ANNALS OF THE CHRYSENE FORMALISM
RESEARCH ARTICLE | AI-AUGMENTED PEER-REVIEWED | VOL. 1, NO. 3 | OCTOBER 2026

Canonical Pairing Without Separation: Dual Tethers, Exact Registry Closure, and the Strand–Coding Gate

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Abstract

A stack of six substituted chrysene units admits twenty classes under the symmetries available to it, and the filing on which the construction rests gives two tethers from the chrysene: one to adenosine at its C2, one to cytosine at its C5. A predecessor uses the first and reads the carrier against four coding bases under pairing that is in three cases non-canonical. This paper uses both, reads it under full Watson–Crick pairing, and does not separate the nucleotides from the chrysene at any stage.

The registry closes exactly. Two of the twenty classes have a constant agreement sequence — the all-agree and the all-disagree extremes — and they are the two tether patterns, so they are consumed rather than chosen. The eighteen remaining meet the eighteen slots with a perfect matching and no spare class, and at one slot the assignment is forced outright. No codon is lost by the consumption: a class seeds a codon and propagation fills its slot.

The heteroatom gate is made rather than inherited. The adenosine tether attaches through an ether at a position on the pairing edge, where an unmodified pair makes a weak third contact; the cytosine tether attaches in the major groove and disturbs nothing. Both tethers perturb the pairs they sit on, so a condition turning on which pair is disturbed does not discriminate between them. What does are two invariants the construction supplies and its predecessor cannot: **which strand carries the tethered base**, and **which member of the pair codes**. The first is the predecessor's own gate, derived here from a construction in which no pair is defective; over twenty-two published tables it covers one hundred and ten of one hundred and thirty-two nitrogen-bearing structures, missing one structure in every table and always the same one. The second covers all one hundred and thirty-two. Their conjunction is necessary at five structures of six and sufficient at five of the six it admits.

Three results are negative and are not caveats. Exact closure leaves one hundred and ninety-two admissible assignments, so the selection problem of the predecessor is narrowed nineteenfold and survives. It does not force the slot set: more than half the slot sets of the right shape close exactly, so the division of the blocks is a choice. And the gate admits seventeen structures of twenty, which is less selective than the eleven of the gate it replaces; a strictly tighter condition exists, necessary on the same six structures, that the construction does not explain. Two of the three were found by running computations the draft had registered as targets. The Watson–Crick partition, which that paper recovers from block structure and reports as its strongest evidence, is here assumed as the tether rule: this paper explains what its predecessor observed, and the explanation costs the observation. Neither reading is derived from the other and the filing does not say which is physical. The two are set side by side and not ranked.

Keywords: Chrysene Formalism; chrysene–adenosine cluster; chrysene–cytosine tether; continuous path; Watson–Crick pairing; registry classes; exact closure; perfect matching; heteroatom gate; ether defect; genetic code mappings.

1 Introduction

1.1 One filing, two readings

The filing on which this corpus rests gives two tethers from the substituted chrysene: one to adenosine at its C2, one to cytosine at its C5. Article 57 uses the first and reads the carrier against four coding bases under pairing that is in three cases non-canonical. This paper uses both, reads it under full Watson–Crick pairing, and does not separate the nucleotides from the chrysene at any stage: the interleaved object formed by the pairing is the object on which the residue is made.

Neither reading is derived from the other and the filing does not say which is physical. Section D sets them side by side and declines to rank them; Target 11.4 names the datum

Citation: Schaper, C. D. (2026). Canonical Pairing Without Separation: Dual Tethers, Exact Registry Closure, and the Strand–Coding Gate. *Annals of the Chrysene Formalism*, 1(3):1432–1452. https://chrysene.com/index.php/acf/article/view/70 © 2026 Charles D. Schaper. Distributed under the CC Attribution-NonCommercial-NoDerivatives 4.0. First published by Schaper Systems Press in the *Annals of the Chrysene Formalism*, Vol. 1, No. 3 (2026). ISSN 3144-2021.

that would.

1.2 What is established

1. **Two classes are consumed, and by an invariant.** Proposition 6.2: exactly two of the twenty have a constant agreement sequence, and they are the two tether patterns.
2. **The registry closes exactly.** Theorem 6.5: the eighteen remaining classes meet the eighteen slots with a perfect matching and no spare.
3. **One slot is forced.** Proposition 9.4: after the tether classes are consumed, one slot has a single admissible class and the assignment there requires no argument.
4. **No codon is lost.** Proposition 6.8: a class seeds a codon and propagation fills its slot, so a class that seeds nothing removes nothing from the table.
5. **Two heteroatom invariants, where the predecessor has none.** Definition 8.3 and Definition 8.4: which strand carries the tethered base, and which member of the pair codes. Both are available only because the pairing is canonical (Scholium 8.6).
6. **The first is the predecessor's gate, derived.** Proposition 8.8. Over twenty-two published tables it covers one hundred and ten of one hundred and thirty-two nitrogen-bearing structures, missing one structure in every table and always the same one (Proposition 8.10).
7. **The second is stronger and holds without exception.** Proposition 8.12: one hundred and thirty-two of one hundred and thirty-two.
8. **The exit follows from the pair.** Corollary 5.8: the 2′-oxygen under one tether, the 3′-oxygen under the other.

1.3 What is not established, and three of these are numbers

1. Exact closure leaves **one hundred and ninety-two** admissible assignments (Theorem 9.1). Article 57's selection problem is narrowed nineteenfold and survives.
2. Exact closure does **not** force the slot set: more than half the slot sets of the right shape close exactly (Proposition 9.10). The division of the blocks is a choice.
3. **Neither condition is a mechanism.** Definition 8.4 says which positions admit a heteroatom and not why (Target 8.22), and Hypothesis 8.7 is hypothesised.
4. **The conjunction fails in both directions** (Proposition 8.15): it misses one structure carrying nitrogen and admits one carrying none. An exchange would remove the first and is not taken (Scholium 8.18).
5. The gate admits **seventeen of twenty** structures and forty-five of sixty-one codons. It is necessary and not determining, and a strictly tighter condition exists that the construction does not explain (Proposition 8.12).
6. The Watson–Crick partition is **assumed** here, as the tether rule, where Article 57 recovers it from block structure. The coincidence that paper reports is unavailable.

Section 3 states these as refusals. **They are not caveats on the results above but the other half of them**, and two were found by computations this paper registered as targets and then ran (Section C).

1.4 What is imported

The cluster, the frame group, the capacity theorem and the triplet; the vessel graph, the retention classification and the fibration; backbone assembly and the entry at C5; the slot-set theorem; parity, the range of the construction, and the two failure modes. All are stated without proof and the source is named at each.

Cysteine and methionine are deferred entirely and no statement here depends on them.

1.5 Organization

Section 2 fixes the register and Section 3 refuses four readings beyond those Article 57 refuses. Section 4 imports the cluster. Section 5 gives the construction, Section 6 the closure; Section 7 imports the vessel. Section 8 is the gate and Section 9 the assignments; these four are the paper. Section 10 records what the construction leaves unchanged. Section 11 states the targets and Section 12 concludes. Appendices: the interpretation, the computations, the ledger, and the concordance with Article 57.

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 and without chemical premise; every such statement here is a computation over a set of at most sixty-four elements, 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. The formal content is unchanged if every scholium is deleted.

2.2 The hypothesis register

hypothesis	stated at	used at
near strand	Hypothesis 8.7	Section 8 only

One hypothesis is added to those imported. Hypothesis 8.7 carries Proposition 8.15 and nothing else; no statement of Section 6 or Section 9 depends on it, and the exact closure of Theorem 6.5 is independent of it entirely. A second hypothesis, turning the gate on the pair rather than the strand, was stated in draft and is withdrawn at Corollary 8.13.

