Soft Protein Architecture Whitepaper

Soft Protein Architecture

Simulated Ribosomal Folding Dynamics Driven by Triplet-Structure Bias

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1. Introduction

Traditional protein folding models are governed by downstream amino acid interactions post-transcription. However, we propose a structural-emulation hypothesis wherein triplet codons, based on their ribosomal spatial positioning, exhibit natural bonding preferences due to geometric and energy constraints.

This model suggests that folding dynamics may be partially pre-determined during translation, rather than purely post-translational.

2. Hypothesis: Triplet Structural Bias

Each codon (triplet) holds not only symbolic meaning (amino acid map), but also a 3D spatial expression when held within the ribosome's active groove.

The physical closeness and angular orientation of neighboring triplets in the ribosome may favor certain chemical bonds between amino acids that are about to form.

This leads to a quasi-deterministic folding pre-pattern, embedded as a bias in the ribosomal path.

3. Simulation Use Case: Soft Protein Architecture

The Soft Protein system emulates folding paths by using a symbolic codon sequence mapped into a geometric vector space, influenced by structure bias tables.

Instead of full folding computation (e.g., AlphaFold), we propose a compressed bias-based shortcut for low-energy AI use cases.

Applications include:

- Early-stage protein shape estimation
- Bio-inspired data compression
- Synthetic biology instruction filters

4. Position in the AGI Architecture

- Works as an internal analog RAM for soft-biological computing frameworks
- Complements Soft Nucleic (DNA/RNA) as an execution-level biological simulator
- May contribute to adaptive memory or self-repair models via misfold/error tracing

5. Use Case Clarification

This hypothesis is intended as a biomimetic augmentation rather than a replacement for protein-folding simulations. It prioritizes computational simplicity and pattern exploration over molecular precision, making it suitable as a tool for AI-driven synthetic bioengineering.

Although currently theoretical, the model proposes that bond length and energy levels--measurable via GTP consumption events--may reveal folding tendencies embedded in the ribosomal process itself.

If validated, this would support the notion that structure-biased folding patterns are present even before post-translational folding begins.