



Rhythmic Biochemistry

Enzyme as a Coherence Instrument and a Practical Index for α in Living Catalysis

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Abstract

Enzymatic catalysis is usually framed as geometry and energetics—"lock-and-key," transition-state stabilization, and conformational selection. Here we recast enzymes as mesoscale coherence instruments within the Temporal Relativity in Multiscale Systems (RTM) framework, where characteristic times scale with size L as a power law $\tau \propto L^\alpha$. We posit that active sites engineer high- α microenvironments that filter reaction pathways by rhythm rather than shape alone. We derive an enzymatic scaling estimator $\alpha_{\text{enz}} = -d(\log k_{\text{app}})/d(\log L)$ with k_{app} the apparent rate constant measured across controlled confinement scales L (nanopores/crowding/cavities), and introduce a Rhythmic Biochemistry Coherence Index (RBCI) (0–1) that integrates slope (α), spin-selective transport (CISS), vibrational coherence, and variance reduction under on-resonance driving.

Computational validation. We implement and validate the RTM enzyme framework through three simulation suites. S1 demonstrates that RTM-modified Michaelis-Menten kinetics ($k_{\text{cat}} \propto L^{(-\alpha)}$) produces distinct kinetic signatures across transport classes, with α recoverable from simulated confinement data within 0.5% error. S2 validates the estimation methodology: the α_{enz} estimator is robust to measurement noise up to $\sigma \approx 0.30$, requires only ≥ 3 confinement scales, and discriminates transport classes (diffusive $\alpha \approx 2.0$ vs. hierarchical $\alpha \approx 2.3$) with Cohen's $d = 3.12$. The data collapse test shows $11\times$ worse coefficient of variation when using incorrect α . S3 predicts confinement-tunable substrate selectivity: for substrates with different α values, selectivity ratios can shift by $2\text{-}3\times$ across the 10–100nm confinement range, with calculable crossover lengths where selectivity inverts.

We outline falsifiable tests—slope stability, data collapse ($k_{\text{app}} \times L^\alpha = \text{constant}$), and class switching under acoustic forcing—together with controls that separate thermal and mixing artefacts. The program predicts bands of α consistent with hierarchical/fractal transport ($\alpha \approx 2.1\text{--}2.5$) and links allosteric regulation, and spin selectivity under a single multiscale law; if refuted, they provide sharp constraints on when and why enzymes deviate from RTM scaling. The framework is operational, preregrowable, and immediately testable with standard biophysical toolkits.

Preliminary empirical validation⇒(APPENDIX B). We validate the Rhythmic Biochemistry framework through a comparative systematic analysis of 153 empirical data points, contrasting global topological processes (protein folding) against localized catalytic events (enzyme kinetics). The analysis demonstrates that the RTM coherence exponent α successfully distinguishes between these two fundamental biological operational regimes.

For protein folding ($n = 84$), where the entire polypeptide chain must structurally coordinate, the system operates in a highly coherent, topology-driven regime yielding $\alpha = +7.2 \pm 0.6$ ($p < 10^{-18}$). This extreme hyper-scaling mathematically captures the highly directed "folding funnel" that resolves Levinthal's paradox. Conversely, enzyme kinetics ($n = 69$) reveals no significant dependence on the global macroscopic size of the enzyme ($\alpha = -0.9 \pm 0.6, p = 0.14$), confirming that catalysis is a highly localized chemical process structurally decoupled from the overall molecular mass. This validates α as a precise diagnostic metric to differentiate between global structural resonance and localized chemical reactions in biological systems.

1. Introduction

1.1 Motivation: from shapes to rhythms

Enzymes accelerate reactions by orders of magnitude, yet purely geometric narratives—lock-and-key, induced fit—do not fully explain rate modulation across crowding, confinement, or long-range allostery. Modern measurements reveal structured fluctuations, long-lived vibrational modes, spin-selective currents in chiral matrices (CISS), and rate variability that narrows under specific driving conditions. These observations suggest that **structure orchestrates time**, not only barriers.

The **Multiscale Temporal Relativity (RTM)** framework treats characteristic times T as scaling with size L via a power law $T \propto L^\alpha$, where the exponent α is an **operational observable** tied to a system's **universality class** (local vs. long-range transport, integer vs. fractal topology, quantum-confined regimes). RTM distinguishes **slope** (the exponent α) from **intercept** (clock/redshift/gain), enabling comparisons across environments without conflating baseline shifts with dynamical mechanism.

1.2 Central hypothesis

We hypothesize that **active sites are mesoscale coherence cavities that raise the local α relative to the surrounding solvent/cell**, thereby filtering reaction trajectories by rhythm. Concretely:

- Smaller, more coherent microenvironments complete characteristic acts faster **by scaling**, not by temperature alone.
- Allostery acts primarily by **tuning α** (coherence/transport class), with conformational changes as the actuator.
- Chiral media exhibiting CISS are empirical signatures of **high- α** transport regimes.

1.3 An operational program

We propose two complementary observables.

1. Enzymatic scaling estimator

$$\alpha_{\text{bio,enz}} = - \frac{d \log k}{d \log L} \Big|_{\text{isothermal, fixed ionic strength, off-resonance control}}$$

obtained by measuring apparent rates k while varying an **effective confinement scale** L (e.g., nanoporous matrices of known pore size, tunable crowding, or engineered cavities). Stability of $\alpha_{\text{bio,enz}}$ over at least one decade in L , plus **data collapse** of k when rescaled by L^{α^*} , is the primary falsification test.

2. Rhythmic Biochemistry Coherence Index (RBCI) (0–1), a composite index that aggregates:

- **Slope:** a normalized map of $\alpha_{\text{bio,enz}}$ over a biologically plausible band;
- **Spin signature (CISS):** polarization/asymmetry of spin-dependent transport through the protein/chiral film;
- **Vibrational coherence:** fraction of spectral power in coherent modes (Raman/IR or pump–probe metrics);
- **Variance reduction under on-resonance driving:** decrease of $\text{Var}(k)$ when applying a non-thermal periodic drive matched to the system’s coherence window, relative to off-resonance.

RBCI complements $\alpha_{\text{bio,enz}}$: slope tests the **law of scale**, whereas RBCI tests **mechanistic coherence** expected to co-vary with high- α transport.

1.4 Predictions and falsifiable outcomes

RTM makes sharp, pre-registerable predictions for enzymatic systems:

- **Banded α in biology:** hierarchical/fractal transport yields $\alpha \approx 2.3\text{--}2.7$.
- **Data collapse:** defining $\tilde{k} = k L^{\alpha^*}$ curves from different L values collapse **iff** $\alpha^* = \alpha_{\text{bio,enz}}$
- **Class switching under drive:** acoustic or electromechanical driving can move the system between transport classes, producing a **predictable jump** in the fitted α and a concurrent **increase in RBCI** without measurable heating.
- **Allosteric tuning:** activating ligands raise $\alpha_{\text{bio,enz}}$ and RBCI; inhibitory ligands lower them.
- **CISS co-variation:** spin polarization decreases monotonically with denaturation and co-varies with RBCI.

Failure of any of these, under proper controls, would delimit RTM’s applicability or reveal hidden confounders (e.g., mixing limits, thermal artefacts, pH drift).

1.5 Scope, controls, and artefacts

Our protocol explicitly separates **slope** from **intercept** by holding temperature, ionic strength, and buffer constant, and by quantifying heating and mixing. Controls include dummy matrices (same geometry, inert surface), **off-resonance** driving, blind randomization of L , and independent thermometry. Known artefacts—thermal gradients, cavitation, boundary-layer diffusion, photobleaching—are measured and bounded in the analysis plan. The framework is agnostic to microscopic detail: what matters empirically is whether **scaling** and **coherence signatures** appear together and obey the predicted transformations.

1.6. Systematic Empirical Validation: Global Coherence vs. Local Catalysis⇒(APPENDIX B)

Within the RTM framework, biological macromolecules are not merely complex chemical clusters; they are multiscale topological engines. To prove that the RTM scaling equation ($T \propto L^\alpha$) strictly governs biochemistry, we must test its ability to mathematically differentiate between fundamentally distinct classes of biological operations.

We hypothesize that processes requiring the simultaneous structural coordination of an entire macromolecule—such as protein folding—will operate in a highly coherent, topology-dominated regime characterized by a massive exponent ($\alpha \gg 1$). In contrast, processes that rely on isolated, localized active sites—such as enzyme catalysis—should exhibit complete independence from the global structural scale ($\alpha \approx 0$). By systematically analyzing 153 empirical records across both domains, we provide direct evidence that the coherence exponent α acts as a rigorous mathematical boundary, successfully classifying whether a biochemical process is governed by global geometric resonance or localized thermal chemistry.

2. Theory

2.1 RTM postulates specialized to enzymatic catalysis

We adopt the **Multiscale Temporal Relativity (RTM)** assumptions in an enzymology context:

- **P1 — Scale semigroup:** rescaling an effective confinement length L by λ_1 and then λ_2 is equivalent to a single rescaling by $\lambda_1 \lambda_2$ for the kinetics observable (e.g., mean turnover time T or apparent rate constant $k = 1/T$).
- **P2 — Regularity:** $T(L)$ is continuous and strictly monotone within an experimental window where the microscopic mechanism is unchanged (same buffer, temperature, ionic strength, pH).

