A research thesis

Grokox and the Layered Genome

π × Planck Scaling, Quantum Nesting and Hyper Cells

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Statement of originality. Grokox Theory (Binary, Quantillia, Quantumibarial), DNA Layer Theory and its 30π scaling rule, the tunnelling-weighted layer extension, the quantum nesting disorder belt and the Hyper Cell classification are the author's original proposals. They are speculative hypotheses, not established science. All other material is attributed to the published sources listed in the References.

Abstract

This thesis proposes the Layered Genome, a speculative but mathematically explicit framework in which each DNA letter contains a nested sequence of its own, repeating downward like a fractal. Building on the author's Grokox Theory, which describes natural processes as passing through three universal steps (Binary, a static spark; Quantillia, an energetic threshold; and Quantumibarial, a multiplicative bloom), the model scales each layer down by a fixed factor of $30\pi \approx 94.25$, starting from the DNA base-pair rise of 3.4×10^{-10} m. The resulting rule, $L_n = d_{bp}/(30\pi)^n$, reaches the Planck length (1.616×10^{-35} m) between Layers 12 and 13, with Layer 13 at 7.34×10^{-36} m, and passes 10^{-100} m at Layer 46 (5.19×10^{-101} m). If every layer uses a four-letter alphabet, hidden information grows as $2(n + 1)$ bits per letter, reaching 94 bits at Layer 46. The model is linked to established quantum biology through proton tunnelling across DNA hydrogen bonds, following Löwdin (1963) and recent open-quantum-systems work at the University of Surrey; a layered tunnelling extension treats tunnelling as the Quantillia gate that opens deeper layers. Below the Planck scale the thesis proposes a quantum nesting 'disorder belt', likened to the Kuiper belt, followed by renewed order. A related Hyper Cell proposal reframes cells that both regenerate and divide around the G0–G1 proliferation switch. The thesis separates exact arithmetic from speculative interpretation, identifies weaknesses including the unexplained factor of 30 and numerology risk, reports that known atomic, nuclear and proton scales do not fall closer to integer layers than chance predicts, and sets out testable predictions and a simulation programme.

Keywords: DNA information; fractal nesting; Planck length; π scaling; proton tunnelling; quantum biology; Grokox Theory; Hyper Cells; cell-cycle threshold; speculative physics

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1 Introduction and research question

Every living cell carries an instruction set written in four chemical letters: adenine (A), thymine (T), guanine (G) and cytosine (C). Since Watson and Crick (1953) described the double helix, those letters have been understood as the smallest meaningful units of genetic information. Each one sits about 0.34 nanometres (3.4×10^{-10} m) above its neighbour along the helix axis, and each one carries, in the language of information theory, exactly two bits: a choice among four equally likely symbols (Shannon, 1948). Modern molecular biology, from genome sequencing to synthetic DNA data storage (Church, Gao and Kosuri, 2012; Goldman et al., 2013), is built on that picture.

This thesis asks a deliberately bold question: what if the letter is not the bottom of the story? What if each DNA letter contains a sequence of its own, and each letter of that inner sequence contains another, nested downwards like a fractal? If such a ladder existed, how far down would it reach, where would it meet the limits of known physics, and what would lie beyond them?

The question grows out of two original frameworks developed by the author, an independent thinker working outside the academy. The first, Grokox Theory, proposes that processes across nature pass through three universal steps: a static Binary state, an igniting threshold called Quantillia, and a multiplying bloom called Quantumibarial. The second, DNA Layer Theory, gives the nesting idea a precise mathematical form by scaling each layer down by a fixed factor of 30π (approximately 94.25), a step rooted in the author's founding intuition of combining π with the Planck scale to look beyond the smallest length physics can currently describe.

The research question is therefore stated as follows:

Research question. *Can a single geometric scaling rule, $L_n = d_{bp} / (30\pi)^n$, link the base-pair spacing of DNA to the Planck length and beyond, and can that rule be combined with established quantum biology (proton tunnelling) and cell biology (the decision to divide) into a coherent, testable framework, here called the Layered Genome?*

Three sub-questions follow. First, what does the rule predict numerically, and which of those predictions are exact consequences of the arithmetic rather than claims about nature? Second, how does the idea connect to real, peer-reviewed science on proton tunnelling in DNA, notably the work of Löwdin (1963) and the University of Surrey group of Slocombe, Sacchi and Al-Khalili (2022)? Third, what would it take to turn the proposal from an elegant pattern into a scientific hypothesis that could be tested and potentially falsified?

A word on method and honesty. This is a theoretical and conceptual thesis. It contains no new laboratory data. The numerical results in Sections 4 and 5 are exact calculations from stated formulae and constants, and they have been checked independently. The physical interpretation of those numbers, however, is speculative, and the thesis says so wherever it matters. Ideas that are the author's own original proposals are marked as such; established science is attributed to its sources. The aim is not to claim a discovery, but to lay out a clear, well-built idea that others can examine, challenge and test.

