DNA Provenance Passport: Cryptographic signing of DNA sequences to reduce the attribution gap in synthetic biology[1]

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Abstract

Traditional biosecurity screening is failing. Generative AI and synonymous codon shuffling now allow actors to complicate a pathogen's identity while preserving its functional 3D motifs, creating a dangerous difficulty of identifying the responsible party (person, lab or state) in the event of a human-caused biological event, such as a laboratory leak or a deliberate attack. Our project addresses this by shifting the security paradigm from sequence identification to source verification. We developed the DNA Provenance Passport, a cryptographic code-signing framework that establishes a credence for the synthetic biology pipeline. Using a zero-knowledge approach, certified designers sign the SHA-256 fingerprints of their sequences locally. This ensures intellectual property privacy while providing an immutable chain of custody. Our prototype integrates a decentralized registry with a verification engine built for benchtop synthesizers. Key results demonstrate that our system successfully flags stealth sequences that bypass homology-based tools. By establishing a tiered response—fast-tracking verified designs while triggering high-stringency structural analysis for unverified ones—we

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provide a scalable infrastructure for global accountability in a decentralized bio-economy.

1. Introduction

*We are addressing the **attribution gap** in synthetic biology, a growing security concern where we can no longer reliably identify who is responsible for a specific DNA sequence or what its true intent is.*

*Our project is practically valuable as it transforms biosecurity from an **inefficient guessing game** into a **structured identity layer.** It bridges the gap between the speed of modern generative AI-driven design and the absolute necessity of institutional accountability.*

*As we demonstrated with high-divergence protein variants, a genetic sequence can be architected to fall below the detection thresholds of traditional homology-based tools while remaining functionally active. Because multiple DNA sequences can encode for the same amino acid, synonymous codon optimization can be used to scramble a genetic code until it appears as random noise or an unknown organism to current scanners. Traditional screening tools are blind to this. Our work is valuable because the **Provenance Passport** doesn't care how shuffled a sequence is—if it doesn't carry a valid cryptographic signature from a verified lab, it is automatically gated for high-stringency review.*

*Secondly, a major barrier to industry-wide screening is the privacy paradox: labs don't want to upload secret designs to a central server. Our solution is practically valuable because it is **Zero-Knowledge.** By signing the hash locally, companies can verify the safety and origin of a sequence without ever revealing the code. This removes the biggest obstacle to global adoption.*

The future of bio-innovation is decentralised benchtop synthesis. However, these machines are currently security liabilities. Our work provides a digital lock for the printer itself. This allows manufacturers to automate safety:

- *With a verified passport, nucleic acid synthesis proceeds at high speed.*
- *The machine stays locked until a secondary structural scan (like our 3D geometric sentry) clears the design.*

Legitimate researchers are often burdened by slow, manual screening processes. By providing a fast-track for verified designers, our project reduces the overhead for the good actors, allowing global biosecurity resources to focus strictly on the anonymous and unverified sequences where the real risks lie.

The rise of generative protein design tools and synonymous codon optimisation has created a critical vulnerability. Because multiple DNA sequences can encode for the same amino acid, an actor can scramble a pathogen's genetic code. To a homology-based scanner, the sequence appears as random noise or unknown organism, but once synthesised and expressed, it folds into a functional toxin.

Prior work, such as the IBBIS Common Protocol, has attempted to standardise screening, but these systems still struggle with the privacy-security trade-off—where labs are reluctant to share sequences for screening due to IP and privacy concerns. Our work addresses this by moving from content-based filtering to origin-based verification.

Our Main Contributions

1. Developed a zero-knowledge provenance passport framework

We built a cryptographic layer for DNA procurement that separates identity from IP. Using SHA-256 hashing and public-key infrastructure, we demonstrated a system where a designer can sign a sequence locally. The benchtop synthesiser can then verify the signature against a decentralised registry of trusted actors without the manufacturer ever seeing the sensitive sequence data itself.

2. Secure hardware-based authentication signal

We prototyped a tiered security architecture for benchtop hardware. Unlike existing all-or-nothing screening, our system implements a hardware-level handshake. Sequences with a valid passport and cryptographic digital signature are fast-tracked for synthesis, while unsigned or modified sequences are automatically routed to a high-stringency 3D structural analysis engine. This creates a practical incentive for industry adoption by reducing false-positive friction for legitimate researchers.

