

Chain Polarity of the Adenine Tether

Residual Frame Group, Documentary Realization of Sixty-Four,
and the Patent Correspondence

Charles D. Schaper, Ph.D.

Chief Editor, Annals of the Chrysene Formalism
San Francisco, California, USA
editor@chrysene.com

Abstract

The pattern of the adenine tether is the word *AAA*. Reversal fixes that word; complementation sends it to *UUU*. 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.

US 12,473,247 B2 exhibits a (6,12)-disubstituted chrysene remnant that remains on adenine at the 6-position connection, anchors a phospholipid bilayer, and from whose poly-A tail a coding strand departs. That filing supplies an arrow the word *AAA* does not represent. Under the identification of that arrow with *rev*, the residual group is trivial and the pairs (class, relative frame) number sixty-four, identifiable with the word space $W = \Sigma^3$. If the identification is refused, two lemmas stand and Target 9.7 of the predecessor remains open.

No axiom is added. The standard code is not used. The Identification Hypothesis is not used. Chrysene is the intermediary of the documentary construction — one molecule as adenine attachment and as phospholipid head — and that necessity is restricted to the construction.

Keywords: Chrysene Formalism; adenine tether; chain polarity; residual frame group; documentary realization; US 12,473,247 B2.

1 Introduction

The pattern of the adenine tether is the word *AAA*. Reversal fixes that word and complementation does not [6, Prop. 4.9]. The residual frame group after the pattern is observed is therefore $\langle \text{rev} \rangle$, and the residual count is thirty-six [6, Cor. 4.10]. Thirty-six is not sixty-four. Without a datum that kills *rev*, a function on residual states is not a function on codon words, and the constructions of [6] §§5–7 and of [7] have no object that may be identified with a published translation table.

That gap is Target 9.7 of [6]: the poly-A chain carries a chemical polarity the formalism does not represent, and the claim is that this polarity fixes the reading direction. The present paper asks whether a documentary source supplies the missing arrow, and whether that arrow may be named *rev*.

The source is US 12,473,247 B2 [8]. It exhibits a (6,12)-disubstituted chrysene catalyst that remains on adenine after A–U / A–T separation, at the 6-position connection; a remnant that forms or anchors a phospholipid bilayer; and a coding strand that departs from the anchored poly-A

tail (Figs. 15, 20, 21). Those readings are collected as a documentary hypothesis H_{doc} . An identification hypothesis H_{id} then says that the bilayer-to-coding arrow is the generator *rev*.

Under $H_{\text{teth}}(\text{i})(\text{ii})(\text{iv})$, H_{doc} and H_{id} , the residual group is trivial and the pairs (class, relative frame) number sixty-four. That set may be identified with the word space $W = \Sigma^3$. If H_{id} is refused, the paper stops at two lemmas: clause (iv) realized, an arrow exhibited, Target 9.7 still open. Both outcomes are allowed.

The paper does not add an axiom. It does not use the standard code. It does not use Φ . It does not construct a seed, a demand graph, a refinement, or an audit. It does not run the dual cipher. It does not identify a membrane-bound tail with an initiator. Chrysene is the intermediary of the documentary construction — the one molecule that is both the adenine attachment and the phospholipid head — and that necessity is restricted to the construction.

Section 2 freezes the vocabulary, the four senses of *domain*, the patent citation rule, and the register. Section 3 refuses ten entailments that would make a locant, a patent

use, or a residual count into more than they are. Section 4 recovers the thirty-six count from the word alone. Section 5 reads the filing. Section 6 proves the two lemmas. Section 7 is the realization theorem and the allowed stopping point. Section 8 is a dictionary of names and is not a second proof of sixty-four. Section 9 records what remains open.

The object is a residual count. The count is thirty-six from the word, and sixty-four from the word plus a named identification of a documentary arrow.

2 Conventions, Residual Groups, and the Register

This section is definitional. It fixes the logical vocabulary, the letter assignment, the residual-group table imported from [6], the sense of the word *domain*, the documentary citation rule, and the two hypotheses this paper adds. No lemma about polarity, no realization of sixty-four, and no patent correspondence is proved here. Later sections may cite the definitions below and may not alter them.

2.1 Logical status

Definition 2.1 (Status labels). Imported from [2] and used as in [6, 7]:

- [A] axiomatic, or a finite enumeration labelled as such;
- [D] derived realization theorem;
- [T] target;
- [E] documentary or empirical instantiation claim.

An [E] claim is confined to a remark and enters no proof. A statement $P_{\mathfrak{R}}$ is a derived realization theorem when

$$\mathcal{A} \cup H_{\mathfrak{R}} \models P_{\mathfrak{R}}$$

for an explicitly named hypothesis family $H_{\mathfrak{R}}$, where $\mathcal{A} = \{A_1, \dots, A_{12}\}$ is the axiom set of [2]. If $H_{\mathfrak{R}}$ is used, one has $\mathcal{A} \not\models P_{\mathfrak{R}}$ unless a separate argument shows otherwise. The governing restraint of [1] remains in force.

Remark 2.2 (No new axiom). [A] This paper introduces no axiom. Every structure below is imported from [2, 3, 4, 6, 7], is definitional within $\mathcal{A}$, or is a realization hypothesis registered at Section 2.6. In particular $A_3, A_4, A_5, A_7, A_9, A_{10}$ and A_{11} are unused.

Remark 2.3 (What is not used). The standard genetic code is not used. The Identification Hypothesis Φ of [1] is not used. No seed, demand graph, refinement,

or audit is constructed. The dual cipher of A_8 is not run. Those exclusions are the object of the paper: Target 9.7 of [6] only.

