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Carbon Traceable Protocell Construction From Substituted Chrysene Stocks

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Abstract

We construct a finite-resource theoretical framework for an externally supplied protocell whose functional carbon is traceable to admitted substituted-chrysene cores and their explicitly constituted organic arms. The initial inventory contains specified 6,12-, 3,6,12-, and 3,6,9,12-substituted stocks, including finite macrocycles, polymers and stacks; a minor 2,5,8,11 pool is optional. Stock manufacture and selection are boundary conditions, rather than tasks performed by the compartment. Persistent atom labels give exact ancestry, open-system balance and no-double-use theorems. Typed preparation and grafting conditions connect the stock boundary to a previously certified constitutional amino-acid grammar without treating open ports as hidden carbon sources. A single explicit uncoded reduced model starts with no peptide, consumes finite donor and release-carrier inventories, produces lumen and retained chains, and reaches a functional retained-product threshold. A matched ablation fails that threshold, establishing a causal productive feedback result under the declared constitutive laws. The same trajectory satisfies positive-invariance, resource, guest-area and idealized water-balance bounds over a finite horizon. Robust operating neighborhoods and resource-aware return-map results distinguish finite operation from repetition. Growth and division are treated through conditional flow–guard–reset statements with normalized daughter-area allocation; physical scission and inheritance are additional requirements. These are constructive mathematical results, including a nonempty assumed-law operating model. They do not assert that its rates, joining chemistry, functional stereochemistry, membrane mechanics and transport have yet been realized by one molecular system. Gene-directed peptide production is an optional extension, not a premise of the base result.

Keywords: protocell; substituted chrysene; carbon ancestry; finite resources; peptide feedback; hybrid dynamics; conditional division.

1 A constructive finite resource result

Constructing a functioning protocell from basic molecular materials requires chemistry and compartment dynamics to work together. A boundary must retain useful products while admitting resources; reactions must replenish material and sustain a compartment-level function under compatible conditions. For a genetically hereditary lineage, template copying must also be coordinated with component production and division. Experiments have demonstrated important parts of this program, including nonenzymatic RNA template copying inside fatty-acid vesicles, coupled vesicle growth and division, and peptide synthesis that promotes membrane growth [AS13b, ZS09, AS13a]. Their integration is a substantive chemical problem. For example, citrate can reconcile magnesium-dependent RNA copying with the stability of fatty-acid membranes [AS13b].

A familiar starting picture is a "primordial soup" containing mixtures of precursors and compartment-forming molecules that become available together at useful local concentrations. Contemporary investigations give this picture several concrete forms. Dehydration–rehydration experiments couple lipid-assisted polymer formation to subsequent encapsulation, thermal-pore models provide concentration mechanisms, and coacervate droplets can concentrate RNA and support catalysis without a membrane [RVB+08, BWD+07, DIALV+18]. Common-source chemistry is also an established objective: cyanosulfidic experiments connect precursors of RNA, proteins and lipids

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through a shared chemical network [PPR+15]. These approaches motivate a general requirement that extends beyond the presence of the right ingredients: their production, localization and use must be mutually compatible in an operating compartment.

Here we investigate a complementary, scaffold-centered construction based on a common chrysene core with specified organic substituents. This is one encodable core family with varied arms and finite assemblies. The orientation-based encoding and reaction-vessel organization disclosed in U.S. Patent No. 12,195,423 B1 provide the starting architectural motivation [Sch25]. The admitted material consists of specified substituted-chrysene stocks and their assemblies; stock preparation and isolation lie outside the present boundary. Within that boundary, we ask whether the same stock family can supply the carbon-bearing structures and products needed for enclosure, transport and productive feedback, with explicit interfaces to subsequent growth, division and information-bearing operation. The longer-term aim is an integrated platform supplying the components of enclosure, replication and division; the present endpoint distinguishes that aim from demonstrated template copying or viable fission. All organic-arm carbon is included in the supply; water, carbon-free inputs and energy remain explicit external resources. This restriction makes the allocation of a common material inventory amenable to exact analysis.

The first operational target is finite, uncoded function. Starting with no peptide, an explicit reduced model consumes finite inventories and produces retained chains that enhance further productive flux. A matched removal of that feedback edge separates this effect from the supplied baseline drive. Atom-level ancestry and allocation results connect this dynamical target to the material construction. Component replenishment, nucleic-acid copying, physical division and heritable function are treated as distinct requirements, each with its own interface. Thus the constructive endpoint is a resource-accounted model of bootstrap and feedback under declared constitutive laws; its molecular realization and hereditary extensions remain further tests. The supplied enclosure, transport, loop and chain-model articles [Sch26i, Sch26f, Sch26n, Sch26g, Sch26l, Sch26m, Sch26k, Sch26j, Sch26a, Sch26c, Sch26e, Sch26d, Sch26h] and the revised Article 75 product grammar [Sch26b] provide the detailed modules developed below.

1.1 The boundary is given stock rather than a prebuilt cell

The admitted carbon-bearing inventory consists of fully specified members of three main substitution families, with their declared arm carbon: 6,12-disubstituted, 3,6,12-trisubstituted and 3,6,9,12-tetrasubstituted chrysene. Finite macrocycles, polymers and stacks of these constituents may be present initially. A separately specified minor 2,5,8,11-substituted pool is permitted but unnecessary for the base model. Later stock batches are admissible under the same predicate and receive fresh origin labels. Water, carbon-free heteroatom and inorganic supplies, and energy can enter through declared channels.

No claim in the present paper explains how these stocks were synthesized, why their locants were selected, how one substitution family progressed into another, how a thermodynamic selection occurred, or how stock self-separation took place. Those questions precede the chosen boundary. Within it, however, a stock label is not a functioning cell. The downstream construction must still account for membrane formation, inward site placement, prepared product packets, joining and release, transport, functional retention and the shared operating environment.

The carbon restriction covers all participating organic material, not only the named output. An organic arm already specified on an admitted stock is eligible; free PEG, adenosine, sugars, amino acids, organic buffers and unlisted organic activation reagents are not additional carbon-free feeds. Coproducts and spent carriers remain in the state. An output formula or a positive carbon balance cannot substitute for atom ancestry.

1.2 Results and their logical level

The paper establishes four connected results. First, persistent labels and typed rewrites give an exact material semantics. In this semantics an ancestry theorem, an open balance identity and a disjoint allocation theorem prevent hidden carbon and duplicate resource use. Formula checks are exact bookkeeping statements for the specified stock graphs. They do not assert a reaction pathway.

Second, the connection to the revised amino-acid repertoire is a genuine composition theorem. A prepared open-module certificate can be used after an origin-preserving preparation and a compatible context graft have been supplied. This identifies an exact sufficient interface and preserves the already proved prepared-input result. It does not invent the preparation map. The baseline needs a functional subset of products, rather than a claim that every standard amino acid must be made simultaneously.

Third, we give a common, explicit reduced-model witness with finite reservoirs and zero initial peptide. Its active retained product crosses a specified functional threshold within the certified horizon; the otherwise matched model with its product-dependent return edge removed does not. The equations include the resource ledger, inactive chains, lumen chains, free failed-joining residues, remnants, spent carriers, guest area and a Donnan water closure. The ex-

istence theorem is established by analytical bounds, with independent arithmetic and trajectory checks. Its rates are assumed nondimensional laws, so its conclusion is a model-existence and feedback result, not a measured chemical parameter fit.

Fourth, sufficient conditions for robust operation, finite repetition and conditional division are stated on complete interfaces. A return map is an operational projection accompanied by a nonperiodic resource ledger. An area-conserving reset is an identity about a stipulated division; it is not the force or pathway causing it. Founder trajectories, repeated lineages and two viable daughters have distinct hypotheses.

1.3 A hierarchy of existence statements

Let $\mathcal{G}$ denote the labelled graph model, $\mathcal{O}$ an assumed-law operating model, and $\mathcal{X}_\theta$ a molecular configuration space at one physical parameter vector θ. The present constructive statements have the forms

$$\exists\, g \in \mathcal{G} :\ \mathsf{Certificate}(g), \qquad \exists\, o \in \mathcal{O} :\ \mathsf{Operation}_{[0,H]}(o),$$

and the conditional transfer

$$\forall\, \theta,\, x \in \mathcal{X}_\theta :\quad \mathsf{CompatibleLift}(x, g, o) \\ \Longrightarrow\ \mathsf{MolecularOperation}_{[0,H]}(x).$$

The first two have explicit witnesses here. The antecedent of the third is a substantive joint chemical and physical condition. It is not discharged by choosing numerical rate constants, by attaching a biological name to a graph, or by observing that each required element occurs somewhere in the stock. Conversely, its unresolved status does not weaken the correctly proved formal results.

1.4 A map of the supplied witnesses

Table 1 locates the three explicit witnesses. They establish nonempty constructions at their respective levels; none is an empty specification awaiting every part of its proof. Their composition into one physical system has separately stated interfaces.

The finite-count construction (Theorem 3.19) supplies an explicit stoichiometric approximation to the operating amounts. The robust-box theorem (Theorem 8.1) supplies a uniform family of operating laws. Neither step is a substitute for the missing chemical interface. Conversely, requiring that interface does not retract the three existence results. Physical division and inherited operation use the additional flow, scission, partition and return conditions of Theorem 10.2.

1.5 Source precedence and notation

The controlling supplied versions are 62 v13, 63 v4, 64 v6, 65 v2, 66 v4, 67 v3, 68 v3, 69 v3, 71 v2, 72 v1, 73 v1, 74 v2 and 76 v6. The revised Article 75 dated 5 October 2026 supplies the formal product grammar. The patent evidence is solely US12195423B1. The audited Pilot02 assessment [pil26] supplies source locators and records corrections; it is not an extra molecular experiment.

Article 71's normalized area reset supersedes the unnormalized older partition. Article 76's chain ledger replaces the older free-residue gain and remnant-consumption mechanism. We do not concatenate superseded mechanisms into a new proof. Article 74's stipulated endpoint geometry can be discussed conditionally, but its least-energy assertion is not imported. The source register at the end gives exact version and section locators; the accompanying data record hashes.

We use amounts for continuous mean-field dynamics and distinct labels for finite atom-level execution. An amount can be fractional; an atom or a complete molecular assembly cannot. A statement transferring between these levels must say which coarse-graining or scaling is used. Throughout, "proved" means proved within the displayed formal premises. "Physical" refers to the further compatible molecular realization, and "experimental" is reserved for an observed system.

2 Typed architecture and downstream assembly

The proposed architecture has an aqueous lumen, a membrane formed from admitted-stock-derived amphiphiles, inward-facing tether or product sites, and a separately constituted pore. A nucleobase-bearing interleave can organize the tethered sites without functioning as a genome. The stock, assembly, preparation, production and functional-operation phases are therefore distinguished before assigning any kinetics.

2.1 Objects and phase interfaces

Definition 2.1 (Assembly interface)**.** An interface is a tuple

$$\mathcal{I} = (\Gamma, \mathcal{L}, \mathcal{U}, \mathcal{C}, \mathcal{O}, \mathcal{E}, \sigma),$$

where Γ is the current atom-and-bond graph; $\mathcal{L}$ assigns immutable origin labels and current molecular ownership; $\mathcal{U}$ lists unused or reserved resource packets; $\mathcal{C}$ gives locations, charge states and boundary-context valences; $\mathcal{O}$ gives orientation, strand direction and accessibility data; $\mathcal{E}$ gives the environment, control schedule

Table 1: Claim-to-witness map. Each row identifies a supplied constructive object and the additional interface required for its molecular use.

Object	Explicit result supplied	Composition frontier
Stock and allocation	An 810-carbon graph inventory with disjoint constitutional reservations (Proposition 3.12); exact ancestry and no-double-use invariants (Theorems 3.5 and 3.6).	This inventory is distinct from the operating model's 130 donors, 30 carriers and reserved scaffold. Prepared connectivity, full contexts and a compatible downstream chemical history must be supplied.
Prepared product repertoire	Eighteen unary certificate words and one joint two-module sulfur word construct twenty constitutional targets from 400 exposed carbons and 1,504 atoms, with 107 product carbons (Theorem 4.2).	Full resident contexts are additional to the exposed counts. The stock-to-prepared map and context graft are required by Theorem 3.14; activity, stereochemistry and reaction feasibility are further molecular questions.
Uncoded operation	One finite-reserve law starts from zero peptide, reaches $p = 1.5$ by $3131/1049 < 2.985$, and its matched ablation stays below 1 (Theorems 7.2 and 7.5).	The rates and product response are stipulated. One compatible molecular history and calibrated observations must satisfy Definition 11.1 and Theorem 11.2.

and admissible continuous configurations; and σ is the current phase. A transition declares its complete read set, write set, guard and output interface. An origin label is never a source of a new atom, and a boundary port is never a resource packet.

A diagram such as "stock → membrane" is a dependency statement until these interface fields are supplied. It can guide a construction without constituting its atom map. At the graph level a transition may have a finite word of guarded rewrites. At the dynamical level it may have an integrated vector field or a guard and reset. At the physical level it needs configurations and admissible paths. The same interface prevents these three meanings from being inadvertently identified.

We use the following phases. Admission gives finite origin-labelled stock. Allocation reserves pairwise disjoint support for structural material, active product packets, release carriers and residual capacity. Assembly establishes a closed boundary and accessible sites. Preparation supplies the full aminoacyl-bearing contexts needed by the product grammar. Production applies extraction, joining and release rules. Operation couples the retained product to later productive flux. An optional information phase supplies a separate template-to-product causal relation; an optional division phase supplies physical fission and daughter initialization. The order can be partly interleaved when a full compatibility proof allows it. The phases need not be physically instantaneous.

Proposition 2.2 (Safe phase composition)**.** *Let $T_1, \dots, T_m$ be finite transitions with interfaces $\mathcal{I}_0, \dots, \mathcal{I}_m$. Suppose each T_j is valid from its stated input; its complete output equals the input of T_{j+1} on all shared atom, resource, location, charge, orientation and environment coordinates; and all persistent invariants are preserved. Then their concatenation is a valid finite execution. A condition declared local to phase j need not hold after an explicit transition retiring it, unless a later guard reads that condition.*

Proof. The first transition is applicable by assumption. Equality of the complete shared interface makes the next guard and input exactly those of its certified instance. Induction gives applicability of every transition. The same induction preserves every declared persistent invariant. A retired phase-local condition is absent from the set being propagated; if it occurs in a later guard, that guard must instead be proved at that later input. Thus no implication is obtained by merely reusing a phase name. □

This distinction matters for product extraction. A backbone-preparation phase can protect all chrysene edges. An extraction phase must explicitly permit its particular boundary scissions. The claim that both phases exist does not mean that all their protection rules hold simultaneously. Likewise a temporary paired-sulfur placement predicate can be required before release without becoming a permanent predicate on an optional final codon table [Sch26b].

2.2 Membrane material and the whole strand condition

The membrane lane uses a specified stock-derived amphiphile constitution. The route-A candidate of Article 62

is an ether-extended phosphate with two C_{18} tails and a four-carbon extended bridge [Sch26i]. Its carbon partition is a useful exact target. Its bilayer phase, bending elasticity, headgroup ionization and insertion free energy are additional molecular properties. No claim that an aromatic precursor becomes a fluid membrane follows solely from the fact that its carbon graph can be cut into tails. The material chapter specifies a mixed-arm input that matches this forty-carbon target without discarding unaccounted arm carbons.

Let $\Sigma \subset \mathbb{R}^3$ be an embedded closed surface separating a bounded lumen component U from the exterior. For the topological statements, Σ is a sufficiently regular embedded sphere; other topologies need the appropriate separation assumptions. A tether anchor has both a membrane location and an aqueous strand attachment point. The latter is specified to lie in U. These are different coordinates. A leaflet tag alone does not locate every segment of the strand.

Proposition 2.3 (Whole strand enclosure)**.** *Let $\gamma : [0,1] \to \mathbb{R}^3 \setminus \Sigma$ be a continuous strand path with $\gamma(t_0) \in U$ at at least one parameter value t_0. Then $\gamma([0,1]) \subset U$. For a finite collection of strand paths, the same conclusion holds componentwise when each connected component has an interior reference point and none intersects Σ.*

Proof. The image of a connected interval under a continuous map is connected. The components of $\mathbb{R}^3 \setminus \Sigma$ are separated. A connected image meeting the component U cannot also meet another component without leaving the complement. Apply this argument to each connected component in the second assertion. □

The no-intersection condition covers terminal tails as well as inter-anchor segments. Equal inward anchor labels supply no such condition: a path can leave and return through two crossings. If the surface and strand move continuously over a time interval, enclosure persists under a no-contact condition and a continuously tracked interior reference. Establishing this geometric condition by steric or energetic means is a separate physical task. In particular, a large transfer-energy estimate does not turn crossings into a logical impossibility.

The footprint ledger includes ordinary membrane amphiphiles and all retained guests: interleave anchors, pore scaffold, switch-bearing units, retained chains, inactive chains, remnants and spent carriers according to the selected localization. A permanent membrane scaffold and consumable product donor cannot use the same core simultaneously. If production severs an anchor, a replacement step or an explicit loss of that site is required. These constraints motivate the separate scaffold reserve in the reduced operating witness.

2.3 A pore must have one linker constitution

The short aryl phosphodiester of Article 66 is Ar–O–P–O–Ar. The extended arm bridge used in the patent-associated tether and Article 62 is Ar–O–CH_2CH_2–O–P–O–CH_2CH_2–O–Ar. They differ in carbon content, contour length and torsional freedom. Consequently, a diameter computed for the former cannot be assigned to the latter without a new geometric model. Our exact stock catalogue contains a phenolic-arm alternative for the short-link pore. A uniform long-link design is also permissible, but its closure and selectivity must be recalculated rather than inherited.

A complete pore interface specifies the finite number of columns and layers, every internal phosphate bridge, terminal groups, membrane orientation, internal charge and possible tether connections. It also specifies a conductance law under the same environment as the product chemistry. Geometric clearance alone neither lower-bounds throughput nor proves retention. A hydrated solute may fail to cross an apparently wide pore; a flexible or defective membrane may leak a species excluded by an idealized static diameter. Carbon-free phosphate supply is part of the resource boundary even when an existing pore retains its phosphorus.

The reduced model below assumes consumption-coupled availability factors and a declared ionic closure. It does not identify these functions with an independently validated chrysene-pore conductance. The value of keeping the exact pore constitution here is to make that later identification a testable interface rather than an unnoticed change of molecule.

2.4 Patent derived interleaves and nucleobase organization

The sole patent foundation describes a disubstituted catalyst paired with a tetrasubstituted substrate, with stacking and optional phosphodiester connections. Its orientation dictionary is ordered catalyst then substrate. With F and B denoting its two faces, the disclosed RNA and DNA dictionaries are

pair	FF	FB	BF	BB
RNA	A	C	G	U
DNA	T	G	C	A

(1)

with the patent's stated $5'$ to $3'$ convention [Sch25, Figs. 4–5]. Equation (1) is a finite encoding definition. To turn it into molecular production one must supply an orientation-

retaining transformation, initialization of RNA or DNA mode, correct atom maps and product identification.

For a three-unit precursor write the proposed pair transformations as

$$\begin{aligned}&(C_1, C_2), (C_3, C_4), (C_5, C_6)\\ \longmapsto\ &(X_1, n_1), (X_2, n_2), (X_3, n_3),\end{aligned}$$

where the six C_j are original admitted cores, the X_j are residual interleave units, and the n_j are produced nucleoside-bearing units. This notation fixes incidence and ancestry roles, not a chemical equation. All arm carbons, nucleotide carbons, caps, coproducts and spectators must occur in the actual map. The stock may contain the original six-core assembly; it does not thereby contain a completed resident adenosine or an active translation system.

