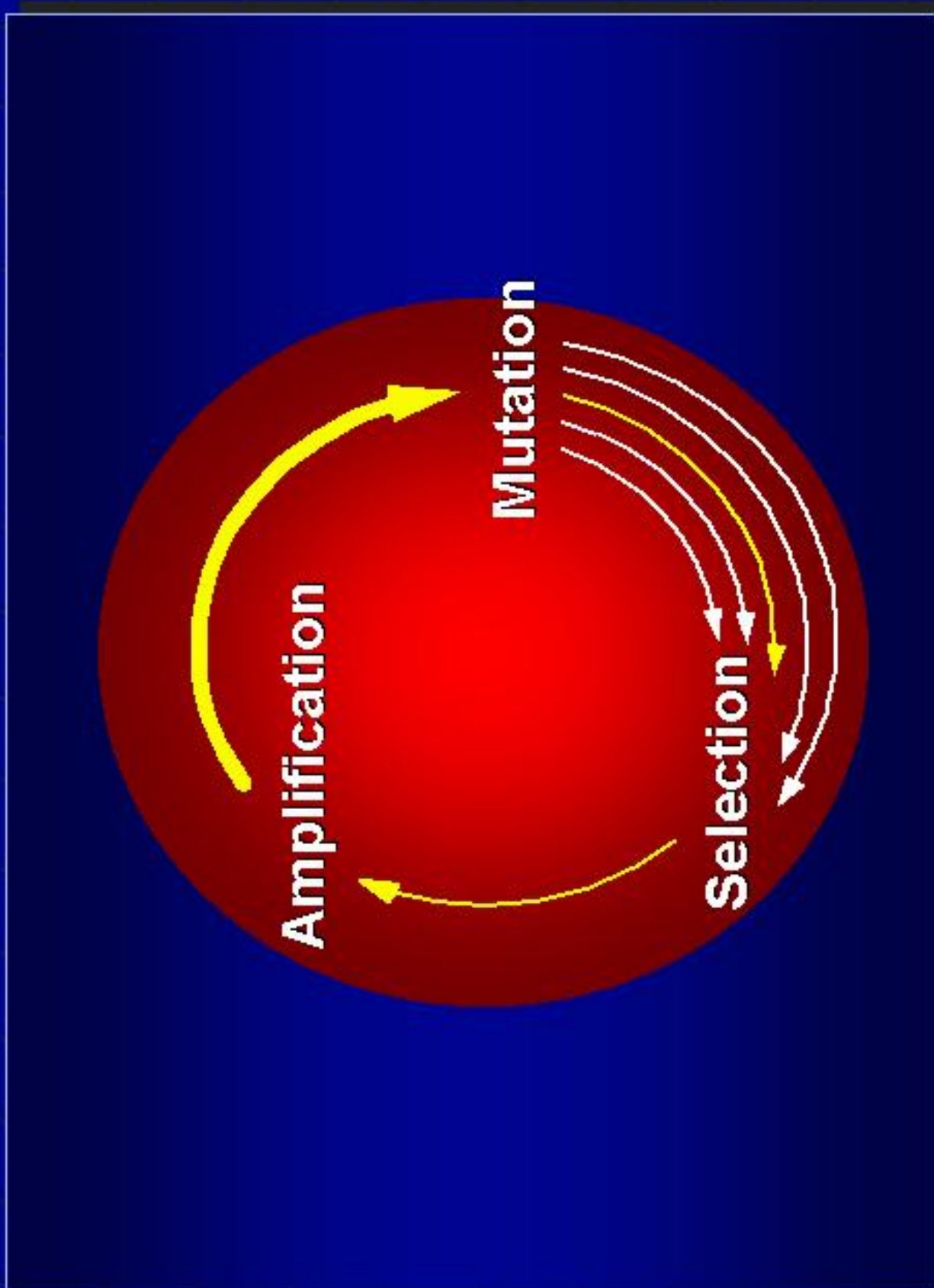


Molecular Ecology Studies with Nucleic Acids

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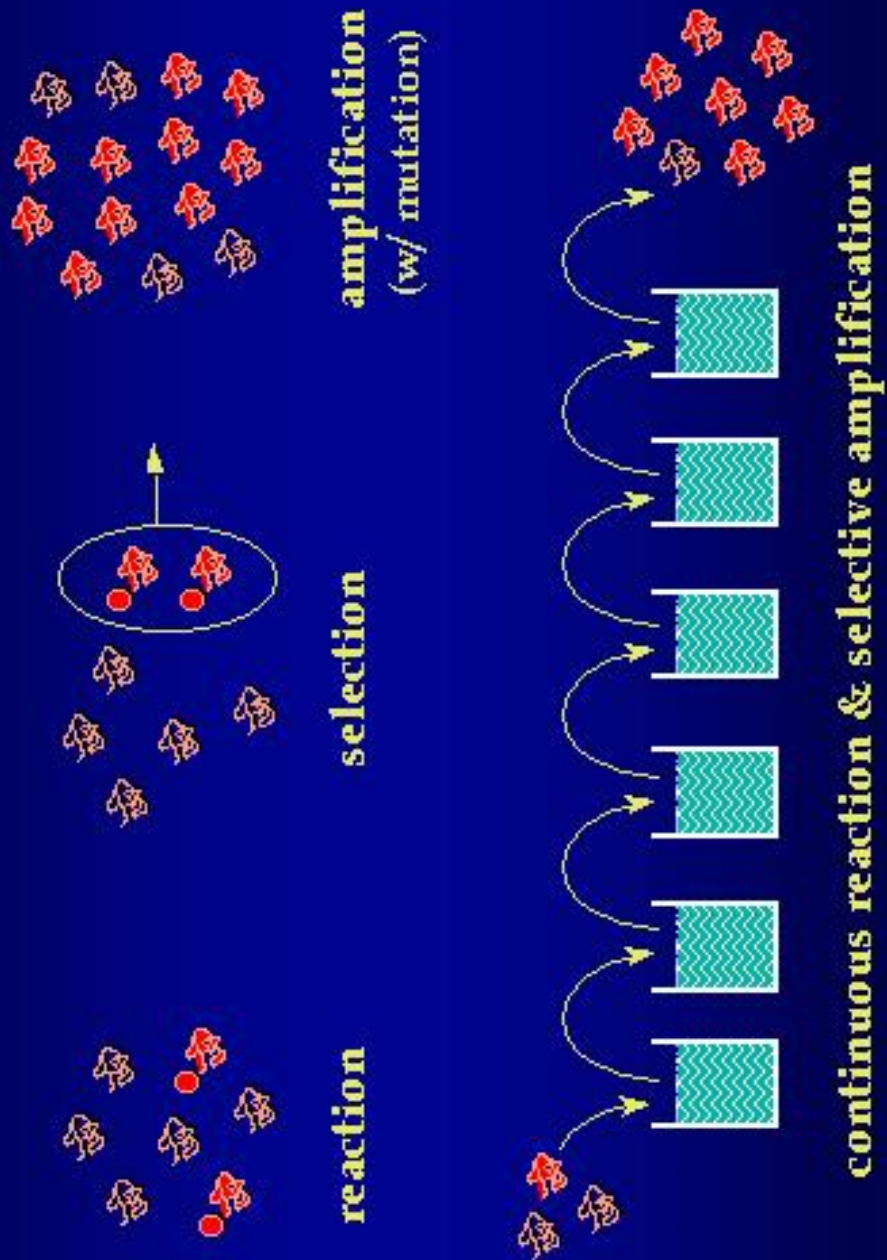
- **A molecular description of the evolution of resistance**

Ordoukhanian, P. and Joyce, G.F. *Chem. Biol.*, **6**, 881-889 (1999)

