

# Uncommon -2 Programmed Translational Frameshift in a Bacteriophage Tripp Transposase Gene

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## *P. larvae* Phage Tripp

Bacteriophage Tripp is a *Siphoviridae* phage that infects *Paenibacillus larvae*, the bacterium responsible for American Foulbrood disease (AFB) in honey bee larvae.

**Phage Tripp**   **Healthy Adult**   **Healthy Pupa**   **Infected Pupa**



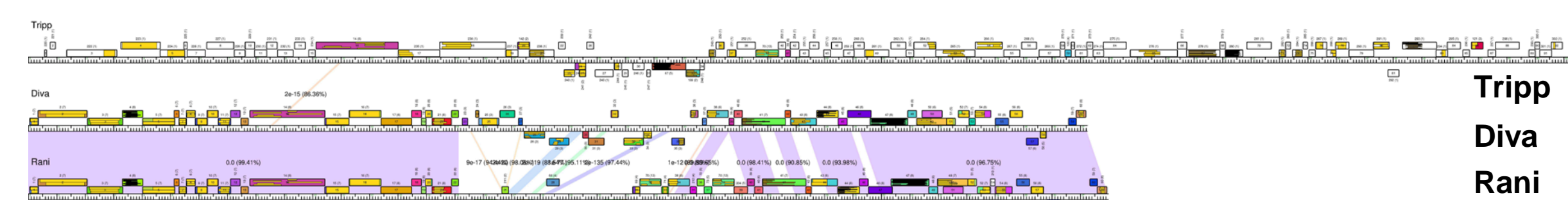
[http://upload.wikimedia.org/wikipedia/commons/e/e0/Honeybee\\_landing\\_on\\_milkthistle02.jpg](http://upload.wikimedia.org/wikipedia/commons/e/e0/Honeybee_landing_on_milkthistle02.jpg)

<http://www.discovery-zone.com/small-creatures-of-the-gods-bee/>

<http://www.caes.uga.edu/departments/ent/bees/disorders/bacterial.html>

Tripp was isolated from an AFB diseased hive in North Carolina. Its genome is 54,441 bp, 48% G+C, has 92 genes, and has 378 bp terminal repeats. It is distinct from all other *P. larvae* phages.

## The Tripp genome and two other *P. larvae* phage genomes

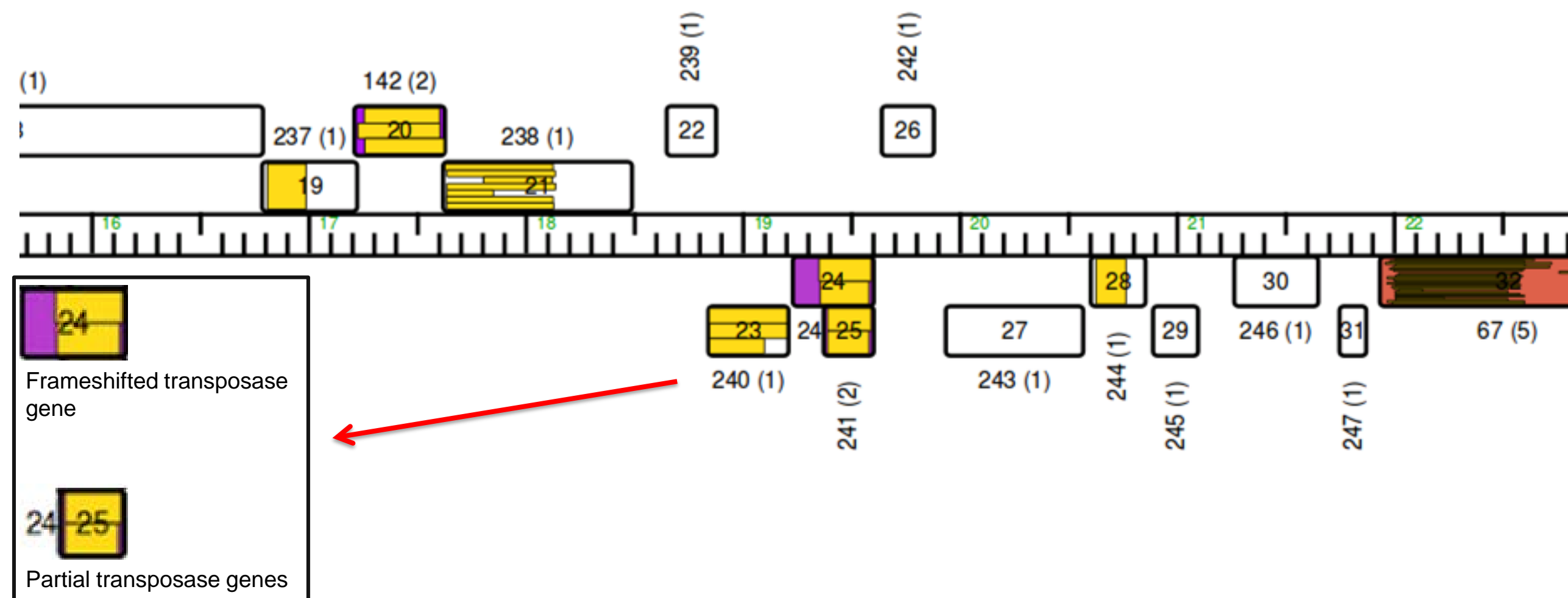


Tripp  
Diva  
Rani

## An Uncommon Frameshift

During annotation of the Tripp genome, we found two consecutive genes (24 & 25) that appeared as partial transposases. If joined, the two genes would encode a typical full-length transposase. We present evidence to suggest there is an uncommon -2 programmed translational frameshift linking these two gene products.