The patent's Example 10 and Figure 15 disclose a membrane-associated poly-A/chrysene arrangement. Examples 15–16 and 18 and Figures 20–23 supply additional interleaved arrangements [Sch25]. These are useful architectural proposals. Precursor synthesis or spectra do not establish sequence-verified conversion of the entire tethered complex. The document also contains differing sugar-closure indices, 20–10 versus 20–16, and differing missing-site descriptions. A new atom-map certificate must select and justify a consistent interpretation. The adenine/cytosine versus adenine/uracil wording discrepancy in Example 15 does not redefine chemical base complementarity.

Three data types are kept separate:

1. the resident word, for example $t = A_1A_2A_3 = AAA$ in a selected post-transformation carrier;
2. the external addressed word $c \in \{A, C, G, U\}^3$, specified by orientation and reference data;
3. the precursor-output word $n = (n_1, n_2, n_3)$, obtained only after a particular atom-mapped precursor transformation has been given.

An external address change does not turn resident adenines into guanines. An immutable original architecture record does not say that its current molecular graph remains intact after extraction. These distinctions allow interleave organization to be part of the base architecture without claiming a working genetic decoder.

2.5 Duplex organization without a genome claim

For an RNA word $u = u_1 \cdots u_N$ written 5′ to 3′, let $\kappa(A) = U$, $\kappa(U) = A$, $\kappa(C) = G$, and $\kappa(G) = C$. A proposed canonical antiparallel partner, also written 5′ to 3′, is

$$\mathsf{RC}(u) = \kappa(u_N) \cdots \kappa(u_1).$$

DNA has the corresponding A/T pairing. Thus an all-A resident tether can have an all-U RNA partner or all-T DNA partner in the relevant mode. Its constant word alone cannot provide arbitrary complementary templates. The partner's carbons need their own eligible origins, and the interleave geometry must leave the pairing sites accessible.

Proposition 2.4 (Complementary strand bookkeeping)**.** *For the displayed involutive complement map,* RC *is an involution on fixed-length words. A pair* (u, v) *with* $v = \mathsf{RC}(u)$ *has the specified antiparallel complementary identities at every position. This identity imposes no replication dynamics and provides no atom allocation for* v*.*

Proof. Reversal and letterwise complementation commute, and each squares to the identity. Their composition therefore squares to the identity. The position relation is $v_{N+1-i} = \kappa(u_i)$ by definition. No transition or atom map appears in this word-level statement. □

A noncanonical docking relation used by an addressed carrier is another object. It should not be relabelled Watson–Crick pairing simply because both use base letters. An optional coding extension must provide its actual docking and readout relation. The present compartment can instead use a chemically or externally timed joining/release rule and retain nucleobase interleaves as organizational scaffolds.

2.6 A common state and the initial condition

A complete state can be represented schematically as

$$Z = (H, \Gamma, \ell, n, u, e, A, V, q, \sigma, \tau; \theta). \tag{2}$$

Here H is immutable admission and architecture history; Γ and ℓ are current molecular bonds and locations; n gives species amounts or counts at the chosen scale; u and e give unused resources and cumulative exported or spent material; A, V are guest-inclusive membrane area and lumen volume; q includes ionic, functional and mechanical coordinates; σ, τ give phase and clock; and θ is one shared environment and constitutive parameter vector. Algebraic closures determine dependent coordinates rather than adding independent freedom.

The admitted initial condition Z_{stock} has no asserted functional feedback loop. A graph-level assembly trace may lead to Z_{ready}, whose coarse-grained coordinates initialize the operating equations. The reduced witness specifies Z_{ready} explicitly, including zero peptide, finite external packets and a separately reserved structural scaffold. Its

existence as an ODE initial condition is proved; a physical stock-to-ready trajectory is the additional preparation and assembly lift. This avoids both mistakes of importing a prebuilt cell into the stock boundary and of pretending that the reduced equations synthesize their own initial pore.

3 Stock constitution and persistent material provenance

The carbon boundary is fixed before any functional assignment. The available material consists of specified substituted-chrysene stocks, including their organic arms and declared finite macrocycles, polymers and stacks. Adequate quantities of the $6, 12$, $3, 6, 12$, and $3, 6, 9, 12$ families are given; $2, 5, 8, 11$ material may be added as a separately specified optional family. Manufacture, progressive enrichment and self-separation of these incoming stocks are outside the problem. Further imports may replenish the same admitted classes. Every other material feed is carbon-free. Consequently, carbon can enter with a declared arm, but cannot enter as an unlisted amino acid, nucleotide, adenosine, lipid, organic catalyst, solvent or free PEG. Preassembled substituted-chrysene stock is permitted; a completed working cell hidden in a stock name is not.

This boundary leaves a positive mathematical task. We construct exact finite stock graphs, prove a provenance invariant and resource-allocation results, and give an explicit nonempty stock-reservation example. We then state the additional downstream certificate required to connect those stocks to the prepared amino-acid modules of Article 75. The distinction is between a completed formal result and an identified molecular obligation; it does not reopen the excluded question of how the incoming stocks were made.

3.1 Molecules, cores, arms and assemblies

Let the core locants, in cyclic order, be

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

The graph has this perimeter and the chords $4a : 12a$, $4b : 10b$, and $6a : 10a$. Its carbon cardinality is eighteen. A declared Kekulé representative may assign alternating perimeter double bonds; an atom identity is not a bond-localization claim. Substitution replaces the hydrogen at a specified peripheral site, rather than adding a new core carbon.

Definition 3.1 (Constitutional stock type)**.** A stock type specifies a finite element-labelled covalent graph, bond orders, formal charge and protonation convention, any required stereochemical tags, and the decomposition of its carbon vertices into one or more named cores and named attached arms. Each attachment has a locant, a complete arm graph, and declared terminal functional groups. Finite assemblies additionally specify their constituent copies, covalent bridges, non-covalent relations, orientation reference and order. A stack relation is not a covalent bond and adds no atoms. An assembly constituent occurs once in its atom inventory, regardless of the number of relations that mention it.

Two attached arms suffice for a compact instance:

$$h = -OH, \qquad e = -O - CH_2 - CH_2 - OH.$$

Their branch formulas are HO and $C_2H_5O_2$, respectively. The two carbon names in an e arm are $e1, e2$ at its specified site. Longer organic or PEG-like arms are allowed only as specified finite graphs, for example a finite explicitly indexed repeat chain with a declared terminal group. The symbol "PEG" alone specifies neither atom count nor molecular endpoint. An arm catalogue records incoming functionalization; it cannot contain a ready nucleotide or prepared aminoacyl carrier solely to discharge the conversion that is being claimed.

Proposition 3.2 (Five exact neutral precursor formulas)**.** *For a chrysene with n_h arms of type h and n_e arms of type e, its neutral unphosphorylated formula is*

$$C_{18+2n_e}H_{12+4n_e}O_{n_h+2n_e}.$$

In particular, the catalogue in Table 2 has the formulas shown there.

Proof. Begin with $C_{18}H_{12}$. Replacing a core hydrogen by h removes one hydrogen and adds HO, for net O. Replacing a core hydrogen by e removes one hydrogen and adds $C_2H_5O_2$, for net $C_2H_4O_2$. Sum these independent substitutions. None changes the eighteen-element core-carbon set. □

The first three types match the patent's hydroxyethoxy examples [Sch25, description anchors p-0138 and p-0208]. T_0 and D_m are explicit catalogue choices within the stipulated substitution families, not asserted patent syntheses. They make the short-link pore and the forty-carbon membrane precursor mutually consistent without requiring them to use the same arm. The optional $2, 5, 8, 11$ family would need its own attachment geometry; replacing its locants by $3, 6, 9, 12$ is not an allowed identification. A finite initial manifest declares a count of each stock and finite upper bounds on polymer length, macrocycle size

Table 2: A concrete admitted stock catalogue. These are neutral precursor formulas; solution charges and counterions are additional data.

Type	Sites	Arms in site order	Formula	Carbon
D_2	$6, 12$	e, e	$C_{22}H_{20}O_4$	22
I_2	$3, 6, 12$	e, e, e	$C_{24}H_{24}O_6$	24
T_2	$3, 6, 9, 12$	e, e, e, e	$C_{26}H_{28}O_8$	26
T_0	$3, 6, 9, 12$	h, h, h, h	$C_{18}H_{12}O_4$	18
D_m	$6, 12$	h, e	$C_{20}H_{16}O_3$	20

and stack height. The admission predicate is unchanged for later fresh imports.

A phosphate diester between two terminal hydroxyl groups changes the sum of their precursor formulas by $-H + O_2P$; a terminal phosphate monoester changes it by $H + O_3P$. These are the neutral-acid balances of

$$2ROH + H_3PO_4 \longrightarrow (RO)_2P(=O)OH + 2H_2O,$$
$$ROH + H_3PO_4 \longrightarrow ROP(=O)(OH)_2 + H_2O.$$

They are constitutional balances, not asserted reaction conditions. A carbon-free reagent inventory can include water, ammonia, phosphate, sulfur sources, metal/mineral species, hydrogen, protons and electrons. It excludes carbon dioxide, bicarbonate, cyanide and organic buffers as extra feeds, even when they would be consumed rather than retained in a target.

3.2 An atom ledger that survives fragmentation and recycling

Definition 3.3 (Origin-labelled material state)**.** An origin is an immutable tuple $\lambda = (b, p, a)$, where b includes the admission event and batch, p identifies one parent constituent copy, and a identifies an atom of its core or one of its arms. Noncarbon reagents have analogous distinct labels. Elements and isotope tags never change. Let $\mathcal{U}_t$ be all carbon origins admitted up to event t. A complete state contains a graph on the admitted atoms and an ownership partition

$$\mathcal{U}_t = F_t \sqcup B_t \sqcup W_t \sqcup R_t \sqcup E_t \sqcup L_t. \qquad \text{(M1)}$$

Here F is free active material, B is functional or bound material, W is residual material, R is recyclable storage, E is material outside the control volume, and L is explicitly tracked inaccessible material. Molecular connected components also form a partition of the atom vertices. These two partitions describe different things and must agree with each component's location and state. An exported or inaccessible atom remains in the ledger. A component spanning an interface has an explicit location assignment at the resolution needed for the balance.

A carbon at locant 6 and the first carbon of its site-6 arm have different labels. Bond scission can move either to a different molecular component without changing its label. Rebuilding a precursor from a remnant requires an actual declared transformation; a recycle flag alone does not restore its graph or available functional groups. A boundary port is a capacity constraint at an omitted interface, not an atom. A complete-molecule claim must replace it by a compatible fully inventoried context.

Definition 3.4 (Admissible material transitions)**.** An internal transition changes bonds, allowed molecular tags or ownership without creating, deleting or relabelling atoms. An export or return moves existing origins between the control volume and its tracked exterior. A carbon-free admission adds no carbon vertex. Admission to the global ledger and crossing the cell control boundary are distinct events. Initial external

reserves are already admitted even before their first inward transport. A fresh stock admission adds exactly the declared core and arm vertices of an eligible stock, disjoint from every previously admitted origin. Reimporting a tracked fragment, when part of the specified boundary protocol, is a return of its old origins and is never counted as fresh stock. The baseline can prohibit such returns; allowing same-class fresh stock does not by itself authorize free-biomolecule returns or imports.

Theorem 3.5 (Persistent provenance and exact open balance)**.** *For every finite execution of Definition 3.4 from a valid initial state, (M1) holds, and every functional carbon has a unique origin in an admitted core or arm. Write C_{in} for the carbon count inside the chosen control volume, I for cumulative new-origin admissions directly inside, $Q_{\mathrm{old,in}}$ for cumulative inward crossings of already-admitted origins, and Q_{out} for cumulative outward crossings. The old-origin term includes both first inward transport of an admitted external reserve and a genuine return after export. Then*

$$C_{\mathrm{in}}(t) = C_{\mathrm{in}}(0) + I(t) + Q_{\mathrm{old,in}}(t) - Q_{\mathrm{out}}(t). \quad \text{(M2)}$$

Crossing counts include repeat crossings of the same atom; the admitted universe counts each origin once. With neither external-reserve entry nor return, the old-origin inward term is zero. Admission of new stock outside the control volume changes the global universe immediately and contributes to the inside balance only on entry.

Proof. At initialization the graph and ownership classes partition the admitted vertices. An internal rewrite preserves this vertex set and merely changes incidences or class membership. A carbon-free admission adds no member to either side of (M1). A fresh eligible admission adds a disjoint set to both sides. A boundary transfer removes precisely the same labelled subset from one class that it adds to another. These observations prove (M1) by induction on the execution length. Fixed elements and immutable labels identify the original core or arm of each carbon uniquely. For (M2), the change in the inside indicator of an atom is $+1$ at an inward crossing, -1 at an outward crossing, and zero otherwise. Sum first over the events of the execution and then over its finite admitted carbon universe. Internal changes cancel. □

No term in (M2) licenses an undeclared carbon input. Export means loss from the control volume, not annihilation. Noncovalent sequestration changes the free/bound partition and can affect activity; it leaves total carbon intact. Likewise, retention of a catalyst is not its production. This sharpens the retention warning and competing-pool accounting in Article 65 [Sch26g, Remarks on retention and the allocation section].

Theorem 3.6 (No double use and the composition of local words)**.** *Suppose distinct simultaneous molecular components $P_1, \dots, P_k$ have injective carbon-origin maps ι_i. They can coexist in a material state only if their images are pairwise disjoint. For such maps their carbon cost is $\sum_i |C(P_i)|$. Sequential use of a catalyst is possible only when the required catalyst state is restored before the next use.*
Two enabled graph words on separately allocated resources commute if every primitive of one preserves all coordinates read by the other's guards and updates, and their write coordinates are disjoint throughout their execution. Under these hypotheses both execution orders are legal and have the same endpoint. Merely disjoint write sets do not suffice.

Proof. Distinct connected components have disjoint vertex sets, so a common image label would represent one atom in two components, contradicting Definition 3.3. Cardinality of a disjoint union gives the cost. The same reasoning applies to a catalyst consumed rather than restored: a historical identity cannot supply its absent endpoint state. For commutation, an interleaving cannot change the values on which the other word's next guard or update depends. Thus each next step remains legal with its original update values. Disjoint writes commute, so swapping adjacent steps from the different words preserves the state. Finitely many such swaps interchange the two entire words. A counterexample without the read condition is a step guarded by a global availability bit that another step changes on a distinct write support. □

This is a statement about simultaneous atom ownership, not a universal ban on useful coproducts. A precursor can be partitioned into two distinct products if both maps and the remaining material are specified. In contrast, one cannot count an extracted core fragment simultaneously as that residue and as the intact aromatic anchor from which it came. A claimed economy from recycling needs a new path with its full resource cost.

3.3 Assembly as a resource-constrained construction

Carbon abundance alone does not select an attachment or make a reaction reachable. The next result separates a finite allocation problem from the subsequent graph and chemical problems.

Definition 3.7 (Certified packets and admissible assignments)**.** A packet is a named collection of available stock and reagent copies with specified atom supports. A component demand specifies the required graph interface and allowed packet assignments. For each demand j, let $\mathcal{H}_j$ be its finite family of certified alternative supports. A joint allocation chooses one $H_j \in \mathcal{H}_j$ for each demand with $H_i \cap H_j = \varnothing$ for $i \neq j$. "Certified" here means a verified interface or production protocol at the claimed level; a carbon count alone does not certify it. Shared catalytic contexts, if used, are factored out and supplied with their own compatibility and restoration certificate.

Theorem 3.8 (Allocation criterion and its unit-slot specialization)**.** *The finite packet problem is equivalent to binary variables x_{jH} obeying*

$$\sum_{H \in \mathcal{H}_j} x_{jH} = 1, \qquad \sum_{j,H:\, u \in H} x_{jH} \leq 1 \quad \text{for every resource } u. \tag{M3}$$

When every demand consumes one eligible resource slot, write $N(J)$ for the union of eligible slots of a demand subset J. A complete allocation exists if and only if $|N(J)| \geq |J|$ for every subset J.

Proof. For (M3), selecting a support sets its binary variable to one. The first constraint selects exactly one alternative and the second forbids repeated resource use. Conversely, the variables equal to one give precisely such a selection, proving equivalence. For unit slots, an allocation injects each J into $N(J)$, so the inequalities are necessary. To prove sufficiency, take a maximum matching. If it leaves a demand j_0 unmatched, explore alternating paths starting there: from demands traverse unmatched eligibility edges and from slots traverse their matched edge, if any. If an unmatched slot is reached, reversing the alternating path increases the matching, a contradiction. Otherwise let J be all reached demands and T all reached slots. Every neighbor of J belongs to T (a matched edge of a reached demand leads to its already reached predecessor slot); every $t \in T$ is matched to a reached demand distinct from j_0. Conversely every reached demand other than j_0 is reached through such a matched slot. Hence $|N(J)| = |T| = |J| - 1$, contradicting the assumed inequalities. The matching is complete. □

Hall inequalities are not sufficient for general multi-resource packets. For example, two demands each with sole support $\{u, v\}$ cannot coexist, although the union of their eligible resources has size two. Equation (M3) retains the missing multiplicity and joint-support information.

Proposition 3.9 (Typed stock and stoichiometric necessary bounds)**.** *Let n_s be available stock counts, c_s their carbon counts, and let d_j components of carbon count c_j be required simultaneously. Let C_{other} count disjoint carbon required in all other retained or unavoidable components. Necessarily*

$$\sum_j c_j d_j + C_{\mathrm{other}} \leq \sum_s c_s n_s. \tag{M4}$$

If a fixed independent protocol uses A_{sj} stock copies of type s for one component j, its disjoint reservation requires $Ad \leq n$, with analogous donor inequalities. These inequalities suffice to allocate copies of that fixed protocol; they do not establish its reachability. For a reaction matrix S on a complete species inventory, any finite reaction word has a nonnegative integer firing vector v with $n' = n + Sv$. Thus existence of such a nonnegative endpoint is necessary but not sufficient for a reaction word to exist.

Proof. Equation (M4) counts distinct admitted carbon origins, including those not in the chosen target components. The typed bounds count whole-copy reservations. If they hold, enumerate the required protocol instances and assign unused copies of each stock and donor type consecutively; the supply inequalities guarantee the assignment never runs out. A fixed protocol's realization is a separate premise. For the final statement, sum each transition's stoichiometric change. The converse fails for the two rules $A + C \to B + C$ and $B \to C$, beginning from one A and no B, C. The formal firing vector $(1, 1)$ gives the nonnegative endpoint C, but neither reaction is initially enabled, so no nonempty word is possible. All three species can have equal carbon count; carbon balance does not repair this reachability failure. □

3.4 A membrane lane with an exact carbon boundary

Article 62's route-A target is the ether-extended phosphate diester

$$R - O - CH_2CH_2 - O - P(=O)(OH) - O - CH_2CH_2 - O - R,$$
$$R = \text{octadecenyl},$$

with formula $C_{40}H_{79}O_6P$ [Sch26i, route-A product and composition ledger]. The target has two eighteen-carbon tails and four linker carbons. Its constitution is not a

conventional phosphatidylcholine and its formula is not a phase-behavior certificate.

