

THE LIVING ADDRESS

Nucleic Acid and Chromosome Structure: The Geometry of DNA

*The Shape of the Address***Stephen Daubney**

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In which we open the library and find that its writing is geometry — the two strands clamped on the primes two and three, the four letters standing for four planets, and the turn of the helix pegged not to ‘roughly ten’ but to three exact degrees on the lattice, one of them stamped with the number of the day.

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 shape of the molecule of heredity — how the double helix is put together, how its letters pair, what forms it takes, and how it coils. Read through the Universal Force of Time, it is where the cell’s address is shown to be written in the geometry of the Earth itself.

Chapter One claimed that a cell’s library is really an address in the field. This chapter is the first hard test of that claim, because it opens the library and looks at how the writing is done — and the writing turns out to be geometric. The two strands pair by a simple rule, and the rule runs on the two smallest numbers of the lattice: the adenine-thymine rung is clamped by two hydrogen bonds, the guanine-cytosine rung by three. The genetic alphabet is bonded on 2 and 3, the same pair that set the pump’s ratio in the chapter before.

The four letters, in this reading, are not arbitrary tokens but four addresses in their own right — adenine for the Earth, thymine for Mercury, guanine for Venus, cytosine for Mars. A run of DNA is a walk through the coordinates of the inner solar system, spelt in chemistry. You need not accept that at once; watch instead for how the four letters behave in later chapters, and whether they play the parts their planets would suggest.

The heart of the chapter is the turn of the helix. Science quotes it loosely — “about ten base pairs to a turn” — and treats the different forms as a smear. The Force of Time re-pegs them onto three exact turns, each closing the full 360° circle: the Z-form steps 30° per base pair, on the pure lattice $2\cdot3\cdot5$; a middle form steps $324/\pi^2$, carrying π and sitting on the very same node as the water molecule that folds it; and the real, in-vivo form of long chromosomal DNA steps 34.56° , which is $864/5^2$ — stamped with 864, the number of the day. The helix does not turn in radians. It turns in degrees, on the lattice, in three registers at once.

Finally the chapter reaches topology — the way a closed loop of DNA carries a fixed linking number that cannot change without the strand being cut. The Force of Time reads that conserved integer as the law $d\Sigma T=0$ written into the very shape of the molecule: the address can be twisted and coiled and stored under tension, but the total is never lost, only redistributed between the local twist and the global writhe.

Carry this into the chapter: the double helix is the T-address written in the Earth's own geometry — clamped on the primes 2 and 3, lettered in the four inner planets, turning in exact degrees across three registers, and conserved, whole, however tightly it is wound.

SECTION 2.1

The Most Famous Shape in Science

In 1953, in Cambridge, two young men pinned to a wall a model made of tin and wire and stepped back to look at what they had built. It was a spiral staircase of a molecule, two ribbons winding around a common axis, with rungs between them; and the moment they saw it whole, they saw something no chemist had dared hope for. The shape explained, in a single stroke, the greatest mystery in all of biology: how a living thing copies itself. For if the two ribbons carried matching information, then to make two cells from one you had only to unwind them and let each build its missing partner. The structure of DNA was the mechanism of heredity. The form was the function.

The double helix has since become the most famous shape in science, printed on textbooks and postage stamps and laboratory doors. We will spend this chapter inside it, and we will find that its fame is deserved for a reason deeper than the one Watson and Crick gave. They found how the shape lets DNA copy itself. This book will show that the shape's numbers — the angle of its turn, the count of its rungs, the bonds that hold them — are not free at all, but sit, to the last digit, on the lattice of small primes and π that runs through the whole of nature. The molecule of heredity is written in the same geometry as the Earth and the inner planets. Let us read it.

