



UNITED NATIONS EDUCATIONAL, SCIENTIFIC AND CULTURAL ORGANIZATION  
INTERNATIONAL ATOMIC ENERGY AGENCY  
INTERNATIONAL CENTRE FOR THEORETICAL PHYSICS  
I.C.T.P., P.O. BOX 586, 34100 TRIESTE, ITALY, CABLE: CENTRATOM TRIESTE



H4.SMR/916 - 36

**SEVENTH COLLEGE ON BIOPHYSICS:**

*Structure and Function of Biopolymers: Experimental and Theoretical  
Techniques.*

*4 - 29 March 1996*

*Photophysics, Protein Physics  
and Myoglobin -*

*the Hydrogen Atom of Biology*

*William A. Eaton  
Laboratory of Chemical Physics  
National Institutes of Health  
20892-0520 Bethesda  
U.S.A.*

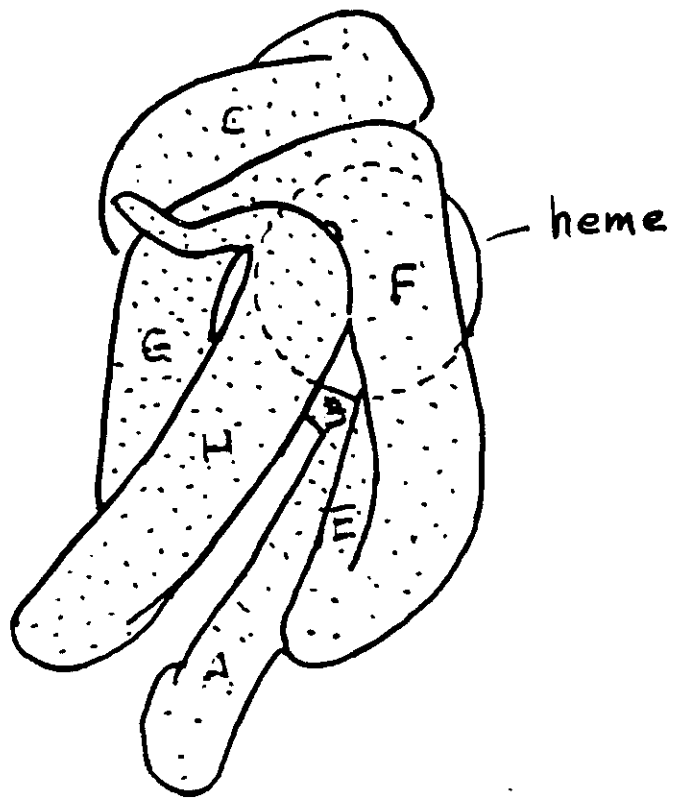
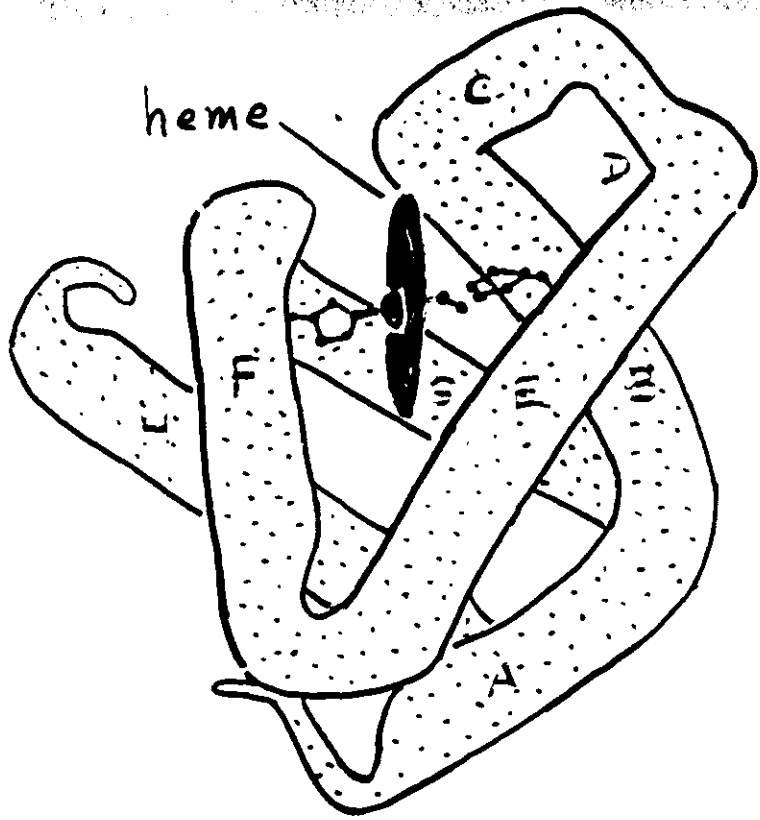
Trieste, March 1996

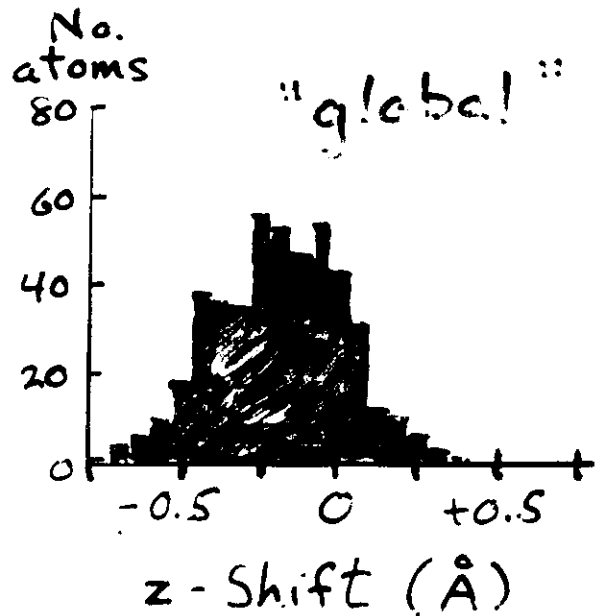
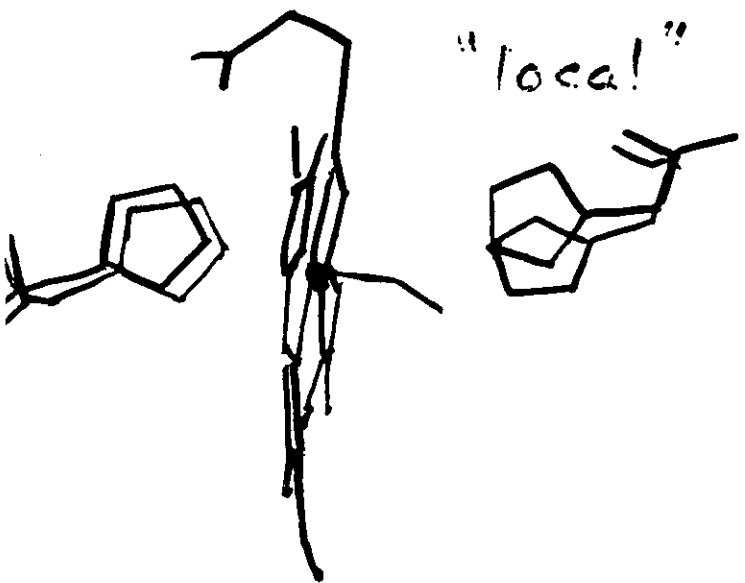
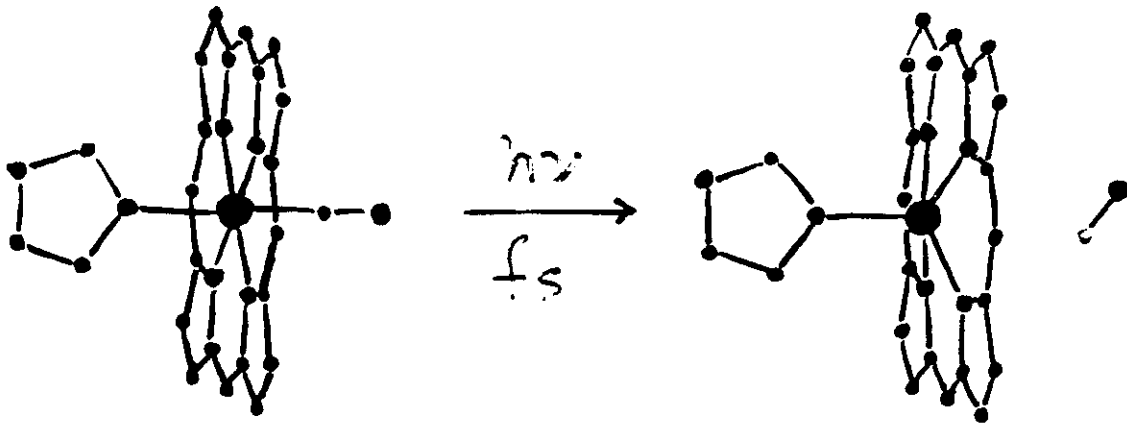
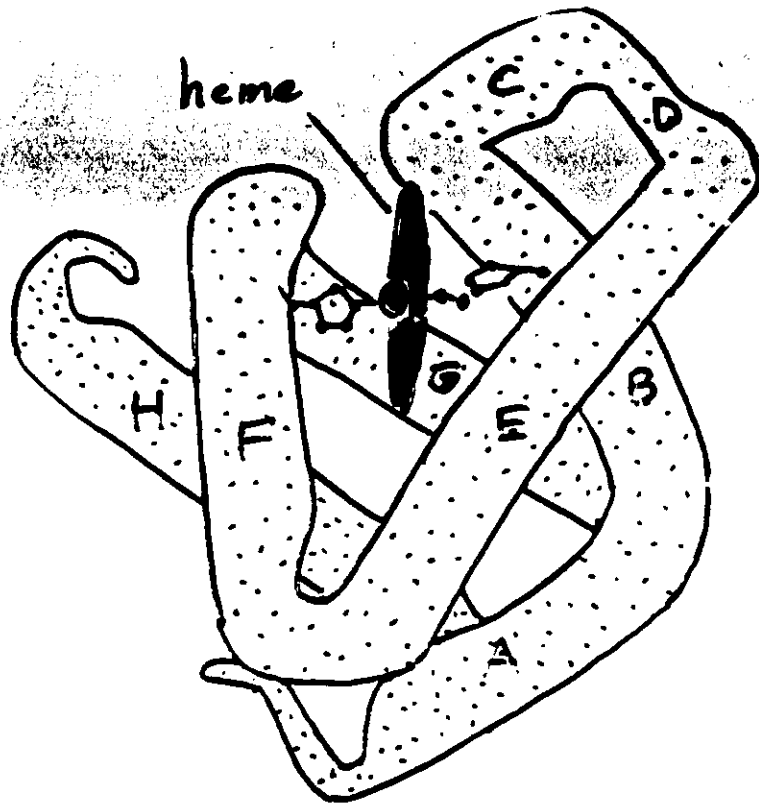
Lecture I

