Fig. S1. Nucleotide and amino acid sequence of SPI1085g2 (GAF2, 216-369aa) from *S. subsalsa* FACHB351. Boxes show the conserved motifs in CBCR GAF domains.

**Fig. S2.** Sequence alignment of SPI1085g2 and reported PEB-binding red/green CBCR GAF domains. Highly conserved residues in red/green CBCR GAF domains, black; CBCR GAF domains with the partially modified PEB, blue; CBCR GAF domains with the unmodified PEB, orange; Residues conserved in the typical red/green CBCR GAF domains, green. The canonical Cys residues that bind bilins are highlighted in red. The residues highlighted in light yellow are presumed to be important for PEB incorporation and high fluorescence quantum yield. The asterisk (*) indicates omitted non-conserved amino acids.