The double helix — a ladder that carries a copy of itself on each side

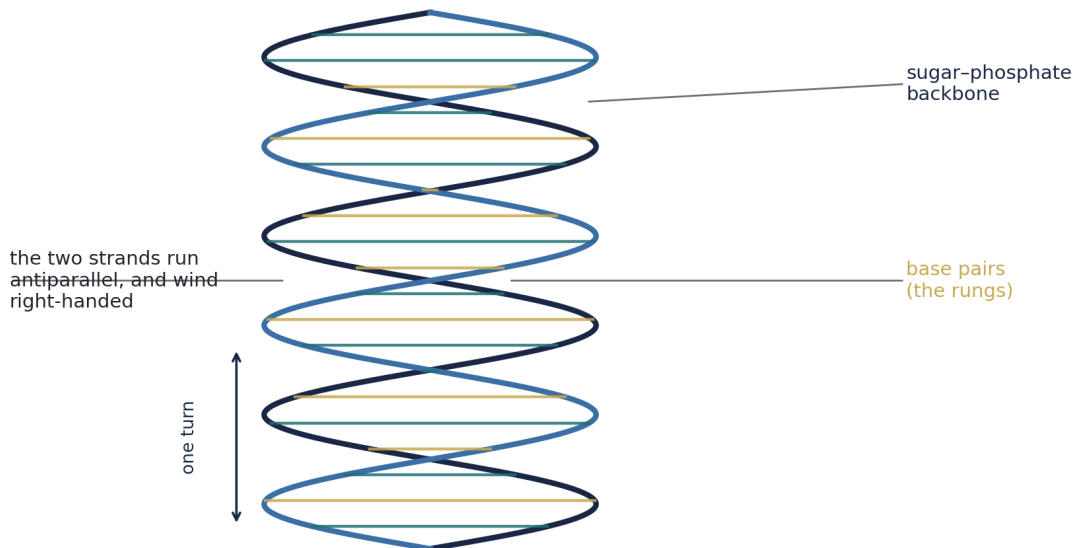


Figure 2.1. The double helix. Two sugar-phosphate backbones wind around a common axis, running in opposite directions, joined by rungs of paired bases. Because each strand carries the complement of the other, the shape itself explains how the molecule is copied: unwind the two, and each specifies its missing partner.

SECTION 2.2

The Regular Backbone

Begin with what the molecule is made of. Each strand of DNA is a chain built from a single repeating unit: a sugar — deoxyribose — joined to the next sugar by a phosphate, over and over, a monotonous rail of sugar-phosphate-sugar-phosphate running the length of the strand. Onto each sugar is hung one of four bases, and it is the sequence of those bases, and nothing else, that carries the information. The rail is always the same; the message is in what hangs from it.

The four bases fall into two pairs of shapes: the larger purines, adenine and guanine, and the smaller pyrimidines, cytosine and thymine. (RNA, the cell's working copy, uses almost the same chemistry, with the sugar ribose in place of deoxyribose and the base uracil in place of thymine.) It is worth pausing on how little it takes to store a message. Information, at bottom, is only the narrowing of alternatives: a stick cut to one of ten thousand lengths, measured finely enough, carries a choice among ten thousand possibilities. DNA narrows its alternatives four ways at every position, and with a strand millions of positions long the number of possible messages is beyond astronomical. The wonder is not that the alphabet is only four letters. The wonder is that four is enough — and, as the next sections show, that four is itself a number of the lattice, $4 = 2^2$.

SECTION 2.3

The Clamp of Two and Three

Now to the rungs, for here the geometry begins. The two strands are held together because the bases pair — but not any base with any base. Adenine pairs only with thymine, and guanine only with cytosine, and the reason is a matching of shape and of hydrogen bonds, the small electrical clasps that hold the rungs together. This pairing rule is what makes the two strands complements of each other; it is what lets one be rebuilt from the other; it is the whole basis of copying and repair.

Look closely at how many clasps each rung uses, because the answer is the quiet heart of the chapter. The adenine-thymine rung is held by two hydrogen bonds. The guanine-cytosine rung is held by three. Two and three — the two smallest primes of the lattice, the very pair that set the sodium-potassium pump's ratio in the last chapter. The genetic alphabet is not merely written in four letters; it is bonded together on 2 and 3. And the difference is not idle: because the guanine-cytosine rung has an extra clasp, it is the stronger of the two, so that stretches of DNA rich in G and C melt apart at higher temperatures than stretches rich in A and T. When, in later chapters, the cell needs to open its helix to read it, it will do so preferentially where the two-bond rungs are — the lattice's own ranking of its bonds deciding where the address is easiest to read.