Remark 2.2 (Imported hypotheses)**.** [A] The accommodation order and the gating loci of Article 57 are imported with the consistency relation and are not restated. They are abstracted from a worked series there and are not derived; the non-implication recording this is clause (v) of that paper's Section 3 and it holds here unamended.

2.3 Nomenclature

A *reading pair* is the object of Definition 5.5 and a *register* is its type. The word *defect* is avoided in this paper's own statements. Article 57 uses it for a pair that pairs badly; under full Watson–Crick pairing no pair does, and Remark 8.2 records that both tethers perturb their pairs without either being defective in that sense. Hypothesis 8.7 turns on the strand and not on the pairing.

A *structure* is the object of Article 57 and never a chemical species; where a species is meant, Section A is cited.

2.4 Scope

Established elsewhere, cited where used, and not restated: the cluster and its frame group; the capacity theorem and the triplet; the vessel graph and the retention classification; the fibration; backbone assembly and stereochemical selection; the slot-set theorem; the compartment layer and the two mappings as two settings.

Cysteine and methionine are deferred entirely. The exogenous pair, the complementarity count and the uniqueness theorem that follows from them are the subject of a companion paper, and no statement here depends on any of them.

3 Traps and non-implications

Article 57 states ten refusals and they hold here unchanged; they are not reprinted. Four further ones belong to this construction, and each guards a place where the present paper is weaker than its predecessor or where a reader will over-read a number.

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

(xi) ***That the Watson–Crick partition is recovered.*** *It is* assumed*, at Proposition 5.1, and used throughout: the tether rule is that partition. Article 57 recovers it from block structure using nothing from its construction, and reports the coincidence as its strongest evidence.* ***Here the coincidence is unavailable, because the partition is a premise.*** *Scholium 5.9 records this at the point of use and Section D returns to it. A reader taking the two papers together should not count the recovery twice.*

(xii) ***That the heteroatom gate is satisfied by the construction, or that it improves on the gate it replaces.*** *It is satisfied by the* standard *mapping and* ***fails against the one the construction outputs*** *(Proposition 8.15), where one structure has no defect at any codon. In the standard mapping it is worse than its predecessor per codon and less discriminating besides.* ***The gate is not offered here as an improvement****, and the exchange that would rescue it is recorded and declined at Scholium 8.18 because a hypothesis rescued by a choice the hypothesis itself motivates is not a test.*

(xiii) ***That exact closure settles either the assignment or the slot set.*** *It settles neither. Theorem 9.1 leaves one hundred and ninety-two admissible assignments, so the selection problem of Article 57 is narrowed nineteenfold and not discharged. And Proposition 9.10 finds that more than half the slot sets of the right shape close exactly, so the division of the blocks is a choice and not a consequence.* ***What closure establishes is the absence of spare classes, and one forced slot.*** *The abstract must not soften either half of this.*

(xiv) ***That the conditions of Section 8 have been com-***

bined. *A conjunction of Proposition 8.15 with Proposition 8.12 selects fewer structures than either and is not stated as a result. It would be fitting and not deriving: the two conditions are necessary on the same six structures, and intersecting them improves the count without supplying a mechanism for either. Target 8.22 asks for the mechanism instead.*

Scholium 3.2 (The two that matter)**.** Clauses (xi) and (xii) are the ones on which this paper is weaker than Article 57, and they should be read together.
That paper recovers a partition and has a gate selecting eleven structures of twenty with one exception. This paper assumes the partition and has a gate selecting seventeen with none. **The exchange is an open problem for a premise, and a discrimination for a coverage.** Whether it is a good exchange is not settled here, and Section D sets the two side by side without ranking them.

4 The cluster and its capacity

Imported without amendment. Stated so that Section 6 has its objects to hand.

Definition 4.1 (Cluster)**.** [C] A stack of six sites alternating in species, with a placement datum at each; its marker assignment lies in $\{F, B\}^6$. Two clusters are identified when no operation available to a unit distinguishes them.

Proposition 4.2 (Twenty classes)**.** [C] *The frame group* $\mathrm{Fr} = \langle \mathrm{flip}, \mathrm{rev} \rangle$ *acts on the sixty-four marker assignments with twenty orbits, eight of size two and twelve of size four [Sch26l].*

Proposition 4.3 (A class is a cluster)**.** [C] *The map from clusters to frame classes is a bijection, so invariance of a product under the frame is a consequence and not a hypothesis.*

Theorem 4.4 (Capacity)**.** [C] *A product of a cluster of* $2N$ *sites takes at most* $2^{2N-2} + 2^{N-1}$ *values, which is twenty at* $N = 3$*; the codon length of three follows from the carrier.*

Scholium 4.5. Nothing in Section 4 is altered by the continuous path. The twenty classes are a property of the stack and are fixed before any pairing is considered; Section 6 removes two of them from the *seeding*, which is a different operation and leaves Proposition 4.2 intact.

5 The continuous path

Article 57 passes from a carrier to a code in stages, and its integrated product is RNA intercalated with tethered chrysene. The residue is then formed on that product. This paper takes the same filing and does not separate the two: the nucleotides remain interleaved with the chrysene throughout, and residue formation continues on the object the pairing leaves behind.

5.1 Two tethers

Proposition 5.1 (The tethers)**.** [C] *The filing gives two tethers from chrysene* C6*. For a pair* $A \cdot U$ *or* $U \cdot A$ *the tether runs to the adenosine at its* C2*; for* $C \cdot G$ *or* $G \cdot C$ *it runs to the cytosine at its* C5*. Both appear in the structural transformation flow of [Sch25a], the second at Figure 6.*

Scholium 5.2. Article 57 used one of the two tethers the filing gives. The restriction was not argued there and nothing in that paper requires it; the present paper uses both, and the difference in what follows is the subject of Section D.

Corollary 5.3 (The vessel sees no difference)**.** [D] *Both tethers leave chrysene at* C6*. The geometry at the vessel is therefore the same under either, and the retention classification and fibration of Article 57 transfer unamended.*

Scholium 5.4. Corollary 5.3 is the construction's economy and it should be read as a constraint rather than a convenience. Had the two tethers left the chrysene at different positions, two fragmentations would be required and the twenty structures would not be one family. That they leave at the same position is a fact about the filing.

5.2 Pairing, and what the reading position is

Definition 5.5 (Reading pair)**.** [D] At each reading position the coding base is paired, in the Watson–Crick sense, with its complement. The *reading pair* is the ordered pair (coding base, complement), so that

$$\mathcal{R} = \{\, A{\cdot}U,\ U{\cdot}A,\ C{\cdot}G,\ G{\cdot}C \,\}.$$

The tethered base is the adenosine in the first two and the cytosine in the last two, whichever strand it lies on.

Remark 5.6 (The cardinality is preserved and the kind is not)**.** [A] $|\mathcal{R}| = 4$, as in Article 57, which is why the gating apparatus of that paper has a form here at all. The invariants differ. Article 57's registers vary by *defect*: they are non-canonical pairs differing in how badly they pair. The registers of Definition 5.5 all pair correctly, and differ by contact count — two against three — by which strand carries the tethered base, and by which groove the tether points into.
What replaces the defect is Section 8, and the replacement is not a relabelling: it is a defect the construction *creates*.

5.3 The exit

Proposition 5.7 (Two exits)**.** [D] *The formed residue is transferred to the ribose of the tethered base: to the* $2'$*-oxygen under the adenosine tether, and to the* $3'$*-oxygen under the cytosine tether.*

Corollary 5.8 (The exit is determined by the pair)**.** [D] *The exit position is a function of the reading pair, hence of the partition* $\{A, U\} \mid \{C, G\}$.

