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Topological Scission of the Chrysene Abiotic Loom: Dual Mastering, Structural Scaffolding, Sequential Catalytic Connectivity, and PCET-Enabled Prototype Enzyme Formation

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Abstract

Papers 1–3 [Sch26a, Sch26c, Sch26d] established that the Chrysene abiotic loom selects secondary-structure geometries, concentrates them in high-resolution public structures, and accommodates their three-dimensional shape, orientation and side-chain packing. The present paper extends the validated lattice into a multi-layer geometric and synthetic compiler. Controlled topological scission simultaneously generates residual voids and liberated fragments that function as dual catalytic masters, while the un-excised towers and rails remain as a rigid residual scaffold that holds every master in absolute spatial register. Successive masters may be placed so that the exit geometry of one coincides with the entrance geometry of the next, realizing metabolon-style sequential connectivity. The residual scaffold preserves the original proton-coupled electron transfer tethers; acting jointly with a scaffold-registered master, those tethers drive cooperative peptide-bond synthesis of a polypeptide conformal to the master. The assembled prototype enzyme is entropically stabilized relative to the disassembled state under aqueous conditions. The constructions are illustrated on segments of the glycolytic pathway (PFK-1 / isomerase) and the G6P–NADPH pathway. The prototype remains a geometric and covalent object only; its genetic tagging and replicative integration are deferred to a future paper. Continuous thermal fluctuations remain fully admissible inside the open cells of the residual lattice; the lattice walls and residual tethers supply absolute spatial and chemical bounds.

Keywords: Chrysene abiotic loom; topological scission; residual void; lattice fragment; residual scaffold; sequential catalytic connectivity; metabolon geometry; PCET; prototype enzyme; dual mastering; structural support.

1 Introduction

The Chrysene abiotic loom was introduced in Paper 1 as a discrete geometric resolution of Levinthal's paradox: continuous conformational exploration is retained inside the open cells of the lattice, while the rigid walls render any trajectory that intersects a wall infinitely costly under a steric Morse function. The only critical configurations admitted by the filtration are right-handed α-helices and extended β-strands; a proton-coupled electron transfer operator then locks these geometrically selected arrangements into covalent permanence. Paper 2 [Sch26c] translated the abstract critical simplices into parameter-free angular windows and demonstrated moderate-to-strong enrichment against a high-resolution public corpus. Paper 3 [Sch26d] elevated the empirical test from local dihedral statistics to higher-order geometric compatibility, showing that native helices and strands align with the lattice frame, admit sterically admissible tethering configurations with positive clearance, and exhibit systematic side-chain organization consistent with lattice contact.

Local and higher-order geometric fidelity, however, do not yet exhaust the architectural competence of the loom. A biologically useful scaffold must also be able to generate functional catalytic sites, to hold those sites in rigid spatial register, to arrange them into sequential metabolic units, and to polymerize polypeptides conformal to the resulting templates. The present paper addresses these further capacities through a single reductive operation—topological scission—and through the residual resources that scission leaves intact.

Topological scission of an admissible lattice subset simultaneously produces three outputs: a residual void, a liberated fragment, and a residual structural scaffold. The void and the fragment function as dual geometric and physico-chemical mas-

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ters for complementary molecular architecture. The residual scaffold, consisting of the un-excised towers and rails, supplies the load-bearing framework that constrains the absolute position and orientation of every master. When two or more masters are registered to the same residual scaffold, their exit and entrance geometries may be aligned so that product channeling becomes possible, realizing a metabolon-style sequential organization. Finally, because admissible scission preserves the original proton-coupled electron transfer tethers, the residual lattice remains chemically competent to drive cooperative peptide-bond synthesis of a polypeptide that is conformationally conformal to its master. The assembled prototype enzyme is stabilized relative to the disassembled state by the hydrophobic/hydrophilic segregation imposed by the lattice: disassembly would release components into mutually non-cooperative bulk solvent.

The four layers—master generation, residual structural support, sequential connectivity, and PCET-enabled prototype formation—are interdependent and are illustrated jointly on two metabolic segments: the glycolytic fragment centered on phosphofructokinase-1 and the subsequent isomerase step, and the glucose-6-phosphate pathway leading to NADPH generation. In each case the lattice-derived masters, the residual scaffold, the sequential geometry and the residual PCET chemistry are examined as a single geometric and synthetic unit.

The prototype enzyme constructed herein is a geometric and covalent object only. The further operations required to tag this prototype, to encode it in a nucleic-acid sequence, and to integrate that sequence into a replicative genetic system constitute a distinct formal development. Those operations are left for a future paper whose geometric premises will be precisely the multi-layer architecture established in the present work.

Continuous thermal fluctuations of backbone, side chains and solvent remain fully admissible inside the open cells of the residual lattice. The lattice walls and residual tethers function solely as absolute spatial and chemical bounds that render the organized metabolic unit preferred to complete disassembly. No claim is made concerning catalytic rate constants or dynamical trajectories; the results are restricted to geometric compatibility, physico-chemical complementarity, residual structural support, sequential register, and PCET-enabled covalent formation of a conformal prototype.

Notation and Standing Assumptions

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

1. **Inheritance from Papers 1–3 [Sch26a, Sch26c, Sch26d].** All definitions, operators and theorems of the Chrysene Tensor Space I_C, the basis tensor Ψ_C, the steric Morse function f_{steric}, the lateral-shift operator $\widehat{R}_{\text{rot}}$, the zero-shift operator $\widehat{R}_0$, the critical simplices Ω_α and Ω_β, the numerical geometric windows W_α and W_β, the local-support theorem, the higher-order compatibility results of Paper 3 [Sch26d], and the proton-coupled electron transfer operator $\widehat{O}_{\text{PCET}}$ are taken as established. No new secondary-structure windows are introduced.

2. **Topological scission.** The topological scission operator is denoted $\widehat{D}_{\text{sciss}}$. Applied to a designated subset of lattice nodes and edges, it produces three simultaneous outputs: a residual void V_{res}, a liberated lattice fragment F_{sciss}, and a residual structural scaffold S_{res} consisting of the un-excised towers and rails. The PCET-capable tethers of the residual scaffold remain active.

3. **Dual mastering maps.** The void-as-master map is written $\mathcal{M}_V$ and the fragment-as-master map is written $\mathcal{M}_F$. Each map sends its geometric master to the set of molecular volumes, charge distributions and solvent structures that are sterically and physico-chemically complementary to it.

4. **Scaffold-support map.** The residual scaffold acts on every catalytic master through the support map $\mathcal{S}$, which constrains the absolute position, orientation and mutual registration of the masters relative to the remaining lattice.

5. **Sequential connectivity.** The sequential-connectivity operator $\widehat{C}_{\text{seq}}$ places two or more catalytic masters inside a common residual scaffold so that the exit geometry of one master coincides, within a prescribed tolerance, with the entrance geometry of the next.

6. **Prototype-enzyme formation.** The prototype-enzyme formation map $\mathcal{E}_{\text{prot}}$ is the composition of a geometric master ($\mathcal{M}_V$ or $\mathcal{M}_F$), the residual scaffold $\mathcal{S}$, and the action of the residual PCET tethers $\widehat{O}_{\text{PCET}}$. It yields a polypeptide conformationally conformal to the master. Conversion of this prototype into a tagged, replicative genetic element is deferred to a future paper.

7. **Complementarity measures.** Steric, electrostatic, hydrophobic/hydrophilic, water-mediated and nucleobase-mediated complementarity are assessed by the corresponding indicator functions and distance thresholds; precise numerical cut-offs are stated when data are introduced.

All continuous thermal fluctuations of backbone, side chains and solvent remain admissible inside the open cells of the residual lattice. The constructions that follow test higher-order geometric and synthetic competence of the scission-derived masters and of the residual scaffold; they do not replace the secondary-structure results of Papers 1–3 [Sch26a, Sch26c, Sch26d][Sch26a, **?**].

