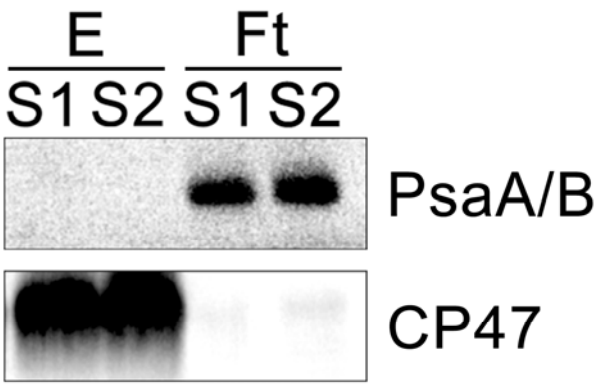
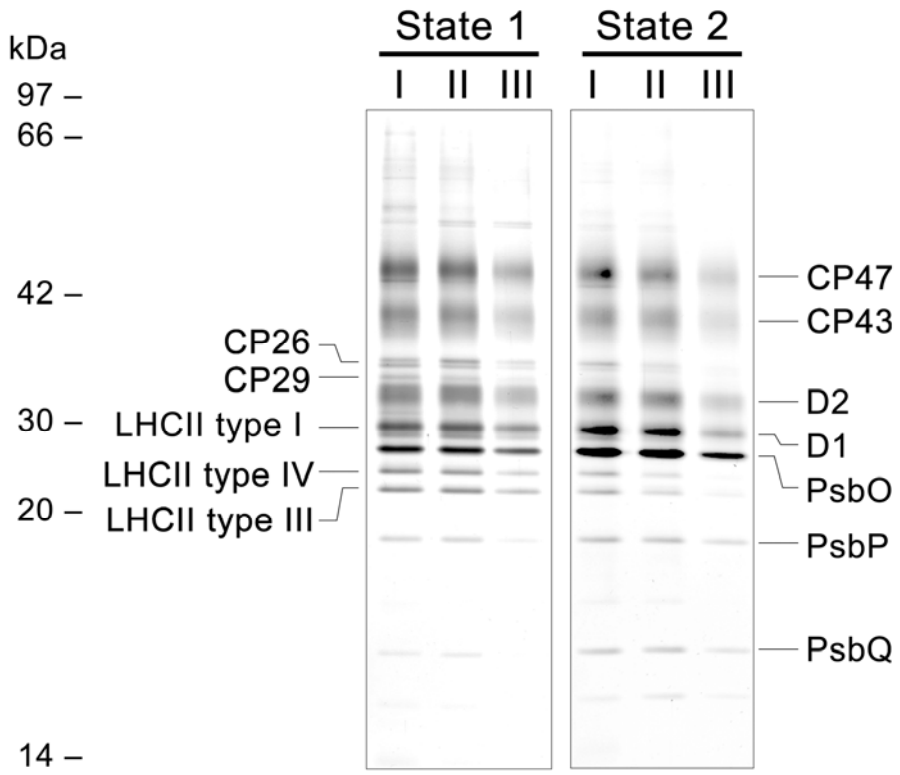
Supplemental Data. Iwai et al. (2008). Molecular Remodeling of Photosystem II during State Transitions in *Chlamydomonas reinhardtii.*



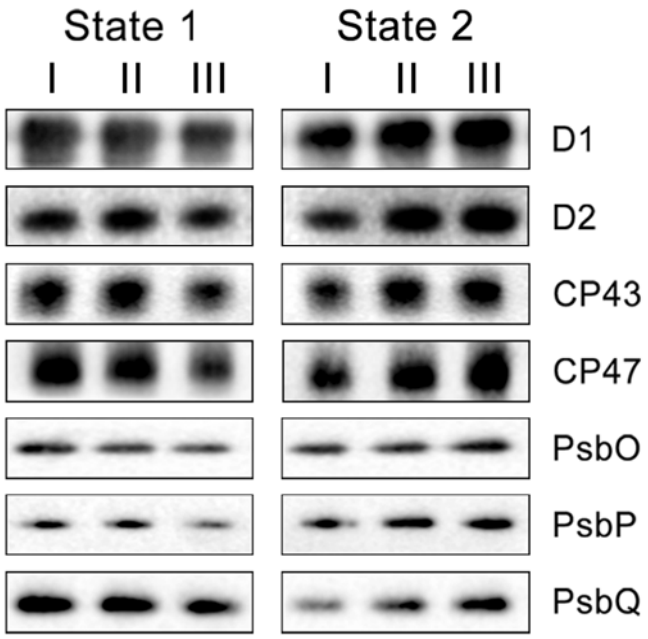
Supplemental Figure 1 online.

Specificity of nickel affinity chromatography. The bound (E) and flow-through (Ft) fractions from the nickel affinity chromatography of State 1 (S1) and State 2 (S2) samples were examined by western blotting. PSI and PSII proteins were identified using antibodies specific for PsaA/B and CP47, respectively.