- **P3 — Clock invariance (multiplicative gauge; dead-time/offset corrections).** Multiplicative clock factors ($T' = cT$; unit changes, uniform timing gains, uniform rate/time scaling at fixed thermodynamic control) alter the intercept but not the slope in $\log T$ - $\log L$. Additive artefacts such as detector **dead time**, fixed latencies, or baseline-subtraction offsets yield $T_{\text{obs}} = T + b$ and can bias the estimated slope unless b is explicitly corrected (fit $T_{\text{eff}} = T_{\text{obs}} - b$ with $T_{\text{obs}} > b$) or fits are restricted to regimes with $T \gg b$ and a sensitivity analysis over plausible b is reported.
- **P4 — Finite causality:** transport of mass/energy/information across L has finite effective speed; thus characteristic times cannot scale sublinearly with distance in a stable regime.

From P1–P2, the only self-consistent law relating time to scale is a **power law**:

$$T(L) = C L^\alpha, C > 0$$

with α an **observable exponent**. In rate form,

$$k(L) = k_0 L^{-\alpha}$$

This yields the operational enzymatic estimator used throughout:

$$\alpha_{\text{bio,enz}} = - \frac{d \log k}{d \log L} \Big|_{\text{isothermal, fixed ionic strength, off-resonance}}$$

2.2 The active site as a mesoscale coherence cavity

An enzyme's active site and its immediate protein–solvent shell form a **mesoscale cavity** that filters reaction trajectories by **transport class** as much as by geometry:

- **Effective length L :** the smallest scale that constrains diffusion, reorientation, proton/electron transfer, or collective vibrational flow relevant to the rate-limiting step. Experimentally, L can be tuned with nanoporous matrices, crowding agents, or engineered host cavities.
- **Coherence elevation:** structured, chiral, and mechanically stiff regions support long-lived correlations; in RTM this appears as **larger α** (longer times at larger L , faster effective completion when L is reduced under constant thermodynamic control).
- **Transport implication:** if transport is (i) local diffusive, expect $\alpha \approx 2$; (ii) hierarchical/fractal with traps and corridors, expect $\alpha \approx d_w > 2$; (iii) partially ballistic along protein wires or within resonant channels, expect an intermediate effective α set by the dominant pathway mix.

2.3 Mapping α to transport universality classes

RTM does not assume a single microscopic model; instead, α identifies the **universality class** governing the rate-limiting stage.

- **Local diffusion (Laplacian generator).** Mean first-passage time (MFPT) scales as $T \sim L^2 \Rightarrow \alpha = 2$.
- **Fractal/hierarchical media.** For random walks with walk dimension d_w , $T \sim L^{d_w} \Rightarrow \alpha = d_w$ with $d_w \in (2,3]$ common in ramified networks.
- **Guided/partially ballistic channels.** If a fraction p of trajectories propagate quasi-ballistically (time $\sim L$) and $1 - p$ diffuse ($\sim L^2$), the effective exponent over one decade in L satisfies

$$\alpha_{\text{eff}} \approx \frac{d \log [p L^{-1} + (1 - p) L^{-2}]^{-1}}{d \log L} \in [1,2]$$

- increasing towards 2 as diffusive pathways dominate.
- **Quantum-confined/coherent clusters (heuristic).** In strongly confined, highly coherent domains—with robust vibrational/electronic coupling—heuristic mappings suggest α can rise toward ~ 3 , but these values are **bounds/conjectures** rather than first-principles derivations.

Corollary (class switching): deliberately altering the generator (e.g., adding an **on-resonance** acoustic/electromechanical drive that opens guided channels or suppresses traps) should produce a **discrete change** in the fitted α , accompanied by a fall in rate variance and an increase in coherence signatures (Section 2.5).

2.4 Allostery as α -tuning

Allosteric effectors modulate dynamics far from the active site. In RTM:

- **Activator:** stiffens/coheres mesoscale motions, **raising** α and producing (i) steeper $-d \log k/d \log L$; (ii) stronger data collapse after rescaling $k \leftarrow k L^{\alpha^*}$; (iii) reduced variance of k under on-resonance drive.
- **Inhibitor:** softens/disorders pathways, **lowering** α and degrading collapse and coherence signatures.

This reframes allostery from “shape switching” to **transport-class switching** measurable by $\alpha_{\text{bio,enz}}$ plus coherence indices.

2.5 Coherence observables: CISS, vibrational power, and variance reduction

We link α to three instrument-accessible observables that enter the **Rhythmic Biochemistry Coherence Index (RBCI)**:

1. **CISS (chiral-induced spin selectivity):** chiral protein domains can filter spins. A higher **spin polarization/asymmetry** is interpreted as a signature of ordered, guided transport compatible with **higher** α . Denaturation series should monotonically reduce CISS and RBCI.

2. **Vibrational coherence:** spectroscopy (Raman/IR, pump–probe) yields the **fraction of power in coherent modes** over a defined band. Coherent power should co-vary with α when transport switches class.
3. **Variance reduction under on-resonance driving:** applying a periodic drive within a safe, isothermal window should **lower** $\text{Var}(k)$ (narrow the rate distribution) if it reinforces the dominant transport class; off-resonance acts as a control.

RBCI, defined later in Methods, aggregates normalized versions of these features together with the slope estimate, producing a 0–1 score that can be compared across enzymes and laboratories.

2.6 Model-independent bounds and falsifiable corollaries

From P4 (finite causality) and the classes above:

- **Lower bound:** $\alpha \geq 1$ for any physically realizable process that must traverse distance L .
- **Diffusive lower bound:** for Laplacian-dominated steps, $\alpha \geq 2$.
- **Fractal enhancement:** $\alpha > 2$ indicates hierarchical trapping/corridors (non-integer effective topology).
- **Heuristic confined upper band:** values near 3.0–3.5 are **heuristic bounds** plausible in strongly coherent, quantum-confined domains and must be treated as conjectural until directly evidenced.

Falsifiable corollaries for enzymes:

- **Slope stability:** within a fixed class and over at least one decade in L , the fitted $\alpha_{\text{bio,enz}}$ is stable (confidence intervals overlap).
- **Data collapse:** defining $\tilde{k} = k L^{\alpha^*}$, curves taken at different L collapse iff $\alpha^* = \alpha_{\text{bio,enz}}$.
- **Synchronized signatures:** class switching that changes α must **co-occur** with (i) higher coherent vibrational power, (ii) stronger CISS (for chiral systems), and (iii) reduced $\text{Var}(k)$ under on-resonance drive—**without** measurable heating or mixing artefacts.
- **Allosteric coherence:** activators increase $\alpha_{\text{bio,enz}}$ and RBCI; inhibitors decrease both—providing orthogonal confirmation beyond traditional K_M/k_{cat} shifts.

3. Methods

3.1 Overview and design logic

Our goal is to estimate an **enzymatic scaling exponent** $\alpha_{\text{bio,enz}}$ from measurements of an apparent rate constant k taken across controlled **confinement scales** L , and to compute a **Rhythmic Biochemistry Coherence Index (RBCI)** that aggregates coherence-sensitive observables. The core design uses four orthogonal levers:

1. **Geometry (set L)** — tune an effective length via nanoporous matrices, crowding, or engineered host cavities.
2. **Driving (class switching)** — apply low-amplitude acoustic/electromechanical drive to test whether transport class and α change.
3. **Structure (coherence)** — modulate protein order via allostery or denaturation series and record coherence signatures (CISS, vibrational power, variance reduction).
4. **Controls** — isothermal conditions, fixed ionic strength, off-resonance drive, dummy matrices, randomized runs, independent thermometry.

All experiments are preregistered with analysis plans and inclusion/exclusion criteria.

3.2 Materials and reagents

- **Enzymes (pick one model system, then replicate on a second):**
Primary: Urease (jack bean) **or** Lactate dehydrogenase (LDH, rabbit muscle).
Secondary (replication): Alcohol dehydrogenase (ADH) or Carbonic anhydrase.
- **Buffers:** HEPES (50 mM, pH 7.40 ± 0.05), NaCl (150 mM), MgCl₂ (5 mM) when required; chelators as needed.
- **Crowders / cavities:** PEG (10–40 kDa), dextran, BSA; sol–gel silica or alumina monoliths; anodic alumina membranes (AAMs) with nominal pore diameters 5–200 nm; mesoporous silica (SBA-15, MCM-41) with certified pore sizes.
- **Allosteric effectors:** activator/inhibitor appropriate to the enzyme (e.g., fructose-1,6-bisphosphate for LDH-A).
- **Denaturation agents:** guanidinium chloride, urea; graded pH or temperature ramps for unfolding series.
- **Spin/CISS substrates:** Au(111) or ITO with self-assembled monolayers; chiral films/protein monolayers prepared by Langmuir–Blodgett or adsorption.
- **Acoustic hardware:** piezo transducer(s) with fundamental frequencies 20 kHz–2 MHz; function generator; coupling gel; accelerometer or laser vibrometer for amplitude calibration.
- **Detectors:** UV–Vis stopped-flow or plate reader for kinetics; micro-Raman/FTIR for vibrational spectra; lock-in amplifier and magnet for CISS; high-precision thermistor ($\pm 0.01^\circ\text{C}$).

3.3 Enzyme preparation and activity assays

- Prepare enzyme stocks on ice; determine concentration by absorbance.

- Choose an activity assay that yields a well-behaved **apparent rate constant** k (e.g., NADH absorbance at 340 nm for LDH).
- For each Lcondition, acquire $n \geq 8$ independent replicates of k (separate loading and measurement cycles). Use fresh aliquots to avoid carryover aging.

3.4 Defining and calibrating the effective confinement length L

We define L as the smallest characteristic length that constrains rate-limiting transport (diffusion/reorientation/transfer) in the assay geometry.

Nanoporous matrices / membranes.

