THE LIVING ADDRESS

Protein Structure and Folding

The Folded Machine

Stephen Daubney
The Daubney Foundation · thedaubneyfoundation@gmail.com

In which the four-letter message is translated into a twenty-letter machine, and we find the machines of the cell folded on quantised angles to the numbers of the lattice — their helix closing the very same degree-circle as the helix of DNA, reciprocal notes struck on one geometry.

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 structure of proteins — the twenty amino acids, the peptide bond, the ways a chain folds, and the forces that hold a fold together. Read through the Universal Force of Time, it is where the message finally becomes a machine, and where the machines of the cell prove to be folded, like everything else, to the numbers of the lattice.

The chapters so far have followed the address — written, copied, read, edited. This chapter turns to what the message finally builds: the proteins, the working machines that do almost everything a cell does. And the first thing to notice is a change of alphabet. The address is written in four letters; the machine is written in twenty. Both counts are powers of the lattice — the four of the bases is 2^2, the twenty of the amino acids is $2^2 \cdot 5$ — and the code that carries one into the other runs through sixty-four codons, which is 2^6. The whole translation from address to machine is arithmetic on the small primes.

Watch the way a protein chain is allowed to bend, because it is not free. One of the bonds along the backbone is rigid and flat and cannot turn at all; only two others rotate, and even those settle into a small handful of allowed angles rather than any angle whatever. The chain cannot take a continuum of shapes; it quantises, folding onto permitted nodes. This is the lattice showing through in the mechanics of folding itself: a T-structure does not smear across all possibilities, it drops onto allowed values, exactly

as the helix twists of Chapter Two formed a rational ladder and not a smear.

The centrepiece is a coincidence that this book says is no coincidence at all. When a protein chain coils into its commonest shape, the α-helix, it turns one hundred degrees at every step and closes its circle in three-point-six steps: 100° × 3.6 = 360°. And the DNA helix, recall, turns thirty-six degrees at every step and closes in ten: 36° × 10 = 360°. Two different helices — the information molecule and the machine — shutting the very same degree-circle, by reciprocal partitions of it, with 36 × 100 = 3600. Both turn in whole degrees, on the master degree-geometry of the field; life turns in degrees at every level, from the address to the machine that reads it.

And when the chain folds, it does not search blindly through its countless possible shapes; it settles, swiftly and reliably, into the one lowest-energy form — T falling to its rest node, each bond formed steadying the next. Folding is not a lucky find but a settling, the field coming to rest in the shape its own numbers determine.

Carry this into the chapter: the four-letter T-address is translated into a twenty-letter machine ($2^2 \to 2^2 \cdot 5$), whose backbone quantises onto allowed folds and whose helix closes the same degree-circle as DNA — and which settles, as it folds, to the lowest node its own lattice numbers set.

SECTION 6.1

The Machines of the Cell

For five chapters we have followed a message: written into the double helix, copied with care, chosen and read, cut and spliced. But a message is only ever a means to an end, and the end is this — to build something that does work. Almost everything a living cell actually does, it does with proteins. They are the enzymes that run its chemistry, the fibres that give it shape, the pumps and channels that guard its wall, the motors that move it, the hands that grip its DNA and read it. If DNA is the library and RNA the working copy, proteins are the machines the copies are made to build. And a machine is defined by its shape.

This chapter is about that shape — how a protein is put together, and how it folds into the precise three-dimensional form that lets it do its one particular job. It is, in a sense, a change of subject: we leave the elegant simplicity of the four-letter helix and enter the messier, richer world of the machines it specifies. But we shall find the lattice waiting for us here too, in the count of the alphabet, in the angles the chain is allowed to bend through, and — most strikingly of all — in the turn of the protein's own helix, which closes the very same circle, in degrees, that the DNA helix closed in Chapter Two. The architect Louis Sullivan said that form ever follows function; in a protein, the two are the same thing, and both are cut to the lattice.

