THE LIVING ADDRESS

Biological Self-Assembly: Ribosomes and Capsids

Building Without a Builder

Stephen Daubney
The Daubney Foundation · thedaubneyfoundation@gmail.com

In which the great machines of the cell — the ribosome that builds every protein, the shell that a virus wraps around its thread — are found to assemble themselves, with no builder standing over them and no blueprint drawn apart from the parts, because the whole is already implicit in the pieces, and the field itself is the plan.

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, biological assembly — how the ribosome and the lambda phage head build themselves from their parts, and the problem of assembly order. Read through the Universal Force of Time, it shows that structure is self-contained: the information for the whole is in the parts because all share one T-address geometry, and building is the field settling into its determined form on a timed schedule. No external blueprint is needed, because the field is the blueprint.

A machine in our world is built by something other than itself, working from a plan held apart from the parts. The cell's machines are not. Put the parts of a ribosome together in a tube and they find one another and assemble into a working ribosome, in the correct order, with no builder and no template. The simplest case is a single protein: made as a floppy chain, it folds into one precise shape determined by its sequence alone — nothing folds it; chaperones only keep it from tangling on the way. Lift that fact from one chain to many parts, and you have self-assembly: pieces shaped to fit in one arrangement only, carrying, distributed among them, the whole of their own design.

The chapter shows the principle in two opposite forms. The ribosome is asymmetric — one copy of each of dozens of different parts — and yet contains the complete information for its own construction, down to the order in which the parts must join. The

lambda phage head is the opposite: a regular icosahedron, one of the five perfect solids, built not from many custom parts but from a few kinds of protein used many times over — a small basis of shapes tiled into a perfect shell. Both build themselves; both need no builder; the difference is only the kind of form the shared design specifies — a bespoke fold in one case, a symmetric tiling in the other. And in both, the parts join in a determined order, each step preparing the next.

Here is the reading. Self-assembly is the one-seed principle at the scale of structure. All the parts of a machine are T configured by the same address, so they carry a shared geometry, cut to one design — which is why they fit, and why the whole is implicit in them. Building is the field settling those co-designed parts into the single form their common address determines; and the order of assembly is a T-schedule, the field reading the parts' addresses in sequence, exactly the timed programme we met in the developing egg, now at the finest scale. The lattice underlies both symmetries: it can raise high symmetry from few generators (the phage coat, few units many times, the {2,3,5,π} economy) and specify a unique irregular fold just as exactly (the ribosome).

This is why self-assembly, which can seem almost miraculous — a machine building itself from a soup of parts with nothing to guide it — is, in this book, not miraculous but inevitable. Parts that are expressions of one address must carry a shared geometry, and shared geometry must fit; a set of pieces cut to one design has the whole of that design distributed among them. The field does not draw a plan and then build to it, because to express one address as a set of parts is already to make them able to find their whole. Life builds without a builder because there is, at bottom, only one thing — the field — and every structure is that one thing settling into a shape it already, in its parts, contains.

The principle reaches the reader in the plainest way: you are assembled, at every level, exactly like this. Your proteins fold themselves; the machines of your cells build themselves; the very ribosomes reading this book into your understanding were put together, inside you, with no builder and no plan but their own parts — which is how a living thing can grow and renew itself endlessly, making its own machines from within. It reaches the reader, too, at the edge where this self-building fails: because a fold is settled without a guide, a protein can settle wrongly, and some of the gravest diseases of the brain are diseases of misfolding — what builds itself so faithfully can, when a part settles wrongly, mis-build itself as surely. To read structure as self-determined is to see both the beauty of the system and its peril, and to see why a young science of designed self-assembly, borrowed from the cell, is so promising: it is learning to do deliberately what life has always done — to build without a builder.

Carry this into the chapter: biological assembly shows structure is self-contained — the information for the whole is in the parts because all share one T-address geometry, and building is the field settling into its determined form on a timed schedule. No external blueprint is needed, because the field is the blueprint.

SECTION 21.1

The Question of the Blueprint

A machine, in the world we know, is built by something other than itself. A watch does not assemble; a watchmaker assembles it, working from a plan held in his head or on paper, apart from the parts. So it is natural to ask, of the intricate machines inside a cell, the same question: where is the builder, and where is the plan? A ribosome is a device of exquisite complexity, a woven cluster of dozens of proteins and several strands of special RNA, folded and fitted together with the precision of a fine watch. Surely, one thinks, something must build it — must hold the design, and put the pieces in their places. This chapter asks that question of the cell's great structures, and returns an answer that is, when you first meet it, astonishing.

