

Evrogen molecular biology services

When it comes to our research efforts, we want them to be both efficient and successful. Given these demands, it makes good sense to commit important or routine stages to those who have years of related experience and constantly develops novel tools to expedite research.

We offer expert and quality services covering common techniques like gene synthesis, site-directed mutagenesis, PCR amplification/cloning as well as modern complex technologies such as full-length-enriched cDNA synthesis, cDNA normalization and subtractive hybridization.



Service	Cat.#	Brief description
cDNA normalization and library construction service	CS010, CS011	Substantial difference in mRNA representation in cells/tissues makes sequence analysis of primary cDNA libraries inefficient, especially for gene discovery projects. Creation of equalized (normalized) cDNA libraries greatly helps to discover rare transcripts. Evrogen normalization technology is a highly efficient and well proved approach to equalizing transcript abundance in cDNA populations enriched with full-length sequences. The flexibility of the normalization procedure allows simple modifications for various purposes.
cDNA depletion and library construction service	CS012	Evrogen depletion technology allows to specifically remove already analyzed transcripts from cDNA populations and prepare depleted full-length-enriched cDNA libraries. Analysis of depleted cDNA libraries significantly accelerates discovery of unknown genes using expression cloning in particular.
cDNA subtraction and library construction service	CS021	If comparison of gene expression in two cDNA populations is required, then Supression Subtractive Hybridization (SSH) is worth to consider. Mirror Orientation Selection (MOS) special approach helps to substantially improve SSH results decreasing number of false-positive clones and increasing number of differential clones in SSH-generated libraries. All procedures are monitored by inventors of the SSH technique.
cDNA synthesis service	CS030	Full-length-enriched ds cDNA is produced using modified SMART technology. Representative cDNA population enriched with full-length sequences is generated from small amounts of starting RNA. Depending on project purposes, cDNA can be flanked by the same (for nondirectional cloning) or different (for directional cloning) adapter sequences.
PCR and RT-PCR cloning service	CS031	Large-scale PCR and RT-PCR cloning of known genes is offered for array preparation and other applications. The service includes PCR amplification of target sequences from DNA/RNA source, cloning of PCR product(s) into required vector, and purification of plasmid DNA with target inserts. Cloned products are confirmed by direct sequencing.
Subcloning service	CS032	Service includes generation of various expression constructs from customer-provided initial plasmid, preparation of chimeric/fusion proteins, any modifications of an existing construct, etc. All procedures can be adjusted to meet your specific research needs. All products are confirmed by direct sequencing.

Service	Cat.#	Brief description
RACE and isolation of full-length cDNA service	CS033	Isolation of full length cDNA(s) correspondent to a known fragment is performed using Step-Out-RACE technology. This method allows fast isolation of the 3'- and 5'-ends of the target transcript with no background noise. The method can be successfully applied to total RNA as well as poly(A)+ RNA and is applicable even if only a short nucleotide (20-30 bp) or protein sequence (8-10 aa) is available.
Genome walking service	CS035	Evrogen provides rapid cloning of promoters and other upstream regulatory elements of target genes using suppression PCR-based genome walking method.
Standard cDNA library construction service	CS040	Full-length-enriched cDNA is usually produced using modified SMART technology. After cDNA synthesis, the double stranded cDNA is size fractionated, cloned into a plasmid vector of choice, and transformed into E. coli. As a quality control measure, a percentage of recombinant clones and average insert size is determined by gel analysis of 33 clones picked at random.
Site-directed mutagenesis service	CS041	Any type of mutations, such as deletion, insertion, or substitution, can be introduced into the gene you are working with. All procedures is conducted to the highest standards and confirmed by direct sequencing.
Gene synthesis service	CS042	Evrogen offers synthesis of genes 300-3 000 bp long by assembly of short oligonucleotides followed by cloning of the synthetic gene into an appropriate vector and confirmation of clone integrity by direct sequencing. In particular, Evrogen offers codon usage optimization for gene expression in various heterological systems.
Custom optimization of Evrogen expression vectors	FPS00	Optimization of Evrogen vectors expressing fluorescent proteins can be performed in accordance with your particular needs.

For more information, please visit our web-site:
www.evrogen.com