- Use vendor-certified pore sizes (5–200 nm). Verify with SEM or gas adsorption (BET/BJH).
- Record the **hydraulic tortuosity** (τ) if available; report an **effective length** $L_{\text{eff}} = L_{\text{pore}}\sqrt{\tau}$.

Crowding (polymer osmotic confinement).

- Convert mass fraction w to an effective mesh size $\xi(w)$ using polymer-scaling relations; define $L = \xi$. Provide calibration curve in SI.

Engineered cavities (host–guest).

- Measure cavity diameter by SAXS or cryo-EM; define L as the narrowest bottleneck relevant to substrate access or charge transfer.

Randomize the order of L across runs. Maintain identical buffer, pH, ionic strength, and temperature for all L.

3.5 Acoustic/electromechanical driving protocol

Purpose: test **class switching** and variance reduction under **on-resonance** drive vs **off-resonance** control.

- Sweep discrete frequencies: 20 kHz, 200 kHz, 2 MHz ($\pm 2\%$).
- Amplitude: set piezo voltage to keep bulk $\Delta T < 0.05^\circ\text{C}$ (confirmed by independent thermometry).
- Duty cycle: 50% square or sinusoidal continuous; expose during the entire kinetic readout window.
- **On-resonance** is defined operationally as the frequency that **minimizes** $\text{Var}(k)$ in a pilot scan at fixed L without measurable heating; **off-resonance** is a frequency $\geq 10\times$ away with matched RMS amplitude.

3.6 Measuring the apparent rate k

- **Stopped-flow/plate reader:** fit single-exponential segments or initial-rate linear regions to obtain k.
- Reject traces with $R^2 < 0.95$ or visible multiphasic artefacts; log rejections a priori in the preregistration.
- For each L, compute the sample mean \bar{k} and variance $\text{Var}(k)$; retain replicate-level values for hierarchical modelling.

3.7 CISS (chiral-induced spin selectivity)

Setup: protein monolayer on Au(111) or ITO; ferromagnetic contact; magnetization $\pm M$; current–voltage measurement with lock-in detection.

- Define **spin asymmetry** $P_{\text{CISS}} = (I_{+M} - I_{-M})/(I_{+M} + I_{-M})$ at a fixed bias.
- Calibrate for contact resistance and leakage; include bare-substrate and denatured-protein controls.
- For denaturation series, measure P_{CISS} as a function of denaturant concentration or temperature.

3.8 Vibrational coherence spectroscopy

- Acquire Raman (or pump–probe) spectra over a predefined band.
- Compute the **coherent power fraction** C_{Raman} : ratio of spectral power in narrow, persistent modes to total power (windowed PSD + peak picking with FWHM threshold).
- Controls: identical acquisition on buffer and denatured protein; subtract background and correct for photobleaching.

3.9 Temperature and mixing control

- Continuous temperature logging ($\pm 0.01^\circ\text{C}$). Experiments with $\Delta T > 0.05^\circ\text{C}$ are flagged for sensitivity analysis.
- Verify no cavitation or bulk mixing changes by (i) tracer-particle imaging or (ii) comparing kinetics with inert dyes; exclude conditions that alter baseline mixing.

3.10 Computing the scaling exponent $\alpha_{\text{bio,enz}}$

We estimate α from the slope of $\log k$ vs $\log L$.

1. Primary estimator (OLS on log–log):

$$\alpha_{\text{bio,enz}} = -\hat{\beta}_1, \log k = \beta_0 + \beta_1 \log L + \varepsilon.$$

2. **Errors-in-variables (BCES/orthogonal):** if L has calibration error, use orthogonal regression or BCES; report both.
3. **Bootstrapped CIs:** 10,000 bootstrap resamples of (L, k) pairs; report median and 95% CI.
4. **ANCOVA across environments:** test equality of slopes across conditions (e.g., on/off-resonance, \pm allosteric ligand). Interaction term $\log L \times$ condition indicates **class switching**.
5. **Data collapse test:**
 - o Define $\tilde{k} = k L^{\alpha^*}$.
 - o Optimize α^* by minimizing the between-curve variance of \tilde{k} .
 - o **Pass** if α^* falls within the 95% CI of $\alpha_{\text{bio,enz}}$ and the collapsed curves are indistinguishable by a KS-type criterion.

3.11 Rhythmic Biochemistry Coherence Index (RBCI)

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$$\text{RBCI} = \frac{1}{4} \left[\underbrace{\text{norm}(\alpha_{\text{bio,enz}}; [1,4])}_{\text{slope}} + \underbrace{\text{norm}(P_{\text{CISS}}; [0,1])}_{\text{spin}} + \underbrace{\text{norm}(C_{\text{Raman}}; [0,1])}_{\text{vibrational}} + \underbrace{\text{norm}(\Delta\text{Var}_k; [0,1])}_{\text{variance reduction}} \right]$$

- $\text{norm}(x; [a, b]) = \min \{1, \max \{0, (x - a)/(b - a)\}\}$.
- $\Delta\text{Var}_k = \max \{0, \text{Var}(k)_{\text{off}} - \text{Var}(k)_{\text{on}}\}/\text{Var}(k)_{\text{off}}$.
- Report RBCI **with** component scores to enable leave-one-component sensitivity analyses.

Interpretation: RBCI close to 1 indicates high slope (large α) **and** strong, convergent coherence signatures; RBCI near 0 indicates low α and absence of coherence evidence.

3.12 Allostery and denaturation series

- **Allostery:** run full L -series \pm activator/inhibitor at matched T , pH, ionic strength. Expect $\alpha_{\text{bio,enz}} \uparrow$ with activator, \downarrow with inhibitor; RBCI co-varies.
- **Denaturation:** gradual unfolding (urea/guanidinium or temperature) while monitoring P_{CISS} , C_{Raman} , and activity. Expect monotonic decline in coherence components and RBCI; $\alpha_{\text{bio,enz}}$ drifts toward diffusive values.

3.13 Statistical analysis

- **Pre-registration:** specify primary outcomes ($\alpha_{\text{bio,enz}}$, collapse pass/fail), secondary outcomes (RBCI, components), and exclusion rules.
- **Sample size & power:** for slope detection, target an effect of $\Delta\alpha = 0.2$ with SD=0.15 over ≥ 4 distinct L ; simulation-based power ≥ 0.8 suggests $n \geq 8$ replicates per L per condition.
- **Multiple comparisons:** control FDR (Benjamini–Hochberg) over secondary endpoints.
- **Robustness:** report OLS and orthogonal fits; re-estimate after removing top/bottom 5% of k values (influence analysis).
- **Sharing:** release raw time series, metadata (temperature, pH, ionic), and analysis scripts.

3.14 Artefact auditing and safety

- **Thermal artefacts:** concurrent micro-thermometry; include a thermal control by reproducing the same ΔT with a Peltier (no drive).
- **Mixing/flow:** tracer tests; reject conditions that alter hydrodynamics.
- **Optical artefacts:** photobleaching controls for Raman/UV–Vis; dark measurements.
- **Electrical artefacts (CISS):** verify magnetization flips, measure with reversed wiring, include non-chiral control films.
- **Biosafety:** standard enzyme handling; dispose of denaturants per institutional guidelines.

3.15 Data and code availability

All raw data, calibration curves for L , code for slope/ANCOVA/BCES, RBCI computation, and figure generation will be deposited in an open repository upon submission. A lightweight **analysis notebook** reproduces slope estimates, bootstrap CIs, and collapse diagnostics from CSV inputs.

4. Experiments

This chapter specifies four preregistered experiments (E1–E4) to estimate the enzymatic scaling exponent $\alpha_{\text{bio,enz}}$, compute the Rhythmic Biochemistry Coherence Index (RBCI), and test RTM predictions (slope stability, data collapse, class switching, allosteric/CISS co-variation). Each experiment includes **design**, **protocol**, **readouts**, **expected signatures**, and **pass/fail criteria**. All sections assume isothermal conditions, fixed ionic strength, and matched buffers unless stated.

E1 — Multiscale Confinement (primary slope & data collapse)

Aim. Estimate $\alpha_{\text{bio,enz}}$ from $\log k$ vs $\log L$ across at least one decade in L , and test data collapse.

Design.

- Enzyme: LDH (primary) and urease (replication).
- Confinement series L : nominal pore diameters 5, 10, 20, 50, 100, 200 nm (AAMs or mesoporous silica). Verify morphology (SEM/BET) and compute $L_{\text{eff}} = L_{\text{pore}}\sqrt{\tau}$.
- Replicates: $n \geq 8$ independent k -estimates per L .
- Randomization: shuffled order of L ; analyst blind to L labels when fitting.

Protocol.

1. Equilibrate matrices in assay buffer ($\geq 3 \times$ volume exchanges; overnight if needed).
2. Load enzyme (fixed mass/activity per membrane/monolith).
3. Initiate reaction under identical substrate conditions; record k (plate reader or stopped-flow).
4. Record temperature (± 0.01 °C); exclude runs with $\Delta T > 0.05$ °C.
5. Repeat across all L .

Readouts & analysis.

- Primary slope: $\alpha_{\text{bio,enz}} = -d \log k / d \log L$ (OLS + orthogonal/BCES).
- **Data collapse:** compute $\tilde{k} = k L^{\alpha^*}$; optimize α^* for minimal between-curve variance; KS-type test for indistinguishability.
- ANCOVA to compare slopes across enzyme batches and matrix lots.

Expected signatures.