SECTION 6.2

Twenty Letters

A protein is a chain, strung together from building blocks called amino acids, and the first fact to hold is how many kinds there are. Where DNA is written in an alphabet of four letters, a protein is written in an alphabet of twenty — twenty different amino acids, each with the same backbone-forming core but a different side-group hanging off it, and it is the sequence of those twenty that makes one protein an enzyme and another a fibre. The change from reading the address to building the machine is a change of alphabet, from four letters to twenty.

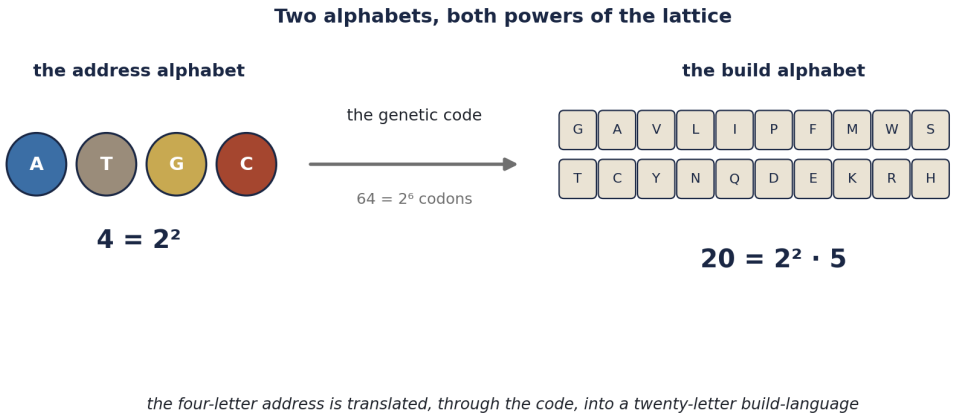

Figure 6.1. The two alphabets of life. The address is written in four bases; the machine in twenty amino acids. Both counts are powers of the lattice — 4 = 2^2 and 20 = $2^2 \cdot 5$ — and the genetic code that carries one into the other runs through 64 = 2^6 codons. The translation from address to machine is arithmetic on the small primes.

Now look at those two numbers through the lens of this book. Four is 2^2. Twenty is $2^2 \cdot 5$. And the genetic code, which we shall meet properly in the next chapter, translates one into the other through sixty-four possible codons — 64 being 2^6. Every count in the whole scheme of translation is a clean product of the lattice's small primes: the address-alphabet a power of two, the build-alphabet a power of two times five, the code between them a power of two. One could shrug this off as the numerology of small numbers — but the claim of this book is that it is not accidental at all, that the alphabets of life are sized to the lattice as surely as the helix is angled to it, and that four and twenty are the counts they are because {2, 5} are the primes the field builds on. The chemistry of life is spelt in powers of two and five.

KEY IDEA

The two alphabets of life are lattice powers: DNA runs on $4 = 2^2$ bases, protein on $20 = 2^2 \cdot 5$ amino acids, and the genetic code between them runs through $64 = 2^6$ codons. The whole translation from address to machine is arithmetic on the small primes 2 and 5.

SECTION 6.3

The Bond That Cannot Turn

String the amino acids together and you have a chain; but a chain that could flop into any shape at all would be useless, for a machine needs a definite form. What gives a protein its definiteness begins with a single, crucial restriction in the bond that joins one amino acid to the next — the peptide bond. You might expect such a bond to swivel freely, like a link in a chain. It does not. For reasons of its electron structure it is locked flat and rigid: the peptide bond cannot turn at all.