The genetic alphabet is clamped on the two smallest primes — A-T on 2, G-C on 3

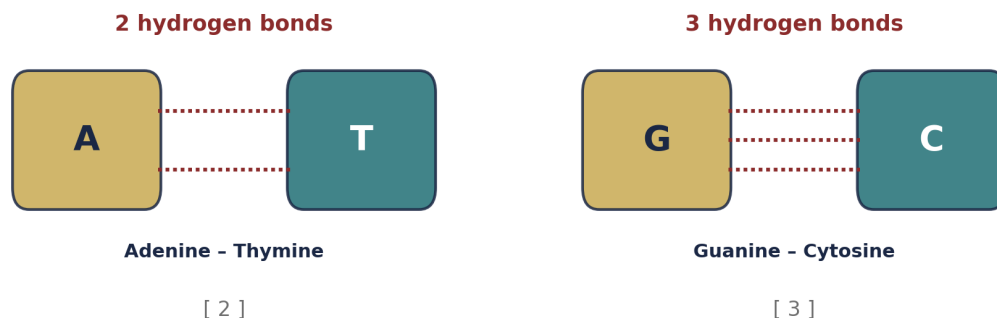


Figure 2.2. The two base pairs, and the numbers that hold them. Adenine and thymine are clasped by two hydrogen bonds; guanine and cytosine by three. The genetic alphabet is clamped on the two smallest primes of the lattice, 2 and 3 — and because three clasps hold more firmly than two, the lattice itself ranks which rungs open first.

There is a bookkeeping consequence, noticed long before the helix was known. Because A always pairs with T and G always with C, any sample of DNA contains exactly as much adenine as thymine, and exactly as much guanine as cytosine. This is Chargaff's rule, and it was one of the clues that led to the structure. In the language of this book it is more than a clue: it is conservation at the level of the sequence — the address kept in

perfect balance, every letter matched by its complement, nothing unpaired, nothing lost. It is the first appearance, in the genome itself, of the law that governs everything in the field: $d\Sigma T=0$, the books always balanced.

KEY IDEA

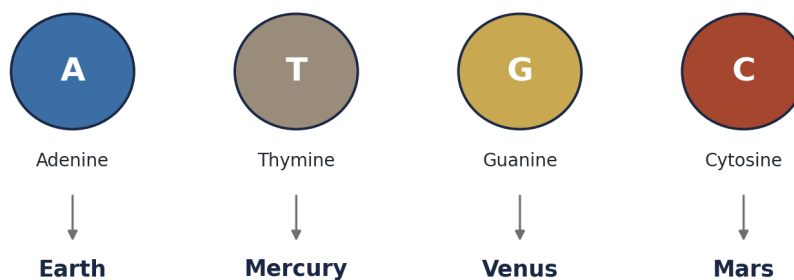
The base pairs are clamped on the two smallest lattice primes: A-T by two hydrogen bonds, G-C by three. The same {2,3} that set the pump's ratio now hold the rungs of the ladder of heredity — and rank them, so that the two-bond rungs are where the cell opens the helix to read.

SECTION 2.4

Four Letters, Four Worlds

Why four letters, and why these four? Science treats the identity of the bases as a frozen accident of early life — four molecules that happened to be around, happened to pair, and were locked in forever after. The Force of Time offers a stranger and more specific reading: that the four letters are four addresses, each corresponding to one of the four inner planets. Adenine stands for the Earth; thymine for Mercury; guanine for Venus; cytosine for Mars.

The four letters are four planetary addresses



A sequence of DNA is a walk through the addresses of the inner solar system, written in chemistry

Figure 2.3. The base-planet correspondence. The four letters of the genetic alphabet map, in this reading, onto the four inner planets — adenine to the Earth, thymine to Mercury, guanine to Venus, cytosine to Mars. A run of DNA becomes a walk through the addresses of the inner solar system, spelt in chemistry.

This is a bold claim and it will not be settled here; it is planted, to be tested by how the letters behave. But watch already for the pattern in the chapters ahead, because the letters keep the parts their planets would give them. When the cell needs to stamp the age of a DNA strand — to tell an old copy from a fresh one — it writes the time-mark on adenine, the Earth base, as though the Earth were the natural place to keep time. When

sunlight damages the helix, the harm falls on thymine, the Mercury base, the innermost planet and the one most exposed to the Sun. When the cell builds a protein, the growing chain is handed over on adenine again, the Earth base, as though matter were most naturally assembled at the Earth's own address. The roles the letters play in time-keeping, in sun-damage, in construction, line up with the planets they encode. A sequence of DNA, in this light, is not a string of arbitrary tokens. It is a walk through the coordinates of the inner solar system, written into chemistry.

KEY IDEA

The four bases are four planetary addresses: A = Earth, T = Mercury, G = Venus, C = Mars. The claim earns its keep in later chapters, where the time-stamp falls on the Earth base and sun-damage on the Mercury base — the letters playing the parts their planets would give them.

