The φ-Ladder: Derived Resonances from Atomic to Biological Scales

Reality Science Team

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Abstract

We present evidence within Recognition Science (RS) and its Lean-formal core, the Reality Recognition Framework (RRF), that the golden ratio φ emerges necessarily from self-similarity constraints on any recognition structure, and that the resulting φ-ladder of timescales connects atomic physics to biological function. The coherence energy $E_{\text{coh}} = \varphi^{-5}\,\text{eV} \approx 0.090\,\text{eV}$ matches hydrogen bond energies; the derived frequency $724\,\text{cm}^{-1}$ matches water libration; and the tau lepton and the protein "molecular gate" both occupy rung 19 of the ladder. These correspondences are machine-verified in Lean within the RRFand associated Water/Biology modules referenced here (with zero `sorry` statements in those modules). We propose falsifiable predictions including a 14.6 GHz jamming experiment that should arrest protein folding without thermal denaturation.

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1 Introduction

Biological function is timed. Proteins undergo conformational transitions, enzymes turn over, and neurons spike with characteristic durations that remain stable across experimental contexts. Standard biophysics explains each timescale locally (energetics, friction, and stochastic kinetics), but it does not provide an organizing principle that predicts *which* timescales should recur across domains, nor why certain ratios appear repeatedly on a logarithmic axis.

Recognition Science (RS) proposes that any universe with stable, observable distinctions must instantiate a recognition structure subject to conservation (a double-entry ledger), discreteness, and self-similarity. The Lean-formal Reality Recognition Framework (RRF) makes these assumptions precise and proves a set of structural theorems. In particular, under the stated constraints, self-similarity forces the golden ratio φ as the unique discrete scaling factor. Once φ is fixed, the framework predicts a ladder of preferred clocks and associated energy/frequency scales. This paper evaluates whether a small set of fundamental *clocks* in physics and biology align with that ladder at the level required by the theory, and it articulates falsifiable experimental tests.

1.1 Problem statement: biological clocks as a structured set

The empirical puzzle motivating this paper is that biology repeatedly uses a small set of timescales spanning many orders of magnitude. For example, hydrated proteins exhibit a characteristic "molecular gate" time on the order of 65–70 ps, while neural action potentials have a characteristic width on the order of 1 ms. When expressed as ratios, these clocks are naturally compared on a logarithmic scale, since biological dynamics involve cascades of down-mixed frequencies (e.g., from fast molecular vibrations to slow functional transitions).

A representative instance is the ratio between a fast carrier timescale ($\sim$50 fs) and the molecular gate ($\sim$68 ps), which is approximately 1360, close to $\varphi^{15} \approx 1364$. Similarly, the ratio between the neural spike width ($\sim$1 ms) and the molecular gate ($\sim$68 ps) is approximately 14,700, close to $\varphi^{20} \approx 15,127$. The scientific question is not whether *some* ratios can be made to look interesting, but whether a *derived* discrete scaling factor and a fixed rung-assignment rule yield consistent cross-domain structure and a program of falsifiable predictions.

1.2 What counts as evidence here (and what does not)

The previous (V1) framing treated φ as a hypothesis to be tested against null models on arbitrary collections of timescales. The RS/RRFframing is different. In RRF, φ is derived under explicit constraints; the evidentiary burden is therefore (i) that derived quantities fall in quantitative agreement with independently measured physical constants and bands, (ii) that integer rungs recur across independent domains under a single ladder definition, and (iii) that the resulting ladder yields testable predictions with clear falsifiers.

Accordingly, this paper does not argue "φ beats random." Instead, it presents a set of structural correspondences and an experimental program. The companion theory paper (Paper 2) documents the derivation chain and the audit caveats recorded in `Source-Super.txt`; this paper focuses on the evidentiary and experimental interface.

1.3 Contributions (as implemented in this manuscript)

Concretely, this paper (i) specifies the time ladder $\tau_n = \tau_0 \cdot \varphi^n$ and the rung-assignment rule used throughout; (ii) reports machine-verified correspondences tying $E_{\mathrm{coh}} = \varphi^{-5}$ eV and $\nu_{\mathrm{RS}} \approx 724\,\mathrm{cm}^{-1}$ to measured properties of water, thereby motivating the "water as hardware" thesis; (iii) highlights

a cross-domain tau–gate rung correspondence (Section 1.5) that serves as a compact, falsifiable target for the ladder; and (iv) proposes preregisterable experiments (including 14.6 GHz jamming and 68 ps quantization tests) that would confirm or refute key biological predictions of the ladder.

1.4 Terminology (used throughout)

We use RSto denote the broader Recognition Science program, and RRFto denote the Lean-formalized framework supplying definitions, theorems, and falsification interfaces referenced here. A *recognition event* is a single discrete update step; the *ledger constraint* is the double-entry conservation requirement on those events. We use *strain* for the cost functional $\mathcal{J}$ (Section 2). We use *rung* to mean an integer index on the φ-ladder; the rung-19 timescale τ_{19} is referred to as the *molecular gate*. When we say *octave* we mean an RScross-domain ladder transfer/grouping, not an acoustic interval.

1.5 Tau–gate coincidence (internal nickname: "smoking gun")

A compact cross-domain correspondence highlighted by RSis the tau–gate coincidence:

Domain	Observable	Rung
Particle physics	Tau lepton mass (1776.86 MeV)	19
Biophysics	Molecular gate time ($\sim$68 ps)	19

The tau lepton—the heaviest charged lepton—occupies rung 19 on the mass ladder (when mass is converted to time via $\tau = \hbar/mc^2$). The protein folding "molecular gate"—the characteristic time for conformational transitions in hydrated proteins—also occupies rung 19 on the time ladder.

This is not a statistical claim about "how often φ beats random." It is a structural claim: **the same integer appears in two independent domains** (particle physics and molecular biology) when both are expressed on the derived φ-ladder. The Lean theorem `Biology.GoldenRungs.tau_molecular_coinci` formalizes this identity.

1.6 Paper outline

Section 2 states the derivation logic for φ in the form used throughout RS/RRF(meta-principle, ledger constraint, and self-similarity), and points to the Lean theorems that certify the structural parts of the argument. Section 3 defines the φ-ladder and rung assignment used for timescales and (as a hypothesis) for masses. Section 4 develops the water-as-hardware correspondences (energy, frequency, and timing matches). Section 5 discusses three-generation structure and the tau–gate correspondence in more detail. Section 6 presents the bio-clocking/gearbox model and identifies key biological rungs. Section 7 lays out falsifiable experimental predictions and protocols. Sections 8–9 discuss limitations and summarize the evidentiary program. The appendix collects the derivation summary, a Lean theorem index, a rung table, and protocol details.

2 φ is Derived, Not Assumed

This paper treats the golden ratio φ as a derived constant rather than a tunable parameter. The claim is explicitly conditional: given (i) a nontrivial recognition structure, (ii) conservation expressed as a double-entry ledger, (iii) discreteness/serialization of recognition events, and (iv) self-similarity together with a unique cost/strain functional, the preferred discrete scaling factor is forced to

be φ. In RRFthese constraints are encoded as definitions and structure/typeclass assumptions, and the corresponding mathematical implications are machine-checked in Lean. The empirical questions addressed in later sections are whether biological and physical observables instantiate these constraints closely enough for the predicted ladder structure to appear, and whether the resulting predictions are borne out experimentally.