"Photophysics, protein physics,  
and Myoglobin -

the hydrogen atom of biology"

# Myoglobin





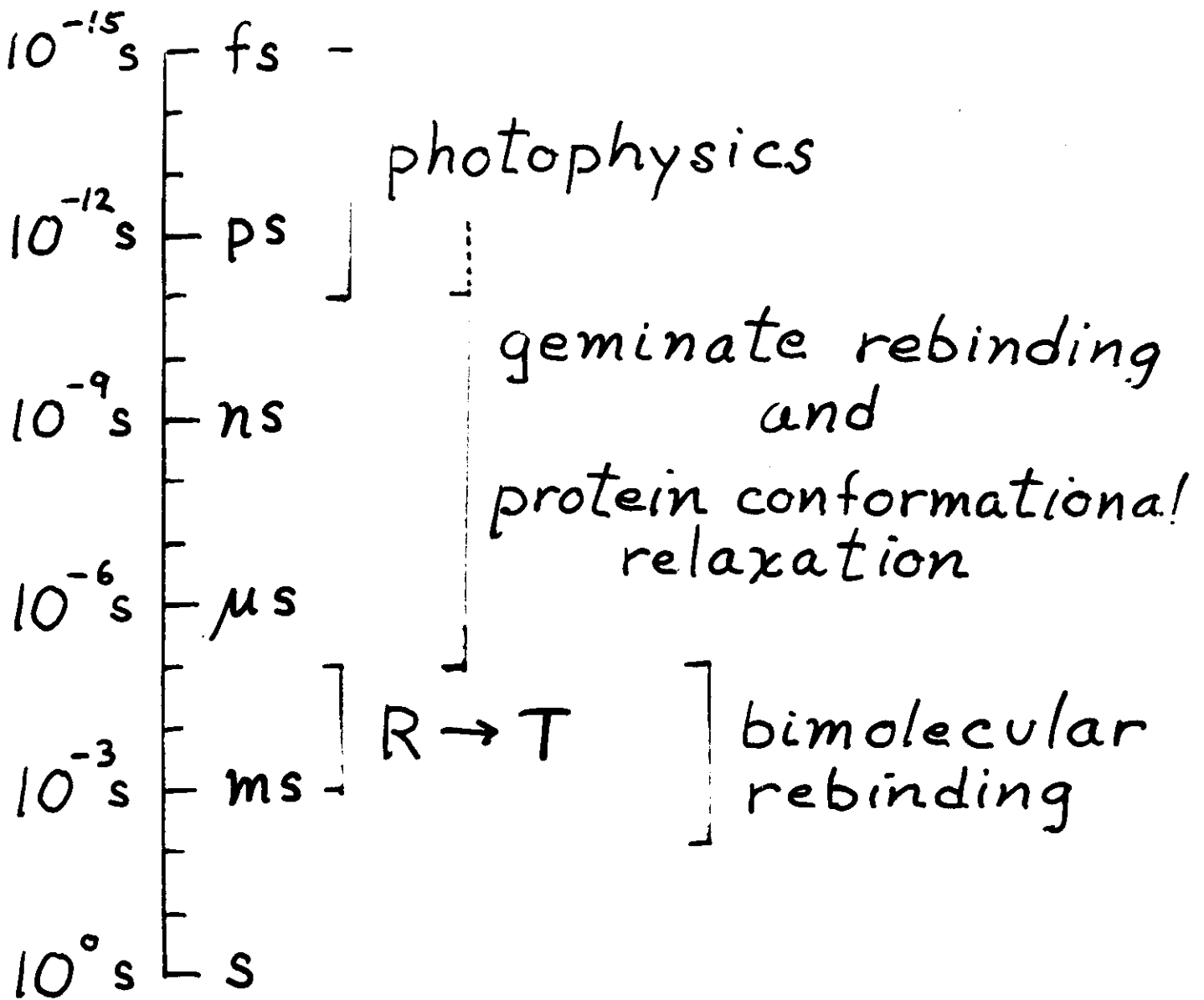
Newer results on myoglobin  
needed to explain more complex  
hemoglobin

1. geminate rebinding
2. conformational substates
3. conformational relaxation  
extended in time ( $\sim e^{-(kt)^\beta}$ ):  
explained by "physical kinetics"
4. relaxation slows geminate  
rebinding

# Pulsed Optical Excitation of Hemes and Heme Proteins

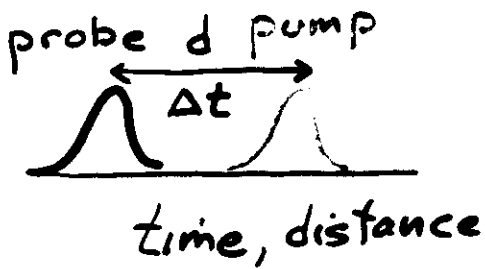
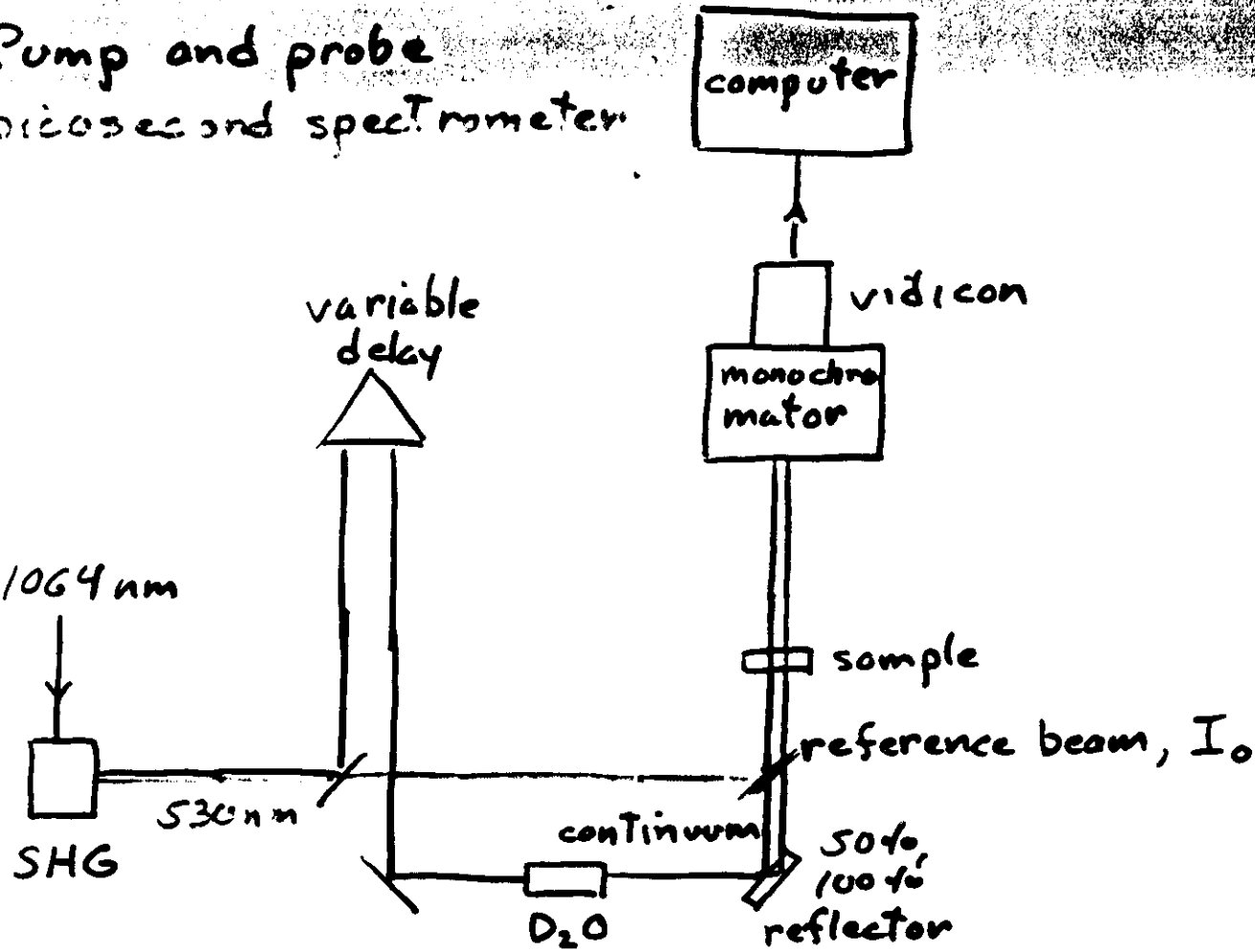
room T

