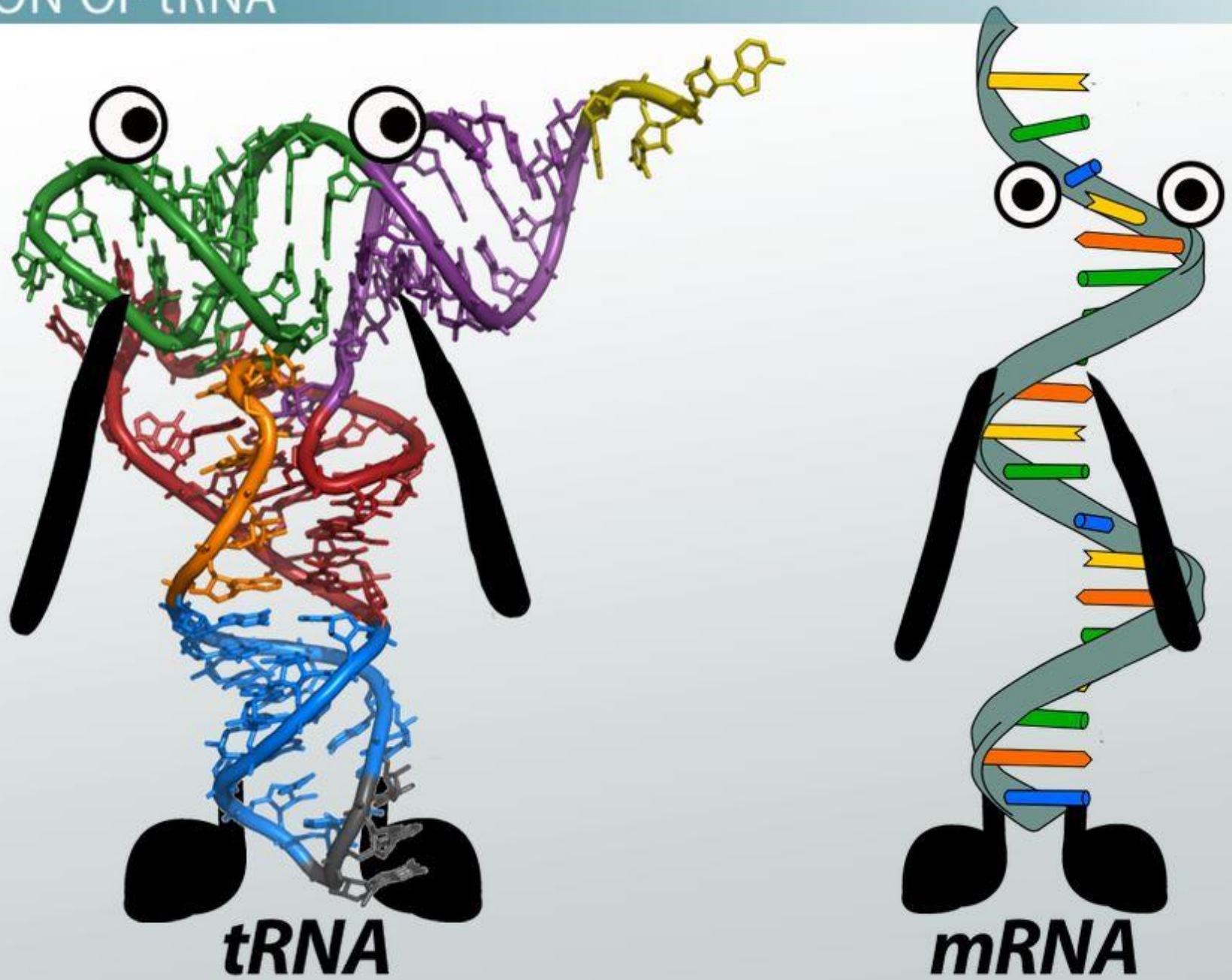
