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The First Pore

Closure, Aperture, and the Reconciliation of Impermeance with Supply

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Abstract. One family of substituted chrysenes is held to supply everything a minimal vessel needs: the nucleic acid, the membrane, the encoding, and the anchor holding one to the other. Earlier articles built the enclosure, read the encoding optically, and showed the vessel's volume to be set by a single impermeant species it makes for itself. *What the account has lacked is any way to move a molecule across its own membrane.* This paper supplies one from the same chemistry.
An aperture is a hole in a patch of surface; a pore is a passage through a bilayer, and the difference is a wall no earlier article names. Here it is built along the one substituted axis the encoding leaves free: units joined end to end along 6–12 by phosphodiester formation into columns spanning the core, closed into rings by the same chemistry along 3–9. Only the tetrasubstituted unit can serve, any other spending both arms on the column. Each column keeps a free terminal arm on the lumen side, which tethers it to the strand — so *the pore is addressed by the sequence it sits in* — and the covalent linkage is what holds a unit in the far leaflet, where no tether reaches.
A torsion scan over the aryl phosphodiester shows that a ring closes at every size without strain, and that the phosphorus lies outside the chord joining two columns in every closing conformer, being the apex of the bend. The bridges therefore set the aperture and never intrude on it: *its size follows from bond geometry and from nothing adjustable*. Closure constrains a trimer and nothing larger — a trimer encloses 0.254 nm, and 0.207 to 0.258 nm over its whole closure set, while a tetramer encloses whatever its conformers give it. Measured as clearances to one van der Waals surface, ammonium passes with 0.050 nm to spare and any residue bearing a side chain is excluded, by 0.021 nm at the smallest, since a minimum enclosing cylinder cannot be reduced by adding atoms. No occupant is required and none would fit.
A pore passing the osmolyte would end the cycle rather than help it, the vessel filling until it can no longer divide; selectivity is the requirement, and geometry alone meets it, with no occupant, condensation or excited state. The ion admitted is consumed on arrival by the excision that makes the osmolyte, so the influx is *a trap and not a leak*: impermeance survives while the particle count is fed. One pore costs two hundredths of a per cent of the pool and is wanted at a millionth of an ion channel's capacity, so what matters is how little it leaks, and no conductance is claimed. The consequence for the programme is a dual function on no new chemistry: *the tetrasubstituted unit, already the precursor of the tethered nucleotide and through it of the phospholipid anchor, is also the only species the filter can be made from*, so one component assembles the vessel and then regulates its volume, addressed by the sequence it helped encode.

Keywords: Chrysene Formalism; transmembrane pore; selectivity; ring closure; phosphodiester bridge; torsion scan; minimum enclosing cylinder; osmotic control; impermeance; dual function

1 Introduction

1.1 What the two preceding papers left open

The signalling paper's mechanical section is short and its statements are about genus. A closed cycle in the adjacency graph of membrane-resident units gives the complement genus one within a patch; the bounded component is an aperture; a ring of six units admits 0.70 nm and of twelve 2.00 nm; and the aperture is lined by the phosphodiester arms of the units that bound it. The paper then recorded, in terms, that these are the dimensions of an ion channel and that the correspondence is used nowhere — no conductance, no selectivity, no gating, and a pore in that sense a hole and not a channel.

The deferral was correct and it was also incomplete in a way the paper did not say. An aperture is a feature of a surface. The object wanted is a passage through a bilayer, and the two differ by a wall. Nothing in the corpus has named what stands between the leaflets, and nothing in it holds a unit in the distal leaflet, every anchor on record being tethered to a strand that lies on one side.

The material ledger, meanwhile, left its own opening. Its

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feasibility inequality has one unsupplied term, the rate at which the environment delivers units; and its source set contains one species attested by no figure, the heteroatom feedstock, imported as a premise and given no route.

1.2 What this paper does, and the order it does it in

It asks whether the architecture can conduct, and the first answer is that a conducting pore is fatal.

The cycle paper's division condition is a statement about excess area, and excess area exists only because the internal particle count is impermeant. A membrane permeable to the osmotically active species, with fixed anionic charge in its leaflets, draws water until the vessel is spherical; the reduced volume is pinned at unity; and the threshold is never reached. That is Section 4, and it converts selectivity from a desirable property into a necessary one.

Sections 5 to 7 then build a selective passage out of the inventory. The construction uses the one substituted axis the encoding does not use, and its central facts are conformational rather than topological: closure is free, the phosphorus is exiled from the lumen by the same geometry that closes the ring, and the aperture is determined at one ring size only.

Section 8 returns the construction to the ledger and computes what it costs. Section 9 shows why the influx is a trap rather than a leak, which is what reconciles the two conditions of the cycle paper that would otherwise exclude each other.

1.3 What is established here, by kind

Recovered. The aperture theorem and its corollary from the signalling paper; the orientation of the unit in a leaflet and the tilt range from the enclosure paper; conditions C1 and C1′, the division threshold and the scale parameters from the cycle paper; the inventory, the digraph and the allocation from the material ledger; the orthogonality of the two substituted axes from the loom paper.

Proved here. That a membrane conducting the osmotically active species cannot reach the division threshold (Theorem 4.2); that only the tetrasubstituted unit can serve in a ring (Proposition 5.2); that the lateral bridge closes a ring at every size without strain (Theorem 6.1); that the phosphorus lies outside the chord in every closing conformer (Theorem 6.3); the trimeric aperture over the whole closure set (Theorem 7.1); that a side chain cannot reduce a minimum enclosing cylinder, so the backbone bounds every residue below (Lemma 7.3); and that the ring is a fourth and negligible demand on the pool (Proposition 8.4).

Found. That impermeance is not incidental to the architecture but is what makes division possible, so that the pore the corpus wanted would have destroyed the cycle it was wanted for (Scholium 4.4); that the geometry which closes a ring is the same geometry that removes its phosphate from the channel (Theorem 6.3); and that the influx is a trap and not a leak, which is what lets C1 and C1′ hold together (Corollary 9.3).

Computed here. Blocks V1 to V5 and W1 to W3 of Appendix B.

Supposed. The cross-section of Convention 2.5, registered as H4, which has reversed this paper's conclusion once; the closure slack of Theorem 7.1; and the solute geometries. *The paper's exposure is the residue's minimum cylinder*, bounded below by glycine and otherwise unknown, on which Corollary 7.5 entirely rests (Scholium 7.6).

Not claimed. Everything at Section 3: no conductance, no gating, no occupant, no sequence, no route for phosphorus, no determinate aperture (Sch. 7.2), and no claim that a ring of three forms rather than merely being the one that would work.

1.4 Organization

Section 2 fixes status and scope and corrects one convention of the material ledger; Section 3 refuses seven readings. Section 4 is the necessity argument. Sections 5, 6 and 7 are the construction, the closure and the aperture. Section 8 is the ledger extension and Section 9 the reconciliation. Sections from 10 are the registers, the precedence entries, the targets and the conclusion.

2 Status, nomenclature, scope

Convention 2.1 (Status labels)**.** [A] As in the coordinating paper. [A] finite or axiom-free; [D] derived under named hypotheses, registered in Appendix A; [C] imported, with the source named; [E] molecular reading, entering no proof.

Convention 2.2 (Patent citation rule)**.** [A] Adopted verbatim from the chain-polarity paper and the material ledger. The documentary source is cited to a figure or an example and never to "the invention"; a sentence that quotes the filing is labelled [E] and does not enter a proof.

Convention 2.3 (Cross-paper reference)**.** [A] Statements of other articles of this corpus are named in prose and never by number. A reader wanting the statement itself is directed to the article; a reader wanting what this paper does with it needs only the name.

Convention 2.4 (The two substituted axes)**.** [C] Chrysene carries two inversion-related pairs of substituted positions, 3–9 and 6–12, and the connectivity vectors they span are orthogonal. Imported from the loom paper, where the orthogonality is an axiom of a tensor space. It is used here only as a statement about the molecular frame and carries no algebraic weight; nothing below depends on that paper's

construction, its operator algebra, or its walls.

Convention 2.5 (The column's cross-section)**.** [A] A column presents a rectangle of 7.0×3.4 Å normal to its axis. The 7.0 Å dimension is the 3–9 axis: it lies along the ring, is consumed by the lateral bridges, and faces neighbouring columns. What faces the enclosed void is the 3.4 Å π-face. *The void is therefore the polygon the inner faces enclose and is not the gap between circumscribed disks.*
This is stated explicitly, and registered as H4 in Appendix A, because an earlier form of this paper took the latter and reversed its own conclusion with every input unchanged (Remark D.1). A premise with that history is the last that should be carried as a convention, and the first draft carried it as one.

Convention 2.6 (Scope)**.** [A] The object is one ring in one bilayer, and the quantities asked of it are geometric. Nothing is asserted about the kinetics of ring formation, about how a unit reaches the distal leaflet, about the environment outside the vessel, or about any conductance.

3 Non-implications

Proposition 3.1 (Non-implications)**.** [A] *None of the following is asserted anywhere below.*

(i) That a ring conducts. *No conductance, no single-channel current, no permeability coefficient and no selectivity ratio is computed. Theorem 7.1 gives a size and Corollary 7.5 an exclusion; neither is a rate.*

(ii) That a ring of three forms. *Theorem 7.1 shows the trimer is the only ring whose aperture is determined. It does not show that larger rings do not form, and no kinetic or thermodynamic argument for closure at three is offered (Target 13.4).*

(iii) That the ring gates. *Nothing opens or shuts. The aperture is fixed by covalent geometry and no state variable acts on it.*

(iv) That an occupant is present. *Corollary 7.5 needs none, and Remark 7.8 records that none would fit.*

(v) That the encoding specifies the ring. *The tether gives a ring a sequence address; it does not follow that a sequence determines where rings are, how many there are, or whether any forms.*

(vi) That phosphorus has a route. *The constriction is cation-selective and passes the nitrogen feedstock. The material ledger's feedstock species must be split and the phosphorus half is unsupplied (Target 13.7).*

(vii) That the loom is presupposed. *Convention 2.4 imports one geometric fact. No construction of this paper requires the tensor space, the Dirichlet walls, or the discrete Morse filtration, and none of this paper's results supports them.*

Scholium 3.2 (Why (i) and (iii) are kept apart)**.** A hole of the right size invites two different over-readings and they fail differently.
The first is that a hole of ion-channel dimension conducts like one. It does not follow: conductance is a rate and this paper computes none, as the signalling paper said when it declined the same step.
The second is that a selective hole is a gate. That is worse, because gating requires a state variable acting on the aperture and the architecture has none — the signalling paper having shown that no loop closes on the orientational state. A selective passage with no gate is a filter, and this paper describes a filter.

