THE LIVING ADDRESS

# RNA Polymerase and Transcription Initiation

*The Reading Head*

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*In which the cell learns to read its own library — sending a molecular scribe to copy out passages into a working script — and we find the reading-head itself cut from the lattice, built on the number thirty-six and the first prime, while the choice of which passage to read is the moment the field decides which address to express.*

*Tau (T) is the living fabric of time itself — the sole substance of which all physical reality is composed. Every particle, force, wavelength, and conscious experience is a structured configuration of T-flow. There is no gravity, no electromagnetic force, no strong nuclear force as separate entities: all are registers of the single T-field operating across dimensional levels. The conservation law $d\Sigma T=0$ governs all change: T is never created or destroyed, only redistributed.*

## Introduction — Through the Force of Time

*The chapter that follows is, in the conventional telling, the machine that transcribes DNA into RNA, and how it chooses where to begin. Read through the Universal Force of Time, it is where the cell reads its address — and the reading-head itself turns out to be cut from the lattice, while the choice of what to read is the field deciding which coordinate to express.*

Chapter Two showed the address written; Chapter Three, copied. This chapter shows it read — and note first how the cell reads. It does not consult the master coordinate directly and risk wearing it out; it sends a scribe to copy the needed passage into a short, disposable working script, the RNA, and works from that. The library that is far too large to use all at once (Chapter One) is read a passage at a time, by copying, so that the address itself is never spent. This is exactly the care you would take with a coordinate you could not afford to lose.

Watch the reading machine itself, because it is built from the same numbers as the thing it reads. The bacterial polymerase carries two copies of a subunit whose mass is thirty-six thousand — and thirty-six is the very number of degrees that B-form DNA turns through at every step, the hub of Chapter Two. The read-head is cut from the address's own geometry: two of the 36, and one each of the larger parts, on the first prime of the

lattice. The machine and the molecule it reads are made to the same protractor.

Watch, too, what reading a gene really is. A promoter is not merely a start signal; it is the point at which the field chooses which address to express, here and now. In the bacterium a detachable selector — the σ factor — picks the promoter, and so picks the passage to be read; in the larger cell, three separate polymerases read three different strata of the registry, the machinery of the read-head, the messages, and the small adaptors, each with its own engine. And as with copying, it is the beginning that is gated. Once reading starts it runs on; the controlled moment is the choice to read at all — the same readout-gate we met at the replication fork, the field deciding which coordinate to bring into expression.

One honest note. The tail of the larger polymerase carries a seven-residue repeat, and seven is not a number of the lattice — the lattice is built on two, three, five and π. The book does not force it. It reads the seven as an off-lattice drift, of exactly the kind the theory expects to sit slightly off a node and be re-pegged, and notes that the number of repeats brackets twenty-five, which is five squared. Where a value does not land on the lattice, this book says so plainly rather than bending it to fit.

*Carry this into the chapter: reading a gene is the field selecting and expressing one address — through a machine built on the same 36 the address turns by, gated at the moment of choosing, and copying each passage into a disposable script so the coordinate itself is never spent.*

SECTION 4.1

## Reading Without Destroying

A great library holds far more than any reader needs on any given day, and a careful librarian does not hand out the original of a rare and irreplaceable manuscript to everyone who wants to consult it. The original is kept safe; a copy is made of the passage required, and the reader works from the copy. The master is never worn, never lost, never marked. We saw in Chapter One that a cell’s library holds far too much information to use all at once, and we have seen since how carefully the master is guarded and copied. It should be no surprise, then, that when the cell comes to use its library — to read out a particular gene and build something from it — it does exactly what the careful librarian does. It does not read the DNA directly and risk wearing out the address. It copies the needed passage into a short, disposable working script, and works from that.

That working script is RNA — ribonucleic acid, a molecule almost identical in chemistry to a single strand of DNA, but built to be temporary. A messenger RNA is made when a gene is to be used, carried to the cell’s workshops, read out to build a protein, and then destroyed. It is the photocopy of the passage, not the passage itself.

