Supporting Information

Structural determinants for light-dependent membrane binding of a photoswitchable polybasic domain

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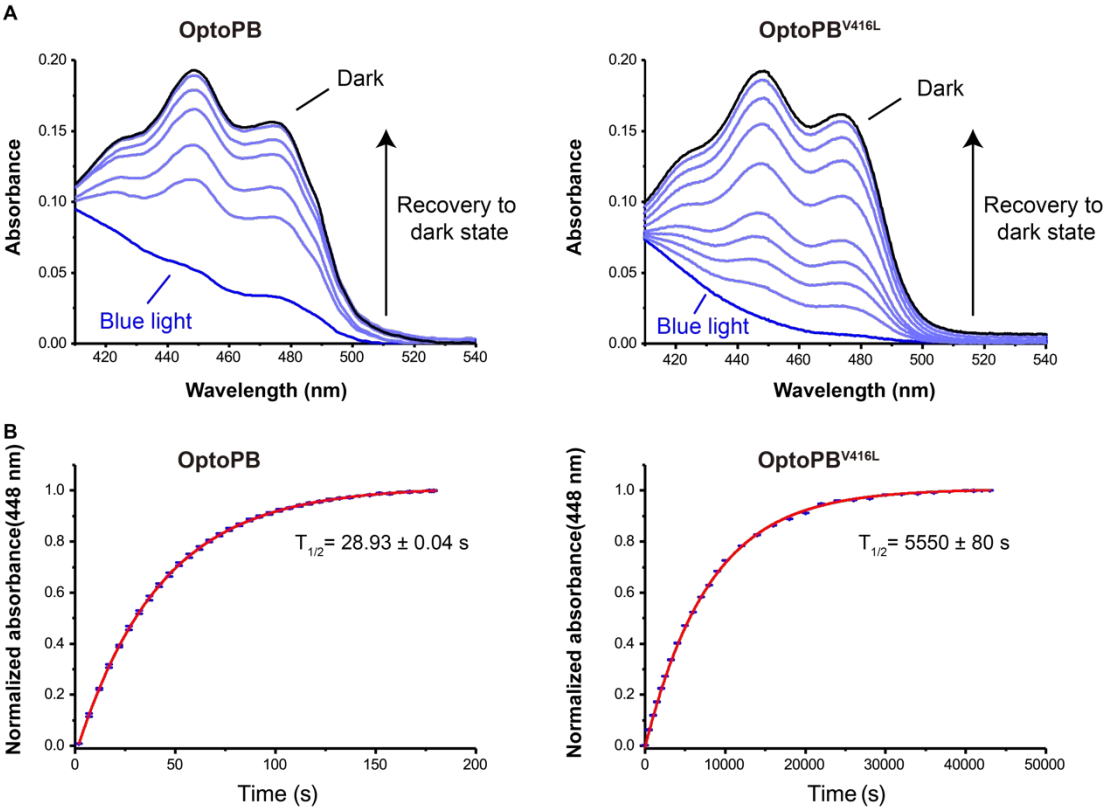

Figure S1. Dark reversion kinetic analysis of OptoPB (left) and OptoPB^{V416L} (right) using UV-VIS spectra. (A) Representative UV-VIS spectra during the process of dark recovering. (B) The half-recovery time $t_{1/2}$ is fitted by the absorbance data at 448 nm using the function of one phase decay.

