



Figure S2. Changes in the abundance of singly and multiply phosphorylated variants of the LHCSR3 peptide $S_{26}VS_{28}GRRT_{32}T_{33}AAEPQTAAPVAAEDVFAYTK$ in response to different light conditions.

Algal cultures were exposed to 200 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$ (A, C, E) or 500 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$ (B, D, F) high light in HS medium and samples were taken at the indicated timepoints. Label-free quantification was performed as described in Figure 1.

(A, B) Singly phosphorylated peptide $S_{26}VS_{28}GRRT_{32}T_{33}AAEPQTAAPVAAEDVFAYTK$
(C, D) Same peptide as in (A,B), doubly phosphorylated.

(E, F) Same peptide as in (A,B), triply phosphorylated.

Data represent mean \pm standard deviation (200 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$: $n=4$; 500 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$: $n=3$ (0h: $n=2$)). Numbers in parentheses indicate the number of data points if low abundances did not permit quantification in all replicates. Welch's t-test (unpaired, two-tailed) was used to analyse the data: Values labelled with identical letters, or no letters, don't show statistically significant differences ($p > 0.05$).

Only kinetics of protein abundance changes but not absolute protein or peptide levels are comparable between the two high light experiments, since samples were analysed with different LC-MS configurations.