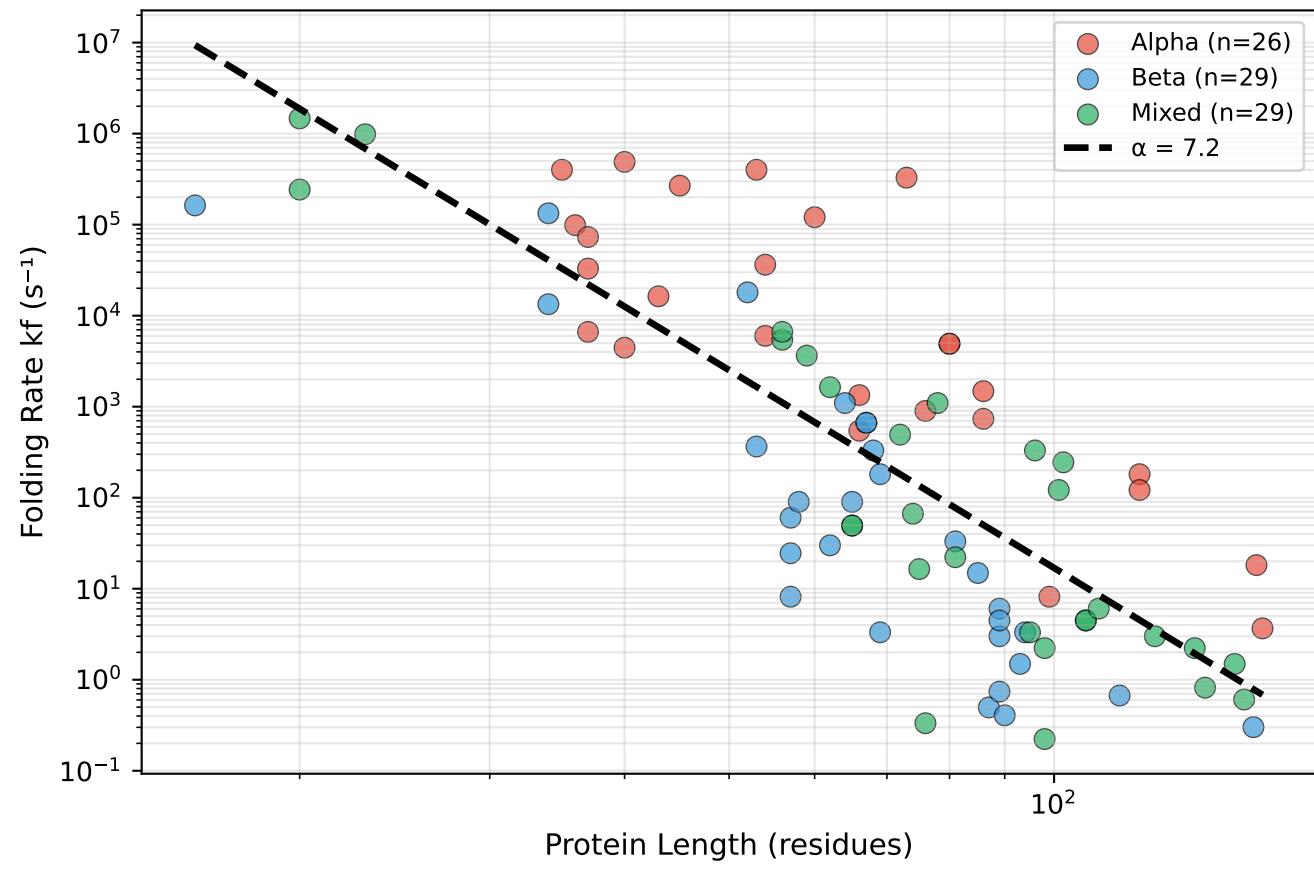
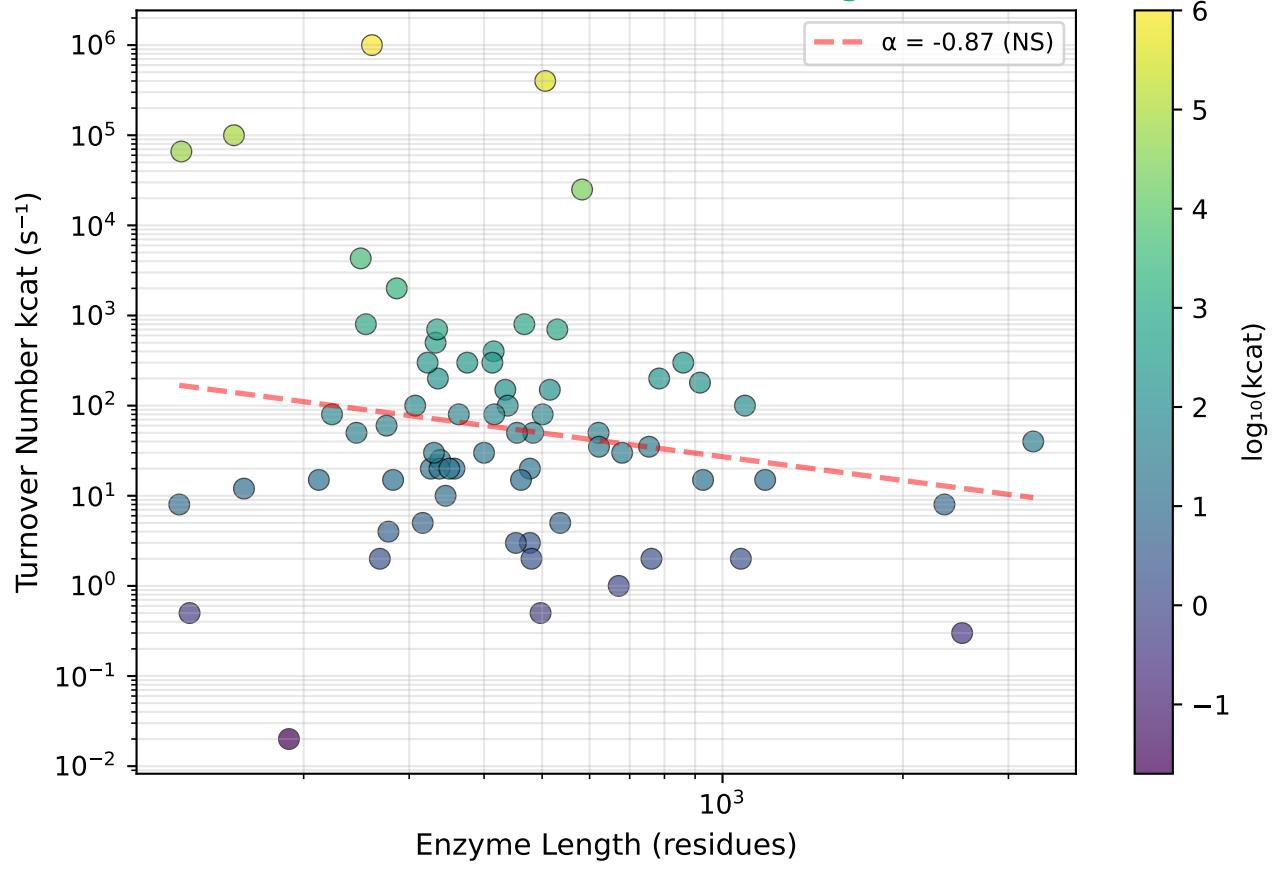


