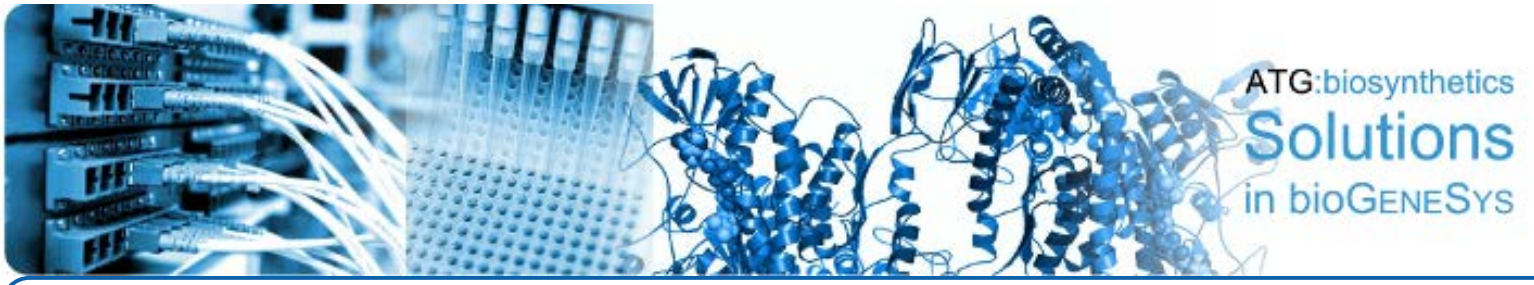

CODONEWS Issue 68

Knowledge Based Deterministic Biodesign

Just try „*Biomorphs* and *PhysioVars*"

Dear Customers,

What is new at ATG:biosynthetics in 2015?

In **2014** more than ever we served our clients with a variety of different design solutions for managing big multi-genetic constructs. Most of these were complete pathway systems, combinatorial gene and vector libraries or (hetero-)protein-complex constructions.

But in addition to the encoded multiple protein information proper gene expression is a function of the genetic background.

Therefore ATG was orienting research and development on genomic analyses for extracting most valuable informationabout the codon use class of a gene and its function in a given genomic background (Publ. in preparation). In **2015** we like to serve you with the highest quality of results and plausibility on the highest rational level possible.

For bio-informatics contracts of constructional and functionally oriented bio-synthetic project consulting you will get the contractual volume for gene synthesis according to the **1st** price table below:

In connection with bioinformatic projects:

<= 3000 bp = €0,20/ bp
<= 8000 bp = €0,22/ bp
<= 10000 bp = €0,23/ bp
>= 15000 please inquire

