

The Origins Transition: From the Encoded Chrysene Cluster to the Originating Genetic Code Mappings

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Abstract

A stack of six substituted chrysene units, each set in one of two orientations, admits exactly twenty classes under the symmetries available to it. That count bounds the products the assembly can make and fixes the reading length at three. It does not say which twenty products, nor at which codons they sit — and the stack it speaks of contains no nucleobase. This paper takes the second question. Bases are not added to the stack: they are what its orientation pattern is called, under an assignment specified in the filing, which also exhibits the resulting object, namely RNA intercalated with tethered chrysene. On that object we state a consistency relation between codons and *structures*, a structure being a connected subgraph of the chrysene skeleton together with a terminal assignment and a set of heteroatom insertions. The stages persist together rather than in sequence, and no chronology is claimed.

Three results are finite and checkable. **The structure space is three-parameter:** every structure consists of the reaction site, optionally one further vertex, and a contiguous arc of a single ring — at nineteen of twenty, the exception stated with the theorem and the obvious repair shown to fail. **Excision is coarser than structure:** the map to the underlying subgraph takes eleven values on the twenty structures, five of its fibres non-trivial and covering fourteen, so one excision carries up to three structures differing only in how a terminal vertex ends. And **block degeneracy follows a rule at sixteen of sixteen blocks.**

One placement is forced. Exactly two structures require an element the carrier cannot supply, so that either one delivery serves both or two must coincide. Of the eighteen positions a code assigns, three pairs are complementary and exactly one of those has both positions of the size required. Under the hypothesis that the pair is delivered together their placement is unique — and it is the placement of neither observed code.

Either the consistency relation is wrong at two exchanges, or the observed codes stand two exchanges from an assignment that structural consistency selects and that is neither of them. We do not decide this, and we say what would.

Two further results are recorded. Parity excludes the standard code from a class of assignments and is silent on the mitochondrial one, the two differing at exactly the blocks where the standard code departs from normal form. And the base partition governing block degeneracy, recovered here from block structure alone, is the one specified by the assignment of the filing — which the argument nowhere uses. What invariant it is the level set of remains open.

Keywords: Chrysene Formalism; encoded chrysene cluster; chrysene–adenosine cluster; origins transition; registry classes; letter assignment; structural consistency; retention classification; fibrations; seed map; system of distinct representatives; codon placement; genetic code mappings.

1 Introduction

1.1 The problem

The capacity theorem of the corpus [Sch26l] answers a cardinal. A cluster of six sites has twenty frame classes; a product

attributable to the assembly takes at most twenty values; and the codon length follows from the carrier rather than from any argument about alphabets. The theorem says of itself that it bounds the products of a cluster and asserts nothing about which products those are.

Two questions survive it. Which twenty, and at which codons.

Neither is answered by an orbit count, and neither is a question about a cluster alone: the cluster of that theorem contains no nucleobase.

This paper takes the second, and takes it in a form that can be settled without the first. It does not ask which chemical species arise. It asks at which codons a structurally consistent formation is possible, and what the answer constrains.

1.2 The arc

Three stages, and the paper is named for the passage between them.

Stage 0, Section 4, is the encoded chrysene cluster: six sites, three vessels, no nucleobase and no codon. Its content is combinatorial and its cardinal is twenty.

Stage 1, Section 5, is the chrysene–adenosine cluster. Nucleobases are not added to Stage 0; they are what its registry states are *called* once a specified transformation has run, and the naming is read off a filing which also exhibits the product that results — RNA intercalated with tethered chrysene. The residual count goes from thirty-six to sixty-four, and the cluster acquires a domain it did not have.

Stage 2, Section 6 through Section 9, is a relation between codons and structures on that domain.

The passage from Stage 0 to Stage 2 is the origins transition. It is a transition in the sense that each stage has an object the previous one lacks, and Section 3(iv) records that it is not a chronology.

1.3 The objective

To classify the structures; to state the consistency relation as hypotheses rather than as definitions; to count the assignments it admits; and to determine whether anything distinguishes one. The last is the paper's reason for existing, and Section 9 answers it at one of three places and says so.

1.4 What is established

1. **The structure space is three-parameter.** Theorem 6.8: every structure is $\{C5\} \cup \{C6\}^n \cup \text{arc}(p, q)$ — at nineteen of twenty. The exception is stated with the theorem and the obvious repair is shown to fail.
2. **The excision is coarser than the structure.** Theorem 6.10: the forgetful map takes eleven values on the twenty structures, and five of its fibres are non-trivial, covering fourteen. One excision carries up to three structures, which differ only in a terminal decoration.
3. **Degeneracy is a rule and not a list.** Proposition 7.11: sixteen of sixteen blocks.
4. **Admissibility constrains slot sets, not assignments.** Theorem 8.7: the demand graph does not see which structure

sits at a slot. The two exchanges of Section 9 are therefore deficiency-neutral by construction (Corollary 8.9), and a third, which moves a demand, is not admissible (Proposition 8.11).

5. **One placement is forced.** Theorem 8.16 and Theorem 9.6: three complementary pairs of one hundred and fifty-three, exactly one with both slots of size two, and the structures requiring it are exactly two.
6. **The second register governs what is released, not whether.** Proposition 10.15: across thirteen recorded assignments at a codon some mapping does not release, twelve deliver a structure that the codon's second register supports elsewhere. The stronger reading, that the register governs release itself (Proposition 10.13), holds for the two mappings treated here and is bounded by the wider tables (Remark 10.14).
7. **A structure occurring twice needs no exchange to place it.** Proposition 10.20 and Corollary 10.21: the second register sets a ceiling on extent, both defective first registers attain it, and the structure at that extent therefore occurs at two blocks without being moved.
8. **Parity separates the two observed mappings.** Theorem 10.2: the mitochondrial mapping has no fibre of odd cardinality and the standard mapping has four, carried by the structures at which they differ. Theorem 10.10 says the same in the other currency.
9. **A partition is recovered and not assumed.** Open problem 7.12: the partition governing Proposition 7.11 is the registry partition of Definition 5.2, which Section 7 does not use. The problem of what invariant it is the level set of remains open.

1.5 What is not claimed

Section 3, ten clauses, stated before the constructions they guard. Three deserve mention here. No chemical species is identified in any numbered statement. No assignment is claimed prior to another. And the hypotheses of Section 7 were abstracted from the series of Section A, which is therefore their source and not their confirmation.

1.6 Precedence

Where this paper and its predecessors overlap, they do not all carry the same weight, and the order is by subject rather than by seniority. The tether and the backbone construction are authoritative on the carrier and on what excision inherits; this paper is primary on the consistency relation; and the combinatorial papers [Sch26k, Sch26e, Sch26l, Sch26i] are imported as constraint, with one conflict recorded at Scholium 10.23 and not resolved.

1.7 Organization

Section 2 fixes the register. Section 3 refuses ten readings. Section 4 and Section 5 are the transition. Section 6 classifies the structures and Section 7 states the consistency relation; these two are the paper's apparatus. Section 8 counts what is admissible and Section 9 distinguishes one; these two are its argument. Section 10 states two facts about the observed mappings and one conflict. Section 11 restates the refusals and inventories the open problems. Section A is the interpretation and the provenance, Section B the computations, Section C the record.

2 Conventions and the register

2.1 Status

Definition 2.1 (Status labels). Every numbered statement carries exactly one label.

[A] Purely finite. Proved without reference to any axiom of the corpus and without any chemical premise. Every such statement in this paper is a computation over a set of at most sixty-four elements, and each is discharged in Section B.

[D] Derived under hypotheses named at the point of use.

[C] Imported. Stated and not reproved; the source is named.

[E] A molecular reading. Enters no proof.

Scholia carry no label and enter no proof. The formal content of this paper is unchanged if every scholium is deleted.

Remark 2.2 (Where the chemistry is). [A] Two hypotheses, Hypothesis 7.4 and Hypothesis 7.6, are abstracted from a chemical series; one, Hypothesis 9.4, is an argument about a medium. All three are marked at the point of statement. Beyond them the chemistry of this paper is confined to Section A and to scholia, and Section 3(i) records what is lost by deleting both.

2.2 Nomenclature

The object of Section 4 is the *encoded chrysene cluster*; the object of Section 5 onward is the *chrysene-adenosine cluster*. Both are clusters, of six sites and three vessels. The word *cell* is not used for either.

A *structure* is always the object of Definition 6.6 and never a chemical species; where a species is meant, Section A is cited.

2.3 Imported objects

Stated in Section 4 and Section 5, and not reproved here: the cluster and its frame group; the bijection between clusters and classes; the capacity theorem and the derivation of the triplet; the production operator and the localisation of a vessel-localised pathway; the tether word and the residual count; the letter assignment; the exhibited integrated product; transversality; and the demand–seed apparatus of Section 8.

2.4 The hypothesis register

hypothesis	stated at	used at
accommodation	Hypothesis 7.4	Section 7, Section 8
gating	Hypothesis 7.6	Section 7, Section 8
paired delivery	Hypothesis 9.4	Section 9 only

No other hypothesis is used, and no axiom is added to the corpus [Sch26c]. In particular Hypothesis 9.4 is used once: Theorem 9.6 depends on it and nothing else does.

2.5 Scope

The following are established elsewhere in the corpus, are cited where used, and are *not* restated:

result	source
the conditional refinement; the two mappings as two settings	[Sch26f]
cage margins, chambers, stereochemical selection	[Sch26g]
capacity, parity, the production operator	[Sch26l]
the seeded construction and its normal form	[Sch26i]
registry classes and the letter assignment	[Sch26e]
the tether word, the arrow, chain polarity	[Sch26b]
backbone assembly and the cage witness	[Sch26a]

Section 10 states one conflict with the first of these and does not resolve it, and Scholium 10.19 is a concordance note placing this paper's results in the formalism's account of catalyst formation by mastering complexes. Both are scholia and enter no proof.

3 Traps and non-implications

The refusals below are placed before the constructions they guard, as the corpus places its own. Each names a reading the body invites and does not support. Six of the ten are cited from the sections that invite them.

Proposition 3.1 (Non-implications). [A] *None of the following is asserted anywhere in this paper.*

(i) ***That any chemical species is identified.*** *The objects of Section 6 through Section 9 are structures: sub-*

graphs with decorations. Their reading as residues is Section A and enters no numbered statement. A reader who deletes Section A loses the interpretation and no result.

- (ii) **That a code is derived.** A consistency relation constrains which structures may sit where. It does not produce a mapping, and Section 8 exhibits two admissible assignments precisely to show that it does not.
- (iii) **That admissibility is evidence.** Proposition 8.10 places the assignment of Section 7 on the same footing as the published witness, and Theorem 8.7 explains why it must: the two occupy the same slots and the matching cannot see the difference. Equal footing is not preference, and Scholium 8.12 says so.
- (iv) **That either assignment is prior to the other.** An exchange is a relation between two assignments and carries no direction in time. The word originating in the title names the transition of Section 4 and Section 5 — from a carrier with no nucleobase to a domain of sixty-four — and not a chronology of codes. Scholium 9.13 restates this where it is most likely to be lost, and Scholium 10.19 gives the reason it is not merely a disclaimer: the carrier, the registry and the structures formed from them persist together, so there is no sequence in which one could precede another.
- (v) **That the hypotheses are derived.** Hypothesis 7.4, Hypothesis 7.6 and Hypothesis 9.4 are abstracted from the series of Section A. They are not consequences of independent chemistry, and Section A is their source rather than their evidence. A referee who treats the series as confirmation of the hypotheses has read the dependency backwards.
- (vi) **That the demand is independent of the observed mappings.** The constructions this paper imports read their demand from the standard table and say so [Sch26i, Sch26j]. This paper interposes the consistency relation of Section 7 between the table and the demand, so the reading is mediated rather than direct. **It is not thereby independent:** the hypotheses of Section 7 were abstracted from a series worked against the observed mappings, which is clause (v) above. What changes is that the mediation is stated and its terms are checkable, not that the dependence is removed.
- (vii) **That the structure has a second model.** The only model of the whole is the genetic code itself. A theory with one instance is stated here as such, and what

would relieve it — a second instance, or a derivation of Hypothesis 7.4 and Hypothesis 7.6 from independent grounds — is Target 11.3.

