FRICTIONAL COEFFICIENT, RATIO

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The translational frictional coefficient, f, is a measure of the resistance to movement of a molecule; this resistance is a function of both the size and the shape of the molecule. It can be measured experimentally either by its rate of diffusion or its rate of sedimentation.

As would be expected, the translational frictional coefficient is inversely proportional to the diffusion coefficient, $D^{\circ}_{20,w}$, under standard conditions of water at 20.0°C and extrapolated to zero concentration:

$$f = \frac{RT}{N_{\rm A}D_{20,\rm w}^{\circ}} = \frac{k_{\rm B}T}{D_{20,\rm w}^{\circ}}$$
 (1)

where R is the gas constant (8.314 imes 10^7 erg mol $^{-1}$ K $^{-1}$) and N_A is Avogadro's number $(6.022 \times 10^{23} \text{ mol}^{-1})$.

Likewise, the frictional coefficient is inversely proportional to the **sedimentation coefficient**, $s^{\circ}_{20,w}$ under the same standard conditions:

$$f = \frac{M_{\rm r}(1 - \overline{v}\rho_{20\rm w})}{N_{\rm A}s_{20\rm ,w}^{\circ}} \tag{2}$$

where \overline{v} is the **partial specific volume** of the macromolecule and $\rho_{20,w}$ is the density of the standard solvent, water at 20°C.

It is usually more informative to use the **frictional ratio**, f/f_0 , which is the dimensionless ratio of the observed translational frictional coefficient to that of an equivalent spherical molecule of the same anhydrous mass and density. This corrects for the size of the molecule and gives an indication of its shape. The greater the frictional ratio, the more asymmetric it is likely to be. The frictional ratio can be calculated from the diffusion coefficient by the following equation:

$$\frac{f}{f_0} = \frac{k_{\rm B}T}{6\pi\,\eta_{20,\rm w}} \cdot \left(\frac{4\pi N_{\rm A}}{3\overline{v}M}\right)^{1/3} \frac{1}{D_{20,\rm w}^{\circ}} \tag{3}$$

The frictional ratio depends intrinsically on the conformation, flexibility, and degree of solvation (by water, salt ions, and any other solvent molecules) of the macromolecule. This degree of water association is termed the hydration of the macromolecule, δ , and is defined as the mass in grams of associated solvent per gram of anhydrous biomolecule. This associated solvent includes both chemically bound solvent and also solvent physically entrained in the interstices in the molecule. The value of δ is typically between 0.2 and 0.5 g/g for proteins, although it is a notoriously difficult parameter to pin down with any accuracy.

The function defining the shape and flexibility of the

biomolecule is the Perrin translational frictional function, P:
$$P = \frac{f}{f_0} \cdot \left(\frac{\overline{v}}{\overline{v} + \delta/\rho_0}\right)^{1/3} \tag{4}$$

where ρ_0 is the density (in grams per milliliter) of the bound solvent. For a molecule that is fairly rigid on a time-averaged basis, the gross conformation can be specified using P in terms of the axial ratio of the equivalent hydrodynamic ellipsoid or in terms of sophisticated arrangements of spheres called hydrodynamic bead models (see **Diffusion**).

Suggestions for Further Reading

- S. E. Harding (1995) On the hydrodynamic characterisation of macromolecular conformation. Biophys. Chem. 55, 69–93.
- K. E. Van Holde (1985) Physical Biochemistry, Prentice-Hall, Englewood Cliffs, N. J. (Chapter 4 gives an excellent introduction).