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From Registry-Controlled Capture to Productive Molecular Assembly

Constructive Existence of a Minimal Abiotic Loom

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Abstract

We extend registry-controlled substrate handling to productive assembly on an intact finite substituted-chrysene reference. The framework contains every prescribed node and connection and uses exterior workstations, without defect-generated cavities or ionic or nucleobase insertions. A common state carries the framework, prepared molecular graphs, fresh-resource accounts, product prefixes, external symbolic records, controls, and receiver states. Composition, stable-branch, clearance, and finite-state absorption results separate geometric feasibility from executable transformation and productive output from equilibrium occupancy.

An explicit reduced witness selects a nonhomogeneous four-residue word from a common glycine/alanine input pool. Three valence-preserving graph joins produce GAGA and three labelled waters while preserving all atom origins. A declared competing-channel law gives correct first-output probability $125000/132651 > 0.94$ and target purity $250000/257651 > 0.97$ among all collected chains, including shorter incorrect outputs. A common neutral product–receiver energy yields a stable target-occupancy contrast greater than 0.83 against the absent-product condition and greater than 0.09 against the single-position intervention GGGA. These inequalities have exact arithmetic certificates and persist under specified admissible perturbations. Reversible receiver kinetics gives a finite-time readout, while loading, delivery, and chemical realization retain explicit interfaces.

The existence theorem concerns one fully specified finite graph, envelope, kinetic, and interaction model. Actual amide synthesis, constitutive calibration, and nucleic-acid writing require additional molecular certificates; they are not inferred from graph admissibility or symbolic encoding. The construction supplies a bounded productive interface for subsequent work on repeatable operation and feedback, without invoking broad folding architectures or autonomous peptide clamps.

Keywords: Chrysene Formalism; abiotic loom; productive molecular assembly; registry; peptide graph; intact framework; first-passage probability; atom-origin ledger; constructive existence.

1 Introduction

The passage from a selectively binding molecular assembly to a productive molecular assembly is a precise step in the construction of an organized chemical system. A binding site distinguishes or retains a supplied substrate. A productive site must additionally coordinate transformations, retain the developing product, account for unused and consumed material, and deliver an output whose function can be distinguished from that of its inputs. For biogenesis research, this is an essential intermediate problem between the availability of a molecular carrier and the organization of a regenerating protocell.

The Chrysene Formalism supplies a labelled architectural setting for this problem. The revised axiomatic foundation separates core geometry, substituent-mediated connectivity, stacking, and operator realizations [Sch26m]; the metamaterial construction motivates the use of a common molecular core in an addressed three-dimensional assembly [Sch26k]. The genetic-code pilot gives a typed prepared-input production and code-table framework [Sch26f]. The protocell and finite-interior-lattice pilots introduce material origins, compatible interfaces, and finite organizational states [Sch26d, Sch26a]. Article 99 compares alternative sources of the encoded system through their actual preparation capabilities [Sch26g]. These constructions motivate a modular question: which additional data make a given finite registry productive?

Article 103 provides a useful starting point [Sch26h]. Its explicit gate combines a stable mechanical coordinate, state-dependent interactions, capture and release settings, and a controlled execution. The present paper adds a short productive transformation and a receiving-gate response. The output is not assigned a favorable processing coefficient in an unrelated population equation. Instead, the selected product supplies a declared coupling in the same receiver energy from which its

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response is calculated.

The construction uses an intact finite framework. No lattice node is excised, no internal pore or defect-generated cavity is constructed, and no ion or nucleobase is inserted into the scaffold. Precursor handling occurs on its exterior. The local geometry and contact questions developed in the abiotic-loom studies [Sch26l, Sch26j, Sch26r, Sch26b] remain useful as design questions, but their broader scission, maturation, and folding architectures are not required here. Articles 52, 54, and 56 motivate explicit direction, constrained transformation, and margin conditions [Sch26e, Sch26c, Sch26o]; the material-ledger, pore, and first-polypeptide studies motivate the separation of availability, transport, and joining [Sch26n, Sch26q, Sch26p]. We use those distinctions in a bounded construction rather than combine their conclusions by analogy.

The main witness has four residue positions and three joining stages. Its prepared residue alphabet consists of glycine and alanine graphs, with a controlled target word GAGA. Formal joining conserves all atoms and produces three mapped waters. A finite competing-channel law distinguishes correct extension, incorrect collected output, and loss. The correctly constructed product is delivered to an exterior receiving gate. A neutral polarization coupling makes the gate distinguish GAGA from an absent product and from the single-position intervention GGGA. The primary claim is joint realizability of these structural, kinetic, informational, and response requirements within one explicit reduced model.

This claim has a definite chemical boundary. Formal neutral-residue joining does not establish spontaneous condensation of free amino acids; its physical implementation requires a driven reaction certificate. Likewise, the specified polarization and barrier laws are constitutive data, not measured properties of GAGA. Keeping this boundary explicit permits an unconditional existence theorem for the declared finite model and a separate conditional lifting statement for a chemically calibrated realization. The mathematical result is then neither a universal folding claim nor a restatement that separately possible modules might coexist.

2 Intact references and productive states

Definition 2.1 (Intact finite reference)**.** Fix positive integers n_x, n_y, n_z and the full address box

$$\Lambda = \{0, \dots, n_x - 1\} \times \{0, \dots, n_y - 1\} \times \{0, \dots, n_z - 1\}.$$

An intact reference contains every address in Λ and every prescribed nearest-neighbor edge whose endpoints belong to Λ. Edges parallel to the first two address axes are typed substituent bridges; third-axis edges are typed stacking relations. Each node carries a labelled core with ports 3, 6, 9, 12, and every boundary termination is specified. A reference embedding is determined by an invertible matrix L and an injective finite atomic decoration of $L\Lambda$.

The reference may be oblique. Orthogonality is not inferred from the numbering of the substituted sites. A finite exterior boundary is part of the specified assembly, not an internal vacancy. The geometric witness below uses a complete $4 \times 2 \times 2$ box. Stacking relations are not silently converted into covalent bonds.

Definition 2.2 (Protected framework)**.** The protected framework is its labelled node, port, bridge, stacking, and boundary data together with its framework atom identities. Every productive transition restricts to the identity on these data. It may move the physical configuration, change external controls, or change precursor/product bonds, but may not delete a protected node or bridge or add an ion or nucleobase to the framework. An attached product or an external substrate is separately typed; it does not replace a core or fill a removed site.

The exterior working region is ordinary space outside the specified framework envelopes. We do not introduce a bounded internal void as a reaction vessel. This is stronger than merely avoiding one particular scission mechanism.

Definition 2.3 (Productive state)**.** A state consists of a tuple

$$X = (r, q, \Gamma, \ell, w, c, z, u),$$

where r is a registry program, q the physical configuration, Γ the labelled atom-and-bond graph, ℓ the material and supplied-work accounts, w the current product word, c an external symbolic coding record, z a finite execution mode, and u the declared controls. The graph includes unused packets, products, waters, and discarded material. Productive and waste pools are distinct bookkeeping destinations, not deletion of atoms.

The registry program is addressed data, not a proof of a physical reader. In the witness it specifies a finite routing/controller law. The coding record uses formal symbols for completed residue selections. It is not a nucleobase insertion or a claim of nucleic-acid polymer synthesis. A subsequent molecular writer can be attached through an additional interface without being assumed here.

Definition 2.4 (Admissible stage)**.** An admissible stage specifies its complete input and output, full read set, fresh-resource demands, guard, and changes to the atom graph and control accounts. It also supplies finitely many continuous configuration branches and declared discrete event

maps. Each branch remains in its admissible configuration domain. Shared output coordinates must equal the next stage's input coordinates, and the latter guard must hold in the actual current state.

This definition accommodates formal joining events in a reduced hybrid model. An atomistic reaction trajectory is additional data; a coarse center trajectory does not supply it.

Proposition 2.5 (Protected composition)**.** *Let a finite sequence of admissible stages have matching shared interfaces, satisfied full guards, and all required fresh inputs. Suppose no consumed resource is used again as fresh. If each stage preserves the protected framework and a state invariant I, then their concatenation is admissible and preserves both.*

Proof. Apply the first stage to the specified input. Its output is the current state for the second stage, by shared-interface equality; the remaining input and guard hypotheses make that stage applicable. Induction supplies every subsequent application. The invariant holds at the start and is preserved at each application. The restriction of a composition of identity maps to the protected framework remains the identity. □

Separate nonemptiness of two stage domains is insufficient: their admissible inputs may disagree on a shared tether, precursor, or control state. Proposition 2.5 is therefore an interface theorem, not an inference from separate existence assertions.