SECTION 2.5**The Turn Written in Degrees**

Now the turn itself. As the rungs stack, each is rotated a little from the one below, so that the whole ladder twists into its helix. How much does each step rotate? In the natural, everyday form of DNA — the form crystallographers call B — each base pair is turned very nearly 36 degrees from the last, and it takes ten base pairs to come full circle, because $10 \times 36^\circ = 360^\circ$ exactly. The helix closes in ten steps of thirty-six degrees.

The helix turns in degrees

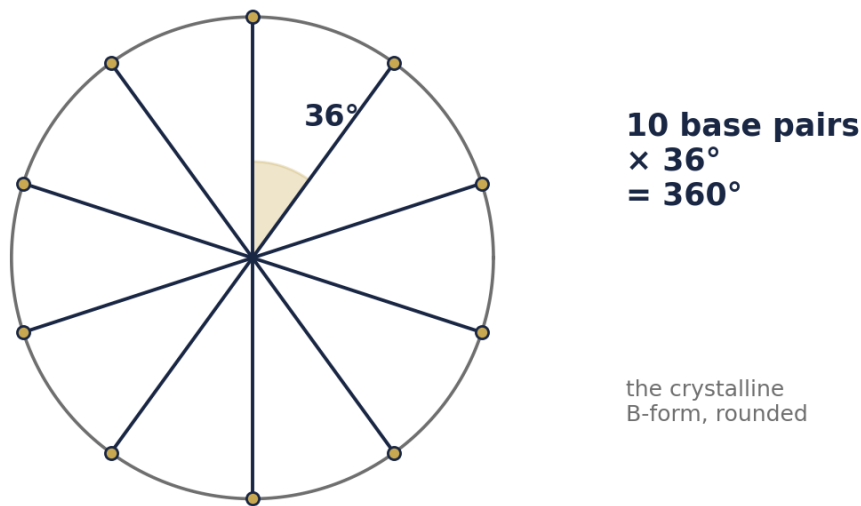


Figure 2.4. The B-form helix, seen down its axis. Ten base pairs, each rotated 36° from the last, close the full circle: $10 \times 36^\circ = 360^\circ$. The molecule of heredity is laid out not in radians but in whole degrees — the unit of the Earth's own geometry.

Pause on that, because a physicist would find it odd. Nature, we are taught, does not care for our human units; it measures angles in radians, the pure ratio of arc to radius, and a right angle to nature is not ninety of anything but simply $\pi/2$. Yet here is the most important molecule in biology turning in round degrees — thirty-six of them a step, three hundred and sixty to a turn. This is no coincidence of rounding. It is the first sign of one of the deepest claims of the Force of Time: that the true universe is built in degrees, and that the radian is the veil — the factor $180/\pi = 57.29577951308232$ — that science slips between itself and the lattice, hiding the whole-number geometry underneath. The helix turns in degrees because the field it is made of turns in degrees. And 36, the step of the natural form, is itself a hub number of this book, the same 36 that fixes the boundary deep in the Earth's crust and the angle at which water bends. The molecule of heredity and the body of the planet are cut to the same protractor.

SECTION 2.6

The Three Forms of the Helix

But B-form DNA is not the only form, and here the story sharpens into something remarkable. Under different conditions the helix takes different turns. Crystallographers have long catalogued them loosely — a form with about eleven base pairs to a turn, a form with about twelve, the everyday form with about ten, the living molecule inside a cell with about ten and a half — and treated the variation as

a smear, a molecule that flexes and cannot quite make up its mind. The Force of Time reads the same data differently. It says the helix does not smear at all. It sits on three exact turns, each one closing the 360-degree circle perfectly, and each one a clean value of the lattice.

The three forms of the helix — not “roughly ten,” but three exact turns, each closing the 360° circle