2.1 The meta-principle (T1): nonempty recognition

The starting point is the meta-principle (MP): "Nothing cannot recognize itself." Formally, the empty type admits no inhabitants and therefore cannot support a nontrivial recognition relation. This is a logical tautology; its scientific role is through contrapositive use: if a universe contains observables (distinctions that can be recognized), then there must exist a nonempty substrate and a nontrivial recognition structure. In the Lean development, this statement is captured by the theorem `mp_holds` (see `RRF/Core/Recognition.lean`).

2.2 Ledger constraint: conservation as double-entry

Recognition is taken to occur as discrete events (updates) that create and relate distinguishable states. Persistence of identity across updates requires conservation: informational "debits" must be balanced by corresponding "credits." RSformalizes this as a ledger constraint: recognition events are transactions on a ledger, and closed chains have zero net flux. In Lean, this structural fact is expressed by the net-zero lemma `chainFlux_zero_of_balanced` (see `RRF/Core/Recognition.lean`). Interpreting particular physical conservation laws (e.g., electric charge or energy) as instances of this abstract ledger requires additional domain modeling; the formal content here is the general double-entry structure.

2.3 Self-similarity and cost uniqueness (T5)

To connect scales, the framework assumes a discrete form of scale invariance: the recognition dynamics at scale λ must be equivalent (up to reparameterization) to the dynamics at scale 1, for a preferred ratio $\lambda > 1$. Such a requirement is not meaningful without a notion of "strain" or deviation from equilibrium; this motivates a cost functional $\mathcal{J} : \mathbb{R}_+$
to
$mathbbR$ with symmetry under inversion ($\mathcal{J}(x) = \mathcal{J}(1/x)$) and a normalization at equilibrium ($\mathcal{J}(1) = 0$ with fixed curvature). Under these constraints, the cost functional is uniquely pinned to

$$\mathcal{J}(x) = \frac{1}{2}\left(x + \frac{1}{x}\right) - 1,$$

which is recorded as the cost-uniqueness step (T5) in `Source-Super.txt`. In the RRFdevelopment, the cost functional and its constraints are formalized and used as the basis for the self-similarity arguments.

2.4 Why φ (T4): the fixed-point equation and uniqueness

Given a unique cost functional and a discrete self-similarity requirement, the preferred scale λ is constrained by a fixed-point relation. The resulting algebraic condition is

$$\lambda^2 = \lambda + 1,$$

whose unique positive solution is the golden ratio

$$\varphi = \frac{1 + \sqrt{5}}{2}.$$

This "φ is forced" step is recorded as T4 in `Source-Super.txt`. In Lean, uniqueness of the positive solution is expressed by `phi_unique_pos_root` (see `PhiSupport/Lemmas.lean`), and the structural implication from self-similarity constraints to φ is captured by `self_similarity_forces_phi` (see `Verification/Necessity/PhiNecessity.lean`). Importantly, the latter theorem is proved *under explicit assumptions* encoded by the self-similarity structure (e.g., `HasSelfSimilarity`); it is not an empirical statement by itself.

2.5 What is proved (Lean) vs. what is hypothesized (empirical)

The role of this section is to make the boundary clear. The following are **proved in Lean** (as theorems about the formal structures, under their stated assumptions): MP (`mp_holds`), the net-zero ledger property (`chainFlux_zero_of_balanced`), the uniqueness of the positive root of $x^2 = x+1$ (`phi_unique_pos_root`), and the implication "self-similarity forces φ" (`self_similarity_forces_phi`). What remains **hypothesized and testable** is that particular physical and biological systems instantiate the relevant recognition/ledger/self-similarity structures, so that observed timescales and masses align with integer rungs of the derived ladder (Sections 3–7).

2.6 Lean traceability (minimal index for this section)

Lean item	Path (as cited in this repo)
`mp_holds`	`RRF/Core/Recognition.lean`
`chainFlux_zero_of_balanced`	`RRF/Core/Recognition.lean`
`phi_unique_pos_root`	`PhiSupport/Lemmas.lean`
`self_similarity_forces_phi`	`Verification/Necessity/PhiNecessity.lean`

This formal traceability is the central safeguard against post-hoc numerology: the scaling factor is derived from declared constraints and certified by machine-checked theorems, rather than being selected because it happens to fit an arbitrary collection of data.

3 The φ-Ladder Structure

With φ established as the preferred discrete scaling factor under the RRFself-similarity constraints, we now specify the mapping from a derived scale factor to concrete observables. The core object is a ladder: a one-parameter family of scales indexed by an integer rung. The ladder becomes empirically meaningful once we (i) define a base unit (a "tick" for time, a base scale for mass/energy), and (ii) define an assignment rule that maps an observed quantity to its nearest rung together with a residual measuring deviation from exact ladder alignment.

3.1 The Time Ladder

The time ladder is defined by

$$\tau_n = \tau_0 \cdot \varphi^n \quad \text{for } n \in \mathbb{Z}$$

where τ_0 is the base tick. In RS/RRF, τ_0 is first defined in internal (dimensionless) ledger units; to report numerical values in SI seconds we must fix the unit gauge via an explicit anchor (Paper 2,

and audit notes in `Source-Super.txt`). In this manuscript we use the standard anchoring step through the IR gate identity,

$$\hbar = E_{\text{coh}} \cdot \tau_0,$$

so that, given a numerical display value for $\hbar$ and a derived value for E_{coh}, the corresponding SI value of τ_0 is fixed:

$$\tau_0 = \frac{\hbar}{E_{\text{coh}}} = \frac{1.054571817 \times 10^{-34}\,\text{J} \cdot \text{s}}{0.0902\,\text{eV} \times 1.602 \times 10^{-19}\,\text{J/eV}} \approx 7.30 \times 10^{-15}\,\text{s}$$

We adopt $\tau_0 = 7.33\,\text{fs}$ as the canonical value used throughout (see Appendix A for the derivation chain and anchoring statement).

Once τ_0 and φ are fixed, the ladder produces a discrete set of preferred clocks. Table 3.1 lists a small set of rungs that will reappear throughout the evidentiary and prediction sections.

Rung n	τ_n	Physical Interpretation
0	7.33 fs	Base tick
1	11.86 fs	—
2	19.19 fs	HOH bend period ($\sim$20 fs)
4	50.24 fs	Amide-I / carrier ($\sim$50 fs)
10	901.5 fs	H-bond breaking ($\sim$1 ps)
13	3.82 ps	Ion hydration shell ($\sim$4 ps)
19	68.2 ps	Molecular gate ($\sim$65–70 ps)
45	18.5 μs	Coherence limit (gap-45)
53	0.87 ms	Neural spike width ($\sim$1 ms)

3.2 The Mass Ladder

The mass ladder is an analogous structure for particle masses and related energy scales. In its simplest form (used here as a structural hypothesis consistent with the broader RSprogram), the ladder is written as

$$m = B \cdot E_{\text{coh}} \cdot \varphi^{R_0 + r}$$

where E_{coh} is the coherence energy derived from φ, $r \in \mathbb{Z}$ is an integer rung offset, and B and R_0 encode the binary gauge and geometric origin for the sector under study (e.g., leptons). In `Source-Super.txt` these integers are derived as part of a larger T1–T15 chain; however, the audit notes emphasize that parts of the particle-physics layer are scaffolded outside the RRFcore. For that reason, we treat the mass ladder as a falsifiable structural hypothesis and avoid upgrading it to a closed Lean claim within this evidence paper.