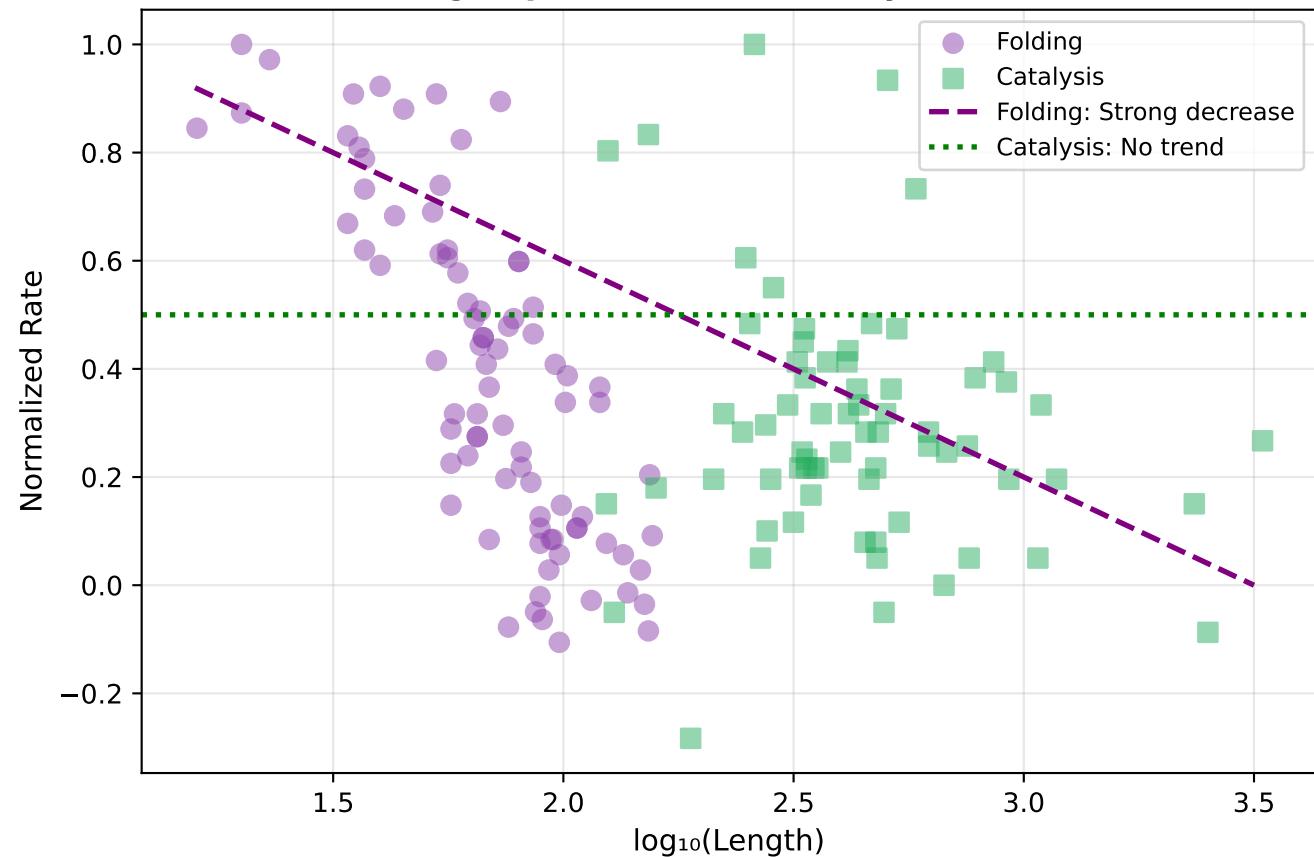
PROTEIN FOLDING: $k_f \propto L^{-\alpha}$
 $\alpha = 7.2 \pm 0.6$, $R^2 = 0.63$ (GLOBAL)



