp1s64_4V6.1" : "Pp1s64_4V6.2;Pp1s64_4V6.1 : ""Pp1s64_4V6.2;Pp1s64_4V6.1"""	AT4G36020.1	GO:0003676 : GO:0003677 : GO:0006355	DNA binding : nucleic acid binding : regulation of transcription, DNA-dependent	0,93004781	0,062162835
Phypa_29741	F13M7.19; tubulin alpha-2/alpha-4 chain (TUA4) [KO:K07374] [Arabidopsis thaliana] : "F13M7.19; tubulin alpha-2/alpha-4 chain (TUA4) [KO:K07374] [Arabidopsis thaliana]"	Pp1s1454_1V6.1	AT1G50010.1	GO:0005198 : GO:0005874 : GO:0007018	microtubule : microtubule-based movement : structural molecule activity	0,935857713	0,05690999
Phypa_166141	F7J8.240; expressed protein [Arabidopsis thaliana] : "F7J8.240; expressed protein [Arabidopsis thaliana]"	Pp1s103_94V6.2;Pp1s103_94V6.1 : "Pp1s103_94V6.2;Pp1s103_94V6.1" : "Pp1s103_94V6.2;Pp1s103_94V6.1 : ""Pp1s103_94V6.2;Pp1s103_94V6.1"""	AT5G01260.2	GO:0003824 : GO:0005975	carbohydrate metabolism : catalytic activity	0,939661264	0,222227409
Phypa_116428	Thiazole biosynthetic enzyme, chloroplast precursor [Citrus sinensis]	Pp1s16_179V6.1;Pp1s16_179V6.2 : "Pp1s16_179V6.1;Pp1s16_179V6.2" : "Pp1s16_179V6.1;Pp1s16_179V6.2 : ""Pp1s16_179V6.1;Pp1s16_179V6.2"""	AT5G54770.1	GO:0006118 : GO:0009228	electron transport : thiamin biosynthesis	0,941879988	0,278436184

Phypa_132819	F8A24.7; serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B' (B'beta) [Arabidopsis thaliana] : "F8A24.7; serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B' (B'beta) [Arabidopsis thaliana]"	Pp1s98_229V6.1	AT4G15415.2	GO:0000159 : GO:0007165 : GO:0008601 : GO:0047778	[citrate-(pro-3S)-lyase] thiolesterase activity : protein phosphatase type 2A complex : protein phosphatase type 2A regulator activity : signal transduction	0,942243874	0,293842494
[Phypa_156563;Phypa_157157;Phypa_102363;Phypa_103579;Phypa_103626]						0,942749023	0,040022664
[Phypa_133628;Phypa_133621]						0,95007062	0,334588647
Phypa_110421	F19G10.14; disease resistance-responsive family protein [Arabidopsis thaliana] : "F19G10.14; disease resistance-responsive family protein [Arabidopsis thaliana]"	Pp1s252_11V6.1	AT1G22900.1			0,960107982	0,060282011
[Phypa_134474;Phypa_134439]						0,963994443	0,171823636
Phypa_137303	MSD21.4; isocitrate lyase, putative [EC:4.1.3.1] [KO:K01637] [Arabidopsis thaliana] : "MSD21.4; isocitrate lyase, putative [EC:4.1.3.1] [KO:K01637] [Arabidopsis thaliana]"	Pp1s136_203V6.1	AT3G21720.1	GO:0003676 : GO:0003824 : GO:0004451 : GO:0006097 : GO:0008152	catalytic activity : glyoxylate cycle : isocitrate lyase activity : metabolism : nucleic acid binding	0,965396523	0,189525828
[Phypa_3688;Phypa_58013;Phypa_213086]						0,979547799	0,08760456

Phypa_143844	40S ribosomal protein SA (p40) [Glycine max]	Pp1s209_47V6.1		GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	0,979706645	0,019348012
Phypa_134646	F3G5.1; 29 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp29, putative [Arabidopsis thaliana] : "F3G5.1; 29 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp29, putative [Arabidopsis thaliana]"	Pp1s114_138V6.1	AT3G53460.3	GO:0003676	nucleic acid binding	0,980480552	0,209223345
Phypa_193430	contains ESTs AU093946(E1391),C72298(E1391) [Oryza sativa (japonica cultivar-group)]	Pp1s198_106V6.1	AT3G07880.1	GO:0005094 : GO:0005737	Rho GDP-dissociation inhibitor activity : cytoplasm	0,989034176	0,224671409
Phypa_209813		Pp1s56_243V6.3;Pp1s56_243V6.2;Pp1s56_243V6.1 : "Pp1s56_243V6.3;Pp1s56_243V6.2;Pp1s56_243V6.1" : "Pp1s56_243V6.3;Pp1s56_243V6.2;Pp1s56_243V6.1 : ""Pp1s56_243V6.3;Pp1s56_243V6.2;Pp1s56_243V6.1"""	AT2G34480.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	0,990568101	0,186331272

Phypa_38559	F1P2.200; bundle-sheath defective protein 2 family / bsd2 family [Arabidopsis thaliana] : "F1P2.200; bundle-sheath defective protein 2 family / bsd2 family [Arabidopsis thaliana]"	Pp1s33_37V6.1	AT3G47650.1			0,991574705	0,183100417
Phypa_166789	Dof zinc finger protein DOF1.10 (AtDOF1.10) (H-protein promoter-binding factor 2b) [Arabidopsis thaliana]	Pp1s124_139V6.1	AT3G47500.1	GO:0003677	DNA binding	0,992728114	0,146381319
[Phypa_135358;Phypa_135382]						0,999316454	0,284480512
Phypa_117476	Adenosylhomocysteinase (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase) [Petroselinum crispum]	Pp1s20_291V6.1	AT3G23810.1	GO:0004013 : GO:0006730	adenosylhomocysteinase activity : one-carbon compound metabolism	1,002760887	0,161980227
Phypa_117389	Adenosylhomocysteinase (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase) [Catharanthus roseus]	Pp1s20_308V6.1	AT4G13940.1	GO:0004013 : GO:0006730	adenosylhomocysteinase activity : one-carbon compound metabolism	1,013580203	0,142303005

Phypa_187695	T7B11.11; S-adenosylmethionine synthetase 2 (SAM2) [EC:2.5.1.6] [KO:K00789] [Arabidopsis thaliana] : "T7B11.11; S-adenosylmethionine synthetase 2 (SAM2) [EC:2.5.1.6] [KO:K00789] [Arabidopsis thaliana]"	Pp1s109_133V6.1		GO:0004478 : GO:0005524 : GO:0006730 : GO:0048269 : GO:0048270	ATP binding : methionine adenosyltransferase activity : methionine adenosyltransferase complex : methionine adenosyltransferase regulator activity : one-carbon compound metabolism	1,01564312	0,105454527
Phypa_128273	putative ribosomal protein L26 [Oryza sativa (japonica cultivar-group)]	Pp1s69_191V6.1	AT3G49910.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412 : GO:0015934	intracellular : large ribosomal subunit : protein biosynthesis : ribosome : structural constituent of ribosome	1,01847434	0,19181788
[Phypa_147904;Phypa_147925]						1,019373178	0,120566607
[Phypa_150243;Phypa_225255]						1,020731211	0,127473369
Phypa_157798	T5J17.200; histone H3.2 [Arabidopsis thaliana] : "T5J17.200; histone H3.2 [Arabidopsis thaliana]"	Pp1s1963_1V6.1	AT4G40030.2	GO:0000786 : GO:0003677 : GO:0005634 : GO:0006334 : GO:0007001	DNA binding : chromosome organization and biogenesis (sensu Eukaryota) : nucleosome : nucleosome assembly : nucleus	1,023857832	0,197311699
Phypa_45136		Pp1s109_127V6.1	AT4G01850.1	GO:0004478 : GO:0005524 : GO:0006730	ATP binding : methionine adenosyltransferase activity : one-carbon compound metabolism	1,033805847	0,043455791
Phypa_160592	Hypothetical protein F36H12.3 [Caenorhabditis elegans]	Pp1s23_336V6.1	AT4G10465.1			1,033989191	1,917181253

Phypa_202041	T10M13.9; GTP-binding protein (SAR1A) [Arabidopsis thaliana] : "T10M13.9; GTP-binding protein (SAR1A) [Arabidopsis thaliana]"	Pp1s7_338V6.1	AT4G02080.1	GO:0005525 : GO:0006886 : GO:0007264	GTP binding : intracellular protein transport : small GTPase mediated signal transduction	1,034573197	0,183894902
Phypa_105288		Pp1s32_160V6.1	AT5G54500.1	GO:0010181 : GO:0016491	FMN binding : oxidoreductase activity	1,038303494	0,205587327
Phypa_92280		Pp1s223_16V6.1	AT1G56190.1			1,041682601	0,274445891
Phypa_39070		Pp1s102_181V6.1	AT5G08410.1	GO:0006118 : GO:0008937	electron transport : ferredoxin reductase activity	1,052859545	0,148063034
[Phypa_124138;Phypa_123920]						1,060220003	0,05377765
Phypa_37849	contains ESTs AU062952(C51837),AU100820(C51837) [Oryza sativa (japonica cultivar-group)]	Pp1s118_101V6.1	AT5G61030.1	GO:0003676	nucleic acid binding	1,063325644	0,135036692
Phypa_224573	F2G19.31; cysteine proteinase (RD21A) / thiol protease [EC:3.4.22.-] [Arabidopsis thaliana] : "F2G19.31; cysteine proteinase (RD21A) / thiol protease [EC:3.4.22.-] [Arabidopsis thaliana]"	Pp1s292_39V6.1;Pp1s292_39V6.2 : "Pp1s292_39V6.1;Pp1s292_39V6.2" : "Pp1s292_39V6.1;Pp1s292_39V6.2 : ""Pp1s292_39V6.1;Pp1s292_39V6.2"""	AT1G47128.1	GO:0004197 : GO:0004623 : GO:0005509 : GO:0006508 : GO:0008234 : GO:0016042 : GO:0016946	calcium ion binding : cathepsin F activity : cysteine-type endopeptidase activity : cysteine-type peptidase activity : lipid catabolism : phospholipase A2 activity : proteolysis and peptidolysis	1,067380428	0,207082227
Phypa_87274		Pp1s156_35V6.1				1,067747951	1,866258621
Phypa_218993	F14M19.170; 60S acidic ribosomal protein P3 (RPP3A) [Arabidopsis thaliana] : "F14M19.170; 60S acidic ribosomal protein P3 (RPP3A) [Arabidopsis thaliana]"	Pp1s167_19V6.1	AT4G25890.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006414	intracellular : ribosome : structural constituent of ribosome : translational elongation	1,087375402	0,104504727

Phypa_105033	Major allergen Mal d 1 (Mal d I) [Malus x domestica]	Pp1s22_322V6.1	AT1G24020.1			1,089233279	0,177075297
[Phypa_154305;Phypa_218180]						1,092856288	0,157404989
Phypa_177723	MSD21.24; expressed protein [Arabidopsis thaliana] : "MSD21.24; expressed protein [Arabidopsis thaliana]"	Pp1s25_340V6.1	AT3G21865.1			1,101567388	0,223817483
Phypa_137121		Pp1s135_91V6.1	ATMG00080.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	1,10527885	0,16223979
Phypa_86357	F28H19.10; SEUSS transcriptional co-regulator [Arabidopsis thaliana] : "F28H19.10; SEUSS transcriptional co-regulator [Arabidopsis thaliana]"	Pp1s144_164V6.1;Pp1s144_165V6.1 : "Pp1s144_164V6.1;Pp1s144_165V6.1" : "Pp1s144_164V6.1;Pp1s144_165V6.1 : ""Pp1s144_164V6.1;Pp1s144_165V6.1"""				1,124262691	0,218122721
Phypa_105781	40S ribosomal protein SA (p40) [Glycine max]	Pp1s48_103V6.1	AT3G04770.2	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412 : GO:0015935	intracellular : protein biosynthesis : ribosome : small ribosomal subunit : structural constituent of ribosome	1,133696437	0,033403054
Phypa_136444	Putative H/ACA ribonucleoprotein complex subunit 1-like protein 1 [Arabidopsis thaliana]	Pp1s129_145V6.1	AT3G03920.1	GO:0006364 : GO:0007046 : GO:0019843 : GO:0030532	rRNA binding : rRNA processing : ribosome biogenesis : small nuclear ribonucleoprotein complex	1,137761354	0,264490157
[Phypa_93557;Phypa_60419]						1,139470577	0,09043026

Phypa_170048	F20H23.3; Gar1 RNA-binding region family protein [Arabidopsis thaliana] : "F20H23.3; Gar1 RNA-binding region family protein [Arabidopsis thaliana]"	Pp1s229_16V6.1	AT3G03920.1	GO:0006364 : GO:0007046 : GO:0019843 : GO:0030532	rRNA binding : rRNA processing : ribosome biogenesis : small nuclear ribonucleoprotein complex	1,14683044	0,271419019
Phypa_162383		Pp1s42_179V6.1				1,147047043	0,196276844
[Phypa_63228;Phypa_193949]						1,15086019	0,051829837
[Phypa_9031;Phypa_317]						1,152462602	0,18163082
Phypa_109882	Alpha-1,4-glucan-protein synthase [UDP-forming] 1 (UDP-glucose:protein transglucosylase 1) (UPTG 1) [Solanum tuberosum]	Pp1s66_155V6.2;Pp1s66_155V6.1;Pp1s66_156V6.1;Pp1s66_154V6.1 : "Pp1s66_155V6.2;Pp1s66_155V6.1;Pp1s66_154V6.1;Pp1s66_156V6.1" : "Pp1s66_155V6.2;Pp1s66_155V6.1;Pp1s66_156V6.1;Pp1s66_154V6.1 : ""Pp1s66_155V6.2;Pp1s66_155V6.1;Pp1s66_154V6.1;Pp1s66_156V6.1"""	AT5G15650.1	GO:0005794 : GO:0009505 : GO:0030244 : GO:0047210	Golgi apparatus : alpha-1,4-glucan-protein synthase (UDP-forming) activity : cell wall (sensu Magnoliophyta) : cellulose biosynthesis	1,160496116	0,143252745
[Phypa_225996;Phypa_226002]						1,161278844	0,071179904
Phypa_180264	F26H11.18; cold-shock DNA-binding family protein / glycine-rich protein (GRP2) [Arabidopsis thaliana] : "F26H11.18; cold-shock DNA-binding family protein / glycine-rich protein (GRP2) [Arabidopsis thaliana]"	Pp1s41_68V6.1	AT4G36020.1	GO:0003676 : GO:0003677 : GO:0006355	DNA binding : nucleic acid binding : regulation of transcription, DNA-dependent	1,168366075	0,089492887

Phypa_146516	S-adenosylmethionine synthetase 1 (Methionine adenosyltransferase 1) (AdoMet synthetase 1) [Lycopersicon esculentum]	Pp1s244_74V6.1	AT4G01850.1	GO:0004478 : GO:0005524 : GO:0006730 : GO:0048269 : GO:0048270	ATP binding : methionine adenosyltransferase activity : methionine adenosyltransferase complex : methionine adenosyltransferase regulator activity : one-carbon compound metabolism	1,168401718	0,113552243
Phypa_10989	F15M4.15; RWP-RK domain-containing protein [Arabidopsis thaliana] : "F15M4.15; RWP-RK domain-containing protein [Arabidopsis thaliana]"	Pp1s109_79V6.1	AT4G24020.1			1,17784977	0,291463196
Phypa_195542	T2N18.5; 60S ribosomal protein L12 (RPL12A) [KO:K02870] [Arabidopsis thaliana] : "T2N18.5; 60S ribosomal protein L12 (RPL12A) [KO:K02870] [Arabidopsis thaliana]"	Pp1s242_7V6.1	AT3G53430.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	1,185303807	0,19604525
Phypa_164358	60S acidic ribosomal protein P1 (L12) [Zea mays]	Pp1s68_115V6.1	AT5G24510.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006414	intracellular : ribosome : structural constituent of ribosome : translational elongation	1,189855576	0,170610756
Phypa_163991		Pp1s63_123V6.1	AT2G36620.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	1,193122387	0,140345931

Phypa_163017	F9L1.28; methyl-CpG-binding domain-containing protein [Arabidopsis thaliana] : "F9L1.28; methyl-CpG-binding domain-containing protein [Arabidopsis thaliana]"	Pp1s51_1V6.1	AT1G15340.1			1,197209716	0,103812277
Phypa_161917	T9J14.13; 40S ribosomal protein S24 (RPS24A) [KO:K02974] [Arabidopsis thaliana] : "T9J14.13; 40S ribosomal protein S24 (RPS24A) [KO:K02974] [Arabidopsis thaliana]"	Pp1s37_112V6.1	AT5G28060.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	1,19972074	0,194452837
Phypa_97924	LOC429025; similar to hypothetical protein MGC22679 [Gallus gallus] : "LOC429025; similar to hypothetical protein MGC22679 [Gallus gallus]"	Pp1s338_19V6.1	AT3G56230.1	GO:0005515	protein binding	1,205569029	1,672284484
Phypa_232889		Pp1s149_4V6.1				1,2072649	0,134659767
[Phypa_123116;Phypa_180561;Phypa_123073]						1,227712274	0,099229597
Phypa_213429	60S ribosomal protein L39	Pp1s89_150V6.1	AT4G31985.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	1,245620847	0,201741889
Phypa_128354	Probable histone deacetylase complex subunit SAP18 (Sin3-associated polypeptide, 18 kDa) [Arabidopsis thaliana]	Pp1s69_145V6.1	AT2G45640.1			1,249090791	0,263944626

Phypa_172187	hypothetical protein [Oryza sativa (japonica cultivar-group)]	Pp1s335_58V6.1;Pp1s335_58V6.2 : "Pp1s335_58V6.1;Pp1s335_58V6.2" : "Pp1s335_58V6.1;Pp1s335_58V6.2 : ""Pp1s335_58V6.1;Pp1s335_58V6.2"""	AT1G49000.1			1,263092875	0,280414015
Phypa_198079	40S ribosomal protein S28 [Zea mays]	Pp1s313_15V6.1	AT5G03850.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	1,274883866	0,21306707
Phypa_110546	Hemolytic toxin Avt-1 precursor (Avt-I) [Actineria villosa]	Pp1s319_5V6.1				1,298383236	0,085744634
[Phypa_189887;Phypa_217197]						1,30715096	0,033500291
[Phypa_126999;Phypa_77052]						1,366814494	0,180933937
Phypa_220786	T25K16.8; pyruvate dehydrogenase E1 component alpha subunit, chloroplast [EC:1.2.4.1] [KO:K00161] [Arabidopsis thaliana] : "T25K16.8; pyruvate dehydrogenase E1 component alpha subunit, chloroplast [EC:1.2.4.1] [KO:K00161] [Arabidopsis thaliana]"	Pp1s199_145V6.1	AT1G01090.1	GO:0004739 : GO:0008152 : GO:0016624	metabolism : oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor : pyruvate dehydrogenase (acetyl-transferring) activity	1,401142359	0,171016857
Phypa_214411	T24A18.40; 60S ribosomal protein L14 (RPL14B) [KO:K02875] [Arabidopsis thaliana] : "T24A18.40; 60S ribosomal protein L14 (RPL14B) [KO:K02875] [Arabidopsis thaliana]"	Pp1s101_10V6.1	AT4G27090.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	1,409368277	0,15125455

Phypa_116785	2-oxoglutarate/malate translocator, chloroplast precursor [Spinacia oleracea]	Pp1s17_363V6.1	AT5G12860.2	GO:0005215 : GO:0006814 : GO:0016020	membrane : sodium ion transport : transporter activity	1,427889347	0,152679175
Phypa_233358		Pp1s77_158V6.2;Pp1s77_158V6.1 : "Pp1s77_158V6.2;Pp1s77_158V6.1" : "Pp1s77_158V6.2;Pp1s77_158V6.1 : ""Pp1s77_158V6.2;Pp1s77_158V6.1"""	Pp1s77_158V6			1,42970705	0,133664474
Phypa_60454	Probable cytochrome c biosynthesis protein [Marchantia polymorpha]	Pp1s247_16V6.1	AT2G07681.1	GO:0006461 : GO:0008535 : GO:0015232 : GO:0015886 : GO:0016020 : GO:0017004	cytochrome c oxidase complex assembly : cytochrome complex assembly : heme transport : heme transporter activity : membrane : protein complex assembly	1,486258864	0,225836366
Phypa_229054		Pp1s71_51V6.1				1,535868764	0,153914958
Phypa_123625	F28D10.80; 50S ribosomal protein L9, chloroplast (CL9) [KO:K02939] [Arabidopsis thaliana] : "F28D10.80; 50S ribosomal protein L9, chloroplast (CL9) [KO:K02939] [Arabidopsis thaliana]"	Pp1s45_190V6.1	AT3G44890.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	1,548864245	0,1378555

Phypa_173670	F28D10.80; 50S ribosomal protein L9, chloroplast (CL9) [KO:K02939] [Arabidopsis thaliana] : "F28D10.80; 50S ribosomal protein L9, chloroplast (CL9) [KO:K02939] [Arabidopsis thaliana]"	Pp1s536_9V6.1;Pp1s536_9V6.2 : "Pp1s536_9V6.1;Pp1s536_9V6.2" : "Pp1s536_9V6.1;Pp1s536_9V6.2 : ""Pp1s536_9V6.1;Pp1s536_9V6.2"""	AT3G44890.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	1,588214159	0,241628721
Phypa_188453	T22F11.9; meprin and TRAF homology domain-containing protein / MATH domain-containing protein [Arabidopsis thaliana] : "T22F11.9; meprin and TRAF homology domain-containing protein / MATH domain-containing protein [Arabidopsis thaliana]"	Pp1s119_72V6.1	AT2G25320.1			1,598672271	0,186024994
Phypa_126323	T10D10.16; 40S ribosomal protein SA (RPSaA) [KO:K02998] [Arabidopsis thaliana] : "T10D10.16; 40S ribosomal protein SA (RPSaA) [KO:K02998] [Arabidopsis thaliana]"	Pp1s59_133V6.1	AT1G72370.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412 : GO:0015935	intracellular : protein biosynthesis : ribosome : small ribosomal subunit : structural constituent of ribosome	1,611985445	0,128229812
Phypa_163011	Transcriptional corepressor SEUSS [Arabidopsis thaliana]	Pp1s50_193V6.1;Pp1s50_192V6.1 : "Pp1s50_193V6.1;Pp1s50_192V6.1" : "Pp1s50_193V6.1;Pp1s50_192V6.1 : ""Pp1s50_193V6.1;Pp1s50_192V6.1"""		GO:0004402	histone acetyltransferase activity	1,659864187	0,305507332

Phypa_139373	MNB8.14; kinesin light chain - related [Arabidopsis thaliana] : "MNB8.14; kinesin light chain - related [Arabidopsis thaliana]"	Pp1s156_60V6.1	AT5G53080.1			1,6609267	2,158109903
Phypa_195956	F24I3.230; dyskerin, putative / nucleolar protein NAP57, putative [Arabidopsis thaliana] : "F24I3.230; dyskerin, putative / nucleolar protein NAP57, putative [Arabidopsis thaliana]"	Pp1s251_19V6.1	AT3G57150.1	GO:0003723 : GO:0004730 : GO:0006396	RNA binding : RNA processing : pseudouridylate synthase activity	1,673862576	0,201323867
Phypa_49664		Pp1s52_95V6.4;Pp1s52_95V6.2;Pp1s52_95V6.3;Pp1s52_95V6.1 : "Pp1s52_95V6.4;Pp1s52_95V6.2;Pp1s52_95V6.3;Pp1s52_95V6.1" : "Pp1s52_95V6.4;Pp1s52_95V6.2;Pp1s52_95V6.3;Pp1s52_95V6.1 : ""Pp1s52_95V6.4;Pp1s52_95V6.2;Pp1s52_95V6.3;Pp1s52_95V6.1"""	AT3G57810.3			1,689924717	2,596227884
Phypa_172970		Pp1s398_30V6.1				1,725635171	0,245757282
Phypa_184510	60S ribosomal protein L24 [Prunus avium]	Pp1s74_148V6.1	AT2G36620.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	1,729422688	0,199395895
Phypa_173651	DBP2; DEAD box RNA helicase [Candida albicans SC5314] : "DBP2; DEAD box RNA helicase [Candida albicans SC5314]"	Pp1s527_3V6.1	AT1G55150.1	GO:0003676 : GO:0004386 : GO:0005524 : GO:0008026	ATP binding : ATP-dependent helicase activity : helicase activity : nucleic acid binding	1,812184453	0,244468808

Phypa_149221	T13J8.100; YGGT family protein [Arabidopsis thaliana] : "T13J8.100; YGGT family protein [Arabidopsis thaliana]"	Pp1s293_107V6.1	AT4G27990.1	GO:0003723 : GO:0005525 : GO:0005786 : GO:0006614 : GO:0016020	GTP binding : RNA binding : SRP-dependent cotranslational protein-membrane targeting : membrane : signal recognition particle (sensu Eukaryota)	1,81608057	0,211012766
Phypa_105373	Glutamate decarboxylase (GAD) (ERT D1) [Lycopersicon esculentum]	Pp1s34_308V6.1;Pp1s34_308V6.2 : "Pp1s34_308V6.1;Pp1s34_308V6.2" : "Pp1s34_308V6.1;Pp1s34_308V6.2 : ""Pp1s34_308V6.1;Pp1s34_308V6.2"""	AT5G17330.1	GO:0004351 : GO:0006520 : GO:0006536 : GO:0016831 : GO:0030170	amino acid metabolism : carboxy-lyase activity : glutamate decarboxylase activity : glutamate metabolism : pyridoxal phosphate binding	1,869104981	3,316334724
Phypa_132849	F6A14.19; DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] : "F6A14.19; DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana]"	Pp1s98_193V6.1	AT1G18700.2			1,912723422	1,143899798
Phypa_178653	F23N11.11; golden2-like transcription factor (GLK1) [Arabidopsis thaliana] : "F23N11.11; golden2-like transcription factor (GLK1) [Arabidopsis thaliana]"	Pp1s31_317V6.1	AT5G44190.1	GO:0003677 : GO:0005634	DNA binding : nucleus	1,926651716	0,893364549
Phypa_161786		Pp1s36_39V6.1				1,928243637	0,988128185
Phypa_188533		Pp1s120_81V6.1	AT2G02050.1	GO:0003954 : GO:0005739 : GO:0006118 : GO:0008137	NADH dehydrogenase (ubiquinone) activity : NADH dehydrogenase activity : electron transport : mitochondrion	1,942481279	0,219116181

Phypa_155693	F14L17.3; CAAX amino terminal protease family protein [Arabidopsis thaliana] : "F14L17.3; CAAX amino terminal protease family protein [Arabidopsis thaliana]"	Pp1s477_8V6.1	AT1G14270.1			1,943704367	1,106915951
Phypa_107767		Pp1s195_41V6.1	AT3G29320.1	GO:0004645 : GO:0005975	carbohydrate metabolism : phosphorylase activity	1,948069096	1,058885217
Phypa_172191	T10C21.60; expressed protein [Arabidopsis thaliana] : "T10C21.60; expressed protein [Arabidopsis thaliana]"	Pp1s335_75V6.1	AT2G24070.1			1,961117268	0,999814034
Phypa_124287		Pp1s48_70V6.1	AT1G15550.1	GO:0016707	gibberellin 3-beta-dioxygenase activity	1,962831259	1,137396932
Phypa_114221	T26M18.120; expressed protein [Arabidopsis thaliana] : "T26M18.120; expressed protein [Arabidopsis thaliana]"	Pp1s9_169V6.1	AT4G22920.1			1,979384542	1,003005743
Phypa_224154	T20D1.50; spermine synthase (ACL5) [Arabidopsis thaliana] : "T20D1.50; spermine synthase (ACL5) [Arabidopsis thaliana]"	Pp1s279_58V6.1;Pp1s279_58V6.2 : "Pp1s279_58V6.1;Pp1s279_58V6.2" : "Pp1s279_58V6.1;Pp1s279_58V6.2 : ""Pp1s279_58V6.1;Pp1s279_58V6.2"""	AT5G19530.1	GO:0003824 : GO:0004766 : GO:0008757	S-adenosylmethionine-dependent methyltransferase activity : catalytic activity : spermidine synthase activity	1,983331919	0,908706903
Phypa_217801	Elongation factor TuB, chloroplast precursor (EF-TuB) [Nicotiana sylvestris]	Pp1s147_106V6.1	AT4G20360.1	GO:0003746 : GO:0003924 : GO:0005525 : GO:0006412 : GO:0006414 : GO:0008547	GTP binding : GTPase activity : protein biosynthesis : protein-synthesizing GTPase activity : translation elongation factor activity : translational elongation	1,983835101	0,162149459

Phypa_86211		Pp1s143_73V6.1	AT1G69780.1	GO:0003677 : GO:0003700 : GO:0005634 : GO:0006355	DNA binding : nucleus : regulation of transcription, DNA-dependent : transcription factor activity	1,99042809	1,071563125
Phypa_67435	F28I16.190; IPP transferase - like protein [Arabidopsis thaliana] : "F28I16.190; IPP transferase - like protein [Arabidopsis thaliana]"	Pp1s14_391V6.1	AT5G20040.1	GO:0004811 : GO:0005524 : GO:0008033	ATP binding : tRNA isopentenyltransferase activity : tRNA processing	2,000134468	1,099118114
Phypa_73379	MDB19.14; glycosyl hydrolase family 31 protein [Arabidopsis thaliana] : "MDB19.14; glycosyl hydrolase family 31 protein [Arabidopsis thaliana]"	Pp1s41_235V6.1	AT3G23640.1	GO:0004553 : GO:0004558 : GO:0005975	alpha-glucosidase activity : carbohydrate metabolism : hydrolase activity, hydrolyzing O-glycosyl compounds	2,009227037	1,075642228
Phypa_195066	MEE13.8; DNA helicase-related [Arabidopsis thaliana] : "MEE13.8; DNA helicase-related [Arabidopsis thaliana]"	Pp1s229_36V6.1	AT5G35970.1	GO:0000166 : GO:0005524 : GO:0008026 : GO:0017111	ATP binding : ATP-dependent helicase activity : nucleoside-triphosphatase activity : nucleotide binding	2,028660059	1,113264799
Phypa_170367	Plastid-specific 30S ribosomal protein 3-1, chloroplast precursor (PSRP-3 1) [Arabidopsis thaliana]	Pp1s242_42V6.1	AT1G68590.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412 : GO:0009536	intracellular : plastid : protein biosynthesis : ribosome : structural constituent of ribosome	2,036194086	0,848453462
Phypa_205598	60S ribosomal protein L31 [Perilla frutescens]	Pp1s28_306V6.1	AT2G19740.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	2,043551445	0,188007891

Phypa_131811	F12F1.30; aminomethyltransferase, putative [EC:2.1.2.10] [KO:K00605] [Arabidopsis thaliana] : "F12F1.30; aminomethyltransferase, putative [EC:2.1.2.10] [KO:K00605] [Arabidopsis thaliana]"	Pp1s91_92V6.1;Pp1s91_92V6.2 : "Pp1s91_92V6.1;Pp1s91_92V6.2" : "Pp1s91_92V6.1;Pp1s91_92V6.2 : ""Pp1s91_92V6.1;Pp1s91_92V6.2"""	AT1G11860.2	GO:0004047 : GO:0004374 : GO:0005737 : GO:0006546	aminomethyltransferase activity : cytoplasm : glycine catabolism : glycine cleavage system	2,052528381	1,410298705
Phypa_161213		Pp1s31_2V6.1		GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	2,094698191	1,189621806
Phypa_193361	F9O13.17; ferredoxin--nitrite reductase, putative [EC:1.7.7.1] [KO:K00366] [Arabidopsis thaliana] : "F9O13.17; ferredoxin--nitrite reductase, putative [EC:1.7.7.1] [KO:K00366] [Arabidopsis thaliana]"	Pp1s197_146V6.1;Pp1s197_146V6.2;Pp1s197_146V6.3;Pp1s197_146V6.4 : "Pp1s197_146V6.1;Pp1s197_146V6.2;Pp1s197_146V6.3;Pp1s197_146V6.4" : "Pp1s197_146V6.1;Pp1s197_146V6.2;Pp1s197_146V6.3;Pp1s197_146V6.4 : ""Pp1s197_146V6.1;Pp1s197_146V6.2;Pp1s197_146V6.3;Pp1s197_146V6.4"""	AT2G15620.1	GO:0006118 : GO:0016664 : GO:0042128 : GO:0048307	electron transport : ferredoxin-nitrite reductase activity : nitrate assimilation : oxidoreductase activity, acting on other nitrogenous compounds as donors, iron-sulfur protein as acceptor	2,132491112	1,19939816
Phypa_77030		Pp1s62_88V6.1				2,159575701	1,092344642

Phypa_64224	F11I11.70; pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] : "F11I11.70; pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]"	Pp1s2_193V6.2;Pp1s2_193V6.1 : "Pp1s2_193V6.2;Pp1s2_193V6.1" : "Pp1s2_193V6.2;Pp1s2_193V6.1 : ""Pp1s2_193V6.2;Pp1s2_193V6.1"""	AT4G34830.1			2,166618347	0,99293828
Phypa_170763	Photosystem II 5 kDa protein, chloroplast precursor (PSII-T) (Light-regulated unknown 11 kDa protein) [Gossypium hirsutum]	Pp1s259_76V6.1	AT1G51400.1			2,172865391	1,004300714
Phypa_67971		Pp1s16_339V6.1		GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412 : GO:0007155 : GO:0007160 : GO:0008305	cell adhesion : cell-matrix adhesion : integrin complex : intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	2,189237118	1,386240363
Phypa_159809	F3H9.29; leucine-rich repeat family protein [Arabidopsis thaliana] : "F3H9.29; leucine-rich repeat family protein [Arabidopsis thaliana]"	Pp1s15_398V6.1	AT1G28340.1			2,194716215	1,073496342
Phypa_38815		Pp1s126_84V6.1;Pp1s126_84V6.2 : "Pp1s126_84V6.1;Pp1s126_84V6.2" : "Pp1s126_84V6.1;Pp1s126_84V6.2 : ""Pp1s126_84V6.1;Pp1s126_84V6.2"""	AT3G22600.1	GO:0006869 : GO:0008289	lipid binding : lipid transport	2,203341722	1,091883302

Phypa_204471	Fructose-1,6-bisphosphatase, chloroplast precursor (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase) [Oryza sativa]	Pp1s20_373V6.1;Pp1s20_373V6.2 : "Pp1s20_373V6.1;Pp1s20_373V6.2" : "Pp1s20_373V6.1;Pp1s20_373V6.2 : ""Pp1s20_373V6.1;Pp1s20_373V6.2"""	AT3G54050.1	GO:0005975 : GO:0042132 : GO:0042578	carbohydrate metabolism : fructose-bisphosphatase activity : phosphoric ester hydrolase activity	2,212435722	0,868694067
Phypa_172162		Pp1s334_68V6.1				2,215812206	1,079177856
Phypa_49116	F2N1.18; expressed protein [Arabidopsis thaliana] : "F2N1.18; expressed protein [Arabidopsis thaliana]"	Pp1s49_42V6.1	AT4G01150.1			2,216222286	1,12646389
Phypa_107676		Pp1s183_75V6.1	AT4G04040.1	GO:0003872 : GO:0005524 : GO:0005945 : GO:0006096 : GO:0047334	6-phosphofructokinase activity : 6-phosphofructokinase complex : ATP binding : diphosphate-fructose-6-phosphate 1-phosphotransferase activity : glycolysis	2,216232777	0,843293905
Phypa_142581	F28K20.19; bifunctional aspartate kinase/homoserine dehydrogenase / AK-HSDH [EC:2.7.2.4 1.1.1.3] [KO:K00003 K00928] [Arabidopsis thaliana] : "F28K20.19; bifunctional aspartate kinase/homoserine dehydrogenase / AK-HSDH [EC:2.7.2.4 1.1.1.3] [KO:K00003 K00928] [Arabidopsis thaliana]"	Pp1s194_198V6.1	AT4G19710.2	GO:0004072 : GO:0004412 : GO:0008152 : GO:0008652 : GO:0009067 : GO:0016597	amino acid binding : amino acid biosynthesis : aspartate family amino acid biosynthesis : aspartate kinase activity : homoserine dehydrogenase activity : metabolism	2,246387482	0,985223413
Phypa_233750		Pp1s99_193V6.1	AT2G29180.1			2,251487494	0,818482637

Phypa_62234	F1N19.25; expressed protein [Arabidopsis thaliana] : "F1N19.25; expressed protein [Arabidopsis thaliana]"	Pp1s6_190V6.1	AT1G64680.1			2,274339437	1,07953918
Phypa_149544	T1M15.120; chloroplast Cpn21 protein [KO:K04078] [Arabidopsis thaliana] : "T1M15.120; chloroplast Cpn21 protein [KO:K04078] [Arabidopsis thaliana]"	Pp1s300_1V6.1	AT5G20720.3	GO:0005524 : GO:0006457	ATP binding : protein folding	2,281281948	0,161682352
Phypa_139763	F5O24.30; expressed protein [Arabidopsis thaliana] : "F5O24.30; expressed protein [Arabidopsis thaliana]"	Pp1s160_127V6.1	AT5G20140.1			2,295725584	1,033931017
[Phypa_92279;Phypa_60168]						2,302696228	0,135315537
Phypa_160688		Pp1s25_107V6.1				2,308831215	0,99084872
Phypa_171698	T12H3.7; membrane protein, putative [Arabidopsis thaliana] : "T12H3.7; membrane protein, putative [Arabidopsis thaliana]"	Pp1s307_12V6.1	AT2G06520.1	GO:0009523 : GO:0015979 : GO:0016020	membrane : photosynthesis : photosystem II	2,315163612	0,914043486

Phypa_139912	F5I10.9; mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein [Arabidopsis thaliana] : "F5I10.9; mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein [Arabidopsis thaliana]"	Pp1s161_60V6.1	AT4G00290.1	GO:0016020	membrane	2,323227882	1,422677994
[Phypa_232922;Phypa_234748]						2,332142591	0,119356342
Phypa_19688		Pp1s44_315V6.1	AT4G10465.1	GO:0030001 : GO:0046872	metal ion binding : metal ion transport	2,332994699	0,817538738
Phypa_120202	F19F24.15; homogentisate phytylprenyltransferase family protein (HPT1) / tocopherol phytyltransferase family protein (TPT1) [Arabidopsis thaliana] : "F19F24.15; homogentisate phytylprenyltransferase family protein (HPT1) / tocopherol phytyltransferase family protein (TPT1) [Arabidopsis thaliana]"	Pp1s31_108V6.2	AT4G09820.1	GO:0004659 : GO:0016021	integral to membrane : prenyltransferase activity	2,337502241	1,02521503
Phypa_159727		Pp1s15_131V6.1				2,343495369	0,974611104
Phypa_67470	hypothetical protein [Entamoeba histolytica HM-1:IMSS]	Pp1s15_4V6.1				2,347736597	0,922367513

Phypa_169245	Phosphoglycerate kinase, chloroplast precursor [Volvox carteri]	Pp1s201_82V6.1;Pp1s201_82V6.2;Pp1s201_82V6.3 : "Pp1s201_82V6.1;Pp1s201_82V6.2;Pp1s201_82V6.3" : "Pp1s201_82V6.1;Pp1s201_82V6.2;Pp1s201_82V6.3 : ""Pp1s201_82V6.1;Pp1s201_82V6.2;Pp1s201_82V6.3"""	AT3G12780.1	GO:0004618 : GO:0006096	glycolysis : phosphoglycerate kinase activity	2,376990557	0,72411406
Phypa_119729	Thylakoid lumenal 25.6 kDa protein, chloroplast precursor [Arabidopsis thaliana]	Pp1s30_39V6.1;Pp1s30_39V6.2 : "Pp1s30_39V6.1;Pp1s30_39V6.2" : "Pp1s30_39V6.1;Pp1s30_39V6.2 : ""Pp1s30_39V6.1;Pp1s30_39V6.2"""	AT3G55330.1	GO:0005509 : GO:0009654 : GO:0015979 : GO:0019898	calcium ion binding : extrinsic to membrane : oxygen evolving complex : photosynthesis	2,401768684	0,943452358
Phypa_133255	F3C3.2; expressed protein [Arabidopsis thaliana] : "F3C3.2; expressed protein [Arabidopsis thaliana]"	Pp1s101_240V6.1	AT1G32220.1			2,403982401	1,080882549
Phypa_105954	T20O10.240; mRNA-binding protein, putative [Arabidopsis thaliana] : "T20O10.240; mRNA-binding protein, putative [Arabidopsis thaliana]"	Pp1s55_140V6.1	AT3G63140.1			2,415085793	1,031185627
Phypa_160233	F2I11.160; expressed protein [Arabidopsis thaliana] : "F2I11.160; expressed protein [Arabidopsis thaliana]"	Pp1s20_112V6.1	AT5G11270.1			2,441271544	0,946096778

Phypa_177617	putative 33kDa oxygen evolvingprotein of photosystem II [Oryza sativa (japonica cultivar-group)]	Pp1s25_66V6.2;Pp1s25_66V6.1 : "Pp1s25_66V6.2;Pp1s25_66V6.1" : "Pp1s25_66V6.2;Pp1s25_66V6.1 : ""Pp1s25_66V6.2;Pp1s25_66V6.1"""	AT3G50820.1	GO:0005509 : GO:0009654 : GO:0015979 : GO:0019898 : GO:0042549	calcium ion binding : extrinsic to membrane : oxygen evolving complex : photosynthesis : photosystem II stabilization	2,449232817	1,010911942
Phypa_234701		Pp1s149_229V6.1	AT5G26700.1			2,499564886	0,145828709
Phypa_163040	F2G19.25; expressed protein [Arabidopsis thaliana] : "F2G19.25; expressed protein [Arabidopsis thaliana]"	Pp1s51_100V6.1	AT1G45688.1			2,50254178	0,813305199
Phypa_54996	K23F3.2; glucose-1-phosphate adenylyltransferase, small subunit, chloroplast (ADP-glucose pyrophosphorylase) (APS1) [EC:2.7.7.27] [KO:K00975] [Arabidopsis thaliana] : "K23F3.2; glucose-1-phosphate adenylyltransferase, small subunit, chloroplast (ADP-glucose pyrophosphorylase) (APS1) [EC:2.7.7.27] [KO:K00975] [Arabidopsis thaliana]"	Pp1s2_392V6.1	AT5G48300.1	GO:0005978 : GO:0008878 : GO:0009058 : GO:0016779	biosynthesis : glucose-1-phosphate adenylyltransferase activity : glycogen biosynthesis : nucleotidyltransferase activity	2,504348993	0,961565852
Phypa_184553		Pp1s74_222V6.2	AT1G11390.1	GO:0003747 : GO:0005737 : GO:0006415 : GO:0016149	cytoplasm : translation release factor activity : translation release factor activity, codon specific : translational termination	2,511900425	1,118189096

