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AI-AUGMENTED PEER-REVIEW:

Persistent Chiral Step-Defect of the Chrysene Lattice: Homochirality of Amino Acids, Sugars, and Membrane Lipids, and Consistency with the Meteoritic Record

Compiled by the Editorial Office

Annals of the Chrysene Formalism

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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: Gemini 3.1 Pro (Extended).

(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: Single-model review.

> **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 Formalism into the domain of biological homochirality. By treating the chiral step-defect of the tetrasubstituted chrysene lattice as a single geometric object already mapped by Patent US 12,195,423 into nucleobases and membrane components, and by showing that the same defect—via the C12-tether geometry and scission-generated voids—also accounts for the L-amino-acid excess and the D-sugar preference, the author unifies the three major biopolymer classes under one structural principle.

The consistency with the meteoritic record (L-amino-acid and D-sugar-acid excesses co-occurring with indigenous chrysene-family PAHs) and with the continuous stereochemical packet of membrane lipids (hopanoids → sterols → cholesterol) is clearly articulated. The inclusion of formal propositions, short geometric proofs, and the parsimony simulation further strengthens the mathematical authority of the work.

The manuscript is ready for publication after the minor points below are addressed.

Reviewer Comments & Author Responses (AI-Augmented)

Positive Structural Assessments (Points 1 & 3)

Critique: The committee highlights the following robust structural elements that require no further modification:

- **Present-day biological boundary condition:** The new opening subsection recording the universal L-amino-acid, D-sugar, and membrane-lipid stereochemistry of contemporary biology correctly frames the geometric constructions as recovering an independent empirical target rather than merely fitting meteoritic data.
- **Scission-generated void for D-fructose:** The link from bay scission → master mould → ghost pocket → D-fructose complementarity → metabolon retention is well drawn. The proof correctly rests on facial selectivity imposed by the steric boundary.

Author's Reply

The committee's positive assessments are noted with gratitude. The present-day biological boundary-condition subsection and the sugar-void argument are retained without change.

2. C12-Tether Mechanism for L-Amino Acids

Critique: The geometric argument is clear and the accompanying proof is appropriately concise. One residual ambiguity remains: the text could more explicitly state that the lattice constraint converts a potentially racemic bay into a statistical L-excess, rather than an absolute stereospecific outcome. A single clarifying sentence would remove any risk of over-reading.

Author's Reply

A clarifying sentence has been added immediately after the statement of the L-amino-acid proposition: "The lattice constraint does not render the bay absolutely stereospecific; it converts a potentially racemic output into a statistical excess of the L-enantiomer."

4. Parsimony Simulation (Simulation A)

Critique: Simulation A provides a useful quantitative illustration of the Occam advantage of a single geometric cause. The vertical layout is appropriate for the two-column format. The caption should explicitly note that the numerical parameters are deliberately generous to the independent-causes model, so that the resulting odds are a lower bound on the advantage of the single-geometry account.

Author's Reply

The caption of Simulation A now explicitly states that the chosen numerical parameters are deliberately generous to the independent-causes model, so that the reported posterior odds constitute a lower bound on the advantage of the single-geometry explanation.

5. Relation to Circularly Polarised Light

Critique: The manuscript correctly treats circularly polarised light (CPL) as a complementary external agent rather than a competing exclusive explanation. A single sentence in the Discussion or Open Questions reminding the reader that the lattice mechanism does not require the absence of photonic bias would further clarify the intended complementarity.

Author's Reply

A sentence has been inserted in the Open Questions subsection affirming that the lattice-derived bias and circularly-polarised-light mechanisms are regarded as complementary rather than exclusive constraints.

6. Minor Residual Points

Critique:

- Ensure that every cross-reference to the patent uses the consistent form "Patent US 12,195,423".
- In the appendix corpus statement, the photosynthetic-macrocycle paper is correctly cited; no change needed.

Author's Reply

All patent citations have been verified to uniformly reflect the format "Patent US 12,195,423" throughout the manuscript.

Author's Concluding Remarks

Dear Members of the Editorial Board and Review Committee,

I thank the Committee for its careful and constructive reading of the manuscript. All recommendations have been implemented. By explicitly defining the statistical nature of the L-enantiomer excess and formalizing the complementarity with external agents like CPL, the geometric model's predictive power is now perfectly aligned with empirical observations. With these corrections, the manuscript is internally consistent and, I believe, ready for publication.

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 treatment of the C12-tether

mechanism as yielding a statistical rather than absolute L-excess, the bounding assumptions of the parsimony simulation, and the framing of circularly polarised light as a complementary rather than competing mechanism was found to be consistent throughout. The unification of the chiral origins of amino acids, sugars, and membrane lipids under a single topological defect was noted as the manuscript's central structural contribution.

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	2026-08-21	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.