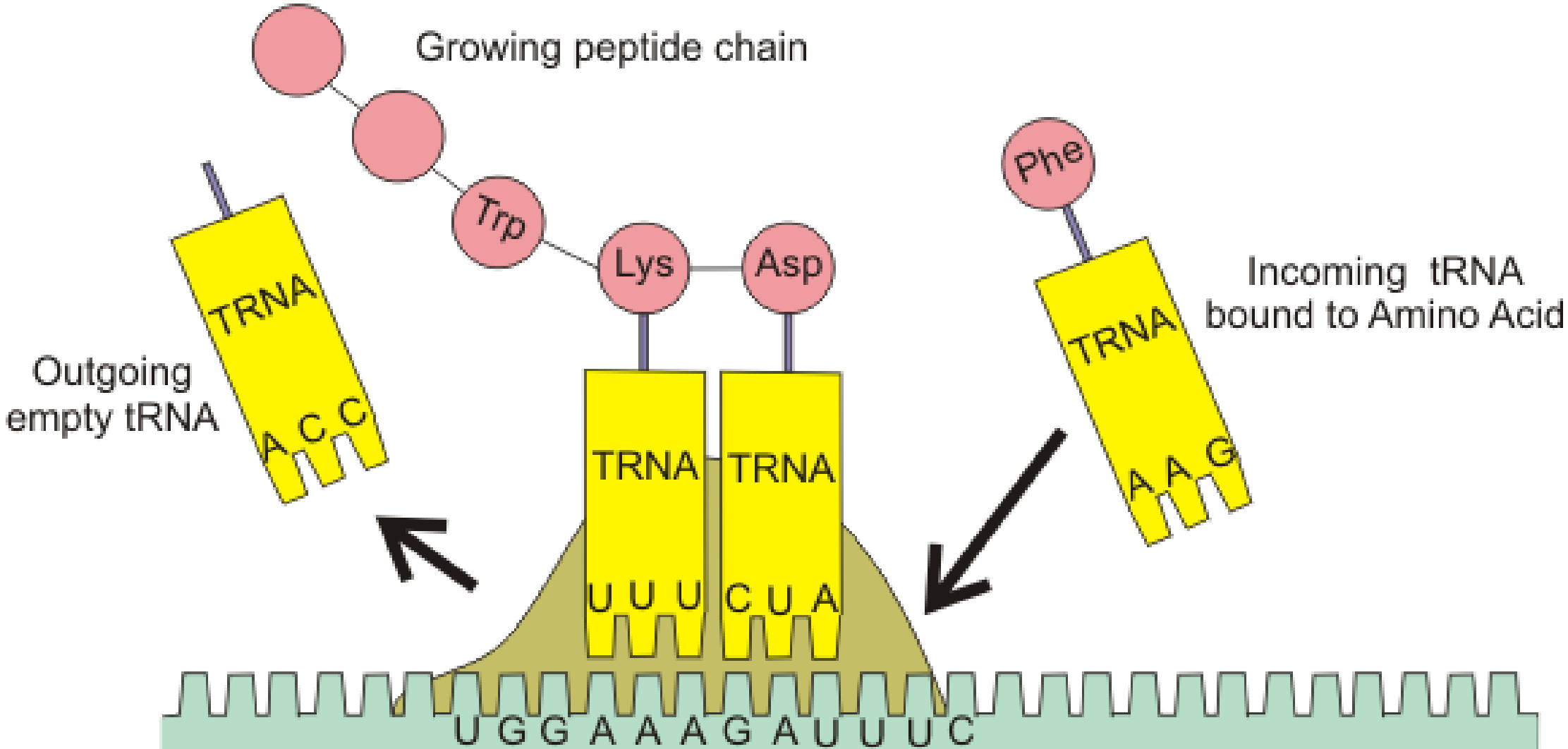
tRNA