Time



# How fast is ligand dissociated?

Pump and probe  
picosecond spectrometer



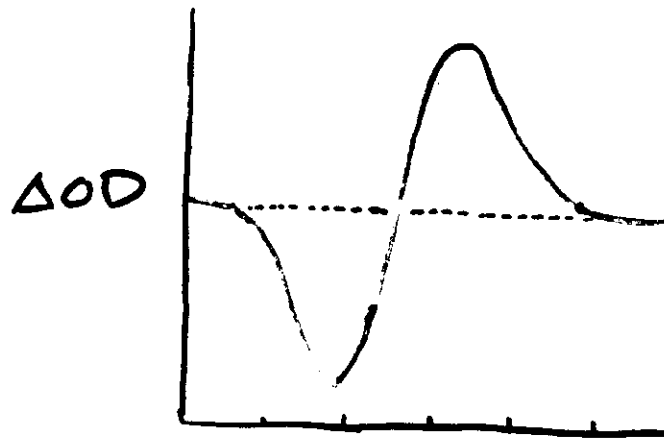
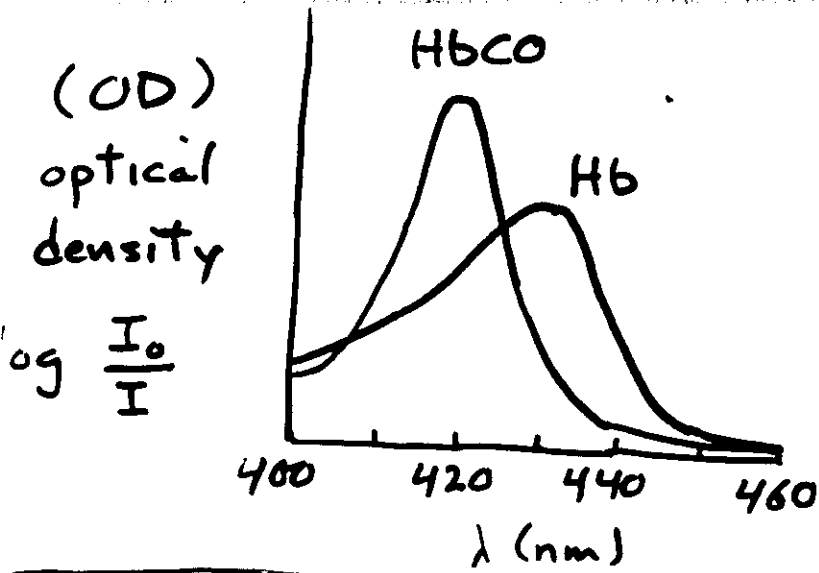
$$\Delta t = \frac{\Delta d}{c}$$

$$c = 3 \times 10^{10} \text{ cm/sec}$$

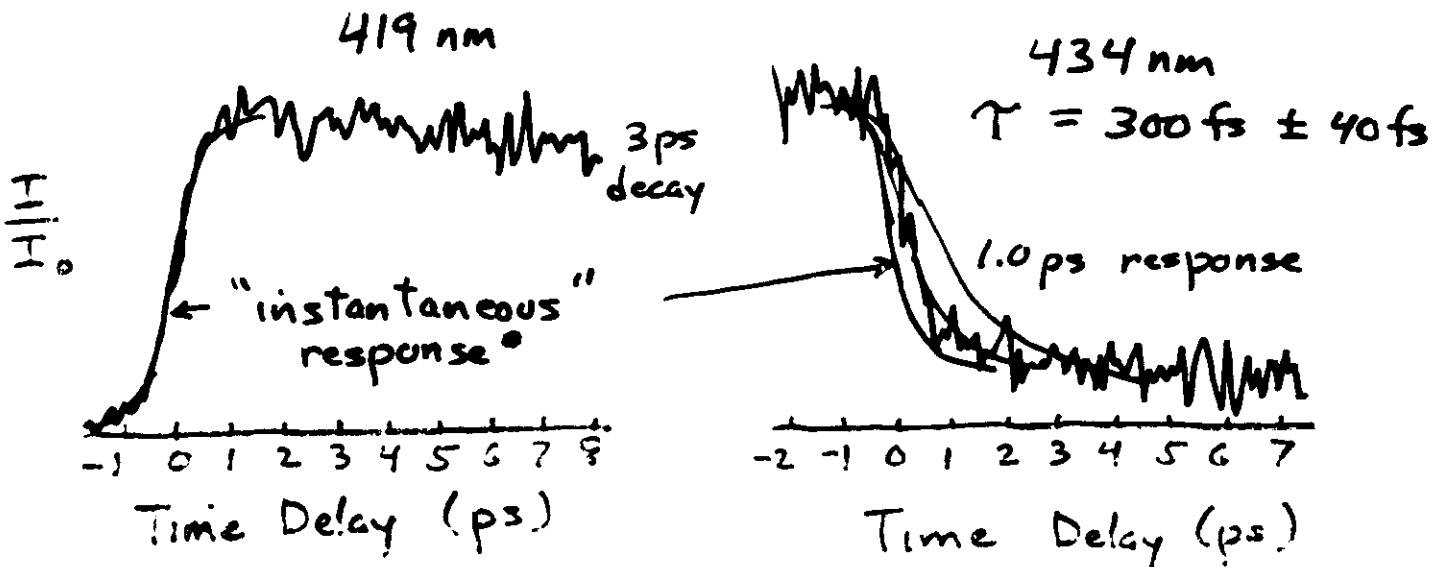
$$1 \text{ ps} = 0.3 \text{ mm}$$

# B (Soret) bands

# Static Difference Spectra



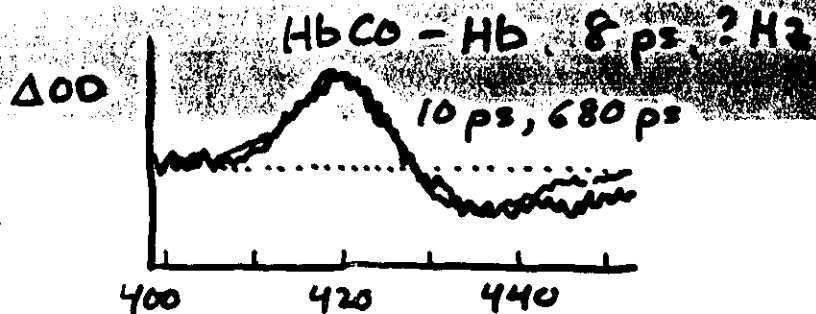
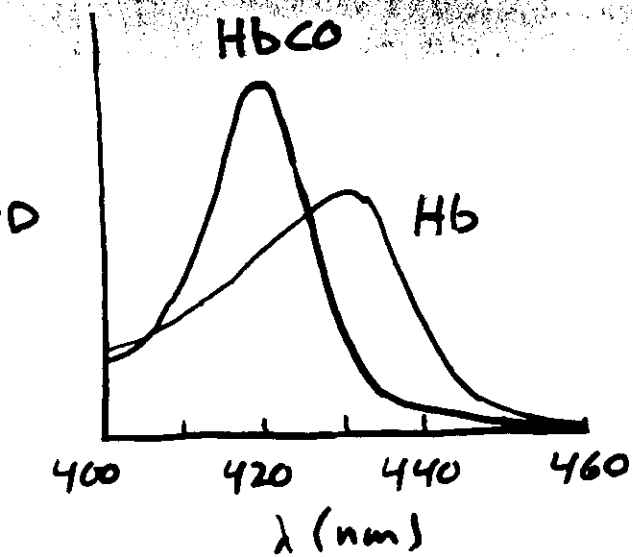
.. Martin Excitation with 0.25 ps pulse



CO has dissociated and iron displaced within 300 fs.

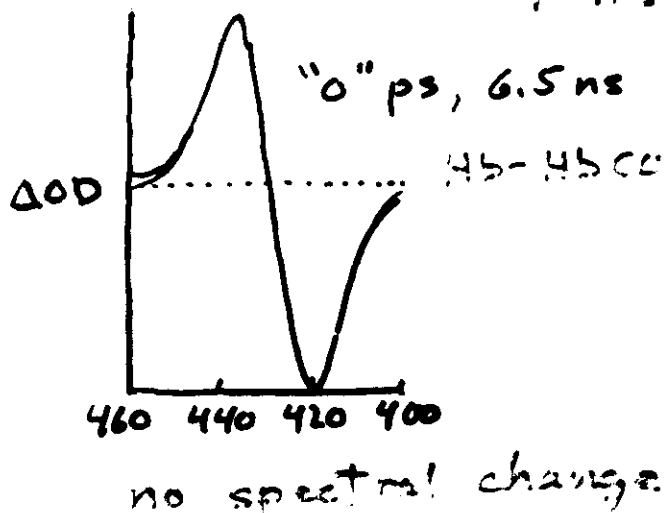
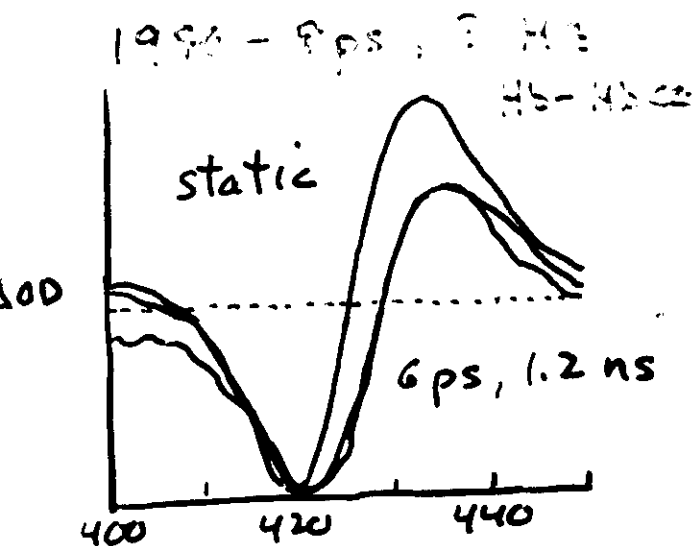


