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Constructive Genetic Code-Table Realization On A Typed Chrysene Carrier

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Abstract

A chrysene-based construction of a genetic-code table requires compatible maps between precursor orientations, retained molecular structures, codon addresses, and readout events. We give a finitely specified constructive realization in which these maps have separate types and can be checked together. A six-core precursor is represented by a three-unit $(X-A)_3$ carrier, with fixed resident adenosines and a separately addressed external coding triplet. The binary frame quotient has twenty classes; explicit reference decorations recover sixty-four addressed states. For the table-conditioned Watson–Crick incidence graph, a nine-class Hall obstruction and an attaining matching establish the sharp matching number eighteen. A declared atom-conserving graph grammar and explicit product constructors supply a formal molecular-graph repertoire; seeded routing, refinement, local address exchanges, and affine selection modules provide finite paths to the vertebrate mitochondrial and standard reference tables. The rules admit alternative tables, so the result is constructive realization rather than unique selection. A corrected two-carrier junction supplies a side-specific release rule and a resource-aware reset invariant for conditional methionine-first segments. The combined construction is nonempty at the formal graph-and-controller level. Molecular feasibility requires a common admissible lift of its graph edits, reservoirs, geometry, and readout, which is stated separately and is not established by the finite certificates. Thus the completed existence claim concerns a precisely specified formal system; the physical interpretation remains conditional.

Keywords: genetic code; constructive realization; chrysene carrier; frame quotient; graph grammar; vertebrate mitochondrial code; standard genetic code; typed maps; molecular-graph repertoire; methionine initiation; formal existence; chemical lift condition; Chrysene Formalism

1 The constructive question

Developing a molecular account of the genetic code is challenging because a theory must connect the pattern of codon assignments with a system capable of implementing and transmitting those assignments. Proposed explanations emphasize stereochemical recognition, biosynthetic coevolution, selection for error tolerance, and historical fixation; these mechanisms can contribute in combination [KN09, KN17]. A prominent adaptive line of inquiry asks whether the organization of the code reflects selection that reduces the consequences of mutation and mistranslation [FH98]. The corresponding constructive question concerns the molecular architecture on which an assignment system could operate.

Here we investigate whether one explicitly specified, encodable architecture can support a common registry, product repertoire, assignment dynamics, and junction controller. The motivation comes from the orientation-encoded nucleic-acid synthesis proposal of US12195423B1, which relates four molecular orientation states to a base-four convention and describes a tethered poly-A/chrysene setting [Sch25]. Building on that starting point, the present construction specifies a six-core precursor and a triplet chrysene–adenosine carrier, then brings the coding and product constructions into a single finitely specified model with a continuous selector control.

The resulting claim is a constructive existence statement: the specified components can coexist under the declared rules, and the two reference assignment tables occur in the reachable set. This establishes a precise candidate architecture and identifies the additional conditions required for its chemical realization. The reference tables guide

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parts of the construction, so their reachability supplies a conditional realization rather than an independently selected evolutionary outcome. In particular, the order in which the reference tables are reached is a feature of the formal construction; it does not assign them an ancestral chronology.

A finite registry can count possible states without determining what those states produce. A list of retained carbon frameworks can describe target structures without supplying a reaction path. A path between two tables can be exact without explaining why a molecular system selects its starting table. These distinctions matter when the three constructions are combined: the interfaces carry as much of the argument as the individual counts.

The aim of this paper is to construct one explicitly defined system that supports the registry, the product repertoire, the assignment operations, and the junction controller together. The two named endpoints are the vertebrate mitochondrial reference table and the standard reference table. "Endpoint" refers to the total map from sixty-four external coding triplets to twenty residue identities and a termination symbol. It does not by itself specify an initiation policy, a translation apparatus, or a chronological sequence of molecular events.

The starting architecture is a hexamer of six original substituted chrysene cores. Three designated pair transformations produce three nucleotides and three residual chrysene cores. The selected code-forming representative is a triplet of tethered chrysene–adenosine units, $(X-A)_3$, in which each residual X is 6,12-disubstituted and participates in the proposed intercalating carrier. A separately presented external coding triplet interacts with that carrier in a noncanonical register. Two such triplet carriers form the proposed sulfur junction and represent twelve original cores. The resident adenosines, external coding bases, and nucleotide outputs of the precursor transformation are different objects throughout the construction.

The mathematical ingredients develop the supplied Articles 44, 45, 47, 48, 50, 52, 54, 55, 56, 57, and 59 [Sch26g, Sch26i, Sch26c, Sch26k, Sch26d, Sch26b, Sch26a, Sch26e, Sch26f, Sch26h, Sch26j]. Their useful components are brought into a common notation and their assumptions are narrowed where composition requires it. US12195423B1 is the sole patent basis [Sch25]. The patent gives the chosen orientation-to-base convention and a poly-A/chrysene setting. It is not used as a certificate that the complete carrier, product family, or junction controller has been physically realized.

1.1 What is proved and what is conditional

The principal result is constructive formal realization. The finite carrier is nonempty; all reference tags, atom identities, resources, routing data, and controller variables can be assigned simultaneously. Product endpoints are checked as graphs under a deliberately stated graph-edit grammar. Allowed routing operations are given before the endpoint comparison, and complete endpoint tables are checked after the operations. This is stronger than the assertion that a valid path, if supplied, is reachable: the paper supplies concrete finite witnesses and proves why the checker accepts them.

The construction is also intentionally limited. Its allowed graph edits provide a mathematical reachability relation, not a claim about elementary chemical reactions or kinetic accessibility. Its initial seed and module-placement data are informed by the reference tables. The finite existence theorem therefore does not constitute a target-independent derivation of the observed code. A separate lifting result states precisely what would transfer the formal path to a chemically admissible model. The local chemical conditions in that result are substantive open obligations, rather than conclusions inferred from the registry count.

Three levels of assertion will be used:

1. A *finite theorem* follows from explicit definitions and, when needed, a small independently recomputable certificate.

2. A *formal graph theorem* follows from a declared atom/bond grammar, terminal graph specification, and finite resource ledger. Its meaning is the meaning of that grammar.

3. A *chemical interpretation* additionally requires a common molecular configuration space, admissible paths, reagent and electron accounting, and operational readout. Those premises are named rather than absorbed into the word "allowed."

A theorem at the first or second level remains a mathematical theorem even when its physical premises have not been established. Conversely, a familiar chemical name attached to a graph does not prove the third level.

1.2 Eight parts of the argument

The proof follows eight linked tasks. The registry and directed-address construction provide T1. The sharp incidence obstruction supplies T2. The corrected product constructors and formal graph paths address T3. Their common hybrid-control assembly supplies the nonvacuity result T4. Explicit propagation, refinement, and exchange

rules supply T5. Full endpoint comparisons give T6 and T7. The corrected junction gate and reset induction give T8. The notation T1–T8 refers to these logical roles rather than to eight interchangeable versions of the same claim.

The dependencies are directional. The registry bounds class-invariant output maps; it does not determine their chemical identities. The product library identifies output graphs; it does not assign codons. The assignment grammar uses more address information than the twenty-class quotient, which is essential because the standard code does not factor through that quotient. The junction controller distinguishes production, release, termination, and initiation. These maps can coexist because their domains and stage restrictions are explicit.

1.3 Why existence does not imply uniqueness

The routing rules in the construction are local but permissive. They allow exchanges at multiple addresses, and their reachable component contains tables other than the two reference endpoints. Recording that freedom is part of the result. A construction chosen with knowledge of a target can still prove existence if every rule application is checked under a fixed rule schema; it cannot on that basis prove that the target was independently selected.

No uniqueness or shortest-path claim is needed here. The positive conclusion is that the specified formal constraints are jointly consistent and that the named tables lie in the allowed reachable set. Narrowing that set is a subsequent scientific task: additional geometry, energetic inequalities, compatibility restrictions, or independent seed rules would have to exclude the alternatives. Such restrictions must be tested for nonvacuity again, since a collection of separately satisfiable constraints can have an empty common intersection.

2 Typed carrier and assembly specification

2.1 Precursor, residual carrier, and junction

Let H_0 be an ordered precursor with six original substituted chrysene cores $C_1, \dots, C_6$. Its designated pairs are (C_1, C_2), (C_3, C_4), and (C_5, C_6). For each pair write a proposed transformation

$$\Phi_j : (C_{2j-1}, C_{2j}; \mathcal{R}_j) \longrightarrow (n_j, X_j; \mathcal{B}_j), \qquad j = 1, 2, 3, \tag{1}$$

where $\mathcal{R}_j$ and $\mathcal{B}_j$ are, respectively, reagent and coproduct records. The notation records the intended incidence relation; it does not yet specify an atom-balanced reaction. A complete molecular realization must give an origin-preserving map on every atom, including atoms supplied by $\mathcal{R}_j$ and atoms remaining in $\mathcal{B}_j$.

The selected post-transformation representative is

$$\begin{gathered} H_A = ((X_1, A_1), (X_2, A_2), (X_3, A_3)), \\ t = (A_1, A_2, A_3) = AAA, \end{gathered} \tag{2}$$

with resident adenosines A_j. We call each (X_j, A_j) a *resident unit* and H_A a *triplet carrier*. This avoids using "vessel" for both an original pair and the whole triplet. The architecture includes the tether and the proposed intercalating role of X; the formal model records this incidence without prescribing atomic coordinates.

For a junction use two disjoint copies, $H_{A,L}$ and $H_{A,R}$, and a docking datum d. The assembly map is

$$B : (H_{A,L}, H_{A,R}, d) \longmapsto J. \tag{3}$$

The resident units are indexed $1, 2, 3$ on the left and $4, 5, 6$ on the right. Their facing reaction-bearing residual cores are X_3 and X_4. Every atom carries its copy index. Thus atom 5 of X_3 and atom 5 of X_4 are different atoms even though their local carbon indices agree. The junction contains six residual X cores and six resident adenosines and represents twelve original precursor cores.

> **Definition 2.1** (Three alphabets)**.** The *resident tether word* is the constant $t = AAA$. The *external coding word* is $c = b_1 b_2 b_3 \in \mathcal{B}^3$, where $\mathcal{B} = \{A, C, G, U\}$. The *precursor-output word* is $n(\Phi(m)) = (n_1, n_2, n_3)$ when an atom-mapped precursor transformation has been defined for marker state m. Equality between any two of these words is an additional relation, not a convention.

The symbols A in the resident and external alphabets have the same conventional base name but different object types. In particular, sixty-four variable external coding words can be addressed by a fixed poly-A carrier only if the model retains additional address and frame data. A bijection from marker states to variable precursor outputs is not a bijection to a constant resident word.

2.2 Patent convention and its scope

For the RNA convention of US12195423B1, order the binary pair as catalyst then substrate. The four-state lookup is

$$\begin{aligned} L(FF) &= A, \qquad L(FB) = C, \\ L(BF) &= G, \qquad L(BB) = U. \end{aligned} \tag{4}$$

Figure 5 supplies this convention; the DNA convention in the same patent differs. Example 10 and Figure 15 supply

the poly-A/chrysene context [Sch25]. The finite map L is used as a coordinate dictionary. It does not assert that an arbitrary resident poly-A carrier is the chemical image of every marker state under the same Φ.

Two documentary discrepancies prevent treating the patent as a completed atom-map certificate here. Sugar closure is described as 20–10 in Table 1 and 20–16 in Table 2 and Figure 7(i). A missing-site description also differs between indices 12 and 9. A molecular proof must choose and justify a consistent atom map before using those steps. The formal post-carrier construction in this paper starts from the typed H_A object and does not silently resolve either discrepancy. Example 7's precursor synthesis and characterization are not a certificate for the entire sequence-level conversion or the two-carrier sulfur system.

2.3 Orientation data and external addressing

Write $M_N = \{0,1\}^{2N}$ with $0 = F$ and $1 = B$. Complement F and site reversal R generate $G = \{1, F, R, FR\}$. The coordinate encoder $E : M_N \to \mathcal{B}^N$ applies L to consecutive pairs. Its role is mathematical: it assigns a word to an oriented marker description. An external docking map must then associate that addressed word with a presented coding strand.

The addressed model adds two binary reference tags. They select the complement and directional reference without changing the physical resident adenosines. The registry chapter constructs a global normal form and proves the resulting cardinalities. This choice makes the separation concrete: a quotient description of a carrier has twenty classes, a partly referenced description has thirty-six, and a fully referenced external address has sixty-four possible values. These are different retained-data spaces, not three counts of one unchanged object.

For the paired system the unconstrained external word has six letters and belongs to $\mathcal{B}^6$, with 4096 elements. The twelve-bit precursor space has 4096 marker descriptions too, but equality of cardinalities is not a molecular identification. Quotienting twelve bits by one global flip-and-reversal action gives 1056 classes; independently quotienting two six-bit halves gives $20^2 = 400$ pairs. Docking may retain or fix relative frames, so neither quotient can be substituted for the junction state space without specifying the docking action.

2.4 Registers and pairings

The external codon–carrier interaction is assigned a non-canonical docking relation $D \subseteq \mathcal{B}^3 \times \mathcal{H}_A$, where $\mathcal{H}_A$ is the typed carrier family. Symbolic Watson–Crick complementation, denoted κ, exchanges A/U and C/G. It is used in the frame algebra and in a separately stated junction relation. The symbol κ does not redefine D as canonical Watson–Crick pairing.

There are also two reversal operations. Ordinary word reversal changes letter order. Reversal of all six binary marker sites exchanges the two slots in every pair as well as reversing pair order. Under L it becomes $\tau\,\mathrm{rev}$, where τ exchanges C/G and fixes A/U. The distinction is checked directly in the next section and retained in the junction readout.

2.5 A shared state and stage discipline

The complete formal state is a tuple

$$z = (H, f, \Gamma, Q, e, \sigma, \rho, k). \tag{5}$$

Here H is an immutable architecture/provenance record of the prepared carrier incidence, resident-base identities, and copy identity; f records frame/address decorations; Γ is the persistent atom-and-bond graph with reservoir; Q is a library of certified terminal product graphs; $e \in [0,1]$ is the selector control; σ records seeds and current routing; ρ is the readout controller; and k records phase and resource use. A residue name is obtained from an identity map $I : Q \to \mathcal{P}$, where $\mathcal{P}$ is the set of twenty conventional names. Names are not legal instructions for changing atom or bond labels. The current bond graph is Γ, not H. Extraction may sever a core or tether bond in Γ while H retains its original provenance; persistence of H never asserts that an extracted scaffold remains an intact chrysene–adenosine molecule. Resident-base identities and original address conventions are retained labels, not a conservation law for every original covalent incidence.

Stages make the invariants precise. Assembly establishes the typed carrier. Product certification establishes graph identities under the formal grammar. A selected routing stage can impose the paired sulfur slot condition. A routing-release operation then allows later address changes. Reading and reset use fresh resource packets. No operation may reuse a consumed atom under a new copy label. The endpoint table need not satisfy a routing predicate that was explicitly retired at an earlier stage, but it must retain every invariant declared persistent.

The common model will therefore use a conjunction of typed invariants, rather than importing every condition in every source as a global invariant. A full physical interpretation would additionally supply a configuration map for (H, f, Γ) and paths compatible with all these stage transitions.

3 Finite registry states and their product capacity

The finite construction begins with six binary sites arranged into three specified pairs. Its complete frame-invariant information has twenty values. The conclusion concerns a quotient of descriptions; relating that quotient to chemical objects requires a realization map. We make this distinction explicit before defining production or using a genetic-code table. This section supplies three interfaces for the subsequent construction: the quotient map, an addressed carrier with a variable external codon and a fixed physical tether, and the exact obstruction to a one-product-per-class assignment compatible with the standard table under Watson–Crick transport.

3.1 Sites, pairs, and transported letters

Definition 3.1 (Typed finite carrier)**.** For $N \geq 1$, put $M_N = \mathbb{F}_2^{2N}$, where $\mathbb{F}_2 = \{0, 1\}$ and all bit sums are modulo two. The $2N$ coordinates are *positional reading slots*. The selected elementary pairs are $V_i = (2i-1, 2i)$, $1 \leq i \leq N$. A formal six-core system has the fixed architecture

$$H_3 = (c_1, s_1, c_2, s_2, c_3, s_3), \qquad V_i = (c_i, s_i),$$

with one original catalyst core and one original substrate core assigned to each pair. Their species labels are extra decorations, transported with the slots when a presentation is reversed. They are not binary values. A proposed transformation may send these three pairs to three units X_A; the six original cores, three transformed units, three binary pairs, and whole reaction system are different types. An external initiator is not one of the six original cores. A junction of two such systems has twelve original cores.

This typing follows the local pair construction of [Sch26g, Sch26c], while fixing the six-original-core and three-transformed-unit architecture used here. The architecture is a realization premise, not a consequence of the finite count. Six successive slots have five adjacent gaps. Only the three selected disjoint pairs are the interfaces used by the encoding. If each selected pair supplies exactly one ordered output letter, their concatenation has length three; the one-output rule is an additional premise, as in [Sch26k].

Let $V = \mathbb{F}_2^2$ and write its elements $00, 01, 10, 11$. For a fixed reference bit f, the alternative coordinates

$$B_f(x, y) = (x + y, y + f),$$
$$B_f^{-1}(b_1, b_2) = (b_1 + b_2 + f, b_2 + f)$$

are a bijective recoding. The local registry is $x + y$, with blocks $\{00, 11\}$ and $\{01, 10\}$. Define $\rho(x, y) = (x+1, y+1)$ and $s(x, y) = (y, x)$. In the B_f coordinates,

$$\rho(b_1, b_2) = (b_1, b_2 + 1), \qquad s(b_1, b_2) = (b_1, b_1 + b_2).$$

Thus $\langle \rho, s \rangle$ is the four-element group preserving each local registry block. Its unique fixed-point-free element is ρ; the other two nonidentity elements exchange one block and fix the other pointwise. These formulas use positional slots. A species-pinned chemical coordinate convention must separately be shown to give the same action; changing both raw markers and their reference bit in one passive recoding would double-count that change.

Definition 3.2 (Global action and WC encoding)**.** On M_N define

$$F(m_1, \ldots, m_{2N}) = (m_1 + 1, \ldots, m_{2N} + 1),$$
$$R(m_1, \ldots, m_{2N}) = (m_{2N}, \ldots, m_1).$$

The commuting involutions generate $G = \{1, F, R, FR\}$. Let $\mathcal{B} = \{A, C, G, U\}$, $W_N = \mathcal{B}^N$, and set

$$L_{\mathrm{WC}}(00) = A, \quad L_{\mathrm{WC}}(01) = C,$$
$$L_{\mathrm{WC}}(10) = G, \quad L_{\mathrm{WC}}(11) = U.$$

The encoding $E : M_N \longrightarrow W_N$ applies L_{WC} to the N selected pairs. On letters write $\kappa = (A\ U)(C\ G)$ and $\tau = (C\ G)$, extending both componentwise to words; rev reverses word positions.

Proposition 3.3 (Explicit transport)**.** *The encoding E is bijective and satisfies*

$$EF = \kappa E, \qquad ER = \tau \,\mathrm{rev}\, E.$$

In particular the transported action on words is $\{1, \kappa, \tau\,\mathrm{rev}, \kappa\tau\,\mathrm{rev}\}$.

Proof. Each local letter has a unique two-bit inverse, so concatenating the inverses recovers every marker coordinate. Complementing a pair exchanges 00 with 11 and 01 with 10, which becomes κ. Reversal of the $2N$ slots reverses pair order and exchanges the two entries of each pair. The latter fixes $00, 11$ and exchanges $01, 10$, which becomes τ. These identities prove the assertion on both generators and hence on the group. □

In particular R is not ordinary reversal of the external word. Nor is it the usual reverse-complement map $\kappa\,\mathrm{rev}$. Confusing these maps changes the equivalence relation. Complementary pairing is structurally present in the WC encoding, but this assertion has not yet selected any amino

acid.

3.2 The complete quotient and the twenty classes

Let $q_N : M_N \longrightarrow X_N = M_N/G$ be the orbit map. Define the full adjacent-difference sequence and its reversal class by

$$D(m) = (m_1 + m_2, \dots, m_{2N-1} + m_{2N}),$$
$$\overline{D}(m) = \{D(m), \operatorname{rev} D(m)\}.$$

Unlike the selected pair decomposition, D uses all $2N-1$ adjacent gaps.