Scholium 5.9 (What Article 57 could not state)**.** Article 57 has one exit and no account of why that one. Here there are two and the choice between them is forced by the pair, so Corollary 5.8 is a statement its predecessor cannot make.
It is also where this paper gives up an evidential item. The partition $\{A, U\} \mid \{C, G\}$ is recovered in Article 57 from block structure, using nothing from its construction, and the coincidence is that paper's strongest evidence. Here the partition *is* the tether rule, assumed at Proposition 5.1 and used throughout. **This paper explains what its predecessor observed, and the explanation costs the observation.** Section 3 records this as a non-implication and Section D returns to it.

6 Exact closure

The registry has twenty classes and the assignment occupies eighteen slots. Article 57 reports three spare classes and offers no account of the slack. Under the two-tether construction the slack is not there to account for: two classes are consumed as the tether patterns themselves, and the remaining eighteen meet the eighteen slots exactly.

6.1 The tether classes

Definition 6.1 (Agreement sequence)**.** [C] For a marker assignment $w \in \{F, B\}^6$ let $D(w) \in \{0, 1\}^5$ record, at each adjacent pair, whether the two orientations agree. D is constant on frame classes up to reversal.

Proposition 6.2 (Two classes, by invariant)**.** [A] *Exactly two of the twenty classes have a constant agreement sequence:*

class 1	{AAA, UUU}	$D = 00000$	*all agree*
class 8	{CCC, GGG}	$D = 11111$	*all disagree*

Proof. A finite check over the twenty classes; Section B, W1. □

Corollary 6.3 (They are the tether patterns)**.** [D] *The two classes of Proposition 6.2 are the homopolymer patterns of the two tethered bases: adenosine at class 1 and cytosine at class 8. They seed no slot and are consumed by Proposition 5.1.*

Scholium 6.4 (The exclusion is not a choice)**.** Article 57 fixes one tether pattern and says so; the pattern is a datum of the filing and the paper does not derive it. Here both tether patterns are *characterised*: they are the two extremes of the agreement sequence, the only classes on which D is constant, and they are therefore identified by an invariant of the registry rather than selected. That the invariant picks out exactly two, and that the construction requires exactly two, is the content of Corollary 6.3.

6.2 The closure

Theorem 6.5 (Exact closure)**.** [A] *The eighteen classes remaining after Corollary 6.3 admit a perfect matching onto the eighteen slots of the assignment. The deficiency is zero and there is no spare class.*

Proof. Bipartite matching on the demand graph, with the two tether classes removed; Section B, W2. □

Corollary 6.6 (Comparison)**.** [A] *Under the twenty classes of Article 57 the same eighteen slots are matched with deficiency zero and* two *classes unused. Removing the tether classes removes exactly the unused ones.*

Scholium 6.7 (What tightness changes)**.** Article 57 reports several hundred seed maps achieving coverage, none distinguished, and asks which the chemistry selects. **Under exact closure that question changes character.** There is no slack within which to select: every class is used, and a seed map is a perfect matching rather than a system of distinct representatives with room to spare.
Whether the count of perfect matchings falls to one is not settled here and is Target 6.10. It is the first computation the sequel should run, because if it falls to one the selection problem is discharged rather than narrowed.
The slot-set theorem of Article 57 continues to apply: the demand graph depends on the slot set alone, so tightness constrains *which slot sets are admissible* and not which structure sits where. Exact closure is therefore a constraint on the construction and not a criterion on assignments, and Section 9 does not appeal to it.
Nor does closure force the division of the blocks. Proposition 9.10 finds that rather more than half the slot sets of the right shape close exactly, so the slot structure of this paper is one choice among many and is not explained by Theorem 6.5. What closure explains is the absence of spare classes and nothing beyond it.

6.3 No codon is lost

Proposition 6.8 (The tether codons are assigned)**.** [A] *The eighteen slots cover fifty-two codons. Of the remaining twelve, four are non-releasing and eight are the purine halves supplied by the refinement. The four codons of the two tether classes are assigned throughout:* `UUU`*,* `CCC` *and* `GGG` *lie in seeded slots, and* `AAA` *is supplied by the refinement at the* `AA` *purine half.*

Proof. Section B, W2c. □

Scholium 6.9 (Why consuming a class costs no codon)**.** The objection Proposition 6.8 answers is natural and should be met before it is raised. A class *seeds* a codon and propagation fills the slot that codon lies in; a class that seeds nothing therefore removes nothing from the table. **The tether classes are withdrawn from the seeding and not from the code.**
This is also why exact closure is possible at all. Were a class required for each codon rather than for each slot, eighteen classes could not carry sixty-four codons, and the construction would fail at the first step.

Target 6.10. The number of perfect matchings of the eighteen classes onto the eighteen slots. Article 57's several hundred is an upper bound; if the number is one, the selection problem of that paper is discharged.

7 The vessel and the structures

Imported without amendment, by Corollary 5.3: both tethers leave chrysene at C6, so the geometry at the vessel is that of Article 57 and the classification transfers.

Proposition 7.1 (Vessel graph)**.** [C] *Eighteen vertices, twenty-one edges, cycle rank four; the perimeter with three chords, and four rings determined by the chord set [Sch26l].*

Theorem 7.2 (Retention)**.** [C] *Every structure satisfies* $S = \{\mathrm{C5}\} \cup \{\mathrm{C6}\}^{\eta} \cup \mathrm{arc}(p, q)$ *at nineteen of twenty; the exception retains a fused ring entire and the obvious repair fails [Sch26l].*

Theorem 7.3 (Fibration)**.** [C] *The map forgetting the decoration takes eleven values on the twenty structures, five of its fibres non-trivial and covering fourteen [Sch26l].*

Remark 7.4 (What would have broken this)**.** [A] Had the two tethers left the chrysene at different positions, the vessel would present two geometries and Theorem 7.2 would classify two families rather than one. **That both leave at** C6 **is a fact about the filing and not a modelling choice**, and it is the condition under which this section is an import rather than a construction.

8 The heteroatom conditions

Article 57 admits a heteroatom where the register is *defective*, and its registers are defective because they are non-canonical. Under Definition 5.5 every pair is canonical. This section supplies what replaces the defect, and what replaces it is not one condition but two.

8.1 Both tethers perturb

Proposition 8.1 (Where the tethers attach)**.** [C] *The adenosine tether attaches at* C2 *through an oxygen; the cytosine tether attaches at* C5*.*

Remark 8.2 (Neither pair is left alone)**.** [E] Adenine C2 lies on the pairing edge between N1 and N3, where an unmodified pair with uracil makes a weak third contact from

C2−H to uracil O2; an ether oxygen there replaces a donor by an acceptor. Cytosine C5 is adjacent to the exocyclic amine at C4, whose hydrogen donates to guanine O6, and a substituent there perturbs that contact sterically — less directly, and not negligibly.
A condition turning on whether the tether disturbs its pair therefore does not discriminate between the two tethers. An earlier form of this section turned on exactly that and failed; Section C records the failure. This remark enters no proof.

8.2 Two invariants

What distinguishes the two tethers is not whether they perturb but where they sit, and the construction supplies two independent answers.

Definition 8.3 (Strand)**.** [D] A reading position is *near* when the tethered base is the coding base itself, and *far* when it lies across the duplex. By Proposition 5.1 the position is near exactly when its coding base is *A* or *C*.

Definition 8.4 (Side)**.** [D] Every reading pair is a purine against a pyrimidine. A position is *purine-coding* when the coding base is the purine of its pair, and *pyrimidine-coding* otherwise; that is, purine-coding exactly when the coding base is *A* or *G*.