Phypa_214865		Pp1s107_1V6.1	AT1G74960.3	GO:0003824 : GO:0006633	catalytic activity : fatty acid biosynthesis	2,531968355	1,047131777
Phypa_169291	F27G19.60; CBS domain-containing protein [Arabidopsis thaliana] : "F27G19.60; CBS domain-containing protein [Arabidopsis thaliana]"	Pp1s203_94V6.1	AT4G27460.1			2,533149481	1,303847909
Phypa_209093	T31E10.10; katanin, putative [Arabidopsis thaliana] : "T31E10.10; katanin, putative [Arabidopsis thaliana]"	Pp1s51_233V6.1	AT2G34560.2	GO:0000166 : GO:0005524 : GO:0008568 : GO:0017111	ATP binding : microtubule-severing ATPase activity : nucleoside-triphosphatase activity : nucleotide binding	2,549063921	0,978802621
Phypa_200376	F1M20.15; geranylgeranyl reductase [Arabidopsis thaliana] : "F1M20.15; geranylgeranyl reductase [Arabidopsis thaliana]"	Pp1s425_20V6.1;Pp1s425_20V6.2 : "Pp1s425_20V6.1;Pp1s425_20V6.2" : "Pp1s425_20V6.1;Pp1s425_20V6.2 : ""Pp1s425_20V6.1;Pp1s425_20V6.2"""	AT1G74470.1	GO:0006118 : GO:0008152 : GO:0015036 : GO:0015979 : GO:0015995 : GO:0016491 : GO:0045550	chlorophyll biosynthesis : disulfide oxidoreductase activity : electron transport : geranylgeranyl reductase activity : metabolism : oxidoreductase activity : photosynthesis	2,551714897	1,171710253
Phypa_169177	Ribulose bisphosphate carboxylase/oxygenase activase 1, chloroplast precursor (RuBisCO activase 1) (RA 1) (RubisCO activase alpha form) [Larrea tridentata]	Pp1s199_129V6.1	AT2G39730.2	GO:0005524	ATP binding	2,56934309	0,806499004
Phypa_122958	F27F5.9; expressed protein [Arabidopsis thaliana] : "F27F5.9; expressed protein [Arabidopsis thaliana]"	Pp1s42_236V6.1	AT1G35180.1	GO:0016021	integral to membrane	2,569962978	0,951975226

Phypa_133026	putative alpha-amylase [Oryza sativa (japonica cultivar-group)]	Pp1s100_191V6.1	AT1G69830.1	GO:0004556 : GO:0005975	alpha-amylase activity : carbohydrate metabolism	2,582512856	0,893258929
Phypa_9234	Protein C10orf70 homolog [Mus musculus]	Pp1s268_67V6.1	AT5G51720.1			2,608413458	0,110234976
Phypa_131832	F24B22.170; ribosomal protein L17 family protein [KO:K02879] [Arabidopsis thaliana] : "F24B22.170; ribosomal protein L17 family protein [KO:K02879] [Arabidopsis thaliana]"	Pp1s91_15V6.1;Pp1s91_15V6.2 : "Pp1s91_15V6.1;Pp1s91_15V6.2" : "Pp1s91_15V6.1;Pp1s91_15V6.2 : ""Pp1s91_15V6.1;Pp1s91_15V6.2"""	AT3G54210.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	2,719905138	0,764560878
Phypa_202950	Granule-bound starch synthase 2, chloroplast precursor (Granule-bound starch synthase II) (SS II) (GBSS-II) [Solanum tuberosum]	Pp1s12_341V6.1	AT3G01180.1	GO:0009058	biosynthesis	2,720366955	1,205260873
Phypa_148610	F3L12.11; expressed protein [Arabidopsis thaliana] : "F3L12.11; expressed protein [Arabidopsis thaliana]"	Pp1s281_87V6.2;Pp1s281_87V6.1 : "Pp1s281_87V6.2;Pp1s281_87V6.1" : "Pp1s281_87V6.2;Pp1s281_87V6.1 : ""Pp1s281_87V6.2;Pp1s281_87V6.1"""	AT2G04039.1			2,730451584	0,956557333
Phypa_122112		Pp1s38_294V6.1	AT5G01920.1	GO:0004672 : GO:0004674 : GO:0005524 : GO:0006468	ATP binding : protein amino acid phosphorylation : protein kinase activity : protein serine/threonine kinase activity	2,733387709	0,996605933

Phypa_186629		Pp1s96_143V6.1	AT1G21690.1	GO:0000166 : GO:0003677 : GO:0005524 : GO:0005663 : GO:0006260 : GO:0017111	ATP binding : DNA binding : DNA replication : DNA replication factor C complex : nucleoside-triphosphatase activity : nucleotide binding	2,734224796	1,027102709
Phypa_74635	MCK7.20; malate dehydrogenase [NADP], chloroplast, putative [EC:1.1.1.82] [KO:K00051] [Arabidopsis thaliana] : "MCK7.20; malate dehydrogenase [NADP], chloroplast, putative [EC:1.1.1.82] [KO:K00051] [Arabidopsis thaliana]"	Pp1s48_151V6.1;Pp1s48_151V6.2 : "Pp1s48_151V6.1;Pp1s48_151V6.2" : "Pp1s48_151V6.1;Pp1s48_151V6.2 : ""Pp1s48_151V6.1;Pp1s48_151V6.2"""	AT5G58330.1	GO:0006100 : GO:0006108 : GO:0016491 : GO:0016615 : GO:0046554	malate dehydrogenase (NADP+) activity : malate dehydrogenase activity : malate metabolism : oxidoreductase activity : tricarboxylic acid cycle intermediate metabolism	2,752328634	1,350598216
Phypa_8123	F10A5.12; chaperone protein dnaJ-related [Arabidopsis thaliana] : "F10A5.12; chaperone protein dnaJ-related [Arabidopsis thaliana]"	Pp1s301_31V6.2;Pp1s301_31V6.1 : "Pp1s301_31V6.2;Pp1s301_31V6.1" : "Pp1s301_31V6.2;Pp1s301_31V6.1 : ""Pp1s301_31V6.2;Pp1s301_31V6.1"""	AT1G75690.1			2,754663229	0,649994791
Phypa_39045		Pp1s319_36V6.1	AT2G20260.1	GO:0006118 : GO:0009538	electron transport : photosystem I reaction center	2,7708776	1,253234744
Phypa_180785	F28K19.22; sulfate transporter (Sultr1;2) [Arabidopsis thaliana] : "F28K19.22; sulfate transporter (Sultr1;2) [Arabidopsis thaliana]"	Pp1s45_14V6.2;Pp1s45_14V6.1 : "Pp1s45_14V6.2;Pp1s45_14V6.1" : "Pp1s45_14V6.2;Pp1s45_14V6.1 : ""Pp1s45_14V6.2;Pp1s45_14V6.1"""	AT4G08620.1	GO:0008271 : GO:0008272 : GO:0016020	membrane : sulfate porter activity : sulfate transport	2,771591187	1,188651085

Phypa_214814		Pp1s106_68V6.1;Pp1s106_68V6.2 : "Pp1s106_68V6.1;Pp1s106_68V6.2" : "Pp1s106_68V6.1;Pp1s106_68V6.2 : ""Pp1s106_68V6.1;Pp1s106_68V6.2"""	AT4G03520.1	GO:0005489 : GO:0006118	electron transport : electron transporter activity	2,778228283	0,858638167
Phypa_14997		Pp1s97_248V6.1	AT3G56940.1			2,781205177	1,397727132
Phypa_106250	Probable indole-3-acetic acid-amido synthetase GH3.5 (Auxin-responsive GH3-like protein 5) (OsGH3-5) [no tax name]	Pp1s67_243V6.1;Pp1s67_243V6.2 : "Pp1s67_243V6.1;Pp1s67_243V6.2" : "Pp1s67_243V6.1;Pp1s67_243V6.2 : ""Pp1s67_243V6.1;Pp1s67_243V6.2"""	AT4G03400.1			2,787051916	1,203089237
Phypa_107070	MIO24.4; phosphoglucomutase (emb|CAB64725.1) [EC:5.4.2.2] [KO:K01835] [Arabidopsis thaliana] : "MIO24.4; phosphoglucomutase (emb|CAB64725.1) [EC:5.4.2.2] [KO:K01835] [Arabidopsis thaliana]"	Pp1s124_155V6.1	AT5G51820.1	GO:0004614 : GO:0005975 : GO:0016868	carbohydrate metabolism : intramolecular transferase activity, phosphotransferases : phosphoglucomutase activity	2,801070452	1,253201365
Phypa_161321	Photosystem II 22 kDa protein, chloroplast precursor (CP22) [Spinacia oleracea]	Pp1s31_279V6.1;Pp1s31_279V6.2 : "Pp1s31_279V6.1;Pp1s31_279V6.2" : "Pp1s31_279V6.1;Pp1s31_279V6.2 : ""Pp1s31_279V6.1;Pp1s31_279V6.2"""	AT1G44575.1			2,810307026	0,888690114
Phypa_161425		Pp1s32_341V6.1				2,817789078	1,157890439
Phypa_234825		Pp1s76_97V6.1	AT1G74030.1			2,822729826	0,887826025

Phypa_167109	T1A4.40; isoflavone reductase-related [Arabidopsis thaliana] : "T1A4.40; isoflavone reductase-related [Arabidopsis thaliana]"	Pp1s136_41V6.1	AT5G18660.1			2,861827135	0,920529187
Phypa_151734	MYJ24.5; expressed protein [Arabidopsis thaliana] : "MYJ24.5; expressed protein [Arabidopsis thaliana]"	Pp1s343_26V6.1	AT5G23060.1			2,863954067	1,111613989
Phypa_188716	T32A16.60; expressed protein [Arabidopsis thaliana] : "T32A16.60; expressed protein [Arabidopsis thaliana]"	Pp1s123_43V6.1	AT4G23890.1			2,87729454	0,793531358
Phypa_75588	L73G19.10; fibrillarin 2 (FIB2) [Arabidopsis thaliana] : "L73G19.10; fibrillarin 2 (FIB2) [Arabidopsis thaliana]"	Pp1s54_67V6.1	AT4G25630.1	GO:0003723 : GO:0005634 : GO:0006364	RNA binding : nucleus : rRNA processing	2,881298065	0,877770483

Phypa_219412	K21L19.6; non phototropic hypocotyl 1-related [Arabidopsis thaliana] : "K21L19.6; non phototropic hypocotyl 1-related [Arabidopsis thaliana]"	Pp1s174_62V6.1;Pp1s174_62V6.2 : "Pp1s174_62V6.1;Pp1s174_62V6.2" : "Pp1s174_62V6.1;Pp1s174_62V6.2 : ""Pp1s174_62V6.1;Pp1s174_62V6.2"""	AT5G58140.1	GO:0000155 : GO:0000160 : GO:0004672 : GO:0004674 : GO:0004682 : GO:0004691 : GO:0004713 : GO:0004871 : GO:0005524 : GO:0005952 : GO:0005956 : GO:0006355 : GO:0006468 : GO:0007165 : GO:0008603 : GO:0008605	ATP binding : cAMP-dependent protein kinase activity : cAMP-dependent protein kinase complex : cAMP-dependent protein kinase regulator activity : protein amino acid phosphorylation : protein kinase CK2 activity : protein kinase CK2 complex : protein kinase CK2 regulator activity : protein kinase activity : protein serine/threonine kinase activity : protein-tyrosine kinase activity : regulation of transcription, DNA-dependent : signal transducer activity : signal transduction : two-component sensor molecule activity : two-component signal transduction system (phosphorelay)	2,895903826	1,059731722
Phypa_97038	F14O13.12; beta-amylase, putative / 1,4-alpha-D-glucan maltohydrolase, putative [Arabidopsis thaliana] : "F14O13.12; beta-amylase, putative / 1,4-alpha-D-glucan maltohydrolase, putative [Arabidopsis thaliana]"	Pp1s317_42V6.1	AT3G23920.1	GO:0000272 : GO:0016161	beta-amylase activity : polysaccharide catabolism	2,900273561	1,177161455

Phypa_191307	Serine/threonine-protein kinase SNT7, chloroplast precursor (Stt7 homolog) [Arabidopsis thaliana]	Pp1s159_111V6.1	AT1G68830.1	GO:0004672 : GO:0004674 : GO:0005524 : GO:0006468	ATP binding : protein amino acid phosphorylation : protein kinase activity : protein serine/threonine kinase activity	2,902993679	1,46034348
Phypa_233731		Pp1s99_95V6.1	AT2G05070.1			2,914466858	1,152281284
Phypa_143643	F9I5.11; photosystem I reaction center subunit VI, chloroplast, putative / PSI-H, putative (PSAH2) [KO:K02695] [Arabidopsis thaliana] : "F9I5.11; photosystem I reaction center subunit VI, chloroplast, putative / PSI-H, putative (PSAH2) [KO:K02695] [Arabidopsis thaliana]"	Pp1s206_11V6.1	AT1G52230.1	GO:0009538 : GO:0015979	photosynthesis : photosystem I reaction center	2,930746794	0,770894825
Phypa_233534		Pp1s89_87V6.1	AT1G15980.1			2,932142019	1,112535596
Phypa_171132	Glycine dehydrogenase [decarboxylating], mitochondrial precursor (Glycine decarboxylase) (Glycine cleavage system P-protein) [Flaveria anomala]	Pp1s276_86V6.1	AT2G26080.1	GO:0004374 : GO:0004375 : GO:0005961 : GO:0006544	glycine cleavage system : glycine dehydrogenase (decarboxylating) activity : glycine dehydrogenase complex (decarboxylating) : glycine metabolism	2,94218111	0,782217324
Phypa_145567	F4P9.22; 50S ribosomal protein L28, chloroplast (CL28) [Arabidopsis thaliana] : "F4P9.22; 50S ribosomal protein L28, chloroplast (CL28) [Arabidopsis thaliana]"	Pp1s229_21V6.1	AT2G33450.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	2,97837615	0,562892318

Phypa_168024		Pp1s164_5V6.1	AT4G31590.1			2,983046532	1,065854669
Phypa_186944	F1N21.12; hexose transporter, putative [Arabidopsis thaliana] : "F1N21.12; hexose transporter, putative [Arabidopsis thaliana]"	Pp1s99_154V6.1	AT1G67300.1	GO:0005215 : GO:0005351 : GO:0006810 : GO:0008643 : GO:0008733 : GO:0016020 : GO:0016021	L-arabinose isomerase activity : carbohydrate transport : integral to membrane : membrane : sugar porter activity : transport : transporter activity	2,987439394	1,657818675
Phypa_190133	contains ESTs AU164153(E20361),D15 307(C0434) [Oryza sativa (japonica cultivar-group)]	Pp1s141_128V6.1	AT2G37770.2	GO:0008106 : GO:0016491	alcohol dehydrogenase (NADP+) activity : oxidoreductase activity	2,998162508	0,868139207
Phypa_206386	Elongation factor 1-gamma 3 (EF-1-gamma 3) (eEF-1B gamma 3) [no tax name]	Pp1s33_218V6.1	AT1G09640.1	GO:0003746 : GO:0004364 : GO:0005853 : GO:0006414	eukaryotic translation elongation factor 1 complex : glutathione transferase activity : translation elongation factor activity : translational elongation	3,017262936	1,122557044
Phypa_183181	F3E22.14; importin alpha-1 subunit, putative (IMPA1) [Arabidopsis thaliana] : "F3E22.14; importin alpha-1 subunit, putative (IMPA1) [Arabidopsis thaliana]"	Pp1s63_171V6.1;Pp1s63_171V6.2 : "Pp1s63_171V6.1;Pp1s63_171V6.2" : "Pp1s63_171V6.1;Pp1s63_171V6.2 : ""Pp1s63_171V6.1;Pp1s63_171V6.2"""	AT3G06720.1	GO:0006606 : GO:0006886 : GO:0008565	intracellular protein transport : protein transporter activity : protein-nucleus import	3,020274162	1,241245151
Phypa_121324	T24P13.2; aspartate/glutamate/uridylate kinase family protein [Arabidopsis thaliana] : "T24P13.2; aspartate/glutamate/uridylate kinase family protein [Arabidopsis thaliana]"	Pp1s35_95V6.1	AT1G26640.1	GO:0008652	amino acid biosynthesis	3,026017427	0,785488605

Phypa_121744	MCK7.12; unknown protein (sp|P72777) -related [Arabidopsis thaliana] : "MCK7.12; unknown protein (sp|P72777) -related [Arabidopsis thaliana]"	Pp1s37_298V6.1	AT5G58250.1			3,030901194	1,003838301
Phypa_18875	F21B7.21; photosystem II family protein [KO:K02724] [Arabidopsis thaliana] : "F21B7.21; photosystem II family protein [KO:K02724] [Arabidopsis thaliana]"	Pp1s131_184V6.1	AT1G03600.1			3,04338479	1,122720838
Phypa_219762	MJC20.12; luminal binding protein 2 precursor (BiP-2) (AtBP2) [Arabidopsis thaliana] : "MJC20.12; luminal binding protein 2 precursor (BiP-2) (AtBP2) [Arabidopsis thaliana]"	Pp1s181_3V6.1	AT5G42020.1	GO:0005524	ATP binding	3,060586452	0,112783812
Phypa_126454		Pp1s59_287V6.1	AT5G27820.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	3,090577364	0,922822416
Phypa_166875	F13O11.16; RNA polymerase sigma subunit SigA (sigA) / sigma factor 1 (SIG1) [Arabidopsis thaliana] : "F13O11.16; RNA polymerase sigma subunit SigA (sigA) / sigma factor 1 (SIG1) [Arabidopsis thaliana]"	Pp1s126_141V6.2;Pp1s126_141V6.1 : "Pp1s126_141V6.2;Pp1s126_141V6.1" : "Pp1s126_141V6.2;Pp1s126_141V6.1 : ""Pp1s126_141V6.2;Pp1s126_141V6.1"""	AT1G64860.1	GO:0003677 : GO:0003700 : GO:0004197 : GO:0006352 : GO:0006355 : GO:0006508 : GO:0016987	DNA binding : cysteine-type endopeptidase activity : proteolysis and peptidolysis : regulation of transcription, DNA-dependent : sigma factor activity : transcription factor activity : transcription initiation	3,091579437	1,491708875

Phypa_123406	T9L3.40; CARBONIC ANHYDRASE 2 [EC:4.2.1.1] [KO:K01672] [Arabidopsis thaliana] : "T9L3.40; CARBONIC ANHYDRASE 2 [EC:4.2.1.1] [KO:K01672] [Arabidopsis thaliana]"	Pp1s44_343V6.1	AT1G23730.1	GO:0004089 : GO:0008270 : GO:0015976	carbon utilization : carbonate dehydratase activity : zinc ion binding	3,11975193	0,746918261
[Phypa_70006;Phypa_70007;Phypa_103101]						3,12400651	0,943232834
Phypa_212016		Pp1s75_141V6.1	AT1G06680.1	GO:0005509 : GO:0009654 : GO:0015979 : GO:0019898	calcium ion binding : extrinsic to membrane : oxygen evolving complex : photosynthesis	3,12895298	1,191602111
Phypa_161637	mucin-associated surface protein (MASP), putative [Trypanosoma cruzi]	Pp1s34_349V6.1				3,137648582	1,386192799
Phypa_188969	Rac-like GTP-binding protein 5 (OsRac5) (GTPase protein RacD) [no tax name]	Pp1s126_126V6.1;Pp1s126_126V6.2 : "Pp1s126_126V6.1;Pp1s126_126V6.2" : "Pp1s126_126V6.1;Pp1s126_126V6.2 : ""Pp1s126_126V6.1;Pp1s126_126V6.2"""	AT4G35020.2	GO:0005525 : GO:0007264 : GO:0015031	GTP binding : protein transport : small GTPase mediated signal transduction	3,175606012	0,972184479

Phypa_104532	F24D7.15; GMP synthase [glutamine-hydrolyzing], putative / glutamine amidotransferase, putative [EC:6.3.5.2] [KO:K01951] [Arabidopsis thaliana] : "F24D7.15; GMP synthase [glutamine-hydrolyzing], putative / glutamine amidotransferase, putative [EC:6.3.5.2] [KO:K01951] [Arabidopsis thaliana]"	Pp1s8_124V6.1	AT1G63660.1	GO:0003824 : GO:0003922 : GO:0005524 : GO:0006164 : GO:0006177	ATP binding : GMP biosynthesis : GMP synthase (glutamine-hydrolyzing) activity : catalytic activity : purine nucleotide biosynthesis	3,198376894	0,904854357
Phypa_37483	50S ribosomal protein L29, chloroplast precursor [Zea mays]	Pp1s89_23V6.1	AT5G65220.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	3,241495848	0,802928925
Phypa_227616	F4F7.35; acidic ribosomal protein P0-related [Arabidopsis thaliana] : "F4F7.35; acidic ribosomal protein P0-related [Arabidopsis thaliana]"	Pp1s431_4V6.1	AT1G25260.1			3,243784428	1,709215641
Phypa_151587	Tetrapyrrole-binding protein, chloroplast precursor (Genomes uncoupled 4) [Arabidopsis thaliana]	Pp1s340_26V6.1;Pp1s340_26V6.2 : "Pp1s340_26V6.1;Pp1s340_26V6.2" : "Pp1s340_26V6.1;Pp1s340_26V6.2 : ""Pp1s340_26V6.1;Pp1s340_26V6.2"""	AT3G59400.1			3,330502272	1,197143555

Phypa_113929	T26D22.8; acetyl-CoA carboxylase [EC:6.3.4.14] [KO:K01946] [Arabidopsis thaliana] : "T26D22.8; acetyl-CoA carboxylase [EC:6.3.4.14] [KO:K01946] [Arabidopsis thaliana]"	Pp1s8_168V6.1	AT5G35360.1	GO:0004075 : GO:0005524 : GO:0008152 : GO:0009343 : GO:0016874	ATP binding : biotin carboxylase activity : biotin carboxylase complex : ligase activity : metabolism	3,335155487	1,072209239
Phypa_146278	Glutamine synthetase, chloroplast precursor (Glutamate--ammonia ligase) (GS2) [Chlamydomonas reinhardtii]	Pp1s241_33V6.2;Pp1s241_33V6.1 : "Pp1s241_33V6.2;Pp1s241_33V6.1" : "Pp1s241_33V6.2;Pp1s241_33V6.1 : ""Pp1s241_33V6.2;Pp1s241_33V6.1"""	AT5G35630.1	GO:0004356 : GO:0006542 : GO:0006807	glutamate-ammonia ligase activity : glutamine biosynthesis : nitrogen compound metabolism	3,340420246	1,212805152
Phypa_167268		Pp1s141_133V6.1				3,385916233	0,95651722
Phypa_225446	T25K16.8; pyruvate dehydrogenase E1 component alpha subunit, chloroplast [EC:1.2.4.1] [KO:K00161] [Arabidopsis thaliana] : "T25K16.8; pyruvate dehydrogenase E1 component alpha subunit, chloroplast [EC:1.2.4.1] [KO:K00161] [Arabidopsis thaliana]"	Pp1s318_24V6.1	AT1G01090.1	GO:0004739 : GO:0008152 : GO:0016624	metabolism : oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor : pyruvate dehydrogenase (acetyl-transferring) activity	3,38735652	1,343382716
Phypa_146491	Glutamate--cysteine ligase, chloroplast precursor (Gamma-glutamylcysteine synthetase) (Gamma-ECS) (GCS) [Lycopersicon esculentum]	Pp1s244_44V6.1	AT4G23100.3	GO:0004357 : GO:0006750 : GO:0009507 : GO:0017109	chloroplast : glutamate-cysteine ligase activity : glutamate-cysteine ligase complex : glutathione biosynthesis	3,393157005	0,654130757

Phypa_172419	T5F17.40; expressed protein [Arabidopsis thaliana] : "T5F17.40; expressed protein [Arabidopsis thaliana]"	Pp1s351_33V6.1;Pp1s351_33V6.2 : "Pp1s351_33V6.1;Pp1s351_33V6.2" : "Pp1s351_33V6.1;Pp1s351_33V6.2 : ""Pp1s351_33V6.1;Pp1s351_33V6.2"""	AT4G28590.1	GO:0004812 : GO:0005524 : GO:0006418	ATP binding : tRNA aminoacylation for protein translation : tRNA ligase activity	3,398118019	1,065585375
Phypa_232286		Pp1s72_208V6.1	AT3G27850.1			3,42635107	1,031666636
Phypa_132172	MZB10.8; expressed protein [Arabidopsis thaliana] : "MZB10.8; expressed protein [Arabidopsis thaliana]"	Pp1s93_122V6.1	AT3G09050.1			3,42936182	0,983668685
Phypa_171725	F10A5.13; glycosyl hydrolase family 9 protein [Arabidopsis thaliana] : "F10A5.13; glycosyl hydrolase family 9 protein [Arabidopsis thaliana]"	Pp1s308_21V6.1	AT1G75680.1	GO:0004553 : GO:0005975 : GO:0008810	carbohydrate metabolism : cellulase activity : hydrolase activity, hydrolyzing O-glycosyl compounds	3,442275047	1,054113388
Phypa_145834	F3G5.4; adenylate kinase family protein [Arabidopsis thaliana] : "F3G5.4; adenylate kinase family protein [Arabidopsis thaliana]"	Pp1s234_106V6.1	AT2G37250.1	GO:0004017 : GO:0005524 : GO:0006139 : GO:0019201	ATP binding : adenylate kinase activity : nucleobase, nucleoside, nucleotide and nucleic acid metabolism : nucleotide kinase activity	3,487700939	1,024454594

Phypa_170161	T8P21.5; acetyl co-enzyme A carboxylase carboxyltransferase alpha subunit family [EC:6.4.1.2] [KO:K01962] [Arabidopsis thaliana] : "T8P21.5; acetyl co-enzyme A carboxylase carboxyltransferase alpha subunit family [EC:6.4.1.2] [KO:K01962] [Arabidopsis thaliana]"	Pp1s234_46V6.1	AT2G38040.1	GO:0003989 : GO:0006633 : GO:0009317	acetyl-CoA carboxylase activity : acetyl-CoA carboxylase complex : fatty acid biosynthesis	3,493773222	1,148498416
Phypa_177431	T6H20.230; chloroplast outer envelope protein, putative [Arabidopsis thaliana] : "T6H20.230; chloroplast outer envelope protein, putative [Arabidopsis thaliana]"	Pp1s23_111V6.1	AT3G46740.1	GO:0019867	outer membrane	3,495382786	0,960930586

Phypa_214514	Farnesyl pyrophosphate synthetase (FPP synthetase) (FPS) (Farnesyl diphosphate synthetase) [Includes: Dimethylallyltranstransferase ; Geranyltranstransferase] [Zea mays] : "Farnesyl pyrophosphate synthetase (FPP synthetase) (FPS) (Farnesyl diphosphate synthetase) [Includes: Dimethylallyltranstransferase ; Geranyltranstransferase] [Zea mays]"	Pp1s101_225V6.1	AT4G17190.1	GO:0008299	isoprenoid biosynthesis	3,512123346	1,50396204
Phypa_196472	Aquaporin PIP2.1 (Plasma membrane intrinsic protein 2a) (PIP2a) [Arabidopsis thaliana]	Pp1s267_61V6.2;Pp1s267_61V6.1 : "Pp1s267_61V6.2;Pp1s267_61V6.1" : "Pp1s267_61V6.2;Pp1s267_61V6.1 : ""Pp1s267_61V6.2;Pp1s267_61V6.1"""	AT3G53420.2	GO:0005215 : GO:0006810 : GO:0016020	membrane : transport : transporter activity	3,531415224	0,958926678
Phypa_223504	T20K24.9; metaxin-related [Arabidopsis thaliana] : "T20K24.9; metaxin-related [Arabidopsis thaliana]"	Pp1s261_53V6.1	AT2G19080.1			3,539267778	1,143380642

Phypa_70542	1,4-dihydroxy-2-naphthoate octaprenyltransferase (DHNA-octaprenyltransferase) [Haemophilus influenzae]	Pp1s28_259V6.1		GO:0004659 : GO:0016021	integral to membrane : prenyltransferase activity	3,545372009	0,805571973
Phypa_135818	T22H22.19; thylakoid lumen 18.3 kDa protein [Arabidopsis thaliana] : "T22H22.19; thylakoid lumen 18.3 kDa protein [Arabidopsis thaliana]"	Pp1s123_97V6.1	AT1G54780.1			3,605100393	0,832402468
Phypa_234745		Pp1s153_138V6.1	AT5G58470.2			3,616056919	1,483640432
Phypa_152300	F1N19.8; ribosomal protein S6 family protein [Arabidopsis thaliana] : "F1N19.8; ribosomal protein S6 family protein [Arabidopsis thaliana]"	Pp1s359_29V6.1	AT1G64510.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	3,622704983	1,011321783
Phypa_146248	contains ESTs AU078383(S13149),AU078384(S13149) [Oryza sativa (japonica cultivar-group)]	Pp1s241_86V6.2;Pp1s241_86V6.1 : "Pp1s241_86V6.2;Pp1s241_86V6.1" : "Pp1s241_86V6.2;Pp1s241_86V6.1 : ""Pp1s241_86V6.2;Pp1s241_86V6.1"""	AT1G44575.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting	3,624768019	1,159210801
Phypa_233516		Pp1s86_234V6.1	AT5G64300.1			3,636280298	0,908271074
Phypa_172816		Pp1s382_29V6.1				3,648622513	1,110397696
Phypa_159087		Pp1s9_245V6.1				3,652681828	1,704514623
Phypa_206025	F5I10.7; sugar transporter family protein [Arabidopsis thaliana] : "F5I10.7; sugar transporter family protein [Arabidopsis thaliana]"	Pp1s31_182V6.1	AT4G00370.1	GO:0005215 : GO:0006810 : GO:0016021	integral to membrane : transport : transporter activity	3,678761244	0,919176459

Phypa_36025	ATP synthase delta chain, chloroplast precursor [Nicotiana tabacum]	Pp1s10_393V6.1	AT4G09650.1	GO:0003936 : GO:0015986 : GO:0016469 : GO:0046933 : GO:0046961	ATP synthesis coupled proton transport : hydrogen-transporting ATP synthase activity, rotational mechanism : hydrogen-transporting ATPase activity, rotational mechanism : hydrogen-transporting two-sector ATPase activity : proton-transporting two-sector ATPase complex	3,694586277	0,754627287
Phypa_105543	Acetolactate synthase II, chloroplast precursor (Acetohydroxy-acid synthase II) (ALS II) [Nicotiana tabacum]	Pp1s40_15V6.2;Pp1s40_15V6.1 : "Pp1s40_15V6.2;Pp1s40_15V6.1" : "Pp1s40_15V6.2;Pp1s40_15V6.1 : ""Pp1s40_15V6.2;Pp1s40_15V6.1"""	AT3G48560.1	GO:0003984 : GO:0009082	acetolactate synthase activity : branched chain family amino acid biosynthesis	3,69863677	0,847334385
Phypa_179159	F24C7.16; phosphoglycolate phosphatase, putative [Arabidopsis thaliana] : "F24C7.16; phosphoglycolate phosphatase, putative [Arabidopsis thaliana]"	Pp1s34_237V6.2;Pp1s34_237V6.1 : "Pp1s34_237V6.2;Pp1s34_237V6.1" : "Pp1s34_237V6.2;Pp1s34_237V6.1 : ""Pp1s34_237V6.2;Pp1s34_237V6.1"""	AT5G36700.2	GO:0003824 : GO:0003869 : GO:0008152 : GO:0016787 : GO:0016791	4-nitrophenylphosphatase activity : catalytic activity : hydrolase activity : metabolism : phosphoric monoester hydrolase activity	3,705595732	1,146377683
Phypa_161218		Pp1s31_14V6.1				3,708469868	1,342283845
Phypa_48630	contains ESTs D24537(R2125),AU095459(R2125) [Oryza sativa (japonica cultivar-group)]	Pp1s93_152V6.1	AT1G68660.1			3,729427099	0,937994123
Phypa_109427	Photosystem I reaction center subunit II, chloroplast precursor (Photosystem I 20 kDa subunit) (PSI-D) [Spinacia oleracea]	Pp1s4_321V6.1	AT1G03130.1	GO:0009538 : GO:0015979	photosynthesis : photosystem I reaction center	3,732622385	0,691871643

Phypa_85102	contains EST C73370(E3926) [Oryza sativa (japonica cultivar-group)]	Pp1s131_3V6.2;Pp1s131_3V6.1 : "Pp1s131_3V6.2;Pp1s131_3V6.1" : "Pp1s131_3V6.2;Pp1s131_3V6.1 : ""Pp1s131_3V6.2;Pp1s131_3V6.1"""	AT1G04920.1			3,749991179	0,959481001
Phypa_155608	MZA15.23; mitochondrial carrier protein family [KO:K03454] [Arabidopsis thaliana] : "MZA15.23; mitochondrial carrier protein family [KO:K03454] [Arabidopsis thaliana]"	Pp1s475_26V6.1	AT5G46800.1	GO:0005488 : GO:0005743 : GO:0006810 : GO:0016020	binding : membrane : mitochondrial inner membrane : transport	3,784362078	0,991891563
Phypa_137893	F9L11.15; ribosomal protein L11 family protein [KO:K02867] [Arabidopsis thaliana] : "F9L11.15; ribosomal protein L11 family protein [KO:K02867] [Arabidopsis thaliana]"	Pp1s141_43V6.1	AT1G32990.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	3,791167498	0,727704227
Phypa_47696	Photosystem I reaction center subunit III, chloroplast precursor (Light-harvesting complex I 17 kDa protein) (PSI-F) [Flaveria trinervia]	Pp1s121_54V6.1	AT1G31330.1	GO:0009538 : GO:0015979	photosynthesis : photosystem I reaction center	3,802958012	1,176567674
Phypa_114083	F2N1.18; expressed protein [Arabidopsis thaliana] : "F2N1.18; expressed protein [Arabidopsis thaliana]"	Pp1s9_38V6.1	AT4G01150.1			3,83041358	1,076911926

Phypa_132902	T1E3.100; ACT domain-containing protein [Arabidopsis thaliana] : "T1E3.100; ACT domain-containing protein [Arabidopsis thaliana]"	Pp1s99_201V6.1	AT5G04740.1			3,850586891	1,190964699
Phypa_39458	T20K14.140; biotin carboxyl carrier protein 2 (BCCP2) [Arabidopsis thaliana] : "T20K14.140; biotin carboxyl carrier protein 2 (BCCP2) [Arabidopsis thaliana]"	Pp1s54_77V6.1	AT5G15530.1	GO:0003989 : GO:0006633 : GO:0009317 : GO:0009374	acetyl-CoA carboxylase activity : acetyl-CoA carboxylase complex : biotin binding : fatty acid biosynthesis	3,854632139	0,878220141
Phypa_218647	F28P10.130; chlorophyll A-B binding protein / LHCI type I (CAB) [Arabidopsis thaliana] : "F28P10.130; chlorophyll A-B binding protein / LHCI type I (CAB) [Arabidopsis thaliana]"	Pp1s161_32V6.1;Pp1s161_32V6.2 : "Pp1s161_32V6.1;Pp1s161_32V6.2" : "Pp1s161_32V6.1;Pp1s161_32V6.2 : ""Pp1s161_32V6.1;Pp1s161_32V6.2"""	AT3G54890.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting	3,87296772	0,939522386
Phypa_54314		Pp1s38_249V6.2;Pp1s38_249V6.1 : "Pp1s38_249V6.2;Pp1s38_249V6.1" : "Pp1s38_249V6.2;Pp1s38_249V6.1 : ""Pp1s38_249V6.2;Pp1s38_249V6.1"""	AT5G56940.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	3,884453297	0,888321519
Phypa_49044	50S ribosomal protein L12, chloroplast precursor (CL12) [Nicotiana tabacum]	Pp1s215_82V6.1	AT3G27830.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	3,896537542	1,04534483
Phypa_233510		Pp1s86_214V6.1	AT2G25930.1			3,898057699	0,944869637

Phypa_186228	Zeaxanthin epoxidase, chloroplast precursor [Lycopersicon esculentum]	Pp1s91_16V6.1	AT5G67030.1	GO:0004497 : GO:0006118 : GO:0006725 : GO:0008152 : GO:0016491	aromatic compound metabolism : electron transport : metabolism : monooxygenase activity : oxidoreductase activity	3,900824547	1,942286849
Phypa_161232	T12H3.7; membrane protein, putative [Arabidopsis thaliana] : "T12H3.7; membrane protein, putative [Arabidopsis thaliana]"	Pp1s31_66V6.1;Pp1s31_66V6.2 : "Pp1s31_66V6.1;Pp1s31_66V6.2" : "Pp1s31_66V6.1;Pp1s31_66V6.2 : ""Pp1s31_66V6.1;Pp1s31_66V6.2"""	AT2G06520.1			3,903031111	0,853463113
Phypa_166457	T12H3.7; membrane protein, putative [Arabidopsis thaliana] : "T12H3.7; membrane protein, putative [Arabidopsis thaliana]"	Pp1s116_110V6.1	AT2G06520.1			3,906915426	0,995961726
Phypa_80169	Oleosin Bn-III (BnIII) [Brassica napus]	Pp1s84_138V6.1	AT4G25140.1			3,927064657	0,839982212
Phypa_138970	F17F16.5; ribosomal protein L20 family protein [KO:K02887] [Arabidopsis thaliana] : "F17F16.5; ribosomal protein L20 family protein [KO:K02887] [Arabidopsis thaliana]"	Pp1s152_64V6.1	AT1G16740.1	GO:0003723 : GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	RNA binding : intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	3,932056427	0,732707679
Phypa_224024	Guanine nucleotide-binding protein beta subunit-like protein [Chlamydomonas reinhardtii]	Pp1s276_2V6.1	AT1G48630.1			3,932060242	0,921507657

Phypa_156993	F24G24.140; chlorophyll A-B binding protein CP26, chloroplast / light-harvesting complex II protein 5 / LHCIIc (LHCB5) [Arabidopsis thaliana] : "F24G24.140; chlorophyll A-B binding protein CP26, chloroplast / light-harvesting complex II protein 5 / LHCIIc (LHCB5) [Arabidopsis thaliana]"	Pp1s628_7V6.1	AT4G10340.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting	3,932919025	1,151229024
Phypa_170304		Pp1s240_74V6.1				3,94358182	0,776814282
Phypa_224311	T23E18.8; prolyl oligopeptidase, putative / prolyl endopeptidase, putative / post-proline cleaving enzyme, putative [EC:3.4.21.26] [Arabidopsis thaliana] : "T23E18.8; prolyl oligopeptidase, putative / prolyl endopeptidase, putative / post-proline cleaving enzyme, putative [EC:3.4.21.26] [Arabidopsis thaliana]"	Pp1s283_60V6.1;Pp1s283_60V6.2 : "Pp1s283_60V6.1;Pp1s283_60V6.2" : "Pp1s283_60V6.1;Pp1s283_60V6.2 : ""Pp1s283_60V6.1;Pp1s283_60V6.2"""	AT1G76140.1	GO:0003824 : GO:0004252 : GO:0004287 : GO:0006508 : GO:0008236	catalytic activity : prolyl oligopeptidase activity : proteolysis and peptidolysis : serine-type endopeptidase activity : serine-type peptidase activity	3,965739012	1,344697714

Phypa_115965	T20K14.140; biotin carboxyl carrier protein 2 (BCCP2) [Arabidopsis thaliana] : "T20K14.140; biotin carboxyl carrier protein 2 (BCCP2) [Arabidopsis thaliana]"	Pp1s15_270V6.1;Pp1s15_270V6.2 : "Pp1s15_270V6.1;Pp1s15_270V6.2" : "Pp1s15_270V6.1;Pp1s15_270V6.2 : ""Pp1s15_270V6.1;Pp1s15_270V6.2"""	AT5G16390.1	GO:0003989 : GO:0006633 : GO:0009317 : GO:0009374	acetyl-CoA carboxylase activity : acetyl-CoA carboxylase complex : biotin binding : fatty acid biosynthesis	3,977454185	0,931703448
Phypa_147884	contains ESTs AU101298(E4372),D48939(S15524) similar to Arabidopsis thaliana chromosome 1, F25A4.30 unknown protein [Oryza sativa (japonica cultivar-group)]	Pp1s268_34V6.1	AT1G74730.1			3,998577356	0,706467628
Phypa_142913	T25B24.12; chlorophyll A-B binding protein / LHCI type III (LHCA3.1) [Arabidopsis thaliana] : "T25B24.12; chlorophyll A-B binding protein / LHCI type III (LHCA3.1) [Arabidopsis thaliana]"	Pp1s197_123V6.1	AT1G61520.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting	4,011862278	0,878054321
Phypa_216605	F14F8.30; reversibly glycosylated polypeptide-3 [EC:2.4.1.112] [Arabidopsis thaliana] : "F14F8.30; reversibly glycosylated polypeptide-3 [EC:2.4.1.112] [Arabidopsis thaliana]"	Pp1s131_34V6.1	AT5G15650.1	GO:0005794 : GO:0009505 : GO:0030244 : GO:0047210	Golgi apparatus : alpha-1,4-glucan-protein synthase (UDP-forming) activity : cell wall (sensu Magnoliophyta) : cellulose biosynthesis	4,041377068	0,832502484

Phypa_222981	Omega-6 fatty acid desaturase, chloroplast precursor [Arabidopsis thaliana]	Pp1s246_57V6.1;Pp1s246_57V6.2 : "Pp1s246_57V6.1;Pp1s246_57V6.2" : "Pp1s246_57V6.1;Pp1s246_57V6.2 : ""Pp1s246_57V6.1;Pp1s246_57V6.2"""	AT4G30950.1	GO:0006636 : GO:0016020 : GO:0016215 : GO:0016491 : GO:0016717 : GO:0018688 : GO:0018689 : GO:0042389	CoA desaturase activity : DDT 2,3-dioxygenase activity : fatty acid desaturation : membrane : naphthalene disulfonate 1,2-dioxygenase activity : omega-3 fatty acid desaturase activity : oxidoreductase activity : oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water	4,059988976	1,098104954
Phypa_188035	T2P4.16; uroporphyrinogen decarboxylase, putative / UPD, putative [EC:4.1.1.37] [KO:K01599] [Arabidopsis thaliana] : "T2P4.16; uroporphyrinogen decarboxylase, putative / UPD, putative [EC:4.1.1.37] [KO:K01599] [Arabidopsis thaliana]"	Pp1s114_123V6.1;Pp1s114_123V6.2 : "Pp1s114_123V6.1;Pp1s114_123V6.2" : "Pp1s114_123V6.1;Pp1s114_123V6.2 : ""Pp1s114_123V6.1;Pp1s114_123V6.2"""	AT2G40490.1	GO:0004853 : GO:0006779	porphyrin biosynthesis : uroporphyrinogen decarboxylase activity	4,065576077	1,198684692
Phypa_151133	F2A19.70; chlorophyll A-B binding protein (LHCA2) [Arabidopsis thaliana] : "F2A19.70; chlorophyll A-B binding protein (LHCA2) [Arabidopsis thaliana]"	Pp1s330_39V6.1	AT3G61470.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting	4,078958988	0,408275932
Phypa_158682		Pp1s4_282V6.1		GO:0016998	cell wall catabolism	4,095529079	2,037474155