# Discovery of geminate recombination

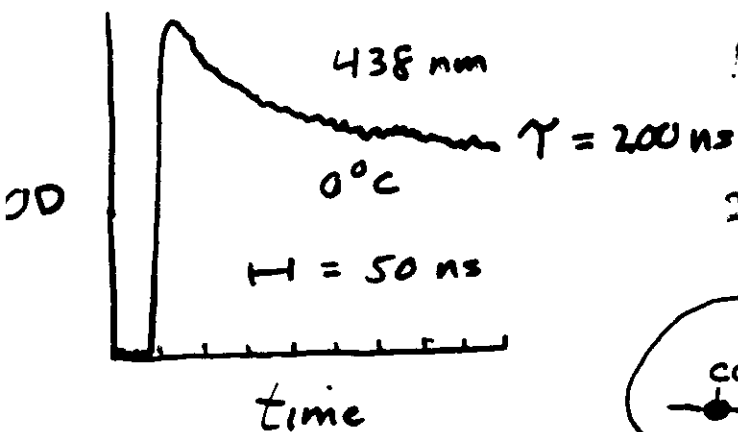


1978 - no geminate rebinding  $\leq 680$  ps

1988 - confirmed, 30 ps. 10 H2

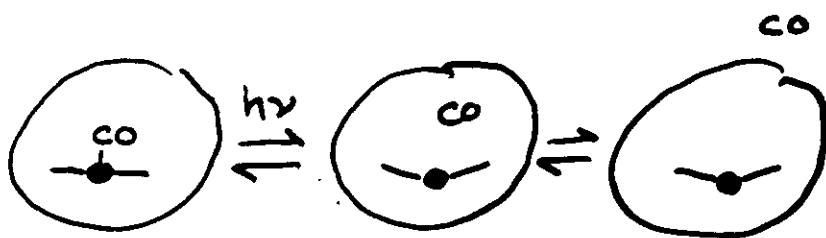


1979 - 30 ns, scope

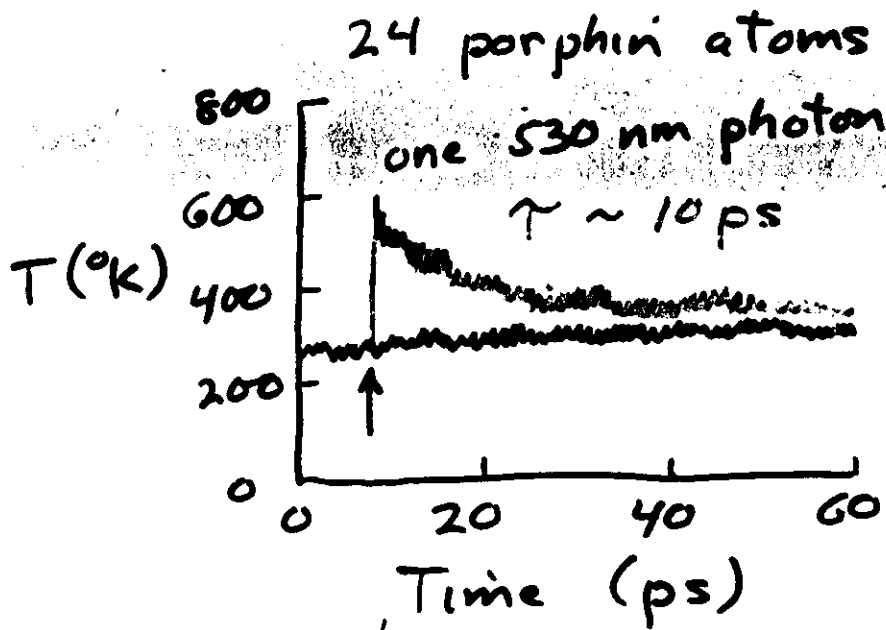


Geminate rebinding because

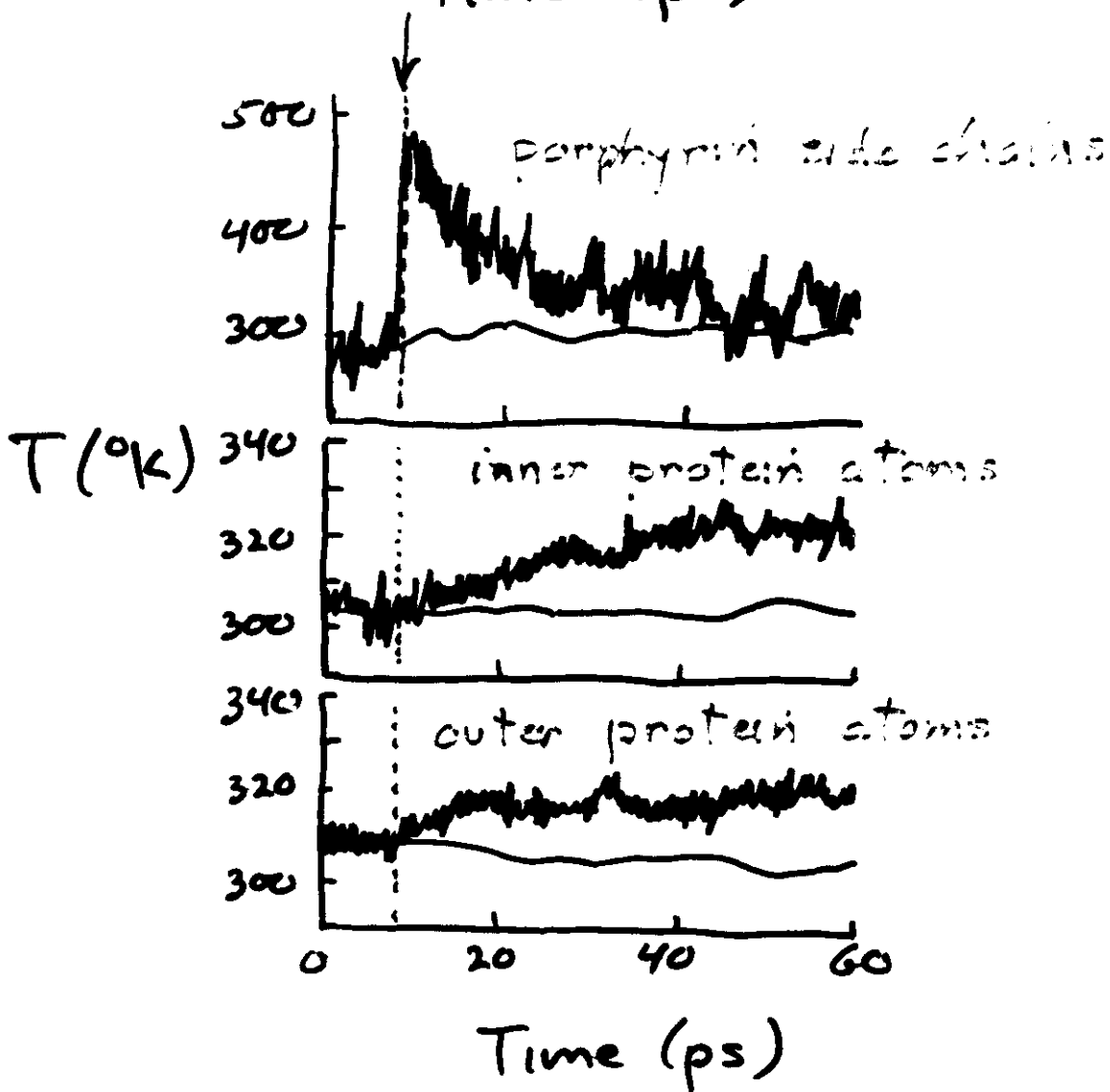
- $5 \times 10^9 \text{ M}^{-1} \text{ s}^{-1}$  too fast for bimolecular
- $\tau$  pressure independent



Eric Henry  
(NIH)



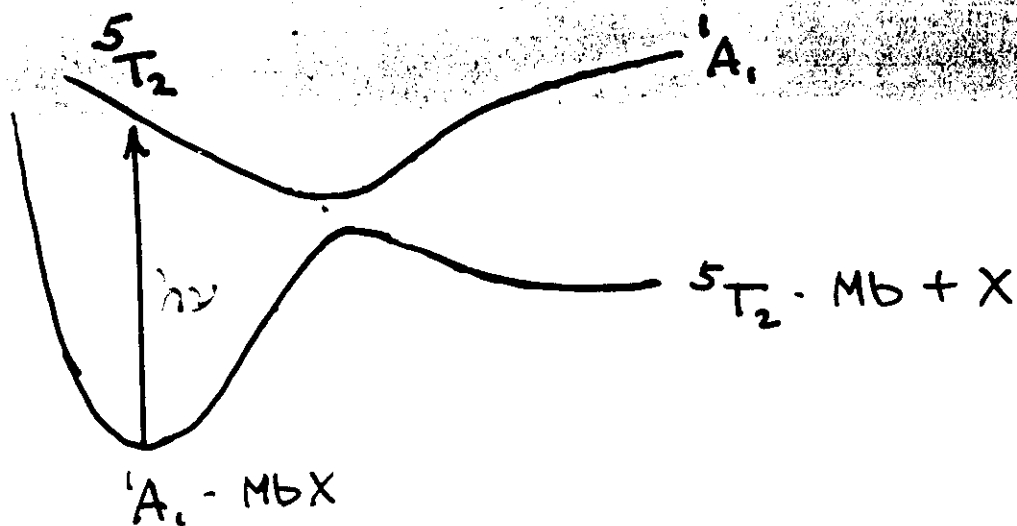
$$\frac{3}{2} N k_B T = \sum_i \frac{1}{2} m_i v_i^2$$



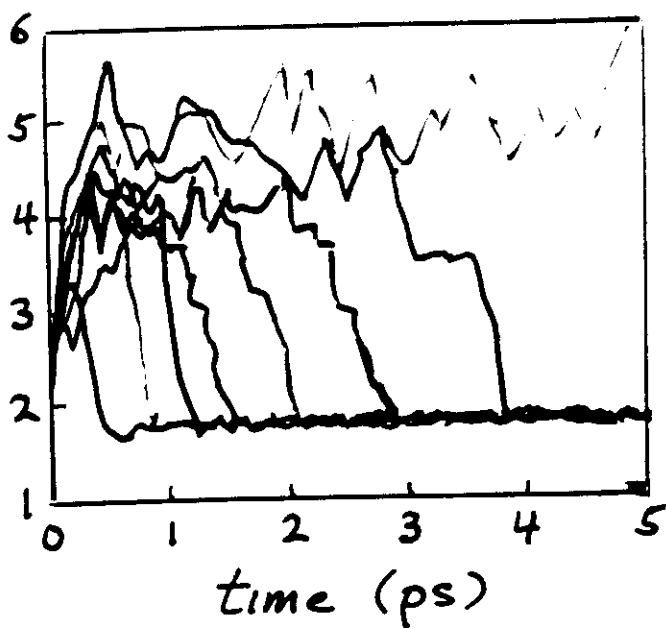
Thermal effects potentially very important  
at times < 20 ps  
QM simulations?