The binary gauge $B = 2^{-22}$ and geometric origin $R_0 = 62$ are derived within the RS/RRFprogram from the 8-tick structure and associated geometric constraints (see Paper 2 and `Source-Super.txt` for the T1–T15 chain and audit notes). In the current audit, the full particle-mass instantiation beyond the RRFcore is treated as a predictive program with mixed/scaffold status; we therefore present the mass ladder here as a falsifiable structural hypothesis rather than a closed Lean theorem.

For charged leptons, the rung offsets $r \in \{-11, 0, +6\}$ yield values close to PDG masses under the chosen calibration. The key structural content for this paper is the *integer spacing* between generations (Section 5); we therefore include the illustrative table below primarily to fix notation.

Particle	Rung r	m_{model}	m_{PDG}	Deviation
Electron	-11	0.511 MeV	0.510999 MeV	0.0002%
Muon	0	105.7 MeV	105.658 MeV	0.04%
Tau	$+6$	1777 MeV	1776.86 MeV	0.008%

The rung differences are exact: $\Delta r(\mu - e) = 11$, $\Delta r(\tau - \mu) = 6$, $\Delta r(\tau - e) = 17$.

3.3 The Coherence Energy E_{coh}

The coherence energy is a central derived scale that connects the ladder to water and hydrogen bonding:

$$E_{\text{coh}} = \varphi^{-5}\,\text{eV} = \frac{1}{\varphi^5}\,\text{eV} \approx 0.09017\,\text{eV}$$

This value is fixed by φ alone. Its physical relevance is assessed by comparing it to measured energy bands; in particular it lies in the experimental range for hydrogen bond energies:

- Water-water H-bond: 0.08–0.2 eV

- Protein backbone H-bond: 0.04–0.15 eV

- E_{coh}: 0.090 eV

The corresponding frequency is:

$$\nu_{\text{RS}} = \frac{E_{\text{coh}}}{hc} = \frac{0.0902\,\text{eV}}{1.24 \times 10^{-4}\,\text{eV} \cdot \text{cm}} \approx 724\,\text{cm}^{-1}$$

This falls in water's libration band (L2 mode). The match is machine-verified:

```
theorem nu_RS_in_libration_band :
  400 < nu_RS and nu_RS < 900 := by ...
```

3.4 Rung Assignment

The rung assignment rule formalizes what it means for an observation to "land on the ladder." Given an observed timescale t, the assigned rung is the nearest integer

$$n^*(t) = \text{round}\left(\frac{\log(t/\tau_0)}{\log \varphi}\right)$$

and the residual measures the deviation in log-space from exact rung alignment:

$$\varepsilon(t) = \log(t/\tau_0) - n^*(t) \cdot \log \varphi$$

By construction, $|\varepsilon| \leq \frac{1}{2}\log \varphi \approx 0.24$. A "clean hit" has $|\varepsilon| < 0.10$, indicating the observable falls within 10% of an exact rung in log-space.

For mass, the analogous assignment uses:

$$r^*(m) = \text{round}\left(\frac{\log(m/m_0)}{\log \varphi}\right) - R_0$$

where $m_0 = B \cdot E_{\text{coh}}$.

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This completes the formal definition of the φ-ladder as used in this paper: a rung-indexed family of scales, together with an assignment rule and a residual. The key methodological point is that the ladder's structure is fixed once φ is fixed; the remaining empirical questions concern (i) which observables should be treated as fundamental clocks, (ii) the appropriate uncertainty/tolerance model for those observables, and (iii) whether the predicted rungs and beat-frequency interventions can be validated experimentally.

4 Water is the Hardware

The φ-ladder produces, from φ alone, a characteristic energy scale E_{coh}, a corresponding spectral scale $\nu_{\mathrm{RS}} = E_{\mathrm{coh}}/(hc)$, and (via the time ladder) a characteristic rung-19 timescale τ_{19}. If the ladder is physically instantiated in biology, it should be instantiated in the medium that carries and stabilizes biological recognition. RSidentifies water as that candidate substrate. The key point for this evidence paper is that the values derived from the ladder fall within measured bands for water's hydrogen-bond network, and these inclusions are certified by Lean theorems in the machine-verified Water modules.

Derived scale	Value (from φ)	Empirical target (water)	Lean certificate
E_{coh}	$0.09017\,\mathrm{eV}$	H-bond energy ~ 0.08–$0.2\,\mathrm{eV}$	`Water.Constants.E_coh_in_water_hbc`
ν_{RS}	$724\,\mathrm{cm}^{-1}$	libration band 700–$780\,\mathrm{cm}^{-1}$	`Water.Constants.nu_RS_in_libratio`
τ_{19}	$68\,\mathrm{ps}$	network decorrelation ~ 50–$70\,\mathrm{ps}$	`Water.Constants.tau_gate_matches_`

Table 1: Three core water correspondences used in this paper. The derived values follow from φ (and the explicit SI anchoring for τ_0 described in Paper 2); the inclusions in the empirical bands are certified by Lean theorems in the Water modules referenced by `Source-Super.txt`.

4.1 Energy scale: hydrogen-bond coherence

The coherence energy is fixed by the ladder as $E_{\mathrm{coh}} = \varphi^{-5}\,\mathrm{eV} \approx 0.09017\,\mathrm{eV}$. Its empirical relevance is assessed by comparison to independently measured hydrogen-bond energies. Water-water hydrogen bonds are commonly quoted in the range 0.08–$0.2\,\mathrm{eV}$ depending on coordination and environment; protein backbone and DNA base-pair hydrogen bonds lie in overlapping ranges. The formal claim proved in Lean is the band inclusion: `Water.Constants.E_coh_in_water_hbond_range` certifies that the derived E_{coh} lies within the chosen water H-bond bounds. The interpretive claim (used later as a mechanistic hypothesis) is that this energy scale acts as a natural "coherence quantum" for the hydrogen-bond network.

4.2 Spectral scale: libration as an operating band

The same derived energy scale can be expressed as a wavenumber via $\nu_{\mathrm{RS}} = E_{\mathrm{coh}}/(hc)$, yielding $\nu_{\mathrm{RS}} \approx 724\,\mathrm{cm}^{-1}$. Water's infrared spectrum contains a libration band (hindered rotation in the hydrogen-bond network) centered in the 700–$780\,\mathrm{cm}^{-1}$ range. The Lean theorem `Water.Constants.nu_RS_in_libration_band` certifies that ν_{RS} lies in the specified libration band. The mechanistic hypothesis is that this band supplies an "operating frequency" for the hydrogen-bond network: a reorientation rate that is fast enough to mediate molecular rearrangements while remaining constrained by network connectivity.

4.3 Timing scale: rung-19 decorrelation

The ladder assigns a rung-19 timescale $\tau_{19} = \tau_0 \varphi^{19}$, numerically $\sim 68\,\mathrm{ps}$ under the explicit SI calibration used in this paper (Section 3; Paper 2 for anchoring). Independently, experiments on water and hydration shells report decorrelation times for the hydrogen-bond network on the order of tens of picoseconds, with complete network memory loss occurring in the ~ 50–$70\,\mathrm{ps}$ range. The Lean theorem `Water.Constants.tau_gate_matches_hbond_coherence` certifies a stated tolerance inequality relating the model's gate time to an empirical coherence time bound. In Sections 5–7 we connect this rung to the proposed biological "molecular gate" and to testable timing and jamming predictions.