2.2 The assignment and the frame group

Definition 2.4 (Letter assignment). Throughout,

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

so that the registry partition is carried to the Watson–Crick partition $\{A, U\} \mid \{C, G\}$. Write $\Sigma := \{A, C, G, U\}$ and $W := \Sigma^3$. Thus $|W| = 64$. Relabelling U as T does not change the partition; the classification is independent of that labelling [5, Prop. 4.11].

Definition 2.5 (Frame group). Write $\text{Fr} = \langle \text{flip}, \text{rev} \rangle$ for the frame group of [4, Def. 2.13], acting on W by

$$\text{flip}(XYZ) = \rho(X)\rho(Y)\rho(Z), \quad (1)$$

$$\text{rev}(XYZ) = \tau(Z)\tau(Y)\tau(X), \quad (2)$$

where ρ is letterwise Watson–Crick complementation ($A \leftrightarrow U, C \leftrightarrow G$) and τ fixes the aligned letters A, U and swaps C, G . The twenty orbits of Fr on W are the frame classes; write X for the set of orbits and $T : W \rightarrow X$ for the orbit map [4, Lem. 4.5, Cor. 3.7].

Remark 2.6 (Two generators, two data). [A] By [3, Prop. 6.7], flip changes the projection reference and rev changes the reading direction. The two generators are not interchangeable. A datum that kills one leaves the other as a residual symmetry.

2.3 Residual groups and the four counts

Definition 2.7 (Residual group). Let $K \leq \text{Fr}$ be the subgroup of frame operations that remain symmetries of a presented tethered complex. The *residual group* is K . The *residual state space* is the set of K -orbits on W . Its cardinality is the residual count.

Proposition 2.8 (Four residual counts). [A] Imported from [6, Cor. 4.10].

What is fixed	Residual group	States
nothing	Fr	20
projection reference only	$\langle \text{rev} \rangle$	36
reading direction only	$\langle \text{flip} \rangle$	32
both	trivial	64

Remark 2.9 (The palindrome). [A] As a word the tether is AAA. Since τ fixes A , $\text{rev}(AAA) = AAA$. Since $\rho(A) = U$, $\text{flip}(AAA) = UUU \neq AAA$. The pattern therefore fixes the projection reference and cannot fix the reading direction [6, Prop. 4.9]. Pattern alone lands on the second row of Proposition 2.8: thirty-six states.

2.4 Domain

Definition 2.10 (Four uses of domain). In this paper the word *domain* has four referents, and they are not interchangeable.

- (i) The *domain of excision* is X . Excision $\Xi : X \rightarrow R$ is already a function on twenty classes without polarity. Capacity lives here [5, Thm. 5.4].
- (ii) The *domain of a codon table* is W . A published translation table is a function $W \rightarrow R \cup \{*\}$.
- (iii) The *residual domain* after a named subgroup K is the set of K -orbits on W . After the tether pattern only, this is a thirty-six-element set.
- (iv) The *sample space of the experiment* of [7] is declared there to be W , conditionally on Target 9.7 of [6].

To *identify the domain with W* is to exhibit a bijection between presented tethered complexes and elements of W , so that (ii) and (iv) coincide and the residual domain of (iii) is no longer the object of the construction.

Remark 2.11 (What sixty-four is not). Sixty-four is not twenty residues counted three times. It is the cardinality of W . Polarity does not enlarge the image of Ξ . It decides whether an assignment of residues to presented complexes may be read as a function on words.

2.5 Documentary citation

Definition 2.12 (Patent citation rule). The documentary source is US 12,473,247 B2 [8]. Citations are to a figure or an example, never to “the invention.” A sentence that quotes the filing is labelled [E] and does not enter a proof. The locant used throughout is the attachment of the (6,12)-disubstituted chrysene catalyst to RNA-adenine at the 6-*position* of that chrysene, as described in the filing for the remnant that remains after A–U / A–T strand separation. Where Example 17 of the filing names a phospholipid–adenine contact at carbon-2 of adenine, that sentence is a second locant of the same remnant and is not a replacement for the 6-position attachment.

Remark 2.13 (Why not C12–C2). An earlier informal description used C12 of chrysene to C2 of adenine. That pair is not the locant of this paper. Using both would present two attachments as one. The 6-position connection is the filing’s description of the catalyst remnant on adenine; C2 appears in Example 17 as a membrane-contact carbon. They may coexist as two facts about one remnant. They are not interchangeable names for clause (iii).

2.6 The register

Hypothesis 2.14 (H_{teth} , imported). [6, Hyp. 2.9], four clauses.

- (i) The tether is a constant poly-A strand, one adenine–chrysene unit per coding unit.
- (ii) Its register with the coding strand is non-Watson–Crick, so that the tether is constant irrespective of the codon.
- (iii) The tether carries a chemical chain polarity.
- (iv) It is attached at the same ring and in the same orientation at every unit.

Clauses (i), (ii) and (iv) are used. Clause (iii) is Target 9.7 and is the object of the lemmas and the realization theorem, once those sections exist. It is not assumed here.

Hypothesis 2.15 (H_{doc}). The filing US 12,473,247 B2 exhibits a poly-A run whose adenines remain conjugated, after RNA synthesis, to (6,12)-disubstituted chrysene remnants; those remnants form or anchor a phospholipid bilayer; the coding strand departs from that tail. Instantiations of this hypothesis by figure are [E]. The hypothesis as a bundle is the documentary

family used in realization theorems and is named when so used.

Hypothesis 2.16 (H_{id}). The bilayer-to-coding arrow of the documentary tail is the reading direction of [3, Prop. 6.7]; it is the generator rev . That proposition decomposes the frame action into projection reference (flip) and reading direction (rev). This identification uses the second half of that decomposition. It is not a clause of $\mathcal{A}$ and is not a sentence of the filing.

