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# Supplementary Materials for

# Photoactivation of *Drosophila melanogaster* cryptochrome through sequential conformational transitions

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## This PDF file includes:

Table S1. TRXSS kinetic modeling.

Table S2. Changes in  $R_{\rm g}$ .

Table S3. SAXS parameters.

Table S4. Rate constants for TRXSS measurements of DmCry at pH 9.

Table S5. Rate constants for TA measurements of *Dm*Cry.

Fig. S1. TRXSS data and the reconstructed data using a kinetic model with different numbers of components.

Fig. S2. SAXS scattering profiles for *Dm*Cry in the dark and under blue-light illumination.

Fig. S3. The RMSD of the FFW motif at each simulation frame.

Fig. S4. TRXSS data and kinetic modeling for wild-type *Dm*Cry and H378A at pH 9.

Fig. S5. Stability analysis of the used samples via SDS-PAGE and SAXS.

# Supplementary materials

# Table S1. TRXSS kinetic modeling.

	n-comp	$k_1$	$k_2$	$k_3$	$k_4$	$k_5$
WT pH 7	4	0.4±0.0 μs <sup>-1</sup>	$2.9\pm0.4 \text{ ms}^{-1}$	$0.3\pm0.0 \text{ ms}^{-1}$	-	-
WT pH 7	5	10.1±0.6 µs <sup>-1</sup>	1.3±0.1 μs <sup>-1</sup>	3.9±0.3 ms <sup>-1</sup>	$0.4\pm0.30$ ms <sup>-1</sup>	-
WT pH 7	6	6.3±25.8 μs <sup>-1</sup> *	6.5±26.3 μs <sup>-1</sup> *	0.9±0.1 μs <sup>-1</sup>	$3.3\pm0.2 \text{ ms}^{-1}$	$0.3\pm0.0$ ms <sup>-1</sup>
H378A pH 7	3	$2.3\pm0.2 \text{ ms}^{-1}$	$0.3\pm0.0 \text{ ms}^{-1}$	-	-	-
H378A pH 7	4	0.2±0.0 µs <sup>-1</sup>	$1.2\pm0.1 \text{ ms}^{-1}$	$0.3\pm0.0 \text{ ms}^{-1}$	-	-
H378A pH 7	5	0.4±0.1 µs <sup>-1</sup>	24.2±2.0 ms <sup>-1</sup>	$0.8\pm0.1 \text{ ms}^{-1}$	$0.4\pm0.1 \text{ ms}^{-1}$	-
WT pH 9	3	0.2±0.0 µs <sup>-1</sup>	$3.5\pm0.2 \text{ ms}^{-1}$	-	-	-
WT pH 9	4	0.2±0.0 µs <sup>-1</sup>	$3.9\pm0.3 \text{ ms}^{-1}$	$0.3\pm0.0 \text{ ms}^{-1}$	-	-
WT pH 9	5	0.6±1.3 µs <sup>-1</sup> *	0.6±1.3 µs <sup>-1</sup> *	$4.4\pm0.2 \text{ ms}^{-1}$	$0.3\pm0.0 \text{ ms}^{-1}$	-
H378A pH 9	2	2.9±0.1 ms <sup>-1</sup>	-	-	-	-
H378A pH 9	3	4.1±0.4 μs <sup>-1</sup>	$1.3\pm0.2 \text{ ms}^{-1}$	-	-	-
H378A pH 9	4	3.0±163.8 μs <sup>-1</sup> *	$2.3\pm0.2 \text{ ms}^{-1}$	-0.5±0.0 ms <sup>-1</sup> *	-	-
*Non-sensible values						

## Table S2. Changes in $R_{\rm g}$ .

	$DmCry_{\alpha}$ (Å)	<i>Dm</i> Cry <sub>β</sub> (Å)	$DmCry_{\gamma}(\text{\AA})$	<i>Dm</i> Cry <sub>δ</sub> (Å)	$DmCry_{\epsilon}^{*}(\text{\AA})$
WT pH 7	-0.02±0.005**	$0.15 \pm 0.004$	$-0.04 \pm 0.004$	$-0.10 \pm 0.004$	$-0.09 \pm 0.004$
H378A pH 7	n/a	$0.09 \pm 0.004$	$-0.17 \pm 0.005$	$-0.09 \pm 0.004$	$-0.07 \pm 0.004$
WT pH 9	n/a	$0.03 \pm 0.004$	$-0.17 \pm 0.004$	$-0.16 \pm 0.004$	$-0.00 \pm 0.004$
H378A pH 9	n/a	n/a	$0.03 \pm 0.004$	$-0.09 \pm 0.004$	$0.00 \pm 0.004$
*For the pH 9 samples this is instead the final state, ** The error ranges represent the statistical					
uncertainty based on the noise level of the data (see Materials and Methods) and does not					

#### Table S3. SAXS parameters.

include experimental uncertainty.