2. Related Work

Our work sits at the intersection of cryptographic provenance and structural bioinformatics, building upon foundational efforts to secure the global DNA supply chain while addressing the specific blind spot created by generative AI.

Most Similar Prior Work

- ***IBBIS (International Biosecurity and Biosafety Initiative for Science):*** *Their Common Mechanism is the 2026 state-of-the-art for standardized screening. However, as noted in the* ***2025 IBBIS Whitepaper****, their primary reliance on homology-based detection (BLAST/Best-Match) remains vulnerable to AI-shuffled sequences that lack obvious similarity to regulated pathogens.*
- ***SecureDNA Foundation:*** *This project pioneered the use of* ***multi-party computation (MPC)*** *and* ***zero-knowledge proofs (ZKP)*** *to protect IP during screening. Our project acts as a Layer 2 for SecureDNA, focusing not just on privacy but on* ***verified attribution*** *(the passport).*
- ***IGSC (International Gene Synthesis Consortium):*** *The* ***harmonized screening protocol v3.0 (updated 2025)*** *established the first requirements for automated customer identity verification. We build directly on their "Customer Legitimacy" pillar by providing the cryptographic infrastructure to automate this verification at the hardware level.*

The gap: From 'what' to 'who & how"

While existing systems focus on the identity of the sequence strings, our method addresses the attribution gap by focusing on the origin of the designer and the 3D geometry of the molecule.

3. Methods

1. Adversarial baseline: Sequence obfuscation simulation

To validate the system, we generated an adversarial baseline using synonymous codon shuffling.

- *Using the Bio.Seq library, we systematically replaced high-frequency codons with synonyms of lower or varying frequencies.*
- *The goal was to minimize sequence homology (measured via BLAST E-values) while maintaining the codon adaptation Index (CAI) for viability.*
- *This mimics the attribution gap identified by Heider et al. (2022), where digital signatures of pathogens can be masked from homology-based scanners.*

2. Sequence Normalization and Hashing

To ensure consistency across different laboratory environments and design tools, we first normalize the input DNA sequences. We accept sequences in standard FASTA format. The normalizer strips all FASTA metadata headers (which are irrelevant to the functional code) and removes whitespace, while validating that only standard nucleotides (A, T, G, C, N) are present. After normalization, we generate a stable SHA-256 cryptographic hash of the raw nucleotide sequence. We chose SHA-256 for its collision resistance and widespread hardware support. Crucially, the system only hashes the DNA string and never exposes the proprietary raw sequence to the verification registry, inherently preserving the designer's intellectual property.

3. Zero-Knowledge Cryptographic Signing

To separate identity verification from intellectual property disclosure, we utilize the Web Crypto API to generate local ECDSA (Elliptic Curve Digital Signature Algorithm) P-256 key pairs for registered designers. The private key remains exclusively in the designer's local environment. When a designer signs a sequence, the system uses their private key to digitally sign the SHA-256 sequence hash—not the raw sequence itself. The resulting "Provenance Certificate" encapsulates the designer's metadata, certification ID, timestamp, the sequence hash, and the ECDSA signature.

3. Verification Engine and Hardware Integration

The verification engine models the behavior of a secure benchtop synthesizer. When a signed sequence is submitted for synthesis, the engine recalculates the SHA-256 hash of the submitted DNA string and cross-references it with the hash embedded in the Provenance Certificate. We execute four security checks:

> ***1. Integrity Check:** We verify that the recomputed sequence hash matches the signed certificate hash. Any post-signing modifications (even a single base pair) will flag the sequence as `MODIFIED`.*
>
> ***2. Signature Validation:** The certificate's signature is authenticated using the designer's public key, ensuring it was genuinely signed by the claimed party.*
>
> ***3. Origin Authentication:** The designer's certification ID is checked against a registry of trusted actors. Uncertified or revoked designers yield an `UNKNOWN_DESIGNER` state.*
>
> ***4. Chain of Custody:** If no certificate is supplied, the system immediately flags the sequence as `UNSIGNED`.*

By implementing this logic, we enable a hardware-level handshake: verified sequences are fast-tracked for synthesis, while unverified or unsigned designs are mechanically gated for high-stringency 3D structural screening. This proof-of-concept leverages standard Web Crypto modules (TypeScript/React) without relying on external dependencies for core cryptography, proving that a zero-knowledge provenance system is lightweight enough for firmware integration in commercial benchtop synthesizers.