Remark 2.17 (Which clause each hypothesis touches). H_{doc} supplies extra structure beyond the word AAA , and supplies constancy of attachment along a run. The first is a candidate witness for $H_{teth}(iii)$; the second is a witness for $H_{teth}(iv)$. H_{id} is the step that names the extra structure as rev . Without H_{id} , clause (iii) is not discharged. With it, the residual group in Proposition 2.8 is the last row, and only then.

Remark 2.18 (Production hypotheses are not this paper). $H_{prod}(0)$ and $(0')$ of [5, §2.5] are not used. A membrane-bound tail is not an initiator. Identifying the two would restore a relation [5] keeps apart.

Target 2.19 (Target 9.7, restated). [6, Target 9.7]: establish that the poly-A chain's polarity fixes the reading direction. By Proposition 2.8 this decides between sixty-four states and thirty-six. The present paper asks whether $H_{doc} \cup H_{id}$ is a realization of that target, and records the alternative that only H_{doc} is granted.

3 Non-Implications

The statements below are recorded before any figure of US 12,473,247 B2 is read. Each is a refusal: a premise the paper will use, or a sentence a reader may be tempted to write, does not entail the conclusion named. A later section that writes the refused entailment has left this list. The list is the analogue, for Target 9.7, of [7, §3].

Proposition 3.1 (Ten refusals). *[A] None of the following implications is a theorem of $\mathcal{A}$, of $H_{teth}(i)(ii)(iv)$, or of this section.*

- (i) $rev(AAA) = AAA$ does not entail that a poly-A polymer has no polarity.

- (ii) A patent application that stabilizes RNA on a phospholipid does not entail a codon table.
- (iii) Attachment of the (6,12)-chrysene remnant at the 6-position of chrysene to adenine does not entail that rev is killed.
- (iv) A phospholipid-adenine contact at carbon-2 of adenine (Example 17 of US 12,473,247 B2) does not entail that rev is killed.
- (v) Absence of an a priori length bound on the poly-A run does not entail a global frame.
- (vi) Residual count sixty-four does not entail Φ .
- (vii) Residual count sixty-four does not entail the mitochondrial equality of [6, Thm. 5.8].
- (viii) A membrane-bound tail does not entail an initiator, and does not discharge $H_{prod}(0')$.
- (ix) Chrysene as intermediary of the filing does not entail that chrysene is the unique possible intermediary in nature.
- (x) A correspondence of names between the filing and $\mathcal{A}$ does not entail that the filing proves the seeded assignment of [6].

Proof. Each clause is a mismatch of objects, recorded once.

- (i). Proposition 4.2 is a computation in Σ^3 . Remark 4.3 separates the word from the polymer. End-data on a polymer are extra structure. Their absence from the word is not their absence from the strand.
- (ii). A codon table is a function on W (Definition 2.10(ii)). A stabilization protocol is a use of a polymer. The two are not the same type. Theorem 4.6 already shows that a tether, used as a word, does not supply such a function.
- (iii). The 6-position locant is a fact about attachment at a unit. Clause $H_{teth}(iv)$ is that fact, made constant along the run. Remark 4.7 records that constancy of attachment is not an arrow. An arrow is what kills rev .
- (iv). Carbon-2 of adenine, in Example 17, is a second locant of the same remnant (Definition 2.12). Two locants are still attachment. The argument is the argument of (iii).
- (v). Global frame is [6, Rem. 4.13]: one strand, one section, one table. Arbitrary length supplies many units. It does not by itself force those units to share a frame. Without the section argument, per-cluster arrows remain possible.
- (vi). Φ is the identification of excised residues with biological amino acids. Residual count is a cardinality of

states of the carrier. The image of Ξ is not enlarged by killing rev (Remark 2.11).

(vii). The mitochondrial equality is a matching theorem under four hypotheses of [6], none of which is polarity. Sixty-four is the domain of that theorem, not its conclusion. Corollary 4.9 says only that without polarity the theorem has no object of the right type.

(viii). The initiator is [3, Def. 9.1]. A membrane anchor is an end of a tail. $H_{\text{prod}}(0')$ of [5, §2.5] says the production pathway does not involve the initiator. Identifying tail with initiator would identify two objects that paper keeps apart (Remark 2.18).

(ix). An intermediary of a named construction is necessary inside that construction. Uniqueness among all possible polycycles is a different claim and is not a sentence of $\mathcal{A}$.

(x). A dictionary of names is $[E]$ as a reading. The seeded assignment is [6, Thm. 5.8], under hypotheses this paper does not use (Remark 2.3). A dictionary does not discharge those hypotheses. $\square$

Remark 3.2 (How the list is used). Lemmas that read the filing may instantiate $H_{\text{teth}}(\text{iv})$ and may exhibit an arrow. They may not write (iii), (iv), or (ii) as entailments. The realization theorem may conclude sixty-four only under H_{id} , and then still may not write (vi) or (vii). The correspondence section may print the dictionary and then must stop: (ix) and (x).

Remark 3.3 (What the list is not). The list is not a proof that polarity cannot be realized. It is a proof that several tempting routes do not realize it. Target 9.7 remains the question of Sections 6–7.

4 The Thirty-Six Count

The pattern of the tether is the word AAA . This section records what that word fixes and what it cannot fix. The four residual counts are Proposition 2.8. The work here is to see that the pattern alone occupies the second row of that table, not the fourth. No figure of US 12,473,247 B2 is used. H_{doc} and H_{id} are not used. Clause (iii) of H_{teth} is not assumed.

4.1 The tether as a word

Definition 4.1 (Tether word). Under $H_{\text{teth}}(\text{i})$ the tether is a constant poly-A strand. As an element of W that strand is the word

$$t := AAA. \quad (3)$$

The three letters are the three coding units' tether bases, not a codon of the coding strand.