2 From Secondary-Structure Fidelity to Multi-Layer Geometric Compilation

Papers 1–3 [Sch26a, **?**, **?**] established that the Chrysene Tensor Space functions as an abiotic loom whose interstitial voids select and stabilize secondary-structure geometries, and that the same lattice accommodates the three-dimensional shape, orientation and side-chain packing of native helices and strands. The present paper extends that validated geometry into a multi-layer compiler capable of four further operations.

1. **Master generation by topological scission.** Controlled excision of lattice material produces both residual voids and liberated fragments. Each class of object functions as a geometric and physico-chemical master for complementary molecular architecture.

2. **Structural support by the residual scaffold.** The unexcised towers and rails remain as a rigid framework that holds every catalytic master in absolute spatial register.

3. **Sequential catalytic connectivity.** Adjacent masters may be placed inside the same residual scaffold so that the product geometry of one site is delivered, within bounded tolerance, to the entrance geometry of the next, realizing a metabolon-style spatial organization.

4. **PCET-enabled prototype enzyme formation.** The original proton-coupled electron transfer tethers remain active on the residual lattice. Acting jointly with a geometric master and the residual scaffold, they drive cooperative peptide-bond synthesis of a polypeptide conformal to the master. Entropic stabilization arises because disassembly would release hydrophobic and hydrophilic components into mutually non-cooperative external environments.

The four layers are interdependent: scission generates the masters, the residual scaffold supports them, sequential placement organizes them into pathways, and residual PCET chemistry converts the geometric template into a covalent prototype enzyme. The resulting prototype is a geometric and synthetic object only. Its subsequent tagging, genetic encoding and integration into a replicative informational system constitute a distinct formal development and are left for a future paper.

The metabolic illustrations employed throughout are drawn from the glycolytic segment centered on phosphofructokinase-1 (PFK-1) and the subsequent isomerase step, and from the glucose-6-phosphate (G6P) pathway leading to NADPH generation. In each case the lattice-derived masters, the residual structural support, the sequential geometry and the PCET-driven prototype formation are examined jointly.

3 The Topological Scission Operator

The higher-order geometric fidelity established in Papers 1–3 [Sch26a, Sch26c, Sch26d] concerns the intact Chrysene Tensor Space. The present section introduces a reductive operation that excises a designated subset of the lattice while preserving the structural and chemical competence of what remains.

Definition 1 (Topological Scission Operator)**.** *Let $\Lambda \subset I_C$ be a finite, connected set of lattice nodes together with the edges that join them. The topological scission operator $\widehat{D}_{\text{sciss}}$ acts on Λ by simultaneous deletion of those nodes and edges. The output of the operator is the ordered triple*

$$\widehat{D}_{\text{sciss}}(\Lambda) = \big(V_{\text{res}},\, F_{\text{sciss}},\, S_{\text{res}}\big),$$

where

- *V_{res} is the residual void—the bounded complementary region whose boundary consists of the newly exposed lattice faces;*
- *F_{sciss} is the liberated fragment—the covalently coherent subset of nodes and edges that has been excised;*
- *S_{res} is the residual structural scaffold—the connected component of $I_C \setminus \Lambda$ that remains after excision.*

Definition 2 (Admissible Scission Set)**.** *A set Λ is admissible for scission when the residual scaffold S_{res} remains path-connected and the PCET-capable tethers incident to the boundary of V_{res} are preserved. Admissibility guarantees that the residual lattice continues to support both mechanical registration and proton-coupled electron transfer.*

Proposition 1 (Void–Fragment–Scaffold Triple)**.** *For every admissible scission set Λ the operator $\widehat{D}_{\text{sciss}}$ produces a well-defined triple $(V_{\text{res}},\, F_{\text{sciss}},\, S_{\text{res}})$ in which*

1. *the boundary of V_{res} is complementary to the surface of F_{sciss},*
2. *S_{res} is rigid relative to the parent lattice metric,*
3. *every PCET tether that terminated on the boundary of Λ remains active on the corresponding boundary of S_{res}.*

Consequently a single scission event simultaneously supplies a geometric master (either the void or the fragment), a complementary partner, and a residual structural framework that holds both in register.

Proposition 2 (Conservation of Local Geometry)**.** *The intrinsic geometry of any secondary-structure element already validated against the intact lattice (Papers 2 and 3) remains admissible inside the residual scaffold S_{res}, provided the element does not intersect the excised set Λ. Scission therefore refines, rather than invalidates, the higher-order compatibility results of the preceding papers.*

Remark 1. *Topological scission is a purely geometric operation. No energetic minimization or side-chain rearrangement is required for the definition of the triple $(V_{\mathrm{res}}, F_{\mathrm{sciss}}, S_{\mathrm{res}})$. Continuous thermal fluctuations remain admissible inside the open cells of the residual scaffold; the newly created void boundary functions solely as an additional absolute steric limit.*

Remark 2 (PCET Persistence)**.** *Because admissible scission preserves the tethers incident to the void boundary, the residual lattice continues to support the cooperative peptide-bond chemistry formalized by $\widehat{O}_{\mathrm{PCET}}$. This persistence is essential for the prototype-enzyme formation map introduced in Section 8.*

4 Residual Voids as Catalytic Masters

The residual void V_{res} generated by topological scission is not merely an empty region; it functions as a geometric and physicochemical master that constrains the admissible shapes, charge distributions and solvent structures of any molecular occupant.

Definition 3 (Residual Void)**.** *Let $\widehat{D}_{\mathrm{sciss}}(\Lambda) = (V_{\mathrm{res}}, F_{\mathrm{sciss}}, S_{\mathrm{res}})$ be the output of an admissible scission. The residual void V_{res} is the bounded, open complement of S_{res} whose boundary $\partial V_{\mathrm{res}}$ consists of the newly exposed faces of the residual lattice. The boundary is an equipotential surface of the steric Morse function f_{steric} inherited from Paper 1 [Sch26a].*

Definition 4 (Geometric Descriptors of the Void)**.** *The residual void is characterized by the following geometric quantities:*

- *volume* $\mathrm{Vol}(V_{\mathrm{res}})$*,*
- *surface area and mean curvature of $\partial V_{\mathrm{res}}$,*
- *topological type (shallow pocket, deep cleft, or through-channel),*
- *minimal and maximal widths measured between opposing boundary faces.*

Definition 5 (Physico-Chemical Descriptors of the Void)**.** *In addition to pure geometry, the void boundary carries:*

- *an electrostatic potential induced by the residual lattice charges,*
- *a hydrophobic/hydrophilic patterning inherited from the local chemical identity of the exposed nodes,*
- *a water-accessible surface that determines structured-solvent capacity,*
- *a nucleobase-interaction capacity when the boundary geometry matches the steric and hydrogen-bonding profile of NAD or related cofactors.*

Definition 6 (Void-as-Master Map)**.** *The void-as-master map $\mathcal{M}_V$ sends the residual void to the set of all molecular volumes Ω that satisfy*

$$\Omega \subset V_{\mathrm{res}} \quad \textit{and} \quad \mathrm{dist}(\Omega, \partial V_{\mathrm{res}}) \geq \delta_{\mathrm{min}}$$

for a prescribed steric tolerance $\delta_{\mathrm{min}} > 0$, together with the electrostatic, hydrophobic/hydrophilic and solvent-complementarity conditions associated with $\partial V_{\mathrm{res}}$. Any molecular entity belonging to $\mathcal{M}_V(V_{\mathrm{res}})$ is said to be void-complementary.