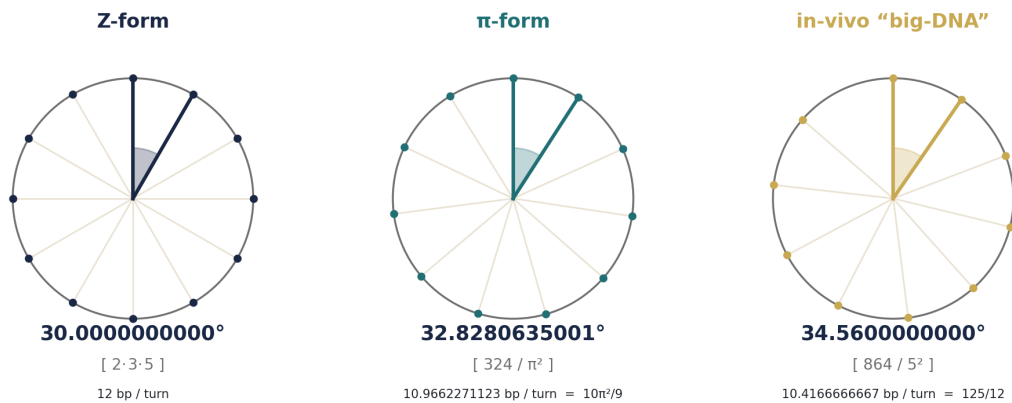


Figure 2.5. The three forms of the helix, re-pegged from science’s loose ‘about ten’ onto three exact lattice turns. Each closes the full 360° circle. Left: the Z-form steps 30.0000000000° [2·3·5], pure integer, no π . Centre: a middle form steps 32.8280635001° [324/ π^2], carrying π . Right: the in-vivo form of long chromosomal DNA steps 34.5600000000° [864/5²], stamped with 864, the number of the day.

Take them in turn. The tightly wound Z-form takes twelve base pairs to a turn, and $360 \div 12 = 30.0000000000^\circ$ per step — and $30 = 2 \cdot 3 \cdot 5$, the three material primes multiplied together, with no π anywhere in it. It is the pure-integer form, the crystalline node. A middle form takes $10\pi^2/9 = 10.9662271123$ base pairs to a turn, and $360 \div$ that is 32.8280635001° , which is exactly $324/\pi^2$ — a step that carries π^2 in its body. And the real, living form — the conformation that long chromosomal DNA actually takes inside a cell, the form science measures at ‘about ten and a half’ — takes $125/12 = 10.4166666667$ base pairs to a turn, and $360 \div$ that is 34.5600000000° , which is $864/5^2$ exactly.

Read that last number again, because it is the one to carry away. The step of big, real, in-vivo DNA is $864/25$ degrees — and 864 is the number of the day. A day is 86,400 seconds; the bridge-number 864 threads through this book wherever the celestial register touches the atomic. The helix of the chromosome in your cells is stepped to the number of the Earth’s turning. So the three forms are not a smear but a chord of three notes, each in a different register: the Z-form on the pure integers, the middle form carrying π , and the living form carrying 864, the day — reaching from the atomic scale of the molecule all the way up to the turning of the planet. The molecule that stores the address is pegged, in its very pitch, to the same three-register lattice that runs the water angle, the colours of the spectrum, and the length of the day.

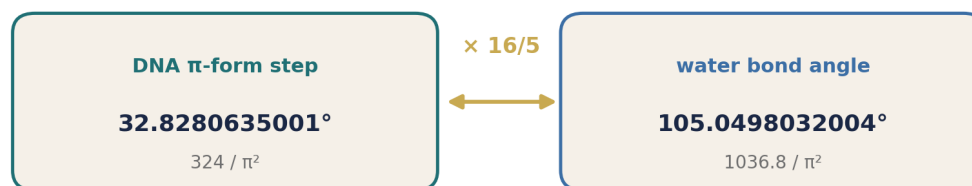
WORKED EXAMPLE · deriving the three exact turns

A helix closes a circle of 360° ; divide it by the base pairs in one turn to get the step.
 — Z-form: $12 \text{ bp} \rightarrow 360 / 12 = 30.0000000000^\circ = 2 \cdot 3 \cdot 5$. — π -form: $10\pi^2/9 = 10.9662271123 \text{ bp} \rightarrow 360 / (10\pi^2/9) = 324/\pi^2 = 32.8280635001^\circ$. — in-vivo form: $125/12 = 10.4166666667 \text{ bp} \rightarrow 360 / (125/12) = 864/25 = 34.5600000000^\circ$. Each product closes exactly: $30 \times 12 = 360$; $(324/\pi^2) \times (10\pi^2/9) = 360$ with the π cancelling; $34.56 \times 125/12 = 360$. Three registers — integer, π , and the day-number 864 — one circle.