4 Why most pores are fatal

The corpus wanted a pore for a reason: the cycle paper's lineage is bounded because the particle count runs down, and a channel that imported particles would appear to fix it. This section shows the appearance is false, and the argument is short enough to be given before anything is built.

Notation 4.1 (What is imported)**.** [C] From the cycle paper: the vessel radius $R = 100$ nm, the external concentration $c_{\mathrm{ext}} = 100$ mM, the particle count $N = 2.52 \times 10^5$, the forcing period $T = 4.32 \times 10^4$ s, the osmotic relaxation time 0.9 s, condition C1 and condition C1′, and the division threshold $v \le Q(\alpha)^{-3/2}$. From the material ledger: that the route-A lipid is a dialkyl phosphate and therefore carries one negative charge. From the enclosure paper: the area per lipid, 0.65 nm^2.

Theorem 4.2 (A conducting membrane is pinned at $v = 1$)**.** [D] *Let the leaflets carry fixed anionic charge at one charge per lipid and let the membrane be permeable to a 1:1 salt. The internal mobile osmolarity at Donnan balance is $\sqrt{c_f^2 + 4c_{\mathrm{ext}}^2}$ against an external $2c_{\mathrm{ext}}$, where c_f is the fixed-charge concentration in the lumen. The excess is positive at every radius:* 14.8 *mM at* $R = 100$ *nm,* 55.9 *at* $R = 50$ *and* 189 *at* $R = 25$.

Water therefore enters until the vessel is spherical and the surplus passes into tension. No division occurs*: the vessel is pinned at* $v = 1$ *where the Donnan tension is sub-lytic and bursts where it is not, and the division thresholds of the cycle paper —* 0.813 *at* $\alpha = 0.10$ *and* 0.707 *symmetrically — are reached in neither case. At a lysis tension of* 5.0 $mN\,m^{-1}$ *the boundary between the two falls at* $R = 31.7$ *nm and at* 7.5 *it falls at* 16.6*. Blocks V1 and W6(a).*

> *Proof.* Finite; Appendix B, blocks V1 and W6(a), computed at six radii. The lysis tension is not supplied by this corpus and the boundary is therefore indicative; the conclusion is insensitive to it, both regimes excluding division. □

Corollary 4.3 (Selectivity is necessary)**.** [D] *A pore compatible with the cycle paper's orbit must not conduct the osmotically active species. Since that species is the residue, the passage must exclude the residue while admitting whatever it is for.*

Scholium 4.4 (The inverse failure)**.** The cycle paper states, at its division geometry, that volume tracks area instantly and that excess area exists *only* because the particle count is impermeant. Read forward, that sentence says what a pore would cost.

The architecture's problem was that its particle count runs down, and a conducting pore does not solve it: it replaces a vessel that shrinks over forty generations with one that cannot divide at all. *Impermeance is not an inconvenience the architecture tolerates; it is the condition that makes division available.* A pore is admissible only where it conducts something the osmotic balance does not count, which is the whole of what Sections 5 to 7 are for.

The two regimes meet near the cycle paper's dilution floor, which is worth recording separately. At $R = 25$ nm the Donnan excess gives 5.9 $\mathrm{mN\,m^{-1}}$, inside the lysis range of a fluid bilayer. *Under a conducting membrane that floor would not be a floor but a boundary*, and a lineage approaching it would not shrink toward a limit but burst at one.

5 The column and the ring

Definition 5.1 (Column and ring)**.** [D] A *column* is a run of units joined end to end along 6–12 by phosphodiester formation, its long axis lying within the tilt range the enclosure paper computes. A *ring* is a closed cycle of columns joined laterally along 3–9 by the same chemistry, one lateral bridge per unit layer.

Proposition 5.2 (Only the tetrasubstituted unit can serve)**.** [A] *A* 6,12*-disubstituted unit spends both arms on the column and has none left for a lateral bridge, so no ring can be built from it. The* 3,6,9,12*-tetrasubstituted unit spends* 6–12 *axially and* 3–9 *laterally.*

The tetrasubstituted unit is the only species in the ledger's inventory from which a ring can be made. *Block V5(a).*

Remark 5.3 (Where the tether can and cannot attach)**.** [A] The 3–9 axis lies in the membrane plane; its arms are directed at neighbouring columns and cannot reach a strand at the lumen interface. No interior unit of a column is tethered.

A column of n units has exactly two free terminal arms, one at each face. The proximal one is the tether and carries the sequence address; the distal one is a phosphate monoester on the outer surface. *The second places fixed anionic charge on the outer leaflet*, which Theorem 4.2 took to be inner only. The correction runs toward symmetry and makes the excess there larger, not smaller, so the necessity argument is unaffected in direction.

Proposition 5.4 (Spanning)**.** [A] *At a unit long axis of* 1.25 *nm and a bilayer core of* 2.7 *nm, three units span the core at tilts to* 30° *and four at* 46°*. The lateral bridges then recur every* 1.25 *to* 0.87 *nm along the normal, so the passage is constricted at two or three rings and is not a bore of constant section. Block V5(b).*

Remark 5.5 (Why the stacking is lateral and the linkage axial)**.** [A] The enclosure paper places the aromatic plane so that it contains the normal, so the π-stacking axis lies in the plane of the membrane. A column cannot be built by face-to-face stacking: that would need 7.9 units and the aromatic plane perpendicular to the normal, which the enclosure paper's footprint corollary excludes. Block V5(a). *π-stacking relates adjacent columns; the covalent linkage of Definition 5.1 builds one.* The linkage is also what holds the distal leaflet's units in register with the proximal, which the tether cannot do and which no earlier paper of this corpus supplied.

6 Closure

Theorem 6.1 (The lateral bridge closes a ring at every size)**.** [A] *The chain* C–O–P–O–C*, built from standard internal coordinates and scanned over its three torsions, admits turns from* 3.8° *to* 178.3° *among the conformers that keep the columns parallel to the normal and in vertical register.*

Closure of an n-ring requires a turn of $360/n$ and is available at $n = 3, 4, 5, 6, 8, 12$, with L_b between 3.8 and 5.0 Å. Block W1.

Proof. Finite; Appendix B, block W1, scanned at 5° over 46,656 conformers, of which 896 satisfy the register constraints. □

Scholium 6.2 (A worry withdrawn)**.** It was argued, in preparing this paper, that the 3 and 9 substituents being inversion-related give collinear linkages; that a chain of columns so linked is straight; that a straight chain bounds no region; and hence that closure required the bridge to bend, in tension with rigidity.
The premises are correct and the conclusion does not follow: the P–O torsions supply the turn without strain. Closure is not the obstruction and no premise about flexibility is needed. The episode is recorded at Remark D.4 because the reasoning was sound and the arithmetic was never done.
What the closure constraints *do* fix, and at $n = 3$ alone, is the bridge angle, which Theorem 7.1 turns to account.

Theorem 6.3 (The phosphate is exiled from the lumen)**.** [A] *In every closing conformer the phosphorus lies on the far side of the chord joining the two columns it bridges: h_P between -1.49 and -1.30 Å at $n = 3$, and between -1.04 and -0.75 Å at $n = 4$, measured positive toward the ring interior. Block W2.*

Proof. The phosphorus is the apex of the bend, and a chain turning inward about a ring carries its apex outside the chord. Finite; Appendix B, block W2, computed over the conformers of block W1. □

Corollary 6.4 (The bridges set the aperture and do not occlude it)**.** [A] *By Theorem 6.3 no bridge atom enters the enclosed void. The aperture is fixed by the column spacing alone, and the lining is anionic by proximity rather than by intrusion.*

Remark 6.5 (What Corollary 6.4 costs and what it buys)**.** [A] It costs the most natural reading of the construction, in which the free arms project into the channel and narrow it to taste. That reading is not available: the arms are spent on bridges and the bridges are outside.
It buys the removal of a premise. An aperture narrowed by a projection depends on the projection's extent, which is a molecular estimate; an aperture set by a covalent bridge depends on the bridge's length, which is computed. The hypothesis register is shorter by one entry on this account (Remark D.3).

7 The aperture

Theorem 7.1 (The trimeric aperture, over the whole closure set)**.** [A] *Under Convention 2.5, and closing the ring over three* independent *bridge conformers rather than three equal ones, the void inradius r_v of a trimer spans* 0.207 *to* 0.258 *nm at one Ångstr"om of positional slack, over* 151 *closures of which* 95 *are scalene. At the tightest slack every closure is equilateral and r_v spans* 0.247 *to* 0.252*; at two Ångstr"oms the span is* 0.165 *to* 0.275*. Blocks W3 and W4.*
At $n \geq 4$ the bridge angle is unconstrained and r_v ranges from 0.13 *to* 0.50 *nm among closing conformers of a single bridge alone.* A tetramer is not a leaky pore but a pore whose size is set by nothing*, which is the worse of the two failures.*

Proof. Finite; Appendix B, blocks W3 and W4, the latter composing three conformers in $SE(2)$ and requiring the product to be the identity. □

Scholium 7.2 (A determinacy claim withdrawn)**.** An earlier form of this theorem reported the aperture as determined to 0.008 nm, on a scan that treated one bridge and asked whether it could turn 120°. A trimer has three, each adopting its own conformer, and the ring closes only if the three are jointly consistent in $SE(2)$.
Composed properly, the equilateral family is recovered at the tightest tolerance and is an artifact of it: admit one Ångstr"om of slack — less than the flex the fixed internal coordinates do not carry — and scalene closures appear, the turn spread reaching 19°. *The aperture of a trimer is not determined; the aperture of a symmetric trimer is.*
What survives is weaker and is the statement Corollary 7.5 actually needs: the aperture remains inside the selective window across the whole closure set at that slack. At two Ångstr"oms it does not, and Target 13.1 asks what the right slack is.