# Simulations of Photolysis Experiments

Olivier Schaad  
(NIH)

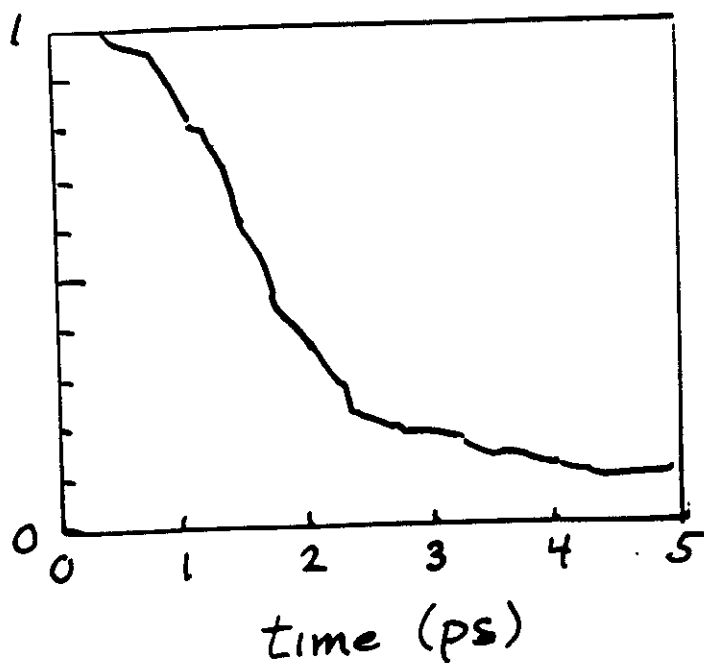


$r$  (Fe-NO)  
Å



barrierless  
trajectories

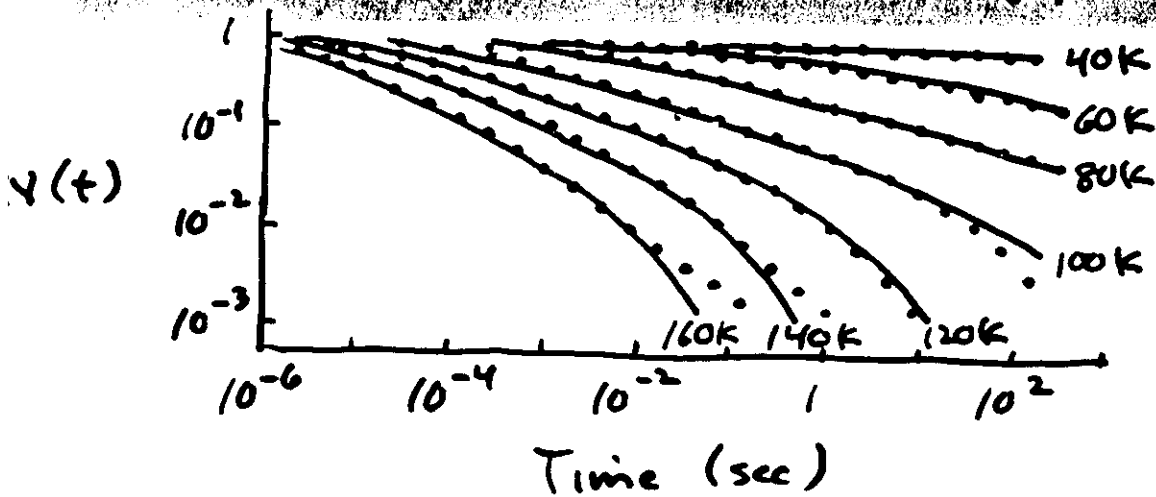
fraction  
unbound



histogram of  
rebinding times

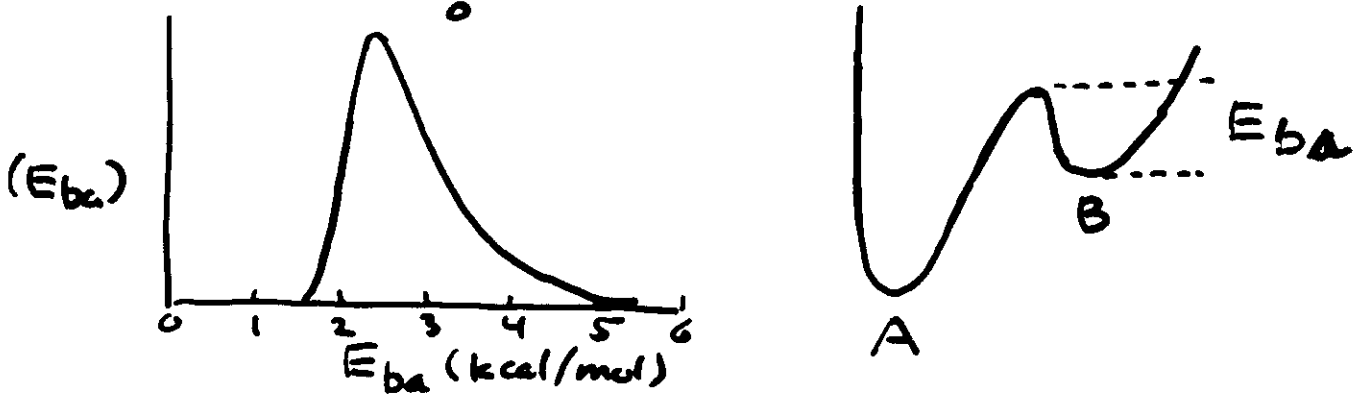
# Conformational Substates - 1975.

MbCO 3:1 glycerol-water



Basic Idea: multiple conformations, each with different activation energy, "frozen" in at low temperature, to produce a distribution of rates.

$$N(t) = \int_0^{\infty} g(E_{ba}) e^{-k_{ba} t} dE_{ba}, \quad k_{ba} = A_{ba} e^{-E_{ba}/RT}$$



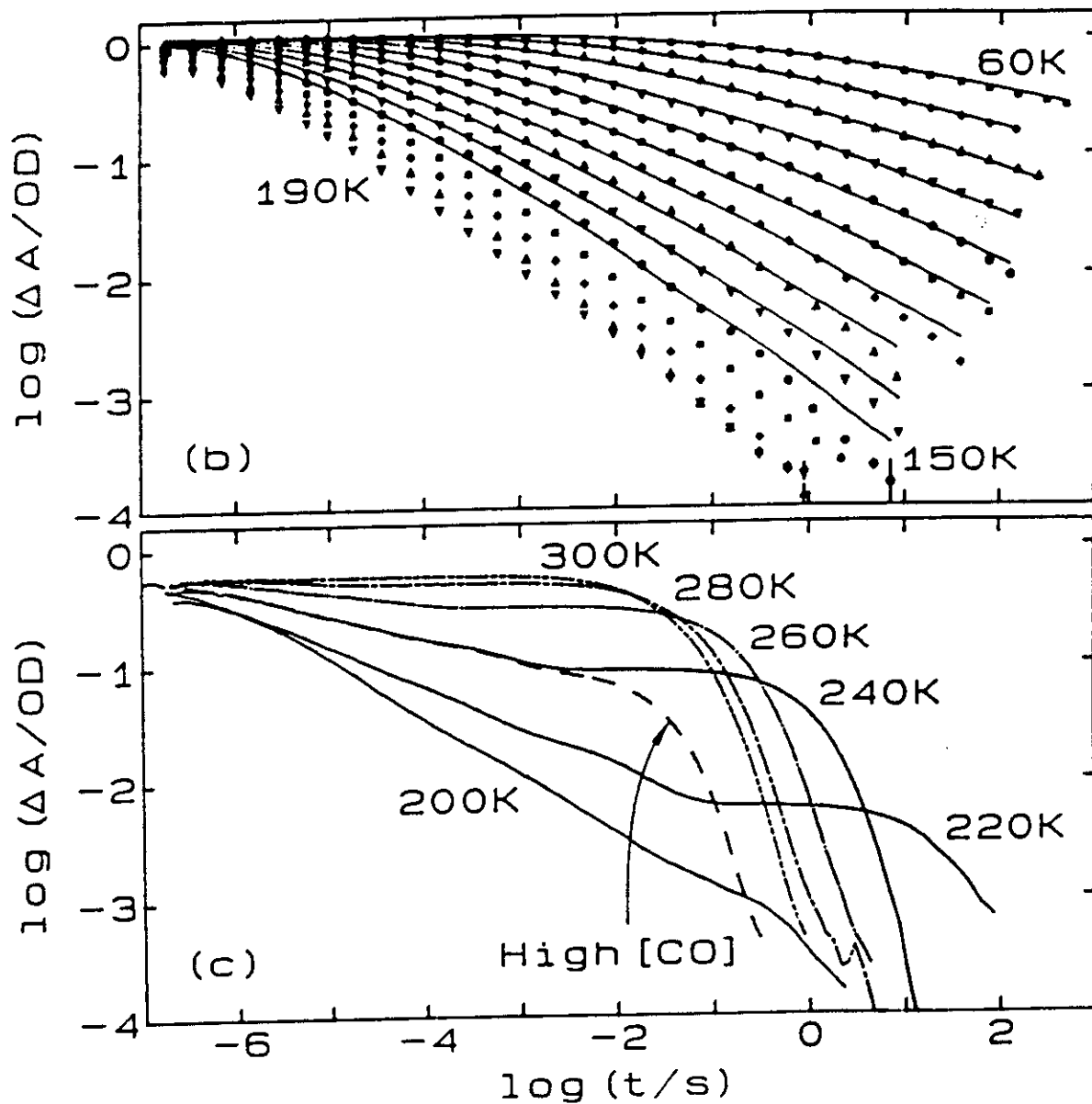
At high temperature, if relaxation among substates is very fast,  $k_r \gg k_{ba}^{\max}$  - rebinding is exponential