This chapter and the next are about how that copy is made — the process called transcription — and about the remarkable machine that makes it. This chapter concerns the machine and the moment it begins; the next follows the copy as it grows and ends. But hold on to the shape of the thing from the start: the cell reads its address by copying, so that the address is never spent. Reading, in a cell, is a kind of careful, temporary transcription — the very word we use for it.

SECTION 4.2

## The Scribe and the Script

The scribe is an enzyme called RNA polymerase, and its work is a cycle of four movements. First it must find and settle onto the right place on the DNA — a landing site, just ahead of the gene, called the promoter. Then it must begin, laying down the first few letters of the RNA copy against the DNA template. Then it elongates, moving down the gene and stringing out the RNA behind it letter by letter, each RNA letter chosen to match the DNA letter it reads. And finally it terminates, releasing the finished RNA and letting go of the DNA, ready to begin again elsewhere. Bind, initiate, elongate, release: the transcription cycle.

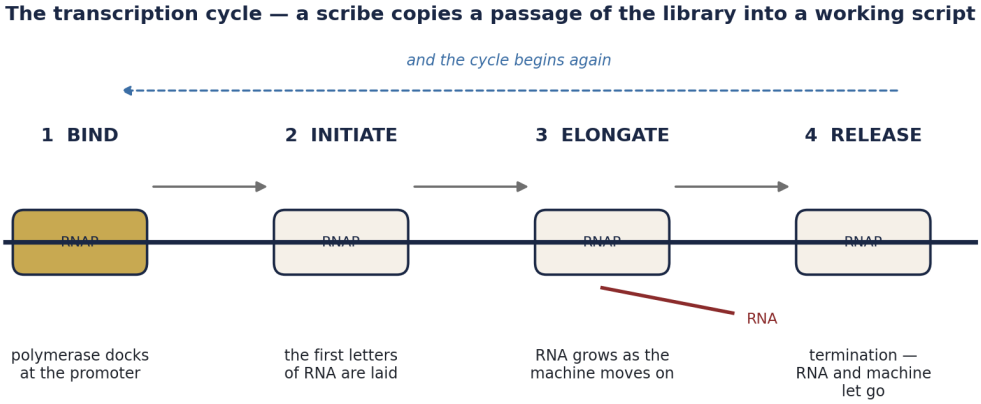


**Figure 4.1.** The transcription cycle. RNA polymerase binds a promoter just ahead of a gene, initiates the RNA copy, elongates it as it moves down the gene, and finally terminates and releases — a scribe copying one passage of the library into a short working script, then moving on to the next.

The RNA that results is a faithful copy of one strand of the gene, differing only in small chemical details of its backbone and in one of its four letters. It carries the same sequence, the same information, the same stretch of the address — but in a form meant to be used and discarded. And because the copy can be made over and over from the same master, the cell can read a gene once or ten thousand times without ever touching the original. A single bacterium holds only a few thousand of these polymerase machines — roughly three thousand — and at any instant about half of them are at work, copying; the rest wait, bound loosely to the DNA or drifting free, until they are needed. The

library is busy, but the master is never at risk.

SECTION 4.3

## The Machine Built on the Lattice

Now look closely at the machine itself, because it holds one of the quiet surprises of this book. The bacterial RNA polymerase is not a single lump of protein but an assembly of several distinct parts, each a subunit with its own job, clipped together into the working whole. Take them apart and weigh them — which biochemists do, by size — and a pattern appears in the numbers that is hard to pass off as accident.

