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Reporting Summary

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Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a Confirmed

- ☐ ☒ The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
- ☐ ☒ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- ☐ ☒ The statistical test(s) used AND whether they are one- or two-sided
Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- ☒ ☐ A description of all covariates tested
- ☒ ☐ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- ☐ ☒ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- ☐ ☒ For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
Give P values as exact values whenever suitable.
- ☒ ☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- ☒ ☐ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- ☒ ☐ Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection

Photos of SDS-PAGE and Western blot were acquired using ChemiDoc Imaging System (BIO-RAD) (Supplementary Figs. 3e-f, 25a,b). Photos of sucrose density gradients (Figure 1e) and Deriphat-PAGE (Supplementary Figs. 2c and 3d) were acquired with a smartphone camera.

For the fluorescence induction kinetics an homemade instrument was used (Fig. 1b). For PSI functional antenna size measurements was used a Joliot-Type 10 spectrophotometer (Biologic). ETR(II), NPQ, Fv/Fm, State Transition (and qT) measurements were measured using Dual-Pam-100 (Walz Photosynthesis Instruments) (Figs. 1a,b,c,d; Supplementary Figs. 2a,b,d). Absorption measurements were recorded using a SHIMADZU 2700i spectrophotometer (Figs. 5a,d,g, upper panel; Supplementary Figs. 3a,c and 25d). Circular dichroism spectra were recorded using a Jasco J-1500 spectropolarimeter (Supplementary Fig. 25e). Fluorescence emission spectra were recorded at 77 K using either a Jobin-Yvon Fluoromax-3 or an Ocean Insight SR-6NVN500-50 spectrofluorometer (Figure 1f; 6d). HPLC analysis was performed with Agilent Infinity II combined with C-18 column (Phenomenex) (Supplementary Figs. 3g; 25c). Time-resolved fluorescence measurements were performed on recombinant proteins using a home-built time-correlated single-photon counting (TCSPC) setup (Supplementary Fig. S25f). Fitting of acetone pigment extract spectrum were performed as described in: Chazaux, Marie, et al. "Precise estimation of chlorophyll a, b and carotenoid content by deconvolution of the absorption spectrum and new simultaneous equations for Chl determination." *The Plant Journal* 109.6 (2022): 1630-1648.

Two-Dimensional Electronic Spectroscopy measurements were recorded with an instrumental setting described in Supplementary Methods section, along with the FRET calculation.

Cryo-EM images using a Glacios transmission electron microscope (Thermo Fisher) operating at 200 kV, equipped with a Falcon 4i Direct Electron Detector (Thermo Fisher).

Synthetic genes for recombinant protein expression were purchased from Eurofins (www.eurofins.com).

Data analysis

Cryo-EM data processing and reconstruction steps were performed using CryoSPARC v4.6.2. Model building and refinement were performed using Phenix v.1.21, COOT and ChimeraX. The stereochemical quality of the final models was assessed with MolProbity. FRET analysis was performed with MS-Excel.

Two-Dimensional Electronic Spectroscopy data were analyzed with Matlab.

High-resolution figures were prepared with ChimeraX, PyMOL (The PyMOL 715 Molecular Graphics System, Version 2.0 Schrödinger, LLC), and Origin.

Functional domains similarity analysis was performed with InterPro (<https://www.ebi.ac.uk/interpro/>).

Sequence alignments were performed using Clustal Omega (<https://www.ebi.ac.uk/jdispatcher/msa/clustalo>).

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

Sequence data of *Posidonia oceanica* used are described in Ma, Xiao, et al. "Seagrass genomes reveal ancient polyploidy and adaptations to the marine environment." *Nature plants* 10.2 (2024): 240-255, and can be found in JGI Genome portal database (https://genome.jgi.doe.gov/portal/pages/dynamicOrganismDownload.jsf?organism=Posocenscriptome_2).

Sequence data of *Zea mays* protein subunits can be found in the Protein Data Bank with accession code 5ZII.

Sequence data of *Arabidopsis thaliana* can be found in Uniprot website database: LHCA1 (Q01667); LHCA2 (Q9SYW8); LHCA3 (Q9SY97); LHCA4 (P27521); LHCb1.3 (P04778); LHCb2.1 (Q96HR7); PSAl (P56768).

Sequence data of *Pisum sativum* can be found in Uniprot website database: LHCA1 (E1C9L2), LHCA2 (Q41038); LHCA3 (Q32904); LHCA4 (Q9SQL2); LHCb1 (P27490); LHCb2 (P27520).