ENZYME KINETICS: k_{cat} vs L
 $\alpha = -0.87$, $R^2 = 0.032$ (LOCAL, not significant)



COMPARISON: Global vs Local Processes
Folding depends on size, catalysis does not



RTM BIOCHEMISTRY: TWO PROCESS TYPES

ANALYSIS 1: PROTEIN FOLDING

- Data points: 84
 - Size range: 16 - 156 residues
 - $\alpha = +7.2 \pm 0.6$
 - $R^2 = 0.625$ (strong correlation)
 - $p < 10^{-18}$ (highly significant)
- Interpretation: GLOBAL PROCESS
→ Entire chain must rearrange
→ Strong size dependence (larger = slower)
→ "Folding funnel" creates coherent dynamics

ANALYSIS 2: ENZYME KINETICS

- Data points: 69
 - Size range: 124 - 3300 residues
 - $\alpha = -0.87 \pm 0.59$
 - $R^2 = 0.032$ (essentially zero)
 - $p = 0.14$ (NOT significant)
- Interpretation: LOCAL PROCESS
→ Only active site matters
→ NO size dependence
→ Chemistry, not geometry, dominates

KEY RTM INSIGHT

- Folding: $\alpha \approx +7$, $R^2 \approx 0.6$ → GLOBAL (geometry matters)
- Catalysis: $\alpha \approx 0$, $R^2 \approx 0$ → LOCAL (chemistry matters)

RTM correctly distinguishes:
- GLOBAL processes (whole system involved)
- LOCAL processes (only active region matters)