Lemma 7.3 (A side chain cannot subtract)**.** [A] *For a fixed conformation the cylinder radius about an axis is the maximum over atoms of the perpendicular distance plus the van der Waals radius. Adding an atom can only raise that maximum, for every axis, and hence can only raise the minimum over axes.* The backbone therefore bounds every α-amino acid from below*, and the bound is essentially attained by glycine.*

Scholium 7.4 (Three and four are the two families, and which one is constrained)**.** Theorem 7.1 selects the trimer for a reason that has nothing to do with what the ring is for. Closure at three constrains the bridge; at four and above it does not, and the aperture is then whatever the conformers give it. *The trimer is not the ring that works best; it is the only ring that is anything in particular.*

That is worth setting beside the loom paper's independent arrival at the same two numbers. Its lattice admits exactly two void families, triangular and rectangular — three-fold and four-fold — and nothing else, and it treats them as mutually exclusive. The agreement at the level of *which two geometries exist* is real and is not trivial: two constructions over the same molecular frame, one by lattice symmetry and one by a torsion scan, find the same pair.

The agreement does not extend to the assignment, and the difference should be recorded rather than smoothed. That paper pairs the three-fold void with its laterally shifted lattice and the four-fold void with exact vertical register; the ring of this paper is three-fold and is built under a register constraint, which is the opposite pairing. The two registers are taken over different axes — successive planes there, laterally adjacent columns here — so there is no formal contradiction, and equally there is no support. Target 13.2 asks whether the two shifts are one operation.

A reader should take from this neither confirmation nor conflict, but a question that now has a definite form, which it did not have before either paper.

Corollary 7.5 (The trimer is selective for any residue bearing a side chain)**.** [D] *Taking every quantity as a clearance to a van der Waals surface — the convention in which the aperture is computed — and minimising each molecule over its own torsions, the minimum enclosing cylinder has radius* 0.255 *nm for the glycine zwitterion,* 0.275 *for alanine,* 0.276 *for serine,* 0.358 *for an aromatic side chain, and* 0.204 *nm for ammonium. The symmetric trimeric aperture is* 0.254 *nm.*

Ammonium passes with 0.050 *nm to spare. At the bound of Lemma 7.3 there is* no *exclusion: glycine clears the aperture by* 0.001 *nm, which is nothing. One methyl buys* 0.021 *nm and an aromatic fragment buys* 0.104.

Since the enclosure paper records that the severed arm releases the side chain *of a residue, glycine is excluded by construction and the smallest admissible case clears by* 0.021 *nm — which survives the aperture's own upper bound of* 0.258 *nm at one Ångstr"om of slack, by* 0.017. *Block W5.*

Scholium 7.6 (A margin withdrawn, and a target that settled itself)**.** An earlier form of this corollary set the aperture, a clearance to a van der Waals surface, against the residue's *Stokes* radius, which is hydrodynamic. The two are not commensurable and they differ by more than the 0.016 nm margin then claimed; that margin is an artifact of mixing conventions and is withdrawn.

What replaced it is not a smaller margin but a different kind of statement. The residue's exact dimension was carried, through two drafts, as the result's principal unknown and its first target. It is not an unknown of that kind. *Lemma 7.3 makes the dependence monotone*, so the question is not what the residue's cylinder is but whether it exceeds the backbone's, and the enclosure paper answers that in four words: the severed arm releases a side chain.

The exact radius would narrow a range already entirely on the safe side. *What is not settled is the aperture's own range*: at one Ångstr"om of closure slack it reaches 0.258 nm and still excludes alanine, and at two it reaches 0.275 and does not. The binding uncertainty of this paper is Target 13.1 and it is not Target 13.3, which the first two drafts had the other way round.

Remark 7.7 (What the margin rests on)**.** [A] The aperture moves by 0.029 nm per half-Ångström of bridge length, by 0.020 nm over an interplanar thickness of 3.0 to 3.8 Å, by 0.014 nm over an in-plane width of 6.5 to 7.5 Å, and by 0.002 nm across the whole pinned range of the bridge angle. Block W3.

The bridge length is computed rather than estimated. Two uncertainties remain and they are of different kinds. The first is the closure slack of Theorem 7.1, which is a modelling parameter and is Target 13.1. The second is the *residue's* minimum cylinder, bounded below at 0.258 nm by glycine and otherwise unknown, which by Scholium 7.6 now carries the whole of Corollary 7.5.

A bulkier residue widens the exclusion and cannot narrow it. That is the only respect in which the result is robust, and it is worth stating plainly rather than leaving to be inferred — as is the fact that it is the only one.

Remark 7.8 (Neither occupant nor condensation)**.** [A] At 0.254 nm the aperture admits no backbone element: an extended strand requires 0.45 nm and a helix 1.00 nm. No occupant is needed by Corollary 7.5 and none would fit.

An earlier development of this paper placed a condensed peptide in the aperture as its filter and supplied an activation chemistry for the condensation. The whole of it is withdrawn at Remark D.2. Nothing here requires a condensation, an excited state, or an oxidizing equivalent, and the signalling paper's convention restricting heteroatom chemistry to the phosphodiester is preserved rather than amended.

Remark 7.9 (What a constriction is, and is not)**.** [A] By Proposition 5.4 the bridges recur two or three times across the core, so the passage is a short constriction repeated, not a long narrow bore. The quantity that bounds a leak through such a passage is the narrowest cross-section and not a permeability per unit length, which is why block V3 computes the former.
That a polygonal constriction discriminates on a solute's smallest cross-section rather than on its Stokes radius is why block W5 computes the minimum enclosing cylinder, minimised over axis directions, and not a hydrodynamic radius. An earlier form of this paper compared the two conventions directly (Scholium 7.6).
What is *not* settled by that computation is the energetics. The dehydration penalty is conceded at Appendix C and used nowhere, and at this aperture it governs (Target 13.5).

8 The ledger extension

Definition 8.1 (Two edges)**.** [D] Two transformations are added to the material ledger's digraph: *axial polymerisation*, taking n tetrasubstituted units and $n-1$ heteroatom units to a column; and *lateral bridging*, taking m columns and m heteroatom units to a ring. Both consume phosphorus and neither is reversed by any edge in the inventory.

Remark 8.2 (A property must be refined)**.** [A] The material ledger carries valence as the number of arms available for further bonding. That is now insufficient: the two axes do different work and are orthogonal, and the construction turns on *which* arms are spent.
Valence is accordingly refined into *axial* valence, on 6–12, and *lateral* valence, on 3–9. The ledger's theorem that valence once spent is restored by no composite survives the refinement with its scope narrowed per axis: no transformation adds an arm on either. This is a refinement and not an overturning, and Ruling 12.4 records it as such.

Proposition 8.3 (The sinks gain two members and the corollary holds)**.** [A] *Column and ring are consumed by no transformation and are therefore sinks. Both are membrane-resident. The material ledger's corollary that every sink leaves the lumen except the residue is unchanged, and with it the osmotic argument that rests on it.*
This is the non-disruption on which the rest of the paper depends*, and it should be checked before anything else: an added sink that stayed in the lumen would enter the osmotic balance and arrest the cycle.*

Proposition 8.4 (A fourth demand, and it is small)**.** [A] *The material ledger's three demands are additive; the ring is a fourth. A trimeric pore of three columns of three units costs nine tetrasubstituted units, six axial bridges and nine lateral ones, hence fifteen phosphorus atoms. One pore is* 0.021% *of the pool at* $\alpha = 0.10$*, ten are* 0.21% *and a hundred are* 2.1%*. The allocation* $(f_{\mathrm{anc}}, f_{\mathrm{res}}, f_{\mathrm{lip}}) = (0.024, 0.664, 0.313)$ *is unchanged at the precision at which it was stated, and a fourth fraction* f_{por} *does not appear at it. Block V5(c).*
A reader will expect a new demand to move the allocation. It does not, and that is worth stating rather than leaving to be noticed.

Remark 8.5 (Where exclusivity is not yet settled)**.** [A] The material ledger proves that no unit serves two of its three demands. The same must be asked of the fourth and is not answered here.
The tetrasubstituted unit was previously consumed by templating alone. A unit in a column has spent 6–12; whether it can still template depends on which positions the sugar-ring formation of Figure 6 uses. If 3 or 9, it cannot, and the four demands are additive as before. If 6 or 12, the question is closed by Proposition 5.2. A unit serving two demands would be the first dual use in the corpus and would *lower* the requirement rather than raise it (Target 13.8).

Remark 8.6 (The feedstock must be split)**.** [A] The material ledger enters nitrogen, oxygen and phosphorus as one species, on the explicit ground that no result there depended on which heteroatom was wanted where. This paper depends on it twice: the constriction is cation-selective and passes nitrogen as ammonium while rejecting phosphate, and the ring itself is built of phosphorus.
The inventory therefore needs Xh resolved into at least Xn and Xp, which carries the ledger's source set from four species to five (Ruling 12.4). This paper supplies a route for the first and none for the second (Target 13.7).

9 Supply, and why the influx is a trap

Remark 9.1 (No conductance is claimed, and none is needed)**.** [A] Condition C1′ at $\alpha = 0.10$ wants 0.648 impermeant particles per second in total, and the excision consumes one feedstock unit per residue, so the feedstock flux wanted is of the same order. One constriction at 10^4 s^{-1} over-supplies it by four orders and one at 10^6 by six. Block V5(d).
The architecture requires a channel run at about a millionth

of an ion channel's capacity. Conduction is therefore not the binding constraint, which is why this paper computes a leak and not a flux, and why the signalling paper's refusal to claim a conductance costs nothing here.

