Supporting Information

A simple method for measuring signs of ${}^{1}H^{N}$ chemical shift differences between ground and excited protein states

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Bloch-McConnell Equations

For a two-site exchange process interconverting states *G* and *E*, $G \frac{k_G}{k_E} E$, the evolution of spin coherence *X* that is not coupled to any other spin can be written as follows

$$
\frac{d}{dt}\left(\begin{array}{c} X_G(t) \\ X_E(t) \end{array}\right) = \left(\begin{array}{cc} -k_G - R_G + i\omega_G & k_E \\ k_G & -k_E - R_E + i\omega_E \end{array}\right) \left(\begin{array}{c} X_G(t) \\ X_E(t) \end{array}\right)
$$
(S1)

where X_i is the 'amount' of coherence X in the exchanging state *i*, ω_i is the Larmor frequency (rad.s⁻¹) of X_i and R_i its relaxation rate (McConnell 1958). The evolution frequencies of *G* and *E*, including contributions from exchange, can be obtained from the imaginary parts of the two eigenvalues of the matrix on the right-hand-side of eq S1. It is thus possible to calculate the shift of the peak corresponding to state *G* in spectra recorded at a different static magnetic fields, $\tilde{\delta}_x$, so long as the parameters of the exchange process are known.

Sample Preparation

[U⁻²H,¹⁵N] enriched Pfl6 I58D was obtained by IPTG-induced protein over-expression in *E*. *coli* BL21(DE3) in M9 minimal medium with 99.9% D_2O and $[^{12}C_6, ^{2}H_7]$ -glucose, following a previously described protocol (Roessler et al. 2008). The NMR sample was 1.4 mM in protein, 2 mM EDTA, 2 mM NaN₃, 50 mM sodium phosphate, pH 6.2, 90% H₂O, 10% D₂O. A sample of 1.2 mM $[U^2H, {}^{13}C, {}^{15}N]$ A39V/N53P/V55L Fyn SH3, 0.2mM EDTA, 0.05% NaN₃, 50 mM sodium phosphate, pH 7.0, 90% $H₂O₁10% D₂O$ was prepared as described in detail previously (Neudecker et al. 2006). A sample of $[U^{-2}H, ^{15}N]$ enriched WT FF domain was generated as previously described (Korzhnev et al. 2007). The sample contained 1.0 mM [U-²H,¹⁵N] protein, 50 mM sodium acetate, 100 mM NaCl, 0.05% (w/v) NaN₃, 0.2 mM EDTA (pH 5.7), 90% H₂O, 10% D₂O.

NMR Spectroscopy and Data Analysis

Single quantum ${}^{1}H^{N}$ relaxation dispersion profiles (Ishima and Torchia 2003) were recorded at 5 °C for Pfl6 I58D, at 30 °C for the WT FF domain and at 20 °C for the A39V/N53P/V55L Fyn SH3 domain. Data were obtained at static magnetic fields strengths of 11.7 and 18.8 T. Relaxation dispersion profiles, $R_{2,\text{eff}}(v_{\text{CPMG}})$, were generated from peak intensities, $I_1(v_{\text{CPMG}})$, in a series of 2D ¹H^N-¹⁵N correlation maps measured as a function of CPMG frequency, $v_{\text{CPMG}} = 1/(4\tau_{\text{CP}})$, where $2\tau_{\text{CP}}$ is the interval between consecutive 180°refocusing pulses of the CPMG sequence. Effective relaxation rates were calculated as $R_{2,\text{eff}}(v_{\text{CPMG}}) = \ln (I_0/I_1(v_{\text{CPMG}}))/T_{\text{CPMG}}$, where I_0 is the peak intensity in a reference spectrum recorded without the relaxation delay T_{CPMG} (Tollinger et al. 2001).