Phypa_125345	F22K18.180; glucose-6-phosphate isomerase, putative [EC:5.3.1.9] [KO:K01810] [Arabidopsis thaliana] : "F22K18.180; glucose-6-phosphate isomerase, putative [EC:5.3.1.9] [KO:K01810] [Arabidopsis thaliana]"	Pp1s54_320V6.1;Pp1s54_320V6.2 : "Pp1s54_320V6.1;Pp1s54_320V6.2" : "Pp1s54_320V6.1;Pp1s54_320V6.2 : ""Pp1s54_320V6.1;Pp1s54_320V6.2"""	AT4G24620.1	GO:0004347 : GO:0006094 : GO:0006096	gluconeogenesis : glucose-6-phosphate isomerase activity : glycolysis	4,113488197	0,98780781
Phypa_29066	F16M14.7; chloroplast 30S ribosomal protein S31 (PSRP4) [Arabidopsis thaliana] : "F16M14.7; chloroplast 30S ribosomal protein S31 (PSRP4) [Arabidopsis thaliana]"	Pp1s29_213V6.1	AT2G38140.1			4,148471832	0,45970726
Phypa_107142	F19K16.17; oxidoreductase family protein [Arabidopsis thaliana] : "F19K16.17; oxidoreductase family protein [Arabidopsis thaliana]"	Pp1s133_69V6.1	AT1G79870.1	GO:0006564 : GO:0016616	L-serine biosynthesis : oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	4,172647476	2,689101934
Phypa_9752	Photosystem II reaction center W protein, chloroplast precursor (PSII 6.1 kDa protein) [Spinacia oleracea]	Pp1s185_110V6.1	AT2G30570.1			4,182356358	0,800451756
Phypa_215021		Pp1s109_97V6.1	AT1G22840.1	GO:0005489 : GO:0006118	electron transport : electron transporter activity	4,190573215	0,579405069

Phypa_165025	F9G14.120; pseudo-response regulator, APRR7 (APRR1/TOC1 family) [Arabidopsis thaliana] : "F9G14.120; pseudo-response regulator, APRR7 (APRR1/TOC1 family) [Arabidopsis thaliana]"	Pp1s81_131V6.3;Pp1s81_131V6.2;Pp1s81_131V6.1 : "Pp1s81_131V6.3;Pp1s81_131V6.2;Pp1s81_131V6.1" : "Pp1s81_131V6.3;Pp1s81_131V6.2;Pp1s81_131V6.1 : ""Pp1s81_131V6.3;Pp1s81_131V6.2;Pp1s81_131V6.1"""	AT5G02810.1	GO:0000156 : GO:0000160 : GO:0003677 : GO:0006355	DNA binding : regulation of transcription, DNA-dependent : two-component response regulator activity : two-component signal transduction system (phosphorelay)	4,207251549	1,115615726
[Phypa_147651;Phypa_110442]						4,208426952	0,801518142
Phypa_58629	MFL8.11; ribosomal protein L3 family protein [KO:K02906] [Arabidopsis thaliana] : "MFL8.11; ribosomal protein L3 family protein [KO:K02906] [Arabidopsis thaliana]"	Pp1s117_86V6.1	AT2G43030.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	4,226840973	0,966731548
Phypa_147622	T9J22.17; cytochrome b6f complex subunit (petM), putative [Arabidopsis thaliana] : "T9J22.17; cytochrome b6f complex subunit (petM), putative [Arabidopsis thaliana]"	Pp1s263_33V6.1	AT2G26500.2			4,244388103	0,559425533
Phypa_171916	T6H20.230; chloroplast outer envelope protein, putative [Arabidopsis thaliana] : "T6H20.230; chloroplast outer envelope protein, putative [Arabidopsis thaliana]"	Pp1s317_51V6.1	AT3G46740.1	GO:0019867	outer membrane	4,259309769	0,605213284

Phypa_126815	Triosephosphate isomerase, chloroplast precursor (TIM) (Triose-phosphate isomerase) [Fragaria x ananassa]	Pp1s61_72V6.1	AT2G21170.1	GO:0004807 : GO:0008152	metabolism : triose-phosphate isomerase activity	4,261455059	0,740836442
Phypa_121098	Cytochrome b6-f complex iron-sulfur subunit 1, chloroplast precursor (Rieske iron-sulfur protein 1) (Plastohydroquinone:plastocyanin oxidoreductase iron-sulfur protein 1) (ISP 1) (RISP 1) [Nicotiana tabacum]	Pp1s35_78V6.1	AT4G03280.1	GO:0006118 : GO:0008121 : GO:0009496 : GO:0016020 : GO:0016491 : GO:0045285	electron transport : membrane : oxidoreductase activity : plastoquinol-plastocyanin reductase activity : ubiquinol-cytochrome-c reductase activity : ubiquinol-cytochrome-c reductase complex	4,283715248	0,948385
Phypa_6728	FCAALL.30; lil3 protein [Arabidopsis thaliana] : "FCAALL.30; lil3 protein [Arabidopsis thaliana]"	Pp1s336_22V6.1	AT4G17600.1			4,289900303	0,809457123
Phypa_115069	Ribulose bisphosphate carboxylase small chain, chloroplast precursor (RuBisCO small subunit) [Marchantia paleacea]	Pp1s12_231V6.1	AT1G67090.1	GO:0009573 : GO:0015977 : GO:0016984	carbon utilization by fixation of carbon dioxide : ribulose bisphosphate carboxylase complex (sensu Magnoliophyta) : ribulose-bisphosphate carboxylase activity	4,30873251	0,875638425
Phypa_206666	T10I14.1; ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein [Arabidopsis thaliana] : "T10I14.1; ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein [Arabidopsis thaliana]"	Pp1s34_345V6.1	AT4G22380.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412 : GO:0030529 : GO:0042254	intracellular : protein biosynthesis : ribonucleoprotein complex : ribosome : ribosome biogenesis and assembly : structural constituent of ribosome	4,322515965	0,630571783

Phypa_176210	T5A14.11; RuBisCO subunit binding-protein beta subunit, chloroplast / 60 kDa chaperonin beta subunit / CPN-60 beta [Arabidopsis thaliana] : "T5A14.11; RuBisCO subunit binding-protein beta subunit, chloroplast / 60 kDa chaperonin beta subunit / CPN-60 beta [Arabidopsis thaliana]"	Pp1s15_485V6.1;Pp1s15_485V6.2 : "Pp1s15_485V6.1;Pp1s15_485V6.2" : "Pp1s15_485V6.1;Pp1s15_485V6.2 : ""Pp1s15_485V6.1;Pp1s15_485V6.2"""	AT1G55490.1	GO:0003763 : GO:0005515 : GO:0005524 : GO:0044267	ATP binding : cellular protein metabolism : chaperonin ATPase activity : protein binding	4,374636173	1,098837256
[Phypa_144392;Phypa_60069]						4,379006386	0,419741035
Phypa_146121	Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase, chloroplast precursor (Mg-protoporphyrin IX monomethyl ester oxidative cyclase) [Euphorbia esula]	Pp1s239_18V6.2;Pp1s239_18V6.1 : "Pp1s239_18V6.2;Pp1s239_18V6.1" : "Pp1s239_18V6.2;Pp1s239_18V6.1 : ""Pp1s239_18V6.2;Pp1s239_18V6.1"""	AT3G56940.1	GO:0048529	magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase activity	4,390359402	1,255268216
Phypa_151155	F2A19.70; chlorophyll A-B binding protein (LHCA2) [Arabidopsis thaliana] : "F2A19.70; chlorophyll A-B binding protein (LHCA2) [Arabidopsis thaliana]"	Pp1s330_37V6.1	AT3G61470.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting	4,396078587	0,856203079
Phypa_109121	K24M7.19; HCF106 (gb|AAD32652.1) [Arabidopsis thaliana] : "K24M7.19; HCF106 (gb|AAD32652.1) [Arabidopsis thaliana]"	Pp1s402_22V6.1	AT5G52440.1	GO:0008565 : GO:0015031 : GO:0016021	integral to membrane : protein transport : protein transporter activity	4,401918411	0,629160821

Phypa_194139	Ferredoxin-dependent glutamate synthase 1, chloroplast precursor (Fd-GOGAT 1) [Arabidopsis thaliana]	Pp1s212_44V6.1	AT5G04140.1	GO:0006537 : GO:0006807 : GO:0008152 : GO:0015930 : GO:0016041 : GO:0016491	glutamate biosynthesis : glutamate synthase (ferredoxin) activity : glutamate synthase activity : metabolism : nitrogen compound metabolism : oxidoreductase activity	4,424654484	1,080395103
Phypa_132698	Glucose-1-phosphate adenylyltransferase large subunit, chloroplast precursor (ADP-glucose synthase) (ADP-glucose pyrophosphorylase) (AGPase S) (Alpha-D-glucose-1-phosphate adenyl transferase) [Beta vulgaris]	Pp1s98_52V6.1	AT5G19220.1	GO:0004672 : GO:0005524 : GO:0005978 : GO:0006468 : GO:0008878 : GO:0009058 : GO:0016779	ATP binding : biosynthesis : glucose-1-phosphate adenylyltransferase activity : glycogen biosynthesis : nucleotidyltransferase activity : protein amino acid phosphorylation : protein kinase activity	4,426646233	1,358536363
[Phypa_98257;Phypa_226175]						4,441209316	0,769474983
Phypa_173108	MOJ9.19; proline-rich protein family [Arabidopsis thaliana] : "MOJ9.19; proline-rich protein family [Arabidopsis thaliana]"	Pp1s411_3V6.1	AT5G07020.1	GO:0031177	phosphopantetheine binding	4,452753544	1,064231515
Phypa_122707	Sedoheptulose-1,7-bisphosphatase, chloroplast precursor (Sedoheptulose-bisphosphatase) (SBPase) (SED(1,7)P2ase) [Arabidopsis thaliana]	Pp1s41_162V6.1	AT3G55800.1	GO:0005975 : GO:0042578	carbohydrate metabolism : phosphoric ester hydrolase activity	4,471050739	0,937295794

Phypa_168546	glpV; Glycogen phosphorylase 1 [EC:2.4.1.1] [KO:K00688] [Dictyostelium discoideum] : "glpV; Glycogen phosphorylase 1 [EC:2.4.1.1] [KO:K00688] [Dictyostelium discoideum]"	Pp1s180_124V6.1	AT3G46970.1	GO:0004645 : GO:0005975 : GO:0008184	carbohydrate metabolism : glycogen phosphorylase activity : phosphorylase activity	4,517593384	0,975420952
Phypa_131582	Photosystem I reaction center subunit VI, chloroplast precursor (PSI-H) (Light-harvesting complex I 11 kDa protein) [Zea mays]	Pp1s89_62V6.1	AT1G52230.1	GO:0009538 : GO:0015979	photosynthesis : photosystem I reaction center	4,519683361	0,721300662
Phypa_175024		Pp1s10_88V6.1	AT3G03341.1			4,535010815	0,763236463
Phypa_232765		Pp1s132_175V6.1	AT1G32060.1			4,570549011	1,027313352
Phypa_190462	Ferredoxin, chloroplast precursor [Physcomitrella patens]	Pp1s146_120V6.1	AT1G60950.1	GO:0005489 : GO:0005506 : GO:0006118	electron transport : electron transporter activity : iron ion binding	4,571412086	0,628564656
Phypa_223248	Chlorophyll a-b binding protein 13, chloroplast precursor (LHCII type III CAB-13) [Lycopersicon esculentum]	Pp1s254_3V6.1;Pp1s254_3V6.2 : "Pp1s254_3V6.1;Pp1s254_3V6.2" : "Pp1s254_3V6.1;Pp1s254_3V6.2 : ""Pp1s254_3V6.1;Pp1s254_3V6.2"""	AT5G54270.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting	4,596272469	1,333962202

Phypa_110579	T22C5.13; glucose-1-phosphate adenylyltransferase large subunit 2 (APL2) / ADP-glucose pyrophosphorylase [EC:2.7.7.27] [KO:K00975] [Arabidopsis thaliana] : "T22C5.13; glucose-1-phosphate adenylyltransferase large subunit 2 (APL2) / ADP-glucose pyrophosphorylase [EC:2.7.7.27] [KO:K00975] [Arabidopsis thaliana]"	Pp1s347_12V6.1	AT5G19220.1	GO:0004672 : GO:0005524 : GO:0005978 : GO:0006468 : GO:0008878 : GO:0009058 : GO:0016779	ATP binding : biosynthesis : glucose-1-phosphate adenylyltransferase activity : glycogen biosynthesis : nucleotidyltransferase activity : protein amino acid phosphorylation : protein kinase activity	4,600771904	1,717450857
Phypa_176684	Chlorophyll a-b binding protein, chloroplast precursor (LHCII type I CAB) (LHCP) [Physcomitrella patens]	Pp1s19_13V6.2;Pp1s19_13V6.1 : "Pp1s19_13V6.2;Pp1s19_13V6.1" : "Pp1s19_13V6.2;Pp1s19_13V6.1 : ""Pp1s19_13V6.2;Pp1s19_13V6.1"""	AT2G05100.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting	4,624107361	0,913616478
Phypa_165954	F1M20.15; geranylgeranyl reductase [Arabidopsis thaliana] : "F1M20.15; geranylgeranyl reductase [Arabidopsis thaliana]"	Pp1s100_107V6.1	AT1G74470.1	GO:0006118 : GO:0008152 : GO:0015979 : GO:0015995 : GO:0016491 : GO:0045550	chlorophyll biosynthesis : electron transport : geranylgeranyl reductase activity : metabolism : oxidoreductase activity : photosynthesis	4,635843754	0,703843594

Phypa_173848	F7J7.220; oxygen-evolving enhancer protein 3, chloroplast, putative (PSBQ1) (PSBQ) [Arabidopsis thaliana] : "F7J7.220; oxygen-evolving enhancer protein 3, chloroplast, putative (PSBQ1) (PSBQ) [Arabidopsis thaliana]"	Pp1s1_461V6.1	AT4G21280.1	GO:0005509 : GO:0009654 : GO:0015979 : GO:0019898	calcium ion binding : extrinsic to membrane : oxygen evolving complex : photosynthesis	4,640904427	1,188246489
Phypa_115956	ATP synthase B' chain, chloroplast precursor (Subunit II) [Spinacia oleracea]	Pp1s15_26V6.1	AT4G32260.1	GO:0015986 : GO:0016469 : GO:0016820	ATP synthesis coupled proton transport : hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances : proton-transporting two-sector ATPase complex	4,649485111	1,277775884
Phypa_150492	Thioredoxin M-type, chloroplast precursor (TRX-M) [Pisum sativum]	Pp1s317_45V6.1;Pp1s317_45V6.2 : "Pp1s317_45V6.1;Pp1s317_45V6.2" : "Pp1s317_45V6.1;Pp1s317_45V6.2 : ""Pp1s317_45V6.1;Pp1s317_45V6.2"""	AT4G03520.1	GO:0005489 : GO:0006118	electron transport : electron transporter activity	4,652883053	1,737393975
Phypa_140416	T6G15.50; expressed protein [Arabidopsis thaliana] : "T6G15.50; expressed protein [Arabidopsis thaliana]"	Pp1s167_136V6.1;Pp1s167_136V6.2 : "Pp1s167_136V6.1;Pp1s167_136V6.2" : "Pp1s167_136V6.1;Pp1s167_136V6.2 : ""Pp1s167_136V6.1;Pp1s167_136V6.2"""	AT4G13500.1			4,688678265	0,888081789

Phypa_228033	T5M16.18; long-chain-fatty-acid--CoA ligase family protein / long-chain acyl-CoA synthetase family protein (LACS9) [EC:6.2.1.3] [KO:K01897] [Arabidopsis thaliana] : "T5M16.18; long-chain-fatty-acid--CoA ligase family protein / long-chain acyl-CoA synthetase family protein (LACS9) [EC:6.2.1.3] [KO:K01897] [Arabidopsis thaliana]"	Pp1s475_12V6.1	AT1G77590.1	GO:0003824 : GO:0004467 : GO:0008152	catalytic activity : long-chain-fatty-acid-CoA ligase activity : metabolism	4,738046646	1,476829171
Phypa_201802	F24J5.20; alpha-xylosidase (XYL1) [Arabidopsis thaliana] : "F24J5.20; alpha-xylosidase (XYL1) [Arabidopsis thaliana]"	Pp1s6_50V6.1	AT1G68560.1	GO:0004553 : GO:0004558 : GO:0005975	alpha-glucosidase activity : carbohydrate metabolism : hydrolase activity, hydrolyzing O-glycosyl compounds	4,77834177	1,377437353
Phypa_121814	T8I13.24; CP12 domain-containing protein [Arabidopsis thaliana] : "T8I13.24; CP12 domain-containing protein [Arabidopsis thaliana]"	Pp1s37_240V6.1	AT2G47400.1			4,78746891	1,221569061
Phypa_107844		Pp1s199_101V6.1	AT5G51820.1	GO:0005975 : GO:0016868	carbohydrate metabolism : intramolecular transferase activity, phosphotransferases	4,799611092	1,301281452

Phypa_176127	K19E20.4; anthranilate N-hydroxycinnamoyl/benzoyltransferase family [Arabidopsis thaliana] : "K19E20.4; anthranilate N-hydroxycinnamoyl/benzoyltransferase family [Arabidopsis thaliana]"	Pp1s15_356V6.1;Pp1s15_356V6.2 : "Pp1s15_356V6.1;Pp1s15_356V6.2" : "Pp1s15_356V6.1;Pp1s15_356V6.2 : ""Pp1s15_356V6.1;Pp1s15_356V6.2"""	AT5G48930.1			4,848741055	1,354837298
Phypa_228299	50S ribosomal protein L9, chloroplast precursor (CL9) [Arabidopsis thaliana]	Pp1s536_10V6.1	AT3G44890.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome	4,856034279	0,857880235
Phypa_206341	5-methyltetrahydropteroyl triglutamate--homocysteine methyltransferase (Vitamin-B12-independent methionine synthase isozyme) (Cobalamin-independent methionine synthase isozyme) [Mesembryanthemum crystallinum]	Pp1s33_110V6.1;Pp1s33_110V6.2 : "Pp1s33_110V6.1;Pp1s33_110V6.2" : "Pp1s33_110V6.1;Pp1s33_110V6.2 : ""Pp1s33_110V6.1;Pp1s33_110V6.2"""	AT5G17920.2	GO:0003871 : GO:0009086	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity : methionine biosynthesis	4,857099533	1,89832902
Phypa_148115	similar to thioredoxin f [Cyanidioschyzon merolae]	Pp1s271_35V6.2;Pp1s271_35V6.1 : "Pp1s271_35V6.2;Pp1s271_35V6.1" : "Pp1s271_35V6.2;Pp1s271_35V6.1 : ""Pp1s271_35V6.2;Pp1s271_35V6.1"""	AT5G16400.1	GO:0004791 : GO:0005489 : GO:0006118	electron transport : electron transporter activity : thioredoxin-disulfide reductase activity	4,885707855	0,968802571

Phypa_162278	T8M16.240; expressed protein [Arabidopsis thaliana] : "T8M16.240; expressed protein [Arabidopsis thaliana]"	Pp1s41_167V6.1				4,892963409	0,90577817
Phypa_163051	fbxl20; F-box and leucine-rich repeat protein 20 [Danio rerio] : "fbxl20; F-box and leucine-rich repeat protein 20 [Danio rerio]"	Pp1s51_143V6.2;Pp1s51_143V6.1 : "Pp1s51_143V6.2;Pp1s51_143V6.1" : "Pp1s51_143V6.2;Pp1s51_143V6.1 : ""Pp1s51_143V6.2;Pp1s51_143V6.1"""	AT3G60350.1			4,935587883	1,275620818
Phypa_170239	F7P1.20; NAD-dependent epimerase/dehydratase family [Arabidopsis thaliana] : "F7P1.20; NAD-dependent epimerase/dehydratase family [Arabidopsis thaliana]"	Pp1s237_14V6.1	AT5G28840.2	GO:0003824 : GO:0008460 : GO:0009225	catalytic activity : dTDP-glucose 4,6-dehydratase activity : nucleotide-sugar metabolism	4,943228245	0,853991508
Phypa_226715	Ribulose bisphosphate carboxylase small chain, chloroplast precursor (RuBisCO small subunit) [Betula pendula]	Pp1s374_50V6.1	AT1G67090.1	GO:0009573 : GO:0015977 : GO:0016984	carbon utilization by fixation of carbon dioxide : ribulose bisphosphate carboxylase complex (sensu Magnoliophyta) : ribulose-bisphosphate carboxylase activity	4,945543766	0,931042612

Phypa_88846	T22C5.13; glucose-1-phosphate adenylyltransferase large subunit 2 (APL2) / ADP-glucose pyrophosphorylase [EC:2.7.7.27] [KO:K00975] [Arabidopsis thaliana] : "T22C5.13; glucose-1-phosphate adenylyltransferase large subunit 2 (APL2) / ADP-glucose pyrophosphorylase [EC:2.7.7.27] [KO:K00975] [Arabidopsis thaliana]"	Pp1s175_26V6.1	AT1G27680.1	GO:0005978 : GO:0008878 : GO:0009058 : GO:0016779	biosynthesis : glucose-1-phosphate adenylyltransferase activity : glycogen biosynthesis : nucleotidyltransferase activity	4,962192535	1,078215003
Phypa_123160	F13G24.250; expressed protein [Arabidopsis thaliana] : "F13G24.250; expressed protein [Arabidopsis thaliana]"	Pp1s43_120V6.1	AT5G08050.1			4,992305279	0,96225667
Phypa_129127	F25O24.9; elongation factor Ts family protein [Arabidopsis thaliana] : "F25O24.9; elongation factor Ts family protein [Arabidopsis thaliana]"	Pp1s74_243V6.1	AT4G29060.1	GO:0003723 : GO:0003735 : GO:0003746 : GO:0005840 : GO:0006412 : GO:0006414	RNA binding : protein biosynthesis : ribosome : structural constituent of ribosome : translation elongation factor activity : translational elongation	5,017736435	0,76835084
Phypa_175594	Chlorophyll a-b binding protein, chloroplast precursor (LHCII type I CAB) (LHCP) [Physcomitrella patens]	Pp1s13_200V6.1	AT2G05100.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting	5,018425465	3,016057491

Phypa_131430	Thylakoid lumenal 21.5 kDa protein, chloroplast precursor [Arabidopsis thaliana]	Pp1s88_182V6.1	AT4G15510.1	GO:0005509 : GO:0009654 : GO:0015979 : GO:0019898	calcium ion binding : extrinsic to membrane : oxygen evolving complex : photosynthesis	5,020479202	0,853200257
Phypa_164715	F25O24.9; elongation factor Ts family protein [Arabidopsis thaliana] : "F25O24.9; elongation factor Ts family protein [Arabidopsis thaliana]"	Pp1s74_242V6.1	AT4G29060.1	GO:0003723 : GO:0003735 : GO:0005840 : GO:0006412	RNA binding : protein biosynthesis : ribosome : structural constituent of ribosome	5,071928501	1,104746699
Phypa_205373	Plastocyanin, chloroplast precursor [Physcomitrella patens]	Pp1s27_130V6.1	AT1G76100.1	GO:0005489 : GO:0005507 : GO:0006118	copper ion binding : electron transport : electron transporter activity	5,08308506	0,646330535
Phypa_129602	T5J8.7; photosystem I reaction center subunit II, chloroplast, putative / photosystem I 20 kDa subunit, putative / PSI-D, putative (PSAD1) [KO:K02692] [Arabidopsis thaliana] : "T5J8.7; photosystem I reaction center subunit II, chloroplast, putative / photosystem I 20 kDa subunit, putative / PSI-D, putative (PSAD1) [KO:K02692] [Arabidopsis thaliana]"	Pp1s77_69V6.1	AT1G03130.1	GO:0009538 : GO:0015979	photosynthesis : photosystem I reaction center	5,158810616	0,888099551

Phypa_164045		Pp1s64_155V6.2;Pp1s64_155V6.1;Pp1s64_155V6.3 : "Pp1s64_155V6.2;Pp1s64_155V6.1;Pp1s64_155V6.3" : "Pp1s64_155V6.2;Pp1s64_155V6.1;Pp1s64_155V6.3 : ""Pp1s64_155V6.2;Pp1s64_155V6.1;Pp1s64_155V6.3"""	AT2G46210.1	GO:0006636 : GO:0016020 : GO:0016491 : GO:0016717	fatty acid desaturation : membrane : oxidoreductase activity : oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water	5,208145142	1,028375983
Phypa_194508	F17I5.140; protein kinase, putative [EC:2.7.1.-] [Arabidopsis thaliana] : "F17I5.140; protein kinase, putative [EC:2.7.1.-] [Arabidopsis thaliana]"	Pp1s218_59V6.1	AT4G33950.1	GO:0004675 : GO:0004676 : GO:0004677 : GO:0004679 : GO:0004680 : GO:0004681 : GO:0004683 : GO:0004686 : GO:0004688 : GO:0004689 : GO:0004690 : GO:0004692 : GO:0004693 : GO:0004694 : GO:0004695 : GO:0004696 : GO:0004697 : GO:0004698 : GO:0004700 : GO:0004701 : GO:0004702 : GO:0004703 : GO:0004704 : GO:0004705 : GO:0004706 : GO:0004707 : GO:0004708 : GO:0004709 : GO:0004710 : GO:0004711 : GO:0004712 : GO:0004713 : GO:0004714 : GO:0004715 : GO:0004716 : GO:0004718 : GO:0005524 : GO:0006468 : GO:0008338 : GO:0008339 : GO:0008349 : GO:0008384 : GO:0008443 : GO:0008545 : GO:0008607 : GO:0008819 : GO:0016307 : GO:0016538 : GO:0016773 : GO:0016908 : GO:0016909 : GO:0018720 : GO:0019199 : GO:0019912 :	dependent protein kinase activity : AMP-activated protein kinase activity : ATP binding : DNA-dependent protein kinase activity : G-protein coupled receptor kinase activity : IkappaB kinase activity : JUN kinase activity : JUN kinase kinase activity : JUN kinase kinase kinase activity : Janus kinase activity : MAP kinase 1 activity : MAP kinase 2 activity : MAP kinase activity : MAP kinase kinase activity : MAP kinase kinase kinase activity : MAP kinase kinase kinase activity : MAP/ERK kinase kinase activity : MP kinase activity : NF-kappaB-inducing kinase activity : SAP kinase activity : atypical protein kinase C activity : cGMP-dependent	5,350483894	2,194253683

Phypa_173789	F14G6.9; 3-hydroxy-3-methylglutaryl-CoA reductase 1 / HMG-CoA reductase 1 (HMG1) [EC:1.1.1.34] [KO:K00021] [Arabidopsis thaliana] : "F14G6.9; 3-hydroxy-3-methylglutaryl-CoA reductase 1 / HMG-CoA reductase 1 (HMG1) [EC:1.1.1.34] [KO:K00021] [Arabidopsis thaliana]"	Pp1s1_155V6.1	AT1G76490.1	GO:0004420 : GO:0006629 : GO:0009058 : GO:0016021	biosynthesis : hydroxymethylglutaryl-CoA reductase (NADPH) activity : integral to membrane : lipid metabolism	5,365731716	0,906204998
Phypa_222462	T4P13.13; glycogen synthase, putative [EC:2.4.1.11] [KO:K00693] [Arabidopsis thaliana] : "T4P13.13; glycogen synthase, putative [EC:2.4.1.11] [KO:K00693] [Arabidopsis thaliana]"	Pp1s234_74V6.1	AT3G01180.1	GO:0004373 : GO:0009058	biosynthesis : glycogen (starch) synthase activity	5,401439667	1,022788286
Phypa_109510	Thylakoid membrane phosphoprotein 14 kDa, chloroplast precursor [Arabidopsis thaliana]	Pp1s15_328V6.1	AT1G52220.1			5,417891979	0,788110316
Phypa_188347	F27K7.6; nucleolin, putative [Arabidopsis thaliana] : "F27K7.6; nucleolin, putative [Arabidopsis thaliana]"	Pp1s118_39V6.1;Pp1s118_39V6.2 : "Pp1s118_39V6.1;Pp1s118_39V6.2" : "Pp1s118_39V6.1;Pp1s118_39V6.2 : ""Pp1s118_39V6.1;Pp1s118_39V6.2"""	AT3G18610.1	GO:0003676	nucleic acid binding	5,419731617	0,573325276

Phypa_165175	fadB; delta 5 fatty acid desaturase [Dictyostelium discoideum] : "fadB; delta 5 fatty acid desaturase [Dictyostelium discoideum]"	Pp1s83_225V6.2;Pp1s83_225V6.1 : "Pp1s83_225V6.2;Pp1s83_225V6.1" : "Pp1s83_225V6.2;Pp1s83_225V6.1 : ""Pp1s83_225V6.2;Pp1s83_225V6.1"""	AT2G46210.1	GO:0006636 : GO:0016020 : GO:0016491 : GO:0016717	fatty acid desaturation : membrane : oxidoreductase activity : oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water	5,546542645	0,769249737
Phypa_211595	T31J12.6; expressed protein [Arabidopsis thaliana] : "T31J12.6; expressed protein [Arabidopsis thaliana]"	Pp1s71_283V6.1	AT1G09340.1	GO:0005975	carbohydrate metabolism	5,586175919	1,135913968
Phypa_115764	T9J22.17; cytochrome b6f complex subunit (petM), putative [Arabidopsis thaliana] : "T9J22.17; cytochrome b6f complex subunit (petM), putative [Arabidopsis thaliana]"	Pp1s14_288V6.1	AT2G26500.1			5,676033974	0,816366911
Phypa_170769		Pp1s259_112V6.1;Pp1s259_112V6.2 : "Pp1s259_112V6.1;Pp1s259_112V6.2" : "Pp1s259_112V6.1;Pp1s259_112V6.2 : ""Pp1s259_112V6.1;Pp1s259_112V6.2"""	Pp1s259_112V6	GO:0003824	catalytic activity	5,711834908	0,463410884
Phypa_223634	MSJ11.24; expressed protein [Arabidopsis thaliana] : "MSJ11.24; expressed protein [Arabidopsis thaliana]"	Pp1s266_2V6.1	AT3G15840.1			5,719340801	1,210547209

Phypa_162911	hypothetical protein, conserved [Trypanosoma cruzi]	Pp1s49_55V6.1		GO:0008757	S-adenosylmethionine-dependent methyltransferase activity	5,758742332	0,595554769
Phypa_123666	Ribulose bisphosphate carboxylase small chain, chloroplast precursor (RuBisCO small subunit) [Marchantia paleacea]	Pp1s46_42V6.1	AT1G67090.1	GO:0009573 : GO:0015977 : GO:0016984	carbon utilization by fixation of carbon dioxide : ribulose bisphosphate carboxylase complex (sensu Magnoliophyta) : ribulose-bisphosphate carboxylase activity	5,768614292	2,164922714
Phypa_196235	F16M14.7; chloroplast 30S ribosomal protein S31 (PSRP4) [Arabidopsis thaliana] : "F16M14.7; chloroplast 30S ribosomal protein S31 (PSRP4) [Arabidopsis thaliana]"	Pp1s258_80V6.1	AT2G38140.1			5,900059223	0,712373257
[Phypa_125887;Phypa_125903;Phypa_125839]						5,978580952	0,706370592
Phypa_214679		Pp1s104_30V6.1	AT4G15770.1	GO:0003723	RNA binding	5,984895706	1,409962416
Phypa_152025	Ribulose bisphosphate carboxylase small chain, chloroplast precursor (RuBisCO small subunit) [Betula pendula]	Pp1s352_14V6.1	AT5G38410.1	GO:0009573 : GO:0015977 : GO:0016984	carbon utilization by fixation of carbon dioxide : ribulose bisphosphate carboxylase complex (sensu Magnoliophyta) : ribulose-bisphosphate carboxylase activity	6,118415356	1,008145928
Phypa_233494		Pp1s86_153V6.2;Pp1s86_153V6.1 : "Pp1s86_153V6.2;Pp1s86_153V6.1" : "Pp1s86_153V6.2;Pp1s86_153V6.1 : ""Pp1s86_153V6.2;Pp1s86_153V6.1"""	AT2G32950.1			6,197117805	1,576609254

Phypa_159676	F8B4.40; expressed protein [Arabidopsis thaliana] : "F8B4.40; expressed protein [Arabidopsis thaliana]"	Pp1s14_348V6.1	AT4G32340.1			6,416001797	6,513771057
[Phypa_52279;Phypa_52281]						6,515311718	0,669872344
Phypa_151854	MRA19.7; immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase [EC:5.2.1.8] [KO:K01802] [Arabidopsis thaliana] : "MRA19.7; immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase [EC:5.2.1.8] [KO:K01802] [Arabidopsis thaliana]"	Pp1s347_30V6.1;Pp1s347_30V6.2 : "Pp1s347_30V6.1;Pp1s347_30V6.2" : "Pp1s347_30V6.1;Pp1s347_30V6.2 : ""Pp1s347_30V6.1;Pp1s347_30V6.2"""	AT5G45680.1	GO:0003755 : GO:0004600 : GO:0006457 : GO:0030051 : GO:0042027	FK506-sensitive peptidyl-prolyl cis-trans isomerase : cyclophilin : cyclophilin-type peptidyl-prolyl cis-trans isomerase activity : peptidyl-prolyl cis-trans isomerase activity : protein folding	6,571975231	1,084416747
Phypa_233882		Pp1s109_92V6.1				6,726111889	0,951481462
Phypa_107666	MJE7.12; expressed protein [Arabidopsis thaliana] : "MJE7.12; expressed protein [Arabidopsis thaliana]"	Pp1s182_93V6.1	AT5G48480.1			6,76736784	0,63120234
Phypa_105126	Chlorophyll a-b binding protein, chloroplast precursor (LHCII type I CAB) (LHCP) [Physcomitrella patens]	Pp1s27_97V6.1	AT2G05100.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting	6,787359238	1,021841526

Phypa_169178	Ribulose bisphosphate carboxylase/oxygenase activase, chloroplast precursor (RuBisCO activase) (RA) [Malus x domestica]	Pp1s199_130V6.3;Pp1s199_130V6.2;Pp1s199_130V6.1 : "Pp1s199_130V6.3;Pp1s199_130V6.2;Pp1s199_130V6.1" : "Pp1s199_130V6.3;Pp1s199_130V6.2;Pp1s199_130V6.1 : ""Pp1s199_130V6.3;Pp1s199_130V6.2;Pp1s199_130V6.1"""	AT2G39730.3	GO:0005524	ATP binding	6,789404869	1,068943143
Phypa_165894	F9I5.10; expressed protein [Arabidopsis thaliana] : "F9I5.10; expressed protein [Arabidopsis thaliana]"	Pp1s98_136V6.1;Pp1s98_136V6.2 : "Pp1s98_136V6.1;Pp1s98_136V6.2" : "Pp1s98_136V6.1;Pp1s98_136V6.2 : ""Pp1s98_136V6.1;Pp1s98_136V6.2"""	AT1G52220.1			6,854888439	0,846050501
Phypa_34885		Pp1s55_65V6.1;Pp1s55_66V6.1;Pp1s55_66V6.2 : "Pp1s55_65V6.1;Pp1s55_66V6.1;Pp1s55_66V6.2" : "Pp1s55_65V6.1;Pp1s55_66V6.1;Pp1s55_66V6.2 : ""Pp1s55_65V6.1;Pp1s55_66V6.1;Pp1s55_66V6.2"""	AT5G44310.2			6,877348423	0,676292598
Phypa_166416	F10M23.190; expressed protein [Arabidopsis thaliana] : "F10M23.190; expressed protein [Arabidopsis thaliana]"	Pp1s114_207V6.1	AT4G26850.1			6,96671629	2,136083603

Phypa_166666	F1L3.19; expressed protein [Arabidopsis thaliana] : "F1L3.19; expressed protein [Arabidopsis thaliana]"	Pp1s121_72V6.1				6,982047558	1,149857402
Phypa_56132	Chlorophyll a-b binding protein CP24 10A, chloroplast precursor (CAB-10A) (LHCP) [Lycopersicon esculentum]	Pp1s28_319V6.1	AT1G15820.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting	7,077290058	0,8992154
Phypa_161636	mucin-associated surface protein (MASP), putative [Trypanosoma cruzi]	Pp1s34_348V6.1;Pp1s34_348V6.2 : "Pp1s34_348V6.1;Pp1s34_348V6.2" : "Pp1s34_348V6.1;Pp1s34_348V6.2 : ""Pp1s34_348V6.1;Pp1s34_348V6.2"""	Pp1s34_348V6			7,086995602	0,64171797
Phypa_196367	Fibrillarin-2 (Fibrillarin-like protein) [Arabidopsis thaliana]	Pp1s263_70V6.1	AT4G25630.1	GO:0003723 : GO:0005634 : GO:0006364	RNA binding : nucleus : rRNA processing	7,102557659	1,067141294
Phypa_146969	Ribulose bisphosphate carboxylase small chain, chloroplast precursor (RuBisCO small subunit) [Betula pendula]	Pp1s251_44V6.1	AT5G38420.1	GO:0009573 : GO:0015977 : GO:0016984	carbon utilization by fixation of carbon dioxide : ribulose bisphosphate carboxylase complex (sensu Magnoliophyta) : ribulose-bisphosphate carboxylase activity	7,263670921	0,949880362

Phypa_39042	F16A16.140; photosystem I reaction center subunit IV, chloroplast, putative / PSI-E, putative (PSAE1) [KO:K02693] [Arabidopsis thaliana] : "F16A16.140; photosystem I reaction center subunit IV, chloroplast, putative / PSI-E, putative (PSAE1) [KO:K02693] [Arabidopsis thaliana]"	Pp1s334_17V6.1	AT2G20260.1	GO:0006118 : GO:0009538	electron transport : photosystem I reaction center	7,389041901	0,637447715
Phypa_172635		Pp1s370_29V6.1	AT2G36640.1			7,52675581	2,268722057
Phypa_170637	Plastocyanin, chloroplast precursor [Physcomitrella patens]	Pp1s254_25V6.1	AT1G76100.1	GO:0005489 : GO:0005507 : GO:0006118	copper ion binding : electron transport : electron transporter activity	7,539018631	0,689661503
Phypa_167599	ASR1; orf19.2344 [Candida albicans SC5314] : "ASR1; orf19.2344 [Candida albicans SC5314]"	Pp1s152_65V6.1				7,561339855	1,246006966
Phypa_182167		Pp1s55_64V6.1				7,871560097	0,807243884
Phypa_163619		Pp1s58_210V6.1				7,9682827	1,542705178
Phypa_139567	Chlorophyll a-b binding protein 6A, chloroplast precursor (LHCI type I CAB-6A) (Light-harvesting complex I 26 kDa protein) [Lycopersicon esculentum]	Pp1s158_109V6.1	AT3G54890.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting	8,006613731	0,875525713
Phypa_95302	long chain polyunsaturated fatty acid elongation enzyme-like protein [Leishmania major]	Pp1s277_79V6.1	AT3G06460.1	GO:0016021	integral to membrane	8,229200363	0,710826635

Phypa_110695	Dmel_CG9682; CG9682 gene product from transcript CG9682-RA [Drosophila melanogaster] : "Dmel_CG9682; CG9682 gene product from transcript CG9682-RA [Drosophila melanogaster]"	Pp1s517_11V6.2;Pp1s517_11V6.1 : "Pp1s517_11V6.2;Pp1s517_11V6.1" : "Pp1s517_11V6.2;Pp1s517_11V6.1 : ""Pp1s517_11V6.2;Pp1s517_11V6.1"""	Pp1s517_11V6			8,384883881	1,477952123
Phypa_200318	putative 33kDa oxygen evolvingprotein of photosystem II [Oryza sativa (japonica cultivar-group)]	Pp1s421_3V6.1	AT3G50820.1	GO:0005509 : GO:0009654 : GO:0015979 : GO:0019898 : GO:0042549	calcium ion binding : extrinsic to membrane : oxygen evolving complex : photosynthesis : photosystem II stabilization	8,529736519	1,355244398
Phypa_178365	Omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 1 [Glycine max]	Pp1s30_149V6.1;Pp1s30_149V6.2 : "Pp1s30_149V6.1;Pp1s30_149V6.2" : "Pp1s30_149V6.1;Pp1s30_149V6.2 : ""Pp1s30_149V6.1;Pp1s30_149V6.2"""	AT3G12120.1	GO:0006636 : GO:0016020 : GO:0016215 : GO:0016491 : GO:0016717 : GO:0018688 : GO:0018689 : GO:0042389	CoA desaturase activity : DDT 2,3-dioxygenase activity : fatty acid desaturation : membrane : naphthalene disulfonate 1,2-dioxygenase activity : omega-3 fatty acid desaturase activity : oxidoreductase activity : oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water	8,576417923	1,763845325

Phypa_85464	Glyceraldehyde-3-phosphate dehydrogenase A, chloroplast precursor (NADP-dependent glyceraldehydephosphate dehydrogenase subunit A) [Spinacia oleracea]	Pp1s135_21V6.1;Pp1s135_21V6.2;Pp1s135_21V6.3 : "Pp1s135_21V6.1;Pp1s135_21V6.2;Pp1s135_21V6.3" : "Pp1s135_21V6.1;Pp1s135_21V6.2;Pp1s135_21V6.3 : ""Pp1s135_21V6.1;Pp1s135_21V6.2;Pp1s135_21V6.3"""	AT1G12900.1	GO:0004365 : GO:0006006 : GO:0006096 : GO:0008943 : GO:0051287	NAD binding : glucose metabolism : glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity : glyceraldehyde-3-phosphate dehydrogenase activity : glycolysis	8,785765648	1,056378722
Phypa_174645	Alpha-glucan water dikinase, chloroplast precursor (Starch-related R1 protein) (Starch excess protein 1) [Arabidopsis thaliana]	Pp1s8_70V6.1	AT1G10760.1	GO:0050521	alpha-glucan, water dikinase activity	8,810492516	2,098016977
Phypa_155603	Fructose-bisphosphate aldolase, chloroplast precursor (ALDP) [no tax name]	Pp1s475_27V6.3;Pp1s475_27V6.2;Pp1s475_27V6.1 : "Pp1s475_27V6.3;Pp1s475_27V6.2;Pp1s475_27V6.1" : "Pp1s475_27V6.3;Pp1s475_27V6.2;Pp1s475_27V6.1 : ""Pp1s475_27V6.3;Pp1s475_27V6.2;Pp1s475_27V6.1"""	AT2G01140.1	GO:0004332 : GO:0006096	fructose-bisphosphate aldolase activity : glycolysis	8,956683159	0,918089271
Phypa_110121	Ferredoxin--NADP reductase, embryo isozyme, chloroplast precursor (FNR) [Oryza sativa]	Pp1s131_175V6.1	AT4G05390.1	GO:0004324 : GO:0006118 : GO:0015039 : GO:0016491	NADPH-adrenodoxin reductase activity : electron transport : ferredoxin-NADP+ reductase activity : oxidoreductase activity	8,988592148	1,335643888

Phypa_109430	Ribulose bisphosphate carboxylase/oxygenase activase 1, chloroplast precursor (RuBisCO activase 1) (RA 1) (RubisCO activase alpha form) [Larrea tridentata]	Pp1s5_83V6.2;Pp1s5_83V6.1 : "Pp1s5_83V6.2;Pp1s5_83V6.1" : "Pp1s5_83V6.2;Pp1s5_83V6.1 : ""Pp1s5_83V6.2;Pp1s5_83V6.1"""	AT2G39730.1	GO:0005524	ATP binding	10,00964165	1,859324932
Phypa_168272		Pp1s171_80V6.1	AT2G43570.1			10,12386608	0,77205652
Phypa_35924	F4H5.23; photosystem II oxygen-evolving complex 23 (OEC23) [KO:K02717] [Arabidopsis thaliana] : "F4H5.23; photosystem II oxygen-evolving complex 23 (OEC23) [KO:K02717] [Arabidopsis thaliana]"	Pp1s11_39V6.2;Pp1s11_39V6.1 : "Pp1s11_39V6.2;Pp1s11_39V6.1" : "Pp1s11_39V6.2;Pp1s11_39V6.1 : ""Pp1s11_39V6.2;Pp1s11_39V6.1"""	AT1G06680.1	GO:0005509 : GO:0009654 : GO:0015979 : GO:0019898	calcium ion binding : extrinsic to membrane : oxygen evolving complex : photosynthesis	10,37664509	0,959047377
Phypa_172642		Pp1s370_52V6.2;Pp1s370_52V6.1 : "Pp1s370_52V6.2;Pp1s370_52V6.1" : "Pp1s370_52V6.2;Pp1s370_52V6.1 : ""Pp1s370_52V6.2;Pp1s370_52V6.1"""	AT2G36640.1			10,84610748	1,393521309
Phypa_168764	Ribulose bisphosphate carboxylase small chain, chloroplast precursor (RuBisCO small subunit) [Betula pendula]	Pp1s188_39V6.1	AT1G67090.1	GO:0009573 : GO:0015977 : GO:0016984	carbon utilization by fixation of carbon dioxide : ribulose bisphosphate carboxylase complex (sensu Magnoliophyta) : ribulose-bisphosphate carboxylase activity	11,21740055	0,941150904