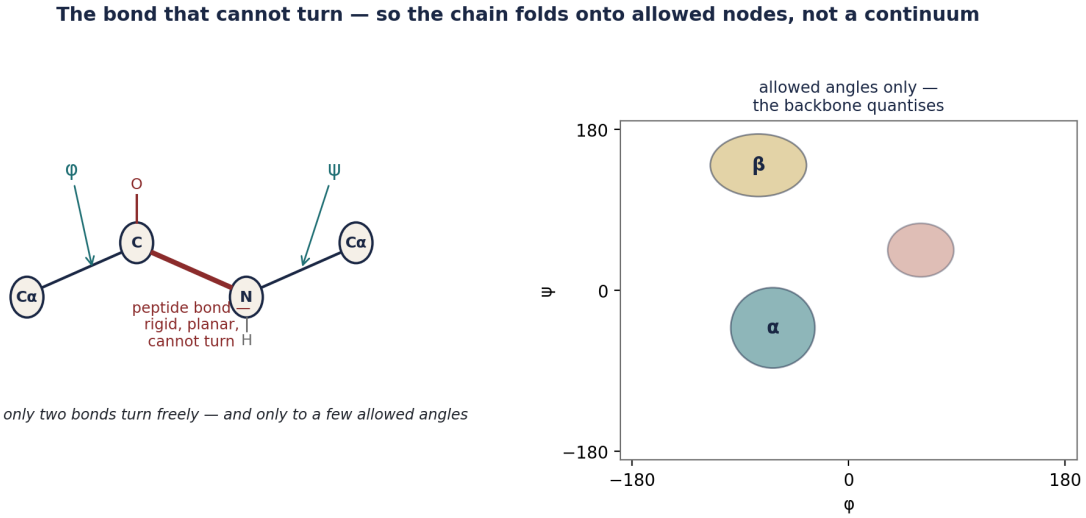

Figure 6.2. The bond that cannot turn. The peptide bond joining one amino acid to the next is rigid and planar — it cannot rotate. Only two other backbone bonds turn freely, and even they settle into a few allowed angles rather than any angle whatever (the shaded islands, right). The chain cannot take a continuum of shapes; it quantises, folding onto permitted nodes.

With the peptide bond frozen, only two other bonds along the backbone can rotate — and here is the deeper point — even those two are not free to take any angle they please. Most combinations of angles jam neighbouring atoms into one another and are forbidden; only a few combinations are allowed, clustering into a small number of permitted islands. Map out which angles a protein backbone can actually adopt and you do not get a smooth continuum; you get a handful of allowed regions, with vast forbidden spaces between them. The chain cannot bend to just any shape. It quantises — it folds only onto permitted nodes.

This is precisely the behaviour the Force of Time expects of any structure made of the field. In Chapter Two we found the DNA helix taking not a smear of twists but a small set of exact ones, a rational ladder of allowed turns. Here the same quantisation governs the folding of the machine: the backbone settles onto lattice-permitted angles, not a continuum of them. A T-structure does not spread itself across all possibilities; it drops onto nodes. That the allowed regions carry the names of the two great folds — the one where the α-helix lives, the one where the β-sheet lives — is our cue to look at those folds directly.

KEY IDEA

The peptide bond joining amino acids is rigid and planar — it cannot rotate — and the two bonds that can rotate settle into only a few allowed angles. The protein backbone therefore quantises, folding onto permitted nodes rather than a continuum, exactly as the DNA helix took a rational ladder of exact twists. A T-structure drops onto nodes.

SECTION 6.4

Three Ways to Fold

Given those allowed angles, a stretch of protein backbone tends to settle into one of a very small number of regular local shapes, called its secondary structures — and remarkably, there are essentially three of them. The first is the α-helix: the chain coils into a tidy spiral, held by a regular ladder of hydrogen bonds running up its length, like the thread of a screw. The second is the β-sheet: several stretches of chain lie side by side, pleated, and hydrogen-bond across to one another to make a broad flat surface. The third is the β-turn: a tight little hairpin that lets the chain reverse direction and fold back on itself.