## The Proposed Frameshift Site in the Genome of Tripp



A programmed translational frameshift in the tail assembly region is conserved among many dsDNA phages, including mycobacteriophages, and is typically a  $\pm 1$  shift. This type of frameshift is not observed in *P. larvae* phages sequenced to date. Among seven *P. larvae* phages from NC, and others, Tripp is the only phage where a programmed frameshift has been seen. Interestingly, the proposed frameshift is in a transposase gene and appears to be a -2 shift.

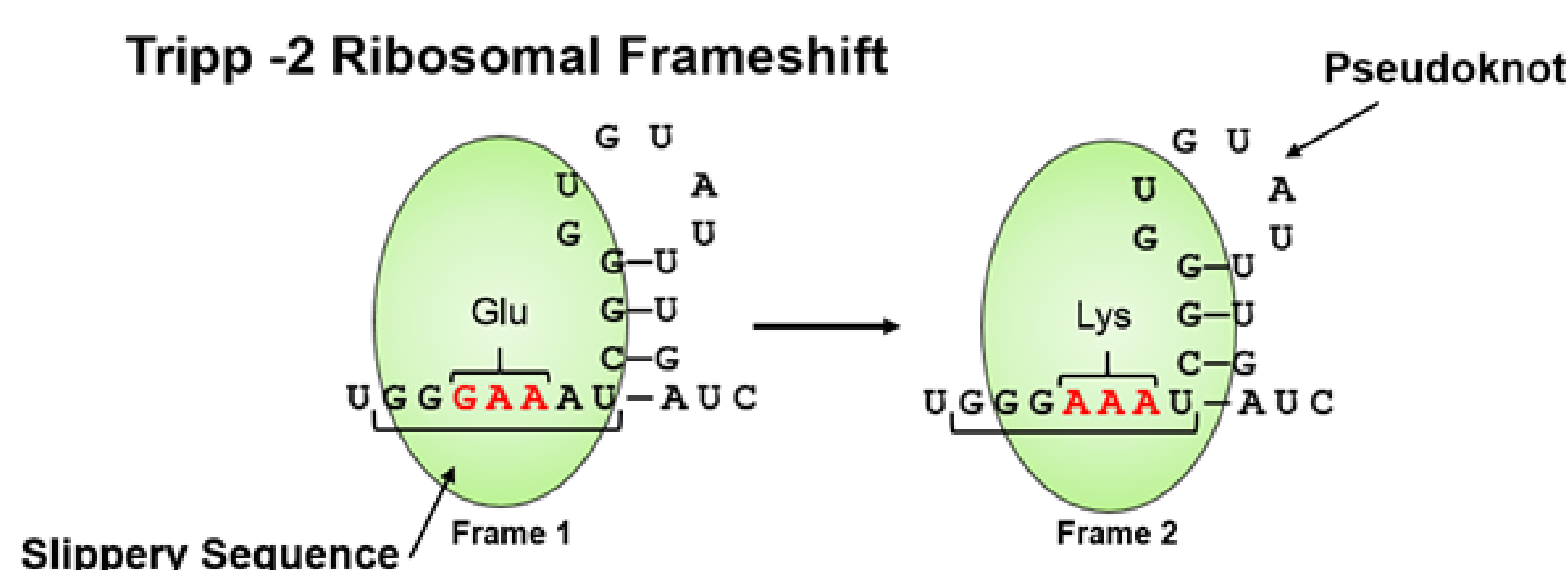
## The -2 Frameshift Sequence

### RNA Sequence of Proposed Frameshift Site

g25 Frame 1: W E I G C I Stop  
**U G G G A A A U C G G G U G U A U U U G A U C A C A U G C U G G A U**  
 g24 Frame 2: K S G V F D H M L D  
 Slippery Sequence      Pseudoknot

- The region spans the end of gene 25 (frame 1) and the beginning of gene 24 (frame 2).
- If joined in this region, the resulting 124 amino acid protein has 98% identity with a *P. larvae* transposase. Transposases with other types of frameshifts have been identified.
- The proposed “shifty region” has features seen in other -2 frameshift sites.

