

*Euglena*. The cells were illuminated at an intensity of  $55 \mu\text{mol m}^{-2} \text{s}^{-1}$ . Samples were taken out at the indicated times and used for the determination of AsA, the assay of ALase, and Northern hybridization. Values are expressed as the mean  $\pm$  SEM for three experiments. *A*, AsA level. *B*, ALase activity. *C*, Northern blot analysis. Ten micrograms of total RNA extracted from each sample was electrophoresed through a formaldehyde-containing agarose gel, capillary blotted onto a nylon membrane, and hybridized with  $^{32}\text{P}$ -labeled cDNA of *Euglena* ALase. Ethidium bromide staining of the rRNA is shown for the equality of loading. Values that were significantly different between control and illuminated cells are indicated <sup>a</sup> $P < 0.05$ , <sup>b</sup> $P < 0.01$ .

### Supplemental Data

The following materials are available in the online version of this article.

**Supplemental FIGURE 1. Sequence alignment of ALase homologues from various photosynthesizing algae.** Position numbers for indicated amino acid residues are from *Euglena* ALase. Sources of sequences: *Euglena* (AB306917), Rat (X69021), *Phaeodactylum tricornutum* (fgenes1\_pg.C\_chr\_22000164) from the *Phaeodactylum* genomic sequence (<http://genome.jgi-psf.org/Phatr2/Phatr2.home.html>), *Ostreococcus lucimarinus* (e\_gwEuk.13.288.1) from the *Ostreococcus* genomic sequence ([http://genome.jgi-psf.org/Ost9901\\_3/Ost9901\\_3.home.html](http://genome.jgi-psf.org/Ost9901_3/Ost9901_3.home.html)), *Thalassiosira pseudonana* (fgenes1\_pg.C\_chr\_7000613) from the *Thalassiosira* genomic sequence (<http://genome.jgi-psf.org/Thaps3/Thaps3.home.html>).