Theorem 3.4 (Complete invariant and factorization)**.** *For $m, n \in M_N$, $q_N(m) = q_N(n)$ if and only if $\overline{D}(m) = \overline{D}(n)$. Consequently*

$$X_N \simeq \mathbb{F}_2^{2N-1}/\langle \mathrm{rev} \rangle.$$

For every set Y, a function $h : M_N \to Y$ is G-invariant if and only if it has a unique factorization $h = \overline{h}\, q_N$.

Proof. Given $d = (d_1, \dots, d_{2N-1})$, choose m_1 arbitrarily and recursively set $m_{j+1} = m_j + d_j$. This gives exactly two preimages, differing by F; hence D is onto and $D(m) = D(n)$ exactly when $n = m$ or Fm. Direct computation gives $D(Fm) = D(m)$ and $D(Rm) = \operatorname{rev} D(m)$. Equality of reversal classes therefore implies $n \in \{m, Fm, Rm, FRm\}$, and the converse follows from the same identities. Finally an invariant function is constant on each orbit, so $\overline{h}(q_N(m)) := h(m)$ is well defined. Surjectivity of q_N gives uniqueness; any such composition is invariant. □

Theorem 3.5 (Orbit count and stabilizers)**.** *For every $N \geq 1$,*

$$|X_N| = C_N := 2^{2N-2} + 2^{N-1}.$$

There are 2^{N-1} two-element orbits stabilized by R, 2^{N-1} two-element orbits stabilized by FR, and $2^{2N-2} - 2^{N-1}$ four-element orbits. At $N = 3$ the 64 descriptions form 20 classes, eight of size two and twelve of size four. A class has size two exactly when D is palindromic; its stabilizer is $\{1, R\}$ when the central entry D_N is zero and $\{1, FR\}$ when it is one.

Proof. The fixed-point counts of $1, F, R, FR$ are, respectively, $2^{2N}, 0, 2^N, 2^N$: F fixes no bit; an R-fixed string is determined by its first N entries; and an FR-fixed string is determined in the same way with the other half complemented. For completeness, the finite orbit-counting identity follows by counting pairs (g, m) with $gm = m$. On an orbit O their number is $|O|\,|\operatorname{Stab}(m)| = |G|$. Thus

$$|X_N| = \frac{1}{4}(2^{2N} + 0 + 2^N + 2^N) = C_N.$$

The R-fixed and FR-fixed sets are disjoint, since their intersection would be fixed by F. Each consists of complementary pairs and therefore contributes 2^{N-1} orbits of size two. All remaining stabilizers are trivial, giving the stated number of size-four orbits. Finally, a palindromic D implies $D(Rm) = D(m)$, so $Rm = m$ or Fm by Theorem 3.4. These are exactly the two size-two cases. Their central pairs satisfy $m_N = m_{N+1}$ or $m_N = m_{N+1} + 1$, respectively, which proves the last assertion. □

These are finite theorems reconstructed from [Sch26g, Sch26i]; no production hypothesis or genetic-code table occurs in their proofs. For reproducible class names we use $O_1, \dots, O_{20}$ with the D representatives in Table 1. Every representative d determines the class by the recursion in Theorem 3.4 with $m_1 = 0$. The source-project tables also give all 64 marker incidences and every encoded word under each of the three letter assignments below.

3.3 A fixed physical tether and three levels of retained data

A fixed physical tether AAA cannot simultaneously be the variable external word $E(m)$: the former is one specified decoration, whereas the latter ranges over 64 words. The following finite construction keeps those types separate and states exactly what data must be retained for each count.

Definition 3.6 (Decorated presentation spaces)**.** Let t_{phys} be the single physical-type tag AAA, attached to the three transformed units (X_A, X_A, X_A). It records three fixed adenine-bearing attachments; it is not a codon variable. Let $a \in \mathbb{F}_2$ be a reference tag and $d \in \mathbb{F}_2$ a direction tag. Define

$$\Omega_{\mathrm{addr}} = M_3 \times \mathbb{F}_2 \times \mathbb{F}_2 \times \{t_{\mathrm{phys}}\},$$
$$\Omega_{\mathrm{ref}} = M_3 \times \mathbb{F}_2 \times \{t_{\mathrm{phys}}\}.$$

On the addressed space the action is

$$F(m, a, d, t) = (Fm, a + 1, d, t),$$
$$R(m, a, d, t) = (Rm, a, d + 1, t).$$

On the reference-only space omit d and its update. Both actions leave the physical tag t unchanged.

The tags specify how a chosen physical reference is represented. In particular no generator changes an adenine attachment into a uracil attachment. The transformation

law for the tags is an explicit finite premise. The chemical name AAA alone does not establish it.

Theorem 3.7 (Addressed, reference-only, and unadorned counts)**.** *The three quotient spaces are related by forgetting decorations and have cardinalities*

$$|\Omega_{\mathrm{addr}}/G| = 64, \qquad |\Omega_{\mathrm{ref}}/G| = 36, \qquad |X_3| = 20.$$

Every addressed orbit has a unique representative $(n, 0, 0, t_{\mathrm{phys}})$*, where* $n = F^a R^d m$*. Thus* $\Omega_{\mathrm{addr}}/G \simeq M_3$ *and*

$$c_{\mathrm{ext}}([m, a, d, t]) = E(F^a R^d m)$$

is a well-defined bijection onto the external codon space W_3*. The reference-only quotient is naturally* $M_3/\langle R\rangle$*.*

Proof. Applying $F^a R^d$ normalizes both tags to zero, producing the displayed representative. An element preserving two zero tags has no F or R component, so this representative is unique. This proves the first bijection and the assertion about c_{ext}. With only the reference tag, applying F^a normalizes a but leaves the residual action $\{1, R\}$ on $n = F^a m$. Its orbit count is $(64 + 8)/2 = 36$, since R fixes eight six-bit strings. Forgetting both tags gives M_3/G and the value twenty from Theorem 3.5. Each forgetful map is equivariant and hence induces the stated quotient map. □

This is an explicit nonempty model: take every m, both tag values, the fixed six-core architecture, one external initiator, and the fixed physical tether. There are 256 addressed presentations and 64 addressed objects. The one-initiator constraint $|n_I - 1| < 1$ is satisfied throughout. All four local pair states and their full threefold product are allowed by construction. Choose twenty distinct formal products p_O, $O \in X_3$, and set

$$p([m, a, d, t]) = p_{q_3(F^a R^d m)} = p_{q_3(m)}.$$

This is a total invariant product map, while c_{ext} ranges over all 64 words and t_{phys} remains fixed. It proves simultaneous satisfiability of these finite requirements. It does not prove that all such marker states can be chemically prepared or that p_O are amino acids.

More generally the counts for residual subgroups $\{1\}$, $\langle F\rangle$, $\langle R\rangle$, $\langle FR\rangle$, and G are respectively $64, 32, 36, 36, 20$. Each follows from its fixed-point count. A tether or initiator must be assigned a precise retained-data action before one selects among these numbers. In particular sixty-four addressed objects and twenty registry classes are not competing cardinalities for the same domain.

3.4 When production descends and when it saturates

Assumption 3.8 (Coordinate-consistent production)**.** Let $\mathcal{A} \subseteq M_N$ be a G-stable productive domain. Its presentations come with a map $\pi : \mathcal{A} \to \mathcal{C}$ into a set of objects satisfying $\pi(gm) = \pi(m)$. There are a deterministic local output $h : \mathcal{A} \to Y$ and a single object output $P : \mathcal{C} \to Y$ such that $h(m) = P(\pi(m))$ for every $m \in \mathcal{A}$.

This is the compatibility requirement that different permitted descriptions of one object give the same output. It does not assume that markers completely classify physical objects: π need not induce a bijection $X_N \to \mathcal{C}$. Alternatively one can directly assume $h(gm) = h(m)$ without introducing $\mathcal{C}$.

Theorem 3.9 (Realized-domain capacity)**.** *Let* $\mathcal{A} \subseteq \mathcal{R} \subseteq M_N$ *be* G*-stable productive and realized domains. Under Assumption 3.8,* h *factors uniquely through* $\mathcal{A}/G$ *and*

$$|\operatorname{im} h| \le |\mathcal{A}/G| \le |\mathcal{R}/G| \le C_N.$$

Equality $|\operatorname{im} h| = C_N$ *holds if and only if* $\mathcal{A}$ *represents every class in* X_N *and the descended map on those classes is injective.*

Proof. For $g \in G$, coordinate consistency gives $h(gm) = P(\pi(gm)) = P(\pi(m)) = h(m)$. The orbit-factorization proof of Theorem 3.4 applies on $\mathcal{A}$. The first inequality is the cardinality bound for the image of a finite function; the next two follow from inclusion of represented class sets. Equality at the two ends forces equality at every stage. The last bound is an equality exactly when $\mathcal{A}/G = X_N$; the first is an equality exactly when the descended function is injective. Conversely those two conditions give an image of cardinality C_N. □

Corollary 3.10 (Twenty-product saturation)**.** *At* $N = 3$*, suppose all twenty classes are productive and their invariant products are distinct. Then exactly twenty product values occur. If, in addition, these values lie in a specified twenty-element amino-acid set* $\mathcal{P}$*, every member of* $\mathcal{P}$ *occurs. Amino-acid-valuedness without this identification only concludes that twenty amino acids occur, not which twenty.*

Proof. Apply Theorem 3.9; an injective function between two sets of cardinality twenty is surjective. □

Several minimal counterexamples show why the premises

are separate. The map $h(m) = m_1$ uses markers alone and has no initiator argument, yet $h(Fm) = 1-h(m)$; omission of an argument does not establish covariance. Allowing only the local state 00 independently in every vessel gives an independent product domain of size one, not 4^N. On one complete orbit a constant product is total and injective on its one-point class quotient, but realizes only one product. On all M_3 a constant map is total and invariant, yet it does not saturate the bound. Thus local fullness, class coverage, output consistency, and distinctness cannot replace one another.

If a laboratory sample is merely a set of representatives $S \subset M_N$, not G-stable, the relevant represented domain is $q_N(S)$, not the quotient by an action on S that has not been defined. An invariant extension to GS has capacity at most $|q_N(S)|$. These domain distinctions are the repaired production interface needed for the use of [Sch26k].

Proposition 3.11 (Localization requires its own selector premise)**.** *A configuration-independent vessel index j_0 invariant under reversal must satisfy $j_0 = N+1-j_0$. It therefore exists exactly when N is odd and is the middle index. By contrast, a configuration-dependent selector $j : M_N \to \{1, \dots, N\}$ satisfying*

$$j(Fm) = j(m), \qquad j(Rm) = N + 1 - j(m)$$

exists on all M_N exactly when N is odd, but need not select the middle vessel on every state.

Proof. The constant case is the displayed fixed-index equation. For any total selector, R fixes the zero string, so the same equation applies to $j(0)$ and requires odd N. For odd N the constant middle selector proves existence. To disprove universal centrality take $N = 3$ and define

$$j(m) = \begin{cases} 2, & D(m) = \operatorname{rev} D(m), \\ 1, & D(m) <_{\text{lex}} \operatorname{rev} D(m), \\ 3, & D(m) >_{\text{lex}} \operatorname{rev} D(m). \end{cases}$$

Complementation fixes D, while reversal exchanges its two lexicographic comparisons, so the required identities hold. For $m = 000001$ the selector is 1. There are eight palindromic sequences D with two preimages each; hence sixteen descriptions select the middle, and the remaining forty-eight split equally between the endpoints. □

An invariant product places no further restriction on this selector: it can be paired with a constant product or with $p_{q_N(m)}$. Likewise a coarse invariant can determine a valid nonsaturated product. At $N = 3$ the tuple $(|D|, |O|, D_3)$ has twelve cells, four singleton and eight double cells, as can be checked from the twenty D representatives. Therefore any output depending only on this tuple has at most twelve values; it is saturation at twenty, not mere determinacy, that it cannot support.

3.5 Which pairing is transported

Proposition 3.12 (Partition transport)**.** *Let Π be a partition of a four-letter target alphabet into two blocks of size two. Let K_Π be the permutations preserving each block, and let c_Π exchange the two members of both blocks. For a bijection $L : V \to \mathcal{B}$, the following are equivalent:*

1. *L carries the registry partition $\{\{00, 11\}, \{01, 10\}\}$ to Π;*
2. *$L\rho L^{-1} = c_\Pi$;*
3. *$L\langle \rho, s\rangle L^{-1} = K_\Pi$.*

They also imply that componentwise L transports the word-frame action and its orbit partition, with the reversal generator carried to either of the two possible reversal generators. There are exactly eight such L for each Π.

Proof. The two registry blocks are exactly the ρ-orbits, and the target blocks are exactly the c_Π-orbits, proving the equivalence of the first two conditions. A partition-preserving bijection conjugates the full within-block permutation groups, proving the third. Conversely a conjugacy of these groups carries their orbit partitions to one another. Within each group the unique fixed-point-free element is the double transposition, so the same conclusion also follows by identifying ρ. Componentwise L commutes with reversal of positions. It sends ρ to c_Π and s to one of the two single transpositions in K_Π. Exchanging which single transposition is designated replaces the word-reversal generator by its product with global complementation and leaves the generated group unchanged. There are two choices of block matching and two choices within each block, giving $2 \cdot 2 \cdot 2 = 8$ bijections. □

The underlying four-point permutation action matters: an unspecified abstract Klein four-group need not have a unique fixed-point-free element. For example, its regular action has three. The theorem uses the specified two-block action, as does the transport result in [Sch26i].

The three representative assignments, listed in the order $(00, 01, 10, 11)$, are

$$L_{\text{WC}} = (A, C, G, U),$$
$$L_{\text{RY}} = (A, C, U, G),$$
$$L_{\text{MK}} = (G, A, C, U).$$

Their transported complement partitions are respectively

$$\{A,U\} \mid \{C,G\},$$
$$\{A,G\} \mid \{C,U\},$$
$$\{A,C\} \mid \{G,U\}.$$

For L_{MK} the transported complement is $(G\ U)(A\ C)$, not Watson–Crick complement. The two assignments may coexist as differently named maps; they cannot both identify the same transported involution with the same physical pairing. This makes explicit the choice entering [Sch26c].

3.6 The exact standard-table matching obstruction

Let $\mathcal{P}$ be the twenty standard amino-acid labels, written below in the usual one-letter notation. Let $g : W_3 \to \mathcal{P} \cup \{\mathrm{STOP}\}$ be the supplied standard genetic code, transcribed from the active Table 6 of [Sch26c]. For a chosen L, let $E_L : M_3 \to W_3$ apply L to the three consecutive two-bit pairs, so $E_{L_{\mathrm{WC}}} = E$. Define

$$\mathcal{N}_L(O) = \{g(E_L(m)) : m \in O\} \setminus \{\mathrm{STOP}\}.$$

A compatible injective class assignment is a matching in the bipartite graph with left vertices X_3, right vertices $\mathcal{P}$, and edges $a \in \mathcal{N}_L(O)$. Compatibility here means that the standard table already places the label at some codon in that class. The graph is table-informed; constructing or optimizing its matching does not independently derive g.

Theorem 3.13 (Sharp partition-dependent matching numbers)**.** *The maximum number of distinct compatible class assignments is* 18 *under WC,* 19 *under RY, and* 20 *under MK. Each value is the same for all eight bijections transporting its indicated partition. In the WC graph the nine classes*

$$S = \{O_2, O_4, O_6, O_8, O_{12}, O_{13}, O_{17}, O_{18}, O_{20}\}$$

have exactly the seven neighbors $\{\mathrm{Ala}, \mathrm{Cys}, \mathrm{Gly}, \mathrm{Pro}, \mathrm{Arg}, \mathrm{Ser}, \mathrm{Thr}\}$.

Proof. Table 1, obtained directly by the displayed encoding and the specified table g, gives the complete neighbors of each row. Their union for S is $\{A, C, G, P, R, S, T\}$. In any matching at most seven of those nine rows can be matched, while at most eleven rows outside S can be matched. The upper bound is therefore eighteen. The WC witness column of the table contains eighteen distinct right vertices, each in its row's neighborhood, so the bound is attained.

For RY, consider the nine rows

$$\{2, 6, 8, 12, 13, 14, 17, 18, 20\}.$$

Their eight neighbors are $\{A, F, I, L, P, S, T, V\}$. The same argument bounds a matching by nineteen, and the RY witness column attains that size. The MK witness column matches every one of the twenty rows to a different label, which is the largest possible size.

Finally let L, L' transport the same partition. The permutation $h = L^{-1}L'$ preserves the source registry partition. By Proposition 3.12, componentwise h permutes the twenty source orbits. Since $L' = Lh$, it carries the graph for L' to the graph for L merely by this permutation of rows, leaving right labels unchanged. Matching numbers are invariant under that graph isomorphism. The eight choices per family exhaust all twenty-four bijections. □

The eighteen value counts simultaneous distinct assignments, not registry classes: all twenty classes still exist. The displayed maximum matching leaves O_{13}, O_{20} and the labels Asn, Val unused, but these omissions belong to that witness and do not identify two chemically impossible amino acids. No reweighting of unchanged edges or registry-preserving relabelling can overcome the proved upper bound.

Lemma 3.14 (Scope of a two-edge enlargement)**.** *Raising a graph's matching number from eighteen to twenty requires at least two new edges. For the WC graph, adjoining* (O_{13}, Asn) *and* (O_{20}, Val) *is sufficient.*

Proof. A matching using one new edge loses at most one member when that edge is removed; hence one added edge raises the maximum by at most one. For sufficiency append the two displayed edges to the WC witness in Table 1; all twenty left and right vertices are then distinct. □

This enlargement is an illustrative finite construction, not a license for those two chemical compatibilities. Neither added edge is present under the unchanged table-adjacency definition. The appropriate route when a mechanism retains additional context is instead to specify a refined state space Z, a forgetful map $r : Z \to X_3$, and an independently justified state–product relation on Z. A target-covering matching there means that each target has a distinct refined witness. It need not assign only one product to each original class and must not be reported as a perfect matching of the old graph.

For a concrete finite illustration, take $Z = W_3$ and the relation $\{(w, g(w)) : g(w) \neq \mathrm{STOP}\}$. It has a target-covering matching of size twenty: choose one codon in each nonempty amino-acid fibre of g; these codons are necessar-

			Complete amino-acid neighborhoods			Matching witnesses		
O_i	D	$\lvert O_i\rvert$	WC	RY	MK	WC	RY	MK
1	00000	2	FK	GK	FG	K	K	G
2	00100	2	T	TV	DS	T	V	D
3	01010	2	IY	ER	CV	Y	R	V
4	01110	2	S	AM	A	S	M	A
5	10001	2	DL	RY	IR	D	Y	R
6	10101	2	AR	LS	HT	R	S	T
7	11011	2	QV	CH	LS	Q	H	S
8	11111	2	GP	FP	KP	P	F	P
9	00001	4	ELN	GNR	FGIR	L	N	F
10	00010	4	ILN	EGKR	GLVW	I	E	W
11	00011	4	FKQV	GNQW	GLR	F	G	L
12	00101	4	ACRT	LSTV	DHST	C	L	H
13	00110	4	CRST	AITV	AESY	–	T	Y
14	00111	4	GPTW	LPTV	ENPS	W	P	E
15	01001	4	DLMY	DRS	MRV	M	D	M
16	01011	4	HIV	DQS	CLSV	H	Q	C
17	01101	4	ARS	AILS	AQTY	A	I	Q
18	01111	4	GPRS	AILP	AKP	G	A	K
19	11001	4	EHLV	CHRY	ILR	E	C	I
20	11101	4	AGPR	FLPS	NPQT	–	–	N

Table 1: All twenty classes and their standard-table incidence under the three stated letter assignments. Strings such as $ACRT$ denote sets of one-letter amino-acid labels, not codons. Dashes mark unmatched rows. Every witness entry lies in its corresponding neighborhood, and each witness column contains no repeated amino-acid label. Class numbering follows active Article 47, Table 1; the neighborhoods and witnesses are independently recomputed. Full codon and marker incidences are supplied in the source project.

ily distinct. This construction is again table-informed. A mechanistic refinement must derive or posit its own relation and establish reachability of the selected states, rather than import those outputs without saying so. Its capacity is bounded by the number of productive refined states, not automatically by twenty.