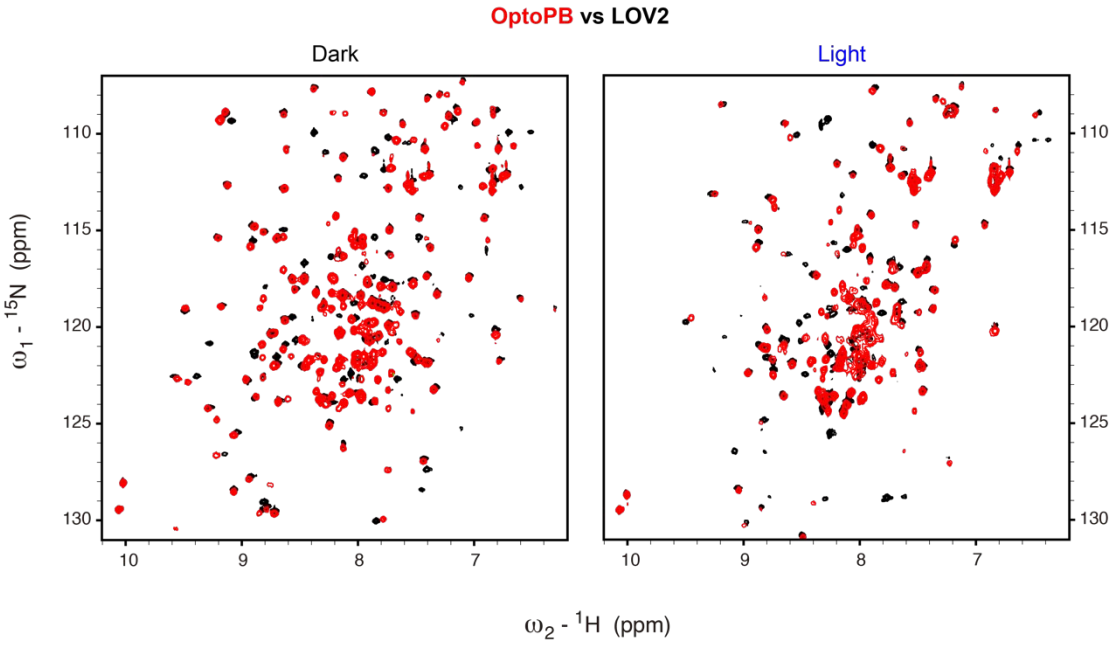

Figure S2. 2D ^{1}H-^{15}N HSQC spectra comparison of OptoPB (red) and LOV2 (black). The conformation of OptoPB was similar to LOV2 in both dark and lit state.

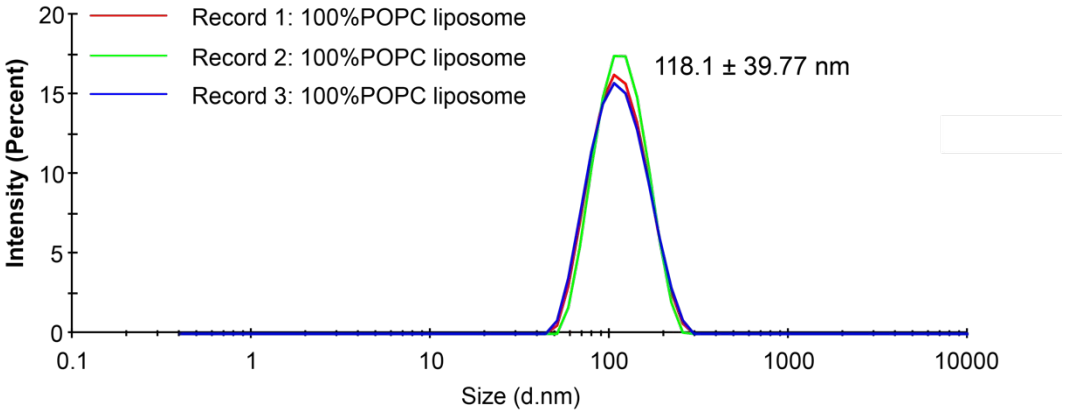

Figure S3. DLS measurements of liposomes used in liposome pulldown assay. The default filter factor of 50% and the default lower threshold of 0.05 and upper threshold of 0.01 were used. The error was obtained by three independent measurements.