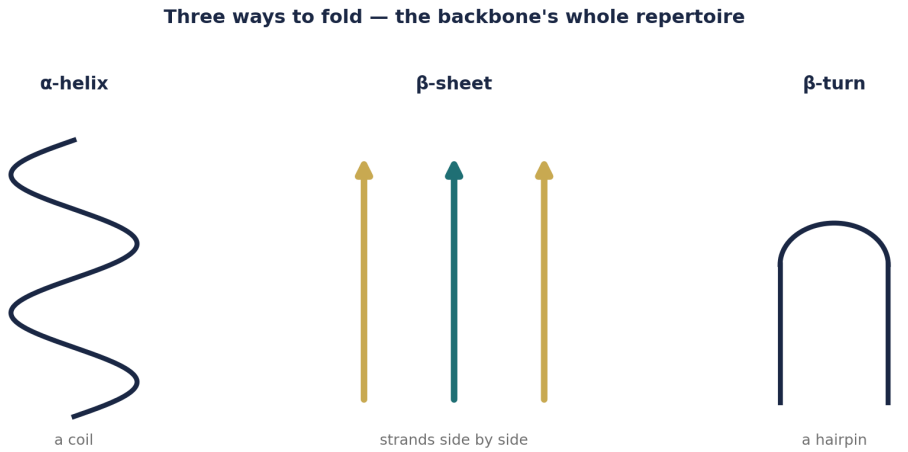

Figure 6.3. Three ways to fold. From the allowed backbone angles the chain settles into essentially three regular local shapes — the coiled α-helix, the pleated β-sheet of strands lying side by side, and the tight β-turn that lets the chain reverse. From these three folds, in endless combination, every machine of the cell is built.

Three folds — and from these three, arranged and combined in endless ways along a chain of twenty letters, every one of the tens of thousands of different proteins in your body is built. It is worth pausing on the economy of it: a build-alphabet of twenty ($2^2 \cdot 5$), a repertoire of three local folds (the lattice's second prime), and out of that small basis, the whole machinery of life. The field builds its endless variety not from endless parts but from a few, combined — the same thrift by which, this book argues, the primes {2, 3, 5} and π span the whole lattice of nature's values. And one of those three folds, the α-helix, hides the chapter's central surprise.

SECTION 6.5

The Two Helices

Look closely at the α-helix, and count its turn. As the chain coils, each amino acid is rotated from the one before it by a fixed angle, and that angle is one hundred degrees. It takes 3.6 amino acids to come full circle — because 100° × 3.6 = 360°, one complete turn. The commonest shape of the protein machine closes its circle in three-and-six-tenths steps of a hundred degrees each.

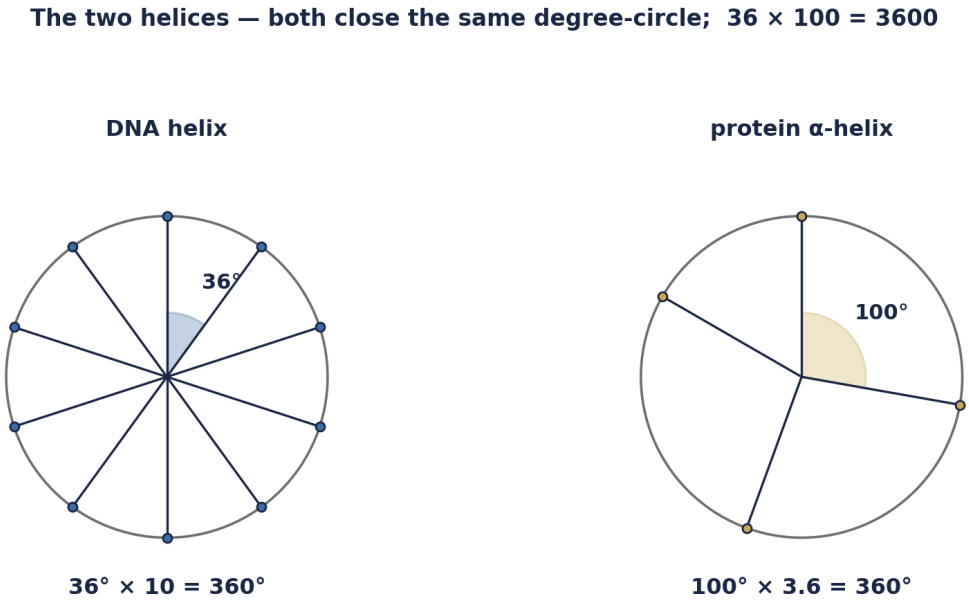

Figure 6.4. The two helices. The DNA helix (left) turns 36° at every step and closes in ten: 36° × 10 = 360°. The protein α-helix (right) turns 100° at every step and closes in 3.6: 100° × 3.6 = 360°. The information molecule and the machine shut the very same degree-circle, by reciprocal partitions of it — and 36 × 100 = 3600.