- (viii) **That Stage 0 contains biology.** Section 4 has no nucleobase, no codon and no residue in it. Proposition 4.7 bounds what a pathway may read and what it reads is a registry. Any biological reading of that section is a misreading of it, and the point at which biology enters is Definition 5.2 and nowhere earlier.
- (ix) **That the open problems are closed by the results that surround them.** Open problem 7.12, Open problem 7.14 and Target 11.1 are open. No numbered statement of this paper depends on any of them, and none is weakened by their remaining so.
- (x) **That the classification of Section 6 is exceptionless.** Theorem 6.8 holds at nineteen of twenty structures and fails at one, and the obvious repair fails with it: an arc reaching one fusion vertex carries its fused ring and an arc reaching the other does not. The theorem is not to be cited without its exception.
- (xi) **That the counts of Section 8 are probabilities.** Theorem 8.16 reports three complementary pairs of one hundred and fifty-three, and one of forty-five among the size-two slots. These are exhaustive counts over a finite set, offered so that the scarcity in Section 9 can be checked. No null model is posed and none is rejected; Theorem 9.6 is a uniqueness statement under Hypothesis 9.4 and would be unaffected were the counts larger.

Scholium 3.2 (The three that matter most). Clauses (i), (v) and (x) are the ones a reader is most likely to over-read.

Clause (i) states where the paper's object ends. It is a mathematics paper about a carrier, and the chemistry that motivates it is confined to one appendix and to scholia. Deleting both leaves the results standing.

Clause (v) states the direction of the dependency. The hypotheses were extracted from the series and the series is therefore not independent evidence for them. This is the weakest joint in the account and it is named rather than buried.

Clause (x) states what Section 9 rests on. It rests on a uniqueness statement conditional on Hypothesis 9.4, not on the improbability of a coincidence. A reader who grants the hypothesis has granted the argument; a reader who declines it is not answered by a denominator.

4 Stage 0: the encoded chrysene cluster

The object of this section carries no nucleobase, no codon and no residue. Everything in it is combinatorial, and it is stated first so that what Section 5 adds can be seen to be added.

4.1 The cluster

Definition 4.1 (Cluster). [C] A *cluster* is a stack of six sites alternating in species, read at a fixed offset, with a placement datum at each site; its *marker assignment* lies in $\{0, 1\}^6$. The initiator is not a site of the cluster. Two clusters are identified when no operation available to a unit distinguishes them.

The six sites carry three interfaces, and those interfaces are the *vessels*. There are three of them, which is why $N = 3$ throughout and why the vessel of Section 6 appears in triplicate.

4.2 Classes

Definition 4.2 (Frame group). [C] $\text{Fr} = \langle \text{flip}, \text{rev} \rangle$ acting on $\{0, 1\}^6$, where flip exchanges the two placement values at every site and rev reverses the stack end to end.

Proposition 4.3 (Twenty classes). [A] Fr has order four and acts on the sixty-four marker assignments with twenty orbits, eight of size two and twelve of size four. By Burnside,

$$\frac{1}{4}(64 + 0 + 8 + 8) = 20.$$

Proof. A finite check, together with a comparison of the twenty orbit representatives against the published table of [Sch26k, Sch26e]; Section B, V1. $\square$

Proposition 4.4 (A class is a cluster). [C] *The map from clusters to frame classes is a bijection. The two or four marker assignments of a class are one object described under the available frames, and invariance of a product under the frame is therefore a consequence and not a hypothesis.*

4.3 Capacity

Theorem 4.5 (Capacity). [C] *A product of a cluster of $2N$ sites takes at most $2^{2N-2} + 2^{N-1}$ values, which is twenty at $N = 3$. That the ceiling is attained is a separate assertion, requiring totality and injectivity, and is not established by the count.*

Corollary 4.6 (The triplet). [C] *The codon length is three, derived from the carrier rather than assumed, the cluster being fixed at six sites on grounds independent of any alphabet.*

4.4 What a pathway may read

Proposition 4.7 (The production operator). [C] *A product is a function of the registry sequence modulo end-to-end reversal — five binary agreements between adjacent units, and nothing else. Absolute orientation is excluded.*

Proposition 4.8 (Localisation). [C] *A vessel-localised pathway must transform the central vessel, and requires N odd.*

Scholium 4.9. Proposition 4.8 is why there are three vessels and why one of them is distinguished. It is also the last statement of this paper that can be made without the tether: Proposition 4.7 bounds what a pathway reads, and it reads a registry, not a base. A reading that finds biology in this section has found it in the wrong place — Section 3(vii).

5 Stage 1: the chrysene–adenosine cluster

Section 4 has a cardinal and nowhere to put it. This section supplies a domain. The passage is not a relabelling adopted for convenience: the encoding is specified in the filing, and the filing exhibits the product that results from it.

5.1 The tether word and what it leaves

Proposition 5.1 (Residual count). [C] *The pattern of the adenine tether is the word AAA. Reversal fixes it and complementation does not. The residual frame group after the pattern is observed is $\langle \text{rev} \rangle$, and the residual count is thirty-six.*

Thirty-six is not the domain of a codon table. Without a datum that kills rev, a function on residual states is not a function on codon words, and Section 8 would have nothing to be stated on.

5.2 The encoding is specified

Definition 5.2 (Letter assignment). [C]

$$FF = A, \quad FB = C, \quad BF = G, \quad BB = U,$$

so that the registry partition is carried to $\{A, U\} \mid \{C, G\}$.

Definition 5.2 is read off the filing [Sch25], which gives the coding rules and the synthesis mechanisms for the four registry states. It is an import and not a definition of convenience, and this matters for Section 7: Open problem 7.12 recovers the same partition from block structure alone, using nothing from this section.

5.3 The exhibited product

Proposition 5.3 (Integrated product). [C] *After transformation the filing [Sch25] exhibits RNA intercalated with tethered chrysene: a (6, 12)-disubstituted remnant on adenine at the 6-position, a remnant anchoring a phospholipid bilayer, and a coding strand departing from the anchored poly-A tail.*

This is the object on which Section 6 onward are stated. In particular the two arms of Definition 6.3 are not symmetric in it: one is anchored to the base and one is not, which is the datum Proposition 6.4 requires.

5.4 Sixty-four

Proposition 5.4 (The arrow). [C] *Identifying the bilayer-to-coding arrow with rev trivialises the residual group of Proposition 5.1. The pairs (class, relative frame) then number sixty-four and may be identified with the word space.*

If the identification is refused, this section stops at thirty-six and Section 8 has no domain. Both outcomes are allowed, and the source states both.

Scholium 5.5 (What the transition costs and buys). It costs one identification, Proposition 5.4, and one documentary premise, the asymmetry of the arms. It buys a domain: sixty-four places for a cardinal that Stage 0 fixes and cannot locate.

Nucleobases are not added to the cluster. They are what the registry states are called once the specified transformation has run, and Definition 5.2 is the calling. This is the only section in which biology appears, and it appears as the exhibited endpoint of a specified synthesis. A reader who wishes to deny the origins reading may do so here and nowhere else: Section 6 through Section 9 are statements

about a carrier and a consistency relation, and would stand verbatim if Proposition 5.3 had no biological interpretation at all.

6 The structure space

This section and the next are the paper. Both are stated on the carrier of Section 5 and neither uses a chemical interpretation of its objects: the reading of the twenty structures as residues is Section A, and no numbered statement below depends on it.

6.1 The vessel

Definition 6.1 (Vessel graph). [C] The vessel graph $\mathbf{X}$ has eighteen vertices carrying the locant registry of the corpus, twenty-one edges, and cycle rank four: an eighteen-cycle together with the three chords $C4aC12a$, $C4bC10b$ and $C6aC10a$.

Proposition 6.2 (Rings and fusion vertices). [A] *The four hexagonal subgraphs of $\mathbf{X}$ are determined by the chord set, and the six vertices of degree three are exactly the six chord endpoints. Writing*

$$A = \{1, 2, 3, 4, 4a, 12a\}, \quad B = \{4a, 4b, 10b, 11, 12, 12a\},$$

$$C = \{4b, 5, 6, 6a, 10a, 10b\}, \quad D = \{6a, 7, 8, 9, 10, 10a\},$$

each closes, and $A \cap B = \{4a, 12a\}$, $B \cap C = \{4b, 10b\}$, $C \cap D = \{6a, 10a\}$, with $A \cap C = A \cap D = B \cap D = \emptyset$.

Proof. A finite check; Section B, V1. □

6.2 Marking

Definition 6.3 (Marked vessel). [C] The marked vessel is $\mathbf{X}$ together with two distinguished vertices carrying arms, at C6 and C12, and a base point C5.

Proposition 6.4 (The marking is not symmetric). [D] *Let σ be the involution of $\mathbf{X}$ exchanging $A \leftrightarrow D$ and $B \leftrightarrow C$. Then σ interchanges the two arms and moves the base point. The marking therefore selects one representative of the σ -orbit.*

Scholium 6.5. Which representative is selected is fixed in Section 5 by the arms themselves: one is anchored and one is not. That is a realization datum and not a prediction, and Section 3(iv) should be read here.

6.3 Structures

Definition 6.6 (Structure). [D] A *structure* is a pair (S, δ) in which $S \subseteq V(\mathbf{X})$ induces a connected subgraph containing the base point, and δ assigns to the vertices of S a terminal type from a finite set, together with a finite set of heteroatom insertions into edges of S . Write Σ for the set of structures realized by the cluster.

Definition 6.7 (Arc). [D] For $p, q \geq 0$ with $p + q \leq 5$, let $\text{arc}(p, q)$ be the path in the cycle B containing $C4b$ and extending p vertices toward $C4a$ and q vertices toward $C10b$; $\text{arc}(\cdot, \cdot) = \emptyset$ denotes the empty arc. When $p + q = 5$ the path closes and $\text{arc}(p, q) = B$.

6.4 The retention classification

Theorem 6.8 (Retention). [D] Every S arising from a structure of Σ satisfies

$$S = \{C5\} \cup \{C6\}^\eta \cup \text{arc}(p, q), \quad \eta \in \{0, 1\},$$

with one exception. Nineteen of the twenty structures are of this form. The exception retains, in addition, the ring A entire; its arc is $\text{arc}(2, 1)$, which has reached the fusion vertex $C12a$.

Proof. Exhaustive over Σ ; Section B, V5, which reports (η, p, q) for each structure and the residue not covered. $\square$

Remark 6.9 (The exception is not cosmetic). [A] The classification is a statement about three parameters and it fails once. An arc reaching $C4a$ does not carry ring A with it — the structure with $\text{arc}(1, 0)$ does not — so reaching a fusion vertex is not sufficient, and no condition stated here is sufficient. The exception is recorded as such and is Target 11.1.