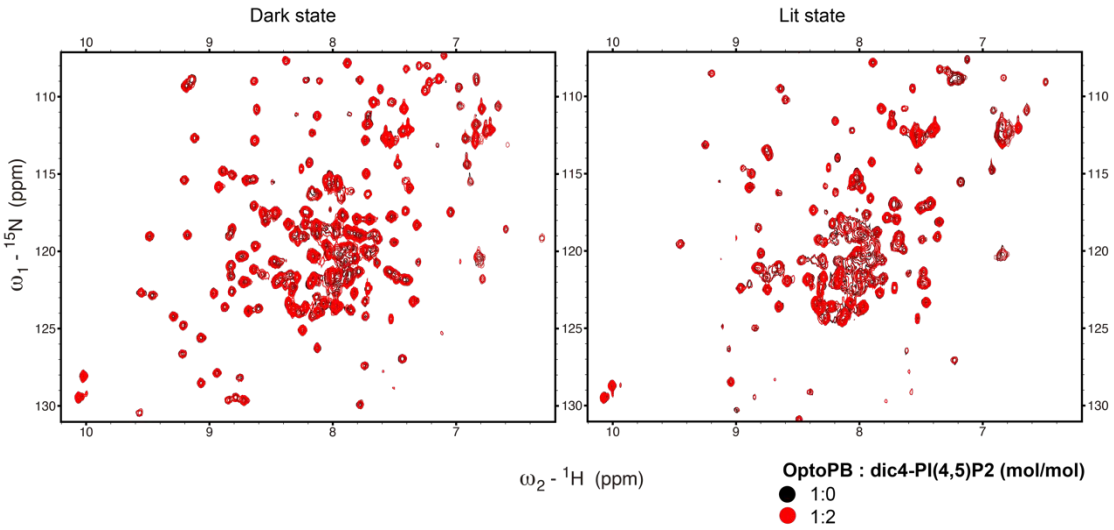

Figure S4. 2D ^{1}H-^{15}N HSQC spectra comparison of OptoPB (0.1 mM) protein only (black) and titrated with dic$_4$-PI(4,5)P$_2$ (0.2 mM) (red). Dic4-PI(4,5)P$_2$ did not bind to OptoPB in both dark and lit states.