Proposition 8.5 (The two are independent and exhaust)**.** [A]

coding A	*near*	*purine-coding*
coding C	*near*	*pyrimidine-coding*
coding G	*far*	*purine-coding*
coding U	*far*	*pyrimidine-coding*

Scholium 8.6 (What each is a property of)**.** Neither invariant is a property of the pairing, which is canonical at every position. Definition 8.3 is a property of *where the vessel sits*: the tether holds it, and the strand decides whether it sits beside the base it reads or across the duplex from it. Definition 8.4 is a property of *which member of the pair codes*, the pair being purine against pyrimidine at every position.
Both are available only because the construction pairs canonically. Article 57, reading one tethered base against four coding bases, has neither: its registers differ by defect, and the question of which member codes does not arise there.

8.3 The strand condition

Hypothesis 8.7 (Near strand)**.** [D] A heteroatom is admitted at a near position and not at a far one.

Proposition 8.8 (The strand condition is Article 57's gate)**.** [A] *Article 57 admits a heteroatom at a defective first register, and its defective registers are those whose coding base is C or A. By Definition 8.3 that is the near condition at the first position.*

Scholium 8.9. This paper therefore does not offer a competing gate. It derives the inherited one from a construction in which no pair is defective, which is a smaller claim than the competition an earlier draft attempted and a more useful one: a second gate would leave the corpus with two and no account of either.

Proposition 8.10 (The strand condition across the published tables)**.** [A] *Over twenty-two published translation tables and one hundred and thirty-two structures carrying side-chain nitrogen, the strand condition at the first position covers one hundred and ten. The twenty-two it misses are one structure,* ***the same one in every table****.*

Proof. Section B, W4b. □

Remark 8.11 (The exception is inherited, not acquired)**.** [A] The structure missed is the one Article 57 carries as a four-outcome locus and an open problem. **The derivation of Proposition 8.8 therefore inherits exactly one open case across twenty-two lineages and acquires none**, which is the strongest thing that can be said for it.

8.4 The side condition

Proposition 8.12 (The side condition across the published tables)**.** [A] *Over the same twenty-two tables, every structure carrying side-chain nitrogen is purine-coding at its second position. One hundred and thirty-two of one hundred and thirty-two, with no exception in any table.*

Proof. Section B, W4b. □

Corollary 8.13 (It is the stronger condition)**.** [A] *It covers every case the strand condition covers and the one it misses, and it admits twenty-eight codons of sixty against the strand condition's thirty.*

Scholium 8.14 (A target discharged, and what it does not supply)**.** An earlier draft registered as a target an invariant of the construction whose level sets are the purine and pyrimidine second positions, and recorded that the condition was tighter than the gate offered and not ours. Definition 8.4 is that invariant and Proposition 8.5 shows it is as much a property of the construction as the strand is. **The target is discharged.**
An invariant is not a mechanism. Definition 8.4 says which positions admit a heteroatom and not why the purine of a pair should admit one where the pyrimidine does not. Target 8.22 asks for that and the paper does not supply it.

8.5 Together

Proposition 8.15 (The conjunction)**.** [A] *Against the mapping the construction outputs, the conjunction of Hypothesis 8.7 at the first position with Proposition 8.12 at the second admits six structures. Five carry side-chain nitrogen; the sixth carries none. One structure carrying side-chain nitrogen is not admitted, and it is the exception of Remark 8.11.*

Proof. Section B, W4b. □

Scholium 8.16 (What the account now is)**.** The conjunction is **necessary at five structures of six and sufficient at five of six admitted**, failing once in each direction. It is sharper than either condition alone, and it is sharper than Article 57's gate, which admits eleven structures of twenty. Two things it is not. It is not a derivation: Hypothesis 8.7 is hypothesised and Proposition 8.12 is an observed regularity with an invariant attached but no mechanism. And it is not exceptionless in either direction, and Section 3 records both failures rather than the better of them.

8.6 An exchange would remove the remaining failure

Proposition 8.17 (Rescue by exchange)**.** [A] *Moving a structure between two slots leaves the slot set unchanged and therefore the deficiency unchanged (Proposition 9.7). Exchanges exist that place every nitrogen-bearing structure at a position satisfying both conditions.*

Scholium 8.18 (Why no exchange is made)**.** Such an exchange is available and it works. It is not adopted.
It is not forced. Several slots would serve and the conditions prefer none of them. An exchange chosen because it satisfies a condition is chosen by that condition, and Article 57 argues its own exchanges from elsewhere — complementarity for one, block coherence for another. No argument of that kind is available here.
It would make the conditions untestable. Proposition 8.15 is the only test they face. Adopting an exchange so that the test passes converts the test into a constraint. **A condition that cannot fail is not evidence for anything.**
Target 11.2 records where an independent argument might come from, and it is not this paper.

8.7 The positions are not interchangeable

Proposition 8.19 (Positional specificity)**.** [A] *Each condition has a preferred position and the preference is strong. At the first position the strand condition covers five nitrogen-bearing structures of six and the side condition two; at the second the side condition covers six and the strand four. The conjunction as stated covers five structures and twelve codons of fourteen; the conjunction with the two positions exchanged covers two structures and four codons.*

Proof. Section B, W4c. □

Scholium 8.20 (A fact with no account)**. The two reading positions are not equivalent, and nothing in either paper says why.** The gating hypothesis imported from Article 57 assigns different roles to the three positions, but it assigns them; it does not derive them, and it says nothing that would predict which of Definition 8.3 and Definition 8.4 attaches where.
Proposition 8.19 is therefore a regularity of the same standing as Proposition 8.12: exact, checkable, and unexplained. It is recorded here because an account of the heteroatom conditions that did not also account for their positions would be incomplete, and because Target 8.21 is the sharper form of Target 8.22.

Target 8.21 (Why these positions)**.** An account of why the strand condition attaches to the first reading position and the side condition to the second. A process that encounters the positions in order would supply one; the construction as stated here is simultaneous at all three and supplies none.

Target 8.22 (Why the purine)**.** A mechanism for Proposition 8.12: why a position at which the coding base is the purine of its pair should admit a heteroatom where one at which it is the pyrimidine does not. Definition 8.4 supplies the invariant and not the reason.

Target 8.23 (The remaining structure)**.** An account of the single structure that carries side-chain nitrogen at a far position, in every published table. It is the four-outcome locus of Article 57 and this paper does not reduce it.

9 Admissible assignments under exact closure

Theorem 6.5 says the construction closes. This section says by how much, and the answer is a number rather than a uniqueness.

9.1 The count

Theorem 9.1 (Assignments under closure)**.** [A] *On the eighteen slots, the twenty classes of the registry admit* 3648 *systems of distinct representatives. The eighteen classes remaining after Corollary 6.3 admit* 192*, all of them perfect matchings.*

Proof. Exhaustive enumeration over the demand graph; Section B, W2b. □

Corollary 9.2. [A] *Consuming the two tether classes removes* 3456 *of the* 3648 *assignments, which is ninety-five per cent of them.*

Remark 9.3 (Target 6.8, answered negatively)**.** [A] Target 6.10 asks whether the count falls to one. It does not: it falls to 192. The selection problem of Article 57 is therefore **narrowed and not discharged**, and the question that paper registers — which admissible assignment the chemistry selects — survives here in the same form over a smaller set.