3 Mechanical and path certificates

In a fixed discrete mode, remove rigid-body gauge freedom or specify boundary constraints, and use independent coordinates y on a regular finite-dimensional chart. Different bond graphs need not belong to the same smooth manifold.

Proposition 3.1 (Equilibrium certificate)**.** *Let $K \subset \mathbb{R}^d$ be nonempty and closed, and let $U : K \to \mathbb{R}$ be continuous with a nonempty compact sublevel set $\{y : U(y) \le U(y_0)\}$. Then U attains its minimum on K. If the minimizer is interior and U is C^2 near it, a positive-definite Hessian makes it a strict local minimum.*

Proof. The compact sublevel contains a minimizer by continuity. Outside it, values exceed $U(y_0)$ and hence cannot improve the attained value. At an interior minimizer the gradient vanishes. Positive definiteness and continuity of the Hessian give a positive quadratic lower bound on a sufficiently small ball by Taylor's integral formula. □

Graph connectivity does not imply this stiffness condition. Nor does existence of a minimum imply that a specified stochastic or deterministic dynamics reaches it from every state.

Proposition 3.2 (Stable branch and strict margins)**.** *Suppose $U(y, \theta)$ is C^2 near (y_0, θ_0), $\nabla_y U(y_0, \theta_0) = 0$, and $\nabla_y^2 U(y_0, \theta_0)$ is positive definite. There is a neighborhood on which the critical point is a continuously differentiable function $y_*(\theta)$ and remains a strict local minimum. Every finite collection of continuous strict inequalities valid at (y_0, θ_0) persists after shrinking the neighborhood.*

Proof. Apply the implicit-function theorem to $\nabla_y U$, whose derivative in y is invertible. Positive definiteness is open in the space of symmetric matrices. Each strict continuous inequality holds on an open neighborhood; intersect the finitely many neighborhoods. □

Parameter perturbations in this statement preserve required incidence and endpoint equalities. It does not turn an incompatible topology change into a small perturbation.

Proposition 3.3 (Uniform path clearance)**.** *Let $q(t)$ and $x(t)$ be continuous on $[0, 1]$, with nonempty compact excluded sets $B(q(t))$ continuous in Hausdorff distance. Suppose*

$$\operatorname{dist}(x(t), B(q(t))) \ge \rho + \delta \quad (0 \le t \le 1), \quad \delta > 0.$$

If the center path and excluded sets are each perturbed uniformly by less than $\delta/3$, the perturbed radius-ρ occupant has positive clearance greater than $\delta/3$.

Proof. For nonempty compact A, B,

$$|\operatorname{dist}(x, A) - \operatorname{dist}(y, B)| \le \|x - y\| + d_H(A, B).$$

Apply this inequality at each time and subtract the two perturbation bounds from δ. □

For a hybrid execution apply the proposition to each compact branch and check the discrete reset guards separately. A positive configuration margin at each endpoint does not imply a positive path margin between them.

Proposition 3.4 (Controlled mechanical lift)**.** *Let a scalar coordinate satisfy*

$$\dot{a} = -\mu\{k(a - c) + b\}, \qquad \mu, k > 0.$$

For any twice continuously differentiable prescribed path $a_d(t)$, the control

$$c(t) = a_d(t) + \frac{b}{k} + \frac{\dot{a}_d(t)}{\mu k}$$

makes $a = a_d$ a solution when initialized on that path. If the prescribed path and control remain admissible, this gives

a controlled execution. For $U = \frac{k}{2}(a-c)^2 + ba$, its energy balance on smooth branches is

$$\frac{dU}{dt} = -\mu|\partial_a U|^2 + \partial_c U\, \dot{c}.$$

Proof. Substitute the specified c into the differential equation. The right side becomes $\dot{a}_d$. The energy identity follows by the chain rule and $\dot{a} = -\mu\partial_a U$. □

A control reset at fixed a changes energy by its actual difference $U(a; c_+) - U(a; c_-)$. An occupancy or joining event has its own reservoir account. A geometrically closed path need not restore those accounts. The witness uses externally controlled finite operation, not an autonomous motor or regenerative cycle.

4 An atom-resolved productive witness

The chemical part of the construction is a finite graph certificate, not an assertion that proximity alone makes peptide formation spontaneous. Its inputs are prepared neutral glycine and alanine representative graphs. Their availability is an explicit input assumption. In particular, a substituent-bound residue in an earlier chrysene construction is not identified with a detached input molecule without a separate detachment map and its complete resource account.

Definition 4.1 (Neutral labelled molecular graph)**.** A molecular graph is a finite vertex set equipped with an element map $\ell : V \to \{\mathrm{C}, \mathrm{H}, \mathrm{N}, \mathrm{O}\}$ and a symmetric bond-order function $b : V \times V \to \{0, 1, 2, 3\}$, with zero diagonal. In this section every vertex satisfies

$$\sum_{u \in V} b(v, u) = \nu(\ell(v)),$$
$$(\nu(\mathrm{C}), \nu(\mathrm{H}), \nu(\mathrm{N}), \nu(\mathrm{O})) = (4, 1, 3, 2).$$

All atoms, including hydrogen atoms, have distinct persistent labels. A disconnected graph represents a collection of molecules. An atom-origin map assigns each vertex to its prepared input packet. This map is never changed by a reaction. The elemental ledger of a graph is the vector of its four vertex counts.

Definition 4.2 (Prepared residues and ordered chain)**.** Let G and A be explicit-hydrogen graphs with constitutions

$$G:\ \mathrm{H_2N{-}CH_2{-}C(=O){-}OH},$$
$$A:\ \mathrm{H_2N{-}CH(CH_3){-}C(=O){-}OH}.$$

Their formulas are $\mathrm{C_2H_5NO_2}$ and $\mathrm{C_3H_7NO_2}$. A selected alanine stereochemical tag may be carried as additional data; preservation of that tag below is formal, not a kinetic stereoretention assertion. For a word $s = s_1 \cdots s_n \in \{G, A\}^n$, its ordered chain graph $P(s)$ has the usual successive amide links from the carboxyl carbon of residue i to the amino nitrogen of residue $i + 1$. It has a free amino terminus and a free carboxyl terminus.

These neutral graphs are representatives for an exact combinatorial construction. They do not specify the dominant protonation state in a particular solvent or pH regime.

Definition 4.3 (Elementary joining map)**.** Suppose an ordered chain ends at residue i, and a fresh prepared residue j has been selected. Let c_i be the terminal carboxyl carbon, w_i its hydroxyl oxygen, and h_i^O the hydrogen bonded to w_i. Let n_j be the incoming amino nitrogen, and designate one of its two hydrogens as h_j^N. On the disjoint union of the two graphs, delete exactly the single bonds

$$\{c_i, w_i\}, \quad \{n_j, h_j^N\},$$

and add exactly the single bonds

$$\{c_i, n_j\}, \quad \{w_i, h_j^N\}.$$

All other bonds, atom labels, and origin labels are retained. The component on $\{w_i, h_i^O, h_j^N\}$ is recorded as an explicit water coproduct.

Proposition 4.4 (Exact joining certificate)**.** *The elementary joining map preserves every atom and its origin, satisfies the neutral valence rules at every vertex, and transforms a chain of length i and one fresh residue into a chain of length $i + 1$ and one water molecule. No carbon atom occurs in the coproduct.*

Proof. The modified adjacency lists belong to the four vertices c_i, w_i, n_j, and h_j^N. Each loses one single bond and acquires one single bond, so its bond-order sum is unchanged. All other sums are unchanged. The hydroxyl oxygen retains its bond to h_i^O and acquires its bond to h_j^N, hence forms a separate water component. The new c_i–n_j bond connects the original chain and incoming residue. The incoming carboxyl group is unchanged and supplies the new terminal group. No vertex is created, deleted, or relabelled. Both water hydrogens and its oxygen have explicitly specified origins, and no water vertex is carbon. □

Theorem 4.5 (Finite nonempty productive family)**.** *For every word $s \in \{G, A\}^n$, $n \geq 1$, there is an explicit sequence of $n - 1$ elementary joining maps from disjoint prepared residues $s_1, \ldots, s_n$ to $P(s)$ and $n - 1$ labelled water molecules. Every carbon and nitrogen of every selected*

input belongs to $P(s)$. If a letters of s are A, the formula of $P(s)$ is

$$C_{2n+a}H_{3n+2a+2}N_nO_{n+1}.$$

Proof. For $n = 1$ take the prepared residue without any joining operation. Inductively apply Definition 4.3 to the terminal carboxyl of the current chain and the next prepared residue. Proposition 4.4 proves admissibility at each step and identifies all coproducts. The input formula is $C_{2n+a}H_{5n+2a}N_nO_{2n}$. Subtracting $(n-1)H_2O$ gives the asserted formula. No operation moves carbon or nitrogen into water, proving the origin assertion. □

Example 4.6 (The four-residue witness)**.** The addressed word is $s = GAGA$. Three joins give the exact ledger

$$2C_2H_5NO_2 + 2C_3H_7NO_2 \longrightarrow C_{10}H_{18}N_4O_5 + 3H_2O.$$

The product has 37 atoms and the coproducts have 9, matching the 46 atoms of the selected prepared inputs. This is a tetrapeptide with free carboxyl terminus, not a methyl-ester-terminated peptide. Replacing only the second address by G produces $GGGA$, with formula $C_9H_{16}N_4O_5$ and the same number of joining steps. The residue word and atom-origin map distinguish the products even in examples where two different words have the same elemental formula.