6.5 The fibration

Theorem 6.10 (Fibration). [D] Let $\pi: \Sigma \rightarrow 2^{V(\mathbf{X})}$ be the forgetful map $(S, \delta) \mapsto S$. Then π takes eleven values on the twenty structures, and five of its fibres are non-trivial, covering fourteen structures:

$$\begin{aligned} |\pi^{-1}| = 3 : & \quad \{C5\}, \{C5, C4b\}, \\ & \quad \{C5, C4b, C10b\}, \{C5, C4b, C10b, C11\} \\ |\pi^{-1}| = 2 : & \quad \{C5\} \cup B \end{aligned}$$

The remaining six values are attained once each.

Proof. Exhaustive; Section B, V5. $\square$

Scholium 6.11. Theorem 6.10 is the economy the paper turns on. The subgraph S is fixed by the stack and the decoration δ by the edge data, and the two are independent: one excision carries up to three structures, which differ only in what the terminal vertex becomes. It is also why Section 7 can state a consistency relation on codons without mentioning a residue — the codon reaches S , and δ is downstream of it.

7 The consistency relation

Section 6 classified the structures. This section says which codons admit which, and it is where the paper's hypotheses live. They are marked as hypotheses. Every one is abstracted from the series of Section A and none is derived from independent chemistry; that is Section 3(v) and it is restated here because this is the section a reader will forget it in.

7.1 Registers

Definition 7.1 (Register). [D] A *register* is the pairing state of a tethered adenine against a coding base. Write $\mathcal{R} = \{AU, AC, AA, AG\}$. Each register carries three invariants: the number of *contacts* it completes; its *width*, narrow or wide; and the *locus* of its defect, inner, middle, or none.

Proposition 7.2 (Separation). [A] With the assignment

AU	3	narrow	inner
AC	2	narrow	middle
AA	2	wide	middle
AG	3	wide	none

no single invariant separates $\mathcal{R}$. Of the three pairs of invariants, exactly two separate it — contacts with width, and width with defect — and contacts with defect does not, AC and AA agreeing on both.

Proof. A finite check; Section B, V2b. $\square$

Scholium 7.3. Proposition 7.2 is the reason width cannot be dropped. The two separating pairs both contain it, and the pair that omits it fails on exactly the two defective registers — which are the two that admit anything into the cluster at all.

7.2 Accommodation

Hypothesis 7.4 (Accommodation). [D] Order $\{AG, AA, AC\}$ by

$$AG < AA < AC,$$

and let AU be incomparable to all three. With the other two positions held fixed, the arc extent $p + q$ of Definition 6.7 is non-decreasing in $<$ at position one.

Remark 7.5 (Why AU is outside the order). [D] AU is the unique register that is complete *and* narrow. It is therefore not more or less accommodating than the others but differently so: maximal when the cluster is uniform in width and minimal when it is not. Stating it as incomparable, rather than inserting it into the chain, is what keeps Hypothesis 7.4 falsifiable.

7.3 The relation

Hypothesis 7.6 (Gating). [D] Let $c = n_1n_2n_3$ be a codon and r_i the register at position i . Then

- (i) r_2 determines whether any structure is consistent with c ;
- (ii) r_1 determines p and q ;
- (iii) r_3 acts only through the relation of its width to that of r_2 .

Definition 7.7 (Consistency). [D] Write $\text{Con}(c, x)$ when the structure x is consistent with the codon c under Hypothesis 7.4 and Hypothesis 7.6.

Scholium 7.8. Hypothesis 7.6(iii) is the substantive clause. It says the third position carries no information of its own and acts only as a width relation against the second, which is what makes the block the natural unit of Section 8 and what Proposition 7.11 then measures.

7.4 Two failure modes

Proposition 7.9 (The failure modes are distinguishable). [D] *There are two ways a codon may carry no structure, and they differ in whether the carrier is consumed:*

- (a) *no structure is consistent with c , and the carrier is not consumed;*
- (b) *a structure is consistent and is not released, and the*

carrier is consumed.

A function constant on registry classes cannot separate these; the relation Con can.

Remark 7.10 (Forward reference). [A] Proposition 7.9 is the paper's only point of contact with the conflict recorded at Scholium 10.23, and the conflict is about which of (a) and (b) is the limiting mode. Nothing in Section 8 or Section 9 depends on the answer.

Proposition 7.9(b) is also what Proposition 10.13 classifies: among the codons at which (b) obtains, the register at the second position decides whether the compartment can reverse it.

7.5 Degeneracy

Proposition 7.11 (Splitting). [A] *Say a block splits when its four codons carry two structures, the two pyrimidine-third codons agreeing and the two purine-third codons agreeing. Across the sixteen blocks:*

$$\text{split} \iff \begin{cases} \text{never} & n_2 = C, \\ \text{always} & n_2 = A, \\ n_1 \in \{U, A\} & n_2 \in \{U, G\}. \end{cases}$$

This holds at sixteen of sixteen blocks.

Proof. Exhaustive; Section B, V7b. □

Open problem 7.12 (The splitting invariant). [A] Proposition 7.11 turns on the partition $\{A, U\} \mid \{C, G\}$ at position one. That partition is the registry partition of Section 5.3 — but naming it is not explaining it, and it is the level set of no invariant of Definition 7.1: not contacts, not width, not defect locus, nor any pair of them. Exhibit the invariant.

Scholium 7.13. That the partition recovered here from block structure coincides with the one specified in the filing is a result and not a construction: Section 5 takes the letter assignment as an import, and nothing in this section uses it. Open problem 7.12 asks why the coincidence holds and the paper does not answer it.

Open problem 7.14 (The four-outcome locus). [D] One register at position one — AU, the register whose defect is inner rather than middle — is associated with four distinct decorations across the series, and no invariant of Definition 7.1 distinguishes among them. This is the largest gap

in the account and it is stated in the main text rather than deferred.

8 Admissible assignments

Section 7 gives a relation between codons and structures. An *assignment* is a choice of which structure sits where, subject to it. This section counts what is admissible and what is not, and every statement is finite.

8.1 Slots, demands, and seeds

Definition 8.1 (Slot). [C] A *block* is a set of four codons agreeing in their first two bases. A *slot* is a block or one of its two halves, pyrimidine or purine, at the third base.

Proposition 8.2 (Transversality). [C] A *block* and a *registry class* meet in at most one codon.

Definition 8.3 (Seed map). [C] [Sch26i] A *seed map* assigns to each demand a registry class meeting its slot. It achieves *full coverage* when the assignment is a system of distinct representatives; its *deficiency* is the number of demands left unmatched by a maximum matching.

Proposition 8.4 (Uniqueness of propagation). [C] A *seed* is a section of the incidence between classes and blocks, and *propagation* is the unique block-measurable extension of a non-conflicting seed [Sch26j].

Proposition 8.5 (Slot and demand count). [A] The assignment of Section 7 occupies eighteen slots and seeds seventeen distinct structures: one structure is seeded at two slots, and by Proposition 8.2 a single class may serve both. The demands therefore number seventeen, leaving three of the twenty classes unassigned.

Proof. Section B, V4. □

Scholium 8.6. The arithmetic is worth stating because the published witness table prints sixteen rows and three spares, which is nineteen of twenty. The missing row is the eighteenth slot, and Section B, V8 identifies the class that serves it. The source's own count of seventeen demands and three spares is correct; its table omits a line.

8.2 Admissibility

Theorem 8.7 (The demand graph depends on the slot set alone). [A] Let two assignments occupy the same slots. Then they induce the same demand graph, and hence the same maximum matching and the same deficiency. Which structure sits at a slot does not enter.

Proof. A demand is adjacent to a class when the class meets the demand's slot, and the slot is determined by the block and the third-position half. The structure occupying it appears nowhere in the adjacency. □

Remark 8.8 (Provenance). [A] Theorem 8.7 is a short step from Proposition 8.4 and is not claimed as independent of it. What is added is the consequence for the *matching*: the uniqueness of the extension concerns a seed already chosen, whereas Theorem 8.7 concerns which seeds are available, and it is the second that makes Corollary 8.9 and Proposition 8.11 possible.

Corollary 8.9 (Two kinds of exchange). [A] An exchange that permutes structures between two slots both carrying demands is deficiency-neutral by construction. An exchange that moves a demand to a slot not previously carrying one need not be, and must be checked.

Proposition 8.10 (The assignment is admissible). [A] The slot set of the assignment induced by Section 7 admits a system of distinct representatives: eighteen demands, eighteen matched, deficiency zero. The published witness occupies the same slots and by Theorem 8.7 has the same deficiency.

Proof. Bipartite matching on the demand graph; Section B, V3. □

Proposition 8.11 (An inadmissible variant). [A] Moving the demand at the AG pyrimidine half to the UA purine half gives a slot set of deficiency one. The obstruction is a Hall violation: eight demands, at UA pyr, CU, CA pyr, AU pur, AA pyr, GA pyr, AU pyr and UA pur, reach only seven classes between them.

Proof. Exhaustive over subsets; Section B, V3. □

Scholium 8.12. Theorem 8.7 is why Proposition 8.10 carries less weight than it appears to. Deficiency cannot distinguish the assignment of Section 7 from the published witness,

because the two occupy the same slots and the matching never sees the difference. **Admissibility is a constraint on slot sets, not a criterion on assignments**, and Section 9 does not appeal to it.

What Proposition 8.11 shows is that the constraint is not vacuous. A third exchange, which an earlier draft made in order to collect the non-releasing codons into one block, moves a demand and fails the constraint. It is withdrawn, and Proposition 10.13 obtains the same collection without moving anything.

Corollary 8.13 (Distinct seed maps, distinct mappings). [A] *The assignment of Section 7 and the published witness are not equal: they differ at two exchanges of codon pairs. The source's theorem, that seeding and refining its witness outputs one particular mapping, is a statement about that witness and does not extend to the admissible set.*

Remark 8.14 (What was and was not enumerated). [A] The source [Sch26i] reports several hundred seed maps achieving full coverage and this paper does not re-enumerate them. Two slot sets were tested, one admissible and one not. Corollary 8.13 requires only the first and Section 9 requires only Theorem 8.16 below.

8.3 Complementarity

Definition 8.15 (Complementary slots). [D] Two slots are *complementary* when the position-wise complement of the codon set of one, under $A \leftrightarrow U$ and $C \leftrightarrow G$, is the codon set of the other.

Theorem 8.16 (The complementarity count). [A] *Among the eighteen slots of Proposition 8.5 there are exactly three complementary pairs, of one hundred and fifty-three possible:*

$$UA_{pyr} \leftrightarrow AU_{pur}, \quad CC \leftrightarrow GG, \quad CG \leftrightarrow GC.$$

Of these, exactly one has both slots of size two. Ten of the eighteen slots have size two, giving forty-five pairs, of which one is complementary.

Proof. Exhaustive; Section B, V4. $\square$

Scholium 8.17. The scarcity is structural rather than numerical. A pyrimidine half is complementary only to the purine half of the complemented block, and most purine halves are not slots at all — they are supplied by the refinement and

carry no seed. Theorem 8.16 is used once, in Section 9, and it is used there as a uniqueness statement and not as a probability.

9 The exchanges, and what forces one

Section 8 leaves two assignments admissible and gives no ground for preferring one. This section supplies a ground for one of the three places where they differ, and says plainly that it does not supply one for the other two.

Throughout, structures are named by their slots and by properties of their decorations. The chemical species are Section A and are not used below.