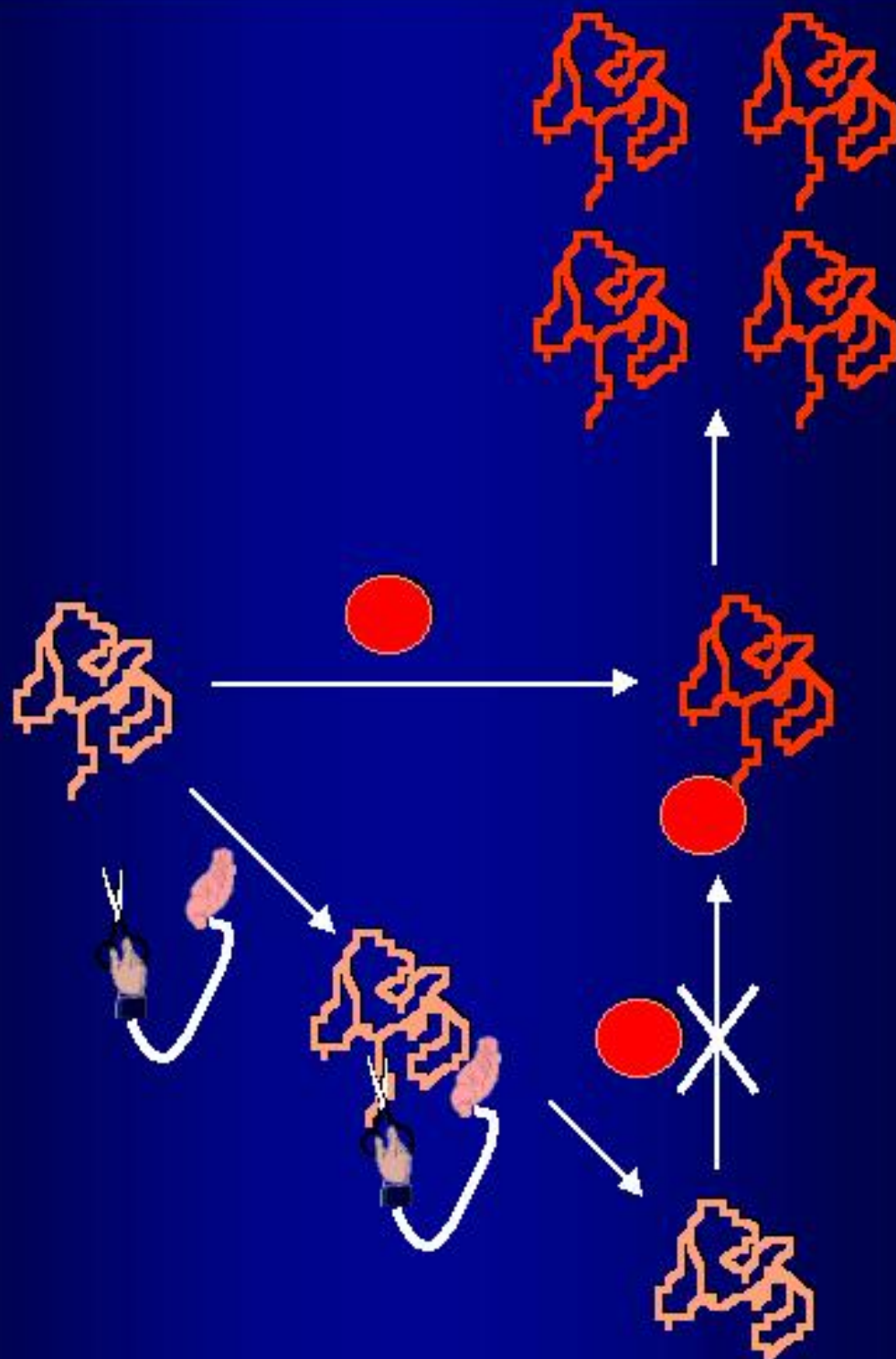
- **Non-unity molecular heritability demonstrated by continuous evolution *in vitro***

Schmitt, T. and Lehman, N. *Chem. Biol.*, **6**, 857-869 (1999)

