**Scap1 Coversheet**

**Gp14** – call is NKF. But there is a possible call of chitosanase from two blast hits to Strep phages OlympicHelado and Rima. However, there are no other Blastp hits at all and HHPred only shows 81.8% prob to a “secreted protein, and 64.8% to xylosidase/xylosidase.” I’m not sure of the Strep calls unless there is data-not-shown that I am unaware of, in which case this call should be made on Scap1. Without that, this is NKF and the Strep calls may be wrong.

**Gp16 and gp17** – call is NKF. These very well may be the tail chaperone genes, but there is no homology to any that have been called that I can find. However, it is notable that gp17 does look strange, it could be a much longer call, but doesn’t have the coding potential per Genemark.hmmp using *Strep. scabiei* 87-22. I have called them as NKF without any evidence that they are the chaperone genes or reference to find the frameshift.

**Gp22** – call is hydrolase. I called the more general hydrolase, not the less supported chitinase or fibronectin, which are in the HHPred and Blast hits.

**Gp37** – call is NKF. The call is very short (126 bp) as called. I considered deleting this feature because it is short and has no (0) blast hits. But it has very strong coding potential, so kept it. Especially in the light of new evidence of short proteins in phages. The next longer call would have a 97 bp overlap for very similar SD scores.

**Gp42, 43** – call is NKF. Both of these are unusual looking, which isn’t unique in this genomem and could both be much longer calls. If they were, they would extend over the previous gene. However, no coding potential in Genemark.hmmp using *Strep. scabiei* 87-22, or apparently in DNAM, so the shorter calls were made. They look odd, though.

Thank you for your assistance,

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