9.2 One slot is determined

Proposition 9.4 (A forced slot)**.** [A] *Under the twenty classes, two meet the* UU *pyrimidine half. One of them is the adenosine tether class, which contains* UUU*. After Corollary 6.3 exactly one class meets that slot, and the assignment there is forced.*

Proof. Section B, W2b. □

Scholium 9.5 (What closure does beyond counting)**.** Proposition 9.4 is the subsection's substantive point and it is easy to miss behind Theorem 9.1. **Exact closure does not merely reduce the number of assignments; at one slot it determines the assignment outright.** No argument from chemistry is required there, and none is offered: the adenosine tether consumes a class, and the slot that class shared has one occupant left.
This is a kind of result Article 57 cannot have. With three spare classes no slot is forced, and every assignment in that paper is a choice among at least two. Here one is not.

Remark 9.6 (And seventeen are not)**.** [A] One slot of eighteen is forced. The other seventeen are not, and Theorem 9.1 is the measure of how free they remain. A reading on which exact closure settles the assignment is not available, and Section 3 records it as a non-implication.

9.3 What transfers

Proposition 9.7 (The slot-set theorem still applies)**.** [C] *The demand graph depends on the slot set alone and not on which structure occupies which slot [Sch26l]. Exact closure is therefore a constraint on admissible slot sets and not a criterion on assignments.*

Corollary 9.8. [A] *No statement of this paper distinguishes two assignments occupying the same slots by appeal to Theorem 6.5 or Theorem 9.1.*

9.4 Closure does not force the slot set

Proposition 9.9 (Two blocks split)**.** [A] *Sixteen blocks carrying eighteen slots force exactly two blocks to contribute two slots each; the other fourteen contribute one.*

Proposition 9.10 (The slot set is not unique)**.** [A] *Hold the split pair fixed and vary which of the remaining fourteen blocks are whole and which carry a single half. Of the* 192 192 *slot sets so obtained,* 169 240 *admit an assignment from twenty classes and* 99 588 *from the eighteen remaining after Corollary 6.3 —* 88.1 *and* 51.8 *per cent respectively.*

Proof. Exhaustive; Section B, W6. □

Scholium 9.11 (What closure constrains, and what it does not)**.** Proposition 9.10 must be read against Theorem 9.1, and the contrast is the point.
Exact closure constrains the assignment sharply: from 3648 to 192, a nineteenfold reduction, ninety-five per cent removed. **It barely constrains the slot set**: from eighty-eight per cent admissible to fifty-two. Rather more than half the slot sets of the right shape still close exactly, and

the one this paper uses is one of ninety-nine thousand. So the slot structure is *chosen* and not forced, and any reading on which exact closure explains why the blocks divide as they do is unavailable. What closure explains is the absence of spare classes, which is a property of the matching and not of the division.

Remark 9.12 (Target withdrawn)**.** [A] An earlier draft registered as a target the question whether the slot set is unique, and recorded that a positive answer would make Theorem 9.1 a statement about the only admissible slot set. Proposition 9.10 answers it negatively and the target is withdrawn.

10 Codes

The results of this section are those of Article 57 and are restated without proof, the objects they concern being unchanged. Two carry a qualification under the present construction and the qualifications are given.

10.1 Parity

Proposition 10.1 (Even fibres)**.** [C] *Every registry class has size two or four, so every fibre of a function constant on classes is of even cardinality. The standard mapping has two fibres of cardinality one and is therefore not such a function [Sch26l].*

Remark 10.2 (The obstruction is unaffected by the closure)**.** [A] Proposition 10.1 is a statement about all twenty classes and does not refer to seeding. Consuming two classes as tether patterns (Corollary 6.3) therefore leaves it unchanged: the two consumed classes have sizes two and two, and no fibre of any mapping is altered by whether a class seeds.

10.2 Regularity

Proposition 10.3 (Normal form is the range)**.** [C] *Refinement at the third position produces only the block patterns* (4) *and* $(2,2)$*, so any mapping the construction admits is regular by construction and the regularity of such a mapping carries no information [Sch26l]. The standard mapping realises also* $(3,1)$ *and* $(2,1,1)$ *and lies outside the range.*

10.3 Initiation and non-release

Proposition 10.4 (Two failure modes)**.** [C] *A codon may carry no structure in two ways, distinguished by whether the carrier is consumed: no structure consistent, the carrier surviving; or a structure formed and not released, the carrier being consumed [Sch26l].*

Remark 10.5 (Unchanged here)**.** [D] The account of initiation and of non-release is that of Article 57 and nothing in the present construction bears on it. The non-releasing codons are the purine halves of Proposition 6.8 that the refinement leaves without a structure, as there.

Scholium 10.6 (What the continuous path does not change)**.** It is worth stating plainly how little of Section 10 is new. The registry classes, the parity obstruction, the range of the construction and the two failure modes are properties of the carrier and of the seeding apparatus, and this paper alters neither. **What it alters is the complex on which the reading is performed**, and the consequences of that are confined to Section 5 through Section 9.
A reader comparing the two papers should therefore not look here for the difference. Section D says where it is.

11 Targets

Two targets registered in draft are discharged, both negatively, and are recorded at Section C rather than here. What remains is four.

Target 11.1 (The strand condition, grounded)**.** Independent evidence for Hypothesis 8.7: that a heteroatom is admitted where the tethered base lies on the strand carrying the coding base, and not where it lies across the duplex. This is the paper's one hypothesis about the world and the only statement in Section C not refuted by a recomputation.

Target 11.2 (The basic structure, deferred)**.** Whether the extent-three basic structure originates at a block other than the one it occupies, and is placed where it is by exchange. Scholium 8.18 declines to choose among the slots that would serve, for want of an argument the gate does not supply. **Such an argument may come from the companion paper**: the two sulfur structures are placed there by complementarity, and the aromatic pair is displaced in consequence. Whether that reorganisation also fixes the basic structure is a question for that paper and not this one.

Target 11.3 (Why the purine)**. Discharged in part.** The invariant asked for is Definition 8.4: every reading pair is a purine against a pyrimidine, so the condition says that the coding base at the second position is the purine of its pair, and Proposition 8.5 shows this to be as much a property of the construction as the strand is.
What remains is the mechanism. Definition 8.4 says which positions admit a heteroatom and not why the purine of a pair should admit one where the pyrimidine does not. That is Target 8.22.

Target 11.4 (Which complex)**.** A datum distinguishing the continuous path from the staged one: whether the nucleotides separate from the chrysene interleaving before residue formation. Target D.4 states this in full. The filing exhibits the product and does not give the order, and no computation in either paper bears on it.

Target 11.5 (The conditions beyond the structures)**. Run, and both conditions survive.** Over twenty-two published tables the strand condition covers one hundred and ten of one hundred and thirty-two nitrogen-bearing structures, missing one structure in every table and the same one; the side condition covers all one hundred and thirty-two.
What remains is the converse. Both conditions are tested here for necessity and neither for sufficiency across the wider tables, and Proposition 8.15 admits one structure carrying no nitrogen even in the mapping this construction outputs.

Scholium 11.6 (What is left)**.** Two of the four targets registered in draft have been run. Target 11.5 was the one most likely to damage the paper and it did not: both conditions survive twenty-two tables, the strand condition with one constant exception and the side condition with none. Target 11.3 is discharged as to the invariant and open as to the mechanism.
What remains cannot be reached by computation. Target 8.22 asks why the purine of a pair should admit a heteroatom; Target 11.1 asks for evidence that the strand decides it; Target 8.23 asks after the one structure that defies both; and Target 11.4 asks which of two complexes is physical and is answered by neither paper. **These four bound what this account can establish**, and three of them are questions about molecules rather than about the construction.

12 Conclusion

The filing gives two tethers. Article 57 uses one and reads the carrier against four coding bases under non-canonical pairing; this paper uses both and reads it under full Watson–Crick pairing, with no separation of the nucleotides from the interleaving at any point.

Three things follow and the third is the smallest.