Phypa_8310	Ribulose bisphosphate carboxylase small chain, chloroplast precursor (RuBisCO small subunit) [Pyrus pyrifolia]	Pp1s459_14V6.1		GO:0009573 : GO:0015977 : GO:0016984	carbon utilization by fixation of carbon dioxide : ribulose bisphosphate carboxylase complex (sensu Magnoliophyta) : ribulose-bisphosphate carboxylase activity	11,47559643	0,321988106
Phypa_161955	Tub; tubby candidate gene [Mus musculus] : "Tub; tubby candidate gene [Mus musculus]"	Pp1s37_306V6.1				11,49256134	1,194284678
Phypa_119427	Chlorophyll a-b binding protein CP24 10A, chloroplast precursor (CAB-10A) (LHCP) [Lycopersicon esculentum]	Pp1s28_315V6.1	AT1G15820.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting	12,07636261	0,868850708
Phypa_159520		Pp1s13_231V6.1				12,58696079	1,658909917
Phypa_109367		Pp1s545_4V6.1	AT5G38410.1	GO:0009573 : GO:0015977 : GO:0016984	carbon utilization by fixation of carbon dioxide : ribulose bisphosphate carboxylase complex (sensu Magnoliophyta) : ribulose-bisphosphate carboxylase activity	12,7453928	1,191422582
Phypa_189346	Ferredoxin--NADP reductase, embryo isozyme, chloroplast precursor (FNR) [Oryza sativa]	Pp1s131_154V6.1	AT4G05390.1	GO:0004324 : GO:0006118 : GO:0015039 : GO:0016491	NADPH-adrenodoxin reductase activity : electron transport : ferredoxin-NADP+ reductase activity : oxidoreductase activity	12,84999943	1,236939073
Phypa_160322	Diflavin flavoprotein A 1 (SsATF573) (NADH:oxygen oxidoreductase) [Synechocystis sp. PCC 6803]	Pp1s21_137V6.1		GO:0006118 : GO:0010181 : GO:0016491	FMN binding : electron transport : oxidoreductase activity	13,37695599	2,539009809

Phypa_173430	F1O19.14; ribulose bisphosphate carboxylase small chain 1A / RuBisCO small subunit 1A (RBCS-1A) (ATS1A) [EC:4.1.1.39] [KO:K01602] [Arabidopsis thaliana] : "F1O19.14; ribulose bisphosphate carboxylase small chain 1A / RuBisCO small subunit 1A (RBCS-1A) (ATS1A) [EC:4.1.1.39] [KO:K01602] [Arabidopsis thaliana]"	Pp1s459_1V6.1;Pp1s459_2V6.2;Pp1s459_2V6.1 : "Pp1s459_1V6.1;Pp1s459_2V6.2;Pp1s459_2V6.1" : "Pp1s459_1V6.1;Pp1s459_2V6.2;Pp1s459_2V6.1 : ""Pp1s459_1V6.1;Pp1s459_2V6.2;Pp1s459_2V6.1"""	AT1G67090.2	GO:0009573 : GO:0015977 : GO:0016984	carbon utilization by fixation of carbon dioxide : ribulose bisphosphate carboxylase complex (sensu Magnoliophyta) : ribulose-bisphosphate carboxylase activity	13,70735168	0,441211224
Phypa_75366	WSI18 protein [Oryza sativa (japonica cultivar-group)]	Pp1s52_212V6.2;Pp1s52_212V6.1 : "Pp1s52_212V6.2;Pp1s52_212V6.1" : "Pp1s52_212V6.2;Pp1s52_212V6.1 : ""Pp1s52_212V6.2;Pp1s52_212V6.1"""	AT2G18340.1			13,93298721	1,027421117
Phypa_225236	Ribulose bisphosphate carboxylase small chain, chloroplast precursor (RuBisCO small subunit) [Marchantia paleacea]	Pp1s312_46V6.1	AT1G67090.1	GO:0009573 : GO:0015977 : GO:0016984	carbon utilization by fixation of carbon dioxide : ribulose bisphosphate carboxylase complex (sensu Magnoliophyta) : ribulose-bisphosphate carboxylase activity	14,2595768	0,819527686
Phypa_109512	Photosystem II 10 kDa polypeptide, chloroplast precursor [Spinacia oleracea]	Pp1s15_409V6.1	AT1G79040.1	GO:0009654 : GO:0015979 : GO:0042651	oxygen evolving complex : photosynthesis : thylakoid membrane	14,46679401	1,14550674

Phypa_169111	MOJ9.19; proline-rich protein family [Arabidopsis thaliana] : "MOJ9.19; proline-rich protein family [Arabidopsis thaliana]"	Pp1s198_75V6.1	AT5G07020.1			15,19991207	1,243998051
Phypa_38875		Pp1s374_42V6.1	AT5G38410.3	GO:0009573 : GO:0015977 : GO:0016984	carbon utilization by fixation of carbon dioxide : ribulose bisphosphate carboxylase complex (sensu Magnoliophyta) : ribulose-bisphosphate carboxylase activity	15,49640751	0,401230395
Phypa_190267	Ferredoxin, chloroplast precursor [Physcomitrella patens]	Pp1s143_176V6.1	AT1G60950.1	GO:0005489 : GO:0005506 : GO:0006118	electron transport : electron transporter activity : iron ion binding	15,51907921	0,571800172
Phypa_202775	Glyceraldehyde-3-phosphate dehydrogenase A, chloroplast precursor (NADP-dependent glyceraldehydephosphate dehydrogenase subunit A) [Spinacia oleracea]	Pp1s11_397V6.5;Pp1s11_397V6.2;Pp1s11_397V6.3;Pp1s11_397V6.4;Pp1s11_397V6.1;Pp1s11_397V6.6 : "Pp1s11_397V6.5;Pp1s11_397V6.2;Pp1s11_397V6.3;Pp1s11_397V6.4;Pp1s11_397V6.1;Pp1s11_397V6.6" : "Pp1s11_397V6.5;Pp1s11_397V6.2;Pp1s11_397V6.3;Pp1s11_397V6.4;Pp1s11_397V6.1;Pp1s11_397V6.6 : ""Pp1s11_397V6.5;Pp1s11_397V6.2;Pp1s11_397V6.3;Pp1s11_397V6.4;Pp1s11_397V6.1;Pp1s11_397V6.6"""	AT1G12900.1	GO:0004365 : GO:0006006 : GO:0006096 : GO:0008943 : GO:0051287	NAD binding : glucose metabolism : glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity : glyceraldehyde-3-phosphate dehydrogenase activity : glycolysis	17,37494278	0,837925971
[Phypa_59935;Phypa_221004]						19,79589462	0,699805617

Phypa_107034	F6N23.1; beta-amylase, putative / 1,4-alpha-D-glucan maltohydrolase, putative [Arabidopsis thaliana] : "F6N23.1; beta-amylase, putative / 1,4-alpha-D-glucan maltohydrolase, putative [Arabidopsis thaliana]"	Pp1s121_168V6.1;Pp1s121_168V6.2 : "Pp1s121_168V6.1;Pp1s121_168V6.2" : "Pp1s121_168V6.1;Pp1s121_168V6.2 : ""Pp1s121_168V6.1;Pp1s121_168V6.2"""	AT4G00490.1	GO:0000272 : GO:0016161	beta-amylase activity : polysaccharide catabolism	21,44999504	6,277317047
Phypa_169593	Chlorophyll a-b binding protein L1818, chloroplast precursor [Chlamydomonas eugametos]	Pp1s213_80V6.1	AT2G05070.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting	93,52127075	0,811689615

Supplemental Dataset 1 - 30 min R down-regulated

Phypa_ID	Funct. descr. BLAST BH	V1.6 CGI	At homolog	GO accession	GO name
Phypa_172732		Pp1s376_9V6.1			
Phypa_117476	Adenosylhomocysteinase (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase) [Petroselinum crispum]	Pp1s20_291V6.1	AT3G23810.1	GO:0004013 : GO:0006730	adenosylhomocysteinase activity : one-carbon compound metabolism
Phypa_169905	grl-25; Hypothetical protein ZK643.8 [Caenorhabditis elegans] : "grl-25; Hypothetical protein ZK643.8 [Caenorhabditis elegans]"	Pp1s224_13V6.1			
Phypa_163011	Transcriptional corepressor SEUSS [Arabidopsis thaliana]	Pp1s50_193V6.1;Pp1s50_192V6.1 : "Pp1s50_193V6.1;Pp1s50_192V6.1" : "Pp1s50_193V6.1;Pp1s50_192V6.1 : ""Pp1s50_193V6.1;Pp1s50_192V6.1"""		GO:0004402	histone acetyltransferase activity
Phypa_65350		Pp1s6_72V6.1			

Phypa_231575		Pp1s134_155V6.2;Pp1s134_155V6.1;Pp1s134_155V6.3 : "Pp1s134_155V6.2;Pp1s134_155V6.1;Pp1s134_155V6.3" : "Pp1s134_155V6.2;Pp1s134_155V6.1;Pp1s134_155V6.3 : ""Pp1s134_155V6.2;Pp1s134_155V6.1;Pp1s134_155V6.3"""	AT5G65170.1		
Phypa_231987		Pp1s148_7V6.1	AT5G58470.1		
Phypa_198924	Glutamine synthetase, cytosolic isozyme (Glutamate--ammonia ligase) (GS1) [Lotus corniculatus var. japonicus]	Pp1s345_10V6.1	AT5G16570.1	GO:0004356 : GO:0006542 : GO:0006807	glutamate-ammonia ligase activity : glutamine biosynthesis : nitrogen compound metabolism
Phypa_219762	MJC20.12; luminal binding protein 2 precursor (BiP-2) (AtBP2) [Arabidopsis thaliana] : "MJC20.12; luminal binding protein 2 precursor (BiP-2) (AtBP2) [Arabidopsis thaliana]"	Pp1s181_3V6.1	AT5G42020.1	GO:0005524	ATP binding

Phypa_152834	MQM1.6; serine C-palmitoyltransferase, putative [EC:2.3.1.50] [KO:K00654] [Arabidopsis thaliana] : "MQM1.6; serine C-palmitoyltransferase, putative [EC:2.3.1.50] [KO:K00654] [Arabidopsis thaliana]"	Pp1s377_35V6.1	AT5G23670.1	GO:0004758 : GO:0008152 : GO:0009058 : GO:0016740 : GO:0016769 : GO:0017059	biosynthesis : metabolism : serine C-palmitoyltransferase activity : serine C-palmitoyltransferase complex : transferase activity : transferase activity, transferring nitrogenous groups
Phypa_16354	Glycine-rich RNA-binding protein 2 [Sorghum bicolor]	Pp1s123_58V6.1	AT4G39260.3	GO:0003676	nucleic acid binding
Phypa_9234	Protein C10orf70 homolog [Mus musculus]	Pp1s268_67V6.1	AT5G51720.1		
Phypa_37849	contains ESTs AU062952(C51837),AU100820(C51837) [Oryza sativa (japonica cultivar-group)]	Pp1s118_101V6.1	AT5G61030.1	GO:0003676	nucleic acid binding
[Phypa_182736;Phypa_182738]					
[Phypa_232463;Phypa_234904]					

Phypa_187695	T7B11.11; S-adenosylmethionine synthetase 2 (SAM2) [EC:2.5.1.6] [KO:K00789] [Arabidopsis thaliana] : "T7B11.11; S-adenosylmethionine synthetase 2 (SAM2) [EC:2.5.1.6] [KO:K00789] [Arabidopsis thaliana]"	Pp1s109_133V6.1		GO:0004478 : GO:0005524 : GO:0006730 : GO:0048269 : GO:0048270	ATP binding : methionine adenosyltransferase activity : methionine adenosyltransferase complex : methionine adenosyltransferase regulator activity : one-carbon compound metabolism
Phypa_234454		Pp1s136_127V6.1	AT3G48050.2		
Phypa_71336	Glycine-rich cell wall structural protein 1.0 precursor (GRP 1.0) [Phaseolus vulgaris]	Pp1s32_87V6.2;Pp1s32_87V6.1 : "Pp1s32_87V6.2;Pp1s32_87V6.1" : "Pp1s32_87V6.2;Pp1s32_87V6.1 : ""Pp1s32_87V6.2;Pp1s32_87V6.1"""		GO:0004308	exo-alpha-sialidase activity

Phypa_182655	contains EST AU029985(E50436) [Oryza sativa (japonica cultivar-group)]	Pp1s59_81V6.1	AT1G55150.1	GO:0003676 : GO:0004003 : GO:0004004 : GO:0004386 : GO:0005524 : GO:0008026 : GO:0008094 : GO:0008186 : GO:0015462 : GO:0015616 : GO:0016887 : GO:0017116 : GO:0042623 : GO:0042624 : GO:0042625 : GO:0042626	ATP binding : ATP-dependent DNA helicase activity : ATP-dependent RNA helicase activity : ATP-dependent helicase activity : ATPase activity : ATPase activity, coupled : ATPase activity, coupled to transmembrane movement of ions : ATPase activity, coupled to transmembrane movement of substances : ATPase activity, uncoupled : DNA translocase activity : DNA-dependent ATPase activity : RNA-dependent ATPase activity : helicase activity : nucleic acid binding : protein-transporting ATPase activity : single-stranded DNA-dependent ATP-dependent DNA helicase activity

Phypa_209813		Pp1s56_243V6.3;Pp1s56_243V6.2;Pp1s56_243V6.1 : "Pp1s56_243V6.3;Pp1s56_243V6.2;Pp1s56_243V6.1" : "Pp1s56_243V6.3;Pp1s56_243V6.2;Pp1s56_243V6.1 : ""Pp1s56_243V6.3;Pp1s56_243V6.2;Pp1s56_243V6.1"""	AT2G34480.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_66696	F25I18.8; expressed protein [Arabidopsis thaliana] : "F25I18.8; expressed protein [Arabidopsis thaliana]"	Pp1s11_386V6.1;Pp1s11_386V6.2 : "Pp1s11_386V6.1;Pp1s11_386V6.2" : "Pp1s11_386V6.1;Pp1s11_386V6.2 : ""Pp1s11_386V6.1;Pp1s11_386V6.2"""	AT2G33180.1		
Phypa_208348	60S ribosomal protein L23A [Fritillaria agrestis]	Pp1s46_72V6.1	AT3G55280.2	GO:0003723 : GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	RNA binding : intracellular : protein biosynthesis : ribosome : structural constituent of ribosome

Phypa_135187	T32M21.100; glycosyltransferase family 47 [Arabidopsis thaliana] : "T32M21.100; glycosyltransferase family 47 [Arabidopsis thaliana]"	Pp1s117_57V6.1	AT5G04500.1		
Phypa_173670	F28D10.80; 50S ribosomal protein L9, chloroplast (CL9) [KO:K02939] [Arabidopsis thaliana] : "F28D10.80; 50S ribosomal protein L9, chloroplast (CL9) [KO:K02939] [Arabidopsis thaliana]"	Pp1s536_9V6.1;Pp1s536_9V6.2 : "Pp1s536_9V6.1;Pp1s536_9V6.2" : "Pp1s536_9V6.1;Pp1s536_9V6.2 : ""Pp1s536_9V6.1;Pp1s536_9V6.2"""	AT3G44890.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_48243		Pp1s108_36V6.1	AT2G37820.1	GO:0005554 : GO:0007242	intracellular signaling cascade : molecular function unknown

Phypa_144932	F6D8.37; formamidopyrimidine-DNA glycolase family protein / mutM, putative (MMH-1) [Arabidopsis thaliana] : "F6D8.37; formamidopyrimidine-DNA glycolase family protein / mutM, putative (MMH-1) [Arabidopsis thaliana]"	Pp1s221_62V6.1	AT1G52500.2	GO:0003723 : GO:0003735 : GO:0005622 : GO:0005840 : GO:0006281 : GO:0006412	DNA repair : RNA binding : intracellular : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_29541	MQK4.29; zinc finger protein 3 (gb|AAD27875.1) [Arabidopsis thaliana] : "MQK4.29; zinc finger protein 3 (gb|AAD27875.1) [Arabidopsis thaliana]"	Pp1s6_324V6.1	AT2G47850.3	GO:0003676	nucleic acid binding
Phypa_105033	Major allergen Mal d 1 (Mal d I) [Malus x domestica]	Pp1s22_322V6.1	AT1G24020.1		
Phypa_114336	50S ribosomal protein L15, chloroplast precursor (CL15) [Pisum sativum]	Pp1s9_435V6.1	AT3G25920.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412 : GO:0015934	intracellular : large ribosomal subunit : protein biosynthesis : ribosome : structural constituent of ribosome

Phypa_213049	F3H11.5; organic cation transporter family protein [Arabidopsis thaliana] : "F3H11.5; organic cation transporter family protein [Arabidopsis thaliana]"	Pp1s85_39V6.1	AT3G20660.1	GO:0005215 : GO:0006810 : GO:0016020 : GO:0016021	integral to membrane : membrane : transport : transporter activity
Phypa_217194	T6H22.13; elongation factor 2, putative / EF-2, putative [EC:3.6.5.3] [KO:K03234] [Arabidopsis thaliana] : "T6H22.13; elongation factor 2, putative / EF-2, putative [EC:3.6.5.3] [KO:K03234] [Arabidopsis thaliana]"	Pp1s138_85V6.1	AT1G56070.1	GO:0003924 : GO:0005525 : GO:0006412 : GO:0008547	GTP binding : GTPase activity : protein biosynthesis : protein-synthesizing GTPase activity
Phypa_219988	T1O24.43; chitinase, putative [Arabidopsis thaliana] : "T1O24.43; chitinase, putative [Arabidopsis thaliana]"	Pp1s184_140V6.1	AT3G54420.1	GO:0004568 : GO:0006032 : GO:0008061 : GO:0008843 : GO:0009613 : GO:0016998	cell wall catabolism : chitin binding : chitin catabolism : chitinase activity : endochitinase activity : response to pest, pathogen or parasite

Phypa_60454	Probable cytochrome c biosynthesis protein [Marchantia polymorpha]	Pp1s247_16V6.1	AT2G07681.1	GO:0006461 : GO:0008535 : GO:0015232 : GO:0015886 : GO:0016020 : GO:0017004	cytochrome c oxidase complex assembly : cytochrome complex assembly : heme transport : heme transporter activity : membrane : protein complex assembly
[Phypa_117402;Phypa_176895]					
Phypa_163991		Pp1s63_123V6.1	AT2G36620.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_71337	Loricrin [Mus musculus]	Pp1s32_94V6.2;Pp1s32_94V6.1 : "Pp1s32_94V6.2;Pp1s32_94V6.1" : "Pp1s32_94V6.2;Pp1s32_94V6.1 : ""Pp1s32_94V6.2;Pp1s32_94V6.1"""	Pp1s32_94V6	GO:0004402	histone acetyltransferase activity
Phypa_22569	MXC17.9; expressed protein [Arabidopsis thaliana] : "MXC17.9; expressed protein [Arabidopsis thaliana]"	Pp1s4_62V6.1;Pp1s4_62V6.2 : "Pp1s4_62V6.1;Pp1s4_62V6.2" : "Pp1s4_62V6.1;Pp1s4_62V6.2 : ""Pp1s4_62V6.1;Pp1s4_62V6.2"""	AT5G24690.1		
Phypa_74339		Pp1s47_2V6.1			

Phypa_148936	F16B3.17; ubiquitin family protein [Arabidopsis thaliana] : "F16B3.17; ubiquitin family protein [Arabidopsis thaliana]"	Pp1s286_52V6.1	AT3G02540.3	GO:0005634 : GO:0006289 : GO:0006464	nucleotide-excision repair : nucleus : protein modification
Phypa_124611		Pp1s50_146V6.1	AT4G12040.2	GO:0003677 : GO:0005554 : GO:0008270	DNA binding : molecular function unknown : zinc ion binding
Phypa_188453	T22F11.9; meprin and TRAF homology domain-containing protein / MATH domain-containing protein [Arabidopsis thaliana] : "T22F11.9; meprin and TRAF homology domain-containing protein / MATH domain-containing protein [Arabidopsis thaliana]"	Pp1s119_72V6.1	AT2G25320.1		
Phypa_66307	T7B11.33; expressed protein [Arabidopsis thaliana] : "T7B11.33; expressed protein [Arabidopsis thaliana]"	Pp1s10_122V6.1			
Phypa_162383		Pp1s42_179V6.1			

Phypa_142157	Sigma factor sigB regulation protein rsbQ [Bacillus subtilis]	Pp1s188_47V6.1	AT4G37470.1	GO:0003824 : GO:0006725 : GO:0016787	aromatic compound metabolism : catalytic activity : hydrolase activity
Phypa_56898	K24M7.20; MATE efflux protein - related [Arabidopsis thaliana] : "K24M7.20; MATE efflux protein - related [Arabidopsis thaliana]"	Pp1s48_46V6.2;Pp1s48_46V6.1 : "Pp1s48_46V6.2;Pp1s48_46V6.1" : "Pp1s48_46V6.2;Pp1s48_46V6.1 : ""Pp1s48_46V6.2;Pp1s48_46V6.1"""	AT5G52450.1	GO:0006855 : GO:0015238 : GO:0015297 : GO:0016020	antiporter activity : drug transporter activity : membrane : multidrug transport
Phypa_151194 [Phypa_63228;Phypa_193949]	F3L17.4; splicing factor RSZp22 (RSZP22) / 9G8-like SR protein (SRZ22) [Arabidopsis thaliana] : "F3L17.4; splicing factor RSZp22 (RSZP22) / 9G8-like SR protein (SRZ22) [Arabidopsis thaliana]"	Pp1s332_29V6.1;Pp1s332_29V6.2 : "Pp1s332_29V6.1;Pp1s332_29V6.2" : "Pp1s332_29V6.1;Pp1s332_29V6.2 : ""Pp1s332_29V6.1;Pp1s332_29V6.2"""	AT4G31580.2	GO:0003676	nucleic acid binding
Phypa_128273	putative ribosomal protein L26 [Oryza sativa (japonica cultivar-group)]	Pp1s69_191V6.1	AT3G49910.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412 : GO:0015934	intracellular : large ribosomal subunit : protein biosynthesis : ribosome : structural constituent of ribosome

Phypa_202041	T10M13.9; GTP-binding protein (SAR1A) [Arabidopsis thaliana] : "T10M13.9; GTP-binding protein (SAR1A) [Arabidopsis thaliana]"	Pp1s7_338V6.1	AT4G02080.1	GO:0005525 : GO:0006886 : GO:0007264	GTP binding : intracellular protein transport : small GTPase mediated signal transduction
[Phypa_53670;Phypa_53669;Phypa_225790]					
Phypa_211705	K7P8.3; expressed protein [Arabidopsis thaliana] : "K7P8.3; expressed protein [Arabidopsis thaliana]"	Pp1s72_271V6.2;Pp1s72_271V6.1 : "Pp1s72_271V6.2;Pp1s72_271V6.1" : "Pp1s72_271V6.2;Pp1s72_271V6.1 : ""Pp1s72_271V6.2;Pp1s72_271V6.1"""	AT1G68140.3		
Phypa_217801	Elongation factor TuB, chloroplast precursor (EF-TuB) [Nicotiana sylvestris]	Pp1s147_106V6.1	AT4G20360.1	GO:0003746 : GO:0003924 : GO:0005525 : GO:0006412 : GO:0006414 : GO:0008547	GTP binding : GTPase activity : protein biosynthesis : protein-synthesizing GTPase activity : translation elongation factor activity : translational elongation

Phypa_195542	T2N18.5; 60S ribosomal protein L12 (RPL12A) [KO:K02870] [Arabidopsis thaliana] : "T2N18.5; 60S ribosomal protein L12 (RPL12A) [KO:K02870] [Arabidopsis thaliana]"	Pp1s242_7V6.1	AT3G53430.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_110421	F19G10.14; disease resistance-responsive family protein [Arabidopsis thaliana] : "F19G10.14; disease resistance-responsive family protein [Arabidopsis thaliana]"	Pp1s252_11V6.1	AT1G22900.1		
Phypa_218993	F14M19.170; 60S acidic ribosomal protein P3 (RPP3A) [Arabidopsis thaliana] : "F14M19.170; 60S acidic ribosomal protein P3 (RPP3A) [Arabidopsis thaliana]"	Pp1s167_19V6.1	AT4G25890.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006414	intracellular : ribosome : structural constituent of ribosome : translational elongation
Phypa_129054	60S ribosomal protein L44 [Gossypium hirsutum]	Pp1s74_73V6.1	AT4G14320.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome

Phypa_183211	Glycine-rich protein 2 [Nicotiana sylvestris]	Pp1s64_4V6.2;Pp1s64_4V6.1 : "Pp1s64_4V6.2;Pp1s64_4V6.1" : "Pp1s64_4V6.2;Pp1s64_4V6.1 : ""Pp1s64_4V6.2;Pp1s64_4V6.1"""	AT4G36020.1	GO:0003676 : GO:0003677 : GO:0006355	DNA binding : nucleic acid binding : regulation of transcription, DNA-dependent
Phypa_219977	contains EST C98236(C1282) [Oryza sativa (japonica cultivar-group)]	Pp1s184_111V6.1	AT2G34480.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_72129	T29H11.150; protein-L-isoaspartate O-methyltransferase / PIMT (PCM) [Arabidopsis thaliana] : "T29H11.150; protein-L-isoaspartate O-methyltransferase / PIMT (PCM) [Arabidopsis thaliana]"	Pp1s35_262V6.1;Pp1s35_262V6.2;Pp1s35_262V6.3;Pp1s35_262V6.4 : "Pp1s35_262V6.1;Pp1s35_262V6.2;Pp1s35_262V6.3;Pp1s35_262V6.4" : "Pp1s35_262V6.1;Pp1s35_262V6.2;Pp1s35_262V6.3;Pp1s35_262V6.4 : ""Pp1s35_262V6.1;Pp1s35_262V6.2;Pp1s35_262V6.3;Pp1s35_262V6.4"""	AT5G50240.1	GO:0004719 : GO:0006464 : GO:0008757	S-adenosylmethionine-dependent methyltransferase activity : protein modification : protein-L-isoaspartate (D-aspartate) O-methyltransferase activity

Phypa_233358		Pp1s77_158V6.2;Pp1s77_158V6.1 : "Pp1s77_158V6.2;Pp1s77_158V6.1" : "Pp1s77_158V6.2;Pp1s77_158V6.1 : ""Pp1s77_158V6.2;Pp1s77_158V6.1"""			
Phypa_214411 [Phypa_135358;Phypa_135382]	T24A18.40; 60S ribosomal protein L14 (RPL14B) [KO:K02875] [Arabidopsis thaliana] : "T24A18.40; 60S ribosomal protein L14 (RPL14B) [KO:K02875] [Arabidopsis thaliana]"	Pp1s101_10V6.1	AT4G27090.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_19427	F9H16.14; RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] : "F9H16.14; RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana]"	Pp1s126_15V6.2;Pp1s126_15V6.1 : "Pp1s126_15V6.2;Pp1s126_15V6.1" : "Pp1s126_15V6.2;Pp1s126_15V6.1 : ""Pp1s126_15V6.2;Pp1s126_15V6.1"""	AT1G76460.1	GO:0003676	nucleic acid binding

Phypa_192417	F2N1.17; acetylesterase, putative [Arabidopsis thaliana] : "F2N1.17; acetylesterase, putative [Arabidopsis thaliana]"	Pp1s179_68V6.1	AT4G01130.1	GO:0003824	catalytic activity
Phypa_172970		Pp1s398_30V6.1			
Phypa_84171	T4C21.160; transketolase, putative [EC:2.2.1.1] [KO:K00615] [Arabidopsis thaliana] : "T4C21.160; transketolase, putative [EC:2.2.1.1] [KO:K00615] [Arabidopsis thaliana]"	Pp1s120_127V6.1	AT3G60750.1	GO:0001584 : GO:0004802 : GO:0007186 : GO:0016021	G-protein coupled receptor protein signaling pathway : integral to membrane : rhodopsin-like receptor activity : transketolase activity

				GO:0004672 : GO:0004674 : GO:0004675 : GO:0004676 : GO:0004677 : GO:0004679 : GO:0004680 : GO:0004681 : GO:0004683 : GO:0004686 : GO:0004688 : GO:0004689 : GO:0004690 : GO:0004692 : GO:0004693 : GO:0004694 : GO:0004695 : GO:0004696 : GO:0004697 : GO:0004698 : GO:0004700 : GO:0004701 : GO:0004702 : GO:0004703 : GO:0004704 : GO:0004705 : GO:0004706 : GO:0004707 :	3-phosphoinositide dependent protein kinase activity : AMP- activated protein kinase activity : ATP binding : DNA-dependent protein kinase activity : G- protein coupled receptor kinase activity : IkappaB kinase activity : JUN kinase activity : JUN kinase kinase activity : JUN kinase kinase kinase activity : Janus kinase activity : MAP kinase 1 activity : MAP kinase 2 activity : MAP kinase activity : MAP kinase kinase activity : MAP kinase kinase kinase activity : MAP kinase kinase kinase kinase activity : MAP/ERK kinase kinase activity : MP kinase activity : NF- kappaB-inducing kinase activity : SAP kinase activity : atypical protein
Phypa_192815	MUK11.19; calcium-dependent protein kinase (CDPK)(AK1) [EC:2.7.1.-] [Arabidopsis thaliana] : "MUK11.19; calcium-dependent protein kinase (CDPK)(AK1) [EC:2.7.1.-] [Arabidopsis thaliana]"	Pp1s187_88V6.1;Pp1s187_88V6.2 : "Pp1s187_88V6.1;Pp1s187_88V6.2" : "Pp1s187_88V6.1;Pp1s187_88V6.2 : ""Pp1s187_88V6.1;Pp1s187_88V6.2"""	AT3G10660.1		
Phypa_55884		Pp1s22_18V6.1	AT4G17520.1		
[Phypa_117940;Phypa_118049]					

Phypa_150088	MXH1.11; auxin-induced protein family [Arabidopsis thaliana] : "MXH1.11; auxin-induced protein family [Arabidopsis thaliana]"	Pp1s310_2V6.1	AT5G35735.1	GO:0004500 : GO:0006584	catecholamine metabolism : dopamine beta-monooxygenase activity
Phypa_38810					
Phypa_149624	F16M14.18; DNA-binding protein-related [Arabidopsis thaliana] : "F16M14.18; DNA-binding protein-related [Arabidopsis thaliana]"	Pp1s301_48V6.1	AT2G38250.1	GO:0003677 : GO:0005634	DNA binding : nucleus
Phypa_168549		Pp1s180_137V6.1	AT1G06330.1	GO:0030001 : GO:0046872	metal ion binding : metal ion transport
Phypa_130931	T9L6.10; trihelix DNA-binding protein, putative [Arabidopsis thaliana] : "T9L6.10; trihelix DNA-binding protein, putative [Arabidopsis thaliana]"	Pp1s85_58V6.1	AT1G76890.2	GO:0003677 : GO:0005634	DNA binding : nucleus

Phypa_126323	T10D10.16; 40S ribosomal protein SA (RPSaA) [KO:K02998] [Arabidopsis thaliana] : "T10D10.16; 40S ribosomal protein SA (RPSaA) [KO:K02998] [Arabidopsis thaliana]"	Pp1s59_133V6.1	AT1G72370.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412 : GO:0015935	intracellular : protein biosynthesis : ribosome : small ribosomal subunit : structural constituent of ribosome
Phypa_128354	Probable histone deacetylase complex subunit SAP18 (Sin3-associated polypeptide, 18 kDa) [Arabidopsis thaliana]	Pp1s69_145V6.1	AT2G45640.1		
Phypa_10989	F15M4.15; RWP-RK domain-containing protein [Arabidopsis thaliana] : "F15M4.15; RWP-RK domain-containing protein [Arabidopsis thaliana]"	Pp1s109_79V6.1	AT4G24020.1		

Phypa_220786	T25K16.8; pyruvate dehydrogenase E1 component alpha subunit, chloroplast [EC:1.2.4.1] [KO:K00161] [Arabidopsis thaliana] : "T25K16.8; pyruvate dehydrogenase E1 component alpha subunit, chloroplast [EC:1.2.4.1] [KO:K00161] [Arabidopsis thaliana]"	Pp1s199_145V6.1	AT1G01090.1	GO:0004739 : GO:0008152 : GO:0016624	metabolism : oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor : pyruvate dehydrogenase (acetyl-transferring) activity
[Phypa_228450;Phypa_227610;Phypa_109208] Phypa_27940		Pp1s3_98V6.1	AT1G79650.4	GO:0006464	protein modification
Phypa_199029	contains EST AU093701(C63333) [Oryza sativa (japonica cultivar-group)]	Pp1s350_28V6.1	AT1G53540.1		
[Phypa_133628;Phypa_133621] Phypa_166789	Dof zinc finger protein DOF1.10 (AtDOF1.10) (H-protein promoter-binding factor 2b) [Arabidopsis thaliana]	Pp1s124_139V6.1	AT3G47500.1	GO:0003677	DNA binding

Phypa_166310 [Phypa_93557;Phypa_60419]	contains EST C28646(C61919) similar to Arabidopsis thaliana chromosome1,At1g27340 unknown protein [Oryza sativa (japonica cultivar-group)]	Pp1s111_44V6.2;Pp1s111_44V6.1;Pp1s111_44V6.3 : "Pp1s111_44V6.2;Pp1s111_44V6.1;Pp1s111_44V6.3" : "Pp1s111_44V6.2;Pp1s111_44V6.1;Pp1s111_44V6.3 : ""Pp1s111_44V6.2;Pp1s111_44V6.1;Pp1s111_44V6.3"""	AT1G27340.1		
Phypa_132819	F8A24.7; serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B' (B'beta) [Arabidopsis thaliana] : "F8A24.7; serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B' (B'beta) [Arabidopsis thaliana]"	Pp1s98_229V6.1	AT4G15415.2	GO:0000159 : GO:0007165 : GO:0008601 : GO:0047778	[citrate-(pro-3S)-lyase] thiolesterase activity : protein phosphatase type 2A complex : protein phosphatase type 2A regulator activity : signal transduction

Phypa_88890	MDC8.9; jacalin lectin family protein [Arabidopsis thaliana] : "MDC8.9; jacalin lectin family protein [Arabidopsis thaliana]"	H/ACA small nucleolar RNP component GAR1		KOG3262	
Phypa_120509	F6I18.170; cytosol aminopeptidase family protein [EC:3.4.11.1 3.4.11.5] [KO:K01259] [Arabidopsis thaliana] : "F6I18.170; cytosol aminopeptidase family protein [EC:3.4.11.1 3.4.11.5] [KO:K01259] [Arabidopsis thaliana]"	Pp1s33_172V6.1	AT2G24200.1	GO:0004177 : GO:0004178 : GO:0005622 : GO:0005737 : GO:0006508 : GO:0019538 : GO:0030145	aminopeptidase activity : cytoplasm : intracellular : leucyl aminopeptidase activity : manganese ion binding : protein metabolism : proteolysis and peptidolysis
Phypa_143844	40S ribosomal protein SA (p40) [Glycine max]	Pp1s209_47V6.1		GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome

Phypa_224573	F2G19.31; cysteine proteinase (RD21A) / thiol protease [EC:3.4.22.-] [Arabidopsis thaliana] : "F2G19.31; cysteine proteinase (RD21A) / thiol protease [EC:3.4.22.-] [Arabidopsis thaliana]"	Pp1s292_39V6.1;Pp1s292_39V6.2 : "Pp1s292_39V6.1;Pp1s292_39V6.2" : "Pp1s292_39V6.1;Pp1s292_39V6.2 : ""Pp1s292_39V6.1;Pp1s292_39V6.2"""	AT1G47128.1	GO:0004197 : GO:0004623 : GO:0005509 : GO:0006508 : GO:0008234 : GO:0016042 : GO:0016946	calcium ion binding : cathepsin F activity : cysteine-type endopeptidase activity : cysteine-type peptidase activity : lipid catabolism : phospholipase A2 activity : proteolysis and peptidolysis
Phypa_234354		Pp1s132_73V6.1;Pp1s132_74V6.1 : "Pp1s132_73V6.1;Pp1s132_74V6.1" : "Pp1s132_73V6.1;Pp1s132_74V6.1 : ""Pp1s132_73V6.1;Pp1s132_74V6.1"""			
Phypa_169977	T14P4.6; lipase class 3 family protein [Arabidopsis thaliana] : "T14P4.6; lipase class 3 family protein [Arabidopsis thaliana]"	Pp1s226_43V6.1	AT3G61680.1	GO:0003824 : GO:0004806 : GO:0006629	catalytic activity : lipid metabolism : triacylglycerol lipase activity
Phypa_116785	2-oxoglutarate/malate translocator, chloroplast precursor [Spinacia oleracea]	Pp1s17_363V6.1	AT5G12860.2	GO:0005215 : GO:0006814 : GO:0016020	membrane : sodium ion transport : transporter activity

Phypa_80245	F6E13.10; La domain-containing protein [Arabidopsis thaliana] : "F6E13.10; La domain-containing protein [Arabidopsis thaliana]"	Pp1s84_286V6.1	AT5G46250.1	GO:0003723 : GO:0005634 : GO:0005737 : GO:0006396 : GO:0006405 : GO:0030529	RNA binding : RNA processing : RNA-nucleus export : cytoplasm : nucleus : ribonucleoprotein complex

Phypa_174734	F1P15.5; amidophosphoribosyltransferase / glutamine phosphoribosylpyrophosphate amidotransferase / phosphoribosyldiphosphate 5-amidotransferase [EC:2.4.2.14] [KO:K00764] [Arabidopsis thaliana] : "F1P15.5; amidophosphoribosyltransferase / glutamine phosphoribosylpyrophosphate amidotransferase / phosphoribosyldiphosphate 5-amidotransferase [EC:2.4.2.14] [KO:K00764] [Arabidopsis thaliana]"	Pp1s8_239V6.1	AT2G16570.1	GO:0004044 : GO:0008152 : GO:0009113 : GO:0009116 : GO:0016740	amidophosphoribosyltransferase activity : metabolism : nucleoside metabolism : purine base biosynthesis : transferase activity

Phypa_67109	T6B20.10; lipase class 3 family protein [Arabidopsis thaliana] : "T6B20.10; lipase class 3 family protein [Arabidopsis thaliana]"	Pp1s13_266V6.1	AT1G51440.1	GO:0003824 : GO:0004806 : GO:0006629	catalytic activity : lipid metabolism : triacylglycerol lipase activity
Phypa_177219	Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplast precursor (Phospho-2-keto-3-deoxyheptonate aldolase 1) (DAHP synthetase 1) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 1) [Nicotiana tabacum]	Pp1s22_79V6.2;Pp1s22_79V6.1 : "Pp1s22_79V6.2;Pp1s22_79V6.1" : "Pp1s22_79V6.2;Pp1s22_79V6.1 : ""Pp1s22_79V6.2;Pp1s22_79V6.1"""	AT1G22410.1	GO:0003849 : GO:0009073	3-deoxy-7-phosphoheptulonate synthase activity : aromatic amino acid family biosynthesis
Phypa_47533	Glycine-rich protein 2 [Nicotiana sylvestris]	Pp1s103_65V6.1	AT4G36020.1	GO:0003676 : GO:0003677 : GO:0006355	DNA binding : nucleic acid binding : regulation of transcription, DNA-dependent
Phypa_27706	contains ESTs D22340(C10768),D15812(C1318),C98241(C1318) [Oryza sativa (japonica cultivar-group)]	Pp1s1_349V6.1	AT1G49950.2	GO:0003677 : GO:0005634	DNA binding : nucleus

Phypa_5536	F15J1.20; ankyrin repeat family protein / AFT protein (AFT) [Arabidopsis thaliana] : "F15J1.20; ankyrin repeat family protein / AFT protein (AFT) [Arabidopsis thaliana]"	Pp1s411_31V6.1	AT4G35450.2		
Phypa_173974	F28O9.190; DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] : "F28O9.190; DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana]"	Pp1s2_417V6.1	AT3G57340.2	GO:0006457 : GO:0031072 : GO:0051082	heat shock protein binding : protein folding : unfolded protein binding
Phypa_148104 [Phypa_225996;Phypa_226002]	F15D2.30; RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] : "F15D2.30; RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana]"	Pp1s271_57V6.2;Pp1s271_57V6.1 : "Pp1s271_57V6.2;Pp1s271_57V6.1" : "Pp1s271_57V6.2;Pp1s271_57V6.1 : ""Pp1s271_57V6.2;Pp1s271_57V6.1"""	AT1G29400.1	GO:0003676	nucleic acid binding

[Phypa_101257;Phypa_101260;Phypa_110814]					
Phypa_159781	hypothetical protein [Dictyostelium discoideum]	Pp1s15_300V6.1	AT1G28070.1		
Phypa_102704		Pp1s698_1V6.1	AT1G63440.1	GO:0004008 : GO:0005524 : GO:0006825 : GO:0016020 : GO:0030001 : GO:0046872	ATP binding : copper ion transport : copper-exporting ATPase activity : membrane : metal ion binding : metal ion transport
Phypa_203561		Pp1s15_268V6.1	AT5G43430.1	GO:0005489 : GO:0006118	electron transport : electron transporter activity
Phypa_157798	T5J17.200; histone H3.2 [Arabidopsis thaliana] : "T5J17.200; histone H3.2 [Arabidopsis thaliana]"	Pp1s1963_1V6.1	AT4G40030.2	GO:0000786 : GO:0003677 : GO:0005634 : GO:0006334 : GO:0007001	DNA binding : chromosome organization and biogenesis (sensu Eukaryota) : nucleosome : nucleosome assembly : nucleus
Phypa_180041	contains EST AU064366(E30232) [Oryza sativa (japonica cultivar-group)]	Pp1s39_288V6.1;Pp1s39_288V6.2 : "Pp1s39_288V6.1;Pp1s39_288V6.2" : "Pp1s39_288V6.1;Pp1s39_288V6.2 : ""Pp1s39_288V6.1;Pp1s39_288V6.2"""	AT3G10950.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome

Phypa_109882	Alpha-1,4-glucan-protein synthase [UDP-forming] 1 (UDP-glucose:protein transglucosylase 1) (UPTG 1) [Solanum tuberosum]	Pp1s66_155V6.2;Pp1s66_155V6.1;Pp1s66_156V6.1;Pp1s66_154V6.1 : "Pp1s66_155V6.2;Pp1s66_155V6.1;Pp1s66_154V6.1;Pp1s66_156V6.1" : "Pp1s66_155V6.2;Pp1s66_155V6.1;Pp1s66_156V6.1;Pp1s66_154V6.1 : ""Pp1s66_155V6.2;Pp1s66_155V6.1;Pp1s66_154V6.1;Pp1s66_156V6.1"""	AT5G15650.1	GO:0005794 : GO:0009505 : GO:0030244 : GO:0047210	Golgi apparatus : alpha-1,4-glucan-protein synthase (UDP-forming) activity : cell wall (sensu Magnoliophyta) : cellulose biosynthesis
Phypa_203817		Pp1s16_334V6.1	AT1G73500.1	GO:0004672 : GO:0004674 : GO:0004713 : GO:0005524 : GO:0006468	ATP binding : protein amino acid phosphorylation : protein kinase activity : protein serine/threonine kinase activity : protein-tyrosine kinase activity
Phypa_166141	F7J8.240; expressed protein [Arabidopsis thaliana] : "F7J8.240; expressed protein [Arabidopsis thaliana]"	Pp1s103_94V6.2;Pp1s103_94V6.1 : "Pp1s103_94V6.2;Pp1s103_94V6.1" : "Pp1s103_94V6.2;Pp1s103_94V6.1 : ""Pp1s103_94V6.2;Pp1s103_94V6.1"""	AT5G01260.2	GO:0003824 : GO:0005975	carbohydrate metabolism : catalytic activity

Phypa_73609	Glycine-rich RNA-binding protein 2 [Sorghum bicolor]	Pp1s42_251V6.2;Pp1s42_251V6.1 : "Pp1s42_251V6.2;Pp1s42_251V6.1" : "Pp1s42_251V6.2;Pp1s42_251V6.1 : ""Pp1s42_251V6.2;Pp1s42_251V6.1"""	AT4G39260.3	GO:0003676	nucleic acid binding
Phypa_8347	K3G17.6; myb family transcription factor [Arabidopsis thaliana] : "K3G17.6; myb family transcription factor [Arabidopsis thaliana]"	Pp1s10_267V6.1	AT3G50060.1	GO:0003677 : GO:0005634	DNA binding : nucleus
Phypa_165037	extremely serine rich protein [Candida albicans SC5314]	Pp1s81_168V6.1			
Phypa_64122		Pp1s1_863V6.1			
Phypa_73571		Pp1s42_188V6.1			
Phypa_71211	MPH15.6; homeobox-leucine zipper protein HAT14 (HD-Zip protein 14) [Arabidopsis thaliana] : "MPH15.6; homeobox-leucine zipper protein HAT14 (HD-Zip protein 14) [Arabidopsis thaliana]"	Pp1s31_272V6.1	AT5G06710.1	GO:0003677 : GO:0003700 : GO:0005634 : GO:0006355	DNA binding : nucleus : regulation of transcription, DNA-dependent : transcription factor activity

Phypa_169504 [Phypa_134474;Phypa_134439]	Immune inhibitor A precursor [Bacillus thuringiensis serovar alesti]	Pp1s211_85V6.2;Pp1s211_85V6.1;Pp1s211_85V6.3;Pp1s211_85V6.4 : "Pp1s211_85V6.2;Pp1s211_85V6.1;Pp1s211_85V6.3;Pp1s211_85V6.4" : "Pp1s211_85V6.2;Pp1s211_85V6.1;Pp1s211_85V6.3;Pp1s211_85V6.4 : ""Pp1s211_85V6.2;Pp1s211_85V6.1;Pp1s211_85V6.3;Pp1s211_85V6.4"""			
Phypa_172497	T6C23.11; TCP family transcription factor, putative [Arabidopsis thaliana] : "T6C23.11; TCP family transcription factor, putative [Arabidopsis thaliana]"	Pp1s356_40V6.1	AT3G47620.1	GO:0004402	histone acetyltransferase activity

Phypa_113830 [Phypa_9031;Phypa_317]	F15J1.30; thioredoxin reductase 1 / NADPH-dependent thioredoxin reductase 1 (NTR1) [EC:1.8.1.9] [KO:K00384] [Arabidopsis thaliana] : "F15J1.30; thioredoxin reductase 1 / NADPH-dependent thioredoxin reductase 1 (NTR1) [EC:1.8.1.9] [KO:K00384] [Arabidopsis thaliana]"	Pp1s8_297V6.1	AT2G17420.1	GO:0004791 : GO:0005737 : GO:0006118 : GO:0015036 : GO:0016491 : GO:0019430	cytoplasm : disulfide oxidoreductase activity : electron transport : oxidoreductase activity : removal of superoxide radicals : thioredoxin-disulfide reductase activity
Phypa_77631	MJM18.1; hypothetical protein [Arabidopsis thaliana] : "MJM18.1; hypothetical protein [Arabidopsis thaliana]"	Pp1s66_143V6.1	AT5G66950.1	GO:0006508 : GO:0008237 : GO:0008270	metallopeptidase activity : proteolysis and peptidolysis : zinc ion binding
Phypa_226674	contains ESTs AU093161(C63864),AU078381(S21490) [Oryza sativa (japonica cultivar-group)]	Pp1s373_11V6.1	AT5G12330.4		

Phypa_38771	hypothetical protein [Oryza sativa (japonica cultivar-group)]	Pp1s91_206V6.1;Pp1s91_206V6.2 : "Pp1s91_206V6.1;Pp1s91_206V6.2" : "Pp1s91_206V6.1;Pp1s91_206V6.2 : ""Pp1s91_206V6.1;Pp1s91_206V6.2"""	AT4G13830.2	GO:0006457 : GO:0031072 : GO:0051082	heat shock protein binding : protein folding : unfolded protein binding

Phypa_138954 [Phypa_105021;Phypa_177288] Phypa_97737	MRP15.9; 2-oxoisovalerate dehydrogenase / 3-methyl-2-oxobutanoate dehydrogenase / branched-chain alpha-keto acid dehydrogenase E1 beta subunit (DIN4) [EC:1.2.4.4] [KO:K00167] [Arabidopsis thaliana] : "MRP15.9; 2-oxoisovalerate dehydrogenase / 3-methyl-2-oxobutanoate dehydrogenase / branched-chain alpha-keto acid dehydrogenase E1 beta subunit (DIN4) [EC:1.2.4.4] [KO:K00167] [Arabidopsis thaliana]"	Pp1s152_53V6.1	AT3G13450.1	GO:0003863 : GO:0017086	3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring) activity : 3-methyl-2-oxobutanoate dehydrogenase (lipoamide) complex

Phypa_122357 [Phypa_201226;Phypa_228370]	Vacuolar sorting receptor 3 precursor (AtVSR3) (Epidermal growth factor receptor-like protein 2a) (AtELP2a) (BP80-like protein a') (AtBP80a') [Arabidopsis thaliana]	Pp1s39_354V6.2;Pp1s39_354V6.1 : "Pp1s39_354V6.2;Pp1s39_354V6.1" : "Pp1s39_354V6.2;Pp1s39_354V6.1 : ""Pp1s39_354V6.2;Pp1s39_354V6.1"""	AT2G14720.2	GO:0005509 : GO:0006508 : GO:0008233	calcium ion binding : peptidase activity : proteolysis and peptidolysis
Phypa_168832 [Phypa_232922;Phypa_234748]	MMG4.16; expressed protein [Arabidopsis thaliana] : "MMG4.16; expressed protein [Arabidopsis thaliana]"	Pp1s190_90V6.1;Pp1s190_91V6.1;Pp1s190_89V6.1 : "Pp1s190_90V6.1;Pp1s190_91V6.1;Pp1s190_89V6.1" : "Pp1s190_90V6.1;Pp1s190_91V6.1;Pp1s190_89V6.1 : ""Pp1s190_90V6.1;Pp1s190_91V6.1;Pp1s190_89V6.1"""		GO:0004402 : GO:0005669 : GO:0006352 : GO:0016986	histone acetyltransferase activity : transcription factor TFIID complex : transcription initiation : transcription initiation factor activity
Phypa_1326	F10B6.24; expressed protein [Arabidopsis thaliana] : "F10B6.24; expressed protein [Arabidopsis thaliana]"	Pp1s228_73V6.1	AT2G01750.1		

Phypa_18892 [Phypa_3688;Phypa_58013;Phypa_213086]	F5H14.27; expressed protein [Arabidopsis thaliana] : "F5H14.27; expressed protein [Arabidopsis thaliana]"	Pp1s87_57V6.1	AT2G40060.1		
Phypa_37877	contains ESTs AU062952(C51837),AU100820(C51837) [Oryza sativa (japonica cultivar-group)]	Pp1s118_100V6.1	AT5G61030.1	GO:0003676	nucleic acid binding
Phypa_99968	F1O17.3; esterase/lipase/thioesterase family protein [Arabidopsis thaliana] : "F1O17.3; esterase/lipase/thioesterase family protein [Arabidopsis thaliana]"	Pp1s405_1V6.1	AT2G36290.1	GO:0003824	catalytic activity
Phypa_168895	contains EST AU033244(S5767) unknown protein [Oryza sativa (japonica cultivar-group)]	Pp1s193_54V6.1;Pp1s193_54V6.2 : "Pp1s193_54V6.1;Pp1s193_54V6.2" : "Pp1s193_54V6.1;Pp1s193_54V6.2 : ""Pp1s193_54V6.1;Pp1s193_54V6.2"""	AT1G80000.1		

Phypa_128382	putative PSTVd RNA-biding protein [Oryza sativa (japonica cultivar-group)]	Pp1s70_77V6.1			
[Phypa_2572;Phypa_2573]					
Phypa_169433		Pp1s209_54V6.2;Pp1s209_54V6.1 : "Pp1s209_54V6.2;Pp1s209_54V6.1" : "Pp1s209_54V6.2;Pp1s209_54V6.1 : ""Pp1s209_54V6.2;Pp1s209_54V6.1"""	Pp1s209_54V6		
Phypa_170048	F20H23.3; Gar1 RNA-binding region family protein [Arabidopsis thaliana] : "F20H23.3; Gar1 RNA-binding region family protein [Arabidopsis thaliana]"	Pp1s229_16V6.1	AT3G03920.1	GO:0006364 : GO:0007046 : GO:0019843 : GO:0030532	rRNA binding : rRNA processing : ribosome biogenesis : small nuclear ribonucleoprotein complex
Phypa_213429	60S ribosomal protein L39	Pp1s89_150V6.1	AT4G31985.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome

Phypa_163017	F9L1.28; methyl-CpG-binding domain-containing protein [Arabidopsis thaliana] : "F9L1.28; methyl-CpG-binding domain-containing protein [Arabidopsis thaliana]"	Pp1s51_1V6.1	AT1G15340.1
Phypa_86357	F28H19.10; SEUSS transcriptional co-regulator [Arabidopsis thaliana] : "F28H19.10; SEUSS transcriptional co-regulator [Arabidopsis thaliana]"	Pp1s144_164V6.1;Pp1s144_165V6.1 : "Pp1s144_164V6.1;Pp1s144_165V6.1" : "Pp1s144_164V6.1;Pp1s144_165V6.1 : ""Pp1s144_164V6.1;Pp1s144_165V6.1"""	
Phypa_166622	T3F17.29; transmembrane protein-related [Arabidopsis thaliana] : "T3F17.29; transmembrane protein-related [Arabidopsis thaliana]"	Pp1s120_82V6.1	AT2G46060.1
Phypa_68756		Pp1s20_156V6.1	AT3G49180.1
[Phypa_126999;Phypa_77052]			

Phypa_143182	F7O18.23; expressed protein (SWP1) [Arabidopsis thaliana] : "F7O18.23; expressed protein (SWP1) [Arabidopsis thaliana]"	Pp1s199_104V6.2;Pp1s199_104V6.3;Pp1s199_104V6.1 : "Pp1s199_104V6.2;Pp1s199_104V6.3;Pp1s199_104V6.1" : "Pp1s199_104V6.2;Pp1s199_104V6.3;Pp1s199_104V6.1 : ""Pp1s199_104V6.2;Pp1s199_104V6.3;Pp1s199_104V6.1"""	AT3G04740.1		
Phypa_105288		Pp1s32_160V6.1	AT5G54500.1	GO:0010181 : GO:0016491	FMN binding : oxidoreductase activity
Phypa_213630	Ubiquitin-conjugating enzyme E2-17 kDa (Ubiquitin-protein ligase) (Ubiquitin carrier protein) [Medicago sativa]	Pp1s91_88V6.1	AT2G02760.1	GO:0004840 : GO:0004842 : GO:0006464 : GO:0006512	protein modification : ubiquitin conjugating enzyme activity : ubiquitin cycle : ubiquitin-protein ligase activity
Phypa_45136		Pp1s109_127V6.1	AT4G01850.1	GO:0004478 : GO:0005524 : GO:0006730	ATP binding : methionine adenosyltransferase activity : one-carbon compound metabolism
Phypa_177723	MSD21.24; expressed protein [Arabidopsis thaliana] : "MSD21.24; expressed protein [Arabidopsis thaliana]"	Pp1s25_340V6.1	AT3G21865.1		

Phypa_29816	AP22.21; G-box binding factor 1 (GBF1) [Arabidopsis thaliana] : "AP22.21; G-box binding factor 1 (GBF1) [Arabidopsis thaliana]"	Pp1s27_273V6.1	AT1G32150.1	GO:0003677 : GO:0005634 : GO:0006355	DNA binding : nucleus : regulation of transcription, DNA-dependent
Phypa_140125	Bcat1; branched chain aminotransferase 1, cytosolic [EC:2.6.1.42] [KO:K00826] [Mus musculus] : "Bcat1; branched chain aminotransferase 1, cytosolic [EC:2.6.1.42] [KO:K00826] [Mus musculus]"	Pp1s163_127V6.1	AT5G65780.1	GO:0003824 : GO:0004084 : GO:0005524 : GO:0008152 : GO:0009081 : GO:0015986 : GO:0016469 : GO:0046933 : GO:0046961	ATP binding : ATP synthesis coupled proton transport : branched chain family amino acid metabolism : branched-chain-amino-acid transaminase activity : catalytic activity : hydrogen-transporting ATP synthase activity, rotational mechanism : hydrogen-transporting ATPase activity, rotational mechanism : metabolism : proton-transporting two-sector ATPase complex

Phypa_152231	T17M13.16; ribonuclease 1 (RNS1) [EC:3.1.27.1] [Arabidopsis thaliana] : "T17M13.16; ribonuclease 1 (RNS1) [EC:3.1.27.1] [Arabidopsis thaliana]"	Pp1s358_60V6.1;Pp1s358_60V6.2 : "Pp1s358_60V6.1;Pp1s358_60V6.2" : "Pp1s358_60V6.1;Pp1s358_60V6.2 : ""Pp1s358_60V6.1;Pp1s358_60V6.2"""	AT2G02990.1	GO:0003723 : GO:0004521	RNA binding : endoribonuclease activity
Phypa_122793	F26K9.200; transport protein-related [Arabidopsis thaliana] : "F26K9.200; transport protein-related [Arabidopsis thaliana]"	Pp1s41_98V6.1	AT3G62770.1		
Phypa_195956	F24I3.230; dyskerin, putative / nucleolar protein NAP57, putative [Arabidopsis thaliana] : "F24I3.230; dyskerin, putative / nucleolar protein NAP57, putative [Arabidopsis thaliana]"	Pp1s251_19V6.1	AT3G57150.1	GO:0003723 : GO:0004730 : GO:0006396	RNA binding : RNA processing : pseudouridylate synthase activity
Phypa_168983		Pp1s195_100V6.1			
Phypa_117389	Adenosylhomocysteinase (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase) [Catharanthus roseus]	Pp1s20_308V6.1	AT4G13940.1	GO:0004013 : GO:0006730	adenosylhomocysteinase activity : one-carbon compound metabolism

[Phypa_156563;Phypa_157157;Phypa_102363;Phypa_103579;Phypa_103626]					
Phypa_9740	MPF21.9; AP2 domain transcription factor, putative [Arabidopsis thaliana] : "MPF21.9; AP2 domain transcription factor, putative [Arabidopsis thaliana]"	Pp1s259_104V6.1	AT2G33710.2	GO:0003700 : GO:0005634 : GO:0006355	nucleus : regulation of transcription, DNA-dependent : transcription factor activity
Phypa_140886 [Phypa_124138;Phypa_123920]	Fructose-bisphosphate aldolase, chloroplast precursor (ALDP) [no tax name]	Pp1s171_150V6.1	AT2G01140.1	GO:0004332 : GO:0006096	fructose-bisphosphate aldolase activity : glycolysis
Phypa_65365	MSL3.12; NTF2-containing RNA-binding protein, putative [Arabidopsis thaliana] : "MSL3.12; NTF2-containing RNA-binding protein, putative [Arabidopsis thaliana]"	Pp1s6_129V6.1	AT5G60980.1	GO:0003676 : GO:0004308 : GO:0005622 : GO:0005634 : GO:0006606 : GO:0008565	exo-alpha-sialidase activity : intracellular : nucleic acid binding : nucleus : protein transporter activity : protein-nucleus import

Phypa_146516	S-adenosylmethionine synthetase 1 (Methionine adenosyltransferase 1) (AdoMet synthetase 1) [Lycopersicon esculentum]	Pp1s244_74V6.1	AT4G01850.1	GO:0004478 : GO:0005524 : GO:0006730 : GO:0048269 : GO:0048270	ATP binding : methionine adenosyltransferase activity : methionine adenosyltransferase complex : methionine adenosyltransferase regulator activity : one-carbon compound metabolism
Phypa_197211	contains EST C98230(C1257) [Oryza sativa (japonica cultivar-group)]	Pp1s287_20V6.1	AT5G02960.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412 : GO:0015935	intracellular : protein biosynthesis : ribosome : small ribosomal subunit : structural constituent of ribosome
Phypa_159184	LOC499168; similar to protein tyrosine phosphatase, receptor type, F [Rattus norvegicus] : "LOC499168; similar to protein tyrosine phosphatase, receptor type, F [Rattus norvegicus]"	Pp1s10_115V6.1			

Phypa_89036	Epstein-Barr nuclear antigen 1 (EBV nuclear antigen 1) (EBNA-1) [Human herpesvirus 4 (strain B95-8)]	Pp1s177_101V6.1;Pp1s177_102V6.1 : "Pp1s177_101V6.1;Pp1s177_102V6.1" : "Pp1s177_101V6.1;Pp1s177_102V6.1 : ""Pp1s177_101V6.1;Pp1s177_102V6.1"""	AT2G19810.1	GO:0004402	histone acetyltransferase activity
Phypa_142560	T19F6.30; glycosyl hydrolase family protein 37 / trehalase, putative [EC:3.2.1.28] [KO:K01194] [Arabidopsis thaliana] : "T19F6.30; glycosyl hydrolase family protein 37 / trehalase, putative [EC:3.2.1.28] [KO:K01194] [Arabidopsis thaliana]"	Pp1s194_104V6.3;Pp1s194_104V6.2;Pp1s194_104V6.1 : "Pp1s194_104V6.3;Pp1s194_104V6.2;Pp1s194_104V6.1" : "Pp1s194_104V6.3;Pp1s194_104V6.2;Pp1s194_104V6.1 : ""Pp1s194_104V6.3;Pp1s194_104V6.2;Pp1s194_104V6.1"""	AT4G24040.1	GO:0004555 : GO:0005991	alpha,alpha-trehalase activity : trehalose metabolism
Phypa_46426	40S ribosomal protein SA (p40) [Daucus carota]	Pp1s173_16V6.1	AT1G72370.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412 : GO:0015935	intracellular : protein biosynthesis : ribosome : small ribosomal subunit : structural constituent of ribosome

Phypa_194318	MMB12.18; pathogenesis-related protein, putative [Arabidopsis thaliana] : "MMB12.18; pathogenesis-related protein, putative [Arabidopsis thaliana]"	Pp1s215_2V6.1	AT3G19690.1	GO:0005576	extracellular region
Phypa_168035		Pp1s164_49V6.1			
Phypa_165920	F8A24.7; serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B' (B'beta) [Arabidopsis thaliana] : "F8A24.7; serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B' (B'beta) [Arabidopsis thaliana]"	Pp1s98_213V6.1;Pp1s98_214V6.2 : "Pp1s98_213V6.1;Pp1s98_214V6.2" : "Pp1s98_213V6.1;Pp1s98_214V6.2 : ""Pp1s98_213V6.1;Pp1s98_214V6.2"""	AT4G15415.1	GO:0000159 : GO:0007165 : GO:0008601 : GO:0047778	[citrate-(pro-3S)-lyase] thiolesterase activity : protein phosphatase type 2A complex : protein phosphatase type 2A regulator activity : signal transduction
Phypa_71025	hypothetical protein [Dictyostelium discoideum]	Pp1s30_337V6.1		GO:0004553 : GO:0005975	carbohydrate metabolism : hydrolase activity, hydrolyzing O-glycosyl compounds

Phypa_172187	hypothetical protein [Oryza sativa (japonica cultivar-group)]	Pp1s335_58V6.1;Pp1s335_58V6.2 : "Pp1s335_58V6.1;Pp1s335_58V6.2" : "Pp1s335_58V6.1;Pp1s335_58V6.2 : ""Pp1s335_58V6.1;Pp1s335_58V6.2"""	AT1G49000.1		
Phypa_169417	hypothetical protein [Oryza sativa (japonica cultivar-group)]	Pp1s208_161V6.1	AT5G13470.1		
Phypa_194737	F5O24.180; 40S ribosomal protein S8 (RPS8A) [KO:K02995] [Arabidopsis thaliana] : "F5O24.180; 40S ribosomal protein S8 (RPS8A) [KO:K02995] [Arabidopsis thaliana]"	Pp1s223_73V6.1	AT5G59240.1	GO:0005622	intracellular
Phypa_116683	F20C19.19; GDSL-motif lipase/hydrolase family protein [Arabidopsis thaliana] : "F20C19.19; GDSL-motif lipase/hydrolase family protein [Arabidopsis thaliana]"	Pp1s17_356V6.1	AT1G54790.2	GO:0003824	catalytic activity
Phypa_234701		Pp1s149_229V6.1	AT5G26700.1		

Phypa_149221	T13J8.100; YGGT family protein [Arabidopsis thaliana] : "T13J8.100; YGGT family protein [Arabidopsis thaliana]"	Pp1s293_107V6.1	AT4G27990.1	GO:0003723 : GO:0005525 : GO:0005786 : GO:0006614 : GO:0016020	GTP binding : RNA binding : SRP-dependent cotranslational protein-membrane targeting : membrane : signal recognition particle (sensu Eukaryota)
Phypa_92280		Pp1s223_16V6.1	AT1G56190.1		
Phypa_76520	Elongation factor 1-alpha (EF-1-alpha) [Glycine max]	Pp1s59_188V6.1;Pp1s59_188V6.2;Pp1s59_188V6.3 : "Pp1s59_188V6.1;Pp1s59_188V6.2;Pp1s59_188V6.3" : "Pp1s59_188V6.1;Pp1s59_188V6.2;Pp1s59_188V6.3 : ""Pp1s59_188V6.1;Pp1s59_188V6.2;Pp1s59_188V6.3"""	AT1G07920.1	GO:0003746 : GO:0003924 : GO:0005525 : GO:0005737 : GO:0006412 : GO:0006414 : GO:0008547	GTP binding : GTPase activity : cytoplasm : protein biosynthesis : protein-synthesizing GTPase activity : translation elongation factor activity : translational elongation
Phypa_180264	F26H11.18; cold-shock DNA-binding family protein / glycine-rich protein (GRP2) [Arabidopsis thaliana] : "F26H11.18; cold-shock DNA-binding family protein / glycine-rich protein (GRP2) [Arabidopsis thaliana]"	Pp1s41_68V6.1	AT4G36020.1	GO:0003676 : GO:0003677 : GO:0006355	DNA binding : nucleic acid binding : regulation of transcription, DNA-dependent

Phypa_164358	60S acidic ribosomal protein P1 (L12) [Zea mays]	Pp1s68_115V6.1	AT5G24510.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006414	intracellular : ribosome : structural constituent of ribosome : translational elongation
[Phypa_189887;Phypa_217197]					
[Phypa_154305;Phypa_218180]					
[Phypa_123116;Phypa_180561;Phypa_123073]					
[Phypa_154682;Phypa_200520;Phypa_154659]					
Phypa_200899	F19K6.12; 60S ribosomal protein L37 (RPL37B) [KO:K02922] [Arabidopsis thaliana] : "F19K6.12; 60S ribosomal protein L37 (RPL37B) [KO:K02922] [Arabidopsis thaliana]"	Pp1s475_18V6.1	AT1G52300.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_205598	60S ribosomal protein L31 [Perilla frutescens]	Pp1s28_306V6.1	AT2G19740.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_19797	Glycine-rich RNA-binding protein 2 [Sorghum bicolor]	Pp1s136_70V6.1	AT4G39260.3	GO:0003676	nucleic acid binding

Phypa_19709	Protein At1g77540 [Arabidopsis thaliana]	Pp1s91_93V6.1;Pp1s91_93V6.2 : "Pp1s91_93V6.1;Pp1s91_93V6.2" : "Pp1s91_93V6.1;Pp1s91_93V6.2 : ""Pp1s91_93V6.1;Pp1s91_93V6.2"""	AT1G21770.1
[Phypa_150243;Phypa_225255]			
Phypa_136723	IMP-specific 5'-nucleotidase 1 [no tax name]	Pp1s131_67V6.1	
Phypa_92771	F17I23.270; expressed protein [Arabidopsis thaliana] : "F17I23.270; expressed protein [Arabidopsis thaliana]"	Pp1s230_66V6.2;Pp1s230_66V6.1 : "Pp1s230_66V6.2;Pp1s230_66V6.1" : "Pp1s230_66V6.2;Pp1s230_66V6.1 : ""Pp1s230_66V6.2;Pp1s230_66V6.1"""	AT4G30390.1
Phypa_97140	T7B11.33; expressed protein [Arabidopsis thaliana] : "T7B11.33; expressed protein [Arabidopsis thaliana]"	Pp1s319_48V6.1;Pp1s319_47V6.2;Pp1s319_47V6.1 : "Pp1s319_48V6.1;Pp1s319_47V6.2;Pp1s319_47V6.1" : "Pp1s319_48V6.1;Pp1s319_47V6.2;Pp1s319_47V6.1 : ""Pp1s319_48V6.1;Pp1s319_47V6.2;Pp1s319_47V6.1"""	

[Phypa_143434;Phypa_157535]					
Phypa_144846	F5N5.17; expressed protein [Arabidopsis thaliana] : "F5N5.17; expressed protein [Arabidopsis thaliana]"	Pp1s220_112V6.1	AT3G22970.1		
Phypa_116428	Thiazole biosynthetic enzyme, chloroplast precursor [Citrus sinensis]	Pp1s16_179V6.1;Pp1s16_179V6.2 : "Pp1s16_179V6.1;Pp1s16_179V6.2" : "Pp1s16_179V6.1;Pp1s16_179V6.2 : ""Pp1s16_179V6.1;Pp1s16_179V6.2"""	AT5G54770.1	GO:0006118 : GO:0009228	electron transport : thiamin biosynthesis
Phypa_194709	T28K15.1; no apical meristem (NAM) family protein [Arabidopsis thaliana] : "T28K15.1; no apical meristem (NAM) family protein [Arabidopsis thaliana]"	Pp1s223_12V6.1;Pp1s223_12V6.2 : "Pp1s223_12V6.1;Pp1s223_12V6.2" : "Pp1s223_12V6.1;Pp1s223_12V6.2 : ""Pp1s223_12V6.1;Pp1s223_12V6.2"""	AT1G12260.1		

Phypa_159009	F15J1.30; thioredoxin reductase 1 / NADPH-dependent thioredoxin reductase 1 (NTR1) [EC:1.8.1.9] [KO:K00384] [Arabidopsis thaliana] : "F15J1.30; thioredoxin reductase 1 / NADPH-dependent thioredoxin reductase 1 (NTR1) [EC:1.8.1.9] [KO:K00384] [Arabidopsis thaliana]"	Pp1s8_302V6.1	AT2G17420.1	GO:0004791 : GO:0005737 : GO:0006118 : GO:0015036 : GO:0016491 : GO:0019430	cytoplasm : disulfide oxidoreductase activity : electron transport : oxidoreductase activity : removal of superoxide radicals : thioredoxin-disulfide reductase activity
Phypa_170328	F18O14.29; expressed protein [Arabidopsis thaliana] : "F18O14.29; expressed protein [Arabidopsis thaliana]"	Pp1s241_42V6.1	AT1G19530.1		
Phypa_173651	DBP2; DEAD box RNA helicase [Candida albicans SC5314] : "DBP2; DEAD box RNA helicase [Candida albicans SC5314]"	Pp1s527_3V6.1	AT1G55150.1	GO:0003676 : GO:0004386 : GO:0005524 : GO:0008026	ATP binding : ATP-dependent helicase activity : helicase activity : nucleic acid binding

Phypa_64463	proteophosphoglycan ppg1 [Leishmania major]	Pp1s2_651V6.1		GO:0031177	phosphopantetheine binding
Phypa_172235		Pp1s337_35V6.1			
[Phypa_92279;Phypa_60168]					
Phypa_170625					
Phypa_105781	40S ribosomal protein SA (p40) [Glycine max]	Pp1s48_103V6.1	AT3G04770.2	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412 : GO:0015935	intracellular : protein biosynthesis : ribosome : small ribosomal subunit : structural constituent of ribosome
Phypa_122336	Chalcone synthase 1B (Naringenin-chalcone synthase 1B) [Pisum sativum]	Pp1s39_349V6.1	AT5G13930.1	GO:0008415 : GO:0009058 : GO:0016747	acyltransferase activity : biosynthesis : transferase activity, transferring groups other than amino-acyl groups
Phypa_56066	MIO24.3; fructokinase, putative [EC:2.7.1.4] [KO:K00847] [Arabidopsis thaliana] : "MIO24.3; fructokinase, putative [EC:2.7.1.4] [KO:K00847] [Arabidopsis thaliana]"	Pp1s27_234V6.2;Pp1s27_234V6.1 : "Pp1s27_234V6.2;Pp1s27_234V6.1" : "Pp1s27_234V6.2;Pp1s27_234V6.1 : ""Pp1s27_234V6.2;Pp1s27_234V6.1"""	AT5G51830.1	GO:0004747 : GO:0006014 : GO:0008865	D-ribose metabolism : fructokinase activity : ribokinase activity

Phypa_137121		Pp1s135_91V6.1	ATMG00080.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_106639		Pp1s88_212V6.2;Pp1s88_212V6.1;Pp1s88_212V6.3 : "Pp1s88_212V6.2;Pp1s88_212V6.1;Pp1s88_212V6.3" : "Pp1s88_212V6.2;Pp1s88_212V6.1;Pp1s88_212V6.3 : ""Pp1s88_212V6.2;Pp1s88_212V6.1;Pp1s88_212V6.3"""	AT3G51880.2	GO:0000785 : GO:0003677 : GO:0005634 : GO:0006355	DNA binding : chromatin : nucleus : regulation of transcription, DNA-dependent
Phypa_136444 [Phypa_73588;Phypa_123042]	Putative H/ACA ribonucleoprotein complex subunit 1-like protein 1 [Arabidopsis thaliana]	Pp1s129_145V6.1	AT3G03920.1	GO:0006364 : GO:0007046 : GO:0019843 : GO:0030532	rRNA binding : rRNA processing : ribosome biogenesis : small nuclear ribonucleoprotein complex

Phypa_42952	MGL6.2; protein phosphatase 2C-related / PP2C-related [Arabidopsis thaliana] : "MGL6.2; protein phosphatase 2C-related / PP2C-related [Arabidopsis thaliana]"	Pp1s66_193V6.2;Pp1s66_193V6.1 : "Pp1s66_193V6.2;Pp1s66_193V6.1" : "Pp1s66_193V6.2;Pp1s66_193V6.1 : ""Pp1s66_193V6.2;Pp1s66_193V6.1"""	AT3G16560.1	GO:0000158 : GO:0003824 : GO:0004721 : GO:0004723 : GO:0004724 : GO:0005963 : GO:0008420 : GO:0008597 : GO:0015071 : GO:0017018 : GO:0017020 : GO:0017023 : GO:0030357	CTD phosphatase activity : calcium-dependent protein serine/threonine phosphatase activity : calcium-dependent protein serine/threonine phosphatase regulator activity : catalytic activity : magnesium-dependent protein serine/threonine phosphatase activity : magnesium-dependent protein serine/threonine phosphatase complex : myosin phosphatase activity : myosin phosphatase complex : myosin phosphatase regulator activity : phosphoprotein phosphatase activity : protein phosphatase type 2A activity : protein phosphatase type 2B activity : protein phosphatase type 2C activity

Phypa_114453	F6F9.7; regulator of chromosome condensation (RCC1) family protein [Arabidopsis thaliana] : "F6F9.7; regulator of chromosome condensation (RCC1) family protein [Arabidopsis thaliana]"	Pp1s10_244V6.1	AT1G19880.1		
Phypa_111068		Pp1s1_845V6.1	AT1G52380.1		
Phypa_73809	F11O4.1; major intrinsic family protein / MIP family protein [Arabidopsis thaliana] : "F11O4.1; major intrinsic family protein / MIP family protein [Arabidopsis thaliana]"	Pp1s44_31V6.1	AT4G01470.1	GO:0005215 : GO:0006810 : GO:0016020	membrane : transport : transporter activity
Phypa_6580		Pp1s77_184V6.1	AT1G69780.1	GO:0003677 : GO:0003700 : GO:0005634 : GO:0006355	DNA binding : nucleus : regulation of transcription, DNA-dependent : transcription factor activity

Phypa_38559	F1P2.200; bundle-sheath defective protein 2 family / bsd2 family [Arabidopsis thaliana] : "F1P2.200; bundle-sheath defective protein 2 family / bsd2 family [Arabidopsis thaliana]"	Pp1s33_37V6.1	AT3G47650.1		
Phypa_29741	F13M7.19; tubulin alpha-2/alpha-4 chain (TUA4) [KO:K07374] [Arabidopsis thaliana] : "F13M7.19; tubulin alpha-2/alpha-4 chain (TUA4) [KO:K07374] [Arabidopsis thaliana]"	Pp1s1454_1V6.1	AT1G50010.1	GO:0005198 : GO:0005874 : GO:0007018	microtubule : microtubule-based movement : structural molecule activity
Phypa_127844	contains ESTs AU093946(E1391),C72298(E1391) [Oryza sativa (japonica cultivar-group)]	Pp1s67_110V6.1	AT3G07880.1	GO:0005094 : GO:0005737	Rho GDP-dissociation inhibitor activity : cytoplasm

Phypa_161917	T9J14.13; 40S ribosomal protein S24 (RPS24A) [KO:K02974] [Arabidopsis thaliana] : "T9J14.13; 40S ribosomal protein S24 (RPS24A) [KO:K02974] [Arabidopsis thaliana]"	Pp1s37_112V6.1	AT5G28060.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_171592	F14F8.90; F-box protein family [Arabidopsis thaliana] : "F14F8.90; F-box protein family [Arabidopsis thaliana]"	Pp1s301_11V6.2;Pp1s301_11V6.1 : "Pp1s301_11V6.2;Pp1s301_11V6.1" : "Pp1s301_11V6.2;Pp1s301_11V6.1 : ""Pp1s301_11V6.2;Pp1s301_11V6.1"""	AT5G15710.1		
Phypa_39070		Pp1s102_181V6.1	AT5G08410.1	GO:0006118 : GO:0008937	electron transport : ferredoxin reductase activity
Phypa_171030	T6G21.26; expressed protein [Arabidopsis thaliana] : "T6G21.26; expressed protein [Arabidopsis thaliana]"	Pp1s271_68V6.1	AT5G21940.1		
Phypa_110546	Hemolytic toxin Avt-1 precursor (Avt-I) [Actineria villosa]	Pp1s319_5V6.1			

Phypa_19276 [Phypa_9662;Phypa_9653]		Pp1s161_109V6.1	AT3G56580.2	GO:0000151 : GO:0004842 : GO:0008270 : GO:0016567	protein ubiquitination : ubiquitin ligase complex : ubiquitin-protein ligase activity : zinc ion binding
Phypa_188533		Pp1s120_81V6.1	AT2G02050.1	GO:0003954 : GO:0005739 : GO:0006118 : GO:0008137	NADH dehydrogenase (ubiquinone) activity : NADH dehydrogenase activity : electron transport : mitochondrion
Phypa_127785	contains ESTs AU093946(E1391),C72298(E1391) [Oryza sativa (japonica cultivar-group)]	Pp1s67_121V6.1	AT3G07880.1	GO:0005094 : GO:0005737	Rho GDP-dissociation inhibitor activity : cytoplasm
Phypa_149544	T1M15.120; chloroplast Cpn21 protein [KO:K04078] [Arabidopsis thaliana] : "T1M15.120; chloroplast Cpn21 protein [KO:K04078] [Arabidopsis thaliana]"	Pp1s300_1V6.1	AT5G20720.3	GO:0005524 : GO:0006457	ATP binding : protein folding

Phypa_162432	F28P22.31; mitochondrial substrate carrier family protein [Arabidopsis thaliana] : "F28P22.31; mitochondrial substrate carrier family protein [Arabidopsis thaliana]"	Pp1s43_27V6.1	AT1G72820.1	GO:0005488 : GO:0005743 : GO:0006810 : GO:0016020	binding : membrane : mitochondrial inner membrane : transport
Phypa_184510	60S ribosomal protein L24 [Prunus avium]	Pp1s74_148V6.1	AT2G36620.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_61245	Auxin response factor 16 [Arabidopsis thaliana]	Pp1s339_42V6.1	AT2G28350.1		
Phypa_132416	putative pumilio/Mpt5 family RNA-binding protein [Oryza sativa (japonica cultivar-group)]	Pp1s96_110V6.1	AT2G29200.1	GO:0003723 : GO:0016071	RNA binding : mRNA metabolism
Phypa_17256	FCAALL.129; DNA-binding protein-related [Arabidopsis thaliana] : "FCAALL.129; DNA-binding protein-related [Arabidopsis thaliana]"	Pp1s58_127V6.2;Pp1s58_127V6.1 : "Pp1s58_127V6.2;Pp1s58_127V6.1" : "Pp1s58_127V6.2;Pp1s58_127V6.1 : ""Pp1s58_127V6.2;Pp1s58_127V6.1"""	AT2G35270.1		

Phypa_141291	F8B4.220; glycine hydroxymethyltransferase, putative / serine hydroxymethyltransferase, putative / serine/threonine aldolase, putative [EC:2.1.2.1] [KO:K00600] [Arabidopsis thaliana] : "F8B4.220; glycine hydroxymethyltransferase, putative / serine hydroxymethyltransferase, putative / serine/threonine aldolase, putative [EC:2.1.2.1] [KO:K00600] [Arabidopsis thaliana]"	Pp1s176_89V6.3	Pp1s176_89V6	GO:0004372 : GO:0006544 : GO:0006563	L-serine metabolism : glycine hydroxymethyltransferase activity : glycine metabolism

Phypa_167013	T10I14.150; expressed protein [Arabidopsis thaliana] : "T10I14.150; expressed protein [Arabidopsis thaliana]"	Pp1s133_17V6.2;Pp1s133_17V6.1;Pp1s133_17V6.3 : "Pp1s133_17V6.2;Pp1s133_17V6.1;Pp1s133_17V6.3" : "Pp1s133_17V6.2;Pp1s133_17V6.1;Pp1s133_17V6.3 : ""Pp1s133_17V6.2;Pp1s133_17V6.1;Pp1s133_17V6.3"""	AT4G22320.1		
[Phypa_147904;Phypa_147925]					
Phypa_232889		Pp1s149_4V6.1			
Phypa_123034	Two-component response regulator ARR2 (Receiver-like protein 5) [Arabidopsis thaliana]	Pp1s42_161V6.1	AT4G16110.1	GO:0000156 : GO:0000160 : GO:0003677 : GO:0005634 : GO:0006355	DNA binding : nucleus : regulation of transcription, DNA-dependent : two-component response regulator activity : two-component signal transduction system (phosphorelay)

Phypa_23467		Pp1s31_291V6.1	AT4G16110.1	GO:0000156 : GO:0000160 : GO:0003677 : GO:0005634 : GO:0006355	DNA binding : nucleus : regulation of transcription, DNA-dependent : two-component response regulator activity : two-component signal transduction system (phosphorelay)
Phypa_92860	F4F15.230; SWAP (Suppressor-of-White-APricot)/surp domain-containing protein / D111/G-patch domain-containing protein [Arabidopsis thaliana] : "F4F15.230; SWAP (Suppressor-of-White-APricot)/surp domain-containing protein / D111/G-patch domain-containing protein [Arabidopsis thaliana]"	Pp1s232_50V6.1	AT3G52120.2	GO:0003723 : GO:0006396	RNA binding : RNA processing
Phypa_93647		Pp1s246_1V6.1			

Phypa_172857	F13H10.2; dehydration-induced protein (ERD15) [Arabidopsis thaliana] : "F13H10.2; dehydration-induced protein (ERD15) [Arabidopsis thaliana]"	Pp1s387_21V6.1	AT2G41430.5	GO:0004497 : GO:0005507	copper ion binding : monooxygenase activity
Phypa_229054		Pp1s71_51V6.1			
Phypa_135141	F27G19.10; no apical meristem (NAM) family protein (RD26) [Arabidopsis thaliana] : "F27G19.10; no apical meristem (NAM) family protein (RD26) [Arabidopsis thaliana]"	Pp1s117_16V6.1	AT4G27410.2		
Phypa_123625	F28D10.80; 50S ribosomal protein L9, chloroplast (CL9) [KO:K02939] [Arabidopsis thaliana] : "F28D10.80; 50S ribosomal protein L9, chloroplast (CL9) [KO:K02939] [Arabidopsis thaliana]"	Pp1s45_190V6.1	AT3G44890.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome

Phypa_216076	F7C8.160; ring-box protein - like [KO:K03868] [Arabidopsis thaliana] : "F7C8.160; ring-box protein - like [KO:K03868] [Arabidopsis thaliana]"	Pp1s123_104V6.1	AT5G20570.1	GO:0000151 : GO:0004842 : GO:0008270 : GO:0016567	protein ubiquitination : ubiquitin ligase complex : ubiquitin-protein ligase activity : zinc ion binding
Phypa_140533 Phypa_159854	Trans-cinnamate 4-monooxygenase (Cinnamic acid 4-hydroxylase) (CA4H) (C4H) (P450C4H) (Cytochrome P450 73) [Populus kitakamiensis]	Pp1s168_84V6.1	AT2G30490.1	GO:0004497 : GO:0006118 : GO:0016710	electron transport : monooxygenase activity : trans-cinnamate 4-monooxygenase activity
Phypa_132376	putative pumilio/Mpt5 family RNA-binding protein [Oryza sativa (japonica cultivar-group)]	Pp1s96_109V6.1	AT2G29200.1	GO:0003723 : GO:0016071	RNA binding : mRNA metabolism