Proposition 3.10 (The forty-carbon input and the four-carbon discrepancy)**.** *Join two D_m copies through their site-12 terminal hydroxyl groups by one phosphate diester. The neutral precursor formula is $C_{40}H_{31}O_8P$, with thirty-six core and four arm carbons. The corresponding single-bridge D_2 dimer has formula $C_{44}H_{39}O_{10}P$, including four further carbon atoms in its two unused site-6 arms. Therefore any origin-preserving map from the latter to the forty-carbon target leaves exactly four carbon atoms outside that target, assuming no additional carbon-bearing input.*

Proof. Twice the D_m formula plus $H_3PO_4 - 2H_2O$ gives the first formula. Twice the D_2 formula with the same bridge gives the second. Their carbon sets have cardinalities forty and forty-four. Injecting the target's forty carbon vertices into the latter set leaves a four-element complement. □

Using D_m is one exact stock choice. Keeping D_2 is also possible if an explicit transformation routes the four additional arm carbons into a coproduct/recycle pool, or if the target itself is changed. Abbreviating an unused hydroxyethoxy arm to "oxygen" is not such a transformation. The neutral arithmetic identity

$$C_{40}H_{31}O_8P + 26H_2 = C_{40}H_{79}O_6P + 2H_2O \qquad \text{(M5)}$$

completes an element ledger but supplies no atom map or mechanism. In particular it does not turn the source's double-bond reduction count into a complete reaction inventory. Route choice, oxygen fate and caps, proton and electron transfers, stereochemistry of the retained double bond, and the actual membrane phase require their own data. The alternative source branch allows $\Delta 9$ or $\Delta 10$ unsaturation; a carbon path alone does not select cis or trans. Supplying glycerol or choline from outside the admitted stock would violate the present boundary. Their use instead requires separate stock-derived maps.

3.5 A short-link pore with complete terminal phosphorus

Article 66's torsion calculation uses the short chain $Ar-O-P-O-Ar$, whereas Article 62's long bridge contains $Ar-O-CH_2CH_2-O-P-O-CH_2CH_2-O-Ar$ [Sch26l, closure section][Sch26i, tether notation]. The latter contains four arm carbons and additional torsions. Their geometry and aperture numbers cannot be interchanged. Separate T_0 pore stock and long-arm membrane/tether stock resolve the constitutional distinction.

Proposition 3.11 (Completed pore inventory)**.** *Take mq copies of T_0, indexed by columns $i \in \{1,\dots,m\}$ and layers $j \in \{1,\dots,q\}$, where $m \geq 3, q \geq 1$. Join $(i,j,12)$ to $(i,j+1,6)$ for $j < q$ and $(i,j,9)$ to $(1 + (i \bmod m), j, 3)$ by short phosphate diesters. There are $b = m(2q-1)$ internal phosphates and $2m$ unspent terminal axial arms. Add p phosphate monoesters on distinct such arms, $0 \leq p \leq 2m$. Before any further tether attachment, the neutral constitutional formula is*

$$C_{18mq}H_{12mq-b+p}O_{4mq+2b+3p}P_{b+p}. \qquad \text{(M6)}$$

For $m = q = p = 3$, this is $C_{162}H_{96}O_{75}P_{18}$.

Proof. Each of the m columns has $q-1$ axial bridges, and each of the q layers has m lateral bridges. Each site is used at most once: interior axial sites meet their predecessor/successor, lateral sites meet the two adjacent columns, and only the first 6 and last 12 sites remain axial terminals. Thus $b = m(q-1) + mq$, leaving $2m$ free terminals. Start from mq copies of $C_{18}H_{12}O_4$, add b copies of H_3PO_4 and remove $2b$ waters, then add p copies of H_3PO_4 and remove p waters. Summation gives (M6). For $(3,3,3)$, $b = 15$, yielding the displayed formula. □

The internal scaffold has $C_{162}H_{93}O_{66}P_{15}$ and comprises six axial plus nine lateral bridges. Article 66 additionally specifies one distal phosphate monoester per column. Completing those three distal termini gives eighteen phosphorus atoms, before proximal tether contexts [Sch26l, terminal-tether remark and fourth-demand proposition]. The stated graph leaves the three proximal arms as hydroxyls. If all three are subsequently phosphate-tethered, the three additional phosphorus atoms and complete contexts must be included. If only one is tethered, the other two still need declared terminal states. Charge after deprotonation and its counterion inventory are distinct from this neutral formula.

The supplied verifier constructs this exact full constitutional graph, including every hydrogen and every terminal phosphate, rather than checking only the integer 18. Its nonempty graph is not proof of a strain-free spatial ring, bilayer spanning, or solute transport. Those tasks require a consistent coordinate model for the selected short-arm constitution, whole ring closure, steric and hydration envelopes, membrane thickness and a transport law. The source's axial-length assumptions and finite torsion samples are not upgraded here to continuous geometric certificates.

3.6 A nonempty stock-reservation witness

Proposition 3.12 (Explicit finite inventory and disjoint reservations)**.** *There is a nonempty formal stock instance with* 810 *distinct carbon atoms and disjoint reservations for one membrane precursor, one completed pore, one three-pair precursor array with a spare initiator, and twenty active module carbon budgets. It uses* $2D_m$, $9T_0$, $23D_2$, $3T_2$ *and* I_2.

Proof. Give every constituent a distinct parent name in one admission batch. Reserve the two D_m copies for the single-bridge membrane precursor (40 carbon), the nine T_0 copies for Proposition 3.11 (162 carbon), three D_2 and three T_2 for the ordered pair list $((D_1,T_1),(D_2,T_2),(D_3,T_3))$, and the I_2 as a separately counted optional initiator. These latter reservations contain $3(22+26)+24 = 168$ carbon. Reserve the remaining twenty D_2 copies for local-module budgets (440 carbon). In each such copy, the eighteen core labels together with the two site-6 arm labels give a distinct twenty-carbon set; the other two arm carbons remain explicitly outside that set. The disjoint parent names prove disjointness and the sum is $40 + 162 + 168 + 440 = 810$.
Each individual stock graph is obtained by the substitutions already specified, with hydrogens saturating the stated valences. The selected pore and membrane bridge graphs are obtained by the explicit finite hydroxyl incidences above; noncarbon phosphate material is counted separately. The pair list and its orientation markers are finite relations on these constituents and add no atoms. These objects are constructed directly by the checker and have no unfilled atomic placeholders. □

The witness proves a stock graph and resource reservation, including the pore's constitutional graph. Its twenty-carbon subsets are *not* already the prepared aminoacyl graphs: choosing site-6 labels for their two-carbon budget gives an injection, not the C5 aminoacyl connectivity. Likewise the three-pair relation is not already three adenosines, nor does a spare I_2 alone close every possible capped array. A full end-to-end molecular assembly is not supplied by the source material and is not asserted by this witness. No minimum-cell or sufficient-quantity claim is attached to its deliberately small inventory.

3.7 The stock-to-prepared-packet bridge

Article 75's product certificates begin with an open prepared module containing eighteen labelled core carbons and two further carbons c_α, c'. The initial local graph includes

$$\begin{gathered} 5 - c_\alpha(H)(n_\alpha H_2) - c'(=o_x) - o_t, \\ 6 - o_6 H, \qquad 12 - o_{12} - B_{12}, \qquad o_t - B_t. \end{gathered} \tag{M7}$$

Here B_{12} and B_t are capacity-one ports, not atoms. The intended o_t context is resident adenosine. The source builder creates the two backbone carbons in the prepared graph and labels their origin class "arm-derived backbone"; it does not name an original admitted stock, arm or site for them [Sch26b, prepared input and product certificates]. An exact origin class is useful evidence about the intended construction, but it does not prove an origin-preserving preparation path.

Assumption 3.13 (Downstream stock preparation certificate)**.** For each active module, a finite explicitly atom-mapped word from reserved admitted stock and carbon-free reagents produces its prepared graph and complete compatible port contexts. It assigns all eighteen core labels to one specified admitted core, assigns c_α, c' to two distinct admitted arm-carbon labels, and inventories all resident sugars, bases, tethers, caps, spectators and coproducts. It does not add carbon at a port. The boundary contexts have the exact valences and bonds required throughout the subsequent extraction word. Different module supports and consumable packets are disjoint, except a declared compatible shared context; the paired sulfur packet is allocated once. The preparation endpoint and the extraction input agree as element-, bond-, resource- and origin-labelled states, not merely in formula or component name.

Theorem 3.14 (Stock-resolved extension of the amino-acid witnesses)**.** *Under Assumption 3.13, each applicable restricted Article 75 extraction word concatenates with its preparation to give an origin-preserving formal path from admitted stock to the same complete constitutional amino-acid product and all coproducts. If S_r is its retained core set, the product carbon map has image exactly $\iota(S_r \sqcup \{c_\alpha, c'\})$. For eighteen separate unary instances and the one two-module sulfur instance, the twenty products contain* $107 = 67 + 40$ *carbon atoms. The active open modules contain* 400 *carbon, leaving* 293 *in their nonproduct components; complete contexts and preparation coproducts add their separate inventories.*

Proof. The preparation endpoint provides an injective labelled identification with the extraction input and its boundary sites. Replace each local atom name in the extraction word by that origin label. The certificate's

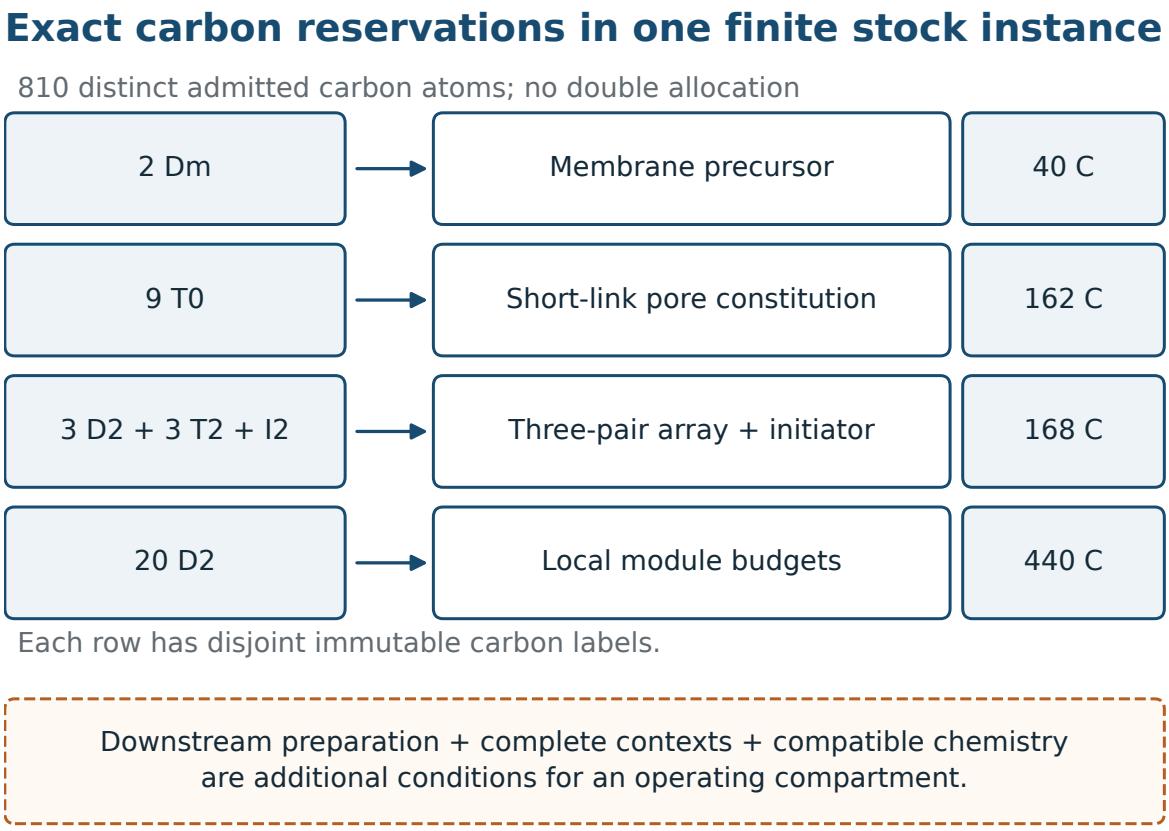


Figure 1: The exact 810-carbon stock-reservation witness. Arrows assign carbon to disjoint roles; they are not chemical reaction arrows. The pore and membrane-precursor graphs are explicit constitutional objects. The local-module reservations are carbon budgets whose downstream preparation and full contexts remain separate conditions. This is not a sufficient minimum-cell inventory.

guards and bond edits are unchanged under injective renaming. A compatible context supplies the boundary capacity without adding local carbon; unchanged context edges stay fixed and any specified boundary-bond changes act on the same inventoried atoms. Hence every subsequent step is legal in the formal enlarged graph. Concatenation with the preparation preserves origins by Theorem 3.5.

The source product carbon sets consist of S_r and the two separate backbone labels, so their images have the asserted form. Allocate eighteen disjoint unary preparations and two disjoint preparations for the joint sulfur word. Full noninterference, or a specified sequential schedule, permits their combination; the sulfur instance is one joint word rather than two separately charged sulfur supplies. Direct summation of the certificate sets gives $\sum_r |S_r| = 67$ and twenty backbone pairs give 40. Each open active module contains twenty carbon, hence $400 - 107 = 293$ remain outside the target products at that exposed-module level. □

The material data-consuming audit independently replays all supplied bond words and verifies these carbon counts and endpoint components. It checks persistent identities, valence capacities and exact endpoint bonds. A separate bundled product-guard verifier replays the full source-specific extraction restrictions and their rejection tests. The two reports retain these distinct scopes; the material replay alone is not the full guard audit. The present stock map is deliberately recorded as unresolved until Assumption 3.13 is supplied. Choosing the twenty D_2 reservations above would add forty unused arm carbons outside their active twenty-carbon subsets even before the full resident contexts were counted. Neither the source's 120 original-core architecture record nor its 1,504 exposed actual atoms including donor packets but excluding ports is a complete stock-resolved cell inventory.

A constitutional graph identifies connectivity, not optical purity. Absolute stereochemistry, tautomer/protonation state and molecular configuration are additional fields; a claimed L product requires their compatible selection.

An orientation marker for a planar chrysene pair is not automatically a stereogenic center or a proof of chiral transfer. The global chemical lift must resolve those fields, reagent balances, endpoints and operating conditions in one common realization.

3.8 Peptide joining and the nucleic-acid interface

Proposition 3.15 (Carbon preservation under specified peptide joining)**.** *Let n identified amino-acid graphs have disjoint atom supports. A specified linear amide-joining word that forms $n-1$ peptide bonds and releases exactly $n-1$ fully mapped waters leaves every monomer carbon in the resulting peptide. If all monomers initially count as distinct retained lumen solute particles, water is excluded from that solute count, and no other particle or counterion change occurs, one retained peptide changes the count by $-(n-1)$. Exporting or otherwise removing that one particle from the counted lumen produces the further change -1.*

Proof. Water contains no carbon. The declared joins change incidences without identifying or removing carbon vertices, so the product carbon set is the disjoint union of the monomer carbon sets. There are initially n counted particles and finally one, or zero after the additional removal; subtraction gives the two particle changes under the stated interpretation. □

This gives an uncoded baseline, consistent with the structural-polymer scope of Article 68 [Sch26k, scope, condensation edge and pool cost]. Accessible amino/carboxyl groups do not by themselves prove amide synthesis, and a formally joined peptide need not have a specified sequence, fold, partition coefficient, aromatic binding strength or activity. Initially tethered residues also do not satisfy the proposition's free-particle premise. Binding a remnant into a co-aggregate preserves remnant carbon; a dynamics model must distinguish reduced activity from removal.

For nucleic-acid organization, allocate separate D_2 catalyst and T_2 substrate copies, plus the explicitly chosen I_2 initiator/cap contexts. The patent's RNA and DNA orientation dictionaries differ; their finite encoding properties do not supply a nucleotide reaction. In particular, every sugar, base, thymine methyl, bridge and cap carbon must occur in one stock-resolved map. The source cap can contain substrate-derived carbon, so assigning all final tether/cap carbon to the catalyst arms is invalid without that map [Sch25, anchors p-0153 and p-0186]. The source's 20–10 versus 20–16 sugar-closure discrepancy and missing-site wording require an explicit model choice and graph validation. A resident poly-A tether, variable coding strand and precursor-output word remain separate objects [Sch26b, typed carrier specification]. The baseline seeks tethered/interleaved organization and uncoded peptide production. It makes no claim of gene-directed sequence synthesis merely because a nucleotide word is present.

3.9 Finite states, open influx and continuous material variables

Theorem 3.16 (Finite discrete state under a finite admission bound)**.** *Suppose all possible atoms over the observation interval belong to a fixed finite labelled universe of size N; vertex tags, bond orders, compartments, assembly relations and discrete controller states range over finite sets. Exclude unbounded chronological event logs and cumulative repeated-crossing counters from this counted state. Then the resulting current discrete material state space is finite. Bounded carbon admission alone proves this only for a correspondingly bounded finite carbon projection, not for unrestricted noncarbon graphs. Unlimited fresh same-class carbon influx does not give a finite full provenance state space.*

Proof. Choose the subset of admitted atoms, vertex tags and compartments, a bond order for each unordered atom pair, and the finitely many relation and controller entries. Each is a choice from a finite set, so their Cartesian product is finite; chemically valid states form a subset. For example, with q vertex tags, k locations and r possible bond orders including absence, $2^N(qk)^N r^{N(N-1)/2}$ bounds the graph/location choices before additional finite relations. If carbon is bounded but arbitrarily many labelled waters can enter, the total-atom cardinality is already unbounded. If fresh carbon can enter indefinitely, the admitted carbon cardinality is unbounded as well. Neither full state space is finite. Repeated outward and inward crossings of the same atom can make cumulative crossing counters unbounded even in this finite universe. Those counters, chronological event logs, continuous coordinates and real control parameters must be treated separately and are not made finite by this counting argument. The finite object is the current discrete state and admitted-origin set, not an unbounded chronological event log. □

Proposition 3.17 (Operational recurrence and cumulative admission)**.** *Let $A(t) = |\mathcal{U}_t|$. Along admissible executions A is nondecreasing, and it increases strictly whenever positive-carbon fresh stock is admitted. No complete provenance state can recur across such an increase. An operational projection that forgets outside*

waste or cumulative admission may nevertheless recur. An exactly repeating control-volume composition with positive fresh input requires compensating net outward carbon over each period.

Proof. Only fresh admission changes the universe, and it adds a disjoint positive set. Equal full states have equal universes and therefore equal A. To exhibit projected recurrence, replace a consumed inside stock packet by an identical fresh type and export its products; the species-level inside counts can repeat while the outside origins and admission record differ. For a repeated inside inventory set the left difference in (M2) to zero; then $Q_{\mathrm{out}} - Q_{\mathrm{old,in}} = I$ on that interval. This is a material balance, not a thermodynamic irreversibility claim or proof of the proposed replacement chemistry. □

Theorem 3.18 (Extensive carbon projection)**.** *Consider a complete species inventory with carbon counts c_i, separating free, bound, stored and external copies when their locations differ. Every origin-preserving internal reaction column $S_{\cdot j}$ satisfies $c^{\mathsf{T}} S_{\cdot j} = 0$. Thus a consistent amount model*

$$\dot{n} = S\,v(n,t) + u(t) - e(t) \quad \Longrightarrow \quad \frac{d}{dt}(c^{\mathsf{T}} n) = c^{\mathsf{T}}(u - e). \tag{M8}$$

For lumen concentrations x_i, use $n_i = V x_i$; for surface densities y_i, use $n_i = A y_i$, with consistent mole or molecule units. The total includes all relevant volume and surface terms and every storage pool.

