Supplemental Table 1. Primer information

Plasmids	Primers	Sequence
pGEM-SlLLP	LLP-S-F	5'-TCCATGTAAGCTCTTCAATATTGTTT-3'
	LLP-S-R	5'-TTTTCTGGTACCAATGAGCTAACA-3'
pThio-SlLLP	LLP-F	5'-GGGCTCGAGATGGAATCACAACTGGGTTT-3'
	LLP-R	5'-CCCGCGGCCGCTTAGTGGTGGTGGTGGTGGTGGGAGGTACTTGCACCCATT-3'
pThio-SlLLP-C295A	LLPSDM1-F	5'-TGGGTCGTAATGCCCGGTTTTTAAG-3'
	LLPSDM1-R	5'-CTTAAAAACCGGGCATTACGACCCA-3'
pThio-SlLLP-R67D	LLPSDM2-F	5'-AGGGAAGAATGGAGATGTATTTCAAGGGC-3'
	LLPSDM2-R	5'-GCCCTTGAAATACCCTTCCATTCTTCCCT-3'
pThio-SlLLP-R296D	LLPSDM3-F	5'-GGGTCGTAATTGCGACTTTTTAAGTGGGGA-3'
	LLPSDM3-R	5'-TCCCCACTTAAAAACCGGCAATTACGACCC-3'
pThio-SlLLP-G66C/R296D	LLPSDM4-F	5'- GTTTTAGGGAAGAATTGCAGGGTATTTCAAGG-3'
	LLPSDM4-R	5'- CCTTGAAATACCCTGCAATTCTTCCCTAAAAC-3'
pGEX-PpLLP1	PpLLP1-F	5'- AAGAATTCATGTTTCTTAGCGGTGGCG -3'
	PpLLP1-R	5'- TTCTCGAGTCACTCTTTGGGCCTGCGT -3'
pGEX-PpLLP2	PpLLP2-F	5'- AAGAATTCATGTCTGTGGGAGATAGTGTT -3'
	PpLLP2-R	5'- TTCTCGAGTCAAGCTTTCGGTATCCGTC -3'
pGEX-PpLLP1-LOV1	PpLLP1-LOV1-F	5'- AAAGAATTCAACTTTGTGTTAAGCGACCC -3'
	PpLLP1-LOV1-R	5'- AAACTCGAGTTAGTCATCAGCAATGGGCGTC -3'
pGEX-PpLLP1-LOV2	PpLLP1-LOV2-F	5'- AAAGAATTCAGTCTTATCCTATCTGATCC -3'
	PpLLP1-LOV2-R	5'- AAACTCGAGTTAAGCTTCACTGACGTTCAGC-3'
pGEX-PpLLP2-LOV1	PpLLP2-LOV1-F	5'- AAAGAATTCAACTTCGTGTTGAGCGACCC -3'
	PpLLP2-LOV1-R	5'- AAACTCGAGTTAGTCCTTAGCAATGGGTGTCT -3'
pGEX-PpLLP2-LOV2	PpLLP2-LOV2-F	5'- AAAGAATTCAGTCTTGTCCTAGCTGATCC-3'
	PpLLP2-LOV2-R	5'- AAACTCGAGTTAGGCGATGCTGACATCCAGC-3'

Supplemental Table 2. Molar ratios of FMN to each of the *Sl*LLP proteins

	Protein	FMN/Protein (measured)[a]	FMN/Protein (expected)[b]	Measured/expected Ratio[c]
*Sl*LLP	WT	0.37	2	0.19
	C295A	0.36	2	0.18
	R67D	0.20	1	0.20
	R296D	0.13	1	0.13
	R67D/R296D	not detected	0	not calculated
	G66C/R296D	0.12	1	0.12

[a] Results are average values of two preparations (WT and R296D) and values of one preparation (C295A, R67D, R67D/R296D and G66C/R296D).

[b] Expected FMN/Protein ratio is the value expected from the number of LOV domain having the potential FMN binding in each protein.

[c] Measured FMN/Protein ratio is divided by expected FMN/Protein ratio.