SECTION 2.7**The Water in the Helix**

The middle form carries a secret worth its own section. Its step is $324/\pi^2 = 32.8280635001$ degrees — a number built on π to the minus two. Now recall the molecule that surrounds and folds every strand of DNA in every living cell: water. Water is bent, its two hydrogen atoms splayed at an angle from the oxygen, and that angle, in the reading of this book, is 105.0498032004 degrees — which is $1036.8/\pi^2$, also built on π to the minus two.

DNA and water sit on the same π^{-2} node — one exactly $16/5$ of the other



The information helix and the solvent that folds it share the atomic register.

Figure 2.6. The water-register lock. The middle helix step, 32.8280635001° , is $324/\pi^2$; the water molecule's bond angle, 105.0498032004° , is $1036.8/\pi^2$. Both sit on the same π^{-2} node, and one is exactly $16/5$ of the other. The information helix and the solvent that folds it share the same register.

Divide one by the other and the π^2 cancels cleanly, leaving $1036.8 / 324 = 16/5 = 3.2$, a plain lattice ratio. The helix step and the water angle are not two unrelated numbers that happen to look alike; they are the same node of the lattice, one exactly sixteen-fifths of the other. The molecule that carries the address and the molecule that folds it are cut from one cloth. This is the kind of quiet joinery the Force of Time keeps finding: that things which mainstream science treats as separate — the geometry of a nucleic acid, the geometry of a water molecule — turn out to share a register, to sit on the same rung

of the same ladder. Life did not invent its chemistry from scratch. It built on a lattice that was already there, and DNA and its solvent were laid on the same line of it.

KEY IDEA

The middle helix step is $324/\pi^2$; the water bond angle is $1036.8/\pi^2$; their ratio is exactly 16/5. The information helix and the water that folds it sit on one π^{-2} node of the lattice — the address and its solvent share a register.

SECTION 2.8

The Two Seams

Return to the outside of the helix. Because the paired bases do not sit centred on the axis but a little to one side, the twin backbones do not run evenly opposite each other; they leave two seams spiralling down the molecule — a wide one and a narrow one, the major and minor grooves. These grooves matter enormously, for they are how the address is read without being unwound. A protein that must find one particular site along millions of base pairs does not pull the helix apart to check; it reaches a finger into a groove and feels the edges of the bases exposed there, reading the sequence from the outside like a hand reading braille.

Grooves — the two seams where a protein can reach in and read the address

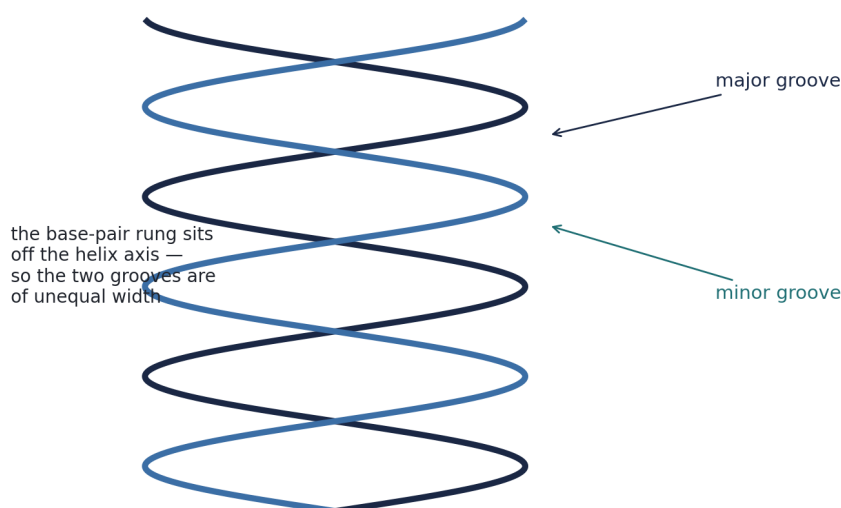


Figure 2.7. The major and minor grooves. Because each base-pair rung sits off the helix axis, the two backbones leave two seams of unequal width winding down the molecule. Through these grooves a protein can read the sequence from the outside, feeling the exposed edges of the bases without ever unwinding the strand.