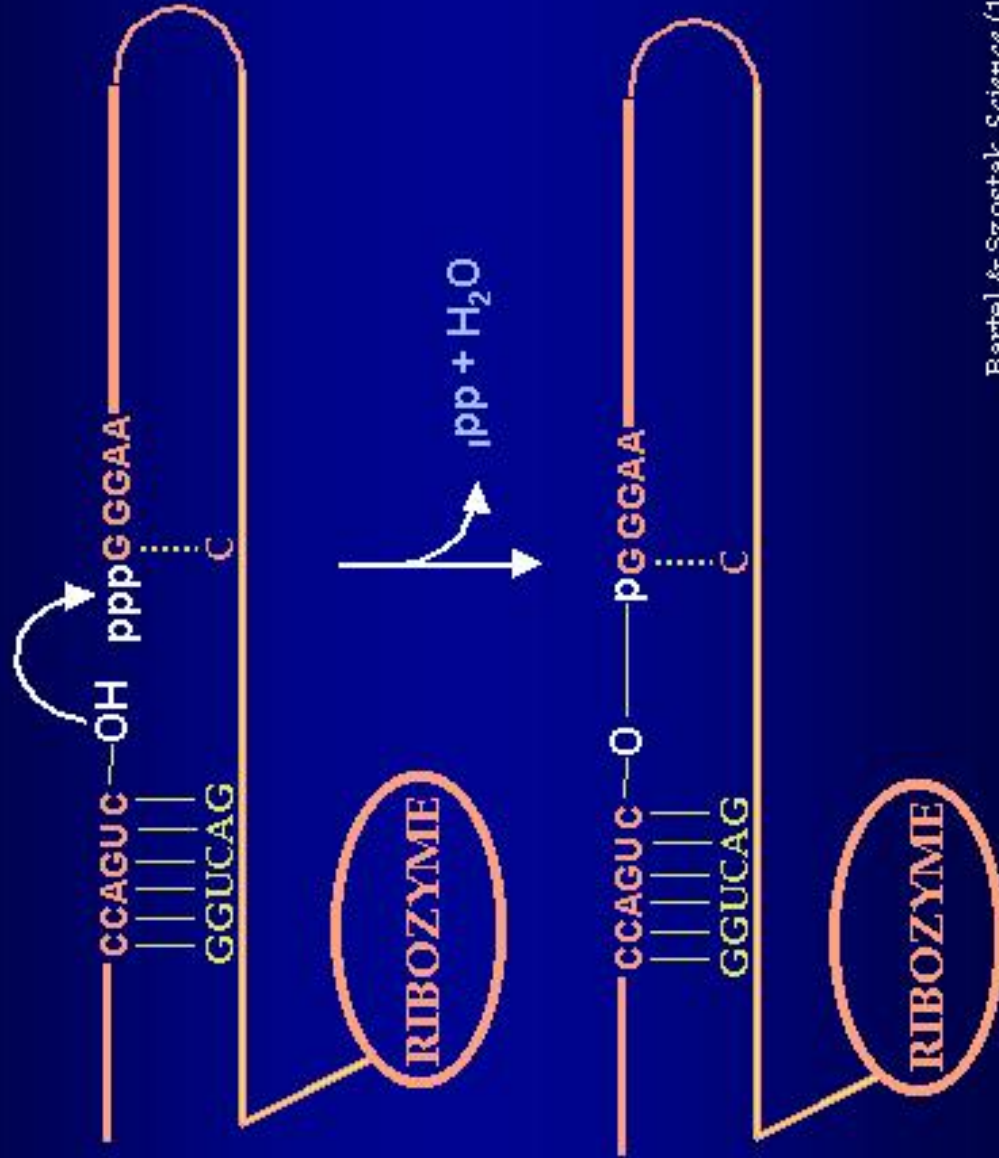
Stepwise vs. Continuous Evolution



Eluding a toxicant for survival

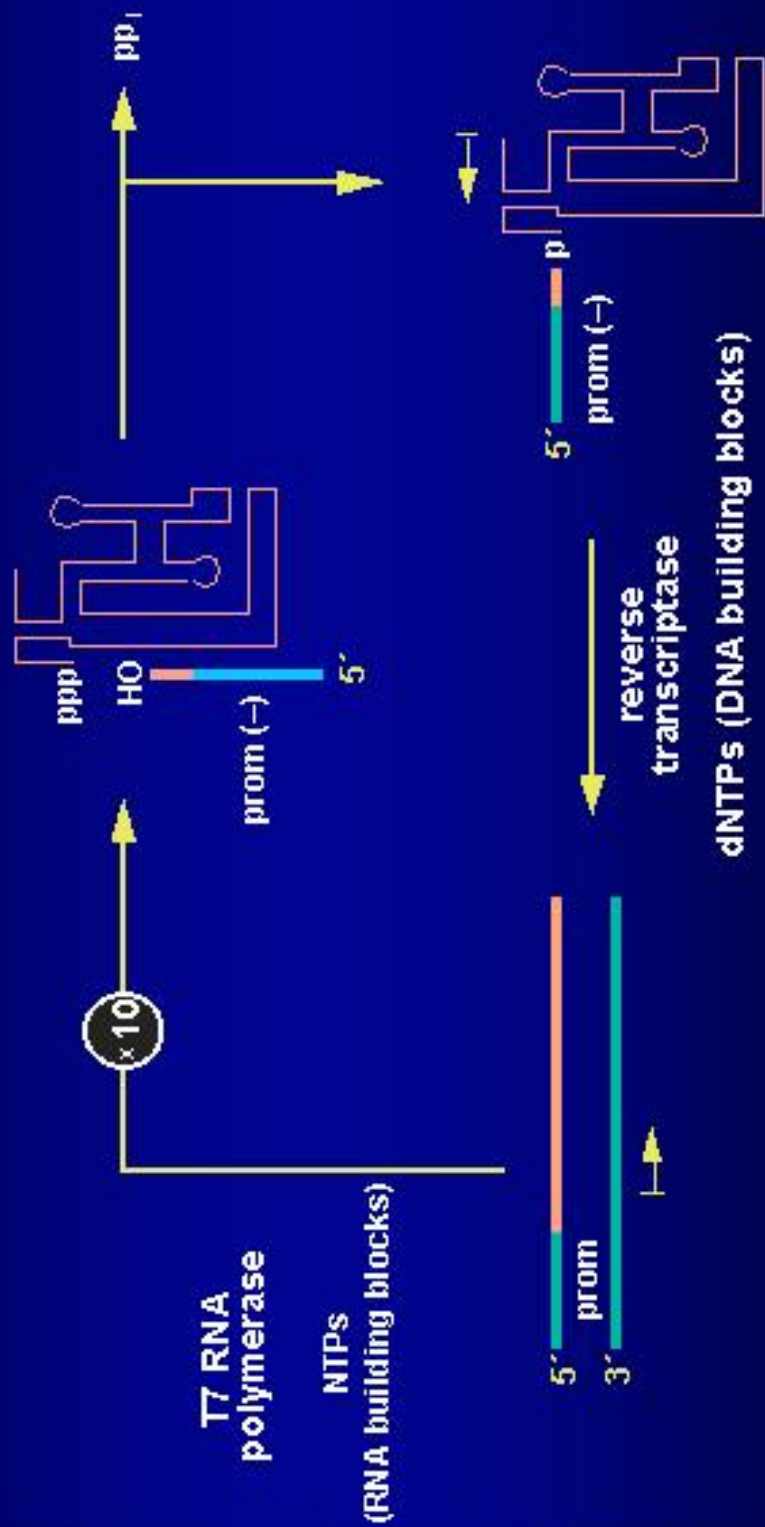


Class I Ligase Ribozymes



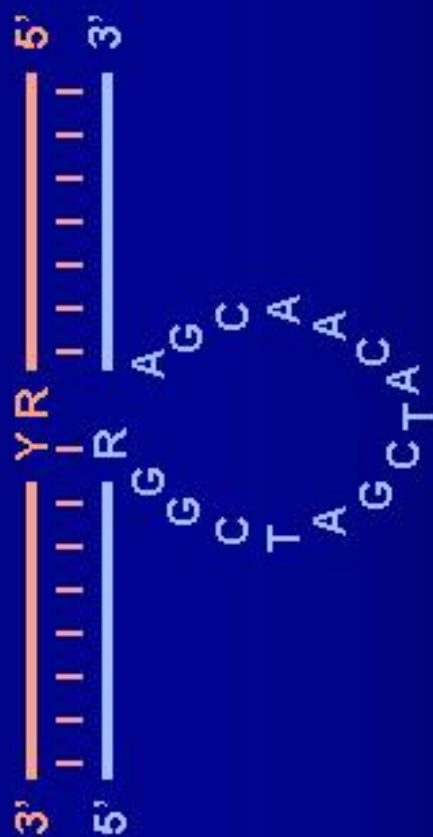
Bartel & Szostak, *Science* (1993)
Eklund, Szostak, and Bartel, *Science* (1995)

