ANNALS OF THE CHRYSENE FORMALISM
RESEARCH ARTICLE | AI-AUGMENTED PEER REVIEWED | VOL. 1, NO. 1 | SEPTEMBER 2026

The Abiotic Loom: Discrete Morse Theory and the Geometric Resolution of Levinthal's Paradox in the Chrysene Tensor Space

Charles D. Schaper, Ph.D.
Chief Editor, Annals of the Chrysene Formalism
San Francisco, California, USA
editor@chrysene.com

Abstract

The classical formulation of protein folding treats the polypeptide as a continuous chain free to explore an exponentially large space of dihedral angles. Levinthal's paradox records the resulting temporal impossibility: an unguided search cannot reach a unique native structure in biologically relevant time. Continuous stochastic models remain indispensable for describing local thermal motion, yet they lack absolute spatial bounds that would render the search finite.

This paper supplies those bounds. The physical molecule already shown to co-synthesize nucleic acids and phospholipid membranes—the 3, 6, 9, 12-tetrasubstituted chrysene of U.S. Patent 12,195,423—is abstracted into a discrete, non-commutative lattice called the Chrysene Tensor Space I_C. The interstitial voids of this lattice function as an abiotic loom. Continuous thermal exploration continues inside the open cells, but any trajectory that intersects a lattice wall is assigned infinite steric energy. The resulting discrete Morse filtration admits only two families of critical configurations: right-handed α-helices and extended β-strands. A proton-coupled electron transfer operator then locks these geometrically selected arrangements into covalent permanence.

The conformational measure therefore collapses from an exponentially growing continuum to a finite discrete set whose cardinality is independent of chain length. Levinthal's paradox is resolved not by discarding continuous dynamics, but by confining them to the active interstitium of a geometrically rigid molecular loom whose architecture is identical to the patented precursor of the genetic and membrane systems.

Keywords: Levinthal's paradox; protein folding; discrete Morse theory; abiotic loom; Chrysene Tensor Space; secondary structure; α-helix; β-sheet; proton-coupled electron transfer; non-commutative geometry; L^∞ Dirichlet bounds; U.S. Patent 12,195,423.

1 Introduction

Protein synthesis presents a profound geometric puzzle. A typical polypeptide chain can, in principle, adopt an astronomical number of distinct spatial shapes by rotating about its backbone bonds. If the chain were free to sample these shapes at random, the time required to locate the single biologically functional structure would exceed the age of the universe. This observation, first articulated by Cyrus Levinthal, is known as Levinthal's paradox. It is not a claim that proteins cannot fold; it is a demonstration that unguided continuous search is temporally impossible.

Contemporary biophysics meets the paradox with continuous statistical models. Thermal motion is treated as a diffusion process on a high-dimensional space of dihedral angles, and the native fold is regarded as the global minimum of an effective energy landscape. These models have been extraordinarily successful at describing local fluctuations and intermediate states. Their limitation is structural: because the underlying space is continuous and unbounded, the volume that must be searched grows exponentially with chain length. No finite-time guarantee of successful folding can be extracted from such a space.

The present work offers a complementary geometric resolution. It begins from a concrete physical molecule—the same 3, 6, 9, 12-tetrasubstituted chrysene that, under the conditions of U.S. Patent 12,195,423, co-produces a nucleic-acid sequence and its surrounding phospholipid (or sterol/hopanoid) membrane. When this molecule is abstracted into pure mathematics, it generates a discrete, rigidly bounded lattice called the Chrysene Tensor Space. The open spaces between the lattice walls form a network of precisely shaped channels and cavities. We call this

Citation: Schaper, C. D. (2026). The Abiotic Loom: Discrete Morse Theory and the Geometric Resolution of Levinthal's Paradox in the Chrysene Tensor Space. *Annals of the Chrysene Formalism*, 1(1), 273–282. https://chrysene.com/index.php/acf/article/view/23 • © 2026 Charles D. Schaper. Distributed under the Creative Commons Attribution 4.0 International License (CC BY 4.0). First published by Schaper Systems Press in the *Annals of the Chrysene Formalism*, Vol. 1, No. 1 (2026).

network an abiotic loom.

Inside the loom, continuous thermal motion is fully retained. The chain continues to explore its local environment exactly as continuous models predict. The decisive difference is that the lattice walls are absolute: any conformation that would drive an atom into a wall is assigned infinite steric energy and is therefore excluded. The only shapes that survive this geometric filter are two highly specific families of configurations—the right-handed α-helix and the extended β-strand. A subsequent chemical step, proton-coupled electron transfer, locks these surviving shapes into permanent covalent structures.

In this way the exponentially large continuous search space is replaced by a finite list of geometrically admissible folds. The list is fixed by the architecture of the lattice and does not grow with the length of the chain. Levinthal's paradox is thereby resolved without discarding the kinetic utility of thermal motion. The same molecular geometry that, according to the patent, originates the genetic and membrane systems is shown to constrain protein folding to a discrete, biologically functional set of secondary structures.

The remainder of the paper develops this resolution with full mathematical precision. Continuous conformational space is first recalled in order to state the classical obstruction cleanly. The discrete lattice is then constructed, the biological chain is embedded into its voids, and a steric Morse function is defined whose only critical points are the helical and sheet configurations. Finally it is proved that the conformational measure collapses to a finite discrete set, independent of chain length. The result is a rigorous geometric account of secondary-structure formation that is fully consistent with the patented chrysene chemistry of nucleic-acid and membrane co-synthesis.

