ANNALS OF THE CHRYSENE FORMALISM

AI-AUGMENTED PEER-REVIEWED | VOL. 1, NO. 4 | ISSN 3144-2021 | OCTOBER 2026

ORTHOGONAL REVIEW RECORD

Constructive Genetic Code-Table Realization On A Typed Chrysene Carrier

Compiled by the Editorial Office
Annals of the Chrysene Formalism
Schaper Systems Press

Paper ID:	ACF-1.4-075
Issue:	Volume 1, Number 4
ISSN:	3144-2021
Review architecture:	Referee report followed by author response and incorporation of all requested changes
Review focus:	Typed carrier, registry, matching obstruction, graph grammar, assignment path, junction controller
Acceptance date:	2026-10-23
Online publication:	2026-10-23
Pages:	1503–1544
Document version:	v1.0
Last audited:	23 October 2026

Citation: Schaper, C. D. (2026). Constructive Genetic Code-Table Realization On A Typed Chrysene Carrier. *Annals of the Chrysene Formalism*, 1(4), 1503–1544. ISSN 3144-2021. `https://chrysene.com/index.php/acf/article/view/75` • © 2026 Charles D. Schaper. Distributed under the CC Attribution-NonCommercial-NoDerivatives 4.0.

Declared conflict

The initial assessment was an AI-assisted referee report on the frozen 54-page working draft dated 5 October 2026. The author accepted all five comments (R1–R5) and incorporated the requested clarifications, validators, and provenance citations into the revised manuscript.

> **Scope of Review**
>
> The manuscript constructs a deliberately specified hybrid formal system whose components are a six-bit frame action, reference-decorated external addresses, an atom-preserving product graph grammar, reference-informed seed and refinement data, permitted routing exchanges and affine selectors, and a resource-aware junction reader. It supplies explicit finite witnesses to

two reference tables and to arbitrarily long finite families of accepted Met-first segments, with a separate finite reservoir for each requested length. It also proves that the routing grammar admits many alternative tables. Physical molecular realization is stated as a compatible-lift obligation rather than inferred from the finite computations. The strongest contribution is the explicit reconciliation of interfaces that are easily conflated: the fixed resident AAA decoration from a variable external codon, a class-invariant production map from an addressed decoder, terminal graph identity from chemical accessibility, and sense absence from release, halt and reset.

Compiled disposition

Accept. The author accepted and incorporated all five requested changes (R1–R5). The formal core is preserved: the twenty-class registry and the 20/36/64 retained-data counts; the sharp Watson–Crick matching bound 18; the 61-state registry-preserving refinement bound; the twenty constitutional product witnesses; the complete guarded assignment/control path; the exact 19 508 428 800-assignment routing orbit; the conditional Met-first safety invariant; and the joint formal realization for every finite requested number of segments. Chemical feasibility, independent selection and historical origin remain distinct, open claims.

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1 Full original referee report

The following is the complete text of the AI-assisted referee report dated 5 October 2026 on the frozen 54-page working draft.

Status of this document. This is an AI-assisted simulated referee report requested for manuscript revision. It is not independent external peer review, a journal decision, or evidence of acceptance. The reviewed object is Charles D. Schaper's frozen 54-page working draft, *Constructive code-table realization on a typed chrysene carrier*, dated 5 October 2026, together with its supplied source and finite certificates. Page numbers below refer to that frozen PDF; source locations identify its corresponding files.

Recommendation and summary

Recommendation: targeted revision before submission, preserving the central formal conclusions. I found no critical counterexample to the stated finite registry, matching, refinement, assignment-path, or controller theorems. Two interfaces need a more exact specification: what remains invariant after extraction, and which written graph-grammar guards the checker actually verifies. Two smaller textual claims should be corrected, and reference-table provenance should be strengthened. These changes can be made without replacing the main result by a weaker catalogue of open questions.

The manuscript constructs a deliberately specified hybrid formal system. Its components are a six-bit frame action, reference-decorated external addresses, an atom-preserving product graph grammar, reference-informed seed and refinement data, permitted routing exchanges and affine selectors, and a resource-aware junction reader. It supplies explicit finite witnesses to two reference tables and to arbitrarily long *finite families* of accepted Met-first segments, with a separate finite reservoir for each requested length. It also proves that the routing grammar admits many alternative tables. Physical molecular realization is stated as a compatible-lift obligation rather than inferred from the finite computations.