Proof. A discrete internal transition partitions the same carbon origins among its reactants and products; counting gives zero change and hence the column identity. Multiply the amount equation by c^{T} and cancel the internal columns. The density substitutions are definitions of extensive amount. Differentiating them includes $V\dot{x}_i + \dot{V} x_i$ or $A\dot{y}_i + \dot{A} y_i$; omitting these size terms would change the balance. Multiplication by carbon's molar mass converts mole-carbon amounts to carbon mass without changing the proof. □

An ODE amount is a real-valued coarse variable. Its value 0.2 is not an individual atom with a fractional identity. Exact labelled graphs project to integer molecule counts; ensembles can project to expected counts, and a justified large-system scaling can project to continuous densities. The expectation equation need not be closed because generally $\mathbb{E}[v(N)] \neq v(\mathbb{E}[N])$ for nonlinear propensities. Accordingly, (M8) is a necessary consistency identity for a coarse dynamics model. It does not prove a microscopic trace, an exact mean-field closure, or a molecular realization of every real-valued trajectory. A combined molecular-operating theorem requires a compatible trace or scaling model and its projection law, in the same chemical regime and assembly state.

For the uncoded operating block used below, a donor B has carbon $C_m + C_r$, a carrier has carbon C_c, each residue has C_m, a remnant has C_r, and a spent carrier retains C_c. Its integer material block is

$$\begin{aligned} &10B + 2\,\text{carrier} \longrightarrow \\ &\quad P_4^{\text{retained}} + P_4^{\text{lumen}} + 2\,\text{residue} \\ &\qquad + 10\,\text{remnant} + 2\,\text{spent carrier}, \end{aligned} \tag{M9}$$

with all noncarbon coproducts separately included. The carbon identity is $10(C_m+C_r)+2C_c = 8C_m+2C_m+10C_r+2C_c$. Using the operating variables b, c, p, w, l, h, r, z, it is equivalently

$$C_{\text{scaffold}} + C_m\{b + 4(p+w+l) + h\} + C_r(b+r) + C_c(c+z). \tag{M10}$$

Here active-to-inactive conversion $p \to w$ preserves the same chain atoms. The scaffold is a separately reserved inventory. The donor symbol B denotes an eligible *derived* atom-mapped packet; it is not permission to import a ready amino acid. The operating parameters cannot establish that packet's stock-to-product chemistry. Formula (M10) states exactly the material interface that any proposed microscopic lift must satisfy.

Theorem 3.19 (A finite count path approximating the operating amounts)**.** *Let $S, w : [0, H] \to \mathbb{R}$ be continuous nondecreasing functions with $S(0) = w(0) = 0$, $0 \le w(t) \le S(t)/10$ and $S(t) \le S_{\max} \le 130$. Suppose the continuous operating amounts are*

$$\begin{aligned} b = 130 - S, \quad c = 30 - S/5, \\ p = S/10 - w, \quad l = S/10, \\ h = z = S/5, \quad r = S. \end{aligned}$$

For each positive integer M, there exists a finite prescribed-time path of integer blocks (M9) and single-chain deactivations, starting from $130M$ donors and $30M$ carriers, whose right-continuous observed amounts, taken after all events at a common timestamp and divided by M, satisfy uniformly

$$\begin{aligned} &|p_M - p|,\ |w_M - w|,\ |l_M - l| < 1/M, \\ &|c_M - c|,\ |h_M - h|,\ |z_M - z| < 2/M, \\ &\quad |b_M - b|,\ |r_M - r| < 10/M. \end{aligned} \tag{M11}$$

The path uses at most $2\lfloor M S_{\max}/10 \rfloor$ block/deactivation events. This is a stoichiometric approximation theorem, not a derivation of its event rates or atom maps.

Proof. Set

$$B_M(t) = \lfloor MS(t)/10 \rfloor, \qquad W_M(t) = \lfloor Mw(t) \rfloor.$$

Both are nondecreasing integer functions and $0 \le W_M \le B_M$. At each increment of B_M, execute one production block; at each increment of W_M, deactivate one produced active chain. When increments coincide, execute production first. The inequality $W_M \le B_M$ ensures that the chain to be deactivated is available after the tie convention. Nondecreasing continuous driving functions cross only finitely many relevant integer thresholds on the bounded interval, so this gives a finite event list. There are at most $\lfloor MS_{\max}/10 \rfloor$ events of each kind.
The exact counts divided by M are

$$b_M = 130 - 10B_M/M, \quad c_M = 30 - 2B_M/M,$$
$$p_M = (B_M - W_M)/M,$$
$$w_M = W_M/M, \quad l_M = B_M/M,$$
$$h_M = z_M = 2B_M/M, \qquad r_M = 10B_M/M.$$

Stocks remain nonnegative because $B_M \le 13M$; carriers even satisfy $c_M \ge 4$. Every production event consumes the declared ten donors and two carriers and produces the displayed components. Deactivation merely moves one retained chain from active to inactive. Write $MS/10 = B_M + \theta$ and $Mw = W_M + \eta$, where $0 \le \theta, \eta < 1$. All bounds follow by substitution; in particular $p_M - p = (\eta - \theta)/M$, whose absolute value is strictly less than $1/M$. The exact block balances prove (M10) at every intermediate event, including between two simultaneous events ordered by the stated convention. The strict error bounds refer to the completed observed state at that timestamp; an intermediate ordered microstep is not separately claimed to satisfy them. □

Corollary 3.20 (Nominal finite-path threshold margin)**.** *For the nominal operating witness of Theorem 7.2, the count path on* $[0, 4]$ *uses at most* $20M$ *events. Where the margin of Corollary 7.4 gives* $p \ge 8/5$*, one has* $p_M > 3/2$ *for every integer* $M > 10$*.*

Proof. The nominal bounds give $S_{\max} = 100$, and hence the event bound is $2\lfloor 10M \rfloor = 20M$. By (M11), $p_M > 8/5 - 1/M > 3/2$ when $M > 10$. The cited nominal margin holds from some time no later than $162812/43813 < 3.717$ through time 4. □

If a complete stock-derived atom-mapped production block and an origin-preserving deactivation map are independently supplied, fresh origin-prefix copies of their consumable supports lift this finite count path to an atom-labelled path. Shared scaffolds additionally require the same restored/compatible state at each event. This conditional step is strictly stronger than the arithmetic construction. The theorem selects event times from the given continuous functions and does not assert that a chemical stochastic process has those times, or that its mass-action or mean-field limit equals the proposed operating ODE.

4 Constitutional amino acid products and uncoded joining

The baseline requires amino-acid-derived peptide material and one product-dependent function. It does not require a genetic code or all twenty conventional amino acids. Nevertheless, the revised Article 75 provides a useful finite constitutional library [Sch26b]. We state its reusable graph construction here because its exact scope determines the preparation interface of the present model.

4.1 Prepared modules and the carbon source gap

Let the chrysene core graph have the perimeter

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

with chords $4a : 12a$, $4b : 10b$ and $6a : 10a$. A declared Kekulé completion alternates doubled perimeter edges, beginning with $6 : 6a$; other core edges have order one. The prepared active module has the additional local motif

$$\begin{gathered} 5 - c_\alpha(H)(n_\alpha H_2) - c'(= o_x) - o_t, \\ 6 - o_6 H, \quad 12 - o_{12} - B_{12}, \quad o_t - B_t. \end{gathered} \tag{3}$$

The symbols B_{12} and B_t are capacity-one boundary ports, not atoms. The intended o_t is a resident adenosine $2'$ oxygen. A real context must supply compatible boundary atoms and all of its remaining valence and carbon. The two carbons c_α, c' have declared arm-backbone roles in the prepared certificate. That declaration does not by itself identify which admitted arm atoms produced them.

Each ordinary module receives three labelled ammonia molecules, three labelled waters and eight labelled hydrogen molecules. The sulfur pair receives one additional labelled *H–S–S–H* packet shared by its two modules. These are finite formal donor packets. They assert neither a laboratory recipe nor a favorable reducing reagent. An exposed ordinary module has inventory $C_{20}H_{44}N_4O_7$, or 75 actual atoms and two ports. The sulfur pair has $C_{40}H_{90}N_8O_{14}S_2$, or 154 actual atoms and four ports. The contexts and spectator cores are outside these exposed counts.

The admitted-stock-to-prepared-module theorem in the material chapter therefore has work to do: it must map the core, two backbone carbons, resident nucleoside, tether,

caps and spectators from separately allocated stock, complete the ports, and account for every coproduct. This is a downstream preparation obligation. It does not reopen the excluded question of manufacturing the admitted incoming stock.

4.2 A restricted finite bond grammar

A formal graph has immutable atoms and bond orders $b_{uv} \in \{0,1,2,3\}$. Neutral capacities are $v(C) = 4$, $v(N) = 3$, $v(O) = v(S) = 2$ and $v(H) = 1$. Unused capacity is $d_a = v(a) - \sum_u b_{au} \geq 0$. A split lowers a positive bond order by one; a join raises it by one when both capacities permit. These are algebraic graph operations. Unused capacities do not designate measured radicals or transition states.

Put $B_6 = \{4a, 4b, 10b, 11, 12, 12a\}$ and $A_6 = \{1, 2, 3, 4, 4a, 12a\}$. An ordinary retained mask has the form $\{5\} \cup \{6\}^\eta \cup I$, where $\eta \in \{0,1\}$ and I is empty or a connected arc of the B_6 cycle containing $4b$; the whole cycle is included once. The other masks are the empty set and the extended set $\{5, 4b, 10b\} \cup A_6$. Up to two neighboring nonretained core vertices may be wholly detached from their original heavy-atom incidences. This means tracked fragments, not deleted atoms.

The guarded grammar has the following persistent restrictions:

1. Product carbon is exactly the retained mask plus c_α, c'. There is no carbon input or transfer between copies during extraction.
2. A changed core edge meets the retained mask or the declared whole-removal support. A new core adjacency must be an original chrysene adjacency. Other remnant core bonds and their orders remain unchanged.
3. Extraction-boundary edges are removed; retained core adjacencies remain except at most one explicitly allowed internal deletion.
4. The bonds $c_\alpha - c'$, $c_\alpha - n_\alpha$ and $c' = o_x$ are protected. The bond $5 - c_\alpha$ is protected except for the empty mask.
5. New side-chain heteroatoms come from the finite labelled packet and attach only within the permitted product support or the specified backbone closure. No atom is renamed as another element.
6. Free-acid completion replaces $c' - o_t$ by $c' - o_0$, retaining the original carbonyl oxygen o_x, and accounts for the displaced hydrogens and context atoms. Ports are never included in the product component.

The initial and terminal graphs and the full rewrite words are bundled as fixed certificate data. They include the hydrogen assignments and all unused donor molecules, rather than an unspecified hydrogen reservoir.

Lemma 4.1 (Finite guarded bond word)**.** *Let b, b' be two bond-order states on the same labelled atom set satisfying the capacity bounds and sharing all protected edges. Suppose every differing edge is permitted by the same support and every inserted adjacency is allowed. Splitting $(b_{uv} - b'_{uv})_+$ units first and joining $(b'_{uv} - b_{uv})_+$ units second gives a finite legal valence path from b to b', of length $\sum_{\{u,v\}} |b_{uv} - b'_{uv}|$.*

Proof. After all splits the bond vector is the componentwise minimum of b, b'. Every subsequent partial join is bounded componentwise by b', so each vertex remains below its terminal capacity. The guards hold edgewise and protected equal edges are unchanged. Atoms and their labels are fixed at every step. The stated length counts precisely the changed bond-order units. □

Without the support and protection hypotheses, this would be a universal bond-reconstruction lemma, too permissive to establish chemical feasibility. Here it is a finite construction within a restricted grammar.

4.3 The constitutional library

Every listed product has the common amino-acid backbone $n_\alpha - c_\alpha - c'(= o_x) - o_0H$, with $c_\alpha - 5$ except in Gly. Table 3 specifies the side-chain heavy-atom connectivity. Unmarked linear edges are single. Hydrogens close neutral valences; aromatic cycles use the certificate's alternating assignment. Each row's core labels belong to its own copy.

Theorem 4.2 (Prepared constitutional repertoire)**.** *In the displayed restricted grammar, eighteen disjoint ordinary prepared modules and one paired two-module sulfur packet admit a finite execution whose endpoint contains the twenty target graphs of Table 3 as disjoint components. Every actual atom and every port is retained in the global accounting, all terminal valences close, and every unmodified remnant core edge retains its order. This is a nonempty formal repertoire, not an assertion that exactly these twenty products exhaust the grammar.*

Proof. For each nonsulfur row choose the retained core set visible in its side-chain connectivity. Ala and Ser use the declared whole-removal neighbors $6, 4b$; the other nonsulfur rows use the permitted boundary cuts. The fixed certificate data specify any internal cut and all hydrogen partners. Every row's inserted heavy-atom edges

Table 3: Twenty constitutional targets in the prepared-input grammar. The final column counts core-derived plus backbone carbon. Stereochemistry is not fixed by these graph rules.

Target	Side-chain connectivity from the backbone	Neutral formula	Carbon origin
Ala	$5H_3$	$C_3H_7NO_2$	$1+2$
Arg	$5-4b-10b-n_1-11(=n_2H)-n_3H_2$	$C_6H_{14}N_4O_2$	$4+2$
Asn	$5-4b(=o_1)-n_1H_2$	$C_4H_8N_2O_3$	$2+2$
Asp	$5-4b(=o_1)-o_2H$	$C_4H_7NO_4$	$2+2$
Cys	$5-s_3H$ on the first sulfur copy	$C_3H_7NO_2S$	$1+2$
Gln	$5-4b-10b(=o_1)-n_1H_2$	$C_5H_{10}N_2O_3$	$3+2$
Glu	$5-4b-4a(=o_1)-o_2H$	$C_5H_9NO_4$	$3+2$
Gly	No retained core carbon; $c_\alpha H_2$	$C_2H_5NO_2$	$0+2$
His	$5-4b$; cycle $4b=10b-n_1H-11=n_2-4b$	$C_6H_9N_3O_2$	$4+2$
Ile	$5(-6)-4b-10b$	$C_6H_{13}NO_2$	$4+2$
Leu	$5-4b(-4a)-10b$	$C_6H_{13}NO_2$	$4+2$
Lys	$5-4b-10b-11-n_1H_2$	$C_6H_{14}N_2O_2$	$4+2$
Met	$5-4b-s_4-10b$ on the second sulfur copy	$C_5H_{11}NO_2S$	$3+2$
Phe	$5-4b$; aromatic cycle $4b,10b,11,12,12a,4a,4b$	$C_9H_{11}NO_2$	$7+2$
Pro	$5-4b-10b-n_\alpha$ closes to backbone nitrogen	$C_5H_9NO_2$	$3+2$
Ser	$5-o_1H$	$C_3H_7NO_3$	$1+2$
Thr	$5(-o_1H)-4b$	$C_4H_9NO_3$	$2+2$
Trp	$5-4b$; fused cycles $4b,10b,n_1H,12a,4a,4b$ and $12a,1,2,3,4,4a,12a$	$C_{11}H_{12}N_2O_2$	$9+2$
Tyr	Phe ring with $12-o_{12}H$, retaining original oxygen	$C_9H_{11}NO_3$	$7+2$
Val	$5(-6)-4b$	$C_5H_{11}NO_2$	$3+2$

use its retained support and the packet heteroatoms, and protect the three backbone edges. The independent data-consuming verifier checks these finite predicates and replays every primitive to the exact terminal graph; it does not import the graph constructor. Lemma 4.1 gives the finite path once these endpoint and support checks hold.

For sulfur the two copies and two sulfur atoms remain distinct. The joint word forms the ordered bridge $5@X_3-s_3-s_4-4b@X_4$, then splits s_3-s_4 and joins $s_4-10b@X_4$, before completing the Cys and Met endpoints. The shared sulfur packet is allocated once. Finally give all nineteen certificate instances disjoint origin prefixes. Their rules read and write only their own support, so sequential composition is legal. The complete terminal atom sets are the disjoint union of their supplied endpoints. □

The twenty diagnostic unary files and the paired sulfur file are not simultaneously consumed twenty-one preparations. For the simultaneous repertoire use eighteen nonsulfur unary paths and the one two-copy sulfur path. The resulting exposed-module count is 1,504 actual atoms and 40 ports; its carbon count is 400. The products contain 107 carbons, 67 from retained core sites and 40 from prepared backbone sites. The other 293 exposed-module carbons remain in tracked nonproduct components. A full twenty-carrier architecture represents 120 original cores, including forty spectator residual cores outside the twenty active local graphs. Resident adenosines, tethers and these spectators are not somehow included in the exposed 1,504-atom total.

The donor upper bound for that repertoire is $60NH_3+60H_2O+160H_2+H_2S_2$. Its mathematical role is finite sufficiency for the graph certificates. It is not a chemical yield, energetic cost or recommended reagent recipe. The usual L configurations, including the separate side-chain configurations of Ile and Thr and the product-priority R descriptor of Cys, require stereochemical data beyond a constitutional graph. Tautomer and protonation choices also require a shared environment.

4.4 What joining adds

A free amino-acid graph, an activated ester and a peptide-transfer complex are different input types. Article 76 proposes adjacent ester transfer and release rules [Sch26h]. Those are candidate local chemistry hypotheses; adjacency alone does not prove reaction, rate or selectivity. The uncoded baseline replaces codon-dependent stopping by a declared chemical or externally timed release rule. It does not infer uncoded production from an IID codon stop formula.

The following identity isolates the material fact that a peptide bond does not require new carbon. It supplies a formal endpoint relation, not the rate law used later.

Proposition 4.3 (Carbon-preserving linear joining identity)**.** *Take $m \geq 1$ disjoint neutral amino-acid graphs with distinct labelled backbone atoms. If each selected next backbone nitrogen has an available N–H bond, the formal operation replacing the current terminal $c'_i - o_i H$ and $n_{i+1} - H_i$ incidences by $c'_i - n_{i+1}$ and $o_i - H_i$ produces a linear peptide graph and $m-1$ labelled waters. It preserves every carbon origin, all atoms and total neutral valence. Its peptide formula is the sum of the input formulas minus $(m-1)H_2O$.*

Proof. At each step split the acyl–hydroxyl bond and the selected N–H bond. The acyl carbon and nitrogen each gain one unused valence, which their new amide edge fills. The hydroxyl oxygen and transferred hydrogen each gain one unused valence, which their new edge fills. The oxygen retains its original hydrogen and therefore becomes a water component. No carbon incidence is replaced by a new atom. Iterate on the terminal carboxyl group of the growing chain, retaining all unused inputs and the water components. Summing the component formulas gives the identity. □

This graph operation is not a claim that free residues condense spontaneously in the compartment. A chemically useful construction needs an activation state, a leaving group, energy and proton accounting, competition control, a molecular path and a rate. An ester-transfer implementation has a different full coproduct context but the same carbon-retention principle. The operating model tracks failed-joining residues as a separate accumulating species and does not consume them in a retired free-residue condensation law.

4.5 Function and sequence remain explicit choices

The four-residue product in the reduced witness is a stoichiometric functional class. Its assigned influence on uptake or processing is a constitutive hypothesis. It is not an identified catalytic tetrapeptide sequence, and the theorem supplies no stereochemical activity measurement. To instantiate it chemically one must choose a specific chain or bounded ensemble, determine its retained fraction and deactivation products, and establish its dose-dependent action under the same environment as joining and transport. A chain that merely occupies membrane area does not yet supply the required return influence.

