## Is there any recent evidence of a tRNA overlapping a protein gene, even by a few bp?

I am asking this question to have this issue settled and possibly suggest that a note be included in the Bioinformatics Resource Guide regarding tRNA annotation.

Phage IkeLoa reverse draft gene 134 at 92938-9390 bp overlaps a tRNA by 27 bp; even if we change the start, it still overlaps by a few bp. Its sequence is: MLYQLSYDGGAAGETSQPSRLRVMSPVCLPSTTIPARVTDEDLTFVKPLSZ

According to <u>the forum post</u>, "How close can one pack protein and tRNA's genes" of Feb 24, 2016, Dr Pope stated that, "*We tend to steer clear of a tRNA and a protein occupying the same space, but there are definitely genomes where they get pretty close*."

We have been following this rule and I am inclined to delete it, but I want to be sure in case something has changed recently, because it is matching recently annotated genes in phagesDB and phamerator (years 2017-2020; see below).

In phagesDB, this hits several recently annotated genes with q1:s1, 100%, e-value such as 6e-22; for example Ronan gp160 (2020), StephanieG, gp162 (2019), Mangeria gp164 (2019), Roots515 gp166 (2017), Chargie21 gp162 (2017), Basquiat gp162 (2017).





## Sample phagesDB hits

Sequences producing significant alignments: (Di	(S) Val	ue
<pre>IkeLoa_Draft_153, function unknown, 50 YemiJoy2021_Draft_162, function unknown, 50 StephanieG_162, function unknown, 50 Roots515_166, function unknown, 50 Ronan_160, function unknown, 50 Mangeria_164, function unknown, 50 Maby2021_Draft_161, function unknown, 50 Jemmno_Draft_163, function unknown, 50 DirtMonster_Draft_158, function unknown, 50 Basquiat_162, function unknown, 50 Jaygup_Draft_162, function unknown, 50 Guwapp_Draft_163, function unknown, 50 Shifa_154, function unknown, 50 HyRo_153, function unknown, 50</pre>	102 101 101 101 101 101 101 101 101 101	2e-22 6e-22 6e-22 6e-22 6e-22 6e-22 6e-22 6e-22 6e-22 6e-22 5e-21 5e-21 1e-20 1e-20