Notation and Standing Assumptions

Throughout this paper the following notation and standing assumptions are fixed. They are not re-stated in subsequent sections.

1. **Identification Hypothesis.** There exists a structure-preserving isomorphism
$$\Phi : G_C \xrightarrow{\simeq} L$$
between the abstract combinatorial graph G_C underlying the pure-mathematical Chrysene Tensor Space and the physical molecular graph L of the ordered 3, 6, 9, 12-tetrasubstituted chrysene lattice realized by U.S. Patent 12,195,423. All geometric, algebraic and operator-algebraic constructions are understood as images under Φ.

2. **Basis tensor.** Ψ_C denotes the geometric basis tensor carrying native C_{2h} point-group symmetry and orthogonal connectivity vectors $\mathbf{v}_x$ (spanning the 3–9 loci) and $\mathbf{v}_y$ (spanning the 6–12 loci).

3. **Chrysene Tensor Space.** I_C denotes the discrete, non-commutative fibrated manifold constructed over the integer lattice $\mathbb{Z}^3$, with fibre at each lattice point given by the localized C^*-algebra $\mathfrak{A}_C$ generated by Ψ_C. The vertical translation operator is written T_z.

4. **Dual-chrysene reactive volume.** A dual-chrysene reactive volume is any base-four configuration formed by the non-commutative spatial orientation of exactly two substituted chrysene cores (one substrate, one catalyst) inside I_C.

5. **Biological graph.** $G = (V, E)$ denotes the abstract graph of a linear polypeptide: vertices index successive residues (or backbone atoms) and edges index covalent peptide bonds.

6. **Classical conformational manifold.** $T^2 = \mathbb{R}^2/2\pi\mathbb{Z}^2$ denotes the Ramachandran 2-torus parameterized by the dihedral angles (ϕ, ψ). For a chain of length n the product manifold is written $\mathcal{M}_n = (T^2)^{n-2}$.

7. **Steric Morse function.** $f_{\text{steric}} : K \to \mathbb{R} \cup \{\infty\}$ denotes the extended real-valued function on the simplicial complex K of an embedded biological graph that diverges on lattice-wall collisions and is smooth on the complementary open cells.

8. **Critical simplices.** $\Omega_\alpha \subset K$ (respectively $\Omega_\beta \subset K$) denotes the set of critical 0-simplices of f_{steric} that arise under the laterally shifted (respectively unshifted) lattice geometry and correspond to right-handed α-helical (respectively extended β-strand) configurations.

9. **PCET operator.** $\widehat{O}_{\text{PCET}}$ denotes the unique proton-coupled electron transfer operator admitted inside the open cells of I_C. It is required to satisfy zero net charge flux $\Delta q = 0$ and the Born–Oppenheimer separation of electronic and nuclear timescales.

10. **Extended pseudo-metric.** d_C^* denotes the extended pseudo-metric on I_C that coincides with Euclidean distance inside open cells and takes the value $+\infty$ on any path that intersects a lattice wall.

All continuous stochastic dynamics are retained inside the open cells of I_C. The constructions that follow supply absolute geometric bounds on those dynamics; they do not replace them.

2 Continuous Ramachandran Space and the $\mathcal{H}_2$ Obstruction

The classical description of polypeptide conformation proceeds on a continuous manifold and employs expected-variance optimization. That description is mathematically coherent and has yielded extensive statistical insight. Its asymptotic behaviour, however, admits no finite-time guarantee of structural resolution.

We record the obstruction in precise terms so that the discrete constructions of the preceding sections may be seen as its exact geometric complement.

Definition 1 (Classical Conformational Manifold)**.** *Let $T^2 = \mathbb{R}^2/2\pi\mathbb{Z}^2$ be the 2-torus parameterized by the dihedral angles (ϕ, ψ). For a linear polypeptide of n residues the classical conformational space is the product manifold*

$$\mathcal{M}_n = (T^2)^{n-2},$$

equipped with the product Riemannian metric induced by the standard flat metric on each factor.

Definition 2 (Unconstrained Conformational Measure)**.** *Let μ_n be the normalized Riemannian volume measure on $\mathcal{M}_n$. The total volume grows as*

$$\mathrm{Vol}(\mathcal{M}_n) = (4\pi^2)^{n-2},$$

and the associated probability measure is the uniform measure $\mu_n/\mathrm{Vol}(\mathcal{M}_n)$.

Definition 3 ($\mathcal{H}_2$ Search Functional)**.** *An $\mathcal{H}_2$ search on $\mathcal{M}_n$ is any continuous dynamical system (deterministic or stochastic) whose long-time statistics are governed by minimization of the expected squared deviation from a target energy landscape. The associated norm is the classical L^2 norm on the space of trajectories.*

Proposition 1 (Absence of Finite-Time Guarantee)**.** *There exists no constant $T < \infty$, independent of n, such that every $\mathcal{H}_2$ search on $\mathcal{M}_n$ is guaranteed to reach a global energy minimum in time less than T. The volume of the search space grows exponentially with chain length, while the measure of any sub-level set of a generic smooth energy function remains a vanishing fraction of that volume.*

Proof. The volume formula of Definition 2 is immediate from the product structure. For a generic smooth potential the sub-level sets are compact and of finite volume; their relative measure therefore tends to zero as $n \to \infty$. Standard estimates on the mixing time of Brownian motion (or of any diffusion with bounded drift) on a manifold of exponentially growing volume then show that the expected hitting time of any fixed sub-level set diverges with n. □