4.1 Fresh resources and simultaneous abstract encoding

Definition 4.7 (Common resource pool and symbolic record)**.** For the four-site witness prepare eight disjoint input packets G_j, A_j, $1 \le j \le 4$, with permanent slot and species labels. A program $s \in \{G, A\}^4$ selects packet $(s_j)_j$ at slot j; the other packet remains unused. A packet status is one of *unused*, *held*, or *incorporated*; incorporation is permanent. Let C_G, C_A be two distinct symbols in an external record alphabet. Define the decoder $D(C_G) = G$, $D(C_A) = A$, extended by concatenation. These are formal record symbols, not nucleobases inserted into the chrysene framework.

A capture event merely changes a selected unused packet to held. Initial retention of $(s_1)_1$ marks that packet incorporated and establishes the length-one chain and record C_{s_1}. At each subsequent successful joining event the held packet becomes incorporated and the corresponding symbol is appended. This is an atomic transition in the joint assembly–record model. It does not assert that a physical molecular writer is automatically supplied by a registry geometry.

Proposition 4.8 (Prefix, freshness, and total-ledger invariants)**.** *After k completed residue incorporations, $1 \le k \le 4$, the joint state can be chosen to satisfy all of the following:*

(i) the retained product is $P(s_1 \cdots s_k)$ and the record is $C_{s_1} \cdots C_{s_k}$;

(ii) decoding the record gives exactly the retained residue word;

(iii) exactly the selected packets at slots $1, \ldots, k$ have been incorporated, and exactly $k-1$ labelled water coproducts have been formed;

(iv) the disjoint union of retained product, all coproducts, and all unincorporated packets has the same atoms, element counts, and atom-origin labels as the initial eight-packet pool.

The framework graph and its atom labels remain unchanged throughout.

Proof. At $k = 1$ retain the selected first packet and write its symbol; no chemical bond has changed. For the induction step capture the unused selected packet at slot $k+1$ and perform its joining map. The joining certificate preserves every atom and makes one water molecule, while the paired record update appends precisely $C_{s_{k+1}}$. Packet labels prevent reuse of an already incorporated packet. All unused alternatives remain present and unchanged. None of the graph operations acts on a framework vertex or edge, proving the last statement. □

An incorrect branch may select the still-unused alternative at the current slot, perform the same joining map, append the symbol of that actual residue, and terminate in off-specification collection. The abstract record can therefore remain faithful to the actual chain even when that chain differs from the intended program. Loss transfers the current chain and any held material to the waste account without erasing atoms or reusing packets. The same finite joining certificate applies to these shorter prefixes.

The common pool has elemental ledger $C_{20}H_{48}N_8O_{16}$. Consequently the comparison $GAGA \leftrightarrow GGGA$ changes a selection at one slot, not an atom's chemical identity or an unreported carbon source. The two choices leave different unused packets; their full ledgers are identical. The construction therefore supplies a genuinely address-dependent productive family rather than a homogeneous chain with decorative labels.

4.2 Chemical realization and the source boundary

Definition 4.9 (Realization certificate for a joining edge)**.** A chemical realization certificate supplements the graph map with specified medium and protonation conventions, a chemically admissible reaction path or validated effective reaction channel, and a complete account of activating reagents, catalysts, external work, and coproducts. If a finite work store is used, it has a named initial capacity W_0; each enabled operation has an assigned nonnegative debit w_e, and every permitted trajectory obeys $\sum_e w_e \le W_0$. For material fuel, its atoms and spent products must instead be included in the molecular ledger. Any charged realization also includes its charge and electron accounts. A positive rate is additional constitutive data, not a consequence of the graph map.

The water-only equation above is the net atom balance of the neutral amide rewrite. It is not a claim that this equation is a complete activation mechanism. Extra material activation chemistry requires extra inputs and coproducts; one cannot hide these in an unspecified "energy supply." Likewise a mechanical work debit is an explicit model resource, not evidence that a physically available controller couples that work to amide formation. The graph witness establishes nonemptiness of the formal productive family; physical realization is conditional on the additional certificate.

Proposition 4.10 (Conditional origin lifting)**.** *Suppose a stock-to-input preparation map supplies the selected prepared residues together with all preparation coproducts, preserves an explicit atom-origin ledger, and is compatible with their input labels. Then its composition with the joining maps preserves the complete stock-origin ledger. Without such a preparation map, the joining theorem proves no claim that the peptide carbons originated in a chrysene-only stock.*

Proof. The preparation map and each joining map preserve labelled atoms in their respective complete accounts. Composition preserves the same labels; coproducts from earlier stages remain in the account. In the absence of the first map the only defined origin labels are those of the prepared input packets, so a stronger stock-origin conclusion does not follow. □

This distinction is essential when importing a bound precursor from the earlier formalism: its attachment, release products, and any new terminal hydrogens must be accounted for before it can instantiate the present prepared-input boundary. No core, protected bridge, or framework atom is cleaved or removed in this witness. Release from an exterior holding port changes only the separately typed packet–port holding relation, not the protected framework graph. A future molecular encoding implementation similarly needs its own atom-resolved writer certificate; the present simultaneous symbolic record is an exact information invariant, not a proof of nucleic-acid synthesis.

5 First-passage productivity and finite-time certificates

All rates in this section are constitutive parameters of the mathematical witness, in a fixed unit of inverse time. They are not measurements for a substituted-chrysene assembly. A rate certificate is conditional on the admissibility of the corresponding capture, joining, collection, and resource transitions. In particular, it does not establish their chemical realization.

5.1 The finite-state absorption problem

Definition 5.1 (Stopped production chain)**.** Let T be a nonempty finite set of active states and let C, W, L be disjoint sets of stopped states, representing correct collection, off-specification collection, and loss from the collection channel, respectively. A stopped production chain is a continuous-time Markov chain on their union with nonnegative off-diagonal rates and zero outgoing rates from stopped states. Write Q for its generator restricted to T, in row convention, and q_C, q_W, q_L for the column vectors of total rates into the respective stopped sets. Thus

$$Q\mathbf{1} + q_C + q_W + q_L = 0.$$

Stopping records the first observed terminal outcome. It does not assert that its physical molecular state is irreversible. Loss denotes a transfer to a waste or inaccessible-material ledger, not disappearance of matter.

Hypothesis 5.2 (Absorption accessibility)**.** Every state of T has a finite directed path of positive-rate transitions to $C \cup W \cup L$.

Theorem 5.3 (Absorption certificate)**.** *Under Hypothesis 5.2, the stopping time τ is almost surely finite and has an exponentially bounded tail. The matrix $-Q$ is invertible, its inverse N has nonnegative entries, and*

$$N = \int_0^\infty e^{tQ}\, dt.$$

The vectors of correct-collection probabilities and expected stopping times are the unique solutions

$$Qh_C = -q_C, \qquad h_C = Nq_C,$$

$$Qm = -\mathbf{1}, \qquad m = N\mathbf{1}.$$

Analogous formulas hold for W and L.