This is a coherent mathematical objective. A target-informed construction can establish existence under declared rules, even though it does not independently explain the target. Similarly, a conditional theorem does not become invalid merely because its chemical premises are unverified. The referee's task is to check that the definitions, witnesses and conclusions have matching scope. The report therefore does not require an experiment, a unique selected code, or a complete prebiotic history as a condition for accepting the formal theorem.

Assessment of the contribution

The strongest contribution is the explicit reconciliation of interfaces that are easily conflated. The manuscript distinguishes the fixed resident AAA decoration from a variable external codon, a class-invariant production map from an addressed decoder, terminal graph identity from chemical accessibility, and sense absence from release, halt

and reset. These distinctions are substantive, because imposing the wrong identification can make the intended conjunction empty.

Several results merit retention in a revision:

1. **Registry and address structure.** The adjacent-difference invariant, Burnside count, stabilizer description and normal-form proof support the twenty-class quotient and the distinct 36- and 64-state retained-data spaces. The capacity theorem correctly states the additional coverage and injectivity assumptions needed for saturation. It does not identify twenty amino acids from the integer twenty alone.
2. **Sharp obstructions.** The WC nine-class/seven-neighbor witness proves an upper bound of eighteen, and the displayed matching attains it. RY and MK are correctly treated as different transported partitions. The 61-state result follows from the minimal joint factorization of the registry map and standard output, including STOP; it is not merely a numerical comparison with the 61 standard sense codons. The existing 64-address model meets this bound.
3. **Constructive structural witnesses.** The product chapter supplies full constitutional graphs, explicitly accounted hydrogens and remnants, and a joint two-sulfur word. Its source-shaped mask and bond restrictions are more informative than unrestricted graph reconstruction. The result is inclusion of the twenty specified targets, not exclusion of all other products. The stereochemical and atom-map limits are appropriately explicit.
4. **An actual assignment path.** Seventeen demands seed eighteen cells; propagation fills 52 addresses; the four refinements add the missing product identities; two exchanges reach the mitochondrial table; and the whole affine-control interval, including its tie wall, reaches the standard table. The permitted moves and reference-informed instance data are distinguished. The exact routing-orbit count 19 508 428 800 is a useful quantitative nonuniqueness result, not an embarrassment to be hidden.
5. **A correctly scoped start invariant.** Met identity is supplied by the outgoing product graph, and the controller allows only that token to establish a new accepted word. Fresh-packet induction prevents reuse. This supports a conditional all-run safety theorem and nonempty finite traces; it does not independently derive biological initiation or unlimited production from a finite batch.

The elementary ingredients include standard orbit counting, matching, graph rewriting and transition induction. I would describe the novelty cautiously as the particular source-guided construction, its repaired interfaces, explicit obstructions and executable composite witnesses. The present review does not establish priority against the entire genetic-code literature.

Major comments

R1 Make the architecture and availability state types explicit

Classification: material specification ambiguity, repairable without weakening the result.

Location. Sections 2.5, 4.2–4.7, 7.2 and 8.1–8.3; especially pp. 16–22, 38–39 and 43–45. Source: `architecture.tex`:54–63; `products.tex`:63–86, 143–173, 392–451; `junction.tex`:456–470; `integration.tex`:8, 49–59.

The common model keeps a carrier record H and a changing atom graph Γ. This separation can make the construction consistent, but the persistent condition (C1) still says that the resident carrier incidence *is* $(X - A)_3$. Extraction changes the active core and removes the aminoacyl ester linkage; for some rows it also changes a boundary attachment. Meanwhile, the proof correctly acknowledges that spectator units, adenosines and tethers are inert typed records rather than fully resolved atom graphs. Readers need to know whether (C1) preserves provenance and address incidence or asserts continuing intact molecular connectivity. The latter is not supplied by the extraction certificates.

There is a related interface issue in FORM and GATE. FORM executes the supplied paired graph certificate and stores two "bound" outputs. That certificate already ends with disconnected, closed-valence free-acid product components. A subsequent GATE can coherently control their availability to the reader, but this is a separate retained/released status; it cannot silently mean the same covalent detachment that was completed by the graph word.

Why it matters. Joint nonemptiness is the central theorem. Its proof must not preserve a literal graph assertion that the graph path destroys, or count the same release operation twice under different names. This is a typing issue within the formal model, not a demand to realize the missing molecular context experimentally.

Requested change. Define H as the persistent architecture/provenance and address-interface record. State which actual incidences belong to the current atom graph and may change during extraction. Define an independent product-token availability status such as retained/unavailable versus released/available, and say explicitly that disconnected graph components can remain unavailable until GATE. Alternatively, split a fully specified formation/release certificate at a suitable intermediate state. Update (C1), FORM and GATE consistently, and preserve the existing physical-lift obligations.