Proposition 3 (Steric Admissibility under Void Mastering)**.** *If a molecular volume Ω lies in the image of $\mathcal{M}_V$, then Ω has empty intersection with the residual scaffold S_{res}. Consequently the placement of any void-complementary ligand or polypeptide segment is sterically admissible by construction.*

Proposition 4 (Void Mastering of Cofactor-Stabilized Architecture)**.** *When the boundary geometry of V_{res} is compatible with the simultaneous coordination of two NAD (or NADP) molecules, the void-as-master map $\mathcal{M}_V$ admits occupants whose stability is enhanced by dual-nucleobase bridging. This geometry supplies the formal setting for the G6P–NADPH pathway illustrations examined in later sections.*

Remark 3. *The residual void does not dictate catalytic chemistry; it supplies absolute spatial, electrostatic and solvation bounds. Continuous conformational and solvent fluctuations remain admissible inside V_{res} provided they respect the boundary conditions encoded by $\mathcal{M}_V$.*

Remark 4 (Relation to the Residual Scaffold)**.** *The void V_{res} is never free-floating. Its boundary is mechanically continuous with the residual scaffold S_{res}, so that every void-complementary occupant remains registered to the larger lattice framework through the support map $\mathcal{S}$ of Section 6.*

5 Liberated Fragments as Catalytic Masters

While residual voids constrain occupants by complementary emptiness, the liberated fragment F_{sciss} functions as a positive geometric and electronic master: a finite, covalently coherent piece of the original lattice that templates complementary molecular surfaces by direct shape, charge and hydrophobic/hydrophilic registry.

Definition 7 (Liberated Lattice Fragment)**.** *Let $\widehat{D}_{\mathrm{sciss}}(\Lambda) = (V_{\mathrm{res}}, F_{\mathrm{sciss}}, S_{\mathrm{res}})$ be the output of an admissible scission. The liberated fragment F_{sciss} is the covalently connected subset of nodes and edges that has been excised. It inherits the local metric, the electronic configuration and the PCET-capable bonding geometry of the parent lattice.*

Definition 8 (Canonical Fragment Classes)**.** *Among the admissible fragments, two classes are of particular metabolic relevance:*

- *five-membered ring systems whose geometry matches the steric and electronic profile of the catalytic cores of phosphofructokinase-type enzymes;*
- *extended aromatic or mixed aromatic-aliphatic fragments capable of templating larger active-site surfaces.*

The five-membered class is denoted F_5 and serves as the prototype for the PFK-1 illustrations of later sections.

Definition 9 (Geometric and Electronic Descriptors of the Fragment)**.** *The liberated fragment is characterized by:*

- *its intrinsic bond-length and bond-angle metric,*
- *the electrostatic potential generated by its residual charge distribution,*
- *the hydrophobic/hydrophilic patterning of its exposed faces,*
- *the set of hydrogen-bond donor and acceptor sites that remain after scission,*
- *the steric volume it excludes when placed against a complementary molecular surface.*

Definition 10 (Fragment-as-Master Map)**.** *The fragment-as-master map $\mathcal{M}_F$ sends the liberated fragment F_{sciss} to the set of all molecular surfaces Σ that satisfy a joint complementarity condition:*

$$\mathrm{dist}(\Sigma,\, F_{\mathrm{sciss}}) \in [\delta_{\min},\, \delta_{\max}]$$

together with matching electrostatic sign, hydrophobic/hydrophilic registry and hydrogen-bond pairing. Any molecular surface belonging to $\mathcal{M}_F(F_{\mathrm{sciss}})$ is said to be fragment-complementary.

Proposition 5 (Steric and Electronic Admissibility under Fragment Mastering)**.** *If a molecular surface Σ lies in the image of $\mathcal{M}_F$, then the complex $F_{\mathrm{sciss}} \cup \Sigma$ is free of steric clash and satisfies the electrostatic and solvation complementarity conditions encoded by the fragment. Consequently the fragment can serve as a geometric template for the formation of a complementary enzymatic surface.*

Proposition 6 (Fragment Mastering of PFK-Type Catalytic Cores)**.** *When F_{sciss} belongs to the five-membered class F_5, the fragment-as-master map $\mathcal{M}_F$ admits complementary surfaces whose geometry, charge distribution and hydrogen-bond pattern are consistent with the active-site architecture of phosphofructokinase-1 and of the immediately downstream isomerase. This supplies the formal setting for the fragment-dominated metabolic illustrations of later sections.*

Remark 5. *The liberated fragment does not itself perform catalysis. It supplies a rigid, chemically patterned master against which a complementary polypeptide surface can be organized. Continuous thermal fluctuations of the complementary surface remain admissible provided they respect the distance and pairing bounds of $\mathcal{M}_F$.*

Remark 6 (Relation to the Residual Scaffold)**.** *Although the fragment has been excised, its original spatial register relative to the residual scaffold S_{res} is retained as a geometric reference. When a complementary enzymatic surface is formed against the fragment, the residual scaffold continues to furnish absolute positional constraints through the support map $\mathcal{S}$, ensuring that the finished prototype enzyme remains mechanically continuous with the larger lattice framework.*

6 The Residual Scaffold as Structural Framework

Topological scission generates catalytic masters (voids or fragments) but does not leave them free-floating. The un-excised portion of the lattice remains as a rigid, load-bearing framework that holds every master in absolute spatial register. This residual scaffold is the principal structural contribution of the Chrysene Tensor Space after scission and is the primary locus for quantitative geometric validation.

Definition 11 (Residual Structural Scaffold)**.** *Let $\widehat{D}_{\text{sciss}}(\Lambda) = (V_{\text{res}}, F_{\text{sciss}}, S_{\text{res}})$ be the output of an admissible scission. The residual structural scaffold S_{res} is the maximal connected component of $I_C \setminus \Lambda$ that remains after excision. It inherits the full metric, the orthogonal connectivity of the parent lattice, and all PCET-capable tethers that were not incident to the excised set.*

Definition 12 (Scaffold-Support Map)**.** *The scaffold-support map $\mathcal{S}$ assigns to every catalytic master $M \in \{V_{\text{res}}, F_{\text{sciss}}\}$ the set of rigid-body placements of M that keep the boundary of M in continuous mechanical contact with S_{res} within a prescribed tolerance $\varepsilon_{\text{reg}} > 0$. Formally,*

$$\mathcal{S}(M) = \left\{ g \in \mathrm{SE}(3) : \operatorname{dist}\left(g \cdot \partial M,\, S_{\text{res}}\right) \le \varepsilon_{\text{reg}} \right\}.$$

Any placement belonging to $\mathcal{S}(M)$ is said to be scaffold-registered.

Definition 13 (Geometric Descriptors of Scaffold Support)**.** *Scaffold support is quantified by the following observables:*

- *tower-to-master clearances—the set of minimum distances from each residual tower to the boundary of the master;*
- *angular registration—the orientation of the master principal axes relative to the lattice frame $\{v_x, v_y, T_z\}$;*
- *rail continuity—the unbroken path length of residual rails that connect successive masters;*
- *inter-master separation—the Euclidean distance between the centroids of two scaffold-registered masters placed inside the same residual lattice.*

Proposition 7 (Absolute Registration of Catalytic Masters)**.** *For every admissible scission the residual scaffold S_{res} is path-connected and rigid with respect to the parent lattice metric. Consequently every catalytic master M generated by the scission admits a non-empty set of scaffold-registered placements $\mathcal{S}(M)$. In all such placements the absolute position and orientation of M are constrained by the residual towers and rails to within the tolerance ε_{reg}.*

Proposition 8 (Mechanical Continuity of Sequential Masters)**.** *Let M_1 and M_2 be two catalytic masters generated by (possibly successive) admissible scissions and registered to a common residual scaffold. Then the inter-master separation and relative orientation are bounded by the geometry of S_{res}. In particular, the residual rails supply a continuous mechanical path linking M_1 to M_2, thereby guaranteeing that sequential catalytic units remain in fixed spatial register.*

Proposition 9 (Persistence of Secondary-Structure Compatibility)**.** *Any secondary-structure element whose placement was sterically admissible in the intact lattice (Papers 2 and 3) remains admissible in the residual scaffold, provided the element does not intersect the excised set. The higher-order geometric compatibility established prior to scission is therefore inherited by S_{res}.*

Remark 7 (Primary Empirical Locus)**.** *The descriptors of Definition 13—tower-to-master clearances, angular registration, rail continuity and inter-master separation—are directly measurable against high-resolution structural data. Section 10 therefore treats these quantities as the principal quantitative tests of the structural-support layer.*

Remark 8 (Relation to Prototype Formation)**.** *Because the residual scaffold preserves PCET-capable tethers, every scaffold-registered master remains chemically competent for the cooperative peptide-bond synthesis formalized by $\widehat{O}_{\text{PCET}}$. Structural support and synthetic competence are consequently inseparable: the same lattice component that holds the master in register also supplies the tethers that polymerize the conformal prototype enzyme.*

7 Sequential Catalytic Connectivity (Metabolon Geometry)

A residual scaffold may host more than one catalytic master. When two (or more) masters are placed so that the exit geometry of one coincides, within a prescribed tolerance, with the entrance geometry of the next, the lattice realizes a spatially sequential catalytic unit of metabolon type. The present section formalizes that sequential connectivity.

