Virtual Expression Arrays

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ABSTRACT

For use in cross-hybridization analysis and cross-species utilization of oligonucleotide expression arrays, we have designed the Virtual Expression Array (VEA). The program uses BLAST to compare the sequences "hybridized" to the virtual chips to a database of ESTs that have been parsed into different expression libraries based upon keywords within the headers . Using pair-wise stretches of sequence homology, the VEA can either be used to estimate levels of gene expression for a specific gene, relative changes in expression levels between two libraries, or cross-hybridization that, under various levels of wash stringency, could potentially occur between the sequences on the array and the EST library.