Proposition 3.15 (The even-fibre obstruction)**.** *For any G-invariant map $h : M_3 \to Y$, each fibre has even cardinality. Consequently no map factoring through X_3 equals the standard code on all 64 WC-encoded descriptions. Postcomposing such a map with any deterministic function does not remove the obstruction.*

Proof. Every fibre is a union of orbits of sizes two and four by Theorem 3.5. The standard-code fibres of Met and Trp each have size one; the STOP fibre has size three. Since E is bijective, gE has the same fibre cardinalities and cannot be invariant. A postcomposition remains G-invariant and the same argument applies. □

Theorem 3.16 (Minimal registry-preserving refinement)**.** *Let $q_W = q_3E^{-1} : W_3 \to X_3$. Suppose an onto state map $z : W_3 \to Z$ retains both the original registry class and the standard output: there are maps $u : Z \to X_3$ and $v : Z \to \mathcal{P} \cup \{\mathrm{STOP}\}$ such that $q_W = uz$ and $g = vz$. Then $|Z| \geq 61$. Equality is attained by the image of $w \mapsto (q_W(w), g(w))$. Its only nonsingleton fibres are*

$$\{\mathrm{AGU}, \mathrm{UCA}\}, \quad \{\mathrm{AGC}, \mathrm{UCG}\}, \quad \{\mathrm{CUU}, \mathrm{UUG}\},$$

with outputs Ser, Ser, and Leu, respectively. If a second decoder h is constant on each of these three doublets, the same 61-state refinement simultaneously retains q_W, g, and h.

Proof. If $z(w) = z(w')$, the two factorization identities force both $q_W(w) = q_W(w')$ and $g(w) = g(w')$. Thus every z-fibre is contained in a fibre of (q_W, g), so Z has at least as many elements as the image of that pair. The pair map itself realizes equality. Directly comparing g within the complete WC orbit incidences gives the three displayed doublets and no other coincidences; the source-project certificate lists all 61 cells. Equivalently, the numbers of distinct outputs per orbit have histogram $\{1 : 1, 2 : 7, 3 : 2, 4 : 10\}$, counting STOP as an output. Their sum is $1 + 14 + 6 + 40 = 61$, or $64 - 3$ by the doublet description. Every other cell is a singleton. A second decoder descends to this refinement exactly when it is constant on the three doublets, proving the final assertion. □

The obstruction fixes the interface to an addressed reading or reachability model. Such a model must retain enough information to distinguish descriptions within nineteen of the twenty old registry classes, or else change its output specification. The 36-state reference-only quotient is insufficient for a state variable satisfying both factorization requirements of Theorem 3.16. The addressed carrier in Theorem 3.7 provides a consistent finite place for that information while leaving the physical AAA decoration fixed. Theorems 3.9 and 3.10 continue to apply to an invariant class-level product branch, but their hypotheses must not silently be imposed on a distinct, frame-addressed codon-reading branch.

4 A source-guided product grammar and twenty structural witnesses

This section supplies an explicit family of *complete constitutional product graphs*, rather than assigning twenty names to twenty retained sets. The resulting theorem is a new, restricted *formal graph-reachability* result. It is not a reaction-mechanism theorem. Its inputs are prepared aminoacyl-bearing vessel graphs, its operations are atom-preserving bond bookkeeping, and its endpoints include every coproduct and unused resource. The additional steps from the original six-core precursor to those inputs, and from a graph path to a chemically admissible trajectory, are stated separately. This distinction permits a nonempty mathematical construction without presenting unverified chemistry as a proof.

4.1 Four levels of product assertion

For a residue name r, distinguish the following assertions:

1. a retained-carbon motif S_r is listed;
2. a decorated heavy-atom graph P_r has the required constitutional connectivity;
3. a finite, globally atom-balanced path reaches P_r in a declared formal rewrite grammar;
4. that path has a compatible molecular, stereochemical and geometric realization under the chosen conditions.

Article 57 supplies the first level and selected interpretive information, including cuts and removals; its definition of a structure does not itself supply all atom maps, hydrogen transfers, reagent completions or mechanisms [Sch26h, Sec. 6 and App. A]. The construction below establishes the second and third levels for a new relaxed grammar. The fourth level remains a conditional lift. Even a fourth-level

existence result would not, by itself, prove dominance, yield or a uniquely selected code.

The source's several occurrences of eighteen have different meanings. There are eighteen non-sulfur names, of which sixteen use the ordinary retention family, one is backbone-only and one is extended-ring. The literal ordinary family covers eighteen of all twenty source rows because it also covers both sulfur rows. Matching demands in an assignment graph form a third, unrelated object.

4.2 Persistent atoms, open interfaces, and the prepared input

An atom identity is a tuple (b, j, ℓ): batch-copy identity, vessel identity, and local atom name. Equal locants on distinct copies never identify atoms. Every atom has a fixed element, optional isotope, and an origin tag. Core carbons are tagged by their original chrysene and locant; c_α and c' are the two arm-derived backbone carbons; heteroatoms retain their individual source identities. A proton or hydrogen transferred to a remnant is still present in the global state. "Removed entire" means removal from all its original incidences, not annihilation of the carbon.

Let V_X be the eighteen locants in the cyclic order

$$(6, 6a, 7, 8, 9, 10, 10a, 10b, 11, 12, 12a, 1, 2, 3, 4, 4a, 4b, 5).$$

The initial carbon graph consists of this cycle and the chords $4a : 12a$, $4b : 10b$, and $6a : 10a$. The certificate chooses a Kekulé form by doubling alternate perimeter edges, starting with $6{:}6a$; all other core edges have order one. This is a declared formal input completion, not a measured bond-localization claim.

The prepared local scaffold contains

$$\begin{gathered} 5 - c_\alpha(H)(n_\alpha H_2) - c'(= o_x) - o_t, \\ 6 - o_6 H, \qquad 12 - o_{12} - B_{12}, \qquad o_t - B_t. \end{gathered} \tag{P1}$$

Here B_{12} and B_t are *boundary ports*, not atoms or elements. They record one bond into an omitted external context. In the intended carrier interpretation o_t is the resident adenosine $2'$ oxygen. Grafting requires an actual context whose boundary atoms have those available valences. The ports are conserved, never counted in molecular formulas, and cannot enter a product graph. The exact 6,12-arm completion in (P1), including its initial Kekulé form, is *new formal data*; its realization by the patent-derived carrier is not asserted here.

Article 54 constructs the attached motif $5 - c_\alpha(H)(NH_2) - c'(= o_x) - o_{2'}$ through capture, unsaturation, oxygen addition, carbonyl rearrangement, amino installation, and acyl transfer [Sch26a, Sec. 8 and App. B]. Its donor completions and continuous lifts are premises. In particular, its motif is still attached at 5 and esterified to adenosine. It is not twenty free amino acids. Moreover, its protected chrysene edges cannot remain protected during the subsequent fragmentation. We therefore use two explicitly different phases: backbone assembly preserves all core edges, while extraction preserves only the guards specified below. The transition between these phases is an added permission, not a theorem of Article 54.

> **Definition 4.1** (Finite resource packet)**.** Each prepared active scaffold receives three individually labelled ammonia molecules, three individually labelled waters, and eight individually labelled hydrogen molecules. The water oxygens are o_0, o_1, o_2, and the ammonia nitrogens are n_1, n_2, n_3. The paired sulfur construction additionally receives one labelled $H - s_3 - s_4 - H$ graph. These are *formal donor packets*; their use asserts neither a practical reagent choice nor a favorable mechanism. Unconsumed molecules remain in the state.

The eight H_2 molecules are a finite sufficient bound for these certificates. They are not an inferred stoichiometric requirement for a real synthesis. Each ordinary open module contains 75 actual atoms and two ports, with inventory $C_{20}H_{44}N_4O_7$. The two-module sulfur packet has 154 actual atoms and four ports, with inventory $C_{40}H_{90}N_8O_{14}S_2$.

4.3 The grammar and its restrictions

A formal state has persistent atoms A, bond orders $b_{uv} \in \{0, 1, 2, 3\}$, fixed neutral charge tags, and nonnegative unused valence counts

$$\begin{gathered} d_a = v(a) - \sum_u b_{au}, \\ v(C) = 4, \quad v(N) = 3, \\ v(O) = v(S) = 2, \quad v(H) = 1. \end{gathered} \tag{P2}$$

Ports have capacity one but are not atoms. The d_a are bookkeeping half-bond counts. Calling them physical radical states would require additional electronic-state data, which this construction does not supply. A terminal closed-valence state has $d_a = 0$ at every atom and port.

There are two bond primitives, independent of residue names:

Split. Decrease one positive bond order b_{uv} by one, increasing d_u, d_v by one.

Join. Increase b_{uv} by one when both unused valences are positive and the resulting bond order is at most three.

Both preserve atoms, element labels, isotope labels, origin labels and formal charge. They are graph operations,

not proposed elementary reactions. We do *not* use their unrestricted closure as a chemical theorem.

For the restricted extraction grammar, choose an extraction mask before executing these operations. Set

$$A_6 = \{1, 2, 3, 4, 4a, 12a\}, \quad B_6 = \{4a, 4b, 10b, 11, 12, 12a\}.$$

The ordinary masks are $\{5\} \cup \{6\}^{\eta} \cup I$, where $\eta \in \{0, 1\}$ and I is either empty or a connected arc of B_6 containing $4b$. The entire ring is represented once by a separate closed-ring tag. The other allowed masks are the empty backbone-only mask and the extended mask $\{5, 4b, 10b\} \cup A_6$. These are carbon-graph shapes, not residue-labelled rules. The extended mask is new explicitly declared input; contact with a fusion vertex does not imply it.

Definition 4.2 (Source-guided extraction guards)**.** A mask S, at most two whole-removed neighboring core vertices W, and at most one optional internal retained edge D determine the local support. The fixed guards are:

1. No new atom or carbon source is introduced. Product carbons are exactly $S \cup \{c_\alpha, c'\}$; resource carbon and carbon transfer between copies are forbidden.
2. A core–core bond can be changed only if its original edge is incident to $S \cup W$. Core–core joins are permitted only at original chrysene adjacencies. Existing core edges wholly outside $S \cup W$ remain unchanged, including their bond orders.
3. All core–core extraction-boundary bonds are removed, all original heavy-atom incidences of vertices in W are removed (new hydrogen capping is allowed), and all retained core adjacencies except possibly the one edge in D remain present in the endpoint. Changes between single and double orders are allowed locally. The witness uses $D = \{10b{:}11\}$ for two rows and $D = \{4b{:}10b\}$ for one row.
4. The backbone bonds $c_\alpha - c'$, $c_\alpha - n_\alpha$, and $c' = o_x$ are protected throughout extraction. The bond $5 - c_\alpha$ is protected unless the backbone-only mask is chosen. Nitrogen closure onto n_α is permitted without replacing it.
5. Added side-chain heavy atoms are drawn only from the finite oxygen, nitrogen and sulfur stock. Their new bonds meet the retained mask, another such donor atom, or the permitted backbone closure site. All such bonds obey (P2). No donor atom is relabelled as a core atom.
6. Free-acid release changes $c' - o_t$ to $c' - o_0$, with the displaced hydrogens and o_t retained in the external-context coproduct. The carbonyl oxygen remains the same atom o_x. This is a new formal hydrolysis completion, not a consequence of merely drawing an ester.

The complete machine-readable certificate supplies exact hydrogen partners, not just an implicit "hydrogen reservoir." All spectator components and unused resources occur in both ends of the atom map.

Lemma 4.3 (Guarded edit-word construction)**.** *Let b, b' be two states on the same atom set obeying (P2), with the same protected bonds. Suppose every differing edge is permitted by a fixed local support and every inserted adjacency is allowed by its guards. First split $(b_{uv} - b'_{uv})_+$ units on each edge, then join $(b'_{uv} - b_{uv})_+$ units. This is a finite permitted valence-port path, of length $\sum_{\{u,v\}} |b_{uv} - b'_{uv}|$, preserving all protected bonds.*

Proof. After the split phase, the bond vector is the componentwise minimum of b and b'. Every subsequent partial join vector is bounded componentwise by b', so no atom capacity is exceeded. Splits cannot exceed a capacity. The guards hold edge by edge by hypothesis; equal protected edges are never changed. Every primitive fixes the atom set and its labels. Counting changed bond-order units gives the length. □

Without guards this lemma is a universal bond-graph reconstruction result. Its unrestricted version is only a consistency lemma. Here the source-shaped mask, protected remnant and backbone, no-new-carbon rule, limited internal cuts and finite heteroatom supply are substantive restrictions. They still allow other products; no exact-twenty exclusion theorem is claimed.

4.4 Exact source operations and completed molecular identities

In Table 2, uv denotes the source core edge $u : v$. A displayed cut is an original core adjacency removed entirely, not a bond-order reduction. Every row also requires ester-release accounting. For the three source whole-removal rows, cutting all incidences of W replaces atom deletion. Glycine additionally requires breaking $5 - c_\alpha$ and supplying the second c_α hydrogen; this is an explicit completion beyond the empty source row. All decorated identities in Table 3 are new completed graph specifications consistent with the retained carbons, not missing source mechanisms.

Every product contains the backbone $c_\alpha - n_\alpha$, $c_\alpha - c'$, $c' = o_x$, $c' - o_0 H$; except Gly it also contains $c_\alpha - 5$. Hy-

Table 2: Retained carbons, exact core cuts, and whole-removed vertices. Article 57 App. A is the source except the declared Article 59 Cys variant. The full operations, including hydrogen atoms, are in the certificates.

Name	S	Core cuts	W
Ala	$\{5\}$	none separately	$\{6, 4b\}$
Arg	$\{5, 4b, 10b, 11\}$	$5:6, 4b:4a, 10b:10a, 11:12, 10b:11$	$\varnothing$
Asn	$\{5, 4b\}$	$5:6, 4b:4a, 4b:10b$	$\varnothing$
Asp	$\{5, 4b\}$	$5:6, 4b:4a, 4b:10b$	$\varnothing$
Gln	$\{5, 4b, 10b\}$	$5:6, 4b:4a, 10b:10a, 10b:11$	$\varnothing$
Glu	$\{5, 4b, 4a\}$	$5:6, 4b:10b, 4a:4, 4a:12a$	$\varnothing$
Gly	$\varnothing$	no core cut; detach backbone	$\varnothing$
His	$\{5, 4b, 10b, 11\}$	$5:6, 4b:4a, 10b:10a, 11:12, 10b:11$	$\varnothing$
Ile	$\{5, 6, 4b, 10b\}$	$6:6a, 4b:4a, 10b:10a, 10b:11$	$\varnothing$
Leu	$\{5, 4b, 4a, 10b\}$	$5:6, 4a:4, 4a:12a, 10b:11, 10b:10a$	$\varnothing$
Lys	$\{5, 4b, 10b, 11\}$	$5:6, 4b:4a, 10b:10a, 11:12$	$\varnothing$
Phe	$\{5\} \cup B_6$	$5:6, 4:4a, 12a:1, 10a:10b$	$\varnothing$
Pro	$\{5, 4b, 10b\}$	$5:6, 4b:4a, 10b:10a, 10b:11$	$\varnothing$
Ser	$\{5\}$	none separately	$\{6, 4b\}$
Thr	$\{5, 4b\}$	$5:6, 4b:4a, 4b:10b$	$\varnothing$
Trp	$\{5, 4b, 10b\} \cup A_6$	$5:6, 10b:10a, 10b:11, 12a:12$	$\varnothing$
Tyr	$\{5\} \cup B_6$	$5:6, 4:4a, 12a:1, 10a:10b$	$\varnothing$
Val	$\{5, 6, 4b\}$	$6:6a, 4b:4a, 4b:10b$	$\varnothing$
Cys	$\{5\}@X_3$	$4b:5, 5:6$ (Article 59 variant)	$\varnothing$
Met	$\{5, 4b, 10b\}@X_4$	$5:6, 4b:4a, 10b:10a, 10b:11, 4b:10b$	$\varnothing$

drogens saturate the displayed neutral valences. Thus n_α is NH_2 except in Pro, where its closure makes it NH. For aromatic cycles, a sequence followed by its first vertex is a closed cycle; the machine certificate fixes a Kekulé assignment. Formula and heteroatom placement both matter. A formula alone does not identify a residue.

The R/S entries use the final product's priority ordering; identical local geometric orientation is not the same as an unchanged R/S label when remote substitution changes priorities. The table specifies the usual L targets, including $(2S, 3S)$ Ile, $(2S, 3R)$ Thr and $(2R)$ Cys. Bare constitutional rewrites neither choose these configurations nor exclude their opposites. The two substituted chiral side chains require their own orientation data.

Proposition 4.4 (Identity and strict carbon accounting)**.** *The completed graphs in Table 3 are twenty distinct rooted constitutional amino-acid graphs. Each contains exactly the retained source carbons S and the two separately identified backbone carbons. No new side-chain carbon is required.*

Proof. The displayed backbone and side-chain edge sets give the complete heavy-atom graph. Saturating the neutral valences gives the formulas displayed in the table; the supplied verifier recomputes these rather than assigning them. All formulas are distinct except those of Ile and Leu. At the side-chain root 5, Ile has three carbon neighbors, including c_α, whereas Leu has two; hence these rooted graphs are not isomorphic. The explicit carbon map is $S \hookrightarrow V_X$, with c_α, c' separate. Inspection of every new edge shows that all retained core–core adjacencies were present in the original chrysene graph. □

Rooting identifies the amino-acid backbone for the decoder; it does not identify equally named locants from different copies. Conventional residue names are applied only *after* this graph identification. The neutral forms fix one protonation and, for His, one tautomeric representative; physiological protonation equilibria are not asserted.

4.5 An actual nonempty restricted witness

The artifact `product_certificates.json` contains each initial graph, complete terminal graph, every mapped hydrogen, atom-origin tags, and every Split/Join instruction. The accompanying standard-library builder/replayer runs without a chemistry toolkit and constructs the fixed endpoints and edit words. A separate data-consuming guard audit, `scripts/validate_product_guards.py`, recognizes the ordinary, empty, and extended mask families; checks neighboring whole-removal vertices, the internal-edge budget, donor-heavy-atom incidences and the release exception; and replays protected-bond, support, atom-identity and valence guards on every unary and paired step. It does not import the builder. Representative mu-

Table 3: Complete neutral side-chain connectivity, added side-chain heavy atoms, free-product formula, and required stereochemistry. Every row also uses the release oxygen o_0 and retains backbone n_α, o_x. A star means that stereochemical realization is a separate obligation, not proved by the bond rules.

Name	Side-chain bonds or groups	Added atoms	Formula	Stereo*
Ala	$5H_3$	none	$C_3H_7NO_2$	$\alpha : S$
Arg	$5-4b-10b-n_1-11(=n_2H)-n_3H_2$	$3N$	$C_6H_{14}N_4O_2$	$\alpha : S$
Asn	$5-4b(=o_1)-n_1H_2$	O, N	$C_4H_8N_2O_3$	$\alpha : S$
Asp	$5-4b(=o_1)-o_2H$	$2O$	$C_4H_7NO_4$	$\alpha : S$
Gln	$5-4b-10b(=o_1)-n_1H_2$	O, N	$C_5H_{10}N_2O_3$	$\alpha : S$
Glu	$5-4b-4a(=o_1)-o_2H$	$2O$	$C_5H_9NO_4$	$\alpha : S$
Gly	no retained core carbon; $c_\alpha H_2$	none	$C_2H_5NO_2$	none
His	$5-4b$; imidazole cycle $4b=10b-n_1H-11=n_2-4b$	$2N$	$C_6H_9N_3O_2$	$\alpha : S$
Ile	$5(-6)-4b-10b$	none	$C_6H_{13}NO_2$	$\alpha : S$ $5 : S$
Leu	$5-4b(-4a)-10b$	none	$C_6H_{13}NO_2$	$\alpha : S$
Lys	$5-4b-10b-11-n_1H_2$	N	$C_6H_{14}N_2O_2$	$\alpha : S$
Phe	$5-4b$; aromatic cycle $4b, 10b, 11, 12, 12a, 4a, 4b$	none	$C_9H_{11}NO_2$	$\alpha : S$
Pro	$5-4b-10b-n_\alpha$, closing the five-membered backbone ring	none	$C_5H_9NO_2$	$\alpha : S$
Ser	$5-o_1H$	O	$C_3H_7NO_3$	$\alpha : S$
Thr	$5(-o_1H)-4b$	O	$C_4H_9NO_3$	$\alpha : S$ $5 : R$
Trp	$5-4b$; fused cycles $4b, 10b, n_1H, 12a, 4a, 4b$ and $12a, 1, 2, 3, 4, 4a, 12a$	N	$C_{11}H_{12}N_2O_2$	$\alpha : S$
Tyr	Phe cycle with $12-o_{12}H$; retain the original arm oxygen	no new side O	$C_9H_{11}NO_3$	$\alpha : S$
Cys	$5-s_3H$ on X_3	S	$C_3H_7NO_2S$	$\alpha : R$
Met	$5-4b-s_4-10b$ on X_4	S	$C_5H_{11}NO_2S$	$\alpha : S$
Val	$5(-6)-4b$	none	$C_5H_{11}NO_2$	$\alpha : S$

tated masks and illegal edits must be rejected. Terminal component membership and formula checks supplement these guard checks. Diagnostic single-product words have 22–48 primitive edits. The shared two-product sulfur word has 174 edits; its longer count includes explicit global hydrogen reassignment and carries no kinetic significance.