Acceptance criterion. A reader can follow one sulfur packet through preparation, graph formation, gating, START and consumption without equating its original architecture record, current covalent graph and readout status. The existing common-model and Met-first conclusions should then remain intact.

R2 Match checker claims to the complete written guards

Classification: reproducibility and proof-assurance gap; no invalid current witness demonstrated.

Location. Definition 4.2 and Theorem 4.5, pp. 17 and 20; Section 7.5, p. 42; Appendix A.1–A.2, p. 50. Source: `products.tex`:143–177, 315–362; `certificates.tex`:8–17. Code: `build_product_certificates.py`:171–206 and paired construction; `verify_junction.py`:130–176; `verify_manuscript.py`:37–51.

The product program both constructs its target graphs and generates their edit words. It checks important properties: valence capacities, atom inventory, selected fixed bonds, original core adjacency/support, retained carbon membership, remnant bonds and the

internal-deletion budget. However, its explicit assertions do not constitute a recognizer for every clause of the written grammar. In particular, the bound $|S| \leq 9$ is not itself membership in the ordinary/empty/extended mask family. Not all whole-removal neighborhood, donor-incidence and paired-path support/protected-bond conditions are replayed as guard predicates. The junction checker independently replays the sulfur word for valence, endpoint projection and bridge ordering, but that is narrower than checking all the source-guided guards.

The combined program's exact regeneration test is useful: changes to packaged output are detected. It does not convert an unimplemented guard into an implemented one. Thus the language that the checker verifies every protected edge and source-shaped restriction needs a more precise basis. This does *not* show that the supplied witnesses violate the restrictions. I separately recognized all twenty current masks and replayed the row paths with the relevant fixed-bond checks; those checks passed.

Why it matters. The manuscript's restriction beyond universal bond-graph reconstruction is central to the value of its structural result. A future modification must not pass only because its generator and expected output changed together. Also, a constructive proof of a particular witness and a general checker for the declared grammar are different deliverables.

Requested change. Preferably add a small data-consuming validator that does not import the product builder: recognize the mask family and whole-removal support, enforce the protected backbone/root bonds and permitted heavy-atom incidences, replay every primitive, check endpoint extraction conditions, and apply the same rules to the joint sulfur support. Include representative invalid-certificate rejection tests. An acceptable narrower remedy is to state exactly which fixed-instance facts are checked and prove the remaining guards directly, without claiming a general recognizer.

Acceptance criterion. The original certificate remains accepted under the stated guards, representative forbidden operations are rejected, and the report distinguishes fixed-instance replay from chemically admissible reaction validation. The repertoire-inclusion theorem need not be weakened if those checks pass.

Minor comments

R3 Correct the account of the first eight sulfur edits

Classification: local factual mismatch between prose and certificate.

Location. Proof of Theorem 4.5, p. 20, and Theorem 7.4, p. 41. Source: `products.tex`:353–357; `junction.tex`:614–624; the paired prefix in `build_product_certificates.py`.

The prose says that the first eight edits transfer the two original sulfur hydrogens, and later describes transfer to available formal ports. In the actual prefix their S–H bonds are split. The labelled hydrogen vertices are retained and temporarily unbonded; their new partners are assigned later. The bridge at step 8 and the topology after step 10 are correctly specified.

Requested change. Say "detach the two sulfur hydrogens while retaining their identities for later reassignment." Reserve "transfer" for the complete split-and-rejoin sequence. This changes neither the endpoint nor the 174-step count.

R4 Do not imply that every controller guard is necessary

Classification: overstrong counterfactual statement following a valid sufficient-condition theorem.

Location. Section 7.3, p. 40; `junction.tex`:551–558.

The paragraph says that the theorem would fail after *any* listed contract change. Some listed changes do defeat particular conclusions, but the RESET example is not generally true. One may allow RESET from Active while discarding the unfinished word, reserving a fresh packet and clearing the phase. All subsequently accepted words can still begin with Met, and the stated no-reuse invariants can remain valid. The additional rule loses unfinished work; it need not create a counterexample to the displayed safety theorem.

Requested change. Replace the universal necessity claim by specific counterexamples attached to the guarantee they violate, or say that these relaxations can invalidate particular guarantees. Distinguish safety from preservation or completion of an unfinished segment. Keep the proved sufficient controller contract.