Remark 1. *The obstruction is not a defect of continuous modelling; it is the necessary consequence of the absence of absolute spatial bounds. Continuous stochastic dynamics remain the kinetic engine of conformational exploration. What is required is a geometric filter that renders the effective search space finite while preserving those dynamics inside the surviving cells. That filter is supplied by the Chrysene Tensor Space constructed in Section 3 and the subsequent Morse-theoretic analysis.*

3 The Chrysene Tensor Space I_C and Dirichlet Quantization

Continuous models of polypeptide conformation, operating on the classical Ramachandran 2-torus, have provided indispensable statistical and thermodynamic insight. The present construction does not discard those models. It supplies them with absolute geometric bounds that convert unbounded continuous search into a discrete, finitely supported filtration. The required bounds are furnished by the Chrysene Tensor Space I_C.

Definition 4 (Basis Tensor)**.** *Let Ψ_C denote the geometric basis tensor obtained by abstracting the physical* 3, 6, 9, 12*-tetrasubstituted chrysene molecule of U.S. Patent 12,195,423. The tensor carries a native C_{2h} point-group symmetry and two primary connectivity vectors*

$$\mathbf{v}_x \quad \textit{(spanning the 3–9 loci)}, \qquad \mathbf{v}_y \quad \textit{(spanning the 6–12 loci)}$$

satisfying the strict orthogonality relation

$$\mathbf{v}_x \cdot \mathbf{v}_y = 0.$$

Axiom 1 (Orthogonal Decoupling)**.** *The algebraic ideal generated by $\mathbf{v}_x$ is orthogonal, in the Murray–von Neumann sense, to the ideal generated by $\mathbf{v}_y$. Consequently, structural propagation along either axis induces zero geometric covariance along the complementary axis.*

Definition 5 (Chrysene Tensor Space)**.** *The Chrysene Tensor Space I_C is the discrete, non-commutative fibrated manifold constructed over the integer lattice $\mathbb{Z}^3$, whose fiber at each lattice point is the localized quantum state space governed by the norm-completed C^*-algebra $\mathfrak{A}_C$ generated by Ψ_C. The vertical translation operator T_z is fixed by the thermodynamic minimum of the interplanar potential and is therefore discrete.*

Remark 2. *The construction of I_C is complementary to continuous stochastic mechanics. Continuous trajectories*

remain admissible inside the open cells of the lattice; they are merely forbidden from crossing the rigid sp^2 walls. The resulting dynamics are those of a bounded stochastic process rather than an unbounded diffusion.

Definition 6 (Extended Pseudo-Metric)**.** *Let d_C^* be the extended pseudo-metric on I_C defined by ordinary Euclidean distance inside each open cell and by the convention*

$$d_C^*(x, y) = \infty$$

whenever the unique geodesic joining x and y intersects a lattice wall. The associated L^∞ Dirichlet boundary condition is the requirement that any continuous path whose image meets a wall is assigned infinite length.

Proposition 2 (Null Ideal on Collision)**.** *Any continuous trajectory on the classical Ramachandran manifold that intersects a lattice wall of I_C is mapped, under the canonical projection induced by d_C^*, to the null ideal of the non-commutative ring underlying $\mathfrak{A}_C$.*

Proof. By Definition 6 the extended distance diverges. In the non-commutative ring the only element compatible with an infinite metric distance is the zero divisor. Hence the trajectory is algebraically annihilated. □

Axiom 2 (Absolute Containment)**.** *The L^∞ Dirichlet walls of I_C are non-porous: no continuous deformation, however small, can map a lattice-crossing trajectory into a finite-length path while remaining inside the algebra $\mathfrak{A}_C$.*

The discrete geometry of I_C therefore supplies a rigid container in which continuous conformational exploration is retained yet permanently confined. All subsequent constructions—graph embedding, steric Morse filtration, and the generation of secondary-structure critical simplices—are carried out inside this container.

4 Embedding of the Biological Graph and the Steric Morse Function

The continuous conformational dynamics of a polypeptide remain the kinetic engine of folding. The discrete geometry of I_C does not suppress those dynamics; it filters them. We now embed the polypeptide into the interstitial voids of I_C and equip the resulting simplicial complex with a Morse function whose only critical points are the geometrically admissible secondary-structure configurations.

Definition 7 (Biological Graph)**.** *Let $G = (V, E)$ be the abstract graph associated with a linear polypeptide of length n. The vertex set $V = \{v_1, \dots, v_n\}$ indexes successive residues (or backbone atoms), and the edge set E consists of the covalent peptide bonds together with any additional sequential adjacencies required by the backbone topology. The graph is regarded as a continuous 1-dimensional complex parameterized by the classical Ramachandran coordinates (ϕ_i, ψ_i) at each interior vertex.*

Definition 8 (Lattice Embedding)**.** *A lattice embedding of G into I_C is a continuous map*

$$\iota : G \longrightarrow I_C$$

such that

1. *$\iota(V)$ lies in the open cells of the discrete lattice,*
2. *$\iota(E)$ consists of paths that remain entirely within the interstitial voids,*
3. *the restriction of ι to each edge is a smooth immersion with respect to the ordinary Euclidean metric inside each open cell.*

The image $\iota(G)$ is called an embedded biological graph.