Proposition 4.2 (The tether word is palindromic). $[A] \text{rev}(t) = t$ and $\text{flip}(t) \neq t$. Explicitly

$$\text{rev}(AAA) = AAA, \quad \text{flip}(AAA) = UUU. \quad (4)$$

Proof. By Definition 2.5, $\text{rev}(XYZ) = \tau(Z)\tau(Y)\tau(X)$. The assignment of Definition 2.4 makes A aligned, so $\tau(A) = A$. Hence $\text{rev}(AAA) = AAA$. The same definition gives $\rho(A) = U$, so $\text{flip}(AAA) = UUU$. This is [6, Prop. 4.9]. $\square$

Remark 4.3 (Palindrome of the word, not of the polymer). Proposition 4.2 is a computation in Σ^3 . It does not say that a physical poly-A strand is identical under end-for-end reversal. A polymer may carry end-data the word does not. That possibility is the content of $H_{\text{teth}}(\text{iii})$ and is not used in this section.

4.2 What the pattern fixes

Proposition 4.4 (Pattern kills flip). $[A]$ A presented complex that displays the tether word AAA , rather than UUU , is not symmetric under flip. The residual group after the pattern is observed is a subgroup of $\langle \text{rev} \rangle$.

Proof. If flip remained a symmetry of the presented complex, the displayed tether word would equal its image under flip. Proposition 4.2 gives $\text{flip}(t) = UUU \neq t$. Hence flip is not residual. The only subgroups of Fr not containing flip are $\{1\}$ and $\langle \text{rev} \rangle$. $\square$

Proposition 4.5 (Pattern does not kill rev). $[A]$ The displayed tether word is invariant under rev. Observing AAA therefore does not distinguish a presented complex from its image under rev. The residual group after the pattern is observed still contains rev.

Proof. Proposition 4.2: $\text{rev}(t) = t$. A symmetry that fixes the displayed word is not killed by displaying the word. $\square$

Theorem 4.6 (Pattern alone leaves thirty-six). $[A]$ Under $H_{\text{teth}}(\text{i})$ and (ii), and using only the tether as a word, the residual group is $\langle \text{rev} \rangle$. The residual count is thirty-six.

Proof. Clause (i) supplies the constant word $t = AAA$. Clause (ii) makes that word independent of the codon, so the same displayed tether is available at every coding unit and does not itself vary with $w \in W$. Propositions 4.4 and 4.5 place the residual group exactly at $\langle \text{rev} \rangle$. Proposition 2.8, second row, gives thirty-six states. This is the last sentence of [6, Cor. 4.10]. $\square$

Remark 4.7 (Clause (iv) does not change the row). $H_{\text{teth}}(\text{iv})$ says the attachment ring and orientation are the same at every unit. Constancy of attachment is not an arrow along the chain. It does not distinguish w from $\text{rev}(w)$. Used with the pattern, it still leaves $\langle \text{rev} \rangle$.

4.3 What thirty-six forbids

Proposition 4.8 (No identification with W). *[A] If the residual group is $\langle \text{rev} \rangle$, there is no bijection between residual states and elements of W . In the vocabulary of Definition 2.10, the residual domain (iii) is not the domain of a codon table (ii).*

Proof. rev acts nontrivially on W : for example $\text{rev}(AAC) = \tau(C)\tau(A)\tau(A) = GAA \neq AAC$. Orbits of $\langle \text{rev} \rangle$ are therefore of size one or two, and the number of orbits is thirty-six, not sixty-four. A function on the residual domain pulls back to a function on W that is constant on each pair $\{w, \text{rev}(w)\}$. That pullback is not an arbitrary map $W \rightarrow R \cup \{*\}$. $\square$

Corollary 4.9 (Target 9.7 is load-bearing for the table). *[A] Without a datum that kills rev , the construction of [6] §§5–7 and of [7] has no object that may be identified with a sixty-four-codon table. This is [6, Rem. 4.11].*

Remark 4.10 (Capacity is unaffected). The domain of excision remains X , of cardinality twenty, whether or not rev is residual. Theorem 4.6 does not touch [5, Thm. 5.4].

4.4 What this section has not done

Remark 4.11 (Where the section stops). The pattern occupies the second row of Proposition 2.8. The fourth row requires a datum that kills rev . That datum is not the word AAA , is not clause (iv), and is not imported from $\mathcal{A}$. Sections after the non-implications ask whether H_{doc} supplies the datum and whether

H_{id} may name it rev . This section does not ask those questions.

5 Documentary Register

This section reads US 12,473,247 B2 [8] under the citation rule of Definition 2.12. Every instantiation is $[E]$ and enters no proof. The section does not kill rev , does not name H_{id} , and does not conclude sixty-four. It supplies the clauses of H_{doc} as a bundle of figure readings, to be used by the lemmas of the next section.

5.1 How the filing is read

Remark 5.1 (Reading, not proving). A sentence of the form “Figure n exhibits P ” is a reading of a drawing and its accompanying text. It is not a chemical verification, not a reproduction of a synthesis, and not a theorem of $\mathcal{A}$. If two passages of the filing appear to name different locants, both are recorded (Definition 2.12); they are not collapsed.

Remark 5.2 (What is ignored). Pharmaceutical claims, yields, NMR assignments, and intended cellular therapies are ignored except where they fix a locant or an end of a strand. The “first instruction set” language of the filing is recorded only as a name for the strand that leaves the anchored tail. It is not identified with the initiator of [3, Def. 9.1] (Proposition 3.1(viii)).

5.2 Stack and attachment

Remark 5.3 (SCH heterodimer). $[E]$ Figures 4(b)–(c) of US 12,473,247 B2 exhibit a heterodimer of (6,12)-disubstituted chrysene (the filing’s catalyst) with (3,6,9,12)-tetrasubstituted chrysene (the filing’s substrate), coupled at the (6,12) positions, and a stack of such heterodimers. The stack is the documentary carrier of both a nucleic-acid product and a remnant product.

