PublisherInfo		
PublisherName	:	BioMed Central
PublisherLocation	:	London
PublisherImprintName	:	BioMed Central

Microbead expression arrays

ArticleInfo		
ArticleID	:	3694
ArticleDOI	:	10.1186/gb-spotlight-20000606-01
ArticleCitationID	:	spotlight-20000606-01
ArticleSequenceNumber	:	131
ArticleCategory	:	Research news
ArticleFirstPage	:	1
ArticleLastPage	:	2
ArticleHistory	:	RegistrationDate : 2000–06–06 OnlineDate : 2000–06–06
ArticleCopyright	:	BioMed Central Ltd2000
ArticleGrants	:	
ArticleContext	:	130591111

William Wells
Email: wells@biotext.com

Strategies for expression analysis range from exhaustive sequencing (and thus counting) of cDNAs to hybridization arrays. In the June issue of Nature Biotechnology Brenner *et al*. describe a method that combines the digital precision of the former with the speed and throughput of the latter (*Nat*. *Biotech*. 2000, **18**:630-634). Brenner et al. attach tagged cDNAs to microbeads and then sequence the overhanging ends of the cDNAs by detecting the hybridization of fluorescently labeled probes. After one overhang is identified, a binding site for a type IIs restriction endonuclease (within the probe) is used to cleave a distant cleavage site (within the cDNA sequence) to expose a new overhang. The coming and going of fluorescent probes is monitored by confocal microscopy of the microbeads, which are immobilized in a flow cell. Hundreds of thousands of mRNAs are identified in a few days, exceeding the throughput per machine of conventional sequencers by over 10-fold.

References

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