$$N(t) = e^{-\int g(E_{ba}) k_{ba} t dE_{ba}} = e^{-k_{ba}^{\text{mean}} t}$$

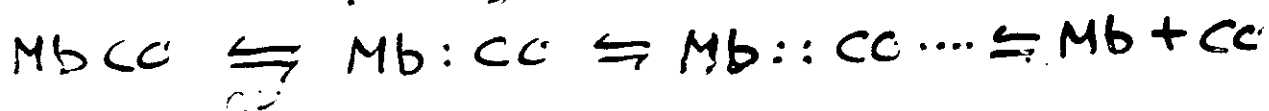
Frauenfelder and coworkers:

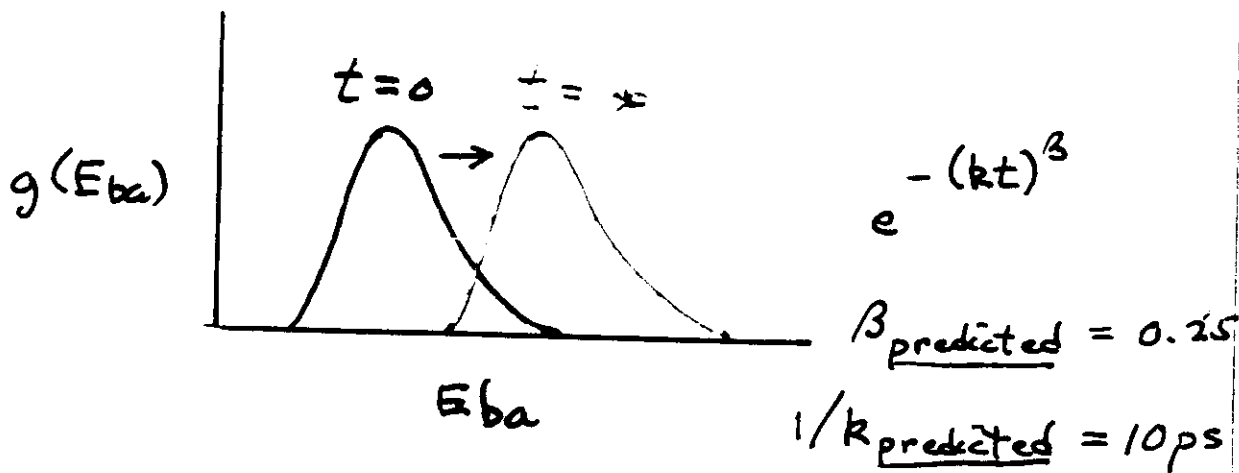
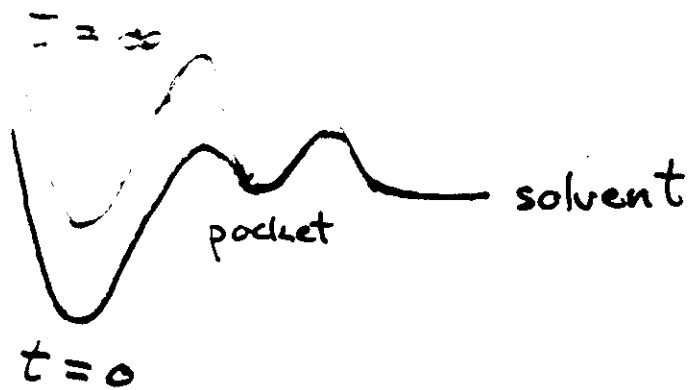
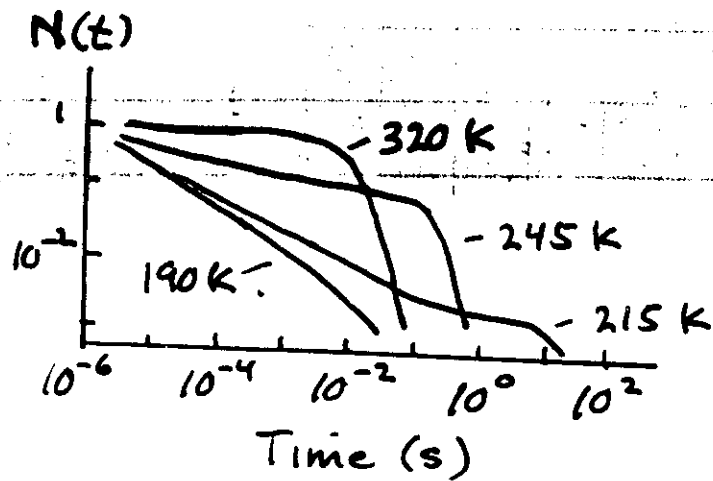
Below  $T_g$ : distribution of rates from "frozen" substates.