Theorem 4.5 (Restricted formal repertoire inclusion)**.** *In the extraction grammar of Definition 4.2, the prepared open scaffolds and finite packets of Definition 4.1 admit finite words to all eighteen non-sulfur constitutional product graphs in Table 3. Two separately indexed prepared scaffolds, with one shared $H-s_3-s_4-H$ packet, admit one finite word whose endpoint contains the Cys and Met graphs as disjoint components. Every atom is accounted for, all endpoint valences close, and all untouched remnant core–core bonds remain unchanged. Thus this restricted formal product model is nonempty.*

Proof. For each row, use its retained set and whole-removal data in Table 2; use the declared boundary-cut Cys variant. Retain all unmodified remnant edges. Install the backbone and side-chain edges of Table 3, using only the labelled stock. Preserve original hydrogen bonds where their endpoint retains spare valence, then assign the remaining mapped hydrogens to unused valences and pair the rest as H_2. The certificate lists the exact resulting assignments. The inventories above supply enough hydrogens and make the remaining count even; direct integer checks establish both assertions for every row. All initial and terminal atoms, including ports, are identical. The finite bond-difference word of Lemma 4.3 then gives the path. Its changed core edges meet the extraction support; none introduces a new core adjacency; the three protected backbone edges do not differ. The retained internal-edge deletion count is at most one. The formulas and connectivities are certified by Proposition 4.4. For sulfur, allocate the two original sulfur atoms once, not once per row. Its first eight edits open the relevant core edges, detach both initial sulfur hydrogens while retaining their identities for later reassignment, and produce the bridge $5@X_3-s_3-s_4-4b@X_4$. The next two edits cleave s_3-s_4 and join s_4 to $10b@X_4$. The remaining guarded word completes the products. The joint certificate places s_3 at $5@X_3$ and s_4 between $4b@X_4$ and $10b@X_4$, and exhaustively accounts for both sets of remnants and all hydrogens. The product components have disjoint origin-labelled vertex sets. These explicit finite objects establish

existence, rather than assuming that an intended path is valid. □

The theorem does not certify that the intermediate valence-port states are stable molecules, transition states or physically traversable configurations. The joint word explicitly visits the ordered disulfide-bridge topology, then cleaves the bridge before completing the thioether. It does not establish a physical disulfide-bridge mechanism; that remains a junction-lift obligation. In particular, no redox balance for Article 59's specified endpoints is automatically inherited by this different formal donor/coproduct completion.

Proposition 4.6 (Substantive exclusions and ablations)**.** *The restricted grammar has the following obstructions.*

1. *Without the extended mask, every product has at most ten carbons; therefore the Trp graph is unreachable.*
2. *Without sulfur stock, both sulfur product graphs are unreachable.*
3. *With the backbone nitrogen protected and no side-chain nitrogen stock, Arg, Asn, Gln, His, Lys and Trp are unreachable.*
4. *A target requiring a new core–core adjacency outside the original chrysene graph, a moved backbone carbonyl oxygen, or altered protected backbone connectivity is unreachable.*

Proof. An ordinary mask has at most eight core vertices: 5, optional 6, and six in B_6. Adding the two backbone carbons gives ten; the Trp target has eleven. The empty mask does not increase this bound. The second and third statements follow from element conservation and the protected nitrogen's fixed backbone incidence. The fourth follows directly from the persistent origin and edge guards, which every primitive preserves. □

These are genuine restrictions but not a characterization of exactly twenty reachable products. The selection and registry chapters must not infer uniqueness, or a twenty-output upper bound, from this theorem alone.

4.6 The sulfur variant and strict batch ownership

The Cys certificate uses the two Article 59 boundary cuts, leaving 17 core carbons in its carbon remnant. Article 57 instead lists whole removal of 6 and 4*b*, leaving a 15-carbon connected remnant plus those two separately accounted-for carbons. Both isolate $S = \{5\}$, but the operations and coproducts differ. The Met certificate retains $5, 4b, 10b$, cuts $4b : 10b$ internally, and joins $4b - s_4 - 10b$. Its unchanged retained bond is $5 - 4b$. Both sulfur maps agree with the junction's specified rooted identities [Sch26j, Sec. 5].

For a common repertoire witness, allocate eighteen disjoint original six-core clusters for the unary constructions and two further six-core clusters for the paired construction. Each cluster supplies three evolved X–A vessels under the separate assembly bridge; only one of its three X graphs is active here. The batch therefore has 120 original cores, 60 remaining X units, 20 active X units and 40 spectator X units. It is a *family of possible preparations*, not a claim that one six-core cluster produces all twenty outputs simultaneously. At the exposed module level the formal batch uses 1,504 actual atoms, plus its 40 ports; the contexts grafted at those ports and the spectator vessels add their own disjoint inventories. The current certificates explicitly resolve only the 20 active open local graphs. The other 40 X units, resident adenosines and tethers are inert typed architecture records until an actual compatible context graph is supplied; their complete atom graphs are not part of the 1,504-atom count. The common donor budget is

$$60NH_3 + 60H_2O + 160H_2 + H_2S_2.$$

Again, this is the certificate's resource bound, not a proposed laboratory recipe. Coproduct components remain owned by their preparation. A later assignment change can transport a product *label* or choose another prepared copy; it cannot reuse an already consumed atom under a new name.

Lemma 4.7 (Context and disjoint-union extension)**.** *A guarded word extends unchanged under grafting of a compatible inert boundary context. Words on disjoint atom sets with disjoint resource packets commute. A paired sulfur word extends on its two-copy support, with its shared packet allocated once.*

Proof. Grafting replaces each capacity-one port by a boundary site having exactly one available valence after its fixed external-context bonds are counted. A local port bond may change: for example, Tyr replaces $o_{12} - B_{12}$ by a bond from that boundary site to a mapped hydrogen. The remaining external-context atoms and edges are unchanged. Every local match and residual-capacity calculation is therefore unchanged. For disjoint unions, the edge and atom coordinates changed by the words are disjoint, so either execution order gives the same state. The sulfur pair is one joint support and does not claim commutation of its two halves. □

An actual carrier context satisfying this port interface remains to be provided; the lemma is not evidence that

the patent supplies every such completion. The source basis remains US12195423B1, especially its Fig. 5 encoding, Fig. 7 atom-map proposals, and Example 10/Fig. 15 poly-A carrier discussion [Sch25]. Its nucleotide-map discrepancies must be resolved in the assembly bridge. No distinct patent is substituted.

4.7 Interface to the common model and the chemical lift

The common state may be written $z = (H, f, G_{\mathrm{at}}, Q, e, \sigma, \rho, k)$. Here G_{at} includes the complete origin-labelled atom graph and resources; Q is the library of terminal graphs just constructed. A fixed identity decoder $I : Q \to \mathcal{A}$ recognizes the backbone and side-chain connectivity, then applies the conventional residue label. Neither I nor the local bond primitives consult the target code table. Assignment operations change σ and perhaps the controller ρ; they do not rewrite atom origins. Product formation changes G_{at} and the resource phase k. In the relaxed model these product words can be available at every $e \in [0, 1]$; a separate selector may choose different members of Q at different values of e. Availability is not selection.

Assumption 4.8 (Common chemical realization of the graph witnesses)**.** For the declared original-core assembly, there exist (i) an atom-conserving assembly/preparation map to the specified open input contexts; (ii) complete reagent-resolved chemical replacements for the formal words in one fixed chemical grammar; (iii) compatible path endpoints, charge, proton, electron, and coproduct balances; (iv) continuous geometric lifts in one common parameter domain; and (v) the required absolute stereochemical selection. The source of every participating atom agrees with the certificate. The Cys variant, sulfur supply and residue-release endpoint are fixed consistently across all these replacements.

Proposition 4.9 (Conditional molecular substitution)**.** *Under Assumption 4.8, substitution of the compatible chemical paths for the formal words yields the same twenty identified products, with the stated atom origins and stereochemical endpoints.*

Proof. Concatenate the substituted local paths using their matching endpoint states and configurations. Identity preservation composes. The protected labels and terminal graph maps agree with the certificates, so the fixed decoder has the same outputs. Compatible continuous endpoints permit actual concatenation of the lifts, while the final stereochemical hypothesis selects the declared configurations. □

This proposition records precisely what remains conditional. Merely making all premises explicit does not establish a physical instance of their conjunction. Conversely, experiments are not required to accept the finite graph theorem already proved. The useful next mathematical advance is a strictly richer, independently specified chemical grammar that realizes some or all certificates and preserves these shared interfaces.

5 Seed routing and a complete assignment path

The preceding carrier and product constructions have different outputs: a framed address space and a library of molecular product types. Neither is a codon assignment. We now supply a finite interface between them and prove an actual path through its permitted states. The endpoint assignments are the archived standard and vertebrate mitochondrial tables used in the source corpus. Both tables agree at all 64 entries with NCBI *The Genetic Codes*, `transl_table=1` and 2, after replacing DNA-alphabet T by RNA-alphabet U [EO24]. We record the page update of 23 September 2024 and access on 5 October 2026; the packaged reference snapshot preserves the two AAs rows and this normalization. The separate NCBI Starts rows are not substituted for internal codon assignments. The data are reference-informed. Consequently the result is a conditional realization theorem, with an explicit nonuniqueness theorem, rather than an independent prediction of either table.

5.1 The fixed interface and the information supplied as data

Let $W = \{A, C, G, U\}^3$ be the variable *external* codon addresses in one normalized frame. Throughout this section the carrier K derives from six original cores and has three residual cores with three resident XA vessels, a separate fixed AAA reference, and the same chosen frame tags. No move below changes a resident reference base into an external coding base. The distinction between a framed domain and a product assignment is essential in the domain theorem of [Sch26b, §7, especially its conditional-domain and global-frame statements]. Write $X_3 = \{O_1, \ldots, O_{20}\}$ for the numbered registry classes, identifying each index with its codon orbit when taking intersections, not for the amino acids. Let $\mathcal{Q}$ be the independently constructed library of twenty identity-checked terminal molecular graph

types, and fix its conventional name map

$$\iota : \mathcal{Q} \longrightarrow \mathcal{P},$$
$$\mathcal{P} = \{A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y\}.$$

The map ι is the identity map I of Section 2, expressed with one-letter residue names. Here the right-hand letters have their conventional amino-acid meanings; they are not nucleobases. We assume ι is a bijection and write p_r for the product with name r. Identity checking of these graph types belongs to the product construction. It is not performed by looking at their intended codons.

A routing record points to a *product type* or a release module. It does not copy atoms, synthesize a new residue, or assert simultaneous production of all products by one hexamer. Molecular instances of different codon queries have separately typed atom universes. A common finite reservoir may be a disjoint union of those instances when a simultaneous formal witness is wanted.

For a two-letter prefix b, write $bY = \{bU, bC\}$, $bR = \{bA, bG\}$ and $bN = \{bU, bC, bA, bG\}$. The fixed cell partition is

$$\begin{aligned}\mathcal{C} = \{&UCN, CUN, CCN, CGN,\\ &ACN, GUN, GCN, GGN\}\\ \cup \{&bY, bR :\\ &b \in \{UU, UA, UG, CA, AU, AA, AG, GA\}\}.\end{aligned} \tag{6}$$

These are eight quartets and sixteen doublets, disjoint and covering W. A blank cell is *unassigned*; it must not be confused with a completed no-release cell.

Definition 5.1 (Fixed data versus move grammar)**.** The instance data consist of $K, \mathcal{Q}, \iota$, the partition (6), the seed roles in Table 4, four refinement records, two initial no-release cells, a protected cell AUR, and the branch modules specified below. These are fixed before executing a path. The move grammar tests incidence, occupation, locality, phase, and explicit control bounds. No move tests equality with either desired reference table.

The residue names, the two special seed anchors UGG and AUG, the refinement names, and the wiring and coefficients of the branch modules are supplied data. The first source seed graph explicitly consults the standard table [Sch26d, §5, seed-map definition and identity caveat]; the selected assignment and two exchanges come from [Sch26h, Appendix A; §9]. Our generic routing law and affine realization are new formal assumptions and constructions. This separation prevents a fitted witness from being advertised as chemically selected merely because its execution is checked.

5.2 Seventeen product demands, eighteen seed cells

For a role d, let B_d be its one or two cells. Define its eligible classes by intersection with every cell, except that the UGR role must meet UGG and the AUR role must meet AUG. Thus the last-base anchors for the two purine roles are narrower than their final propagated cells. In symbols,

$$E_d = \bigcap_{s \in B_d} \{q \in X_3 : q \cap A_s \neq \varnothing\},$$
$$A_{UGR} = \{UGG\}, \quad A_{AUR} = \{AUG\},$$
$$A_s = s \text{ otherwise.}$$

This gives the exact anchored graph of the source computation [Sch26d, verification supplement, demand construction and V4–V6]. Pure cell incidence would instead allow class 2 at UGR and class 3 at AUR, and would be a different graph. The selected initial assignment changes the names at the UAY and UGY roles, not these incidence sets. It therefore is not an instance of the source's original, standard-name eligibility rule without that explicitly declared change.

Theorem 5.2 (An explicit matching and its proper type)**.** *Table 4 is an injective system of distinct representatives for seventeen demands. It leaves classes* $11, 17, 20$ *unused and seeds eighteen cells. This graph has* 840 *SDRs, with* 87 *different unused triples.*

Proof. Each last-column entry occurs in its eligible set, and the seventeen entries are distinct. Concrete seed addresses in row order are

$$\begin{aligned}&UUU;\ (UCA, AGU);\ UAU;\ UGU;\ UGG;\\ &CUU;\ CCA;\ CAC;\ CGA;\ AUC;\ AUG;\\ &ACU;\ AAU;\ GUC;\ GCG;\ GAC;\ GGG.\end{aligned}$$

Their classes are exactly the last column. In particular class 4 contains both UCA and AGU, so it serves the merged serine demand. There are seventeen rows but eighteen addresses and eighteen cells.
For completeness the finite enumeration uses the recurrence

$$N(k, U) = \sum_{q \in E_{d_k} \setminus U} N(k+1, U \cup \{q\}), \qquad N(18, U) = 1,$$

where rows are numbered 1 through 17. Every SDR chooses exactly one term at each level; conversely each completed branch gives an SDR. Thus the recurrence is exact, with no symmetry division. The supplied independent verifier evaluates $N(1, \varnothing) = 840$ and groups

Cell(s)	Selected product name	Eligible classes	Chosen class
UUY	F	$1, 11$	1
UCN, AGY	S	$4, 17$	4
UAY	C	$3, 15$	3
UGY	Y	$12, 13$	13
UGR	W	14	14
CUN	L	$5, 9, 15, 19$	9
CCN	P	$8, 14, 18, 20$	18
CAY	H	$16, 19$	19
CGN	R	$6, 12, 17, 20$	12
AUY	I	$10, 16$	16
AUR	M	15	15
ACN	T	$2, 12, 13, 14$	2
AAY	N	$9, 10$	10
GUN	V	$7, 11, 16, 19$	7
GCN	A	$6, 12, 17, 20$	6
GAY	D	$5, 15$	5
GGN	G	$8, 14, 18, 20$	8

Table 4: The anchored seventeen-demand graph and an explicit SDR for the selected assignment. Serine serves two cells; names at UAY, UGY are the selected, rather than the reference-mitochondrial, names.

its leaves by $X_3 \setminus U$, obtaining 87 triples. It also checks every incidence directly from the six-marker orbit action rather than importing the listed classes. The explicit SDR already proves existence independently of these totals. □

Remark 5.3 (Two graphs must not be conflated). The eighteen-independent-cell graph used by the matching routine in [Sch26h, verification supplement, V3] has a separate vertex for each serine cell. Its matching and its Hall obstruction are not the seventeen-merged-demand calculation above. The claim that labels never affect adjacency applies to a fixed geometric cell graph; it does not remove independently imposed class–product chemistry or the two anchored restrictions.

Lemma 5.4 (Propagation only on seeded cells)**.** *Let $a : D \to \mathcal{Q}$ be a partial assignment and let $\mathcal{C}_0$ be the cells containing at least one assigned address. A cell-constant extension of a to $\bigcup \mathcal{C}_0$ exists exactly when all assigned addresses in each cell have the same product. When it exists, it is unique on that union. It imposes no value on a cell outside $\mathcal{C}_0$.*

Proof. Necessity follows by restricting any cell-constant extension to the assigned addresses. Under the condition, give a cell the common product of its assigned addresses. This is well-defined because the cells are disjoint, agrees with a, and is forced on each occupied cell. No input address lies in any other cell, so constancy places no condition on its product. In particular blank cells cannot be filled by appealing to uniqueness on occupied cells. □

Class–block transversality prevents two addresses from the *same* class in a block; it does not prevent conflicting products from distinct classes. The explicit matching and disjoint cells remove those conflicts here. The extension fills eight quartets and ten doublets, hence 52 addresses. It leaves the following six cells blank. Four are completed by the explicit refinement records

$$\begin{aligned} UUR &\mapsto p_L, & CAR &\mapsto p_K, \\ AAR &\mapsto p_Q, & GAR &\mapsto p_E, \end{aligned} \tag{7}$$

and UAR, AGR are completed as initial no-release cells. The conventional reference-mitochondrial refinement has $CAR \mapsto p_Q$ and $AAR \mapsto p_K$; (7) deliberately gives the selected assignment instead.

Proposition 5.5 (Correct repertoire accounting)**.** *The completed selected assignment has 22 sense cells, namely eight quartets and fourteen doublets, and two no-release doublets. Its sense image contains exactly twenty product identities.*

Proof. There are $18 + 4 = 22$ sense cells; together with the last two cells they partition all 64 addresses. The seed names are seventeen distinct elements of $\mathcal{P}$. Refinement reuses L and adds exactly K, Q, E, giving twenty. All outputs lie in $\mathcal{Q}$ by construction. A general repertoire bound of twenty would require closure in that fixed palette; it does not follow from the incorrect claim that

every refinement product had an initial seed. □

5.3 A fixed grammar, its guards, and the selected-to-reference path

A compatible state is

$$s = (K, \mathcal{Q}, \iota, \varphi, m, a, L, \mathcal{J}, \mathcal{M}, u),$$

where φ is a phase; m is a partial injection from demands to classes; a is a partial baseline address assignment at $u = 0$; L is its seed-origin ledger; $\mathcal{J}$ is an optional closed production certificate; $\mathcal{M}$ is a cell-indexed family of branch modules; and $u \in [0, 1]$ is an environment control. The first three entries are immutable. After module installation, a records the baseline routing and current readout is computed from $(\mathcal{M}, u)$; therefore a control change need not change a. The following schemas define the allowed moves independently of a desired endpoint.

1. *Seed*(d, q), in the seed phase, requires $q \in E_d$, an unused class and blank cells B_d. It registers $m(d) = q$, assigns p_{r_d} to the specified addresses $q \cap A_s$, and adds their origins to L.

2. *Propagate*(s) requires an origin in L and agreement of every already assigned address in s. It assigns that product only to the remaining addresses of s.

3. *Advance*(seed, refinement) requires all seventeen demands registered and all eighteen seed cells fully propagated. *Advance*(refinement, production) requires every cell completed according to its seed, refinement or no-release record. These are the only permitted pre-routing phase advances.

4. *Refine*(s, p), in the refinement phase, requires a blank cell and an available record (s, p) in the fixed refinement catalogue. It fills that cell. A separate completion schema records the initial no-release cells. Neither schema follows merely from the existence of the seed matching.

5. *Equip*, in the production phase with modules not yet installed, installs the predeclared branch modules, with the guard that their readout at $u = 0$ agrees with the completed assignment. The universal branch syntax is (p, α, β) with affine margin $\alpha + \beta u$; its coefficients and destination product are instance data.

6. *Close*, in the equipped production phase, stores a valid production certificate $\mathcal{J}$ and changes from the production/selection phase to the routing phase. It leaves all products unchanged. Any hypothesis used only to create that certificate is thereafter a statement about the recorded production state.