The registry closes exactly. Two classes have a constant agreement sequence — the all-agree and the all-disagree extremes — and they are the two tether patterns. The eighteen that remain meet the eighteen slots with no spare, and at one slot the assignment is forced outright. Article 57 has three spare classes, no account of them, and no forced slot.

The heteroatom gate is made rather than inherited. The adenosine tether attaches through an oxygen at a position on the pairing edge, where an unmodified pair makes a weak third contact; the cytosine tether attaches in the major groove and disturbs nothing. Both tethers perturb their pairs, so what discriminates is not the perturbation but two invariants the canonical pairing makes available: which strand carries the tethered base, and which member of the pair codes. The first is the predecessor's gate derived; the second is stronger and holds across twenty-two published tables without exception. **Neither is a mechanism**, and their conjunction fails once in each direction.

The exit is determined by the pair, to the 2′-oxygen under one tether and the 3′-oxygen under the other. Article 57 has one exit and does not say why.

What the paper does not establish is stated throughout and is collected at Section 3. Exact closure leaves one hundred and ninety-two admissible assignments and does not force the division of the blocks; the gate admits seventeen structures of twenty and is necessary rather than determining; and the partition that Article 57 recovers is here assumed, so the coincidence that paper reports is unavailable.

Scholium 12.1 (What the two papers are to each other)**.** Not a succession. **They are two readings of one filing**, and the filing does not say which is physical. Article 57 uses one tether and obtains a recovery; this paper uses both and obtains a closure. Each has something the other cannot state, and Section D sets them side by side without ranking them because no measure ranks them.
Target 11.4 names the datum that would decide between them, and neither paper contains it.

A The structure series and its interpretation

A.1 Status, and what is imported

This appendix is the only place in the paper where a chemical species is named. Section 6 through Section 10 are stated on structures, and deleting this appendix costs the interpretation and no numbered result.

The series itself is not restated. The twenty structures, their retained vertices, their severed edges and the vertices removed entire are those of Article 57, and transfer by Corollary 5.3: the vessel geometry is the same under either tether, so the fragmentation is the same and the structures are the same objects.

A.2 The decoration record

The terminal type at each retained vertex and the heteroatoms inserted into edges of the retained set are imported from [Sch26k], where they are printed in full and where each row is checked against the reconstituted side-chain formula.

> **Remark A.1** (The proline field)**.** [C] That record carries a third field on the decoration — a set of closures from retained vertices to the backbone, empty for nineteen structures. It is required because proline's nitrogen is the backbone amine and the distinctive datum is that the retained set closes onto it, a bond running from a retained vertex to a vertex outside the retained set. **The present paper inherits the field and uses it in one place**: Proposition 8.15 counts side-chain heteroatoms, and proline's nitrogen is not one, which is why proline is not among the six.

A.3 What this paper adds to the interpretation

Two items, both consequences of the two tethers.

> **Remark A.2** (The exit)**.** [E] Under Proposition 5.7 the formed residue is transferred to the 2′-oxygen where the pair carries the adenosine tether and to the 3′-oxygen where it carries the cytosine. Article 57 has one exit and does not account for it. This remark enters no proof.

> **Remark A.3** (The ether)**.** [E] The adenosine tether attaches through an oxygen at C2, which lies on the pairing edge; the cytosine tether attaches at C5, which lies in the major groove and takes no part in the pairing contacts. Both perturb the pairs they sit on, which is why Hypothesis 8.7 turns on the strand rather than on the pairing. This remark enters no proof.

A.4 Deferred

Cysteine and methionine are named nowhere in this paper, here included. The structures exist in the series and are interpreted there; what is deferred is the argument about their joint formation, which requires a premise about the medium that this paper does not make.

B Combinatorics and verification

```
======================================================================
W1  The two tether classes, by invariant
======================================================================
  class 1   AAA UUU      agreement sequence ['00000']
  class 8   CCC GGG      agreement sequence ['11111']
  exactly 2 classes have a constant agreement sequence: [1, 8]
  these are the all-agree and all-disagree extremes, and they are the
  adenosine (AAA/UUU) and cytosine (CCC/GGG) tether patterns.

======================================================================
```

```
W2  Exact closure
======================================================================
  twenty classes  : 18 of 18 slots matched, deficiency 0, spare 2
  eighteen classes: 18 of 18 slots matched, deficiency 0, spare 0
  perfect matching with no spare: True
  -> eighteen slots, eighteen classes, the construction is exactly tight.

======================================================================
W2c  No codon is lost when the tether classes are consumed
======================================================================
  codons covered by the eighteen slots : 52
  not covered                          : 12
    AA pur    AAA AAG  -> refinement
    AG pur    AGA AGG  -> non-releasing
    CA pur    CAA CAG  -> refinement
    GA pur    GAA GAG  -> refinement
    UA pur    UAA UAG  -> non-releasing
    UU pur    UUA UUG  -> refinement
  the four tether codons:
    AAA  refinement at AA pur
    UUU  seeded slot UU pyr
    CCC  seeded slot CC all
    GGG  seeded slot GG all
  a class seeds a codon and propagation fills its slot, so a class that
  seeds nothing removes no codon from the table.

======================================================================
W3  The ether-defect gate
======================================================================
  Art.57  defective first register   covers 5 of 6, predicts 11 of 20, missed: Trp
  Art.70  ether defect at 1 or 2     covers 6 of 6, predicts 17 of 20, missed: none
  structures the Article 70 gate excludes: Ala, Gly, Pro
  none carries side-chain nitrogen (proline's is the backbone amine).
  BOTH GATES ARE NECESSARY AND NEITHER IS SUFFICIENT.

======================================================================
W2b  How much exact closure constrains
======================================================================
  assignments on the eighteen slots, twenty classes available :  3648
  the same with the two tether classes removed                 :   192
  reduction 19.0x -- 95% of the assignments are removed

  FORCED: slot UU pyr    -> class 11   (was [1, 11])
  the adenosine tether class contains UUU; removing it leaves exactly
  one class meeting the UU pyrimidine half.  Closure determines a slot.

======================================================================
W3b  The gates read per codon
======================================================================
  codons carrying a nitrogen-bearing structure: 15
  Art.57 defective first register  covers 14 of 15, admits 32 of 61
      missed: UGG(Trp)
  Art.70 ether defect at 1 or 2    covers 11 of 15, admits 45 of 61
```

```
      missed: CGA(Arg), CGC(Arg), CGG(Arg), CGU(Arg)
  PER STRUCTURE the comparison favours this paper, 6 of 6 against 5.
  PER CODON it REVERSES: Article 57 misses one codon, this paper four.
  The four are the CG block entire, carrying a structure that the AG
  block reaches defectively.

======================================================================
W3c  The gate against the mapping the construction OUTPUTS
======================================================================
  standard                     codons covered 11 of 15   structures with NO defective codon: none
  mitochondrial (the output)   codons covered 10 of 14   structures with NO defective codon: Arg

  THE CONSTRUCTION OUTPUTS THE MITOCHONDRIAL MAPPING, in which the AG
  purine half does not release.  Arginine is then at CG alone, where no
  codon carries a defect.  THE GATE FAILS FOR ARGININE OUTRIGHT THERE,
  per structure as well as per codon.  The six-of-six count holds only
  for the standard mapping, which the construction does not output.

  SINGLE EXCHANGES THAT WOULD RESCUE IT
  exchanging Arg to a fully defective slot whose occupant carries no
  nitrogen: 11 such slots
    UU pyr, UC all, UA pyr, UG pyr, CU all, AU pyr, AU pur, AC all, AG pyr, GU all, GA pyr
  the gate is rescued by any of them and forced by none.

======================================================================
W3d  Pair type against strand: which reading of the tether
======================================================================
  coding base A or U -> adenosine tether; C or G -> cytosine tether.
  coding base A or C -> the tethered base is on the NEAR strand.

  pair type: ether defect at 1 or 2        structures 5/6  codons 10/14  admits 44/60
      missed: CGA(Arg), CGC(Arg), CGG(Arg), CGU(Arg)
  strand: tethered base near at position 1 structures 5/6  codons 12/14  admits 30/60
      missed: UGA(Trp), UGG(Trp)

  THE STRAND READING IS STRICTLY BETTER: more codons covered and fewer
  admitted.  It is also Article 57's gate -- its defective first
  registers are coding base C or A, which is the near-strand condition.

======================================================================
W4  The unexplained regularity
======================================================================
  purine at the second position: covers 6 of 6, predicts 12 of 20
  tighter than either gate, and it does not follow from the tether rule.
  carries no nitrogen yet predicted: Asp, Cys, Glu, Gly, Ser, Tyr

======================================================================
W4b  The strand gate and the purine-second condition, wider tables
======================================================================
  across 22 published tables, 132 nitrogen-bearing structures in all:
    strand at position one : 110 of 132 covered, 22 missed
    purine at position two : 132 of 132 covered, 0 missed
  the structure the strand condition misses, every time: [('Trp', 22)]
```

```
  PURINE AT POSITION TWO IS AN INVARIANT OF THE CONSTRUCTION.  Every
  reading pair is purine against pyrimidine, so the condition says that
  THE CODING BASE AT POSITION TWO IS THE PURINE OF ITS PAIR -- a property
  of which member of the pair codes, as the strand condition is.
  The two are independent and together name the four bases:
     coding base A: tethered base near , coding base is the purine
     coding base C: tethered base near , coding base is the pyrimidine
     coding base G: tethered base far  , coding base is the purine
     coding base U: tethered base far  , coding base is the pyrimidine

  THE CONJUNCTION, against the mapping the construction outputs:
    admits  : Arg, Asn, Gln, His, Lys, Ser
    covers  : Arg, Asn, Gln, His, Lys
    missed  : Trp
    admitted carrying no nitrogen: Ser
  six structures admitted, five carrying nitrogen; the sixth carries none
  and the one missed is the same exception as before.

======================================================================
W5  The two exits
======================================================================
  pair at a reading position -> tether -> exit
    A.U / U.A    adenosine at C2      2'-OH
    C.G / G.C    cytosine at C5       3'-OH
  the exit is determined by the pair type, hence by the partition
  {A,U} | {C,G}, which Article 57 recovered and this paper assumes.

======================================================================
W6  Does exact closure force the slot set?
======================================================================
  sixteen blocks and eighteen slots force exactly two blocks to split.
  Holding the split pair at {UG, AU} and varying which of the remaining
  fourteen are whole and which carry one half:
    slot sets of this shape                    192192
    admitting an assignment, twenty classes    169240  (88.1%)
    admitting an assignment, eighteen classes   99588  (51.8%)
  the slot set is NOT unique.  Exact closure constrains the ASSIGNMENT
  (3648 -> 192) and barely constrains the SLOT SET (88%% -> 52%%).
```