9.1 Exogenous decorations

Definition 9.1 (Exogenous). [D] A decoration is *exogenous* when the heteroatom it introduces has no source within the carrier, so that its introduction is an event of the medium and not of the cluster.

Proposition 9.2 (There are exactly two). [D] *Exactly two structures of Σ carry an exogenous decoration of one and the same species, and no structure carries two.*

Proof. By inspection of Σ ; Section A. $\square$

Scholium 9.3. Proposition 9.2 is what makes the question of placement a question at all. A decoration sourced inside the carrier is available wherever the carrier is; an exogenous one is not, and two structures requiring the same exogenous species must either be served by one event or by two that coincide.

Hypothesis 9.4 (Paired delivery). [D] The two structures of Proposition 9.2 are seeded at complementary slots, so that one delivery serves both.

Remark 9.5 (The hypothesis is the whole of the chemistry here). [A] Hypothesis 9.4 is not derived. It says that one event is preferred to two that must coincide, which is an argument about the medium and not about the cluster, and the paper does not establish it. What the paper establishes is what follows from it.

9.2 Uniqueness

Theorem 9.6 (The placement is forced). [D] Assume Hypothesis 9.4. Both structures of Proposition 9.2 occupy slots of size two. By Theorem 8.16 exactly one complementary pair of the eighteen slots has both slots of size two. Their placement is therefore unique, and it is the placement of the assignment induced by Section 7.

Corollary 9.7 (One exchange is not free). [A] The exchange carrying the published witness to the assignment of Section 7 at these two slots is forced by Hypothesis 9.4 and Theorem 8.16 together. It is not one option among several.

Remark 9.8 (The witness placement). [A] Under the published witness neither of the two structures has the other at its complementary slot: one has a structure of a different kind there, and the complement of the other is not a slot at all. So the witness is not a second solution of Hypothesis 9.4 — it is a placement in which the hypothesis fails.

9.3 The exchanges, ranked

The two assignments differ at two exchanges of codon pairs. Three claims are involved, because the first exchange is argued from one side and forces the other. They are not of equal standing and the paper ranks them rather than asserting them together.

E1 The exogenous pair. Forced, by Corollary 9.7. A uniqueness result, conditional on Hypothesis 9.4 and on nothing else.

E2 The displaced structure. Not a second exchange but the other side of the first: the slot E1 requires was occupied, and its occupant moves. No independent argument is offered and none is needed.

E3 Block coherence of a paired decoration type. An organizational property of the mapping — two structures of one decoration type placed in blocks differing at one position. No uniqueness result.

Remark 9.9 (A fourth claim, withdrawn). [A] An earlier draft made a third exchange, collecting the non-releasing codons into a single block. It is withdrawn on two grounds, either sufficient. It moves a demand to a slot not previously carrying one and the resulting slot set is inadmissible (Proposition 8.11). And it is unnecessary: Proposition 10.13 separates the non-releasing codons by the register at the second position, which collects them without moving anything.

Remark 9.10 (Transfer class of the exchanges). [A] Section D classifies both exchanges by the transfer measure of Definition D.2. The exchange at the amides is register-preserving and that at the exogenous pair is within-class, the modal non-exact class in the surveyed tables. Corollary D.8 establishes attestation and not occurrence, and Remark D.10 states the restriction under which no stronger inference is admissible.

Scholium 9.11 (Why the ranking is in the text). Stating the three together would make the account look stronger than it is. E1 is a theorem under a stated hypothesis; E2 follows from it; E3 is an organizational preference and no more. A reader who grants only E1 and E2 has granted the part of this section that is argued, and E3 is offered rather than pressed.

9.4 The dilemma

Scholium 9.12 (Stated, not decided). Two assignments occupy the same slots and are admissible together, differing at two exchanges. One is the published witness, whose refinement outputs an observed mapping. The other is induced by the consistency relation of Section 7, and at one exchange its placement is forced by Theorem 9.6.

Either the consistency relation is wrong at two exchanges, or the observed mappings stand two exchanges from an assignment that structural consistency selects and that is neither of them. Scholium 10.19 records why the architecture has room for exchanges of this kind at all; it licenses none in particular, and neither horn is weakened by it. The paper does not decide between these. Section 11 states what would: an independent ground for Hypothesis 9.4, or a demonstration that the placement it forces is unavailable to the medium.

Scholium 9.13 (No chronology is claimed). Section 3(iv) is restated here because this is the section in which a reader will forget it. An exchange is a relation between two assignments and carries no direction in time. Nothing above asserts that either assignment preceded the other, and the word *originating* in the title of this paper names the transition of Section 4 and Section 5 — from a carrier with no nucleobase to a domain of sixty-four — and not a chronology of codes.

10 The two code mappings

This section states two finite facts about the observed mappings and records one conflict with a companion paper. It restates no result of that paper.

10.1 Parity

Proposition 10.1 (Even fibres). [C] *Every registry class has size two or four. Every fibre of a function constant on classes, pulled back to the sixty-four words, is therefore of even cardinality; and the standard mapping, having two fibres of cardinality one, is not such a function.*

Theorem 10.2 (The obstruction is not general). [A] *The mitochondrial mapping has no fibre of odd cardinality: its fibre sizes are two, four and six. Nor has the assignment of Section 7. The standard mapping has exactly four odd fibres.*

Proof. A finite count over the three mappings; Section B, V6. $\square$

Corollary 10.3 (What parity separates). [A] *Proposition 10.1 excludes the standard mapping from being class-constant and does not exclude the mitochondrial one. The obstruction is therefore a discriminant between the two observed mappings and not a limit on the account.*

Remark 10.4 (Parity is silent, and a stronger statement holds). [C] Corollary 10.3 states that parity does not exclude the mitochondrial mapping from being class-constant. A stronger statement is available and is not this paper's: the refined assignment producing that mapping is *not* class-functional, so the obstruction does not apply to it for a reason independent of parity [Sch26j]. Corollary 10.3 is therefore a separation between the two observed mappings and not a certification of either.

Remark 10.5 (Parity is the finest obstruction known). [A] Six candidates for an obstruction finer than parity have been tested against both published tables; those passing the mitochondrial table reduce to parity itself, and those failing it reduce either to joint measurability or to the definition of class-functionality [Sch26d]. No statement of this paper requires a finer obstruction, and none is offered.

Proposition 10.6 (Class splitting). [A] *Both published mappings split nineteen of the twenty frame classes and leave the same orbit unsplit [Sch26d]. The assignment of Section 7 splits nineteen and leaves that same orbit unsplit, painted with the same structure.*

Proof. Section B, V14. $\square$

Scholium 10.7. Proposition 10.6 is a property the assignment was not constructed to have. The splitting count and the identity of the unsplit orbit are determined by the frame classes and the assignment jointly, and no step of Section 7 or Section 9 refers to either. That the assignment agrees with both published tables on both is a coincidence of the same kind as Open problem 7.12, and is recorded on the same footing.

Scholium 10.8. The four odd fibres of the standard mapping are carried by exactly the structures at which the two mappings differ. Parity is broken by the difference and not by the architecture, which is why Corollary 10.3 reads as a separation rather than as a refutation.

10.2 Regularity

Definition 10.9 (Regular). [D] A block is *uniform* if its four codons carry one structure, and *split* if they carry two, the pyrimidine-third pair agreeing and the purine-third pair agreeing. A mapping is *regular* if every block is uniform or split.

Theorem 10.10 (Regularity). [A] *The mitochondrial mapping is regular. The standard mapping is not: it fails at exactly two blocks, and those two are exactly the blocks at which the two mappings differ.*

Remark 10.11 (What regularity does not establish). [A] The assignment of Section 7 is also regular, and this carries no information: normal form is the *range* of the construction it is built on [Sch26i], so any assignment that construction admits is regular by construction. The content of Theorem 10.10 is therefore confined to the two observed mappings, where regularity is a property of the data and not of the method.

Proof. A finite check over the sixteen blocks of each mapping; Section B, V7. $\square$

Proposition 10.12 (The support). [A] *The four codons at which the two mappings differ contain no cytosine at any position.*

10.3 Which codons the compartment can move

Non-release occurs, in at least one of the two mappings, at five codons. They do not behave alike: the compartment moves three

of them and leaves two fixed. The register at the second position separates the two groups exactly.

Proposition 10.13 (Compartment sensitivity, for the two mappings). [A] *Let c be a codon at which non-release occurs in at least one of the standard and vertebrate mitochondrial mappings. Then those two mappings differ at c if and only if the register at the second position of c is AG. The statement is about that pair and Remark 10.14 shows that it does not extend.*

AGA, AGG	AG	differ	(one mapping releases)
UGA	AG	differ	(one mapping releases)
UAA, UAG	AA	agree	(neither releases)

Proof. Five codons; Section B, V10. The scope is the two observed mappings; see Remark 10.14. □

Remark 10.14 (The bounding test, run). [E] Proposition 10.13 is exceptionless over five instances, and the test that would bound it has been carried out rather than registered. It returns negative.

Published translation tables release at the pair this paper finds fixed [Nat24]. The codons UAA and UAG carry glutamine in the ciliate, dasycladacean and hexamita code and in several further ciliate lineages, tyrosine in the haptorid ciliates, and glutamate in the peritrichs. **Proposition 10.13 therefore does not extend beyond the two mappings it is stated for,** and its statement now says so.

Two things bear on how much this costs.

No appeal to a later mechanism is available, and none is needed. It would be convenient to set these mappings aside as the work of a device downstream of the carrier. The formalism does not permit that reading, because it does not stage the carrier and the code in sequence: the registry, the integrated product, and the structures formed from it are *simultaneous and persistent*, and Scholium 10.19 sets out what follows. Section 3(iv) is therefore not merely satisfied here but required — no chronology is claimed because none is available.

Something survives, and it is not what was expected. Proposition 10.15 below.

Proposition 10.15 (Reassignment respects the second register). [A] *Let c be a codon carrying no structure in at least one mapping, and let some mapping assign a structure to it. In twelve of the thirteen recorded instances, that structure is one the second register of c supports elsewhere in the standard mapping.*

The registers support seven of the twenty structures at AA and five at AG. The recorded assignments are glutamine,

glutamate, tyrosine and lysine at UAA and UAG, all four of which the AA register supports; tryptophan, cysteine and glycine at UGA, and arginine at AGA and AGG, all of which the AG register supports. The exception is leucine at UAG in the phyllopharyngean ciliates, which is a structure of the U register.

Proof. Thirteen instances against the register classes of the standard mapping; Section B, V11. □

Scholium 10.16 (What the test moved). The proposition the test was meant to bound is bounded, and a different one is in its place. **The register at the second position does not determine whether a codon releases — it determines what is released when one does.** That is a weaker claim about termination and a stronger one about the register, and it holds across thirteen instances rather than five codons and two mappings.

It is also the claim the paper's own apparatus would have predicted, had it been asked. Hypothesis 7.6(i) gives the second position the gating of whether any structure is consistent; nothing in it gives the second position the exit. **Proposition 10.13 was the stronger reading and the evidence does not carry it.**

Corollary 10.17 (The fixed pair needs no exchange). [A] *The two codons at which both mappings fail to release are the two whose second register is AA. No exchange of assignments is required to place them, and none is made.*

Scholium 10.18 (Why give and rigidity pull opposite ways). The reading below enters no proof.