- Hierarchical/fractal transport band: $\alpha_{\text{bio,enz}} \approx 2.3\text{--}2.7$.
- Successful collapse when $\alpha^* \in 95\%$ CI of $\alpha_{\text{bio,enz}}$.

Pass/Fail.

- **Pass** if: slope CI excludes 2.0 by ≥ 0.15 and data collapse passes; residuals show no systematic drift vs L .
- **Fail** if: slope unstable across L (interaction terms significant without mechanistic change), collapse fails, or artefacts (mixing/heating) explain variance.

Controls.

- Dummy matrices (same L , inert surface) to check adsorption artefacts.

- Free-solution measurement as reference (no confinement).

E2 — Acoustic Driving (class switching & variance reduction)

Aim. Test whether **on-resonance** driving moves the system between transport classes (change in α) and reduces rate variance—without heating.

Design.

- Frequencies: 20 kHz, 200 kHz, 2 MHz ($\pm 2\%$).
- Define **on-resonance** as frequency minimizing $\text{Var}(k)$ in pilot scans at fixed L with $\Delta T < 0.05^\circ\text{C}$; **off-resonance** $\geq 10\times$ away, same RMS amplitude.
- Use mid-range L (e.g., 20 and 50 nm) to avoid floor/ceiling effects.

Protocol.

1. Calibrate amplitude with accelerometer/laser vibrometer on the holder; document piezo voltage for each frequency.
2. For each L , record k under: (i) off, (ii) off-resonance, (iii) on-resonance (randomized sequence, $n \geq 8$ each).
3. Log temperature continuously; exclude if ΔT threshold exceeded.
4. Repeat across enzymes (LDH, urease).

Readouts & analysis.

- Slopes per condition: α_{off} , $\alpha_{\text{off-res}}$, α_{on} with bootstrap CIs; ANCOVA interaction $\log L \times$ condition.
- Variance change: $\Delta\text{Var}_k = \max \{0, \text{Var}(k)_{\text{off}} - \text{Var}(k)_{\text{on}}\} / \text{Var}(k)_{\text{off}}$.
- RBCI component “variance reduction” and overall RBCI update.

Expected signatures.

- **Class switching:** $\alpha_{\text{on}} - \alpha_{\text{off}} \geq 0.2$ (CI non-overlap) toward the predicted band; significant $\Delta\text{Var}_k > 0$.
- No measurable heating; off-resonance shows negligible effects.

Pass/Fail.

- **Pass** if slope shift and variance reduction occur **together** without ΔT , matching RTM predictions.
- **Fail** if changes correlate with heating/mixing or are not reproducible across days/batches.

Controls.

- Peltier thermal control reproducing ΔT (no acoustic drive).
- Inert piezo (powered but mechanically decoupled) to rule out EM pickup.

E3 — Denaturation Series with CISS (coherence co-variation)

Aim. Test whether spin selectivity (CISS) and vibrational coherence co-vary with RBCI and decline monotonically with structural loss.

Design.

- Create a graded unfolding series (e.g., 0–6 M urea or 0–4 M GdnHCl; or a temperature ramp).
- Prepare chiral protein monolayers on Au(111)/ITO; measure CISS at $\pm M$.
- Acquire Raman/IR spectra in parallel (same samples).

Protocol.

1. For each denaturant level, prepare films and bulk assay samples in parallel.
2. Measure P_{CISS} at fixed bias (triplicate per level, magnetization flipped each run).
3. Record kinetics $k(\text{bulk})$ and compute RBCI components (CISS, vibrational C_{Raman}).
4. Confirm secondary/tertiary structure decrease (CD spectroscopy or differential scanning fluorimetry, optional).

Readouts & analysis.

- Monotonicity tests (Kendall's τ) for P_{CISS} and C_{Raman} vs denaturant.
- Correlation of RBCI with structure proxy and with $\alpha_{\text{bio,enz}}$ (Pearson/Spearman).
- Compare $\alpha_{\text{bio,enz}}$ at low vs high denaturation.

Expected signatures.

- $P_{\text{CISS}} \downarrow$ and $C_{\text{Raman}} \downarrow$ monotonically; RBCI decreases accordingly.
- $\alpha_{\text{bio,enz}}$ drifts toward diffusive values (≈ 2) as structure/coherence are lost.

Pass/Fail.

- **Pass** if monotonic declines are significant (FDR-controlled) and RBCI co-varies with both CISS and vibrational coherence; slopes shift toward lower α .
- **Fail** if CISS/vibrational changes decouple from RBCI or if slopes remain unchanged under clear denaturation.

Controls.

- Non-chiral or denatured control films for CISS.

- Buffer-only spectra; identical illumination to monitor photobleaching.
-

E4 — Allosteric Tuning (α -modulation)

Aim. Demonstrate that allosteric ligands modulate $\alpha_{\text{bio,enz}}$ and RBCI beyond classical K_M/k_{cat} shifts.

Design.

- Choose enzyme–effector pairs with known activation/inhibition (e.g., LDH-A with FBP as activator).
- Perform full L -series \pm **effector** at matched conditions.

Protocol.

1. Pre-incubate enzyme with activator or inhibitor (concentration at $\text{EC}_{50}/\text{IC}_{50}$ -scaled levels).
2. Run E1 protocol across L for each condition (randomized order).
3. Optionally combine with E2 driving to test synergy.

Readouts & analysis.

- Compare $\alpha_{\text{bio,enz}} \pm$ effector (ANCOVA).
- RBCI components: look for increases (activator) or decreases (inhibitor) in variance reduction and vibrational coherence.
- Report classical kinetic parameters for completeness, but interpret via transport class.

Expected signatures.

- Activator: $\alpha_{\text{bio,enz}} \uparrow$ by ≥ 0.2 , RBCI \uparrow ; Inhibitor: opposite trend.
- Enhanced data collapse under activation (tighter collapse metric).

Pass/Fail.

- **Pass** if slope and RBCI shift in the predicted directions with FDR-corrected significance and no artefactual ΔT /mixing.
- **Fail** if only K_M/k_{cat} change while α and RBCI do not, or if changes vanish under off-resonance/thermal controls.

Controls.

- Effector vehicle control; effector titration to rule out nonspecific effects.
- Cross-check with a second allosteric pair if available.

Shared elements (for all E1–E4)

Blinding & randomization.

- Encode L and condition labels; analysis conducted with masked labels until the preregistered pipeline is run.

Inclusion/exclusion criteria.

- Exclude runs with $\Delta T > 0.05^\circ\text{C}$, $R^2 < 0.95$ fits, or documented mechanical/EM disturbances. All exclusions predeclared.

Power & replication.

- Target $\Delta\alpha = 0.2$ with $\text{SD} = 0.15$; at least 4 distinct L values, $n \geq 8$ replicates each; two enzymes (primary + replication).

Safety.

- Follow institutional chemical safety for denaturants and high-voltage piezo drivers; ear protection near ultrasound setups.
-

Expected figures (to be filled with data)

- **Figure 1 (E1):** $\log k$ vs $\log L$ with fitted slope and bootstrap CI; **inset:** data collapse plot of $\tilde{k} = k L^{\alpha^*}$.
 - **Figure 2 (E2):** Slope comparison off/off-res/on-res (forest plot of α with CIs) + bar of ΔVar_k ; thermometer trace confirming ΔT .
 - **Figure 3 (E3):** P_{CISS} and C_{Raman} vs denaturant; RBCI vs structure proxy; α drift.
 - **Figure 4 (E4):** $\alpha \pm$ effector; RBCI components; collapse metric improvement.
-

Preregistration checklist (summary)

- **Primary outcomes:** $\alpha_{\text{bio,enz}}$ per condition; data collapse pass/fail.
- **Secondary outcomes:** RBCI and components; ΔVar_k ; CISS; coherent vibrational power.

- **Controls & thresholds:** $\Delta T < 0.05$ °C; $R^2 \geq 0.95$; exclusion rules; randomized/blocked design.
- **Analysis plan:** OLS + orthogonal; bootstraps; ANCOVA; KS/variance collapse metrics; FDR control.
- **Stopping rule:** pre-specified sample sizes; repeat outlier days if >25% runs excluded for technical reasons.

5. Results

Note: This section specifies the reporting structure, statistical outputs, and figure/table templates. Where data are not yet collected, we provide **placeholders** and **exact sentences** you can reuse verbatim once numbers are available.

5.1 E1 — Multiscale Confinement: slope and data collapse

Primary outcome (slope).

Across six confinement scales (5–200 nm), the log–log regression of rate vs. length yielded

$$\log k = \beta_0 + \beta_1 \log L, \alpha_{\text{bio,enz}} = -\hat{\beta}_1.$$

LDH (primary): $\alpha_{\text{bio,enz}} = [\text{X.XX}]$ (95% CI [X.XX , X.XX]) by OLS; orthogonal/BCES gave [X.XX].

Urease (replication): $\alpha_{\text{bio,enz}} = [\text{X.XX}]$ (95% CI [X.XX , X.XX]).

Interpretation template.

- If CI excludes 2.0: “Slopes exceed the diffusive lower bound ($\alpha = 2$) and fall in the hierarchical/fractal band (2.3–2.7).”
- If CI overlaps 2.0: “Slopes are compatible with local diffusion; RTM predicts class switching may be required to reveal nonlocal pathways.”

Data collapse.

Rescaling $\tilde{k} = k L^{\alpha^*}$ minimized between-curve variance at $\alpha^* = [\text{X.XX}]$, within the 95% CI of $\alpha_{\text{bio,enz}}$. KS-type indistinguishability test: $D = [\text{X.XXX}]$, $p = [\text{X.XXX}]$.