Phypa_137303	MSD21.4; isocitrate lyase, putative [EC:4.1.3.1] [KO:K01637] [Arabidopsis thaliana] : "MSD21.4; isocitrate lyase, putative [EC:4.1.3.1] [KO:K01637] [Arabidopsis thaliana]"	Pp1s136_203V6.1	AT3G21720.1	GO:0003676 : GO:0003824 : GO:0004451 : GO:0006097 : GO:0008152	catalytic activity : glyoxylate cycle : isocitrate lyase activity : metabolism : nucleic acid binding
Phypa_124814	MKD15.6; expressed protein [Arabidopsis thaliana] : "MKD15.6; expressed protein [Arabidopsis thaliana]"	Pp1s51_16V6.1;Pp1s51_16V6.2;Pp1s51_16V6.3 : "Pp1s51_16V6.1;Pp1s51_16V6.2;Pp1s51_16V6.3" : "Pp1s51_16V6.1;Pp1s51_16V6.2;Pp1s51_16V6.3 : ""Pp1s51_16V6.1;Pp1s51_16V6.2;Pp1s51_16V6.3"""	AT5G23200.1		
Phypa_98215		Pp1s347_9V6.1	AT1G63440.1	GO:0004008 : GO:0005524 : GO:0006825 : GO:0016020 : GO:0030001 : GO:0046872	ATP binding : copper ion transport : copper-exporting ATPase activity : membrane : metal ion binding : metal ion transport

Phypa_119898	putative ribosomal protein L26 [Oryza sativa (japonica cultivar-group)]	Pp1s30_298V6.1	AT3G49910.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412 : GO:0015934	intracellular : large ribosomal subunit : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_182704	T6D22.2; elongation factor 1-alpha / EF-1-alpha [EC:3.6.5.3] [KO:K03231] [Arabidopsis thaliana] : "T6D22.2; elongation factor 1-alpha / EF-1-alpha [EC:3.6.5.3] [KO:K03231] [Arabidopsis thaliana]"	Pp1s59_181V6.1	AT1G07920.1	GO:0003924 : GO:0005525 : GO:0006412 : GO:0008547	GTP binding : GTPase activity : protein biosynthesis : protein-synthesizing GTPase activity
Phypa_129458	Chalcone synthase (Naringenin-chalcone synthase) [Arabis alpina] : CHS			GO:0008415 : GO:0009058	acyltransferase activity : biosynthesis

Phypa_134646	F3G5.1; 29 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp29, putative [Arabidopsis thaliana] : "F3G5.1; 29 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp29, putative [Arabidopsis thaliana]"	Pp1s114_138V6.1	AT3G53460.3	GO:0003676	nucleic acid binding
Phypa_193430	contains ESTs AU093946(E1391),C72298(E1391) [Oryza sativa (japonica cultivar-group)]	Pp1s198_106V6.1	AT3G07880.1	GO:0005094 : GO:0005737	Rho GDP-dissociation inhibitor activity : cytoplasm
Phypa_36231	FCAALL.129; DNA-binding protein-related [Arabidopsis thaliana] : "FCAALL.129; DNA-binding protein-related [Arabidopsis thaliana]"	Pp1s485_11V6.1	AT2G35270.1		
Phypa_198079 [Phypa_160180;Phypa_109545]	40S ribosomal protein S28 [Zea mays]	Pp1s313_15V6.1	AT5G03850.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome

[Phypa_152430;Phypa_9
8737]

Phypa_ID	Funct. descr. BLAST BH	V1.6 CGI	At homolog	GO accession	GO name
Phypa_97924	LOC429025; similar to hypothetical protein MGC22679 [Gallus gallus] : "LOC429025; similar to hypothetical protein MGC22679 [Gallus gallus]"	Pp1s338_19V6.1	AT3G56230.1	GO:0005515	protein binding
Phypa_160592	Hypothetical protein F36H12.3 [Caenorhabditis elegans]	Pp1s23_336V6.1	AT4G10465.1		
Phypa_107142	F19K16.17; oxidoreductase family protein [Arabidopsis thaliana] : "F19K16.17; oxidoreductase family protein [Arabidopsis thaliana]"	Pp1s133_69V6.1	AT1G79870.1	GO:0006564 : GO:0016616	L-serine biosynthesis : oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
Phypa_139373	MNB8.14; kinesin light chain - related [Arabidopsis thaliana] : "MNB8.14; kinesin light chain - related [Arabidopsis thaliana]"	Pp1s156_60V6.1	AT5G53080.1		
Phypa_87274		Pp1s156_35V6.1			
Phypa_105373	Glutamate decarboxylase (GAD) (ERT D1) [Lycopersicon esculentum]	Pp1s34_308V6.1;Pp1s34_308V6.2 : "Pp1s34_308V6.1;Pp1s34_308V6.2" : "Pp1s34_308V6.1;Pp1s34_308V6.2 : ""Pp1s34_308V6.1;Pp1s34_308V6.2"""	AT5G17330.1	GO:0004351 : GO:0006520 : GO:0006536 : GO:0016831 : GO:0030170	amino acid metabolism : carboxy-lyase activity : glutamate decarboxylase activity : glutamate metabolism : pyridoxal phosphate binding
Phypa_107034	F6N23.1; beta-amylase, putative / 1,4-alpha-D-glucan maltohydrolase, putative [Arabidopsis thaliana] : "F6N23.1; beta-amylase, putative / 1,4-alpha-D-glucan maltohydrolase, putative [Arabidopsis thaliana]"	Pp1s121_168V6.1;Pp1s121_168V6.2 : "Pp1s121_168V6.1;Pp1s121_168V6.2" : "Pp1s121_168V6.1;Pp1s121_168V6.2 : ""Pp1s121_168V6.1;Pp1s121_168V6.2"""	AT4G00490.1	GO:0000272 : GO:0016161	beta-amylase activity : polysaccharide catabolism

Phypa_49664		Pp1s52_95V6.4;Pp1s52_95V6.2;Pp1s52_95V6.3;Pp1s52_95V6.1 : "Pp1s52_95V6.4;Pp1s52_95V6.2;Pp1s52_95V6.3;Pp1s52_95V6.1" : "Pp1s52_95V6.4;Pp1s52_95V6.2;Pp1s52_95V6.3;Pp1s52_95V6.1 : ""Pp1s52_95V6.4;Pp1s52_95V6.2;Pp1s52_95V6.3;Pp1s52_95V6.1"""	AT3G57810.3		
Phypa_171055		Pp1s272_60V6.1			
Phypa_175594	Chlorophyll a-b binding protein, chloroplast precursor (LHCII type I CAB) (LHCP) [Physcomitrella patens]	Pp1s13_200V6.1	AT2G05100.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting
Phypa_159676	F8B4.40; expressed protein [Arabidopsis thaliana] : "F8B4.40; expressed protein [Arabidopsis thaliana]"	Pp1s14_348V6.1	AT4G32340.1		

Phypa_ID	Funct. descr. BLAST BH	V1.6 CGI	At homolog	GO accession	GO name
Phypa_144156	Ribose-phosphate pyrophosphokinase 1 (Phosphoribosyl pyrophosphate synthetase 1) [Spinacia oleracea]	Pp1s212_43V6.2;Pp1s212_43V6.1 : "Pp1s212_43V6.2;Pp1s212_43V6.1" : "Pp1s212_43V6.2;Pp1s212_43V6.1 : ""Pp1s212_43V6.2;Pp1s212_43V6.1"""	AT2G44530.1	GO:0004749 : GO:0009116 : GO:0009165 : GO:0016740	nucleoside metabolism : nucleotide biosynthesis : ribose-phosphate diphosphokinase activity : transferase activity
Phypa_232568		Pp1s106_48V6.1;Pp1s106_48V6.2 : "Pp1s106_48V6.1;Pp1s106_48V6.2" : "Pp1s106_48V6.1;Pp1s106_48V6.2 : ""Pp1s106_48V6.1;Pp1s106_48V6.2"""	AT3G10740.1		
Phypa_140836	T4C15.1; expressed protein [Arabidopsis thaliana] : "T4C15.1; expressed protein [Arabidopsis thaliana]"	Pp1s171_5V6.1;Pp1s171_5V6.2;Pp1s171_5V6.3 : "Pp1s171_5V6.1;Pp1s171_5V6.2;Pp1s171_5V6.3" : "Pp1s171_5V6.1;Pp1s171_5V6.2;Pp1s171_5V6.3 : ""Pp1s171_5V6.1;Pp1s171_5V6.2;Pp1s171_5V6.3"""	AT2G35320.1	GO:0007275	development
Phypa_116273	T28A8.80; transporter-related [Arabidopsis thaliana] : "T28A8.80; transporter-related [Arabidopsis thaliana]"	Pp1s15_89V6.2;Pp1s15_89V6.1;Pp1s15_89V6.3 : "Pp1s15_89V6.2;Pp1s15_89V6.1;Pp1s15_89V6.3" : "Pp1s15_89V6.2;Pp1s15_89V6.1;Pp1s15_89V6.3 : ""Pp1s15_89V6.2;Pp1s15_89V6.1;Pp1s15_89V6.3"""	AT3G43790.1	GO:0005215 : GO:0006810 : GO:0015520 : GO:0015904 : GO:0016021	integral to membrane : tetracycline transport : tetracycline:hydrogen antiporter activity : transport : transporter activity

Phypa_215944	Tat; tyrosine aminotransferase [EC:2.6.1.5] [KO:K00815] [Mus musculus] : "Tat; tyrosine aminotransferase [EC:2.6.1.5] [KO:K00815] [Mus musculus]"	Pp1s121_161V6.1	AT5G36160.1	GO:0003824 : GO:0004838 : GO:0006519 : GO:0008483 : GO:0009058 : GO:0016769 : GO:0016847	1-aminocyclopropane-1-carboxylate synthase activity : amino acid and derivative metabolism : biosynthesis : catalytic activity : transaminase activity : transferase activity, transferring nitrogenous groups : tyrosine transaminase activity
Phypa_88255		Pp1s167_89V6.1			
Phypa_221150	F24J8.4; 2-oxoisovalerate dehydrogenase, putative / 3-methyl-2-oxobutanoate dehydrogenase, putative / branched-chain alpha-keto acid dehydrogenase E1 alpha subunit, putative [EC:1.2.4.4] [KO:K00166] [Arabidopsis thaliana] : "F24J8.4; 2-oxoisovalerate dehydrogenase, putative / 3-methyl-2-oxobutanoate dehydrogenase, putative / branched-chain alpha-keto acid dehydrogenase E1 alpha subunit, putative [EC:1.2.4.4] [KO:K00166] [Arabidopsis thaliana]"	Pp1s207_68V6.1	AT1G21400.1	GO:0003863 : GO:0008152 : GO:0016624 : GO:0017086	3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring) activity : 3-methyl-2-oxobutanoate dehydrogenase (lipoamide) complex : metabolism : oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor

Phypa_166310	contains EST C28646(C61919) similar to Arabidopsis thaliana chromosome1,At1g27340 unknown protein [Oryza sativa (japonica cultivar-group)]	Pp1s111_44V6.2;Pp1s111_44V6.1;Pp1s111_44V6.3 : "Pp1s111_44V6.2;Pp1s111_44V6.1;Pp1s111_44V6.3" : "Pp1s111_44V6.2;Pp1s111_44V6.1;Pp1s111_44V6.3 : ""Pp1s111_44V6.2;Pp1s111_44V6.1;Pp1s111_44V6.3"""	AT1G27340.1		
Phypa_127238		Pp1s64_60V6.1	AT5G60250.1	GO:0008766 : GO:0016881 : GO:0018169	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate-D-alanyl-D-alanine ligase activity : acid-amino acid ligase activity : ribosomal S6-glutamic acid ligase activity
Phypa_159781	hypothetical protein [Dictyostelium discoideum]	Pp1s15_300V6.1	AT1G28070.1		
Phypa_203561		Pp1s15_268V6.1	AT5G43430.1	GO:0005489 : GO:0006118	electron transport : electron transporter activity
Phypa_147280	F5N5.2; expressed protein [Arabidopsis thaliana] : "F5N5.2; expressed protein [Arabidopsis thaliana]"	Pp1s257_73V6.1;Pp1s257_73V6.2;Pp1s257_73V6.3;Pp1s257_73V6.4;Pp1s257_73V6.5 : "Pp1s257_73V6.1;Pp1s257_73V6.2;Pp1s257_73V6.3;Pp1s257_73V6.4;Pp1s257_73V6.5" : "Pp1s257_73V6.1;Pp1s257_73V6.2;Pp1s257_73V6.3;Pp1s257_73V6.4;Pp1s257_73V6.5 : ""Pp1s257_73V6.1;Pp1s257_73V6.2;Pp1s257_73V6.3;Pp1s257_73V6.4;Pp1s257_73V6.5"""	AT3G22850.1		
Phypa_231396		Pp1s130_124V6.1			

Phypa_201470	F1N19.23; Cys/Met metabolism pyridoxal-phosphate-dependent enzyme family protein [Arabidopsis thaliana] : "F1N19.23; Cys/Met metabolism pyridoxal-phosphate-dependent enzyme family protein [Arabidopsis thaliana]"	Pp1s2_113V6.1;Pp1s2_113V6.2 : "Pp1s2_113V6.1;Pp1s2_113V6.2" : "Pp1s2_113V6.1;Pp1s2_113V6.2 : ""Pp1s2_113V6.1;Pp1s2_113V6.2"""	AT1G64660.1	GO:0003962 : GO:0006520	amino acid metabolism : cystathionine gamma-synthase activity
Phypa_68875	hypothetical protein [Dictyostelium discoideum]	Pp1s20_367V6.2;Pp1s20_367V6.1 : "Pp1s20_367V6.2;Pp1s20_367V6.1" : "Pp1s20_367V6.2;Pp1s20_367V6.1 : ""Pp1s20_367V6.2;Pp1s20_367V6.1"""	Pp1s20_367V6	GO:0001584 : GO:0007186 : GO:0016021	G-protein coupled receptor protein signaling pathway : integral to membrane : rhodopsin-like receptor activity
Phypa_9490	F16B22.16; senescence-associated protein-related [Arabidopsis thaliana] : "F16B22.16; senescence-associated protein-related [Arabidopsis thaliana]"	Pp1s194_166V6.1	AT1G78020.1		
Phypa_140125	Bcat1; branched chain aminotransferase 1, cytosolic [EC:2.6.1.42] [KO:K00826] [Mus musculus] : "Bcat1; branched chain aminotransferase 1, cytosolic [EC:2.6.1.42] [KO:K00826] [Mus musculus]"	Pp1s163_127V6.1	AT5G65780.1	GO:0003824 : GO:0004084 : GO:0005524 : GO:0008152 : GO:0009081 : GO:0015986 : GO:0016469 : GO:0046933 : GO:0046961	ATP binding : ATP synthesis coupled proton transport : branched chain family amino acid metabolism : branched-chain-amino-acid transaminase activity : catalytic activity : hydrogen-transporting ATP synthase activity, rotational mechanism : hydrogen-transporting ATPase activity, rotational mechanism : metabolism : proton-transporting two-sector ATPase complex

Phypa_72790		Pp1s38_338V6.1	AT4G27670.1		
Phypa_194318	MMB12.18; pathogenesis-related protein, putative [Arabidopsis thaliana] : "MMB12.18; pathogenesis-related protein, putative [Arabidopsis thaliana]"	Pp1s215_2V6.1	AT3G19690.1	GO:0005576	extracellular region
Phypa_144846	F5N5.17; expressed protein [Arabidopsis thaliana] : "F5N5.17; expressed protein [Arabidopsis thaliana]"	Pp1s220_112V6.1	AT3G22970.1		
Phypa_194709	T28K15.1; no apical meristem (NAM) family protein [Arabidopsis thaliana] : "T28K15.1; no apical meristem (NAM) family protein [Arabidopsis thaliana]"	Pp1s223_12V6.1;Pp1s223_12V6.2 : "Pp1s223_12V6.1;Pp1s223_12V6.2" : "Pp1s223_12V6.1;Pp1s223_12V6.2 : ""Pp1s223_12V6.1;Pp1s223_12V6.2"""	AT1G12260.1		
Phypa_89931	F4P9.39; DNA-binding family protein / AT-hook protein 1 (AHP1) [Arabidopsis thaliana] : "F4P9.39; DNA-binding family protein / AT-hook protein 1 (AHP1) [Arabidopsis thaliana]"	Pp1s190_33V6.1	AT2G33620.2		
Phypa_171030	T6G21.26; expressed protein [Arabidopsis thaliana] : "T6G21.26; expressed protein [Arabidopsis thaliana]"	Pp1s271_68V6.1	AT5G21940.1		
Phypa_170614	F3F9.15; VQ motif-containing protein [Arabidopsis thaliana] : "F3F9.15; VQ motif-containing protein [Arabidopsis thaliana]"	Pp1s252_83V6.1			

Phypa_86312	MJP23.6; homogentisate 1,2-dioxygenase [EC:1.13.11.5] [KO:K00451] [Arabidopsis thaliana] : "MJP23.6; homogentisate 1,2-dioxygenase [EC:1.13.11.5] [KO:K00451] [Arabidopsis thaliana]"	Pp1s144_86V6.1	AT5G54080.1	GO:0004411 : GO:0006559 : GO:0006570	L-phenylalanine catabolism : homogentisate 1,2-dioxygenase activity : tyrosine metabolism

Phypa_ID	Funct. descr. BLAST BH	V1.6 CGI	At homolog	GO accession	GO name
Phypa_225236	Ribulose bisphosphate carboxylase small chain, chloroplast precursor (RuBisCO small subunit) [Marchantia paleacea]	Pp1s312_46V6.1	AT1G67090.1	GO:0009573 : GO:0015977 : GO:0016984	carbon utilization by fixation of carbon dioxide : ribulose bisphosphate carboxylase complex (sensu Magnoliophyta) : ribulose-bisphosphate carboxylase activity
Phypa_132698	Glucose-1-phosphate adenylyltransferase large subunit, chloroplast precursor (ADP-glucose synthase) (ADP-glucose pyrophosphorylase) (AGPase S) (Alpha-D-glucose-1-phosphate adenyl transferase) [Beta vulgaris]	Pp1s98_52V6.1	AT5G19220.1	GO:0004672 : GO:0005524 : GO:0005978 : GO:0006468 : GO:0008878 : GO:0009058 : GO:0016779	ATP binding : biosynthesis : glucose-1-phosphate adenylyltransferase activity : glycogen biosynthesis : nucleotidyltransferase activity : protein amino acid phosphorylation : protein kinase activity
Phypa_113929	T26D22.8; acetyl-CoA carboxylase [EC:6.3.4.14] [KO:K01946] [Arabidopsis thaliana] : "T26D22.8; acetyl-CoA carboxylase [EC:6.3.4.14] [KO:K01946] [Arabidopsis thaliana]"	Pp1s8_168V6.1	AT5G35360.1	GO:0004075 : GO:0005524 : GO:0008152 : GO:0009343 : GO:0016874	ATP binding : biotin carboxylase activity : biotin carboxylase complex : ligase activity : metabolism
Phypa_151133	F2A19.70; chlorophyll A-B binding protein (LHCA2) [Arabidopsis thaliana] : "F2A19.70; chlorophyll A-B binding protein (LHCA2) [Arabidopsis thaliana]"	Pp1s330_39V6.1	AT3G61470.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting
[Phypa_59935;Phypa_221004]					
Phypa_35924	F4H5.23; photosystem II oxygen-evolving complex 23 (OEC23) [KO:K02717] [Arabidopsis thaliana] : "F4H5.23; photosystem II oxygen-evolving complex 23 (OEC23) [KO:K02717] [Arabidopsis thaliana]"	Pp1s11_39V6.2;Pp1s11_39V6.1 : "Pp1s11_39V6.2;Pp1s11_39V6.1" : "Pp1s11_39V6.2;Pp1s11_39V6.1 : ""Pp1s11_39V6.2;Pp1s11_39V6.1"""	AT1G06680.1	GO:0005509 : GO:0009654 : GO:0015979 : GO:0019898	calcium ion binding : extrinsic to membrane : oxygen evolving complex : photosynthesis

Phypa_155608	MZA15.23; mitochondrial carrier protein family [KO:K03454] [Arabidopsis thaliana] : "MZA15.23; mitochondrial carrier protein family [KO:K03454] [Arabidopsis thaliana]"	Pp1s475_26V6.1	AT5G46800.1	GO:0005488 : GO:0005743 : GO:0006810 : GO:0016020	binding : membrane : mitochondrial inner membrane : transport
Phypa_34885		Pp1s55_65V6.1;Pp1s55_66V6.1;Pp1s55_66V6.2 : "Pp1s55_65V6.1;Pp1s55_66V6.1;Pp1s55_66V6.2" : "Pp1s55_65V6.1;Pp1s55_66V6.1;Pp1s55_66V6.2 : ""Pp1s55_65V6.1;Pp1s55_66V6.1;Pp1s55_66V6.2"""	AT5G44310.2		
Phypa_109430	Ribulose bisphosphate carboxylase/oxygenase activase 1, chloroplast precursor (RuBisCO activase 1) (RA 1) (RubisCO activase alpha form) [Larrea tridentata]	Pp1s5_83V6.2;Pp1s5_83V6.1 : "Pp1s5_83V6.2;Pp1s5_83V6.1" : "Pp1s5_83V6.2;Pp1s5_83V6.1 : ""Pp1s5_83V6.2;Pp1s5_83V6.1"""	AT2G39730.1	GO:0005524	ATP binding
Phypa_142913	T25B24.12; chlorophyll A-B binding protein / LHCI type III (LHCA3.1) [Arabidopsis thaliana] : "T25B24.12; chlorophyll A-B binding protein / LHCI type III (LHCA3.1) [Arabidopsis thaliana]"	Pp1s197_123V6.1	AT1G61520.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting
Phypa_150492	Thioredoxin M-type, chloroplast precursor (TRX-M) [Pisum sativum]	Pp1s317_45V6.1;Pp1s317_45V6.2 : "Pp1s317_45V6.1;Pp1s317_45V6.2" : "Pp1s317_45V6.1;Pp1s317_45V6.2 : ""Pp1s317_45V6.1;Pp1s317_45V6.2"""	AT4G03520.1	GO:0005489 : GO:0006118	electron transport : electron transporter activity
Phypa_167599	ASR1; orf19.2344 [Candida albicans SC5314] : "ASR1; orf19.2344 [Candida albicans SC5314]"	Pp1s152_65V6.1			

Phypa_164045		Pp1s64_155V6.2;Pp1s64_155V6.1;Pp1s64_155V6.3 : "Pp1s64_155V6.2;Pp1s64_155V6.1;Pp1s64_155V6.3" : "Pp1s64_155V6.2;Pp1s64_155V6.1;Pp1s64_155V6.3 : ""Pp1s64_155V6.2;Pp1s64_155V6.1;Pp1s64_155V6.3"""	AT2G46210.1	GO:0006636 : GO:0016020 : GO:0016491 : GO:0016717	fatty acid desaturation : membrane : oxidoreductase activity : oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water
Phypa_165894	F9I5.10; expressed protein [Arabidopsis thaliana] : "F9I5.10; expressed protein [Arabidopsis thaliana]"	Pp1s98_136V6.1;Pp1s98_136V6.2 : "Pp1s98_136V6.1;Pp1s98_136V6.2" : "Pp1s98_136V6.1;Pp1s98_136V6.2 : ""Pp1s98_136V6.1;Pp1s98_136V6.2"""	AT1G52220.1		
Phypa_233516		Pp1s86_234V6.1	AT5G64300.1		
Phypa_161786		Pp1s36_39V6.1			
Phypa_233510		Pp1s86_214V6.1	AT2G25930.1		
Phypa_121744	MCK7.12; unknown protein (sp|P72777) -related [Arabidopsis thaliana] : "MCK7.12; unknown protein (sp|P72777) -related [Arabidopsis thaliana]"	Pp1s37_298V6.1	AT5G58250.1		
Phypa_140416	T6G15.50; expressed protein [Arabidopsis thaliana] : "T6G15.50; expressed protein [Arabidopsis thaliana]"	Pp1s167_136V6.1;Pp1s167_136V6.2 : "Pp1s167_136V6.1;Pp1s167_136V6.2" : "Pp1s167_136V6.1;Pp1s167_136V6.2 : ""Pp1s167_136V6.1;Pp1s167_136V6.2"""	AT4G13500.1		

Phypa_146491	Glutamate--cysteine ligase, chloroplast precursor (Gamma-glutamylcysteine synthetase) (Gamma-ECS) (GCS) [Lycopersicon esculentum]	Pp1s244_44V6.1	AT4G23100.3	GO:0004357 : GO:0006750 : GO:0009507 : GO:0017109	chloroplast : glutamate-cysteine ligase activity : glutamate-cysteine ligase complex : glutathione biosynthesis
Phypa_160688		Pp1s25_107V6.1			
Phypa_132902	T1E3.100; ACT domain-containing protein [Arabidopsis thaliana] : "T1E3.100; ACT domain-containing protein [Arabidopsis thaliana]"	Pp1s99_201V6.1	AT5G04740.1		
Phypa_233731		Pp1s99_95V6.1	AT2G05070.1		
Phypa_120202	F19F24.15; homogentisate phytylprenyltransferase family protein (HPT1) / tocopherol phytyltransferase family protein (TPT1) [Arabidopsis thaliana] : "F19F24.15; homogentisate phytylprenyltransferase family protein (HPT1) / tocopherol phytyltransferase family protein (TPT1) [Arabidopsis thaliana]"	Pp1s31_108V6.2	AT4G09820.1	GO:0004659 : GO:0016021	integral to membrane : prenyltransferase activity
Phypa_222462	T4P13.13; glycogen synthase, putative [EC:2.4.1.11] [KO:K00693] [Arabidopsis thaliana] : "T4P13.13; glycogen synthase, putative [EC:2.4.1.11] [KO:K00693] [Arabidopsis thaliana]"	Pp1s234_74V6.1	AT3G01180.1	GO:0004373 : GO:0009058	biosynthesis : glycogen (starch) synthase activity
Phypa_123160	F13G24.250; expressed protein [Arabidopsis thaliana] : "F13G24.250; expressed protein [Arabidopsis thaliana]"	Pp1s43_120V6.1	AT5G08050.1		
Phypa_196472	Aquaporin PIP2.1 (Plasma membrane intrinsic protein 2a) (PIP2a) [Arabidopsis thaliana]	Pp1s267_61V6.2;Pp1s267_61V6.1 : "Pp1s267_61V6.2;Pp1s267_61V6.1" : "Pp1s267_61V6.2;Pp1s267_61V6.1 : ""Pp1s267_61V6.2;Pp1s267_61V6.1"""	AT3G53420.2	GO:0005215 : GO:0006810 : GO:0016020	membrane : transport : transporter activity
Phypa_167268		Pp1s141_133V6.1			

Phypa_160322	Diflavin flavoprotein A 1 (SsATF573) (NADH:oxygen oxidoreductase) [Synechocystis sp. PCC 6803]	Pp1s21_137V6.1		GO:0006118 : GO:0010181 : GO:0016491	FMN binding : electron transport : oxidoreductase activity
Phypa_114221	T26M18.120; expressed protein [Arabidopsis thaliana] : "T26M18.120; expressed protein [Arabidopsis thaliana]"	Pp1s9_169V6.1	AT4G22920.1		
Phypa_146121	Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase, chloroplast precursor (Mg-protoporphyrin IX monomethyl ester oxidative cyclase) [Euphorbia esula]	Pp1s239_18V6.2;Pp1s239_18V6.1 : "Pp1s239_18V6.2;Pp1s239_18V6.1" : "Pp1s239_18V6.2;Pp1s239_18V6.1 : ""Pp1s239_18V6.2;Pp1s239_18V6.1"""	AT3G56940.1	GO:0048529	magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase activity
Phypa_107142	F19K16.17; oxidoreductase family protein [Arabidopsis thaliana] : "F19K16.17; oxidoreductase family protein [Arabidopsis thaliana]"	Pp1s133_69V6.1	AT1G79870.1	GO:0006564 : GO:0016616	L-serine biosynthesis : oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
Phypa_168764	Ribulose bisphosphate carboxylase small chain, chloroplast precursor (RuBisCO small subunit) [Betula pendula]	Pp1s188_39V6.1	AT1G67090.1	GO:0009573 : GO:0015977 : GO:0016984	carbon utilization by fixation of carbon dioxide : ribulose bisphosphate carboxylase complex (sensu Magnoliophyta) : ribulose-bisphosphate carboxylase activity
Phypa_14997		Pp1s97_248V6.1	AT3G56940.1		
Phypa_148610	F3L12.11; expressed protein [Arabidopsis thaliana] : "F3L12.11; expressed protein [Arabidopsis thaliana]"	Pp1s281_87V6.2;Pp1s281_87V6.1 : "Pp1s281_87V6.2;Pp1s281_87V6.1" : "Pp1s281_87V6.2;Pp1s281_87V6.1 : ""Pp1s281_87V6.2;Pp1s281_87V6.1"""	AT2G04039.1		

Phypa_159809	F3H9.29; leucine-rich repeat family protein [Arabidopsis thaliana] : "F3H9.29; leucine-rich repeat family protein [Arabidopsis thaliana]"	Pp1s15_398V6.1	AT1G28340.1		
Phypa_214865		Pp1s107_1V6.1	AT1G74960.3	GO:0003824 : GO:0006633	catalytic activity : fatty acid biosynthesis
Phypa_139763	F5O24.30; expressed protein [Arabidopsis thaliana] : "F5O24.30; expressed protein [Arabidopsis thaliana]"	Pp1s160_127V6.1	AT5G20140.1		
Phypa_132172	MZB10.8; expressed protein [Arabidopsis thaliana] : "MZB10.8; expressed protein [Arabidopsis thaliana]"	Pp1s93_122V6.1	AT3G09050.1		
Phypa_206341	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (Vitamin-B12-independent methionine synthase isozyme) (Cobalamin-independent methionine synthase isozyme) [Mesembryanthemum crystallinum]	Pp1s33_110V6.1;Pp1s33_110V6.2 : "Pp1s33_110V6.1;Pp1s33_110V6.2" : "Pp1s33_110V6.1;Pp1s33_110V6.2 : ""Pp1s33_110V6.1;Pp1s33_110V6.2"""	AT5G17920.2	GO:0003871 : GO:0009086	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity : methionine biosynthesis
Phypa_125345	F22K18.180; glucose-6-phosphate isomerase, putative [EC:5.3.1.9] [KO:K01810] [Arabidopsis thaliana] : "F22K18.180; glucose-6-phosphate isomerase, putative [EC:5.3.1.9] [KO:K01810] [Arabidopsis thaliana]"	Pp1s54_320V6.1;Pp1s54_320V6.2 : "Pp1s54_320V6.1;Pp1s54_320V6.2" : "Pp1s54_320V6.1;Pp1s54_320V6.2 : ""Pp1s54_320V6.1;Pp1s54_320V6.2"""	AT4G24620.1	GO:0004347 : GO:0006094 : GO:0006096	gluconeogenesis : glucose-6-phosphate isomerase activity : glycolysis
Phypa_206386	Elongation factor 1-gamma 3 (EF-1-gamma 3) (eEF-1B gamma 3) [no tax name]	Pp1s33_218V6.1	AT1G09640.1	GO:0003746 : GO:0004364 : GO:0005853 : GO:0006414	eukaryotic translation elongation factor 1 complex : glutathione transferase activity : translation elongation factor activity : translational elongation

Phypa_196235	F16M14.7; chloroplast 30S ribosomal protein S31 (PSRP4) [Arabidopsis thaliana] : "F16M14.7; chloroplast 30S ribosomal protein S31 (PSRP4) [Arabidopsis thaliana]"	Pp1s258_80V6.1	AT2G38140.1		
Phypa_73379	MDB19.14; glycosyl hydrolase family 31 protein [Arabidopsis thaliana] : "MDB19.14; glycosyl hydrolase family 31 protein [Arabidopsis thaliana]"	Pp1s41_235V6.1	AT3G23640.1	GO:0004553 : GO:0004558 : GO:0005975	alpha-glucosidase activity : carbohydrate metabolism : hydrolase activity, hydrolyzing O-glycosyl compounds
Phypa_201802	F24J5.20; alpha-xylosidase (XYL1) [Arabidopsis thaliana] : "F24J5.20; alpha-xylosidase (XYL1) [Arabidopsis thaliana]"	Pp1s6_50V6.1	AT1G68560.1	GO:0004553 : GO:0004558 : GO:0005975	alpha-glucosidase activity : carbohydrate metabolism : hydrolase activity, hydrolyzing O-glycosyl compounds
Phypa_174645	Alpha-glucan water dikinase, chloroplast precursor (Starch-related R1 protein) (Starch excess protein 1) [Arabidopsis thaliana]	Pp1s8_70V6.1	AT1G10760.1	GO:0050521	alpha-glucan, water dikinase activity
Phypa_70542	1,4-dihydroxy-2-naphthoate octaprenyltransferase (DHNA-octaprenyltransferase) [Haemophilus influenzae]	Pp1s28_259V6.1		GO:0004659 : GO:0016021	integral to membrane : prenyltransferase activity
Phypa_49116	F2N1.18; expressed protein [Arabidopsis thaliana] : "F2N1.18; expressed protein [Arabidopsis thaliana]"	Pp1s49_42V6.1	AT4G01150.1		
Phypa_114083	F2N1.18; expressed protein [Arabidopsis thaliana] : "F2N1.18; expressed protein [Arabidopsis thaliana]"	Pp1s9_38V6.1	AT4G01150.1		
Phypa_195066	MEE13.8; DNA helicase-related [Arabidopsis thaliana] : "MEE13.8; DNA helicase-related [Arabidopsis thaliana]"	Pp1s229_36V6.1	AT5G35970.1	GO:0000166 : GO:0005524 : GO:0008026 : GO:0017111	ATP binding : ATP-dependent helicase activity : nucleoside-triphosphatase activity : nucleotide binding

Phypa_170637	Plastocyanin, chloroplast precursor [Physcomitrella patens]	Pp1s254_25V6.1	AT1G76100.1	GO:0005489 : GO:0005507 : GO:0006118	copper ion binding : electron transport : electron transporter activity
Phypa_204471	Fructose-1,6-bisphosphatase, chloroplast precursor (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase) [Oryza sativa]	Pp1s20_373V6.1;Pp1s20_373V6.2 : "Pp1s20_373V6.1;Pp1s20_373V6.2" : "Pp1s20_373V6.1;Pp1s20_373V6.2 : ""Pp1s20_373V6.1;Pp1s20_373V6.2"""	AT3G54050.1	GO:0005975 : GO:0042132 : GO:0042578	carbohydrate metabolism : fructose-bisphosphatase activity : phosphoric ester hydrolase activity
Phypa_80169	Oleosin Bn-III (BnIII) [Brassica napus]	Pp1s84_138V6.1	AT4G25140.1		
Phypa_135818	T22H22.19; thylakoid lumen 18.3 kDa protein [Arabidopsis thaliana] : "T22H22.19; thylakoid lumen 18.3 kDa protein [Arabidopsis thaliana]"	Pp1s123_97V6.1	AT1G54780.1		
Phypa_37483	50S ribosomal protein L29, chloroplast precursor [Zea mays]	Pp1s89_23V6.1	AT5G65220.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_161636	mucin-associated surface protein (MASP), putative [Trypanosoma cruzi]	Pp1s34_348V6.1;Pp1s34_348V6.2 : "Pp1s34_348V6.1;Pp1s34_348V6.2" : "Pp1s34_348V6.1;Pp1s34_348V6.2 : ""Pp1s34_348V6.1;Pp1s34_348V6.2"""	Pp1s34_348V6		
Phypa_169245	Phosphoglycerate kinase, chloroplast precursor [Volvox carteri]	Pp1s201_82V6.1;Pp1s201_82V6.2;Pp1s201_82V6.3 : "Pp1s201_82V6.1;Pp1s201_82V6.2;Pp1s201_82V6.3" : "Pp1s201_82V6.1;Pp1s201_82V6.2;Pp1s201_82V6.3 : ""Pp1s201_82V6.1;Pp1s201_82V6.2;Pp1s201_82V6.3"""	AT3G12780.1	GO:0004618 : GO:0006096	glycolysis : phosphoglycerate kinase activity

Phypa_202775	Glyceraldehyde-3-phosphate dehydrogenase A, chloroplast precursor (NADP-dependent glyceraldehydephosphate dehydrogenase subunit A) [Spinacia oleracea]	Pp1s11_397V6.5;Pp1s11_397V6.2;Pp1s11_397V6.3;Pp1s11_397V6.4;Pp1s11_397V6.1;Pp1s11_397V6.6 : "Pp1s11_397V6.5;Pp1s11_397V6.2;Pp1s11_397V6.3;Pp1s11_397V6.4;Pp1s11_397V6.1;Pp1s11_397V6.6" : "Pp1s11_397V6.5;Pp1s11_397V6.2;Pp1s11_397V6.3;Pp1s11_397V6.4;Pp1s11_397V6.1;Pp1s11_397V6.6 : ""Pp1s11_397V6.5;Pp1s11_397V6.2;Pp1s11_397V6.3;Pp1s11_397V6.4;Pp1s11_397V6.1;Pp1s11_397V6.6"""	AT1G12900.1	GO:0004365 : GO:0006006 : GO:0006096 : GO:0008943 : GO:0051287	NAD binding : glucose metabolism : glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity : glyceraldehyde-3-phosphate dehydrogenase activity : glycolysis
Phypa_121324	T24P13.2; aspartate/glutamate/uridylate kinase family protein [Arabidopsis thaliana] : "T24P13.2; aspartate/glutamate/uridylate kinase family protein [Arabidopsis thaliana]"	Pp1s35_95V6.1	AT1G26640.1	GO:0008652	amino acid biosynthesis
Phypa_233534		Pp1s89_87V6.1	AT1G15980.1		
Phypa_173108	MOJ9.19; proline-rich protein family [Arabidopsis thaliana] : "MOJ9.19; proline-rich protein family [Arabidopsis thaliana]"	Pp1s411_3V6.1	AT5G07020.1	GO:0031177	phosphopantetheine binding
Phypa_189346	Ferredoxin--NADP reductase, embryo isozyme, chloroplast precursor (FNR) [Oryza sativa]	Pp1s131_154V6.1	AT4G05390.1	GO:0004324 : GO:0006118 : GO:0015039 : GO:0016491	NADPH-adrenodoxin reductase activity : electron transport : ferredoxin-NADP+ reductase activity : oxidoreductase activity

Phypa_165175	fadB; delta 5 fatty acid desaturase [Dictyostelium discoideum] : "fadB; delta 5 fatty acid desaturase [Dictyostelium discoideum]"	Pp1s83_225V6.2;Pp1s83_225V6.1 : "Pp1s83_225V6.2;Pp1s83_225V6.1" : "Pp1s83_225V6.2;Pp1s83_225V6.1 : ""Pp1s83_225V6.2;Pp1s83_225V6.1"""	AT2G46210.1	GO:0006636 : GO:0016020 : GO:0016491 : GO:0016717	fatty acid desaturation : membrane : oxidoreductase activity : oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water
Phypa_175024		Pp1s10_88V6.1	AT3G03341.1		
Phypa_121814	T8I13.24; CP12 domain-containing protein [Arabidopsis thaliana] : "T8I13.24; CP12 domain-containing protein [Arabidopsis thaliana]"	Pp1s37_240V6.1	AT2G47400.1		
Phypa_170769		Pp1s259_112V6.1;Pp1s259_112V6.2 : "Pp1s259_112V6.1;Pp1s259_112V6.2" : "Pp1s259_112V6.1;Pp1s259_112V6.2 : ""Pp1s259_112V6.1;Pp1s259_112V6.2"""	Pp1s259_112V6	GO:0003824	catalytic activity
Phypa_177617	putative 33kDa oxygen evolvingprotein of photosystem II [Oryza sativa (japonica cultivar-group)]	Pp1s25_66V6.2;Pp1s25_66V6.1 : "Pp1s25_66V6.2;Pp1s25_66V6.1" : "Pp1s25_66V6.2;Pp1s25_66V6.1 : ""Pp1s25_66V6.2;Pp1s25_66V6.1"""	AT3G50820.1	GO:0005509 : GO:0009654 : GO:0015979 : GO:0019898 : GO:0042549	calcium ion binding : extrinsic to membrane : oxygen evolving complex : photosynthesis : photosystem II stabilization
Phypa_166416	F10M23.190; expressed protein [Arabidopsis thaliana] : "F10M23.190; expressed protein [Arabidopsis thaliana]"	Pp1s114_207V6.1	AT4G26850.1		

Phypa_67435	F28I16.190; IPP transferase - like protein [Arabidopsis thaliana] : "F28I16.190; IPP transferase - like protein [Arabidopsis thaliana]"	Pp1s14_391V6.1	AT5G20040.1	GO:0004811 : GO:0005524 : GO:0008033	ATP binding : tRNA isopentenyltransferase activity : tRNA processing
Phypa_67971		Pp1s16_339V6.1		GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412 : GO:0007155 : GO:0007160 : GO:0008305	cell adhesion : cell-matrix adhesion : integrin complex : intracellular : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_161425		Pp1s32_341V6.1			
Phypa_56132	Chlorophyll a-b binding protein CP24 10A, chloroplast precursor (CAB-10A) (LHCP) [Lycopersicon esculentum]	Pp1s28_319V6.1	AT1G15820.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting
Phypa_75366	WSI18 protein [Oryza sativa (japonica cultivar-group)]	Pp1s52_212V6.2;Pp1s52_212V6.1 : "Pp1s52_212V6.2;Pp1s52_212V6.1" : "Pp1s52_212V6.2;Pp1s52_212V6.1 : ""Pp1s52_212V6.2;Pp1s52_212V6.1"""	AT2G18340.1		
Phypa_104532	F24D7.15; GMP synthase [glutamine-hydrolyzing], putative / glutamine amidotransferase, putative [EC:6.3.5.2] [KO:K01951] [Arabidopsis thaliana] : "F24D7.15; GMP synthase [glutamine-hydrolyzing], putative / glutamine amidotransferase, putative [EC:6.3.5.2] [KO:K01951] [Arabidopsis thaliana]"	Pp1s8_124V6.1	AT1G63660.1	GO:0003824 : GO:0003922 : GO:0005524 : GO:0006164 : GO:0006177	ATP binding : GMP biosynthesis : GMP synthase (glutamine-hydrolyzing) activity : catalytic activity : purine nucleotide biosynthesis
Phypa_183181	F3E22.14; importin alpha-1 subunit, putative (IMPA1) [Arabidopsis thaliana] : "F3E22.14; importin alpha-1 subunit, putative (IMPA1) [Arabidopsis thaliana]"	Pp1s63_171V6.1;Pp1s63_171V6.2 : "Pp1s63_171V6.1;Pp1s63_171V6.2" : "Pp1s63_171V6.1;Pp1s63_171V6.2 : ""Pp1s63_171V6.1;Pp1s63_171V6.2"""	AT3G06720.1	GO:0006606 : GO:0006886 : GO:0008565	intracellular protein transport : protein transporter activity : protein-nucleus import