Definition 14 (Sequential-Connectivity Operator)**.** *Let M_1 and M_2 be catalytic masters (voids or fragments) registered to a common residual scaffold S_{res} via the support map $\mathcal{S}$. The sequential-connectivity operator $\widehat{C}_{\mathrm{seq}}$ acts on the ordered pair $(M_1,\ M_2)$ by imposing the geometric handover condition*

$$\mathrm{dist}\big(\mathrm{Exit}(M_1),\ \mathrm{Entrance}(M_2)\big) \le \delta_{\mathrm{hand}}$$

together with a relative-orientation tolerance θ_{hand}. The output of the operator is the sequential pair $(M_1 \to M_2)$ when the handover condition is satisfied, and is undefined otherwise.

Definition 15 (Exit and Entrance Geometry)**.** *For a catalytic master M the exit set $\mathrm{Exit}(M)$ is the subset of ∂M through which a product molecule is sterically permitted to leave; the entrance set $\mathrm{Entrance}(M)$ is the subset of ∂M through which a substrate molecule is sterically permitted to enter. Both sets are determined by the local geometry and physicochemical patterning of the master boundary.*

Definition 16 (Product-Channeling Tolerance)**.** *The handover tolerances δ_{hand} and θ_{hand} are chosen so that a molecular species leaving M_1 remains within the capture radius of M_2 under ordinary thermal diffusion. Structured water or nucleobase cofactors may further reduce the effective tolerances by providing transient bridging interactions.*

Proposition 10 (Existence of Lattice-Compatible Sequential Pairs)**.** *There exist admissible scission sequences such that the residual scaffold S_{res} simultaneously supports two scaffold-registered masters M_1 and M_2 satisfying the handover condition of Definition 14. In particular, sequential pairs corresponding to the PFK-1→isomerase segment and to successive steps of the G6P–NADPH pathway are geometrically realizable inside a single residual lattice.*

Proposition 11 (Mechanical and Chemical Continuity of Sequential Units)**.** *If $(M_1 \to M_2)$ is a sequential pair registered to S_{res}, then:*

1. *the residual rails of S_{res} furnish a continuous mechanical path linking M_1 to M_2;*
2. *the PCET-capable tethers of the residual scaffold remain available at both masters, permitting cooperative prototype formation at each site;*
3. *the inter-master separation and relative orientation are bounded by the geometry of S_{res}, independent of continuous thermal fluctuations inside the open cells.*

Proposition 12 (Guided Handover by Physico-Chemical Patterning)**.** *When the exit face of M_1 and the entrance face of M_2 carry complementary electrostatic, hydrophobic/hydrophilic or nucleobase-mediated patterns, the effective capture radius of the sequential pair is enlarged relative to pure steric handover. Structured water layers or bridging NAD/NADP molecules may further stabilize the transit geometry.*

Remark 9. *Sequential connectivity does not require covalent fusion of the two masters. The residual scaffold supplies the spatial register; the masters themselves remain distinct geometric objects. Continuous diffusion of intermediate species between the masters is admissible provided the handover tolerances are respected.*

Remark 10 (Relation to Prototype Formation)**.** *Because each master in a sequential pair remains PCET-competent and scaffold-registered, a conformal prototype polypeptide can be synthesized at every site of the sequence. The resulting multi-site prototype inherits the spatial organization of the metabolon geometry while remaining a purely geometric and synthetic object; genetic tagging and replicative integration are deferred.*

8 PCET-Enabled Formation of the Prototype Enzyme

The residual scaffold does not merely hold catalytic masters in register; it retains the proton-coupled electron transfer tethers of the parent lattice. Acting jointly with a geometric master, those tethers drive the cooperative synthesis of a polypeptide that is conformationally conformal to the master. The resulting object is termed a prototype enzyme. Its subsequent genetic tagging and replicative integration lie outside the present scope and are reserved for a future paper.

Definition 17 (Residual PCET Competence)**.** *Let S_{res} be the residual scaffold produced by an admissible scission. Every PCET-capable tether that was not incident to the excised set remains active on S_{res}. The restriction of the operator $\widehat{O}_{\mathrm{PCET}}$ to these residual tethers is denoted $\widehat{O}_{\mathrm{PCET}}\big|_{S_{\mathrm{res}}}$ and is called the residual PCET operator.*

Definition 18 (Prototype-Enzyme Formation Map)**.** *Let M be a catalytic master (void or fragment) registered to S_{res} via the support map $\mathcal{S}$. The prototype-enzyme formation map $\mathcal{E}_{\mathrm{prot}}$ is the composition*

$$\mathcal{E}_{\mathrm{prot}}(M) = \widehat{O}_{\mathrm{PCET}}\big|_{S_{\mathrm{res}}} \circ \mathcal{S}(M).$$

Its value is a polypeptide chain whose backbone and side-chain geometry lie inside the complementarity bounds of $\mathcal{M}_V(M)$ or $\mathcal{M}_F(M)$, and whose peptide bonds have been formed by residual PCET chemistry. The resulting chain is called a prototype enzyme conformal to M.

Definition 19 (Entropic Stabilization Relative to Disassembly)**.** *Consider the assembled prototype enzyme $E = \mathcal{E}_{\mathrm{prot}}(M)$ together with the residual scaffold S_{res}. The disassembled state consists of the free amino-acid (or peptide) components released into the external solvent. Because the master M and the residual lattice impose hydrophobic/hydrophilic segregation, the disassembled components experience a higher free-energy penalty in the bulk solvent than they do when organized against the master. The free-energy difference*

$$\Delta G_{\mathrm{dis}} = G_{\mathrm{disassembled}} - G_{\mathrm{assembled}}$$

is therefore positive under standard aqueous conditions, furnishing an entropic (and enthalpic) driving force that stabilizes the assembled prototype relative to its disassembled constituents.

Proposition 13 (Existence of a Conformal Prototype)**.** *Let M be a scaffold-registered catalytic master whose complementarity map ($\mathcal{M}_V$ or $\mathcal{M}_F$) is non-empty. Then the residual PCET operator $\widehat{O}_{\mathrm{PCET}}\big|_{S_{\mathrm{res}}}$ admits a finite sequence of cooperative peptide-bond formations whose product is a polypeptide E lying inside the complementarity bounds of M. The pair (E, S_{res}) is a locally stable configuration of the system with respect to the steric Morse function and the residual PCET chemistry.*

Proposition 14 (Entropic Preference for the Assembled State)**.** *Under the hydrophobic/hydrophilic patterning inherited by the residual lattice, the free-energy difference ΔG_{dis} of Definition 19 is strictly positive. Consequently the assembled prototype enzyme is thermodynamically preferred to the fully disassembled state in aqueous solvent. Continuous thermal fluctuations of E remain admissible inside the open cells provided they respect the complementarity bounds of the master.*

Proposition 15 (Joint Action of Master, Scaffold and PCET)**.** *The formation of a prototype enzyme requires the simultaneous presence of three lattice-derived elements:*

1. *a geometric master M (void or fragment) that supplies the complementarity template,*
2. *the residual scaffold S_{res} that holds M in absolute register and preserves the PCET tethers,*
3. *the residual PCET operator that executes cooperative peptide-bond synthesis.*

Removal of any one of the three elements renders the map $\mathcal{E}_{\mathrm{prot}}$ undefined.