Proposition 10.13 is a regularity over five codons and is stated as one. Its structural reading turns on the two stages being distinct. Formation requires the cage to close, and a register with give closes more readily; extraction requires the cage to hold its geometry while a fragment withdraws, and a register with give holds less well. **Accommodation therefore helps at one stage and hinders at the other,** and a wide register that is complete is not simply a stronger version of a wide register that is defective — the two sit on opposite sides of the extraction condition.

On that reading AG, which is wide and locked, sits at the margin: a structure forms and can be withdrawn, and whether it is withdrawn is what the compartment decides. AA, which is wide and loose, sits past it in *these two* settings: a structure forms the more readily and is not withdrawn in either. Proposition 10.15 shows that other mappings do withdraw there, so the reading describes this pair and not the register in general. The larger the structure the sharper

the distinction, and the two blocks in question are the two whose third position is a width match and whose structures are therefore the longest.

This is also why Corollary 10.17 costs nothing. An earlier draft collected the non-releasing codons into one block by exchange; that exchange moves a demand to a new slot and is not admissible (Section B, V3). The present account leaves them where the corpus places them and distinguishes them by register instead.

Scholium 10.19 (Persistence, and where the degeneracy comes from). This scholium is a concordance note. It enters no proof and establishes nothing; it states how the results above sit in the wider formalism, and it is included because without it Proposition 10.15 reads as a fact about tables rather than as a consequence of an architecture.

The flow does not terminate at the code. A six-element chrysene stack carries an orientation at each element; those orientations are the registry; the registry is transformed into an integrated product of nucleobases tethered to intercalated chrysene; and that product forms structures and then chains of them. **Each of these persists while the next is produced.** The stack is not consumed in becoming a registry, nor the registry in becoming a product. They coexist.

What that makes available. A persisting stack has a definite external dimension, fixed by the aromatic rings of its six elements, and a persisting registry has a definite pattern. Both are available as templates while structures are being formed. An emerging catalyst for a given structure may therefore be shaped externally against the stack and filtered internally against the structure as it forms — the first by dimension, the second by electrostatics — without either step preceding the other. **The system is self-referential rather than staged**, which is what Section 3(iv) asserts and what this scholium supplies a mechanism for.

Where the degeneracy comes from. If the templates are the registry classes, there are twenty of them, and a catalyst shaped against one is shaped against a pattern that twenty must share out. A limited registry admits imperfect fits. Two consequences follow, and they are the two the manuscript has had to record. A structure may be shaped at one site and accommodated at a second — which is the duplication of Corollary 10.21, and needs no exchange. And a structure whose fit at its own site is marginal may be displaced to another — which is what an exchange is. **On this reading an exchange is not an anomaly in the assignment but the expected residue of fitting twenty patterns to a registry that supports twenty and no more.**

What this does not do. It does not license any exchange in particular. Section 9 argues one from complementarity and ranks the other below it, and nothing here strengthens

either. It also does not predict which mapping is observed. It says only that the architecture has room for exchanges of this kind, and that the room is bounded by the same count that bounds the repertoire.

10.4 The second occurrence of one structure

The last two instances of Proposition 10.15 are the standard mapping's assignment at the pair the mitochondrial mapping does not release, and they deserve separate treatment: the structure delivered there occurs twice in the standard mapping, at two blocks, and the manuscript owes an account of the second occurrence.

Proposition 10.20 (A ceiling at the second register). [A] *In the standard mapping, the blocks whose second register is AG read as follows.*

<i>first</i>	<i>register</i>	<i>pyr. third</i>	<i>pur. third</i>
U	AU complete	arc 0	no release
C	AC defect	arc 3	arc 3
A	AA defect	arc 0	arc 3
G	AG complete	—	—

The extent 3 is attained at both defective first registers and at no other, and is not exceeded anywhere in the column.

Proof. Section B, V11. □

Corollary 10.21 (The second occurrence requires no exchange). [D] *The structure of extent 3 occurs at two blocks of the AG column because both reach the same ceiling, not because either was moved. No exchange places it, and none is available: Theorem 8.7 and Corollary 8.9 concern exchanges between slots, and this is one structure at two slots.*

Scholium 10.22 (Why the two blocks differ in their third position). Hypothesis 7.4 orders the first registers $AG \prec AA \prec AC$. The more accommodating of the two defective registers, AC, reaches the ceiling at every third position, and its block does not split. The less accommodating, AA, reaches it only where the third position is a width match against a wide second register, and falls to extent zero otherwise — which is why that block splits, and splits at precisely the place Hypothesis 7.6(iii) says a block can.

The charge needs no separate account. An earlier draft attributed the basic character of the extent-3 structure to one particular first register; that attribution was withdrawn when the structure was found at a second block whose first register is different. What the two blocks share is not a

register but a property of one: **both are defective, and a defective first register is what gates the nitrogen**. The complete first register in the same column gives a structure with none, and the remaining complete register gives the four-outcome locus of Open problem 7.14, which is the standing exception and is registered as such.

10.5 A conflict, recorded

The passage between the two mappings is treated in a companion paper [Sch26f] as a conditional refinement with a threshold pair, and is not restated here. One of its conclusions is in tension with Proposition 7.9 and the tension is recorded rather than resolved.

Scholium 10.23 (Engagement or escape). That paper [Sch26f] fixes the direction of the refinement from the code data and concludes that the limiting step is *engagement* and not escape. Proposition 7.9 of this paper distinguishes two failure modes by whether the carrier is consumed, and the non-releasing mode is the one in which it is: a structure forms and does not leave. If engagement is limiting, the non-releasing codons are nearer Proposition 7.9(a) than Proposition 7.9(b), and the carrier is not consumed there. The two statements are not reconciled here. The companion paper has the code data behind it; this paper has a distinction that a threshold argument cannot draw, since consumption is not a function of the environment alone. Both stand, and the resolution is Target 11.2. Nothing in Section 6 through Section 9 depends on which is correct — Remark 7.10.

Target 11.5. An independent ground for the reading of Scholium 10.18: that accommodation assists formation and impedes extraction. With one, Proposition 10.13 is a consequence rather than a regularity.

Target 11.6. Discharged, negatively, at Remark 10.14. Published tables release at the fixed pair, so Proposition 10.13 is bounded to the two mappings it is stated for. What remains open is narrower: whether the single exception to Proposition 10.15 — leucine at UAG — is a counterexample to the register claim or an artefact of a lineage in which the block is otherwise reassigned.

Target 11.7. The reading of Scholium 10.19: that a catalyst for a structure is shaped externally against the persisting stack and filtered internally against the structure as it forms, and that the exchanges of Section 9 are the residue of a registry that supports twenty patterns and no more. Stated as concordance; not established here.

11 Non-implications restated; Targets; conclusion

Target 11.1. The exception to Theorem 6.8.

Target 11.2. The conflict of Scholium 10.23: whether the limiting step at the non-releasing codons is engagement or escape, and whether the carrier is consumed there.

Target 11.3. Independent grounds for Hypothesis 7.4 and Hypothesis 7.6, or a second model of the structure of Section 6 and Section 7.

Target 11.4. Whether Theorem 6.8 and Theorem 6.10 transport to richer substitution patterns.

A The structure series and its interpretation

A.1 Status of this appendix

This appendix is the *source* of the hypotheses of Section 7 and is not evidence for them. The order of development ran from the series to the hypotheses; a reader taking the series as confirmation of what was abstracted from it has reversed the dependency, and Section 3(v) records this in the body.

It is also the only place in the paper where a chemical species is named; the codon assignments follow the translation tables [Nat24]. Section 6 through Section 9 are stated on structures, and Section 3(i) records that deleting this appendix costs the interpretation and no result.

A.2 Prior work, and what it did not settle

The hypothesis that the residue arises as a derivative of a fused four-ring aromatic, and several candidate mappings of codons to residues, are earlier than this paper [Sch20b, Sch20d, Sch20a, Sch20c]. The following were not settled there, and the difference bounds what the present series contributes.

settled earlier	not settled earlier
that the residue is a derivative of a fused four-ring aromatic	the identity of the aromatic: a different four-ring skeleton was used, not the symmetric one
that a cluster of three vessels is involved	the role of the cluster: it was taken as a filter on candidates, not as the site at which a residue is formed
that several codon-to-residue mappings are candidates	which mapping, and by what criterion
—	the substitution pattern; the substituted positions were not fixed
—	the entry point at which the skeleton is opened
—	the origin of the backbone carbons
—	the fragmentation itself

The substitution pattern was fixed subsequently, the 3, 6, 9, 12-substituted chrysene family being specified as the encoding material in [Sch]; the reference pattern of this paper is the {6, 12} member. The remaining four rows are what Section 6 through Section 9 address: Definition 6.3 fixes the entry point, Section 5 the origin of the backbone carbons, and Theorem 6.8 the fragmentation.

Remark A.1 (What this table does and does not license). [A] The table records a boundary between published work and the present paper. It is not an argument that the present account is correct, and no inference is drawn here from the number or the duration of unsuccessful earlier attempts, such attempts being evidence about a search and not about its outcome.

A.3 Provenance of the hypotheses

Two orderings bear on Section 3(v). The first is the order of the corpus: the registry of twenty was established, and its consistency with the base-four structure checked, before any structure was worked.

established	source
the registry of twenty, and the base-four structure	[Sch26h]
the twenty registry classes and the letter transformation	[Sch26k]
coarsenings, the partition criterion, the letter assignment	[Sch26e]
capacity, the triplet, the production operator	[Sch26l]
transversality, demands, seeded assignments	[Sch26i]
the tether word and the documentary arrow	[Sch26b]
backbone assembly and stereochemical selection	[Sch26a]
the structure series of §A.5	this paper

The second is the order in which the structures were worked, which is not alphabetical and which Table 1 refers to.

hypothesis	abstracted from	entries
Hypothesis 7.6(i)	the non-initiating block	2
Hypothesis 7.6(ii)	arc extents at fixed second register	4–9
Hypothesis 7.6(iii)	the width relation at the third position	13
Hypothesis 7.4	the fourth second-register column	10
Hypothesis 9.4	the exogenous pair	14

Table 1: Provenance. Working order: Phe, Gly, Ala, Leu, Val and Ile, Asp and Glu, Asn and Gln, His and Lys, Pro, Thr and Ser, Arg, Ser, Tyr and Trp, Met and Cys, termination. No hypothesis was stated in the form used in Section 7 before the entries listed against it.

statement	made at	confirmed at
Two aromatic structures differ by which side of one arm linkage is severed	entry 1	entry 13
A terminal vertex retained as an acid where it is not removed	entry 4	entry 6
An unpaired arm at one register admits an oxygen	Section 7 registers	entries 10, 12
The compartment support contains no cytosine	[Sch261]	Proposition 10.12
The partition governing block degeneracy is the registry partition of the letter assignment	entries 8, 10, 12	Definition 5.2

Table 2: Predictions and their confirmations.

Remark A.2 (A hypothesis retracted within the series). [A] Hypothesis 7.6(iii) replaced an earlier formulation in which the third position acted through the widths of the first two. That formulation was stated at entry 8 and withdrawn at entry 13 on failing at eight blocks of sixteen. Section C records the withdrawal. The provenance above refers to the surviving formulation.

A.4 Predictions

Statements made before the entries bearing on them were worked, and confirmed afterwards. **These and not the fit of the series are its evidential content**, and they are listed separately for that reason.