Phypa_206025	F5I10.7; sugar transporter family protein [Arabidopsis thaliana] : "F5I10.7; sugar transporter family protein [Arabidopsis thaliana]"	Pp1s31_182V6.1	AT4G00370.1	GO:0005215 : GO:0006810 : GO:0016021	integral to membrane : transport : transporter activity
Phypa_165025	F9G14.120; pseudo-response regulator, APRR7 (APRR1/TOC1 family) [Arabidopsis thaliana] : "F9G14.120; pseudo-response regulator, APRR7 (APRR1/TOC1 family) [Arabidopsis thaliana]"	Pp1s81_131V6.3;Pp1s81_131V6.2;Pp1s81_131V6.1 : "Pp1s81_131V6.3;Pp1s81_131V6.2;Pp1s81_131V6.1" : "Pp1s81_131V6.3;Pp1s81_131V6.2;Pp1s81_131V6.1 : ""Pp1s81_131V6.3;Pp1s81_131V6.2;Pp1s81_131V6.1"""	AT5G02810.1	GO:0000156 : GO:0000160 : GO:0003677 : GO:0006355	DNA binding : regulation of transcription, DNA-dependent : two-component response regulator activity : two-component signal transduction system (phosphorelay)
Phypa_121098	Cytochrome b6-f complex iron-sulfur subunit 1, chloroplast precursor (Rieske iron-sulfur protein 1) (Plastohydroquinone:plastocyanin oxidoreductase iron-sulfur protein 1) (ISP 1) (RISP 1) [Nicotiana tabacum]	Pp1s35_78V6.1	AT4G03280.1	GO:0006118 : GO:0008121 : GO:0009496 : GO:0016020 : GO:0016491 : GO:0045285	electron transport : membrane : oxidoreductase activity : plastoquinol-plastocyanin reductase activity : ubiquinol-cytochrome-c reductase activity : ubiquinol-cytochrome-c reductase complex
Phypa_143643	F9I5.11; photosystem I reaction center subunit VI, chloroplast, putative / PSI-H, putative (PSAH2) [KO:K02695] [Arabidopsis thaliana] : "F9I5.11; photosystem I reaction center subunit VI, chloroplast, putative / PSI-H, putative (PSAH2) [KO:K02695] [Arabidopsis thaliana]"	Pp1s206_11V6.1	AT1G52230.1	GO:0009538 : GO:0015979	photosynthesis : photosystem I reaction center
Phypa_169291	F27G19.60; CBS domain-containing protein [Arabidopsis thaliana] : "F27G19.60; CBS domain-containing protein [Arabidopsis thaliana]"	Pp1s203_94V6.1	AT4G27460.1		
Phypa_232765		Pp1s132_175V6.1	AT1G32060.1		

Phypa_169111	MOJ9.19; proline-rich protein family [Arabidopsis thaliana] : "MOJ9.19; proline-rich protein family [Arabidopsis thaliana]"	Pp1s198_75V6.1	AT5G07020.1		
Phypa_161213		Pp1s31_2V6.1		GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_190267	Ferredoxin, chloroplast precursor [Physcomitrella patens]	Pp1s143_176V6.1	AT1G60950.1	GO:0005489 : GO:0005506 : GO:0006118	electron transport : electron transporter activity : iron ion binding
Phypa_159520		Pp1s13_231V6.1			
Phypa_146278	Glutamine synthetase, chloroplast precursor (Glutamate--ammonia ligase) (GS2) [Chlamydomonas reinhardtii]	Pp1s241_33V6.2;Pp1s241_33V6.1 : "Pp1s241_33V6.2;Pp1s241_33V6.1" : "Pp1s241_33V6.2;Pp1s241_33V6.1 : ""Pp1s241_33V6.2;Pp1s241_33V6.1"""	AT5G35630.1	GO:0004356 : GO:0006542 : GO:0006807	glutamate-ammonia ligase activity : glutamine biosynthesis : nitrogen compound metabolism
Phypa_105954	T20O10.240; mRNA-binding protein, putative [Arabidopsis thaliana] : "T20O10.240; mRNA-binding protein, putative [Arabidopsis thaliana]"	Pp1s55_140V6.1	AT3G63140.1		
Phypa_170161	T8P21.5; acetyl co-enzyme A carboxylase carboxyltransferase alpha subunit family [EC:6.4.1.2] [KO:K01962] [Arabidopsis thaliana] : "T8P21.5; acetyl co-enzyme A carboxylase carboxyltransferase alpha subunit family [EC:6.4.1.2] [KO:K01962] [Arabidopsis thaliana]"	Pp1s234_46V6.1	AT2G38040.1	GO:0003989 : GO:0006633 : GO:0009317	acetyl-CoA carboxylase activity : acetyl-CoA carboxylase complex : fatty acid biosynthesis
Phypa_188035	T2P4.16; uroporphyrinogen decarboxylase, putative / UPD, putative [EC:4.1.1.37] [KO:K01599] [Arabidopsis thaliana] : "T2P4.16; uroporphyrinogen decarboxylase, putative / UPD, putative [EC:4.1.1.37] [KO:K01599] [Arabidopsis thaliana]"	Pp1s114_123V6.1;Pp1s114_123V6.2 : "Pp1s114_123V6.1;Pp1s114_123V6.2" : "Pp1s114_123V6.1;Pp1s114_123V6.2 : ""Pp1s114_123V6.1;Pp1s114_123V6.2"""	AT2G40490.1	GO:0004853 : GO:0006779	porphyrin biosynthesis : uroporphyrinogen decarboxylase activity

Phypa_223504	T20K24.9; metaxin-related [Arabidopsis thaliana] : "T20K24.9; metaxin-related [Arabidopsis thaliana]"	Pp1s261_53V6.1	AT2G19080.1		
Phypa_159727		Pp1s15_131V6.1			
Phypa_161321	Photosystem II 22 kDa protein, chloroplast precursor (CP22) [Spinacia oleracea]	Pp1s31_279V6.1;Pp1s31_279V6.2 : "Pp1s31_279V6.1;Pp1s31_279V6.2" : "Pp1s31_279V6.1;Pp1s31_279V6.2 : ""Pp1s31_279V6.1;Pp1s31_279V6.2"""	AT1G44575.1		
Phypa_126454		Pp1s59_287V6.1	AT5G27820.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_58629	MFL8.11; ribosomal protein L3 family protein [KO:K02906] [Arabidopsis thaliana] : "MFL8.11; ribosomal protein L3 family protein [KO:K02906] [Arabidopsis thaliana]"	Pp1s117_86V6.1	AT2G43030.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_86211		Pp1s143_73V6.1	AT1G69780.1	GO:0003677 : GO:0003700 : GO:0005634 : GO:0006355	DNA binding : nucleus : regulation of transcription, DNA-dependent : transcription factor activity
Phypa_151155	F2A19.70; chlorophyll A-B binding protein (LHCA2) [Arabidopsis thaliana] : "F2A19.70; chlorophyll A-B binding protein (LHCA2) [Arabidopsis thaliana]"	Pp1s330_37V6.1	AT3G61470.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting
Phypa_151587	Tetrapyrrole-binding protein, chloroplast precursor (Genomes uncoupled 4) [Arabidopsis thaliana]	Pp1s340_26V6.1;Pp1s340_26V6.2 : "Pp1s340_26V6.1;Pp1s340_26V6.2" : "Pp1s340_26V6.1;Pp1s340_26V6.2 : ""Pp1s340_26V6.1;Pp1s340_26V6.2"""	AT3G59400.1		
Phypa_161218		Pp1s31_14V6.1			

[Phypa_147651;Phypa_110442]					
Phypa_224154	T20D1.50; spermine synthase (ACL5) [Arabidopsis thaliana] : "T20D1.50; spermine synthase (ACL5) [Arabidopsis thaliana]"	Pp1s279_58V6.1;Pp1s279_58V6.2 : "Pp1s279_58V6.1;Pp1s279_58V6.2" : "Pp1s279_58V6.1;Pp1s279_58V6.2 : ""Pp1s279_58V6.1;Pp1s279_58V6.2"""	AT5G19530.1	GO:0003824 : GO:0004766 : GO:0008757	S-adenosylmethionine-dependent methyltransferase activity : catalytic activity : spermidine synthase activity
Phypa_171725	F10A5.13; glycosyl hydrolase family 9 protein [Arabidopsis thaliana] : "F10A5.13; glycosyl hydrolase family 9 protein [Arabidopsis thaliana]"	Pp1s308_21V6.1	AT1G75680.1	GO:0004553 : GO:0005975 : GO:0008810	carbohydrate metabolism : cellulase activity : hydrolase activity, hydrolyzing O-glycosyl compounds
Phypa_122112		Pp1s38_294V6.1	AT5G01920.1	GO:0004672 : GO:0004674 : GO:0005524 : GO:0006468	ATP binding : protein amino acid phosphorylation : protein kinase activity : protein serine/threonine kinase activity
Phypa_172419	T5F17.40; expressed protein [Arabidopsis thaliana] : "T5F17.40; expressed protein [Arabidopsis thaliana]"	Pp1s351_33V6.1;Pp1s351_33V6.2 : "Pp1s351_33V6.1;Pp1s351_33V6.2" : "Pp1s351_33V6.1;Pp1s351_33V6.2 : ""Pp1s351_33V6.1;Pp1s351_33V6.2"""	AT4G28590.1	GO:0004812 : GO:0005524 : GO:0006418	ATP binding : tRNA aminoacylation for protein translation : tRNA ligase activity
Phypa_186228	Zeaxanthin epoxidase, chloroplast precursor [Lycopersicon esculentum]	Pp1s91_16V6.1	AT5G67030.1	GO:0004497 : GO:0006118 : GO:0006725 : GO:0008152 : GO:0016491	aromatic compound metabolism : electron transport : metabolism : monooxygenase activity : oxidoreductase activity

Phypa_173789	F14G6.9; 3-hydroxy-3-methylglutaryl-CoA reductase 1 / HMG-CoA reductase 1 (HMG1) [EC:1.1.1.34] [KO:K00021] [Arabidopsis thaliana] : "F14G6.9; 3-hydroxy-3-methylglutaryl-CoA reductase 1 / HMG-CoA reductase 1 (HMG1) [EC:1.1.1.34] [KO:K00021] [Arabidopsis thaliana]"	Pp1s1_155V6.1	AT1G76490.1	GO:0004420 : GO:0006629 : GO:0009058 : GO:0016021	biosynthesis : hydroxymethylglutaryl-CoA reductase (NADPH) activity : integral to membrane : lipid metabolism
Phypa_148115	similar to thioredoxin f [Cyanidioschyzon merolae]	Pp1s271_35V6.2;Pp1s271_35V6.1 : "Pp1s271_35V6.2;Pp1s271_35V6.1" : "Pp1s271_35V6.2;Pp1s271_35V6.1 : ""Pp1s271_35V6.2;Pp1s271_35V6.1"""	AT5G16400.1	GO:0004791 : GO:0005489 : GO:0006118	electron transport : electron transporter activity : thioredoxin-disulfide reductase activity
Phypa_77030		Pp1s62_88V6.1			
Phypa_107676		Pp1s183_75V6.1	AT4G04040.1	GO:0003872 : GO:0005524 : GO:0005945 : GO:0006096 : GO:0047334	6-phosphofructokinase activity : 6-phosphofructokinase complex : ATP binding : diphosphate-fructose-6-phosphate 1-phosphotransferase activity : glycolysis
Phypa_124287		Pp1s48_70V6.1	AT1G15550.1	GO:0016707	gibberellin 3-beta-dioxygenase activity
Phypa_190133	contains ESTs AU164153(E20361),D15307(C0434) [Oryza sativa (japonica cultivar-group)]	Pp1s141_128V6.1	AT2G37770.2	GO:0008106 : GO:0016491	alcohol dehydrogenase (NADP+) activity : oxidoreductase activity

Phypa_166875	F13O11.16; RNA polymerase sigma subunit SigA (sigA) / sigma factor 1 (SIG1) [Arabidopsis thaliana] : "F13O11.16; RNA polymerase sigma subunit SigA (sigA) / sigma factor 1 (SIG1) [Arabidopsis thaliana]"	Pp1s126_141V6.2;Pp1s126_141V6.1 : "Pp1s126_141V6.2;Pp1s126_141V6.1" : "Pp1s126_141V6.2;Pp1s126_141V6.1 : ""Pp1s126_141V6.2;Pp1s126_141V6.1"""	AT1G64860.1	GO:0003677 : GO:0003700 : GO:0004197 : GO:0006352 : GO:0006355 : GO:0006508 : GO:0016987	DNA binding : cysteine-type endopeptidase activity : proteolysis and peptidolysis : regulation of transcription, DNA-dependent : sigma factor activity : transcription factor activity : transcription initiation
Phypa_170304		Pp1s240_74V6.1			
Phypa_131811	F12F1.30; aminomethyltransferase, putative [EC:2.1.2.10] [KO:K00605] [Arabidopsis thaliana] : "F12F1.30; aminomethyltransferase, putative [EC:2.1.2.10] [KO:K00605] [Arabidopsis thaliana]"	Pp1s91_92V6.1;Pp1s91_92V6.2 : "Pp1s91_92V6.1;Pp1s91_92V6.2" : "Pp1s91_92V6.1;Pp1s91_92V6.2 : ""Pp1s91_92V6.1;Pp1s91_92V6.2"""	AT1G11860.2	GO:0004047 : GO:0004374 : GO:0005737 : GO:0006546	aminomethyltransferase activity : cytoplasm : glycine catabolism : glycine cleavage system
Phypa_179159	F24C7.16; phosphoglycolate phosphatase, putative [Arabidopsis thaliana] : "F24C7.16; phosphoglycolate phosphatase, putative [Arabidopsis thaliana]"	Pp1s34_237V6.2;Pp1s34_237V6.1 : "Pp1s34_237V6.2;Pp1s34_237V6.1" : "Pp1s34_237V6.2;Pp1s34_237V6.1 : ""Pp1s34_237V6.2;Pp1s34_237V6.1"""	AT5G36700.2	GO:0003824 : GO:0003869 : GO:0008152 : GO:0016787 : GO:0016791	4-nitrophenylphosphatase activity : catalytic activity : hydrolase activity : metabolism : phosphoric monoester hydrolase activity
Phypa_147884	contains ESTs AU101298(E4372),D48939(S15524) similar to Arabidopsis thaliana chromosome 1, F25A4.30 unknown protein [Oryza sativa (japonica cultivar-group)]	Pp1s268_34V6.1	AT1G74730.1		
Phypa_172816		Pp1s382_29V6.1			
Phypa_172162		Pp1s334_68V6.1			
Phypa_48630	contains ESTs D24537(R2125),AU095459(R2125) [Oryza sativa (japonica cultivar-group)]	Pp1s93_152V6.1	AT1G68660.1		

Phypa_200376 [Phypa_70006;Phypa_70007;Phypa_103101]	F1M20.15; geranylgeranyl reductase [Arabidopsis thaliana] : "F1M20.15; geranylgeranyl reductase [Arabidopsis thaliana]"	Pp1s425_20V6.1;Pp1s425_20V6.2 : "Pp1s425_20V6.1;Pp1s425_20V6.2" : "Pp1s425_20V6.1;Pp1s425_20V6.2 : ""Pp1s425_20V6.1;Pp1s425_20V6.2"""	AT1G74470.1	GO:0006118 : GO:0008152 : GO:0015036 : GO:0015979 : GO:0015995 : GO:0016491 : GO:0045550	chlorophyll biosynthesis : disulfide oxidoreductase activity : electron transport : geranylgeranyl reductase activity : metabolism : oxidoreductase activity : photosynthesis
Phypa_145834	F3G5.4; adenylate kinase family protein [Arabidopsis thaliana] : "F3G5.4; adenylate kinase family protein [Arabidopsis thaliana]"	Pp1s234_106V6.1	AT2G37250.1	GO:0004017 : GO:0005524 : GO:0006139 : GO:0019201	ATP binding : adenylate kinase activity : nucleobase, nucleoside, nucleotide and nucleic acid metabolism : nucleotide kinase activity
Phypa_218647	F28P10.130; chlorophyll A-B binding protein / LHCI type I (CAB) [Arabidopsis thaliana] : "F28P10.130; chlorophyll A-B binding protein / LHCI type I (CAB) [Arabidopsis thaliana]"	Pp1s161_32V6.1;Pp1s161_32V6.2 : "Pp1s161_32V6.1;Pp1s161_32V6.2" : "Pp1s161_32V6.1;Pp1s161_32V6.2 : ""Pp1s161_32V6.1;Pp1s161_32V6.2"""	AT3G54890.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting
Phypa_164715	F25O24.9; elongation factor Ts family protein [Arabidopsis thaliana] : "F25O24.9; elongation factor Ts family protein [Arabidopsis thaliana]"	Pp1s74_242V6.1	AT4G29060.1	GO:0003723 : GO:0003735 : GO:0005840 : GO:0006412	RNA binding : protein biosynthesis : ribosome : structural constituent of ribosome

Phypa_110579	T22C5.13; glucose-1-phosphate adenylyltransferase large subunit 2 (APL2) / ADP-glucose pyrophosphorylase [EC:2.7.7.27] [KO:K00975] [Arabidopsis thaliana] : "T22C5.13; glucose-1-phosphate adenylyltransferase large subunit 2 (APL2) / ADP-glucose pyrophosphorylase [EC:2.7.7.27] [KO:K00975] [Arabidopsis thaliana]"	Pp1s347_12V6.1	AT5G19220.1	GO:0004672 : GO:0005524 : GO:0005978 : GO:0006468 : GO:0008878 : GO:0009058 : GO:0016779	ATP binding : biosynthesis : glucose-1-phosphate adenylyltransferase activity : glycogen biosynthesis : nucleotidyltransferase activity : protein amino acid phosphorylation : protein kinase activity
Phypa_122958	F27F5.9; expressed protein [Arabidopsis thaliana] : "F27F5.9; expressed protein [Arabidopsis thaliana]"	Pp1s42_236V6.1	AT1G35180.1	GO:0016021	integral to membrane
Phypa_132849	F6A14.19; DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] : "F6A14.19; DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana]"	Pp1s98_193V6.1	AT1G18700.2		
Phypa_109510	Thylakoid membrane phosphoprotein 14 kDa, chloroplast precursor [Arabidopsis thaliana]	Pp1s15_328V6.1	AT1G52220.1		
Phypa_176210	T5A14.11; RuBisCO subunit binding-protein beta subunit, chloroplast / 60 kDa chaperonin beta subunit / CPN-60 beta [Arabidopsis thaliana] : "T5A14.11; RuBisCO subunit binding-protein beta subunit, chloroplast / 60 kDa chaperonin beta subunit / CPN-60 beta [Arabidopsis thaliana]"	Pp1s15_485V6.1;Pp1s15_485V6.2 : "Pp1s15_485V6.1;Pp1s15_485V6.2" : "Pp1s15_485V6.1;Pp1s15_485V6.2 : ""Pp1s15_485V6.1;Pp1s15_485V6.2"""	AT1G55490.1	GO:0003763 : GO:0005515 : GO:0005524 : GO:0044267	ATP binding : cellular protein metabolism : chaperonin ATPase activity : protein binding
Phypa_194139	Ferredoxin-dependent glutamate synthase 1, chloroplast precursor (Fd-GOGAT 1) [Arabidopsis thaliana]	Pp1s212_44V6.1	AT5G04140.1	GO:0006537 : GO:0006807 : GO:0008152 : GO:0015930 : GO:0016041 : GO:0016491	glutamate biosynthesis : glutamate synthase (ferredoxin) activity : glutamate synthase activity : metabolism : nitrogen compound metabolism : oxidoreductase activity

Phypa_47696	Photosystem I reaction center subunit III, chloroplast precursor (Light-harvesting complex I 17 kDa protein) (PSI-F) [Flaveria trinervia]	Pp1s121_54V6.1	AT1G31330.1	GO:0009538 : GO:0015979	photosynthesis : photosystem I reaction center
Phypa_232286		Pp1s72_208V6.1	AT3G27850.1		
Phypa_165954	F1M20.15; geranylgeranyl reductase [Arabidopsis thaliana] : "F1M20.15; geranylgeranyl reductase [Arabidopsis thaliana]"	Pp1s100_107V6.1	AT1G74470.1	GO:0006118 : GO:0008152 : GO:0015979 : GO:0015995 : GO:0016491 : GO:0045550	chlorophyll biosynthesis : electron transport : geranylgeranyl reductase activity : metabolism : oxidoreductase activity : photosynthesis
Phypa_106250	Probable indole-3-acetic acid-amido synthetase GH3.5 (Auxin-responsive GH3-like protein 5) (OsGH3-5) [no tax name]	Pp1s67_243V6.1;Pp1s67_243V6.2 : "Pp1s67_243V6.1;Pp1s67_243V6.2" : "Pp1s67_243V6.1;Pp1s67_243V6.2 : ""Pp1s67_243V6.1;Pp1s67_243V6.2"""	AT4G03400.1		
Phypa_200318	putative 33kDa oxygen evolvingprotein of photosystem II [Oryza sativa (japonica cultivar-group)]	Pp1s421_3V6.1	AT3G50820.1	GO:0005509 : GO:0009654 : GO:0015979 : GO:0019898 : GO:0042549	calcium ion binding : extrinsic to membrane : oxygen evolving complex : photosynthesis : photosystem II stabilization
Phypa_54996	K23F3.2; glucose-1-phosphate adenylyltransferase, small subunit, chloroplast (ADP-glucose pyrophosphorylase) (APS1) [EC:2.7.7.27] [KO:K00975] [Arabidopsis thaliana] : "K23F3.2; glucose-1-phosphate adenylyltransferase, small subunit, chloroplast (ADP-glucose pyrophosphorylase) (APS1) [EC:2.7.7.27] [KO:K00975] [Arabidopsis thaliana]"	Pp1s2_392V6.1	AT5G48300.1	GO:0005978 : GO:0008878 : GO:0009058 : GO:0016779	biosynthesis : glucose-1-phosphate adenylyltransferase activity : glycogen biosynthesis : nucleotidyltransferase activity

Phypa_216605	F14F8.30; reversibly glycosylated polypeptide-3 [EC:2.4.1.112] [Arabidopsis thaliana] : "F14F8.30; reversibly glycosylated polypeptide-3 [EC:2.4.1.112] [Arabidopsis thaliana]"	Pp1s131_34V6.1	AT5G15650.1	GO:0005794 : GO:0009505 : GO:0030244 : GO:0047210	Golgi apparatus : alpha-1,4-glucan-protein synthase (UDP-forming) activity : cell wall (sensu Magnoliophyta) : cellulose biosynthesis
Phypa_107767		Pp1s195_41V6.1	AT3G29320.1	GO:0004645 : GO:0005975	carbohydrate metabolism : phosphorylase activity
Phypa_9752	Photosystem II reaction center W protein, chloroplast precursor (PSII 6.1 kDa protein) [Spinacia oleracea]	Pp1s185_110V6.1	AT2G30570.1		
Phypa_223248	Chlorophyll a-b binding protein 13, chloroplast precursor (LHCII type III CAB-13) [Lycopersicon esculentum]	Pp1s254_3V6.1;Pp1s254_3V6.2 : "Pp1s254_3V6.1;Pp1s254_3V6.2" : "Pp1s254_3V6.1;Pp1s254_3V6.2 : ""Pp1s254_3V6.1;Pp1s254_3V6.2"""	AT5G54270.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting
Phypa_160233	F2I11.160; expressed protein [Arabidopsis thaliana] : "F2I11.160; expressed protein [Arabidopsis thaliana]"	Pp1s20_112V6.1	AT5G11270.1		
Phypa_211595	T31J12.6; expressed protein [Arabidopsis thaliana] : "T31J12.6; expressed protein [Arabidopsis thaliana]"	Pp1s71_283V6.1	AT1G09340.1	GO:0005975	carbohydrate metabolism
Phypa_18875	F21B7.21; photosystem II family protein [KO:K02724] [Arabidopsis thaliana] : "F21B7.21; photosystem II family protein [KO:K02724] [Arabidopsis thaliana]"	Pp1s131_184V6.1	AT1G03600.1		

Phypa_85102	contains EST C73370(E3926) [Oryza sativa (japonica cultivar-group)]	Pp1s131_3V6.2;Pp1s131_3V6.1 : "Pp1s131_3V6.2;Pp1s131_3V6.1" : "Pp1s131_3V6.2;Pp1s131_3V6.1 : ""Pp1s131_3V6.2;Pp1s131_3V6.1"""	AT1G04920.1		
Phypa_188716	T32A16.60; expressed protein [Arabidopsis thaliana] : "T32A16.60; expressed protein [Arabidopsis thaliana]"	Pp1s123_43V6.1	AT4G23890.1		
Phypa_163619		Pp1s58_210V6.1			
Phypa_109121	K24M7.19; HCF106 (gb|AAD32652.1) [Arabidopsis thaliana] : "K24M7.19; HCF106 (gb|AAD32652.1) [Arabidopsis thaliana]"	Pp1s402_22V6.1	AT5G52440.1	GO:0008565 : GO:0015031 : GO:0016021	integral to membrane : protein transport : protein transporter activity
Phypa_172635		Pp1s370_29V6.1	AT2G36640.1		
Phypa_214514	Farnesyl pyrophosphate synthetase (FPP synthetase) (FPS) (Farnesyl diphosphate synthetase) [Includes: Dimethylallyltranstransferase ; Geranyltranstransferase] [Zea mays] : "Farnesyl pyrophosphate synthetase (FPP synthetase) (FPS) (Farnesyl diphosphate synthetase) [Includes: Dimethylallyltranstransferase ; Geranyltranstransferase] [Zea mays]"	Pp1s101_225V6.1	AT4G17190.1	GO:0008299	isoprenoid biosynthesis
Phypa_156993	F24G24.140; chlorophyll A-B binding protein CP26, chloroplast / light-harvesting complex II protein 5 / LHCIIc (LHCB5) [Arabidopsis thaliana] : "F24G24.140; chlorophyll A-B binding protein CP26, chloroplast / light-harvesting complex II protein 5 / LHCIIc (LHCB5) [Arabidopsis thaliana]"	Pp1s628_7V6.1	AT4G10340.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting
Phypa_158682		Pp1s4_282V6.1		GO:0016998	cell wall catabolism

Phypa_152025	Ribulose bisphosphate carboxylase small chain, chloroplast precursor (RuBisCO small subunit) [Betula pendula]	Pp1s352_14V6.1	AT5G38410.1	GO:0009573 : GO:0015977 : GO:0016984	carbon utilization by fixation of carbon dioxide : ribulose bisphosphate carboxylase complex (sensu Magnoliophyta) : ribulose-bisphosphate carboxylase activity
Phypa_215021		Pp1s109_97V6.1	AT1G22840.1	GO:0005489 : GO:0006118	electron transport : electron transporter activity
Phypa_178653	F23N11.11; golden2-like transcription factor (GLK1) [Arabidopsis thaliana] : "F23N11.11; golden2-like transcription factor (GLK1) [Arabidopsis thaliana]"	Pp1s31_317V6.1	AT5G44190.1	GO:0003677 : GO:0005634	DNA binding : nucleus
Phypa_170239	F7P1.20; NAD-dependent epimerase/dehydratase family [Arabidopsis thaliana] : "F7P1.20; NAD-dependent epimerase/dehydratase family [Arabidopsis thaliana]"	Pp1s237_14V6.1	AT5G28840.2	GO:0003824 : GO:0008460 : GO:0009225	catalytic activity : dTDP-glucose 4,6-dehydratase activity : nucleotide-sugar metabolism
Phypa_233750		Pp1s99_193V6.1	AT2G29180.1		
Phypa_169178	Ribulose bisphosphate carboxylase/oxygenase activase, chloroplast precursor (RuBisCO activase) (RA) [Malus x domestica]	Pp1s199_130V6.3;Pp1s199_130V6.2;Pp1s199_130V6.1 : "Pp1s199_130V6.3;Pp1s199_130V6.2;Pp1s199_130V6.1" : "Pp1s199_130V6.3;Pp1s199_130V6.2;Pp1s199_130V6.1 : ""Pp1s199_130V6.3;Pp1s199_130V6.2;Pp1s199_130V6.1"""	AT2G39730.3	GO:0005524	ATP binding
Phypa_131582	Photosystem I reaction center subunit VI, chloroplast precursor (PSI-H) (Light-harvesting complex I 11 kDa protein) [Zea mays]	Pp1s89_62V6.1	AT1G52230.1	GO:0009538 : GO:0015979	photosynthesis : photosystem I reaction center

Phypa_223634	MSJ11.24; expressed protein [Arabidopsis thaliana] : "MSJ11.24; expressed protein [Arabidopsis thaliana]"	Pp1s266_2V6.1	AT3G15840.1		
Phypa_171698	T12H3.7; membrane protein, putative [Arabidopsis thaliana] : "T12H3.7; membrane protein, putative [Arabidopsis thaliana]"	Pp1s307_12V6.1	AT2G06520.1	GO:0009523 : GO:0015979 : GO:0016020	membrane : photosynthesis : photosystem II
Phypa_172191	T10C21.60; expressed protein [Arabidopsis thaliana] : "T10C21.60; expressed protein [Arabidopsis thaliana]"	Pp1s335_75V6.1	AT2G24070.1		
Phypa_169593	Chlorophyll a-b binding protein L1818, chloroplast precursor [Chlamydomonas eugametos]	Pp1s213_80V6.1	AT2G05070.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting
Phypa_145567	F4P9.22; 50S ribosomal protein L28, chloroplast (CL28) [Arabidopsis thaliana] : "F4P9.22; 50S ribosomal protein L28, chloroplast (CL28) [Arabidopsis thaliana]"	Pp1s229_21V6.1	AT2G33450.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_39458	T20K14.140; biotin carboxyl carrier protein 2 (BCCP2) [Arabidopsis thaliana] : "T20K14.140; biotin carboxyl carrier protein 2 (BCCP2) [Arabidopsis thaliana]"	Pp1s54_77V6.1	AT5G15530.1	GO:0003989 : GO:0006633 : GO:0009317 : GO:0009374	acetyl-CoA carboxylase activity : acetyl-CoA carboxylase complex : biotin binding : fatty acid biosynthesis
Phypa_107666	MJE7.12; expressed protein [Arabidopsis thaliana] : "MJE7.12; expressed protein [Arabidopsis thaliana]"	Pp1s182_93V6.1	AT5G48480.1		
Phypa_234825		Pp1s76_97V6.1	AT1G74030.1		
Phypa_161232	T12H3.7; membrane protein, putative [Arabidopsis thaliana] : "T12H3.7; membrane protein, putative [Arabidopsis thaliana]"	Pp1s31_66V6.1;Pp1s31_66V6.2 : "Pp1s31_66V6.1;Pp1s31_66V6.2" : "Pp1s31_66V6.1;Pp1s31_66V6.2 : ""Pp1s31_66V6.1;Pp1s31_66V6.2"""	AT2G06520.1		
Phypa_119427	Chlorophyll a-b binding protein CP24 10A, chloroplast precursor (CAB-10A) (LHCP) [Lycopersicon esculentum]	Pp1s28_315V6.1	AT1G15820.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting

Phypa_138970	F17F16.5; ribosomal protein L20 family protein [KO:K02887] [Arabidopsis thaliana] : "F17F16.5; ribosomal protein L20 family protein [KO:K02887] [Arabidopsis thaliana]"	Pp1s152_64V6.1	AT1G16740.1	GO:0003723 : GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	RNA binding : intracellular : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_6728	FCAALL.30; lil3 protein [Arabidopsis thaliana] : "FCAALL.30; lil3 protein [Arabidopsis thaliana]"	Pp1s336_22V6.1	AT4G17600.1		
Phypa_109427	Photosystem I reaction center subunit II, chloroplast precursor (Photosystem I 20 kDa subunit) (PSI-D) [Spinacia oleracea]	Pp1s4_321V6.1	AT1G03130.1	GO:0009538 : GO:0015979	photosynthesis : photosystem I reaction center
Phypa_170367	Plastid-specific 30S ribosomal protein 3-1, chloroplast precursor (PSRP-3 1) [Arabidopsis thaliana]	Pp1s242_42V6.1	AT1G68590.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412 : GO:0009536	intracellular : plastid : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_193361	F9O13.17; ferredoxin--nitrite reductase, putative [EC:1.7.7.1] [KO:K00366] [Arabidopsis thaliana] : "F9O13.17; ferredoxin--nitrite reductase, putative [EC:1.7.7.1] [KO:K00366] [Arabidopsis thaliana]"	Pp1s197_146V6.1;Pp1s197_146V6.2;Pp1s197_146V6.3;Pp1s197_146V6.4 : "Pp1s197_146V6.1;Pp1s197_146V6.2;Pp1s197_146V6.3;Pp1s197_146V6.4" : "Pp1s197_146V6.1;Pp1s197_146V6.2;Pp1s197_146V6.3;Pp1s197_146V6.4 : ""Pp1s197_146V6.1;Pp1s197_146V6.2;Pp1s197_146V6.3;Pp1s197_146V6.4"""	AT2G15620.1	GO:0006118 : GO:0016664 : GO:0042128 : GO:0048307	electron transport : ferredoxin-nitrite reductase activity : nitrate assimilation : oxidoreductase activity, acting on other nitrogenous compounds as donors, iron-sulfur protein as acceptor
Phypa_168272		Pp1s171_80V6.1	AT2G43570.1		
Phypa_139912	F5I10.9; mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein [Arabidopsis thaliana] : "F5I10.9; mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein [Arabidopsis thaliana]"	Pp1s161_60V6.1	AT4G00290.1	GO:0016020	membrane

Phypa_172642		Pp1s370_52V6.2;Pp1s370_52V6.1 : "Pp1s370_52V6.2;Pp1s370_52V6.1" : "Pp1s370_52V6.2;Pp1s370_52V6.1 : ""Pp1s370_52V6.2;Pp1s370_52V6.1"""	AT2G36640.1		
Phypa_224024	Guanine nucleotide-binding protein beta subunit-like protein [Chlamydomonas reinhardtii]	Pp1s276_2V6.1	AT1G48630.1		
Phypa_129602	T5J8.7; photosystem I reaction center subunit II, chloroplast, putative / photosystem I 20 kDa subunit, putative / PSI-D, putative (PSAD1) [KO:K02692] [Arabidopsis thaliana] : "T5J8.7; photosystem I reaction center subunit II, chloroplast, putative / photosystem I 20 kDa subunit, putative / PSI-D, putative (PSAD1) [KO:K02692] [Arabidopsis thaliana]"	Pp1s77_69V6.1	AT1G03130.1	GO:0009538 : GO:0015979	photosynthesis : photosystem I reaction center
Phypa_163051	fbxl20; F-box and leucine-rich repeat protein 20 [Danio rerio] : "fbxl20; F-box and leucine-rich repeat protein 20 [Danio rerio]"	Pp1s51_143V6.2;Pp1s51_143V6.1 : "Pp1s51_143V6.2;Pp1s51_143V6.1" : "Pp1s51_143V6.2;Pp1s51_143V6.1 : ""Pp1s51_143V6.2;Pp1s51_143V6.1"""	AT3G60350.1		
Phypa_49044	50S ribosomal protein L12, chloroplast precursor (CL12) [Nicotiana tabacum]	Pp1s215_82V6.1	AT3G27830.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_131430	Thylakoid lumenal 21.5 kDa protein, chloroplast precursor [Arabidopsis thaliana]	Pp1s88_182V6.1	AT4G15510.1	GO:0005509 : GO:0009654 : GO:0015979 : GO:0019898	calcium ion binding : extrinsic to membrane : oxygen evolving complex : photosynthesis

Phypa_166457	T12H3.7; membrane protein, putative [Arabidopsis thaliana] : "T12H3.7; membrane protein, putative [Arabidopsis thaliana]"	Pp1s116_110V6.1	AT2G06520.1		
Phypa_225446	T25K16.8; pyruvate dehydrogenase E1 component alpha subunit, chloroplast [EC:1.2.4.1] [KO:K00161] [Arabidopsis thaliana] : "T25K16.8; pyruvate dehydrogenase E1 component alpha subunit, chloroplast [EC:1.2.4.1] [KO:K00161] [Arabidopsis thaliana]"	Pp1s318_24V6.1	AT1G01090.1	GO:0004739 : GO:0008152 : GO:0016624	metabolism : oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor : pyruvate dehydrogenase (acetyl-transferring) activity
Phypa_209093	T31E10.10; katanin, putative [Arabidopsis thaliana] : "T31E10.10; katanin, putative [Arabidopsis thaliana]"	Pp1s51_233V6.1	AT2G34560.2	GO:0000166 : GO:0005524 : GO:0008568 : GO:0017111	ATP binding : microtubule-severing ATPase activity : nucleoside-triphosphatase activity : nucleotide binding
Phypa_228033	T5M16.18; long-chain-fatty-acid--CoA ligase family protein / long-chain acyl-CoA synthetase family protein (LACS9) [EC:6.2.1.3] [KO:K01897] [Arabidopsis thaliana] : "T5M16.18; long-chain-fatty-acid--CoA ligase family protein / long-chain acyl-CoA synthetase family protein (LACS9) [EC:6.2.1.3] [KO:K01897] [Arabidopsis thaliana]"	Pp1s475_12V6.1	AT1G77590.1	GO:0003824 : GO:0004467 : GO:0008152	catalytic activity : long-chain-fatty-acid-CoA ligase activity : metabolism
Phypa_206666	T10I14.1; ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein [Arabidopsis thaliana] : "T10I14.1; ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein [Arabidopsis thaliana]"	Pp1s34_345V6.1	AT4G22380.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412 : GO:0030529 : GO:0042254	intracellular : protein biosynthesis : ribonucleoprotein complex : ribosome : ribosome biogenesis and assembly : structural constituent of ribosome

Phypa_115965	T20K14.140; biotin carboxyl carrier protein 2 (BCCP2) [Arabidopsis thaliana] : "T20K14.140; biotin carboxyl carrier protein 2 (BCCP2) [Arabidopsis thaliana]"	Pp1s15_270V6.1;Pp1s15_270V6.2 : "Pp1s15_270V6.1;Pp1s15_270V6.2" : "Pp1s15_270V6.1;Pp1s15_270V6.2 : ""Pp1s15_270V6.1;Pp1s15_270V6.2"""	AT5G16390.1	GO:0003989 : GO:0006633 : GO:0009317 : GO:0009374	acetyl-CoA carboxylase activity : acetyl-CoA carboxylase complex : biotin binding : fatty acid biosynthesis
Phypa_152300	F1N19.8; ribosomal protein S6 family protein [Arabidopsis thaliana] : "F1N19.8; ribosomal protein S6 family protein [Arabidopsis thaliana]"	Pp1s359_29V6.1	AT1G64510.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_19688		Pp1s44_315V6.1	AT4G10465.1	GO:0030001 : GO:0046872	metal ion binding : metal ion transport
Phypa_139567	Chlorophyll a-b binding protein 6A, chloroplast precursor (LHCI type I CAB-6A) (Light-harvesting complex I 26 kDa protein) [Lycopersicon esculentum]	Pp1s158_109V6.1	AT3G54890.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting
Phypa_142581	F28K20.19; bifunctional aspartate kinase/homoserine dehydrogenase / AK-HSDH [EC:2.7.2.4 1.1.1.3] [KO:K00003 K00928] [Arabidopsis thaliana] : "F28K20.19; bifunctional aspartate kinase/homoserine dehydrogenase / AK-HSDH [EC:2.7.2.4 1.1.1.3] [KO:K00003 K00928] [Arabidopsis thaliana]"	Pp1s194_198V6.1	AT4G19710.2	GO:0004072 : GO:0004412 : GO:0008152 : GO:0008652 : GO:0009067 : GO:0016597	amino acid binding : amino acid biosynthesis : aspartate family amino acid biosynthesis : aspartate kinase activity : homoserine dehydrogenase activity : metabolism
Phypa_161637	mucin-associated surface protein (MASP), putative [Trypanosoma cruzi]	Pp1s34_349V6.1			
Phypa_177431	T6H20.230; chloroplast outer envelope protein, putative [Arabidopsis thaliana] : "T6H20.230; chloroplast outer envelope protein, putative [Arabidopsis thaliana]"	Pp1s23_111V6.1	AT3G46740.1	GO:0019867	outer membrane

Phypa_186629		Pp1s96_143V6.1	AT1G21690.1	GO:0000166 : GO:0003677 : GO:0005524 : GO:0005663 : GO:0006260 : GO:0017111	ATP binding : DNA binding : DNA replication : DNA replication factor C complex : nucleoside-triphosphatase activity : nucleotide binding
Phypa_222981	Omega-6 fatty acid desaturase, chloroplast precursor [Arabidopsis thaliana]	Pp1s246_57V6.1;Pp1s246_57V6.2 : "Pp1s246_57V6.1;Pp1s246_57V6.2" : "Pp1s246_57V6.1;Pp1s246_57V6.2 : ""Pp1s246_57V6.1;Pp1s246_57V6.2"""	AT4G30950.1	GO:0006636 : GO:0016020 : GO:0016215 : GO:0016491 : GO:0016717 : GO:0018688 : GO:0018689 : GO:0042389	CoA desaturase activity : DDT 2,3-dioxygenase activity : fatty acid desaturation : membrane : naphthalene disulfonate 1,2-dioxygenase activity : omega-3 fatty acid desaturase activity : oxidoreductase activity : oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water
Phypa_180785	F28K19.22; sulfate transporter (Sultr1;2) [Arabidopsis thaliana] : "F28K19.22; sulfate transporter (Sultr1;2) [Arabidopsis thaliana]"	Pp1s45_14V6.2;Pp1s45_14V6.1 : "Pp1s45_14V6.2;Pp1s45_14V6.1" : "Pp1s45_14V6.2;Pp1s45_14V6.1 : ""Pp1s45_14V6.2;Pp1s45_14V6.1"""	AT4G08620.1	GO:0008271 : GO:0008272 : GO:0016020	membrane : sulfate porter activity : sulfate transport

Phypa_224311	T23E18.8; prolyl oligopeptidase, putative / prolyl endopeptidase, putative / post-proline cleaving enzyme, putative [EC:3.4.21.26] [Arabidopsis thaliana] : "T23E18.8; prolyl oligopeptidase, putative / prolyl endopeptidase, putative / post-proline cleaving enzyme, putative [EC:3.4.21.26] [Arabidopsis thaliana]"	Pp1s283_60V6.1;Pp1s283_60V6.2 : "Pp1s283_60V6.1;Pp1s283_60V6.2" : "Pp1s283_60V6.1;Pp1s283_60V6.2 : ""Pp1s283_60V6.1;Pp1s283_60V6.2"""	AT1G76140.1	GO:0003824 : GO:0004252 : GO:0004287 : GO:0006508 : GO:0008236	catalytic activity : prolyl oligopeptidase activity : proteolysis and peptidolysis : serine-type endopeptidase activity : serine-type peptidase activity
Phypa_74635	MCK7.20; malate dehydrogenase [NADP], chloroplast, putative [EC:1.1.1.82] [KO:K00051] [Arabidopsis thaliana] : "MCK7.20; malate dehydrogenase [NADP], chloroplast, putative [EC:1.1.1.82] [KO:K00051] [Arabidopsis thaliana]"	Pp1s48_151V6.1;Pp1s48_151V6.2 : "Pp1s48_151V6.1;Pp1s48_151V6.2" : "Pp1s48_151V6.1;Pp1s48_151V6.2 : ""Pp1s48_151V6.1;Pp1s48_151V6.2"""	AT5G58330.1	GO:0006100 : GO:0006108 : GO:0016491 : GO:0016615 : GO:0046554	malate dehydrogenase (NADP+) activity : malate dehydrogenase activity : malate metabolism : oxidoreductase activity : tricarboxylic acid cycle intermediate metabolism
Phypa_133255	F3C3.2; expressed protein [Arabidopsis thaliana] : "F3C3.2; expressed protein [Arabidopsis thaliana]"	Pp1s101_240V6.1	AT1G32220.1		
Phypa_167109	T1A4.40; isoflavone reductase-related [Arabidopsis thaliana] : "T1A4.40; isoflavone reductase-related [Arabidopsis thaliana]"	Pp1s136_41V6.1	AT5G18660.1		
Phypa_212016		Pp1s75_141V6.1	AT1G06680.1	GO:0005509 : GO:0009654 : GO:0015979 : GO:0019898	calcium ion binding : extrinsic to membrane : oxygen evolving complex : photosynthesis