Proposition 9.2 (The charge balance closes)**.** [D] *Ammonium enters the lumen; the excision fixes its nitrogen as the residue's ammonium terminus and releases a proton as the carboxylate forms. The net event is an ammonium in and a proton out through the same cation-selective constriction:* 28,000 *of each per period at* $\alpha = 0.10$ *and* 5,143 *at* $\alpha = 0.02$*, which is* 0.648 *and* 0.119 *per second, for a net charge of zero in both cases. No anion pathway is required and no membrane potential accumulates. Block W6(b).*

Corollary 9.3 (C1 and C1′ hold together)**.** [D] *The arriving ion is consumed on arrival and does not equilibrate, so the influx is a trap and not a leak, and the impermeant population it feeds is the residue. The cycle paper's condition C1 survives for the residue by Corollary 7.5, while C1′ is discharged by the excision, and the reduced volume is not pinned.*
Selectivity is what reconciles two conditions that would otherwise exclude each other*, and Theorem 7.1 supplies it from covalent geometry with no premise behind it.*

Scholium 9.4 (What the pore is for)**.** It is worth saying plainly what has and has not changed about the cycle.
The material ledger discharged C1′ by finding the osmolyte. It left unsupplied the rate at which the environment delivers what the osmolyte is made of. This paper does not make particles and does not import them: it supplies a route by which one of the feedstock heteroatoms crosses the membrane, at a rate the architecture can use, without the crossing itself entering the osmotic balance.
The pore is a supply line and not a pump. Nothing here moves a solute against its gradient, and the appearance of doing so is an artifact of the arriving species being destroyed at the far end.

10 Consolidated register

Does a conducting pore help the cycle?
No. It pins the reduced volume at unity above a lysis boundary near 32 nm and bursts the vessel below it, removing the division condition it was wanted to supply.
Rests on: Finite (Thm. 4.2), blocks V1 and W6(a).
Standing: [D] Computed. Rests on the dialkyl-phosphate reading of the head group, registered as H1.

What can a ring be built from?
The tetrasubstituted unit alone; the disubstituted unit has no arm left for a lateral bridge.
Rests on: Finite (Prop. 5.2), block V5(a).
Standing: [A] Computed.

Where is a ring tethered?
At the free terminal arm of the lumen-side unit of a column, and nowhere else; the lateral arms lie in the plane and cannot reach the strand.
Rests on: Rem. 5.3.
Standing: [A] Geometric.

Can the lateral bridge close a ring?
Yes, at every size from three to twelve, without strain.
Rests on: Finite (Thm. 6.1), block W1.
Standing: [A] Computed over 46,656 conformers.

Does the bridge phosphate narrow the channel?
No. It lies outside the chord in every closing conformer, being the apex of the bend.
Rests on: Finite (Thm. 6.3), block W2.
Standing: [A] Computed.

What aperture does a ring enclose?
0.254 nm in the symmetric trimer; 0.207 to 0.258 nm over the closure set at one Ångstr"om of slack. Set by nothing at $n \geq 4$.
Rests on: Finite (Thm. 7.1), blocks W3 and W4.
Standing: [A] Computed. Rests on the cross-section, H4, and on the slack, Target 13.1.

Is the trimeric aperture selective?
Ammonium passes with 0.050 nm to spare. Any residue bearing a side chain is excluded, by 0.021 nm at the smallest and 0.104 for an aromatic fragment; the bare backbone is not.
Rests on: Cor. 7.5, Lem. 7.3, block W5.
Standing: [D] Rests on the closure slack, Target 13.1, and not on the residue's exact dimension.

What does a ring cost the pool?
Nine units and fifteen phosphorus atoms; a hundred pores are 2.1% of the pool and the allocation is unchanged.
Rests on: Finite (Prop. 8.4), block V5(c).
Standing: [A] Computed. Rests on the scale parameters, H3.

How is C1 reconciled with C1′?
The admitted ion is consumed on arrival, so the influx is a trap; impermeance holds for the residue and the particle count is fed, at 0.648 ions per second each way and zero net charge.
Rests on: Cor. 9.3, Prop. 9.2, block W6(b).
Standing: [D] Rests on Cor. 7.5.

Nine entries. Five are finite or geometric. Four rest on H1 to H4 of Appendix A, and *one of the four — the selectivity — rests on a quantity this paper does not have*. None rests on a premise about mechanism.

11 Falsification register

Theorem 4.2
A head-group reading on which the leaflets carry no net charge — the phosphatidyl reading the enclosure paper entertains — which would reduce the fixed charge to the strand's 0.17 mM and remove the pinning. *This is the entry that matters for Section 4*, and Scholium 13.11 says what survives it.

Proposition 5.2
A ring built from disubstituted units, or a tether borne by an interior unit of a column.

Theorem 6.1
A bond geometry for the aryl phosphodiester admitting no turn of $360/n$ for any n among register-preserving conformers.

Theorem 6.3
A closing conformer with the phosphorus inside the chord.

Theorem 7.1
A closed triple of bridge conformers, within whatever slack the bond geometry actually permits, whose inradius falls outside 0.207 to 0.258 nm; or a cross-section for the column other than the plank of H4, which has already reversed a statement of this paper once (Rem. D.1).

Corollary 7.5
A closure slack above two Ångstr"oms, at which Theorem 7.1's upper end reaches even the smallest admissible residue. Also: a residue bearing no side chain, which the enclosure paper's account of the severed arm excludes; or a feedstock cation retaining enough hydration to exceed the aperture.

Lemma 7.3
An atom whose addition lowers a minimum enclosing cylinder, which the definition forbids; or a residue conformation in which the backbone atoms do not form a subset of the whole.

Proposition 8.3
A transformation consuming a column or a ring; or a reading on which either is not membrane-resident, which would put a new sink in the lumen and arrest the cycle.

Proposition 8.4
A pore count above about a thousand, at which the ring's demand becomes comparable to the encoding's.

Corollary 9.3
A feedstock species not consumed at the rate it enters. The influx is then a leak, and the pinning of Theorem 4.2 returns through the pore this paper built.

12 Precedence

Ruling 12.1 (Against the signalling paper). 🄰 *Consistent;* no deferral lifted. *That paper computed apertures and declined a conductance, and this paper declines it too (Rem. 9.1). Nor is that paper's aperture inherited: its apertures belong to an in-plane aggregate of units and this paper's to a transmembrane ring of columns, which are different objects whose numbers are not comparable (Appendix E). That paper offered its frame as one a later architecture would find already built; this paper does not find it, and builds another.*
What is supplied is what neither paper had: a wall between the leaflets.
Its convention restricting heteroatom chemistry to the phosphodiester, with no metal, cofactor or oxidizing equivalent in a numbered statement, is preserved unamended. *An earlier development of this paper would have required amending it; that development is withdrawn (Rem. D.2).*

Ruling 12.2 (Against the enclosure paper). 🄰 *Consistent; one orientation result load-bearing in a new way. That paper's placement of the aromatic plane with the normal in it is what forbids a face-to-face column and forces the axial linkage (Rem. 5.5). Its tilt range sets the unit count per column (Prop. 5.4) and its area per lipid sets the fixed charge (Thm. 4.2). Nothing of that paper is revised.*

Ruling 12.3 (Against the cycle paper). 🄰 *Consistent; one scope qualification and one condition jointly discharged. Its scholium that size homeostasis is unavailable rests on its dilution theorem, which assumes no particle source; the qualification is already in that paper and is not a revision here.*
What is new is that C1 and C1′ are shown to be jointly satisfiable, which that paper left as two separate requirements with no argument that one did not exclude the other (Cor. 9.3).

Ruling 12.4 (Against the material ledger). 🄰 *Consistent, extending; one property refined, two edges added, one species to be split. Valence is refined per axis and the no-restoration theorem survives with its scope narrowed (Rem. 8.2). Two sinks are added and the corollary that every sink but the residue leaves the lumen is unchanged (Prop. 8.3). The heteroatom feedstock must be split into at least a nitrogen and a phosphorus species, which that paper entered as one on the explicit ground that nothing then depended on the distinction (Rem. 8.6).*
That makes its source set five and not four, *and the point*

should be claimed rather than absorbed: that paper's own falsification register names "a fifth species consumed and unproduced" as the likelier direction of error, and records that the theorem had already been wrong once in that direction. This paper supplies the fifth.
Its free-residue hypothesis is neither used nor relaxed *here. An earlier development of this paper relaxed it; that development is withdrawn.*

Ruling 12.5 (Against the loom paper)**.** [A] *One fact imported, nothing inherited. Convention 2.4 takes the orthogonality of the two substituted axes as a statement about the molecular frame. Nothing here uses that paper's tensor space, its Dirichlet walls, its Morse filtration or its identification hypothesis, and nothing here supports them.*
One correspondence is recorded and is not used. That paper's lattice admits exactly two void families, three-fold and four-fold, and Theorem 7.1 finds the same two and constrains only the first. The agreement is on which geometries exist and not on how they arise, and the two accounts assign them oppositely to a register condition (Sch. 7.4, Target 13.2).
The relation is otherwise worth stating in this direction rather than the other. That paper is axiomatic where this corpus is ledgered: it carries no status labels, no falsification register and no verification blocks, and several of its statements are not of a kind an observation could refute. A result of this paper may not rest on one of its statements beyond the [C] *import above, and the correspondence just recorded is* [E] *and enters no proof.*

13 Targets, and conclusion

13.1 Targets

Target 13.1 (The closure slack)**.** Determine how much positional slack the aryl phosphodiester actually permits, by relaxing the bond lengths and angles that block W4 holds fixed. At one Ångstr"om the trimeric aperture reaches 0.258 nm and still excludes the smallest admissible residue; at two it reaches 0.275 and does not. *This is the first target of this paper and the binding one*: it decides whether Theorem 7.1 supports Corollary 7.5 at all.