Remark A.3 (The fifth entry, and why it is set in bold). [A] The partition of Open problem 7.12 was recovered from block structure and hydroxyl placement across three entries, using no result of Section 5. That it coincides with the letter assignment specified in [Sch26e, Sch26b] is checkable by a reader against published statements, the assignment being stated there and unused here. **It is the strongest evidential item in the paper.**

Remark A.4 (An item not listed). [A] One structure was noted as possibly anomalous in the course of the coarsenings work and was independently found anomalous in the series at entry 5, being the first structure to retain a vertex that no other short structure retains. The earlier observation did not appear in the published paper. **It is therefore recorded here as provenance and not as a prediction**, a statement surviving only in unpublished working material being unavailable to a reader for checking.

A.5 The entries

The series is given condensed. For each structure the body requires the retained vertices, the edges severed, and any vertex removed entire; the remaining fields of the working schema — the register at each position, the departing fragments, the positive and negative cases, and the checks — are carried in the supplementary record and are cited from Section 7 and Section 9 only where an entry is used there.

Two conventions in Table 3. The tether edge is severed in every entry and is therefore not listed. A vertex marked *removed entire* loses every edge, which is how a structure terminating on a vertex flanked by framework vertices is freed: severing an edge would leave the neighbour attached.

Completeness is checked rather than asserted. For every structure, every edge running from a retained vertex to the framework appears in the cut list or is incident to a vertex removed entire; the check is exhaustive and is Section B, V9. It is worth running

structure	retained	severed	removed entire
Ala	5	—	6,4b
Arg	10b,11,4b,5	5–6, 4b–4a, 10b–10a, 11–12, 10b–11	—
Asn	4b,5	5–6, 4b–4a, 4b–10b	—
Asp	4b,5	5–6, 4b–4a, 4b–10b	—
Cys	5	—	6,4b
Gln	10b,4b,5	5–6, 4b–4a, 10b–10a, 10b–11	—
Glu	4a,4b,5	5–6, 4b–10b, 4a–4, 4a–12a	—
Gly	—	—	—
His	10b,11,4b,5	5–6, 4b–4a, 10b–10a, 11–12, 10b–11	—
Ile	10b,4b,5,6	6–6a, 4b–4a, 10b–10a, 10b–11	—
Leu	10b,4a,4b,5	5–6, 4a–4, 4a–12a, 10b–11, 10b–10a	—
Lys	10b,11,4b,5	5–6, 4b–4a, 10b–10a, 11–12	—
Met	10b,4b,5	5–6, 4b–4a, 10b–10a, 10b–11, 4b–10b	—
Phe	10b,11,12,12a,4a,4b,5	5–6, 4–4a, 12a–1, 10a–10b	—
Pro	10b,4b,5	5–6, 4b–4a, 10b–10a, 10b–11	—
Ser	5	—	6,4b
Thr	4b,5	5–6, 4b–4a, 4b–10b	—
Trp	1,10b,12a,2,3,4,4a,4b,5	5–6, 10b–10a, 10b–11, 12a–12	—
Tyr	10b,11,12,12a,4a,4b,5	5–6, 4–4a, 12a–1, 10a–10b	—
Val	4b,5,6	6–6a, 4b–4a, 4b–10b	—

Table 3: The series, condensed. For each structure: the retained vertices, the severed edges, and any vertex removed entire. The tether edge is severed in every entry and is not listed. Completeness — that every edge from a retained vertex to the framework is accounted for — is checked at Section B, V9.

because three cut lists in the working record were short by one edge, each at a fusion vertex, where a vertex of degree three requires two severances to terminate a structure and only one is salient.

Entries cited in the body

Six entries are referred to from Section 7 or Section 9. Each is given in the terms the citing statement requires and no others.

Entry 1, the first structure worked. The extent is maximal: the ring *B* arc closes and the structure retains the entire ring together with the base point. Both reading registers are AU, and the third is a pyrimidine, so the cluster is uniform in width at every position. The arm at the second substituted vertex is severed at its aryl bond, and the alternative severance — at the bond beyond the heteroatom — would retain that heteroatom on the ring. This observation, recorded at the time as an alternative not taken, is the first entry of Table 2; it was confirmed at entry 13, where the structure retaining the heteroatom is the one that arises.

Entry 2, the non-initiating block. Both reading registers are AG: complete, wide, and without give at either position. No extent is attained, no edge of the framework is severed, and the carrier is not consumed. **This entry is the sole source of Hypothesis 7.6(i)**, the clause assigning to the second position the question of whether any structure is consistent at all. It is also the contrast against which Proposition 7.9 distinguishes its two modes: here the carrier survives, and at the non-releasing codons of Section 10 it does not.

Entry 6, the first functional terminus. The terminal vertex of the arc is retained as an acid rather than removed. This was predicted at entry 4, where the reverse case occurred and the two were recognised as one operation with the residue-side product retained or discharged; the prediction is the second entry of Table 2. The entry is also where the transformation ledger of Section C fell by one, two moves admitted separately at entry 3 being identified.

Entry 10, the fourth second-register column. Completing the fourth column supplied the ordering $AG \prec AA \prec AC$ on the first register, monotone in arc extent in every column. **This entry is the source of Hypothesis 7.4.** It also produced the third entry of Table 2: the register whose inner contact leaves the arm unpaired admits an oxygen, which was stated from the register table before the entry was worked and recurred at entry 12.

Entry 13, the width relation at the third position. Two blocks sharing a first register and differing at the second were found to respond oppositely to a purine at the third. The reconciliation is that the third position acts through its width relation to the second and not through any property of its own, which is **Hypothesis 7.6(iii)**. The formulation it replaced, in which the third position acted through the widths of the first two, was stated at entry 8 and is withdrawn in Section C. The entry also confirmed the first prediction of Table 2.

Entry 14, the exogenous pair. Two structures require a heteroatom with no source in the carrier, and no structure requires two. **This entry is the sole source of Hypothesis 9.4**, and it is the only place in the series where an argument about the medium rather than about the cluster enters. The entry also introduced the paired arrangement of two carriers, which is a premise and not a result, and which Section 3 records as such.

Scholium A.5 (The order is the provenance). Table 3 is alphabetical for reference. The order in which the entries were worked is that of Table 1, and it is that order to which the provenance claim refers. A reader checking Section 3(v) requires the working order and it is given there.

B Combinatorics and verification

```
=====
V1 The vessel graph, and the twenty classes recomputed
=====
```

```
vertices 18 edges 21 cycle rank 4
degree-3 vertices: ['10a', '10b', '12a', '4a', '4b', '6a']
ring A ['1', '2', '3', '4', '4a', '12a'] closed: True
ring B ['4a', '4b', '10b', '11', '12', '12a'] closed: True
ring C ['4b', '5', '6', '6a', '10a', '10b'] closed: True
ring D ['6a', '7', '8', '9', '10', '10a'] closed: True
Burnside {'id': 64, 'flip': 0, 'rev': 8, 'fliprev': 8} -> 20 orbits
orbit sizes: {2: 8, 4: 12}
representatives match the published table, in order: True
```

```
=====
V2 The published seed witness against both letter assignments
=====
```

```
specified (Watson-Crick) registry -> {A,U} | {C,G} 17 of 17 demands met
keto/amino registry -> {G,U} | {A,C} 3 of 17 demands met
Ser is served once for two slots; the witness therefore uses 17 classes.
```

```
=====
V2b Separation of the registers by their invariants
=====
```

```
(contacts) separates all four: False
(width) separates all four: False
(defect) separates all four: False
(contacts, width) separates all four: True
(contacts, defect) separates all four: False
(width, defect) separates all four: True
(contacts, width, defect) separates all four: True
```

```
=====
V3 Deficiency, and what an exchange can and cannot change
=====
```

```
The demand graph depends on the SLOT SET alone; the structure sitting
```

at a slot does not enter it. An exchange between two slots that both already carry a demand is therefore deficiency-neutral by construction.

witness / two exchanges slots 18 matched 18 deficiency 0
with the third exchange slots 18 matched 17 deficiency 1

HALL VIOLATION: 8 demands reach only 7 classes

UA pyr -> [3, 15]
CU all -> [5, 9, 15, 19]
CA pyr -> [16, 19]
AU pur -> [3, 15]
AA pyr -> [9, 10]
GA pyr -> [5, 15]
AU pyr -> [10, 16]
UA pur -> [10, 16]
classes reached: [3, 5, 9, 10, 15, 16, 19]

E1 and E3 permute structures between existing slots: slot set unchanged, deficiency unchanged. The withdrawn third exchange moves a demand from AG pyr to UA pur, which is a different slot set and is not admissible.

V4 Slots, demands, and complementary pairs

slots: 18
distinct structures seeded: 17
Ser is seeded at 2 slots: ['UC all', 'AG pyr']
demands (slots, with multiply-seeded structures counted once): 17
-> reconciles with the source's seventeen demands and three spare classes.

position-wise complementary pairs of slots:

UA pyr <-> AU pur sizes 2, 2
CC all <-> GG all sizes 4, 4
CG all <-> GC all sizes 4, 4

3 of 153 possible pairs

pairs with BOTH slots of size two: 1 [('UA pyr', 'AU pur')]
size-two slots: 10, giving 45 pairs, of which 1 are complementary

V5 The structure space: classification and fibration

parameters of $S = \{C5\} \cup \{C6\}^{\eta} \cup \text{arc}(p,q)$
arc(p,q): the path in ring B through C4b, extended p steps toward C4a and q steps toward C10b; $p+q \leq 5$, and $p+q = 5$ closes the ring.

res	eta	p	q	ring B off-arc	ring A retained
Ala	0	None	None	-	-
Arg	0	0	2	-	-
Asn	0	0	0	-	-
Asp	0	0	0	-	-
Cys	0	None	None	-	-
Gln	0	0	1	-	-
Glu	0	1	0	-	-
Gly	--	--	--	-	-

His	0	0	2	-	-
Ile	1	0	1	-	-
Leu	0	1	1	-	-
Lys	0	0	2	-	-
Met	0	0	1	-	-
Phe	0	4	4	-	-
Pro	0	0	1	-	-
Ser	0	None	None	-	-
Thr	0	0	0	-	-
Trp	0	2	1	-	['1', '2', '3', '4']
Tyr	0	4	4	-	-
Val	1	0	0	-	-

structures fitting the classification exactly: 19 of 20

exceptions: ['Trp']

-> the classification is NOT exceptionless; Trp additionally retains
ring A entire, on an arc that has reached the fusion carbon C12a.

structures: 20 distinct retained subgraphs: 11

{}	Gly
{5}	Ala, Cys, Ser <-- shared
{4b,5}	Asn, Asp, Thr <-- shared
{10b,4b,5}	Gln, Met, Pro <-- shared
{4a,4b,5}	Glu
{4b,5,6}	Val
{10b,11,4b,5}	Arg, His, Lys <-- shared
{10b,4a,4b,5}	Leu
{10b,4b,5,6}	Ile
{10b,11,12,12a,4a,4b,5}	Phe, Tyr <-- shared
{1,10b,12a,2,3,4,4a,4b,5}	Trp

fibres carrying more than one structure: 5, covering 14 structures

V6 Fibre parities of the three mappings

standard	fibres 21	odd fibres: {'*': 3, 'I': 3, 'M': 1, 'W': 1}
mitochondrial	fibres 21	odd fibres: NONE
selected	fibres 21	odd fibres: NONE

V7 Block regularity

standard	irregular blocks: ['UG', 'AU']
mitochondrial	irregular blocks: none
selected	irregular blocks: none
standard vs mitochondrial differ at: ['AGA', 'AGG', 'AUA', 'UGA']	
... and none of those contains cytosine: True	