7. *Exchange*(s, t), in the routing phase at $u = 0$, requires occupied sense cells, the same suffix Y, R or N, prefixes differing in exactly one coordinate, and $s, t \notin \{AUR\}$. It exchanges their entire modules using the same third-base ports. It does not exchange atoms, molecular identities, or the physical reference. The initial no-release cells are excluded.

8. *Control*(u, v), from routing or control phase at the current value u, requires $0 \le u \le v \le 1$, enters or remains in the control phase, and fixes every non-control field while traversing the whole segment. All values in the segment, including equality walls, are permitted control states. Readout may be set-valued or absent during this motion.

The initial state has m, a, L empty, $u = 0$, and the fixed carrier and product library. Its reader is inactive. The seed moves in table order, eighteen propagations, the guarded advance to refinement, four refinements, two initial no-release records, and the guarded advance to production are all permitted by their guards. They produce a fully assigned state C_{sel}. Only after completion is translation readout enabled.

In this state the sulfur-bearing pair has the assignment $UAY \mapsto C$, $AUR \mapsto M$. The two cells are complements under $A \leftrightarrow U$, $C \leftrightarrow G$. The production-stage hypothesis of [Sch26h, §9, paired delivery] can therefore be certified here, with the ordered product identities supplied by the junction construction. Among the 18 seed cells, the complete list of complementary pairs is

$$(UAY, AUR), \quad (CCN, GGN), \quad (CGN, GCN).$$

Thus the first is the unique size-two pair. That fact fixes a pair of cells; it does not, without an ordering predicate, decide which of the two distinct products goes at which end.

Theorem 5.6 (Two guarded exchanges)**.** *From the completed selected state, after closing its production certificate, the permitted path*

$$C_{\mathrm{sel}} \xrightarrow{\text{Exchange}(UAY,UGY)} C_1 \xrightarrow{\text{Exchange}(AAR,CAR)} C_{\mathrm{mito}} \tag{8}$$

reaches the archived vertebrate mitochondrial assignment. Two is the minimum number of exchange moves for these fixed endpoint routings. Every completed state along the path has $AUG \mapsto M$ and the same product identities, carrier, frame and stored production certificate.

Proof. The first exchange is between two occupied Y cells whose prefixes UA, UG differ in one coordinate. Neither is locked. It sends UAY from C to Y and UGY

from Y to C. The second is between occupied R cells with prefixes AA, CA, also differing in one coordinate; it sends AAR from Q to K and CAR from K to Q. All other values are unchanged. After these moves the block values in third-base order U, C, A, G, listed in first- and second-base order U, C, A, G, are

	U	C	A	G
U	$FFLL$	$SSSS$	$YY{*}{*}$	$CCWW$
C	$LLLL$	$PPPP$	$HHQQ$	$RRRR$
A	$IIMM$	$TTTT$	$NNKK$	$SS{*}{*}$
G	$VVVV$	$AAAA$	$DDEE$	$GGGG$

where $*$ denotes no selected sense product at this stage. This is exactly the archived mitochondrial comparison string, checked at every address by the verifier. Neither exchange touches AUR, and neither changes any immutable field. The selected and mitochondrial routings differ on four cells, whereas one exchange changes at most two cells. Thus at least two exchanges are necessary, and the displayed path attains that bound. The remaining claims follow directly from the move definitions. □

Remark 5.7 (A staged hypothesis is not a preserved assignment predicate). At the endpoint, C is assigned to UGY, whose complement is ACR, not AUR. Requiring the production-stage complementary assignment to hold also of every later codon-routing table would therefore contradict the stated endpoint. Our common model instead preserves the produced molecular pair and its certificate while permitting a later change of reading assignment. This is an additional interface choice. It is not a claim that a geometric frame change alone realizes either exchange; the two slot-specific operations are not the global Klein-group frame action.

5.4 Reachability, selection, and the obstruction to nested singletons

We use the finite reachability construction of [Sch26f, §§4–6], retaining its useful mathematics while separating feasibility from continuous molecular motion. Let V be a finite state set and E a finite set of *matched* transitions. A rule name alone does not identify a transition. Each $e \in E$ has a continuous real margin $\mu_e(u)$ and is admitted exactly when $\mu_e(u) > 0$. Fix an initial state o outside the decoded terminal set. For each terminal T, define

$$\Phi_T(u) = \max_{p: o \rightsquigarrow T} \min_{e \in p} \mu_e(u), \qquad \max \varnothing = -\infty,$$

and group terminals by the fixed molecular decoder:

$$\Psi_r(u) = \max_{\iota(T)=r} \Phi_T(u), \qquad K^*(u) = \arg\max_{r: \Psi_r(u) > 0} \Psi_r(u).$$

Here the decoder notation includes the terminal's product-graph projection. The last set is empty when there is no positive residue score. It is not an assertion that there are no reachable states, since o is always reachable. The maximum-margin selection rule is a modelling premise, not a kinetic law.

Lemma 5.8 (Finite maximum-bottleneck reachability). *If a terminal is graph-reachable, its Φ_T is a finite maximum of finite minima of continuous margins and is continuous. It has an admitted path exactly when $\Phi_T > 0$. Off margin-zero loci the admitted graph is constant on each connected component; on components avoiding both margin-zero loci and positive score ties the selected product is also constant.*

Proof. A path visits a finite subset of E, and its minimum depends only on that subset. There are finitely many such subsets, so the maximum is attained. Equivalently, deleting loops cannot lower a path's minimum, and finitely many simple paths suffice. Finite maxima and minima preserve continuity. A positive maximum supplies a path every one of whose margins is positive; any admitted finite path gives a positive lower bound on the maximum. On a connected component avoiding zeroes, each continuous edge margin has constant sign, proving the graph assertion. The residue scores of structurally reachable products are continuous; their positive set is fixed there. A unique positive maximizer cannot change without a tie, which proves the last assertion. □

Proposition 5.9 (Nested-singleton obstruction). *Suppose $K(w, t') \subseteq K(w, t)$ for $t \le t'$ and $|K(w, t)| \le 1$. If a doublet has the common nonempty singleton $\{r\}$ at t', it has that same singleton at both addresses at every earlier t. Consequently a discriminating doublet cannot become uniformly nonempty under these two assumptions.*

Proof. Each earlier set contains r by inclusion and contains at most one element, so it equals $\{r\}$. Apply this to both addresses. □

Thus the strictly decreasing-margin, singleton-reachability combination in [Sch26f, §5, H_{relax} and H_{det}] cannot furnish the required nondegenerate discrimination-to-uniform transition. Replacing raw reachability by selection requires a new witness; merely saying that determinism is retired does not prove such a witness exists.

Proposition 5.10 (A strict score-crossing repair)**.** *There is a two-port, finite-graph model with strictly decreasing affine margins, constant multi-product reachability, and a selected transition from discrimination to uniformity.*

Proof. At port a, use one-edge branches to distinct products p_r, p_s with scores $3-2t$ and $2-t/2$ on $0 \le t \le 1$. At port g use only the p_s branch with score $2-t/2$. All scores strictly decrease and stay positive. The raw reachable sets are constantly $\{r,s\}$ and $\{s\}$. Their score difference at a is $1-3t/2$: selection is r for $t < 2/3$, $\{r,s\}$ at $2/3$, and s for $t > 2/3$. The selected doublet therefore passes from (r,s) to (s,s) through the stated tie. This violates the raw singleton assumption, exactly as required, while satisfying nested raw reachability. □

5.5 One explicit control path to the standard assignment

For each branch take a singleton compact configuration space $X_e = \{0\}$, one constraint, and $g_e(0,u) = \mu_e(u)$. This realizes the abstract maximum-margin formalism without assuming any molecular lift. The module syntax is uniform: a finite list of product references and affine scores at each third-base port. Constant occupied cells have their assigned product's score 1 at every port; unlisted branches are absent. The exceptional modules are

cell	port	product	score
AUR	A	I	$1+3u$
AUR	A	M	$2+u$
AUR	G	M	$2+u$
UGR	A	W	$1-2u$
UGR	G	W	1
AGR	A,G	R	$2u-1$

$0 \le u \le 1.$ (9)

The UAR module has no sense branch. At $u=0$ these modules agree with the completed selected assignment before exchange, and with the mitochondrial assignment after exchange. Notice that I is already *reachable* at AUA at $u=0$; its lower score prevents its selection. No raw-singleton hypothesis is imposed.

The coefficients and the placement of these general branch forms are an explicit reference-informed design. In particular the AGR product name R is data, not a consequence of the word "uniform." The distinction between outcome type and product content is already explicit in [Sch26e, §8, two resolutions and what is imported].

For a reader with a separate stop-and-release controller, adopt the explicit absence-to-stop policy

$$\mathrm{StopSignal}(w) \iff K^*(w,u) = \varnothing. \tag{10}$$

This is a separate formal signal policy, not a halt transition. The reader still requires its guarded observe, release and halt steps. Interpreting them as actual biochemical termination needs the termination certificate stated below. A positive path to one sense product cannot prove absence of all competing products.

Theorem 5.11 (The full compatible-state control path)**.** *The fixed instance above has a path from its empty seed register, through the selected assignment and the two exchanges, to the mitochondrial assignment at $u=0$ and then to the standard assignment at $u=1$. Its control suffix is the entire curve $u(t)=t$, $0 \le t \le 1$, in the same state space. The endpoint tables differ at exactly four codons, in exactly three purine cells:*

$$AGA, AGG : \ * \longrightarrow R,$$
$$AUA : M \longrightarrow I, \qquad UGA : W \longrightarrow *.$$

Every fully initialized state in the displayed path retains $AUG \mapsto M$; the physical carrier, product identities, decoder and production certificate are invariant. Readout at the intermediate wall is explicitly permitted but is not a deterministic genetic code.

Proof. The seed and refinement prefix was verified above; the two exchanges satisfy Theorem 5.6. Freeze their resulting modules. The control rule admits every $t \in [0,1]$ and changes no immutable field, so its continuous parameter curve is a path of compatible control states, not merely two independently chosen parameter values. At AUA the score difference $\Psi_I - \Psi_M = 2u-1$ is negative below $1/2$ and positive above it, while both scores are positive throughout. At AUG only M occurs and its score is positive. At UGA the W score is positive below $1/2$ and nonpositive at and above it; at UGG it is constantly 1. At AGA, AGG the R score is positive exactly above $1/2$. Every other sense module is constant, and UAR remains empty. Hence

	$0 \le u < 1/2$	$u = 1/2$	$1/2 < u \le 1$
AUA	$\{M\}$	$\{I,M\}$	$\{I\}$
AUG	$\{M\}$	$\{M\}$	$\{M\}$
UGA	$\{W\}$	$\varnothing$	$\varnothing$
UGG	$\{W\}$	$\{W\}$	$\{W\}$
AGA, AGG	$\varnothing$	$\varnothing$	$\{R\}$

These are all score zeroes or positive ties in the control interval. In particular the wall is a legitimate state with an explicit set-valued interpretation; it is not silently discarded. At $u=1$ the changes turn the mitochondrial block strings into $AU : IIIM$, $UG : CC{*}W$, and $AG : SSRR$ and leave the other thirteen blocks unchanged. This is the archived standard string at all

64 addresses. The invariant claims follow because the control rule changes only u. □

Corollary 5.12 (Robust endpoint readings and finite certificates)**.** *Both endpoint readings persist on relative neighborhoods of their control values. Across the two endpoint tables there are exactly* 63 *distinct sense pairs* (w, r) *requiring molecular realization certificates.*

Proof. The regime calculation gives constant readout throughout $[0, 1/2)$ and $(1/2, 1]$. More generally positive witness margins and strictly positive selection gaps for finitely many branches persist under small continuous perturbations. For the pair count, 60 addresses agree between endpoints: 58 sense and two no-release. The changed addresses contribute five sense pairs: one each at AGA, AGG, UGA and two at AUA. Thus $58+5 = 63$. This count does not include absence, termination, routing, or junction certificates, which have different types. □

There is no assertion that the same monotone physical quantity makes every margin decrease: (9) contains increasing and decreasing margins. Nor does an argmax score determine yields or kinetic dominance. Those are separate requirements on a chemical interpretation.

5.6 Exactly how much freedom the routing law leaves

The two-exchange theorem is existential. The general exchange grammar permits many other choices even with the initiation cell protected. This can be quantified without enumerating trillions of tables.

Theorem 5.13 (A large, exact routing orbit)**.** *With* $u = 0$*, the completed cell set, the two initial no-release cells fixed, and* AUR *locked, the exchange grammar has exactly*

$$8!\,8!\,3!\,2! = 19\,508\,428\,800$$

distinct codon assignments in the orbit of the mitochondrial configuration. All preserve its palette, cell sizes and $AUG \mapsto M$*. In particular the model does not uniquely select either named code.*

Proof. Form a graph on the unlocked sense cells, with an edge exactly when an exchange is permitted. Its connected components are

$$\{UUY, UAY, UGY, CAY, AUY, AAY, AGY, GAY\},$$
$$\{UCN, CUN, CCN, CGN, ACN, GUN, GCN, GGN\},$$
$$\{CAR, AAR, GAR\}, \qquad \{UGR, UUR\}.$$

The first component is connected, for example, through UAY and AAY; the second is connected through CCN, GCN; the last two are visibly connected. There are no edges between the displayed components because the third-base suffix must be unchanged, and the omitted AUR is locked.
Edge transpositions in a connected graph generate the full symmetric group on its vertices. To see this directly, along a path $v_0, \ldots, v_k$, conjugating the last edge transposition by the preceding edge swaps gives $(v_0\ v_k)$; hence arbitrary transpositions are generated. Each component contains distinct product names at $u = 0$, so different permutations give different codon assignments. The components act independently, yielding the product of factorials. The locked cell and initial no-release cells are unchanged. As a concrete counterexample, the legal exchange (UUY, UAY) interchanges F and Y, preserves $AUG \mapsto M$ and every immutable certificate, and gives neither named reference table. □

This count measures the freedom of our deliberately permissive new routing assumption, not the number of chemically feasible or naturally occurring codes. If all equal-size cells could be permuted without the local and lock guards, the freedom would be larger still. To obtain an independently selective theory one must justify stronger compatibility or selection constraints and test them against alternative mappings. The two desired endpoints alone cannot supply those constraints.

5.7 What lifts to molecular reachability, and what does not

Theorem 5.14 (Compatible witness substitution)**.** *Fix one target-independent molecular rewrite grammar, persistent atom universe, resource and charge ledger, protected graph invariants, and molecular decoder. Take a finite abstract assignment/release path. Suppose each abstract generating edge is replaced by a finite admitted molecular path with the following properties:*

1. *its source and target project to the corresponding abstract states;*
2. *adjacent replacement paths have exactly compatible molecular boundary states and resource ledgers;*

3. *every matched molecular step preserves the declared atom identities, elements, charge accounting and protected invariants;*
4. *geometric lifts, when claimed, have common endpoint configurations, or are joined by explicitly permitted configuration paths;*
5. *each endpoint sense readout has a positive witness margin and a positive selection gap against every competing decoded product; each no-release readout excludes all such sense products, with a separate termination path when STOP is claimed.*

Then concatenation gives a molecular path realizing the abstract endpoints. With the geometric clause it also gives a continuous, piecewise-geometric lift. The same conclusion applies to a control suffix if a continuous molecular implementation of that whole suffix, including its wall states, is supplied.

Proof. List the abstract edges in order and replace each by its certified finite word. Source–target equality in the second clause makes their concatenation a well-defined molecular word. Induction over its steps preserves each invariant and the ledger, proving molecular admissibility. The decoder and selection clauses identify its sense endpoints and distinguish absence from termination. For geometric lifts, choose the specified common boundary configurations and insert any certified joining paths. Rescale the finitely many parameter intervals and concatenate. Each piece is continuous and adjacent endpoints agree, so the pasting lemma gives a continuous path. The asserted control implementation may be appended by the same argument. No conclusion about geometric lift follows when that implementation has not been supplied. □

The geometric hypothesis is stronger than static feasibility. In [Sch26a, §5, geometric lifts], a lift is a path with compatible reactant and product endpoints. The inequality test on a compact local configuration space in [Sch26f, §4] guarantees only a feasible point unless that space already parameterizes certified paths. For example, the discrete configuration space $\{x, y\}$, a constant positive constraint, and prescribed distinct endpoints x, y satisfy static positivity but admit no continuous connecting path. Likewise, two individually liftable rewrites can land in disconnected components of an intermediate state's configuration space. Independent nonemptiness of their lift spaces does not solve that compatibility problem.

One sound strengthened margin is

$$\widehat{\mu}_e(u) = \max_{\gamma \in \Gamma_e} \min_{(t,c) \in [0,1] \times C_e} g_{e,c}(\gamma(t), u),$$

where Γ_e is a nonempty compact family of continuous paths with the required fixed endpoints and the integrand is jointly continuous. A positive value now certifies a whole admissible path, not merely a point. Shared endpoints or joining certificates are still needed across different edges.

The local six-generator motif of [Sch26a, §8] is useful as one candidate replacement word; its chemical-admissibility, balanced-completion and lift packages are expressly separate assumptions there. The mathematical assignment path proved here does not establish those packages for all 63 sense pairs, the routing exchanges, or the changing termination behavior. Conversely, lack of experimental instantiation does not erase the nonempty formal model: all of its finite guards, affine regimes, and reference-table equalities have explicit witnesses. The scope of the central conclusion is therefore precise: a shared framed carrier and independently identified product library support a complete, checked conditional realization path under declared routing and control laws; a continuous chemical realization requires the additional, separately typed substitution certificates.

6 A directed sulfur junction and its readout

This section constructs a nonempty formal junction module and proves a Met-first invariant for its accepted output sequences. Its conclusions are conditional on a declared formation grammar, directed atom map, register transport, and controller. A complement calculation alone proves none of formation, release, initiation, or termination. We therefore specify these as separate operations and prove their composition. The distinction between an atom-preserving formal rewrite and a molecularly admissible reaction remains in force throughout. In particular, the construction does not establish a reaction rate, a measurable yield, or a mechanism for physical propagation.

6.1 Objects and directed support

A precursor representative consists of six original substituted chrysene cores, with three designated core pairs. The chosen conversion takes each pair to one nucleotide and one remaining 6, 12-disubstituted chrysene unit. Thus one converted representative has three nucleotides and three remaining units. Its resident poly-A representative is

$$K_A = ((X_1, A_1), (X_2, A_2), (X_3, A_3)).$$

Each (X_i, A_i) is one evolved vessel. An external coding base h_i is a separate object from resident adenosine A_i; their stipulated interaction is noncanonical. Symbolic Watson–Crick complementation below is an operation on letters,

not an assertion about that physical interaction. The conversion and its incidence/atom map are modeling premises; neither the counts nor the letter encoding supply a chemical proof of the conversion.

A junction joins two such representatives. It therefore has twelve original precursor cores, six remaining chrysene units, six resident nucleotides, and six evolved vessels. Number its remaining units $X_1, \dots, X_6$, with facing units X_3, X_4. The six external letters range in $\mathcal{B}^6$, where $\mathcal{B} = \{A, C, G, U\}$; this is a 4096-element domain, distinct from the 64-element triplet domain. The twenty-class count for one precursor does not apply to the twelve-core junction as a whole. These conventions resolve the six-core/six-vessel ambiguity in the source definitions [Sch26j, `article59-sec04.tex`, definitions `def:strand` and `def:cell`].

Lemma 6.1 (What parity supplies)**.** *Reversal of N ordered vessels has a fixed vessel exactly when N is odd. For $N = 6$ its central interface is between X_3 and X_4.*

Proof. A fixed index satisfies $i = N + 1 - i$, hence $i = (N + 1)/2$. This is an integer exactly for odd N. For even N the two middle indices are $N/2$ and $N/2+1$. □

The lemma locates an interface; it does not produce a reaction or two residues. Both three-vessel halves still have a central vessel. Moreover, $\{X_2, X_3, X_4\}$ and $\{X_3, X_4, X_5\}$ have centers X_3 and X_4. We use a separate binary support condition rather than the contrary claims in [Sch26j, `article59-sec04.tex`, `prop:whysix` and `cor:onecell`].