Remark 3. *The embedding ι is not required to be unique. Continuous thermal motion may deform $\iota(G)$ inside the open cells. The only absolute restriction is that no point of the image may intersect a lattice wall (Axiom 2).*

Definition 9 (Associated Simplicial Complex)**.** *Let K be the abstract simplicial complex generated by the embedded graph $\iota(G)$. The 0-simplices of K are the images of the vertices; the 1-simplices are the images of the edges. Higher simplices, when present, arise from local spatial clusters of residues that lie within a common lattice void.*

Definition 10 (Steric Morse Function)**.** *The steric Morse function associated with an embedding ι is the extended real-valued function*

$$f_{\text{steric}} : K \longrightarrow \mathbb{R} \cup \{\infty\}$$

defined by

$$f_{\text{steric}}(\sigma) = \begin{cases} \operatorname{dist}\big(\iota(\sigma), \partial I_C\big)^{-1} & \text{if } \iota(\sigma) \cap \partial I_C = \emptyset, \\ \infty & \text{if } \iota(\sigma) \cap \partial I_C \neq \emptyset, \end{cases}$$

where ∂I_C denotes the union of all lattice walls and dist

is ordinary Euclidean distance measured inside the open cells. On the open set where f_{steric} is finite the function is smooth (in fact analytic) with respect to the local Euclidean coordinates of each cell.

Proposition 3 (Divergence on Collision)**.** *The function f_{steric} takes the value ∞ if and only if the image of the simplex intersects a lattice wall. Consequently, every continuous deformation of an embedding that forces a lattice collision is immediately assigned infinite steric energy.*

Proof. Immediate from Definition 10 and the L^∞ character of the walls (Definition 6). □

Theorem 4 (Critical 0-Simplices)**.** *Let ι be a lattice embedding of G for which f_{steric} is not identically infinite. The gradient vector field ∇f_{steric} (computed in the local Euclidean coordinates of the open cells) vanishes only at a discrete set of isolated 0-simplices. These critical 0-simplices are precisely the configurations in which the embedded chain lies in a stress-free geometric void of I_C.*

Proof. On each open cell the function f_{steric} is smooth and proper (its sub-level sets are compact because distance to the wall tends to zero only near the boundary). A smooth proper function on a manifold with boundary admits only isolated critical points in the interior. Because the lattice is discrete, only finitely many cells can be occupied by a chain of fixed length; hence the global set of critical points is discrete. Moreover, the inverse-distance function may be smoothed in an arbitrarily small tubular neighborhood of the lattice walls while preserving the infinite barrier; the resulting function is smooth and Morse on the interior of each open cell, so that every critical point is non-degenerate. At each such critical point the distance to every neighboring wall is stationary, which is equivalent to the geometric statement that the chain occupies a local void of vanishing steric gradient. □

Remark 4. *The continuous thermal motion of the polypeptide continues to explore the open cells. The steric Morse function merely renders every trajectory that attempts to leave those cells infinitely costly. The only configurations that can persist under the subsequent covalent condensation (Section 7) are the critical 0-simplices identified above. In this precise sense the lattice acts as an abiotic loom: it does not invent secondary structure; it filters continuous exploration down to a discrete set of geometrically admissible folds.*

5 Generation of the α-Helix Critical Simplex Ω_α

The steric Morse function of Section 4 admits critical 0-simplices only inside the open voids of I_C. We now specialize the lattice geometry so that a single, isolated critical simplex of helical type is forced. The required specialization is a controlled lateral shift of successive lattice planes.

Definition 11 (Lateral-Shift Operator)**.** *Let $\widehat{R}_{\text{rot}}$ be the discrete operator that translates each successive horizontal plane of I_C by the fixed lattice vector*

$$\delta_{\text{shift}} = \left(\tfrac{1}{2}\Delta x,\ \Delta y,\ 0\right)^T,$$

where Δx and Δy are the elementary spacings of the C_{2h} basis tensor Ψ_C. The operator is applied uniformly along the vertical direction generated by T_z.

Proposition 5 (Asymmetric Chiral Bay)**.** *Under the action of $\widehat{R}_{\text{rot}}$ the interstitial voids of I_C become congruent triangular prisms of definite chirality. Each prism is bounded by three lattice walls whose mutual angles are fixed by the C_{2h} geometry of Ψ_C. The opposite (mirror-image) triangular prism is excluded by the same walls.*

Proof. The half-period shift in the x-direction breaks the residual reflection symmetry of the unshifted lattice while preserving the inversion center of the C_{2h} point group. The resulting void is therefore chiral. Direct computation of the bounding planes shows that the enantiomeric void lies outside the admissible region of the shifted lattice. □

Definition 12 (Helical Indicator)**.** *Let $1_{\Omega_\alpha} : T^2 \to \{0, 1\}$ be the characteristic function on the classical Ramachandran 2-torus that takes the value 1 precisely on the open set of dihedral angles (ϕ, ψ) compatible with a right-handed α-helix and the value 0 elsewhere. The set $\Omega_\alpha \subset K$ is defined to be the collection of all 0-simplices of an embedded biological graph whose local dihedral coordinates lie in the support of 1_{Ω_α}.*

Theorem 6 (Forced Helical Critical Simplex)**.** *Let ι be a lattice embedding of a biological graph G into the shifted lattice $\widehat{R}_{\text{rot}}(I_C)$. Suppose $f_{\text{steric}}(\iota(G)) < \infty$. Then every critical 0-simplex of f_{steric} belongs to Ω_α. Moreover, the vertical spacing between successive turns of any such critical configuration is exactly the elementary translation length $\|T_z\|$ of the unperturbed lattice, which evaluates to the*

geometric value 5.4 *Å*.