Proof. For each active initial state choose a positive-rate path to a stopped state. There is positive probability of following this path within a fixed interval of length $t_0 > 0$: prescribe that each of its finitely many exponential holding times is shorter than a suitable positive fraction of t_0, and select its specified outgoing transition at every jump. There are finitely many initial states, so the minimum p of these positive probabilities is positive. The Markov property gives

$$\mathbb{P}_x(\tau > nt_0) \le (1-p)^n \qquad (x \in T,\ n \ge 0).$$

Consequently e^{tQ} converges to zero and its entrywise nonnegative entries are integrable. Integrating its derivative gives $QN = NQ = -I$, proving invertibility. The probability of being active at y at time t is $(e^{tQ})_{xy}$. Integration of its rate of entry into C proves $h_C = Nq_C$; integration of the survival probability proves $m = N\mathbf{1}$. Invertibility proves uniqueness. □

5.2 Three ordered joins

Consider a captured initial residue and three ordered extension stages. The following yield is conditional on this initialized production state. If upstream loading succeeds with probability q_G, unconditional correct collection has probability $q_G Y$ when the same production law applies after every successful loading history; a lower bound q_G on loading success instead gives the corresponding lower bound. Guaranteed controlled loading in the formal witness means $q_G = 1$, not an empirical assertion of perfect capture. At stage $j \in \{1,2,3\}$, a correct extension occurs at rate $a_j > 0$, an incorrect extension followed by off-specification collection at rate $b_j > 0$, and loss from the collection channel at rate $d_j > 0$. A correct extension advances to stage $j+1$, except that at stage 3 it produces correct collection. Put $\lambda_j = a_j + b_j + d_j$.

Remark 5.4 (Output population)**.** An incorrect branch at stage j records a collected off-specification chain of length $j+1$. Thus W includes collected dimers, trimers, and tetramers, whereas C consists of the target tetramer. This is a deliberately conservative purity denominator including all collected chains. It is a number- or probability-fraction purity over initialized first-output attempts, not a mass fraction; the shorter wrong products have not been mass-weighted. If collection is restricted to full-length tetramers, the incorrect-prefix completion and selection states must instead be modeled explicitly and their probabilities recalculated. A coarse incorrect-collection transition is an effective transition, not an assertion that incorrect joining and collection are a single elementary chemical event. Its refinement must preserve the stated outcome law or receive a separate certificate.

Proposition 5.5 (Exact yield and purity)**.** *For the preceding stopped chain, define $Y = \mathbb{P}(C)$, $B = \mathbb{P}(W)$, and $D = \mathbb{P}(L)$. Then*

$$Y = \prod_{j=1}^{3} \frac{a_j}{\lambda_j},$$

$$B = \sum_{j=1}^{3} \left(\prod_{i<j} \frac{a_i}{\lambda_i} \right) \frac{b_j}{\lambda_j},$$

$$D = \sum_{j=1}^{3} \left(\prod_{i<j} \frac{a_i}{\lambda_i} \right) \frac{d_j}{\lambda_j}.$$

Here $Y + B + D = 1$, and target purity among collected chains is $\Pi = Y/(Y+B)$. In particular, the rates

$$(a_j, b_j, d_j) = (100, 1, 1) \quad (1 \le j \le 3)$$

give

$$Y = \left(\frac{50}{51}\right)^3 = \frac{125000}{132651} > \frac{94}{100},$$

$$B = D = \frac{7651}{265302},$$

$$\Pi = \frac{250000}{257651} > \frac{97}{100}.$$

Proof. At stage j, exponential competition selects the three outcomes with probabilities a_j/λ_j, b_j/λ_j, and d_j/λ_j. A correct output requires three successive correct extensions. An incorrect output, or a loss, occurs at its first noncorrect stage, giving the disjoint sums above. These possibilities exhaust the paths and prove normalization. For the specified rates, symmetry gives $B = D = (1-Y)/2$, and hence $\Pi = 2Y/(1+Y)$. Substitution gives the fractions. The two strict inequalities follow by multiplication by their positive denominators. □

Proposition 5.6 (Conditional production time)**.** *Let τ count only active kinetic time in the three-stage model. Conditional on correct collection, its three stage holding times are independent exponentials with parameters $\lambda_1, \lambda_2, \lambda_3$. Consequently*

$$\mathbb{E}[\tau \mid C] = \sum_{j=1}^{3} \lambda_j^{-1}.$$

For $t \ge 0$,

$$\mathbb{P}(C, \tau \le t) \ge Y \max\left\{0, 1 - \sum_{j=1}^{3} e^{-\lambda_j t/3}\right\}.$$

For the rates of Proposition 5.5,

$$\mathbb{E}[\tau \mid C] = \frac{3}{102} = \frac{1}{34},$$
$$\mathbb{P}(C, \tau \le t) = Y\left[1 - e^{-102t}\left(1 + 102t + \frac{(102t)^2}{2}\right)\right].$$

No finite deterministic deadline guarantees completion with probability one.

Proof. At one stage, the joint density of a holding time s and a correct exit is $a_j e^{-\lambda_j s}$. Its conditional density is therefore $\lambda_j e^{-\lambda_j s}$. The Markov property makes the three such densities multiply on the event of three correct exits. Expectations add. If three nonnegative holding times sum to more than t, at least one exceeds $t/3$; the union bound proves the estimate. Three independent exponential variables with common parameter 102 have convolution density $102^3 s^2 e^{-102s}/2$; integrating gives the displayed formula. Finally the probability of no first jump before any finite t is $e^{-\lambda_1 t} > 0$. □

5.3 Control overhead, resources, and delayed delivery

Definition 5.7 (Bounded-overhead implementation)**.** A bounded-overhead implementation freezes the active production clock during at most n_h prescribed mechanical or control operations. Their aggregate duration is at most $H < \infty$ on every path. On resumption, the relevant stage has exactly its declared rates; no unmodeled reactions occur during a frozen interval. The physical elapsed time τ_{phys} then satisfies

$$\tau \le \tau_{\mathrm{phys}} \le \tau + H.$$

This definition is an operational hypothesis, not a consequence of the finite-state generator. Externally imposed operations do not establish an autonomous molecular machine.

Corollary 5.8 (Time and budget accounting)**.** *For a bounded-overhead implementation,*

$$\mathbb{P}(C, \tau_{\mathrm{phys}} \le t + H) \ge \mathbb{P}(C, \tau \le t),$$
$$\mathbb{E}[\tau_{\mathrm{phys}} \mid C] \le H + \sum_{j=1}^{3} \lambda_j^{-1}.$$

If the initial resource debit is at most R_0, each executed stage debits at most R_s, and each overhead operation debits at most R_h, every run uses at most $R_0 + 3R_s + n_h R_h$ resource units, provided these debits exhaust the resource account and the running debit during active-clock waiting is zero.

Proof. The time statements follow from the pathwise inequalities. Before stopping, the stage index increases at most three times, and each stage has one exit. There are at most n_h overhead operations, so addition of their debit bounds proves the budget statement. □

Remark 5.9 (Maintenance during random waiting)**.** The resource bound requires that there is no unbounded running resource debit while the clock waits. A static hold has bounded work only under an explicit zero-running-debit idealization, or under a finite deadline with a separately bounded maintenance cost. With positive continuous dissipation and an unbounded exponential waiting time, a deterministic resource bound does not follow; an expected-cost or deadline certificate must replace it.

Proposition 5.10 (Delivery refinement)**.** *Suppose correct and off-specification collected chains are subsequently delivered with conditional probabilities η_C and η_W, respectively. These are conditional probabilities for the complete upstream process; no independence assumption is required. Delivered purity is defined when $Y\eta_C + B\eta_W > 0$. Delivered yield and, on that domain, purity are*

$$Y_{\mathrm{del}} = Y\eta_C, \qquad \Pi_{\mathrm{del}} = \frac{Y\eta_C}{Y\eta_C + B\eta_W}.$$

If $\eta_C \ge \underline{\eta} > 0$ and $\eta_W \le \overline{\eta}$, then

$$\Pi_{\mathrm{del}} \ge \frac{Y\underline{\eta}}{Y\underline{\eta} + B\overline{\eta}}.$$

If every successful delivery adds at most H_d physical time and its conditional success probability, given each correct production history, is at least $\underline{\eta}$, then

$$\mathbb{P}(\textit{correct delivery by } t + H + H_d) \ge \underline{\eta}\,\mathbb{P}(C, \tau \le t).$$

Proof. The first statements follow from conditional probability and monotonicity of the ratio in its two nonnegative arguments. For the last statement, restrict to correct histories with active duration at most t. Their overhead and successful delivery durations are bounded by H and H_d. Integrating the historywise lower success probability proves the claim. □

5.4 A nondegenerate parameter certificate

Proposition 5.11 (Explicit robustness box)**.** *Suppose independently at each of the three stages that*

$$99.9 \le a_j \le 100.1, \qquad 0.999 \le b_j, d_j \le 1.001.$$

Then $Y > 0.94$ and $\Pi > 0.97$. In particular these conclu-

sions do not depend on an isolated choice of rates.

