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Supporting Information

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Fluorescent Probes to Characterise FK506-Binding Proteins

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Appendix 1:

The equation:

$$[EC_{50}] = \frac{1}{2}[L]_t + K_d \quad (1.)$$

Equation (1.) can be deduced as follows: At equilibrium, $K_d = [L] \times [R] / [LR]$ (2.), $[L]_t = [L] + [LR]$ (3.), and $[R]_t = [R] + [LR]$ (4.), with $[L]$, $[R]$, and $[LR]$ being the concentrations of free ligand, free receptor and the ligand-receptor complex and $[L]_t$ and $[R]_t$ being the total concentrations of ligand and receptor, respectively.

In FP binding experiments, the EC_{50} is defined as the total concentration $[R]_t^{50}$ where equal amounts of free ligand and bound ligand are present, assuming identical intrinsic fluorescence intensities for free and bound ligands. Therefore, at the EC_{50} , equation (3.) simplifies to $[L] = [LR] = \frac{1}{4}[L]_t$ (5.) and equation (2.) to $K_d = [R]$ (6.). At the EC_{50} , equations (4.), (5.) and (6.) therefore yield $[R]_t^{50} = K_d + \frac{1}{4}[L]_t$ (1.).

Appendix 2:

A mathematical term describing the ligand-receptor complex (LR) in binding assays was described by Wang et. al. 1992^[45].

$$[LR] = \{([R]_t + [L]_t + K_d)/2 - \{([R]_t + [L]_t + K_d)/2\}^2 - [L]_t[R]_t\}^{0.5} \quad (7.)$$

The fluorescence anisotropy (A) is direct proportional to the increase of $[LR]$ ^[46]. This relation is represented by a linear function, raising from the minimal measured anisotropy (A_{min}) to the maximal measured anisotropy (A_{max}) with a slope of $\Delta A/[L]_t$

$$A = (\Delta A / [L]_t) [LR] + A_{min} \quad (8.)$$

Eq.(9.) follows from inserting (7.) into (8.) and was used to fit K_d values from binding curves.

$$A = [(A_{max} - A_{min}) / [L]_t] \times \{([R]_t + [L]_t + K_d)/2 - \{([R]_t + [L]_t + K_d)/2\}^2 - [L]_t[R]_t\}^{0.5} + A_{min} \quad (9.)$$

Appendix 3:

A mathematical expression describing competitive binding of two different ligands to a protein molecule was described by Wang et. al. 1995^[30].

The mathematical term for the competition of a titrated compound with a tracer for the binding to a protein was used to describe competition curves. The conversion into anisotropy values was done by insertion into (8.), the resulting formula was used to fit K_i values.

$$A = (A_{\max} - A_{\min}) / [L]_t \times (([L]_t \times ((2x((K_{\text{lig}} + K_{\text{comp}} + [L]_t + [I]_t - [R]_t)^2 - 3x(K_{\text{comp}} \times ([L]_t - [R]_t) + K_{\text{lig}} \times ([I]_t - [R]_t) + K_{\text{lig}} \times K_{\text{comp}}))^0.5 \times \cos(\arccos((-2x(K_{\text{lig}} + K_{\text{comp}} + [L]_t + [I]_t - [R]_t)^3 + 9x(K_{\text{lig}} + K_{\text{comp}} + [L]_t + [I]_t - [R]_t) \times (K_{\text{comp}} \times ([L]_t - [R]_t) + K_{\text{lig}} \times ([I]_t - [R]_t) + K_{\text{lig}} \times K_{\text{comp}}) - 27x(-1x K_{\text{lig}} \times K_{\text{comp}} \times [R]_t)) / (2x(((K_{\text{lig}} + K_{\text{comp}} + [L]_t + [I]_t - [R]_t)^2 - 3x(K_{\text{comp}} \times ([L]_t - [R]_t) + K_{\text{lig}} \times ([I]_t - [R]_t) + K_{\text{lig}} \times K_{\text{comp}}))^3)^{0.5}))) / 3)) - (K_{\text{lig}} + K_{\text{comp}} + [L]_t + [I]_t - [R]_t))) / ((3x K_{\text{lig}}) + ((2x((K_{\text{lig}} + K_{\text{comp}} + [L]_t + [I]_t - [R]_t)^2 - 3x(K_{\text{comp}} \times ([L]_t - [R]_t) + K_{\text{lig}} \times ([I]_t - [R]_t) + K_{\text{lig}} \times K_{\text{comp}}))^0.5 \times \cos(\arccos((-2x(K_{\text{lig}} + K_{\text{comp}} + [L]_t + [I]_t - [R]_t)^3 + 9x(K_{\text{lig}} + K_{\text{comp}} + [L]_t + [I]_t - [R]_t) \times (K_{\text{comp}} \times ([L]_t - [R]_t) + K_{\text{lig}} \times ([I]_t - [R]_t) + K_{\text{lig}} \times K_{\text{comp}}) - 27x(-1x K_{\text{lig}} \times K_{\text{comp}} \times [R]_t)) / (2x(((K_{\text{lig}} + K_{\text{comp}} + [L]_t + [I]_t - [R]_t)^2 - 3x(K_{\text{comp}} \times ([L]_t - [R]_t) + K_{\text{lig}} \times ([I]_t - [R]_t) + K_{\text{lig}} \times K_{\text{comp}}))^3)^{0.5}))) / 3)) - (K_{\text{lig}} + K_{\text{comp}} + [L]_t + [I]_t - [R]_t)))) + A_{\min} \quad (10.)$$

In this equation K_{lig} and K_{comp} stand for the K_d values of the used tracer or competing inhibitor, $[I]_t$ is referring to the total concentration of the titrated inhibitor.