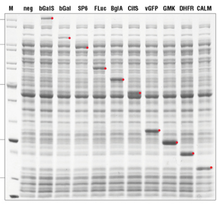
New product:

NEBExpress® Cell-free *E. coli* Protein Synthesis System

The NEBExpress Cell-free *E. coli* Protein Synthesis System is a new coupled transcription/translation system designed to synthesize proteins encoded by a DNA or mRNA template under the control of a T7 RNA Polymerase promoter. The system offers high expression levels, the ability to produce high molecular weight proteins, scalability, and is cost-effective for high throughput expression applications. The speed and robustness of the system facilitates protein synthesis in applications such as protein engineering, mutagenesis studies and enzyme screening.

The NEBExpress Cell-free *E. coli* Protein Synthesis System can be used to express a wide range of proteins



50 µl reactions containing 250 ng template DNA were incubated at 37°C for 3 hours. The red dot indicates the protein of interest. M = Unstained Protein Standard, Broad Range (NEB #P7717), "neg" = negative control, no DNA

View Product Details | Request a free Sample from your local distributor

Interested in protein expression? Visit the free webinar for tips & tricks:

Tips to Maximize the Potential of *E. coli* to Produce Challenging Proteins

NEB has been producing recombinant proteins for over 40 years, and today, over 600 individual proteins are produced using microbial expression systems. This webinar is designed to share many of the solutions that have been developed by NEB scientists for producing various classes of proteins. This session includes guidelines for generating properly-folded recombinant protein. Challenges such as protein toxicity, disulfide bond formation and insolubility will be addressed. After years of dedicated research, we have found that maltose binding protein (MBP) remains a first choice for expression level enhancement and target protein solubility enhancement. A newly updated MBP fusion system will be introduced which enables a simplified, animal-free approach for target protein isolation.

Date: Wednesday, March 11th at 15:00 (03:00 PM) CET
Your Speaker: James C. Samuelson, Senior Scientist

In case you can't make it, still register and watch recorded version later on demand.

Register here!

NEB's Monarch Genomic DNA Purification kit enables fast and simple purification of highly-pure, long DNA from a variety of samples. Even challenging samples are easily processed with the Monarch workflow, with no need to purchase additional reagents; proteinase K, various lysis buffers, and RNase A are all included. Optimized buffer chemistry ensures yields are excellent and DNA is long and intact (peak sizes typically >50kb), making it an excellent choice upstream of NGS.

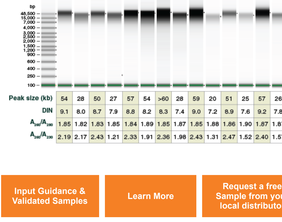
Blood: Fresh or frozen, nucleated or mammalian…the Monarch kit can purify high quality, highly-intact DNA from all (properly collected/stored) blood samples; purified DNA is typically > 50 kb. Utilizing a single lysis step, highly-pure DNA samples can be purified in under 20 minutes with our user-friendly protocol.

Fibrous Tissue (e.g. muscle): Fibrous tissues are challenging for many silica kits, but are easily processed with the Monarch kit. An additional spin after lysis helps clear out residual fibers, ensuring a highly pure gDNA prep.

Mouse Tail: Achieve excellent yields with peak DNA size >60 kb, all with the convenience of a silica kit. A brief post-lysis centrifugation step removes tail fibers, maximizing sample purity and prevents membrane clogging.

Fatty Tissue (e.g brain): Often troublesome for silica kits, fatty tissues are no problem for the Monarch kit's optimized buffers.

Genomic DNA purification with the Monarch Genomic DNA Purification Kit compared against the Qiagen DNeasy Mini Kit



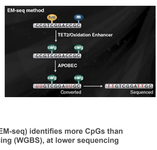
Input Guidance & Validated Samples | Learn More | Request a free Sample from your local distributor

Where methylome analysis is concerned, gentler is better.

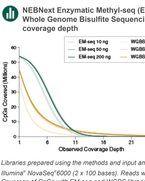
Historically, bisulfite sequencing has been the gold standard method for methylome analysis. But now, there is a new enzyme-based solution for 5mC and 5hmC detection that avoids the DNA damage caused by sodium bisulfite treatment and dramatically improves performance, including detection sensitivity, GC coverage and mapping efficiency.

The NEBNext® Enzymatic Methyl-seq Kit includes reagents for the protection of 5mC and 5hmC sites, conversion of non-protected cytosines, and high-quality library preparation (Ultra™ II DNA), in one convenient kit.

To learn the important differences between whole genome bisulfite sequencing (WGBS) and EM-seq view our EM-seq tutorial.



NEBNext Enzymatic Methyl-seq (EM-seq) identifies more CpGs than Whole Genome Bisulfite Sequencing (WGBS), at lower sequencing coverage depth

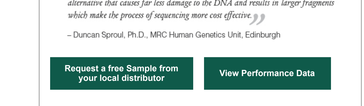


Libraries prepared using the methods and input amounts shown, and were sequenced on an Illumina® NovaSeq®6000 (2 x 100 bases). Reads were aligned to hg38 using bwa-meth 0.2.2. Coverage of CpGs with EM-seq and WGBS libraries was analyzed using 324 million paired end reads. Each top and bottom strand CpGs were counted independently, yielding a maximum of 56 million possible CpG sites. EM-seq identifies more CpGs at lower depth of sequencing.

What users are saying about the NEBNext EM-seq:

> *"Whole genome bisulfite sequencing is the workhorse technique in our laboratory and we have tested range of different kits. NEB's EM-seq kit provides an excellent alternative that causes far less damage to the DNA and results in larger fragments which make the process of sequencing more cost effective."*
>
> – Duncan Sproul, Ph.D., MRC Human Genetics Unit, Edinburgh

Request a free Sample from your local distributor | View Performance Data



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