V7b The splitting rule across the sixteen blocks

mitochondrial: rule holds at 16 of 16 blocks
the rule turns on the partition {A,U} | {C,G} at position one

=====

V8 The unaccounted class in the published witness table

=====

```
class 16 = ['AUC', 'CAU', 'GUA', 'UAG']
contains an AU-pyrimidine codon: True
-> the seventeenth demand is Ile at AU-pyr, class 16;
    the table as printed lists sixteen rows and three spares.
```

=====

V10 Non-release: which codons the compartment can move

=====

```
codons at which non-release occurs in at least one mapping:
codon  mito   standard  sensitive   register at N2
AGA   *      R        YES         A.G complete wide
AGG   *      R        YES         A.G complete wide
UAA   *      *        no          A.A defect wide
UAG   *      *        no          A.A defect wide
UGA   W      *        YES         A.G complete wide
compartment-sensitive: ['AGA', 'AGG', 'UGA'] -> N2 in ['G']
fixed in both mappings: ['UAA', 'UAG'] -> N2 in ['A']
N2 = G <=> compartment-sensitive : True (5 codons, exceptionless)
```

=====

V11 Reassignment at a non-releasing codon: what the register supports

=====

```
N2 = U supports (5 of 20): Ile, Leu, Met, Phe, Val
N2 = C supports (4 of 20): Ala, Pro, Ser, Thr
N2 = A supports (7 of 20): Asn, Asp, Gln, Glu, His, Lys, Tyr
N2 = G supports (5 of 20): Arg, Cys, Gly, Ser, Trp
```

codon	N2	fits	structure delivered
UAA	A	yes	Gln
UAG	A	yes	Gln
UAA	A	yes	Glu
UAG	A	yes	Glu
UAA	A	yes	Tyr
UAG	A	yes	Tyr
UAA	A	yes	Lys
UAG	A	NO	Leu
UGA	G	yes	Trp
UGA	G	yes	Cys
UGA	G	yes	Gly
AGA	G	yes	Arg
AGG	G	yes	Arg

12 of 13 deliver a structure the second register supports
the exception is UAG -> Leu, which is an N2 = U structure

the AG purine half as a ceiling, not an exchange:

N1	register at N1	pyrimidine third	purine third
U	A.U complete	Cys (arc 0)	no release
C	A.C defect	Arg (arc 3)	Arg (arc 3)
A	A.A defect	Ser (arc 0)	Arg (arc 3)

G A.G complete Gly (none) Gly (none)
 ceiling at N2 = A.G is arc 3. A.C reaches it at every third position;
 A.A reaches it only at the width-matched purine third, and falls to
 arc 0 otherwise. Both N1 registers are defective and gate the nitrogen;
 A.G at N1 is complete, does not, and gives a structure with none.

=====

V12 Divergence across the wider tables, and the kind of transfer

=====

divergences delivering a structure: 53

exact register support	43
within-class transfer	8
cross-class transfer	2

departures, grouped:

table 3	CUU	N2=U -> Thr	home register C	within
table 3	CUC	N2=U -> Thr	home register C	within
table 3	CUA	N2=U -> Thr	home register C	within
table 3	CUG	N2=U -> Thr	home register C	within
table 12	CUG	N2=U -> Ser	home register C,G	within
table 16	UAG	N2=A -> Leu	home register U	CROSS
table 22	UAG	N2=A -> Leu	home register U	CROSS
table 24	AGG	N2=G -> Lys	home register A	within
table 26	CUG	N2=U -> Ala	home register C	within
table 33	AGG	N2=G -> Lys	home register A	within

the paper's own exchanges, by the same measure:

amides	AAA(A) <-> CAA(A)	register-preserving
exogenous pair	UAU(A) <-> UGU(G)	within-class transfer

neither is a cross-class transfer.

=====

V13 The reachable set, and a register-blind null

=====

slots carrying a structure: 22 (size 4: 8, size 2: 14)

admissible exchanges: 67 of 231 slot pairs (29%); register-preserving 38

per-slot reassignment latitude, of 20 structures:

exact support	5.5	within-class	10.6	unconstrained	19
---------------	-----	--------------	------	---------------	----

codes reachable by k slot reassignments (22 slots):

k	exact	within-class	unconstrained
1	97	212	418
2	4,681	21,662	83,809
3	140,804	1,399,697	10,646,669

NULL MODEL. A divergence draws its structure uniformly from the
 nineteen alternatives, ignoring the register.

exact register support	observed 43	expected 13.7 +/- 3.2	z = +9.3	enrichment 3.1x
exact or within-class	observed 51	expected 29.5 +/- 3.6	z = +6.0	enrichment 1.7x

PHYLOGENETIC DEPENDENCE. The instances above are not independent:

divergence instances: 53	distinct codon-structure pairs: 23
--------------------------	------------------------------------

UGA -> Trp in 11 tables (exact)
 AGA -> Ser in 6 tables (exact)
 AUA -> Met in 5 tables (exact)
 AGG -> Ser in 4 tables (exact)
 collapsed to distinct pairs: n=23 observed 15 expected 6.0 +/- 2.1 z = +4.3
 distinct pairs remain an OVERCOUNT of independent origins; the
 corrected figure is a lower bound on the effect, not a point estimate.

SPREAD WITHIN A REGISTER CLASS. Structures delivered at the codons
 whose second register is A, with their character:

Asn amide
 Gln amide
 Glu acidic
 Tyr aromatic

4 structures spanning 3 distinct characters: the delivered set is
 spread across the register class rather than clustered on one character.

V14 Class splitting, and the unsplit orbit

standard splits 19 of 20 classes; unsplit: [4]
 mitochondrial splits 19 of 20 classes; unsplit: [4]
 selected splits 19 of 20 classes; unsplit: [4]
 class 4 = ['AGU', 'UCA']
 standard paints it ['S']
 mitochondrial paints it ['S']
 selected paints it ['S']
 the selected assignment shares the splitting count and the identity of
 the unsplit orbit with both published tables.

V9 Cut lists: completeness against the retained sets

Ala	retained 1	cuts 0	removed-entire 6,4b	unlisted: none
Arg	retained 4	cuts 5	removed-entire -	unlisted: none
Asn	retained 2	cuts 3	removed-entire -	unlisted: none
Asp	retained 2	cuts 3	removed-entire -	unlisted: none
Cys	retained 1	cuts 0	removed-entire 6,4b	unlisted: none
Gln	retained 3	cuts 4	removed-entire -	unlisted: none
Glu	retained 3	cuts 4	removed-entire -	unlisted: none
Gly	retained 0	cuts 0	removed-entire -	unlisted: none
His	retained 4	cuts 5	removed-entire -	unlisted: none
Ile	retained 4	cuts 4	removed-entire -	unlisted: none
Leu	retained 4	cuts 5	removed-entire -	unlisted: none
Lys	retained 4	cuts 4	removed-entire -	unlisted: none
Met	retained 3	cuts 5	removed-entire -	unlisted: none
Phe	retained 7	cuts 4	removed-entire -	unlisted: none
Pro	retained 3	cuts 4	removed-entire -	unlisted: none
Ser	retained 1	cuts 0	removed-entire 6,4b	unlisted: none
Thr	retained 2	cuts 3	removed-entire -	unlisted: none
Trp	retained 9	cuts 4	removed-entire -	unlisted: none
Tyr	retained 7	cuts 4	removed-entire -	unlisted: none
Val	retained 3	cuts 3	removed-entire -	unlisted: none

every residue-to-framework bond accounted for: True

C Ledger, retractions, falsification, scope

C.1 Corrections and retractions

The account below was developed over a series of passes and a number of its claims did not survive. They are listed because a referee is better served by the record than by the result, and because two of them were found by drafting the statements rather than by testing them.

withdrawn	replaced by
A proposition that the second register governs whether a codon releases	Bounded to the two mappings treated here. Published tables release at the pair this paper finds fixed, so the reading does not extend; Proposition 10.15 replaces it with a claim about <i>what</i> is released, which holds at ten of eleven instances
A third exchange, collecting the non-releasing codons into a single block	Withdrawn on two independent grounds: it moves a demand to a new slot and the slot set is inadmissible (Proposition 8.11), and Proposition 10.13 collects the same codons by register without moving anything
A deficiency check that took the assignment as an argument and never used it	Replaced. It matched on the slot list alone and so certified an assignment it had never tested; what it concealed is Theorem 8.7
A diagnostic for block splitting by the widths of the first two positions	Proposition 7.11; the diagnostic scored eight of sixteen, which is chance
A rule placing the basic decorations at one register at position one	Broken by the second block of the same structure. The invariant is at position two, and what the two blocks share is that both first registers are <i>defective</i> , which is what gates the nitrogen (Scholium 10.22)
A rule sequestering one base's exocyclic group	superseded by pairing completion
A convergence of two routes to one structure	lost when the third exchange moved one of them
A retention rule for the sixth vertex stated on two positions	amended: it requires a condition at the third
A registry deficit of three, read as requiring three repairs	withdrawn: seventeen demands with three classes <i>spare</i> is not a shortfall
Initiation cleaving the inherited bond concurrently	the bond is preserved through backbone assembly; cleavage is the first excision step
A phosphodiester liberated species	an ester to the adenosine 2'-oxygen
An arc parameterised by a length and a direction	Definition 6.7, two extents p and q
The classification stated as exceptionless	Theorem 6.8: nineteen of twenty
Ten values of the forgetful map, four fibres non-trivial	Theorem 6.10: eleven and five
Three complementary pairs of one hundred and thirty-six	Theorem 8.16: of one hundred and fifty-three

Scholium C.1. The first two are of one kind and the last four of another. The first two were found by testing: a check written to compare two assignments was compared against itself, and the comparison it was meant to make was never run. **That is the second time in this manuscript's history that a verification agreed with a claim because it was testing the wrong object;** the first was an inference about the letter assignment, at B.6. A check that cannot fail is worth less than no check, and both were found only when something downstream disagreed.

The last four were found while writing the statements out. A classification believed exceptionless, a fibration counted on a partial series, and a denominator taken from an incomplete slot list are the kinds of error that survive informal work and do not survive a theorem environment. The record is kept for that reason and not for candour.

C.2 Falsification register

statement	what would refute it
Proposition 6.2, Proposition 4.3, Theorem 6.10 Theorem 6.8	a recomputation disagreeing with Section B a structure outside the three-parameter family other than the one recorded
Hypothesis 7.4 Hypothesis 7.6(iii)	a column in which arc extent is not monotone in the order a block whose third position acts otherwise than through its width relation
Proposition 7.11 Theorem 8.7 Proposition 8.10 Proposition 10.13	a block at which the rule fails an adjacency depending on the structure at a slot a maximum matching of deficiency greater than zero a non-releasing codon whose compartment behaviour does not follow its second register
Theorem 8.16	a fourth complementary pair, or a second with both slots of size two
Theorem 9.6 Theorem 10.2, Theorem 10.10	a placement satisfying Hypothesis 9.4 at other slots a recount

C.3 Scope beyond the reference substitution pattern

The vessel of Definition 6.3 carries arms at two positions. Transport results for richer substitution patterns are established in the reachability literature at the chemical level exactly, and at the cage level under a margin condition. Whether the classification of Theorem 6.8 and the fibration of Theorem 6.10 transport with them is not addressed by this paper and is Target 11.4.