Assumption 6.2 (Directed junction certificate)**.** A packet j contains disjoint indexed atoms for two converted representatives, a designated incoming/outgoing boundary, and one indexed two-sulfur precursor. Its allowed paired rewrite is supported on X_3, X_4 and the declared reagent reservoir. It has a certificate Γ_j with the following properties:

1. Terminal sulfur is delivered to $5@X_3$ on the incoming side. The outgoing side retains $\{5, 4b, 10b\}@X_4$, removes the internal edge $4b - 10b$, and inserts its sulfur between $4b@X_4$ and $10b@X_4$.
2. The two sulfur atoms have distinct persistent identifiers, come from the same indexed S–S precursor, and retain their assigned sides. The precursor bond is absent before two separate output components are released.
3. Each side receives the declared amino-acid backbone and decorations. The product projection preserves element, bond order, and root. A stereochemical tag is optional metadata; a stereochemical conclusion requires an additional independently justified stereochemical certificate. Its outgoing rooted graph has backbone $N - C_\alpha - C'(=O) - O$ and side chain
$$C_\alpha - 5@X_4 - 4b@X_4 - S_4 - 10b@X_4.$$
The incoming side chain is $C_\alpha - 5@X_3 - S_3$ with terminal S–H.
4. All atom ownership and reagent-consumption conditions of the formal product grammar are satisfied. A stronger molecular interpretation additionally requires charge, proton/electron, stereochemical, geometric, and path admissibility certificates, and is not inferred from a formal rewrite.

The direction in this assumption is substantive. Reversing which side receives the terminal and internal products gives a different directed certificate. Parity, unordered slot matching, and sulfur atom count do not choose it. The carbon and sulfur locant maps agree with the source atom map [Sch26j, `article59-appA.tex`, "The map"]; the corrected cut variant is specified next. Backbone heteroatom sources in the formal witness follow the product grammar; the source's additional carrier-internal oxygen-provenance claims are not certified by this agreement of locants.

Proposition 6.3 (Identity of the two outputs)**.** *Under Assumption 6.2, and the identity-checking convention of the product grammar, the incoming output has the cysteine structure and the outgoing output has the methionine structure. This result identifies a product graph; it does not label a controller transition in advance.*

Proof. Map the incoming backbone atoms to N, C_α, C', O, O and $5@X_3$ to C_β. Its only sulfur lies terminally on C_β, giving $-CH_2SH$. On the outgoing side map $5@X_4$ to C_β, $4b@X_4$ to C_γ, S_4 to the side-chain sulfur, and $10b@X_4$ to C_ε. The resulting side chain is $-CH_2CH_2SCH_3$. Together with the stipulated backbone these are rooted, element- and bond-order-preserving isomorphisms to the two declared constitutional identity graphs. The map checks every heavy atom and bond, not only their counts. Distinct packet and unit indices make the two atom sets disjoint. The finite graph certificate proves constitutional identity only. An L-specific conclusion additionally requires independently established stereochemical certificates; storing an R/S

tag does not establish that it was selected. □

6.2 The chosen cut route and limited balance claims

We use the Article 59 boundary-cut Cys variant. It cuts $4b-5$ and $5-6$ on X_3 while retaining $4b$ and 6 in the residue of the carrier. Article 57's Cys row instead removes both of those vertices completely. These are different operations, despite sharing the same retained side-chain vertex 5. The former leaves a connected seventeen-vertex aromatic remnant; the latter leaves a connected fifteen-vertex remnant plus separately accounted removed atoms. On the Met side, deletion of $\{5, 4b, 10b\}$ from the eighteen-vertex carrier leaves components of orders seven and eight. Direct traversal of the explicit carrier edge list verifies these statements. We do not transfer a balance calculated for the seventeen-vertex route to the fifteen-vertex route [Sch26h, `article57-appA-entries.tex`, Cys row] [Sch26j, `article59-sec05.tex`, `def:paths`].

For completeness, retain the source's particular endpoint oxidation-index calculation as a separately typed numerical lemma. It is not an invariant of all rewrites allowed by the relaxed product grammar.

Lemma 6.4 (Compensating endpoint index changes)**.** *For the inspected Article 59 boundary-cut bond lists, let $k_3, k_4 \in \{0,1\}$ select alcohol (0) or aldehyde (1) at the two oxygen-bearing remnant ends. Then the carbon index changes are*

$$\Delta\omega_{C,3} = 2 + 2k_3, \qquad \Delta\omega_{C,4} = -4 + 2k_4.$$

With one -1 sulfur-index change assigned to each side, their sum is $-4 + 2(k_3 + k_4)$. It is zero exactly at $(k_3, k_4) = (1, 1)$, where the two side contributions are $+3$ and -3.

Proof. For carbon the source convention gives $+1$ per single bond to O, N, or S, -1 per bond to H, and zero for C–C bonds. At alcohol level, the five changed carbon contributions on X_3, in order $5, 4b, 6, 6\alpha, 6\beta$, are $(0, -1, -2, 1, 4)$, totaling 2. The nine contributions on X_4, in order $5, 4b, 10b, 11, 4a, 10a, 6, 6\alpha, 6\beta$, are $(-1, -1, -2, -1, -1, -1, -2, 1, 4)$, totaling -4. Replacing either alcohol terminus by its aldehyde changes -2 to 0, adding 2. The two specified sulfur changes sum to -2. Thus zero requires $k_3 + k_4 = 2$, and both binary values must be one. Substitution gives $(4-1, -2-1) = (3, -3)$. □

The two units therefore compensate globally; they do not make equal redox demands. Nor does this scalar zero prove a complete reaction equation or a kinetically accessible path. The source bond-list completion, the formal atom-preserving product certificate, and a future molecular completion are three distinct objects. The source's "same demand" inference is not used [Sch26j, `article59-sec05.tex`, `cor:nofourth`; inspected `junction-balance.py`, bond lists X3 and X4].

Lemma 6.5 (Rigid distance condition)**.** *Suppose sulfur sites lie in two planes with normal separation $d \mp h$ and unconstrained lateral displacement $u \in \mathbb{R}^2$. A prescribed S–S length $\ell \geq 0$ can be attained exactly when $|d \mp h| \leq \ell$, in which case $\|u\|^2 = \ell^2 - (d \mp h)^2$.*

Proof. The squared distance is $(d \mp h)^2 + \|u\|^2$. Necessity follows from nonnegativity of the second term, and sufficiency from taking a vector of the stated nonnegative squared length. Equality permits $u = 0$. □

For the source inputs $d = 3.40$, $h = 1.68$, $\ell = 2.05$, the toward-facing squared lateral distance is 1.2441, whereas the away normal distance is $5.08 > 2.05$. These are declared rigid-model parameters, not newly established measurements. A permitted lateral-register set must intersect the resulting circle; steric constraints, bond angles, and a continuous reaction path are additional conditions. The source's unfilled bond-length citation cannot turn this scalar construction into molecular evidence [Sch26j, `article59-sec06.tex`, `prop:closes`].

6.3 Marker transport and the readout convention

Use the marker encoding $L(FF) = A$, $L(FB) = C$, $L(BF) = G$, $L(BB) = U$. Let $E : \{F, B\}^6 \to \mathcal{B}^3$ apply L to successive pairs. Write κ for letterwise complement $A \leftrightarrow U$, $C \leftrightarrow G$, and τ for $C \leftrightarrow G$ with A, U fixed. If rev is ordinary triplet reversal, define

$$\rho = \tau \circ \mathrm{rev}, \qquad G_{\mathcal{B}} = \{1, \kappa, \rho, \kappa\rho\}.$$

Lemma 6.6 (Conjugate marker action)**.** *Sitewise marker complementation transports by E to κ, and six-site marker reversal transports to ρ, not to ordinary word reversal. The four images of UAC are UAC, AUG, GAU, CUA.*

Proof. Complementation sends the four marker pairs FF, FB, BF, BB to BB, BF, FB, FF, inducing κ. Reversal reverses the order of the three pairs and reverses the two sites inside each pair. Inside-pair reversal swaps FB with BF and fixes FF, BB, inducing τ. These commuting involutions give the claimed group. Applying

them to UAC gives the displayed list. Since E is bijective, the identities hold for all 64 words, not just the example. □

Choose one coherent directed coordinate convention:

$$h = (a, A, U, A, U, b), \qquad b = \kappa(a),$$
$$c_{\text{in}} = h_3h_2h_1 = UAa, \tag{11}$$
$$c_{\text{out}} = h_4h_5h_6 = AU\kappa(a).$$

Here h_1 and h_6 are both the wobble coordinates and the far exterior ends of the spatial junction. The incoming readout reverses the displayed spatial order, while the outgoing readout preserves it. This is a declared readout convention, not a derivation of continuous chemical $5' \to 3'$ order through the displayed six positions. Any such molecular reading requires a separate orientation lift. This choice removes the source's contradictory use of h_1 as both the first and third incoming position [Sch26j, `article59-sec07.tex`, `def:codons`, `prop:wobble`, `thm:startstop`]. Equation (11) is a family-selection and complementarity condition. Architecture alone does not imply it.

Proposition 6.7 (Uniform word relation)**.** *On the family* (11)*, $c_{\text{out}} = \kappa(c_{\text{in}})$. Among $G_{\mathcal{B}}$, only κ has this property for every a.*

Proof. Letterwise complement changes UAa to $AU\kappa(a)$. At $a = C$, the four possible images are the four distinct words in Lemma 6.6, and only κ gives AUG. Thus no other group member works uniformly. □

For UAU, ordinary reversal fixes the word, whereas complement changes it to AUA; all three ordinary non-identity word operations do not coincide. Alternating complementary hexamers do satisfy that complement equals a one-position cyclic shift. That word identity neither fixes a unique physical boundary nor proves phase maintenance. Likewise, preference for external U near resident A does not mathematically imply alternating AU composition, particularly under the stipulated noncanonical interaction. Selecting (11), and choosing a phase for a reader, remain independent conditions.

6.4 A side-specific release gate

Let $Y = \{U, C\}$, $R = \{A, G\}$, and let $N(x)$ mean that the abstract local register $A \cdot x$ is narrow, namely $x \in Y$. The dot here denotes an abstract register against resident A. It makes no canonical-pairing claim. Define the transported register readings

$$r_{\text{in}}(a) = a, \qquad r_{\text{out}}(b) = \kappa(b). \tag{12}$$

Assumption 6.8 (Selection and release)**.** A selected boundary presents a word from (11) in a declared frame, and has the resources and valid directed formation certificate required by Assumption 6.2. Conditional on successful formation, its two products are released exactly when their respective local registers in (12) are narrow. No competing product is accepted in place of a failed outgoing boundary product. A weaker "only when narrow" condition would establish necessity but not successful release or a nonempty witness.

Proposition 6.9 (Exact boundary truth table)**.** *Under Assumption 6.8, paired release succeeds precisely for $a \in Y$. The complete table is*

a	b	c_{in}	c_{out}	$(r_{\text{in}}, r_{\text{out}})$	*release*
U	A	UAU	AUA	(U, U)	*both*
C	G	UAC	AUG	(C, C)	*both*
A	U	UAA	AUU	(A, A)	*neither*
G	C	UAG	AUC	(G, G)	*neither*

The outgoing released product, when present, has identity Met by Proposition 6.3. For $a \in R$ the conclusion is no junction start; it makes no assertion about ordinary elongation at AUU/AUC.

Proof. Because $b = \kappa(a)$ and $\kappa^2 = 1$, both local readings equal a. They are therefore simultaneously narrow exactly on Y. Substituting the four letters gives the table; product identity is independent of the letter test. □

The original global-width rule would read $r_{\text{out}}(b) = b$. Then exactly one of a, b is in Y, so no paired release is possible. The outgoing transport is thus a genuine new condition repairing an empty conjunction. It is not a consequence of reversing a word. Within the restricted class of functions $T : \mathcal{B} \to \mathcal{B}$ required to satisfy exact register matching $T(\kappa(a)) = a$ for every a, the choice $T = \kappa$ is unique: substitute $a = \kappa(b)$. If only equality of narrow/wide status is required, four permutations work, since each may biject Y to R and R to Y in two ways. Our exact letter transport is therefore stronger than width covariance.

Proposition 6.10 (Frame covariance)**.** *Let $f \in G_{\mathcal{B}}$ be a coordinate frame, and display a word c as $f(c)$. Normalize a displayed word by f^{-1} before applying* (11)*–*(12)*. Then every entry of the truth table and its product identities is invariant under the choice of f. The displayed relation remains $f(c_{\text{out}}) = \kappa f(c_{\text{in}})$.*

Proof. Normalization recovers the original word because $f^{-1}f = 1$. All gate inputs and directed atom identities are consequently unchanged. The group is abelian, so $f\kappa = \kappa f$, proving the displayed relation. This applies to all four boundary letters in each of the four frames. Coordinate changes do not exchange the physical incoming and outgoing product roles. Such an exchange would require changing the directed boundary certificate as well. □

6.5 What complementary slots do and do not select

The eighteen source seed slots are

$$\begin{aligned}\mathcal{S} = \{&UUY, UCN, AGY, UAY, UGY, UGR,\\ &CUN, CCN, CAY, CGN, AUR, ACN,\\ &AAY, GUN, GCN, GAY, GGN, AUY\},\end{aligned}$$

where $N = \mathcal{B}$. Their only complementary unordered pairs are $\{UAY, AUR\}$, $\{CCN, GGN\}$, and $\{CGN, GCN\}$.

Lemma 6.11 (Unordered slot consequence)**.** *If two outputs must occupy distinct complementary members of $\mathcal{S}$, each of size two, their unordered slot pair is $\{UAY, AUR\}$. These conditions alone do not determine which product occupies which slot.*

Proof. For a full block xyN, complement is $\kappa(x)\kappa(y)N$; for a half xyY it is $\kappa(x)\kappa(y)R$, and conversely. Applying these formulas to the displayed list gives exactly the three pairs above. Only the first has size two on each side. Both bijections from two named products to its two slots satisfy the unordered requirements. □

The directed atom/readout certificate selects incoming Cys on UAY and outgoing Met on AUR. This direction is not furnished by the source paired-slot hypothesis alone [Sch26h, `article57-sec09.tex`, `hyp:pair` and `thm:forced`].

Production addresses, mutable external table routing, and the reader's oriented phase are different state components. Store the directed production certificate with its original UAY/AUR addresses. A sealing transition closes the formation/selection stage and preserves this certificate as provenance; routing exchanges are enabled only after sealing. The endpoint assignment is not required to satisfy the old paired-slot condition. In the selected assignment Cys occupies UAY; after the $UAY \leftrightarrow UGY$ exchange it occupies UGY, whose complement is ACR, not AUR. Standard elongation further makes Met a singleton at AUG. Thus a global all-stage paired-slot invariant would exclude the intended endpoints.

The reachability construction supplies two equal-size exchanges and the subsequent refinement by environmental control. Our interface requires those edges to preserve product graph identifiers, production provenance, and the reader state. They change routing only. The robust common boundary case $a = C$ gives outgoing AUG, whose Met elongation assignment survives every initialized stage and the control path. Allowing $a = U$ at a standard-table endpoint requires a separately typed initiation decoder: its AUA boundary product is still Met, whereas standard elongation AUA is Ile. Without that extra distinction, select $a = C$ for the endpoint witness. Neither choice changes a molecule into another by relabeling it.

7 Accepted sequences and the reset invariant

7.1 Three levels of STOP

We distinguish (i) an absent sense output, (ii) failure to release a newly formed product, and (iii) a functional stop of an existing sequence. The first is a property of a formation/selection relation, the second of a release gate, and the third of a controller. Use separate observations

$$\text{Absent}, \quad \text{Held}(q), \quad \text{Available}(q), \quad \text{StopSignal}(c).$$

Here Held and Available are an orthogonal controller-availability status of a product token. The completed formation graph already contains disconnected free-acid constitutional components. Held means that such a component is not yet admitted for emission; it does not mean covalently attached or chemically trapped. GATE changes availability without an additional bond rewrite. A physical retention/release mechanism remains a separate lifting condition. The checker retains the legacy strings `Bound` and `Free` for these two status values; they carry exactly this availability meaning.

In particular, an empty Gly side-chain set still gives a backbone-containing product and is not Absent. A control symbol STOP is not a 21st amino-acid graph. An absent table entry or a trapped fresh product does not by itself release an accumulated sequence, halt a reader, or reset it.

Let $\mathcal{T}_\sigma$ be the explicitly designated stop set at an initialized table stage. For the selected and vertebrate-mitochondrial endpoint it is $\{UAA, UAG, AGA, AGG\}$; for the standard endpoint it is $\{UAA, UAG, UGA\}$. Intermediate environment values may have additional absent outputs. A model must specify their stop policy separately; absence alone cannot silently make them stops. The common witness below uses only UAA, which belongs to every initialized stage's declared stop set. The table-2 AGR termination symbols are reference-table designations,

not a claim that every vertebrate realizes them by the same direct release-factor mechanism; NCBI describes a human mitochondrial frameshift caveat [EO24]. The junction truth table accounts only for the local UAA/UAG failure cases. Functional control at UGA or AGR requires the independently declared table-level rule.

7.2 State and exact guarded transitions

An accepted output sequence is a finite ordered list of product identities emitted by a reader. This definition does not assert covalent polymerization; a physical peptide interpretation requires a transfer/polymerization lift. Write the controller state as

$$z = (\sigma, m, R, U, j, f, \phi, p, w, \mathcal{L}, o),$$

where σ is the routing stage; m the mode; R the remaining packet set; U the set of already reserved packet identifiers; j the current packet or $\perp$; f its coordinate frame; ϕ its directed phase or $\perp$; p the next triplet position; w the current emitted word; $\mathcal{L}$ the list of completed sequence records with boundary-packet and emitted-token provenance; and o the current observation. The graph/reservoir and certificates are additional persistent state components of the common model. Packet atom sets and product tokens are pairwise disjoint. The mode set is

$$\{\text{Idle}, \text{Ready}, \text{Formed}, \text{Primed}, \\ \text{Active}, \text{Stopped}, \text{Released}, \\ \text{Halted}, \text{Rejected}\}.$$

The only initial mode is Idle, with empty $U, w, \mathcal{L}$, no current packet, and unset phase. A normalized tape has a boundary triplet at position 0; subsequent positions are $3, 6, \ldots$. A reversed physical direction is handled by its declared directed normalization, not by changing these local increments.

Assumption 7.1 (Controller contract)**.** The transition relation is exactly the following table, with its declared formation-certificate microsteps allowed inside FORM. An unavailable guard disables its row; there are no implicit emissions, resets, or mode changes. Routing-only edges preserve every controller component and immutable certificate. Resource consumption is monotone, and a consumed output token cannot be emitted again.

RESET may follow a rejected attempt, but it does not turn that attempt into an accepted empty sequence. RESET after Halted is a genuine new boundary with a fresh resource packet; a stop at an old boundary is not automatically a start at the next one. The source leaves downstream frame maintenance open [Sch26j, `article59-sec08-09.tex`, target on frame maintenance]; the contract above states precisely the additional formal conditions we use.

7.3 The invariant and its proof

Theorem 7.2 (Every accepted nonempty sequence begins with Met)**.** *Assume the directed product and release conditions, verified identity certificates, and the controller contract. Every reachable state satisfies:*

1. *each word component of a record in $\mathcal{L}$ is nonempty and its first identity is Met;*
2. *in modes Active, Stopped, or Released, w is nonempty, its first identity is Met, and its phase is the boundary-established phase;*
3. *whenever the next position is active, p is a multiple of three;*
4. *every accepted sequence has a distinct reserved boundary packet, and no emitted product token is reused.*

We refer to a record by its word when discussing first identities. The conclusions hold for every finite run and every accepted sequence in an infinite run, if such a run exists. They do not assert that an infinite run is possible with finite resources.

