SUPPLEMENTARY MATERIAL

Table S1. Oligomers used for preparation of the ΔH324 mutant.

1. HemHf: 5′-GCGATGTAAATCCACTAAGG-3′
2. HemHr: 5′-CATCAATTGGAGGAAGCCTG-3′
3. HemHZeo1: 5′-ACATTAATTGCGTTGCGCTCACTGC**CTAAAGCAAGCCGACAAAATG**-3′
4. HemHZeo2: 5′-CAACTTAATCGCCTTGCAGCACATC**GTTAGGGCATAAATTGGAGC**-3′
5. HemHΔ324: 5′-GATTCCCTCAAC**TAG**GATCCTCCCTGCACC-3′

1,2 - Forward and reverse primers amplifying *hemH* gene with ~400 base pairs of the up- and downstream regions. **3,4** - Fusion primers, parts in bold are complementing to the zeocin resistance cassette, the rest of the primers are complementing to *hemH* gene. Used for insertion of zeocin cassette behind the *hemH* gene. **5** - Primer used for generation of the stop codon in *hemH* gene at amino acid position 324 (bolded).

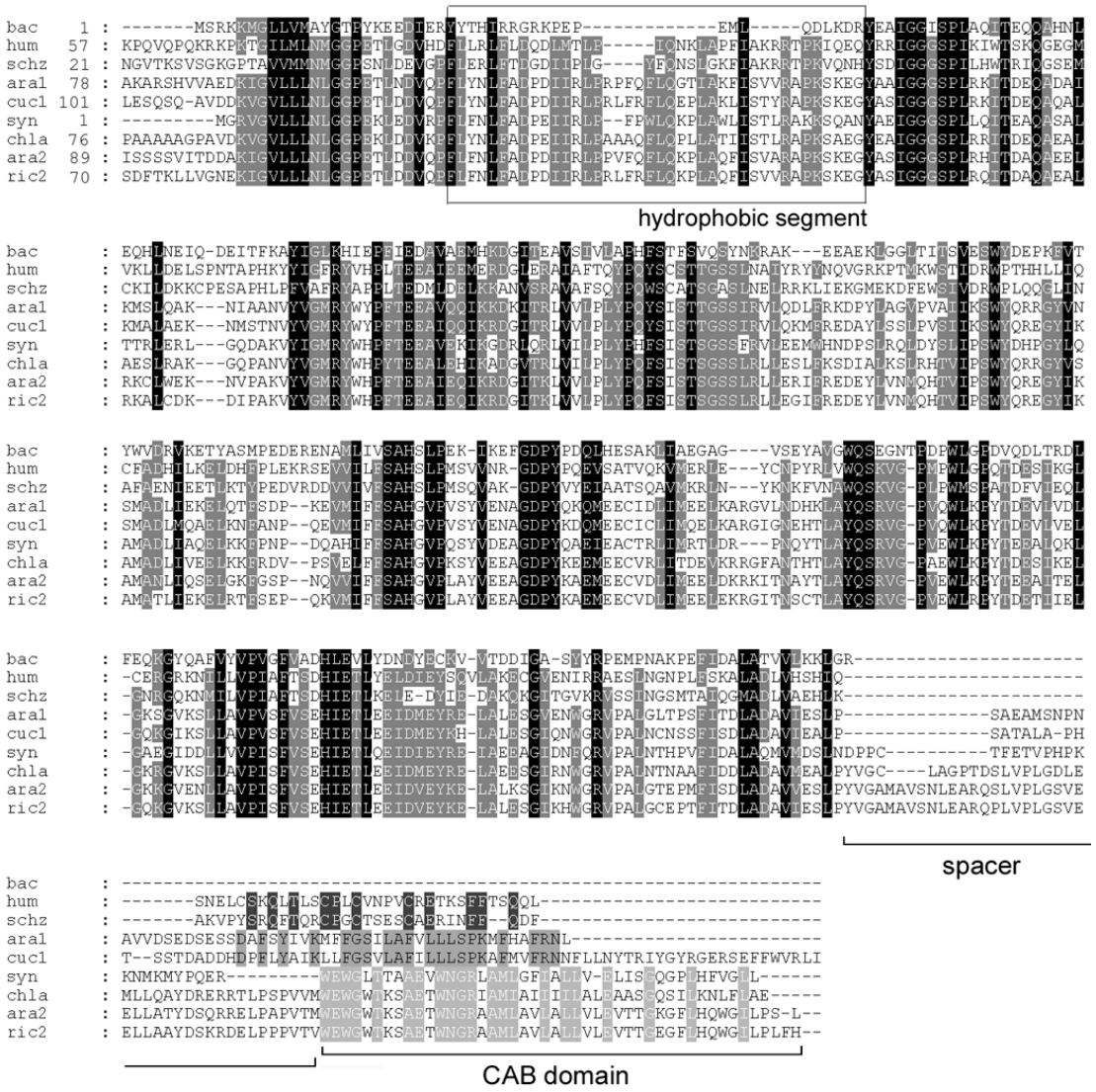

Figure S1. A) Amino acid alignment among FeCH proteins form *Bacillus subtilis* (bac), human (hum), *Schizosaccharomyces pombe* (schz); Arabidopsis isoform I (ara1), cucumber isoform I (cuc1), *Synechocystis* (syn), *Chlamydomonas* (chla), Arabidopsis isoform II (ara2) and rice isoform II (ric2). The targeting sequences in eukaryotic FeCHs have been omitted for clarity. The hydrophobic region at the N-terminus is boxed and the spacer region and the C-terminal CAB domain in *Synechocystis* FeCH are also shown.