List of regular pricing

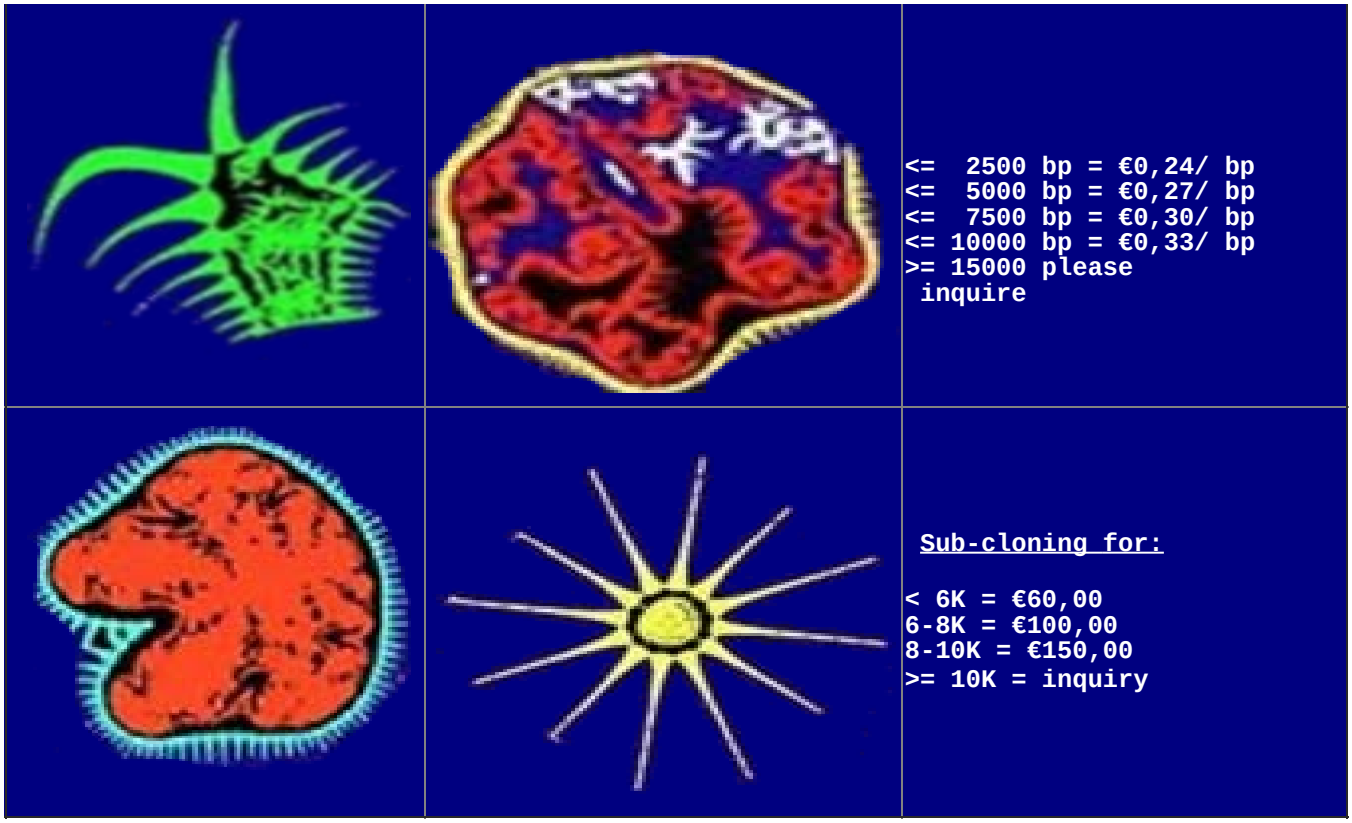

Figure-1: Biomorphs like indicated here are very different in it's genesis but you can try just BioDesign with suppoert of ATG - we are looking forward to you inquiry.

FREE! - *Sub-cloning for >10 gene orders (price list valid till March 31st)*

Today we can support you with all aspects of genomic and functional bioinformatics analysesof the genetic background functions of natural genes, gene clusters and pathways. In order to learn about genetic background and to design the individual genes according to itas well as the affected pathways – ***per se*** it is not possible to separate both from each other.

Experience all support of ATG in molecular biodesigns.

Initially ATG:biosynthetics started 2001 with service syntheses of double-stranded DNA mostly ordered as single or multiple coding sequences for cloning it into commercial or proprietary vector systems.

1. ***Parts of genes(coding sequences, leader sequences, promoters, regulatory CIS-elements, terminators)***
2. ***Complete functional genes(coding sequences + leader sequences + promoters + regulatory CIS-elements + (polyA-) terminators***
3. ***Multiple gene libraries (2.)***
4. ***Gene sequence variant libraries (point mutations)***
5. ***Combinatorial gene libraries (macro-sequence (re-) arrangements)***
6. ***GeneClusters (multiple genes in one construct)***
7. ***Gene cluster - vector systems (one to multiple genes)***
7. **Gene cluster - vector systems (one to multiple genes)**

What is quality of DNA in terms of gene function?

Is quality just providing the DNA chemically in terms of sequence identity or is it the detailed composition of

sequences in its terms of semi predictable function?

Gene function is mediated by RNA always dependent from RNA stability, high transitional initiation rates, ribosomal packing, smooth during the elongation but correct co-translational folding and so on.In the end the RNA design is the most important for the physiological function of the proteins and for many genes the major quality feature is not primarily the yield of product generated but its fraction of functional product in terms of its specific activity which will make the final value.

The DNA level,the RNA level and the protein level are closely interdependent.Based on genomic data we are performing semi-rational computer aided analytical genomic explorations in order to adapt the molecular synthetic designs on all based on EvoMAG our proprietary software.

Heuristic experimental work will not be completely abolished in future Biodesign activities and iterative cycles of incremental improvement might still be necessary.But the number of iterative improvement cycles necessary in order to improve the results can be reduced to reasonable scales if experimental design controls the experimental outcomes.For this purpose the experimental responses such as protein yield or specific activity are computationally mapped to the set of points in sequence (construct) feature space.The information thereby gained makes it possible to predict the most promising candidates for the next iteration of experimentation and model development.

In short ,the so called " ***Design of Experiments(DoE)*** " is a set of statistically designed experimental trials that concurrently evaluates multiple variables of alternative designs in a single set of experiments, employing a minimum number of trials.

Special requirements arising from the fact that the adjustment of the multiple variables itself is an optimization problem (on the level) in the framework of (the) formal sequences or pathway design.In contrast to more easily adjustable parameters of the fermentation process.

More than ever in the history of ATG the customers are interested in the best possible design of complex gene systems.

The prediction of the best orchestrated gene functionality is increasingly becoming the ***focus of our work***.

Sincerest regards,

Dr. Hubert S. Bernauer
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ATG - Your Partner in Synthetic Biology