## COMMUNICATIONS

## Improved Estimation of Protein Rotational Correlation Times from <sup>15</sup>N Relaxation Measurements

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In the study of protein backbone dynamics by <sup>15</sup>N relaxation measurements, an initial estimation of the isotropic global correlation time,  $\tau_{\rm m}$ , is usually obtained from the average  $T_1/T_2$  ratio of nuclear spins that do not exhibit slow internal motion and with  $T_2$ values not significantly shortened by chemical or conformational exchange processes. Different methods have been used for identification of the rates of internal motion. However, the number of nuclear spins included in the  $\tau_m$  estimation is often larger than the number that ultimately can be fitted to a single-order parameter,  $S^2$ , implying that some nuclear spins involved in the initial  $au_{\mathbf{m}}$  estimation actually have an effective internal correlation time,  $\tau_{\rm e}$ , not as fast as assumed. As a consequence,  $\tau_{\rm m}$  is underestimated, since internal motion reduces the  $T_1/T_2$  ratio. This situation becomes more obvious if the molecule has a large  $\tau_{\rm m}$  value because the reduction in  $T_1/T_2$  ratio arising from internal motion is more significant than for molecules with smaller  $\tau_{\rm m}$  and the same degree of internal motion. This Communication describes a more reliable method for identifying nuclear spins which should be excluded from the  $\tau_{\rm m}$  estimation because of insufficiently rapid internal motion. This results in an improved  $\tau_m$  value, giving a much better agreement between the number of nuclear spins fitted successfully to a single-order parameter,  $S^2$ , and those used in the  $\tau_m$  estimation. © 1998 Academic Press

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<sup>15</sup>N relaxation measurements have been used widely to gain information on the backbone dynamics of proteins in solution (1-8). Although most molecules exhibit some degree of anisotropy of their global motion, and fully anisotropic analyses of the <sup>15</sup>N relaxation data have been reported recently (9-13), <sup>15</sup>N relaxation data (<sup>15</sup>N  $T_1$ ,  $T_2$  and {<sup>1</sup>H} – <sup>15</sup>N NOE) are often interpreted with the approximation of isotropic global motion because of the significant simplification of data analysis afforded. Under this isotropic approximation, the motional parameters are usually obtained by using the model-free formalism (14), with the isotropic

global correlation time of the molecule being determined from the  $T_1/T_2$  ratio (1, 2).

Nuclear spins with an effective internal correlation time,  $\tau_{\rm e}$ , much faster than the global correlation time of the molecule have a spectral density function, as adopted by the model-free formalism (14), of

$$J(\omega) = S^{2} \tau_{\rm m} / [1 + (\omega \tau_{\rm m})^{2}], \qquad [1]$$

where  $S^2$  is the order parameter, reflecting the extent of spatial restriction of the NH bond, and  $\tau_{\rm m}$  is the global correlation time of the molecule. Using Eq. [1],  $\tau_{\rm m}$  can be determined from the average  $T_1/T_2$  ratio, provided that nuclear spins with slow internal motion or with  $T_2$  values that are significantly shortened due to chemical or conformational exchange are excluded (1). As internal motion results in a reduction in both the  $T_1/T_2$  ratio and the NOE (see below), whereas a significant contribution from exchange processes leads to an increase in the  $T_1/T_2$  ratio, alternative methods have been used to identify nuclear spins for the estimation of  $\tau_{\rm m}$  values. Thus, nuclear spins with slow internal motion can be identified by their small NOE values (for example, a lower limit in the range 0.6-0.7 is frequently adopted), whereas nuclear spins having a significantly shortened  $T_2$  due to chemical or conformational exchange are identified by a  $T_1/T_2$  ratio greater than the average (over the nuclear spins with NOE larger than the preselected value) plus one standard deviation (1). Alternatively, nuclear spins exhibiting either slow internal motion or chemical or conformational exchange can be identified exclusively from the  $T_1/T_2$  ratio (for example, only nuclear spins with a  $T_1/T_2$  ratio within one standard deviation of the averaged value are used for the  $\tau_{\rm m}$  estimation (2), or, equivalently, a trimmed weighted average value of the  $T_1/T_2$  ratio can be used (6)). These methods are used widely for identification of the character of internal motion of nuclear spins before making an initial estimation of the isotropic global correlation time, although an estimation of  $\tau_{\rm m}$  obtained by making

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Comparison of the Number of Nuclear Spins Used in the $\tau_m$ Estimation with Those Fitted to a Single S <sup>e</sup> Value for Several Proteins from the Literature where Both Numbers Were Reported						
Protein	No. of spins used in $\tau_{\rm m}$ estimation	Estimated $\tau_{\rm m}$ (ns)	Critical value <sup>a</sup>	No. of spins fitted to a single $S^2$	Referen	
Interleukin-1 $\beta$ SH2 domain:	113	8.3 ± 0.05	$T_1/T_2 = \langle T_1/T_2 \rangle - $ SD	54	2 5	
Free	67	$9.3 \pm 0.4$	$T_1/T_2 = \langle T_1/T_2 \rangle - SD$	4		

 $T_1/T_2 = \langle T_1/T_2 \rangle - \mathrm{SD}$ 

NOE = 0.65

TABLE 1

<sup>a</sup> Nuclear spins with  $T_1/T_2$  ratios or NOE values smaller than the critical values are considered to have insufficiently rapid internal motion.