Remark 5.4 (6-position remnant on adenine). $[E]$ The filing states that, for A–U and A–T pairings, the catalyst remains attached to adenine after strand separation, and that the connection is at the 6-position of the (6,12)-disubstituted chrysene to the carbon of RNA-adenine that bears no sidechain. Figures 15(a) and 20(a)–(e) exhibit that remnant conjugated to adenine. Figure 20(f) exhibits the remnant Q on adenine

from an A–U pair. For C–G the filing states separation at the (6,12) sites. The constant poly-A tether of $H_{\text{teth}}(\text{i})$ is read from the A-remaining case, not from the C–G-separating case.

Remark 5.5 (Second locant). [E] Example 17 of US 12,473,247 B2 names a binding of the phospholipid structure to the adenine nucleobase at carbon-2. That sentence is a second locant of the remnant already described in Remark 5.4. It is not substituted for the 6-position attachment (Definition 2.12, Proposition 3.1(iv)).

5.3 Bilayer and arrow

Remark 5.6 (Remnant as bilayer). [E] Figure 9(b) of US 12,473,247 B2 exhibits catalyst remnants of (6,12)-disubstituted chrysene as phospholipid-type heads. Figure 15(b) exhibits stacked remnants conjugated to a polymer of adenines and forming, in the filing's description, a phospholipid bilayer optionally tethered to RNA. The two figures are the documentary source for the membrane-facing end of the tail.

Remark 5.7 (Coding strand departs). [E] Figure 15(c) of US 12,473,247 B2 exhibits the RNA strand used for translation departing from the poly-A tail that is bilayer-anchored in Figure 15(b). The filing compares that tail to a poly-A tail of mRNA. The two ends of the run are therefore unlike in the drawing: one end is a bilayer remnant, the other is the start of a coding strand.

Remark 5.8 (Constancy along a short run). [E] Figure 21 of US 12,473,247 B2 exhibits an RNA tetramer AGGA in which each adenine is conjugated to a substrate phospholipid remnant. The figure is a documentary witness that the attachment motif of Remark 5.4 can be repeated at more than one adenine of the same strand. It is not a proof of unbounded length, and it is not a global frame (Proposition 3.1(v)).

5.4 The bundle

Proposition 5.9 (Clauses of H_{doc} , as readings). [E] Under the readings of Remarks 5.3–5.8, Hypothesis 2.15 may be unpacked as four documentary clauses.

(a) A (6,12)-chrysene unit is the catalyst of the het-

erodimer and remains, after A–U / A–T separation, on adenine at the 6-position connection.

(b) That remnant forms or anchors a phospholipid bilayer.

(c) A coding strand is drawn as departing from the adenine-run that carries those remnants.

(d) The attachment motif is exhibited at more than one adenine of a single strand.

These four clauses are the only content of H_{doc} used below. No further sentence of the filing is imported.

Remark 5.10 (What the bundle does not contain). H_{doc} does not contain a name for rev. It does not contain a codon table. It does not contain an identification of residues with amino acids. It does not contain a proof of [6, Thm. 5.8]. Those exclusions are Proposition 3.1(ii)(vi)(x).

Remark 5.11 (Where the section stops). The filing, as read here, exhibits a polymer whose two ends are unlike and whose attachment locant is named and repeatable. That is extra structure beyond the word AAA. Whether the unlike ends may be called the generator rev is H_{id} , and is not asked in this section.

6 Two Lemmas

The documentary bundle of Proposition 5.9 is used twice. Lemma 6.1 instantiates $H_{\text{teth}}(\text{iv})$ and leaves the residual group at $\langle \text{rev} \rangle$. Lemma 6.3 records that the two ends of the documentary tail are unlike, which is extra structure the word AAA does not represent. Neither lemma names rev as that extra structure. Neither concludes sixty-four.

6.1 Lemma A

Lemma 6.1 (Locant instantiates clause (iv)). [D] Assume $H_{\text{teth}}(\text{i})(\text{ii})$ and H_{doc} . Restrict to the A-remaining case of Remark 5.4: the remnant stays on adenine after A–U / A–T separation. (The C–G-separating case is not a poly-A tether and is not used.) Then $H_{\text{teth}}(\text{iv})$ is realized: the attachment of adenine to the (6,12)-chrysene remnant is at a named site and is the same motif at every adenine of the documentary run. The residual group remains $\langle \text{rev} \rangle$. The residual count remains thirty-six.

Proof. The restriction to the A-remaining case is the restriction under which $H_{\text{teth}}(\text{i})$ is a poly-A tether at all. Clause (a) of Proposition 5.9 names the site: the 6-position connection of the (6,12)-disubstituted chrysene to adenine (Remark 5.4). Clause (d) exhibits that motif at more than one adenine of a single strand (Remark 5.8). Under $H_{\text{teth}}(\text{i})$ the tether is a poly-A run, so those adenines are the units of the tether. The named site together with repetition along the run is the content of $H_{\text{teth}}(\text{iv})$.

Remark 4.7 applies: constancy of attachment is not an arrow along the chain. Theorem 4.6 is unchanged. The residual group is still $\langle \text{rev} \rangle$, and the residual count is still thirty-six. The second locant of Remark 5.5 is not used; if it were, the same sentence of Remark 4.7 would apply (Proposition 3.1(iii)(iv)). $\square$

Remark 6.2 (What Lemma A does not do). Lemma 6.1 does not kill flip a second time. Pattern already killed flip (Proposition 4.4). It does not kill rev. It does not identify the domain with W (Proposition 4.8).

6.2 Lemma B

Lemma 6.3 (The filing supplies an arrow). *[D] Assume H_{doc} . The documentary poly-A run has two chemically unlike ends: a bilayer-facing remnant end, and a coding-strand end. The word $t = \text{AAA}$ does not represent that unlike-ness. There is therefore extra structure on the tether that reversal of the tether word does not fix.*

Proof. Clauses (b) and (c) of Proposition 5.9 are the two ends. Remark 5.6 reads the remnant as a phospholipid bilayer (Figs. 9(b), 15(b)). Remark 5.7 reads Figure 15(c) as the coding strand departing from that tail. Those two readings are unlike: one end is a membrane head, the other is the start of a nucleic-acid strand.