## The -2 Frameshift Site Includes a Pseudoknot



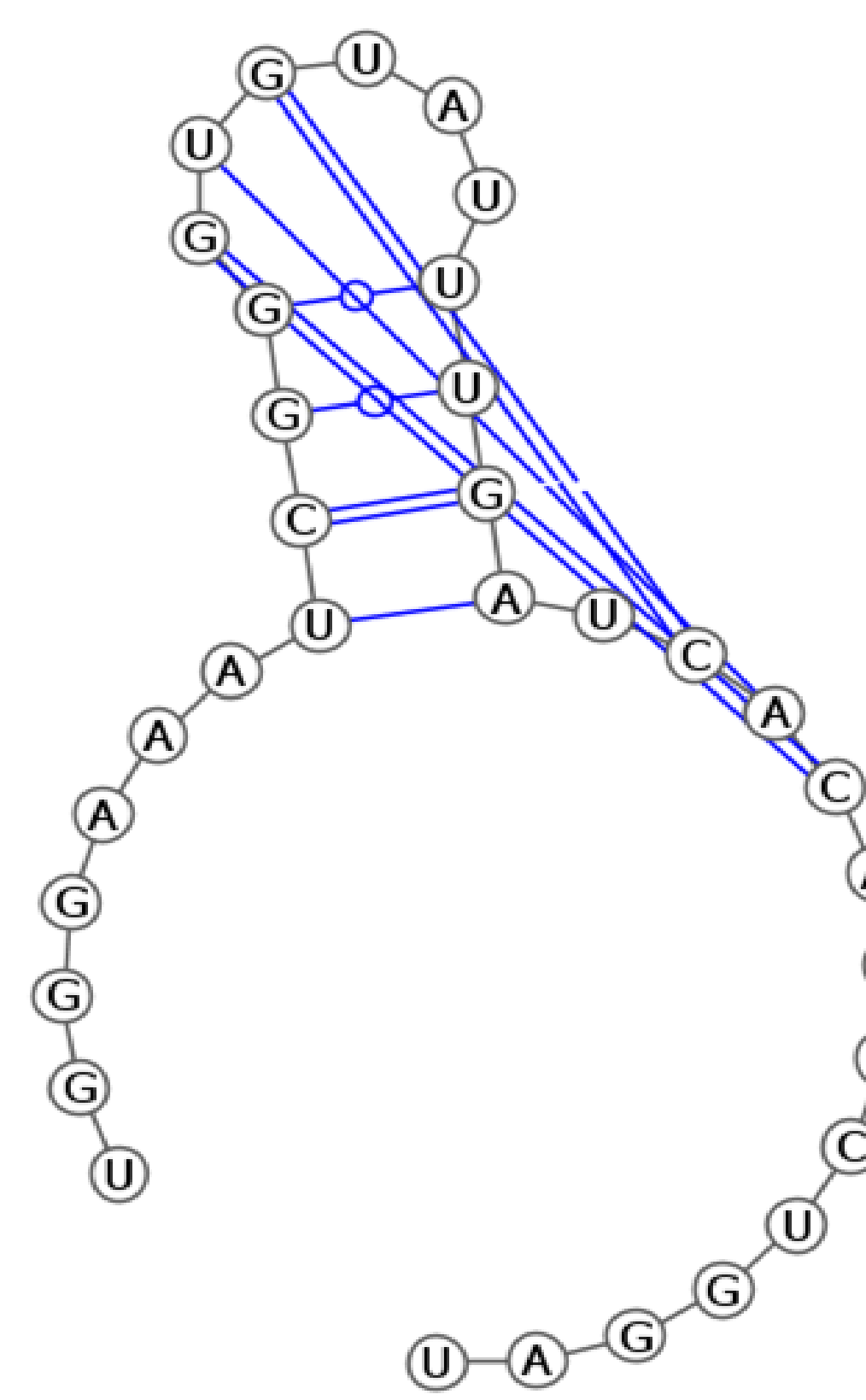
**Slippery sequence** - a motif of nucleotides where the ribosome slips and frameshifts often occur.

**Pseudoknot** - RNA helical structure that can cause ribosomes to stall during translation. Pseudoknot-prediction software strongly suggests the formation of a pseudoknot immediately following the slippery sequence.

Together, the slippery sequence, RNA pseudoknot, stop codon in frame 1 and the alignment of the joined protein to other transposases strongly suggest the presence of a -2 programmed translational frameshift in phage Tripp.

**Transposases** are enzymes which facilitate the movement of genes within and across genomes. If only 1 - 5% of translating ribosomes change reading frames at a typical programmed frameshift site, the infrequent frameshift would allow for low level transposase expression and some genetic variation without greatly altering the genome.

### mRNA Pseudoknot



<http://rips.dna.bio.keio.ac.jp/ipknot/>

Longer range base pairing is shown with the blue lines.

## Conclusions & Future Work

The slippery sequence, pseudoknot, and alignment with a *P. larvae* transposase strongly suggest the presence of a -2 programmed translational frameshift between genes 24 and 25 of bacteriophage Tripp.

The transposase gene with its frameshift may have been acquired from the *P. larvae* host.

Characterizing the frameshift features may aid in understanding the unique aspects of this frameshift.

We hope to analyze the pseudoknot and experimentally demonstrate the frameshift product.

## References

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## Acknowledgments

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