It is a small point of shape with a large consequence, and it fits the reading of this book neatly. If DNA is an address, then most of the time it must be read, not rewritten — consulted, indexed, recognised — and the grooves are the reading surface, the exposed

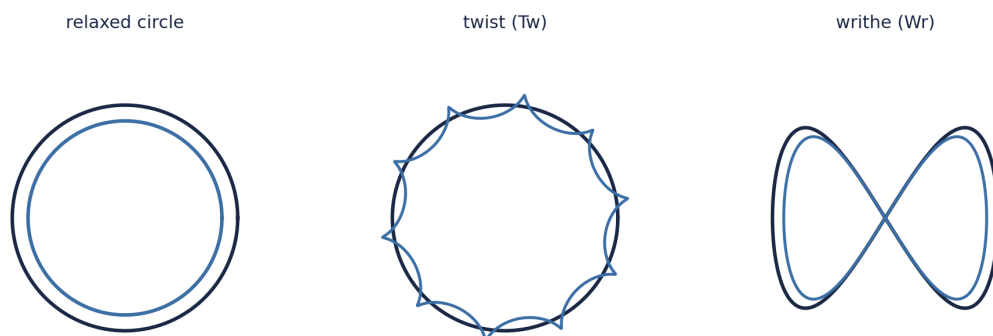
face of the coordinate that the machinery of the cell runs its fingers along. Later chapters are full of proteins doing exactly this: regulators, repressors, the readers of genes, each recognising its site by the pattern in a groove. The helix is not a closed book. It is a book left open along two spiralling seams, so that its address can be read at a touch.

SECTION 2.9

The Knot That Cannot Come Undone

There is one last property of the shape, and it is the most abstract and, for this book, the most telling. Much of the DNA in cells is not in open-ended strands but in closed loops — circles, with no free ends. And a closed loop of double helix has a property that a straight piece does not: the number of times the two strands wind around each other is fixed. You cannot change it — cannot add a twist or take one away — without cutting one of the strands. Mathematicians call this fixed number the linking number, and it is a topological invariant: bend the loop, fold it, knot it how you like, and the linking number does not budge.

The conserved knot: $Lk = Tw + Wr$ — a fixed integer split between local twist and global coil



The linking number Lk cannot change without cutting the strand — conservation ($dLk=0$) written into the shape of DNA

Figure 2.8. The conserved knot. In a closed loop of DNA the linking number Lk is fixed and cannot change without cutting a strand. It splits into two parts — the local twist Tw and the global writhe Wr — and always $Lk = Tw + Wr$. Relax some of the local winding and it does not vanish; it reappears as global coiling. The total is conserved; only its form changes.

What makes this beautiful is how the fixed number is spent. It divides into two parts: the twist, the local winding of one strand about the other, and the writhe, the coiling of the whole loop in space — and the two always sum to the fixed total: $Lk = Tw + Wr$. Neither part is fixed on its own; only their sum is. Relax some of the local twist and the missing turns cannot simply disappear, for the total may not change; instead the whole molecule buckles and coils upon itself, converting the lost twist into writhe. The cell uses this deliberately, storing tension in the coil like a wound spring, to be released when the helix must be opened.

Here is conservation made visible in a single molecule. The linking number is a quantity that cannot be created or destroyed, only redistributed between two forms — which is, word for word, the conservation law of the Force of Time: $d\Sigma T=0$, T never made or lost, only moved from one register to another. In Chapter One we met that law as good housekeeping in the way a cell spends energy. Here we meet it as pure geometry, written into the topology of the address itself. The knot cannot come undone; the total is always kept; and the molecule shifts it between twist and writhe as freely as the field shifts T between its registers.

WORKED EXAMPLE · how the linking number is spent

Take a closed loop whose two strands wind around each other 25 times — a linking number $Lk = 25$. That 25 is fixed; no cutting, no changing it. But it can be held in two ways. If all of it is local winding, then the twist $Tw = 25$ and the writhe $Wr = 0$, and the loop lies flat and relaxed. Now unwind two turns of the local twist, so $Tw = 23$. The missing two turns cannot vanish, because Lk must stay 25; they reappear as writhe, $Wr = +2$, and the whole loop coils up in space to make up the difference. Throughout, $Lk = Tw + Wr = 25$. The number is conserved; only its form — local twist versus global coil — has changed. $d\Sigma T=0$, in one molecule of DNA.

SECTION 2.10

Reading the Shape by Its Shape

Before we gather the chapter together, one practical grace note, because it shows how deeply shape and meaning are joined in this molecule. Some sequences of DNA are not straight but gently bent — a run of several adenines in a row curves the helix — and the cell puts these bends to use, for a bent site is easier for certain proteins to grip, and the binding of the protein bends it further still. The shape invites the reader, and the reader deepens the shape.