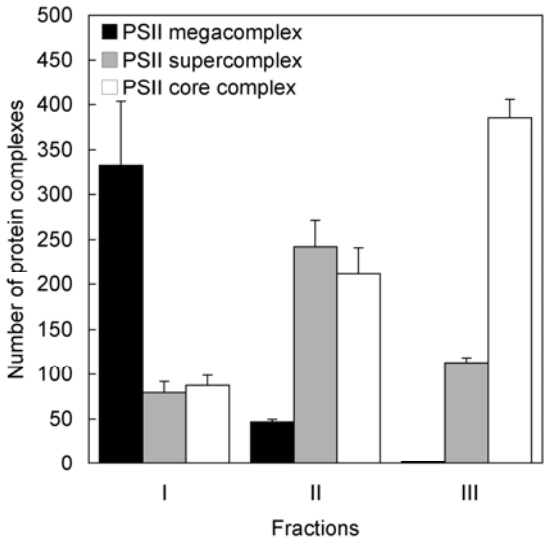
Supplemental Figure 2 online.

Polypeptide composition in the gel-filtration fractions I–III in State 1 and 2. Polypeptides in 15 µL of each fraction were separated by SDS-PAGE and silver stained.



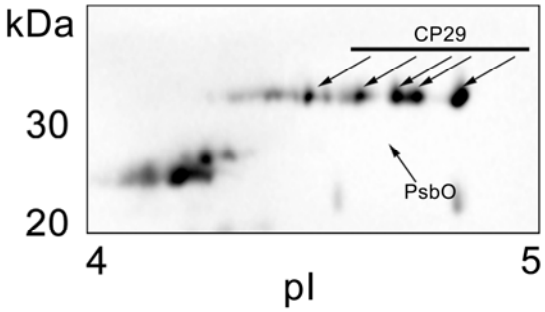
Supplemental Figure 3 online.

Relative abundance of the PSII core subunits in the gel-filtration fractions from State 1- and State 2-locked samples. Major subunits of PSII core in the State 1 and 2 samples were identified by western blotting using the specific antibodies as indicated. **I**, **II**, and **III** indicate the corresponding fractions isolated using gel-filtration (Figure 3). Ten µL from each fraction was loaded.



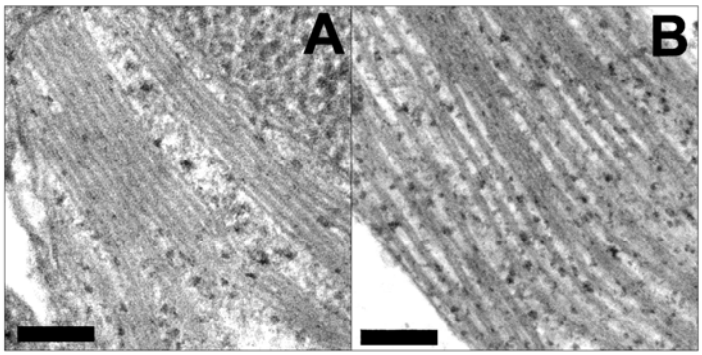
Supplemental Figure 4 online.

Distribution of PSII particle projections on electron micrographs. Particles corresponding to PSII-LHCII megacomplexes, PSII-LHCII supercomplexes, and PSII core were counted in randomly selected 500 particles on electron micrographs of Fractions I–III. A representative set of electron micrographs is shown in Figure 6. Data represent an average of two independent countings and are expressed as mean ± SD.



Supplemental Figure 5 online.

Evidence for the correspondence between spot #12 in Figure 8D and CP29.
Protein spot #12 on the 2-DE gel (Figure 8D) was identified by western blotting with an anti-CP29 antibody. Shown is the region between 20–40 kDa and pH 4.0–5.0 on the 2-DE gel.



Supplemental Figure 6 online.

Structure of thylakoid membranes in State 1 and State 2. Membrane layers of the thylakoids in the cells locked in State 1 **(A)** and 2 **(B)** were observed under an electron microscope. Scale bars represent 100 nm.

Supplemental Table 1 online. Relative protein levels of the PSII core subunits in the three PSII fractions.

PSII fraction	D1 (%)[a]	CP47 (%)[a]	PsbO (%)[a]
State 1			
I	100	100	100
II	86 ± 3	93 ± 17	81 ± 12
III	65 ± 10	73 ± 19	54 ± 16
State 2			
I	100	100	100
II	125 ± 24	133 ± 19	148 ± 42
III	135 ± 38	146 ± 71	163 ± 27

[a] Protein levels detected by western blotting (Supplemental Figure 3 online) were quantified using ImageJ software. Values shown are means of three measurements ± SD normalized to the value of Fraction I.