 $6.7 \pm 0.2$ 

 $6.50 \pm 0.04$ 

use of structural information (for example, from the  $T_1/T_2$ ratios of nuclear spins located in regions that are well defined in the solution structure) has also been reported (15).

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It has often been found, however, that the number of nuclear spins included in the  $\tau_{\rm m}$  determination is larger than the number finally fitted to a single, internal motion-related parameter,  $S^2$  (2, 5, 7), as shown in Table 1. In other words, if the original model-free formalism is followed (fitting to  $S^2$  and  $\tau_{\rm e}$ ), the number of nuclear spins exhibiting extremely fast effective internal correlation times in the final results is usually less than that used in the  $\tau_{\rm m}$  determination. This implies that these methods may have failed to identify some nuclear spins for which effective internal motion correlation times are not as fast as assumed and for which Eq. [1] is therefore not strictly valid. As a consequence, the global correlation time of the molecule is underestimated (see below). This is significant because the initial value of  $\tau_{\rm m}$  might dominate the final fitting results for particular residues. For example, an underestimated  $\tau_{\rm m}$  value will result in the data for some nuclear spins being satisfactorily fitted only with the addition of an explicit exchange term,  $R_{ex}$ . Furthermore, a final optimization of the  $\tau_{\rm m}$  value, after the best combination of parameters related to internal motion has been determined for each individual nuclear spin, usually gives only a very limited improvement in the  $\tau_{\rm m}$  value itself. Thus, the value of the global correlation time is important in the analysis of <sup>15</sup>N relaxation data, and an improvement in its estimation is desirable.

An improved  $\tau_{\rm m}$  value can be obtained if nuclear spins for which internal motions are not sufficiently rapid (i.e., where Eq. [1] becomes invalid) can be identified and then excluded from the estimation of  $\tau_{\rm m}$ . Figures 1A and 1B compare the theoretical predictions of the  $T_1/T_2$  ratio and  ${^{1}H} - {^{15}N}$  NOE for an  ${^{15}N}$  spin as a function of  $\tau_m$  for different rates and amplitudes of internal motion, with the spectral density function taking the form used in the modelfree formalism (14). This illustrates that: (i) internal motion gives rise to a reduction in both the  $T_1/T_2$  ratio and NOE, but the extent of reduction is much more significant for the NOE, (ii) for the same magnitude of internal motion this

effect is more pronounced for molecules with larger global correlation times, and (iii) the NOE value is much less sensitive to  $\tau_{\rm m}$  than the  $T_1/T_2$  ratio. From Figs. 1A and 1B, it is clear, first, that inclusion of nuclear spins with internal effective correlation times that are not sufficiently rapid will result in an underestimated  $au_{\mathrm{m}}$  because internal motion causes a decrease in the  $T_1/T_2$  ratio. Second, since the <sup>15</sup>N NOE exhibits a much higher sensitivity to internal motion, the NOE should serve as a better identifier of internal motion than the  $T_1/T_2$  ratio; i.e., nuclear spins with relatively slow internal motion may not be obvious from their  $T_1/T_2$  ratio, but should be detectable from their NOE value. Finally, even though the <sup>15</sup>N NOE is also independent of  $S^2$  when the spectral density function takes the form of Eq. [1], its high sensitivity to internal motions and insensitivity to  $\tau_{\rm m}$  makes it less favorable for an independent determination of the global correlation time.

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When the NOE is used for identification of the rates of internal motion, it is obvious that the outcome of the  $\tau_{\rm m}$ estimation will depend strongly on the selection of the critical NOE value, NOE<sub>c</sub> (nuclear spins with an NOE value larger than this value are considered to have relatively rapid internal motion and thus the use of Eq. [1] is valid), and use of a higher NOE<sub>c</sub> value will improve the performance for the estimation of  $\tau_{\rm m}$ . In practice, however, the  $T_1/T_2$ ratios of those few nuclear spins with the largest NOE values are not suitable for the  $\tau_{\rm m}$  estimation due to experimental error in the NOE measurements, even though in theory a larger NOE value implies less effect from internal motion. In addition, NOE<sub>c</sub> is molecule- and field-dependent. A uniform value does not exist.