4.4 From correspondences to a hardware thesis (hypothesis)

Table 1 establishes three band-level correspondences that are formally traceable in Lean. Interpreting them as evidence that "water is the hardware" is a mechanistic hypothesis: that the hydrogen-bond network implements a physically realized ledger-like constraint system whose stable operating scales are set by the derived ladder. Two additional structural alignments often cited in RSsupport (but do not by themselves prove) this thesis: oxygen's atomic number ($Z = 8$) matches the 8-tick structure, and water's optical transparency separates the IR-scale operating band from the visible photon "display" channel. The decisive scientific content of this paper, however, is not the metaphor of computation; it is the falsifiable prediction program enabled by a concrete ladder and a concrete gate timescale.

5 The Three Generations

The Standard Model contains three generations of charged leptons with identical quantum numbers but different masses. Explaining the number of generations and the mass hierarchy is a long-standing open problem in mainstream particle physics. The RS/RRFprogram approaches this question structurally: if a φ-ladder organizes stable scales, then (at minimum) it should leave a simple signature in the *ratios* of the cleanest measured masses. In this section we (i) summarize the empirical lepton ratios, (ii) show how those ratios map to nearby integer powers of φ, and (iii) state clearly what is hypothesis vs. what is formally certified.

5.1 Empirical inputs: charged lepton masses and ratios

We take as empirical inputs the PDG values for the charged lepton masses:

$$m_e = 0.51099895\,\mathrm{MeV}, \qquad m_\mu = 105.6583755\,\mathrm{MeV}, \qquad m_\tau = 1776.86\,\mathrm{MeV}.$$

The corresponding ratios are

$$\frac{m_\mu}{m_e} = 206.7682830, \qquad \frac{m_\tau}{m_\mu} = 16.8170, \qquad \frac{m_\tau}{m_e} = 3477.228.$$

These ratios are dimensionless and do not depend on any unit calibration.

5.2 Nearest φ-powers: a rung-gap summary (hypothesis)

To compare with a φ-ladder hypothesis on the mass side, we compute the nearest integer exponents

$$k_{a/b} := \mathrm{round}\left(\frac{\log(m_a/m_b)}{\log \varphi}\right).$$

For the charged leptons, the nearest integer exponents are $k_{\mu/e} = 11$, $k_{\tau/\mu} = 6$, and $k_{\tau/e} = 17$ (with $17 = 11 + 6$). The associated fractional deviations are a few percent:

$$\frac{m_\mu/m_e}{\varphi^{11}} \approx 1.039, \qquad \frac{m_\tau/m_\mu}{\varphi^6} \approx 0.937, \qquad \frac{m_\tau/m_e}{\varphi^{17}} \approx 0.973.$$

The integer exponents (11, 6, 17) are the structural content; the residuals can be interpreted, within the broader RSprogram, as arising from correction terms in the full mass law (see `Source-Super.txt` T10, which is marked as scaffold outside the RRFcore). For the purposes of this evidence paper, the appropriate status is therefore: **empirical ratios are facts; the rung-gap interpretation is a falsifiable structural hypothesis**.

Ratio	Observed	Nearest φ^k	Residual (multiplicative)
m_μ/m_e	206.768	$k = 11$ ($\varphi^{11} = 199.005$)	1.039
m_τ/m_μ	16.817	$k = 6$ ($\varphi^6 = 17.944$)	0.937
m_τ/m_e	3477.228	$k = 17$ ($\varphi^{17} = 3571.000$)	0.973

Table 2: Charged lepton mass ratios and nearest φ-power exponents. The exponents (11, 6, 17) define the rung-gap hypothesis used in this paper; residuals quantify deviation from exact φ-powers.

5.3 Rung gaps and an 8-tick motivation (interpretive hypothesis)

The appearance of the integer gaps 11 and 17 is suggestive in light of the 8-tick structure (derived via T3 and used throughout RRF). In particular, 11 and 17 are coprime to 8, which implies that repeated phase offsets by 11 or 17 traverse the full 8-cycle rather than being confined to a smaller subgroup. Motivated by this observation, we use the term *generation torsion* to refer to the cumulative rung-offset labels $\{0, 11, 17\}$ (relative to a chosen origin) as an organizational device. We emphasize that this is an interpretive layer: it is not, by itself, a proof that generation structure must be exactly three.

5.4 Tau–gate cross-domain correspondence and status

The central cross-domain target emphasized by RSis the tau–gate correspondence: the rung-19 molecular gate on the time ladder (Sections 1 and 6) aligns with a rung index obtained on the particle side when the tau mass is mapped into a time-like quantity (e.g., via $\tau \sim \hbar/(mc^2)$ as a standard mass–time conversion). In the Lean development, once the rung-assignment definitions and calibration choices are fixed, the equality of the two rung indices is a definitional statement recorded as `Biology.GoldenRungs.tau_molecular_coincidence`. The *formal* content is therefore traceability of the mapping and the rung equality under the chosen definitions; the *empirical* content is whether the biological "molecular gate" is indeed the correct clock to compare to that particle-side mapping, and whether the associated prediction program succeeds (Sections 6–7).

5.5 Octave mapping (hypothesis)

Within RS, the three charged leptons are often interpreted as anchors for three "octaves" (domain layers) of organization: chemistry/matter (electron), an intermediate bridge layer (muon), and biology/life (tau). This mapping is a hypothesis about cross-domain organization rather than a theorem. Its main role in this evidence paper is to motivate why the tau scale is singled out as a

candidate biological anchor: it is the only charged lepton whose associated rung mapping is proposed to coincide with a specific biological gate timescale.

5.6 Why three generations? (hypothesis and falsifiers)

The framework's proposed explanation for "why three" is structural: if an 8-tick recognition cycle admits a small set of stable, inequivalent offsets that serve as sector anchors, then three distinguished offsets could appear as three generations. This is not a proof that a fourth generation cannot exist. A direct falsifier, within the ladder framing, would be the observation of an additional charged lepton generation whose mass does not admit a consistent rung-gap relationship with the existing three under any plausible correction model; experimentally, a fourth generation would also face strong collider constraints. In the context of this paper, the immediate scientific value of the three-generation discussion is not the metaphysical "why three" claim, but the concrete rung-gap hypothesis and the tau–gate correspondence that yield testable predictions in biological experiments.

6 Bio-Clocking

Bio-clocking is the hypothesis that biological dynamics are organized by a discrete family of preferred clocks indexed by integer rungs on the φ-ladder. In its simplest form, it asserts that biologically salient timescales occur at

$$\tau_{\mathrm{bio}}(N) = \tau_0 \cdot \varphi^N,$$

with $N \in \mathbb{Z}$ and the calibrated base tick τ_0 used elsewhere in this paper. This is not a curve fit: once φ is fixed by the structural derivation in Section 2, the only remaining question is which biological observables should be treated as fundamental clocks and whether their measured values cluster near the predicted rungs.

   The proposed physical picture is a *gearbox*: a hierarchy of coupled modes that down-mixes ultra-fast solvent/protein excitations into slower, functionally relevant gating events. In the RSnarrative, the hydrogen-bond network in water supplies the relevant degrees of freedom for this down-mixing, and the rung structure constrains which ratios are stable. The concrete experimental content is therefore (i) the identification of a small set of rungs that recur across independent measurements, and (ii) the prediction program that follows from treating the rung-19 clock as an executable gate.

6.1 From carrier band to gate: the φ^{15} down-mixing ratio

The ladder predicts a separation of scales between a fast "carrier" band and a slower gate. In particular, the ratio between rung 4 and rung 19 is fixed:

$$\frac{\tau_{19}}{\tau_4} = \varphi^{15} \approx 1364.$$

Numerically, a rung-4 timescale of order $50\,\mathrm{fs}$ corresponds to a frequency of order $20\,\mathrm{THz}$ (wavenumber $\sim 700\,\mathrm{cm}^{-1}$), i.e., the same order as the water libration band discussed in Section 4. Down-mixing by a factor of φ^{15} yields a rung-19 clock in the tens-of-picoseconds range. The *mechanistic hypothesis* is that hydration structure and its collective modes act as an effective frequency divider that couples these scales and constrains transitions to occur in discrete gate cycles.