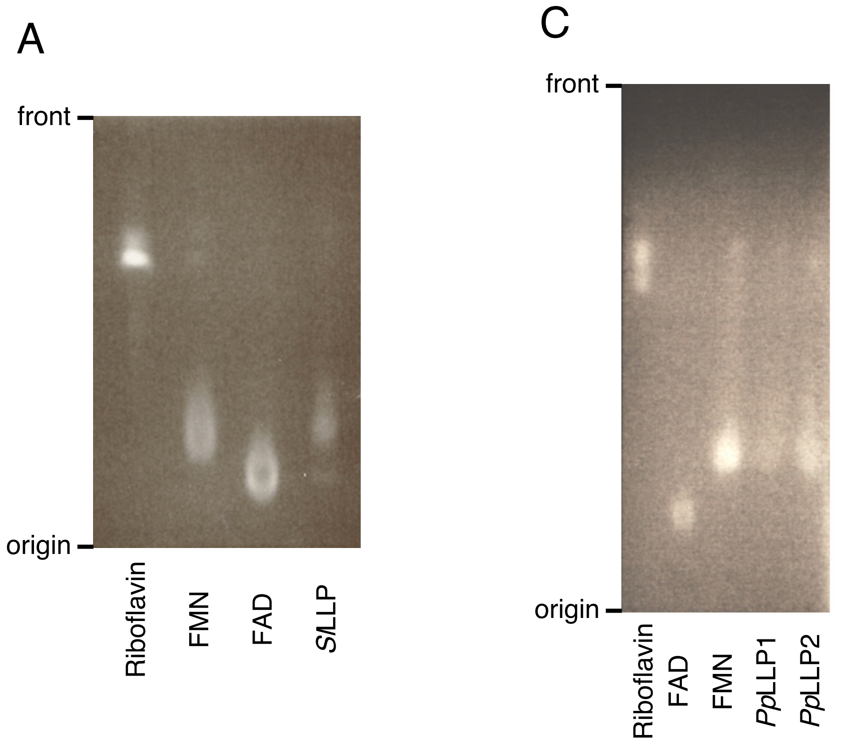
Supplemental Table 3. Molar ratios of FMN to each of the *Pp*LLP1 and *Pp*LLP2 proteins

	Protein	FMN/Protein (measured)[a]	FMN/Protein (expected)[b]	Measured/expected Ratio[c]
*Pp*LLP1	Full-length	0.37	2	0.19
	LOV1	0.07	1	0.07
	LOV2	0.15	1	0.15
*Pp*LLP2	Full-length	0.38	2	0.19
	LOV1	0.21	1	0.21
	LOV2	0.23	1	0.23

[a] Results are average values of two preparations (*Pp*LLP1 Full-length; *Pp*LLP2 Full-length, LOV1 and LOV2) and values of one preparation (*Pp*LLP1 LOV1 and LOV2).

[b] Expected FMN/Protein ratio is the value expected from the number of LOV domain having the potential FMN binding in each protein.

[c] Measured FMN/Protein ratio is divided by expected FMN/Protein ratio.



B

Flavin	Rf
Riboflavin	0.67
FMN	0.26
FAD	0.18
*Sl*LLP	0.26

D

Flavin	Rf
Riboflavin	0.65
FMN	0.30
FAD	0.12
*Pp*LLP1	0.30
*Pp*LLP2	0.30

FIGURE S1. Identification of the chromophore associated with LLPs. (A) Thin-layer chromatogram of the chromophore associated with *Sl*LLP and flavin standards, riboflavin, FMN and FAD. (B) Rf values calculated from the chromatogram shown in A. (C) Thin-layer chromatogram of the chromophore associated with *Pp*LLP1, *Pp*LLP2 and flavin standards, riboflavin, FMN and FAD. (D) Rf values calculated from the chromatogram shown in C.