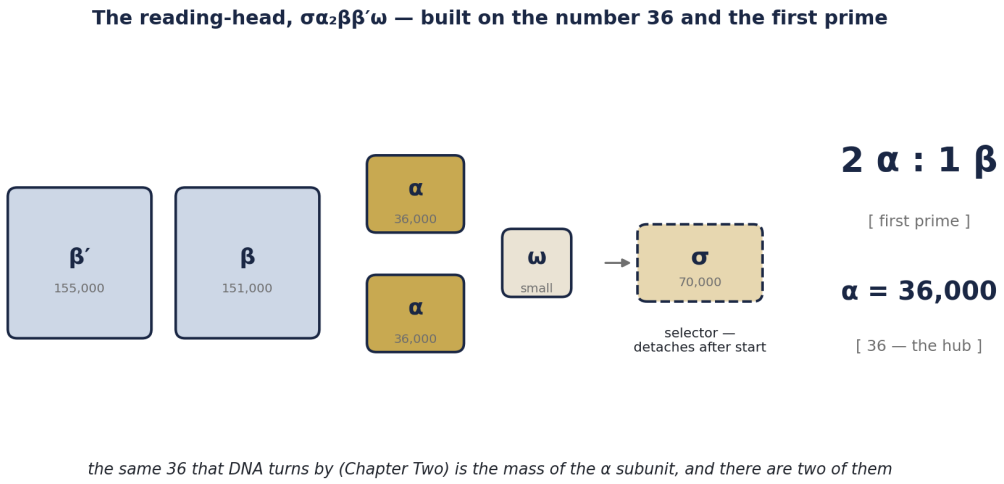


**Figure 4.2.** The bacterial reading-head, written $\sigma\alpha_2\beta\beta'\omega$. It carries two copies of the α subunit, each of mass 36,000, together with the larger β (151,000) and β′ (155,000), a small ω, and a detachable σ (70,000) that selects where to begin. The machine that reads the address is built on the number 36 — the very step, in degrees, by which DNA turns — and there are two of them, on the first prime of the lattice.

The assembly is written, in the biochemist's shorthand, $\sigma\alpha_2\beta\beta'\omega$. There is one large β subunit of mass 151,000, one slightly larger β′ of 155,000, a small ω whose presence is not even essential, and a loosely bound σ of 70,000 that we will come to. And there are two copies of a subunit called α, each of mass 36,000. Two α to one of everything else; and the α whose mass is thirty-six thousand.

Recall Chapter Two. The natural, everyday form of DNA turns through exactly thirty-six degrees at every step of its helix, ten steps to a full turn. Thirty-six is the hub of the helix's geometry, and it is a hub of the whole lattice besides — the same number that fixes a boundary deep in the Earth's crust and the angle at which water bends. And here it is again, in the mass of the subunit the polymerase carries two of: the machine that reads the address is cut from the address's own number. Two of the 36, on the first prime of the lattice, and one each of the larger parts. One could dismiss a single such coincidence; but this book's claim is that these are not coincidences at all, that the true values of nature — the turn of a helix, the mass of a protein subunit, the ratio of parts in

a machine — are laid on a single lattice of small primes and π, and that the reading-head and the molecule it reads are made, quite literally, to the same protractor.

**KEY IDEA**

The bacterial reading-head is $\sigma\alpha_2\beta\beta'\omega$: two α subunits, each of mass 36,000, to one each of the larger parts. The 36 is the same hub the DNA helix turns by (Chapter Two), and the 2:1 is the first prime of the lattice. The machine that reads the address is built from the address's own numbers.

SECTION 4.4

## Three Heads for Three Strata

The simple bacterium makes do with one kind of RNA polymerase for all its reading. The larger, compartmented cells of animals and plants — the eukaryotes of Chapter One — do something more telling: they keep three different polymerases, each dedicated to a different class of the library. It is a division of labour worth pausing on, because of how the labour is divided.