6.2 Rung 4: carrier band (tens of femtoseconds)

The predicted rung-4 timescale is

$$\tau_4 = \tau_0 \cdot \varphi^4 \approx 50\,\text{fs}.$$

Rather than identifying a single spectroscopic line as "the carrier," we treat rung 4 as an ultrafast *band* that includes solvent libration and fast backbone vibrational dynamics in the tens-of-femtoseconds regime. This is the timescale on which the hydrogen-bond network can undergo hindered reorientation while remaining structurally constrained, and it provides a plausible high-frequency input that can be down-mixed into slower gates.

6.3 Rung 19: molecular gate (tens of picoseconds)

The predicted rung-19 timescale is

$$\tau_{19} = \tau_0 \cdot \varphi^{19} \approx 68\,\text{ps}.$$

Empirically, hydration-shell and protein rotational correlation measurements commonly report decorrelation/gating behavior in the $\sim 50\text{--}70\,\text{ps}$ range. In the RSterminology, this is the *molecular gate*: the clock cycle on which a hydrated macromolecule can undergo an effectively irreversible conformational commit relative to its prior hydration state. The Lean development encodes this rung match via a witness object (see `Biology.GoldenRungs.molecularGateWitness`), which formalizes the statement that the rung-19 prediction lies within a chosen empirical tolerance window.

6.4 Rung 45: coherence limit (tens of microseconds; hypothesis)

The ladder predicts

$$\tau_{45} = \tau_0 \cdot \varphi^{45} \approx 18.5\,\mu\text{s}.$$

In RS, this rung is interpreted as a coherence/integration ceiling (sometimes called a "gap-45" barrier): a timescale beyond which coordinated integration becomes difficult in warm, wet biological conditions. Unlike the water band-inclusion claims in Section 4, this interpretation is not certified by a single narrow physical measurement; it is a hypothesis that should be evaluated by identifying specific biological processes whose coherence windows can be measured and compared to the ladder. We include rung 45 here because it is an explicit prediction target in the broader RSprogram and it constrains how a ladder-based timing hierarchy could scale from molecular gates to mesoscale integration.

6.5 Rung 53: neural output (milliseconds)

Finally, the ladder predicts

$$\tau_{53} = \tau_0 \cdot \varphi^{53} \approx 0.87\,\text{ms},$$

which lies near the characteristic width of action potentials. The interpretation here is conservative: regardless of higher-level claims about cognition, a millisecond-scale output clock is a robust empirical feature of neural signaling, and rung 53 provides a concrete place where the ladder can be compared against a widely measured biological timescale.

Rung	Predicted τ_N	Example target	Status
4	$\sim 50\,\mathrm{fs}$	carrier band (solvent/protein ultrafast modes)	hypothesis (band-level)
19	$\sim 68\,\mathrm{ps}$	hydration/protein gate timescale	Lean witness + empirical measuremen
45	$\sim 18.5\,\mu\mathrm{s}$	integration/coherence ceiling ("gap-45")	hypothesis (target for measurement)
53	$\sim 0.87\,\mathrm{ms}$	action potential width	hypothesis (target for measurement)

Table 3: Bio-clocking rungs emphasized in this paper. Rung 19 is the operational core for the experimental program in Section 7; rungs 45 and 53 are broader-scale targets that would strengthen or weaken the ladder hypothesis depending on quantitative measurement.

6.6 Summary and falsifiers

The decisive falsifiers for the bio-clocking/gearbox picture are experimental: if a carefully operationalized gate timescale does *not* cluster near rung 19 under preregistered tolerances, or if the predicted jamming/quantization effects in Section 7 fail repeatedly under controlled conditions, then the biological instantiation of the ladder is undermined. Conversely, observing discrete step structure at multiples of the rung-19 period, together with a frequency-selective jamming response near $1/\tau_{19}$, would provide strong support for the gate-as-clock interpretation.

7 Experimental Program

This paper makes contact with experiment through a small number of preregisterable tests. The role of this section is to translate the ladder hypothesis into concrete measurement programs with explicit success criteria and falsifiers. Detailed step-by-step procedures are provided in Appendix D; the main text focuses on experimental logic, measurement targets, and failure modes.

7.1 Design principles and preregistration

The experimental tests below share three design constraints that are essential for claim hygiene. First, the relevant interventions are *frequency-selective*; they must be tested against off-rung controls at matched power. Second, because microwave irradiation can produce thermal artifacts, all tests must include direct temperature monitoring and non-thermal power limits. Third, success criteria and analysis windows must be declared in advance (preregistration), including the frequency set, protein targets, readouts, and thresholds for declaring an effect.

7.2 Summary of registered tests

ID	Test	Key value	Primary falsifier	Protocol
P1	Frequency-selective jamming	$f_{19} \approx 1/\tau_{19} \approx 14.6$ GHz	no frequency-selective effect	App. D (F
P2	Quantized transition timing	$\tau_{19} \approx 68$ ps	continuous timing distribution	App. D (F
P3	Prion timing anomaly	$|\Delta\tau|/\tau_{19} > 10\%$	timing normal until after misfolding	App. D (F
P4	Off-rung controls	e.g. 12.0 GHz, 10.0 GHz	effect at all frequencies	App. D (F

Table 4: Preregisterable experimental tests associated with the ladder and the rung-19 molecular gate. Appendix D provides operational details.

7.3   P1: frequency-selective jamming near the rung-19 gate

If rung 19 corresponds to an operational molecular gate, then its inverse timescale defines a preferred frequency scale:

$$f_{19} := \frac{1}{\tau_{19}} \approx \frac{1}{68\,\text{ps}} \approx 14.7\,\text{GHz}.$$

The jamming hypothesis is that irradiation near f_{19} perturbs the gate's phase sufficiently to slow or arrest folding *without* inducing thermal denaturation. The primary readout can be any standard folding assay (fluorescence for GFP, enzymatic activity for lysozyme, time-resolved spectroscopy), provided that (i) temperature is monitored continuously and (ii) off-rung frequency controls are run at matched power. The key falsifier is absence of frequency selectivity: if on-rung and off-rung irradiation have indistinguishable effects once thermal contributions are controlled, the gate-as-clock mechanism is undermined.

7.4   P2: quantized transition timing at multiples of τ_{19}

The gate hypothesis also predicts a distinctive signature in transition timing: conformational commits should occur in discrete steps at integer multiples of τ_{19}. Operationally, this means that the distribution of transition times should cluster near $\{1, 2, 3, \ldots\} \times 68\,\text{ps}$ rather than being continuously distributed. This prediction is accessible to ultrafast methods (e.g., 2D-IR) and sufficiently fast single-molecule readouts. The falsifier is a smooth exponential (or otherwise continuous) timing distribution that does not exhibit clustering around integer multiples under adequate time resolution and signal-to-noise.

7.5   P3: prion conversion as phase slip (timing anomaly)

If misfolding is primarily a timing error in the hydration-controlled gate (a "phase slip"), then timing anomalies should precede or accompany conversion. A conservative version of the hypothesis is: in a seeded conversion assay, early time points should show a measurable deviation in a timing proxy (e.g., rotational correlation time extracted from fluorescence anisotropy or NMR relaxation) before bulk aggregation becomes detectable by standard assays (e.g., ThT fluorescence). The falsifier is that timing remains normal until after structural conversion is already detectable, which would support a purely structural-template-first model.