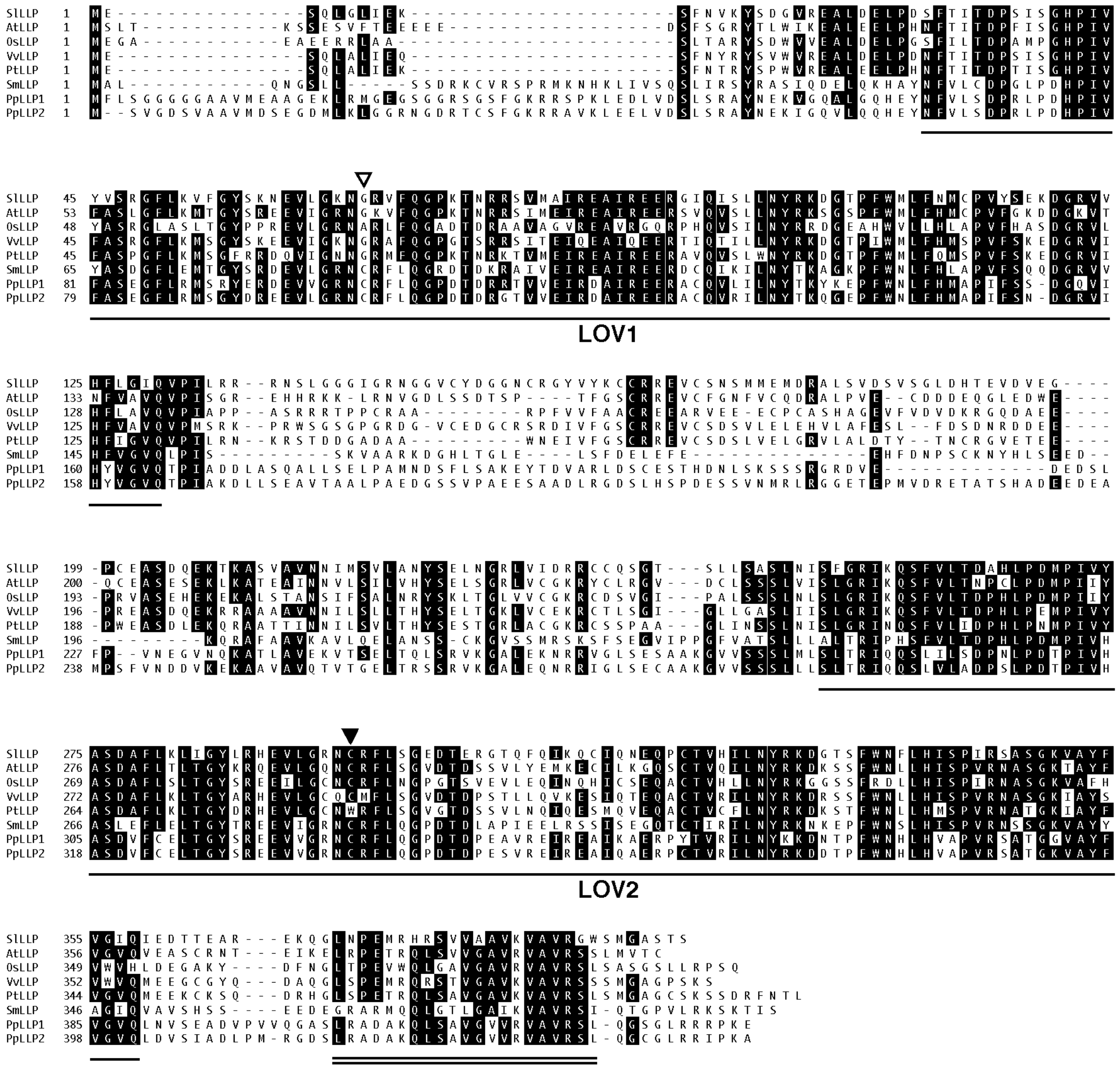


FIGURE S2. Amino acid alignment of LLPs. Alignment of the amino acid sequences of LLPs of *Solunum lycopersicum* (SlLLP), *Arabidopsis thaliana* (AtLLP), *Oryza sativa* (OsLLP), *Vitis vinifera* (VvLLP), *Populus trichocarpa* (PtLLP), *Selaginella moellendorffii* (SmLLP) and *Physcomitrella patens* (PpLLP1 and PpLLP2). Amino acid residues identical in more than five sequences are shaded. Gaps introduced for good alignment are indicated by dashes. Numbers are amino acid positions for each amino acid sequence. Single lines indicate LOV1 and LOV2 domains. The highly conserved cysteines in the LOV2 domains are indicated by the solid arrowhead. The corresponding amino acids in the LOV1 domains are indicated by the open arrowhead. A highly conserved C-terminal region is indicated by a double line.