Target 13.2 (The two shifts)**.** Determine whether the loom paper's lateral shift between successive lattice planes and the lateral register between adjacent columns required here are the same operation taken on different axes. That paper pairs its three-fold void with the shifted lattice and its four-fold void with exact register; this paper's three-fold ring is built under register (Scholium 7.4). If the two are one operation the accounts disagree and one is wrong; if they are two, the three-fold selection has been reached twice by unrelated routes and is worth more than either reaching alone.

Target 13.3 (The residue's side chain)**.** Identify the side chain the severed arm releases, and with it the residue's minimum enclosing cylinder. By Lemma 7.3 this can only widen the exclusion, and the smallest admissible value already clears the aperture, so the target is *confirmatory rather than gating* — which the first two drafts of this paper had the other way round (Scholium 7.6). It remains worth settling because the margin it supplies is what absorbs any widening of the slack.

Target 13.4 (What selects the trimer)**.** Exhibit a reason for closure at three. Theorem 7.1 shows the trimer is the only ring with a determined aperture; it does not show that larger rings do not form. A kinetic or thermodynamic argument would convert a geometric singularity into a mechanism, and without one the paper describes the only ring that *would* work rather than the one that does.

Target 13.5 (The dehydration term)**.** Carry the dehydration penalty and its repayment by the lining into the selectivity statement. At an aperture of a quarter of a nanometre it is the energetics and not the clearance that decide whether anything crosses, and Corollary 7.5 is a necessary condition on size with the energetic condition outstanding (Appendix C).

Target 13.6 (The head group)**.** Settle whether the route-A lipid is the anionic dialkyl phosphate the material ledger names or the zwitterionic phosphatidyl the enclosure paper entertains. It decides Theorem 4.2 and with it whether selectivity is necessary or merely useful.

Target 13.7 (Phosphorus)**.** Split the heteroatom feedstock and supply a route for the phosphorus half. The constriction passes nitrogen and rejects phosphate, while the ring itself consumes fifteen phosphorus atoms (Rem. 8.6).

Target 13.8 (Dual use)**.** Determine whether a tetrasubstituted unit in a column can still template, by settling which positions the sugar-ring formation of Figure 6 uses. A unit serving two demands would be the first dual use in the corpus and would lower the material ledger's requirement rather than raise it (Rem. 8.5).

13.2 Conclusion

Proposition 13.9 (What is established)**.** [A] *Subject to Appendix A:*

(i) That a membrane conducting the osmotically active species is pinned at unit reduced volume and cannot reach the division threshold, so that selectivity is necessary rather than desirable (Theorem 4.2, Corollary 4.3).

(ii) That a ring can be built only from the tetrasubstituted unit, and is tethered only at a column's terminal arm (Proposition 5.2, Remark 5.3).

(iii) That the covalent axial linkage, and not π-stacking, is what spans the bilayer and holds the distal leaflet in register (Remark 5.5).

(iv) That the lateral bridge closes a ring at every size without strain (Theorem 6.1).

(v) That the phosphorus lies outside the chord in every closing conformer, so the bridges set the aperture and never occlude it (Theorem 6.3, Corollary 6.4).

(vi) The trimeric aperture over its whole closure set, 0.207 *to* 0.258 *nm at one Ångstr"om of slack, against a tetramer's which is set by nothing (Theorem 7.1).*

(vii) That a minimum enclosing cylinder is monotone under atom addition, so the backbone bounds every α-amino acid below (Lemma 7.3).

(viii) That the aperture admits ammonium with 0.050 *nm to spare and excludes any residue bearing a side chain, by* 0.021 *nm at the smallest, requiring no occupant (Corollary 7.5).*

(ix) That the ring is a fourth demand on the pool and does not move the allocation (Proposition 8.4).

(x) That the influx is a trap rather than a leak, so that C1 and C1′ hold together (Proposition 9.2, Corollary 9.3).

Remark 13.10 (What is not established)**.** [A] No conductance is computed and no rate of any kind, and no dehydration energetics, which at this aperture govern. No argument is given that a ring of three forms rather than being the one that would serve. No chemistry is derived: both new edges are phosphodiester formation, named and not obtained. The phosphorus half of the feedstock has no route, and the exclusivity of the fourth demand is unsettled.
And the closure slack is not bounded, which leaves Theorem 7.1's upper end — and with it Corollary 7.5 — resting on a modelling parameter rather than on a computed one.

Scholium 13.11 (What would overturn the paper)**.** Two findings, and they take different amounts with them.
A phosphatidyl head group would remove the fixed charge and with it Theorem 4.2. Section 4 would go, and selectivity would become useful rather than necessary. *The construction would survive*: a determined aperture that excludes the residue is a better object than an indeterminate one whatever the motivation for wanting it, and Corollary 9.3 would still be the reason the influx does not equilibrate.
A closure slack above two Ångstr"oms would carry the aperture to 0.275 nm, where it admits even the smallest residue bearing a side chain, and would remove Corollary 7.5 and with it everything the construction is for. *This is the entry to watch.* It is a question about how much the aryl phosphodiester's bond geometry actually flexes, it is settled by relaxing what block W4 holds fixed, and nothing in this paper bounds it.
The residue's own dimension, which the first two drafts put in this position, is not a risk of the same kind. Lemma 7.3 makes the dependence monotone and the enclosure paper's account of the severed arm supplies the side chain, so the requirement is not that the residue be large but that it exist, and it does.
A third possibility is not a finding but an absence. If nothing selects the trimer (Target 13.4), the paper does not fail — it becomes a statement about which ring *could* serve, with no claim that any does. That is a weaker paper than this one and it is not a refuted one, and the difference should be kept clear.

A Hypothesis register

	premise	what rests on it	what survives its failure
H1	The route-A lipid is the anionic dialkyl phosphate named in the material ledger, carrying one negative charge per lipid, rather than the zwitterionic phosphatidyl the enclosure paper entertains.	Theorem 4.2 and, through it, Corollary 4.3 — that is, the whole of Section 4.	The construction. Sections 5 to 7 are geometry and are indifferent to the head group; what fails is the argument that selectivity is *necessary*, not the demonstration that it is available (Sch. 13.11).
H2	The solute geometries: bond lengths, angles and van der Waals radii from which block W5 builds each molecule, and the backbone dimensions of an extended strand and a helix. Standard values, sourced at Appendix E.	Corollary 7.5 and Remark 7.8.	Theorems 6.1, 6.3 and 7.1, which give a closure, an exclusion of the phosphate and an aperture without reference to what passes through it; and Lemma 7.3, which is about sets and not about radii.
H3	The scale parameters: R, N, T, c_{ext} and the area per lipid, imported from the cycle and enclosure papers (Not. 4.1).	Every number in Theorem 4.2, Proposition 8.4 and Remark 9.1.	All three statements, each holding as a formula in the imported quantities rather than at their values.
H4	The column's cross-section is the plank of Conv. 2.5: 3–9 along the ring and the 3.4 Å π-face toward the void.	Theorem 7.1 and, through it, Corollary 7.5 — that is, every number in Sections 7.	Nothing of the aperture. On the disk reading the trimeric void is 0.278 nm and the ring leaks, with every input unchanged (Rem. D.1). *This premise has reversed the paper's conclusion once and is registered for that reason.*

Remark A.1 (Four premises, and where the weight sits)**.** [A] H1 carries the motivation, H2 the solute geometries, H3 the numbers, H4 the aperture.
An earlier form of this register held three entries and observed that the paper's principal result rested on none of them, the cross-section being carried as a convention. That was bookkeeping in the paper's favour: a convention which reverses a conclusion when changed is a premise, and it is now H4.
A reader allocating scepticism should spend most of it on H4 and on Target 13.3, which between them carry Corollary 7.5 entirely. H1 carries only the argument that the corollary is *needed*; H3 carries no statement.

B Verification

Each block recomputes its claim from an explicit structure and emits its own numbers. Nothing quantitative in the body is asserted. The V series carries the ledger and flux quantities and the W series the bridge conformational geometry. Blocks V2, V4 and V6 are superseded and are listed at Appendix D rather than reproduced here; blocks W4 to W6 were added at revision and replace the aperture and selectivity statements of the first draft.

V1 [COMPUTED] **A non-selective pore pins the reduced volume at one**

Donnan balance with fixed anionic head groups at one charge per lipid, against the division thresholds of the cycle paper.

```
Donnan balance with fixed anionic head groups, 1 charge per lipid.
internal mobile osmolarity = sqrt(c_f^2 + 4 c_ext^2);  external = 2 c_ext

  R (nm)     fixed Z   c_f (mM)  excess (mM)  dPi (kPa)  tension (mN/m)
-------------------------------------------------------------------------
      25   1.023e+04      333.2       188.64     470.50           5.881
      50   4.454e+04      159.7        55.92     139.47           3.487
     100   1.857e+05       78.2        14.75      36.78           1.839
     150   4.235e+05       51.8         6.60      16.45           1.234
     200   7.579e+05       38.7         3.71       9.26           0.926
```

```
     400   3.062e+06       19.3         0.92       2.31           0.461
-------------------------------------------------------------------------

DIVISION THRESHOLD, Art. 64 block V5
   alpha = 0.50   Q = 1.2599   v must fall to 0.7071
   alpha = 0.30   Q = 1.2365   v must fall to 0.7273
   alpha = 0.10   Q = 1.1476   v must fall to 0.8134
   alpha = 0.05   Q = 1.1021   v must fall to 0.8643

READING.  The excess is positive at every radius, so water enters until the
vesicle is spherical and the surplus goes into tension.  Osmotic relaxation
is 0.9 s against a period of 4.3e4 s, so the pinning is immediate.  A vessel
at v = 1 reaches no threshold in the table above.

Art. 64 block V5 states the same thing from the other side: excess area
exists ONLY because N is impermeant.  Hence a pore that conducts the
osmotically active species does not relieve the dilution limit, it removes
the division condition.  SELECTIVITY IS NECESSARY, not a refinement.

At R = 25 nm -- Art. 64's dilution floor -- the tension is at the lysis range
of a fluid bilayer.  Under this reading the floor is a lysis boundary.
```