Structure, function, evolution and annotation

FUNCTION OF tRNA



tRNA function



tRNA-Phe primary structure

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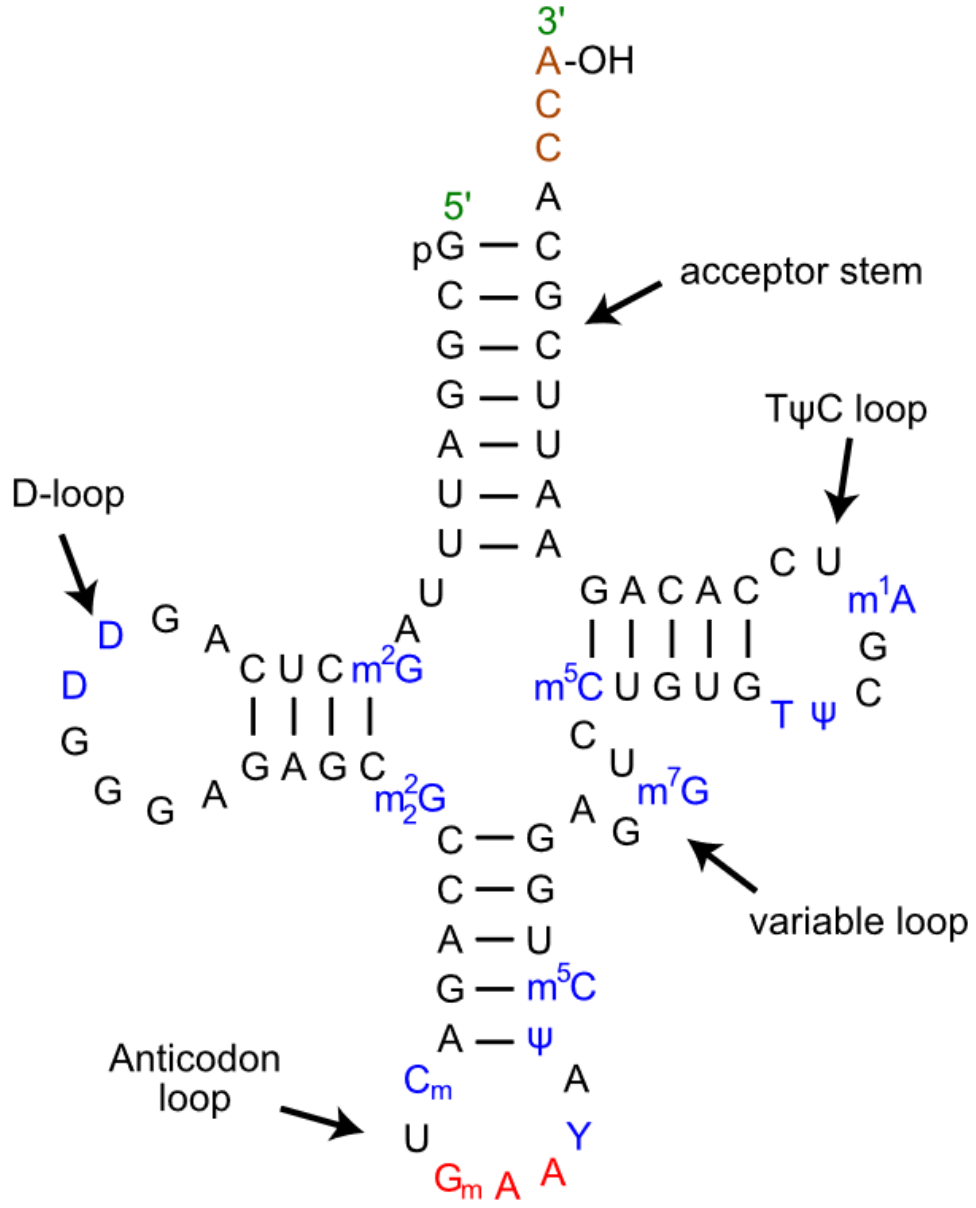
GGTTGGATAGCTCAGTCGGTAGAGCAGCAGACTGAAAATCTGCGTGTCGGCA
GTTCGATTCTGCCTCTAACCACCA

Secondary structure

Anticodon loop – contains the anticodon
D-loop –a recognition site for aminoacyl-tRNA synthetase. Contains dihydrouracil,
Acceptor stem – 3’ end attaches to the amino acid
T-loop – recognition site for the ribosome