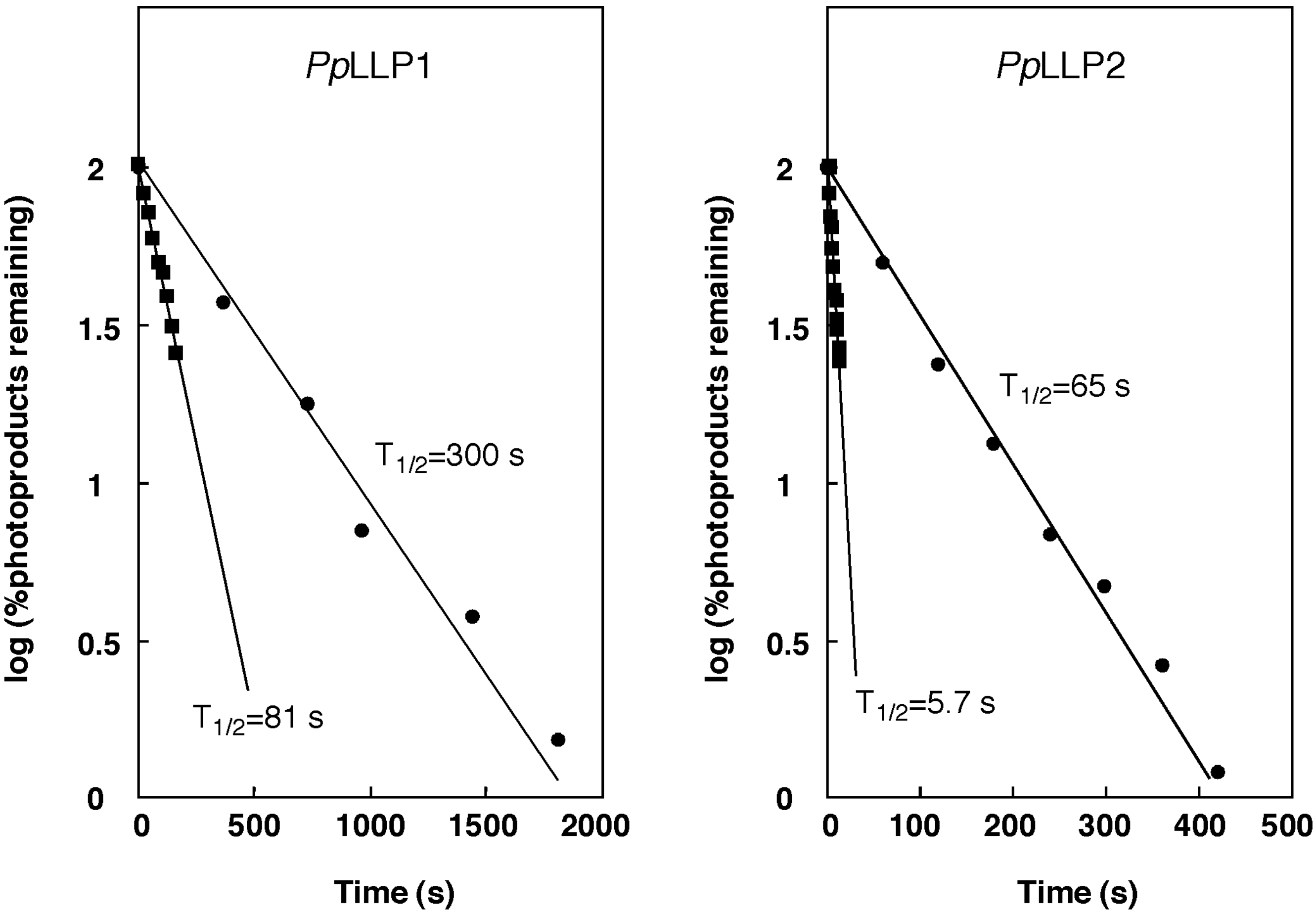


FIGURE S3. Effect of imidazole on dark reversion kinetics of *Pp*LLP1 (left) and *Pp*LLP2 (right). The amount of photoproduct remaining after dark incubation is plotted against the duration of dark incubation in the presence (square) or the absence (circle) of 100 mM imidazole. Half lives ($T_{1/2}$) are shown.

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