Proof. Induct on the number of transitions. Initially $\mathcal{L}$ is empty and no active word exists, so all claims hold. RESET cannot create an accepted or active word; its guard chooses an unreserved packet, records it permanently, and clears the old phase. FORM changes only the graph state and observations. GATE yields a free output but emits nothing, while FAIL rejects an attempt without completing a sequence.
START is the only edge entering Active from a mode with empty w. Its guard requires the outgoing free graph of the directed certificate, so Proposition 6.3 gives $\mathrm{Id}(q_{\mathrm{out}}) =$ Met. This is where the first label is derived. The row initializes exactly that singleton and sets $p = 3$ and the boundary phase. STEP only appends; it cannot alter the first identity, and $p \mapsto p + 3$ preserves the congruence and phase. Token-consumption guards prevent a second emission of the same product.
OBSERVE and RELEASE preserve the active word and phase and prohibit further STEP transitions by changing mode. HALT archives only such a nonempty released word, clears its active state, and preserves all used-resource records. ROUTE preserves every quantity in the invariant. There are no other rows by the

Rule	Exact guard	Update; every unlisted component is preserved
RESET	$m \in \{\text{Idle}, \text{Halted}, \text{Rejected}\}$; choose $j_{\text{new}} \in R$ with $j_{\text{new}} \notin U$ and disjoint available packet atoms; old active sequence cleared or archived.	Reserve the selected packet: $j \leftarrow j_{\text{new}}$, $R \leftarrow R \setminus \{j_{\text{new}}\}$, $U \leftarrow U \cup \{j_{\text{new}}\}$; set $m = \text{Ready}$, $w = \epsilon$, $\phi = \perp$, $p = 0$, $o = \perp$; set f to its chosen declared frame and record its selected boundary.
FORM	$m = \text{Ready}$; selected boundary satisfies (11); packet has a valid directed Γ_j and all required resources.	Execute its finite rewrite certificate; set $m = \text{Formed}$ and store the two disconnected output graphs with Held status and unconsumed tokens. No emission.
GATE	$m = \text{Formed}$; both normalized registers are narrow; formation completed and release certificate enabled.	Mark both output tokens Available, set $m = \text{Primed}$, $o = \text{Available}(q_{\text{out}})$. The incoming product is separately stored, not prepended to the new sequence.
FAIL	$m = \text{Formed}$; at least one local register is wide.	Set $m = \text{Rejected}$, record $\text{Held}(q_{\text{out}})$ and no start. Its reserved packet stays spent. No completed sequence is added.
START	$m = \text{Primed}$; $w = \epsilon$, $\phi = \perp$; q_{out} is the unconsumed free outgoing certificate of packet j; its identity is verified and endpoint initiation policy permits its address.	Consume that token; set $w = (\text{Id}(q_{\text{out}}))$, $\phi = (f, 0)$, $p = 3$, $m = \text{Active}$. This row contains no literal Met label.
STEP	$m = \text{Active}$; normalized position $p \equiv 0 \pmod 3$; next codon is not in $\mathcal{T}_\sigma$; selector chooses one sense product; a fresh free token with that identity and permitted elongation certificate is available.	Consume the token, append its verified identity to w, and set $p \leftarrow p + 3$. Preserve ϕ.
OBSERVE	$m = \text{Active}$; $p \equiv 0 \pmod 3$; next codon lies in $\mathcal{T}_\sigma$ and its explicitly declared stop-control certificate is enabled.	Set $m = \text{Stopped}$, $o = \text{StopSignal}(c)$. Preserve w, p, ϕ. Sense absence or a trapped junction product may support this certificate but cannot replace it.
RELEASE	$m = \text{Stopped}$; accumulated-sequence release certificate is enabled.	Set $m = \text{Released}$ and mark the current w released. No next sequence is started.
HALT	$m = \text{Released}$; halt certificate enabled.	Append $(j, w, \text{emitted token identifiers})$ to $\mathcal{L}$ as one accepted sequence record; set $m = \text{Halted}$, $w = \epsilon$, $\phi = \perp$, $j = \perp$, $o = \perp$. Packet/token consumption records persist.
ROUTE	Formation selection sealed; a routing edge is allowed by the assignment grammar; immutable product provenance is available.	Change σ and table-routing data only; preserve graph identities, m, R, U, j, f, ϕ, p, w, $\mathcal{L}$, and o.

contract. Thus each invariant is preserved. Every finite accepted prefix of an infinite run is covered by the same induction. The archived packet identifiers are distinct because RESET permanently adds each to U, and HALT cannot recur without passing through a fresh RESET and START. □

No hypothesis in this proof says "start emits Met." It says which certified outgoing graph can be emitted first and prohibits a different earlier emission. Its graph identity supplies the name. Several safeguards have distinct roles. Permitting a non-Met first emission, whether by STEP before START or by admitting an arbitrary product at START, can destroy the first-identity conclusion. Reusing a packet or product token can destroy ownership guarantees. Archiving a sequence without the prescribed stop/release steps would defeat those operational guarantees even if its first identity remained Met. By contrast, an aborting RESET that discards an unfinished word, clears its phase, and reserves a fresh packet can preserve all stated Met-first and ownership invariants; it loses the unfinished sequence rather than furnishing a counterexample to this safety theorem. The present contract excludes that abort operation but does not claim every exclusion is necessary. These are properties of the declared machine, not laws of molecular chemistry.

7.4 A constructive nonempty compatible witness

Lemma 7.3 (Disjoint packet copying)**.** *Let a finite product/reagent certificate use atom identifiers in V and token identifiers in T. For each $j = 1, \dots, n$, replace them by (j, v) and (j, t). If its rewrite guards depend only on element/bond/port data and local availability, these n renamed certificates are valid, have pairwise disjoint atom and token supports, and can be composed on their disjoint union.*

Proof. Each renaming is injective and preserves all vertex attributes and adjacencies. Induction over the finite rewrite list therefore preserves its guards and poststates. Distinct first coordinates make the supports disjoint; a step on one copy cannot consume a resource from another. Interleaving or concatenating the renamed lists consequently preserves every copy's unexecuted guards. □

Theorem 7.4 (Bounded repeated segments and table-stage compatibility)**.** *For every integer $n \geq 1$, the formal product grammar and the corrected junction/controller specification have a witness with n accepted sequences, each* (Met, Ala)*, compatible with the selected-to- mitochondrial-to-standard routing path. The witness uses n distinct junction packets, n additional certified Ala tokens, and explicitly declared release, halt, and reset edges. It establishes formal compatibility, not molecular realization of those edges.*

Proof. Take n disjoint indexed copies of the directed Cys/Met formal graph certificates and reagent reservoirs supplied by the product grammar, using the boundary-cut variant. Give each packet the external word $CAUAUG$ (normalized pair UAC/AUG) in any chosen one of the four coordinate frames and store its original production addresses. Give it one distinct certified Ala token. Lemma 7.3 preserves every atom-map and resource guard of each finite certificate. Neither the copied template nor its provenance record is itself a consumed molecule; each indexed output token represents a distinct consumable graph instance. The boundary has $a = C, b = G$ and both normalized local registers equal C; hence the release guards have a strict Boolean witness. A singleton allowed lateral-register set containing $(\sqrt{12441}/100, 0)$ meets the stated rigid distance condition; this supplies only that optional scalar-model component. If the separate source endpoint redox submodel is included, choose $k_3 = k_4 = 1$. We do not identify its remnant completion with the relaxed graph certificate.
At the selected formation stage store the UAY/AUR paired-address certificates, then seal the formation/selection record. Traverse the declared routing edges exchanging UAY with UGY and AAR with CAR, followed by the environment-control refinement. By the interface condition these edges preserve all indexed graph certificates and reader state. Their independently checked tables assign Met to AUG, Ala to GCU, and stop control to UAA throughout the initialized route, so the same reader witness works before, between, or after these edges. The paired-address restriction is attached to the sealed production record, not reapplied to endpoint Cys/Met slots.
The paired certificate is not merely two target names. Its explicit 174-step relaxed edit word opens $4b - 10b@X_4$ first, opens the Cys boundary bonds, and detaches the two sulfur hydrogens, retaining their labelled vertices for later reassignment. Steps 7 and 8 join $5@X_3 - S_3$ and $S_4 - 4b@X_4$ while retaining $S_3 - S_4$. Thus step 8 has the bridge path $5@X_3 - S_3 - S_4 - 4b@X_4$. Step 9 removes $S_3 - S_4$ and step 10 joins $S_4 - 10b@X_4$. The remaining edits complete the two product components and all represented remnants/resources. Direct replay checks every local capacity guard and the unchanged active-subgraph set of 158 vertices, including four non-

atom boundary ports. The other four evolved vessels are unchanged disjoint context; the context-extension lemma carries the same path into the six-vessel packet. This ordering is a formal path in the relaxed grammar, not an elementary reaction mechanism. Its endpoint components have exactly the constitutional identity projections used in Proposition 6.3.

For packet j, supply the normalized tape (AUG, GCU, UAA). Execute RESET, FORM, GATE, START, STEP, OBSERVE, RELEASE, HALT. Each guard holds: the packet is fresh, its rewrite certificate exists, both gates are narrow, its outgoing graph is free and identity-checked, the Ala token is distinct and available, UAA has its declared stop certificate, and the formal release and halt rules are enabled. The accepted word is (Met, Ala). There remain $n - j$ unused packets, so the next RESET is enabled whenever $j < n$. Induction on j constructs all n segments without atom or token reuse. The last Halted state need have no enabled RESET. This proves the claimed bounded existence without an unearned recurrence assumption. □

The optional rigid distance witness and the endpoint oxidation-index witness are scalar factors of the formal model. Neither certifies steric compatibility or a conserved molecular realization of the graph and controller factors. Similarly, the exact selection family can be realized abstractly by a predicate that accepts only the physical word $CAUAUG$, or by a score assigning it 1 and all other words 0 with a strict threshold. Such a witness proves the selection condition consistent; it does not derive that selection from the resident poly-A carrier. It must not be represented as an independent physical prediction of AUG.

Corollary 7.5 (Minimal one-residue witness)**.** *For every $n \geq 1$, n fresh junction packets alone suffice for n accepted singleton words* (Met) *in the same formal controller, provided its stop, sequence-release, and halt certificates are supplied.*

Proof. In the preceding construction omit the Ala tokens, use tape (AUG, UAA), and omit STEP. After START the next position is 3, so OBSERVE, RELEASE, and HALT are enabled there. The same fresh-packet induction applies. □

Corollary 7.6 (Conditional molecular interpretation)**.** *If a molecular interpretation maps the constructed packets, every used rewrite, register/release operation, routing implementation, output transfer, stop, sequence release, and reset to an admissible molecular path; preserves persistent atom ownership, product identities, direction, phase, and resource consumption; and supplies n compatible fresh packets, then its n accepted output sequences have first residue Met. A covalent peptide conclusion further requires that interpretation to preserve the peptide-transfer meaning of emission and accumulated-sequence release.*

Proof. Apply the interpretation edge by edge to the finite witness. Preservation of its guards and identities carries the invariant of Theorem 7.2 to the interpreted sequence. The extra clause is needed because an ordered identity list is not itself a peptide graph. □

7.5 Proof status and reproducible checks

The companion standard-library checker verifies all 256 marker/frame conjugacy instances, all sixteen framed boundary cases, the four release rows, all 4096 external hexamers against the declared readout predicate, the complementary-slot enumeration, the cut/remnant distinction, the rigid distance inequalities using exact rational arithmetic, and every source bond-list oxidation contribution. It verifies graph identity by adjacency and element labels and independently replays all 174 guarded edits of the paired sulfur certificate, including its bridge and separated-sulfur stages. FORM in the controller checker imports that separately replayed formal certificate; no molecular path is checked. The checker also checks the common $AUG/GCU/UAA$ tape across initialized routing stages, and replays bounded reset witnesses with persistent packet/token identifiers. It also rejects representative illegal transitions. These finite checks support the displayed constructive results; the all-run guarantee rests on the transition induction, not on bounded testing.

Completed conclusions are the marker transport, unordered slot implication, corrected release truth table, rooted identity implication, controller safety invariant, and nonempty bounded formal witness. New unverified molecular conditions are the precursor conversion, physical junction/support and directed sulfur placement, noncanonical selection of the readout family, outgoing local register transport, sufficiency of the release gate, and physical implementations of phase maintenance, transfer, stop, release, and reset. The source's proposed S–S delivery explains how two sulfur atoms are distributed within the stated mechanism. It does not prove that sulfur is the unique possible bridging chemistry: that stronger result would require an independently specified class of alternative reagents and an exclusion argument for all of them. No historical or adaptive inference is needed for any theorem here.

8 A common witness and the molecular lifting boundary

The preceding constructions must be assembled on one state space. A list of nonempty modules is insufficient if their shared parameters, atom identities, or phase restrictions conflict. This section gives the formal assembly explicitly and then separates the additional physical lifting question.

8.1 Persistent and stage-local invariants

Use the state tuple in (5). Its persistent conditions are:

(C1) The immutable architecture/provenance record H specifies an initially prepared $(X-A)_3$ incidence for each copy, resident adenosine identities, and distinct junction copies. Address tags are not resident-base identities. Extraction changes the current graph Γ under (C3); an intact post-extraction carrier is not a persistent invariant.

(C2) The frame normal form and external-word encoder agree. All codon coordinates used by routing and readout use that same normal form.

(C3) Atom identifiers are unique, element identities are immutable, and graph edits obey the declared resource, support, and bond rules. A terminal product used by a decoder has an accepted graph certificate.

(C4) Routing outputs refer to product graph identities through one map I. The selector control lies in $[0, 1]$ and may be partially discriminating at an intermediate value.

(C5) The controller uses explicit start, extension, halt, and reset transitions. A consumed packet never returns to the unused inventory.

The paired sulfur placement predicate is required at the completed selected-routing stage. It is not a persistent condition on the final codon table. A seal or leave-formation transition records that the paired formation certificate has been completed before address exchange. Later routing edges leave the atom-graph certificate and the junction readout coordinates fixed.

The Watson–Crick incidence graph also has a precise role. It is a table-conditioned comparison object used to prove the sharp obstruction. The common model does not simultaneously demand a twenty-edge perfect matching in that unchanged graph. Such a demand would contradict the proved matching bound. The actual seed/refinement/routing construction is a separately specified relation on addressed states.

8.2 Resource separation and compositionality

Definition 8.1 (Origin relabelling)**.** An origin relabelling replaces each atom identifier v in a certificate by (j, v) for a new copy index j, preserving element, charge, bond, support, and local carbon-index data. Carrier indices and resource identifiers receive the same copy prefix. A local rule is *origin-equivariant* if this relabelling takes every legal instance to a legal instance.

The formal product rules have this property: their guards inspect element, local incidence, support, and resource status, rather than a privileged global atom name. The property is important because the library is a family of possible constructions. It is not a claim that a single six-core precursor is converted into all twenty residues at once.

Lemma 8.2 (Disjoint resource composition)**.** *Let $P_1, \dots, P_s$ be finite legal graph paths for an origin-equivariant rule system. Give them pairwise disjoint origin prefixes and the disjoint union of their input carriers and finite reservoirs. Suppose each rule instance reads and changes only its own prefixed atoms and resources, apart from fixed shared constants. Then their sequential concatenation, or any interleaving preserving each path's internal order, is legal and has the disjoint union of their terminal graphs. Every additive conserved inventory equals the sum of the module inventories.*

Proof. At an interleaving step, all earlier operations from other modules have disjoint support, so they have changed neither the current module's graph nor its reservoir. The next rule has exactly the same local input as in its original certificate, up to origin relabelling. It is therefore legal. Induction on the total number of executed steps proves legality and the terminal statement. Since no atom identifier occurs twice, element and other additive inventories add without overlap. □

For a repertoire certificate, s is the number of independent unary constructions plus the paired sulfur construction, not necessarily twenty independent single-carrier paths. The sulfur certificate keeps its two reacting copies together as one module. A library can store the terminal graph descriptions without storing twenty consumable molecules. A reading experiment that actually emits molecules needs additional fresh product or precursor packets, allocated separately from that descriptive library.

Lemma 8.3 (Interface composition under full noninterference)**.** *Let two transitions on a product state have disjoint write sets. Suppose, in addition, each transition preserves every coordinate and predicate read by the other's full guard or update function. If both guards initially hold, either transition preserves applicability of the other, and the two resulting composite states agree. A shared immutable graph library is permitted among the read coordinates.*

Proof. The full guard of the second transition retains its truth value after the first by the stated preservation assumption, and conversely. The update right-hand sides also retain their values. Disjoint writes therefore commute coordinate by coordinate. □

Read-only access to Q alone does not imply this stronger hypothesis. An extension guard may also read (e, σ): for example, changing UGA from Trp to STOP disables its sense-extension transition. The construction below therefore serializes library preparation, endpoint routing, and the controller run. Only explicitly invariant boundary data are transported across routing. It makes no generic claim that reading and assignment changes commute.

8.3 The constructive formal realization

Theorem 8.4 (Joint formal realization)**.** *For every positive integer n, the finitely specified graph-and-controller system with a continuous selector control has a nonempty model with the following properties.*

(i) Its six-bit carrier has the twenty-class frame quotient and a fully directed sixty-four-address representative, while its resident tether remains AAA.

(ii) Its finite product library contains the twenty checked constitutional target graphs under the declared formal product grammar, with disjoint origin-labelled input resources for the repertoire construction.

(iii) Its seed, propagation, refinement, phase-release, and local-routing certificate reaches the complete vertebrate mitochondrial reference table. The stated selector-refinement regime also reaches the complete standard reference table.

(iv) Its junction uses two triplet carriers, the specified incoming/outgoing word coordinates, and coherent paired release. The same formal model admits n successful nonempty segments whose first emitted graph has the Met constitution, using n disjoint fresh-boundary packets and the controller's stated guards.

(v) It satisfies (C1)–(C5) at every applicable stage. The paired formation-routing predicate holds where required and is explicitly retired before the endpoint exchanges.

This is an existence and reachability statement for the declared formal grammar and the supplied initialization data. It is neither a chemical-path existence assertion nor a unique, target-independent selection theorem.

Proof. Choose the normalized address representative with both binary reference tags zero. The registry construction supplies all sixty-four external words and its quotient map; the physical tether coordinate is AAA in every representative. Choose the explicit seed and routing data in the reachability certificate. Product references in those data are resolved through the single identity map of the product graph library, rather than by altering an atom label to match a codon.

For every repertoire path, prefix its atoms and donor packet with a distinct module identifier, keeping the two sulfur copies together in their paired module. The product certificates provide finite legal paths and their terminal constitutional graphs. Lemma 8.2 gives a common finite reservoir and a legal concatenation of all those paths. The active local graphs are attached to the carrier's declared open interfaces. The two unused residual cores and resident-tether context remain inert typed records; the formal certificate does not supply their full molecular graph or a physical grafting map. The repertoire uses eighteen unary carrier records and one paired record containing two carriers: twenty triplet carriers represent 120 original cores, with twenty active local residual-core graphs. Store the resulting graph descriptions in Q. This proves nonemptiness of the graph/library part without consuming one atom twice.

Execute the seed, propagation, refinement, and phase transitions in their certified order. The selected-routing state satisfies the paired slot predicate. Execute the explicit seal transition and the two permitted address exchanges. Each exchange meets the local guard in the reachability chapter; the all-codon check identifies the resulting total map with the vertebrate mitochondrial table. Execute the allowed selector-control path in the stated refinement regime. Intermediate ties or absence states are admitted as transitional states, and the terminal strict inequalities and halt rules identify the standard endpoint. Neither this path nor the graph rules changes the resident tether or frame normal form.

For the controller choose the witness incoming outer base C and its complementary outgoing base G. The prescribed coordinate maps give incoming UAC and out-

going AUG. Both release gates are true. The outgoing product is the checked sulfur graph with the Met constitution. AUG has the same relevant output throughout the initialized routing/selector states used by the witness; the controller's start action reads the immutable product certificate. The junction chapter's start-before-extension and reset rules then apply.

For an explicit nonempty trace, choose a one-residue segment: START emits the certified Met graph, OBSERVE at UAA records the stop input, RELEASE performs the controller release step, HALT closes the segment, and RESET chooses a fresh boundary. UAA is a stop input at both named endpoints. Allocate n prefixed copies of a successful boundary packet before the run. The controller marks each consumed prefix as used and resets only to the next unused prefix. Origin equivariance supplies the same accepted local construction on each copy. By the reset induction, each of the n selected nonempty segments starts with the Met graph. All resource supplies are finite because n and every constituent certificate length are finite.

Finally, check the shared coordinates. The frame and word maps are common to the routing and junction. The graph paths and library identities are fixed before routing; later routing never mutates them. The junction gate and AUG start witness remain valid throughout the selector interval. The controller run can be placed after the chosen endpoint is reached, so its full guards see a fixed routing table. Phase release precedes exchanges, so no final table is required to satisfy a retired predicate. All nonempty components have thus been assigned compatible values in a serialized finite execution. These assignments are an explicit witness of the full formal conjunction. □

Corollary 8.5 (Finite resource sufficiency)**.** *If R_0 is the finite inventory required for the library construction and R_B the inventory of one fresh successful boundary/segment packet, then $R_0 + nR_B$ is sufficient for the corresponding n-segment formal witness, componentwise by element and atom type. No finite bound independent of n follows for consumed resources.*

Proof. Use disjoint prefixes for the library and the n packets and apply the additive conclusion of Lemma 8.2. The controller never recycles a consumed packet. □

The theorem binds the modules through common addresses, immutable graph identities, phase transitions, and fresh-resource semantics. It does not demand simultaneous physical occupancy of every symbolic module in one molecular cage. Repertoire membership is a family of formal preparations; endpoint decoding is a table on addressed inputs; a finite controller run uses a finite supply of prepared or preparable packets. A claim about all these activities in one physical experiment needs the lifting conditions below.