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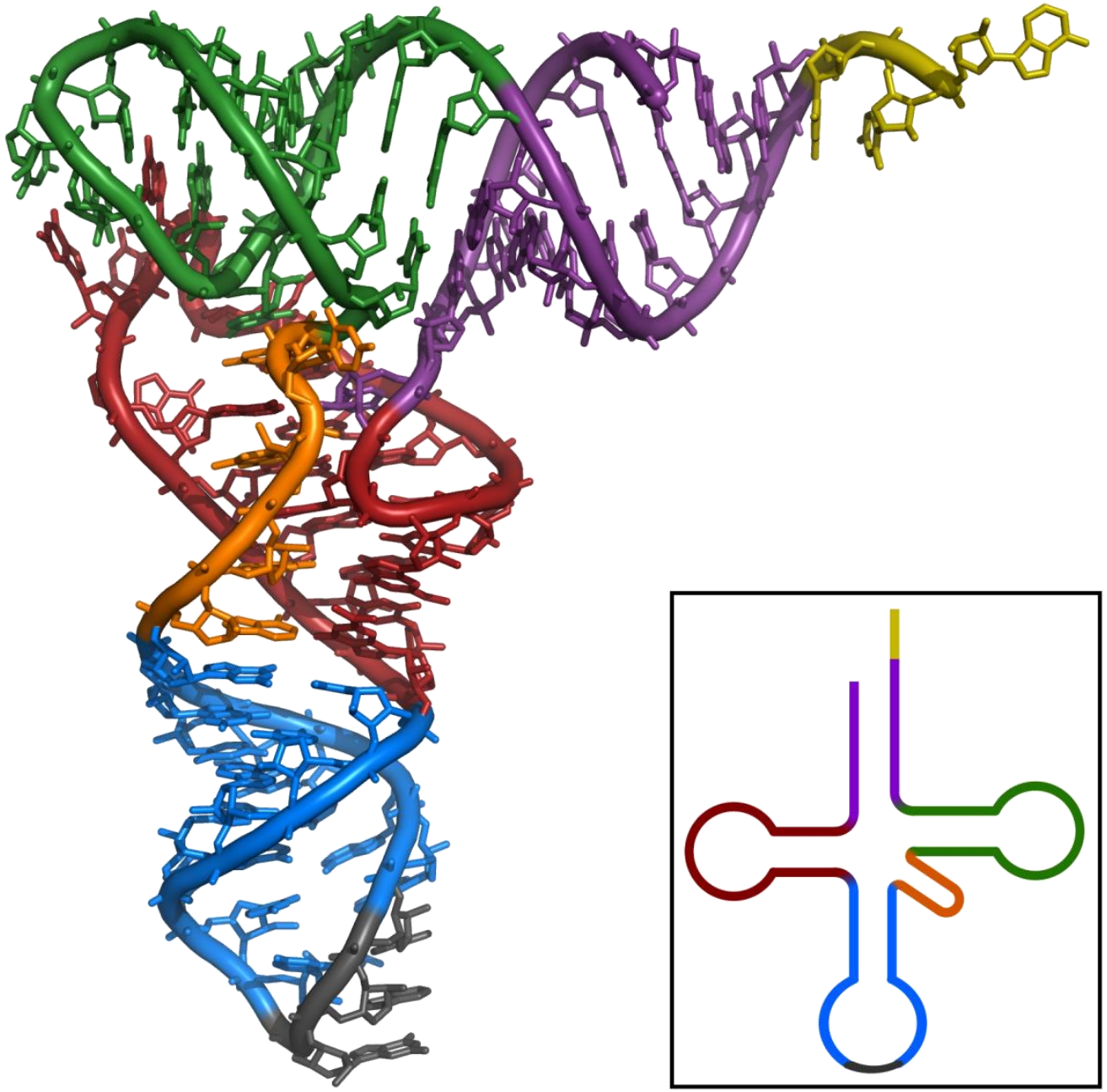
Tertiary structure

- 3-d folding



tRNA annotation in DOGMA

- There should be ~22 tRNA genes
- It may be hard to find some of them
- To determine if a tRNA is good –
  - Is it complete?
  - Does it align well to other species' version of that tRNA?
  - Does it have a good **COVE score**?

  The log of the ratio of the probability of the sequence given the tRNA covariance model used (developed from hand-alignment of 1415 tRNAs), and the probability of the sequence given a simple random sequence model. tRNAscan-SE counts any sequence that attains a score of 20.0 bits or larger as a tRNA (based on empirical studies conducted by Eddy & Durbin 1994)

Once you have checked all individual tRNAs

- Look at the “tRNA list” to see which amino acids are missing
- We can look for them in other ways…

tRNA prediction

- Homology (BLAST)
- De novo
  - tRNAscan
    - Older version in DOGMA – will miss some tRNAs!
    - Better version online – use this to look for missing tRNAs

  http://trna.ucsc.edu/tRNAscan-SE/

trna.ucsc.edu/tRNAscan-SE/

Search options

Sequence source	Mixed (general tRNA model)
Search mode	Legacy (tRNAscan + EufindtRNA -> Cove)
Query sequence	(•) Formatted (FASTA) ( ) Raw Sequence
	Sequence name (optional): (no spaces)
	(Queries are limited to a total of less than 5 million nucleotides at any one time)
	or submit a file:
	Choose File Phlyctis_boliviensis_mt_corrected.txt
	Clear Sequence
Output	[ ] Output BED format

Run tRNAscan-SE Reset Form

Homework

- Finish annotating your tRNA genes!
  - make sure the genes in DOGMA look good
  - add genes that are missing, based on the BLAST and tRNA-scan
- Complete the annotation for as many protein-coding genes as possible, and be ready for Thursday with questions
- Try to annotate the rRNA genes, and be ready with any questions if you have them