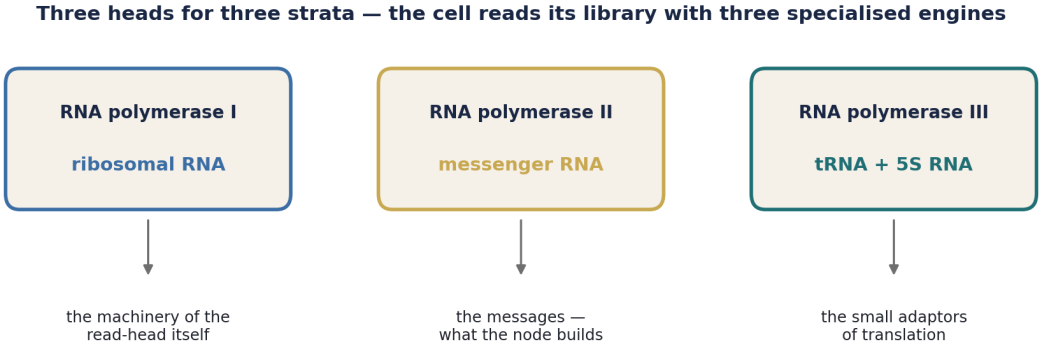


**Figure 4.3.** The three eukaryotic reading-heads. Polymerase I reads out the ribosomal RNA — the substance of the read-heads themselves; polymerase II reads the messenger RNAs — the instructions for what the cell builds; polymerase III reads the small transfer and 5S RNAs — the adaptors of protein synthesis. The registry is read in three strata, by three engines.

The first polymerase reads only the genes for ribosomal RNA — the RNA that forms the very machines, the ribosomes, that will later read the messages. The second reads the messenger RNAs — the working copies of the genes for the cell's proteins, the instructions for what the cell is to build. The third reads the small RNAs, the transfer RNAs and their kin, the little adaptors that the ribosome uses to turn a message into a protein. Three engines, three strata: the machinery of the reader itself, the messages, and the adaptors between them.

In the language of this book the stratification is the point. The cell does not read its whole registry with one undifferentiated head; it separates the reading of the apparatus — the parts of the reading machine — from the reading of the messages that the apparatus will build, and it gives each its own dedicated engine. This is the register-structure of the field showing through in the organisation of reading itself: different strata of the address are read by different machines, as though the coordinate had layers, and each layer wanted its own reader. The same three-fold division will echo, in later chapters, in the way the field itself is built in registers — the subatomic, the atomic, the celestial — each with its own scale and its own laws.

**KEY IDEA**

Eukaryotic cells read their library with three polymerases — one for the ribosomal RNA (the read-head's own machinery), one for the messenger RNAs (the messages), one for the small adaptor RNAs. The registry is read in strata, by dedicated engines — the field's register-structure surfacing in the organisation of reading.

SECTION 4.5

## The Promoter, Where the Address Is Chosen

Return to that landing site, the promoter, for it is far more than a place to park. The promoter is where the cell decides. Of the thousands of genes in the library, only some are wanted at any moment — the ones whose products the cell needs, under the conditions it faces now — and the decision about which to read is made at the promoter, by which promoters the polymerase is allowed to settle upon and begin from. To read a gene is to choose it; and the choosing happens here.