For a gene-directed extension, a template-to-product map must be causally implemented. The revised Article 75 supplies a finite addressed product/controller framework after prepared inputs and specified routing; it does not make a fixed resident AAA tether into an arbitrary genome. The extension needs a carbon-traceable template and decoder, a faithful readout, start/extension/termination rules, fresh resource semantics and a matched template intervention that changes the product as predicted. Copying, error control and segregation add further requirements if heredity is claimed. None of those is needed for the productive feedback theorem of the uncoded base model.

5 A common state for constructive operation

The first operating question is whether admitted material can support a bounded, productive compartment without assuming a genetic instruction system. We answer that question for a specified reduced constitutive model. Its initial peptide amount is zero, its donor and carrier supplies are finite, and its own retained product increases productive processing. The answer is positive for four forcing periods. Every assertion of chemical or physical realization remains conditional on a common material and constitutive certificate. The numbers below are normalized model choices, not measured parameters of a chrysene protocell.

This distinction also fixes the source precedence. Article 71 version 2 corrects area creation in the division reset, but its residue–remnant condensation law is not our chemistry. Article 76 version 6 replaces that law by tethered-chain joining, released chains, and hydrolysis before joining [Sch26a, Convention on the reset][Sch26h, H2–H9 and precedence rulings]. We retain that compartmental distinction without importing a codon distribution, a genome, or a stop-word mechanism into this uncoded example.

5.1 Extensive amounts and one compartment boundary

Write the general operating state as

$$x = (n, b, \ell, V, s, \tau, m; \theta).$$

Here n lists internal amounts, including free, bound, membrane, growing-chain, released-chain and stored-waste species; b lists finite outside reserves; ℓ records cumulative admissions and exports; V is lumen volume; s is switch state; τ is forcing phase; and m is a discrete mode. All modules use the same parameter vector θ, the same inventories, and the same bath. Area is derived from the membrane inventory, or from an explicitly declared elastic constitutive relation. Algebraically determined ion amounts are outputs of the closure, not extra independent coordinates.

For a reaction matrix S and boundary fluxes, the amount equation is

$$\dot{n} = S r(t, n, b, V, s; \theta) + j_{\text{in}} - j_{\text{out}}. \tag{4}$$

If c is the row of carbon counts and $cS = 0$, then

$$\frac{\mathrm{d}}{\mathrm{d}t}(cn) = cj_{\mathrm{in}} - cj_{\mathrm{out}}, \qquad cn + \ell_{\mathrm{out}} - \ell_{\mathrm{in}} = cn(0). \quad (5)$$

External reserves satisfy the matching withdrawal equation. A carrier cannot cross the boundary without appearing in that equation. If a concentration is used instead, $n_i = Vx_i$ gives $\dot{x}_i = \dot{n}_i/V - x_i\dot{V}/V$; omitting the dilution term loses the amount ledger. Surface densities similarly require the changing area.

Equation (5) is a real-valued projection. Atom labels belong to a discrete reaction realization, or to an explicitly defined measure model. A fractional ODE amount is not a fractional labelled carbon atom, and a conserved scalar carbon count alone does not prove admissible ancestry. The material certificate must separately provide eligible starting graphs, atom-preserving transformations, and a justified coarse-graining relation. Nothing here produces incoming stock, advances its prehistory, or makes it self-separate before admission.

5.2 What counts as a lumen particle

An independently translating ideal solute contributes one particle regardless of its residue count. A free four-residue chain therefore contributes one, whereas four independently released residues contribute four. A residue esterified to an immobilized carrier contributes no additional freely translating lumen particle. A soluble complex contributes one complex particle, not one per bound constituent. An immobilized complex affects membrane area, charge and mechanics; its constituent charges may still affect ionic osmotics. These are different accounting operations.

Let N_{free} count the declared ideal nonpermeant lumen particles, with complexation already resolved. For an ideal permeant monovalent salt of bath concentration $c_s > 0$, and fixed negative charge of magnitude $Q \geq 0$, the fast-equilibrium closure is

$$n_+ - n_- = Q, \qquad n_+ n_- = c_s^2 V^2,$$
$$n_\pm = \frac{\sqrt{Q^2 + 4c_s^2V^2} \pm Q}{2}. \quad (6)$$

The positive root is unique: eliminating n_+ produces a quadratic in n_- whose other root is negative. The excess mobile-ion concentration is

$$D(Q, V, c_s) = \sqrt{(Q/V)^2 + 4c_s^2} - 2c_s, \qquad 0 \leq D \leq \frac{Q^2}{4c_sV^2}. \quad (7)$$

The bound follows by rationalizing the square root; its denominator is at least $4c_s$. For $Q > 0$ the excess is positive even though the ions permeate. Thus permeability cannot by itself justify deleting the counterion contribution. Nor may one add a second copy of the same mobile ions as "chain counterions." Article 76's H15 is an additional exclusion assumption; we do not use it [Sch26h, H15].

A compatible illustrative water law is

$$\dot{V} = \kappa A \left[\frac{N_{\mathrm{free}}}{V} + D(Q, V, c_s) - \omega - e(t, x) \right], \qquad \kappa > 0. \quad (8)$$

The carbon-free excluded bath solute contributes ω. The term e can represent mechanical pressure divided by the osmotic conversion constant and other declared closure error. This equation is an assumption about transport; its use for a physical membrane requires permeability, ionic equilibration, retention and pressure estimates at the same operating point. A finite-rate ion model instead requires its own transport equations and charge ledger.

6 An explicit uncoded finite-stock model

The outside reserve b consists of donor packets, each containing a residue-equivalent moiety and a complementary skeletal remnant. The outside reserve c consists of release-carrier packets. Their unused contents are outside the lumen and do not count as internal osmolytes or membrane guests. The flux J means consumption-coupled admission and processing. In this zero-residence-time approximation no separate internal donor pool is assumed; a finite residence time would require adding that pool to all inventories.

The internal product coordinates are active retained four-residue chains p, inactive retained chains w, released lumen chains l, free residues from failed joining h, membrane remnants r, and membrane spent carriers z. Deactivation $p \to w$ preserves all material and footprint. The processing rule joins a fraction $q = 4/5$ of residue equivalents, releases $\rho = 1/5$ chains per acceptance, and allocates half of those chains to the lumen. In particular, $4\rho = q$. This is a stipulated uncoded local yield, not an inference from independent codons. No free-residue condensation sink is present.

Set the forcing period to one. For $t \in [k, k+1)$, let $I(t) = 1$ on $[k, k+1/2)$ and $I(t) = 0$ on $[k+1/2, k+1)$. Equivalently, $\dot{\tau} = 1$ with a phase reset $\tau \mapsto 0$ at $\tau = 1$. The half-period event changes the input but resets no molecular coordinate. The equations are

$$J = \left(10 + \frac{20p}{1+p}\right) \frac{b}{1+b} \frac{c}{1/10 + c} \left(\frac{19}{20} + \frac{s}{20}\right), \quad (9)$$

$$\dot{b} = -J, \qquad \dot{c} = -J/5, \quad (10)$$
$$\dot{p} = J/10 - p, \qquad \dot{w} = p,$$
$$\dot{l} = J/10, \qquad \dot{h} = J/5,$$

$$\dot r = J, \qquad \dot z = J/5,$$
$$\dot s = 2I(t)(1-s) - s. \tag{11}$$

Guest-inclusive area and freely translating neutral particles are

$$A = 500 + 4(p+w) + r + z, \qquad N_{\mathrm{free}} = 20 + l + h. \tag{12}$$

The area 500 represents a finite assembled scaffold, including the pore, switch and fixed sites. Its carbon is separately reserved from eligible starting stock. It is not a new stock class or an uncounted prebuilt input. The initial 20 particles are carbon-free nonpermeant species; their retention and charge states must be specified in any realization. Their net fixed negative charge, together with any other declared immobilized charge, is $Q = 2$. Organic products are neutral in this example. With $c_s = 1$, $\omega = 1/10$, $\kappa = 1/100$, and $e = 0$, the volume equation is

$$\dot V = \frac{A}{100}\left[\frac{20 + l + h}{V} + \sqrt{4 + 4/V^2} - 2 - \frac{1}{10}\right]. \tag{13}$$

The initial condition is

$$\begin{aligned}&(b, c, p, w, l, h, r, z, s, V)(0)\\ &= (130, 30, 0, 0, 0, 0, 0, 0, 0, 200), \qquad H = 4.\end{aligned} \tag{14}$$

Thus neither a functional peptide seed nor a genome is supplied.

6.1 Explicit supply and service ledgers

Put $S(t) = \int_0^t J(u)\,\mathrm{d}u$. Direct integration gives

$$\begin{aligned} b = 130 - S, \quad c = 30 - S/5,\\ p + w = l = S/10, \quad h = z = S/5,\\ r = S, \quad A = 500 + 8S/5,\\ N_{\mathrm{free}} = 20 + 3S/10. \end{aligned} \tag{15}$$

Consequently

$$b + 4(p+w+l) + h = 130, \qquad b + r = 130, \qquad c + z = 30. \tag{16}$$

If the actual donor graph has C_m carbons in its residue-equivalent moiety and C_r in its complementary remnant, and a carrier has C_c, the conserved carbon projection is

$$C_{\mathrm{scaffold}} + C_m[b + 4(p+w+l) + h] + C_r[b + r] + C_c[c + z]. \tag{17}$$

This requires an atom-mapped donor satisfying $C_B = C_m + C_r$, with the carrier, scaffold, products and any coproducts matched to the same material certificate. No export occurs in this particular model. An export extension must add its cumulative carbon to (17), rather than delete spent material.

A compatible integer stoichiometric block consumes ten donors and two carriers and produces one retained and one lumen four-residue chain, two free residues, ten remnants and two spent carriers. Its residue balance is $4 + 4 + 2 = 10$. The reserve pays for at most thirteen complete donor blocks. This is an integer balance example, not a molecular mechanism or an exact realization of every continuous trajectory.

Energy capacity is also finite over the claimed experiment. To make the service assumption explicit, allocate $E(0) = 160$ normalized usable-work units and require that the stipulated processing, activation and maintenance services cost at most

$$\begin{aligned} P(t) &= J(t) + 2I(t)(1 - s(t)) + p(t),\\ E(t) &= 160 - \int_0^t P(u)\,\mathrm{d}u. \end{aligned} \tag{18}$$

These are declared unit costs and a capacity ledger, not measured quantum yields or a thermodynamic proof. In a realization, reaction free energies, coupling, photochemical losses and bath work must fit the budget. The analysis below gives $P \le 30$, hence $E \ge 40$ on $[0, 4]$. No energetic exhaustion mode is reached there. Any continuation past the funded experiment requires a new budget or a specified shutdown rule. Carbon-free auxiliary feeds and the salt/water bath remain explicitly declared boundary services.

7 Well posedness and the finite operating theorem

Theorem 7.1 (Continuous-mode and hybrid well posedness)**.** *In each mode let $f(t, x)$ be measurable in t, continuous in x for almost every t, and locally Lipschitz in x. On every compact state set and bounded time interval assume integrable magnitude and Lipschitz bounds $M(t), L(t)$. Assume that f extends to an open neighborhood of the allowed state domain, all algebraic closures are uniquely solvable with locally Lipschitz solutions, and $f_i(t, x) \ge 0$ when a constrained species coordinate $x_i = 0$ and the other species are nonnegative. Then each admissible initial state has a unique local Carathéodory solution and its species remain nonnegative.*

For a hybrid extension, event times must be prescribed separated times or attained first hits of closed guards given by continuous guard functions. Specify a unique reset and deterministic priorities at simultaneous events. Exclude grazing from the claimed domain, or give a separate well-posed grazing rule. Each reset must preserve the allowed domain and complete ledger.

Assume the resulting concatenation is non-Zeno and remains in a compact subset of the regular domain. Then it has a unique continuation to every specified finite horizon satisfying those assumptions.

Proof. On a sufficiently short interval, integrability permits $\int L < 1$ and $\int M$ smaller than the radius of a chosen local ball. The integral operator $Tx = x_0 + \int f(u, x(u))\,\mathrm{d}u$ maps the corresponding closed space of continuous paths into itself and is a contraction in the uniform norm. Its fixed point is absolutely continuous and satisfies the ODE almost everywhere. Two such solutions have distance bounded by the integral of L times that distance, hence coincide by the integral Gronwall argument. Repeating this construction gives the maximal local solution.

For positivity, let x^+ replace negative constrained coordinates by zero, and let q be the sum of their negative parts. Wherever a coordinate is negative, quasi-positivity at x^+ and the local Lipschitz bound give $-f_i(t,x) \le L(t)\|x - x^+\|$, up to a fixed finite-dimensional norm factor. Thus $q' \le CL(t)q$ almost everywhere. Since $q(0) = 0$, $q = 0$. Local extension permits this argument before any putative first exit.

At an attained first event the unique reset gives a new initial condition. Uniqueness on each segment and deterministic priority give uniqueness of every finite concatenation. The non-Zeno assumption leaves finitely many events on any compact time interval. On a regular compact state set the integrable magnitude bound gives a limiting state at a finite maximal endpoint; local existence there extends the trajectory unless a prescribed terminal event has been reached. This proves continuation. Closedness or an explicit attained-hit rule is essential: the open guard $t > 0$ has infimum zero but no first hit after $t = 0$. □

The theorem concerns uniqueness for fixed initial state, parameters and input. It says nothing about uniqueness of architecture, viable parameter choice, or attractor. Time measurability without integrable bounds is insufficient. For (9)–(13), the only discontinuities are the prescribed half-period changes of I; $V > 0$ and nonnegative species keep all state denominators away from singularities locally. Hence these hypotheses hold as soon as the bounds below are established.

Theorem 7.2 (Bounded operation and bootstrap from zero peptide)**.** *Equations (9)–(14) have a unique solution on* $[0, 4]$*. Every material amount is nonnegative and*

$$0 \le p \le 3, \quad b \ge 30, \quad c \ge 10,$$
$$500 \le A \le 660, \quad 100 \le V \le 600, \tag{19}$$
$$0 \le s \le 1.$$

Production is strictly positive on this interval. The active retained-chain amount reaches the functional threshold $p_{\mathrm{fun}} = 3/2$ *no later than*

$$t_{\mathrm{fun}} \le \frac{3131}{1049} < \frac{597}{200} = 2.985 \tag{20}$$

and cannot fall below that threshold before $t = 4$*. The service budget in (18) remains positive.*

Proof. At $b = 0$ or $c = 0$ the availability factor makes $J = 0$. At $p = 0$ its derivative is nonnegative; all other product coordinates have nonnegative sources. At $s = 0$ the derivative is $2I \ge 0$ and at $s = 1$ it is -1, so the switch interval is invariant. Theorem 7.1 gives local positivity. First $J \le 30$, whence $\dot p + p \le 3$ and integration after multiplication by e^t gives $p(t) \le 3(1 - e^{-t}) \le 3$. Substitution into the saturation term improves the flux bound to $J \le 25$. Therefore $S(t) \le 25t$, and for $t \le 4$ the reserve lower bounds in (19) follow.

Each availability factor is now bounded uniformly from below:

$$\frac{b}{1+b}\frac{c}{1/10+c}\left(\frac{19}{20} + \frac{s}{20}\right) \ge \mu := \frac{19}{20}\frac{30}{31}\frac{100}{101} = \frac{2850}{3131}. \tag{21}$$

For $0 \le p \le 3/2$,

$$\dot p \ge F(p) := \mu\left(1 + \frac{2p}{1+p}\right) - p.$$

Here $F''(p) = -4\mu/(1+p)^3 < 0$. A concave function on an interval is at least the smaller endpoint value, so

$$F(p) \ge \min\{\mu, (11/5)\mu - 3/2\} = \frac{3147}{6262} =: \delta > 0.$$

If the threshold had not been reached by $(3/2)/\delta = 3131/1049$, integrating $\dot p \ge \delta$ would contradict $p < 3/2$. The rational comparison $626200 < 626253$ proves $3131/1049 < 597/200$. The same positive lower derivative at and just below the boundary forbids a downward crossing on the remaining horizon. This is a uniform differential inequality, so no differentiability at a light-switch instant is needed.

The exact identities (15) give $A \le 660$ and $N_{\mathrm{free}} \le 50$. At $V = 100$ the water bracket is at least $20/100 - 1/10 = 1/10 > 0$. At $V = 600$, the rational Donnan bound gives the strict upper bound

$$\frac{50}{600} + \frac{1}{600^2} - \frac{1}{10} = -\frac{5999}{360000} < 0.$$

The scalar boundary inequalities preserve $100 \le V \le 600$. The product identities bound every other coordinate, yielding a compact regular operating tube. The continuation part of Theorem 7.1 now extends the local solution through $H = 4$.

Since the reserves stay positive, $J \ge 10\mu > 0$. Thus $S(t) > 0$ for $t > 0$, and l, h, r, z become positive. The integrating-factor expression for p makes $p(t) > 0$ for $t > 0$, and then $w(t) = \int_0^t p > 0$ for $t > 0$. Finally $P \le 25 + 2 + 3 = 30$, so $E(t) \ge 160 - 30t \ge 40$. □

Corollary 7.3 (Global mathematical continuation of the material model)**.** *With the prescribed bounded forcing continued, the material, switch and volume subsystem has a unique solution for every $t \ge 0$. It obeys $S \le 130$, $A \le 708$, $N_{\text{free}} \le 59$, and $100 \le V \le 600$. This is a mathematical continuation, not an indefinitely funded operation.*

Proof. Nonnegativity of $b = 130 - S$ gives $S \le 130$; the identities bound all material coordinates and give $c \ge 4$. At the upper volume boundary the bracket is at most $59/600 + 1/360000 - 1/10 = -599/360000 < 0$; the lower-bound sign is unchanged. Every finite interval has finitely many clock events, so the compactness argument proves continuation. The service reserve (18) was only certified on $[0, 4]$ and is not asserted to pay for this continuation. □

Corollary 7.4 (A strict terminal functional margin)**.** *The nominal trajectory reaches $p = 8/5$ by $162812/43813 < 3.717$ and stays at least $8/5$ through $t = 4$. In particular, its terminal margin above p_{fun} is at least $1/10$.*

Proof. Repeat the concavity argument on $[0, 8/5]$. The smaller endpoint is $\mu(1 + 2(8/5)/(1 + 8/5)) - 8/5 = 87626/203515 > 0$. Dividing $8/5$ by that lower speed gives $162812/43813 < 3.717$. The positive boundary derivative again prevents a subsequent downward crossing. □

This strict margin permits an independently justified approximation error smaller than $1/10$ in the active amount to transfer the terminal functional predicate. It does not itself supply a molecular approximation theorem.

7.1 Geometry and function are separately testable

For the reduced volume $v = 6\sqrt{\pi}V/A^{3/2}$, the operating tube gives

$$v^2 \le \frac{36(22/7)600^2}{500^3} < \frac{1}{3} < 1, \qquad \frac{3V}{A} \ge \frac{300}{660} = \frac{5}{11} > \frac{2}{5}. \tag{22}$$

We used the elementary upper bound $\pi < 22/7$. These are a spherical-capacity screen and a global length proxy. They do not bound the narrowest local lumen gap, prove a stable membrane shape, or show that any particular carbon-derived bilayer tolerates its guests. Those interfaces must hold on the same trajectory.