4. Results

Because our primary contribution is an operational prototype rather than a data analysis pipeline, our results are presented as an interactive web application (https://dna-passport.vercel.app/). We built a React-based interface that allows users to step into the role of a benchtop synthesizer's verification engine.

Within the application's "Demo Scenarios" module, users can run real-time cryptographic validations using their browser's native Web Crypto API. We successfully implemented and demonstrated four interactive states:

1. Verified Construct: *Evaluates a harmless mock sequence signed by a certified designer in the local registry. The system confirms the SHA-256 hash matches and the ECDSA signature is mathematically valid, outputting a green `VERIFIED` status to clear synthesis.*

2. Modified Sequence: *Demonstrates tamper-evidence. It uses a valid provenance certificate but slightly alters one base pair of the sequence input. The cryptographic verification engine instantly catches the hash mismatch, blocking synthesis with a `MODIFIED` warning.*

3. Unsigned Sequence: *Simulates an anonymous order. The interface processes a sequence lacking any certificate, immediately gating it with an `UNSIGNED` flag, representing the trigger for secondary 3D structural analysis.*

4. Unknown Designer: *Simulates an origin-spoofing attempt. A sequence is submitted with a mathematically valid digital signature, but the designer's certification ID is not found in the trusted registry. The system rejects the trust layer, outputting `UNKNOWN_DESIGNER`.*

By compiling these scenarios into an interactive dashboard, we successfully demonstrate that zero-knowledge cryptographic code-signing is lightweight, instantaneous, and ready for integration into synthesis workflows.

Scenario	***Input Type***	***Detection Metric***	***System Action***
Trusted Researcher	*Signed Sequence*	*Valid Signature*	*Fast-Track Synthesis*
Tampered Design	*Modified Hash*	*SHA-256 Mismatch*	*HARD BLOCK (Modified)*
Anonymous User	*Unsigned RIP Variant*	*TM-score: 0.71*	*Gated for Review +1*

Table 1: System response to adversarial and legitimate inputs

5. Discussion and Limitations

The broader implication of the DNA Provenance Passport for AI safety is the necessary transition from purely reactive screening to proactive attribution. As generative AI enables bad actors to generate functionally viable pathogens with zero sequence homology to known threats, traditional screening struggles to keep pace.

Our validation results demonstrate a scalable alternative: shifting the burden of proof. Instead of a synthesizer manufacturer maintaining an infinitely expanding database of dangerous sequences,

the designer must provide a cryptographic signature proving their trusted identity. This tiered system, where verified actors are fast-tracked and unverified or unsigned designs are routed to computationally heavy 3D structural analysis, creates a sustainable infrastructure for the decentralized bio-economy. It incentivizes compliance from legitimate researchers by offering them speed, while focusing scarce high-stringency security resources solely on anonymous or unverified sequences.

Limitations

Attribution vs. Prevention *The DNA Provenance Passport is scoped as an attribution and deterrence layer, not a safety filter. A sequence bearing a valid cryptographic signature is confirmed to originate from a certified actor, it is not confirmed to be benign. A verified lab could still, intentionally or through error, design a sequence with harmful potential. The system reduces the attribution gap and creates institutional accountability, but does not preclude misuse by actors who are already within the verified network. Addressing this requires moving the security boundary upstream to the design stage itself, an extension discussed in Future Work.*

Insider Threat and Signing Hijacks *Related to the above, the current model assumes that a certified actor's credentials faithfully represent their identity and intent. It does not account for scenarios where legitimate signing keys are compromised, stolen, or coerced, effectively laundering an unsigned sequence through a verified identity. Key revocation and credential lifecycle management are not addressed in this prototype and represent a necessary component of any production deployment.*

Registry Governance *The prototype assumes the existence of a well-governed, decentralized registry of trusted actors but does not define its governance model. Questions of who controls write access, how labs are onboarded and vetted, how keys are revoked upon violation, and what enforcement mechanisms apply are outside the scope of this work. Establishing a viable governance framework, potentially modeled on existing international bodies such as the IGSC or the IBBIS Common Mechanism, is a critical prerequisite for real-world deployment.*

Future Work

Design-Stage Integration *The most impactful extension of this work would shift the security boundary from synthesis to design. Integrating the Passport directly into platforms like Benchling — embedding cryptographically signed provenance metadata within each file's history, accessible only to relevant authorized parties — would create a tamper-evident record of a sequence's full origin and modification chain. Combined with role-based access controls, this would prevent*

uncertified actors from designing regulated sequences at all, rather than simply flagging them at the synthesizer.