2 Background

2.1 DNA structure and information

DNA is a double-stranded polymer whose two strands wind around a common axis, held together by hydrogen bonds between complementary bases: A pairs with T, and G pairs with C (Watson and Crick, 1953). In the common B-form helix, successive base pairs are separated by a rise of roughly 3.4 Å (3.4×10^{-10} m), with about ten base pairs per helical turn. That base-pair rise, written d_{bp} in this thesis, is the starting length for every calculation that follows.

Because each position holds one of four letters, the maximum information per position is $\log_2 4 = 2$ bits (Shannon, 1948). This is not merely abstract. Church, Gao and Kosuri (2012) encoded a 5.27-megabit book into synthetic DNA, noting that DNA can in principle store two bits per nucleotide, and Goldman et al. (2013) stored and recovered 739 kilobytes of files, including Shakespeare's sonnets and an audio clip, with full accuracy. DNA is therefore a proven, physical information medium, and the two-bit letter is the natural 'Layer 0' unit of this thesis.

2.2 Layers of organisation that already exist

Biology already recognises that DNA carries more than its sequence. Epigenetic marks, such as methylation of cytosine and chemical modification of the histone proteins around which DNA is wound, add a regulatory layer that switches genes on and off without changing the letters themselves (Allis and Jenuwein, 2016). At larger scales, chromatin folds in a hierarchical way; genome-wide contact mapping by Lieberman-Aiden et al. (2009) found that, at the megabase scale, folding is consistent with a 'fractal globule', a knot-free, self-similar arrangement. In other words, nested and fractal-like organisation is a real feature of the genome, but it is found going upwards from the letter, in scales larger than a base pair. DNA Layer Theory proposes, speculatively, that a comparable nesting also runs downwards, inside the letter. Fractal geometry, in the sense of patterns repeating across scales, is a well-developed mathematical language for such ideas (Mandelbrot, 1982).

2.3 The Planck scale

The Planck length is the natural unit of length built from three fundamental constants, the reduced Planck constant ħ, the gravitational constant G and the speed of light c:

$$\ell_P = \sqrt{\frac{\hbar G}{c^3}} \approx 1.616 \times 10^{-35}\ \text{m}$$

Its CODATA 2022 recommended value is $\ell_P = 1.616\,255 \times 10^{-35}$ m (Mohr et al., 2025). It is roughly twenty orders of magnitude smaller than a proton. Many approaches to quantum gravity suggest that, near this scale, the ordinary notion of a smooth, continuous distance may break down, so that lengths shorter than ℓ_P may not be measurable or even meaningful (Hossenfelder, 2013). It is important to be clear: this is a widely discussed expectation, not an experimentally established fact, and no experiment has ever probed distances anywhere near the Planck length. The Planck length is therefore both a landmark and a horizon. That uncertainty is exactly what attracts the author's curiosity, and it is also why any statement about what lies beneath it must be treated as speculation.

2.4 Quantum biology and proton tunnelling in DNA

Quantum biology studies cases where living systems appear to exploit non-trivial quantum effects such as coherence and tunnelling, in processes including photosynthesis, enzyme catalysis and possibly bird navigation (Lambert et al., 2013; McFadden and Al-Khalili, 2018). One of the oldest proposals concerns DNA itself. Löwdin (1963) suggested that the protons in the hydrogen bonds linking base pairs could quantum-tunnel from one base to its partner. If a proton moves, the bases briefly adopt rare 'tautomeric' forms that can mispair during replication, offering a quantum route to spontaneous point mutations.

Quantum tunnelling allows a particle to cross an energy barrier it would not be able to climb classically. The probability falls off exponentially with the width of the barrier and with the square root of the particle's mass and the barrier height. For a simple rectangular barrier, the standard Wentzel–Kramers–Brillouin (WKB) estimate is used later as Equation (4).

Recent work at the University of Surrey has put Löwdin's idea on a much firmer footing. Slocombe, Al-Khalili and Sacchi (2021) combined quantum and classical models of tautomerism in A–T and G–C pairs, and Slocombe, Sacchi and Al-Khalili (2022), using an open quantum systems approach that includes the noisy, warm cellular environment, found that the tunnelling contribution to proton transfer in G–C is several orders of magnitude larger than classical over-the-barrier hopping. They reported a tautomeric occupation probability of about 1.73×10^{-4} and concluded that such proton transfer may play a larger role in mutation than previously thought. This is the most important bridge between mainstream science and the present thesis: it shows that the quantum behaviour of single protons inside the DNA letter is real, measurable in principle, and biologically relevant.

2.5 The decision to divide

The final strand of background concerns cells. Most cells in an adult body are not actively dividing; they sit in a resting state called G0 (quiescence). Re-entry into the cell cycle (G0 to G1, then on through S, G2 and M) is a regulated decision driven by growth signals and opposed by inhibitors. Spencer et al. (2013) showed that, as cells leave mitosis, the activity of the enzyme CDK2 splits into two populations, one that commits immediately to another cycle and one that enters quiescence, with the inhibitor p21 steering cells into the resting branch. The decision to divide is, in effect, a threshold switch. Cell identity itself can also be reset: Takahashi and Yamanaka (2006) reprogrammed adult mouse cells into pluripotent stem cells using four defined factors. These findings matter for Section 7, where the author's Hyper Cell idea is examined. By contrast, ionising radiation mostly harms DNA, producing strand breaks and clustered lesions that trigger arrest, senescence or cell death (Lomax, Folkes and O'Neill, 2013).