Now set that beside Chapter Two. The DNA helix turns thirty-six degrees at every step and closes its circle in ten steps: 36° × 10 = 360°. The protein α-helix turns one hundred degrees at every step and closes in three-point-six: 100° × 3.6 = 360°. Two entirely different helices — one the molecule that stores the address, the other the machine the address builds — and they shut the very same degree-circle, each by its own

partition of it. The one takes ten steps of thirty-six; the other three-and-six-tenths steps of a hundred; and the two step-angles multiply to 36 × 100 = 3600. Both turn in whole degrees, on the master degree-geometry this book holds the true universe to be built in — the geometry Chapter Two found hidden behind science's radians by the veil, the factor 180/π. Life turns in degrees at every level: the address turns in degrees, and so does the machine that reads it. That two such different helices should close one circle, in round degrees, is exactly what a single underlying degree-lattice predicts, and exactly what a world of arbitrary chemistry would not.

KEY IDEA

The protein α-helix turns 100° per step and closes in 3.6 steps (100 × 3.6 = 360°); the DNA helix turns 36° per step and closes in ten (36 × 10 = 360°). The machine and the message shut the same degree-circle, by reciprocal partitions, with 36 × 100 = 3600. Both turn in whole degrees — life's geometry, at every level, is the degree-lattice.

SECTION 6.6

The Forces That Fold

What holds a fold together, once formed? Four kinds of force, all of them weak, all of them working together. There are electrostatic attractions between oppositely charged side-groups; there are hydrogen bonds, the same small clasps that rung the DNA ladder and coil the α-helix; there are dispersion forces, feeble and very short-ranged, between atoms pressed close; and there is the hydrophobic effect, the tendency of oily side-groups to huddle together away from the surrounding water, which is less a force than a shunning, but which drives much of folding all the same.

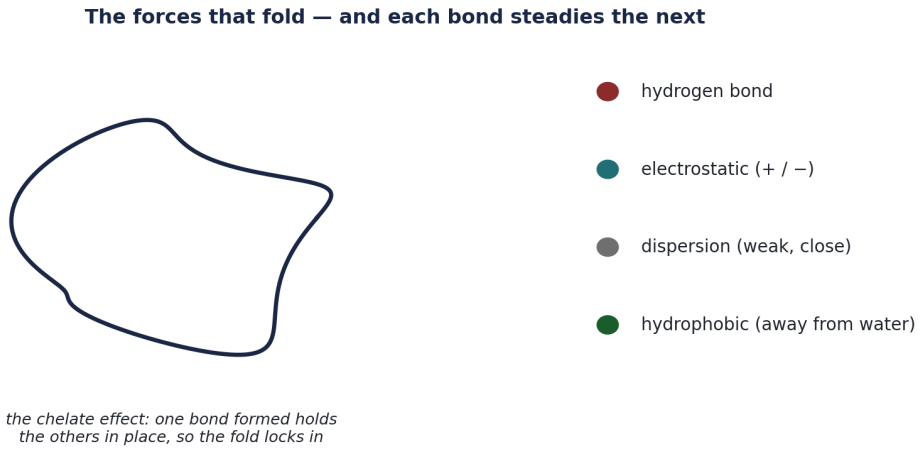

Figure 6.5. The forces that fold. Four weak forces — electrostatic, hydrogen-bonding, dispersion, and the hydrophobic huddling away from water — together hold a protein in its shape. And by the chelate effect, each bond once formed steadies the others, so that many weak holds combine into one firm fold.