Coupled Catalysis / Amplification



M. Wright and G.F. Joyce, *Science*, **276**, 614-7 (1997)

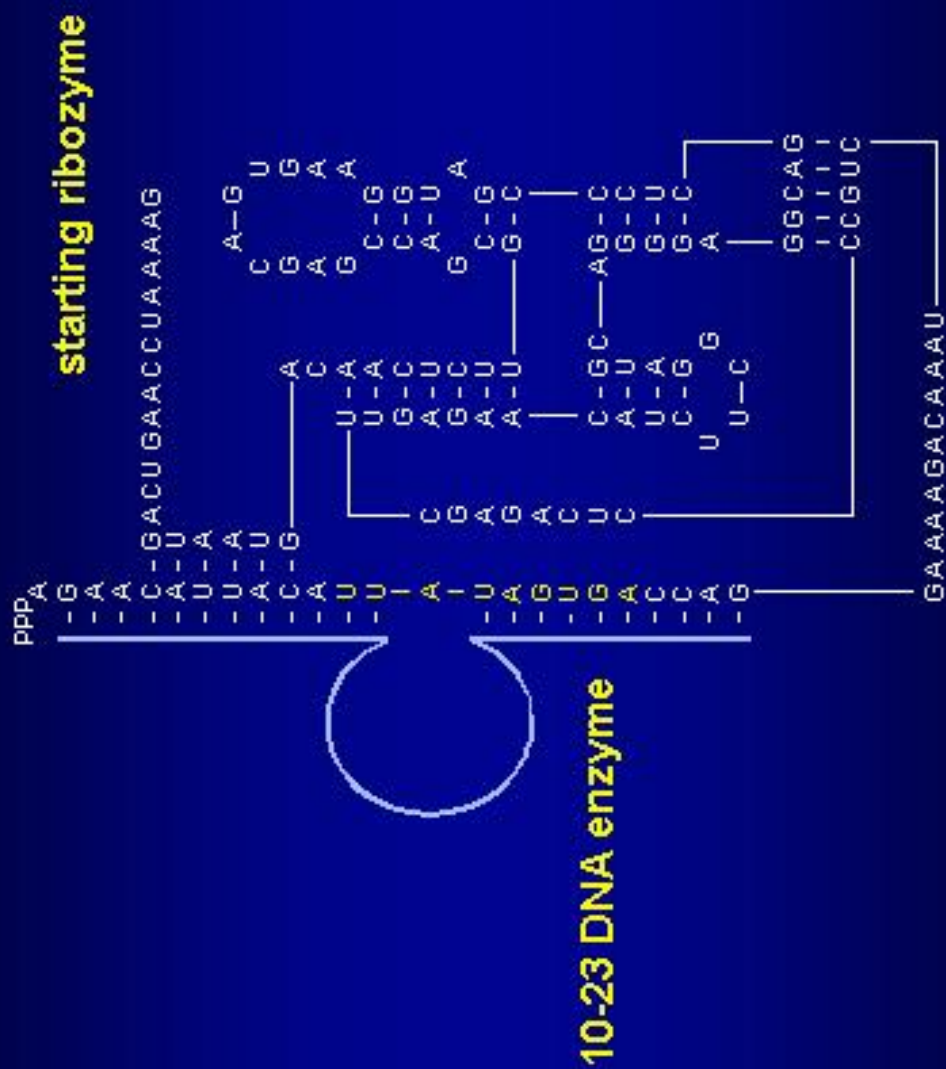
10-23 DNA enzyme

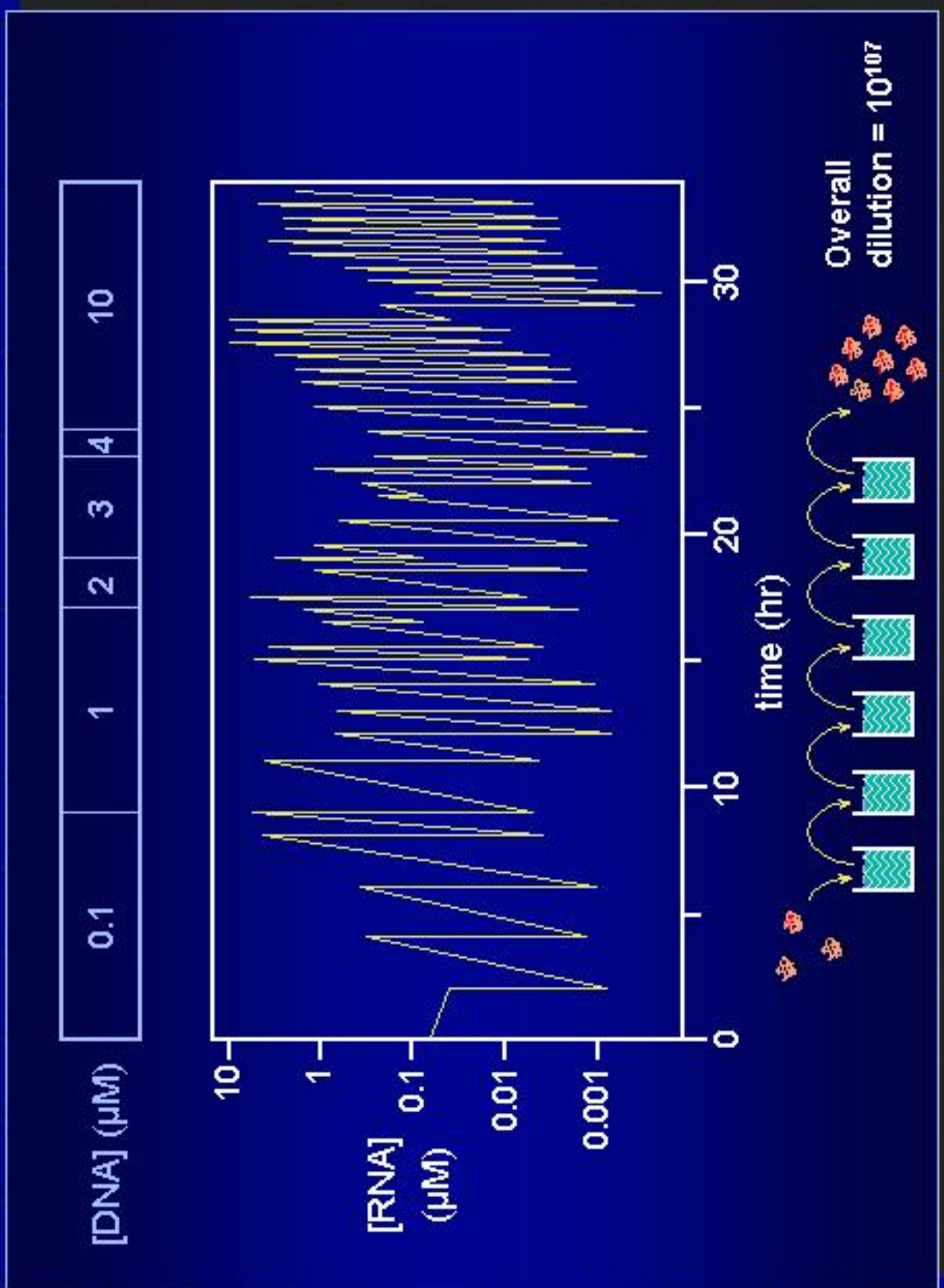


Y = U or C

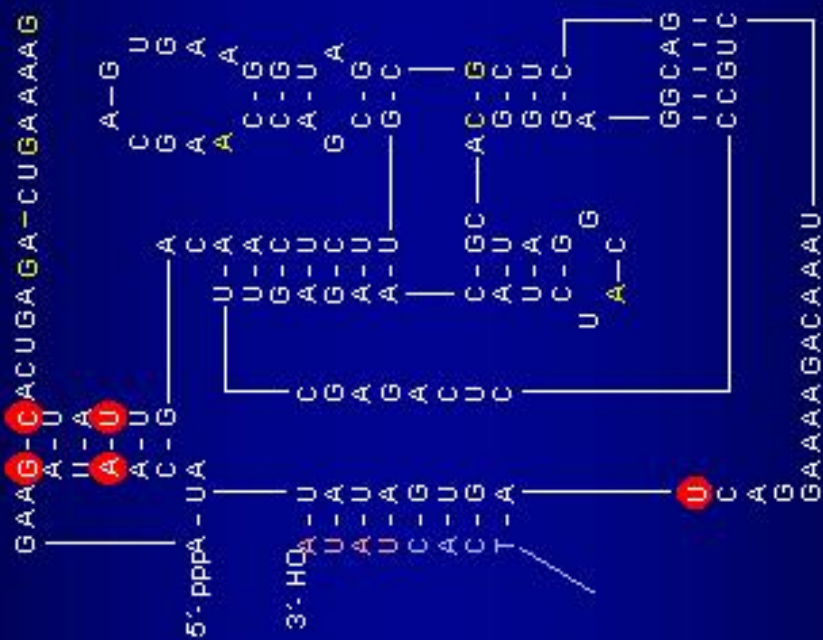
R = A or G

S. Santoro and G.F. Joyce, *PNAS*, **94**, 4262-6 (1997)

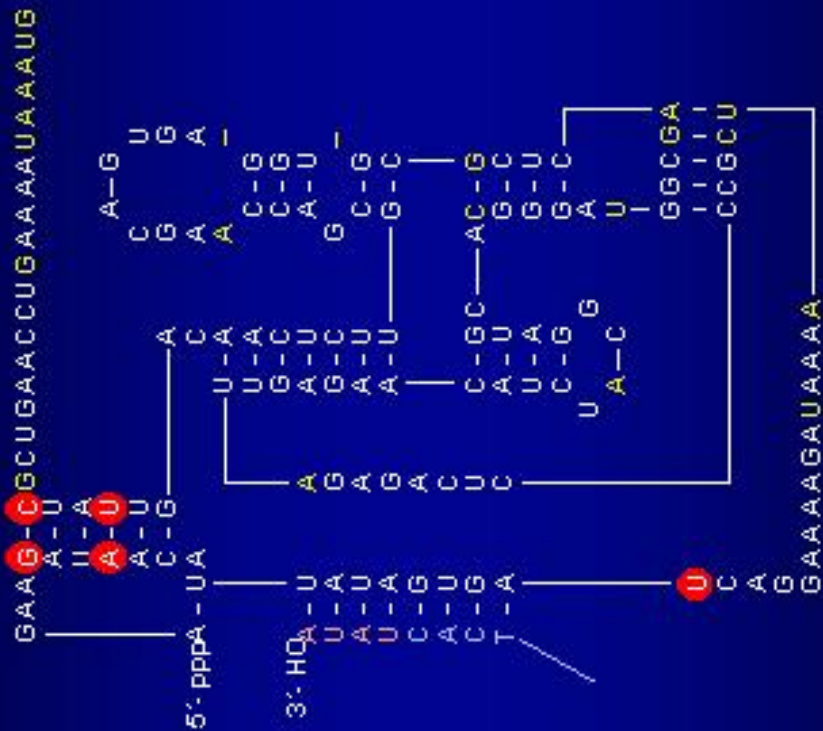


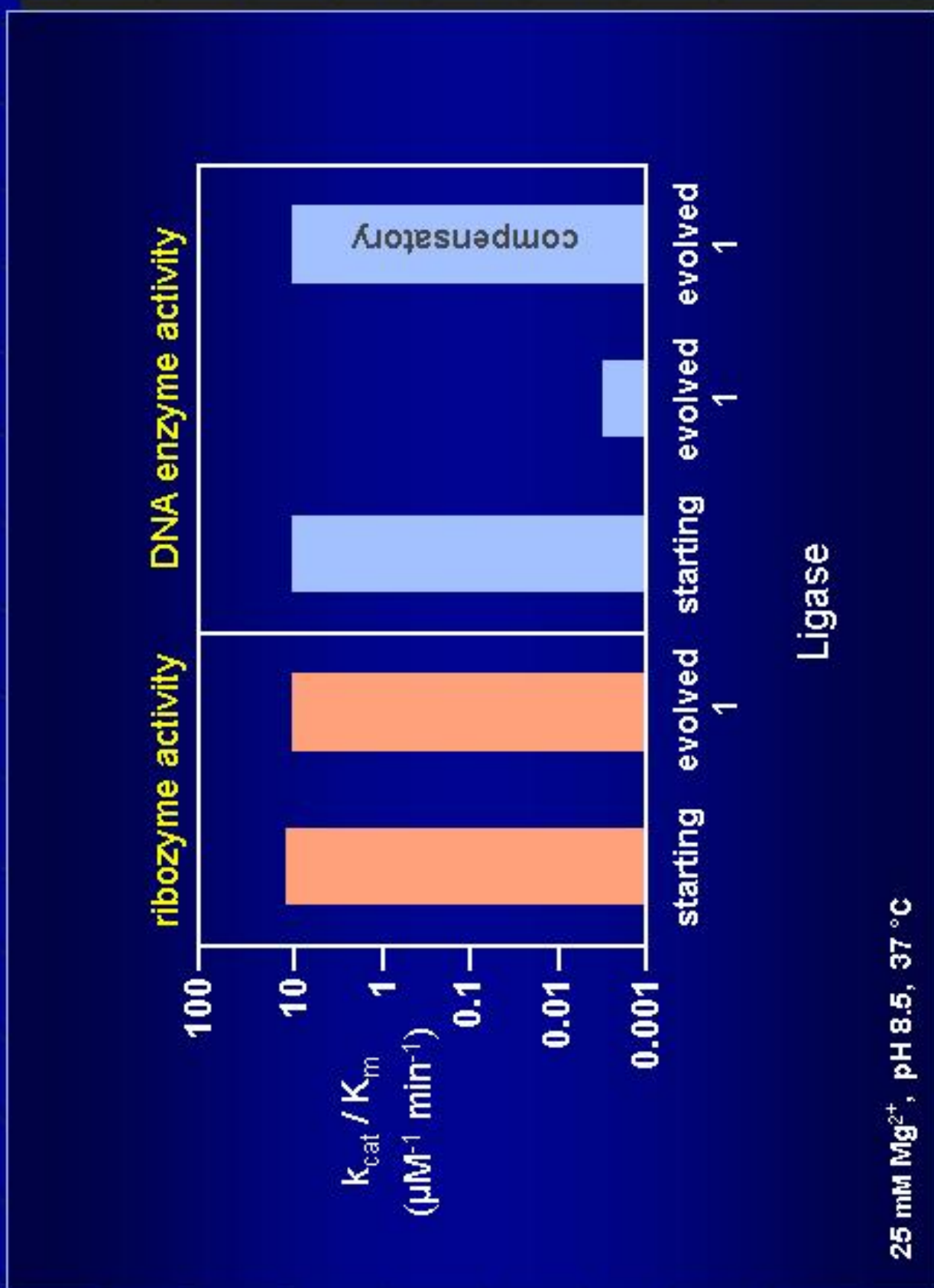


Evolved ligase 1

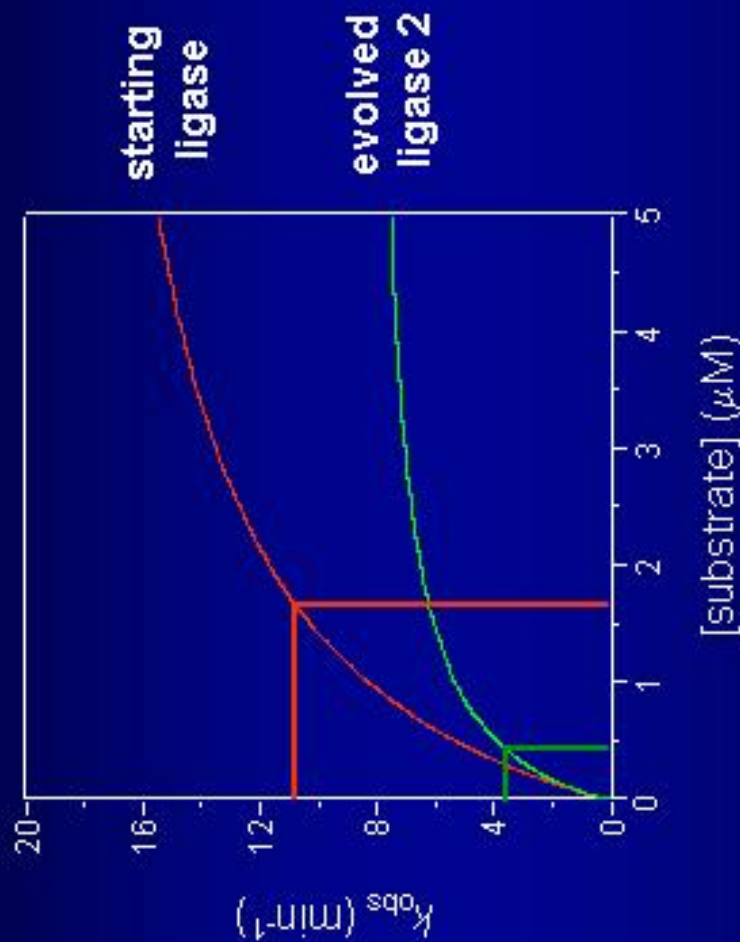


Evolved ligase 2





Comparison of K_m 's for Starting and Evolved Ligase 2



$[\text{substrate}]_0 = 2.5 \mu\text{M}$

starting

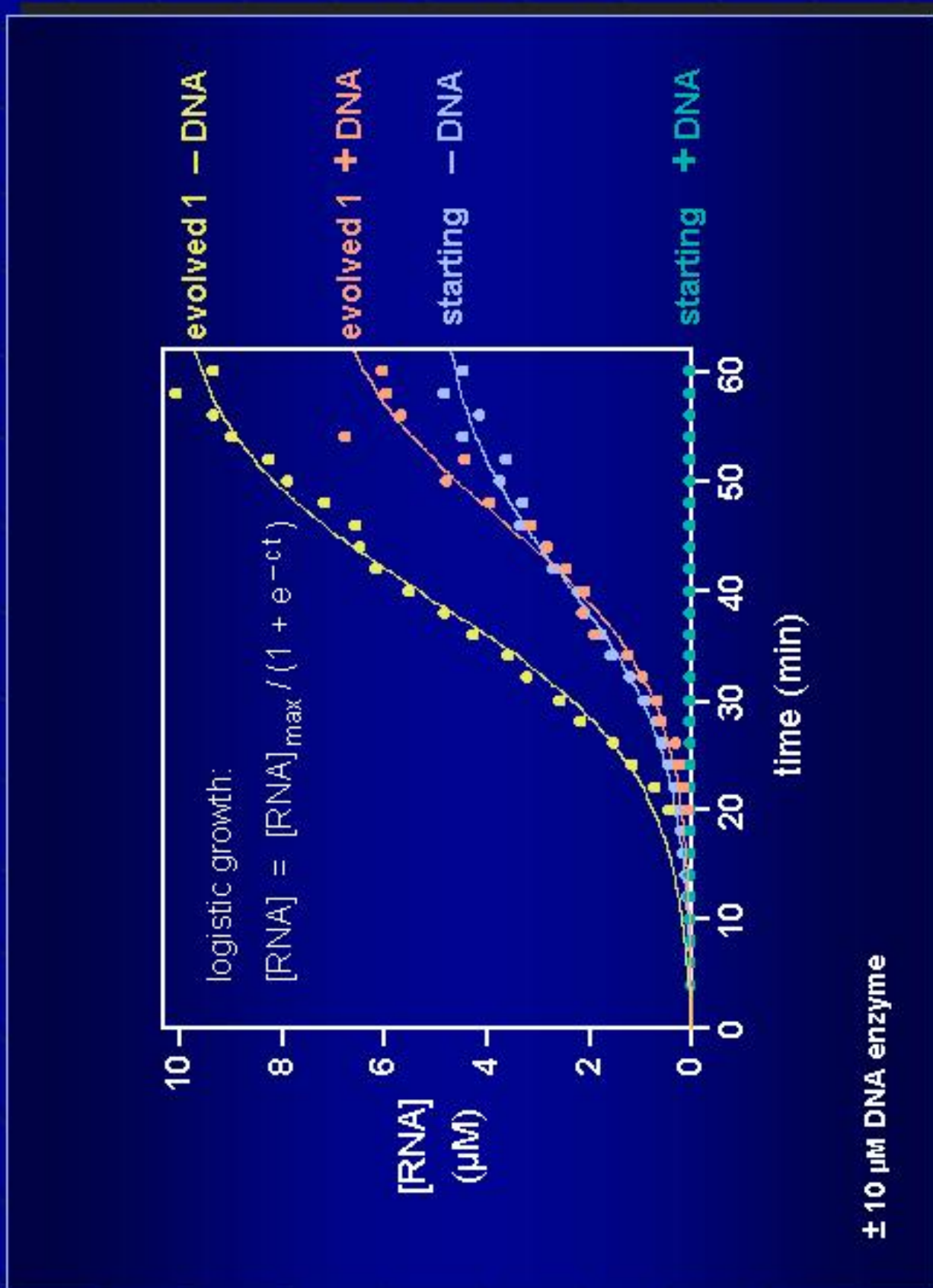
evolved 2

60% saturated

80% saturated

25 mM Mg^{2+} , pH 8.5, 37 °C

K_m = concentration of substrate where the rate is half maximal.



Predicting the Growth Rate in the Presence of the DNA enzyme

- The growth rate is dependent upon the catalytic efficiency of the ligase and the DNA enzyme.