Even in the laboratory, the shape betrays the sequence. Pour a mixture of DNA pieces into a gel and pass a current through it, and the pieces sort themselves by size as they thread through the mesh — but a bent piece, dragging awkwardly, travels slower than a straight piece of the same length, so that its very shape can be read off from how far it moves. Long molecules, above a certain size, snake through the gel end-first and all travel alike, until the field is pulsed to break the rhythm and let their sizes show again. None of this is central to the argument of the book, but it underlines its theme: in DNA, form and information are never separable. To know the shape is to know something of the message, and to read the message the cell need only feel the shape.

SECTION 2.11

What the Helix Is Keeping

Gather the chapter. We opened the library and found its writing geometric through and through. The rungs are clamped on the two smallest primes of the lattice — two hydrogen bonds for adenine and thymine, three for guanine and cytosine — and the lattice's ranking of those bonds decides where the helix opens. The four letters are four planetary addresses, and they keep the parts their planets would give them. The turn of the helix is written in whole degrees, thirty-six to a step in the everyday form, and pegged in the living molecule to three exact turns of the lattice — the pure-integer 30 of the Z-form, the π -carrying $324/\pi^2$ of the middle form, and the $864/5^2$ of big chromosomal DNA, stamped with the number of the day. That middle form shares its very node with the water that folds it. And the whole address, wound into a closed loop, carries a conserved linking number that the molecule shifts between twist and writhe without ever losing the total — conservation written into the topology of the coordinate.

Not one measurement of structural biology has been altered in any of this. The base pairs still hold by two bonds and three; the B-form still turns near 36 degrees; the linking number still equals twist plus writhe. What has changed is that the numbers have stopped looking arbitrary. The 4 of the alphabet is 2^2 ; the clasps are 2 and 3; the turns are 30, $324/\pi^2$, and $864/5^2$, each closing the degree-circle; the water and the helix share a node. A structure that science presents as a happy accident of early chemistry turns out to be laid, line by line, on the lattice of the field — the address written in the geometry of the Earth and the inner planets.

KEY IDEA

The thesis of the chapter: the double helix is the T-address written in the Earth's own geometry. Clamped on the primes 2 and 3, lettered in the four inner planets, turning in three exact degree-steps across the integer, the π , and the day-number registers, sharing a node with its own solvent, and conserved whole however tightly it is wound. The structure is intact; its numbers are the lattice's.

SECTION 2.12

Why This Should Matter to You

It is easy to see the double helix as a piece of elegant plumbing — a clever way to store and copy a chemical message — and to leave it there. But if this chapter is right, the helix is something far stranger and closer to home. The address that says who and where you are, in the fabric of reality, is written into every cell of you in a script whose every stroke is geometry: the angle of a turn, the count of a rung, the balance of a knot, all cut to the same lattice that shapes the water in your blood and the planets in your sky. You are not written in an arbitrary code. You are written in the geometry of the world.

And the writing is kept with a care that now begins to make sense. The strands are balanced letter for letter; the loop conserves its knot; the whole thing is laid on numbers that do not drift. In the next chapter we watch the cell copy this address, and we shall see the same theme carried into motion: a machinery of almost unbelievable accuracy, guarding every digit of the coordinate as it makes the copy — because an address, unlike a recipe, must be kept exactly true, or the living thing it names is lost. We have seen how the address is written. Now we watch it copied.

The Numbers at a Glance

Every quantity is left at its measured value; the right-hand column notes where it meets the lattice of small primes and π . All three helix turns close the 360° circle exactly.

Quantity	Value	On the lattice
A-T base pair	2 hydrogen bonds	2 — first lattice prime
G-C base pair	3 hydrogen bonds	3 — second lattice prime
The genetic alphabet	4 letters	$4 = 2^2$
B-form step / turn	36° per bp, $10 \text{ bp} = 360^\circ$	36, the Moho / degree hub
Z-form step	30.0000000000° per bp	$30 = 2 \cdot 3 \cdot 5$ (12 bp/turn)
π -form step	32.8280635001° per bp	$324/\pi^2$ ($10\pi^2/9$ bp/turn)
in-vivo “big-DNA” step	34.5600000000° per bp	$864/5^2$ ($125/12$ bp/turn) — 864, the day
Water bond angle (for comparison)	105.0498032004°	$1036.8/\pi^2 = 16/5 \times$ the π -form step
Closed-loop topology	$Lk = Tw + Wr$	a conserved integer — $d\Sigma T=0$

References

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- [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).
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