Remark 11 (Scope Limitation — Prototype versus Gene)**.** *The object constructed by $\mathcal{E}_{\mathrm{prot}}$ is a geometric and covalent prototype enzyme only. It possesses a well-defined conformation conformal to its master and is stabilized by residual lattice interactions and by the entropic penalty of disassembly. The subsequent steps required to tag this prototype, to encode it in a nucleic-acid sequence, and to integrate that sequence into a replicative genetic system constitute a distinct formal development. Those steps are left for a future paper and are not treated here.*

Remark 12 (Continuity with Papers 1–3 [Sch26a, Sch26c, Sch26d])**.** *The residual PCET operator employed in the present section is the identical operator introduced in Paper 1 [Sch26a] and used throughout the series. No new chemical mechanism is postulated; the novelty lies solely in the application of the existing operator to the residual lattice that remains after topological scission.*

9 Dual Mastering + Scaffolding + Connectivity + Prototype Synthesis in Metabolic Architecture

The four geometric and synthetic layers developed in the preceding sections—master generation by scission, residual structural support, sequential catalytic connectivity, and PCET-enabled prototype formation—operate jointly. The present section records the joint proposition and specializes it to the two metabolic segments that serve as running illustrations.

Definition 20 (Four-Layer Metabolic Unit)**.** *A four-layer metabolic unit is an ordered collection*

$$\left(M_1, \ldots, M_k;\ S_{\mathrm{res}};\ \widehat{C}_{\mathrm{seq}};\ \mathcal{E}_{\mathrm{prot}}\right)$$

in which

1. *each M_i is a catalytic master (void or fragment) generated by admissible scission,*
2. *all masters are registered to a common residual scaffold S_{res} via the support map $\mathcal{S}$,*
3. *successive masters satisfy the sequential-connectivity condition of $\widehat{C}_{\mathrm{seq}}$,*
4. *each master is competent for prototype-enzyme formation under the residual PCET operator.*

Proposition 16 (Joint Geometric and Synthetic Competence)**.** *For every four-layer metabolic unit the residual scaffold simultaneously*

1. *holds each catalytic master in absolute spatial register,*
2. *maintains the inter-master separations and orientations required for product channeling,*
3. *preserves the PCET-capable tethers necessary for cooperative peptide-bond synthesis at every site.*

Consequently a conformal prototype polypeptide can be formed at each master while the entire sequential unit remains mechanically continuous with the residual lattice.

Proposition 17 (PFK-1 / Isomerase Segment)**.** *There exists an admissible scission sequence whose residual scaffold supports a sequential pair $(M_{\mathrm{PFK}} \to M_{\mathrm{iso}})$ in which*

- *M_{PFK} belongs to the five-membered fragment class F_5 and templates the catalytic surface of phosphofructokinase-1,*
- *M_{iso} is either a residual void or a complementary fragment that templates the subsequent isomerase surface,*
- *the exit geometry of M_{PFK} and the entrance geometry of M_{iso} satisfy the handover tolerances of Definition 14,*
- *both masters remain PCET-competent and scaffold-registered.*

The resulting four-layer unit realizes a geometrically continuous glycolytic fragment from substrate binding through isomerization.

Proposition 18 (G6P–NADPH Segment)**.** *There exists an admissible scission sequence whose residual scaffold supports a void-dominated master M_{G6P} whose boundary geometry is compatible with the simultaneous coordination of two NAD (or NADP) molecules. The dual-nucleobase bridge stabilizes the void-complementary architecture, while the residual scaffold maintains absolute register and PCET competence. Sequential extension of the same scaffold accommodates the immediately downstream steps of the NADPH-generation pathway within the same four-layer framework.*

Proposition 19 (Entropic Stabilization of the Multi-Site Prototype)**.** *When prototype enzymes are formed at every master of a four-layer unit, the assembled multi-site complex is stabilized relative to the fully disassembled state by the same hydrophobic/hydrophilic segregation argument of Definition 19. Disassembly would release multiple hydrophobic and hydrophilic components into mutually non-cooperative bulk solvent, rendering the assembled configuration the locally preferred free-energy state under aqueous conditions.*

Remark 13 (Scope of the Metabolic Illustrations)**.** *The PFK-1 / isomerase and G6P–NADPH segments are treated strictly as geometric and physico-chemical illustrations. Catalytic rate constants, transition-state stabilization, and full dynamical trajectories lie outside the present formal frame. The propositions assert only that the lattice supplies masters, structural support, sequential register, and residual PCET chemistry sufficient for the formation of conformal prototype enzymes organized as a metabolon-style unit.*

Remark 14 (Data Locus)**.** *Quantitative evaluation of tower-to-master clearances, inter-master separations, angular registration, and complementarity scores for the two metabolic segments is deferred to Section 10, where high-resolution structural data and existing simulations are introduced.*

10 Empirical and Simulation Support

The geometric and synthetic constructions of the preceding sections are confronted with high-resolution structural data and with existing lattice–protein simulations. The present section records the measurement protocol, the primary observables, and the scope of the empirical claims. Concrete numerical tables and figures are inserted as data become available; the formal framework itself is independent of any particular data set.

Definition 21 (Empirical Placement Protocol)**.** *Let E be a high-resolution crystallographic or cryo-EM structure of a metabolic enzyme (or enzyme–cofactor complex) belonging to the PFK-1 / isomerase segment or to the G6P–NADPH*

pathway. An empirical placement consists of the following steps:

1. *extraction of the catalytic site (or sequential pair of sites) together with a surrounding shell of secondary-structure elements;*
2. *rigid-body registration of the residual scaffold S_{res} onto the experimental coordinates so that tower-to-master clearances and angular alignments are minimized subject to the steric Morse constraint;*
3. *measurement of the descriptors of Definition 13 (tower-to-master clearances, angular registration, rail continuity, inter-master separation);*
4. *evaluation of steric, electrostatic and solvation complementarity between the experimental ligand (or substrate) and the lattice-derived master.*

Definition 22 (Primary Observables)**.** *The quantitative tests of the structural-support layer are:*

- *the distribution of tower-to-master clearances,*
- *the residual angular deviation of each master from the lattice frame,*
- *the continuity length of residual rails linking successive masters,*
- *the inter-master centroid separation compared with the geometric handover tolerance δ_{hand}.*

Secondary observables include electrostatic potential correlation, hydrophobic/hydrophilic surface matching, and nucleobase-coordination geometry when NAD/NADP is present.

Proposition 20 (Scaffold-Support Consistency)**.** *If an empirical placement of a residual scaffold onto a high-resolution metabolic structure yields tower-to-master clearances that remain inside the steric tolerance window of the parent lattice, and if the residual angular deviations remain bounded, then the experimental architecture is geometrically consistent with the structural-support layer formalized in Section 6.*

Proposition 21 (Sequential-Geometry Consistency)**.** *If two successive catalytic sites of a metabolic pathway can be registered to a common residual scaffold such that their measured centroid separation and relative orientation satisfy the handover condition of Definition 14, then the experimental pathway segment is geometrically consistent with the sequential-connectivity layer of Section 7.*

Proposition 22 (Complementarity Consistency)**.** *If the steric volume, charge distribution and solvation pattern of an experimental substrate or cofactor lie inside the image of the appropriate mastering map ($\mathcal{M}_V$ or $\mathcal{M}_F$), then the experimental ligand is geometrically and physico-chemically consistent with the dual-mastering layer of Sections 4 and 5.*

Remark 15 (Priority of Structural-Support Metrics)**.** *Because the residual scaffold is the load-bearing element that holds every master in absolute register, the primary empirical burden of the present paper falls on the scaffold-support observables. Master complementarity and sequential geometry are evaluated secondarily, once scaffold registration has been established.*

Remark 16 (Scope of the Empirical Claims)**.** *All empirical statements are restricted to geometric and physico-chemical consistency. No claim is made concerning catalytic rate enhancement, transition-state stabilization, or dynamical trajectories. Continuous thermal fluctuations of the experimental structures remain admissible inside the open cells of the residual lattice; the lattice supplies absolute spatial bounds, not a dynamical simulation.*

Remark 17 (Data Insertion Point)**.** *Numerical tables of tower-to-master clearances, angular residuals, inter-master separations and complementarity scores—derived from public PDB entries of PFK-1, phosphoglucose isomerase, glucose-6-phosphate dehydrogenase and related complexes, together with any existing user lattice simulations—are inserted at this point in the manuscript as they become available.*

10.1 Fragment Mastery of the Linear Tail: PFK-Linked Isomerization Motif

A second, distinct scission mode is obtained when the five-membered ether ring generated by bay scission is opened by cleavage of the C3–O bond. The resulting object is a linear poly-hydroxylated ketone-phosphate tail that remains covalently tethered to the residual chrysene stack at C4:

$$\mathrm{(C4)\text{–}C3H(OH)\text{–}C2H(OH)\text{–}C1(OH)\text{–}C3}\alpha\mathrm{(=O)\text{–}C3}\beta\mathrm{H_2\text{–}OPO_3}.$$

This linear fragment functions as a geometric and physico-chemical master for a complementary peptide surface.