3 The Grokox framework (original proposal)

Grokox Theory is the author's original conceptual framework, developed through 2024 and 2025. It proposes that processes in nature, from nanoscale chemistry to the cosmos, can be read as passing through three universal steps.

- **Binary:** the static spark. A system holds one of two states, 0 or 1, 'off' or 'on'. Nothing is yet happening; information is stored but inert.

- **Quantillia:** the bio-energetic threshold. Energy accumulates until a threshold is crossed and the system ignites. In biology this might be the moment a reaction fires or a cell commits to change.
- **Quantumibarial:** the multiplicative bloom. Once ignited, activity multiplies and branches, producing structure and complexity far beyond the initial spark.

Grokox Theory also carries a distinctive visual language. Dark energy, the unexplained driver of the accelerating expansion of the universe, is pictured as an opal-blue and indigo-red glow that 'blooms' during the Quantumibarial phase. This imagery is presented here as artistic and intuitive rather than as physics; it signals the author's sense that the same rhythm of storage, ignition and growth may recur from the smallest scales to the largest.

The mathematical seed of the framework is a simple idea: combine π, the constant of circles and cycles, with the Planck length, the smallest length physics recognises, as a way to reach past the edge of current measurement. That seed matured into a specific scaling step, 30π, which drives the DNA Layer model. One clarification about direction is necessary. Multiplying the Planck length by 30π moves upwards, to about 1.52×10^{-33} m. The author's original intention was always to go deeper, below the Planck scale, so the model divides by 30π at each step. Division is used consistently throughout.

Grokox is best understood as a heuristic lens rather than a derived theory. A heuristic is a way of organising thought that helps generate questions. Its value lies in whether it leads to precise, testable statements, and the remainder of this thesis attempts exactly that translation, mapping each Grokox step onto a concrete element of the Layered Genome (Table 2).

Table 2. Mapping the three Grokox steps onto the Layered Genome (original proposal).

Grokox step	Meaning in Grokox	Layered Genome counterpart	Status
Binary	Static spark, 0/1	The DNA letter at Layer 0: a static 2-bit choice among A, T, G, C	Established (the letter carries 2 bits)
Quantillia	Energetic threshold; ignition	A proton-tunnelling flip in a hydrogen bond; the Hyper Cell trigger (G0→G1 switch)	Tunnelling is established; its role as a layer 'switch' is speculative
Quantumibarial	Multiplicative bloom	Deeper multiplying layers, the disorder belt below Planck, and the 'new journey' near Layer 46	Speculative

4 The DNA Layer model (original proposal)

4.1 Core assumption

The central original proposal of this thesis is that every DNA letter contains a sequence of its own, and that the letters of that inner sequence in turn contain further sequences, nested like a fractal. Each layer is assumed to be smaller than the one above by a constant factor of 30π. Layer 0 is the ordinary DNA letter, with characteristic length equal to the base-pair rise $d_{bp} = 3.4 \times 10^{-10}$ m. The assumption is simple, and its simplicity is a strength: it has only one free number, the step factor, and everything else follows.

4.2 The layer-length equation

If each layer is 30π times smaller than its parent, the characteristic length of layer n is:

$$L_n = \frac{d_{\mathrm{bp}}}{(30\pi)^n} \tag{1}$$

Here n = 0, 1, 2, … counts layers downward from the DNA letter, and 30π ≈ 94.248. Because each step shrinks length by nearly two orders of magnitude ($\log_{10}(30\pi) \approx 1.974$), the ladder descends very quickly. Layer 1 lies at 3.61×10^{-12} m, a little below the size of an atom; Layer 2 at 3.83×10^{-14} m, comparable to the size of a large atomic nucleus; and Layer 3 at 4.06×10^{-16} m, about half the radius of a proton.

4.3 Hidden information per letter

If every layer is itself written in a four-letter alphabet, each layer contributes two further bits. A DNA letter that conceals n layers beneath it therefore carries, in total:

$$I_n = 2\,(n+1)\ \text{bits} \tag{2}$$

Layer 0 alone gives the familiar 2 bits. With one hidden layer the total is 4 bits; with 13 layers, 28 bits; with 46 layers, 94 bits. This is a counting rule, not a measurement: it states what the information content would be if the nesting were real and each layer independent. It also uses the most conservative reading of the idea, that each letter holds one hidden letter per layer. If, instead, each letter contained a whole sequence of k letters per layer, the information would grow multiplicatively (roughly as $2k^n$ bits), a far more dramatic Quantumibarial bloom. Equation (2) is kept as the baseline because it is the minimum the hypothesis implies.