Theorem 7.5 (Causal productive feedback and matched ablation)**.** *In the full model the retained product increases processing at fixed remaining state, and the functional threshold of Theorem 7.2 is attained. Under the intervention that deletes only $20p/(1 + p)$ from (9), with the same initial state, bath, light, yields and other constants, the active amount satisfies $p(t) \le 1 - e^{-t} < 1$ at every finite $t > 0$ and never reaches $3/2$.*

Proof. At $b, c > 0$,

$$\frac{\partial J}{\partial p} = \frac{20}{(1+p)^2}\frac{b}{1+b}\frac{c}{1/10+c}\left(\frac{19}{20} + \frac{s}{20}\right) > 0.$$

The full-model threshold claim was proved independently above. In the ablated system $J \le 10$, so $\dot{p} + p \le 1$ with $p(0) = 0$. Multiplying by e^t and integrating gives the stated bound. The resource trajectories need not remain equal after intervention; they result from the same laws and initial resources. Holding them artificially equal would be a different intervention. □

A positive feedback arrow alone would not establish function. Here the declared predicate is both crossed in the full system and impossible in the matched ablation. Identifying a real four-residue product with the assumed saturating uptake effect and threshold remains a chemical test. Deterministic RK4 traces included with the manuscript give crossing near 1.611 and $p(4) \approx 2.16440$; the ablation gives $p(4) \approx 0.94266$. These are numerical illustrations. The certified time bound is the rational, more conservative $3131/1049 \approx 2.98475$.

8 An explicit robust operating box

The nominal example is not protected merely by plotting it away from a boundary. The following family has a uniform

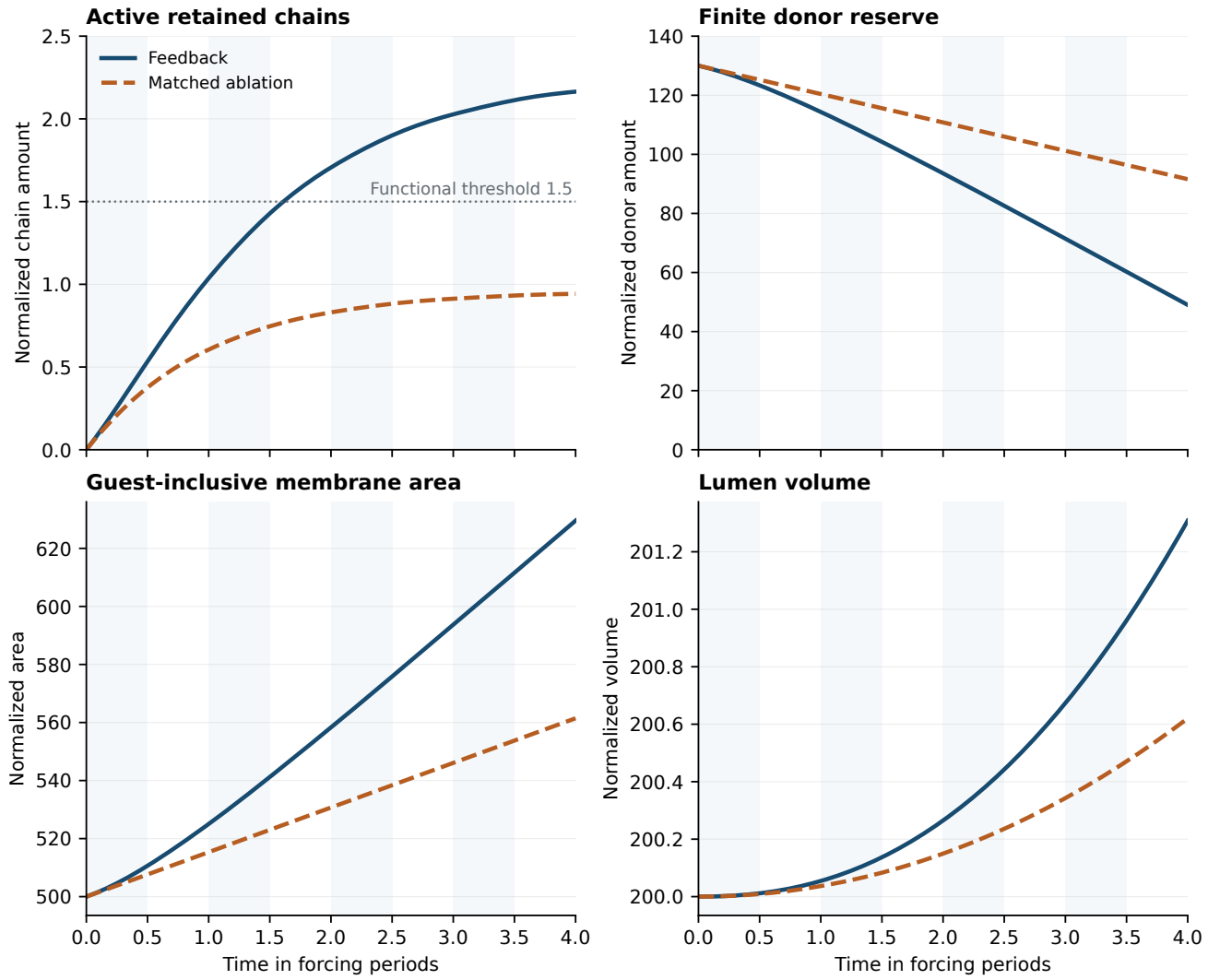


Figure 2: Numerical illustrations of the nominal equations with feedback (solid) and its matched return-edge ablation (dashed). Shaded half-periods have illumination. The retained-product threshold is 1.5; the formal proof gives crossing by $3131/1049 < 2.985$, independently of the earlier numerical crossing near 1.611. All coordinates use the model's normalized units. The reserve is finite, and area and volume are evaluated from the same trajectory. These RK4 curves are sanity checks, not physical rate measurements or proofs of chemical realization.

analytic certificate. Keep all yields and compartment assignments in (10), replacing deactivation by $\dot p = J/10 - kp$, $\dot w = kp$, and let

$$J = \left(a_0 + a_1\frac{p}{1+p}\right)\frac{b}{K_b+b}\frac{c}{K_c+c}\left(\frac{19}{20}+\frac{s}{20}+\eta(t)\right). \tag{23}$$

All disturbances are fixed bounded measurable input paths. Require the intervals

$$\begin{aligned} &a_0 \in [9.9, 10.1], \quad a_1 \in [19.8, 20.2],\\ &k \in [0.99, 1.01], \quad K_b \in [0.99, 1.01],\\ &K_c \in [0.099, 0.101], \quad |\eta(t)| \le 0.005,\\ &b(0) \in [129, 131], \quad c(0) \in [29, 31]. \end{aligned}$$

Let $0 \le I(t) \le 1$ be any measurable input in the same switch equation, $s(0) \in [0,1]$, $V(0) \in [100, 600]$, and all initial peptide/product amounts be zero. Replace the area law by

$$\begin{aligned} A = A_0 + a_P(p+w) + a_r r + a_z z,\\ A_0 \in [499, 501], \quad a_P \in [3.9, 4.1],\\ a_r, a_z \in [0.99, 1.01]. \end{aligned}$$

Use (8) with $N_{\text{free}} = N_0 + l + h$ and

$$\begin{aligned} &N_0 \in [19.9, 20.1], \quad Q \in [1.9, 2.1],\\ &c_s \in [0.99, 1.01], \quad \omega \in [0.099, 0.101],\\ &\kappa \in [0.009, 0.011], \qquad |e(t,x)| \le 0.001. \end{aligned}$$

Assume the stated Carathéodory and locally integrable Lipschitz conditions for state-dependent e. The intervals are parameter uncertainty, not measurements.

Theorem 8.1 (Uniform four-period robustness)**.** *Every system in this family has a unique nonnegative solution on* $[0,4]$ *and*

$$\begin{aligned} p \le 3.1, \quad J \le 26, \quad b \ge 25, \quad c \ge 8.2,\\ 499 \le A < 670, \quad 100 \le V \le 600. \end{aligned}$$

Starting from zero peptide, it reaches $p = 3/2$ *by*

$$t \le \frac{239898900}{70245111} < 3.416, \tag{24}$$

and remains above that threshold through $t = 4$*. Every matched feedback ablation stays below* 1.026*. With the same service-cost convention and* $E(0) = 160$*,* $E(t) > 35$ *on the horizon.*

Proof. The multiplier involving s and η lies in $[189/200, 201/200]$. At first, $J \le (10.1 + 20.2)1.005 = 30.4515$. At $p = 3.1$ this gives $\dot p \le 3.04515 - 0.99(3.1) < 0$, preserving $p \le 3.1$. Inserting that upper bound improves the estimate to

$$J \le \left(\frac{101}{10} + \frac{101}{5}\frac{31}{41}\right)\frac{201}{200} = \frac{2091003}{82000} < 26.$$

Hence $S \le 104$, $b \ge 129 - 104 = 25$ and $c \ge 29 - 104/5 = 41/5$. On this tube the three availability factors have product at least

$$\widehat\mu = \frac{189}{200}\frac{25}{25 + 101/100}\frac{41/5}{41/5 + 101/1000} = \frac{717500}{799663}.$$

For $p \in [0, 3/2]$,

$$\dot p \ge \widehat\mu\left(\frac{99}{100} + \frac{99}{50}\frac{p}{1+p}\right) - \frac{101}{100}p.$$

This concave function has minimum at $p = 3/2$, equal to $\widehat\delta = 70245111/159932600 > 0$; its other endpoint is larger. The same integration and no-downward-crossing argument as before gives $(3/2)/\widehat\delta = 239898900/70245111 < 3.416$.

The identities $p + w = l = S/10$, $h = z = S/5$, $r = S$ still hold. Thus $A \le 501 + (0.41 + 1.01 + 0.202)104 = 669.688 < 670$ and $N_{\text{free}} \le 20.1 + 0.3(104) = 51.3$. At $V = 100$, the water bracket is at least $19.9/100 - 0.101 - 0.001 = 0.097 > 0$. At $V = 600$ it is at most

$$\frac{51.3}{600} + \frac{2.1^2}{4(0.99)600^2} - 0.099 + 0.001 < 0.$$

These rational strict inequalities give the volume bounds and regular compact continuation. The capacity and global-length screens remain strict because $36(22/7)600^2/499^3 < 1/3$ and $300/670 > 2/5$. For the ablation, $J \le 10.1(1.005) = 10.1505$ and $\dot p \le 1.01505 - 0.99p$, so $p \le 1.01505/0.99 < 1.026$. Lastly $P \le 26 + 2 + 3.1 = 31.1$, whence $E \ge 160 - 4(31.1) = 35.6$. □

The box preserves the discrete compartment assignment and stoichiometric yields. It certifies a nontrivial neighborhood of rate, transport, footprint, initial reserve and osmotic parameters within that model class. It does not certify unmodelled chemical reactions, a changed charge state, altered chain length, new organic feed, or a neck pathway.

Proposition 8.2 (Pathwise perturbations and nearby initial conditions)**.** *On a common regular tube, suppose* f *has Lipschitz bound* $L(t)$ *and* $\|\widetilde f(t,x) - f(t,x)\| \le \epsilon(t)$*, where both bounds are integrable. For initial discrepancy* d_0*, solutions with the same prescribed clock*

event times satisfy

$$\|\widetilde{x}(t) - x(t)\| \le e^{\int_0^t L} \left[d_0 + \int_0^t e^{-\int_0^u L} \epsilon(u)\, \mathrm{d}u \right] \quad (25)$$

up to their first tube exit. If this bound is smaller than the relevant strict boundary margins, the corresponding safety and threshold inequalities persist.

Proof. Subtract the integral equations, apply the Lipschitz and perturbation bounds, and multiply the resulting scalar comparison equation by $\exp(-\int_0^t L)$. Integration gives (25). If an alleged first exit requires a discrepancy greater than the bound, it is impossible. Identity resets at fixed clock times do not change the discrepancy. Non-identity resets require their own Lipschitz factors, and state-dependent event-time shifts are not covered by this fixed-time formula. □

For a fixed bounded measurable noise path, these results are deterministic and pathwise. A random input satisfies them on the event that it obeys the stated bounds. They make no claim that all realizations of an unbounded noise law do so, and white-noise forcing is not an ordinary bounded input function. The periodic clock is external; safe operation under it does not establish an endogenous clock or an autonomous organism.

9 What a repeatable operation would require

The four-period theorem establishes a productive trajectory from specified stocks. It does not yet establish a renewal cycle: membrane guests accumulate, outside reserves decrease, and no regeneration or division reset has been constructed. We now give sufficient conditions for the stronger conclusion, keeping these material changes visible.

9.1 A periodic switch is only one periodic coordinate

For the nominal square-wave forcing, write s_0 for the switch fraction at phase zero. Solving (11) on the two half-periods gives

$$R_s(s_0) = e^{-2} s_0 + \frac{2}{3} e^{-1/2} (1 - e^{-3/2}). \quad (26)$$

Indeed, the illuminated solution is $s(1/2) = 2/3 + (s_0 - 2/3)e^{-3/2}$, and darkness multiplies this by $e^{-1/2}$. The map preserves $[0, 1]$, has contraction factor e^{-2}, and has the unique fixed point

$$s_* = \frac{(2/3)e^{-1/2}(1 - e^{-3/2})}{1 - e^{-2}}.$$

Thus the switch alone approaches a forced periodic response. This elementary calculation proves neither periodic materials nor successful division. For a fixed aperiodic bounded input path one instead has a nonautonomous response; there need not be a single repeated one-period map.

Definition 9.1 (Operational state and resource history)**.** An operational projection $z = \pi(x)$ records the quantities required to perform the declared service at a fixed forcing phase. It may forget the names of fresh atom labels and cumulative counters. Any quantity needed to predict the next operation must remain in z or in the accompanying history. A resource history h records remaining outside stocks, all used labels, cumulative admissions and exports, and any other omitted variable that can affect the next cycle. A history-dependent cycle map is

$$(z, h) \longmapsto \big(R_h(z), \mathcal{H}(h, z)\big).$$

It is the composition of an actual flow, attained events, partition or reset, and a specified replenishment policy. Replenishment withdraws named eligible packets from reserves; export increments the export ledger. Neither operation may erase a cumulative history.

Theorem 9.2 (Finite renewal with a uniform resource certificate)**.** *Let K be a nonempty operational section. For every reachable history with the required reserve floor, suppose the certified cycle is defined for every $z \in K$, stays in its common viable tube, and satisfies $R_h(z) \in K$. Suppose its complete withdrawal vector obeys $0 \le d(h, z) \le \bar{d}$, including initial assembly or refurbishment when needed. If the initial reserve is componentwise at least $N\bar{d} + b_{\mathrm{floor}}$ and the replenishment policy leaves that floor available for the last cycle, then the operation can be performed N times. Its full ledger remains consistent on every cycle.*
If a single history-independent map R is justified on a compact convex $K \subset \mathbb{R}^d$ and is continuous, it has an operational fixed point. If K is complete and R is a contraction with factor $q < 1$, that fixed point is unique and every iteration from K converges to it, with error at most q^j times the initial error.

Proof. Before cycle $j+1$, at most $j\bar{d}$ has been withdrawn, so the reserve is at least $(N-j)\bar{d} + b_{\mathrm{floor}}$. The hypotheses therefore apply to the next cycle. The self-map condition gives its next operational state in K and the ledger-preserving flow and reset give its updated resource history. Induction proves all N cycles. This argument requires

the certificate uniformly over reachable histories; a proof for one undepleted reservoir is insufficient.
For a continuous self-map of compact convex K, the finite-dimensional fixed-point theorem gives a fixed point. Under contraction, successive iterates have differences bounded by $q^j\|Rz - z\|$. The geometric series makes them Cauchy; completeness gives a limit z_*, continuity gives $Rz_* = z_*$, and two fixed points have distance at most q times that distance, so must coincide. Applying contraction to $R^j z$ and z_* gives the claimed error estimate. □

The reserve-dependent uptake law (9) does not automatically descend to a history-independent map on a projection that omits b, c. To obtain one, a separate delivery policy must restore the same accessible supply conditions at each cycle, drawing from a finite master reserve, or the operational state must retain all relevant reserve coordinates. Such a policy is an additional material and transport requirement, not a change of notation.

Proposition 9.3 (No productive periodic orbit of a finite consuming state)**.** *If a full state includes a reserve b satisfying $\dot{b} = -J$, with $J \geq 0$ and strictly positive integrated consumption on each productive cycle, and no admitted replenishment, the full state cannot be periodic. More generally, a strictly increasing cumulative-admission or export counter cannot be periodic on a cycle with a positive corresponding increment.*

Proof. A period T would require $0 = b(t+T) - b(t) = -\int_t^{t+T} J(u)\,\mathrm{d}u < 0$, a contradiction. The counter statement follows by reversing the sign. A relabelling of fresh atoms cannot change either inequality. □

For a single descendant lineage, $N\bar{d}$ can bound N renewal cycles. If every cell divides and each of N complete generations consumes $\bar{d}$ per parent, there are $1 + 2 + \cdots + 2^{N-1} = 2^N - 1$ serviced parents. A sufficient withdrawal allowance is therefore $(2^N - 1)\bar{d}$, together with all simultaneously required reserve floors. A shared master-reserve floor is counted once; daughter-owned reserve floors must be funded for every concurrent daughter unless already included in $\bar{d}$. Because $\bar{d}$ is an upper cost bound, this allowance is sufficient, not a necessary lower bound on actual use. A certificate for one branch is not a whole-population resource certificate. Likewise, proving an independently funded finite-horizon example for each H does not produce one indefinitely funded trajectory.

10 Conditional division with inherited resources

A dividing extension must turn a connected parent into two sealed daughters, assign complete usable machinery to both, and put their operational states in a certified next-cycle section. This is stronger than an area inequality or an endpoint energy difference. The present manuscript gives an exact interface for that extension; it does not claim the source corpus supplies its physical path certificate.

10.1 The corrected geometric partition

Let A and V be the actual guest-inclusive parent area and volume and put $v = 6\sqrt{\pi}V/A^{3/2}$. For a daughter volume share $\alpha \in (0, 1/2]$, define

$$Q(\alpha) = \alpha^{2/3} + (1-\alpha)^{2/3}, \quad a_1 = \frac{\alpha^{2/3}}{Q(\alpha)}, \quad a_2 = 1 - a_1. \tag{27}$$

Proposition 10.1 (Area-conserving two-daughter geometry)**.** *If $1/\sqrt{2} \leq v < 1$, there is a unique $\alpha \in (0, 1/2]$ satisfying $Q(\alpha) = v^{-2/3}$. The assignment*

$$(A_1, A_2) = (a_1 A, a_2 A), \qquad (V_1, V_2) = (\alpha V, (1-\alpha)V)$$

conserves area and volume and gives two spherical-capacity-equality daughters. If $0 < v < 1/\sqrt{2}$, symmetric area and volume halving gives each daughter reduced volume $\sqrt{2}v < 1$. Both statements are geometric compatibility statements.