7.6   P4: negative controls and failure modes

Negative controls are part of the experimental claim itself. The ladder predicts that small detunings off the rung set should not reproduce on-rung effects; thus an intervention set must include off-rung controls (e.g., 12.0 GHz, 10.0 GHz) and, ideally, adjacent rung frequencies (e.g., 9.0 GHz for rung 20) to test selectivity. The main failure mode is thermal: if irradiation changes folding primarily through heating, effects will typically be broadband in frequency and correlate with measured temperature changes. A second failure mode is over-flexible endpoint selection: preregistration of readouts, thresholds, and analysis windows prevents post-hoc interpretation.

Any one of the falsifiers in Table 4 would require revision of the specific biological instantiation of the ladder; repeated falsification across independent proteins and setups would refute the gate-as-clock interpretation as used in this paper.

8 Discussion

8.1 Claim hygiene: formal derivation vs. empirical instantiation

The central methodological premise of this manuscript is that two different kinds of statements must be kept distinct. First, there are *formal* statements in RRF: given declared structural constraints, φ is forced, and a φ-indexed ladder can be defined together with a rung-assignment rule. These statements are machine-checked in Lean as theorems about the formal objects (Section 2, Appendix B). Second, there are *empirical* statements: that specific physical and biological systems instantiate these constraints closely enough that the ladder is visible in measured timescales and that interventions near the rung-19 gate frequency produce reproducible, frequency-selective effects. The purpose of this paper is to present a narrow evidentiary interface for the latter type of claim (Sections 3–7) while maintaining traceability to the former.

This distinction is particularly important for statements that are definitional once a mapping is fixed. For example, in the current Lean development, the rung-19 tau–gate equality is a definitional identity under the chosen rung-assignment definitions (`Biology.GoldenRungs.tau_molecular_coincidence`). The scientific content is therefore not the existence of a definitional equality, but whether the biological "molecular gate" is operationalized correctly and whether the gate-as-clock intervention program succeeds experimentally.

8.2 Why this is not numerology

The standard objection to golden-ratio claims is post-hoc selection: choosing a constant because it looks good on a hand-picked set of numbers. The RS/RRFframing avoids this failure mode in three ways. First, φ is not introduced as a tunable parameter; it is derived under explicit structural constraints, and the derivation is machine-checked (Section 2). Second, the ladder and rung-assignment rule are fixed before looking at biological outcomes; this converts the empirical question into a measurement question (do specific clocks land near specific rungs under preregistered tolerances?). Third, the framework proposes intervention-level falsifiers (Section 7) that are difficult to satisfy by coincidence: frequency-selective jamming near f_{19}, timing quantization at multiples of τ_{19}, and off-rung negative controls at matched power.

8.3 Relationship to standard physics and biophysics

Nothing in this paper modifies quantum mechanics, statistical mechanics, or general relativity. The ladder hypothesis is best read as a proposed *selection rule* for which clocks recur in biology and as a proposed organizational constraint on cross-domain scale transfer. At the level of standard biophysics, the ladder does not replace energetic or kinetic models; rather, it proposes that a subset of observed rates and gating events are stabilized by a discrete hierarchy that becomes visible once the correct fundamental clocks are isolated (as opposed to lumping together arbitrary "timescales" from heterogeneous processes). At the level of particle physics, the mass-side ladder discussed here is treated as a falsifiable structural hypothesis with mixed/scaffold status outside the RRFcore (Section 3; Paper 2 for audit caveats).

8.4 Limitations and key risks

Several limitations should be explicit. First, numerical values in SI units require an explicit unit anchor (Paper 2); therefore, claims should preferentially be expressed in dimensionless form (e.g., rung indices and ratios), and sensitivity to anchoring should be reported where relevant. Second, the

biological gate must be operationalized carefully. "Protein folding time" is not a fundamental clock; the hypothesis is about a specific hydration-mediated gating event. If the operational definition of the gate drifts, the rung comparison loses meaning. Third, the strongest water results are currently band-inclusion certificates (Table 1); moving from band-level correspondence to a mechanistic gearbox model requires additional experimental work that directly measures coupling and phase response near the predicted frequencies.

8.5 Near-term priorities

The immediate way to strengthen or refute the ladder's biological instantiation is to run preregistered experiments that directly probe rung-19 selectivity and discretization, across multiple proteins and assay types. The highest value tests are P1 and P2 in Table 4: frequency-selective jamming near f_{19} with strict thermal controls, and high-time-resolution detection of quantized transition timing. These experiments would clarify whether "gate-as-clock" is a physically instantiated mechanism or merely a convenient organizational metaphor.

9 Conclusion

9.1 Summary

This paper has presented an evidence-and-test interface for the φ-ladder hypothesis. On the formal side, RRFsupplies a machine-checked derivation showing that, under explicit structural constraints, φ is a forced discrete scaling factor and a rung-indexed ladder can be defined (Section 2). On the empirical side, we focused on a small set of candidate *clocks* rather than heterogeneous process times: (i) a calibrated base tick τ_0 together with the rung assignment rule (Section 3), (ii) water band correspondences for the derived coherence scales (Table 1), (iii) a rung-gap hypothesis for charged lepton ratios and the tau–gate cross-domain target (Section 5), and (iv) a bio-clocking hierarchy organized around the rung-19 molecular gate (Section 6). These elements together motivate a concrete experimental program with explicit falsifiers (Section 7).

9.2 Central correspondence: tau–gate (internal nickname: "smoking gun")

The tau–gate correspondence provides a compact cross-domain target for the ladder:

> **Tau-Gate Coincidence**: The tau lepton mass and the protein molecular gate both correspond to rung 19 on the φ-ladder. The same integer appears in particle physics and molecular biology.

As emphasized above, the Lean statement is definitional under the chosen rung-assignment mapping; the scientific content is whether the biological gate is operationalized correctly and whether the associated intervention-level predictions succeed.

9.3 Decisive experiments

The ladder hypothesis becomes scientifically meaningful only to the extent that it survives preregistered tests. The most decisive near-term experiments are: (i) frequency-selective jamming near f_{19} with strict thermal controls and off-rung negative controls, and (ii) time-resolved detection of quantized transition timing at integer multiples of τ_{19}. A third test class concerns whether timing anomalies precede misfolding in prion conversion assays. These tests are all feasible with standard

instrumentation (microwave sources and folding assays; ultrafast spectroscopy or fast single-molecule methods; NMR/anisotropy readouts) and are specified in Appendix D.

If these predictions fail robustly under controlled conditions, the biological instantiation of the ladder should be rejected or revised. If they succeed, the φ-ladder would become a generator of new, cross-domain experimental targets rather than a retrospective pattern description.

A Full Derivation Chain

This appendix records, in prose, the logical path from the Meta-Principle to the ladder definitions used throughout the paper and to the corresponding empirical test interface. The Lean symbols listed below are intended as traceability pointers: they certify formal claims about the *model objects*. They do not, by themselves, certify empirical adequacy of any mapping from those objects to laboratory measurements.

Meta-Principle (MP). The framework begins from the claim that "nothing cannot recognize itself," i.e., that existence requires nontrivial recognition structure rather than an empty fixed point. This appears in the Lean development as `mp_holds` in `RRF/Core/Recognition.lean`.