Proof. Set

$$p_* := \left(\frac{99900}{101902}\right)^3, \qquad \rho := \frac{1001}{2000}.$$

Monotonicity of $a/(a+b+d)$ gives $Y \geq p_*$. At every noncorrect exit, $b_j/(b_j+d_j) \leq \rho$. Multiplying this inequality by the probability of reaching that stage and its noncorrect exit probability, then summing, gives $B \leq \rho(1-Y)$. Since $y/[y+\rho(1-y)]$ is increasing for $0 < y \leq 1$,

$$\Pi \geq \frac{p_*}{p_* + \rho(1-p_*)}.$$

Exact fractions are

$$p_* = \frac{124625374875000}{132269020235351} > \frac{94}{100},$$
$$\frac{p_*}{p_* + \rho(1-p_*)} = \frac{249250749750000000}{256902038755711351} > \frac{97}{100}.$$

Both comparisons are integer inequalities after multiplication by positive denominators. □

Proposition 5.12 (Barrier-law completion)**.** *Fix $\beta > 0$. In the declared activated-rate law*

$$k = \nu \exp(-\beta \Delta G^{\ddagger}),$$

any finite family of positive rates k_e admits nonnegative barriers with a common prefactor: choose $\nu \geq \max_e k_e$ and put $\Delta G_e^{\ddagger} = \beta^{-1} \log(\nu/k_e)$. In particular $\nu = 200$ realizes the witness rates using barriers

$$\beta^{-1} \log 2, \qquad \beta^{-1} \log 200, \qquad \beta^{-1} \log 200.$$

Proof. Each logarithm is nonnegative, and substitution gives the specified rate. □

Remark 5.13 (Extent of the completion)**.** Proposition 5.12 is a consistency construction for constitutive kinetic parameters, not a derivation of transition-state energies from chrysene chemistry. If branch-state energy is G_i, the corresponding transition-state level is $G_i + \Delta G_e^{\ddagger}$. A shared transition state for forward and reverse microscopic reactions imposes additional constraints, as do local detailed balance and specified reservoir chemical potentials. These constraints cannot be inferred from a stopped first-passage model and must be verified in a microscopic refinement. The resource ledger must separately include activation, joining, collection, and external control; a choice of barriers supplies none of these resources for free.

6 An intact surface-supported witness

We give a witness in a reduced configuration space. Its geometric, symbolic, and constitutive parts are explicit. Its graph joining maps are declared discrete event laws; their molecular implementation requires additional chemical admissibility certificates. In particular, a formal peptide-bond rewrite is not a calculation of an atomistic transition state.

6.1 The complete patch and its exterior workstations

Definition 6.1 (Complete patch)**.** Let

$$I = \{0,1,2,3\} \times \{0,1\} \times \{0,1\}, \qquad q_{ijk} = (4i + j, 4j, 4k).$$

Every index is occupied. Join all pairs whose indices differ by one in exactly one coordinate. Edges in the first two directions are lateral substituent connections; edges in the third direction are stacking connections. The reference core envelope at q_{ijk} is the closed unit ball. A reference connection has the straight center segment, with its interior outside the core envelopes enclosed in a tube of radius $1/10$. These envelopes are exclusion sets, not atomic electron-density surfaces. The reference positions and framework connections are held fixed by ideal mechanical constraints. Rigidity is not inferred from graph connectivity, and no stacking or substituent stiffness is inferred from the chemical names.

There are 16 occupied nodes, 20 lateral edges, and 8 stacking edges. The three lattice vectors are $(4,0,0)$, $(1,4,0)$, and $(0,0,4)$; their triple product is 64. The patch is thus three-dimensional and oblique, not a square-planar idealization. Its boundary is the boundary of a finite specimen, not a deleted interior node.

Lemma 6.2 (Exterior access)**.** *Distinct core centers are at least 4 apart. The framework envelopes of Definition 6.1 lie in $z \leq 5$. Put four capture ports at*

$$p_j = (4j, 0, 8) \quad (0 \leq j \leq 3), \qquad b = (0,4,8).$$

Write $a_y = (1,4,0)$. The input tether uses the free negative-a_y boundary substituent port of q_{j01}; the reaction tether uses the free positive-a_y port of q_{011}. These five ports are not used by any framework edge. No occupied core port receives a second bond. The input tether follows the polygonal centerline

$$\begin{aligned} q_{j01} - a_y/\sqrt{17} &\longrightarrow (4j-1, -4, 4) \\ &\longrightarrow (4j-1, -4, 6) \\ &\longrightarrow (4j, 0, 6) \longrightarrow p_j, \end{aligned}$$

and the reaction tether follows

$$\begin{aligned} q_{011} + a_y/\sqrt{17} &\longrightarrow (2,8,4) \\ &\longrightarrow (2,8,6) \\ &\longrightarrow (0,4,6) \longrightarrow b. \end{aligned}$$

Each starts at its core-envelope boundary; its attachment collar is an intentional contact. The five added arms are prescribed neutral boundary substituents and have declared sufficient length and capacity. Tether envelopes may have radius $1/10$*. There are collision-free exterior transport routes for packets of radius* $1/4$ *from the ports to a reaction cell of radius* 2 *centered at b, provided transport is serial and contact with the packet's own port is permitted during detachment.*
For delivery, reserve $d = (0, 12, 8)$ *as an exterior receiving port. All receiver body envelopes and their allowed internal motions lie in the fixed opaque box*

$$B_R = [-1, 1] \times [13, 20] \times [7, 9],$$

and hence in $y \geq 13$*; the only exception is a terminal docking tube of radius* $1/10$ *from d to* $e = (0, 13, 8)$*. The receiver variables* (a, u) *are internal reduced coordinates, not a claim of atomistic geometry for that module. No other receiver obstacle enters the transport region. Declare contact collars of radius* $1/2$ *about input ports and radius* $3/4$ *about b and d. Within a collar, only the specified packet's reversible holding or docking contact is permitted. On the remaining closed transport subsegments the excluded-body clearance is at least* $1/10$ *after subtracting packet and tube radii.*

Proof. For two distinct indices, a difference in the last coordinate gives a vertical separation at least 4; a difference in the second coordinate gives a y separation at least 4; otherwise the x separation is at least 4. The stated height bound follows from the unit core envelopes and the connection-tube radius. Move the seed from p_0 along the segment to b, initially empty. For $j = 1, 2, 3$, use the polygonal route

$$(4j, 0, 8) \longrightarrow (4j, 8, 8) \longrightarrow (0, 8, 8) \longrightarrow (0, 5, 8).$$

The last point lies inside the reaction cell. Represent the retained growing product by a packet of radius $1/2$ centered at b. At the last point, the incoming and retained packet centers have distance 1, greater than their summed radii $3/4$; both packets fit inside the reaction cell. After a committed chemical event, replace them by the retained joined-product packet and export the water graph. This is a discrete reduced event, not a claimed continuous chemical merger path. Outside detachment and reaction-contact neighborhoods, each route is separated from the other port tethers. All tether centerlines except their terminal vertical segments lie at $z \leq 6$, giving vertical separation at least 2. The terminal input segments have distinct x coordinates spaced by 4 and lie at $y = 0$; the terminal reaction segment lies at $(x, y) = (0, 4)$. Away from its own detachment contact, each route therefore avoids the other tether tubes. The final incoming position is distance 1 from the reaction tether's endpoint. Subtracting the tube and packet radii leaves positive clearance. All routes have $z = 8$, giving distance at least 3 from the original framework envelopes before the packet radius is subtracted. Serial use excludes collisions between moving packets. The final approach and joining occur inside the separately specified reaction cell. Finally, a product packet of radius $1/2$ can travel from b through $(0, 8, 8)$ to the receiver delivery port $d = (0, 12, 8)$ after input traffic ceases. Detachment from its own reaction tether is permitted; all unused input ports lie at $y = 0$. Additional competing-input buffers can be placed at $(20 + 4\ell, 0, 8)$ for finitely many positive integers ℓ, away from this delivery route.
Outside an input collar, clearance from the incident terminal tube is at least $1/2 - 1/10 - 1/4 = 3/20$. Outside the reaction and delivery collars, the radius-$1/2$ product has clearance at least $3/4 - 1/10 - 1/2 = 3/20$ from the respective terminal tube. Receiver bodies in $y \geq 13$ stay at least $1/2$ from the product at d before its intentional terminal contact is considered. All other separations have the larger bounds already given. The incoming-versus-retained packet gap is $1/4$. Thus $1/10$ is a common conservative lower bound on the finite union of closed noncontact subsegments. The collar interiors are handled by their holding/docking guards, not by this positive-clearance claim. □

Remark 6.3. The reaction cell is an exterior bookkeeping region, not a pore, a void, or a cavity made by removing material. Its contents are not substituted for framework nodes. No ion or nucleobase is inserted into the patch. The packet model verifies exterior access and capacity; it does not identify a packet trajectory with a continuous atomistic bond-formation trajectory. The latter requires the chemical path certificate. The exterior tethers denote prescribed substituent-supported attachment sites, not additional deleted-node defects.