Supplemental Table 2 online. MS/MS analysis of the LHCII proteins bound to the PSII complexes[a].

Spot[b]	Peptide sequence	Predicted protein	Position[c]
1	YRENELLHAR	CP26	100–109
	HVADPFGYNLLTVLGAEER	CP26	267–285
2	GWLGGQGGAADLDKWYGPDR	CP26	38–57
	GWLGGQGGAADLDKWYGPDRK	CP26	38–58
	KLFLPSGLYDR	CP26	58–68
	LFLPSGLYDR	CP26	59–68
	SEIPEYLNGELAGDYGYDPLGLGK	CP26	69–92
	YRENELLHAR	CP26	100–109
	WAMLAAAGILIPEGLQANGANIK	CP26	110–132
	NGTGPAGYSPGIGK	CP26	185–198
	HVADPFGYNLLTVLGAEER	CP26	267–285
3	LAPYSEVFGLAR	CP29	121–132
4	SGTQFGEAVWFK	LhcbM3	113–124
	GPIQNLDDHLSNPTVNNAFAFATK	LhcbM3	229–252
	SGTKFGEAVWFK	LhcbM4/6	110–121
5	SSGVEFYGPNR	LhcbM4/6 /9	32–42
6	VNGGPLGEGLDK	LhcbM1	168–179
	LYPGGSFDPLGLADDPDTFAELK	LhcbM1	180–202
	GPLQNLSDHLANPGTNNAFAYATK	LhcbM1	229–252
7	LYPGGSFDPLGLADDPDTFAELK	LhcbM1	180–202
	GPLQNLSDHLANPGTNNAFAYATK	LhcbM1	229–252
8	GPIQNLDDHLANPTAVNAFAYATK	LhcbM2/7	221–244

9	GPIQNLDDHLANPTAVNAFAYATK	LhcbM2/7	221–244

[a] PSII complexes were isolated from State 2-locked samples

[b] Numbered spots correspond to those shown in Figure 5.

[c] Amino acid position in the corresponding protein.

Supplemental Table 3 online. MS/MS analysis of the free LHCII proteins in the nickel affinity chromatography flow-through[a].

Spot[b]	Peptide sequence	Predicted protein	Position[c]
10	YRENELLHAR	CP26	100–109
	HVADPFGYNLLTVLGAEER	CP26	267–285
11	GWLGGQGGAADLDKWYGPDR	CP26	38–57
	GWLGGQGGAADLDKWYGPDRK	CP26	38–58
	KLFLPSGLYDR	CP26	58–68
	LFLPSGLYDR	CP26	59–68
	SEIPEYLNGELAGDYGYDPLGLGK	CP26	69–92
	YRENELLHAR	CP26	100–109
	WAMLAAAGILIPEGLQANGANIK	CP26	110–132
	NGTGPAGYSPGIGK	CP26	185–198
	HVADPFGYNLLTVLGAEER	CP26	267–285
12	Confirmed by western blotting (Supplemental Figure 5 online)	CP29	
13	SGTQFGEAVWFK	LhcbM3	113–124
	GPIQNLDDHLSNPTVNNAFAFATK	LhcbM3	229–252
14	SGTKFGEAVWFK	LhcbM4/6	110–121
15	SSGVEFYGPNR	LhcbM4/6/9	32–42
16	VNGGPLGEGLDK	LhcbM1	86–95
17	LYPGGSFDPLGLADDPDTFAELK	LhcbM1	180–202
	GPLQNLSDHLANPGTNNAFAYATK	LhcbM1	229–252
18	LYPGGSFDPLGLADDPDTFAELK	LhcbM1	86–95

	GPLQNLSDHLANPGTNNAFAYATK	LhcbM1	229–252
19	GPIQNLDDHLANPTAVNAFAYATK	LhcbM2/7	221–244
20	VNGGPLGEGLDK	LhcbM1	86–95
	LYPGGSFDPLGLADDPDTFAELK	LhcbM1	180–202
	GPLQNLSDHLANPGTNNAFAYATK	LhcbM1	229–252
21	AAIEWYGPDRPK	LhcbM2	28–39
	NGIPFGEAVWFK	LhcbM2/7	105–116
	ANGGPLGEGLDPLHPGGAFDPLGLADDPD TFAELK	LhcbM2/7	160–194
	GPIQNLDDHLANPTAVNAFAYATK	LhcbM2/7	221–244
22	NGIPFGEAVWFK	LhcbM2/7	105–116
	ANGGPLGEGLDPLHPGGAFDPLGLADDPD TFAELK	LhcbM2/7	160–194
	GPIQNLDDHLANPTAVNAFAYATK	LhcbM2/7	221–244

[a] PSII complexes were isolated from a State 2-locked sample

[b] Numbered spots correspond to those shown in Figure 8.

[c] Amino acid position in the corresponding protein.