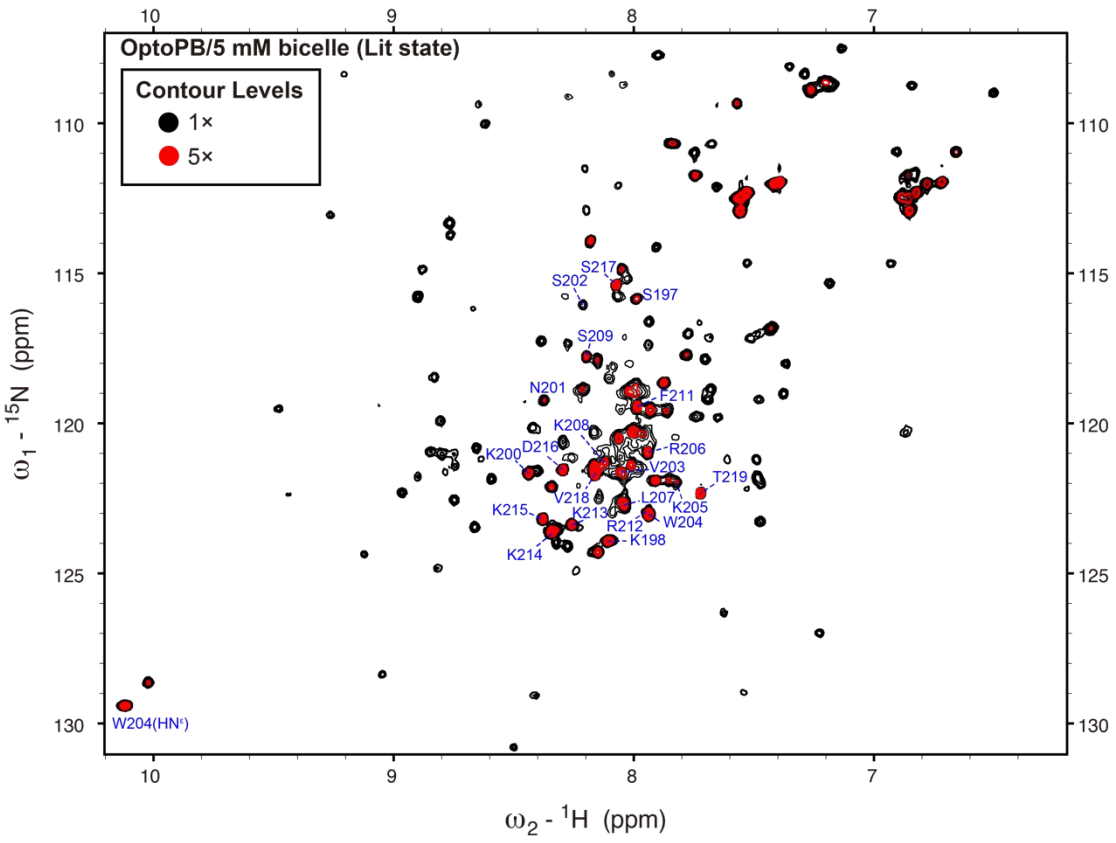

Figure S5. 2D ^{1}H-^{15}N HSQC spectrum of OptoPB in the lit state indicating the assignments of the Rit-PB residues. The peaks of Rit-PB can be identified more easily upon the increasing of the spectral contour levels.