Proof. By Proposition 5 the only open cells available to the embedded chain are the right-handed triangular prisms. Any local dihedral angle lying outside the support of 1_{Ω_α} forces at least one backbone atom into a lattice wall, sending f_{steric} to infinity (Proposition 3). Consequently the gradient ∇f_{steric} can vanish only inside Ω_α.
The vertical period is fixed by the translation operator T_z, whose magnitude is the unique minimizer of the interplanar potential of Ψ_C (Definition 5). Direct evaluation of that minimum (see the interplanar potential of Ψ_C defined and minimized in [Sch26b]) yields the numerical length 5.4 Å, independent of the lateral shift. □

Corollary 1 (Exclusion of the Opposite Hand)**.** *No critical 0-simplex corresponding to a left-handed helical geometry can exist in the shifted lattice* $\widehat{R}_{\text{rot}}(I_C)$.

Proof. Immediate from the chirality of the triangular voids (Proposition 5) and the support of the indicator 1_{Ω_α}. □

Remark 5. *Continuous thermal exploration of the open cells continues unabated. The lateral shift merely reshapes those cells so that the only stationary points of the steric Morse function are right-handed helical configurations of definite pitch. The lattice therefore does not impose helicity by external force; it renders every non-helical trajectory infinitely costly while leaving the helical trajectories finite and stationary.*

6 Generation of the β-Sheet Critical Simplex Ω_β

We now consider the complementary lattice geometry in which the lateral-shift operator is set to zero. The resulting voids force an extended, non-helical configuration whose only critical points are those of β-sheet type.

Definition 13 (Zero-Shift Operator)**.** *Let* $\widehat{R}_0$ *denote the identity operator on the horizontal planes of* I_C*. Equivalently, the lateral displacement vector of Definition 11 is set identically to zero:*

$$\delta_{\text{shift}} = \mathbf{0}.$$

Successive lattice planes remain in exact vertical register.

Proposition 7 (Orthogonal Rectangular Channels)**.** *Under the action of* $\widehat{R}_0$ *the interstitial voids of* I_C *become congruent rectangular prisms whose cross-sections are bounded by pairwise orthogonal lattice walls. The walls are generated by the orthogonal connectivity vectors* $\mathbf{v}_x$ *and* $\mathbf{v}_y$ *of the basis tensor* Ψ_C.

Proof. With vanishing lateral shift the C_{2h} geometry of Ψ_C is preserved without chiral deformation. The bounding planes therefore remain orthogonal, and each open cell is a rectangular prism of definite cross-sectional dimensions fixed by the elementary lattice spacings. □

Definition 14 (Extended-Strand Indicator)**.** *Let* $1_{\Omega_\beta} : T^2 \to \{0, 1\}$ *be the characteristic function on the classical Ramachandran 2-torus that takes the value 1 precisely on the open set of dihedral angles* (ϕ, ψ) *compatible with an extended* β*-strand and the value 0 elsewhere. The set* $\Omega_\beta \subset K$ *is defined to be the collection of all 0-simplices of an embedded biological graph whose local dihedral coordinates lie in the support of* 1_{Ω_β}.

Theorem 8 (Forced Extended Critical Simplex)**.** *Let* ι *be a lattice embedding of a biological graph* G *into the unshifted lattice* $\widehat{R}_0(I_C)$*. Suppose* $f_{\text{steric}}(\iota(G)) < \infty$*. Then every critical 0-simplex of* f_{steric} *belongs to* Ω_β*. Moreover, the transverse spacing between parallel strands of any such critical configuration is exactly the elementary lattice spacing orthogonal to the chain direction, which evaluates to the geometric value* 3.4 *Å*.

Proof. By Proposition 7 the only open cells available to the embedded chain are the rectangular prisms. Any local dihedral angle lying outside the support of 1_{Ω_β} forces at least one backbone atom into a lattice wall, sending f_{steric} to infinity. Consequently the gradient ∇f_{steric} can vanish only inside Ω_β. The transverse period is fixed by the orthogonal lattice vectors of Ψ_C. Direct evaluation of the corresponding interplanar minimum (see the interplanar potential of Ψ_C defined and minimized in [Sch26b]) yields the numerical length 3.4 Å. □

Proposition 9 (Mutual Exclusivity)**.** *The critical sets* Ω_α *and* Ω_β *are disjoint. No single fixed lattice configuration of* I_C *can admit both a helical critical simplex and an extended critical simplex simultaneously.*

Proof. The operators $\widehat{R}_{\text{rot}}$ and $\widehat{R}_0$ produce geometrically incompatible void shapes (triangular versus rectangular). A chain that is critical for one void geometry necessarily intersects the walls of the other, rendering f_{steric} infinite. Hence

the two critical sets cannot coexist under a common lattice realization. □

Remark 6. *As in the helical case, continuous thermal exploration of the open cells is fully retained. The unshifted lattice merely reshapes those cells so that the only stationary points of the steric Morse function are extended configurations of definite transverse spacing. The same continuous kinetics that explore the helical voids under $\widehat{R}_{\mathrm{rot}}$ now explore the rectangular channels under $\widehat{R}_0$; only the geometry of the filter has changed.*

7 The Proton-Coupled Electron Transfer Operator as Kinematic Engine

The discrete Morse filtration of Sections 4–6 selects a finite set of geometrically admissible configurations. We now introduce the unique chemical operator that is permitted to act inside those configurations, thereby converting a critical geometric arrangement into a covalently locked secondary-structure element.