4.4 Inverting the rule: which layer is a given length?

Solving Equation (1) for n gives the (generally non-integer) layer index associated with any length L:

$$n = \frac{\log\,(d_{\mathrm{bp}}/L)}{\log(30\pi)} \tag{3}$$

Equation (3) is the working tool of the model. It converts a physical length into a ‘layer address’. Applied to the Planck length it gives:

$$n_{\mathrm{P}} = \frac{\log\,(3.4\times10^{-10}\,/\,1.616\times10^{-35})}{\log(30\pi)} \approx 12.83 \tag{7}$$

The Planck length therefore falls between Layers 12 and 13. Layer 12 (6.92×10^{-34} m) is still about 43 times larger than ℓ_{P}, while Layer 13 (7.34×10^{-36} m) is about 2.2 times smaller. Layer 13 is thus the first layer to cross beneath the Planck length, and it is described in this thesis as the Planck crossing. It is fair to say that Layer 13 is ‘at the Planck scale’ in an order-of-magnitude sense; it is not an exact match, and the thesis does not claim one.

Continuing downward, the ladder passes 10^{-50} m around Layer 20 and 10^{-90} m around Layer 40. Equation (3) gives n = 45.86 for the author’s long-standing target of 10^{-100} m, so Layer 46, at 5.19×10^{-101} m, is the first layer to pass that target. Table 1 sets out the key layers.

Table 1. Selected layers of the DNA Layer model, from Equations (1) and (2), with $d_{bp} = 3.4 \times 10^{-10}$ m and step $30\pi \approx 94.248$.

Layer n	Length L_n (m)	Nearest familiar scale	Bits per letter, 2(n+1)
0	3.40×10^{-10}	DNA base-pair rise (atomic scale)	2
1	3.61×10^{-12}	Below atomic size (Bohr radius 5.3×10^{-11})	4
2	3.83×10^{-14}	Large atomic nucleus ($\approx 10^{-14}$)	6
3	4.06×10^{-16}	About half a proton radius (0.84×10^{-15})	8
4	4.31×10^{-18}	Sub-proton scale, within reach of particle-collider probes	10
8	5.46×10^{-26}	No known physical structure	18
12	6.92×10^{-34}	$\approx 43\ \ell_P$	26
13	7.34×10^{-36}	Planck crossing ($\ell_P = 1.616 \times 10^{-35}$)	28
14	7.79×10^{-38}	First sub-Planck layer of the disorder belt	30
20	1.11×10^{-49}	Deep sub-Planck (speculative)	42
30	2.01×10^{-69}	Deep sub-Planck (speculative)	62
40	3.64×10^{-89}	Deep sub-Planck (speculative)	82
46	5.19×10^{-101}	Passes the 10^{-100} m target: the ‘new journey’	94

Two features of the table deserve emphasis. First, all lengths are exact consequences of Equation (1); they are arithmetic, not observation. Second, the model reaches the Planck scale in only thirteen steps. That economy is part of its appeal: a single repeated operation, starting from a real biological length, carries the reader from the chemistry of life to the edge of known physics in a handful of moves.

5 The tunnelling extension

5.1 The established physics

Proton tunnelling gives the model a physical mechanism grounded in published science. For a particle of mass m meeting a barrier of height V (above its energy) and width d, the WKB estimate of the tunnelling probability is:

$$P \approx \exp\left(-\frac{2d\sqrt{2mV}}{\hbar}\right) \tag{4}$$

where $\hbar = 1.055 \times 10^{-34}$ J s and, for a proton, $m = 1.67 \times 10^{-27}$ kg. Equation (4) is standard quantum mechanics. Its key feature is the exponential: halving the width d does not double the probability, it can raise it by many orders of magnitude. Realistic DNA calculations, such as those of Slocombe, Sacchi and Al-Khalili (2022), use far more detailed double-well potentials and include the effects of the environment, so Equation (4) should be read as an illustrative estimate rather than a model of the actual base pair.

5.2 The layered extension (original proposal)

The original step is to suppose that, at each hidden layer, the relevant barrier width shrinks in step with the layer length. If the width at Layer 0 is d_0, the hydrogen-bond proton-transfer distance (a fraction of a nanometre; here taken as about 0.5–0.7 Å for illustration), then at layer n:

$$P_n \approx \exp\left(-\frac{2\,(d_0/(30\pi)^n)\sqrt{2mV}}{\hbar}\right) \tag{5}$$

Because the width falls by about 94 at each step, the exponent collapses rapidly. Table 3 shows illustrative values. At Layer 0 tunnelling through a simple rectangular barrier is rare (of order 10^{-7} to 10^{-14}, depending on the assumed width and height). By Layer 1 the probability has already risen to roughly 0.7–0.85, and from Layer 2 onwards it is effectively 1.