R5 Add direct reference-table provenance

Classification: source transparency and biological interpretation, not a numerical correction.

Location. Section 5.1, pp. 23–24; Section 7.1, p. 38; bibliography, pp. 53–54; embedded reference strings in the registry and reachability checkers.

The supplied-corpus provenance is valuable, but a journal reader should also be able to identify the biological comparison tables directly. NCBI's *The Genetic Codes*, tables 1 and 2, supplies the same two amino-acid strings and the same four differences after replacing DNA T by RNA U. It separately records initiation information. Its table-2 commentary also cautions against treating the AGR designation as a universal direct termination mechanism in humans. This supports the manuscript's existing separation of table entries from initiation and halt mechanisms.

Requested change. Cite that primary reference-table resource, identify table numbers and the T-to-U normalization, and retain the exact archived strings as immutable inputs. If adding biological interpretation, explicitly distinguish a table's STOP designation from the molecular mechanism implementing termination. No change to the four-codon difference theorem is indicated.

Objections that would not justify weakening the result

- **Lack of experiments.** Experiments test a physical realization of the premises. They are not needed to prove the finite conditional statements already supplied. The molecular lift must remain unproved unless supported, as it currently is.
- **Use of target-informed data.** This limits explanatory or predictive scope, but does not invalidate a checked realization under fixed, disclosed data. The appropriate response is provenance and an exact conclusion, not deletion of the endpoint theorem.

- **Failure of uniqueness.** The manuscript proves nonuniqueness and quantifies it. Unique selection would be a new result under stronger independently motivated restrictions.
- **The WC matching obstruction.** Eighteen is a bound for the particular table-conditioned class graph. It does not forbid twenty structural products or an addressed refinement. Requiring a perfect matching in that unchanged graph would contradict the manuscript's own theorem and misstate its construction.
- **A permissive chemical grammar.** The Split/Join grammar is intentionally formal. Its restrictions and their ablations should be checked and clearly attributed. A criticism should identify an incorrect claimed restriction, or an unjustified chemical inference, rather than demand that a formal primitive already be an elementary reaction.
- **Conditional Met-first behavior.** Identifying the required outgoing graph before START is more informative than inserting a residue-name string into an update. The chosen support, direction and start-precedence contract remain premises. The theorem is a valid invariant under those premises, not a historical explanation of why biological initiation evolved.

Review method and final assessment

I read the complete source of the 54-page manuscript, its tables and appendices, and the four certificate programs plus the combined verifier. I reran the inspected combined verifier on a separate copy; all four modules and the shared-interface checks passed, including deterministic regeneration. I checked the arguments rather than treating a PASS string as a proof, and added the fixed-instance mask and protected-bond spot checks described in R2. All 54 PDF pages were rendered and visually inspected in page-contact views; the large tables, equations and page transitions showed no material layout obstruction. This review does not claim an exhaustive audit of every external source manuscript or a proof-assistant formalization.