C Ledger, retractions, falsification

C.1 Corrections made during drafting

Two, both found by computing a claim the draft had stated.

withdrawn	replaced by
That exact closure might determine the assignment, registered as a target with the note that a positive answer would discharge the selection problem of Article 57	Theorem 9.1: one hundred and ninety-two assignments, not one. The problem is narrowed nineteenfold and survives
That the eighteen-slot set might be the unique set of its size admitting a perfect matching, registered as a target with the note that a positive answer would force the slot structure	Proposition 9.10: more than half the slot sets of the right shape close exactly. The slot structure is chosen, not forced; the target is withdrawn at Remark 9.12

Scholium C.1. Both corrections went against the draft, and both were found by running a computation the draft had already named as worth running. **Neither was found by reading the draft**, and the second in particular was invisible to inspection: the slot set is one of ninety-nine thousand that close, and nothing about its appearance indicates that.
The consequence for Section 6 is that its headline is narrower than it was drafted: exact closure establishes the absence of spare classes and one forced slot, and explains neither the assignment nor the division of the blocks. Section 3(xiii) carries the restriction and the abstract must not relax it.

withdrawn	replaced by
That the heteroatom gate covers every structure carrying side-chain nitrogen, six of six with no exception	Proposition 8.15: that count is for the *standard* mapping. Against the mapping the construction outputs it is five of six, and the sixth has no defective codon at all. The earlier statement tested the hypothesis against a mapping the construction does not produce

Scholium C.2. This correction is of a different kind from the two above. Those were numbers that came out otherwise than the draft expected. This one is a **test run against the wrong object**: the gate was checked against the standard mapping while the construction outputs the mitochondrial one, and the difference is exactly where the gate fails.
It was found while preparing Target 11.5, which proposed to test the gate against the *wider* tables and had not yet tested it against the paper's own.

withdrawn	replaced by
A gate turning on whether the tether *defects the pair* it sits on	Hypothesis 8.7, turning on which *strand* carries the tethered base. Both tethers perturb their pairs (Remark 8.2), so the pair reading does not discriminate; the strand reading covers two more nitrogen-bearing codons and admits fourteen fewer in all (Corollary 8.13)

Scholium C.3. This is the fourth correction and the one that changes the paper's claim. The draft offered a gate *competing* with Article 57's and better than it. What survives is a gate *identical* to Article 57's, derived from a construction in which no pair is defective.
That is a smaller claim and a more useful one. A second gate would have left the corpus with two; a derivation leaves it with one and an account of where it comes from.

C.2 Falsification register

statement	what would refute it
Proposition 6.2	a third class with constant agreement sequence, or a recomputation disagreeing with Section B
Theorem 6.5	a maximum matching of the eighteen classes onto the eighteen slots of size less than eighteen
Theorem 9.1	a recount
Proposition 9.4	a second class meeting the `UU` pyrimidine half after the tether classes are removed
Hypothesis 8.7	evidence that a heteroatom is admitted where the tethered base lies across the duplex, or withheld where it lies on the coding strand
Proposition 8.15	a structure carrying side-chain nitrogen with no ether defect at either reading position
Proposition 8.12	a structure carrying side-chain nitrogen with a pyrimidine at the second position
Corollary 5.3	a tether leaving the chrysene at a position other than C6

Remark C.4 (The one that is not finite)**.** [A] Every row above is refuted by a recomputation except Hypothesis 8.7, which is refuted by evidence about two molecules. That asymmetry is the shape of this paper: one hypothesis about the world, and the rest finite.

D Concordance with Article 57

D.1 Scope

The two papers take the same carrier, the same vessel, the same entry point and the same fragmentation, and differ in the complex on which those are stated. This appendix sets them side by side. **It does not rank them**, and Scholium D.3 says why not.

Four statements in the body point here: Scholium 5.9 on the partition, Scholium 8.16 on the gate, Scholium 3.2 on the two places this paper is weaker, and Scholium 5.2 on the choice of tether.

D.2 What is common

Imported here and not reproved, identical in both: the cluster and its frame group; the twenty orbits and the capacity ceiling; the derivation of the triplet; the vessel graph, its symmetry and its marking; the retention classification and its single exception; the fibration, with eleven values and five non-trivial fibres; entry at C5; the two-stage account of backbone assembly and excision; the slot-set theorem and the two kinds of exchange; and the treatment of initiation and of non-release.

Nothing in the list above is at issue between the two papers. The comparison below concerns the complex and what follows from it.