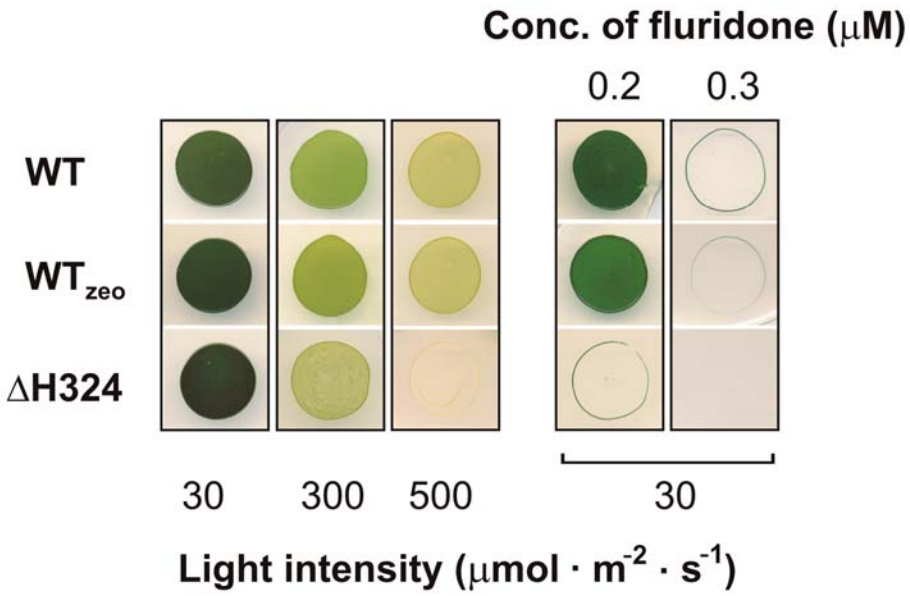

Figure S2. The growth of mutants exposed to high light and photooxidative stress. Cells in the logarithmic growth phase were diluted to OD_{730} ~0.05 and 50 μl of diluted culture was pipetted onto a BG 11 plate. Cells were grown six days at different light intensities or at several concentrations of fluridone.

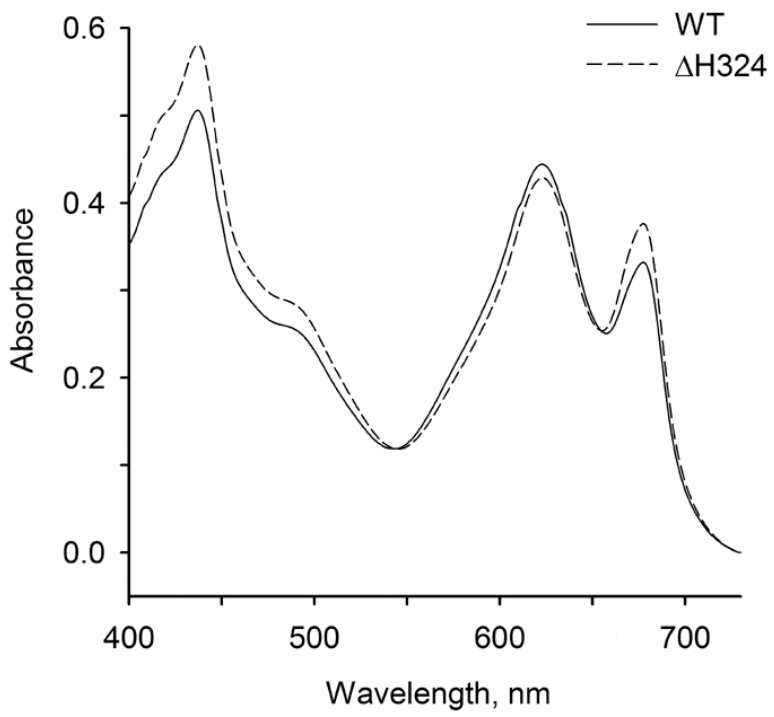

Figure S3. A) Absorbance spectra of *Synechocystis* 6803 whole cells. Chl *a* is represented by 682 and 440 nm peaks, phycobilinoproteins are represented by 625 nm peak. Strains were grown aerobically at normal light. Spectra were measured with cells in the logarithmic phase of growth (OD_{730} = ~ 0.4) and normalized to light scattering at 730 nm.