

Table S1. Kinetic parameters of NADPH diaphorase reaction for several FNRs and the dissociation constants for complexes with NADP<sup>+</sup>

FNR	$K_m$ ( $\mu\text{M}$ )	$k_{\text{cat}}$ ( $\text{s}^{-1}$ )	$k_{\text{cat}}/K_m$ ( $\mu\text{M}^{-1} \text{s}^{-1}$ )	$K_d$ ( $\mu\text{M}$ )
<i>X. axonopodis</i> <sup>a</sup>	10.8±0.5	121.9±1.8	11.3	9.7±0.4
pea <sup>a</sup>	15.3±4.3	374.3±18	24.5	10.9±3.1
<i>E.coli</i> <sup>a</sup>	8.3±1.3	38.2±3.5	4.6	5.9±0.6
<i>R. capsulatus</i>	80 <sup>b</sup>	7.2 <sup>b</sup>	0.09	222±5 <sup>c</sup>
<i>P. putida</i> <sup>d</sup>	4.79±0.08	4.77±0.17	1.03±0.02	-
	3.97±0.04	4.51±0.06	1.14±0.08	-

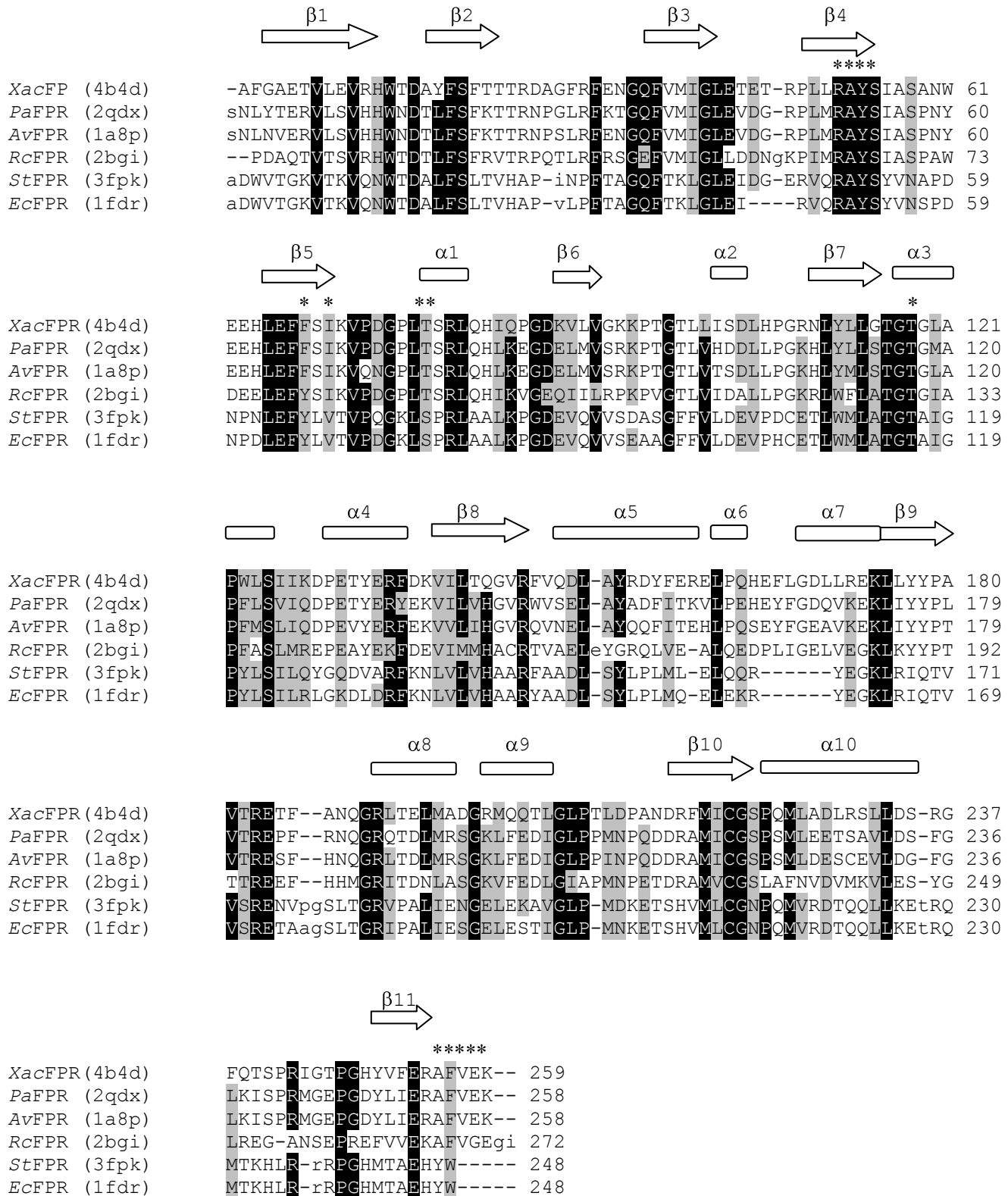
<sup>a</sup> Data from Tondo M.L. et al., PLoS One 2011; 6: e27124.

<sup>b</sup> Data from Bittel C. et al., FEBS Lett 2003; 553: 408–412.

<sup>c</sup> Data from Bortolotti A. et al., BBA 2009; 1794: 199-210.

<sup>d</sup> Data from Yeom J. et al., J. Biochem 2009; 145: 481-491. Data for FprA (first line), homologue with the *A. vinelandii* FPR and FprB (second line), homologue with the *E.coli* FPR.

Figure S1



**Figure S1:** Structure-based sequence alignment of several bacterial FPRs by DALI Server. Secondary structure for *XacFPR* stated by the SMM server. Pa, *P. aeruginosa* (subclass IA); Av, *A. vinelandii* (subclass IA); Rc, *R. capsulatus* (subclass IB); St, *Salmonella typhimurium* (subclass II); Ec, *E. coli* (subclass II). Residues of *XacFPR* that interact with FAD are pointed with an asterisk on top.