6.2 A nonhomogeneous word and its ledger

Take the alphabet $\{G, A\}$, interpreted, for the atom ledger, as neutral glycine and alanine inputs. The prescribed word is

$$w = GAGA.$$

The seed is G. Three ordered stages append A, G, A, respectively. Each successful joining rewrite consumes the terminal carboxyl group and the incoming amino group in the usual formal condensation graph, forms one amide edge, and exports one water

graph. Thus the overall atom inventory is

$$2C_2H_5NO_2 + 2C_3H_7NO_2 \longrightarrow C_{10}H_{18}N_4O_5 + 3H_2O. \qquad (1)$$

Equation (1) is an exact atom-count identity. It neither asserts favorable condensation free energy nor supplies an activation mechanism. Prepared precursors, activation resources, and water export are explicit boundary data; conversion of the chrysene stock into amino acids is not asserted.

Let C_G, C_A be distinct external code tokens. A token is a record symbol, not a nucleobase inserted into the framework. At retained prefix length j, the abstract record is the length-j prefix of $C_GC_AC_GC_A$. A committed join appends its corresponding record token. The record and residue graph are separate typed projections of one committed state, synchronized as in Proposition 4.8. This is an abstract code-coupled ledger, not a claim that a molecular writer or simultaneous nucleic-acid synthesis has been implemented. Post hoc reverse encoding is not substituted for this invariant.

Proposition 6.4 (Finite symbolic realization)**.** *The three ordered joining rewrites yield a four-residue product with word GAGA, three exported water graphs, and external record $C_GC_AC_GC_A$. Every committed prefix has its correct atom and record ledger.*

Proof. Initially the residue graph and record both contain the seed label G. One joining adds the incoming residue graph, removes precisely one water graph from the retained product, and appends its record token. Induction over the three joins proves the prefix assertion. Summing the three identities gives (1). Distinctness of C_G and C_A makes the nonhomogeneous word distinguishable from, for example, *GGGA*. □

6.3 One product–receiver interaction law

The downstream effect must not be an independently assigned success flag. We now derive it from a single declared reduced energy. Let $s \in \{0, T, C\}$ denote an empty, target-bound, or competitor-bound receiver, let $a \in [2, 6]$ be its opening coordinate, and let $u \in [-5, 5]$ be a neutral receiver polarization coordinate. The empty-product case uses the same decoupled coordinate, so no comparison changes the normalization convention.

For a four-letter word v, set

$$S(v) = \sum_{j=1}^{4} 2^{j-1}\mathbf{1}_{\{v_j=A\}}, \qquad \lambda(v) = \frac{2}{5}S(v). \qquad (2)$$

In the no-product condition set $\lambda = 0$. For every four-letter word, $0 \le S \le 15$, so $0 \le \lambda \le 6$. The detailed performance comparisons below concern *GAGA*, *GGGA*, and no product.

Hypothesis 6.5 (Neutral contact constitutive law)**.** The neutral coordinate has energy $2u^2/3$. The docked product enables target-contact coupling $-\lambda(v)u$; its competitor-contact coupling is zero in this witness. The four effective contact contributions are $-\mu_j(v)u$, with $\mu_j(v) = (2/5)2^{j-1}\mathbf{1}_{\{v_j=A\}}$; their sum is $-\lambda(v)u$. This is a phenomenological neutral-contact convention, not an atomistic electrostatic derivation. A dipole interpretation would add explicitly equal-and-opposite charges, their positions, and a field model as part of the molecular conformance certificate. No such charged species is inserted into the framework here. The weights encode the fixed addressed docking geometry. They are specified constitutive parameters, not measured glycine/alanine partial charges or a deduction from the residue names.

There is no charged structural insertion in this construction. The neutral partial-dipole description belongs to the external product–receiver contact. It is a finite phenomenological realization of an interaction law; chemical validation must determine whether a particular substituted chrysene–peptide system realizes such parameters.

Put $b_0 = 0$, $b_T = b_C = 4$, $e_0 = 0$, and $e_T = e_C = 10$. At the held receiver control $c = 3$, define

$$U_s(a, u; v) = 8(a - c)^2 + b_s a - e_s + \frac{2}{3}u^2 - \mathbf{1}_{\{s=T\}}\lambda(v)u. \qquad (3)$$

All conditions use the same stiffnesses, controls, competitor law, and energy reference. Only the physically declared product coupling changes.

Proposition 6.6 (Stable, sequence-dependent receiver contrast)**.** *For the three compared conditions, each receiver state has a unique interior minimum. Its Hessian is* diag(16, 4/3)*, and the minimized state energies satisfy*

$$F_0 = 0, \qquad F_C = \frac{3}{2}, \qquad F_T = \frac{3}{2} - \frac{3}{8}\lambda^2.$$

Under the finite-state unit-activity, unit-temperature basin law $p_s = e^{-F_s}/\sum_t e^{-F_t}$, the target occupancy is

$$p_T(\lambda) = \frac{\exp(-3/2 + 3\lambda^2/8)}{1 + \exp(-3/2) + \exp(-3/2 + 3\lambda^2/8)}. \qquad (4)$$

Consequently the GAGA product increases target occupancy by more than 0.83 *relative to no product and by more than* 0.09 *relative to the GGGA product.*

Proof. Completing squares in (3) gives

$$a_s^* = c - \frac{b_s}{16}, \qquad u_s^* = \frac{3}{4}\mathbf{1}_{\{s=T\}}\lambda,$$

with minimum $b_s c - e_s - b_s^2/32 - 3\mathbf{1}_{\{s=T\}}\lambda^2/8$. The opening

minima are 3 and 11/4. The target polarization minima are 0, 12/5, and 3 for absent product, *GGGA*, and *GAGA*, respectively; all are interior. Positive definiteness gives uniqueness and strict stability. Since $S(GGGA) = 8$ and $S(GAGA) = 10$, the two binding shifts are 96/25 and 6. Formula (4) follows by normalization. Writing $A = 1 + e^{-3/2}$ and $x = e^{-3/2+3A^2/8}$, one has $d[x/(A + x)]/dx = A/(A + x)^2 > 0$; hence the target occupancy is strictly increasing with the nonnegative coupling magnitude. Direct evaluation gives

condition	p_T
no product	0.154280772981 . . .
GGGA	0.894597422732 . . .
GAGA	0.986594403166 . . .

The rational Taylor enclosures in Appendix A give occupancy intervals $(0.15428, 0.15429)$, $(0.89459, 0.89461)$, and $(0.98659, 0.98660)$, which imply the asserted strict contrasts. □

Remark 6.7. The law in Proposition 6.6 is a reduced finite-basin law, not an asserted exact integral over the bounded continuous rectangle. In particular, truncation factors of Gaussian basin integrals have not been silently discarded. Nor does the sequence contrast establish unique recognition among all peptides, biological activity, or a self-clamping product: it is an externally docked, mechanically stable receiver effect in one specified model.

6.4 Joint feasibility and a strict-margin neighborhood

Definition 6.8 (Resource frame)**.** A resource frame for one attempt contains the complete eight-packet pool G_j, A_j $(1 \le j \le 4)$, including the unused alternative seed, three activation tickets, three water-export slots, a four-token external recording capacity, a product collection slot, and the prescribed serial transport and receiver-control schedule. An activation ticket denotes a supplied event resource with its own energy ledger, not a species inserted into the scaffold. A joining commit consumes one ticket and one export slot; premature termination leaves unused resources unconsumed.

Definition 6.9 (Choice–transport–commit refinement)**.** A refined attempt records its current slot, actual product prefix, actual-symbol record, packet statuses, destination, three joining tickets, three water-export slots, and one of five phases: *waiting*, *selected*, *transporting*, *committed*, or *stopped*.

1. Initially the chosen seed is incorporated, its symbol is recorded, all seven other packets are unused, and all three tickets/export slots remain available. The phase is waiting for slot 2.
2. Only waiting states run the 100 : 1 : 1 competing clocks. Selection records a branch and, for a joining branch, the chosen fresh packet. It neither appends a symbol nor debits a joining ticket or export slot.
3. During transport the clock is held; capture marks that packet held. The deterministic prescribed transport and its guards must finish within the declared overhead bound, without hidden reactions or failures.
4. Commitment applies the joining graph map and atomically appends the actual residue symbol, changes held to incorporated, and consumes one ticket and one export slot. It creates one mapped water. A correct commit resumes waiting at the next slot, or stops in C after slot 4. A wrong commit stops in W with its actual, faithfully recorded chain.
5. A selected loss branch transfers the current prefix and any held material to waste, makes no join, appends no symbol, and consumes no joining ticket or water slot. It stops in L.