- Comparing the specificity of ligase with its substrate vs. the DNA enzyme for cleaving the ligase .

$$\begin{aligned} \frac{v_{\text{ligase}}}{v_{\text{DNA enzyme}}} &= \frac{(k_{\text{cat}} / K_m)_{\text{ligase}} \bullet [\text{substrate}]}{(k_{\text{cat}} / K_m)_{\text{DNA enzyme}} \bullet [\text{DNA enzyme}]} \\ &= \frac{(20 \text{ min}^{-1} / 1.7 \times 10^{-6} \text{ M}^{-1} \text{ min}^{-1})(2.5 \text{ } \mu\text{M})}{(0.4 \text{ min}^{-1} / 4.8 \times 10^{-8} \text{ M}^{-1} \text{ min}^{-1})(10 \text{ } \mu\text{M})} \\ &= \underline{\underline{0.3}} \end{aligned}$$

- Growth rate in the absence of DNA enzyme = 0.13 min^{-1}
- Predicted growth rate with DNA enzyme = $(0.3)(0.13) = \underline{\underline{0.04 \text{ min}^{-1}}}$
- Observed growth rate with DNA enzyme = $\underline{\underline{0.06 \text{ min}^{-1}}}$

Summary

Two mechanisms of ligase resistance

- **Alteration of toxicant binding site, without disruption of the substrate binding site or catalytic function, resulted in a 2,000-fold lower susceptibility to the toxicant.**