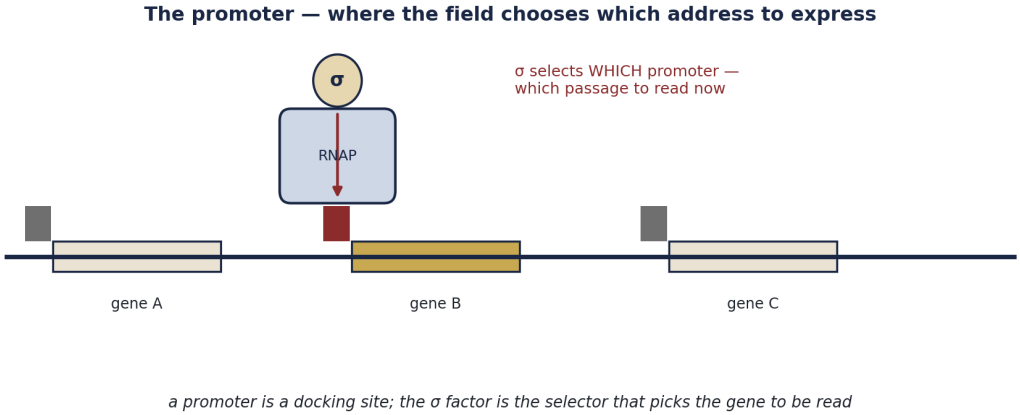


**Figure 4.4.** The promoter, where the field chooses. A promoter is a docking site just ahead of a gene; the detachable σ factor is the selector that picks which promoter the polymerase settles on, and so which passage of the library is read now. To express one gene rather than another is to choose one address over the rest.

In the bacterium the choosing is done in part by the detachable σ subunit — the loosely bound part of the machine we set aside earlier. It is σ that recognises the promoter, that steers the polymerase to the right landing site, and that is released once reading has begun, its selecting job done. Different σ factors recognise different sets of promoters, so that by swapping which σ is in play the cell can switch whole classes of genes on or off at a stroke — reading one set of addresses under one condition, another set under another. The σ factor is, quite exactly, a selector: a molecular hand that reaches into the library and picks the passage to be read.

This is the deepest reading of the chapter, and it will govern everything in the regulation chapters ahead. If the genome is an address registry, then the central act of a living cell — moment to moment, the thing it is always doing — is choosing which of its addresses to express. The promoter is where that choice is made physical, and the σ factor and its many cousins are how the field, sensing its conditions, selects the coordinate to bring into expression. Regulation, which fills the middle of this book, is nothing but the elaboration of this one act: the choosing, at the promoter, of which address to read.

**KEY IDEA**

A promoter is not merely a start-signal but the point where the field chooses which address to express. The σ factor is the selector that picks the promoter, and so the gene; swapping σ factors switches whole classes of genes at once. The central, ceaseless act of a living cell is choosing which of its addresses to read.

SECTION 4.6

## The Gate at the Beginning

There is a pattern here that we have met before and will meet again, and it is worth naming plainly. In the copying of DNA, Chapter Three, we found that the cell regulates not the speed of copying but the decision to begin. In the reading of DNA it is the same. Once the polymerase has settled on a promoter and started, the reading simply runs; what is controlled, elaborately and at length, is the step of starting — the binding, the selecting, the initiation. Elongation, once under way, is not where the decisions are made.

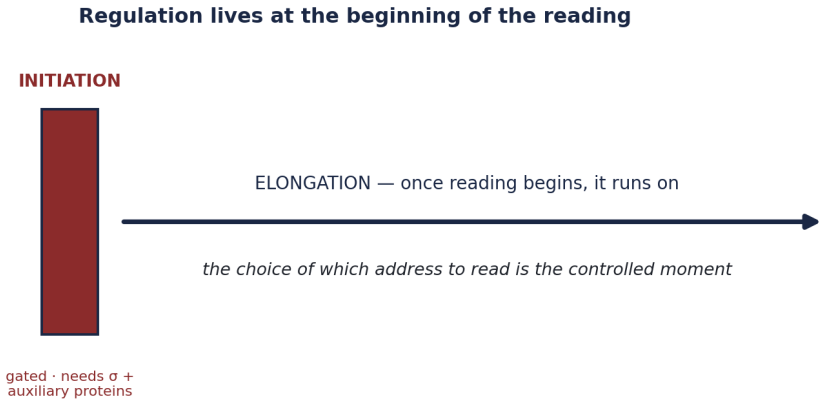


**Figure 4.5.** Regulation at the beginning. As in copying, so in reading: once initiation has occurred, elongation runs on. What the cell controls — with σ factors and a host of auxiliary proteins — is the decision to begin reading a given address. The controlled moment is the choice to read.