	<i>Dm</i> Cry (dark)	<i>Dm</i> Cry (light)
$R_g$ (Guinier analysis)	30.3±0.3 Å	30.8±0.3 Å
I(q=0) (Guinier analysis)	21.9±0.12	22.8±0.13
$MW(Q_r)$	61 kDa	61 kDa

## Table S4. Rate constants for TRXSS measurements of *Dm*Cry at pH 9.

	$k_1$	$k_2$	$k_3$
WT pH 9	$0.2\pm0.0 \ \mu s^{-1}$	$3.9\pm0.3 \text{ ms}^{-1}$	$0.3\pm0.0 \text{ ms}^{-1}$
H378A pH 7	n/d	4.1±0.4 ms <sup>-1</sup>	1.3±0.2 ms <sup>-1</sup>

Table S5. Rate constants for TA measurements of *Dm*Cry.

	$k_{I}(\mu s^{-1})*$	$k_2(\mu s^{-1})*$	$k_{3}(\mu s^{-1})^{**}$	$k_4(\mu s^{-1})*$	$k_5 (ms^{-1})$	$k_6 (ms^{-1})$	$k_{recom.}$ *** (ms <sup>-1</sup> )
WT pH 7	$3.1 \cdot 10^3 \pm 9.97 \cdot 10^7$	$8.68 \pm 0.39$	0.37±4.3·10 <sup>-3</sup>	$0.7 \cdot 10^{-3} \pm 1.2 \cdot 10^{-3}$	$0.5 \pm 1.97 \cdot 10^{-2}$	$0.069 \pm 2.54 \cdot 10^{-3}$	0.0998
H378A pH 7	217.7±22	218±22	$0.4\pm5.173\cdot10^{-3}$	$9.48 \cdot 10^{-3} \pm 7.2 \cdot 10^{-4}$	2.85±0.7	0.14±0.06	0.213
WT pH 9	146.1±2.55	$4.44 \pm 0.16$	$0.80\pm6.0\cdot10^{-3}$	2·10 <sup>-3</sup> ±0.3·10 <sup>-3</sup>	$0.63 \pm 1.65 \cdot 10^{-2}$	$0.098 \pm 1.0 \cdot 10^{-3}$	0.099
H378A pH 9	139±22	3.19±0.19	$0.73 \pm 21 \cdot 10^{-3}$	$8.0 \cdot 10^{-3} \pm 8.5 \cdot 10^{-4}$	12.35±2.87	0.12±0.01	0.1648
* $k_1$ , $k_2$ and $k_4$	remain unassigned i	n this paper. V	Ve follow Ref. (19	) for assignments			

\*\*  $k_3$  is the time constant assigned to deprotonation of W394

\*\*\*The time constant for radical pair recombination is calculated as  $k_{recom} = (k_5 + w_5 + k_6 * w_6)/(w_5 + w_6)$ 



**Fig. S1. TRXSS data and the reconstructed data using a kinetic model with different numbers of components.** Wild type *Dm*Cry at pH 7 with 4 (A), 5 (B) or 6 (C) components. H378A *Dm*Cry at pH~7 with 3 (D), 4 (E) or 5 (F) components. Wild type *Dm*Cry at pH 9 with 3 (G), 4 (H) or 5 (I) components. H378A *Dm*Cry at pH 9 with 2 (J), 3 (K) or 4 (L) components. Shaded areas highlight the regions where too few species result in systematic deviations.



Fig. S2. SAXS scattering profiles for *Dm*Cry in the dark and under blue-light illumination.



**Fig. S3. The RMSD of the FFW motif at each simulation frame.** (A) Four simulations with oxidized FAD, (B) four simulations with reduced FAD, (C) four simulations with oxidized FAD and H378A mutation, (D) four simulations with reduced FAD and H378A mutation.(E) Existence of a hydrogen bond between H378 and W536 or H378 and FAD for wild type trajectories using oxidized (ox) or reduced (red) chromophore parameters



Fig. S4. TRXSS data and kinetic modeling for wild-type DmCry and H378A at pH 9. Scattering data (A,B), transient populations (C,D), species associated spectra (E,F) and  $\Delta P(r)$  (G,H). The coloring is according to the similar spectra that are found in Fig. 3, with the exception of the DmCry<sub> $\varepsilon$ </sub> state (magenta), which is significantly different at pH 9.



Fig. S5. Stability analysis of the used samples via SDS-PAGE and SAXS. (A) SDS-PAGE analysis of DmCry WT and H378A performed under non reducing conditions (without beta-mercaptoethanol), with and without ferricyanide, in the dark and directly after 5 minutes of blue-light. No presence of DmCry dimer can be observed. (B) Concentration dependence of scattering profile, measured during TRXSS experiment. S(q) is the ratio between the 24 mg/ml and the infinite dilution scattering curves.