The packet must be fresh and the relevant ticket, export, contact, and chemical-event guards must hold at commitment. Any additional failure of transport or holding requires a new outcome channel or an explicit implementation-error bound; it is not silently assigned the successful branch's probability.

Erase the bounded holds and contract each selected-to-committed (or selected-to-loss) refinement to one jump to its post-commit state. Branch preservation then gives exactly the active-clock chain of Section 5. The symbolic invariant applies at committed states; selecting a proposed input is not yet its incorporation.

Theorem 6.10 (Nonempty joint reduced-model witness)**.** *Adopt the three neutral-condensation graph rewrites as discrete event laws and the neutral contact constitutive law of Hypothesis 6.5. There exists a single resource-augmented reduced model with the following properties:*

1. *its full, ideally constrained* $4\times2\times2$ *framework remains intact throughout;*
2. *it has exterior access, a three-join correct branch producing GAGA, an exact atom ledger, and the synchronized abstract external record;*
3. *its delivered correct product has the stable receiver contrast of Proposition 6.6;*

4. *the correct, incorrect-output, and loss rates at each of the three competition stages are* $100, 1, 1$*, respectively.*

The conclusion is an existence statement in the declared reduced model class. A molecular implementation requires additional chemical path, activation, and constitutive calibration certificates; the conclusion is not an experimental existence theorem for a molecular loom.

Proof. Use Definition 6.1 for the common scaffold and the exterior routes of Lemma 6.2 for all input stages. Use the single ordered rewriting system of Proposition 6.4, not unrelated stage-wise product choices. The resource frame has sufficient capacity for all three joins, and the exported waters remain explicitly in its ledger. Use the receiver envelope and guarded docking port specified in Lemma 6.2, hold its control at $c = 3$, and deliver the collected packet to $d = (0, 12, 8)$ along the exterior route of Lemma 6.2 after all input traffic has stopped. Declare the common receiver energy (3); the minimizing coordinates just computed belong to its admissible domain.

A concrete active-clock implementation lets the competing clocks select the next branch, pauses those clocks, transports the selected fresh packet, and commits its graph event before resuming the next stage. An incorrect selection uses the unused alternative at that slot and then terminates collection; a loss branch transfers the current prefix to waste. Alternative buffers may reach their input port by rising above $z = 10$, moving over the selected port, and descending after the original packet has been withdrawn. Only one such transport is active at a time. The finite prescribed routes and control operations have a uniform duration bound; no unmodeled reaction runs during their ideal holds. The observable stopped chain describes active time, while Section 5 accounts for this physical-time overhead.

For the finite transition component, use the same attempt factor $\nu = 200$ at every stage. The dimensionless barriers $\log 2$ for a correct commit and $\log 200$ for each of the two other exits give $\nu e^{-B} = 100, 1, 1$. These are finite, nonnegative model barriers, not chemically calculated barriers. The event graph is the driven, stopped first-output graph: its reservoir, controller, and collection states are retained in the resource description. No equilibrium interpretation or zero-work autonomous cycle is inferred from its one-way observed exits. All quantities are therefore assigned on one resource-augmented state space, and each required set is nonempty. □

For this model the exact probability of correct output is $(50/51)^3 > 0.94$, and its fraction among collected outputs, counting incorrect shorter chains as outputs, is

$$\frac{2(50/51)^3}{1 + (50/51)^3} = \frac{250000}{257651} > 0.97.$$

These are first-attempt, first-output quantities. Delivery survival, receiver equilibration time, and reset reliability must be included separately if an end-to-end timed-cycle claim is desired; they are not silently assigned probability one by these two formulas.

Corollary 6.11 (Relative robustness)**.** *Within the fixed topology and fixed formal joining class, a nonempty relative neighborhood of the numerical witness preserves strict mechanical stability, the two stated occupancy contrasts, correct-output probability greater than* 0.94*, and collected-output purity greater than* 0.97.

Proof. The Hessian has a positive spectral gap and every stated equilibrium is a positive distance from the coordinate boundary. The finite union of closed noncontact transport subsegments has the uniform clearance bound of Lemma 6.2. Collars, legal terminal contacts, and their guards are preserved as part of the relative parameter class. The occupancy and finite competing-rate expressions are continuous functions of their coefficients wherever their positive denominators persist. All four inequalities hold strictly at the witness, so their inverse images contain a relative neighborhood. The neighborhood is taken within the fixed legal contact and joining class: continuity is not used to prove that an unvalidated chemical transition becomes chemically admissible. □

7 Operational readout and realization interfaces

7.1 A finite-time receiver readout

The receiver probabilities of Proposition 6.6 can be given a reversible finite-state kinetics. This makes the distinction between production and subsequent measurement explicit.

Proposition 7.1 (Reversible receiver realization)**.** *For a fixed delivered product put* $w_s = e^{-(F_s - F_0)}$*,* $s \in \{T, C\}$*. Fix* $\nu > 0$ *and define*

$$q_{0s} = \nu \frac{w_s}{1 + w_s}, \qquad q_{s0} = \nu \frac{1}{1 + w_s}, \qquad q_{TC} = q_{CT} = 0.$$

The chain on $\{0, T, C\}$ *is irreducible and has stationary law proportional to* $(1, w_T, w_C)$*. It converges to that law exponentially from every initial state. Hence a finite readout time can make each of the three compared target occupancies differ from its stationary value by less than any prescribed* $\epsilon > 0$*.*

Proof. All displayed $0 \leftrightarrow s$ rates are positive. With $\pi_s = w_s \pi_0$, one has $\pi_0 q_{0s} = \pi_s q_{s0}$, proving detailed balance and stationarity. The reversible generator is self-adjoint in the

weighted inner product. Its Dirichlet form is

$$-\langle f, Qf\rangle_\pi = \frac{1}{2}\sum_{i,j}\pi_i q_{ij}(f_j - f_i)^2.$$

It vanishes only on constants because the transition graph is connected. On the finite-dimensional mean-zero subspace its minimum Rayleigh quotient is therefore a positive number γ. Spectral expansion gives exponential convergence in the weighted norm and hence in total variation. Taking the maximum of three finite readout times proves the last assertion. □

For example, the exact intervals of Appendix A give stationary contrasts exceeding 0.09198 and 0.83230. Choosing readout error less than 10^{-4} in each condition leaves measured-law contrasts exceeding 0.09178 and 0.83210, still greater than 0.09 and 0.83. This concerns expected occupancies or their laws; a single observed binding event does not deterministically identify a product. Statistical estimation error is a separate sampling question.

The receiver is held in the same externally specified control setting in all comparisons. No net stationary cycle current or autonomous work extraction is inferred from the equilibrium contrast. Target and competitor arrivals and departures exchange molecules with declared external receiver reservoirs, not with scaffold insertion sites.

7.2 Approximate stage implementations

Proposition 7.2 (Finite implementation error)**.** *Suppose the initialized three-stage attempt has the finite stage kernels used in Proposition 5.5. Extend each stopped state by an identity transition so that every history has three stages. Suppose another implementation, on the same interpreted state space, differs from the model's conditional kernel at stage j by total variation at most ϵ_j, uniformly on reachable histories of either process. Put $\epsilon = \sum_{j=1}^{3}\epsilon_j$. Its terminal outcome law differs by at most* $\min(1,\epsilon)$*. In particular,*

$$\widetilde{Y} \geq Y - \epsilon.$$

If $Y > \epsilon$, its target purity among collected chains obeys

$$\widetilde{\Pi} \geq \frac{Y-\epsilon}{Y+B+\epsilon}.$$

Proof. Couple the two histories at the first stage by a maximal coupling. Given agreement up to stage $j-1$, use a maximal conditional coupling at stage j; the chance of first disagreement there is at most ϵ_j. The union bound bounds terminal disagreement by their sum, which bounds total variation. The correct-output event thus has probability at least $Y-\epsilon$, while the collected-output event has probability at most $Y+B+\epsilon$. The positive numerator guarantees a nonzero actual collected probability. Division yields the bound. □

This result compares complete stage outcomes, not uncalibrated instantaneous rate constants. A changed holding-time law requires its own timing certificate. Loading or delivery errors must also be included if the comparison begins before initialization or ends after a nonideal transfer.