V3 [COMPUTED] The leak bound

What a residue leak costs the C1′ gain, and what effective aperture satisfies it.

```
C1' at alpha = 0.10 requires a NET gain of 0.648 particles/s.
The residue is the osmolyte, so c_res(in) ~= c_ext = 100 mM,
and c_res(out) ~= 0.  Any residue leak subtracts from that gain.

Single-pore permeability of a right cylinder, with access resistance:
    p = H(lambda) . D . pi r^2 / (l + pi r / 2)

 r_eff (nm)   lambda   H(lambda)   leak /s /pore   pores affordable
-------------------------------------------------------------------
       0.35     0.77   4.015e-03       1.432e+04           4.53e-05
       0.30     0.90   6.904e-04       1.840e+03           3.52e-04
       0.28     0.96   6.769e-05       1.583e+02           4.09e-03
       0.26     1.04   0.000e+00       0.000e+00          unbounded
       0.24     1.12   0.000e+00       0.000e+00          unbounded
       0.20     1.35   0.000e+00       0.000e+00          unbounded
       0.15     1.80   0.000e+00       0.000e+00          unbounded
       0.10     2.70   0.000e+00       0.000e+00          unbounded
-------------------------------------------------------------------

READING.  At the geometric aperture of the smallest ring (r = 0.35 nm) a
single pore leaks residues some six orders faster than the cell makes them.
Partial hindrance does not help: the budget admits fewer than one pore until
the effective radius falls below the residue's own.  THE EXCLUSION MUST BE
STERIC AND ESSENTIALLY COMPLETE.

That is available, and from the lining already named.  Cor. (aperture)
computes the gap between UNIT EDGES; the phosphodiester arms that line it
project inward and occlude it.  Writing delta for the radial projection:

  delta (nm)       n=6       n=8      n=12
---------------------------------------------
        0.00     0.350     0.565     1.002
        0.05     0.300     0.515     0.952
        0.10     0.250     0.465     0.902
        0.15     0.200     0.415     0.852
        0.20     0.150     0.365     0.802
        0.25     0.100     0.315     0.752
---------------------------------------------

The window wanted is  r_eff < 0.27 nm (excludes the residue) and
r_eff > 0.15 nm (passes a partially dehydrated cation).

  n =  6 : open for delta between about 0.08 and 0.20 nm
  n =  8 : open only above delta = 0.30 nm, beyond a plausible arm
  n = 12 : never open -- the aperture exceeds the residue at every delta

THE SELECTIVE PORE IS THE MINIMAL RING AND ONLY THE MINIMAL RING.  Since the
ring size is the run length of consecutive engaged anchors, selectivity is a
property of the sequence, and a run of eight or more is a leak rather than a
pore.  That is a falsifiable statement about the genome and not about the
lipid.

CONSEQUENCE FOR THE FEEDSTOCK.  A cation-selective aperture passes the
```

```
nitrogen feedstock as ammonium and rejects the phosphorus feedstock as an
anion.  Article 66 supplies one of the two heteroatoms of thm:sources and
not both.  The phosphorus route is a TARGET, and should be stated as one.
```

V5 [COMPUTED] The column as a polymer, and what it costs the pool

The two axes, column and pore stoichiometry, the fourth demand, the flux wanted, and the charge balance.

```
(a) THE TWO AXES.  Chrysene carries two inversion-related substituted
    pairs: 3-9 and 6-12.  Polymerising along 6-12 by phosphodiester
    formation builds a column END-TO-END along the long axis -- the
    geometry block V4(a) requires -- and leaves 3-9 free.

    A 6,12-DISUBSTITUTED unit spends both arms on the column and can carry
    no tether: a column of D units is NOT sequence-addressed.
    A 3,6,9,12-TETRASUBSTITUTED unit spends 6-12 on the column and keeps
    3 and 9: one to tether, one to project into the interstitium.
    The tetrasubstituted unit is therefore the only inventory species that
    can be both a column member and an anchor.

(b) COLUMN AND PORE STOICHIOMETRY
    tilt   0 deg : 3 units per column, 2 axial phosphodiester bridges, constriction every 1.25 nm
    tilt  30 deg : 3 units per column, 2 axial phosphodiester bridges, constriction every 1.08 nm
    tilt  46 deg : 4 units per column, 3 axial phosphodiester bridges, constriction every 0.87 nm

    minimum bounded interstitium: 3 columns, 9 units, 6 bridges per pore

(c) THE FOURTH DEMAND ON THE POOL
       pores    units   P atoms   % of pool, a=0.10   % of pool, a=0.02
    ------------------------------------------------------------------
           1        9         6              0.021%              0.047%
          10       90        60              0.213%              0.466%
         100      900       600              2.133%              4.663%
        1000     9000      6000             21.327%             46.632%
    ------------------------------------------------------------------

    READING.  Article 65's three demands are additive and the column is a
    fourth.  It is also negligible: a hundred pores cost two per cent of the
    pool at alpha = 0.10.  The allocation of Thm. (feasible) is unchanged to
    the stated precision, and that should be said plainly -- a reader will
    assume a new demand moves it.

(d) THE FLUX THE PORE MUST CARRY, AND WHY NO CONDUCTANCE IS CLAIMED
    C1' at alpha = 0.10 : 0.648 feedstock ions per second, total.
       1 pore(s) at j = 1e+06/s deliver 1e+06/s -- over-supply 1.5e+06
       1 pore(s) at j = 1e+04/s deliver 1e+04/s -- over-supply 1.5e+04
      10 pore(s) at j = 1e+04/s deliver 1e+05/s -- over-supply 1.5e+05

    The architecture needs a channel run at about a millionth of an ion
    channel's capacity.  Conduction is therefore NOT the binding constraint
    and no conductance is computed here; what is computed is the leak
    (block V3) and the geometry that bounds it (block V4).

(e) CHARGE BALANCE, WHICH CLOSES WITHOUT A COUNTER-ANION PATHWAY.
    Ammonium enters; excision fixes its nitrogen into the residue's
    -NH3+ and releases a proton as the carboxylate forms.  The net event
    is NH4+ in, H+ out through the same cation-selective constriction.
    No anion pathway is required and no membrane potential accumulates.
    The arriving ion is CONSUMED, so the influx is a trap and not an
    equilibrating leak -- which is why block V1's pinning does not follow.
```

W1 [COMPUTED] Closure of a ring by the lateral bridge

Torsion scan over the aryl phosphodiester, retaining conformers that keep the columns parallel to the normal and in vertical register.

```
Chain C1-O1-P-O2-C2 built from standard internals (C(ar)-O 1.36 A,
O-P 1.60 A, C-O-P 120 deg, O-P-O 104 deg); all three torsions scanned at
5 deg; conformers retained only if they keep the columns parallel to the
normal and in vertical register.

    ring n    turn needed    closing conformers    L_b (A)    bridge angle
    ------------------------------------------------------------------
       3         120 deg              96          3.80-3.91     53-66 deg
       4          90 deg             128          4.33-4.48      free
       5          72 deg             608          4.04-4.74      free
       6          60 deg             508          4.15-4.91      free

CLOSURE IS NOT THE OBSTRUCTION.  The P-O torsions supply the turn at every
```

```
ring size without strain, so the rigidity worry is withdrawn.  What the
closure constraints DO fix, and only at n = 3, is the bridge angle.
```

W2 [COMPUTED] The phosphate is exiled from the lumen

The phosphorus offset from the chord, over the closing conformers of block W1.

```
h_P, the phosphorus offset from the chord joining two columns, is
NEGATIVE -- away from the ring interior -- in every closing conformer at
n = 3 (-1.49 to -1.30 A) and n = 4 (-1.04 to -0.75 A).

This is structural and not accidental: the phosphorus is the apex of the
bend, and a chain turning inward around a ring carries its apex outside the
chord.  THE GEOMETRY THAT CLOSES THE RING PUTS THE PHOSPHATE OUT OF THE
CHANNEL.  The bridges line the void from outside it and do not occlude it,
so the aperture is whatever the column spacing leaves.
```

W3 [COMPUTED] The void, with the column taken as a plank

The enclosed polygon under Convention 2.5, with the sensitivity of the trimeric aperture to each input.

```
CORRECTION TO BLOCKS V4 AND V6.  Those blocks took the column's
cross-section as a disk of diameter 0.70 nm.  That is wrong.  The 0.70 nm
dimension is the 3-9 axis, which lies ALONG the ring and is consumed by the
bridges; what faces the void is the 0.34 nm pi-face.  The column is a plank
of 7.0 x 3.4 A, not a disk, and the void is the polygon its inner faces
enclose.

       n     L_b   angle   r_v (nm)   verdict
    ------------------------------------------------
       3    3.87    60.0      0.256   SELECTIVE
       4    4.40     0.0      0.400   leaks
       5    4.40     0.0      0.615   leaks
       6    4.50     0.0      0.826   leaks
    ------------------------------------------------

    Over the 96 closing conformers of ONE bridge at n = 3 the void spans
    0.250 to 0.258 nm.  THAT SPREAD IS NOT THE APERTURE OF A TRIMER: a
    trimer has three bridges and block W4 composes them.  At n >= 4 the
    bridge angle is free and the void ranges from 0.13 to 0.50 nm even for
    a single bridge, so no ring but the trimer is constrained at all.

SENSITIVITY AT n = 3, around L_b = 3.87 A and bridge angle 60 deg
    base r_v = 0.256 nm;  residue 0.270 nm;  cation 0.150 nm

    input                        perturbation   r_v (nm)   change
    ------------------------------------------------------------
    bridge length L_b                    4.37      0.284   +0.029
    bridge length L_b                    3.37      0.227   -0.029
    pi thickness T                       3.80      0.236   -0.020
    pi thickness T                       3.00      0.276   +0.020
    in-plane width W                     7.50      0.270   +0.014
    in-plane width W                     6.50      0.241   -0.014
    bridge angle                        53.00      0.254   -0.002
    bridge angle                        66.00      0.254   -0.001
    ------------------------------------------------------------

    READING.  The margin that mattered was never a physical constant.  An
    earlier form of this analysis reported the trimer as marginally LEAKY at
    0.278 nm; the whole of the difference was the cross-section model, and
    the correction moves the void to 0.254 nm by changing a modelling choice
    rather than by refitting an input.  Recorded at Appendix D.

    The residue figure of 0.270 nm used in the sensitivity table above is a
    STOKES radius and is superseded by block W5, which recomputes every
    solute as a clearance to the same van der Waals surface as the aperture.
    The margin is smaller there.
```

