



ATG:biosynthetics
Solutions
in biosynthetics

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Comparative genomics and **synthetic genes** are synergistic in improving DNA mediating RNA and protein gene product function by design.

In general calculating complex sequence features of bio-molecules like DNA, RNA or protein sequences is time consuming and the work on it is often on a stony path compared to the finally expected excellence of results.

Sometimes there is no solution for bioinformatics tasks on-site because of lack of expertise, resources, time and/ or due to missing tools.

For the most cases ATG:biosynthetics can provide the right solution for you in time - just inquire.

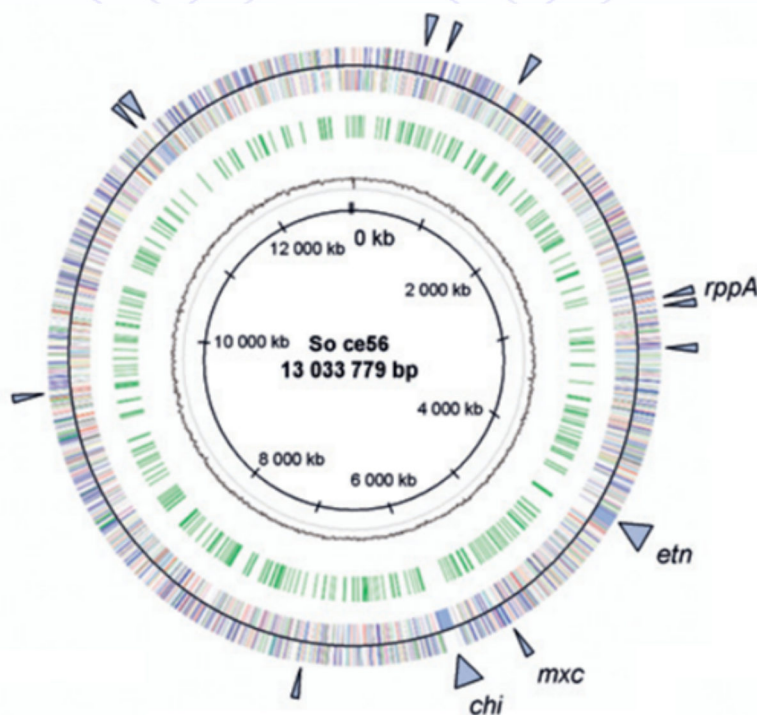


Figure-1. Example of a widely explored genome.

Comparative genomics is informative on many molecular levels and has many faces.

Combined with RNAseq and/ or mass spectroscopy analyses it can make the decisive difference for analytical and constructive application developments with improved properties.

So with comparative genomics we can learn about the design of molecular function and construction.

Consistently and consequently applying existing and new acquired knowledge on synthetic constructions can reduce complexity and support functional improvements of synthetic genes and in addition to the gene products protein and RNA on a rational basis.

ATG is strong in:

- functional and pure comparative genomic analytics (orthologs, paralogs, CAI, ACE, and operon identification, pathway identification (e.g. specific compounds).
- detailed multi-targeted *in silico* optimization of formal-functional gene features (specific codon tables, RNA secondary

structure calculations).

- RNAseq data computational analyses
- MS data computational analyses

On all molecular function levels from Genome to individual proteins from pathways to bio-peptide libraries we perform:

- Just tell us what you like ATG to be calculated and where your problems are.
- We will make a proposal and offer to you how we can provide a solution.
- After the project you can see the visualization of our results on your individual web-space you share with ATG – classify and discuss the results with your experts by Skype, Google hang out, etc.

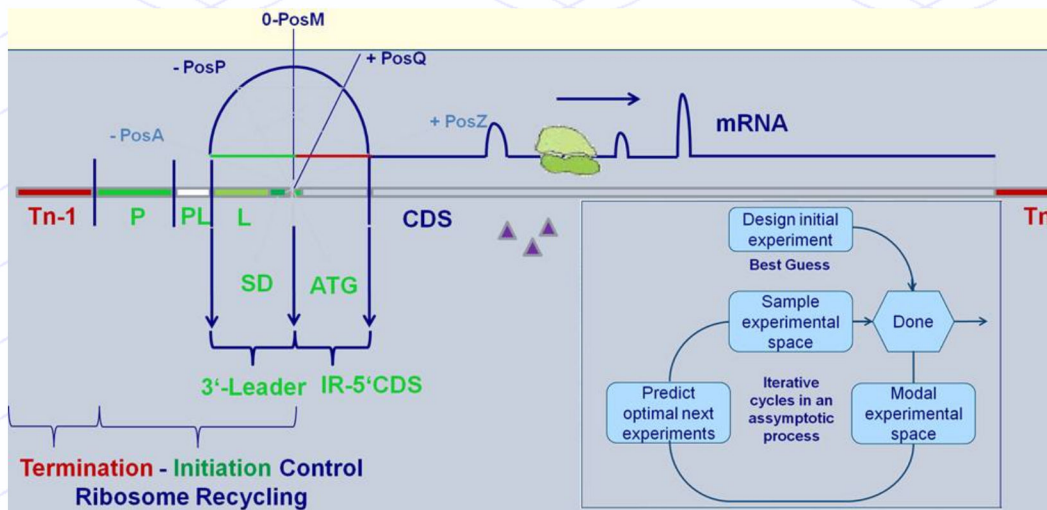


Figure-2. Gene expression influencing factors and integrated iterative improvement scheme of gene expression features by use of ATG: *EvoMAG* proprietary software package.

For more information or a quote, just ask our experts at
<https://www.atg-biosynthetics.com/Optimizations/InfoRequestOpt.html>
or give us a call: +497618889424

ATG:biosynthetics ... experts in synthetic biology and bioinformatics