The answer is that there is no builder, and no plan apart from the parts. The structures build themselves. Put the pieces of a ribosome together in a tube, under the right conditions, and they find one another and assemble into a working ribosome, in the correct order, with no machine to guide them and no blueprint to consult. The information for the whole is not held somewhere outside, to be imposed upon the parts; it is carried within the parts, in their very shapes, so that when they are present together they fall into their determined arrangement of their own accord. In the reading of this book, this is not a surprise but an inevitability — and the reason is the deepest idea this book has to offer about form.

SECTION 21.2

A Fold With No Folder

Begin with the simplest case, one we touched on chapters ago: the folding of a single protein. A protein is made as a long, floppy chain of amino acids, strung out in the order the gene dictates. To do its work it must fold — collapse from a limp thread into a precise, compact three-dimensional shape, the same shape every time. And here is the first marvel: nothing folds it. There is no machine that takes the chain and bends it to the correct form. The shape is determined entirely by the sequence of the chain itself. Given its order of amino acids, the chain will find its one proper fold, spontaneously, because that fold is the arrangement its own sequence makes most stable — the resting shape toward which it naturally settles.

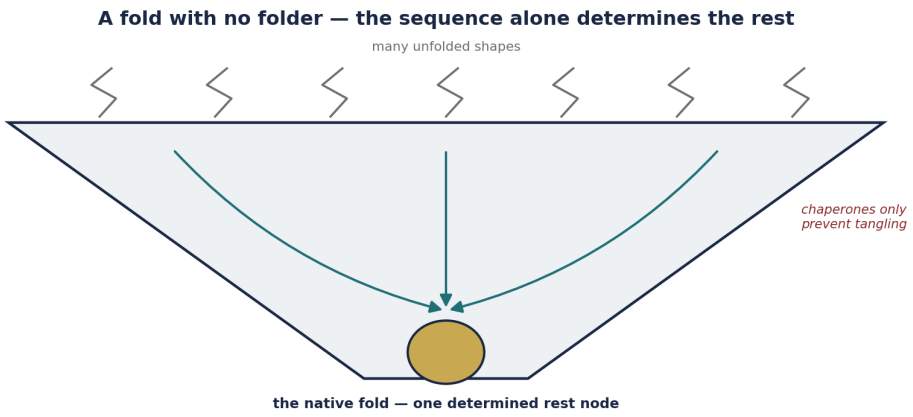

Figure 21.1. A fold with no folder. A protein chain, made floppy and extended, settles spontaneously into one determined shape — the fold its own sequence makes most stable. No machine bends it; the information for the fold is in the sequence. (Chaperone proteins only keep chains from tangling on the way, not direct the fold.)

There are helpers, called chaperones, but they do not do the folding — they only keep a freshly made chain from sticking to its neighbours and tangling before it has folded, like hands that keep a skein of wool from knotting while it unwinds. The fold itself is the chain's own doing. In the reading of this book, this is the folding-to-a-rest-node we met in the chapter on protein structure: a T-configured chain settling into the one form its own sequence determines, the shape of least resistance in its own landscape. The information for the shape is in the parts — here, in the single chain — and the shape emerges without any hand imposing it. This chapter's whole argument is this one fact, carried upward from a single chain to a whole machine.

SECTION 21.3

The Whole Implicit in the Parts

Now lift the idea from one chain to a structure of many parts. If a single protein carries, in its sequence, the information for its own fold, then a structure built of many such proteins might carry, in the shapes of its parts, the information for its own assembly — and this is exactly what the cell's great machines do. The parts are shaped so that they fit together in only one way, like the pieces of a three-dimensional puzzle cut so precisely that they can be assembled in one arrangement and no other. Present the parts, and they find their fits and lock into the whole. The design of the whole is distributed across the parts, written into their surfaces; there is no separate copy of it, and no builder needed to read one.

This is self-assembly, and in the reading of this book it is the one-seed principle at the scale of structure. Recall the book's founding image: one particle, one address, re-instanced — the field expressing a single coordinate. Here, all the parts of a machine

are T configured by the same address, and so they carry a shared geometry, cut to one common design. That shared geometry is why they fit: they are not strangers brought together by an outside plan, but expressions of one coordinate, made to belong to one another. Assembly is the field settling those co-designed parts into the single form their shared address determines. No blueprint sits outside the machine, because the machine's parts are already the blueprint, each carrying its piece of the one design.

