Title :
Thermodynamics of a Tetra-Stranded Genome: Stability, Thresholds, and Entropic Constraints

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Abstract

The existence of a canonical tetra-stranded hereditary polymer requires more than structural plausibility: it must satisfy **thermodynamic conditions** that favor a genome-scale four-strand state over duplex or partially folded alternatives. In this work, I develop a **minimal thermodynamic framework** for Q-DNA, decomposing the free energy of a tetra-stranded genome into enthalpic interactions, electrostatic contributions, and entropic penalties associated with strand confinement and ordering. I derive **stability thresholds** as functions of temperature, ionic composition, and molecular crowding, and I predict the existence of **environmental stability windows** in which Q-DNA dominates the free-energy landscape. This framework provides quantitative criteria for canonicality and establishes testable predictions for experimental and synthetic realizations of tetra-stranded genomes.

Keywords: Q-DNA, tetra-stranded genome, thermodynamics, free energy, entropy, electrostatics, molecular crowding

1. Introduction

1.1 Why thermodynamics is decisive for Q-DNA

Structural classification and topology define what **can** exist geometrically, but **thermodynamics decides what actually exists**. For duplex DNA, the dominance of the double helix reflects a balance between base-pairing enthalpy, electrostatic repulsion, and entropic costs. Any alternative hereditary architecture must satisfy an analogous balance.

A tetra-stranded genome faces an immediate challenge:

- increased backbone charge density,
- reduced conformational entropy,
- and stronger coupling between strands.

I therefore treat thermodynamics as the **gatekeeper** of Q-DNA existence.

1.2 Scope of this paper

This paper does not attempt to compute exact free energies for a specific chemical implementation. Instead, I aim to:

1. Define a **minimal free-energy decomposition** applicable to any tetra-stranded candidate.

2. Identify **stability thresholds** relative to duplex DNA.

3. Predict **environmental windows** (temperature, ions, crowding) where Q-DNA is favored.

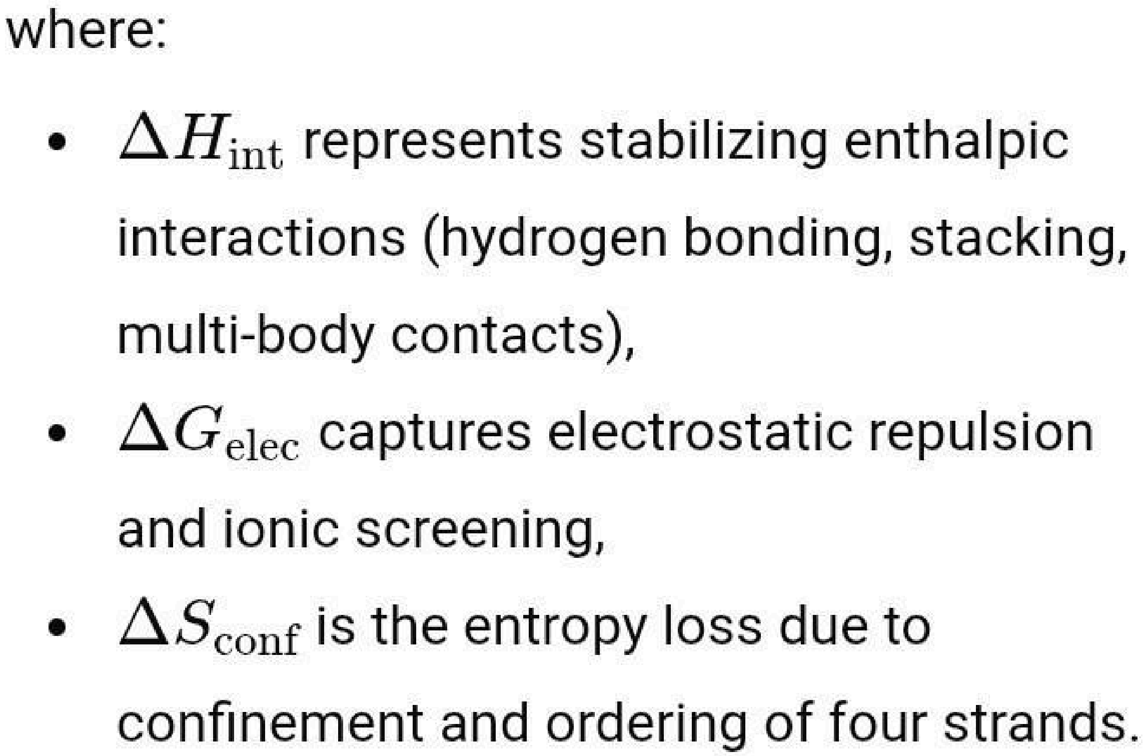
4. Provide falsifiable criteria that separate canonical Q-DNA from marginal or metastable states.