Proof. For $0 < \alpha < 1/2$, $Q'(\alpha) = \frac{2}{3}[\alpha^{-1/3} - (1-\alpha)^{-1/3}] > 0$. Its limiting value at zero is 1 and its value at $1/2$ is $2^{1/3}$, so the intermediate-value theorem and strict monotonicity give the unique root. The daughter reduced volume is $v_i = v\alpha_i/a_i^{3/2} = vQ(\alpha)^{3/2} = 1$. The normalized shares sum to one. In the symmetric case direct substitution gives $v_i = \sqrt{2}v$. The proof constructs numerical area–volume assignments; it contains no force law, neck evolution or scission step. □

This is the area-preserving reset of Article 71 version 2 and the conditional geometry of Article 72[Sch26a, Convention on the reset] [Sch26c, Definition of division and geometric proposition]. The unnormalized rule $A_i = \alpha_i^{2/3}A$ would create total area $Q(\alpha)A > A$ and is not used. Exact spheres with fixed total A, V occur at the appropriate equality. An inequality below that value permits excess area in nonspherical daughters, rather than proving those same spheres are present.

For a linear area law $A = \sum_{j \in M} a_j n_j$, where M includes the structural scaffold and every membrane guest, proportional membrane allocation $n_{j,i} = a_i n_j$ reproduces $A_i = a_i A$. Proportional lumen allocation $n_{j,i} = \alpha_i n_j$ preserves each lumen concentration immediately at the cut. These proportional rules are continuum allocation assumptions. Actual integer allocations must be separately exhibited, and a membrane-bound charge need not split by the same ratio as lumen volume. Each daughter's Donnan closure must therefore be recomputed from its own charge and volume. Instantaneous osmotic equilibrium after asymmetric partition cannot be presumed.

10.2 A division certificate with an exact reset map

Fix a compact operational section K, a same-phase lift $\iota_h(z)$ to the full state at resource history h, and a cycle time or attained event time $T(z, h)$. The proposed complete cycle is

$$R_{i,h}(z) = \pi\, U_{i,h}\, P_{i,h}\, \Psi_h\, \Phi_{T(z,h)}\, \iota_h(z), \qquad i = 1, 2. \quad (28)$$

Here Φ is the predivision operating flow; Ψ is the certified finite neck-and-sealing evolution; P_i is the material partition; and U_i is a specified replenishment or equilibration procedure. Each factor carries its own elapsed time, resource withdrawals and exports. The next phase is specified in π; a delayed firing time is not silently treated as exact dusk.

The following conditions make this formula substantive and checkable.

1. *Attained gate.* There is a unique allowed event in a specified window, with a hold condition before it. The gate includes an actual retained-active-product threshold, the required switch state, sufficient accessible energy and packets, and any required geometric condition. Clock permission alone does not ensure the remaining conditions. A refractory state prevents another fission until a new cycle has been armed.

2. *Common physical path.* For every admitted starting state in the section, Ψ_h is a uniquely specified evolution lasting at most $\bar{t}_{\mathrm{neck}}$ and ending in exactly two sealed components. It obeys the same material, charge and energy ledgers; retains or accounts for the pore, products and solutes; keeps all safety constraints along the path; and consumes at most the stated budget. This is a named path-certificate assumption where no physical neck dynamics are available.

3. *Complete partition.* For every discrete molecular species and assembly, nonnegative integer allocations and discarded amounts obey $n_{j,1} + n_{j,2} + n_{j,\mathrm{out}} = n_j^{\mathrm{pre}}$, with disjoint atom labels. Here n_j^{pre} is the inventory supplied by Ψ_h immediately before partition, after any neck or sealing chemistry. The allocation must be the one realized by Ψ_h; a feasible abstract split alone does not supply a physical sorting mechanism. Any assembly treated as indivisible remains complete in its recipient. The same allocation determines area, fixed charge and free-particle counts. Each daughter has enough complete pores, switch assemblies, active sites and other required structures; means alone cannot certify this.

4. *Paid replenishment.* The amounts admitted by U_i are named eligible packets withdrawn from the shared reserve. If a deficient assembly is made after the cut, its construction path and ingredients are included. Carbon-bearing cleaning, repair or activation reagents are not free services. The combined path and both daughters' replenishments cost at most $\bar{d}$.

5. *Verified return inequalities.* The resulting state for each daughter satisfies every defining inequality of K, including reserve floors, retained activity, scaffold and pore minima, free/bound particle counts, charge, volume and area constraints. Bound all of these on the entire section, rather than at a single nominal point.

For example, if species j is indispensable and cannot be rebuilt during U_i, both-daughter survival requires $n_j^{\mathrm{pre}} \geq m_{j,1} + m_{j,2}$, where $m_{j,i}$ is its daughter's minimum complete count. With only one indivisible pore and a requirement of one pore per daughter, the certificate fails immediately. If counts of all independent indivisible required species exceed the sums of their minima, assigning the minima first and any remainder arbitrarily constructs a feasible allocation for those count constraints. Coupled complexes, area, charge and location constraints still have to be checked on that same allocation.

Theorem 10.2 (Resource-inheriting conditional division)**.** *If all five conditions above hold on K for every reachable funded history, then (28) is a well-defined ledger-preserving daughter map and each daughter returns to K. With the budget of Theorem 9.2, any chosen daughter branch can perform the specified finite number of cycles. With the corresponding branching budget, the statement holds for the full finite binary descendant tree.*

Proof. The operating theorem and attained gate define the input to Ψ_h uniquely. The common-path condition gives two sealed components and all intervening costs. The partition equalities place every retained label in exactly one daughter or the export ledger and create

none. Their complete-assembly minima give the required functional hardware. Paid replenishment preserves these ledgers by transferring named outside packets and applies only certified transformations. Finally the return inequalities put each complete daughter state in K. Thus every factor of (28) is defined and the result is a self-map for each daughter and history. The renewal induction then applies. Summing the number of parent operations over the binary tree gives the branching budget stated above. □

This theorem does not assume that daughters are viable merely because they have received fractions of a parent. It identifies the simultaneous inequalities, integer assignments and common path that constitute a viability certificate. The four-period witness has not supplied this certificate and is not called a dividing cell. The source corpus likewise leaves the neck mechanism and several inheritance interfaces open[Sch26h, Non-implications and switch target].

10.3 Derivative bounds for an actual return map

A stability claim needs derivatives of the complete map, including the event time and the reset. The following estimate provides a usable sufficient test. Use a fixed norm and its induced operator norm throughout.

Theorem 10.3 (Return-map derivative and robust attraction)**.** *Let K be a closed convex section on a single smooth branch of the funded cycle. Suppose its flow is continuously differentiable in initial state, is jointly continuously differentiable in time and state near any variable-time hit, and $\|D_x f\| \le L$ for elapsed time at most $\bar{T}$. For a state-dependent event given by $g(t,x) = 0$, assume the first hit is unique, g is continuously differentiable near it,*

$$|g_t + g_x f| \ge \gamma > 0, \qquad \|g_x\| \le G, \qquad \|f\| \le M.$$

Let the entire post-hit state map, including its partition and paid return, be $\Delta(t,x)$ with $\|D_x\Delta\| \le B_x$ and $\|\partial_t\Delta\| \le B_t$. Then the return derivative obeys

$$\|DR\| \le e^{L\bar{T}}\left[B_x + \frac{(B_t + B_x M)G}{\gamma}\right]. \tag{29}$$

For a fixed-clock event the event-time term is absent and the bound is $B_x e^{L\bar{T}}$. Include derivatives of the initial lift and final projection if they are not identity coordinates. Products of these bounds cover finitely many smooth events. If an established self-map $R : K \to K$ has a uniform bound $q < 1$, it has the unique attracting operational fixed point of Theorem 9.2.

More quantitatively, suppose K is a closed radius-r ball about z_c and $\|R(z_c) - z_c\| + qr \le r - \delta$ with $\delta > 0$. A perturbed map with $\sup_K\|\widetilde{R} - R\| \le \epsilon < \delta$ and $\sup_K\|D\widetilde{R} - DR\| \le \epsilon_D < 1 - q$ is also a contracting self-map of K.

Proof. The variational equation for the fixed-time flow derivative Y is $\dot{Y} = D_x f\, Y$, $Y(0) = \mathrm{id}$, hence $\|Y(t)\| \le e^{Lt}$ by the integral inequality. Let $T(z)$ be the event time and $x_e = \Phi_{T(z)}(z)$. The implicit-function theorem applies because the stated denominator is nonzero. Differentiating $g(T(z), x_e) = 0$ gives

$$DT = -\frac{g_x Y(T)}{g_t + g_x f}.$$

Differentiating $R(z) = \Delta(T(z), x_e)$ then gives the exact formula

$$DR = \left[D_x\Delta - \frac{(\partial_t\Delta + D_x\Delta f)g_x}{g_t + g_x f}\right] Y(T). \tag{30}$$

The triangle and operator-norm inequalities give (29). For fixed event time, $DT = 0$. Chain differentiation covers compositions. On convex K, integrate the derivative along the segment between two points to obtain the Lipschitz bound q. The contraction theorem applies only after the actual self-map and resource conditions have been verified.
For the perturbation, any $z \in K$ satisfies $\|\widetilde{R}(z) - z_c\| \le \epsilon + \|R(z_c) - z_c\| + q\|z - z_c\| < r$. Its derivative norm is at most $q + \epsilon_D < 1$, proving the last statement. □

The geometric branch deserves care. On the asymmetric taut branch,

$$\frac{\mathrm{d}\alpha}{\mathrm{d}v} = -\frac{(2/3)v^{-5/3}}{Q'(\alpha)}.$$

Since $Q'(1/2) = 0$, a derivative bound cannot be asserted uniformly through the symmetric endpoint. One may work strictly below the symmetric capacity threshold, where the symmetric partition is fixed, or restrict the asymmetric branch to $\alpha \in [\alpha_-, 1/2 - \varepsilon]$ and bound Q' away from zero. Likewise, a change of integer allocation is not differentiable; either fix the allocation branch or use a direct Lipschitz/self-map argument. An eigenvalue calculation at one point does not replace these requirements.

For the commonly used scalar mean-area map $R(\Lambda) = (\Lambda + G(\Lambda))/2$, the derivative is $(1 + G')/2$. Strict linear attraction therefore requires $-3 < G'(\Lambda_*) < 1$, not merely $G'(\Lambda_*) < 1$. To prove a contraction on an interval, bound $|(1 + G'(\Lambda))/2|$ strictly below one throughout that interval and establish the interval self-map. At derivative magnitude one, nonlinear analysis is required. This repairs

the omitted negative-slope condition in the environmental-supply map[Sch26e, Environmental lipid set point].

10.4 A gate needs a path and absolute timing

For a fixed-hazard Poisson escape model, let k_h be the holding-phase rate for length t_h and k_f the firing-window rate for length t_f. The exact probability requirements are

$$k_h t_h \le -\log(1-\varepsilon), \qquad k_f t_f \ge \log(1/\delta), \tag{31}$$

for early-firing probability at most ε and no-fire probability at most δ, conditional on reaching the firing window. These follow directly from the survival probability e^{-kt}. In this piecewise-hazard model the probability of holding and then firing is at least $(1-\varepsilon)(1-\delta)$. This remains a probabilistic timing claim, not the deterministic path certificate required above. A constant rate can meet both only if

$$\frac{\log(1/\delta)}{t_f} \le \frac{-\log(1-\varepsilon)}{t_h}.$$

The conservative sufficient holding condition $k_h t_h \le \varepsilon$ may be used, but is not the exact equivalence.

If both rates have the same attempt prefactor and the Arrhenius form $k = k_0 e^{-B/(k_B T)}$, dividing the rate inequalities yields the necessary barrier change

$$B_h - B_f \ge k_B T \log\left(\frac{t_h \log(1/\delta)}{t_f[-\log(1-\varepsilon)]}\right). \tag{32}$$

The absolute inequalities (31) must still hold; a barrier difference alone does not fix either absolute rate. Different prefactors require their ratio in the formula. The first fission must enter an absorbing or refractory mode to ensure at most one event per cycle. This is the timing distinction emphasized by Article 76's holding/firing analysis[Sch26h, Timing and neck barrier].

An equilibrium end-state energy difference is not a transition barrier or a path certificate. In particular, the touching-sphere endpoint in Article 74 may be compared with two separated spheres only after specifying that parent shape[Sch26d, Conditional marginal cost of fission]. Its H3 identification of that shape as the unconstrained bending-energy minimizer is not used; the prior source assessment found a lower-energy prolate competitor for the written area–volume problem[pil26]. Neither that disputed minimizer claim nor a favorable Gaussian endpoint term provides Ψ_h in (28). A physically accomplished neck pathway, complete resource inheritance and verified daughter return remain the named conditions for the stronger dividing-system theorem.

11 Transfer to one molecular operating system

The material and dynamical results give a constructive theoretical framework with a nonempty operating example. To interpret that example as a particular molecular protocell, the same molecular history must satisfy both the labelled material semantics and the operating observables. This section makes that transfer precise, including the difference between integer molecule counts and continuous mean-field amounts.

11.1 The common parameter requirement

Let θ collect temperature, solvent composition, pH, ionic strength, light schedule, redox supply, charge conventions, molecular structures, rate and binding parameters, transport and membrane mechanics. For each required module j, let Θ_j denote parameter values admitting the stated module with its specified interfaces. Separate nonemptiness of the Θ_j does not imply nonemptiness of their intersection. For example, $(0, 1/2)$ and $(1/2, 1)$ are both nonempty but have empty intersection. Even a common numerical parameter value is insufficient if adjacent modules assign different conformations to the same interface or different owners to the same carbon.

The required compatibility is therefore not merely $\theta_* \in \bigcap_j \Theta_j$. It also includes a common set of atom identities, compatible configurations at each handoff, and one schedule that supplies all consumed resources. A pore evaluated in one membrane composition and a joining reaction evaluated in another do not establish this conjunction. Nor does a parameter vector manufactured by freely choosing favorable rate constants establish a physical member of the intersection.

11.2 Compatible finite molecular realization

Definition 11.1 (Compatible microscopic realization)**.** Fix a finite labelled graph execution g, a reduced trajectory $y : [0, H] \to \mathbb{R}^d$, a scale $M > 0$, and one parameter vector θ. A compatible microscopic realization consists of an admissible molecular history x and an observation map Π_M such that:

(L1) The initial history begins at admitted stock, rather than a prebuilt functional cell. Its assembly and preparation segments reach the stated ready interface, with exactly tracked atom identities, charge, reagents, energy inputs, locations and coproducts. The clock $t = 0$ of the reduced operation is as-

signed to that ready interface.

(L2) All graph-rule occurrences in g have the same atom and product interpretation in x. Neighboring segments share their full terminal and initial molecular interface, including conformations and phase data. No consumed support is duplicated. All participating organic carbon has admitted origin, including catalysts, activation carriers and solvents when such organic components participate.

(L3) The same θ governs preparation, joining, release, transport, retention, functional action, ionic response and membrane mechanics during the claimed experiment, allowing only its explicitly declared controls. Each segment obeys the stipulated physical admissibility conditions.

(L4) The observation $\widehat{y}(t) = \Pi_M x(t)$ has a declared scale and meaning for every coordinate. Its amount, localization, area and volume errors are bounded in one chosen norm by $\sup_{0\le t\le H} \|\widehat{y}(t) - y(t)\| \le \varepsilon$.

(L5) Each transferred functional or geometric predicate has the same operational meaning in x as in y, up to a separately stated observation/model discrepancy. Where a retained amount represents activity, the selected molecular product actually has the specified action at that amount, charge, stereochemistry and localization.

Condition (L4) deliberately permits finite-count observations. A nonconstant smooth amount trajectory cannot be identical at every instant to a finite integer count divided by a finite M. The explicit count-path approximation in Theorem 3.19 is a nonempty formal bridge at this level. It is not a stochastic chemical kinetic derivation: prescribing reaction times from a reference trajectory does not identify physical propensities. Similarly, an expected molecular count does not independently satisfy a nonlinear mean-field equation, because generally $\mathbb{E}f(X) \neq f(\mathbb{E}X)$.

The scale M also changes required supplies. An amount model with 130 donor units and 30 carrier units becomes the integer reserve $130M, 30M$ when M is an admissible integer scaling. It does not become an unlimited reservoir. A small concentration error can coexist with a large absolute particle number; its validity must be judged against the chosen experimental size and amount convention.

Theorem 11.2 (Finite molecular transfer with margins)**.** *Fix a reduced witness y and a compatible realization as in Definition 11.1. Let ε be its observation-error bound and define the closed observation tube*

$$\mathcal{T}_\varepsilon = \{z : \operatorname{dist}(z, y([0,H])) \le \varepsilon\}.$$

Let g_j be finitely many reduced operating predicates, each defined and K_j-Lipschitz on $\mathcal{T}_\varepsilon$. More generally, a common set containing both the reference and observed paths suffices if the same Lipschitz estimate holds for every compared pair. Suppose the reference satisfies $g_j(y(t)) \ge m_j > 0$ on its specified time set $T_j \subseteq [0,H]$. If the molecular interpretation differs from $g_j(\widehat{y}(t))$ by at most $\delta_j \ge 0$, and

$$K_j\varepsilon + \delta_j < m_j \quad \text{for every } j,$$

then the corresponding molecular predicates are positive on every T_j. Every molecular product also has the exact admitted carbon ancestry specified in (L1)–(L2).

Proof. For each $t \in T_j$, the observation bound places both $y(t)$ and $\widehat{y}(t)$ in the stated domain. Lipschitz continuity therefore gives $g_j(\widehat{y}(t)) \ge g_j(y(t)) - K_j\varepsilon \ge m_j - K_j\varepsilon$. Subtracting the interpretation discrepancy δ_j leaves a strictly positive value. The material assertion follows from the origin-preserving microscopic execution, independently of the approximation used for amounts. Apply the argument to the finite family of predicates. □

This is a conditional theorem for every supplied compatible realization. If at least one such realization is exhibited with the stated margins, it yields a molecular operating witness. The theorem proves the transfer; it does not supply the antecedent. In particular, an unverified chemical path cannot be repaired by choosing a larger numerical safety margin.

For the retained-function predicate $g(y) = p - 1.5$, the norm can be chosen so that $K = 1$. A certified reference interval with $p \ge 1.6$ provides margin 0.1. Thus an amount-observation error and functional calibration discrepancy summing to less than 0.1 transfer the threshold on that interval. This is why the strengthened nominal bound in the dynamics chapter is more informative for realization than a trajectory that only touches 1.5 at a single time. The near-boundary volume and area screens require their own margins in their own units.

11.3 An explicit residual test for approximate kinetics

A proximity assumption can itself be tested. Let $f(t, y)$ be the reduced vector field, including its prescribed light schedule, and suppose it is uniformly L-Lipschitz in y on a

common tube. Let a bounded measurable observation $\widehat{y}$ satisfy the integral residual relation

$$\widehat{y}(t) = \widehat{y}(0) + \int_0^t f(s, \widehat{y}(s))\,\mathrm{d}s + r(t), \qquad r(0) = 0. \quad (33)$$

The residual may have jumps; it can therefore include the staircase error of finite molecule counts. It is not assumed to be an unmodelled carbon source. The microscopic material ledger must remain exactly balanced.

Proposition 11.3 (Uniform observation error from residuals)**.** *Assume the reference and observed paths remain in the common tube, and* $\|\widehat{y}(0) - y(0)\| \le e_0$, $\sup_{[0,H]} \|r(t)\| \le \eta$. *Then*

$$\sup_{0 \le t \le H} \|\widehat{y}(t) - y(t)\| \le (e_0 + \eta)e^{LH}.$$

If instead the observation is absolutely continuous with an a.e. differential residual of norm at most η_d*, the sharper bound is* $e_0 e^{LH} + \eta_d(e^{LH} - 1)/L$ *for* $L > 0$*, and* $e_0 + H\eta_d$ *for* $L = 0$.