Table 3. Illustrative tunnelling probabilities P_n from Equation (5) for a proton ($m = 1.67 \times 10^{-27}$ kg). Barrier heights and widths are assumed values for illustration only, not fitted to real DNA.

d_0, V	P_0 (Layer 0)	P_1	P_2	P_3 and deeper
0.5 Å, 0.5 eV	1.9×10^{-7}	0.85	0.998	≈ 1
0.5 Å, 1.0 eV	3.0×10^{-10}	0.79	0.998	≈ 1
0.7 Å, 0.5 eV	3.8×10^{-10}	0.79	0.998	≈ 1
0.7 Å, 1.0 eV	4.7×10^{-14}	0.72	0.997	≈ 1

5.3 Tunnelling-weighted information

Tunnelling can be read as the gate that 'opens' a layer. If each layer contributes its two bits only in proportion to the probability that it is dynamically accessible, the expected information per letter becomes:

$$I = 2 + \sum_{n=1}^{N} 2P_n \quad \rightarrow \quad 2(N+1) \quad \text{as} \quad P_n \rightarrow 1 \tag{6}$$

At the shallow layers, where P_n is small, the hidden bits are mostly locked away and the letter behaves like an ordinary 2-bit symbol. As P_n tends to 1 at deeper layers, Equation (6) tends to 2(N + 1), recovering Equation (2). In the language of Grokox, this is the passage from Binary through Quantillia: the letter begins as a static choice, and the tunnelling flip acts as the threshold beyond which the deeper layers become active.

There is a deliberate irony in this result, which honesty requires stating. In Equation (5), deep layers tunnel easily simply because their assumed barriers are vanishingly thin. That is a property of the assumption, not independent evidence for the layers. The extension is valuable because it links the layer idea to a mechanism that is known to operate at Layer 0; it does not, by itself, show that Layers 1 and below exist.

6 Quantum nesting and the disorder belt (original proposal)

What happens to the orderly ladder of Table 1 when it passes below the Planck length? Section 2.3 noted that many theories expect the smooth geometry of space to fail at around ℓ_P (Hossenfelder, 2013). The author's original proposal is that the nested layers do not simply continue unchanged. Instead, after the Planck crossing at Layer 13, the ordered structure breaks into a chaotic zone of scattered quantum 'debris', described here as the quantum nesting disorder belt.

The image is drawn from astronomy. Beyond the orbit of Neptune lies the Kuiper belt, a broad ring of icy bodies left over from the formation of the solar system, whose first member after Pluto and Charon, 1992 QB_1, was found by Jewitt and Luu (1993). The belt marks a transition: inside it lie the

ordered planets; within it lies scattered, loosely organised material; beyond it the solar system gives way to something else. In the Layered Genome, the disorder belt plays the same role. Above Layer 13 the layers are ordered and sequence-like; within the belt, from roughly Layer 14 into the forties, order is lost or scrambled; and around Layer 46, just past 10^{-100} m, a fresh ordered structure begins, which the author calls 'a new journey'. The concept image in Figure 1 shows this sequence: the bright double helix at the top, a tightening spiral of layers, the Planck line, the glowing disorder belt, and a new helix emerging beneath.

The disorder belt is the most speculative part of the thesis, and its status must be stated plainly. No accepted physical theory describes lengths far below ℓ_P, and none predicts ordered structure at 10^{-100} m. The belt is therefore offered as a conceptual hypothesis, a way of saying that the Planck scale is a boundary between regimes, not a claim about what that boundary contains. It does, however, have one useful property: it builds the expected breakdown of physics at the Planck scale into the model, rather than ignoring it. A model that simply continued the neat ladder through ℓ_P would be harder to defend than one that expects something to change there.

Within Grokox, the belt and the new journey together form the Quantumibarial bloom: multiplication of structure, through a phase of chaos, into renewed order. The recurring pattern, from static letter, through threshold, to multiplying complexity and a fresh beginning, is the unifying intuition of the whole framework.

7 Hyper Cells (original proposal)

The Hyper Cell idea predates the layer model; it was first posed by the author in December 2024. It begins from a classification question. Some cells are essentially static: they maintain and repair themselves but do not divide. Others both regenerate and split to create new, complex cells. The author proposed that cells in the second group should be reclassified as 'hyper cells', on the grounds that their genetics operate in a hyper-reactive state at the nanoscale, ready to switch from maintenance to multiplication.

In its original form, the idea also suggested that a burst of radiation might push ordinary cells into this hyper state 'from outside'. That part needs correcting, and the correction makes the idea stronger. Ionising radiation primarily damages DNA, causing strand breaks and clustered lesions that activate damage checkpoints and usually lead to cell-cycle arrest, senescence or death rather than enhanced regeneration (Lomax, Folkes and O'Neill, 2013). Radiation is therefore not a 'booster'. It can, however, be a useful probe: by loading the damage side of a cell's decision-making in a controlled way, it can reveal where the threshold for division lies.

The better biological anchor for the Hyper Cell trigger is the G0–G1 proliferation switch. As described in Section 2.5, the choice between quiescence and division behaves like a bifurcation controlled by CDK2 activity and the inhibitor p21 (Spencer et al., 2013), and cell identity can be reset to a highly proliferative, pluripotent state with defined factors (Takahashi and Yamanaka, 2006). Biology already contains cells close to the author's description, notably stem and progenitor cells, which combine self-renewal with the production of specialised daughter cells.