- **Greater initial substrate saturation of the evolved 2 ligase protects the ribozyme by blocking the toxicant binding site.**

- **A molecular description of the evolution of resistance**

Ordoukhanian, P. and Joyce, G.F. *Chem. Biol.*, **6**, 881-889 (1999)

- **Non-unity molecular heritability demonstrated by continuous evolution *in vitro***

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Heritability of a Trait

$$0 \leq H^2 \leq 1$$

It is a measure of the response of a population's phenotypic variation of a trait after an evolutionary period, which is dependent upon the genotypic variation that existed before the period.

$H^2 = 1$, the trait is more easily affected by natural selection during the evolution process.

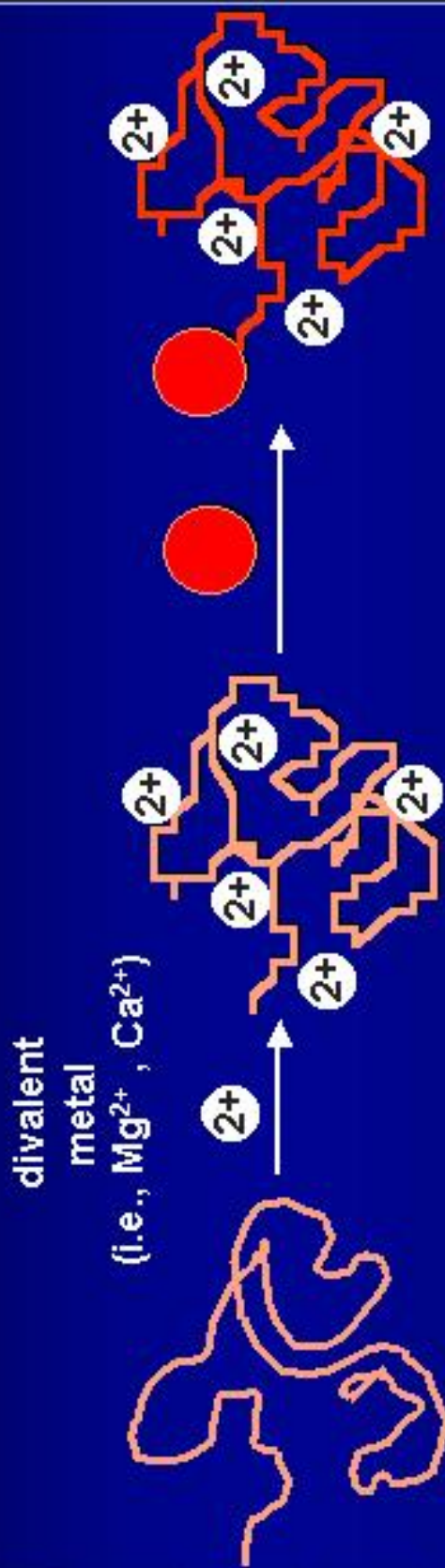
Non-unity heritability, the trait responds slower to natural selection in the evolution process.