2. Free-Energy Decomposition of a Tetra-Stranded Genome

2.1 Minimal thermodynamic model

I express the free energy per genome segment as:

$$\Delta G_Q = \Delta H_{\text{int}} + \Delta G_{\text{elec}} - T\Delta S_{\text{conf}}$$



where:

- ΔH_{int} represents stabilizing enthalpic interactions (hydrogen bonding, stacking, multi-body contacts),
- ΔG_{elec} captures electrostatic repulsion and ionic screening,
- ΔS_{conf} is the entropy loss due to confinement and ordering of four strands.

This decomposition mirrors classical treatments of duplex DNA thermodynamics while making explicit the additional penalties of multistranded confinement.

2.2 Enthalpic contributions: multi-strand stabilization

In Q-DNA, stabilization is not limited to pairwise base pairing. Instead:

- multi-body hydrogen-bond networks,
- cooperative stacking across strands,
- and topologically enforced contacts

can provide **superlinear enthalpic gains**.

I therefore treat ΔH_{int} as potentially more favorable than a simple sum of duplex interactions, provided cooperativity is strong.

2.3 Electrostatics: the dominant destabilizing term

Four negatively charged backbones in close proximity dramatically increase electrostatic repulsion. The electrostatic free energy depends strongly on:

- ionic strength,
- cation valency,
- and ion correlation effects

I treat ΔG_{elec} as a function:

$\Delta G_{elec}=f([K+],[Mg2+],dielectric,geometr)$

Multivalent cations and crowding agents are therefore **not optional** but central to Q-DNA stability.

2.4 Entropic confinement penalty

Bringing four polymer chains into a single ordered structure imposes a severe entropic cost:

- reduced translational freedom,
- reduced conformational entropy,
- suppression of thermal fluctuations.

This term scales with genome length and defines a **fundamental size limit** unless compensated by enthalpy or electrostatics.

3. Stability Thresholds and Canonicality

3.1 Definition of thermodynamic canonicality

I define Q-DNA as thermodynamically canonical if, over genome-scale lengths:

$$\Delta G_Q < \Delta G_D - \delta$$

where ΔG_D is the free energy of the best competing duplex-dominant state and δ is a finite stability margin.

This criterion parallels, but generalizes, the notion of duplex dominance in classical DNA thermodynamics.

3.2 Temperature dependence

Increasing temperature:

- weakens enthalpic interactions,
- increases entropic penalties.

I predict that Q-DNA will be favored only below a **maximum temperature threshold**, likely lower than that of duplex DNA unless enthalpy is unusually strong.

3.3 Ionic thresholds

I predict **sharp ionic thresholds**:

- monovalent ions **(K^+)** stabilize via screening,
- divalent ions **(Mg^{2+})** enable ion-correlation effects that can overcompensate repulsion.

Below critical ion concentrations, Q-DNA is unstable regardless of sequence.

3.4 Molecular crowding effects

Crowding agents effectively reduce the entropy of unfolded states, favoring compact, ordered conformations. I therefore predict that **crowded environments shift stability boundaries** in favor of Q-DNA.

4. Phase Diagram of Q-DNA Stability

4.1 Environmental stability windows

Combining temperature, ionic strength, and crowding, I predict **finite stability windows** where:

- Q-DNA is globally stable,
- duplex DNA is metastable or unfavorable,
- and transitions are reversible.

Outside these windows, Q-DNA either unfolds or converts to duplex states.

4.2 Absence of universality

Unlike duplex DNA, which is stable across a wide range of conditions, Q-DNA is expected to occupy **narrower but well-defined niches**. This has implications for:

- synthetic implementation,
- astrobiology,
- and early-Earth or non-aqueous environments.

5. Testable Predictions

Prediction 1 — Ionic window dominance

There exist regimes of **[Mg^{2+}]** and **[K^{+}]** where tetra-stranded constructs are thermodynamically favored over duplex constructs of equal sequence length.

Prediction 2 — Temperature-dependent collapse

Q-DNA undergoes cooperative collapse/unfolding at a characteristic temperature distinct from duplex melting.

Prediction 3 — Crowding-induced stabilization

Addition of inert crowding agents expands the Q-DNA stability window.

Prediction 4 — Length-dependent threshold

Below a minimum genome length, Q-DNA is unstable due to entropic penalties; above it, cooperativity dominates.

6. Discussion

6.1 Why duplex DNA usually wins

Duplex DNA represents an optimal compromise between stability and entropy. Q-DNA must overcome additional penalties, explaining why it is not observed in extant biology under standard conditions.

6.2 Why Q-DNA is still plausible

Thermodynamics does not forbid Q-DNA; it restricts it to specific regimes. Synthetic systems and alternative chemistries can exploit these regimes deliberately.

6.3 Implications for origins of life and astrobiology

If early or extraterrestrial environments featured:

- high ionic strength,
- strong crowding,
- or alternative solvents,

Q-DNA-like systems could have been viable competitors to duplex heredity.

7. Conclusion

I have established a **minimal thermodynamic framework** for evaluating the feasibility of a canonical tetra-stranded genome. By decomposing free energy into enthalpic, electrostatic, and entropic contributions, I identify **stability thresholds** and predict **environmental windows** where Q-DNA can dominate. This work provides quantitative criteria that any candidate tetra-stranded hereditary system must satisfy and sets the stage for detailed simulations and experimental tests.