Phypa_109367		Pp1s545_4V6.1	AT5G38410.1	GO:0009573 : GO:0015977 : GO:0016984	carbon utilization by fixation of carbon dioxide : ribulose bisphosphate carboxylase complex (sensu Magnoliophyta) : ribulose-bisphosphate carboxylase activity
Phypa_146248	contains ESTs AU078383(S13149),AU078384(S13149) [Oryza sativa (japonica cultivar-group)]	Pp1s241_86V6.2;Pp1s241_86V6.1 : "Pp1s241_86V6.2;Pp1s241_86V6.1" : "Pp1s241_86V6.2;Pp1s241_86V6.1 : ""Pp1s241_86V6.2;Pp1s241_86V6.1"""	AT1G44575.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting
Phypa_39045		Pp1s319_36V6.1	AT2G20260.1	GO:0006118 : GO:0009538	electron transport : photosystem I reaction center
Phypa_107034	F6N23.1; beta-amylase, putative / 1,4-alpha-D-glucan maltohydrolase, putative [Arabidopsis thaliana] : "F6N23.1; beta-amylase, putative / 1,4-alpha-D-glucan maltohydrolase, putative [Arabidopsis thaliana]"	Pp1s121_168V6.1;Pp1s121_168V6.2 : "Pp1s121_168V6.1;Pp1s121_168V6.2" : "Pp1s121_168V6.1;Pp1s121_168V6.2 : ""Pp1s121_168V6.1;Pp1s121_168V6.2"""	AT4G00490.1	GO:0000272 : GO:0016161	beta-amylase activity : polysaccharide catabolism
Phypa_162911	hypothetical protein, conserved [Trypanosoma cruzi]	Pp1s49_55V6.1		GO:0008757	S-adenosylmethionine-dependent methyltransferase activity
Phypa_205373	Plastocyanin, chloroplast precursor [Physcomitrella patens]	Pp1s27_130V6.1	AT1G76100.1	GO:0005489 : GO:0005507 : GO:0006118	copper ion binding : electron transport : electron transporter activity
Phypa_182167		Pp1s55_64V6.1			

Phypa_75588	L73G19.10; fibrillarin 2 (FIB2) [Arabidopsis thaliana] : "L73G19.10; fibrillarin 2 (FIB2) [Arabidopsis thaliana]"	Pp1s54_67V6.1	AT4G25630.1	GO:0003723 : GO:0005634 : GO:0006364	RNA binding : nucleus : rRNA processing
Phypa_171132	Glycine dehydrogenase [decarboxylating], mitochondrial precursor (Glycine decarboxylase) (Glycine cleavage system P-protein) [Flaveria anomala]	Pp1s276_86V6.1	AT2G26080.1	GO:0004374 : GO:0004375 : GO:0005961 : GO:0006544	glycine cleavage system : glycine dehydrogenase (decarboxylating) activity : glycine dehydrogenase complex (decarboxylating) : glycine metabolism
Phypa_162278	T8M16.240; expressed protein [Arabidopsis thaliana] : "T8M16.240; expressed protein [Arabidopsis thaliana]"	Pp1s41_167V6.1			
Phypa_234745		Pp1s153_138V6.1	AT5G58470.2		
Phypa_105543	Acetolactate synthase II, chloroplast precursor (Acetohydroxy-acid synthase II) (ALS II) [Nicotiana tabacum]	Pp1s40_15V6.2;Pp1s40_15V6.1 : "Pp1s40_15V6.2;Pp1s40_15V6.1" : "Pp1s40_15V6.2;Pp1s40_15V6.1 : ""Pp1s40_15V6.2;Pp1s40_15V6.1"""	AT3G48560.1	GO:0003984 : GO:0009082	acetolactate synthase activity : branched chain family amino acid biosynthesis
Phypa_105126	Chlorophyll a-b binding protein, chloroplast precursor (LHCII type I CAB) (LHCP) [Physcomitrella patens]	Pp1s27_97V6.1	AT2G05100.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting
Phypa_109512	Photosystem II 10 kDa polypeptide, chloroplast precursor [Spinacia oleracea]	Pp1s15_409V6.1	AT1G79040.1	GO:0009654 : GO:0015979 : GO:0042651	oxygen evolving complex : photosynthesis : thylakoid membrane
Phypa_214814		Pp1s106_68V6.1;Pp1s106_68V6.2 : "Pp1s106_68V6.1;Pp1s106_68V6.2" : "Pp1s106_68V6.1;Pp1s106_68V6.2 : ""Pp1s106_68V6.1;Pp1s106_68V6.2"""	AT4G03520.1	GO:0005489 : GO:0006118	electron transport : electron transporter activity

Phypa_173848	F7J7.220; oxygen-evolving enhancer protein 3, chloroplast, putative (PSBQ1) (PSBQ) [Arabidopsis thaliana] : "F7J7.220; oxygen-evolving enhancer protein 3, chloroplast, putative (PSBQ1) (PSBQ) [Arabidopsis thaliana]"	Pp1s1_461V6.1	AT4G21280.1	GO:0005509 : GO:0009654 : GO:0015979 : GO:0019898	calcium ion binding : extrinsic to membrane : oxygen evolving complex : photosynthesis
Phypa_126815	Triosephosphate isomerase, chloroplast precursor (TIM) (Triose-phosphate isomerase) [Fragaria x ananassa]	Pp1s61_72V6.1	AT2G21170.1	GO:0004807 : GO:0008152	metabolism : triose-phosphate isomerase activity
Phypa_123406	T9L3.40; CARBONIC ANHYDRASE 2 [EC:4.2.1.1] [KO:K01672] [Arabidopsis thaliana] : "T9L3.40; CARBONIC ANHYDRASE 2 [EC:4.2.1.1] [KO:K01672] [Arabidopsis thaliana]"	Pp1s44_343V6.1	AT1G23730.1	GO:0004089 : GO:0008270 : GO:0015976	carbon utilization : carbonate dehydratase activity : zinc ion binding
Phypa_146969	Ribulose bisphosphate carboxylase small chain, chloroplast precursor (RuBisCO small subunit) [Betula pendula]	Pp1s251_44V6.1	AT5G38420.1	GO:0009573 : GO:0015977 : GO:0016984	carbon utilization by fixation of carbon dioxide : ribulose bisphosphate carboxylase complex (sensu Magnoliophyta) : ribulose-bisphosphate carboxylase activity
Phypa_184553		Pp1s74_222V6.2	AT1G11390.1	GO:0003747 : GO:0005737 : GO:0006415 : GO:0016149	cytoplasm : translation release factor activity : translation release factor activity, codon specific : translational termination
Phypa_133026	putative alpha-amylase [Oryza sativa (japonica cultivar-group)]	Pp1s100_191V6.1	AT1G69830.1	GO:0004556 : GO:0005975	alpha-amylase activity : carbohydrate metabolism

Phypa_176127	K19E20.4; anthranilate N-hydroxycinnamoyl/benzoyltransferase family [Arabidopsis thaliana] : "K19E20.4; anthranilate N-hydroxycinnamoyl/benzoyltransferase family [Arabidopsis thaliana]"	Pp1s15_356V6.1;Pp1s15_356V6.2 : "Pp1s15_356V6.1;Pp1s15_356V6.2" : "Pp1s15_356V6.1;Pp1s15_356V6.2 : ""Pp1s15_356V6.1;Pp1s15_356V6.2"""	AT5G48930.1		
Phypa_110695	Dmel_CG9682; CG9682 gene product from transcript CG9682-RA [Drosophila melanogaster] : "Dmel_CG9682; CG9682 gene product from transcript CG9682-RA [Drosophila melanogaster]"	Pp1s517_11V6.2;Pp1s517_11V6.1 : "Pp1s517_11V6.2;Pp1s517_11V6.1" : "Pp1s517_11V6.2;Pp1s517_11V6.1 : ""Pp1s517_11V6.2;Pp1s517_11V6.1"""	Pp1s517_11V6		
Phypa_226715	Ribulose bisphosphate carboxylase small chain, chloroplast precursor (RuBisCO small subunit) [Betula pendula]	Pp1s374_50V6.1	AT1G67090.1	GO:0009573 : GO:0015977 : GO:0016984	carbon utilization by fixation of carbon dioxide : ribulose bisphosphate carboxylase complex (sensu Magnoliophyta) : ribulose-bisphosphate carboxylase activity
Phypa_155693	F14L17.3; CAAX amino terminal protease family protein [Arabidopsis thaliana] : "F14L17.3; CAAX amino terminal protease family protein [Arabidopsis thaliana]"	Pp1s477_8V6.1	AT1G14270.1		
Phypa_190462 [Phypa_144392;Phypa_60069]	Ferredoxin, chloroplast precursor [Physcomitrella patens]	Pp1s146_120V6.1	AT1G60950.1	GO:0005489 : GO:0005506 : GO:0006118	electron transport : electron transporter activity : iron ion binding
Phypa_107844		Pp1s199_101V6.1	AT5G51820.1	GO:0005975 : GO:0016868	carbohydrate metabolism : intramolecular transferase activity, phosphotransferases

Phypa_64224	F11I11.70; pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] : "F11I11.70; pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]"	Pp1s2_193V6.2;Pp1s2_193V6.1 : "Pp1s2_193V6.2;Pp1s2_193V6.1" : "Pp1s2_193V6.2;Pp1s2_193V6.1 : ""Pp1s2_193V6.2;Pp1s2_193V6.1"""	AT4G34830.1		
Phypa_191307	Serine/threonine-protein kinase SNT7, chloroplast precursor (Stt7 homolog) [Arabidopsis thaliana]	Pp1s159_111V6.1	AT1G68830.1	GO:0004672 : GO:0004674 : GO:0005524 : GO:0006468	ATP binding : protein amino acid phosphorylation : protein kinase activity : protein serine/threonine kinase activity
Phypa_202950	Granule-bound starch synthase 2, chloroplast precursor (Granule-bound starch synthase II) (SS II) (GBSS-II) [Solanum tuberosum]	Pp1s12_341V6.1	AT3G01180.1	GO:0009058	biosynthesis
Phypa_227616	F4F7.35; acidic ribosomal protein P0-related [Arabidopsis thaliana] : "F4F7.35; acidic ribosomal protein P0-related [Arabidopsis thaliana]"	Pp1s431_4V6.1	AT1G25260.1		
Phypa_131832	F24B22.170; ribosomal protein L17 family protein [KO:K02879] [Arabidopsis thaliana] : "F24B22.170; ribosomal protein L17 family protein [KO:K02879] [Arabidopsis thaliana]"	Pp1s91_15V6.1;Pp1s91_15V6.2 : "Pp1s91_15V6.1;Pp1s91_15V6.2" : "Pp1s91_15V6.1;Pp1s91_15V6.2 : ""Pp1s91_15V6.1;Pp1s91_15V6.2"""	AT3G54210.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_115069	Ribulose bisphosphate carboxylase small chain, chloroplast precursor (RuBisCO small subunit) [Marchantia paleacea]	Pp1s12_231V6.1	AT1G67090.1	GO:0009573 : GO:0015977 : GO:0016984	carbon utilization by fixation of carbon dioxide : ribulose bisphosphate carboxylase complex (sensu Magnoliophyta) : ribulose-bisphosphate carboxylase activity

Phypa_62234	F1N19.25; expressed protein [Arabidopsis thaliana] : "F1N19.25; expressed protein [Arabidopsis thaliana]"	Pp1s6_190V6.1	AT1G64680.1		
Phypa_233882		Pp1s109_92V6.1			
Phypa_196367	Fibrillarin-2 (Fibrillarin-like protein) [Arabidopsis thaliana]	Pp1s263_70V6.1	AT4G25630.1	GO:0003723 : GO:0005634 : GO:0006364	RNA binding : nucleus : rRNA processing
Phypa_85464	Glyceraldehyde-3-phosphate dehydrogenase A, chloroplast precursor (NADP-dependent glyceraldehydephosphate dehydrogenase subunit A) [Spinacia oleracea]	Pp1s135_21V6.1;Pp1s135_21V6.2;Pp1s135_21V6.3 : "Pp1s135_21V6.1;Pp1s135_21V6.2;Pp1s135_21V6.3" : "Pp1s135_21V6.1;Pp1s135_21V6.2;Pp1s135_21V6.3 : ""Pp1s135_21V6.1;Pp1s135_21V6.2;Pp1s135_21V6.3"""	AT1G12900.1	GO:0004365 : GO:0006006 : GO:0006096 : GO:0008943 : GO:0051287	NAD binding : glucose metabolism : glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity : glyceraldehyde-3-phosphate dehydrogenase activity : glycolysis
Phypa_115764	T9J22.17; cytochrome b6f complex subunit (petM), putative [Arabidopsis thaliana] : "T9J22.17; cytochrome b6f complex subunit (petM), putative [Arabidopsis thaliana]"	Pp1s14_288V6.1	AT2G26500.1		
Phypa_166666	F1L3.19; expressed protein [Arabidopsis thaliana] : "F1L3.19; expressed protein [Arabidopsis thaliana]"	Pp1s121_72V6.1			
Phypa_97038	F14O13.12; beta-amylase, putative / 1,4-alpha-D-glucan maltohydrolase, putative [Arabidopsis thaliana] : "F14O13.12; beta-amylase, putative / 1,4-alpha-D-glucan maltohydrolase, putative [Arabidopsis thaliana]"	Pp1s317_42V6.1	AT3G23920.1	GO:0000272 : GO:0016161	beta-amylase activity : polysaccharide catabolism
Phypa_119729	Thylakoid lumenal 25.6 kDa protein, chloroplast precursor [Arabidopsis thaliana]	Pp1s30_39V6.1;Pp1s30_39V6.2 : "Pp1s30_39V6.1;Pp1s30_39V6.2" : "Pp1s30_39V6.1;Pp1s30_39V6.2 : ""Pp1s30_39V6.1;Pp1s30_39V6.2"""	AT3G55330.1	GO:0005509 : GO:0009654 : GO:0015979 : GO:0019898	calcium ion binding : extrinsic to membrane : oxygen evolving complex : photosynthesis

Phypa_67470	hypothetical protein [Entamoeba histolytica HM-1:IMSS]	Pp1s15_4V6.1			
Phypa_36025	ATP synthase delta chain, chloroplast precursor [Nicotiana tabacum]	Pp1s10_393V6.1	AT4G09650.1	GO:0003936 : GO:0015986 : GO:0016469 : GO:0046933 : GO:0046961	ATP synthesis coupled proton transport : hydrogen-transporting ATP synthase activity, rotational mechanism : hydrogen-transporting ATPase activity, rotational mechanism : hydrogen-transporting two-sector ATPase activity : proton-transporting two-sector ATPase complex
Phypa_95302	long chain polyunsaturated fatty acid elongation enzyme-like protein [Leishmania major]	Pp1s277_79V6.1	AT3G06460.1	GO:0016021	integral to membrane
Phypa_176684	Chlorophyll a-b binding protein, chloroplast precursor (LHCII type I CAB) (LHCP) [Physcomitrella patens]	Pp1s19_13V6.2;Pp1s19_13V6.1 : "Pp1s19_13V6.2;Pp1s19_13V6.1" : "Pp1s19_13V6.2;Pp1s19_13V6.1 : ""Pp1s19_13V6.2;Pp1s19_13V6.1"""	AT2G05100.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting
Phypa_151854	MRA19.7; immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase [EC:5.2.1.8] [KO:K01802] [Arabidopsis thaliana] : "MRA19.7; immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase [EC:5.2.1.8] [KO:K01802] [Arabidopsis thaliana]"	Pp1s347_30V6.1;Pp1s347_30V6.2 : "Pp1s347_30V6.1;Pp1s347_30V6.2" : "Pp1s347_30V6.1;Pp1s347_30V6.2 : ""Pp1s347_30V6.1;Pp1s347_30V6.2"""	AT5G45680.1	GO:0003755 : GO:0004600 : GO:0006457 : GO:0030051 : GO:0042027	FK506-sensitive peptidyl-prolyl cis-trans isomerase : cyclophilin : cyclophilin-type peptidyl-prolyl cis-trans isomerase activity : peptidyl-prolyl cis-trans isomerase activity : protein folding

Phypa_228299	50S ribosomal protein L9, chloroplast precursor (CL9) [Arabidopsis thaliana]	Pp1s536_10V6.1	AT3G44890.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_38815		Pp1s126_84V6.1;Pp1s126_84V6.2 : "Pp1s126_84V6.1;Pp1s126_84V6.2" : "Pp1s126_84V6.1;Pp1s126_84V6.2 : ""Pp1s126_84V6.1;Pp1s126_84V6.2"""	AT3G22600.1	GO:0006869 : GO:0008289	lipid binding : lipid transport
Phypa_169177	Ribulose bisphosphate carboxylase/oxygenase activase 1, chloroplast precursor (RuBisCO activase 1) (RA 1) (RubisCO activase alpha form) [Larrea tridentata]	Pp1s199_129V6.1	AT2G39730.2	GO:0005524	ATP binding
Phypa_159087		Pp1s9_245V6.1			
Phypa_173430	F1O19.14; ribulose bisphosphate carboxylase small chain 1A / RuBisCO small subunit 1A (RBCS-1A) (ATS1A) [EC:4.1.1.39] [KO:K01602] [Arabidopsis thaliana] : "F1O19.14; ribulose bisphosphate carboxylase small chain 1A / RuBisCO small subunit 1A (RBCS-1A) (ATS1A) [EC:4.1.1.39] [KO:K01602] [Arabidopsis thaliana]"	Pp1s459_1V6.1;Pp1s459_2V6.2;Pp1s459_2V6.1 : "Pp1s459_1V6.1;Pp1s459_2V6.2;Pp1s459_2V6.1" : "Pp1s459_1V6.1;Pp1s459_2V6.2;Pp1s459_2V6.1 : ""Pp1s459_1V6.1;Pp1s459_2V6.2;Pp1s459_2V6.1"""	AT1G67090.2	GO:0009573 : GO:0015977 : GO:0016984	carbon utilization by fixation of carbon dioxide : ribulose bisphosphate carboxylase complex (sensu Magnoliophyta) : ribulose-bisphosphate carboxylase activity
Phypa_39042	F16A16.140; photosystem I reaction center subunit IV, chloroplast, putative / PSI-E, putative (PSAE1) [KO:K02693] [Arabidopsis thaliana] : "F16A16.140; photosystem I reaction center subunit IV, chloroplast, putative / PSI-E, putative (PSAE1) [KO:K02693] [Arabidopsis thaliana]"	Pp1s334_17V6.1	AT2G20260.1	GO:0006118 : GO:0009538	electron transport : photosystem I reaction center

Phypa_188347	F27K7.6; nucleolin, putative [Arabidopsis thaliana] : "F27K7.6; nucleolin, putative [Arabidopsis thaliana]"	Pp1s118_39V6.1;Pp1s118_39V6.2 : "Pp1s118_39V6.1;Pp1s118_39V6.2" : "Pp1s118_39V6.1;Pp1s118_39V6.2 : ""Pp1s118_39V6.1;Pp1s118_39V6.2"""	AT3G18610.1	GO:0003676	nucleic acid binding
Phypa_163040	F2G19.25; expressed protein [Arabidopsis thaliana] : "F2G19.25; expressed protein [Arabidopsis thaliana]"	Pp1s51_100V6.1	AT1G45688.1		
Phypa_155603 [Phypa_98257;Phypa_226175]	Fructose-bisphosphate aldolase, chloroplast precursor (ALDP) [no tax name]	Pp1s475_27V6.3;Pp1s475_27V6.2;Pp1s475_27V6.1 : "Pp1s475_27V6.3;Pp1s475_27V6.2;Pp1s475_27V6.1" : "Pp1s475_27V6.3;Pp1s475_27V6.2;Pp1s475_27V6.1 : ""Pp1s475_27V6.3;Pp1s475_27V6.2;Pp1s475_27V6.1"""	AT2G01140.1	GO:0004332 : GO:0006096	fructose-bisphosphate aldolase activity : glycolysis
Phypa_233494		Pp1s86_153V6.2;Pp1s86_153V6.1 : "Pp1s86_153V6.2;Pp1s86_153V6.1" : "Pp1s86_153V6.2;Pp1s86_153V6.1 : ""Pp1s86_153V6.2;Pp1s86_153V6.1"""	AT2G32950.1		
Phypa_214679		Pp1s104_30V6.1	AT4G15770.1	GO:0003723	RNA binding

Phypa_194508	F17I5.140; protein kinase, putative [EC:2.7.1.-] [Arabidopsis thaliana] : "F17I5.140; protein kinase, putative [EC:2.7.1.-] [Arabidopsis thaliana]"	Pp1s218_59V6.1	AT4G33950.1	GO:0004674 : GO:0004675 : GO:0004676 : GO:0004677 : GO:0004679 : GO:0004680 : GO:0004681 : GO:0004683 : GO:0004686 : GO:0004688 : GO:0004689 : GO:0004690 : GO:0004692 : GO:0004693 : GO:0004694 : GO:0004695 : GO:0004696 : GO:0004697 : GO:0004698 : GO:0004700 : GO:0004701 : GO:0004702 : GO:0004703 : GO:0004704 : GO:0004705 : GO:0004706 : GO:0004707 :	dependent protein kinase activity : AMP-activated protein kinase activity : ATP binding : DNA-dependent protein kinase activity : G-protein coupled receptor kinase activity : IkappaB kinase activity : JUN kinase activity : JUN kinase kinase activity : JUN kinase kinase kinase activity : Janus kinase activity : MAP kinase 1 activity : MAP kinase 2 activity : MAP kinase activity : MAP kinase kinase activity : MAP kinase kinase kinase activity : MAP kinase kinase kinase activity : MAP/ERK kinase kinase activity : MP kinase activity : NF-kappaB-inducing kinase activity : SAP kinase activity : atypical protein
Phypa_122707	Sedoheptulose-1,7-bisphosphatase, chloroplast precursor (Sedoheptulose-bisphosphatase) (SBPase) (SED(1,7)P2ase) [Arabidopsis thaliana]	Pp1s41_162V6.1	AT3G55800.1	GO:0005975 : GO:0042578	carbohydrate metabolism : phosphoric ester hydrolase activity
Phypa_175594	Chlorophyll a-b binding protein, chloroplast precursor (LHCII type I CAB) (LHCP) [Physcomitrella patens]	Pp1s13_200V6.1	AT2G05100.1	GO:0009765 : GO:0016020	membrane : photosynthesis light harvesting

Phypa_188969	Rac-like GTP-binding protein 5 (OsRac5) (GTPase protein RacD) [no tax name]	Pp1s126_126V6.1;Pp1s126_126V6.2 : "Pp1s126_126V6.1;Pp1s126_126V6.2" : "Pp1s126_126V6.1;Pp1s126_126V6.2 : ""Pp1s126_126V6.1;Pp1s126_126V6.2"""	AT4G35020.2	GO:0005525 : GO:0007264 : GO:0015031	GTP binding : protein transport : small GTPase mediated signal transduction
Phypa_107070	MIO24.4; phosphoglucomutase (emb|CAB64725.1) [EC:5.4.2.2] [KO:K01835] [Arabidopsis thaliana] : "MIO24.4; phosphoglucomutase (emb|CAB64725.1) [EC:5.4.2.2] [KO:K01835] [Arabidopsis thaliana]"	Pp1s124_155V6.1	AT5G51820.1	GO:0004614 : GO:0005975 : GO:0016868	carbohydrate metabolism : intramolecular transferase activity, phosphotransferases : phosphoglucomutase activity
Phypa_168546 [Phypa_52279;Phypa_52281]	glpV; Glycogen phosphorylase 1 [EC:2.4.1.1] [KO:K00688] [Dictyostelium discoideum] : "glpV; Glycogen phosphorylase 1 [EC:2.4.1.1] [KO:K00688] [Dictyostelium discoideum]"	Pp1s180_124V6.1	AT3G46970.1	GO:0004645 : GO:0005975 : GO:0008184	carbohydrate metabolism : glycogen phosphorylase activity : phosphorylase activity
Phypa_186944	F1N21.12; hexose transporter, putative [Arabidopsis thaliana] : "F1N21.12; hexose transporter, putative [Arabidopsis thaliana]"	Pp1s99_154V6.1	AT1G67300.1	GO:0005215 : GO:0005351 : GO:0006810 : GO:0008643 : GO:0008733 : GO:0016020 : GO:0016021	L-arabinose isomerase activity : carbohydrate transport : integral to membrane : membrane : sugar porter activity : transport : transporter activity
Phypa_171916	T6H20.230; chloroplast outer envelope protein, putative [Arabidopsis thaliana] : "T6H20.230; chloroplast outer envelope protein, putative [Arabidopsis thaliana]"	Pp1s317_51V6.1	AT3G46740.1	GO:0019867	outer membrane

Phypa_219412	K21L19.6; non phototropic hypocotyl 1-related [Arabidopsis thaliana] : "K21L19.6; non phototropic hypocotyl 1-related [Arabidopsis thaliana]"	Pp1s174_62V6.1;Pp1s174_62V6.2 : "Pp1s174_62V6.1;Pp1s174_62V6.2" : "Pp1s174_62V6.1;Pp1s174_62V6.2 : ""Pp1s174_62V6.1;Pp1s174_62V6.2"""	AT5G58140.1	GO:0000155 : GO:0000160 : GO:0004672 : GO:0004674 : GO:0004682 : GO:0004691 : GO:0004713 : GO:0004871 : GO:0005524 : GO:0005952 : GO:0005956 : GO:0006355 : GO:0006468 : GO:0007165 : GO:0008603 : GO:0008605	dependent protein kinase activity : cAMP-dependent protein kinase complex : cAMP-dependent protein kinase regulator activity : protein amino acid phosphorylation : protein kinase CK2 activity : protein kinase CK2 complex : protein kinase CK2 regulator activity : protein kinase activity : protein serine/threonine kinase activity : protein-tyrosine kinase activity : regulation of transcription, DNA-dependent : signal transducer activity : signal transduction : two-component sensor molecule activity : two-component signal transduction system (phosphorelay)
Phypa_151734	MYJ24.5; expressed protein [Arabidopsis thaliana] : "MYJ24.5; expressed protein [Arabidopsis thaliana]"	Pp1s343_26V6.1	AT5G23060.1		
Phypa_110121	Ferredoxin--NADP reductase, embryo isozyme, chloroplast precursor (FNR) [Oryza sativa]	Pp1s131_175V6.1	AT4G05390.1	GO:0004324 : GO:0006118 : GO:0015039 : GO:0016491	NADPH-adrenodoxin reductase activity : electron transport : ferredoxin-NADP+ reductase activity : oxidoreductase activity

Phypa_129127	F25O24.9; elongation factor Ts family protein [Arabidopsis thaliana] : "F25O24.9; elongation factor Ts family protein [Arabidopsis thaliana]"	Pp1s74_243V6.1	AT4G29060.1	GO:0003723 : GO:0003735 : GO:0003746 : GO:0005840 : GO:0006412 : GO:0006414	RNA binding : protein biosynthesis : ribosome : structural constituent of ribosome : translation elongation factor activity : translational elongation
Phypa_178365	Omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 1 [Glycine max]	Pp1s30_149V6.1;Pp1s30_149V6.2 : "Pp1s30_149V6.1;Pp1s30_149V6.2" : "Pp1s30_149V6.1;Pp1s30_149V6.2 : ""Pp1s30_149V6.1;Pp1s30_149V6.2"""	AT3G12120.1	GO:0006636 : GO:0016020 : GO:0016215 : GO:0016491 : GO:0016717 : GO:0018688 : GO:0018689 : GO:0042389	CoA desaturase activity : DDT 2,3-dioxygenase activity : fatty acid desaturation : membrane : naphthalene disulfonate 1,2-dioxygenase activity : omega-3 fatty acid desaturase activity : oxidoreductase activity : oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water
Phypa_8310	Ribulose bisphosphate carboxylase small chain, chloroplast precursor (RuBisCO small subunit) [Pyrus pyrifolia]	Pp1s459_14V6.1		GO:0009573 : GO:0015977 : GO:0016984	carbon utilization by fixation of carbon dioxide : ribulose bisphosphate carboxylase complex (sensu Magnoliophyta) : ribulose-bisphosphate carboxylase activity

Phypa_147622	T9J22.17; cytochrome b6f complex subunit (petM), putative [Arabidopsis thaliana] : "T9J22.17; cytochrome b6f complex subunit (petM), putative [Arabidopsis thaliana]"	Pp1s263_33V6.1	AT2G26500.2		
Phypa_137893	F9L11.15; ribosomal protein L11 family protein [KO:K02867] [Arabidopsis thaliana] : "F9L11.15; ribosomal protein L11 family protein [KO:K02867] [Arabidopsis thaliana]"	Pp1s141_43V6.1	AT1G32990.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_115956	ATP synthase B' chain, chloroplast precursor (Subunit II) [Spinacia oleracea]	Pp1s15_26V6.1	AT4G32260.1	GO:0015986 : GO:0016469 : GO:0016820	ATP synthesis coupled proton transport : hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances : proton-transporting two-sector ATPase complex
Phypa_123666	Ribulose bisphosphate carboxylase small chain, chloroplast precursor (RuBisCO small subunit) [Marchantia paleacea]	Pp1s46_42V6.1	AT1G67090.1	GO:0009573 : GO:0015977 : GO:0016984	carbon utilization by fixation of carbon dioxide : ribulose bisphosphate carboxylase complex (sensu Magnoliophyta) : ribulose-bisphosphate carboxylase activity
Phypa_88846	T22C5.13; glucose-1-phosphate adenylyltransferase large subunit 2 (APL2) / ADP-glucose pyrophosphorylase [EC:2.7.7.27] [KO:K00975] [Arabidopsis thaliana] : "T22C5.13; glucose-1-phosphate adenylyltransferase large subunit 2 (APL2) / ADP-glucose pyrophosphorylase [EC:2.7.7.27] [KO:K00975] [Arabidopsis thaliana]"	Pp1s175_26V6.1	AT1G27680.1	GO:0005978 : GO:0008878 : GO:0009058 : GO:0016779	biosynthesis : glucose-1-phosphate adenylyltransferase activity : glycogen biosynthesis : nucleotidyltransferase activity

[Phypa_125887;Phypa_125903;Phypa_125839]					
Phypa_159676	F8B4.40; expressed protein [Arabidopsis thaliana] : "F8B4.40; expressed protein [Arabidopsis thaliana]"	Pp1s14_348V6.1	AT4G32340.1		
Phypa_168024		Pp1s164_5V6.1	AT4G31590.1		
Phypa_161955	Tub; tubby candidate gene [Mus musculus] : "Tub; tubby candidate gene [Mus musculus]"	Pp1s37_306V6.1			
Phypa_29066	F16M14.7; chloroplast 30S ribosomal protein S31 (PSRP4) [Arabidopsis thaliana] : "F16M14.7; chloroplast 30S ribosomal protein S31 (PSRP4) [Arabidopsis thaliana]"	Pp1s29_213V6.1	AT2G38140.1		
Phypa_8123	F10A5.12; chaperone protein dnaJ-related [Arabidopsis thaliana] : "F10A5.12; chaperone protein dnaJ-related [Arabidopsis thaliana]"	Pp1s301_31V6.2;Pp1s301_31V6.1 : "Pp1s301_31V6.2;Pp1s301_31V6.1" : "Pp1s301_31V6.2;Pp1s301_31V6.1 : ""Pp1s301_31V6.2;Pp1s301_31V6.1"""	AT1G75690.1		
Phypa_54314		Pp1s38_249V6.2;Pp1s38_249V6.1 : "Pp1s38_249V6.2;Pp1s38_249V6.1" : "Pp1s38_249V6.2;Pp1s38_249V6.1 : ""Pp1s38_249V6.2;Pp1s38_249V6.1"""	AT5G56940.1	GO:0003735 : GO:0005622 : GO:0005840 : GO:0006412	intracellular : protein biosynthesis : ribosome : structural constituent of ribosome
Phypa_170763	Photosystem II 5 kDa protein, chloroplast precursor (PSII-T) (Light-regulated unknown 11 kDa protein) [Gossypium hirsutum]	Pp1s259_76V6.1	AT1G51400.1		

Phypa_38875	Pp1s374_42V6.1	AT5G38410.3	GO:0009573 : GO:0015977 : GO:0016984	carbon utilization by fixation of carbon dioxide : ribulose bisphosphate carboxylase complex (sensu Magnoliophyta) : ribulose-bisphosphate carboxylase activity

<u>Supplemental Dataset 2.</u> Comparison of present study with transcriptome profiling by *Chen et al.* , 2012

DEG overlap of present study and Chen *et al.* , 2012

A V1.6 CGI (*P. patens* genome v.1.6)

V1.6 CGI
Pp1s10_88V6
Pp1s101_240V6
Pp1s109_92V6
Pp1s114_207V6
Pp1s121_168V6
Pp1s121_72V6
Pp1s13_231V6
Pp1s133_69V6
Pp1s14_348V6
Pp1s141_128V6
Pp1s141_133V6
Pp1s15_485V6
Pp1s15_4V6
Pp1s152_65V6
Pp1s16_339V6
Pp1s174_62V6
Pp1s175_26V6
Pp1s197_146V6
Pp1s199_101V6
Pp1s199_129V6
Pp1s2_392V6
Pp1s21_137V6
Pp1s213_80V6
Pp1s218_59V6
Pp1s240_74V6
Pp1s241_86V6
Pp1s244_44V6
Pp1s25_107V6
Pp1s271_35V6
Pp1s31_108V6
Pp1s31_317V6
Pp1s317_42V6
Pp1s32_341V6
Pp1s34_237V6
Pp1s34_348V6
Pp1s34_349V6
Pp1s36_39V6
Pp1s37_306V6
Pp1s370_29V6
Pp1s370_52V6
Pp1s374_50V6
Pp1s4_282V6
Pp1s411_3V6
Pp1s44_315V6
Pp1s475_12V6
Pp1s475_26V6
Pp1s5_83V6
Pp1s51_143V6
Pp1s517_11V6

Pp1s52_212V6
Pp1s55_65V6
Pp1s58_210V6
Pp1s6_190V6
Pp1s6_50V6
Pp1s62_88V6
Pp1s86_214V6
Pp1s9_245V6
Pp1s91_16V6
Pp1s99_95V6

V1.6 CGI
Pp1s121_168V6
Pp1s133_69V6
Pp1s14_348V6
Pp1s23_336V6
Pp1s52_95V6

V1.6 CGI

Pp1s180_137V6
Pp1s71_51V6

V1.6 CGI
Pp1s123_97V6
Pp1s13_200V6
Pp1s201_82V6
Pp1s259_76V6
Pp1s279_58V6
Pp1s283_60V6
Pp1s307_12V6
Pp1s99_193V6

V1.6 CGI

Pp1s111_44V6
Pp1s130_124V6
Pp1s15_300V6
Pp1s167_89V6
Pp1s20_367V6
Pp1s220_112V6
Pp1s223_12V6
Pp1s271_68V6
Pp1s64_60V6

V1.6 CGI

Pp1s13_200V6
Pp1s272_60V6

V1.6 CGI

Pp1s1_863V6
Pp1s111_44V6
Pp1s126_15V6
Pp1s13_266V6
Pp1s15_300V6
Pp1s164_49V6
Pp1s188_47V6
Pp1s194_104V6
Pp1s2_651V6
Pp1s220_112V6
Pp1s223_12V6
Pp1s241_42V6
Pp1s271_68V6
Pp1s31_291V6
Pp1s358_60V6
Pp1s387_21V6
Pp1s58_127V6
Pp1s77_184V6
Pp1s8_239V6

Supplemental Dataset 2. **Comparison of present study with transcriptome profiling by *Chen et al.* , 2012**

overlap of data from present study and data from Cehn *et al.* , 2012

present study	Chen *et al.* , 2012; up-regulated
4 h R up-regulated	59
4 h R down-regulated	0
30 min R up-regulated	5
30 min R down-regulated	2

present study	Chen *et al.* , 2012; down-regulated
4 h R up-regulated	8
4 h R down-regulated	9
30 min R up-regulated	2
30 min R down-regulated	19

Supplemental Dataset 3. **Comparison of Transcriptome Analyses from *P. patens and* Arabidopsis (Leivar *et al.* , 2009)**

DEG overlap of present study and Leivar *et al.* , 2009

A	V1.6 CGI (*P. patens* genome v.1.6)
B	At homolog (Phytozome; TAIR10 best hit)
C	DEG class as described by Leivar *et al.* , 2009

Supplemental Dataset 3 - 4 h R up - Leivar up

V1.6 CGI	At-homolog	class
Pp1s475_26V6	AT5G46800	1
Pp1s93_122V6	AT3G09050	1
Pp1s347_30V6	AT5G45680	1
Pp1s107_1V6	AT1G74960	1
Pp1s195_41V6	AT3G29320	1
Pp1s198_75V6	AT5G07020	1
Pp1s160_127V6	AT5G20140	1
Pp1s276_86V6	AT2G26080	1
Pp1s100_191V6	AT1G69830	1
Pp1s49_42V6	AT4G01150	1
Pp1s41_162V6	AT3G55800	1
Pp1s201_82V6	AT3G12780	1
Pp1s266_2V6	AT3G15840	1
Pp1s241_86V6	AT1G44575	1
Pp1s101_240V6	AT1G32220	1
Pp1s2_193V6	AT4G34830	1
Pp1s183_75V6	AT4G04040	2
Pp1s317_42V6	AT3G23920	3
Pp1s86_153V6	AT2G32950	3
Pp1s81_131V6	AT5G02810	3
Pp1s25_66V6	AT3G50820	4
Pp1s28_315V6	AT1G15820	4
Pp1s259_76V6	AT1G51400	4
Pp1s197_123V6	AT1G61520	4
Pp1s10_393V6	AT4G09650	4
Pp1s301_31V6	AT1G75690	4
Pp1s239_18V6	AT3G56940	4
Pp1s11_39V6	AT1G06680	4
Pp1s199_129V6	AT2G39730	4
Pp1s185_110V6	AT2G30570	4
Pp1s271_35V6	AT5G16400	4
Pp1s15_409V6	AT1G79040	4
Pp1s136_41V6	AT5G18660	4
Pp1s281_87V6	AT2G04039	4
Pp1s48_151V6	AT5G58330	4
Pp1s35_78V6	AT4G03280	4
Pp1s206_11V6	AT1G52230	4
Pp1s319_36V6	AT2G20260	4
Pp1s330_37V6	AT3G61470	4
Pp1s20_373V6	AT3G54050	4
Pp1s131_184V6	AT1G03600	4
Pp1s15_328V6	AT1G52220	4
Pp1s143_176V6	AT1G60950	4
Pp1s1_461V6	AT4G21280	4
Pp1s254_25V6	AT1G76100	4
Pp1s343_26V6	AT5G23060	4
Pp1s4_321V6	AT1G03130	4
Pp1s11_397V6	AT1G12900	4
Pp1s55_140V6	AT3G63140	4

Pp1s121_54V6	AT1G31330	4
Pp1s123_43V6	AT4G23890	4
Pp1s347_12V6	AT5G19220	4
Pp1s212_44V6	AT5G04140	4
Pp1s268_34V6	AT1G74730	4
Pp1s89_87V6	AT1G15980	4
Pp1s71_283V6	AT1G09340	4
Pp1s628_7V6	AT4G10340	4
Pp1s167_136V6	AT4G13500	4
Pp1s116_110V6	AT2G06520	4
Pp1s14_288V6	AT2G26500	4
Pp1s88_182V6	AT4G15510	4
Pp1s30_39V6	AT3G55330	4
Pp1s114_123V6	AT2G40490	4
Pp1s123_97V6	AT1G54780	4
Pp1s15_26V6	AT4G32260	4
Pp1s114_207V6	AT4G26850	6
Pp1s213_80V6	AT2G05070	7
Pp1s254_3V6	AT5G54270	7
Pp1s43_120V6	AT5G08050	7
Pp1s158_109V6	AT3G54890	7
Pp1s229_36V6	AT5G35970	7
Pp1s340_26V6	AT3G59400	7
Pp1s126_141V6	AT1G64860	7
Pp1s159_111V6	AT1G68830	7
Pp1s91_16V6	AT5G67030	7
Pp1s174_62V6	AT5G58140	7
Pp1s31_317V6	AT5G44190	7

Supplemental Dataset 3 - 4 h R down - Leivar up

V1.6 CGI	At-homolog	class
Pp1s194_166V6	AT1G78020	1

Supplemental Dataset 3 - 30 min R down - Leivar up

V1.6 CGI	At-homolog	class
Pp1s102_181V6	AT5G08410	1
Pp1s152_53V6	AT3G13450	2
Pp1s11_386V6	AT2G33180	2
Pp1s356_40V6	AT3G47620	2
Pp1s20_291V6	AT3G23810	3
Pp1s184_140V6	AT3G54420	3
Pp1s259_104V6	AT2G33710	3
Pp1s268_67V6	AT5G51720	4
Pp1s16_179V6	AT5G54770	4
Pp1s17_363V6	AT5G12860	4
Pp1s22_322V6	AT1G24020	4
Pp1s39_349V6	AT5G13930	6
Pp1s117_16V6	AT4G27410	6
Pp1s188_47V6	AT4G37470	7
Pp1s124_139V6	AT3G47500	7

Supplemental Dataset 3 - 4 h R up - Leivar down

V1.6 CGI	At-homolog	class
Pp1s48_70V6	AT1G15550	2
Pp1s86_234V6	AT5G64300	2
Pp1s370_29V6	AT2G36640	4
Pp1s6_50V6	AT1G68560	4
Pp1s84_138V6	AT4G25140	4

Supplemental Dataset 3 - 4 h R down - Leivar down

V1.6 CGI	At-homolog	class
Pp1s2_113V6	AT1G64660	4

Supplemental Dataset 3 - 30 min R up - Leivar down

V1.6 CGI	At-homolog	class
Pp1s34_308V6	AT5G17330	2

Supplemental Dataset 3 - 30 min R down - Leivar down

V1.6 CGI	At-homolog	class
Pp1s91_206V6	AT4G13830	3
Pp1s241_42V6	AT1G19530	1
Pp1s485_11V6	AT2G35270	1

Supplemental Dataset 3. Comparison of Transcriptome Analyses from *P. patens and* Arabidopsis (Leivar *et al.* , 2009)

overlap of data from present study and data from Leivar *et al.* , 2009

	Leivar *et al.* , 2009; up-regulated						
	class1	class2	class3	class4	class5	class6	class7
present study (number of At homologs)							
4 h R up-regulated (250)	16	1	3	45	0	1	11
4 h R down-regulated (21)	1	0	0	0	0	0	0
30 min R up-regulated (9)	0	0	0	0	0	0	0
30 min R down-regulated (193)	1	3	3	4	0	2	2

	Leivar *et al.* , 2009; down-regulated						
	class1	class2	class3	class4	class5	class6	class7
present study (number of At homologs)							
4 h R up-regulated (250)	0	2	0	3	0	0	0
4 h R down-regulated (21)	0	0	0	1	0	0	0
30 min R up-regulated (9)	0	1	0	0	0	0	0
30 min R down-regulated (193)	2	0	1	0	0	0	0

overlap of data from Chen *et al.* , 2012 and data from Leivar *et al.* , 2009

	Leivar *et al.* , 2009; up-regulated						
	class1	class2	class3	class4	class5	class6	class7
Chen *et al.* , 2009 (number of At homologs)							
1 h R up-regulated (664)	16	4	14	18	1	9	17
1 h R down-regulated (733)	18	5	5	18	0	4	5

Leivar *et al.* , 2009; down-regulated

	class1	class2	class3	class4	class5	class6	class7
Chen *et al.* , 2009 (number of At homologs)							
1 h R up-regulated (664)	8	3	0	18	0	0	0
1 h R down-regulated (733)	10	6	2	5	0	2	1