
Frequently Asked Questions: Gene Synthesis Service

Version 3.2, Revision 2011-08-05



This is a collection of frequently asked questions about our gene synthesis service. If you have any question not answered here, feel free to drop us a line at info@biomatik.com.

1. Can Biomatik synthesize "difficult" DNA sequences?

Our synthesis platform allows us to produce very "complex" genes with high GC content, repetitive elements, or wobble bases.

2. What's the difference between oligo synthesis and gene synthesis?

Oligo Synthesis only creates single-stranded DNA with very limited length (normally up to around 100 - 200 bases). Oligos are not cloned into a vector. Gene has a length of 100 - 10,000 bp or longer, and it is double-stranded synthesis and cloned into a vector for delivery.

3. Can I use the same synthetic gene in two different organisms?

Yes, you can use a mixed codon table computed from the codon usage tables of the two organisms. Codon usage adjustments are very easy using fully synthetic genes.

4. Isn't it less expensive to synthesize the gene on my own?

Unless you have a method considerably simpler than that invented by Khorana in the 1970's, you will need many ligation and cloning steps requiring several weeks, if not months, of work. A Biomatik gene with up to 2000 bp requires around 3-4 weeks for delivery. It is not only economical, but it will also save your precious time.

5. What accuracy does Biomatik guarantee?

We guarantee a sequence accuracy of 100%, i.e. every gene will be shipped with the sequence exactly as ordered. You will receive complete sequence chromatograms, which document the identity of the delivered sequence and the ordered gene.

6. Can Biomatik optimize a gene for specific expression tasks?

Expression in different organisms or tissue types is often enhanced by the use of a special subset of codons. For many organisms and tissues, codon usage tables have been computed from genes with high expression in these target organisms and tissues. By adjusting the codon usage of your synthetic gene to the codon usage of your host organism, you will likely increase its expression efficiency and consequently the yield of the expressed protein.

7. Is a high GC content a problem?

Our method is very reliable across a large range of AT to GC ratios. We have already synthesized genes with a GC content of over 85% successfully. If, however, your gene has a high GC content of >70%, and additional critical features such as many repetitive elements, you should contact our support team prior to ordering a gene.

8. How long do I have to wait for a Biomatik gene?

After we have received your order, we will send you a confirmation. From the time of receiving our confirmation, the estimated delivery time is 3-4 weeks for the cloned gene (of up to 2000 bp). For genes longer than 2000 bp, the delivery time will be prolonged by approximately 1-2 additional weeks for each extra kb. If a sequence is particularly complicated or very long, the synthesis might take considerably longer. In such a case, we will discuss the delivery time with you ahead of accepting the order.

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9. How much does it cost?

We would be happy to send you an individual price quote on the basis of your gene or protein sequence. Please send your inquiry to custom@biomatik.com or via our webpage.

10. What maximum length can Biomatik synthesize?

Although our gene synthesis method has no theoretical limits, however longer genes require extra planning and have longer turnaround time, thus create high risk in production. We typically encourage our customers to synthesize no more than 10kb in length.

11. What vectors can be used to clone the gene?

Basically we can subclone the synthesized gene into any vector of your choice. Biomatik provides a few standard vectors for subcloning, free of charge: 1) pBMH; 2) pBME; 3) pBluescript II SK (+); 4) pUC19; 5) pUC18; 6) pUC57. We can also subclone your gene into any other vector of your choice. If you wish to use any specific vector other than our free standard vectors, we will be happy to do it at an additional cost.

12. How is an online order verified?

We will send you written confirmation by email or fax. If you order via our online form, you can check an option to request a copy of the sequence by email, so that you can confirm the sequence.

Please note, however, that the transfer of textual information by email is inherently insecure. If you request the sequence to be included with the confirmation, you will accept any data security risks involved. Alternatively, you can request a confirmation by fax, in which case we will fax the original sequence to you.

13. Is gene modification or gene synthesis preferable?

It depends on the complexity of the necessary modifications. If they are scattered across the whole gene and abundant, a complete synthesis is probably advisable. A synthesis also gives you the opportunity to optimize many other features of the gene such as codon usage, restriction sites, introns adapted to the expression host, etc. Modification of an existing gene, on the other hand, is preferable, if the modifications are few, or are clustered in a small part of the gene. Simple hybrids should also be made by conventional modification procedures.

14. What is the difference between complete genes and ligation products?

The ligation product is the immediate product of the gene synthesis. It is then being sequenced and check for any errors. You must ligate this product into a vector. Since a small amount of wrong bases at any base position can not be seen during sequencing (it is overshadowed by the large number of correct bases at that position), you have to transform a host with the vector and screen for correct clones. This is compensated by the much lower price of the ligation product.

For the complete gene, we handle the ligation, transformation and screening. You receive complete plasmids with the correct sequence. This is the reason why the complete gene is more expensive. You get complete documentation, including sequence chromatograms.

15. Can I also use degenerated base positions (which contain more than one nucleotide, i.e. wobble bases)?

Of course you can. We offer this service for completely degenerated positions (all four nucleotides in roughly the same amount) without additional fee. Please ask for more complex degenerations (e.g. only A and T) - they are also possible without problems. Please note that the exact ratio of all bases at a degenerated position cannot be predicted.

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16. Do you have a comparison reference between PCR cloning and gene synthesis?

Comparison	PCR Cloning for 1000bp Gene	Gene Synthesis for 1000bp Gene
Cost	Total cost is over \$2150: -one marathon-Ready cDNA libraries: \$450 -PCR product may have three mutations from SNPs, which need to be corrected: 3 X \$350 -PCR cloning kit, primers, sequencing, enzyme etc: \$650	Much cheaper
Codon Optimization	PCR Cloning won't have the same advantage way as gene synthesis.	
Delivery	No guaranteed delivery time frame	10-15 business days.