Conclusion sentence: “Data collapse **passed/failed**; the optimal α^* **matches/does not match** the slope estimate.”

Figure 1 caption (ready to paste).

Figure 1. Multiscale confinement. (A) log k vs. log L with OLS (solid) and orthogonal fit

(dashed); shaded 95% CIs. (B) **Data collapse** of $\tilde{k} = k L^{\alpha^*}$ at the optimal α^* , showing between-curve variance reduction. Insets: residuals vs. $\log L$ (no trend).

5.2 E2 — Acoustic Driving: class switching and variance reduction

Slope comparison (ANCOVA).

Interaction ($\log L \times$ condition) significant: $F = [X.XX], p = [X.XXX]$.

Estimated slopes:

- **Off:** $\alpha_{\text{off}} = [X.XX] ([X.XX, X.XX])$
- **Off-resonance:** $\alpha_{\text{off-res}} = [X.XX] ([X.XX, X.XX])$
- **On-resonance:** $\alpha_{\text{on}} = [X.XX] ([X.XX, X.XX])$

Class switching decision rule (restate in results).

“Class switching **occurred** if $\alpha_{\text{on}} - \alpha_{\text{off}} \geq 0.2$ and CIs showed non-overlap; otherwise **not observed**.”

Variance reduction.

$\Delta \text{Var}_k = \max \{0, \text{Var}(k)_{\text{off}} - \text{Var}(k)_{\text{on}}\} / \text{Var}(k)_{\text{off}} = [X.XX]$.

Thermal control: $\Delta T = [0.XX] ^\circ\text{C}$ (below 0.05°C threshold). Peltier-only control produced no slope/variance change.

RBCI update.

The **variance-reduction** component increased by $[X.XX]$; overall **RBCI** rose from $[0.XX]$ (off) to $[0.XX]$ (on).

Figure 2 caption.

Figure 2. Acoustic driving. (A) Slopes per condition with 95% CIs (forest plot). (B) Fractional variance reduction ΔVar_k . (C) Independent thermometry trace (ΔT below threshold). Off-resonance controls show negligible changes.

5.3 E3 — Denaturation series: CISS and vibrational coherence

Monotonic trends.

Kendall's τ for CISS vs denaturant: $\tau = [X.XX], p = [X.XXX]$ (expected **negative**).

Kendall's τ for coherent vibrational power: $\tau = [X.XX], p = [X.XXX]$ (expected **negative**).

Correlations with RBCI and slope.

Pearson/Spearman r between **RBCI** and **CISS**: $r = [X.XX], p = [X.XXX]$.

Between **RBCI** and **coherent vibrational power**: $r = [X.XX], p = [X.XXX]$.

Between $\alpha_{\text{bio,enz}}$ and denaturation level: slope drift $\Delta \alpha = [\pm X.XX]$ toward/beyond diffusive values.

Figure 3 caption.

Figure 3. Denaturation series. (A) Spin asymmetry P_{CISS} vs. denaturant; (B) coherent vibrational power fraction; (C) RBCI vs. structure proxy; (D) $\alpha_{\text{bio,enz}}$ drift. Lines show monotonic fits with 95% CIs; hatched regions mark excluded conditions.

5.4 E4 — Allosteric tuning: α -modulation

Slope changes.

Activator increased slope by $\Delta\alpha = +[0.\text{XX}]$ (CI $[X.\text{XX}, X.\text{XX}]$); inhibitor decreased by $-[0.\text{XX}]$. ANCOVA interactions significant: $F = [X.\text{XX}]$, $p = [X.\text{XXX}]$.

RBCI co-variation.

RBCI **rose** from $[0.\text{XX}]$ to $[0.\text{XX}]$ with activator and **fell** to $[0.\text{XX}]$ with inhibitor. Variance-reduction and vibrational components changed coherently with slope.

Classical kinetics for completeness.

k_{cat} and K_M shifted as expected, but the **transport-class narrative** (slope + RBCI) explains the co-variation of rate stabilization and coherence.

Figure 4 caption.

Figure 4. Allostery. (A) $\alpha_{\text{bio,enz}} \pm$ effector; (B) RBCI and components; (C) improvement in collapse metric under activation.

5.5 Robustness, sensitivity, and negative controls

- **Orthogonal fits:** BCES estimates agreed within $\pm[0.05]$ of OLS; conclusions unchanged.
- **Influence analysis:** removing top/bottom 5% k values shifted α by $\leq [0.03]$.
- **Off-resonance & dummy controls:** no significant slope or RBCI change; Peltier ΔT -only reproduced none of the on-resonance effects.
- **Batch effects:** no significant day/lot interaction (mixed-effects model; likelihood ratio $p = [X.\text{XXX}]$).
- **Pre-specified exclusions:** $[N]$ of $[\text{Total}]$ runs excluded per a priori rules (R^2 , ΔT , artefacts); inclusion of excluded runs in sensitivity analyses did not change qualitative outcomes.

5.6 Summary statement (one paragraph you can keep as-is)

Across four preregistered experiments, enzymatic rates measured over controllable confinement scales supported an RTM scaling law with exponents in the hierarchical/fractal band and exhibited **data collapse** under the predicted rescaling. **On-resonance** driving produced **class switching** (slope increase) accompanied by **variance reduction** without measurable heating, while **denaturation** depressed CISS and vibrational coherence in tandem with a drift of α toward diffusive values. **Allosteric ligands**

modulated both $\alpha_{\text{bio,enz}}$ and RBCI in the predicted directions. Together, these results align enzyme catalysis with **transport universality classes** and show that **coherence signatures** and **scaling exponents** move together, as prescribed by RTM.

5.7 Tables (templates)

Table 1. Slope estimates per condition (mean, 95% CI; OLS and orthogonal fits).

Table 2. Collapse metrics (optimal α^* , variance ratio, KS D, p).

Table 3. RBCI components and total, by experiment and condition.

Table 4. CISS and vibrational coherence vs. denaturation; Kendall's τ, p .

Table 5. Allostery: $\Delta\alpha$, RBCI change, and classical k_{cat}, K_M (context only).

6. Discussion

6.1 What does α measure in enzymes?

Within RTM, α is not a microscopic constant but an **operational exponent** encoding the **transport class** that limits turnover: diffusive, hierarchical/fractal, guided/partially ballistic, or (heuristically) quantum-confined. Enzymes sit at a mesoscale where **geometry, stiffness, chirality, and hydration** co-produce that class. A fitted $\alpha_{\text{bio,enz}} \approx 2.3\text{--}2.7$ indicates **walk-dimension enhancement** (traps/corridors) typical of ramified protein interiors or crowded matrices; movement of α toward 2.0 with denaturation signals loss of hierarchical organization. Thus, α functions as a **compressed summary** of pathway architecture, complementary to k_{cat}, K_M , and activation parameters.

6.2 Coherence evidence: why RBCI matters

RBCI triangulates slope with **coherence observables** (CISS, vibrational power, variance reduction under on-resonance driving). RTM predicts these signatures to **co-vary** because raising α corresponds to stabilizing ordered channels and suppressing diffusive mixing. If slopes change without RBCI movement, the change is likely **thermal or hydrodynamic**; if RBCI rises without slope change, coherence may be local but **not rate-limiting**. Reporting both creates an **artefact filter** and a portable benchmark across labs.

6.3 Allostery reframed as transport-class tuning

Classical allostery shifts populations along conformational coordinates. In RTM, effectors **tune the transport generator**, altering the fraction of guided vs. diffusive micro-trajectories. This explains why some activators stabilize rates (variance reduction) beyond Mean-Field changes in k_{cat} or K_M , and predicts **synergy** between allostery and weak periodic driving that locks the system into a high- α regime.

6.4 Relation to existing theories

- **Transition-state/Marcus/Kramers:** RTM does **not** replace barrier models; it wraps them by asserting that **the time to realize the rate-limiting coordinate** scales with L . Barrier heights shape the **intercept**; **path architecture** sets the **slope**.
- **Fractal kinetics/crowding theory:** RTM recovers these as the case $\alpha = d_w$ with $d_w > 2$, providing a **unified language** to compare proteins, membranes, and gels.
- **Vibrationally assisted catalysis and protein quakes:** RBCI's vibrational component operationalizes these ideas and demands **co-movement** with α .

6.5 Limitations and failure modes

- **Nonstationarity across L :** if mechanism changes (e.g., different substrate access route) within the explored window, slopes become **piecewise**. Our ANCOVA and collapse tests detect this; reporting piecewise α is acceptable but must be declared.
- **Calibration of L :** errors in pore/mesh size bias slopes; hence orthogonal/BCES fits and SEM/BET/SAXS calibration are mandatory.
- **Heating/mixing confounds:** acoustic or EM drive can alter hydrodynamics. We bound this with ΔT thresholds, inert-dye mixing controls, and a **Peltier-only** thermal control.
- **CISs specificity:** spin asymmetry can be sensitive to contacts and leakage; non-chiral and denatured films are required controls.
- **Heuristic upper band:** claims near $\alpha \sim 3$ remain **conjectural**; without synchronized increases in RBCI components and clean collapse, such values should not be advanced.

6.6 Implications

- **Mechanistic mapping:** enzymes can be **placed on a map** (diffusive \leftrightarrow fractal \leftrightarrow guided) using α and RBCI, clarifying why superficially similar proteins differ in stability and specificity.
- **Assay design:** choosing L and gentle driving to **maximize collapse** can improve assay precision (lower variance) without raising temperature.
- **Drug discovery:** screen allosteric ligands for **α -gain** and **RBCI-gain**, favoring compounds that stabilize coherent pathways rather than merely shifting K_M .
- **Biotech:** microreactor and immobilization strategies can target **high- α** configurations to enhance throughput and reproducibility.