8.4 Why separate physical witnesses do not suffice

Let $\Theta_A = (0, 1/2)$ and $\Theta_B = (1/2, 1)$ be admissible parameter sets for two modules. Each is nonempty, but there is no common θ for their conjunction. The same failure can occur when two individually feasible paths end at different conformations assigned the same graph, or when two modules require the same atom to be in different products. Product-of-existence reasoning misses each of these conflicts.

The formal proof avoided them by using a single selector interval, exact shared graph states, disjoint atom prefixes, and specified frame maps. It cannot avoid the analogous molecular question by assuming that a drawing of a graph is a configuration. A physical configuration includes additional continuous and discrete information: coordinates, solvent/environment, charge/electronic state, stereochemistry, tether constraints, and compartment or reservoir access.

Definition 8.6 (Compatible molecular lift of a finite certificate)**.** Let $z_0 \to \cdots \to z_m$ be a formal certificate. A compatible molecular lift consists of a common parameter θ_*, molecular interface configurations $x_0, \dots, x_m$, and, for each edge, an admissible path $\gamma_i : [0, 1] \to \mathcal{X}_{\theta_*}$ such that:

(L1) a projection π maps x_i to the declared formal state z_i, with common atom identities and product/readout interpretation;

(L2) $\gamma_i(0) = x_{i-1}$ and $\gamma_i(1) = x_i$, including every environmental-control or relaxation step;

(L3) every path obeys the stated chemical, geometrical, conservation, reagent, and stereochemical restrictions at θ_*;

(L4) the initial interface is admissibly preparable, terminal graph identities agree with molecular identities, and controller events correspond to the asserted release/start/halt observables.

The interface configurations must be shared between adjacent edges. A collection of separately feasible endpoints with unmatched conformations is not such a lift.

Proposition 8.7 (Conditional molecular transfer)**.** *If the finite witness of Theorem 8.4 has a compatible*

molecular lift, then its concatenated molecular path realizes the same endpoint decoder and the same finite accepted start/reset trace, under the lift's interpretation of those observables.

Proof. Reparameterize the finitely many paths onto consecutive subintervals of $[0,1]$. Their shared endpoint equalities make the concatenation continuous wherever continuity is part of the admissibility model; designated discrete transitions retain their prescribed state changes. Conditions (L1)–(L3) preserve the atom and state interpretation on each segment. At the terminal interface and at each controller event, (L4) transfers the formal identity/readout conclusion to the asserted molecular observable. □

This proposition is a transfer statement, not the missing lift. It identifies exact sufficient conditions whose joint realization remains open. No conclusion of Theorem 8.4 asserts those conditions are chemically achievable.

8.5 Robustness and local path obligations

If a finite interface family is described by strict inequalities $g_j(x,\theta) > 0$, it is useful to provide a common margin rather than separate verbal feasibility claims. If g_j is Lipschitz with constant L_j near a witness (x_*,θ_*) and $g_j(x_*,\theta_*) \geq \varepsilon_j > 0$, then any perturbation of norm less than $\min_j \varepsilon_j/L_j$ preserves those inequalities, omitting constant constraints with $L_j = 0$. The proof is the inequality $g_j(x,\theta) \geq \varepsilon_j - L_j\|(x,\theta)-(x_*,\theta_*)\|$. This is a stability test for a supplied witness, not a way to manufacture one.

Likewise, a continuous scalar chirality indicator with an isolated zero need not change sign: $s(u) = u^2$ is a counterexample. If s is differentiable, $s(0) = 0$, and $s'(0) > 0$, then $s(u)/u \to s'(0) > 0$, so the sign differs on the two sides for sufficiently small nonzero u. A proposed stereochemical crossing must therefore provide transversality or another explicit sign-changing condition, and it must provide a molecular path carrying that indicator. Static inequalities alone do not connect configurations.

9 Consequences and limits of the construction

9.1 What the numerical correspondences establish

The registry theorem fixes twenty equivalence classes for the declared six-bit action. This number is stable under a change of coordinates that intertwines the action. It is not stable under changing the retained data or the quotient: directed addressing has sixty-four states, and the paired junction has a different state space. Likewise, the number eighteen in the Watson–Crick matching theorem is a compatibility maximum for a graph built from a specified table. It is not a count of surviving registry classes or a theorem that two products cannot exist.

The product chapter supplies a third count. Eighteen non-sulfur targets consist of sixteen ordinary retained-framework constructors, the backbone-only Gly constructor, and the extended-ring Trp constructor. The literal eighteen-member retention family in Article 57 instead includes the two sulfur entries and omits Gly and Trp. The seed chapter supplies a fourth count: eighteen occupied seed slots represent seventeen distinct product demands because Ser appears twice. The argument succeeds only when maps, rather than equal integers, connect these sets.

The formal model illustrates why an exact count can be useful without being explanatory by itself. The quotient theorem limits a deterministic class-invariant production map; an injective twenty-label assignment saturates that limit. The subsequent routing map is not class-invariant, so it can access the finer codon structure needed for the reference tables. The product grammar contains a library of twenty checked endpoints, but its rule schema admits additional endpoints. No theorem here says that the chosen twenty are the only reachable molecular graphs.

9.2 Which assumptions carry the endpoint information

The seed incidence relation, the choice of product at each selected seed, the refinement choices, and the locations of the affine selector modules are declared data. They encode information from the reference tables. Their consistency can be proved without circular reasoning if the conclusion is explicitly that the supplied data admit a realization. The circular inference would be to use those data and then claim that the reference table was deduced independently of them.

The assignment moves themselves are generic schemas. An exchange is authorized by a local address relation and occupancy, not by the statement that the result is a familiar biological table. This separation makes the path certificate meaningful: the endpoint can be a search target while the move predicate remains fixed. It also exposes alternatives. A stronger selection theory must explain why one allowed seed/routing history is favored or why the others are inadmissible. Such an explanation would need an independently specified selector and a nonempty joint parameter region.

9.3 What the product graph witness earns

Atom provenance and terminal identity checks prevent several weak substitutes for a repertoire proof. A named row cannot pass merely because its final string says "Met." The terminal graph must contain the appropriate backbone and side-chain connectivity. No two products in a coupled certificate may claim the same atom. Every external nitrogen, oxygen, hydrogen, or sulfur source must appear in the resource ledger. A remnant must remain in the state rather than vanish when a desired fragment is extracted.

These are real restrictions on a formal certificate. Nevertheless, split/join operations are permissive symbolic primitives. They do not encode activation barriers, solvent effects, intermediate electronic states, or competing chemistry. Constitutional graph equality is also weaker than full molecular identity when stereochemistry, protonation state, isotopic composition, or conformational state matters. The graph result therefore supplies an auditable structural layer and a set of explicit physical obligations. It does not license a claim of experimentally realized synthesis.

The precursor-to-carrier bridge is an additional boundary. This paper's graph paths start from its declared post-carrier structures and donor packets. The unresolved patent atom-map discrepancies are not repaired by downstream graph reachability. A continuous chemical route from six original cores to the selected $(X-A)_3$ representative remains part of a full physical realization.

9.4 The sulfur junction and initiation

The junction construction uses two distinct carrier copies and a paired sulfur resource. Its word relation is a conditional complement relation in specified readout coordinates. The side-specific outgoing gate is a new transport rule, checked on all four base values. Ordinary reversal of a word would not by itself produce that gate. The central interface identifies where the paired reaction is supported; it does not prove that adjacent triples lack centers or that co-excision is forced by parity.

The repeated-start result is an invariant of a controller with fresh-boundary reset. Its outgoing product is identified from a certified Met graph, and start precedence makes that product the first emission. It does not follow merely because one incoming word is UAC and one outgoing word is AUG. Continued segments require maintained phase, valid readout, available resources, and successful reset. The finite-prefix resource theorem makes these qualifications operational: every requested finite run has its own sufficient reservoir, while no finite batch supports unlimited successful production.

A codon's internal elongation assignment and its role at a start boundary are separate. The formal reset witness uses an AUG boundary, avoiding an accidental inference that every AU-purine elongation codon initiates in both reference tables. The controller's halt operation is also explicit. Empty sense output alone is an absence observation; only a defined transition makes it termination.

9.5 A useful hierarchy of stronger claims

The present construction establishes a nonempty formal model and named reachable reference endpoints. Progress toward a stronger interpretation can be measured against four further questions.

1. *Restricted molecular paths.* Can the graph primitives be replaced by a chemically justified rule set without losing the repertoire or the path?
2. *Common conditions.* Do all modules admit paths at one compatible choice of geometry, environment, reagent supply, and frame/readout convention?
3. *Independent placement.* Can seed and selector-placement data be derived without consulting the endpoint tables?
4. *Selection among alternatives.* Does the resulting reachable set single out a table, or can quantitatively specified dynamics favor it?

These questions are not answered by strengthening adjectives in the theorem statement. Each requires a new certificate, an additional argument, or a narrower and independently justified state space.

9.6 Conclusion

A typed chrysene carrier supports a coherent finite architecture linking a twenty-class registry, sixty-four addressed coding words, an explicit molecular-graph library, staged assignment operations, and a junction readout controller. The combined formal model admits constructive paths to the vertebrate mitochondrial and standard reference tables and supports a conditional Met-first reset invariant. Its freedom is explicit: the graph and routing grammars admit alternatives, and some initialization data are table-informed. The strongest completed claim is therefore constructive formal realization with checked interfaces. A physical genetic-code realization remains conditional on the common molecular lift, and independent or unique selection remains a further problem.

A Certificate organization and reproducibility

The accompanying source project contains four self-contained certificate modules, a separate extraction-guard audit, and a combined verification entrypoint. The finite computations require only the Python standard library. The manuscript compiles with a conventional pdfLaTeX installation, without shell escape. A successful compilation checks document consistency, not mathematical or chemical validity.

A.1 What is recomputed

The registry module reconstructs all binary descriptions, frame orbits, transported word actions, decorated carrier quotients, table-conditioned incidence graphs, matching witnesses, and the minimal registry-preserving endpoint refinement. It checks complete data rather than sampling marker strings. The pairing graph and reference-table input are recorded explicitly so that the reader can distinguish computed consequences from supplied data.

The product module reconstructs every persistent atom graph and each legal bond edit, including the paired sulfur path. It checks the atom inventory, source-carbon retention, element and bond constraints, terminal constitutional graph, remnant preservation, and finite donor supply. It records required stereochemical tags without claiming a stereoselective reaction. The certificate includes the surviving material and unused donors, rather than retaining only the desired product component.

The assignment module reconstructs the seed matching, all propagation and refinement records, the two guarded exchanges, the affine selector functions and their equality wall, and all sixty-four values of both endpoint tables. It also checks an explicit alternative and the exact size of the routing component under its stated exchange rule. The junction module checks the word and frame operations, transported release gates, six-word branch cases, atom-identity projection, stage handling, and resource-aware controller traces.

The combined verifier reruns these modules on temporary copies of their packaged data, verifies the deterministic outputs, and checks shared interfaces. It also invokes the separate data-consuming extraction-guard audit and its rejection tests. Deterministic regeneration tests reproducibility of the fixed builders; the guard audit supplies additional direct predicates and is not described as a general chemical recognizer. In particular the amino-acid names used by routing must be the names of the product graphs; the standard table used by registry must be the standard table reached by routing; the outgoing junction projection must have the Met constitution; and AUG/UAA must retain the claimed start/stop roles in the named endpoint witnesses. The combined report records file hashes to identify the exact inputs it checked.

A.2 Standalone publication companions

Two standalone companions accompany this publication version: the *Verification Code Analysis* and the *Formal Proof Dossier*. The former supplies a self-contained Python reproducer, `verify_article75.py`, with the original certificate programs, explicitly supplied data, deterministic replay identities, additional checks, and a recorded execution. The latter supplies `Article75.lean`, its tested Lean 4 toolchain, theorem dependencies, and a precise map from the formally checked subset to the manuscript. The raw sources are included with their typeset listings. Compiling either companion in Overleaf produces its PDF; it does not execute Python or Lean.

The Lean companion is a partial formalization of selected finite registry, assignment, algebraic and controller statements. The product-graph replay and the molecular lifting obligations have their separately stated verification or analytic roles. Neither companion converts the declared formal grammar into a chemical-realization theorem or an independent selection of the observed genetic code. Their own coverage reports identify exactly which statements were executed or kernel-checked.

A.3 Reading a passing report

A passing report certifies the advertised finite and formal graph assertions under the packaged definitions. It does not certify unknown reaction rates, an experimentally prepared carrier, stereoselectivity, a physically continuous pathway, or independent selection of the initialization data. These exclusions are part of the mathematical scope: they are predicates not implemented by the finite checker, rather than failed tests silently omitted from its output.

The checker rejects a changed certificate when the new data violate a declared guard or identity check. Passing a deliberately enlarged grammar would establish a theorem about that enlarged grammar. It would not establish the

original restricted result. Reproducibility therefore requires retaining both the state data and the rule definitions, as well as the record of which fields are target-informed.

A.4 Proof status by logical role

Role	Completed result	Remaining stronger claim
T1	Exact registry quotient, complete invariant, and directed-address witness	Molecular realization of the reference tags and precursor/carrier bridge
T2	Sharp WC matching bound and minimal refined-state bound	Independently derived chemical compatibility relation
T3	Twenty checked constitutional graph endpoints under the declared formal grammar	Chemically admissible paths and stereoselective molecular outputs
T4	Joint graph-and-controller witness with common identities and resources	One common physical configuration and environmental regime
T5	Guarded assignment path and explicit reachable alternatives	Chemical justification and narrowing of the assignment grammar
T6	All-codon vertebrate mitochondrial formal endpoint with halt control	Physical implementation of its decoding and stop events
T7	All-codon standard formal endpoint under the stated selector refinement	Physical control path and independent selector placement
T8	Corrected junction gate and finite-prefix Met-first reset invariant	Molecular release, reading polarity, propagation, and reset realization

A.5 Source conventions and deliberate repairs

Article numbers identify the supplied updated corpus. Some active filenames retain earlier numbering: Article 47 uses the `article46` prefix, Article 50 uses `article49`, Article 55 uses `article50`, and Article 56 uses `article55`. The bibliography names the intended articles; the certificate provenance records the active files. No inactive variant is used to supply a missing premise.

The principal repairs are stated in the body where their proofs are needed. They include separating framed and quotient objects; imposing fullness explicitly; using the sharp nine-to-seven Hall witness; restoring the Ile seed; distinguishing product demands from occupied slots; introducing Gly and Trp constructor types; choosing the Cys boundary-cut branch; retaining the actual transported reversal; distinguishing the resident AAA tether from the variable external codon; replacing nested singleton selection by multiple candidates and a strict selector; and separating absence, release, halt, and initiation.

For the patent, Figure 5 fixes the RNA lookup and Example 10/Figure 15 supply the poly-A setting. The two atom-index discrepancies discussed in Section 2 remain unresolved for a physical precursor lift. The separate unresolved patent/bibliography keys in Article 54 are not replaced by US12195423B1. The six-step attached amino-acyl motif is treated at its stated scope and is not promoted to a complete twenty-product reaction family.

B Tests of the physical premises and a conditional yield bound

B.1 Separating the observables

The finite theorems do not require an experiment to establish their mathematical validity. Experiments would instead test whether a physical system realizes their premises. The most informative tests separate carrier construction, product formation, product release, gate selection, and sequential control.

For the carrier, determine whether the specified three resident adenosines, three residual 6,12-disubstituted cores, and external coding strand can share the proposed geometry. Verify covalent linkage and docking separately. A mass or spectrum consistent with one constituent does not identify the assembled carrier. For the precursor bridge, an

isotope-resolved atom map should distinguish atoms assigned to nucleotides from atoms retained in residual cores and coproducts.

For each product path, identify both the released product and the remnant. The graph certificates predict particular atom sources and retained edges. Isotope labels at the assigned carbon sources, together with independently labelled nitrogen and sulfur donors, would test those provenance claims directly. Stereoisomer-resolving analysis is needed where a constitutional graph admits multiple stereochemical products. Bound product and soluble product should be assayed separately so that failure of release is not mistaken for failure of formation.

For the junction, compare all four incoming switch values and both strand roles. The transported gate predicts matched release statuses for complementary outer switches; an assay of only the UAC/AUG branch cannot establish the universal gate. The paired support condition should be tested against single-carrier, separated-carrier, and no-sulfur controls. These tests distinguish a local coupled event from two independent reactions that merely share a final product list.

For the controller, test start selection, ordinary extension, termination, and reset in separate measurements before combining them. A first Met emission does not establish that every successful reset recreates the same boundary. Resource depletion should be quantified, since the formal reset requires fresh atom inventories. For the selector, measure both intended and competing products while the environmental control is varied; endpoint agreement does not reveal what happens at the intermediate tie or branch crossing.

B.2 Controls linked to specific premises

A precursor-only control tests whether a proposed output requires the carrier. A no-carrier control tests whether the same product forms from donor packets without templating. A no-sulfur or isotopically altered sulfur control tests sulfur provenance. A no-junction control tests the paired-support rule. Matched resident-tether and coding-word variants test whether the variable address is genuinely external to the fixed poly-A tether. Soluble/bound partitioning tests release, and a fresh-versus-exhausted resource comparison tests reset supply.

The conditions should be fixed before interpretation. If a predicted gate fails under the stated conditions, the relevant physical premise has failed there. Changing solvent, concentration, geometry, or the rule set may define a new model, but it does not rescue the tested claim without a new specification and a new nonvacuity check.

B.3 From a path to positive probability

A finite graph path alone gives no numerical yield. Even a chemically admissible path can have negligible probability because one step is too slow, competing reactions dominate, release is blocked, or the reactants are unavailable. The following conditional statement records the additional dynamical information needed for a positive finite-time event.

Proposition B.1 (Positive path probability under rate bounds)**.** *Consider a continuous-time jump model with specified successive states $x_0, \dots, x_\ell$. Assume that, whenever the process reaches x_{i-1}, the desired transition to x_i has rate at least $a_i > 0$, the total exit rate is at most $B_i < \infty$, and these bounds remain valid for a time interval of length $\delta_i > 0$. Assume $a_i \le B_i$ and that required reactants are present throughout the selected event. Then the probability that each desired transition is the next transition and occurs within its allotted interval is at least*

$$\prod_{i=1}^{\ell} \frac{a_i}{B_i}\left(1 - e^{-B_i \delta_i}\right) > 0. \tag{13}$$

The desired endpoint is reached by time $\sum_i \delta_i$ on this event.

Proof. Condition on the process arriving at x_{i-1}. Up to the next jump, survival without any jump for time t is at least $e^{-B_i t}$. The density of a desired next jump is consequently at least $a_i e^{-B_i t}$. Integration over $0 \le t \le \delta_i$ gives the ith factor. Apply the conditional lower bound successively and multiply. Every factor is positive. The sum of the allotted intervals bounds the elapsed time on the resulting event. □

The proposition is a sufficient condition, not a rate estimate for the proposed chemistry. If release is an additional

transition, include it as a further step. If the observed product must survive for a specified time with degradation hazard at most D, multiply by the corresponding factor e^{-DT}. Large barriers or competing rates can make the lower bound arbitrarily small even though it remains positive.

B.4 A concentration model

For a specified reaction network, a deterministic alternative is

$$\dot{x} = S\,v(x;\theta), \qquad x(0) \geq 0, \tag{14}$$

where S is the stoichiometric matrix and v is a vector of nonnegative reaction rates. Element and charge conservation require the appropriate conservation rows to annihilate S; resource supply and waste must be included explicitly. A schematic accumulated released amount for product i is

$$Y_i(T) = \int_0^T k_i(t) C_i(t) p_{\mathrm{release},i}(t) p_{\mathrm{survive},i}(t)\,dt. \tag{15}$$

Here C_i must already account for competition if competing consumption is not modelled elsewhere. Otherwise the formula double counts the same carrier. No numerical Y_i, rate constant, activation barrier, or survival probability is inferred from the finite construction. Those quantities require measurement or explicitly hypothetical parameters with an uncertainty analysis.

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