Multiple Conformations vs. a Single Conformation on a Fitness Landscape

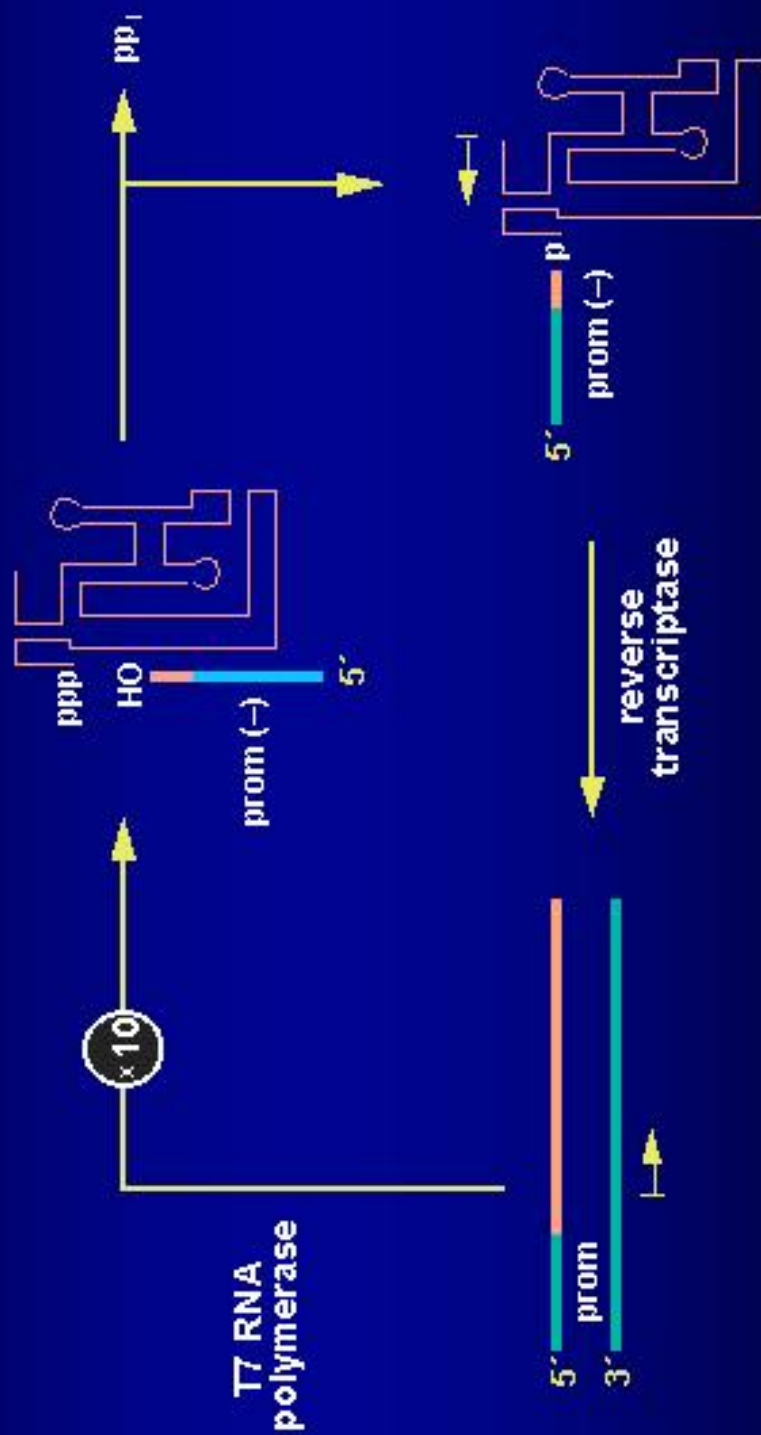


Phenotype = Fitness = Σ (fraction of conformer)(conformer reactivity)

**Nucleic acid catalysts typically require divalent
Metals for activity**

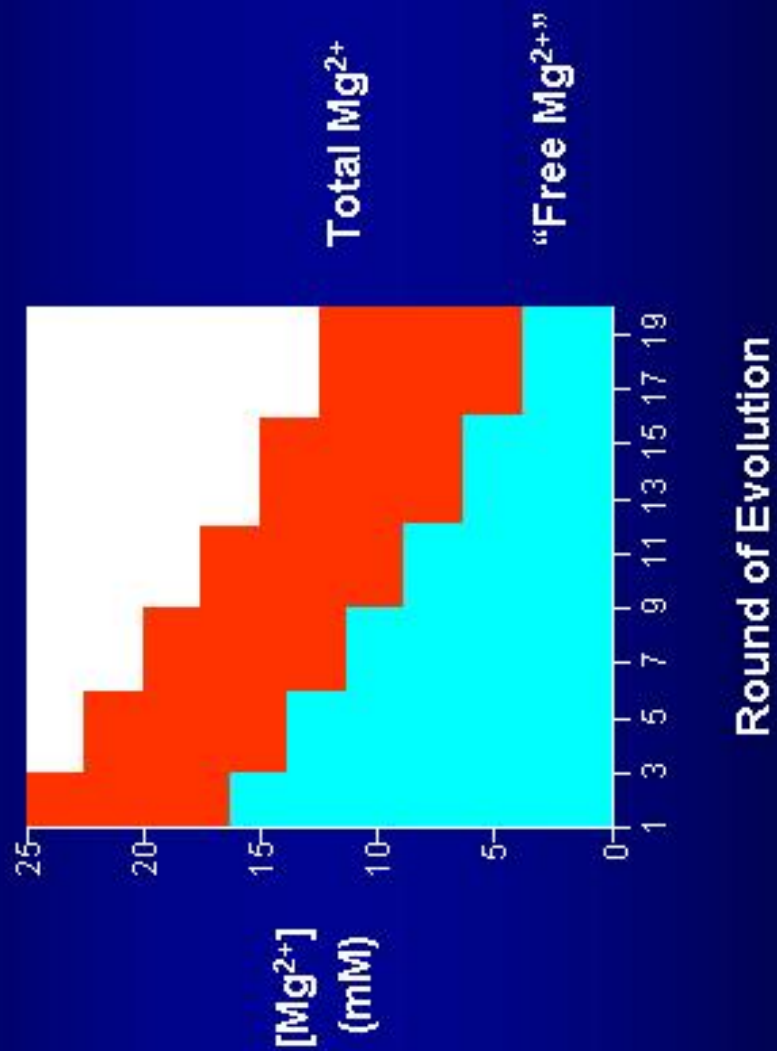


In vitro Continuous Evolution Process



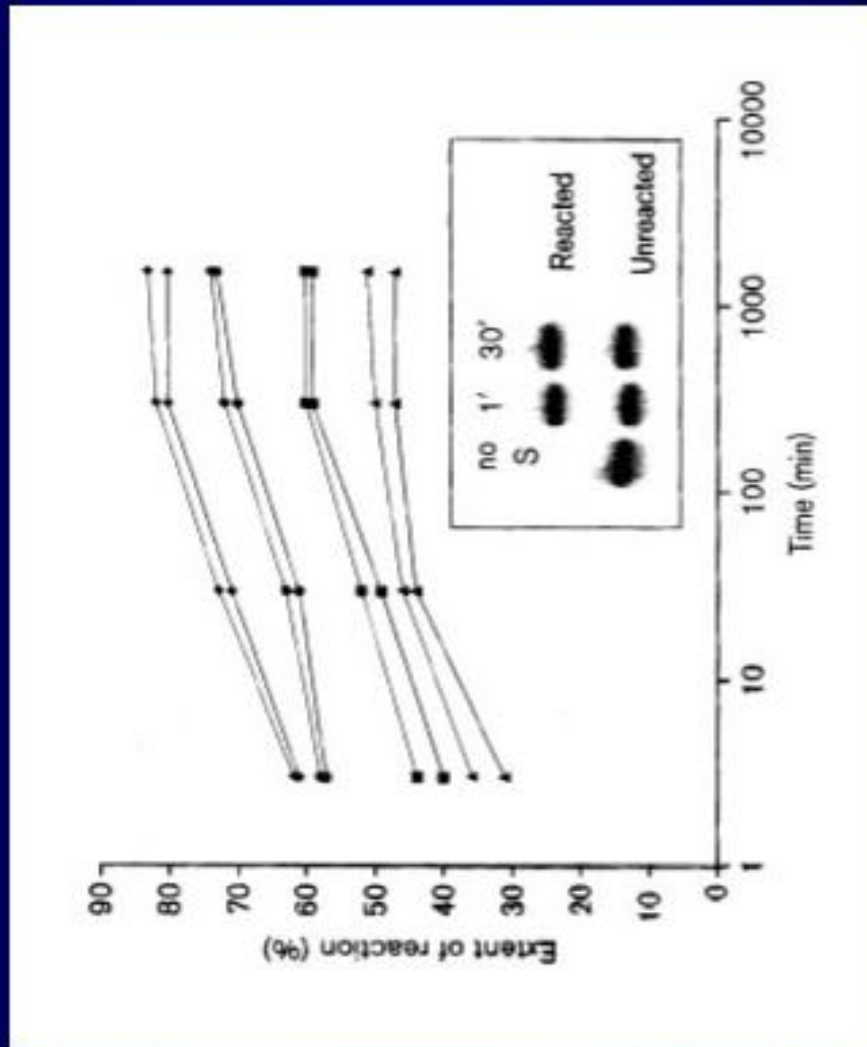
M. Wright and G.F. Joyce, *Science*, **276**, 614-7 (1997)