KEY IDEA

The cell's great machines assemble themselves. A protein's fold is fixed by its sequence alone — no folder; and a structure of many proteins is fixed by the shapes of its parts — no builder, no blueprint apart from the parts. The ribosome (asymmetric, one copy of many proteins and RNAs) and the lambda phage head (a regular icosahedron from a few proteins in many copies) each fall into their determined form when their parts are present, joining in a set order. In this book: self-assembly is the one-seed principle at the scale of structure — all the parts are T configured by the same address, so they carry a shared geometry that snaps together; building is the field settling into the form its own parts determine. No external blueprint is needed, because the field is the blueprint.

SECTION 21.4

The Ribosome Assembles Itself

Take the ribosome, the most important machine in any cell — the factory on which every protein is built. It is not a simple or symmetric thing: it is a large, irregular, asymmetric structure, made of several strands of ribosomal RNA and dozens of different proteins, each present in just a single copy, each with its own particular place. One might think that so intricate and lopsided an object, with no repeating pattern to guide it, would surely need a template or a machine to put it together. It does not. Its RNA strands and its dozens of proteins, mixed together in the right conditions, assemble into a complete, working ribosome on their own — and they do so in a definite order, each protein binding only after certain others are already in place, so that the structure builds up through a determined pathway from first piece to last.

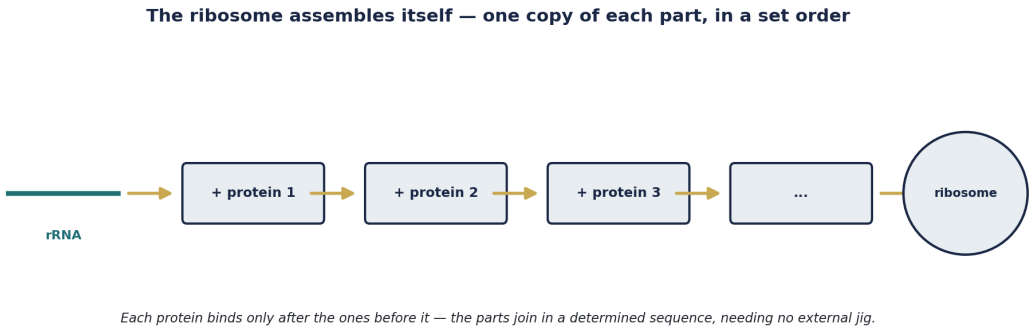

Figure 21.2. The ribosome assembles itself. Its several RNA strands and dozens of proteins — one copy of each — find their places and build a complete, working ribosome with no external machine, and in a definite order: each protein binds only after the ones before it. The asymmetric machine carries its own assembly plan.

Consider what this means. An asymmetric machine of great complexity, with no repeated motif to lean on, nonetheless contains within its own parts the complete information for its own construction — not only which pieces go where, but in what order they must come together. In the reading of this book, the ribosome is the field expressing one coherent address as a bespoke form: every part cut to the one design, so that the parts know their fits and their sequence without being told. The order of assembly, we shall see, is itself a kind of schedule — but the point to hold here is that even a one-of-a-kind, irregular machine is fully self-determined. It needs no blueprint, because it is one: a single address, worn as a structure.

SECTION 21.5

The Phage Builds a Perfect Shell

Now set beside the ribosome a structure of the opposite character, and watch the same principle produce a very different beauty. When the lambda phage of our earlier chapters builds itself, it must wrap its thread of DNA in a protective coat — a head. And the head it builds is a thing of geometric perfection: a regular icosahedron, one of the five perfect solids of the ancient geometers, a shell of twenty identical triangular faces. But here is the economy of it. The phage does not carve this shell from a hundred different custom parts. It builds it from a few kinds of protein, used many times over — the same small units, repeated again and again, tiling themselves into the regular polyhedron. A handful of shapes, copied and fitted edge to edge, closes into a perfect enclosing form.

