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AI-AUGMENTED PEER-REVIEW:

Topological Scission of the Chrysene Abiotic Loom: Dual Mastering, Structural Scaffolding, Sequential Catalytic Connectivity, and PCET-Enabled Prototype Enzyme Formation

Compiled by the Editorial Office

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Review Scope and Objective

Prior to submission, this article underwent a Level 1 AI-Augmented review. Under Level 1, the author conducted an AI-augmented review of the manuscript, using review instructions provided by the editorial committee that restrict the AI system's task to identifying mathematical and logical flaws. Under Level 1, the AI-augmented review may also issue specific recommendations on how to correct identified flaws.

Upon submission, the editorial board evaluated the manuscript using the same review instructions provided to the author, in order to confirm the author-side findings. Human review was used to judge whether the manuscript adhered to the principles of the Chrysene Formalism, and whether it was grounded in the invariant chemistry that forms the axiomatic framework and tensorial space of the Chrysene Formalism. A more rigorous tier of AI-augmented peer review is currently in development and is being implemented for papers that will be published soon. It is anticipated that Level 1-reviewed papers will be subject to future audit, and, where warranted, updated versions of the manuscript may be issued.

Disclosure of AI Use

The author claims the use of AI in the development and writing of the manuscript.

AI-Augmented Review Procedure

This submission was evaluated under the journal's basic Level 1 AI-augmented review protocol, consisting of two independent stages:

(1) **Author-Side Draft Check.** During manuscript preparation, the author employed an AI-augmented review system to screen the draft for mathematical and logical flaws prior to submission.
Model(s) used: Grok 4.6 [internal review — not shown]; Grok 4.6 and Gemini 3.1 Pro (Extended) [final meta-review response].

(2) **Editorial Meta-Review.** Following submission, the editorial office conducted a second, independent check for mathematical and logical flaws, also using AI-augmentation, to verify consistency with the foundational formalism prior to acceptance.
Model(s) used: Gemini 3.1 Pro (Extended).

Review workflow: Author-side: an internal AI-augmented review pass was conducted using Grok 4.6 during manuscript development; this internal pass is not individually reproduced. The author's final meta-review response was drafted jointly using Grok 4.6 and Gemini 3.1 Pro (Extended). Editorial meta-review conducted independently using Gemini 3.1 Pro (Extended).

> **Scope of Review**
>
> AI-augmented review at this tier evaluates internal consistency, notational coherence, and alignment with previously established results in the formalism. It does not constitute independent verification of novel mathematical claims by a subject-matter expert, and it does not certify that a cross-field analogy invoked in the manuscript (e.g. between a result native to one field and the formalism's invariants) is mathematically valid beyond the level of internal consistency and stated falsifiability. Readers evaluating a specific applied claim

> in this paper are encouraged to consult a domain specialist in the relevant field.

Editorial Board & Review Committee Summary

Recommendation: Accept with Minor Revisions

The manuscript successfully extends the Chrysene abiotic loom from a secondary-structure selection engine (Papers 1–3) into a multi-layer geometric and synthetic compiler. The introduction of the topological scission operator, the dual mastering maps (void and fragment), the residual-scaffold support map, the sequential-connectivity operator, and the residual-PCET prototype-formation map is formally coherent and continuous with the earlier papers.

The two metabolic illustrations (PFK/Glyco-Wire linear-tail motif and G6PD dual-NADP motif) supply concrete geometric realizations of all four layers, and the newly added experimental reference distances from human G6PD (PDB 2bhl) provide a first quantitative anchor against a public high-resolution structure. The committee regards the work as a natural and necessary next step in the series. The mathematical scaffolding is rigorous, the scope limitations (especially the explicit deferral of genetic tagging) are stated with appropriate clarity, and the cooperative stance toward continuous models is maintained throughout.

The minor revisions listed below are intended solely to sharpen presentation and to make the empirical claims as precise as the formal claims.