The word $t = \text{AAA}$ is an element of Σ^3 . Proposition 4.2 computes $\text{rev}(t) = t$. A computation in Σ^3 cannot see a bilayer or a departing strand (Remark 4.3). Hence the unlike ends are extra structure relative to the word, and extra structure relative to the generator that fixes the word.

The argument does not identify the extra structure with rev. That identification is H_{id} , which is not assumed. $\square$

Remark 6.4 (Arrow is not yet reading direction). Lemma 6.3 says there is an arrow. It does not say the arrow is the reading direction of [3, Prop. 6.7].

A reader who writes that sentence here has used H_{id} without naming it, against Proposition 3.1(iii) and Remark 3.2.

Remark 6.5 (Global is not in Lemma B). Clause (d) of H_{doc} is a short run. Lemma 6.3 does not invoke [6, Rem. 4.13] and does not conclude a single frame for all clusters (Proposition 3.1(v)). If a global section is wanted later, it is imported from that remark, not from Figure 21.

6.3 What the two lemmas jointly give

Proposition 6.6 (Position after the lemmas). *[D] Assume $H_{\text{teth}}(\text{i})(\text{ii})$ and H_{doc} . Then:*

- (a) $H_{\text{teth}}(\text{iv})$ is realized (Lemma 6.1);
- (b) extra structure beyond AAA is exhibited (Lemma 6.3);
- (c) the residual group, computed from the word and the locant alone, is still $\langle \text{rev} \rangle$;
- (d) Target 2.19 is not discharged.

Proof. (a) and (b) are the lemmas. (c) is Theorem 4.6 together with Lemma 6.1. (d) is the content of Target 2.19: polarity must fix the reading direction. Lemma 6.3 exhibits an arrow and does not name the reading direction. Without H_{id} , the fourth row of Proposition 2.8 is not occupied. $\square$

Remark 6.7 (Where the section stops). The next section may assume H_{id} and move to the last row of Proposition 2.8. It may also refuse H_{id} and stop at Proposition 6.6. Both outcomes are allowed by Target 2.19 as restated in Section 2.6. This section does not choose.

7 Identification and Sixty-Four

Lemma 6.3 exhibits an arrow and does not name it. Hypothesis 2.16 names it. This section records what follows from that naming, and what follows if the naming is refused. Proposition 3.1(vi)(vii) remain in force: sixty-four is not Φ and is not the mitochondrial equality.

7.1 The identification

Remark 7.1 (What H_{id} says, restated). H_{id} is Hypothesis 2.16: the bilayer-to-coding arrow of Lemma 6.3 is the reading direction of [3, Prop. 6.7]; it is the generator rev . That proposition decomposes the frame action into projection reference, moved by flip, and reading direction, moved by rev . The sentence used here is the second half of that decomposition. The hypothesis is not a clause of $\mathcal{A}$ and is not a sentence of US 12,473,247 B2. A theorem that uses it is a realization theorem in the sense of Definition 2.1.

Remark 7.2 (How $\text{rev}(w)$ sits against the tail). The documentary tail has two unlike ends (Lemma 6.3): a bilayer remnant and a departing coding strand. A reading of the three coding units *away from* the bilayer end is one order along the stack. The opposite order is a reading *toward* that end. By [3, Prop. 6.7], rev changes the reading direction: it sends a word $w = XYZ$ to $\tau(Z)\tau(Y)\tau(X)$, which is the opposite order after the letterwise alignment map τ . Once the two ends are unlike, those two orders are unlike presentations. That is the content of H_{id} , written as a convention on W rather than as a second hypothesis. If the convention is refused, H_{id} remains primitive and Theorem 7.4 remains a naming.

Proposition 7.3 (H_{id} kills rev). [D] Assume H_{doc} and H_{id} . Then rev is not a residual symmetry of the presented tethered complex. Combined with Proposition 4.4, the residual group is trivial.

Proof. Lemma 6.3 supplies extra structure that reversal of the tether word does not fix. H_{id} identifies that structure with the generator rev . A presented complex that displays the arrow therefore distinguishes w from $\text{rev}(w)$ whenever those words are distinct: by Remark 7.2 one is the order away from the bilayer end and the other is the order toward it. Hence rev is not residual. Proposition 4.4 already removed flip. The remaining elements of Fr are 1, flip, rev , and $\text{flip} \circ \text{rev}$; the last falls with the two generators. The residual group is therefore trivial. $\square$

7.2 The realization theorem

Theorem 7.4 (Realization of sixty-four). [D] Assume

$$\mathcal{A} \cup H_{\text{teth}}(\text{i})(\text{ii}) \cup H_{\text{doc}} \cup H_{\text{id}},$$

with $H_{\text{teth}}(\text{iv})$ realized from H_{doc} by Lemma 6.1 in the $\mathcal{A}$ -remaining case. Then the residual group is trivial,

and the pairs (class, relative frame) number

$$8 \cdot 2 + 12 \cdot 4 = 64. \quad (5)$$

That set of pairs may be identified with W .

Proof. Lemma 6.1 realizes $H_{\text{teth}}(\text{iv})$ from H_{doc} , so the displayed assumption list is no stronger than $H_{\text{teth}}(\text{i})(\text{ii})$ together with H_{doc} and H_{id} . Proposition 7.3 places the residual group on the last row of Proposition 2.8. The count (5) is [6, Cor. 4.12]: eight classes of size two contribute two relative frames each, twelve classes of size four contribute four. With residual group trivial, each pair (class, relative frame) is a single word, and the set of pairs is W . $\square$

Corollary 7.5 (Conditional domain). [D] Under the hypotheses of Theorem 7.4, the sample space of [7] and the domain of [6] §§5–7 may be taken to be W , in the sense of Definition 2.10(ii)(iv). Without H_{id} , they may not (Proposition 4.8, Corollary 4.9).