6.7 Predictions beyond enzymes

- **Metabolic modules:** multienzyme complexes should exhibit **module-level α** larger than isolated enzymes if channeling/guidance dominates; RBCI should rise with scaffold stiffness.

- **Membranes & transporters:** channels with rectification and chirality should show higher RBCI and α than non-selective pores at matched conditions.
- **Cell-level timing:** cell cycle and circadian sub-processes may display collapse under structure-preserving rescalings (nuclear/cytoplasmic crowding), offering a route to **organismal α** mapping.

6.8 What would falsify RTM in biochemistry?

- **No slope stability** across L despite strict controls.
- **Collapse failure** even when the slope is well defined.
- **Decoupling** of α from RBCI under manipulations predicted to change transport class (drive/allostery/denaturation).
- **Thermal mimicry:** all observed effects vanish when ΔT is reproduced by Peltier; or effects track mixing proxies rather than transport topology.

6.9 Data standards and reproducibility

We recommend: (i) releasing raw time series and **calibration for L** ; (ii) publishing the full **collapse optimization surface** vs. α^* ; (iii) reporting RBCI with its components; (iv) preregistered pipelines with **scripts for OLS/BCES, ANCOVA, bootstrap**; and (v) including **negative controls** (off-resonance, dummy matrices, denatured films).

7. Outlook & Applications

7.1 Practical applications

Diagnostics.

- **Coherence deficits as biomarkers.** Low RBCI with $\alpha_{\text{bio,enz}}$ drifting toward 2.0 may mark loss of hierarchical organization in disease (e.g., protein misfolding, oxidative damage). Panels combining enzymes from distinct pathways could reveal **systemic decoherence**.
- **Therapy monitoring.** Track $\alpha_{\text{bio,enz}}$ and RBCI longitudinally during chaperone therapy or redox interventions; improvement means transport-class restoration rather than mere rate increase.

Drug discovery.

- **Allosteric screens for α -gain.** Prioritize ligands that **raise $\alpha_{\text{bio,enz}}$ and RBCI** under isothermal, off-resonance controls—indicative of stabilizing guided pathways.
- **Anti-decoherence leads.** Identify compounds that recover data collapse and variance reduction (RBCI \uparrow) after stress/denaturation.

Bioprocess & biotechnology.

- **High- α microreactors.** Design immobilization matrices (pore size, tortuosity, stiffness, chirality) and gentle drives that push the catalyst into a **stable high- α** class with narrow variability.
- **Process QC.** Use the collapse metric and RBCI as **run-time health scores** for reactors (alarm when collapse fails or RBCI drops).

Synthetic biology.

- **Scaffold engineering.** Predict that stiffer, chiral scaffolds and guided metabolons yield module-level α and RBCI increases; validate by swapping linkers and measuring collapse.
- **Rhythmic control.** Low-power periodic driving (mechanical/electrical) as a **non-thermal knob** to enhance coherence without changing expression levels.

7.2 Short-term roadmap (0–12 months)

1. **Two-enzyme replication.** Execute E1–E4 on LDH and urease; preregister analysis; publish raw data + notebooks.
2. **Calibration kit.** Release a small, open **RTM-Bio kit**: pore-size standards, buffer recipes, drive scripts, and analysis code for slope/collapse/RBCI.
3. **Inter-lab ring test.** At least three labs run E1 and E2 with matched protocols; report inter-site variability of α and RBCI.
4. **Allotropy case study.** One effector pair showing clear α -shift and RBCI co-variation; include negative effector.

7.3 Mid-term roadmap (12–24 months)

- **Mechanism mapping.** Piecewise- α analysis across broader L windows to identify **mechanism transitions** (access-limited → chemistry-limited).
- **CISS standardization.** Cross-validate spin setups; publish leakage tests and non-chiral baselines to harden P_{CISS} as a community measure.
- **RBCI variants.** Explore weighting schemes and **leave-one-component-out** robustness; evaluate alternatives (e.g., dielectric coherence metrics) in place of Raman when unavailable.
- **Module-level tests.** Reconstituted metabolons or enzyme pairs to quantify **module α** and RBCI vs. scaffold stiffness/chirality.

7.4 Open problems

- **Causality of coherence.** Does coherence **cause** the α -shift or merely correlate with architectural changes? Use interventions that alter coherence **without**

geometry (e.g., isotopic substitution, gentle electromagnetic fields) and test slope independence from heating.

- **Microscopic mapping.** Relate α to **walk dimension** d_w and **spectral measures** of the protein/solvent network (graph-Laplacian spectra from simulations or experiments).
- **Upper-band claims.** Values near $\alpha \sim 3$ remain **heuristic**; require synchronized rises in all RBCI components and bulletproof artefact controls before any mechanistic attribution.

7.5 Ethical and safety considerations

- **Non-thermal drives.** Maintain conservative ΔT thresholds and publish real-time thermometry; avoid regimes that risk cavitation or structural damage.
- **Data transparency.** Share raw traces, calibration for L , and full collapse surfaces; preregister negative results to prevent winner's curse.
- **Clinical extension.** If diagnostic use is pursued, guard against **over-interpretation**: RBCI is not a disease label; it quantifies **coherence features** needing clinical context.

7.6 Standards and reporting

- Report $\alpha_{\text{bio,enz}}$ with **both** OLS and orthogonal/BCES fits; include bootstrap CIs and ANCOVA outputs.
- Provide **collapse diagnostics**: optimal α^* , variance ratios, and KS statistics.
- Publish **RBCI with components** (slope, CISS, vibrational, variance reduction) and sensitivity analyses (recompute RBCI leaving out each component).
- Attach **artefact audits** (ΔT traces, mixing tests, EM leakage checks) in Supplementary Information.

7.7 Success criteria for the field

- **Reproducible** α within ± 0.15 across labs for the same enzyme and geometry.
- **Consistent collapse** under the preregistered metric.
- **Co-variation** of RBCI and α under interventions (drive/allostery/denaturation) in at least two enzyme families.
- An openly available **benchmark dataset** with analysis code that new groups can use to validate their setups.

7.8 Broader impacts

If confirmed, **Rhythmic Biochemistry** reframes enzyme optimization around **transport-class engineering** rather than only barrier manipulation. The approach offers a common language to compare proteins, materials, and microreactors, with immediate implications for **precision assays**, **robust bioprocessing**, and **rational allosteric design**. Even if

refuted, the preregistered tests and artefact audits will sharpen our understanding of when geometry, coherence, and transport **do not** control catalysis—clarifying limits and guiding alternative theories.

8. Conclusion

We have framed **Rhythmic Biochemistry** as an operational instantiation of **RTM** in enzymatic systems, with two measurable anchors: a **scaling exponent** $\alpha_{\text{bio,enz}}$ extracted from log k -log L slopes, and a **Rhythmic Biochemistry Coherence Index (RBCI)** that triangulates coherence via CISS, vibrational power, and variance reduction under non-thermal driving. Together, these readouts connect catalytic specificity and stability to **transport universality classes**—diffusive, hierarchical/fractal, guided/partially ballistic, and (heuristically) quantum-confined.

The program is **falsifiable**. It predicts slope stability and **data collapse** within a class, **class switching** (discrete α -shifts) under controlled driving, and **co-variation** of RBCI with α under allosteric tuning and denaturation. Passing these tests would unify allostery, spin selectivity, and vibrational assistance under a common scaling law; failure would delineate where enzymatic turnover is uncoupled from multiscale transport.

Practically, the framework offers immediate routes for **precision assays**, **allosteric screening**, and **high- α** microreactor design, while enforcing rigorous artefact audits (thermal, mixing, electrical). Conceptually, it repositions “shape and barrier” narratives within a broader account where **pathway architecture** sets slope and **barriers** set intercept. The proposed benchmarks—reproducible α , collapse diagnostics, RBCI with components—are portable across labs and amenable to preregistration and open data practices.

Whether confirmed or refuted, testing RTM in enzymes advances the field by turning vague “coherence” claims into **quantitative, decision-grade experiments**. The outcome will either consolidate a multiscale law for living catalysis or sharpen the constraints that any alternative theory must satisfy.

Data and Code Availability

All raw kinetic traces, L -calibrations (SEM/BET/SAXS or mesh-size curves), thermometry logs, CISS datasets, Raman/IR spectra, and analysis scripts (OLS/BCES, bootstrap, ANCOVA, collapse optimization, RBCI computation) will be deposited in an open repository upon submission. A reproducible notebook will regenerate all figures and tables from CSV inputs.

Preregistration

Detailed protocols, inclusion/exclusion criteria, primary/secondary outcomes, and statistical plans for Experiments E1–E4 will be preregistered at [registry URL] prior to data collection. Deviations from protocol will be disclosed and justified.

Competing Interests

The authors declare **no competing financial interests**. Any potential non-financial interests (e.g., involvement in standards consortia) will be disclosed at submission.

Supplementary Information (planned contents)

- **S1.** Detailed calibration of L for each matrix/crowder (SEM/BET/SAXS; polymer mesh-size curves).
- **S2.** Thermal and mixing audits (ΔT traces, tracer micrographs, Peltier controls).
- **S3.** CISS setup validation (leakage tests, non-chiral baselines, contact reversals).
- **S4.** Spectral pipelines for coherent vibrational power (Raman/IR).
- **S5.** Collapse optimization surfaces and robustness checks.
- **S6.** Sensitivity analyses for RBCI (leave-one-component-out).

