



Figure 1. A) An AlphaFold2 model of P22 scaffolding protein (left). The dashed pink ellipse indicates the C-terminal helix-turn-helix domain that binds to coat protein. This domain replaced the phiBB1 helix 8 (right) in the chimeric scaffolding protein. B) Negative stain TEM of the particles made with P22 coat protein and the chimeric scaffolding protein. Notice the ring-like density on the interior of the particle. C) Particles of P22 coat protein assembled by P22 scaffolding protein. When comparing the particles, both appear to be about the same diameter. However, there is no ring-like density on the inside of the P22 particles (C) and the edges appear thicker, suggesting the particles made with the chimeric scaffolding protein will be different than P22 procapsid-like particles.

#### References:

- Jumper, J.; et al., Highly accurate protein structure prediction with AlphaFold. *Nature* 2021, 596 (7873), 583-589.
- Rumnieks, J.; Fuzik, T.; Tars, K., Structure of the *Borrelia* Bacteriophage phiBB1 Procapsid. *J Mol Biol* 2023, 435 (24), 168323.