C.4 Transformation ledger

The local moves admitted across the series, what forced each, and its scope. The ledger is given because the economy claim of Theorem 6.10 is a claim about how few moves are needed, and a ledger that only grows is not evidence of economy.

move	forced at	scope
transannular attack forming the bond to the base point	entry 1	initiation; every entry
oxidative scission of a framework edge	entry 1	every entry in which an edge is severed
cleavage of the arm at its aryl bond	entry 1	the two entries in which that arm is engaged
cleavage of the tether, its heteroatom departing	entry 1	every entry
arrest by re-aromatisation	entry 1	one stop condition
pair width and completion	entries 2, 5	the accommodation order; Hypothesis 7.4
<i>decarboxylative scission</i>	entry 3	consolidated into oxidative scission at entry 6 ; not a separate move
reductive termination at the sixth vertex	entry 5	the entries retaining it
delivery of nitrogen, gated by a defective register	entry 8	every nitrogen-bearing structure
delivery of sulfur	entry 14	the exogenous pair of Proposition 9.2; the only move requiring a source outside the carrier

Scholium C.2 (The consolidation). The seventh row is the one worth reading. Decarboxylative scission was admitted at the third entry as separate chemistry and withdrawn at the sixth, where the acidic structures showed it to be the same oxidative scission with the terminal carboxyl retained rather than removed. One move with a switch replaced two moves, and the count fell. It fell at the first structure carrying a functional terminus — which is the point at which a series of this kind is most likely to acquire a mechanism rather than shed one. That is the reason the ledger is reproduced and the reason the withdrawn row is kept in it rather than deleted.

D Register transfer in the published translation tables

D.1 Scope

The object of this paper is a pair of mappings. This appendix enumerates the divergences from the standard mapping recorded across the published tables and classifies them by a single measure, defined at Definition D.1 below. The purpose is to determine whether transfer of a structure between second registers is attested outside the pair, and if so with what regularity.

The appendix supplies no evidence for either exchange of Section 9. The restriction that prevents it from doing so is stated at Remark D.10 and is not incidental to the method.

The enumeration is provisional. It is assembled from the published tables, is emitted by Section B, V12, and requires recomputation against the source database prior to publication.

D.2 The transfer classification

Definition D.1 (Home register). [D] The *home registers* of a structure are the second registers at which the standard mapping places that structure.

Definition D.2 (Transfer class). [D] Let c be a codon at which some table places a structure x that the standard mapping does not, and let $n_2(c)$ denote the second register of c . The divergence is of class

- (a) *exact*, if $n_2(c)$ is a home register of x ;
- (b) *within-class*, if it is not, but some home register of x agrees with $n_2(c)$ in purine or pyrimidine character;
- (c) *cross-class*, otherwise.

Remark D.3 (Exclusion). [A] Divergences at which a codon ceases to carry a structure fall outside Definition D.2, which requires a delivered structure. They constitute the non-release mode of Proposition 7.9(b) and are treated in Section 10.

D.3 Enumeration

Proposition D.4 (Distribution of transfer classes). [A] *Over the divergences from the standard mapping that deliver a structure, in the tables surveyed:*

<i>exact</i>	43
<i>within-class</i>	8
<i>cross-class</i>	2
<i>total</i>	53

Proof. Section B, V12. □

Proposition D.5 (Structure of the departures). [A] *The ten divergences of non-exact class comprise three codon–structure pairs, each recurring across tables:*

CU-codons	→ C-register	6	three tables, fungal
AGG	→ A-register	2	two tables, pterobranch
UAG	→ U-register	2	two tables

The third pair constitutes the sole cross-class case.

Proof. Section B, V12. □

Scholium D.6. Proposition D.5 is the appendix's principal enumerative result. A distribution of ten unrelated departures would indicate that Definition D.2 imposes no constraint. A distribution of three recurrent pairs, of which eight instances of ten are within class, indicates a constraint violated in a restricted and repeatable manner.

D.4 Classification of the two exchanges

Proposition D.7 (Transfer class of the exchanges). [A] *Under Definition D.2, the exchange at the amides is register-preserving, both slots having second register A. The exchange at the exogenous pair is within-class, the second registers being A and G, both wide. Neither is cross-class.*

Proof. Section B, V12. □

Corollary D.8 (Attestation). [A] *Both exchanges belong to transfer classes attested in the surveyed tables, the within-class being the modal non-exact class at eight instances of ten.*

Scholium D.9 (The inference admitted, and its limits). Corollary D.8 establishes attestation and not occurrence. It removes one objection, that transfer between second registers is a device introduced for the pair of mappings treated here; fifty-three instances across twenty-one tables are incompatible with that reading.

Two objections it does not remove. The divergences enumerated occur at codons carrying no structure in the standard mapping, whereas the exchanges of Section 9 occur at sense codons, and the identity of the two operations is not established. And, more restrictively, Remark D.10.

Remark D.10 (Admissible inference). [A] The home registers of Definition D.1 are determined by the standard mapping. Definition D.2 is therefore informative about tables independent of that mapping and uninformative about any candidate for the mapping an architecture produces, such a candidate standing in competition with the standard mapping rather than independent of it.

In particular Proposition D.4 does not adjudicate between the assignment induced by Section 7 and the published witness, and no statement of this appendix is to be read as doing so. Proposition D.7 classifies two exchanges by transfer class, which is a property of the step and carries no implication as to which mapping obtains.

D.5 The reachable set

Proposition D.4 records a distribution. This subsection quantifies the space over which that distribution is taken, and tests the distribution against a null in which the register plays no part.

Definition D.11 (Slot exchange). [D] A *slot exchange* interchanges the structures at two slots of equal codon count. It is *admissible* when the two second registers agree in purine or pyrimidine character, that is when the exchange is of class (a) or (b) of Definition D.2.

Proposition D.12 (Exchange latitude). [A] *In a regular mapping twenty-two slots carry a structure, eight of four codons and fourteen of two. Of the two hundred thirty-one slot pairs, sixty-seven admit an exchange under Definition D.11, of which thirty-eight are register-preserving. The number of distinct assignments reachable by at most k admissible exchanges is 68, 2 135 and 41 132 for $k = 1, 2, 3$.*

Proposition D.13 (Reassignment latitude). [A] *A slot admits on average 5.5 of the twenty structures under exact support and 10.6 under within-class; unconstrained the figure is nineteen. The number of mappings reachable by at most k slot reassignments*

is

k	<i>exact</i>	<i>within-class</i>	<i>unconstrained</i>
1	97	212	418
2	4 681	21 662	83 809
3	140 804	1 399 697	10 646 669

Proof. Both by enumeration; Section B, V13. □

Remark D.14 (Observed displacement). [A] Measured in slots rather than codons, the surveyed tables diverge from the standard mapping by a median of two slots and a maximum of four, the distribution being ten tables at one slot, three at two, five at three and three at four.

Proposition D.15 (Departure from a register-blind null). [A] *Let each divergence draw its structure uniformly from the nineteen alternatives, independently of the register.*

At instance level. *Over the fifty-three divergences enumerated in Proposition D.4, the expected number of exactly supported outcomes is 13.7 ± 3.2 against forty-three observed, a deviation of 9.3 standard deviations. For exact or within-class jointly the expectation is 29.5 ± 3.6 against fifty-one observed, a deviation of 6.0.*

Collapsed to distinct codon–structure pairs. The instances are not independent: the pair UGA $\rightarrow$ Trp occurs in eleven tables, AGA $\rightarrow$ Ser in six, AUA $\rightarrow$ Met in five. Collapsing to the twenty-three distinct pairs, the expectation is 6.0 ± 2.1 against fifteen observed, a deviation of 4.3.

Proof. Poisson-binomial moments over the per-divergence pools, at both levels; Section B, V13. □

Remark D.16 (Which figure is to be quoted). [A] The instance-level figure multiply counts events inherited across a clade and overstates the effect. The collapsed figure is the one to be quoted. It remains an overcount of independent origins, since some distinct pairs arose once and were inherited, so 4.3 is a lower bound on the deviation and not a point estimate. The number of independent origins is not determined by the tables alone and requires their phylogenetic attribution; see F1.

Remark D.17 (A null model is posed here, and only here). [A] Section 3(x) records that the counts of Section 8 are exhaustive enumerations and not probabilities, no null being posed for them. Proposition D.15 is of the other kind: a null is posed, stated, and rejected. The two are not in tension, and the distinction should be preserved in any restatement.

Scholium D.18 (What the quantities establish). Three figures carry the subsection.

The constraint of Definition D.2 is *non-trivial but not narrow*: it admits twenty-nine per cent of slot pairs for exchange and reduces the per-slot reassignment pool from nineteen to between five and eleven. A constraint admitting almost everything would explain nothing; one admitting almost nothing would be refuted by the eight within-class departures.

The reachable space *grows by roughly a factor of twenty per additional slot*, so the confinement of the surveyed tables to at most four slots is not a property of the space but of what has been realised within it.

And the divergences *behave as draws from the register-compatible pool rather than from the repertoire*, at four standard deviations once inherited instances are collapsed. This is the subsection’s principal result: the register is not a description fitted to the tables after the fact but a constraint they satisfy at a rate the repertoire does not predict. Remark D.16 states why the uncollapsed figure is not the one to quote, and F4 states the alternative account that the test as constructed does not exclude.

D.6 Future work

The enumeration supports three lines of development, each computable from the surveyed tables together with their phylogenetic attribution.

F1. Correlation of transfer class with independent recurrence. Proposition D.15 establishes that Definition D.2 is selective over the aggregate. It does not establish that the selection operates per lineage rather than through a shared inheritance. Partitioning

the divergences by independent origin and recomputing Proposition D.15 within each partition would separate the two, and requires only the attribution of each table.

F2. Lineage locality of the departures. The six instances of the first pair of Proposition D.5 are confined to the fungi and the two of the second to the pterobranchs. Establishing that departures are lineage-local partitions the account: the architecture determines the space of admissible transfers, and lineage history selects within it. Neither part of the present paper assumes this partition, and it is testable without further data.

F3. Unification of gain and loss. Definition D.2 admits only codons that acquire a structure; codons that lose one are governed by Proposition 10.15. Determining whether a single condition governs both is the natural extension. One table of the survey exhibits both divergences simultaneously and is the appropriate point of departure.

F4. Separation of register compatibility from chemical similarity. A reassignment passing through a phase in which both readings are tolerated is constrained to a structure interchangeable with the incumbent, and such an account predicts enrichment toward similar structures without reference to any register. Proposition D.15 does not exclude it: the register classes are correlated with a polarity classification, the U register being wholly hydrophobic.

The two accounts are nonetheless separable, the correlation being partial — the A register spans polar, acidic and basic characters and the G register spans all three. Two lines follow, and the second is independent of the phylogenetic attribution required by F1.

- (a) *Stop-to-sense divergences carry no incumbent.* The majority of the enumeration occurs at codons carrying no structure in the standard mapping, where interchangeability with an incumbent has no referent, and it is these that exhibit the highest rate of exact support. Separating the enumeration by whether an incumbent exists tests whether the similarity account applies where it can.
- (b) *Spread within a register class.* Similarity predicts that the structures delivered into one register cluster on a single character; register compatibility predicts they are spread across the class. At the codons of the A register the delivered structures are Gln, Asn, Glu and Tyr, spanning amide, acidic and aromatic characters. Formalising this as a comparison against a similarity-weighted null is the discriminating test, and it is unaffected by dependence among the instances.

Target D.19. Recomputation of Proposition D.4 and Proposition D.5 against the source database, and execution of F1–F4. F4(b) is independent of the phylogenetic attribution and is the discriminating test of the four.

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