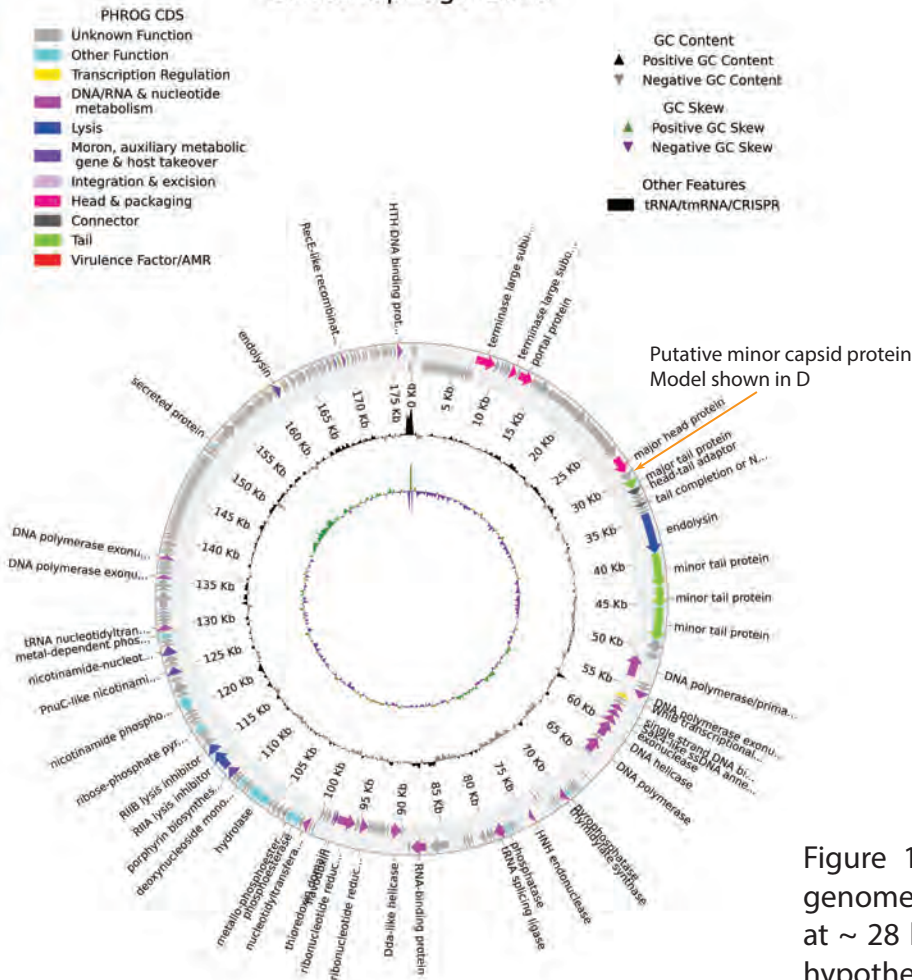


Bacteriophage Eonti

A



B

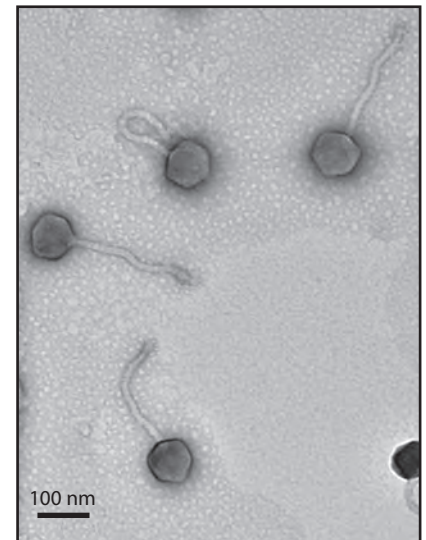
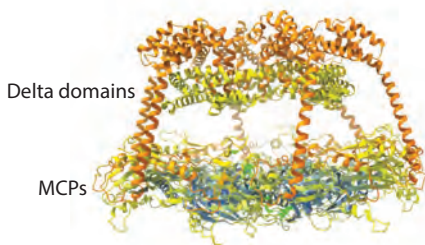
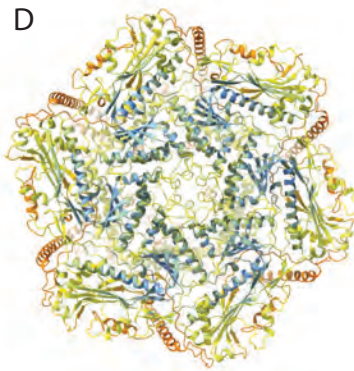


Figure 1. A) Preliminary annotation of Eonti's genome. The major capsid protein (MCP) gene is at ~ 28 kb. Next to it is a gene for a protein we hypothesize is a minor capsid protein, indicated by the orange arrow. B) Negative stain TEM micrograph of a diluted Eonti phage prep. It is a siphophage with a large head, ~ 900Å. C) An AlphaFold3 prediction of a hexamer arrangement of the MCP colored by confidence levels, shown from the side. The orange and yellow helices show one prediction for the delta domains. The delta domain predictions are always helical but the arrangements of the helices vary, and always have poor confidence. D) Top view of the MCPs' HK97 fold, which is predicted with good confidence. E) An AlphaFold3 prediction of a pentameric arrangement of the minor capsid protein, colored by confidence levels. The protein has a typical HK97 fold, as shown in F, which is the prediction for a monomer. Note the absence of a delta domain.

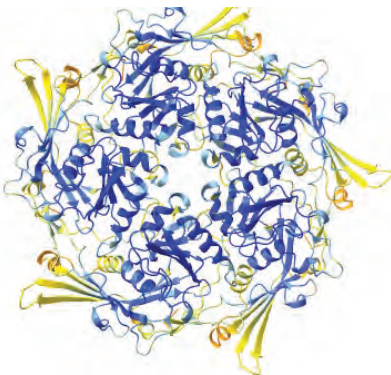
C



D



E



F

