you could esstimate the energy required to add amino acids to proteins (per amino acid), then quantify for dimer, trimer, tetramer.... then add tehse energies for # of -mer units required to form capside of volumes x y ans z

Now you're thinking like a scientist rather than a reviewer.

This is exactly the sort of thing that could transform the paper from a pedagogical review into a genuine research article.

The key insight is that the author's current argument is qualitative:

> pentamers and hexamers seem attractive.

But you are proposing:

> quantify the assembly cost of different architectures and compare them.

That immediately creates a falsifiable hypothesis.

First approximation

Suppose:

$$E_p$$

= energetic cost of assembling one pentamer

$$E_h$$

= energetic cost of assembling one hexamer

A T=1 capsid might require:

$$12E_p$$

A larger capsid:

$$12E_p + nE_h$$

Now compare against alternative architectures.

Triangle-based architecture

Suppose closure requires 4 trimeric curvature units.

At first glance:

$$4E_t$$

looks cheaper.

But to reach the same enclosed volume, many additional expansion units may be required.

The relevant quantity is not closure cost.

It is:

$$\frac{\text{Assembly Cost}}{\text{Enclosed Volume}}$$

or

$$\frac{\text{Assembly Cost}}{\text{Genome Capacity}}$$

Potential novelty

The author could define:

$$\eta = \frac{V}{E}$$

where

- V = enclosed volume
- E = assembly cost

and compare:

- trimer-based
- tetramer-based
- pentamer–hexamer
- hypothetical alternatives

If pentamer–hexamer systems consistently maximize V/E, that would be a publishable result.

But there is a deeper issue

Simply counting amino acids is probably not enough.

Evolution does not pay primarily for:

> amino acids per oligomer

It pays for:

- protein synthesis
- folding
- assembly
- error correction
- failed intermediates
- genome encoding costs

For example:

A pentamer and hexamer built from the same protein differ by only one subunit.

That may be evolutionarily cheaper than maintaining separate trimeric and decameric proteins.

So the relevant metric might be:

$$\text{Assembly Information Content}$$

rather than just ATP cost.

The strongest version

I would define something like:

$$\Phi = \frac{\text{Accessible Volume States}}{\text{Distinct Protein Types} \times \text{Assembly Cost}}$$

Now compare architectures.

Then the claim becomes:

> Pentamer–hexamer systems maximize architectural versatility per unit assembly investment.

That is a genuinely new hypothesis.

Why this is interesting

Notice what happened.

We started with Euler's theorem.

Euler's theorem gives:

> closure is possible.

Your proposed framework asks:

> among all possible closure architectures, which gives the most enclosed volume and design flexibility per unit assembly investment?

That is exactly the type of optimization question evolution could plausibly care about.

If the author actually performed such calculations—even approximate scaling analyses—the paper would move from:

> educational review

to

> hypothesis-driven theoretical study.

That would be a much stronger claim to novelty than the current manuscript's re-derivation of known geometric results. The challenge, of course, is that the model would need to be carefully justified and compared against biological reality, but at least it would generate quantitative predictions rather than descriptive observations.