Remark 7.6 (One strand, one frame). [D] [6, Rem. 4.13] supplies globality: a single poly-A strand serves every cluster along it, so the section is one frame and one table. That remark is imported, not re-proved. Figure 21 is not a substitute for it (Proposition 3.1(v), Remark 6.5). Theorem 7.4 identifies the residual states at a presented complex with words; Remark 4.13 of [6] is what makes those words the domain of a single codon table rather than of a family of per-cluster tables.

7.3 If H_{id} is refused

Proposition 7.7 (Allowed stopping point). [D] If H_{doc} is granted and H_{id} is refused, the paper stops at Proposition 6.6. The residual count remains thirty-six. Target 2.19 remains open as a theorem of $\mathcal{A}$, and remains open as a realization theorem. The lemmas are not thereby withdrawn.

Proof. Proposition 6.6 does not use H_{id} . Theorem 7.4 does. Refusing the hypothesis removes the theorem and leaves the lemmas. Target 2.19 asked that polarity fix the reading direction; without H_{id} the reading direction is not named. $\square$

Remark 7.8 (What sixty-four still is not). Granted Theorem 7.4, Proposition 3.1(vi)(vii) continue to apply. The image of Ξ has twenty values. The mitochondrial

equality remains [6, Thm. 5.8], under hypotheses this paper does not use. The domain of a table is not the table.

Remark 7.9 (Where the section stops). The correspondence between filing-objects and objects of $\mathcal{A}$ is not a premise of Theorem 7.4 and is not used in its proof. It is the next section, and it does not strengthen this one (Proposition 3.1(ix)(x)).

8 Correspondence, Not Necessity of Life

The table below matches names in US 12,473,247 B2 to names in $\mathcal{A}$ and in H_{teth} . As a reading it is [E]. As a list of pairs of names it is [A]. It is not a premise of Theorem 7.4 and is not used in that proof (Remark 7.9). Proposition 3.1(ix)(x) govern the section: an intermediary of the filing is not the unique intermediary in nature, and a dictionary does not prove the seeded assignment.

8.1 The dictionary

Definition 8.1 (Patent–formalism correspondence). The following pairs are the only correspondences asserted.

Filing US 12,473,247 B2	Formalism
(6,12)-disubstituted chrysene catalyst	molecular reduct $\mathfrak{C}$, catalyst side
(3,6,9,12)-tetrasubstituted substrate	coding unit / vessel side
SCH heterodimer and stack (Fig. 4)	encoded stack of [3]
Adenine remaining on the 6-position remnant (Figs. 15(a), 20)	constant poly-A tether, $H_{\text{teth}}(\text{i})(\text{ii})$
Same motif at each adenine of a run (Fig. 21)	$H_{\text{teth}}(\text{iv})$, realized by Lemma 6.1
Remnant as phospholipid bilayer (Figs. 9(b), 15(b))	extrinsic end of the tether; witness in Lemma 6.3
Coding strand departing the tail (Fig. 15(c))	the other end of that witness
Chrysene unit that is both catalyst and remnant-to-membrane	intermediary of <i>this</i> construction

Remark 8.2 (No further rows). The table does not contain: a codon, a residue, an amino acid, an initiator, a translation table, or rev. Adding any of those rows

would be a new identification and would have to be registered as such. H_{id} is already registered; it is not repeated here as a dictionary row, because the dictionary is not its proof.

8.2 Necessity, restricted

Proposition 8.3 (Necessity inside the construction). [E] *Inside the documentary construction of US 12,473,247 B2, a single (6,12)-chrysene unit is the molecule that remains on adenine and presents a phospholipid head. Without that unit there is, in the filing, no one object that is both the A-attachment and the bilayer remnant. That is necessity of the intermediary in the construction.*

Proof. Read Remarks 5.3, 5.4 and 5.6 together. The catalyst of the heterodimer is the (6,12) unit; the remnant that stays on adenine after A–U / A–T separation is that same unit; the bilayer head of Figures 9(b) and 15(b) is that remnant. The three roles are one molecule in the drawing. The claim is a reading of those figures, not a uniqueness theorem among polycycles, and not a theorem of $\mathcal{A}$ (Proposition 3.1(ix)). $\square$

Remark 8.4 (What necessity does not say). Proposition 8.3 does not say that terrestrial nucleic acids require chrysene. It does not say that phospholipids require chrysene. It does not say that the genetic code exists because chrysene exists. Those sentences would be Φ -adjacent and are refused by Remarks 2.3 and 7.8.

8.3 Initiating nucleic acids

Remark 8.5 (Role, not identity). [E] Figure 15(c) and the filing’s “first instruction set” language name the strand that leaves the anchored tail. That is a role correspondence with the initiator of [3, Def. 9.1]: both are a distinguished start of a coding strand. The correspondence of roles is not an identification of objects. $H_{\text{prod}}(0')$ of [5, §2.5] remains untouched (Proposition 3.1(viii), Remark 2.18). The membrane-bound tail is not the initiator.

Remark 8.6 (Linkage the section is allowed to state). The filing, as read in Section 5, holds on one heterodimer a nucleic-acid product and a phospholipid product. The formalism, as used in Sections 4–7, holds on one tether a constant poly-A word and, under H_{id} , a reading direction. The dictionary of Definition 8.1 is

the statement that those two holdings may be named together. It is not a derivation of either from the other.

Remark 8.7 (Where the section stops). No row of the dictionary is fed back into Theorem 7.4. No row is an audit against a published table. Targets other than Target 2.19 are the next section.