On many genes the σ factor alone is not enough; the polymerase needs the help of further proteins, auxiliary factors that bind near the promoter and either assist the machine to settle and start, or block it from doing so. These are the sensors and switches of the cell, the proteins that read the conditions — is there food of this kind, is there danger of that kind — and translate what they sense into a decision about whether this or that address shall be read. We will meet them, one celebrated system at a time, in the chapters on the operons. For now the shape is enough: the gate is at the beginning. The field decides, at the moment of initiation, which coordinate to bring into expression, and having decided, lets the reading run. It is the readout-gate of Chapter Three in a new guise — the controlled moment always the choosing, never the running.

SECTION 4.7

## The Heptad and the Off-Lattice Drift

Honesty requires a section on a number that does not fall neatly on the lattice, because a theory that only ever reported its hits would not be worth trusting. The largest subunit of the eukaryotic messenger-reading polymerase carries, at one end, a curious tail: a short sequence of seven amino acids, repeated over and over — between twenty-five and fifty times in different organisms. And seven is not a number of the lattice. The lattice of this book is built on two, three, five and π; seven is a prime it does not use.

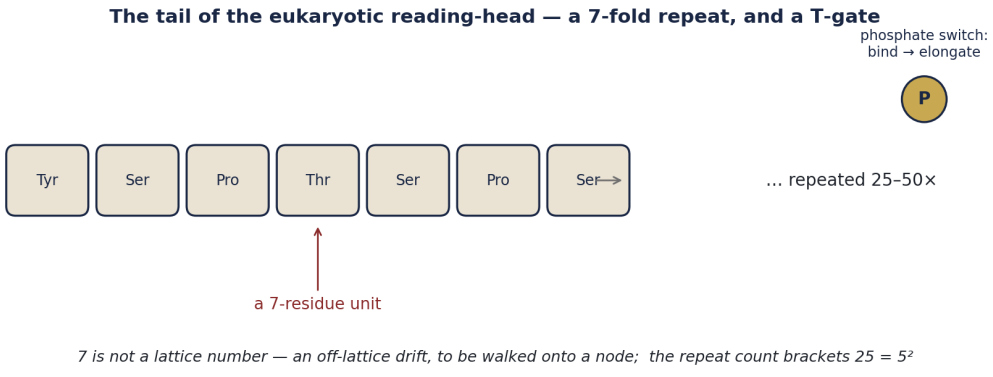


**Figure 4.6.** The tail of the eukaryotic messenger-reading polymerase: a seven-residue unit (Tyr-Ser-Pro-Thr-Ser-Pro-Ser) repeated 25 to 50 times, switched between binding and elongating by the addition of phosphate groups. Seven is not a lattice number — this book reads it as an off-lattice drift to be re-pegged, and notes that the repeat count brackets 25 = 5².

So what does the book say about it? Not that seven is secretly a lattice number — it is not — and not that the heptad is meaningless. It says that a value which does not land on a node is an off-lattice drift: a quantity to be walked back onto the nearest lattice value by a principled adjustment, exactly as an astronomer walks a slightly-off measurement onto its true position. It notes, without forcing anything, that the number of repeats — twenty-five to fifty — brackets twenty-five, which is five squared, a clean lattice value; and that the tail's real work is a switch, flipped by the adding and removing of phosphate groups, that turns the polymerase from its settling-and-binding mode into its free-running elongating mode. That switch is a T-gate, a clean on-and-off. But the seven itself the book leaves flagged, as a drift, not a node. Where a value sits off the lattice, this book says so, plainly, rather than bending the lattice to reach it.

**KEY IDEA**

The eukaryotic messenger polymerase carries a seven-residue repeat — and 7 is not a lattice number. The book does not force it: it reads the seven as an off-lattice drift to be re-pegged, notes that the repeat count brackets 25 = 5², and treats the phosphate on/off as a clean T-gate. A theory worth trusting reports where a value fails to land, not only where it lands.