D.3 What differs

	Article 57	this paper
complex	adenosine tether against four coding bases, non-canonical pairing	two tethers, full Watson–Crick pairing
tethers of the filing used	one	both
path	integrated product formed, then the residue	continuous; no separation
registers	$A{\cdot}U$, $A{\cdot}C$, $A{\cdot}A$, $A{\cdot}G$	$A{\cdot}U$, $U{\cdot}A$, $C{\cdot}G$, $G{\cdot}C$
vary by	defect	contacts, strand, groove
classes available	twenty	eighteen
unused on these slots	two	**none**
assignments	3648	192
slots forced	none	**one**
$\{A,U\} \mid \{C,G\}$	**recovered** from block structure	assumed, as the tether rule
heteroatom gate	defective first register	ether defect at position one or two
structures covered, standard mapping	five of six	**six of six**
structures covered, mapping output	**five of six**	five of six, the sixth with *no* defective codon
codons covered, standard mapping	**fourteen of fifteen**	eleven of fifteen
codons missed	`UGG`	`CGN`
selects	**eleven** of twenty structures, thirty-two of sixty-one codons	seventeen, and forty-five
exits	one, unaccounted	two, determined by the pair
purine at position two	unexplained	unexplained

Remark D.1 (On the spare count)**.** [A] Article 57 reports three spare classes. The figure here is two, because that paper counts demands and this one counts slots, and one structure is seeded at two slots. The two counts agree; the editorial ruling on which object is matched is at [Sch26k].

D.4 What each buys

Scholium D.2 (Four exchanges, stated as exchanges)**. Closure for recovery.** This paper's registry closes exactly and forces a slot; its predecessor's does neither. Against that, its predecessor recovers the partition that this paper assumes, and the recovery is the strongest evidential item either paper has. The closure is a result about the construction; the recovery is evidence that the construction is right. **They are not commensurable and neither substitutes for the other.**
Coverage for discrimination, and the direction depends on the reading. Per structure the gate here covers all six and its predecessor five. Per codon the order reverses: eleven of fifteen against fourteen, and the four missed are one block entire where the one missed is a single codon. **The per-codon reading is the mechanistic one** (Scholium 8.16), so on the reading that matters this paper's gate is the weaker, and it is the less discriminating besides. **This comparison favours Article 57 and is recorded as such.**
A made defect for an inherited one. Article 57's defects are properties of pairs that pair badly, and the carrier has them before the construction acts. The defect here is created by the tether, at a pair that pairs correctly. The second is the more specific claim and therefore the more exposed: it stands or falls with Proposition 8.1 and Remark 8.2.
Two exits for one. This paper determines the exit from the pair and its predecessor does not account for its single exit. This is the one comparison with no cost on either side, and it is the smallest of the four.

D.5 Why no ranking is offered

Scholium D.3. A ranking would require a measure, and the four exchanges of Scholium D.2 do not share one. Two of them trade a result for evidence, one trades coverage for selectivity, and one is a gain with no loss. Summing them is not available. What *is* available is the observation that the two papers are not successive drafts of one account. **They are two readings of one filing**, which gives two tethers and does not say that one is used alone. Article 57 uses one and obtains a recovery; this paper uses both and obtains a closure. A reader is entitled to hold that one complex is the physical one and the other is not, and nothing in either paper settles that.
Target D.4 states what would.

Target D.4. A datum distinguishing the two complexes: evidence that the nucleotides do or do not separate from the chrysene interleaving before residue formation. On the continuous reading they do not, and the two tethers are simultaneous; on the reading of Article 57 the integrated product is formed first. **The filing exhibits the product and does not settle the order**, and no computation in either paper bears on it.

E The corpus, and where this paper sits in it

A reader arriving at this paper without the volume needs three things: what the registry is, what has been established about it, and which of those results this paper uses rather than reproves. This appendix supplies them. It argues nothing.

E.1 Before the formalism

The hypothesis that a residue arises as a derivative of a fused four-ring aromatic, and several candidate codon-to-residue mappings, are earlier than the corpus [Sch20b, Sch20a]. That work used a different four-ring skeleton, did not fix the substitution pattern, and treated the three-vessel arrangement as a filter rather than as the site at which a residue forms. The substitution pattern was fixed subsequently, the $3, 6, 9, 12$-substituted chrysene family being specified as the encoding material in [Sch25a]; the adenosine tether, the integrated product and the anchored coding strand are in [Sch25b], and the cytosine tether of this paper is at Figure 6 of the first. A survey of the first volume is [Sch26g].

E.2 The registry

The object underneath the whole corpus is a stack of six substituted chrysene units, each set in one of two orientations. The orientation pattern is the *registry*. Three results fix its size and its reading length.

The classes.
The frame group — generated by reversing the stack and by exchanging the two orientations at every site — acts on the sixty-four patterns with **twenty** orbits, eight of size two and twelve of size four [Sch26m]. The orbits are the *registry classes*.

The base-four structure.
The registry carries a base-four encoding, and the stack is shown to admit the sequence algebra that makes a letter assignment possible [Sch26j].

The cardinal and the length.
A product attributable to the assembly takes at most $2^{2N-2} + 2^{N-1}$ values, which is **twenty** at $N = 3$; and the reading length of **three** follows from the carrier rather than from any argument about alphabets [Sch26n]. The same paper supplies the production operator and the parity obstruction.

Remark E.1 (What the registry is not)**.** [A] A registry class is not a codon block. The two partitions of the sixty-four words are *transverse*, meeting in at most one word, so a structure attached to a class is not thereby attached to a codon [Sch26e, Sch26f]. Everything in the corpus about seeding exists to cross that gap, and Section 6 and Section 9 of this paper are statements about the crossing.

E.3 From registry to code

The letter assignment.
Which of the admissible assignments carries the registry partition to the Watson–Crick partition $\{A, U\} \mid \{C, G\}$, and the partition criterion that selects it [Sch26d]. **This paper assumes that partition as the tether rule**; Scholium 5.9 records the cost.

Seeding.
A seed places a class's structure at one codon, propagation fills the block, and a refinement divides a block at the third base. Seventeen seeds suffice with three classes to spare, and eight hundred and forty seed maps achieve coverage with none distinguished [Sch26e]. The sufficiency framing, and the uniqueness of propagation as the block-measurable extension, are [Sch26f].

Obstructions.
Parity excludes the standard mapping from the class-functional assignments and is silent on the mitochondrial one; six candidates for a finer obstruction have been tested and none survives [Sch26n, Sch26c].

The chain polarity.
The tether word, the residual frame group, and the documentary arrow that carries the residual count from thirty-six to sixty-four [Sch26b].

The cage.
Backbone assembly, the constructive witness, and the stereochemical selection that fixes the configuration at the α-carbon [Sch26a]. This paper imports the backbone and states nothing about configuration.

The compartment.
The two observed mappings as two settings of a conditional refinement, with a threshold pair on an effective vessel volume [Sch26h, Sch26i]. The mappings themselves are [Nat24], Table 1 and Table 2.

E.4 The immediate predecessor

Article 57 [Sch26l] states the structure space, the retention classification and its exception, the fibration, the slot-set theorem and the two kinds of exchange. **This paper imports all of them and reproves none.** What it changes is the complex on which they are stated, and Section D is the comparison.

E.5 What this paper adds

Three items, and Section 1 gives them with their qualifications.

1. The two tether classes, characterised by an invariant of the registry, and the exact closure that follows (Section 6).
2. A heteroatom gate made by the tether rather than inherited from a defective pair (Section 8).
3. An exit determined by the reading pair (Proposition 5.7).

Scholium E.2 (The one thing a new reader should carry away)**.** The corpus establishes a cardinal — twenty — from a carrier that contains no nucleobase, and a reading length of three from the same carrier. Everything after that is an attempt to say *which* twenty and *where*, and no paper in the volume claims to have settled both. This one settles neither and narrows one of them.

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