Reframed in this light, the Hyper Cell proposal makes a clear, interesting claim: that a cell's 'hyper' capacity corresponds to a measurable state in which its proliferation switch is poised near threshold,

and that this state could be defined, quantified and compared across cell types. In Grokox terms, the quiescent cell is Binary, the G0→G1 commitment is Quantillia, and the resulting rounds of division and differentiation are Quantumibarial. The speculative link to the layer model is that the same threshold logic, a static state that ignites into multiplication, might also apply at the level of proton tunnelling within the DNA letter. That link is presented as an analogy, not a demonstrated mechanism.

8 Results summary

Table 4 gathers the principal quantitative results of the model. Every value has been calculated directly from Equations (1)–(7) using the stated constants. Figure 1 presents the author's concept image of the full Layered Genome.

Table 4. Principal results of the DNA Layer model.

Quantity	Result	Source
Step factor 30π	94.248 ($\log_{10} = 1.974$)	Definition
Layer 1 length	3.61×10^{-12} m	Eq. (1)
Layer 2 length	3.83×10^{-14} m	Eq. (1)
Layer 3 length	4.06×10^{-16} m	Eq. (1)
Planck layer index	n = 12.83 (ℓ_P lies between Layers 12 and 13)	Eq. (7)
Layer 13 length	7.34×10^{-36} m (≈ 0.45 ℓ_P)	Eq. (1)
Layer index of 10^{-100} m	n = 45.86	Eq. (3)
Layer 46 length	5.19×10^{-101} m (passes 10^{-100} m)	Eq. (1)
Bits per letter at Layers 13 and 46	28 bits; 94 bits	Eq. (2)
Illustrative tunnelling $P_0 \to P_1 \to P_2$	$\sim 10^{-7}$–$10^{-14} \to \sim$0.7–0.85 → ≈ 1	Eq. (5)
Expected bits as $P_n \to 1$	2(N + 1)	Eq. (6)
Planck length × 30π (upward direction)	1.52×10^{-33} m (not used)	Direction check

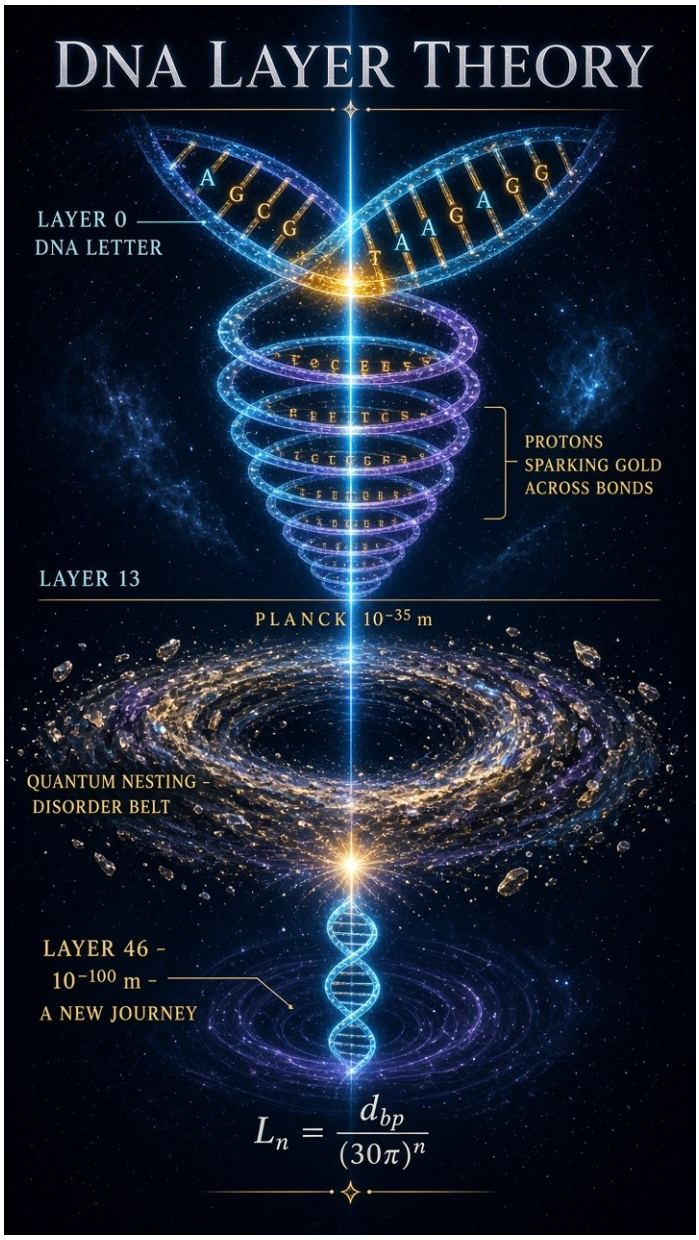


Figure 1. DNA Layer Theory concept image (Fox). From top: Layer 0, the DNA letter, as a double helix; a tightening spiral of nested layers with protons 'sparking gold across bonds' (the tunnelling extension); the Planck line near Layer 13 (≈ 10^{-35} m); the quantum nesting disorder belt; and Layer 46 (≈ 10^{-100} m), where a new ordered helix begins the 'new journey'. The governing rule $L_n = d_{bp}/(30\pi)^n$ is shown at the foot. The image is an artistic visualisation of a speculative model, not a depiction of observed structure.