No one of these forces is strong; a single hydrogen bond is easily broken. The strength of a fold comes from their number, and from a subtle bootstrapping the chemists call the chelate effect: once a few of these weak holds have formed, they pin the chain in place so that the next ones form more easily, and so on, each bond steadying the next until the whole structure locks. It is why a protein, whose every individual bond could be undone by a passing jostle, nonetheless holds a shape stable enough to work as a machine. In the reading of this book the many-weak-holds-make-one-firm-fold is conservation showing through once more: the fold is the configuration in which the greatest number of the field's little tensions are satisfied at once, each locking the rest, the whole settling into a self-consistent knot of T that will not easily come undone.

SECTION 6.7

Settling to the Lowest Node

This raises the deepest question about a protein, and one science has wrestled with for decades: how does a chain, freshly made and floppy, ever find its one correct shape? The number of shapes a protein chain could in principle adopt is beyond astronomical; if it had to try them one by one it would take longer than the age of the universe to fold even once. Yet a real protein folds in a fraction of a second, reliably, to the same shape every time. It plainly does not search blindly. So what does it do?

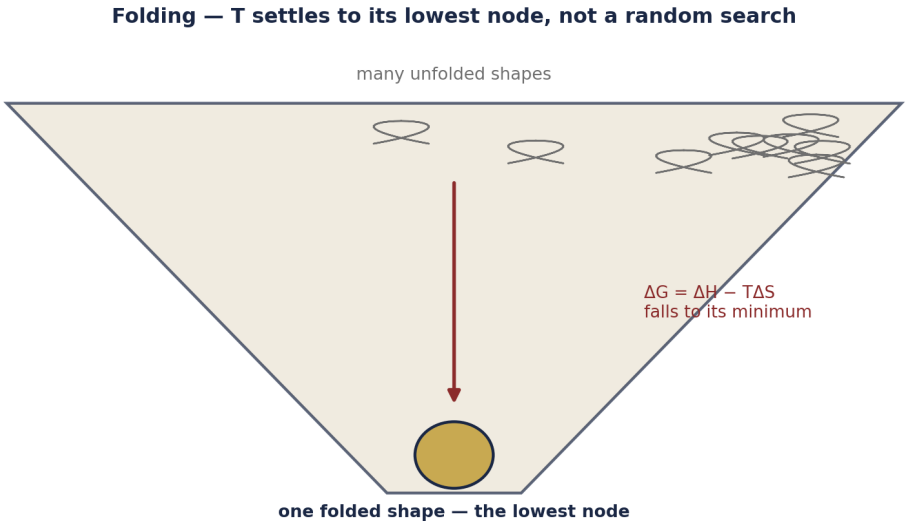

Figure 6.6. Folding as settling. A freshly made chain does not search its countless possible shapes one by one; it settles, swiftly and reliably, down a funnel of falling free energy (ΔG = ΔH − TΔS) into the single lowest-energy form. Folding is not a lucky find but a settling — T coming to rest at its lowest node.

It settles. The chain slides downhill, energetically, toward the one shape in which its free energy — the balance the chemists write as ΔG = ΔH − TΔS, with T the absolute temperature — is lowest, the way a ball released on a slope rolls to the bottom of the valley without needing to visit every other point on the hillside first. There is a funnel in the energy landscape, and the folding chain runs down it to the single lowest node. In

the language of this book that is exactly what a T-structure does: it comes to rest at its lowest permitted node, the configuration that best redistributes its tensions, and it finds that node not by search but by settling — the field flowing downhill to its resting shape, on a landscape its own lattice numbers have carved. Folding is not a lucky discovery. It is T coming to rest, and the shape it comes to rest in is the machine.

KEY IDEA

A protein does not search its countless possible shapes; it settles down a funnel of falling free energy ($\Delta G = \Delta H - T\Delta S$) to the single lowest-energy form, in a fraction of a second, every time. Folding is T coming to rest at its lowest node — the field flowing downhill to the resting shape its own lattice numbers set, which is the working machine.