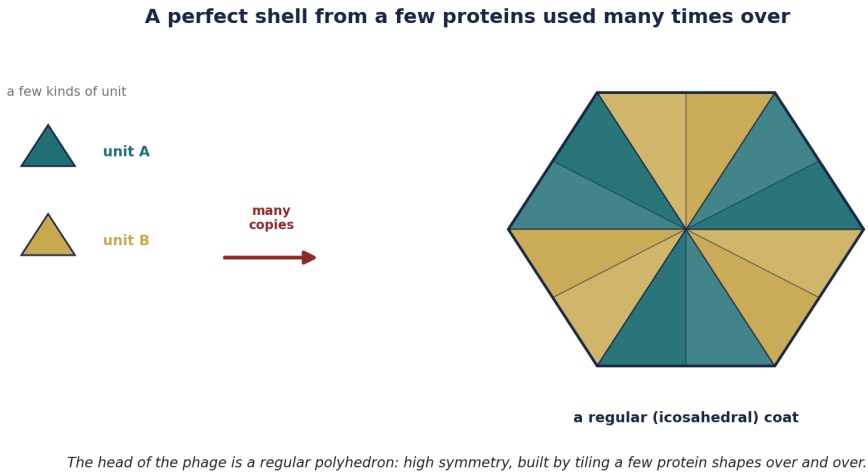

Figure 21.3. A perfect shell from a few proteins used many times over. The phage head is a regular icosahedron — high symmetry — built not from many custom parts but by tiling a few kinds of protein unit over and over. A small basis of shapes, repeated, closes into a perfect enclosing solid.

This too is self-assembly, and it too needs no builder: the units are shaped to fit one another in just the way that closes the shell, and present them together and they tile into the icosahedron of their own accord. But its economy is of a different kind from the ribosome's. Where the ribosome is bespoke — one copy of each of many parts — the phage coat is a tiling: a few generators, endlessly repeated, spanning the whole surface. In the reading of this book, the coat is a symmetric T-form, built by the same lattice economy we have met again and again: few generators, vast coverage. A small set of protein shapes, like a small set of lattice numbers, is enough to build a large and perfectly regular whole.

SECTION 21.6

Two Symmetries, One Principle

Set the two side by side, for the contrast is illuminating. The phage coat is regular, symmetric, tiled — a few units many times over. The ribosome is irregular, asymmetric, bespoke — many units, one time each. They could hardly look more different: one a crystal of a shell, the other a lopsided machine. And yet they are built on one and the same principle, and it is the principle of the whole chapter. Each is a single coherent structure whose complete assembly information is carried within its own parts. Neither needs an external plan; each falls into its determined form when its pieces are present. The difference between them is only in the kind of form the shared design specifies — a symmetric tiling in the one case, a bespoke fold in the other.

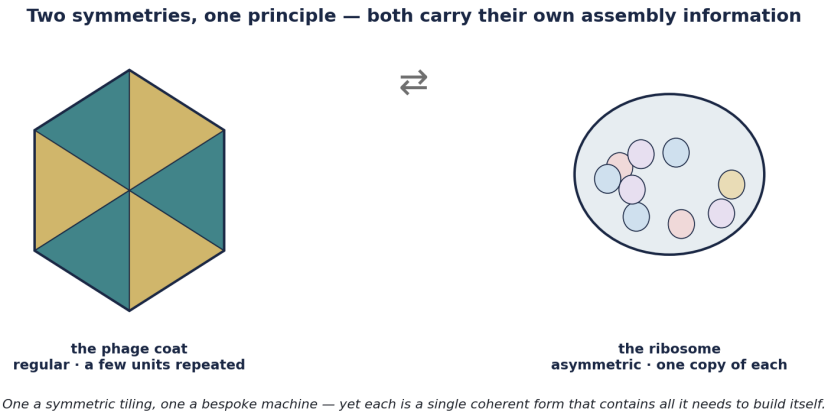

Figure 21.4. Two symmetries, one principle. The phage coat is regular — a few units repeated into a symmetric shell; the ribosome is asymmetric — one copy of each of many parts. Opposite in symmetry, yet each is a single coherent form that contains all it needs to build itself.

In the reading of this book, both are T-forms — both are the field expressing one coherent address as a structure — and the two symmetries are simply two kinds of address. Some coordinates specify a regular, repeating shape, like a crystal or a virus coat, cheaply built from a few generators; others specify a unique, irregular one, like an enzyme or a ribosome, each part bespoke. The lattice underlies both: it can generate high symmetry from few generators, and it can specify a particular one-of-a-kind fold just as exactly. What the two structures share — self-containment, self-assembly, no external builder — is the deep thing, and it holds whether the form the address wears is symmetric or unique. Structure, of either kind, is the field settling into what its own parts determine.

SECTION 21.7

The Order of Assembly Is a Schedule

Return to a detail we passed over: that the parts assemble in a set order. This is not incidental — it is essential, and it is the second half of the chapter's idea. A complex structure cannot, in general, have its parts thrown together all at once and left to sort themselves out; the pieces must come together in sequence, each creating the surface on which the next can bind. The first proteins settle onto the RNA scaffold; only then does a second set find its footholds on the growing structure; only then a third. The pathway is determined — there is a right order, and the assembly follows it — so that building a machine is not only a matter of what fits where, but of what comes when.