SECTION 4.8

## What the Reading Head Is

Gather the chapter. We found that a cell reads its address the way a careful librarian reads a rare manuscript — not by handling the original, but by copying the needed passage into a short, disposable working script, the RNA, so that the master coordinate is never spent. We watched the scribe that makes the copy, the RNA

polymerase, work its cycle of binding, initiating, elongating and releasing. We took the scribe apart and found it built on the lattice: two α subunits of mass 36,000 — the very 36 the DNA helix turns by — to one each of the larger parts, on the first prime. We found the larger cell reading its registry in three strata, with three dedicated engines. We found the promoter to be the place where the field chooses which address to express, and the σ factor to be the selector that makes the choice. We found the gate, as ever, at the beginning — the controlled moment the choosing, not the running. And we found one number, the seven of the heptad, that does not land on the lattice, and we flagged it honestly as a drift rather than forcing it to fit.

Not one measurement has been altered. The polymerase still has two α subunits; they still weigh what they weigh; the eukaryote still has three of them; the tail still repeats seven residues. What has changed is the meaning: these facts, laid together, describe not merely a copying enzyme but the field's own reading-head — a machine cut from the lattice, reading the registry in strata, and choosing, at every promoter, which coordinate to bring into expression. The act of reading a gene, which biology describes as transcription, is in this light the field selecting and expressing one address of the many it holds. And that act of selection — the choosing, at the promoter, of what to read — is the whole subject of the chapters to come.

**KEY IDEA**

The thesis of the chapter: reading a gene is the field selecting and expressing one address. The reading-head is cut from the lattice (the α subunit's 36, the 2:1 first prime), reads the registry in three strata, and chooses at the promoter which coordinate to express — copying each passage into a disposable script so the address itself is never spent.

SECTION 4.9

## Why This Should Matter to You

Every difference between the cells of your body — the difference between a cell of your eye and a cell of your liver, though both carry the identical library — comes down to this chapter's single act: which addresses each chooses to read. They differ not in what they know but in what they are reading. A muscle cell and a nerve cell hold the same coordinate registry, letter for letter, and are as unlike as any two things in nature, because each has settled its polymerases on a different set of promoters — is expressing a different selection of the shared address. You are not one reading of your library. You are trillions of different readings of the same library, each cell a different choice of passages, and the choosing is the making of you.

This is why the promoter, and the selecting done there, will matter so much in the chapters ahead, and why it matters to a human life. When a cell reads the wrong passages — switches on an address it should keep closed, or silences one it needs — the consequences run from the trivial to the fatal, and much of disease, read in this book's terms, is a misreading: the wrong addresses expressed. To understand how the cell chooses what to read is therefore to understand how a body builds itself rightly, and how it goes wrong. We have watched the reading-head settle and begin. In the next chapter we follow the copy it makes as it grows, ends, and is made ready for use — and find, in the tempo of the reading, a clock set by the field itself.

## The Numbers at a Glance

*The reading machine and its numbers. Every biological value is left exactly as measured; the right column notes where it meets the lattice — and where, honestly, it does not.*

| Feature | Value | On the lattice |
|---|---|---|
| α subunit (two of them) | mass 36,000 | 36 — the hub the DNA helix turns by |
| Subunit ratio | 2 α : 1 of each larger part | the first prime, 2 |
| β and β′ subunits | 151,000 and 155,000 | the larger parts of the read-head |
| σ selector | 70,000; detaches after start | the hand that chooses the address |
| Eukaryotic polymerases | three (I, II, III) | the registry read in three strata |
| Polymerases per bacterium | ~3,000, about half at work | the library busy, the master safe |
| Messenger-polymerase tail | 7-residue repeat, 25–50× | 7 is OFF-lattice — a drift; count brackets 25 = $5^2$ |
| What is regulated | initiation, not elongation | the choosing is the gated moment |

## References

[1] S. Daubney, The Universal Force of Time — Master Compendium v5, The Daubney Foundation (2026).

[2] R. Schleif, Genetics and Molecular Biology, 2nd ed., Johns Hopkins University Press, Baltimore (1993).

[3] S. Daubney, The Force of Time — Where It Departs From Current Science, The Daubney Foundation (2026).