



THE BUILDING BLOCKS OF LIFE. BUILT FOR YOU.

Dear Fellow Scientist,

Welcome to **DNA 2.0's Gene Synthesis & Protein Engineering Newsletter**. This Newsletter will keep you up to date on trends and breakthroughs affecting molecular biologists who are interested in achieving their project goals faster and at lower cost.

- **New tool for the RNAi field: RNAissance genes ensure that the correct gene target is identified using RNAi.** [Read more.](#)
- **Smart use of protein sequence/activity relationship data lets you forget about HTP screening and large gene libraries.** [Read about](#) our new paper on modern protein engineering.
- **Recent trend in the gene synthesis market; a need for sets of gene variants.** [Read more.](#)

RNAissance genes give you full control over your RNAi experiments

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RNAi is a great way of identifying gene function in mammalian cells. You design your siRNA, introduce it into your cells, and when you see the desired phenotype you assume it's related to gene silencing of your target gene. Well, that's not always the case. Several recent publications have shown that RNAi doesn't always have the laser-like specificity once thought. The observed "silencing" is often a non-specific effect.

That's why we developed RNAissance genes, a new tool that will serve as an unambiguous control, ensuring that the correct gene target is identified. RNAissance DNA sequences are only 60-65% identical with the original human gene, and are not recognized by siRNA-complexes targeted toward the chromosomal gene copy. The same protein is produced from the RNAissance gene, but using a very different nucleotide sequence. The RNAissance gene will restore normal gene function in the presence of siRNA that silences the chromosomal copies. If the RNAissance gene does not restore the wild-type phenotype, the siRNA causes non-specific effects. All of a sudden, you can do genetics with RNAi. Think of the possibilities!

Visit **PlanetGene** to view the full offering of [twentyfive thousand RNAi-resistant human genes](#).

Engineered proteins where the commercial properties are center stage

Protein engineering today is a multi-billion dollar industry and includes anything from laundry detergent enzymes to pharmaceuticals. In a recently published paper, we discuss how

Genes Encoding Fluorescent Proteins
What's your favorite color?

Have your pick of fluorescent proteins from every color of the rainbow.

Catalog #	Color	Sequence Information
FP-1	Cyan	monomerizing AAV97923
FP-2	Green	improved folding monomerizing AAC53663
FP-3	Green	absorption spectral shift improved folding monomerizing AAC53663
FP-4	Yellow	improved folding monomerizing 1MYWA
FP-5	Yellow	AY678271 (mHoneydew)
FP-6	Yellow/ Orange	AY678267 (mBanana)
FP-7	Orange	AY678265 (mOrange)
FP-8	Orange/ Red	AY678270 (mTangerine)
FP-9	Red/ Orange	AY678266 (mStrawberry)
FP-10	Red	AAM54544 (mRFP1)
FP-11	Red	AAV65051 (mRFPmars)
FP-12	Red	AY678264 (mCherry)
FP-13	Red	AAV65486 (mRaspberry)
FP-14	Red	AAV65487 (mPlum)

exploiting protein activity/sequence relationships will free you from the expenses and inaccuracies of high throughput screens, and allow you to directly measure the protein properties you really care about.

The big problem with high throughput screening is that you are forced to set up assays where you can measure many thousands of variants at the same time and hope that a hit remains a hit when tested in the commercial application. Instead, we are using the predictive power of computational methods to derive maximal information from protein sequence differences compared to screening data. Taking this approach you can forget about low quality high throughput assays, and focus your resources on high quality low throughput assays. This also means that large gene libraries are no longer needed. A small set of defined gene variants will suffice.

If you want to improve a protein using sequence/activity relationship modeling provided by DNA2.0, your success rate will be much higher, cost will be much lower and your IP much stronger.

Just published: **Predicting enzyme function from protein sequence.** Minshull et al. (2005) Current Opinion in Chemical Biology 9:202-209. [Let us know](#) if you want a copy.

Read more about [DNA2.0's protein engineering](#) platform.

Outsource the dirty work so you can do the fun stuff

What we're seeing in the gene synthesis market right now is a need for sets of synthetic gene variants. It can be sets of 10-15 natural gene variants or sets of mutants derived from computational analysis. We saw this trend up close at the recent Protein Society meeting in San Diego, where protein scientists presented protein activity studies of such variant sets. Strikingly often, 90% of the time had been spent creating these variants and only 10% of the time actually measuring protein activities.

This is where DNA2.0 fits in the picture. Making gene variants is a large part of DNA2.0 technology and filling orders of 100s of variants in two weeks is not a problem for us. If you need a gene variant set each gene is much cheaper than when ordered individually. Wouldn't you rather spend your time characterizing your proteins than synthesizing gene variants?

As always, time is money, and there is **no faster way to get your synthetic genes** than ordering them directly from DNA2.0. [How we can help.](#)

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Then you just need to decide on your favorite host because we've codon-optimized each fluorescent protein gene sequence for optimal expression in three hosts.

- *Escherichia coli*
- *Homo sapiens*
- *Bacillus subtilis*

Order Genes Encoding Fluorescent Proteins from the PlanetGene gene catalog and receive a 20% discount when mentioning the June Newsletter.

[Find out more about genes encoding fluorescent proteins](#)

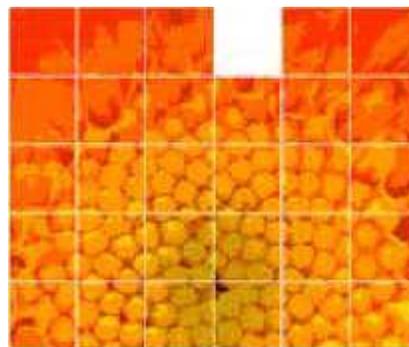
A new version of Protein-2-DNA free software is coming soon. It will be a complete suite of gene designing capabilities, and it will be beautiful. We'll let you know when it's available for download at our website www.dnatwopointo.com

We would be delighted to hear your thoughts, ideas and questions about our products, what your needs are and **how we can serve you better.**



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