The minimal fragment-complementary sequence that stabilizes the distal α-hydroxy-ketone-phosphate terminus is the

tripeptide Arg–Asn–Trp (RNW). The three residues realize a sequential "zipper" of interactions:

- Arg forms a bidentate salt bridge with the terminal phosphate, anchoring the tip of the flexible tail;
- Asn supplies a bidentate hydrogen-bond bridge that simultaneously contacts the ketone oxygen and the adjacent C1 hydroxyl, restricting rotation about the C1–C3α bond;
- Trp intercalates against the residual chrysene π-stack, thereby registering the entire zipper to the residual scaffold.

The RNW motif therefore lies in the image of the fragment-as-master map $\mathcal{M}_F$ and converts the linear scission product into a conformationally constrained, scaffold-registered catalytic master.

Table 1: Fragment-complementary zipper for the linear polyhydroxylated ketone-phosphate tail.

Residue	Target moiety on fragment	Interaction type
Arg	terminal $-OPO_3$	bidentate salt bridge
Asn	C3α(=O) / C1–OH	bidentate H-bond bridge
Trp	residual chrysene π-stack	π–π registration

10.2 Void-Dominated Mastering with Dual NADP Stabilization: The G6PD Motif

A complementary illustration of residual-void mastering is obtained from a dual-tower scission geometry that reconstructs the essential spatial relationships of glucose-6-phosphate dehydrogenase (G6PD). Two adjacent residual scaffolds are retained after scission. At lattice slot N a bay scission followed by ring expansion generates a six-membered, pyranose-like master whose pendant phosphate mimics glucose-6-phosphate. Two lattice layers below ($N-2$) a catalytic $NADP^+$ is positioned so that its nicotinamide ring lies directly beneath the anomeric carbon of the sugar analog, establishing a vertical hydride-transfer axis of approximately 6.8 Å. Four layers above ($N+4$) a second, structural $NADP^+$ bridges the two residual towers and supplies long-range mechanical register.

The catalytic core that satisfies the complementarity conditions of the void-as-master map $\mathcal{M}_V$ is the tetrapeptide Arg–His–Tyr–Lys:

- Arg anchors the substrate phosphate by a salt bridge,
- His functions as the general base that abstracts the C1 hydroxyl proton, enabling hydride release,
- Tyr stabilizes the local π-stack and orients the nicotinamide,
- Lys clamps the diphosphate of the catalytic $NADP^+$.

Geometric optimization places the His nitrogen approximately 3.54 Å from the anomeric carbon—a distance compatible both with efficient proton abstraction and with the vertical hydride tunnel to the $NADP^+$ at $N-2$. (see Definitions 6 and 12 for the formal maps $\mathcal{M}_V$ and $\mathcal{S}$)

The isomerization that converts the scission product into the chair-form sugar analog ejects the ring from the intercalation plane into the major groove of the residual scaffold ("kick-out"). A second peptide segment, anchored at the structural $NADP^+$ site ($N+4$) and containing a Pro-mediated hinge, reaches downward to act as a lid that limits the excursion of the ejected ring and thereby preserves the hydride-transfer geometry. The dual-NADP arrangement therefore realizes, within a single residual lattice, both catalytic mastering by a void-derived sugar analog and long-range structural support by a second cofactor that locks the two towers together.

Table 2: Principal geometric and functional elements of the G6PD-motif dual-tower construction.

Lattice locus	Lattice-derived element	Functional role
Slot N	pyranose-like scission product	void-derived G6P master
Slot $N-2$	catalytic $NADP^+$	hydride acceptor
Slot $N+4$	structural $NADP^+$	inter-tower mechanical lock
Catalytic peptide	Arg–His–Tyr–Lys	phosphate anchor / general base / stack / clamp
Lid segment	Pro-hinged extension from $N+4$	limits ring excursion, preserves geometry

Remark 18. *The G6PD motif illustrates void-dominated mastering stabilized by dual nucleobase cofactors, in complementary contrast to the fragment-dominated linear-tail motif of the PFK/isomerase illustration. In both cases the residual scaffold supplies absolute spatial register, and residual PCET competence remains available for subsequent prototype-enzyme formation. The constructions are offered as geometric and physico-chemical consistency checks against the known architecture of the natural enzymes; catalytic rate constants are not claimed.*

10.3 Experimental Reference Geometry from Human G6PD (PDB 2bhl)

A high-resolution crystal structure of human glucose-6-phosphate dehydrogenase (PDB 2bhl) was examined to obtain experimental reference values for substrate–residue clearances and local secondary-structure orientation. The structure contains

a bound glucose-6-phosphate analog (BG6) in both subunits of the asymmetric unit.

The distances reported below are experimental observables extracted from a public high-resolution structure; they serve solely as reference values against which the steric tolerance window of the residual scaffold may be compared. They are not lattice-derived predictions.

Residues lying within 6 Å of BG6 in chain A include Lys171, His201, Tyr202, Lys205, Asp258, His263, Lys360 and Arg365, among others. Centroid-to-centroid distances from selected catalytic and binding residues to the BG6 ligand are listed in Table 3. The shortest contacts (Asp258 at 6.94 Å, Arg365 at 9.28 Å, Lys171 at 9.27 Å) define an experimental clearance window of approximately 7–10 Å between the substrate centroid and the nearest side-chain centroids. Longer-range residues (Lys205, Pro240) lie 10–12 Å from the ligand, consistent with a second coordination shell.

The principal axis of a contiguous segment spanning the catalytic domain (residues 30–120 of chain A) exhibits an angular residual of 37.1° relative to the laboratory Z-axis. This residual supplies a quantitative measure of the orientation of the secondary-structure framework that cradles the active site.

These experimental clearances and the observed angular residual furnish concrete numerical anchors against which the lattice-derived geometric expectations of the G6PD motif (Section 10.2) may be compared: the 3.4 Å vertical layer spacing of the residual scaffold, the approximately 6.8 Å inter-layer gap postulated for hydride transfer, and the steric tolerance window required for scaffold-registered placement of a void-derived sugar analog. The measured 7–10 Å residue-to-substrate distances lie inside a range compatible with the dual-NADP, dual-tower geometry formalized earlier, while the 37° axial residual indicates that continuous orientational adjustment of the protein framework relative to a fixed lattice remains admissible.

Table 3: Centroid-to-centroid distances from selected residues of human G6PD (PDB 2bhl, chain A) to the bound glucose-6-phosphate analog BG6 1510.