SECTION 6.8

What the Machine Is

Gather the chapter. We turned from the address to the machine the address builds, and found the lattice waiting at every step. The build-alphabet is twenty letters, $2^2 \cdot 5$, translated from the four-letter (2^2) address through a code of sixty-four (2^6) codons — the whole scheme sized to the small primes. The chain cannot bend freely: its peptide bond is locked flat, its other bonds settle onto a few allowed angles, so the backbone quantises onto permitted nodes rather than a continuum. From those angles it forms just three regular folds — helix, sheet, and turn — from which every machine of the cell is combined. Its commonest fold, the α-helix, turns a hundred degrees a step and closes the same degree-circle the DNA helix closes at thirty-six a step, the two step-angles multiplying to 3600. And the whole thing holds together by many weak forces locking one another, settling — not searching — to the single lowest node of its energy, which is its working shape.

Not one measurement has been altered. There are still twenty amino acids; the peptide bond is still planar; the α-helix still turns a hundred degrees a residue; folding still minimises the free energy. What has changed is that these facts, laid together, stop describing a merely complicated molecule and begin describing something of a piece with everything before it: a machine whose alphabet is a lattice power, whose folding quantises onto nodes, and whose helix turns in the same degrees, on the same geometry, as the address it is built from. The message and the machine are not two unrelated things. They are two expressions of one lattice — the four-letter coordinate and the twenty-letter tool, both turning in degrees, both settling onto the field's allowed nodes. Form follows function in a protein because both follow the lattice.

KEY IDEA

The thesis of the chapter: the machine is the message made three-dimensional, and both are cut to the lattice. A twenty-letter ($2^2 \cdot 5$) build-alphabet, a backbone that quantises onto allowed folds, an α-helix closing the same degree-circle as DNA, and a fold found by settling to the lowest node — the protein is the address expressed as a working shape, on the same geometry.

SECTION 6.9

Why This Should Matter to You

The shape of a protein is not a detail; it is, quite literally, a matter of life and death, and never more plainly than when the folding goes wrong. Some of the cruellest diseases known are diseases not of the message but of the fold — where a protein whose sequence is perfectly correct nonetheless settles into the wrong shape, and that wrong shape does harm. In the dementias, misfolded proteins clump into the tangles and plaques that choke the brain. In the prion diseases, a single misfolded protein can even coax its correctly folded neighbours to misfold in turn, a wrong shape spreading like a rumour through the tissue. The letter of the address was right; the machine it built came to rest at the wrong node, and a life unravels from it.

Read in this book's terms, these are failures of settling — the field coming to rest in a shape it should not have taken, a T-structure caught in the wrong valley of its landscape. And that framing carries, at its far end, a hope the medical chapters will take up: that if disease can be a matter of a structure settling wrongly, then healing can be a matter of helping it settle rightly — of restoring the fold, as elsewhere of restoring the address, to the node it should have kept. For now it is enough to see how much rides on the shape, and how deeply the shape is written into the lattice. We have watched the address written, copied, read, edited, and now built into a folded machine. In the next chapter we watch the building itself — the machine that reads the message and lays the twenty letters down in order — and find the genetic code, the very dictionary that turns address into machine, is itself a structure of the lattice.

The Numbers at a Glance

The machine and its numbers. Every biological value is left exactly as measured; the right column notes where it meets the lattice. Both helix turns close the 360° circle.

Feature	Value	On the lattice
Amino-acid (build) alphabet	20 amino acids	$20 = 2^2 \cdot 5$
Base (address) alphabet	4 bases	$4 = 2^2$
Genetic code	64 codons	$64 = 2^6$
Peptide bond	rigid, planar — cannot rotate	backbone quantises onto allowed nodes
Secondary structures	3 (α-helix, β-sheet, β-turn)	3 — the second lattice prime
Protein α-helix step	100° per residue, 3.6 per turn	$100 \times 3.6 = 360°$
DNA helix step (Ch. 2)	36° per base pair, 10 per turn	$36 \times 10 = 360°$; $36 \times 100 = 3600$
Folding	settles to lowest $\Delta G = \Delta H - T\Delta S$	T coming to rest at its lowest node

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