Axiom 3 (Exclusive Condensation Operator)**.** *Inside the open cells of I_C, the only admissible process that forms or rearranges covalent bonds of the polypeptide backbone is the proton-coupled electron transfer operator $\widehat{O}_{\mathrm{PCET}}$.*

Definition 15 (Zero Net Charge Flux)**.** *The operator $\widehat{O}_{\mathrm{PCET}}$ is required to satisfy the global charge-conservation condition*

$$\Delta q = 0$$

on every open cell in which it acts. Equivalently, the total charge flux tensor associated with the simultaneous transfer of a proton and an electron vanishes identically.

Definition 16 (Born–Oppenheimer Separation)**.** *The action of $\widehat{O}_{\mathrm{PCET}}$ is required to respect the Born–Oppenheimer separation of electronic and nuclear timescales: the electronic rearrangement is treated as instantaneous relative to nuclear motion, so that the nuclear coordinates remain fixed during the charge-transfer step itself.*

Proposition 10 (Action Restricted to Critical Simplices)**.** *Let ι be a lattice embedding of a biological graph G. The operator $\widehat{O}_{\mathrm{PCET}}$ can act non-trivially on $\iota(G)$ only at those 0-simplices that are critical for the steric Morse function f_{steric}. On every non-critical configuration the operator is identically zero. This restriction follows directly from the joint requirements of zero net charge flux ($\Delta q = 0$) and vanishing nuclear force at equilibrium, both of which are already present in the standing axioms.*

Proof. Suppose a configuration is not critical. Then $\nabla f_{\mathrm{steric}} \neq \mathbf{0}$, so there exists a direction of strictly decreasing steric energy. Any covalent rearrangement that attempted to lock the chain in such a non-stationary geometry would produce a residual force incompatible with the equilibrium condition required by the Born–Oppenheimer separation (Definition 16). The only configurations compatible with both zero net charge flux and vanishing nuclear force are the critical 0-simplices already selected by f_{steric}. □

Theorem 11 (Deterministic Zero-Entropy Condensation)**.** *The composition of the discrete Morse filtration with the operator $\widehat{O}_{\mathrm{PCET}}$ yields a deterministic map*

$$G \longmapsto \textit{covalently locked secondary-structure element}$$

whose image is supported exclusively on the critical sets Ω_α and Ω_β. The map is independent of the continuous thermal measure on the open cells and therefore carries zero conformational entropy.

Proof. By Theorem 4 the Morse filtration reduces the continuous conformational space to a discrete set of critical 0-simplices. By Proposition 10 the operator $\widehat{O}_{\mathrm{PCET}}$ acts only on that discrete set. Once a critical simplex has been selected, the simultaneous requirements of zero net charge flux and Born–Oppenheimer separation fix the covalent outcome uniquely. No residual continuous degrees of freedom survive, and the resulting map is therefore deterministic and entropy-free. □

Remark 7. *Continuous thermal motion remains the kinetic engine that explores the open cells of I_C. The steric Morse function filters that exploration down to a finite set of stationary geometries; the PCET operator merely locks those geometries into covalent permanence. Geometry selects; chemistry records. The two stages remain cleanly separated, and neither stage requires an exhaustive search of the classical Ramachandran continuum.*

8 Collapse of the Conformational Measure and Resolution of Levinthal's Paradox

The discrete geometry of I_C, the steric Morse filtration, the forced critical simplices Ω_α and Ω_β, and the restricted action of the PCET operator together replace the continuous search space of Section 2 by a finite discrete set. We now record the precise

measure-theoretic statement of that replacement.

Definition 17 (Discrete Conformational Measure)**.** *Let $C(G)$ denote the (finite) set of all critical 0-simplices of f_{steric} that arise from lattice embeddings of a fixed biological graph G into any admissible configuration of I_C (shifted or unshifted). Define the discrete conformational measure ν_G to be the normalized counting measure on $C(G)$:*

$$\nu_G = \frac{1}{|C(G)|} \sum_{\sigma \in C(G)} \delta_\sigma.$$

Theorem 12 (Finite Local Support Independent of Length)**.** *For every biological graph G of finite length the support of ν_G is a discrete set of critical 0-simplices. The local geometric repertoire of admissible critical configurations (i.e., the distinct void geometries that can host a secondary-structure element) is finite and bounded by a constant that depends only on the local geometry of the basis tensor Ψ_C. This local bound is independent of the number of residues. Consequently the exponential volume growth of the classical manifold $\mathcal{M}_n$ is replaced by a discrete set whose local cardinality remains uniformly bounded.*

Proof. By Theorems 6 and 8 every critical 0-simplex belongs to either Ω_α or Ω_β. By Proposition 9 these two sets are disjoint and arise from mutually exclusive lattice geometries. Inside each fixed lattice geometry the number of distinct voids that can be occupied by a chain of any length is finite, because the lattice is discrete and the local cross-section of each void is fixed by Ψ_C. The PCET operator (Theorem 11) acts only on this already finite set and introduces no additional continuous degrees of freedom. Hence $|C(G)|$ admits a uniform upper bound independent of chain length. □

Corollary 2 (Resolution of the Continuous Obstruction)**.** *The continuous $\mathcal{H}_2$ search on the exponentially growing manifold $\mathcal{M}_n$ is replaced by a discrete, deterministic evaluation of a finite set of critical simplices. The expected hitting time of a geometrically admissible secondary-structure configuration is therefore finite and independent of polypeptide length.*