The frozen PDF is identified by SHA-256

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02e3176a24e993162c1dcc80f1f7ebf2077
cbcd5ccf583af581241dd7bc7555a
```

This report addresses that version, not any later revisions.

Overall judgment. The formal core is worth preserving. R1 and R2 should be resolved before submission because they affect the exact interpretation and auditability of the composite witness. R3 and R4 correct local overstatements, and R5 improves the scientific reference boundary. A reasoned response may defend the existing formal scope against stronger empirical or uniqueness demands. The revised manuscript should make the same positive result easier to verify: one explicitly specified, nonempty formal graph-and-controller system has the claimed registry structure, structural repertoire, reachable reference tables and finite Met-first reset traces. Chemical feasibility, independent selection and historical origin remain distinct, open claims.

2 Original findings and author responses

R1 – Architecture and availability state types

Finding. The common model keeps a carrier record H and a changing atom graph Γ. The persistent condition (C1) could be read as requiring an intact chrysene–adenosine carrier after extraction. FORM imported a certificate with disconnected free-acid product components and then called its outputs Bound before GATE released them.

Author response (accepted). Section 2.5 defines H as the immutable architecture/provenance record and Γ as the current atom-and-bond graph. Condition (C1) now preserves that provenance record; an intact post-extraction carrier is expressly not an invariant. Section 7.1 introduces Held and Available as orthogonal controller-token status values. FORM stores disconnected components with Held status; GATE marks their tokens Available without another bond rewrite. Theorems 8.4 and 7.2 remain intact.

R2 – Match checker claims to the complete written guards

Finding. The product program constructs its target graphs and generates their edit words, but its explicit assertions do not constitute a recognizer for every clause of the written grammar. The combined program's exact regeneration test does not convert an unimplemented guard into an implemented one.

Author response (accepted). Added `scripts/validate_product_guards.py`, a data-consuming validator that imports no builder function. It recognizes the mask family, checks whole-removal support and protected bonds, and replays every primitive of all twenty diagnostic row certificates and the joint sulfur certificate. Seven representative rejection tests are included. The combined verifier invokes this audit. All current witnesses pass. Theorem 4.5 retains its repertoire-inclusion conclusion.

R3 – Account of the first eight sulfur edits

Finding. The prose said that the first eight edits transfer the two original sulfur hydrogens, but in the actual prefix their S–H bonds are split and the labelled hydrogen vertices are retained for later reassignment.

Author response (accepted). The proof of Theorem 4.5 and the witness proof of Theorem 7.4 now say that those hydrogens are detached with their identities retained for later reassignment. The 174-step paired certificate and terminal identities are unchanged.

R4 – Do not imply that every controller guard is necessary

Finding. The paragraph after Theorem 7.2 claimed that the theorem would fail after any listed contract change. An aborting RESET can discard an unfinished word and still preserve the stated Met-first and ownership invariants.

Author response (accepted). Section 7.3 replaces the overbroad paragraph with separate consequences for particular relaxations. It explicitly acknowledges that an aborting fresh-

packet RESET may preserve all stated safety invariants while losing an unfinished sequence. The transition table and its induction are unchanged.

R5 – Direct reference-table provenance

Finding. A journal reader should be able to identify the biological comparison tables directly. NCBI's *The Genetic Codes*, tables 1 and 2, supplies the same two amino-acid strings and the same four differences after T-to-U normalization.

Author response (accepted). Section 5 now cites NCBI *The Genetic Codes*, translation tables 1 and 2 (page update 23 September 2024, accessed 5 October 2026), and states the T-to-U normalization. Added `data/ncbi_reference_tables.json`. The combined verifier reconstructs both 64-entry maps and compares them with the packaged endpoints. The prose distinguishes table entries from initiation and halt mechanisms. The four differing codons remain AGA, AGG, AUA, and UGA.

Preserved conclusions

The revision preserves the twenty-class registry and the 20/36/64 retained-data counts; the sharp Watson–Crick matching bound 18; the 61-state registry-preserving refinement bound; the twenty constitutional product witnesses; the complete guarded assignment/control path; the exact 19 508 428 800-assignment routing orbit; the conditional Met-first safety invariant; and the joint formal realization for every finite requested number of segments. The existing atom-graph, routing, registry, and controller certificates remain byte-for-byte unchanged. The manuscript still distinguishes these proved formal results from a compatible chemical lift, stereoselective synthesis, kinetic dominance, and independent evolutionary selection, none of which is claimed.

Recommendation

Accept. All five requested changes were accepted and incorporated. The formal core is worth preserving and is now easier to verify. Chemical feasibility, independent selection and historical origin remain distinct, open claims.

References

[NCBI] A. Elzanowski and J. Ostell. The Genetic Codes. National Center for Biotechnology Information. Translation tables 1 and 2; page updated 23 September 2024, accessed 5 October 2026.

Revision history

Version	Date	Notes
v1.0	2026-10-23	Review record published with Article 75.

Living Document Notice

As with any actively developing field, the mathematical and applied claims in this article are subject to periodic re-evaluation as the surrounding formalism matures and as the journal's AI-augmented review tooling advances. Consistent with standard scientific practice for provisional or fast-moving frameworks, this article and its review record may be re-audited by subsequent review systems, and a revised version bearing an updated review history may be issued to reflect developments in the field. Readers should consult the Revision History table above, and the journal's records, for the current version number and audit date of this article.

Editorial Disclaimer

The *Annals of the Chrysene Formalism* aims to develop the Chrysene Formalism through the application of advanced mathematics, using AI systems selected as well suited to this task. In pursuing this aim, it is possible that errors occur during the mathematical progression and analysis of the formalism, including within the review and editing process itself. However, the formalism is constructed within a multidisciplinary, horizontal framework that is grounded in a specific instantiation of molecular matter and its associated networks, an instantiation that is invariant and falsifiable. For this reason, the editorial office considers the formalism well suited to an AI-augmented approach, and anticipates that this approach will continue to be adapted as AI models and the surrounding mathematical understanding advance.