Here we describe a method for the determination of NOE<sub>c</sub> solely from the relaxation data. An initial  $\tau_{\rm m}$  is obtained from the  $T_1/T_2$  ratio of all nuclear spins with an NOE larger than a preselected value, say  $NOE_c = 0.6$  (excluding, as usual, nuclear spins with  $T_2$  values shortened significantly by chemical or conformational exchange). A corresponding estimate of the global correlation time,  $\tau'_{\rm m}$ , is then derived from the measured NOEs of the same nuclear spins in a similar manner. As  $\tau'_{\rm m}$  will be smaller than  $\tau_{\rm m}$ , the procedure

Complexed

Interleukin-3





**FIG. 1.** Theoretical plots of the  $T_1/T_2$  ratio and  $\{{}^{1}H\} - {}^{15}N$  NOE value for an  ${}^{15}N$  spin versus global correlation time, in a typical range of  $\tau_m$  values, 5.0–15.0 ns, for a number of  $S^2$  and  $\tau_e$  values. The spectral density function takes the form adopted by the model-free formalism, and the  ${}^{15}N$  resonance frequency is -60.81 MHz. (A) For a constant effective internal correlation time,  $\tau_e$ , of 20 ps, from top to bottom with  $S^2 = 1.0$  (solid line), 0.85 (dashed line), 0.7 (dotted line), and 0.55 (single dotted and dashed line), respectively. (B) For a constant order parameter,  $S^2$ , of 0.8, from top to bottom with  $\tau_e = 0$  ps (solid line), 20 ps (dashed line), 50 ps (dotted line), and 100 ps (single dotted and dashed line), respectively.

is repeated with NOE<sub>c</sub> increased by a small step, e.g., 0.02. The whole process is then continued in an iterative manner until a minimum difference between  $\tau_m$  and  $\tau'_m$  is obtained or  $\tau'_m$  becomes greater than  $\tau_m$ .

The variation of  $\tau_{\rm m}$  and  $\tau_{\rm m}'$  as a function of NOE<sub>c</sub> for relaxation data from the 20-kDa cytokine leukaemia inhibitory factor (LIF), as measured at an  $^{15}$ N frequency of -60.81MHz, is shown in Fig. 2. It is clear that the global correlation times derived from the ratio of  $T_1/T_2$  and the NOE value approach the same value as NOE<sub>c</sub> increases, i.e., as more nuclear spins with relatively slow internal motion (where Eq. [1] is not strictly valid) are excluded. As a result,  $\tau_{\rm m}$ increased from 9.47  $\pm$  0.62 to 9.75  $\pm$  0.46 ns. The global correlation time of 9.47  $\pm$  0.62 ns was derived from the average  $T_1/T_2$  ratio of 113 nuclear spins (from a total of 143 measured nuclear spins) using an  $NOE_c = 0.6$ , but subsequently only 70 spins were fitted satisfactorily to a single-order parameter,  $S^2$  (indicating they had sufficiently rapid internal motions). In comparison, when the global correlation time of 9.75  $\pm$  0.46 ns was used, 49 nuclear spins from the 50 involved in the estimation of  $\tau_{\rm m}$  were fitted satisfactory to a single  $S^2$  value. It is obvious that even though the value of  $\tau_m$  changed by only a small amount (within the range of the error), use of the new  $\tau_{\rm m}$  value gave a much better agreement between the number of nuclear spins fitted successfully to a single-order parameter,  $S^2$ , and those used in the estimation of  $\tau_{\rm m}$ .

Table 2 compares the results obtained by fitting the relaxation data with the model selection approach using  $\tau_m$  values



**FIG. 2.** Dependence of the isotropic global correlation time of leukaemia inhibitory factor (LIF) determined from the  $T_1/T_2$  ratio (open circles) and NOE value (closed circles) as a function of different critical NOE values (see text). The dashed line represents the theoretical dependence of the {<sup>1</sup>H} - <sup>15</sup>N NOE value on the global correlation time,  $\tau_m$ , for a rigid molecule with the spectral density function taking the form of Eq. [1] and with an <sup>15</sup>N frequency of -60.81 MHz. Note that the offset between the curve traced by the solid dots and the theoretical dashed line reflects largely the contribution of possible internal motions, even though they are very rapid in comparison with  $\tau_m$ .