W4 [COMPUTED] Closure over independent bridge conformers

Three bridges composed in $SE(2)$, with the product required to be the identity; the equilateral family is a slice of the result.

```
Block W1 asked whether ONE bridge can turn 360/n.  A trimer has three,
each adopting its own conformer, and closure requires the composition of
the three in SE(2) to be the identity -- turns summing to 360 deg AND the
displacements closing.  The symmetric family is a slice of that set.
```

```
Scanned over 184 distinct planar conformers; closure accepted within a
positional tolerance that stands for the flex the fixed internal
coordinates do not carry.

    tolerance     closures   max turn spread   inradius (nm)   scalene
    ------------------------------------------------------------------
    0.4 A, 2 deg       14          1.7 deg      0.247 - 0.252     0
    1.0 A, 4 deg      151         19.1 deg      0.207 - 0.258    95
    2.0 A, 6 deg      813         28.3 deg      0.165 - 0.275   725

READING, AND IT COSTS THE PAPER A CLAIM.  At the tightest tolerance every
closure is equilateral and the aperture is determined to 0.005 nm.  That is
an artifact of the tolerance: admit one Angstrom of slack -- less than the
flex of a phosphodiester -- and scalene closures appear, the turn spread
reaches 19 deg and the aperture spans 0.207 to 0.258 nm.

The determinacy claim of the first draft is WITHDRAWN.  What survives is
weaker and still useful: ACROSS THE WHOLE CLOSURE SET AT ONE ANGSTROM OF
SLACK THE APERTURE REMAINS INSIDE THE SELECTIVE WINDOW.  At two Angstroms
the upper end reaches the residue and the ring leaks.
```

W5 [COMPUTED] **The solutes, in the aperture's own convention**

Minimum enclosing cylinder of each solute's van der Waals surface, minimised over axis directions, against the clearance of block W3.

```
Block W3's inradius is a clearance to a van der Waals surface: the plank
half-thickness of 1.7 A is the aromatic carbon vdW radius.  A Stokes radius
is hydrodynamic and is NOT that quantity.  Comparing the two, as the first
draft did, mixes conventions by more than the margin it claimed.

Recomputed as the minimum cylinder enclosing each solute's vdW surface,
minimised over axis directions:

    solute                      min cylinder radius
    ------------------------------------------------
    glycine zwitterion               0.258 nm
    ammonium NH4+                    0.204 nm
    bare K+                          0.138 nm
    bare Na+                         0.102 nm

    aperture, symmetric trimer       0.254 nm
    aperture, closure set at 1 A     0.207 - 0.258 nm

READING.  The margin of 0.016 nm claimed in the first draft is an artifact
and is withdrawn.  In one convention the symmetric aperture stands 0.004 nm
inside GLYCINE, which is the smallest amino acid there is.

THE RESULT LEANS ON THE SIDE CHAIN, AND THE DEPENDENCE IS MONOTONE.
For a fixed conformation the cylinder radius about an axis is the maximum
over atoms of (perpendicular distance + vdW radius); adding an atom can only
raise that maximum, for every axis, and hence can only raise the minimum
over axes.  THE BACKBONE THEREFORE BOUNDS EVERY ALPHA-AMINO ACID FROM BELOW
and the bound is essentially attained by glycine.  A side chain cannot
subtract.

Minimised over each molecule's own torsions:

    residue                              min cylinder   vs aperture 0.254
    ------------------------------------------------------------------
    glycine, side chain H                    0.255 nm        +0.001 nm
    alanine, side chain CH3                  0.275 nm        +0.021 nm
    serine,  side chain CH2OH                0.276 nm        +0.022 nm
    aromatic side chain, benzyl proxy        0.358 nm        +0.104 nm

READING, AND IT SETTLES THE TARGET WITHOUT COMPUTING THE RESIDUE.  At the
bound there is no exclusion: glycine clears the aperture by a thousandth of
a nanometre, which is nothing.  ONE METHYL BUYS 0.021 nm AND AN AROMATIC
FRAGMENT BUYS 0.104.  The enclosure paper records that the severed arm
RELEASES THE SIDE CHAIN of a residue, so glycine is excluded by
construction and the smallest admissible case already clears by 0.021.

The exact radius of the actual residue would narrow a range that is already
entirely on the safe side.  What is NOT settled is the aperture's own range:
at one Angstrom of closure slack it reaches 0.258 and still excludes alanine
by 0.017, but at two Angstroms it reaches 0.275 and does not.  THE BINDING
UNCERTAINTY IS THE SLACK, NOT THE RESIDUE.

Ammonium at 0.204 nm passes the symmetric aperture with 0.050 nm to spare
```

```
and the tightest closures of block W4 by 0.003.
```

W6 [COMPUTED] **The pinning boundary, and the charge balance**

Where a pinned vessel lyses, and the per-period ammonium influx against the proton efflux.

```
(a) WHERE THE PINNED VESSEL LYSES.  Block V1 gives the Donnan tension; a
fluid bilayer lyses between about 5 and 10 mN/m.

    R (nm)      20     25     30     35     40     50    100
    tension   6.75   5.88   5.20   4.65   4.19   3.49   1.84   mN/m

    at a lysis tension of 5.0 mN/m the boundary falls at R = 31.7 nm
    at 7.5 mN/m it falls at R = 16.6 nm

So a conducting vessel is pinned at v = 1 above the boundary and bursts
below it.  The cycle paper's dilution floor at 25 nm lies inside the
bursting range for any lysis tension under about 5.9 mN/m.  EITHER WAY NO
DIVISION OCCURS, which is what the corollary needs; the theorem must not
say 'pinned' uniformly.

(b) THE CHARGE BALANCE, COMPUTED.

    alpha    NH4+ in / period   H+ out / period    each /s    net charge
    ------------------------------------------------------------------------
    0.10          28,000             28,000         0.648          0
    0.02           5,143              5,143         0.119          0

One proton leaves for each ammonium that enters, so the lumen gains no net
charge and no potential accumulates.  The first draft argued this in prose
inside a block and emitted no numbers.
```

C Molecular commentary, isolated

Remark C.1 (Status of this appendix)**.** [A] Nothing here enters a numbered statement and no result is weakened by its removal.

Remark C.2 (The aryl phosphodiester)**.** [E] The linkage used on both axes is an aryl phosphodiester, Ar–O–PO_2^-–O–Ar′, which is the same connection the signalling paper uses as its tether and bridge. That the architecture should build its wall out of the chemistry it already uses to carry its encoding is a convenience of the account and not an argument for it.

Remark C.3 (Dehydration at a constriction)**.** [E] A cation crossing a constriction narrower than its hydration shell must shed part of that shell, and the cost is repaid by coordination to the lining. The lining here is anionic by Corollary 6.4. Nothing in this paper computes either term, and the radius of 0.150 nm used at Corollary 7.5 assumes partial dehydration rather than deriving it.

Remark C.4 (Why the residue is the species to exclude)**.** [E] The material ledger's commentary notes that an α-amino acid is zwitterionic near neutrality, that its bilayer permeability is low but not zero, and that nothing there estimates the leak. This paper estimates it at a constriction (block V3) and not across a bilayer, which is a different quantity; the background permeability of the intact membrane is unaffected by anything here and remains unestimated.

Remark C.5 (The outer-leaflet monoester)**.** [E] Remark 5.3 leaves a free phosphate monoester at each column's distal face. On the outer surface of a vessel this is a small addition to the exterior charge; it is noted because Theorem 4.2 was computed with inner-leaflet charge only, and a reader checking that block should know the omission is in the conservative direction.

D What was withdrawn in preparing this paper

Remark D.1 (The column modelled as a disk)**.** [A] The aperture was first computed as the gap between three circumscribed disks of diameter 0.70 nm, that being the unit width the enclosure paper records. The trimeric void came out at 0.278 nm against a residue radius of 0.270, and the pore was reported as marginally leaky. Blocks V4 and V6 carried that reading and are superseded by block W3.

The 0.70 *nm dimension is the* 3–9 *axis and lies along the ring.* It is consumed by the lateral bridges and faces neighbouring columns, not the void. What faces the void is the 3.4 Å π-face, so the column is a plank and the void is the polygon its inner faces enclose. Recomputed on that reading the void is 0.254 nm and the pore is selective. The margin then reported with it, 0.016 nm, was wrong for a second and unrelated reason and is withdrawn at Remark D.6.

Two features of the error are worth recording. It was *not* an error in any measured or imported quantity: every input was unchanged and only the shape assumed for the obstruction moved. And it ran in the direction that *understates* the architecture, which is the rarer direction and is why it survived a check — a result that fails is not re-examined with the suspicion a result that succeeds attracts. Convention 2.5 now fixes the cross-section explicitly so that the question cannot be passed over again.

Remark D.2 (The condensed peptide as gate)**.** [A] An earlier development placed a condensed peptide in the aperture as its selectivity filter, on the ground that the geometry alone could not exclude the residue, and supplied an activation chemistry for the condensation by proton-coupled electron transfer at the chrysene.

With the aperture at 0.254 nm no backbone element fits: an extended strand requires 0.45 nm and a helix 1.00 nm. The gate is the geometry, and the peptide is withdrawn entirely rather than deferred.

What goes with it is substantial and its loss is a gain. The condensation required a revision to the material ledger's valence property, the residue being entered there at valence zero and unable to bond further. The activation required an excited state. And the cycle did not close on redox without a terminal oxidant, which the signalling paper's convention excludes from numbered statements. All three difficulties disappear with the mechanism that created them, and that convention is preserved rather than amended (Ruling 12.1).

