engine the biomarker company

engine Protein Macroarrays
a powerful tool for high throughput and multiplexed protein analysis, made of >> 10.000 of recombinant proteins derived from selected human tissues.

engine Protein Macroarrays for:

- autoantibody screening
- antibody specificity determination
- epitope mapping of antibodies
- protein interaction-identification
- determination of protein functions
- functional assays
- identification of DNA/RNA binding proteins

Features of engine Protein Macroarrays

- highly sensitive
- multiplexed
- generate large amounts of data in a single experiment
- parallel screening of thousands of interactions, such as:
  - protein-antibody
  - enzyme-substrate
  - protein-ligand
  - protein-drug
  - protein-protein
- direct identification of recognized proteins (no need of further sequencing)

For further information on engine Protein Macroarrays and related services, please contact us by e-mail or by phone:

info@engine-gmbh.de +49 (0)3302 5519983

Specifications

With *E. coli* expressed proteins derived from cDNA libraries from different human tissues (foetal brain, lymphocytes, lung), **engine** offers one of the largest collection of arrayed proteins for screening experiments. Clones for the production of Protein Macroarrays are sequenced and have undergone a stringent in-frame analysis. The expression vector adds a HIS-Tag to each expressed protein. All proteins on the arrays have been verified for expression by detecting this HIS-Tag using an anti-HIS antibody. Protein Arrays are delivered with an accompanying annotation table and respective spotting positions.

engine Protein Macroarrays consist of up to 27,648 clones, which are printed in duplicate (totalling to 55,296 protein spots) onto 22 cm x 22 cm PVDF membranes.

Types of Protein Macroarrays

engine offers different types of Protein Macroarrays. The corresponding cDNA expression libraries were validated and advanced based on many years of experience in the field.

hEX1 engine Protein Macroarray

The hEX1 protein expression library was constructed by preparing cDNA from human fetal brain poly(A)+ RNA, using oligo (dT)-priming. The resulting fragments (larger than 500 bp) were cloned into a modified expression vector (pQE30NST) allowing protein expression to be induced by addition of IPTG to the growth medium. The resulting expressed proteins include an N-terminal RGS-HIS-Tag, which can be used for detection and purification purposes.
193,536 clones were picked, spotted and induced on PVDF-membranes and thereafter assayed for protein expression using an anti-HIS-antibody. Based on this screen, 37,830 putative expression clones were selected and re-arrayed into 384 well microtiter plates which constitute the hEX1-library. Spotted on high-density protein filters on two PVDF-membranes, the library is available as hEX1 part 1 and part 2 (Büssow et al., NAR 1998). Most clones of this library have been 5'tag sequenced and annotated. The clone collection contains full-length as well as shorter cDNA clones representing full-length along with partial proteins. Some clones express artificial sequences derived from out-of-frame cDNA-construct as well as 5' and 3'UTRs.

hEXselect engine Protein Macroarray

The hEXselect protein expression library was derived from the hEX1 library by in silico analysis and re-arraying. Genes which were available in a high clone number were reduced to decrease redundancy. Expressed proteins, which were available only as a single copy were doubled for successive production of high density protein macroarrays. The hEXselect protein expression library contains 23,806 clones. Like the hEX1-library, it comprises full-length as well as shorter cDNA clones. All clones have been 5'tag sequenced and are fully annotated. The size of the low redundancy collection allows a complete spotting in duplicates onto a single Protein Array, which saves processing time and hybridisation probe volume.

UniPEx engine Protein Macroarray

The UniPEx protein expression library consists of 2 Arrays representing clones in 2 different modified vectors. In total, more than 100,000 sequenced clones from different protein expression libraries (human fetal brain, T-cells, lung) were analysed in depth for their coding potential. After in-frame analysis only clones with a confirmed in-frame ORF were selected and redundancy with respect to clones per gene was minimized (< 3 fold). In total, 15,456 UniPEx clones represent 7,390 distinct human proteins.

Custom-made engine Protein Arrays

Arrays can be generated from subsets of these libraries in the range of 500 to 13,000 clones spotted in duplicates.