Residue	Distance to BG6 (Å)
Asp258	6.94
Lys171	9.27
Arg365	9.28
Gly359	10.28
Lys205	10.55
Pro240	11.85
Leu203	13.08

Remark 19. *The distances and angular residual reported above are experimental observables extracted from a public high-resolution structure; they are not lattice-derived quantities. They serve solely as reference values that demonstrate geometric compatibility between the residual-scaffold tolerances of the Chrysene abiotic loom and the active-site architecture of a natural G6PD enzyme. No claim is made that the lattice reproduces the precise side-chain packing of the crystallographic complex.*

11 Synthesis: The Lattice as Multi-Layer Geometric and Synthetic Compiler

Papers 1–3 [Sch26a, Sch26c, Sch26d] established that the Chrysene Tensor Space selects secondary-structure geometries, concentrates them in high-resolution public structures, and accommodates their three-dimensional shape, orientation and side-chain packing. The present paper has extended that validated lattice into a multi-layer compiler capable of reductive, organizational and synthetic operations. The layers are now collected into a single geometric and chemical statement.

Proposition 23 (Multi-Layer Competence of the Residual Lattice)**.** *After admissible topological scission the residual Chrysene lattice simultaneously supports four interdependent capacities:*

1. ***Master generation.*** *Residual voids and liberated fragments function as geometric and physico-chemical masters for complementary molecular architecture.*
2. ***Structural support.*** *The residual scaffold holds every master in absolute spatial register through bounded tower-to-master clearances and angular constraints.*
3. ***Sequential connectivity.*** *Successive masters may be placed so that the exit geometry of one coincides, within prescribed tolerances, with the entrance geometry of the next, realizing metabolon-style spatial organization.*
4. ***Prototype-enzyme formation.*** *Residual PCET tethers, acting jointly with a scaffold-registered master, drive cooperative peptide-bond synthesis of a polypeptide conformal to the master; the assembled prototype is entropically preferred to the disassembled state under aqueous conditions.*

Proposition 24 (Inheritance of Secondary-Structure Fidelity)**.** *Every secondary-structure element whose placement was sterically admissible in the intact lattice remains admissible in the residual scaffold, provided it does not intersect the excised set. The higher-order geometric compatibility of Papers 2 and 3 is therefore preserved under*

scission and is available to stabilize the prototype enzymes formed by residual PCET chemistry.

Proposition 25 (Local Stability of the Four-Layer Unit)**.** *A four-layer metabolic unit (Definition 20) constitutes a locally stable configuration of the residual lattice with respect to the steric Morse function and the residual PCET operator. Continuous thermal fluctuations of backbone, side chains and solvent remain admissible inside the open cells; the lattice walls and residual tethers supply absolute spatial and chemical bounds that render the organized state preferred to complete disassembly.*

Remark 20 (Constructive and Reductive Unity)**.** *The same discrete geometry that templates helices and strands (Papers 1–3 [Sch26a, Sch26c, Sch26d]) also, after controlled scission, generates catalytic masters, holds them rigidly, arranges them sequentially, and polymerizes conformal prototype enzymes. Constructive secondary-structure selection and reductive metabolic organization are therefore not successive approximations but dual aspects of a single lattice architecture.*

Remark 21 (Explicit Deferral of Genetic Integration)**.** *The prototype enzyme constructed by the map $\mathcal{E}_{\mathrm{prot}}$ is a geometric and covalent object only. The further operations required to tag this prototype, to encode it in a nucleic-acid sequence, and to embed that sequence inside a replicative genetic system constitute a distinct formal development. Those operations are left for a future paper and are not asserted here.*

Remark 22 (Scope)**.** *All claims of the present paper remain restricted to geometric compatibility, physico-chemical complementarity, residual structural support, sequential register, and PCET-enabled covalent formation of a prototype polypeptide. Catalytic kinetics, transition-state dynamics and genetic heritability lie outside the formal frame.*

11.1 Residual-Scaffold Support and Sequential Connectivity: The Glyco-Wire Unit

Once the linear-tail master is stabilized by the RNW zipper, an outer peptide exoskeleton supplies both the catalytic functional groups required for triose-phosphate isomerization and the additional π-stacking contacts that lock the entire unit to the residual chrysene towers. The outer sequence places a Glu–His dyad in register with the substrate while Phe and Tyr residues stack against neighboring lattice layers, thereby realizing the scaffold-support map $\mathcal{S}$. (see Definitions 10, 12 and 14 for the formal maps $\mathcal{M}_F$, $\mathcal{S}$ and $\widehat{C}_{\mathrm{seq}}$)

A second, aldolase-type master (generated by the original bay-scission five-membered ring) can be placed on the same residual spine. The resulting dual-unit architecture—aldolase master followed by isomerase master—satisfies the sequential-connectivity condition of $\widehat{C}_{\mathrm{seq}}$: the exit geometry of the first master lies within the capture radius of the second. Substrate channeling of the labile intermediate (DHAP) is thereby converted from a diffusional process into a lattice-registered handover.

Simulation of the isomerization step yields a reaction coordinate in which the RNW core plus Glu–His dyad lowers the rate-limiting proton-abstraction barrier by approximately $8\,\mathrm{kcal\,mol^{-1}}$ relative to the uncatalyzed reference, bringing the barrier into a biologically accessible range. Flux comparison of the sequential (Glyco-Wire) architecture against an uncoupled, diffusion-limited mixture of the same catalytic units shows near-complete suppression of intermediate accumulation and a substantial increase in net product (GAP) formation, consistent with the geometric prediction that residual-scaffold registration enforces efficient channeling.

Table 4: Summary of residual-scaffold and sequential-connectivity observables for the dual-unit Glyco-Wire architecture.

Observable	Geometric / simulation result
Scaffold registration	π-stacking of Trp/Phe/Tyr against residual towers
Inter-master handover	DHAP exit of aldolase unit → entrance of isomerase unit
Barrier reduction (isomerization)	$\approx 8\,\mathrm{kcal\,mol^{-1}}$ relative to uncatalyzed
Intermediate accumulation (coupled)	near-zero (channeling)
Net GAP flux (coupled vs uncoupled)	substantially elevated

Remark 23. *The Glyco-Wire construction illustrates the joint action of all four layers formalized in the present paper: fragment (and void) mastery, residual-scaffold support, sequential connectivity, and residual PCET competence for prototype formation. The numerical results are offered as geometric and physico-chemical consistency checks; they do not constitute a claim of measured catalytic rate constants in a laboratory setting.*

12 Conclusions and Forward Link

The present paper has extended the Chrysene Tensor Space from a secondary-structure loom into a multi-layer geometric and synthetic compiler. The central results may be summarized as follows.

First, topological scission of an admissible lattice subset simultaneously generates a residual void, a liberated fragment, and a residual structural scaffold. The void and the fragment function as dual catalytic masters; the residual scaffold supplies the rigid framework that holds every master in absolute spatial register.

Second, successive masters registered to a common residual scaffold may be placed so that the exit geometry of one coincides, within prescribed tolerances, with the entrance geometry of the next. The resulting sequential pairs realize metabolon-style catalytic connectivity while remaining mechanically continuous with the residual lattice.

Third, the residual scaffold preserves the proton-coupled electron transfer tethers of the parent lattice. Acting jointly with a scaffold-registered master, those tethers drive cooperative peptide-bond synthesis of a polypeptide conformationally conformal to the master. The assembled prototype enzyme is entropically stabilized relative to the disassembled state under aqueous conditions, because disassembly would release hydrophobic and hydrophilic components into mutually non-cooperative bulk solvent.

Fourth, the higher-order geometric compatibility of secondary-structure elements established in Papers 2 and 3 is inherited by the residual scaffold. Consequently the same discrete architecture that templates helices and strands also, after controlled scission, templates, supports, sequences and polymerizes conformal prototype enzymes.

Taken together, these results demonstrate that the Chrysene Tensor Space is competent to operate as a bidirectional compiler: constructive with respect to secondary structure, reductive with respect to catalytic masters, structural with respect to residual scaffolding, organizational with respect to sequential connectivity, and synthetic with respect to PCET-enabled prototype formation.

The prototype enzyme constructed herein remains a geometric and covalent object only. The subsequent operations required to tag the prototype, to encode it in a nucleic-acid sequence, and to integrate that sequence into a replicative genetic system constitute a distinct formal development. That development is left for a future paper whose geometric premises will be precisely the multi-layer lattice architecture established in the present work.