In the reading of this book, the order of assembly is a T-schedule. We met such a schedule before, in the developing frog's egg that made one part of its ribosomes months ahead of the rest — the field keeping time, expressing its addresses in a determined sequence. Here is the same principle at the finest scale: the field building one structure

by reading its parts' addresses in a set order, each step preparing the next. Form, in living things, is not only a matter of shape but of timing — of the parts arriving in their proper succession — and the timing, like the shape, is carried within the parts themselves, in the surfaces that each step creates for the step that follows. The blueprint that is the parts includes, in this way, not just the plan of the whole but the order of its making.

WORKED EXAMPLE · who tells the parts what to do?

Trace the causes and see that none is external. The fold: a protein chain settles into one shape — cause: its own sequence, the fold of least resistance. No folder. The fit: two proteins join in one arrangement — cause: their complementary shapes, cut to one design. No jig. The order: protein 2 binds only after protein 1 — cause: protein 1 creates the surface protein 2 needs. No scheduler. The whole: a ribosome or a phage coat forms — cause: all the parts, co-designed by one address, settling into the form and sequence their own shapes determine. At every step the cause is in the parts. In this book: the parts share one T-address geometry, so the whole is implicit in them — the field is the blueprint, and building is it settling into its determined form on a determined schedule.

SECTION 21.8

The Field Is the Blueprint

Gather the chapter into its single sentence, for it is one of the most important in this book. The information for a biological structure is not held apart from the structure, in some plan or template or builder; it is held within the parts, in their shapes and their order of assembly, because all the parts are the field expressing one coherent address, and so are cut to one shared design. There is no blueprint outside the machine because the field is the blueprint — the coordinate the parts share is at once what makes them fit and what makes them a whole. To assemble is simply for the field to settle its co-designed parts into the form, and the sequence, that their common address determines.

This is why self-assembly, which can seem almost miraculous — a machine building itself out of a soup of parts, with nothing to guide it — is, in the reading of this book, not miraculous at all but inevitable. Parts that are expressions of one address must carry a shared geometry, and shared geometry must fit; and a set of pieces cut to one design has, distributed among them, the whole of that design. The wonder is real, but it is the wonder of a deep economy, not of magic: the field does not need to draw a plan and then build to it, because to express one address as a set of parts is already to make those parts able to find their whole. Life builds without a builder because, at bottom, there is only one thing — the field — and its every structure is that one thing settling into a shape it already, in its parts, contains.

SECTION 21.9

Why This Should Matter to You

You are assembled, at every level, in exactly this way. The proteins of your body fold themselves; the machines of your cells build themselves; the very ribosomes reading this book's account into your understanding were put together, inside your cells, with no builder and no plan but their own parts. Nothing stands over your molecules directing their construction. They carry their assembly within them, because they are all expressions of the one address that is you — and that is why a living thing can grow and renew itself endlessly, making its own machines from within, with no external factory and no imposed design. You are a structure that contains, in its parts, the whole of its own making.

And it matters, too, at the edge where this self-building fails. Because the fold of a protein is determined by its own sequence and settled without a guide, a protein can, on rare occasion, settle into a wrong fold — and some of the gravest diseases of the brain and body are diseases of misfolding, in which proteins take a shape they should not and clump where they should not, and the cell cannot easily undo it. To understand that structure is self-determined is to understand both the beauty of the system and its peril: what builds itself so faithfully can, when a part settles wrongly, mis-build itself as surely. And on the hopeful side, having learned that structures assemble from co-designed parts, science has begun to build in the same way — to design molecules that assemble themselves into wanted shapes, a young craft of building without a builder, borrowed from the cell. Hold, then, this: you are not made by a maker standing apart from you; you are the field, settling into the form your own parts contain — a blueprint that builds itself, and needs no other.

The Numbers at a Glance

The parts of self-assembly, and the reading the Force of Time gives each. Every biological fact is left exactly as measured.

The fact	What it is	The Force of Time reading
Protein folding	fixed by the sequence alone	a T-chain settling to its determined rest node
Chaperones	prevent tangling, do not fold	helpers, not builders — the fold is the chain's own
The ribosome	asymmetric, one copy of each part	a bespoke T-form — self-determined, self-built
The phage head	regular icosahedron, few proteins × many	a symmetric tiling — few generators, vast coverage
Assembly order	a determined pathway, part by part	a T-schedule — the parts read in set sequence
No external blueprint	structure implicit in the parts	the field is the blueprint (the one-seed principle)
Misfolding	a protein settling to a wrong shape	a self-built form mis-built — the peril of the beauty

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