



RTM BIOCHEMISTRY: TWO PROCESS TYPES	
ANALYSIS 1: PROTEIN FOLDING	
<ul style="list-style-type: none">• Data points: 84• Size range: 16 - 156 residues<ul style="list-style-type: none">• $\alpha = +7.2 \pm 0.6$• $R^2 = 0.625$ (strong correlation)• $p < 10^{-18}$ (highly significant) <p>Interpretation: GLOBAL PROCESS</p> <ul style="list-style-type: none">→ Entire chain must rearrange→ Strong size dependence (larger = slower)→ "Folding funnel" creates coherent dynamics	
ANALYSIS 2: ENZYME KINETICS	
<ul style="list-style-type: none">• Data points: 69• Size range: 124 - 3300 residues<ul style="list-style-type: none">• $\alpha = -0.87 \pm 0.59$• $R^2 = 0.032$ (essentially zero)• $p = 0.14$ (NOT significant) <p>Interpretation: LOCAL PROCESS</p> <ul style="list-style-type: none">→ Only active site matters→ NO size dependence→ Chemistry, not geometry, dominates	
KEY RTM INSIGHT	
<ul style="list-style-type: none">• Folding: $\alpha \approx +7, R^2 \approx 0.6$ → GLOBAL (geometry matters)• Catalysis: $\alpha \approx 0, R^2 \approx 0$ → LOCAL (chemistry matters) <p>RTM correctly distinguishes:</p> <ul style="list-style-type: none">- GLOBAL processes (whole system involved)- LOCAL processes (only active region matters)	