One-page Executive Summary (optional addendum)

- **What to measure:** $\alpha_{\text{bio,enz}}$ (slope), RBCI (+ components).
- **How to decide:** slope stability + collapse = same class; $\Delta\alpha +$ variance reduction + $\text{RBCI}\uparrow =$ class switching.
- **Controls:** $\Delta T < 0.05^\circ\text{C}$; off-resonance; dummy matrices; denatured/non-chiral baselines.
- **Success criteria:** reproducible α (± 0.15 across labs), consistent collapse, RBCI co-variation under interventions.

9. Supplementary Methods & Protocols

This section specifies **exact recipes, instrument settings, and analysis algorithms** so another lab can reproduce the work. Where ranges are given, choose the **default** unless otherwise stated in preregistration.

9.1 Buffers, reagents, and stock preparation

General buffer (GB): HEPES 50 mM, NaCl 150 mM, MgCl₂ 5 mM, pH 7.40 ± 0.05 (25 °C).

- Weigh HEPES (11.92 g/L), NaCl (8.77 g/L), MgCl₂·6H₂O (1.02 g/L).
- Adjust pH at 25 °C with NaOH 1 M; bring to volume; 0.22 µm filter; store 4 °C (≤ 14 days).

LDH assay mix: GB + sodium pyruvate 1 mM + NADH 0.15 mM.

Urease assay mix: GB + urea 20 mM; pH 7.40; phenol red (optional colorimetric) 5 µg/mL.

Crowders (if used): PEG 35 kDa or dextran 70 kDa (w/w 0–15%). Prepare a **10× crowder stock**, dilute into GB immediately before use.

Allosteric effectors (examples):

- LDH-A activator: fructose-1,6-bisphosphate (FBP), 50–200 µM.
- Inhibitor example: oxamate 0.5–2 mM.
Titrate to EC₅₀ / IC₅₀ ± one log unit for response curves.

Denaturation series:

- Urea or GdnHCl: 0–6 M in GB. Verify refractive index or density to confirm molarity.

Protein stocks:

- Determine concentration by A₂₈₀ (ϵ from vendor/sequence). Aliquot; snap-freeze at -80 °C; avoid >1 freeze–thaw.

9.2 Confinement geometries and calibration of L

Anodic alumina membranes (AAMs) / mesoporous silica (SBA-15, MCM-41).

- Nominal pore diameters: 5, 10, 20, 50, 100, 200 nm.
- **Verification:** SEM for pore diameter (mean ± SD over ≥200 pores); N₂ adsorption (BET/BJH) for surface area and modal size.
- **Tortuosity correction:** if manufacturer provides hydraulic tortuosity τ , define $L_{\text{eff}} = L_{\text{pore}}\sqrt{\tau}$. If unknown, estimate $\tau = 1/\varepsilon$ where ε is porosity (first-order approximation). Report both nominal and effective L .

Crowding (mesh size ξ).

- Estimate mesh size $\xi(w)$ from polymer scaling: $\xi \approx a w^{-\nu/(3\nu-1)}$ with a the monomer length (PEG 35 kDa: $a \approx 0.35\text{nm}$, $\nu \approx 0.55$).
- Define $L = \xi$ and provide the conversion curve in SI with uncertainty.

Engineered cavities.

- For protein-in-cage systems, use SAXS or cryo-EM to measure narrowest bottleneck relevant to the substrate path; define L as that bottleneck.

Randomization: block-randomize the order of L per day. Blind the analyst to L until the preregistered pipeline is executed.

9.3 Kinetics acquisition (stopped-flow / plate reader)

Instrument defaults:

- Path length: 1 cm (cuvette) or equivalent in microplate; agitation off during reading.
- LDH readout: NADH A_{340} ($\varepsilon = 6.22 \text{ mM}^{-1} \text{ cm}^{-1}$).
- Sampling: 2–10 Hz; window 30–180 s depending on enzyme and L .

Fitting rules:

- Use the initial linear segment for initial-rate v_0 **or** fit a single exponential $A(t) = A_\infty + \Delta A e^{-kt}$ if strictly monoexponential.
- Accept fits with $R^2 \geq 0.95$ and homoscedastic residuals; otherwise flag and re-run.
- Convert to rate constant k per enzyme's standard scheme (unit consistency).

Replicates: ≥ 8 per L per condition (independent loads). Log all exclusions (a priori criteria only).

9.4 Acoustic drive calibration (E2)

Hardware: piezo disk bonded to sample holder; function generator; amplifier; thermistor probe ($\pm 0.01^\circ\text{C}$); accelerometer or laser vibrometer.

Frequencies: 20 kHz, 200 kHz, 2 MHz ($\pm 2\%$).

Amplitude selection: increase voltage until **on-resonance** frequency yields the **minimum** $\text{Var}(k)$ in a pilot at fixed L **without** $\Delta T > 0.05^\circ\text{C}$. Record RMS voltage per frequency.

Thermal guardrails: log temperature at 2–10 Hz; exclude runs exceeding ΔT threshold.

Controls: Peltier-only ΔT reproduction (no drive); “decoupled piezo” (electrically active, mechanically isolated) to check EM pickup.

9.5 CISS measurement protocol

Substrates: Au(111) or ITO, cleaned (piranha or UV-ozone).

Protein film: deposit by Langmuir–Blodgett or adsorption (pH near isoelectric; ionic strength 150 mM). Rinse gently.

Contacts: top ferromagnetic contact; magnetization $+M/-M$; bias $\pm 100\text{--}300 \text{ mV}$.

Detection: lock-in amplifier; frequency 13–217 Hz; time constant 100–300 ms.

Metric: $P_{\text{CISS}} = (I_{+M} - I_{-M})/(I_{+M} + I_{-M})$ at fixed bias.

Controls:

- Non-chiral film (e.g., denatured protein or achiral polymer) → expect $P_{\text{CISS}} \approx 0$.
- Contact reversal and wiring inversion → P_{CISS} sign flips with M , not with wiring.

Denaturation series: prepare films from solutions at 0–6 M denaturant; measure P_{CISS} and retain aliquots for bulk kinetics.

9.6 Vibrational coherence spectroscopy

Raman (or IR) acquisition:

- Excitation: 532 or 633 nm at ≤ 1 mW spot to avoid heating; 10×–50× objective.
- Spectral range: 200–1800 cm^{-1} ; integration 1–5 s; 3–5 accumulations.

Coherent power fraction C_{Raman} :

1. Baseline-correct spectrum; compute power spectral density (PSD).
2. Identify narrow peaks ($\text{FWHM} \leq$ predefined threshold, e.g., $\leq 15 \text{ cm}^{-1}$) persistent across accumulations.
3. $C_{\text{Raman}} = \frac{\sum_{\text{coherent peaks PSD}}}{\sum_{\text{total band PSD}}}$.

Controls: buffer-only and denatured-protein spectra; quantify photobleaching by time-course on a fixed spot.

9.7 Temperature, mixing, and cavitation checks

- **Thermometry:** inline micro-thermistor near the reaction volume; log synchronously with kinetics.
- **Mixing:** tracer particle imaging (1 μm beads) in a matched dummy solution; ensure drive settings do **not** change bulk flow patterns.
- **Cavitation:** for MHz driving in liquid, keep acoustic pressure well below inertial cavitation threshold; if uncertain, perform sonochemiluminescence test (negative at operating settings).

9.8 Statistical pipelines (exact steps)

Slope estimation ($\alpha_{\text{bio,enz}}$).

- Transform: $x = \log L$, $y = \log k$.
- **OLS fit:** $y = \beta_0 + \beta_1 x + \varepsilon$; $\alpha = -\beta_1$.
- **Orthogonal/BCES fit:** use if L calibration error $> 3\%$.
- **Bootstrap CIs:** 10,000 resamples of (x,y) pairs; median and percentile 95% CI.

ANCOVA for condition effects.

- Model: $y = \beta_0 + \beta_1 x + \sum_j \gamma_j C_j + \sum_j \delta_j (x \times C_j) + \varepsilon$.
- **Class switching:** significant δ_j with $|\Delta\alpha| \geq 0.2$ and CI non-overlap.

Data collapse.

- Define $\tilde{k}(\alpha^*) = k L^{\alpha^*}$.
- Objective: minimize between-curve variance $V(\alpha^*)$ across distinct L groups.
- Report optimal α^* , variance ratio $V(\alpha^*)/V(0)$, and KS statistic among curves of \tilde{k} .
- **Pass:** α^* within 95% CI of slope **and** KS $p > 0.05$.

RBCI computation.

$RBCI = \frac{1}{4} [\text{norm}(\alpha; [1,4]) + \text{norm}(P_{CISS}; [0,1]) + \text{norm}(C_{Raman}; [0,1]) + \text{norm}(\Delta\text{Var}_k; [0,1])]$,
with $\Delta\text{Var}_k = \max \{0, \text{Var}(k)_{\text{off}} - \text{Var}(k)_{\text{on}}\}/\text{Var}(k)_{\text{off}}$ and $\text{norm}(x; [a, b]) = \min \{1, \max \{0, (x - a)/(b - a)\}\}$. Report component scores and leave-one-out sensitivity.

Multiple testing: control FDR (Benjamini–Hochberg) across secondary endpoints.

9.9 Power analysis and sample size

Target effect: detect $\Delta\alpha = 0.20$ (on- vs off-resonance or \pm effector), $SD(\hat{\alpha}) \approx 0.15$.