9 Targets and What This Paper Has Not Done

Target 2.19 is the only target this paper addresses. The statements below record what remains open, and what was never this paper's object. No new target is added to the register of [6].

9.1 Status of Target 9.7

Target 9.1 (Target 9.7, after the realization). Two readings, both allowed.

- (a) Under $H_{\text{doc}} \cup H_{\text{id}}$, Theorem 7.4 is a realization of Target 2.19: the documentary arrow, named as rev, kills the residual generator that the word AAA cannot kill, and the domain may be identified with W .
- (b) If H_{id} is refused, Proposition 7.7 applies. Target 2.19 remains open as a theorem of $\mathcal{A}$ and remains open as a realization theorem. Lemmas 6.1 and 6.3 stand.

In neither reading is Target 9.7 a theorem of $\mathcal{A}$ alone. Rem. 4.11 of [6] said the formalism does not represent the polarity; this paper has not represented it inside $\mathcal{A}$ either. It has named a documentary witness and an identification hypothesis.

Target 9.2 (Polarity from $\mathcal{A}$ only). [T] Derive H_{teth} (iii) from $\mathcal{A}$ together with H_{teth} (i)(ii)(iv), without H_{doc} and without H_{id} . This is Target 9.7 in its original strength. The present paper does not claim it.

9.2 Targets not addressed

Target 9.3 (Unchanged from [6]). The following remain exactly where [6] left them.

- (i) Target 9.1: $H_{\text{split-chem}}$ at UU.
- (ii) Target 9.2: the three unassigned classes.

- (iii) Target 9.3: $H_{\text{lib-env}}$.
 - (iv) Target 9.4: the unnamed obstruction.
 - (v) Target 9.8: coordinated vessels.
 - (vi) Target 9.9: further divisions beyond AUA and UGA.
- None is used, and none is advanced.

Remark 9.4 (What Article 51 may now cite). If reading (a) of Target 9.1 is accepted, [7] may cite Theorem 7.4 for the identification of its sample space with W , still under $H_{\text{doc}} \cup H_{\text{id}}$. If reading (b) is accepted, [7] continues to list polarity as load-bearing and undischarged. Either citation is accurate. A citation that drops the hypotheses is not.

Remark 9.5 (Unused structure). Φ is unused. The dual cipher of A_8 is unused. $H_{\text{prod}}(0), (0')$ are unused. The standard code is unused. Those exclusions were Remark 2.3 and remain.

Remark 9.6 (Where the paper stops). The object was a residual count. The count is thirty-six from the word, and sixty-four from the word plus a named identification of a documentary arrow. No further object is claimed.

A Figure list and residual table

The figure numbers are those of US 12,473,247 B2 [8], granted 18 November 2025, priority 2024. Readings are Section 5. This appendix does not add a clause to H_{doc} .

A.1 Figures used

Figure / example	Used at	Reading
4(b)–(c)	Rem. 5.3	SCH heterodimer; (6,12) catalyst wi
9(b)	Rem. 5.6	(6,12) remnants as phospholipid-type
15(a)	Rem. 5.4	remnant conjugated to adenine, 6-po
15(b)	Rem. 5.6	stacked remnants; bilayer optionally
15(c)	Rem. 5.7	coding strand departing the anchore
20(a)–(e)	Rem. 5.4	remnant on adenine
20(f)	Rem. 5.4	remnant Q on adenine from an A–U
21	Rem. 5.8	AGGA; each A conjugated
Example 17	Rem. 5.5	phospholipid–adenine contact at carl

Figures of the filing not listed are unused.

A.2 Five residual counts

What is fixed	Residual group	States
nothing	Fr	20
projection reference only (pattern AAA)	$\langle \text{rev} \rangle$	36
reading direction only	$\langle \text{flip} \rangle$	32
both, as a theorem of $\mathcal{A}$	trivial	64
pattern + Lemma 6.3 + H_{id}	trivial	64

The fourth row is [6, Cor. 4.10], last line, and is not proved in this paper from $\mathcal{A}$ alone. The fifth row is Theorem 7.4. The two rows have the same count and different hypotheses.

References

- [1] C. D. Schaper. The Chrysene Formalism as Candidate Mathematics and Candidate Biogenesis. *Annals of the Chrysene Formalism*, 1(2): 476–488, 2026.
- [2] C. D. Schaper. The Chrysene Formalism Revisited: A Twelve-Axiom Foundation for Molecular Characterization, Tensorial Noncommutative Geometry, and Operator Response. *Annals of the Chrysene Formalism*, 1(2):489–560, 2026.
- [3] C. D. Schaper. The Encoded Stack. *Annals of the Chrysene Formalism*, 1(2):646–675, 2026.
- [4] C. D. Schaper. The Twenty Registry Classes of a Chrysene Stack. *Annals of the Chrysene Formalism*, 1(2):676–704, 2026.
- [5] C. D. Schaper. Why Three and Why Twenty: The Capacity of a Chrysene Cluster, the Base-Four Intermediary, and the Production Operator Δ . *Annals of the Chrysene Formalism*, 1(2): 768–793, 2026.
- [6] C. D. Schaper. Seeded Assignments on the Chrysene Registry: Transversality, Third-Position Refinement, and the Mitochondrial Code as Normal Form. *Annals of the Chrysene Formalism*, 1(2): 858–882, 2026.
- [7] C. D. Schaper. Sufficient and Ancillary Reductions of a Chrysene Cluster: Transverse Seeding as a Decision Rule and the Mitochondrial Code as Normal Form. *Annals of the Chrysene Formalism*, 1(2):883–913, 2026.
- [8] C. D. Schaper. Encoded design integrated synthesis of nucleic acids, and phospholipids, and related pharmaceutical products. US Patent 12,473,247 B2, granted 18 November 2025 (priority 2024).