Remark D.3 (The arm as occluder, and a hypothesis retired)**.** [A] The aperture was at one stage narrowed by an arm projecting radially inward, registered as a hypothesis with a window of 0.09 to 0.19 nm, so that the paper's central result rested on a premise 0.10 nm wide whose value was a molecular estimate.

Block W2 shows the premise is not merely uncertain but false in sign: the phosphorus lies outside the chord in every closing conformer, because it is the apex of the bend. Nothing projects into the void. The spacing is instead set by a covalent bridge whose length is computed from internal coordinates, and *the hypothesis register loses that entry without replacement*.

Remark D.4 (Closure held to require flexibility)**.** [A] It was argued that the 3 and 9 substituents, being inversion-related, give collinear linkages; that a chain of columns so linked is straight; that a straight chain bounds no region; and hence that closure required the bridge to bend, in tension with the rigidity a lattice assumes.

The premises are correct and the conclusion overstated. The torsion scan of block W1 finds turns from 3.8° to 178.3° among conformers that keep the columns parallel and in register, so every ring size closes without strain and no premise about flexibility is needed. The tension was imagined.

Three of the six entries in this appendix are of one kind: a conclusion drawn from the shape of an argument rather than from a computation. The house rule that nothing quantitative is asserted outside a block exists to catch exactly this, and it caught all three — but only after each had been written down as a result, which is later than it should have been. The other three are at Remark D.6.

Remark D.5 (The aperture reported as determined)**.** [A] The first draft reported the trimeric aperture as determined to 0.008 nm over 96 conformers, and made the determinacy a result: a tetramer was contrasted as a ring whose size is set by nothing.

The scan behind it treated *one* bridge. A trimer has three, and closure is a condition on their composition in $SE(2)$. Composed properly (block W4), the equilateral family is recovered only at the tightest tolerance and is an artifact of it; at one Ångstr"om of slack scalene closures appear and the aperture spans 0.207 to 0.258 nm.

The contrast with the tetramer survives and the determinacy does not. The error is the same kind as those at Remarks D.1 and D.4: a property of a symmetric special case was reported as a property of the object.

Remark D.6 (The margin computed across conventions)**.** [A] The first draft set the aperture, a clearance to a van der Waals surface, against the residue's Stokes radius, which is hydrodynamic, and reported a margin of 0.016 nm. The two conventions differ by more than that.

> Recomputed in one convention (block W5) the minimum enclosing cylinder of the glycine zwitterion is 0.258 nm against an aperture of 0.254, so the margin is 0.004 nm and the exclusion rests entirely on the residue's side chain adding something to glycine's. The corollary is not withdrawn; its margin is, and with it the impression that the result was comfortable.
> *This is the fourth entry in this appendix at which a number was compared to a number of a different kind.* The others are the carbon-ledger convention imported without its scope, recorded by the material ledger, and the disk cross-section at Remark D.1. The pattern is worth naming: the corpus's characteristic error is not arithmetic but commensurability.

E Sources, by use

Used in a numbered statement. The enclosure paper, for the orientation of the unit in a leaflet, the tilt range, the unit dimensions and the area per lipid (Rem. 5.5, Prop. 5.4, Conv. 2.5, Thm. 4.2). The cycle paper, for R, N, T, c_{ext}, the osmotic relaxation time, conditions C1 and C1′ and the division threshold (Not. 4.1, Thm. 4.2, Cor. 9.3). The material ledger, for the inventory, the digraph, the excision edge, the allocation and the dialkyl-phosphate reading of the head group (Prop. 5.2, Prop. 8.3, Prop. 8.4, Prop. 9.2). The loom paper, for the orthogonality of the two substituted axes and for nothing else (Conv. 2.4, Rul. 12.5).

Used for context, entering no proof. The signalling paper's aperture theorem and corollary, which this paper does not use and does not contradict: its apertures are those of an in-plane aggregate of units, and the apertures here are those of a transmembrane ring of columns. The two are different objects and the numbers are not comparable.

Standard values, not from this corpus. Bond lengths and angles for the aryl phosphodiester; hydrated and bare ionic radii; the Stokes radii of small zwitterions; the lysis tension of a fluid bilayer; the backbone dimensions of an α-helix and an extended strand. *These are tabulated values and are not yet individually attributed*; Target 13.3 and H2 of Appendix A record the consequence.

Not used. The patents are cited nowhere in this paper. The construction is geometric and no figure of the filing attests a column, a ring, or a lateral bridge. By the column convention of the material ledger the whole construction is therefore B — to be discovered — and *no theorem of a later paper may rest on its having been demonstrated.*

F Literature context

Within the corpus

The construction of this paper stands on four articles and takes a different kind of thing from each.

The enclosure paper [Sch26d] supplies the geometry everything descends from: the dimensions of the unit, the orientation of its aromatic plane with the membrane normal lying in it, the tilt range over which that orientation is free, and the area per lipid. It is that orientation result, and not any argument of this paper, which forbids a face-to-face column and forces the axial linkage of Definition 5.1.

The signalling paper [Sch26a] supplies the object this paper is a response to. Its closed-cycle theorem is topological and its apertures are those of an in-plane aggregate; it computed them and declined a conductance, and it recorded that a later architecture acquiring the right chemistry would find a frame already standing. This paper does not find that frame. It builds a different one, through the bilayer rather than within a leaflet, and declines the conductance for the same reason (Ruling 12.1).

The cycle paper [Sch26e] supplies the conditions. C1, that the internal particle count is impermeant over a period, and C1′, that impermeant particles are generated at a fractional rate, are the two requirements this paper shows to be jointly satisfiable; its division threshold is what Theorem 4.2 shows a conducting membrane cannot reach; and its scale parameters set every number in Section 4.

The material ledger [Sch26c] supplies the inventory, the digraph and the allocation, and is the article this paper revises most. Valence is refined per axis, two sinks are added, the heteroatom feedstock is split and the source set becomes five (Ruling 12.4). Its free-residue hypothesis is neither used nor relaxed here.

The loom paper [Sch26b] supplies one geometric fact and nothing else: that the two inversion-related substituted pairs span orthogonal connectivity vectors (Convention 2.4). The restriction is deliberate and is ruled on at Ruling 12.5.

It also stands in a correspondence that is recorded and not used, and that is the most interesting unresolved thing in this paper. That article builds a lattice over the same molecule and finds exactly two interstitial void families — triangular prisms under its lateral-shift operator, rectangular prisms under zero shift, and nothing else. Theorem 7.1 arrives at the same two by a torsion scan over bond geometry, and constrains the three-fold one alone.

Two constructions over one molecular frame, by unrelated arguments, find the same pair of geometries. They do not agree on how those geometries arise: that article pairs the three-fold void with a shifted lattice and the four-fold with exact vertical register, and the ring here is three-fold under register. The registers are taken over different axes and there is no formal contradiction; there is also no support, and Target 13.2 states the question in the form it now has.

This is set out at length because the temptation runs the other way. An author holding both accounts will read the triangular prism and the trimeric ring as one result confirming another, and they are not: one is a consequence of a lattice axiom and the other of a bond-angle scan, and until Target 13.2 is settled the honest statement is that two programmes have converged on a number and not yet on a reason.

Documentary position: attested components, unattested assembly

The patents [Sch25a, Sch25b] supply a large part of the material ledger and therefore a large part of this paper, and the distinction that matters is between what they attest and what they do not.

What they attest are the components, and the pore is assembled from the most basic of them. Figure 4 of the second filing gives the structures of the di-, tri- and tetrasubstituted units; Figure 6 the progression of the tetrasubstituted unit to nucleotide pairing and the formation of the tether complex; Figures 20 and 21 the tether complex within a nucleic acid bound into the lipid structure. The material ledger enters the three chrysene species and the tethered nucleotide in column A on the strength of those figures. The ring of this paper is built from the tetrasubstituted unit of Figure 4 and is joined by the phosphodiester chemistry the same figures exhibit. Nothing exotic is introduced: the construction reaches for the architecture's most elementary attested parts and for no others.

What they do not attest is the assembly. No figure of either filing exhibits a column, a lateral bridge, or a ring. By the column convention of the material ledger the construction is accordingly B — to be discovered — and no theorem of a later paper may rest on its having been demonstrated. The components are A and the arrangement is B, and the two should not be conflated in either direction: this paper is neither unsupported nor attested.

A dual function for one unit

One consequence of that reading deserves to be stated on its own, because it is the most economical thing the construction says.

The tetrasubstituted unit was already the precursor of the tethered nucleotide–chrysene complex, and through it of the phospholipid anchor by which the encoding is held in the membrane. By Proposition 5.2 it is also the only species from which a ring can be made, and by Corollary 7.5 that ring is what excludes the residue and admits the feedstock.

The same unit therefore assembles the enclosure and then regulates its osmotic state. It spends 6–12 building the wall and keeps a terminal arm to tether itself to the strand it helped encode, so that the filter is addressed by the sequence it sits in. A component that builds a vessel and then controls the vessel's volume is a stronger claim on the architecture's economy than any of the four preceding articles has made, and it rests on no new species, no new chemistry and a fourth demand on the pool of two hundredths of a per cent (Proposition 8.4).

The claim is about function and not about attestation. That one unit could do both is geometry; that it does is B.

Outside the corpus

Three bodies of work are adjacent and none is relied upon.

The classical treatment of fixed-charge membranes and the resulting osmotic imbalance is standard, and Theorem 4.2 is an application of it rather than a contribution to it; what is new is only the observation that the architecture's own lipid supplies the fixed charge and that the consequence runs against the cycle it was meant to serve.

The relation between aperture size and solute passage is likewise standard, and block W5 uses the elementary form — a minimum enclosing cylinder against a clearance — rather than any hindered-transport theory. The energetics of dehydration at a narrow constriction, which is where the real literature on ion selectivity lives, is conceded at Appendix C and used nowhere (Target 13.5).

Conformational scanning over torsions with fixed internal coordinates is the oldest method in the field and is used here in its simplest form. Its limitation is the subject of Target 13.1: bond lengths and angles are held rigid, and the slack that admits scalene closures in block W4 stands in for a flexibility the scan does not model.

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