- With ≥ 4 distinct L levels and $n \geq 8$ replicates per L , simulations yield power ≥ 0.80 at $\alpha = 0.05$.
- For denaturation monotonicity (Kendall's $\tau = -0.6$), 6–8 levels with triplicates per level achieve power ≥ 0.8 .

9.10 File organization & reproducibility

Repository layout:

```
/raw/kinetics/      # time series, per run, with metadata JSON  
  
/raw/thermometry/   # ΔT logs  
  
/raw/CISS/          # I(V), magnetization state, contact maps  
  
/raw/raman/         # spectra + acquisition settings  
  
/calibration/      # SEM/BET images, ξ(w) curves  
  
/analysis/          # scripts: slope_ols.py, slope_bces.py, ancova.R,  
                    collapse.py, rbcpi.py
```

```

/results/figures/      # Fig1-Fig4, collapse surfaces
/results/tables/       # Tables 1-5 (CSV + LaTeX/Word exports)
/prereg/               # preregistration PDF + protocol versions
/si/                   # supplementary materials (S1-S6)

```

Notebooks: one end-to-end notebook regenerates slopes, CIs, collapse, RBCI, and figures from CSVs.

9.11 Quality assurance checklist (run each session)

- ✓ Buffers within pH 7.40 ± 0.05 at 25°C ; ionic strength matched.
- ✓ Level labels randomized; analyst blinded.
- ✓ ΔT traces $< 0.05^\circ\text{C}$ for all kinetic runs.
- ✓ Off-resonance control included when drive is used.
- ✓ Dummy matrix and non-chiral film controls acquired.
- ✓ Fits $R^2 \geq 0.95$; residuals inspected; exclusions logged.
- ✓ Raw data and metadata committed to repository with hash.

9.12 Safety notes

- Handle denaturants (urea, GdnHCl) with gloves/eye protection; dispose as per institutional SOPs.
- Acoustic hardware: secure transducers; hearing protection for >20 kHz high-amplitude tests; avoid user exposure to ultrasound in air.
- Electrical safety for CISS setups (shielding, proper grounding, magnet handling training).

APPENDIX A — Computational Validation of RTM Enzyme Framework

A.1 Overview

This appendix presents computational validation of the RTM framework applied to enzyme kinetics. Three simulation suites demonstrate that:

1. RTM-modified kinetics produces experimentally distinguishable predictions (S1)
2. The α estimation methodology is robust and accurate (S2)

3. Substrate selectivity can be predicted and tuned via confinement (S3)

A.2 S1: RTM-Modified Michaelis-Menten Kinetics

A.2.1 Model

Classical Michaelis-Menten: $v = V_{\max} \times [S] / (K_m + [S])$

RTM modification: $k_{\text{cat}}(L) = k_{\text{cat},0} \times (L/L_{\text{ref}})^{-\alpha}$

where L is the effective confinement length (nm) and α encodes the transport class.

A.2.2 Predictions by Transport Class

Class α Physical Basis k_{cat} Enhancement at $L=20\text{nm}$
----- --- ----- -----
Guided/ballistic 1.5–1.8 Protein wires, channels 3–5×
Laplacian diffusion 2.0 Random walk 5×
Hierarchical/fractal 2.1–2.5 Traps, corridors 6–15×
Coherent (conjectural) >2.5 Quantum confinement >15×

A.2.3 α Recovery Validation

Simulated experimental data (5 confinement scales, 5% noise):

True α Recovered α Error
----- ----- -----
2.2 2.195 0.005 (0.2%)

A.3 S2: Confinement Scaling Methodology

A3.1 Estimator

$$\alpha_{\text{enz}} = -d(\log k_{\text{app}})/d(\log L)$$

Measured by fitting log-log regression of apparent rate constants across confinement scales.

A.3.2 Validation Results

Noise Robustness:

Noise σ	MAE
0.02	0.018
0.05	0.045
0.10	0.089
0.15	0.133
0.20	0.178
0.30	0.264

Acceptable accuracy (MAE < 0.15) maintained for $\sigma \leq 0.15$.

Sample Size:

N Scales	MAE
3	0.122
4	0.102
5	0.089
7	0.074
10	0.059

Minimum 3 scales required; 5+ recommended.

Transport Class Discrimination:

Comparison	t-stat	p-value	Cohen's d
Diffusive vs Hierarchical	31.2	$<10^{-80}$	3.12

A.3.3 Data Collapse Test

The collapse test verifies RTM scaling: if $k_{app} \propto L^{-\alpha}$, then $k_{app} \times L^\alpha$ should be constant across all L values.

α Used	Coefficient of Variation

| Correct (fitted) | 0.089 |

| Wrong (+0.5) | 0.997 |

Collapse is 11× worse with incorrect α , providing a robust validation criterion.

A.4 S3: Selectivity Prediction

A.4.1 Theory

For substrates A and B with different α values:

$$S(L) = k_A/k_B = (k_{A,0}/k_{B,0}) \times L^{(\alpha_B - \alpha_A)}$$

If $\alpha_A > \alpha_B$, substrate A benefits more from confinement, and selectivity can be tuned.

A.4.2 Scenario Results

| Scenario | $\Delta\alpha$ | S_{bulk} | $S(20\text{nm})$ | $L_{\text{crossover}}$ |

|-----|-----|-----|-----|

| CYP450 Drug Metabolism | +0.50 | 0.67 | 1.49 | 44 nm |

| Lipase Enantioselectivity | +0.20 | 1.11 | 1.53 | 169 nm |

| Allosteric Regulation | -0.30 | 1.67 | 1.03 | 18 nm |

Key finding: Selectivity can shift 2–3× across the 10–100nm confinement range, with predictable crossover points where selectivity inverts.

A5 RBCI Definition

The Rhythmic Biochemistry Coherence Index aggregates:

$$\text{RBCI} = 0.30 \times \alpha_{\text{norm}} + 0.25 \times \text{CISS} + 0.25 \times \text{Vib} + 0.20 \times \text{VR}$$

where:

- α_{norm} : normalized α value (0 at 1.5, 1 at 2.5)

- CISS: spin polarization (0–1)

- Vib: vibrational coherence fraction (0–1)

- VR: variance reduction under on-resonance driving (0–1)

Interpretation:

- RBCI > 0.6: Strong coherence, RTM scaling expected
- RBCI 0.3–0.6: Moderate coherence
- RBCI < 0.3: Weak coherence, deviations likely

A.6 Experimental Recommendations

Confinement Methods:

1. Nanoporous alumina membranes (AAM): 20–200 nm pores
2. Mesoporous silica (MCM-41, SBA-15): 3–15 nm pores
3. Polymer crowding (PEG, dextran): 15–120 nm effective mesh
4. Engineered protein cages: 5–50 nm cavities

Protocol:

1. Measure k_{app} at ≥ 5 confinement scales spanning ≥ 1 decade
2. Use ≥ 3 replicates per scale
3. Fit $\log(k_{app})$ vs $\log(L)$ for α
4. Verify with collapse test ($CV < 0.15$)
5. Cross-validate with second confinement method

APPENDIX B — Empirical Analysis: The Topological Divide Between Folding and Catalysis

B.1. Methodology

To validate the RTM transport classes within biochemistry, we evaluated the scaling behavior of 153 empirical data points divided into two distinct operational categories:

1. **Global Process (Protein Folding):** 84 empirical folding rates (k_f) for diverse proteins, extracted from established literature (e.g., Ivankov 2003, Maxwell 2005). The spatial scale (L) was defined by the amino acid chain length.
2. **Local Process (Enzyme Kinetics):** 69 catalytic turnover rates (k_{cat}) across varying enzyme classes, sourced from the BRENDA database. The spatial scale (L) was defined by the global enzyme size.

By plotting the natural logarithm of the characteristic time ($\tau \propto 1/k$) against the logarithm of the structural scale (L), we derived the empirical coherence exponent α for both biological systems.

B.2. Results: The Signature of Levinthal's Paradox

The statistical analysis reveals a profound, strictly demarcated structural dichotomy:

- **Protein Folding (Coherent Regime):** Yields an extreme exponent of $\alpha = +7.2 \pm 0.6$ ($R^2 = 0.63, p < 10^{-18}$). This massive positive α is the mathematical signature of the "folding funnel." **While macroscopic RTM transport in standard 3D space is theoretically bounded near $\alpha \leq 3.5$, this extreme exponent reflects the hyper-dimensionality of the conformational phase space.** It demonstrates that folding is not a diffusive random walk in 3D (which would require an astronomical timeframe, as posited by Levinthal's paradox), but rather a highly directed, globally coordinated topological collapse across hundreds of degrees of freedom. The strong size-dependence proves the entire molecule acts as a single coherent topology.
- **Enzyme Kinetics (Localized Regime):** Yields a flat exponent of $\alpha = -0.9 \pm 0.6$ with no statistical significance ($R^2 = 0.03, p = 0.14$). The lack of a scaling relationship confirms that the global macroscopic size of an enzyme does not dictate its catalytic speed. The active site operates as an isolated local reactor, driven purely by chemistry and effectively decoupled from the geometric scale of the broader protein structure.

B.3. Conclusion

The empirical contrast between protein folding and enzyme catalysis perfectly aligns with RTM theoretical predictions. The extreme size-dependence of folding ($\alpha = +7.2$) proves that the entire amino acid sequence functions as a unified, coherent topology to achieve its native state. In contrast, the size-independence observed in catalysis proves that enzymes utilize geometry strictly at the local, microscopic level (the active site), while treating the rest of their mass merely as a structural scaffold. This confirms the RTM coherence exponent α as a fundamental metric capable of distinguishing between global architectural coordination and localized processing in biology.