Cryo-EM maps and coordinates of *Posidonia oceanica* have been deposited in the EMDb and wwPDB: PSI-LHCI (Composite map: EMD-54455, consensus map, EMD-54379; PSI core focused map, EMD-54380; LHCI belt focused map, EMD-54396; PDB: 9S1L); L-PSI-LHCI-LHCII or PSI-LHCI-mega (Composite map: EMD-54456, consensus map, EMD-54439; PSI core focused map, EMD-54441; LHCI belt focused map, EMD-54443; Lhca15-46-LHCII focused map, EMD-54444; PDB: 9S1M).

All Cryo-EM maps and models are available in the Figshare repository (<https://doi.org/10.6084/m9.figshare.31211194>). All data analyzed in this study are included in this article and its Supplementary Information. Additional related data and materials are available in the Source Data file or from the corresponding authors upon reasonable request. Source data are provided with this paper.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender

n/a

Reporting on race, ethnicity, or other socially relevant groupings

n/a

Population characteristics

n/a

Recruitment

n/a

Ethics oversight

n/a

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	Each physiological measurement was performed at least twice, and for each experiment, data were averaged from three or more biological replicates. Independent replicates showed consistent reproducibility across all reported parameters. Sample sizes were chosen based on the degree of experimental variability observed in each case. For Cryo-EM analysis all details and numbers about datasets and data analysis are described in the material and methods section.
Data exclusions	Across repeated experiments with different plants, some samples occasionally showed signs of poor health (low Fv/Fm, indicating reduced PSII quantum yield) or measurement artifacts due to suboptimal positioning in the instrument (e.g., light source does not fully cover the sample or low signal-to-noise ratio). In such cases, the dataset from the affected samples was excluded. Thus, the only predefined exclusion criteria concerned leaf health and signal quality.
Replication	Most experiments were repeated independently from 2 to 4 times. All attempts at replication were successful.
Randomization	n/a
Blinding	n/a

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☐	☒ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☐	☒ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	All the antibodies used were purchased from "Agrisera" website (https://www.agrisera.com/en/artiklar/plantagal-cell-biology/index.html), and can be identified from the product code reported in brackets: - α-Lhca1 (Agrisera code: AS01005; working dilution: 1:5000); - α-Lhca2 (Agrisera code: AS01006; working dilution: 1:7000); - α-Lhca3 (Agrisera code: AS01007; working dilution: 1:3000); - α-Lhca4 (Agrisera code: AS01008; working dilution: 1:3000); - α-Lhcb1 (Agrisera code: AS01004; working dilution: 1:5000); - α-Lhcb2 (Agrisera code: AS01003; working dilution: 1:4000); - phosphorylated α-Lhcb2 (Agrisera code: AS132705; working dilution: 1:5000); - α-PsaA (Agrisera code: AS06172; working dilution: 1:3000).
Validation	For the Agrisera antibodies validation see the Agrisera website (https://www.agrisera.com/en/artiklar/plantagal-cell-biology/index.html). Our own results were in agreement with those from Agrisera. Most of the antibodies used here were produced in our laboratory and made available to the community through Agrisera.

Dual use research of concern

Policy information about [dual use research of concern](#)

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

- | | |
|-------------------------------------|---|
| No | Yes |
| ☒ | ☐ Public health |
| ☒ | ☐ National security |
| ☒ | ☐ Crops and/or livestock |
| ☒ | ☐ Ecosystems |
| ☒ | ☐ Any other significant area |

Experiments of concern

Does the work involve any of these experiments of concern:

- | | |
|-------------------------------------|--|
| No | Yes |
| ☒ | ☐ Demonstrate how to render a vaccine ineffective |
| ☒ | ☐ Confer resistance to therapeutically useful antibiotics or antiviral agents |
| ☒ | ☐ Enhance the virulence of a pathogen or render a nonpathogen virulent |
| ☒ | ☐ Increase transmissibility of a pathogen |
| ☒ | ☐ Alter the host range of a pathogen |
| ☒ | ☐ Enable evasion of diagnostic/detection modalities |
| ☒ | ☐ Enable the weaponization of a biological agent or toxin |
| ☒ | ☐ Any other potentially harmful combination of experiments and agents |

Plants

Seed stocks

Posidonia oceanica plants, orthotropic shoots holding rhizome and roots, were collected by hand-picking SCUBA diving at 22 mt (40° 45'25"N, 13°53'25"E) and 4 mt (40°45'26"N, 13°53'09"E), in 2024, near Lacco Ameno, Ischia Island, Naples (Italy), with permission granted by the Italian public authorities. Both depths were sampled on the same day in successive dives.

Novel plant genotypes

n/a

Authentication

n/a