Ledger constraint. Recognition events are constrained by a conservation-like balancing condition (the "ledger"): for a closed chain, the signed ledger flux sums to zero (one representative formalization is $\sum_i \phi(u_i) = 0$). A corresponding Lean statement is `chainFlux_zero_of_balanced` in `RRF/Core/Recognition.lean`. In the empirical interface of Paper 1, this constraint motivates looking for stable clocks (gates) that act as repeatable commit events rather than for arbitrary process times.

Dimension and the 8-tick schedule (T3). Within the Recognition Science derivation chain summarized in `Source-Super.txt`, the spatial dimension $D = 3$ is claimed to be derived as the unique dimension supporting the relevant nontrivial linking/synchronization condition; one formal hook is the gap-45 synchronization criterion $\text{lcm}(2^D, 45) = 360$, which holds iff $D = 3$. A Lean anchor cited in that chain is `onlyD3_satisfies_RSCounting_Gap45_Absolute`. The practical role of this step, for this manuscript, is that $2^D = 8$ supplies the 8-tick schedule used in later structural statements (RRF/RS) and that the "gap-45" motif becomes a recurring candidate rung in the biological clocking hierarchy.

Self-similarity and the forcing of φ. The ladder depends on discrete scale invariance: self-similarity under multiplicative rescaling with a preferred ratio. In the RRFdevelopment, this is expressed via the uniqueness of a cost functional on $\mathbb{R}_+$ (one representative form is $\mathcal{J}(x) = \frac{1}{2}(x + 1/x) - 1$) and a fixed-point condition of the form $\lambda^2 = \lambda + 1$. A Lean statement encoding this step is `self_similarity_forces_phi` (see `Verification/Necessity/PhiNecessity.lean`).

Golden ratio. Given the fixed-point equation, the preferred ratio is the golden ratio $\varphi = (1 + \sqrt{5})/2$, the unique positive root of $x^2 = x + 1$. In Lean, this corresponds to a lemma such as `phi_unique_pos_root` (see `PhiSupport/Lemmas.lean`).

From φ to coherence scales and a base tick. With φ fixed, the framework defines a coherence energy scale $E_{\text{coh}} = \varphi^{-5}\,\text{eV}$ (numerically $E_{\text{coh}} \approx 0.09017\,\text{eV}$). Mapping this dimensionless expression into SI units requires an explicit unit anchor; in this paper we use $\hbar$ (CODATA) to define a

base tick $\tau_0 = \hbar/E_{\text{coh}}$ via the "IR gate" identity $\hbar = E_{\text{coh}} \cdot \tau_0$. Using this anchoring yields $\tau_0 \approx 7.3 \times 10^{-15}$ s, with a canonical display value $\tau_0 \approx 7.33$ fs after documented corrections (see Paper 2 and `Source-Super.txt` audit notes for the anchoring caveat).

Time ladder. The time ladder is defined by $\tau_n = \tau_0 \varphi^n$ for integer rungs $n \in \mathbb{Z}$. The scientific use of this definition is not that "all timescales must lie on the ladder," but that certain *clocks* (gating events) may recur as stable rungs across systems and may support intervention-level tests (Section 7).

Mass-side ladder (hypothesis interface). On the mass side, the paper discusses a structural hypothesis of the form $m = B \cdot E_{\text{coh}} \cdot \varphi^{R_0+r}$ with a binary gauge factor B (e.g., 2^{-22}), a baseline exponent R_0 (e.g., 62 for a lepton construction), and integer rung offsets $r \in \mathbb{Z}$. The mass-side program is treated as scaffold/conditional outside the core RRFmodule; for Paper 1, its main role is to supply testable cross-domain rung targets (notably rung 19) that connect to biological intervention proposals.

Prediction program and falsifiers. Once the ladder definition and its anchoring are fixed, the framework becomes predictive in the following sense: it proposes a small set of rung-indexed clocks and intervention frequencies, together with off-rung negative controls, that should exhibit frequency-selective effects if the biological instantiation is correct. The decisive tests are summarized in Section 7, with operational details in Appendix D.

B Lean Theorem Index

This section provides symbol-level traceability to the Lean developments referenced by this manuscript. File paths are given relative to the companion Lean repository, and the entries should be interpreted as certificates of formal statements about the model objects (not as certificates of empirical adequacy).

Theorem	File	Status
mp_holds	RRF/Core/Recognition.lean	PROVED
chainFlux_zero_of_balanced	RRF/Core/Recognition.lean	PROVED
phi_squared	PhiSupport/Lemmas.lean	PROVED
phi_unique_pos_root	PhiSupport/Lemmas.lean	PROVED
self_similarity_forces_phi	Verification/Necessity/PhiNecessity.lean	PROVED
E_coh_in_water_hbond_range	Water/Constants.lean	PROVED
nu_RS_in_libration_band	Water/Constants.lean	PROVED
tau_gate_matches_hbond_coherence	Water/Constants.lean	PROVED
water_is_special	Water/Basic.lean	PROVED
tau_molecular_coincidence	Biology/GoldenRungs.lean	PROVED
bio_clocking_theorem	Biology/BioClocking.lean	PROVED
wtoken_cardinality_eq_amino_acid	Water/WTokenIso.lean	PROVED

The repository containing these developments is available at https://github.com/jonwashburn/reality. Readers can independently verify the status claims by building the Lean project at the revision corresponding to this manuscript.

C Time ladder table (rungs 0–60)

For convenience, we list the derived time ladder values used in this manuscript. The values are computed from $\tau_n = \tau_0\varphi^n$ with $\tau_0 \approx 7.33\,\mathrm{fs}$ and $\varphi = (1 + \sqrt{5})/2$, and we define $f_n = 1/\tau_n$. This table is purely numerical; interpretive associations (which physical or biological processes correspond to which rungs) are discussed in the main text. Negative rungs (optical/UV scales) can be generated analogously but are omitted here.

n	τ_n (s)	τ_n (display)	f_n (Hz)	f_n (display)
0	7.330e-15	7.330 fs	1.364e+14	136.426 THz
1	1.186e-14	11.860 fs	8.432e+13	84.316 THz
2	1.919e-14	19.190 fs	5.211e+13	52.110 THz
3	3.105e-14	31.050 fs	3.221e+13	32.206 THz
4	5.024e-14	50.241 fs	1.990e+13	19.904 THz
5	8.129e-14	81.291 fs	1.230e+13	12.301 THz
6	1.315e-13	131.532 fs	7.603e+12	7.603 THz
7	2.128e-13	212.822 fs	4.699e+12	4.699 THz
8	3.444e-13	344.354 fs	2.904e+12	2.904 THz
9	5.572e-13	557.176 fs	1.795e+12	1.795 THz
10	9.015e-13	901.530 fs	1.109e+12	1.109 THz
11	1.459e-12	1.459 ps	6.855e+11	685.539 GHz
12	2.360e-12	2.360 ps	4.237e+11	423.686 GHz
13	3.819e-12	3.819 ps	2.619e+11	261.852 GHz
14	6.179e-12	6.179 ps	1.618e+11	161.834 GHz
15	9.998e-12	9.998 ps	1.000e+11	100.019 GHz
16	1.618e-11	16.177 ps	6.181e+10	61.815 GHz
17	2.618e-11	26.175 ps	3.820e+10	38.204 GHz
18	4.235e-11	42.353 ps	2.361e+10	23.611 GHz
19	6.853e-11	68.528 ps	1.459e+10	14.593 GHz
20	1.109e-10	110.881 ps	9.019e+09	9.019 GHz
21	1.794e-10	179.409 ps	5.574e+09	5.574 GHz
22	2.903e-10	290.290 ps	3.445e+09	3.445 GHz
23	4.697e-10	469.699 ps	2.129e+09	2.129 GHz
24	7.600e-10	759.989 ps	1.316e+09	1.316 GHz
25	1.230e-09	1.230 ns	8.132e+08	813.214 MHz
26	1.990e-09	1.990 ns	5.026e+08	502.594 MHz
27	3.219e-09	3.219 ns	3.106e+08	310.620 MHz
28	5.209e-09	5.209 ns	1.920e+08	191.974 MHz
29	8.428e-09	8.428 ns	1.186e+08	118.646 MHz
30	1.364e-08	13.637 ns	7.333e+07	73.327 MHz
31	2.207e-08	22.066 ns	4.532e+07	45.319 MHz
32	3.570e-08	35.703 ns	2.801e+07	28.009 MHz
33	5.777e-08	57.769 ns	1.731e+07	17.310 MHz
34	9.347e-08	93.472 ns	1.070e+07	10.698 MHz
35	1.512e-07	151.242 ns	6.612e+06	6.612 MHz
36	2.447e-07	244.714 ns	4.086e+06	4.086 MHz
37	3.960e-07	395.956 ns	2.526e+06	2.526 MHz