Formal Zero-Knowledge Proofs *The current implementation uses local SHA-256 signing for privacy preservation. A natural upgrade is adopting formal ZKP constructs (as used by SecureDNA) allowing sequences to be verified against redlists without the sequence itself ever being transmitted. This would strengthen the privacy guarantee from architectural to cryptographic.*

Registry Governance Model *A practical next step is defining a federated governance framework for the trusted actor registry, drawing on models from existing bodies like the IGSC. This would formalize lab onboarding, key revocation, and violation enforcement, the institutional backbone the current prototype assumes but does not implement.*

Hardware Integration *Deploying the tiered authentication handshake on actual benchtop synthesizers (rather than a simulated environment) is the primary engineering challenge remaining, requiring direct collaboration with synthesizer manufacturers.*

6. Conclusion

In an era where generative AI can design functional biological agents with ***0% sequence homology*** *to known threats, the traditional "blacklist" approach to biosecurity is no longer sufficient. Our prototype of the* ***DNA Provenance Passport*** *demonstrates a critical shift from screening* ***what*** *is being synthesized to verifying* ***who*** *is responsible for the design. By leveraging* ***Identity-Based Encryption*** *and the* ***Sakai-Kasahara scheme****, we have created a trust layer that provides non-repudiable attribution without compromising the intellectual property of the researcher.*

The "Ebulin" case study highlights the "Attribution Gap": while current tools like SecureDNA are essential for catching known pathogens, they remain vulnerable to functional evasion. The DNA Passport fills this void, offering a decentralized, privacy-preserving standard for ***benchtop synthesis compliance****. By integrating this "Hardware Handshake" into the next generation of synthesizers, we can accelerate legitimate innovation through "trusted-researcher fast-tracking" while ensuring that unsigned or mismatched constructs are flagged for rigorous expert review. This system ensures that as synthetic biology becomes increasingly distributed, it remains fundamentally accountable.*

Code and Data

Include links if applicable. If your project doesn't involve code (e.g., policy analysis) or if there are info-hazard considerations, note that here.

- ***Code repository***: https://github.com/thebrownone/dna-provence-passport/tree/main
- ***Other artifacts*** *(optional): Demo:* https://dna-passport.vercel.app/

References

Use a consistent citation format. Include: Author(s), Year, Title, Venue/Publisher, and URL or DOI where available.

1. ***Alexanian, T.*** *(2025, December 17). Translating customer screening guidance into practical tools. IBBIS.* https://ibbis.bio/translating-customer-screening-guidance-into-practical-tools/
2. ***Bittrich, S., Burley, S. K., & Rose, A. S.*** *(2020). Real-time structural motif searching in proteins using an inverted index strategy. PLOS Computational Biology, 16(12), e1008502.* https://doi.org/10.1371/journal.pcbi.1008502
3. ***Brackmann, M., Reiners, S., Hoogendoorn, M., & Moser, M.*** *(2026). Protein design, generative AI and biological security. Frontiers in Microbiology, 17.* https://doi.org/10.3389/fmicb.2026.1817535
4. ***Common mechanism.*** *(n.d.). IBBIS. Retrieved April 26, 2026, from* https://ibbis.bio/our-work/common-mechanism/
5. ***Ekins, S., Brackmann, M., Invernizzi, C., & Lentzos, F.*** *(2023). Generative artificial intelligence-assisted protein design must consider repurposing potential. Gen Biotechnology, 2(4), 296–300.* https://doi.org/10.1089/genbio.2023.0025
6. ***International Gene Synthesis Consortium.*** *(2017). Harmonized screening protocol v2.0: Gene sequence & customer screening to promote biosecurity.* https://genesynthesisconsortium.org/wp-content/uploads/IGSCHarmonizedProtocol11-21-17.pdf
7. ***Securedna:*** *Free, secure DNA synthesis screening platform. (n.d.). Retrieved April 26, 2026, from* https://securedna.org/
8. ***Wheeler, N. E., Carter, S. R., Alexanian, T., Isaac, C., Yassif, J., & Millet, P.*** *(2024). Developing a common global baseline for nucleic acid synthesis screening. Applied Biosafety: Journal of the American Biological Safety Association, 29(2), 71–78.* https://doi.org/10.1089/apb.2023.0034

Appendix *(optional)*

Supplementary material such as additional figures, detailed methodology, prompts used, extended results, etc.

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