Proof. Immediate from Theorem 12 and the deterministic character of the composition of Morse filtration with $\widehat{O}_{\text{PCET}}$ (Theorem 11). □

Remark 8. *Continuous thermal motion continues to operate inside every open cell of I_C. The lattice geometry, the steric Morse function, and the PCET operator together ensure that the only configurations that survive as stationary and covalently locked are drawn from a finite list fixed by the basis tensor Ψ_C. The classical search is not abolished; it is rendered finite by absolute geometric bounds. In this precise sense the abiotic loom resolves Levinthal's paradox without discarding the kinetic utility of continuous stochastic dynamics.*

9 Conclusions

The classical continuous formulation of polypeptide conformation, while indispensable for describing local thermal motion, admits no finite-time guarantee that a unique native structure will be reached. The volume of the Ramachandran product manifold grows exponentially with chain length, and any search governed by expected-variance criteria therefore remains asymptotically open.

The constructions of this paper close that openness by absolute geometric means. The same 3, 6, 9, 12-tetrasubstituted chrysene molecule that, under the conditions of U.S. Patent 12,195,423, co-synthesizes nucleic acids and phospholipid membranes is abstracted into the discrete Chrysene Tensor Space I_C. The interstitial voids of this lattice function as an abiotic loom: continuous exploration continues inside the open cells, yet every trajectory that intersects a lattice wall is assigned infinite steric energy. The resulting discrete Morse filtration admits only two families of critical 0-simplices—those corresponding to right-handed α-helices and those corresponding to extended β-strands. A proton-coupled electron transfer operator, required to act solely at these critical configurations and to conserve net charge, then locks the selected geometries into covalent permanence.

The conformational measure consequently collapses from an exponentially growing continuum to a finite discrete set whose cardinality is independent of polypeptide length. Levinthal's paradox is thereby resolved without the abandonment of continuous stochastic dynamics. Geometry selects; chemistry records. The same molecular architecture that originates the genetic and membrane systems is shown to constrain secondary-structure formation to a rigorously finite, biologically functional repertoire.

The framework developed here is deliberately limited to the generation of secondary structure. The same lattice geometry, once secondary elements are in place, supplies natural routes to tertiary packing, active-site voids, and higher-order assemblies. Those extensions lie beyond the present scope and will be treated in subsequent work. What has been established is the foundational geometric step: continuous conformational space, when confined to the active interstitium of the chrysene loom, becomes finite, deterministic, and consistent with the patented chemistry of biological co-synthesis.

A Literature Context

The observation that an unguided random search through the space of polypeptide conformations cannot reach a unique native structure in biologically relevant time was first articulated by Levinthal [Lev69]. The resulting temporal obstruction has become known as Levinthal's paradox. Anfinsen's thermodynamic hypothesis [Anf73] established that, under physiological conditions, the native conformation of a small globular protein is determined by the amino-acid sequence as the state of lowest free energy; the hypothesis is silent on the kinetic route by which that state is reached.

Subsequent theoretical work has sought to reconcile the thermodynamic hypothesis with finite folding times. Zwanzig, Szabo and Bagchi [ZSB92] showed that a modest energetic bias against locally unfavourable configurations is sufficient to reduce the search time to a biologically plausible scale. The energy-landscape perspective developed by Bryngelson, Onuchic, Socci and Wolynes, and by Dill and Chan [DC97, BOSW95], reframed folding as motion on a funnel-shaped landscape in which the native basin is reached by progressive reduction of conformational entropy rather than by exhaustive enumeration. Lattice models [CD90, LD89] further demonstrated that steric constraints alone, when a chain is driven to compactness, generate substantial secondary structure.

Discrete Morse theory, introduced by Forman [For98, For02], supplies a purely combinatorial analogue of classical Morse theory that assigns real values to the cells of a simplicial complex and identifies critical cells whose number is related to the topology of the complex. Applications of discrete Morse theory to biomolecular data analysis have appeared, yet a systematic geometric embedding of the polypeptide backbone into a rigid molecular lattice whose voids enforce secondary-structure critical cells has not previously been developed.

The present work belongs to this discrete geometric tradition while remaining complementary to the continuous energy-landscape programme. Continuous thermal exploration is retained inside the open cells of the lattice; the lattice walls merely render every trajectory that leaves those cells infinitely costly. The resulting filtration admits only the critical geometries corresponding to α-helices and β-strands. The same molecular architecture that, under the conditions of U.S. Patent 12,195,423 [Sch25], co-synthesizes nucleic acids and phospholipid membranes is thereby shown to constrain secondary-structure formation to a finite, deterministic set.

B Background within the Chrysene Formalism

The geometric constructions of the present paper rest on a coherent mathematical and physical framework developed across the Chrysene Formalism. That framework begins with the empirical observation that a single polycyclic aromatic architecture—the 3, 6, 9, 12-tetrasubstituted chrysene—can serve as the generative precursor for the co-synthesis of nucleic-acid sequences and phospholipid (or sterol/hopanoid) membrane components under the conditions of U.S. Patent 12,195,423. The mathematical abstraction of this molecule into a discrete, non-commutative lattice supplies the absolute spatial bounds required for deterministic biological assembly.

The pure-mathematical foundations are set out in two complementary volumes. The first develops the cohomological invariants, operator algebras, and discrete non-commutative state space of the Chrysene Tensor Space I_C [Sch26b]. The second constructs the universal algebraic geometry and maximal-entropy survival principles that govern the lattice under topological strain [Sch26e]. Together these works establish I_C as a bounded fibrated manifold over $\mathbb{Z}^3$ whose C_{2h}-symmetric basis tensor enforces orthogonal decoupling and L^∞ Dirichlet walls.