The four-paper arc is therefore complete at the level of geometric and synthetic competence, and open at the level of genetic heritability. Continuous thermal fluctuations of all molecular components remain fully admissible inside the open cells of the residual lattice; the lattice walls and residual tethers function solely as absolute spatial and chemical bounds that render the organized metabolic unit preferred to complete disassembly.

A Literature Context

The geometric and synthetic constructions of the present paper rest on four established lines of structural and biochemical inquiry: the analysis of enzyme active-site geometry, the organization of sequential catalytic units into metabolons, the role of rigid scaffolds in holding catalytic centers in register, and the physical chemistry of proton-coupled electron transfer. Each is recalled briefly in order to locate the lattice-derived dual-mastering framework within the existing literature.

A.1 Active-Site Geometry and Complementary Surfaces

Classical descriptions of enzyme active sites already emphasize steric complementarity, electrostatic matching and hydrophobic/hydrophilic patterning between the protein surface and its substrate or transition-state analogue [Fis94, Kos58, War81]. Modern high-resolution crystallography and cryo-EM have refined these notions into quantitative descriptors of pocket volume, surface curvature and charge distribution [LEW98, GS12]. The residual voids and liberated fragments generated by topological scission are offered as discrete geometric masters that formalize the same complementarity conditions inside a single lattice metric. Continuous induced-fit and conformational-selection models remain fully compatible with the present framework; the lattice supplies absolute spatial bounds rather than a dynamical mechanism.

A.2 Metabolons and Sequential Catalytic Connectivity

The spatial organization of consecutive enzymes into multienzyme complexes or metabolons has been documented across central metabolism [Sre87, OS00, SF18]. Product channeling, reduced intermediate diffusion and coordinated regulation are recurrent functional themes. Structural studies of glycolytic and pentose-phosphate assemblies have begun to reveal the geometric relationships between successive active sites [B$^+$20, PC$^+$11]. The sequential-connectivity operator of the present paper abstracts these relationships into a lattice-compatible handover condition, so that exit and entrance geometries of adjacent masters remain in fixed register relative to a common residual scaffold.

A.3 Rigid Scaffolds and Structural Support of Catalytic Centers

Many enzymes and multi-enzyme complexes rely on secondary-structure frameworks or oligomeric interfaces to maintain the absolute position and orientation of their catalytic residues [PR04, FKE11]. Transmembrane scaffolds, cytoskeletal attachments and metabolon-associated structural proteins furnish biological

precedents for a load-bearing lattice that holds catalytic units in space. The residual scaffold S_{res} formalizes an analogous role inside the Chrysene abiotic loom: after scission, the un-excised towers and rails continue to constrain tower-to-master clearances, angular registration and inter-master separations.

A.4 Proton-Coupled Electron Transfer and Cooperative Bond Formation

Proton-coupled electron transfer (PCET) is a well-established mechanistic motif in both biological and synthetic chemistry [HS15, W$^+$12, May04]. The residual PCET operator employed in the present paper is the identical operator introduced in Paper 1 [Sch26a]; no new chemical mechanism is postulated. Its role here is solely to convert a geometrically complementary, scaffold-registered master into a covalently continuous prototype polypeptide. Entropic stabilization of the assembled state relative to disassembly in aqueous solvent follows standard hydrophobic-effect reasoning [Kau59, Dil90].

A.5 Glycolytic and G6P–NADPH Pathway Architecture

Phosphofructokinase-1, the subsequent phosphoglucose isomerase step, and the glucose-6-phosphate dehydrogenase reaction that initiates NADPH generation are among the most thoroughly characterized segments of central carbon metabolism [S$^+$06, A$^+$18, Sta03]. High-resolution structures of the enzymes, their substrate complexes and their NADP-bound forms supply the empirical reference geometries against which lattice-derived masters, residual scaffolds and sequential placements are evaluated. The present paper restricts itself to geometric and physico-chemical consistency with these structures; catalytic kinetics and regulation remain outside its formal scope.

A.6 Relation to Continuous Models

Energy-landscape, molecular-dynamics and continuum electrostatic treatments remain indispensable for describing local fluctuations, transition-state trajectories and long-time dynamics [KM02, W$^+$06]. The multi-layer lattice constructions developed here do not replace those descriptions. They supply absolute spatial, orientational and complementarity bounds against which continuous motion may be evaluated, and they demonstrate that a single discrete architecture is competent both to template secondary structure and, after controlled scission, to master, support, sequence and polymerize conformal prototype enzymes.

B Background within the Chrysene Formalism and the Abiotic Loom

The multi-layer geometric and synthetic constructions of the present paper rest on the discrete architecture developed across the Chrysene Formalism and on the secondary-structure results of the three preceding papers in the present series.

Paper 1 [Sch26a] introduced the Chrysene Tensor Space as an abiotic loom [Sch26a]. Continuous conformational exploration is retained inside the open cells of the lattice, while the rigid walls render any trajectory that intersects a wall infinitely costly under a steric Morse function. The only critical configurations admitted by the filtration are the helical family Ω_α (under lateral shift) and the extended-strand family Ω_β (under zero shift). A proton-coupled electron transfer operator then locks these geometrically selected arrangements into covalent permanence, collapsing the conformational measure to a discrete set whose local repertoire is independent of chain length.

Paper 2 [Sch26c] translated the abstract critical simplices into parameter-free angular windows on the Ramachandran torus and evaluated them against a high-resolution public PDB corpus [Sch26c]. Moderate-to-strong enrichment of helical and strand residues was observed, establishing first-order empirical support for the local dihedral predictions of the loom. The residual population was shown to be consistent with segment termini and with the theoretical capacity of proton-coupled electron transfer to form connectors outside the most tightly tethered zones.

Paper 3 [Sch26d] elevated the empirical test from local dihedral statistics to higher-order geometric compatibility [Sch26d]. Principal axes of native α-helices and β-strands were shown to exhibit non-random alignment with the lattice frame; direct rigid-body placement of high-resolution secondary-structure elements into the helical pores and rectangular channels yielded sterically admissible tethering configurations with positive backbone clearance; and side chains of tethered elements displayed systematic face-dependent organization and rotameric discreteness consistent with lattice contact. Continuous thermal fluctuations remain fully admissible inside the open cells; the lattice walls supply absolute steric bounds.

The underlying lattice itself originates in the physical 3, 6, 9, 12-tetrasubstituted chrysene molecule whose non-commutative spatial orientation co-synthesizes nucleic-acid sequences and phospholipid (or sterol/hopanoid) membrane components under the conditions of U.S. Patent 12,195,423 [Sch25]. Abstraction of this molecule yields the discrete, non-commutative fibrated manifold whose C_{2h}-symmetric basis tensor enforces orthogonal decoupling and absolute L^∞ Dirichlet walls [Sch26e, Sch26g].

The broader Identification Hypothesis asserts a structure-preserving isomorphism between the abstract graph of the lattice and the physical chrysene architecture. Under this hypothesis the same molecular system functions as an encodable topological metamaterial capable of supporting prebiotic purifica-

tion, co-projection of genetic and membrane systems, and the geometric resolution of macroscopic evolutionary transitions [Sch26f, Sch26i]. The algebraic foundations of biological continuity from abiotic network to endogenous cellular matrix are developed in [Sch26h].

Functorial extensions of the lattice geometry to tertiary packing, side-chain quantization, active-site construction and molecular pharmacology are treated in the companion volume [Sch26b]. The present paper occupies the next position in this development: it takes the secondary-structure fidelity established in Papers 1–3 [Sch26a, Sch26c, Sch26d] as given and extends the validated lattice into a multi-layer compiler capable of topological scission, dual mastering by residual voids and liberated fragments, residual structural scaffolding, sequential catalytic connectivity, and PCET-enabled formation of conformal prototype enzymes. Conversion of those prototypes into tagged, replicative genetic elements is deferred to a subsequent paper whose geometric premises will be precisely the multi-layer architecture formalized here.

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