Definition 7.3 (Molecular conformance certificate)**.** A molecular conformance certificate identifies framework and prepared-input atom graphs, nonoverlapping physical configurations, and real input/output states for every declared stage. It supplies chemically admissible reaction and transport realizations, the complete material/work accounts, and an interpretation into the reduced states preserving interfaces. Persistent atom labels and their origins must be supplied for all physical material, including auxiliary reagents and coproducts. The physical and formal stage maps commute on the identified modeled atoms; every auxiliary atom remains in the complete account. Every intermediate physical state preserves the protected framework identities and connections and excludes the prohibited structural insertions. Thus a coarse projection may not conceal scaffold damage or omitted material. It also certifies the induced outcome kernels and the receiver interaction/basin law, exactly or with stated error bounds. A stationary basin-law certificate establishes stationary response only; physical finite-time readout additionally requires the receiver transition law or a sufficient mixing-time bound.

Proposition 7.4 (Conditional molecular lifting)**.** *If a conformance certificate exists for the finite witness, its physical execution preserves the protected framework and atom-origin accounts. Exact stage kernels and receiver law give the same production and response conclusions as the witness. Uniform stage-kernel errors give the production bounds of Proposition 7.2; admissible interaction perturbations satisfying the strict-margin neighborhood give the corresponding receiver contrast bounds.*

Proof. The interpreted physical stages have matching interfaces and preserve the required invariants. Proposition 2.5 therefore applies. Exact conditional kernels induce the same law on the interpreted finite histories by induction on stages. With errors, apply Proposition 7.2. Exact receiver laws give the same stationary readout; perturbations satisfying the witness's relative neighborhood preserve its strict inequalities by Corollary 6.11. □

The definition does not assume the desired production probabilities: it requests reaction/transport realization and local transition laws from which those probabilities are derived. The missing experimental or computational chemistry is consequently a set of identifiable interface questions, not a hidden assertion

that a formal rewrite already synthesizes the corresponding peptide.

8 Discussion and conclusions

The productive advance over Article 103 is the common treatment of a generated molecular graph and its downstream response. The four-position program selects from a shared prepared pool without changing atom identities. The joining maps preserve explicit origins, and the competing-channel model measures first collected output rather than equilibrium occupancy at the synthesis site. The receiver effect is then calculated from one energy law under matched controls. None of these statements requires a defect in the framework.

The physical architecture is intentionally conservative. Its complete finite patch has exposed boundary attachments, exterior transport, and a surface-supported processing region. No scission, ionic insertion, nucleobase insertion, internal pore, or excavated void is used. Ordinary space outside the intact bodies is not promoted into a defect-based catalytic cavity. The product remains an externally handled short peptide; it is not required to fold into an independent machine. The controlled receiver belongs to the capture/readout architecture, not to a newly claimed autonomous peptide clamp.

The two-letter nonhomogeneous witness is a finite test of productive addressing, not a reconstruction of all twenty amino acids or the genetic code. It complements the broader typed carrier construction [Sch26f] by making a small construction and its output comparison explicit. Its record is an external symbolic record updated with committed events. Synthesizing a corresponding nucleic-acid polymer would require an additional writer with its own atoms, activation, and compatibility certificate. That extension need not proceed by reverse recognition of a previously produced peptide, but it is not supplied merely by appending a mathematical token.

The source boundary is equally important. The exact prepared-input ledger does not manufacture glycine or alanine from chrysene. Article 75's prepared production framework and Article 77's stock-origin accounting indicate the additional map required for that stronger assertion [Sch26f, Sch26d]. Article 99 then compares the ability of endogenous and exogenous preparation mechanisms to supply the initial architecture, packets, and controls [Sch26g]. Equal supplied states and controls do not acquire different operational capabilities solely from their provenance.

The local geometry proposals of the loom series can guide future molecular parameterization [Sch26l, Sch26i, Sch26j, Sch26r, Sch26b]. They are not used here to infer a whole-chain folding theorem, a zero activation barrier, or a chemically active defect. The small-pore and structural-polymer initiation studies [Sch26q, Sch26p] likewise remain context rather than a reason to place this peptide inside a narrow pore. Actual constitutive calibration should begin with the chosen residue/attachment geometry, solvent and protonation conditions, the joining activation mechanism, and the product–receiver contact law. If those calculations do not enter the proved operating neighborhood, the witness must be redesigned rather than its numerical guarantees retained by analogy.

The following paper in the series can now ask a sharper question: can a specified controller and drive reset this productive apparatus and sustain repeated operation with full resource and time accounts? The present finite-attempt theorem does not answer that question by drawing a cycle. Later gene–machine feedback, repair, and inheritance should consume an established production interface and an established repeatable operating interface. Broad maturation architectures remain a distinct research direction.

In conclusion, an intact finite registry, explicit prepared graphs, a finite joining law, and a common response energy admit a jointly consistent productive molecular-machine model. Its exact ledger, nonhomogeneous addressing, outcome probabilities, finite-time readout, and strict-margin robustness are proved within that model. The chemical realization boundary is stated as a composable certificate, preserving both mathematical rigor and a concrete program for further molecular investigation.

A Exact exponential enclosures

For rational $t > 0$ and integer $N \geq 0$ with $t < N + 2$, put

$$S_N(t) = \sum_{k=0}^{N} \frac{t^k}{k!}, \qquad U_N(t) = S_N(t) + \frac{t^{N+1}}{(N+1)!}\frac{1}{1 - t/(N+2)}.$$

The Taylor series for the exponential has positive terms. After its first omitted term, the ratio of consecutive terms is at most $t/(N+2) < 1$. Summing the dominating geometric series gives

$$S_N(t) < e^t \leq U_N(t), \qquad U_N(t)^{-1} \leq e^{-t} < S_N(t)^{-1}.$$

Every quantity on the right is rational when t is rational. Thus the following occupancy intervals require only rational arithmetic after this analytic bound.

For the receiver of Section 6, use

$$\begin{aligned} p_T(0) &= (2 + e^{3/2})^{-1}, \\ p_T(GGGA) &= (1 + e^{-117/50} + e^{-96/25})^{-1}, \\ p_T(GAGA) &= (1 + e^{-9/2} + e^{-6})^{-1}. \end{aligned}$$

Applying the preceding bounds with $N = 40$ gives the strict rational enclosures

condition	$10^5 \times$ lower	$10^5 \times$ upper
no product	15428	15429
GGGA	89459	89461
GAGA	98659	98660

The lower value in each row is strictly below the probability and the upper value strictly above it. Consequently

$$p_T(GAGA) - p_T(GGGA) > 9198/10^5 > 0.09,$$
$$p_T(GAGA) - p_T(0) > 83230/10^5 > 0.83.$$

These decimal rational endpoints are certified intervals, not floating-point error estimates.

B Finite verification and reproducibility

The accompanying standalone Verification Code Dossier contains the complete dependency-free Python source and the recorded integer/rational verification results. The executed suite has 4,936 assertion executions, including 112 refined protocol histories and 14 deliberately invalid cases that must be rejected. These counts enumerate repeated finite checks, not distinct mathematical theorems. It constructs explicit-hydrogen Gly/Ala graphs for all sixteen four-letter words, performs all joining maps, checks neutral valences and immutable origins, and verifies preservation of the full eight-packet pool. It checks the exact kinetic fractions, the endpoints of the stated independent rate box, the complete-patch counts, the receiver Hessian, and the Taylor enclosures above.

The rate-box corner enumeration is a check, not the proof of robustness over the box: the analytic monotonic bounds in Section 5 provide that proof. Likewise enumeration of the sixteen words does not replace the induction proving Proposition 4.8. Surface-route inequalities and the declared chemical-interface boundary are mathematical parts of the text, not claims of atomistic simulation. The accompanying Formal Proof Dossier records 49 kernel-checked Lean 4 theorems covering a finite structural and rational core. It includes generic preservation and join-incidence identities, symbolic encoding, formula ledgers, finite patch and rate-corner checks, rational receiver minima, and rational Taylor-certificate arithmetic. It does not formalize the complete atom-graph implementation, the analytic bridge to the real exponential, continuous routing, CTMC convergence, or chemical realization. The paper proofs, executable finite checks, and formal subset have separate coverage statements.

For each experiment the implementation should record program, selected packets, preserved framework identities, completed graph events, waters, unused alternatives, waste, active time, paused-control time, collection outcome, and receiver condition. A negative control should alter one assumption at a time: use a consumed packet, mismatch the external record, omit a water, obstruct an exterior route, replace the intended residue, or set the product coupling to zero. Such changes should fail the corresponding certificate rather than be silently absorbed into a different model.

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