Above  $T_g$ : geminate rebinding slows with increasing temperature



Models: multiple geminate states

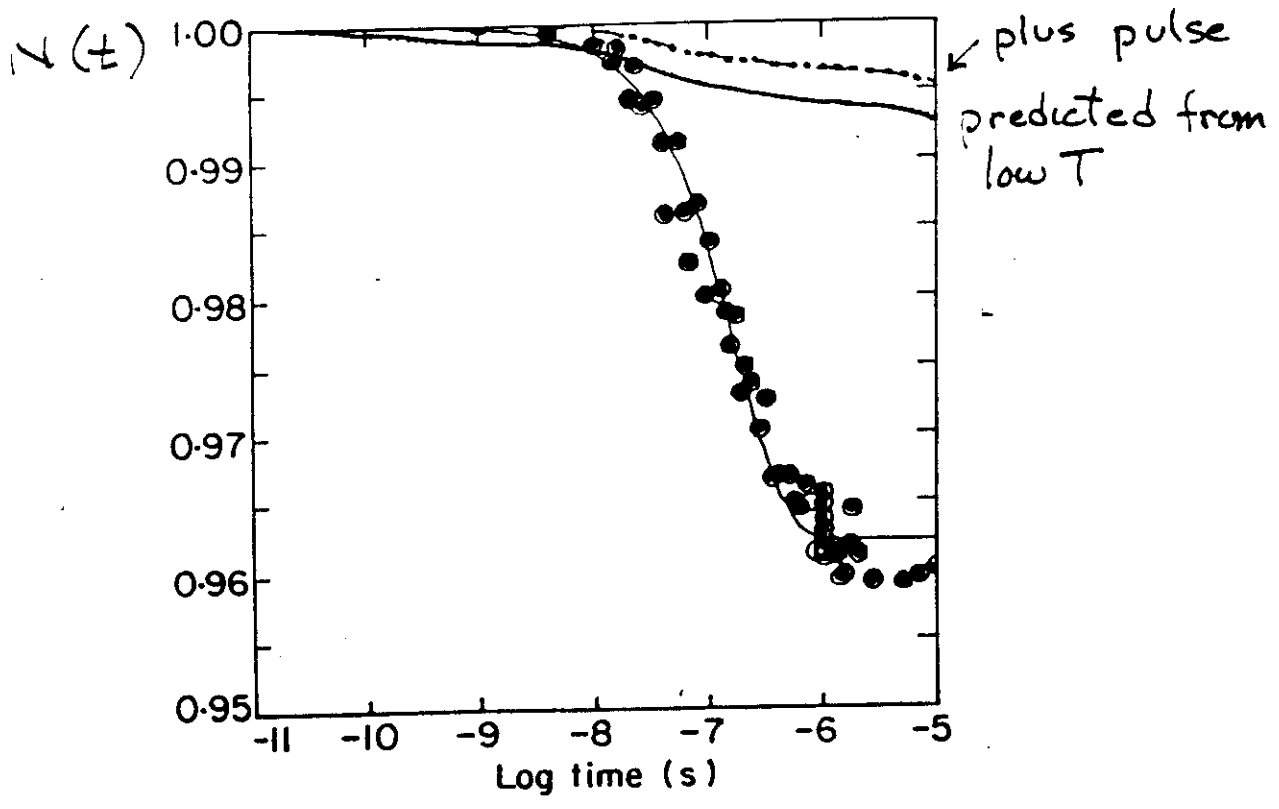




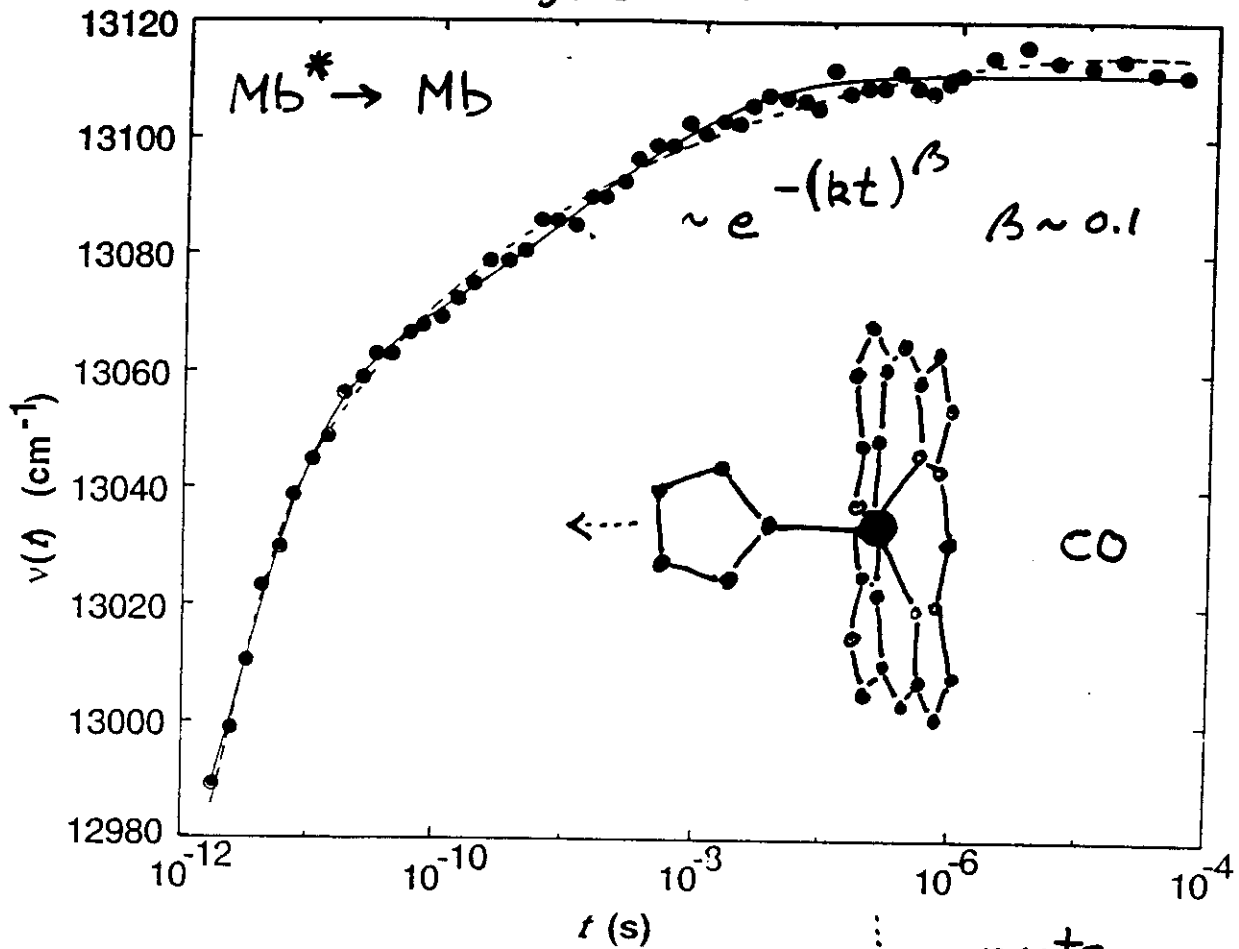
An alternative view (Agmon & Hopfield, 1983)  
 - protein relaxation shifts barrier height distribution.

Stembach, Frauenfelder et al. 1991 -  
predicted kinetics of protein relaxation 12

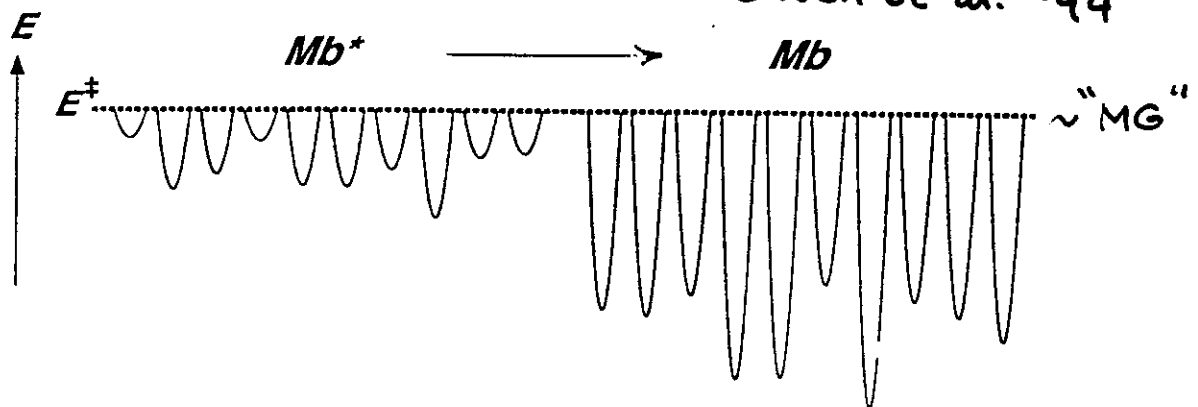
# Discovery of geminate rebinding of CO in liquid Mb solution



Stephen Hagen (NIH); Data of Philip Anfinrud (Harvard)  
 $a_{2u}(\pi) \rightarrow Fe(dxz)$  charge transfer

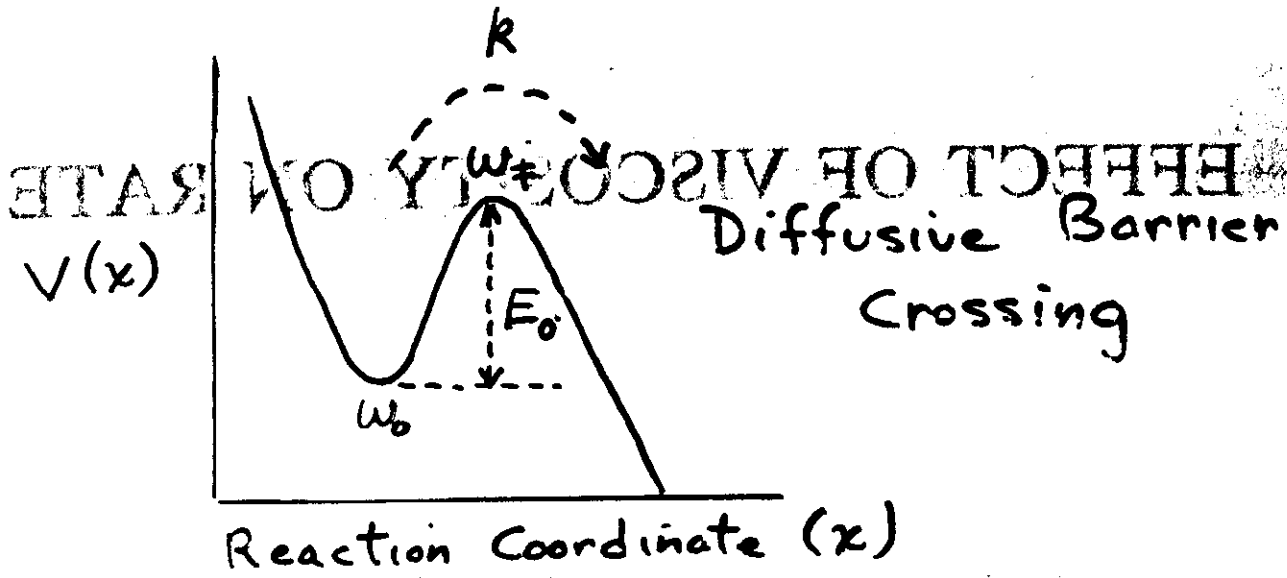


roots  
 De Dominicis et al. '85  
 Koper & Hillhorst '87  
 Shakhnovich & Gutin '89  
 Frauenfelder et al. '91  
 Saven et al. '94



$$k_{ij}(T) = k_0 g(E_j) dE \exp[-(E^\ddagger - E_i)/RT]$$





Dynamics described by Langevin equation:

$$M \frac{d^2x}{dt^2} = -\frac{dV}{dx} - \zeta \frac{dx}{dt} + R(t)$$

which, in high friction limit, yields Kramers' equation:

$$k = \frac{M \omega_0 \omega_{\ddagger}}{2\pi\zeta} \exp\left(-\frac{E_0}{k_B T}\right)$$

Assuming that protein friction and solvent friction are additive, Kramers' equation is:

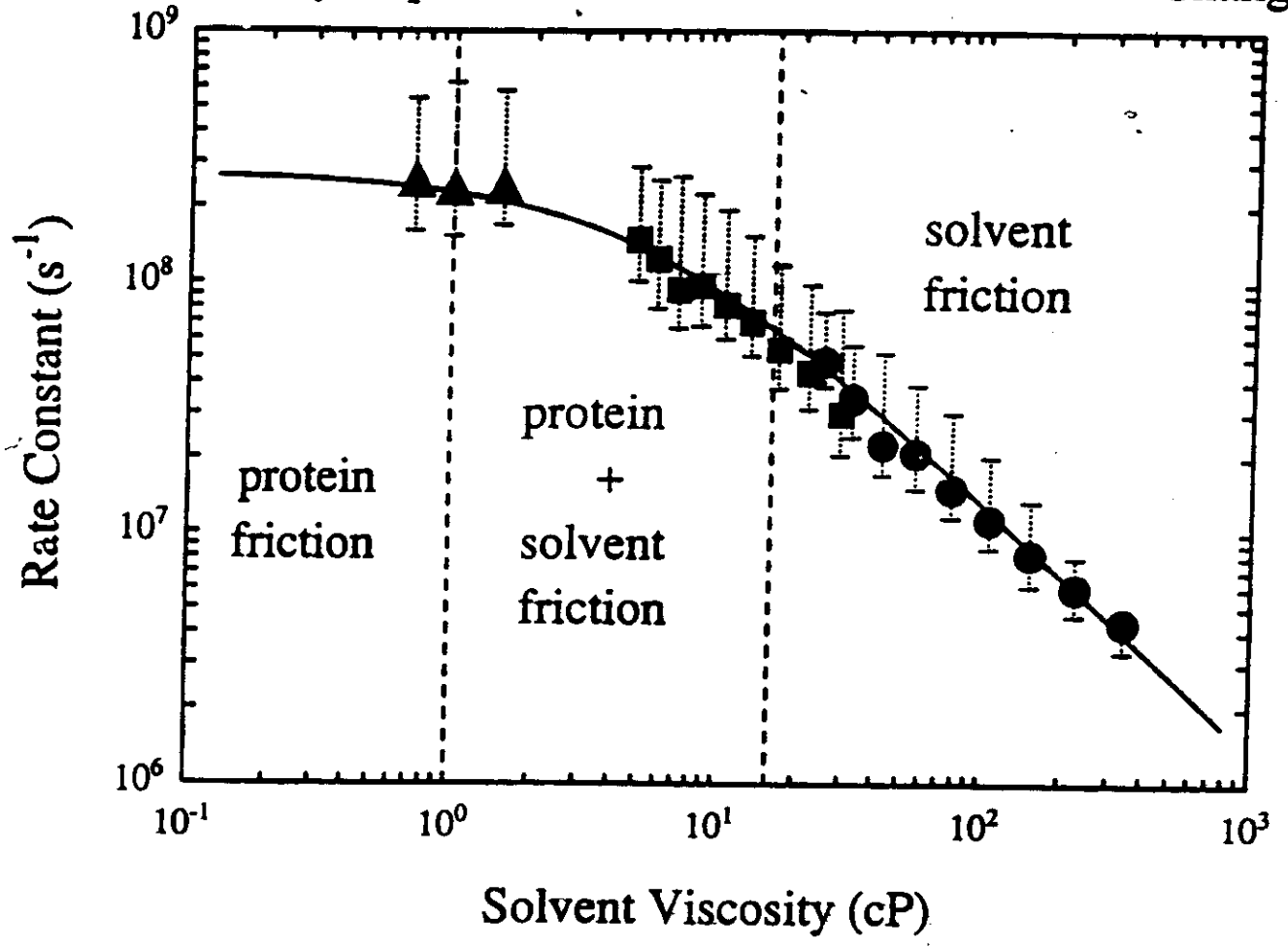
$$k = \frac{B}{\alpha\zeta_p + (1-\alpha)\zeta_s} \exp\left(-\frac{E_0}{k_B T}\right)$$

which, using Stokes' law, becomes:

$$k = \frac{C}{\sigma + \eta_s} \exp\left(-\frac{E_0}{k_B T}\right)$$

Rate (M<sup>-1</sup>s<sup>-1</sup>)

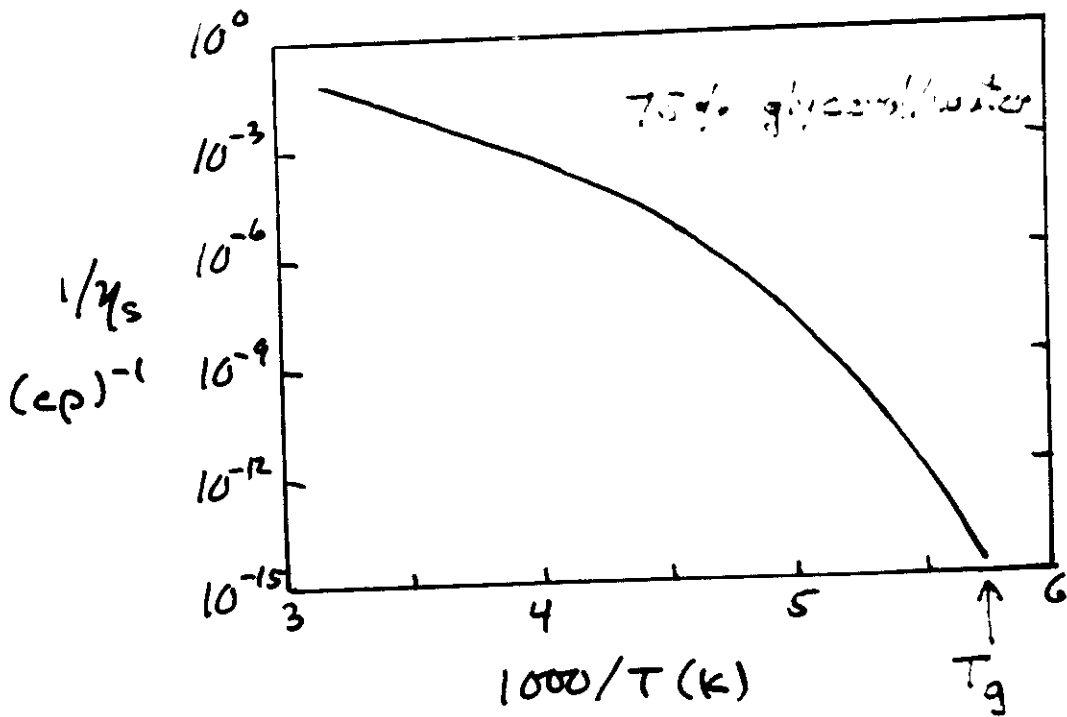
### Viscosity Dependence of Protein Conformational Change



$$k = \frac{c}{\sigma + \eta} \exp(-E_a/RT)$$

protein "viscosity"      solvent viscosity

$$k = \frac{c}{\sigma + \eta_s} e^{-E_0/RT}$$



$$\sigma \sim 4 \text{ cp}, \quad E_0 \sim 2 \text{ kcal/mole}$$

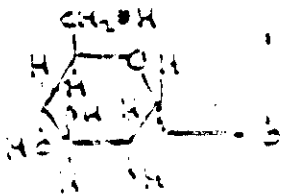
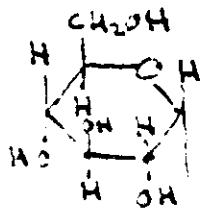
Slowing near  $T_g$  due to solvent viscosity  
 (not glass transition of protein)

$$\eta_s \sim 10^{11}$$

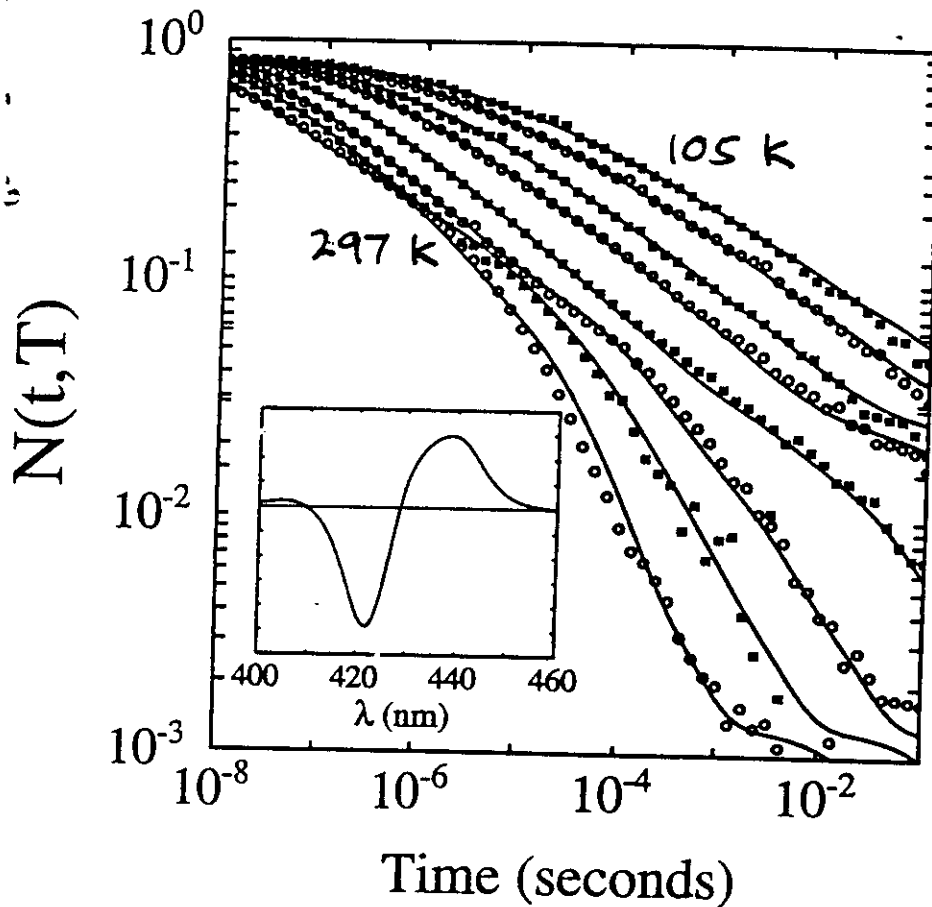
$$e^{-E_0/RT} \sim 10^2$$

Stephen Hagen  
(NIH)

# Myoglobin in a trehalose glass



/U2/figures/hagen\_PRL\_1994/figure\_1



Recall:

$$N(t) = \exp\left[-\int g(E_{ba}) k_{ba} t dE_{ba}\right]$$

$$= \exp\left[-k_{ba}^{\text{mean}} t\right]$$

$k_{ba}^{\text{mean}} = 5 \times 10^7 \text{ s}^{-1}$  unrelaxed protein

$k_{ba}^{\text{water}} = 2 \times 10^4 \text{ s}^{-1}$  relaxed protein

Protein "stuck" in relaxed (fast reactive)  
conformational subsites.