Reviewer Comments & Author Responses (AI-Augmented)

1. Clarification of Empirical Status in Section 10

Critique: The experimental distances from PDB 2bhl are valuable, yet the text should more explicitly distinguish "experimental reference clearances" from "lattice-derived predictions."
Recommendation: A single sentence stating that the 7–10 Å window is an observed experimental range against which lattice tolerances may be compared (rather than a lattice prediction itself) would eliminate any possible ambiguity.

Author's Reply

A new sentence has been inserted at the opening of the PDB 2bhl subsection: "The distances reported below are experimental observables extracted from a public high-resolution structure; they serve solely as reference values against

which the steric tolerance window of the residual scaffold may be compared." The remark that closes the subsection has been strengthened to the same effect.

2. Table Formatting Consistency

Critique: Tables 1–3 and the new G6PD distance table employ slightly different column-width conventions.
Recommendation: Harmonize the use of `\small` and `\toprule`/`\midrule`/`\bottomrule` so that all empirical tables share a uniform appearance in the two-column layout.

Author's Reply

All empirical tables (the RNW zipper table, the G6PD-motif element table, the Glyco-Wire observables table, and the new 2bhl distance table) now employ an identical preamble (`\small`, `\toprule`/`\midrule`/`\bottomrule`, and consistent column alignment). The two-column layout is preserved without overflow.

3. Cross-Reference Density in the Metabolic Illustrations

Critique: The Glyco-Wire and G6PD subsections are rich in geometric detail.
Recommendation: A few additional forward/backward references to the formal definitions of $\mathcal{M}_F$, $\mathcal{M}_V$, $\mathcal{S}$, and $\widehat{C}_{\mathrm{seq}}$ would help the reader keep the four-layer architecture in view while reading the concrete examples.

Author's Reply

Explicit parenthetical references to Definitions 6, 10, 12 and 14 ($\mathcal{M}_V$, $\mathcal{M}_F$, $\mathcal{S}$, $\widehat{C}_{\mathrm{seq}}$) have been added at the first substantive mention of each concept inside the Glyco-Wire and G6PD illustration subsections.

4. Minor Typographic Polish

Critique: Two residual instances of "Paper 1" (instead of the series citation style used elsewhere) remain in the introduction.

Recommendation: Align them with the citation format adopted for Papers 2 and 3.

Author's Reply

The two residual instances of the bare phrase "Paper 1" in the introduction have been replaced by the series-consistent citation form used for Papers 2 and 3. In addition, a final pass has removed a duplicated phrase in Remark 18 and standardized the spelling of "$NADP^+$" throughout.

Author's Concluding Remarks

Dear Members of the Editorial Board and Review Committee,

I am grateful for the careful reading and for the constructive recommendations. All four points have been addressed in the revised manuscript. By cleanly separating experimental observables from theoretical predictions and systematically linking the abstract topology maps back into the concrete metabolic illustrations, the text is now highly cohesive.

I believe the manuscript now satisfies the committee's recommendations and is ready for publication in the *Annals of the Chrysene Formalism*.

Sincerely,
Charles D. Schaper, Ph.D.
Chief Editor, Annals of the Chrysene Formalism

Final Remarks from the Editorial Review Committee Chair

The editorial meta-review of this manuscript has been completed. Using the journal's AI-augmented evaluation protocol, the editorial office assessed the submission's alignment between its stated mathematical formalism and its applied biochemical claims, and confirmed that the manuscript satisfies the journal's standard for internal consistency at this review tier. The manuscript's separation of experimental PDB observables from lattice-derived theoretical predictions, the formatting consistency of the empirical tables, the cross-referencing of the four-layer topological architecture within the metabolic illustrations, and the citation consistency across the paper series was found to be consistent throughout.

The manuscript is formally accepted for publication in the *Annals of the Chrysene Formalism*, Volume 1, Number 1.

Revision History

Version	Date	Notes
v1.0	2026-08-26	Initial publication.

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.