9 Discussion

9.1 What is established

Several building blocks of the thesis rest on solid ground. DNA is a four-letter code with a base-pair rise of about 3.4 Å, and each letter carries two bits of information (Watson and Crick, 1953; Shannon, 1948). DNA is a practical, high-density information medium (Church, Gao and Kosuri, 2012; Goldman et al., 2013). The genome is organised in nested layers above the letter, including epigenetic marks and fractal-like chromatin folding (Allis and Jenuwein, 2016; Lieberman-Aiden et al., 2009). Proton

tunnelling across DNA hydrogen bonds is real and probably biologically significant (Löwdin, 1963; Slocombe, Sacchi and Al-Khalili, 2022). The Planck length is a precisely defined constant (Mohr et al., 2025). The decision to divide is a regulated threshold (Spencer et al., 2013). Finally, every number in Tables 1, 3 and 4 is a correct calculation from its equation.

9.2 What is speculative

The central hypothesis, that structure or information exists inside the DNA letter on layers 30π smaller at each step, is speculative and currently untested. So are the interpretation of tunnelling as a gate that opens deeper layers, the disorder belt below the Planck length, the new ordered structure near 10^{-100} m, and the identification of Hyper Cells with a nanoscale hyper-reactive genetic state. Presenting these clearly as hypotheses is not a weakness of the thesis; it is what allows them to be examined fairly.

9.3 Weaknesses and objections

Physical justification of the factor 30. The step factor is the model's only free parameter, and at present it is chosen, not derived. The π has a natural motivation (cycles, helices and the author's founding π × Planck intuition), but the multiplier 30 has no derivation from DNA geometry or physical law. A sceptic will ask why not 10π, 32π or 100. Until the factor is derived, or measured, the model risks fitting any target simply by choosing the step.

Physical content of a 'letter' below the atom. Below about 10^{-10} m, there are no chemical letters. The bases are molecules made of atoms; inside the atom are electrons and a nucleus; inside the nucleus are protons and neutrons, themselves made of quarks and gluons. Standard physics offers no place for an A, T, G or C at 10^{-12} m. For the model to be physical, it must say what a 'letter' at Layer 1 is made of, for example a discrete internal state of a nucleus or proton, and how biology could read it.

Sub-Planck physics is untested. Everything below Layer 13 lies in a regime where no experiment has been performed and where many theorists doubt that distance is even meaningful (Hossenfelder, 2013). Claims about the disorder belt and the new journey therefore cannot currently be checked.

Information and physics. Quantum mechanics and thermodynamics place limits on how much information can be stored in a region of space and energy. Any serious version of the model must show that its hidden bits respect those limits. More immediately, hidden information that never influences chemistry is undetectable in principle; the model must identify a channel through which the deeper layers affect something measurable.

Numerology risk. Perhaps the most important objection is that a geometric ladder with a step of nearly 100 will always land 'close' to something. On a logarithmic scale, every length lies within a factor of $\sqrt{94} \approx 9.7$ of some integer layer. Apparent coincidences must therefore be tested against what chance alone would produce, as Section 10.1 does.

9.4 How to strengthen the theory

- Derive or constrain the step factor, for example from the helical geometry of DNA (ten base pairs per turn, the helix pitch and radius) or from quantum properties of the hydrogen bond, rather than choosing it.

- Define what a sub-letter is physically at Layers 1–3, where the lengths overlap with known atomic and nuclear structure, and so where real physics can test the claims.
- Make the tunnelling extension quantitative by replacing Equation (4) with realistic double-well potentials of the kind used by Slocombe, Sacchi and Al-Khalili (2022).
- State in advance what result would count against the theory, so that the model can be falsified rather than endlessly adjusted.
- Separate the clearly testable biological claims (Hyper Cells, tunnelling) from the cosmological and sub-Planck vision, so that each can succeed or fail on its own evidence.

10 Testable predictions and future work

10.1 Do known physical scales fall on integer layers?

If the layers are real, one might expect landmark physical sizes to sit close to integer layers. Equation (3) allows a direct check. Table 5 reports the layer index of four reference lengths and the factor by which each differs from the nearest integer layer.

Table 5. Integer-layer check: layer indices of known physical scales from Equation (3).