**Concentration of Magnesium available to the ribozyme
was lowered during the Evolution**

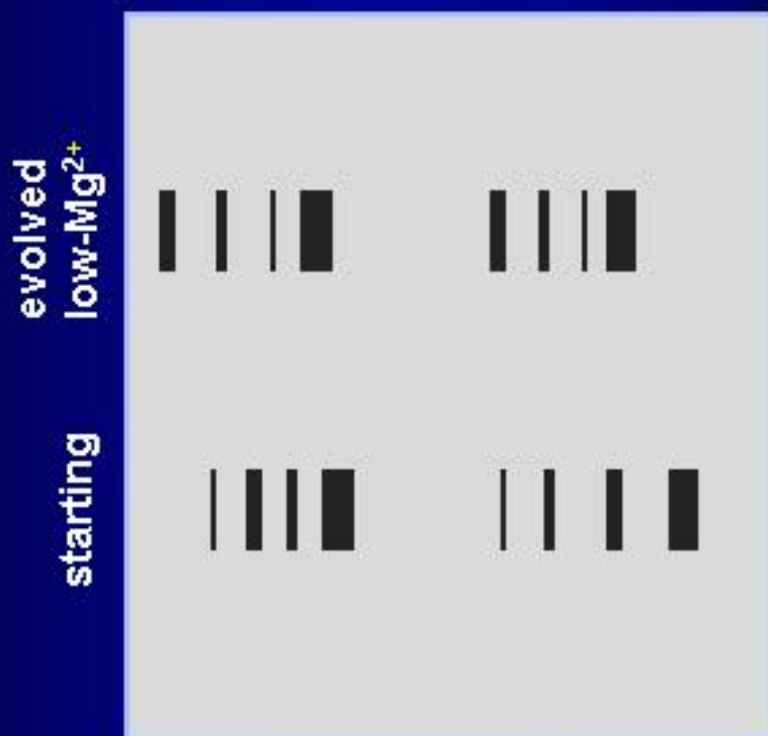


Maximum Extent of the Ligases

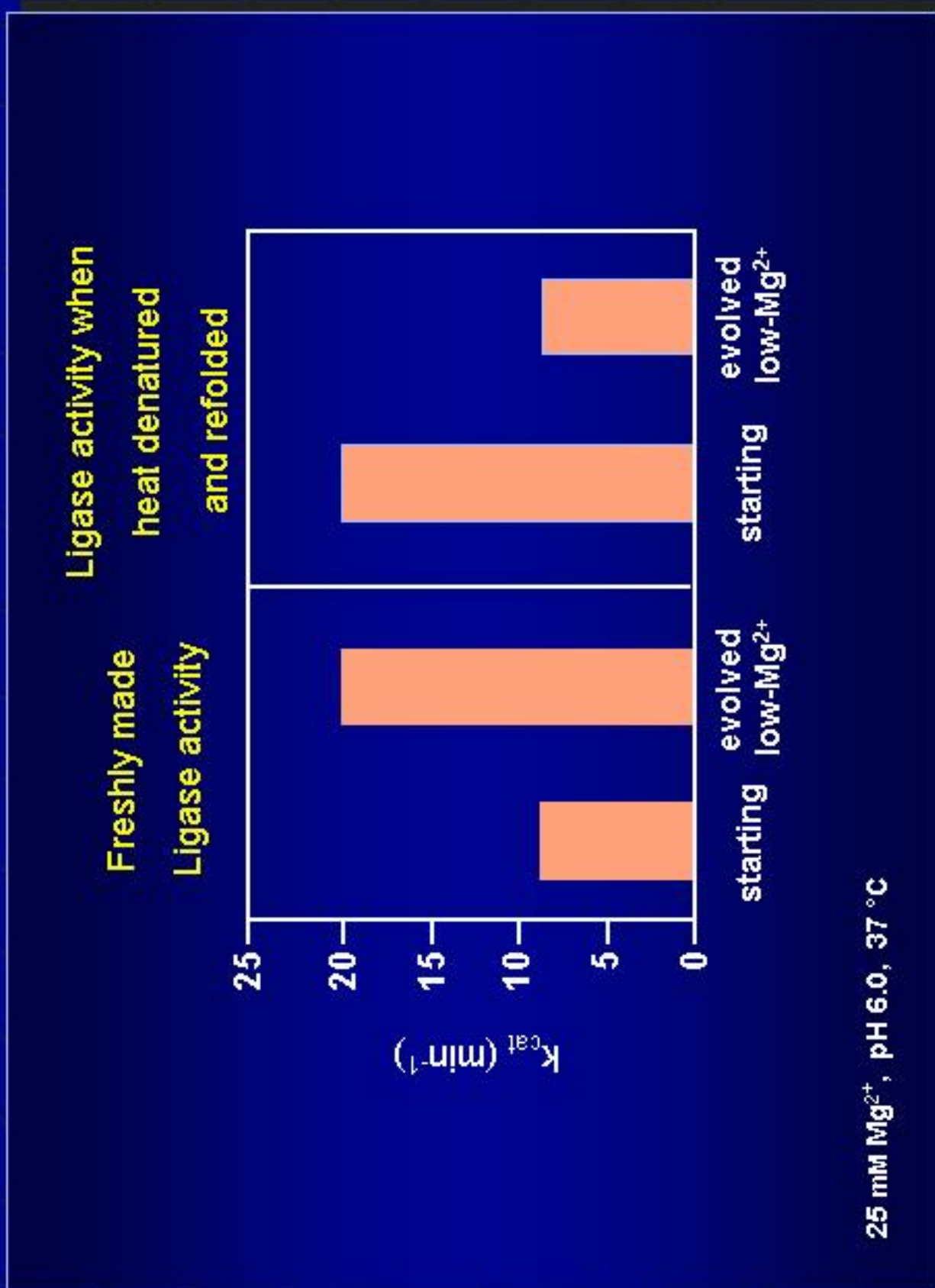
<u>Ligase</u>	<u>[Mg²⁺]</u>
evolved low-Mg ²⁺	25 mM
evolved low-Mg ²⁺	10 mM
starting	25 mM
starting	10 mM



Both the starting and the evolved low-Mg²⁺ ligases have multiple conformations with varying reactivity



Non-denaturing Polyacrylamide gel electrophoresis



Activity of the Dominant Conformer when Transcribed in the Presence and Absence of Substrate

	substrate	
	(+)	(-)
starting ligase	inactive	active
Evolved low-Mg ²⁺	active	active

Calculating the Heritability of the Trait

$$H^2 = R / S$$

Mean phenotype, z = Σ (amount of conformer)(conformer reactivity)

Starting ligase, $z_{\text{before}} = 2.1\%$

Evolved low-Mg²⁺ ligase, $z_{\text{after}} = 5.9\%$

Where **R** is the response to the evolution.

R = (mean phenotype after the evolution) — (mean phenotype before the evolution)
= 5.9% — 2.1% = 3.8%

And **S** is the maximum possible response to the evolution.

S = total max. response — starting response
= 100% — 2.1% = 97.9%

So, $H^2 = 0.038 / 0.979 = \underline{0.04}$

Summary

- $H^2 = 0.04$, is close to zero.
- The overall response to the evolution experiment was small, and so, the heritability of the trait of conformational reactivity responds slowly to evolutionary pressures.
- However, there was a measurable response:
 - 1) The starting ligase and the evolved low-Mg²⁺ were both conformationally heterogeneous and the various conformers had differing reactivity.
 - 2) The evolved low-Mg²⁺ ligase was able to adopt more active conformations as shown by the maximum extent experiment.
 - 3) The evolved low-Mg²⁺ was able to fold better “on the fly” during transcription.
 - a) Kinetics: the evolved low-Mg²⁺ ligase was faster when transcribed and slower when denatured and refolded. The reverse was true for the starting ligase.
 - b) The substrate was able to inhibit the folding of the starting ligase if present during transcription, but not the evolved low-Mg²⁺ ligase.

Conclusions

- The use of isothermal amplification methods can be used to study a variety of ecological problems on reasonable time scales.
- Since these methods make use of nucleic acids, whose sequence can be obtained and activity quantitated, it allows for a molecular level of description of the changes that occurred during the course of the evolution experiment.
- As a result, mechanisms can be proposed to account for these changes.

**Gerald F. Joyce and
the other members of the Joyce Laboratory**