Figures

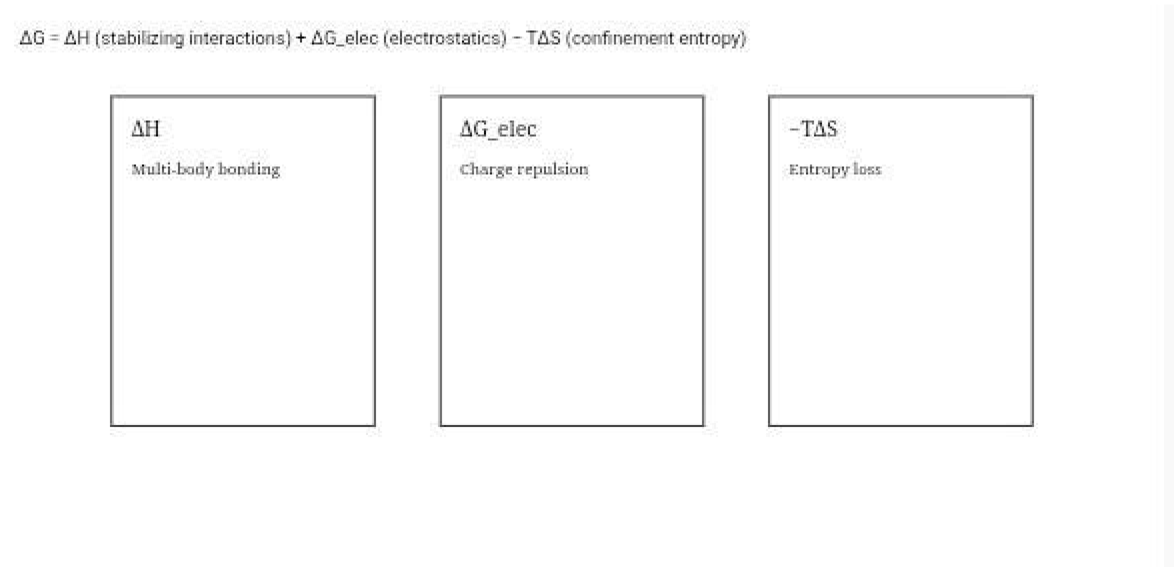


Figure 1 — Free-Energy Decomposition of a Tetra-Stranded Genome

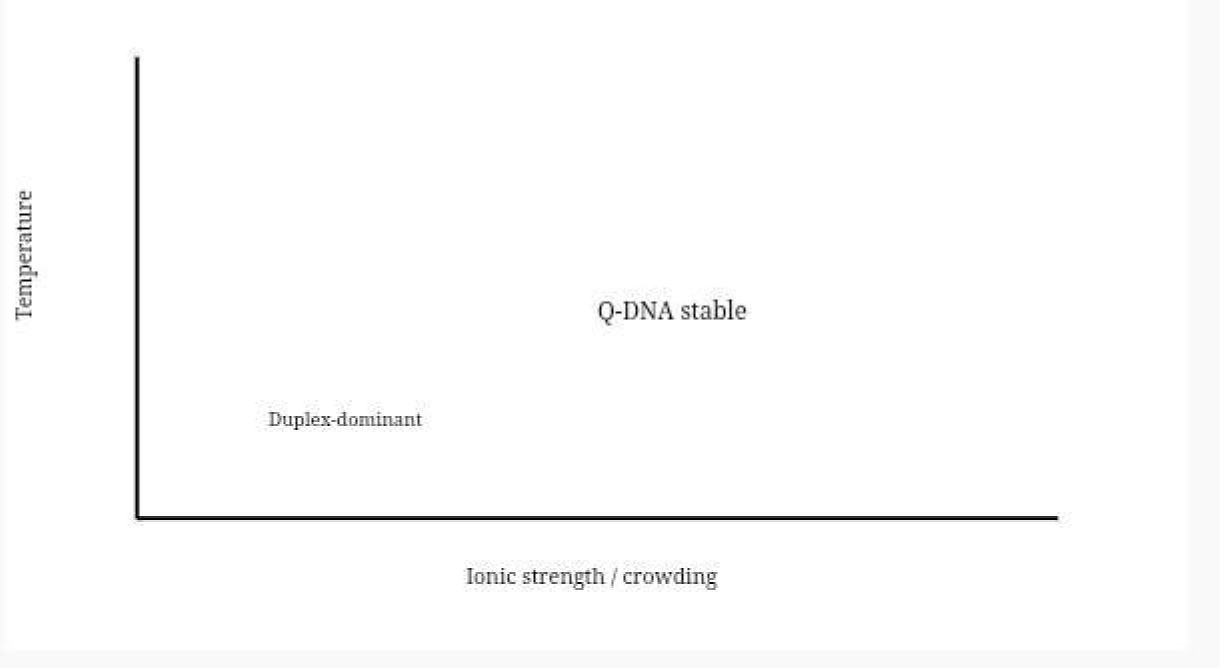


Figure 2 — Thermodynamic Phase Diagram (Conceptual)

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