 TABLE 2

 Distribution of the Number of Residues Fitted Satisfactorily

 to Each Combination of Model-Free Parameters for the 20-kDa

 Cytokine Leukaemia Inhibitory Factor (LIF)<sup>a</sup>

Demonsterre	Residues fitted satisfactorily		
optimized	$\tau_{\rm m}$ 9.47 ns	$\tau_{\rm m}$ 9.75 ns	
$S^2$	71 (71/103) <sup>b</sup>	67 (49/50)	
$S^2$ , $\tau_{\rm f}$	12	14	
$S^2$ , $R_{\rm ex}$	16	9	
$S^2$ , $\tau_{\rm f}$ , $R_{\rm ex}$	1	3	
$S_{ m f}^2,S_{ m s}^2, au_{ m s}$	35	42	

<sup>*a*</sup> In the model selection approach (6), using the extended model-free formula (16) for the expression of the spectral density function, up to three parameters related to the internal motion are fitted, while the effects of the remaining parameters are assumed to be negligible. Previously described selection criteria were followed for the determination of model-free parameter combinations for each individual residue (6).

<sup>b</sup> The number of nuclear spins exhibiting sufficiently rapid internal motion in the final results vs that assumed initially to have rapid internal motion is shown in parentheses.

obtained with NOE<sub>c</sub> = 0.6 and those obtained with the approach proposed here. The previously described selection criteria of Mandel *et al.* (6) were followed. It is clear that upon using the  $\tau_{\rm m}$  value obtained with the method described in the present paper, the number of residues requiring an explicit contribution of chemical or conformation exchange (Rex) for a satisfactory fit was reduced, as anticipated. Furthermore, more residues were fitted satisfactorily with relatively slower effective internal correlation times, as a consequence of the increased  $\tau_{\rm m}$  value.

In summary, we have shown that an underestimated  $\tau_m$  value (due to the inclusion of nuclear spins with relatively slow internal motion in the  $\tau_m$  estimation) is responsible for the discrepancy between the number of nuclear spins that can be fitted to a single  $S^2$  value and the number used in the estimation of  $\tau_m$ . Although the intrinsically high sensitivity of the <sup>15</sup>N NOE value to internal motion when compared with the  $T_1/T_2$  ratio limits its utility as an independent determination of the global correlation time, it can be used to obtain a better identification of the magnitude of internal motion and thus to obtain an improved initial estimation of the global correlation time from the  $T_1/T_2$  ratio in the study of protein dynamics by <sup>15</sup>N relaxation measurements. This

improvement is readily achievable from existing <sup>15</sup>N relaxation data. It will be more significant for molecules with longer global correlation times since the same degree of internal motion will give a relatively larger reduction in the  $T_1/T_2$  ratio. Therefore, if a molecule has a relatively long global correlation time and isotropic overall motion is assumed, the method described in this Communication should give a better estimate of the global correlation time.

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## REFERENCES

- 1. L. E. Kay, D. A. Torchia, and A. Bax, Biochemistry 28, 8972 (1989).
- G. M. Clore, P. C. Driscoll, P. T. Wingfield, and A. M. Gronenborn, Biochemistry 29, 7383 (1990).
- M. J. Stone, W. J. Fairbrother, A. G. Palmer III, J. Reizer, M. H. Saier, Jr., and P. E. Wright, *Biochemistry* **31**, 4394 (1992).
- 4. J. W. Peng and G. Wagner, Biochemistry 31, 8571 (1992).
- N. A. Farrow, R. Muhandiram, A. U. Singer, S. M. Pascal, C. M. Kay, G. Gish, A. E. Shoelson, T. Pawson, J. D. Forman-Kay, and L. E. Kay, *Biochemistry* 33, 5984 (1994).
- A. M. Mandel, M. Akke, and A. G. Palmer III, J. Mol. Biol. 246, 144 (1995).
- Y. Feng, B. K. Klein, and C. A. McWherter, J. Mol. Biol. 259, 524 (1996).
- E. T. Olejniczak, M.-M. Zhou, and S. W. Fesik, *Biochemistry* 36, 4118 (1997).
- N. Tjandra, S. E. Feller, R. W. Pastor, and A. Bax, J. Am. Chem. Soc. 117, 12,562 (1995).
- Z. Zheng, J. Czaplicji, and O. Jardetzky, *Biochemistry* 34, 5212 (1995).
- N. Tjandra, P. Wingfield, S. Stahl, and A. Bax, J. Biomol. NMR 8, 273 (1996).
- J. P. Mackay, G. L. Shaw, and G. F. King, *Biochemistry* 35, 4867 (1996).
- N. Tjandra, D. S. Garrett, A. M. Gronenborn, A. Bax, and G. M. Clore, *Nature Struct. Biol.* 4, 443 (1997).
- 14. G. Lipari and A. Szabo, J. Am. Chem. Soc. 104, 4546 (1982).
- J.-W. Cheng, C. A. Lepre, S. P. Chambers, J. R. Fulghum, J. A. Thomson, and J. M. Moore, *Biochemistry* 32, 9000 (1993).
- G. M. Clore, A. Szabo, A. Bax, L. E. Kay, P. C. Driscoll, and A. M. Gronenborn, *J. Am. Chem. Soc.* **112**, 4989 (1990).