Proof. Subtract the reference integral equation from (33). The norm difference $E(t)$ satisfies $E(t) \le e_0 + \eta + L\int_0^t E(s)\,\mathrm{d}s$. The integral comparison inequality gives the first bound. For a bounded differential residual, retain the integral of η_d and solve the scalar inequality $E' \le LE + \eta_d$, which gives the stated expressions. All integrations use the same forcing schedule; scheduled vector-field jumps do not alter the argument. □

For state-dependent switching, independently shifted event times or material resets, the residual or a hybrid error estimate must also include those discrepancies. A continuous-mode estimate cannot simply be carried through a discontinuous division reset. Likewise a parameter uncertainty test is distinct from a chemical realization test: it shows that a specified family of laws tolerates changes, not that those laws are physical.

11.4 Exact conservation with approximate observables

Let c be the carbon-count row vector for the coarse species. An exact microscopic history always satisfies the labelled open balance. Its projection can satisfy $c^T\widehat{y} + E_C = C_0 + I_C$ exactly if the species partition is exhaustive and normalized consistently. If unobserved residual material is omitted, the same identity may appear to fail even though the microscopic history is valid. Conversely, a coarse identity can pass while atom identities are replaced illegally. We therefore keep three separate records: an exhaustive labelled ledger, a chosen observable projection and a residual/error certificate between that projection and the reduced law.

The reduced model's Donnan ions illustrate why this matters beyond carbon. An ideal salt equilibrium counts free mobile ions through its algebraic closure. Counterions already included in those free-ion numbers cannot be added again merely because a product formula includes charge. Bound counterions have a different particle contribution. A valid physical lift must choose an ionic binding and charge convention compatible with both the stoichiometric and osmotic counts. "Carbon-free" does not remove this requirement.

11.5 Testable implementation conditions

The preparation condition is an atom-map and chemistry problem. Each backbone carbon, nucleoside carbon, tether and spectator needs an origin; its transformation needs a compatible chemical path and state. The joining condition is an activation, selectivity and release problem. The function condition is a causal product-response problem. The transport condition requires supply and retention at the demanded rates. The membrane condition requires one phase and mechanical regime at the actual guest composition. These are joint conditions because changing one can alter all others.

A particularly discriminating physical test compares a functioning candidate to an intervention that removes the retained product's action while matching stock, illumination and all independently controllable conditions. The dynamical ablation theorem predicts a threshold loss for its specified intervention. A practical experiment must verify that the intervention did not instead disable all chemistry or change the membrane in an unrelated way. The causal interpretation is strongest when the intervention changes the named return edge and the other measured inputs remain matched.

None of these conditions requires spontaneous stock synthesis, selection of substitution patterns, or an autonomous origin scenario. Externally supplied eligible stock and carbon-free forcing are legitimate boundary conditions. The burden is narrower and more precise: one actual molecular system must implement the downstream interfaces and the desired finite-horizon function.

12 Consequences and limits of the construction

The constructive result has two nonempty mathematical components. The labelled graph formalism supports finite constitutional products and exact resource accounting after stated preparation interfaces. The explicit uncoded

operating model supports bootstrap from zero peptide, productive feedback, and finite-horizon bounds using one common state and finite reserves. These components can be connected through exact material maps and controlled coarse-graining. Their molecular connection is a separate compatible-realization condition rather than an unspoken assumption.

12.1 What the finite witness establishes

A supplied functional product need not be encoded to participate in a feedback loop. In the present witness, retained active chains increase productive uptake or processing, subsequent production creates more retained chains, and deactivation transfers all product material to an inactive pool. Both lumen products and retained products occur in the same model. The matched edge deletion changes the attainable functional threshold. This is a positive constructive result within the declared constitutive laws, not merely a list of desired properties.

The result is also resource-bounded. The reservoirs are outside the lumen, the consumption factors vanish at exhaustion, and spent material remains in the state. The structural scaffold is separately reserved. No residual core is simultaneously a consumed amino-acid precursor and an intact permanent pore. The integer-block approximation shows how the mean amount ledger has a finite count interpretation without asserting exact smooth molecule counts.

The water and geometric bounds serve as consistency screens within an explicit idealization. A reduced volume below one prevents a simple sphere-capacity contradiction, but does not construct a low-energy shape or guarantee local hydration. A positive flux variable does not identify a physical pore. The significance of including those coordinates is that the assumptions and resource consequences are testable together.

12.2 What repetition and division add

Finite operation and indefinite operation have different quantifiers. For each n one can reserve a finite stock for n admissible returns, but that does not provide one finite stock for all n. A compact operational return set can remain invariant while its provenance ledger accumulates new labels, exports and consumed packets. A periodic projection is therefore compatible with an open material process; a periodic finite-reserve full state is incompatible with strictly positive net consumption.

Division is a further dynamical event with a physical path. The corrected area normalization preserves area for asymmetric daughters. Its exactness must not be diluted merely because a neck mechanism is unknown. Equally, that exact geometric identity does not prove that a parent crosses an activation barrier, seals two daughters, or gives each daughter enough complete machinery. A mean fractional pore in each daughter is not an integer viable allocation. The division theorem consequently includes actual scission, complete partition and a viable birth set as hypotheses. It cannot be established by iterating an older fixed line that omits area, resources or the reset.

A gate's increased probability of at least one escape event is not an exactly-one viable binary fission result. A first-event absorbing or refractory reset, absolute rates and the relevant transition state are required. The source-derived founder calculations further show why a recurrence derived after prior divisions cannot establish the first division from an unreset founder. These distinctions preserve useful geometry and timing mathematics while preventing an incorrect lineage claim.

12.3 Information is an extension of the base function

Tethered bases and interleaves organize material; an addressed code table organizes symbolic correspondences; a physical gene-directed apparatus causally couples a template to a product sequence. These are separate levels. The revised product grammar supplies constitutional identities that a decoder may refer to. It does not supply the template copying, physical readout, error suppression and segregation required for a hereditary lineage.

The base construction gains clarity by ending earlier. It asks for a particular uncoded product or bounded ensemble with a measurable compartment function. A later information extension can use the same carbon ledger and prepared-product interfaces, but needs new causal and kinetic evidence. A sequence intervention that changes a product as predicted would address gene direction; a daughter that inherits and reuses a copied template would address heredity. Neither follows from the four-letter orientation dictionary alone.

12.4 A bounded implementation program

The next molecular realization should close named interfaces rather than add favorable assumptions independently. First, identify one exact stock-derived prepared packet, including all nucleoside and spectator carbon. Second, establish joining and release for the chosen product at conditions compatible with its retention and function. Third, test the same enclosure and pore under the required flux, charge and guest load. Fourth, compare measured trajectories and interventions with the reduced law and quantify the observation residual. This sequence can reject a candidate for a specific reason without refuting the entire family

of architectures.

An experimentally identified molecular witness would strengthen the conclusion by satisfying the transfer theorem's antecedent. It would not retroactively change a graph rewrite into an elementary reaction, nor make a prior symbolic address a resident base identity. Keeping the interfaces typed allows replacement of an unsuccessful molecular module while retaining exact bookkeeping and theorems that remain applicable.

12.5 Conclusion

Admitted substituted-chrysene stock supports a rigorous construction problem with an explicit carbon boundary. Exact provenance, allocation, formula and prepared-product results can be composed without hiding organic inputs. A finite uncoded dynamical model exhibits bootstrap and feedback under one set of laws, and its ablation distinguishes that function from externally supplied forcing alone. Robustness, resource-aware repetition and corrected conditional division extend the mathematics without asserting a completed physical cell. The remaining molecular question is concrete: whether one compatible stock-to-ready history, product chemistry, functional response, transport law and membrane regime realizes the certified operating predicates. The present manuscript establishes the formal construction and its testable transfer conditions, with chemical realization, gene-directed operation and physical division retained as distinct stronger claims.

A Material certificates and source audit

A.1 Reproducible finite checks

The portable material verifier uses only the Python standard library. It constructs all five complete precursor graphs, saturates their neutral valences, constructs the bridged D_m and D_2 dimers, and constructs the terminal-complete short-link pore with every atom explicitly present. Forty-eight (m, q, p) pore instances independently check the general formula. A separate labelled-carbon trace checks internal redistribution, fresh imports, export, first inward entry of an already-admitted external reserve, and a tracked return without double admission. The return is a test of the general balance and not an inferred permission in the baseline protocol.

The same verifier exhausts all 512 eligibility graphs on three unit demands and three unit slots, comparing direct matching with every Hall inequality. It tests the general packet collision and the catalyst-gated example in which the net stoichiometric endpoint is nonnegative but no first reaction is enabled. The supplied Article 75 data are consumed without importing its builder: all twenty diagnostic graph words and the joint sulfur word are replayed, and the product components, formulas and carbon sets are checked. This material replay and the separately bundled full extraction-guard audit have explicitly distinct scopes.

Table 4: Independent material checks and what they establish.

Check	Verified finite result
Five stock graphs	Exact atoms, bonds, neutral formulas and closed valences
Forty-eight pore graphs	Internal/terminal phosphorus, arm capacities and formula (M6)
Two membrane precursor graphs	D_m: 40 C; D_2: 44 C; exact oxygen/hydrogen ledgers
Global stock reservation	810 disjoint carbon origins in four role reservations
Carbon transfer trace	Open balance, export retention and old-origin inward entry
512 eligibility graphs	Unit-slot matching agrees with all Hall inequalities
Article 75 material replay	668 diagnostic edits, 174 joint sulfur edits; 107 product C
Sixty rational projection cases	Exact block carbon and bounds (M11)
Fourteen rejection tests	Representative origin, formula, capacity and scope errors rejected

The negative tests reject duplicate stock admission, a free-adenosine input, an organic extra feed, carbon deletion, an equal-count swap to an unadmitted origin, double allocation, hidden carbon-bearing port contexts, an origin class substituted for a stock map, deletion of an Article 75 backbone atom, an incorrect Ala formula, terminal-arm overuse, the D_2 forty-carbon miscount, the completed-pore fifteen-phosphorus miscount, and deactivation before production. A passing material report is neither a reaction-path certificate nor a geometry, transport, stereochemical or gene-directed synthesis test. Those flags are explicitly false in the report.

A.2 Exact source entrypoints and logical roles

The selected source versions are Article 62 version 13, Article 65 version 2, Article 66 version 4 and Article 68 version 3. Article 65 version 2 is the explicitly selected source; no alternate version repairs it implicitly. The Article 75 input is the revised manuscript and its original product certificate data. The patent source is US12195423B1. Table 5 records the specific claims used, with a byte-hash read manifest supplied alongside the verifier. Originals were read-only.

A.3 Stock-resolved tasks that remain molecular obligations

The existing formal results constrain the missing downstream work rather than certify its completion. A stock-to-prepared-module certificate must supply the exact original arm identities of both backbone carbons and the complete resident nucleotide and port graphs. A nucleotide certificate must resolve the source index discrepancies, map every sugar/base/tether/cap carbon and close all noncarbon balances. A membrane certificate must map core scission, retained unsaturation, oxygen fate and any four-carbon D_2 complement. A pore realization must use the selected arm constitution and a consistent three-dimensional geometry with all termini. Peptide function requires an actual joining mechanism and its sequence/composition, stereochemical, binding and partition properties. These are downstream functional transformations and assembly conditions. The manufacture or self-separation of the admitted initial stocks is not one of them.

Table 5: Read sources and their use in the material construction.

Source	Read locations	Use and boundary
Article 62 v13	Tether notation; reference architecture; route-A product; carbon ledger	Long-link constitution and targets; molecular and phase claims remain separate
Article 65 v2	Species; retention; allocation; source and sink graph	Typed resources and retained-versus-produced distinction; tabulated transformations do not prove chemistry
Article 66 v4	Axes; column; terminal tether; closure; fourth demand	Short-link architecture; add three distal phosphates to the 15-P internal count
Article 68 v3	Scope; functional valence; condensation; pool cost	Uncoded joining and conditional particle interpretation
Article 75 revised	Products; architecture; certificates; product JSON and builder excerpts	Complete formal product endpoints; prepared carbon origins do not supply a stock map
US12195423B1	Anchors 0133, 0137–0138, 0149, 0153, 0156, 0158, 0186–0187, 0208, 0230–0231	Given stock examples, proposed maps and tethers; discrepancies remain explicit

B Verification objects and reproducibility

The portable project contains the complete source, fixed certificate data and independent executable checks. The checks use Python's standard library for material and analytic predicates. Numerical trajectories are sanity checks of the displayed laws; they do not replace the proofs of invariance or bootstrap. Plot generation is separate from verification. The PDF build uses ordinary pdfLaTeX with shell escape disabled and requires no external source archive or network access.

B.1 Finite certificates

The material verifier constructs exact stock graphs, checks formulas and carbon-origin sets, and tests disjoint allocation and open balance. Representative invalid cases are required to fail: hidden carbon, duplicate origins, double ownership, reuse of a consumed packet and untracked exports. Its small graph fixture is a witness of a stock and reservation model, not a molecular operating protocell.

The product guard verifier consumes the fixed revised Article 75 graph JSON without importing its constructor. It recognizes permitted masks, whole-removal neighbors, core support, allowed original adjacencies, protected backbone edges, the internal-cut budget, heteroatom incidences and the free-acid exception. It replays every primitive, compares the terminal bond map, checks valence and actual product components, and rejects representative illegal mutations. Twenty diagnostic row paths plus the paired sulfur path are checked. Only eighteen nonsulfur rows and the paired sulfur path belong to the simultaneous twenty-product repertoire. An additional independent identity audit compares the terminal heavy-atom connectivity and formula against Table 3.

The operating verifier evaluates the exact rational bounds for the nominal and perturbed families, the matched ablation ceiling, resource and water inequalities, and the corrected daughter-area identities. It integrates the displayed ODE separately as a sanity check and exports the trajectory data used in the figure. No simulation outcome is used as a substitute for the all-time inequalities in the theorems.

B.2 Evidence levels of the output

The checker output distinguishes a verified assertion from a physical interpretation. A formula check establishes a formula of a specified graph. A graph replay establishes legality in a specified grammar. A rational inequality check confirms arithmetic in a proof. A numerical integration checks implementation consistency at selected resolution. None by itself establishes reaction feasibility, yield, stereoselection, transport rates, a membrane phase or physical scission.

The source manifest identifies the controlling manuscript versions and hashes, together with the revised Article 75 certificate and the sole patent. Original source files are not changed by any verification or build. Archive-relative source paths are audit locators; the portable project uses the fixed data included within it. Rebuilding in a relocated directory does not purport to reread a source archive that is absent there.

B.3 Reproducing and modifying the example

Run the project check script and then the build script from the project root. Their generated results and compilation files remain in separate results and build directories. Changing a stock formula requires changing its complete graph, not only a printed count. Changing an operating rate requires rechecking the rational bounds and may invalidate the threshold time. Changing a pore linker requires a new geometry and transport model. Changing a division reset requires recomputing its invariants, daughter allocation and return-map conditions.

The model fixes a finite species and constant-parameter structure; its bounded time-dependent disturbances form a separate function class. Its resource types, forcing convention and closures are explicitly specified. Adding an untracked organic reagent or an independent molecular module is a model change, not a harmless numerical perturbation. Likewise replacing a prepared-module label by an admitted-stock name does not close the preparation interface without the atom map and compatible context.

B.4 Publication companions

The standalone companions `Article77_Verification_Code` and `Article77_Formal_Proof` provide executable source and reproducibility records. The formalization covers the explicitly listed finite and rational statements, not the entire analytical argument or chemical realization claims. Compiling the companion LaTeX files in Overleaf typesets the listings; it does not execute the Python verifiers or the Lean checker.

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[Sch26f] Charles D. Schaper. Structural Adequacy for Signalling: The Chrysene–Nucleic Acid Complex as a Hybrid Channel, Scaffold Succession, and the Continuity of Directed Pathways. *Annals of the Chrysene Formalism*, 1(3):1321–1347, 2026. Article 63, version 4. DOI: https://doi.org/10.68366/0e3gsg12. Signalling and moving-window results require the binary-feasibility and actual-readout conditions.

[Sch26g] Charles D. Schaper. The Chrysene-Reachable Material Ledger: Species, Properties, and the Allocation of a Single Pool. *Annals of the Chrysene Formalism*, 1(3):1371–1383, 2026. Article 65, version 2. DOI: https://doi.org/10.68366/dwqk8m15. Material ledger: conv:chem, sec:ledger, prop:nonimp and rem:notinbundle.

[Sch26h] Charles D. Schaper. The Division of the Vessel: The Coded Chain, the Photochrome Brake, and the Genome that Selects Itself. *Annals of the Chrysene Formalism*, 1(4):1545–1566, 2026. Article 76, version 6. DOI: https://doi.org/10.68366/s7zef416. Revised chain model and gates: hyp:ester, thm:count, thm:gain, thm:brake, hyp:gate76, prop:invariant and thm:interior.

[Sch26i] Charles D. Schaper. The Enclosure via the Encoded Chrysene Cluster: Integrated Synthesis of Nucleic Acids and Phospholipids, and the Orientational Encoding of the Membrane. *Annals of the Chrysene Formalism*, 1(3):1279–1320, 2026. Article 62, version 13. DOI: https://doi.org/10.68366/24m3wx88. Use thm:encaps, thm:capacityfull, thm:ratio, and thm:elimination only with the enclosure, transfer and unsaturation corrections stated here.

[Sch26j] Charles D. Schaper. The First Loop: The Remnant Fixed Point, the Division Period, and the Self-Tuning Lineage. *Annals of the Chrysene Formalism*, 1(3):1423–1431, 2026. Article 69, version 3. DOI: https://doi.org/10.68366/11czsz09. Historical loop module; its subsystem fixed line is not a division-invariant full state.

[Sch26k] Charles D. Schaper. The First Polypeptide: Condensation, Sequestration, and the Discharge of the Remnant. *Annals of the Chrysene Formalism*, 1(3):1414–1422, 2026. Article 68, version 3. DOI: https://doi.org/10.68366/jw1axc69. Structural polymer and particle-count module; joining chemistry remains conditional.

[Sch26l] Charles D. Schaper. The First Pore: Closure, Aperture, and the Reconciliation of Impermeance with Supply. *Annals of the Chrysene Formalism*, 1(3):1384–1404, 2026. Article 66, version 4. DOI: https://doi.org/10.68366/en23gq52. Short-link pore: thm:closure, thm:aperture, tgt:dehydration and W1. Geometry and transport are separate.

[Sch26m] Charles D. Schaper. The Persistent Lineage: Composition of the Pore, the Cycle, and the Remnant. *Annals of the Chrysene Formalism*, 1(3):1405–1413, 2026. Article 67, version 3. DOI: https://doi.org/10.68366/h6d6b415. Historical lineage module, subject to later area-reset and chain-ledger corrections.

[Sch26n] Charles D. Schaper. The Photoentrained Cycle: Existence and Stability of a Periodic Orbit in a Forced Hybrid Protocell. *Annals of the Chrysene Formalism*, 1(3):1348–1370, 2026. Article 64, version 6. DOI: https://doi.org/10.68366/h9rzkd75. Forced cycle and necessary division geometry; no unqualified recurrent molecular cycle is imported.

[ZS09] Ting F. Zhu and Jack W. Szostak. Coupled Growth and Division of Model Protocell Membranes. *Journal of the American Chemical Society*, 131(15):5705–5713, 2009. DOI: https://doi.org/10.1021/ja900919c.