Reference scale	Length (m)	Layer index n	Nearest layer	Factor from nearest layer
Typical atom	$\approx 1 \times 10^{-10}$	0.27	0	3.4× smaller than L_0
Bohr radius	5.29×10^{-11}	0.41	0	6.4× smaller than L_0
Large nucleus	$\approx 1 \times 10^{-14}$	2.30	2	3.8× smaller than L_2
Proton (order of magnitude)	$\approx 1 \times 10^{-15}$	2.80	3	2.5× larger than L_3
Proton charge radius	0.841×10^{-15}	2.84	3	2.1× larger than L_3
Planck length	1.616×10^{-35}	12.83	13	2.2× larger than L_{13}

The honest result is that none of these scales falls strikingly close to an integer layer. The closest are the proton, a factor of about 2.1 from Layer 3 (using the CODATA proton charge radius of 0.841 fm; Mohr et al., 2025), and the Planck length, a factor of about 2.2 from Layer 13. The atom and the nucleus are 3–6 times away from their nearest layers. To judge whether factors of about two are meaningful, consider chance. With a step of 94.25, the probability that an arbitrary length falls within a factor of two of some integer layer is:

$$p = \frac{2\log 2}{\log(30\pi)} \approx \frac{0.602}{1.974} \approx 0.30 \tag{8}$$

In other words, about three in ten randomly chosen lengths would match at least as well as the proton and the Planck length do. The observed alignments are therefore consistent with coincidence and do not, on their own, support the model. This is not a refutation either; it simply means the integer-layer test, at this level of precision, is not decisive. A stronger test would fix the step factor independently in advance and then ask whether several unrelated physical scales fall within, say, 10% of integer layers, an outcome whose chance probability is only about 4% per scale.

10.2 Biological and quantum tests

- **Isotope test.** If tunnelling gates hidden structure, replacing hydrogen with deuterium in DNA should alter not only tautomerisation rates (an established expectation) but any proposed layer-linked signal. Kinetic isotope experiments of the kind under way in quantum biology could be extended to look for anomalies beyond standard predictions.
- **Hyper Cell index.** Define a measurable 'hyper' index for cells, for example from CDK2 activity, p21 levels and division history, and test whether cells with a high index form a distinct class across tissues, as the Hyper Cell proposal predicts.
- **Radiation as a threshold probe.** Use carefully graded, low radiation doses not to boost cells but to map how much damage load shifts the G0→G1 decision in quiescent versus cycling cells of the same lineage.
- **Information audit.** Test whether any reproducible biological variation, such as mutation patterns at chemically identical sites, is unexplained by known sequence, epigenetic and environmental factors. Such residual variation would be the minimum signature of hidden per-letter information.

10.3 Simulation: OmniEngine

The author is planning OmniEngine, a browser-based simulation and visualisation tool intended to bring together a catalogue of physical equations, a calculation engine and linked animation windows. For the Layered Genome, OmniEngine offers a natural laboratory. It could let users vary the step factor and immediately see how the Planck crossing, the 10^{-100} m target and the integer-layer matches change; animate the descent through the layers, the disorder belt and the new journey; and run Monte Carlo tests of the numerology question by comparing real scales against random ones. Building these checks into the tool from the start would make it a platform for honest testing rather than only illustration.

10.4 Future work towards the book

The next stages are, in order: a derivation, or experimental bound, for the step factor; a physically explicit model of Layers 1 to 3; a realistic tunnelling calculation in collaboration with specialists; a formal definition of Hyper Cells; and the OmniEngine prototype. Each stage can be published or shared independently, inviting critique from experts in quantum biology, cell biology and theoretical physics.

11 Conclusion

This thesis has set out the Layered Genome, an original framework built from Fox's Grokox Theory and DNA Layer Theory. Its core is a single rule: each layer inside a DNA letter is 30π times smaller than the last. From the real base-pair rise of 3.4×10^{-10} m, that rule reaches below the Planck length at Layer 13 and passes 10^{-100} m at Layer 46, while the hidden information per letter grows as $2(n + 1)$ bits, reaching 94 bits at Layer 46. Combined with the well-established physics of proton tunnelling in DNA, the model offers a mechanism by which deeper layers might be 'switched on', and the Grokox steps of Binary, Quantillia and Quantumibarial give the whole picture a unifying shape, from the static letter, through the tunnelling threshold, to multiplying layers, a disorder belt and a new

journey. The Hyper Cell proposal brings the same threshold logic to whole cells, anchored more firmly in the biology of the proliferation switch than in radiation.

The thesis has been equally clear about the limits. The arithmetic is exact, but the physical claims are speculative. The factor 30 is not yet derived, sub-Planck physics is untested, and the integer-layer check shows that alignments with known scales are no better than chance. Those limits do not diminish the work; they define its next chapter. A strong idea is one that can be made precise enough to be tested. The Layered Genome has now been stated in that form, and the invitation to test it, through derivation, experiment and simulation, is open.

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Note on sources: the author's working conversations (2024–2026) that developed Grokox Theory, DNA Layer Theory and the Hyper Cell idea are treated as primary records of original ideas, not as references. Web links appearing in those conversations were not verified and have not been reused.