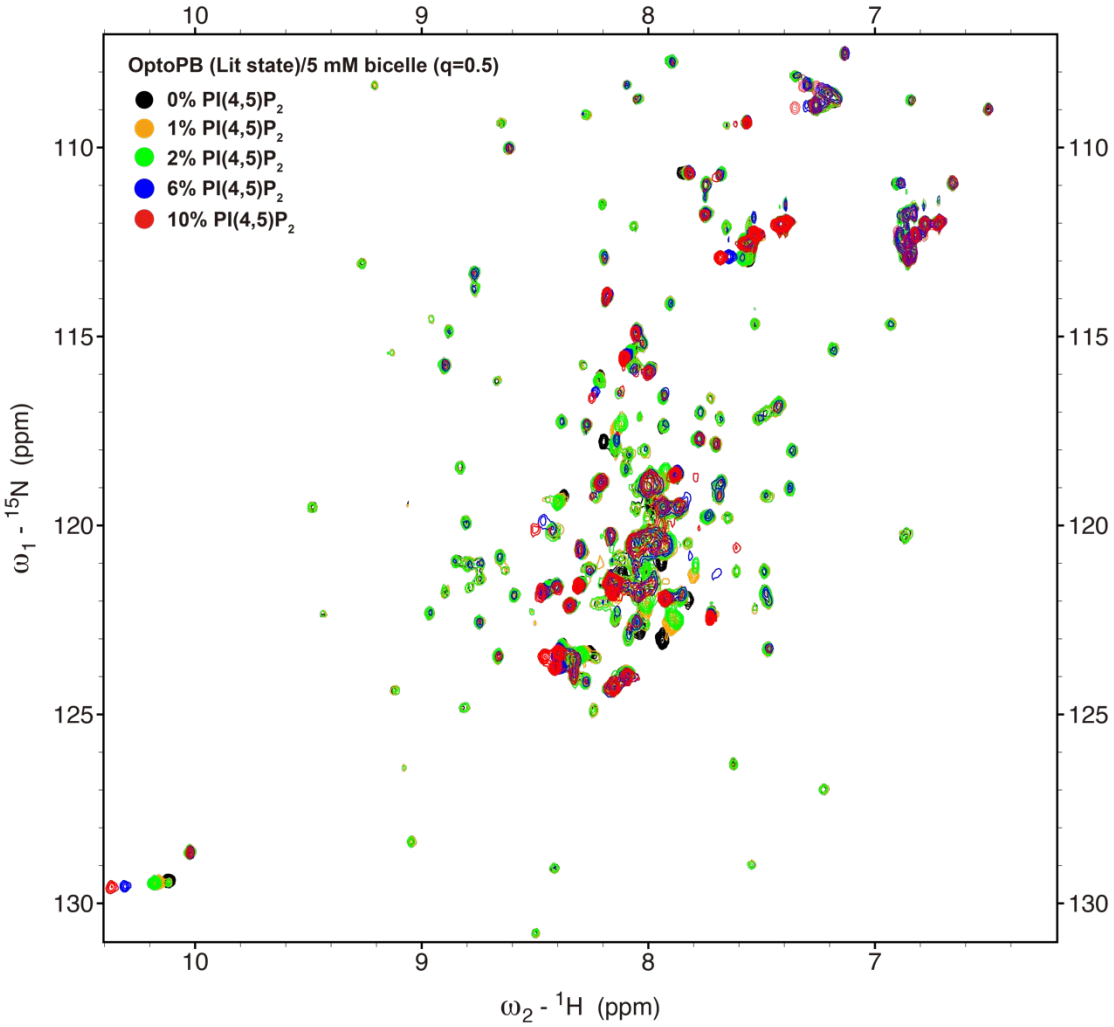

Figure S6. Full view of 2D ^{1}H-^{15}N HSQC spectra of light-excited OptoPB titrated with bicelles with varying PI(4,5)P_2 concentration. See Figure 5A for the individual illustration of each pronouncedly perturbed residue.

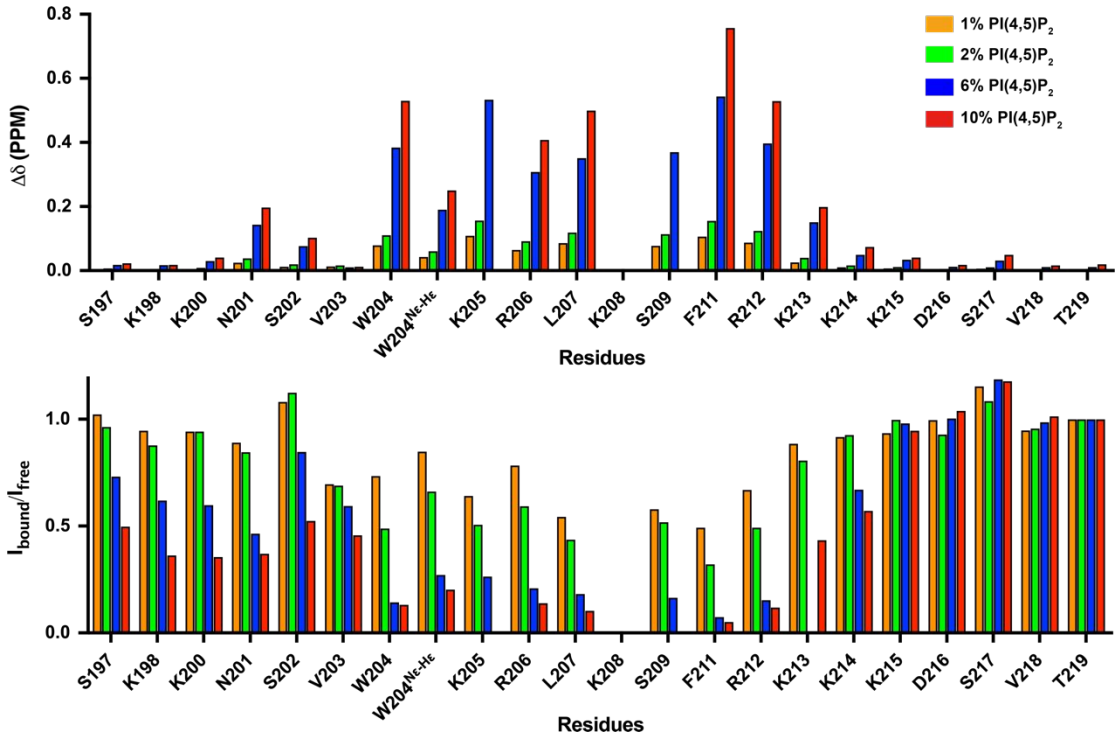

Figure S7. Chemical shift perturbations (Δδ) (top) and intensity reduction ratios (I_{bound}/I_{free}) (bottom) of Rit-PB residues upon the titration with bicelles with varying PI(4,5)P_2 concentration.