All data sets were processed and analyzed with the NMRPipe program (Delaglio et al. 1995) and signal intensities were quantified using the program FuDA (http://pound.med.utoronto.ca/software.html) or MUNIN (Korzhnev et al. 2001; Orekhov et al. 2001). Relaxation dispersion data were analyzed using a two-state exchange model and the best-fit model parameters were extracted as described previously (Hansen et al. 2008) using the program CATIA, which is available from http://pound.med.utoronto.ca/software.html. Briefly, the parameters are obtained by minimization of the target function,

$$
\chi^2(\xi) = \sum \left(\frac{R_{2,\text{eff}}^{\text{calc}}(\xi) - R_{2,\text{eff}}^{\text{exp}}}{\Delta R_{2,\text{eff}}^{\text{exp}}} \right)^2 \tag{S2}
$$

where $R_{2,\text{eff}}^{\text{exp}}$ and $\Delta R_{2,\text{eff}}^{\text{exp}}$ are experimental effective relaxation rates and their uncertainties, respectively, $R_{2,\text{eff}}^{\text{calc}}(\xi)$ are calculated relaxation rates obtained by numerical integration of the Bloch-McConnell equation (McConnell 1958), $\zeta = \{x_1, \ldots, x_n\}$ denotes the set of adjustable model parameters (including $\Delta\tilde{\omega}$) and the summation in eq S2 is over the number of experimental data points.

 $[$ ¹H, ¹⁵N]-HSQC spectra were recorded with the following parameters: (1) Pfl6 I58D $(t_1, t_2) = (103.0, 64.0)$ ms at 11.4 T and $(t_1, t_2) = (89.5, 64.0)$ ms at 18.8 T, (2) WT FF domain $(t_1, t_2) = (117.8, 64.0)$ ms at 11.4 T and $(t_1, t_2) = (99.5, 64.0)$ ms at 18.8 T, (3) A39V/N53P/V55L Fyn SH3 domain $(t_1, t_2) = (145.2, 64.0)$ ms at 11.4 T and $(t_1, t_2) = (121.0,$ 64.0) at 18.8 T. $\left[{}^{1}H, {}^{15}N \right]$ -HMQC spectra were recorded on the Pfl6 I58D sample with (t_1, t_2) values identical to those used for the HSQC spectra. After extensive zero-filling, peak positions were determined by two-dimensional parabolic interpolation (Press et al. 2007). Overlapped peaks for which no maximum could be defined were discarded from the analysis.

Bootstrap Analysis

Errors on fitted $|\Delta \omega_{\text{H}}|$ and calculated $|\Delta \tilde{\delta}_{H}^{calc}|$ values were determined by a standard bootstrap analysis (Press et al. 2007):

1) 1000 're-sampled' data sets of the same size as the original ${}^{1}H^{N}$ relaxation dispersion data set were generated by randomly picking $R_{2,\text{eff}}(v_{\text{CPMG}})$ points from the original data set – the same point could be picked once, several times or not at all.

2) The dispersion profiles $i \in \{1,...,1000\}$ generated in step (1) were independently fitted to extract $|\Delta \omega_{H,i}|$ for each residue, assuming previously fitted values for p_E and k_{ex} . Simultaneously, exchange-induced shifts $|\Delta \tilde{\delta}_{H,i}^{\text{calc}}|$ were calculated for each profile

 $i \in \{1,...,1000\}$ by numerically solving the Bloch-McConnell equations, S1, using the exchange parameters $\left(p_{\text{\tiny E}}, k_{\text{\tiny ex}}, \left| \Delta \omega_{\text{\tiny H,i}} \right| \right)$.

4) Errors on fitted $|\Delta \omega_{\text{H}}|$ and calculated $|\Delta \tilde{\delta}_{\text{H}}^{calc}|$ values were estimated as the standard deviation of $\left\{ \left| \Delta \omega_{H,i} \right| \right\}_{i \in \left\{ 1,...,1000 \right\}}$ and $\left\{ \left| \Delta \tilde{\delta}_{H}^{calc} \right| \right\}_{i \in \left\{ 1,...,1000 \right\}}$, respectively, for each residue.

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