A subsequent categorical refinement elevates the manifold to a discrete non-commutative topos. Operator algebras are mapped into characteristic-2 sequence spaces over $\mathbb{F}_4$ via the ring of Witt vectors, and uncompensated topological derivations are shown to resolve by algebraic excision into the null ideal while preserving global Betti numbers [Sch26c]. The same work proves that the C_{2h} chiral step-defect graph is the unique finite topology capable of generating the required braided monoidal category without spectral degeneracy.

On the biological side, the Identification Hypothesis asserts a structure-preserving isomorphism between the abstract graph of I_C and the physical chrysene lattice. Under this hypothesis the lattice functions as an encodable topological metamaterial whose interstitial architecture simultaneously accounts for prebiotic purification, co-projection of nucleic acids and membrane lipids, and the geometric resolution of macroscopic evolutionary transitions [Sch26g, Sch26d]. The broader algebraic foundations of the biosphere, including the continuity from abiotic network to endogenous cellular matrix, are developed in [Sch26f].

The present paper applies this established geometry to the specific problem of secondary-structure formation. Continuous conformational exploration is retained inside the open cells of the lattice; the rigid walls convert the exponentially large Ramachandran continuum into a discrete Morse filtration whose only critical simplices are the α-helical and β-strand geometries. The same molecular architecture that originates the genetic and membrane systems is thereby shown to constrain polypeptide folding to a finite, deterministic repertoire. Extensions of the lattice geometry to tertiary packing, active-site voids, and pharmacological stabilization are treated in the companion volume on functorial mappings in protein synthesis [Sch26a].

References

[Anf73] Christian B. Anfinsen. Principles that govern the folding of protein chains. *Science*, 181(4096):223–

230, 1973.

[BOSW95] Joseph D. Bryngelson, José N. Onuchic, Nicholas D. Socci, and Peter G. Wolynes. Funnels, pathways, and the energy landscape of protein folding: A synthesis. *Proteins: Structure, Function, and Bioinformatics*, 21(3):167–195, 1995.

[CD90] Hue Sun Chan and Ken A. Dill. Origins of structure in globular proteins. *Proceedings of the National Academy of Sciences*, 87(16):6388–6392, 1990.

[DC97] Ken A. Dill and Hue Sun Chan. From levinthal to pathways to funnels. *Nature Structural Biology*, 4(1):10–19, 1997.

[For98] Robin Forman. Morse theory for cell complexes. *Advances in Mathematics*, 134(1):90–145, 1998.

[For02] Robin Forman. A user's guide to discrete morse theory. *Séminaire Lotharingien de Combinatoire*, 48:Article B48c, 35 pp., 2002.

[LD89] Kit Fun Lau and Ken A. Dill. A lattice statistical mechanics model of the conformational and sequence spaces of proteins. *Macromolecules*, 22(10):3986–3997, 1989.

[Lev69] Cyrus Levinthal. How to fold graciously. In J. T. P. Debrunner, J. C. Tsibris, and E. Munck, editors, *Mossbauer Spectroscopy in Biological Systems*, pages 22–24. University of Illinois Press, 1969.

[Sch25] Charles D. Schaper. Encoded design integrated synthesis of nucleic acids, and phospholipids, and related pharmaceutical products, 2025. Patent US 12,195,423.

[Sch26a] Charles D. Schaper. *Designing Therapeutics with The Chrysene Formalism: Functorial Mappings in Protein Synthesis and Molecular Pharmacology*. Schaper Systems Press, San Francisco, CA, 2026. ISBN: 979-8-950371-10-3.

[Sch26b] Charles D. Schaper. *Foundations of the Chrysene Formalism: Cohomological Invariants, Operator Algebras, and the Discrete Noncommutative State Space*. Schaper Systems Press, San Francisco, CA, 2026. ISBN: 979-8-950371-08-0.

[Sch26c] Charles D. Schaper. On the foundations of discrete non-commutative topoi: Operator algebras, $\mathbb{F}_4$ sequence spaces, and the c_{2h} bipartite isomorphism. *Annals of the Chrysene Formalism*, 1:130–142, 2026.

[Sch26d] Charles D. Schaper. Programmable topological metamaterials: Self-assembly and quantum information encoding in the tetrasubstituted chrysene lattice. *Annals of the Chrysene Formalism*, 1:169–177, 2026.

[Sch26e] Charles D. Schaper. *Tensorial Framework of the Chrysene Formalism - Universal Algebraic Geometry and Maximal-Entropy Survival*. Schaper Systems Press, San Francisco, CA, 2026. ISBN: 979-8-950371-03-5.

[Sch26f] Charles D. Schaper. *The Geometric Origins and Continuity of Life: The Chrysene Formalism and the Algebraic Foundations of the Biosphere*. Schaper Systems Press, San Francisco, CA, 2026. ISBN: 979-8-950371- 02-8.

[Sch26g] Charles D. Schaper. The universal blueprint: One encodable topological metamaterial to explain the origin, intelligence, and evolution of life. *Annals of the Chrysene Formalism*, 1:178–195, 2026.

[ZSB92] Robert Zwanzig, Attila Szabo, and Biman Bagchi. Levinthal's paradox. *Proceedings of the National Academy of Sciences*, 89(1):20–22, 1992.