n	τ_n (s)	τ_n (display)	f_n (Hz)	f_n (display)
38	6.407e-07	640.670 ns	1.561e+06	1.561 MHz
39	1.037e-06	1.037 us	9.647e+05	964.668 kHz
40	1.677e-06	1.677 us	5.962e+05	596.198 kHz
41	2.714e-06	2.714 us	3.685e+05	368.471 kHz
42	4.391e-06	4.391 us	2.277e+05	227.727 kHz
43	7.105e-06	7.105 us	1.407e+05	140.743 kHz
44	1.150e-05	11.496 us	8.698e+04	86.984 kHz
45	1.860e-05	18.601 us	5.376e+04	53.759 kHz
46	3.010e-05	30.098 us	3.322e+04	33.225 kHz
47	4.870e-05	48.699 us	2.053e+04	20.534 kHz
48	7.880e-05	78.797 us	1.269e+04	12.691 kHz
49	1.275e-04	127.497 us	7.843e+03	7.843 kHz
50	2.063e-04	206.294 us	4.847e+03	4.847 kHz
51	3.338e-04	333.790 us	2.996e+03	2.996 kHz
52	5.401e-04	540.084 us	1.852e+03	1.852 kHz
53	8.739e-04	873.874 us	1.144e+03	1.144 kHz
54	1.414e-03	1.414 ms	7.072e+02	707.235 Hz
55	2.288e-03	2.288 ms	4.371e+02	437.095 Hz
56	3.702e-03	3.702 ms	2.701e+02	270.140 Hz
57	5.990e-03	5.990 ms	1.670e+02	166.955 Hz
58	9.691e-03	9.691 ms	1.032e+02	103.184 Hz
59	1.568e-02	15.681 ms	6.377e+01	63.771 Hz
60	2.537e-02	25.372 ms	3.941e+01	39.413 Hz

D   Experimental Protocols

D.1   Protocol P1: 14.6 GHz Jamming Experiment

Objective and readout.   This protocol tests whether irradiation near $f_{19} \approx 14.6$ GHz produces a frequency-selective slowdown or arrest of refolding, relative to matched-power off-rung irradiation. A convenient readout is GFP fluorescence recovery (or, for other proteins, an activity assay or a structural proxy).

Equipment and setup.   Use a microwave source covering approximately 10–20 GHz (typical output power 1–100 mW), coupled to the sample via a waveguide or horn antenna. Maintain the sample in a temperature-controlled chamber and continuously monitor temperature (e.g., IR thermometry). Measure folding progress with a fluorescence spectrometer or equivalent assay instrumentation.

Sample.   Prepare a denatured protein solution (e.g., GFP or lysozyme) in a standard refolding buffer; choose concentrations compatible with the readout.

Procedure.

1. Prepare denatured protein at 1 mg/mL in 6M GuHCl

2. Dilute 10-fold into refolding buffer at $t = 0$

3. Apply microwave irradiation at specified frequency (14.6 GHz or control)

4. Monitor folding by fluorescence (GFP) or activity (lysozyme) every 30 s

5. Measure sample temperature continuously; abort if $\Delta T > 1\,°\mathrm{C}$

Controls and decision rule. Run at least three controls: no irradiation (baseline), and two off-rung frequencies (e.g., 10 GHz and 20 GHz) at matched power. A nearby-rung condition at ≈ 9.0 GHz (rung 20) can be included as a secondary prediction. Define success as a $> 50\%$ reduction in folding rate at 14.6 GHz relative to off-rung frequencies at matched power *and* matched temperature history. The hypothesis is falsified if no frequency-selective effect is observed (i.e., effects are indistinguishable across frequencies once thermal confounds are controlled).

D.2 Protocol P2: Quantized Folding Detection

Objective and readout. This protocol tests whether conformational transition times cluster near integer multiples of the rung-19 tick, $\tau_{19} \approx 68$ ps, rather than following a continuous exponential distribution. The readout can be ultrafast spectroscopy (e.g., 2D-IR) or high-time-resolution single-molecule measurements.

Equipment and sample. Use an ultrafast 2D-IR instrument with $\lesssim 50$ ps time resolution, or a single-molecule FRET setup with $\lesssim 100$ ps effective timing. Choose a fast-folding protein (e.g., a WW domain with $\tau_{\mathrm{fold}} \sim 10\,\mu\mathrm{s}$) and an initiation method such as a temperature jump or rapid mixing.

Procedure.

1. Initiate folding via T-jump or rapid mixing

2. Collect time-resolved spectra at 10 ps intervals

3. Extract transition times from spectral changes

4. Histogram transition times with 20 ps bins

Decision rule. Define success as reproducible histogram peaks near 68 ± 10 ps, 136 ± 15 ps, and 204 ± 20 ps with troughs between, across repeated runs and (ideally) across proteins. The hypothesis is falsified if the transition-time distribution remains consistent with a smooth exponential (or otherwise continuous) distribution after controlling for instrument response and binning artifacts.

D.3 Protocol P3: Prion Timing Anomaly

Objective and readout. This protocol tests whether measurable timing/relaxation anomalies precede overt aggregation in seeded prion conversion assays. The readout can be NMR relaxation (T_1/T_2) or time-resolved fluorescence anisotropy, used to estimate correlation times that are hypothesized to be perturbed if rung-19 gate timing slips.

Equipment and samples. Use an NMR spectrometer (e.g., 600 MHz or higher) for T_1/T_2 measurements and/or a fluorescence anisotropy setup with picosecond-scale resolution. Measure three conditions: PrP^C (baseline), PrP^C seeded with PrP^{Sc} sampled at early time points (e.g., < 1 hour post-seeding), and PrP^{Sc} as a positive control.

Procedure.

1. Measure rotational correlation time τ_{rot} via NMR relaxation or anisotropy

2. Compare to expected molecular gate time (68 ps)

3. Track τ_{rot} over time post-seeding

Decision rule. Define success as a reproducible deviation in the inferred correlation time (e.g., $|\tau_{rot} - 68\,\text{ps}| > 7\,\text{ps}$ as a representative 10% threshold) that appears *before* aggregation becomes detectable by conventional assays (e.g., ThT fluorescence). The hypothesis is falsified if τ_{rot} remains consistent with baseline until after structural conversion/aggregation is detectable, or if deviations occur equally in unseeded controls.

References