

AI-AUGMENTED PEER-REVIEW:
*Higher-Order Geometry of the Abiotic Loom: Axis
Alignment, Pore Tethering, and Side-Chain Packing
of Secondary-Structure Elements in the Chrysene
Tensor Space*

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: Grok 4.6.

- (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: Grok 4.6.

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. Only the author’s final meta-review response, also drafted using Grok 4.6, is included in this review record. Editorial meta-review conducted independently using Grok 4.6.

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 elevates the empirical examination of the Chrysene Tensor Space from the local dihedral enrichment established in Papers 1 and 2 to a coherent set of higher-order geometric tests. Three independent lines of evidence—axis alignment, direct pore/channel tethering, and side-chain packing/rotameric organization—are developed with quantitative measurements drawn from high-resolution public structures (primarily GluA2 AMPA receptor M3 helix and a TREM2 β -strand).

The residue-by-residue tether-gap tables (especially Table 6) and the χ_1 rotamer analysis (Table 7 and Remarks 12–13) supply concrete numerical support that was previously only promissory. The reframing of the rotamer data in the direction of *de novo* nucleation by a pre-existing lattice is particularly effective and consistent with the overall logic of the series. Continuous thermal fluctuations are correctly retained inside the open cells; the lattice is required only to supply absolute steric bounds.

The paper is structurally complete, mathematically coherent with the preceding works, and ready for publication after a small number of clarifications.

REVIEWER COMMENTS & AUTHOR RESPONSES (AI-AUGMENTED)

1. Scope of Side-Chain Contact Claims (Props. 6–8)

Critique: The side-chain adjacency propositions still rest partly on geometric proxies (radial distance and binary face classification) rather than explicit distances between side-chain heavy atoms and lattice-wall atoms.

Recommendation: Soften the language of “systematic contacts” and “adjacency matrix” to reflect the proxy nature of the current measurements, or note explicitly that full atom-to-wall distances remain a task for subsequent work.

Author’s Reply

The language of Propositions 6–8 and the surrounding prose has been revised to emphasize that the present measurements are geometric proxies (radial distance from the helical axis and binary face classification). Explicit atom-to-wall distance matrices are noted as a natural extension for subsequent work. The claims now read as demonstrations of systematic face differentiation and amphipathic organization consistent with lattice contact, rather than as fully resolved adjacency statistics.

2. Statistical Characterization of Axis Alignment

Critique: Proposition 1 asserts non-random vertical alignment on the basis of a single detailed example (AMPA M3) plus qualitative remarks.

Recommendation: A brief quantitative statement of the residual θ_z distribution (or at least an explicit acknowledgment that the broader ensemble statistics are deferred) would strengthen the claim.

Author's Reply

A clarifying sentence has been added to Section 3.1 stating that the AMPA M3 analysis supplies a concrete, residue-resolved illustration of the alignment principle, while a full ensemble distribution of residual θ_z angles across the curated corpus remains a task for later quantitative surveys. The proposition itself is unchanged in substance.

3. Rotamer Enrichment Language (Props. 9–11)

Critique: The observed face-dependent bias (lattice face $\sim 79\%$ *trans*) is real and valuable, yet the manuscript occasionally uses the stronger language of “lattice-induced enrichment.”

Recommendation: Clarify that the present data demonstrate native discreteness and face-dependent organization that are consistent with lattice templating, while a direct contact-versus-free ensemble comparison remains future work.

Author's Reply

The wording of Propositions 9–11 and Remarks 12–13 has been adjusted. The data are now described as demonstrating native rotameric discreteness and a clear face-dependent bias that are geometrically consistent with templating by a pre-existing lattice. Direct statistical comparison of contact versus free ensembles is explicitly deferred.

4. Table 6 Window Statement

Critique: The text states that minimum gaps “lie predominantly inside the functional window of approximately 5–7.5 Å.” A minority of core residues fall slightly below 5 Å.

Recommendation: A one-sentence qualification noting that the majority of core positions remain inside or near the window would improve precision.

Author's Reply

The relevant sentence has been revised to: “The minimum gap to the nearest tower remains positive for every residue and, for the majority of core positions, lies inside or immediately adjacent to the functional window of approximately 5–7.5 Å.”

5. Minor Typographical / Consistency Points

Critique:

- Ensure uniform use of “Paper 1 / Paper 2” versus citation keys.
- Confirm that all table captions correctly identify the PDB entry and residue range.

Recommendation: The recommended revisions are minor, clarifying, and do not affect the central geometric conclusions of the work.

Author's Reply

Citation style has been standardized across the manuscript to uniformly reference “Paper 1” and “Paper 2,” and all table captions have been rigorously checked for accurate PDB and residue-range identification.

AUTHOR'S CONCLUDING REMARKS

Dear Members of the Editorial Board and Review Committee,

I thank the committee for its careful and constructive evaluation of the manuscript. Each recommendation has been addressed. These revisions sharpen the precision of the empirical claims without altering the central conclusion: the discrete geometry of the Chrysene Tensor Space accommodates the three-dimensional shape, orientation, and side-chain organization of native secondary-structure elements at the level of residue-resolved measurements.

I believe the manuscript is now 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 structural-biology claims, and confirmed that the manuscript satisfies the journal’s standard for internal consistency at this review tier. The manuscript’s treatment of the proxy-based scope of the side-chain contact claims, the statistical characterization of axis alignment, the qualified framing of rotamer enrichment as consistent with (rather than proven to be caused by) lattice templating, and the precision of the Table 6 window statement 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	2026-08-25	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.