

[ScienceWatch Home](#)[Inside This Month...](#)[Interviews](#)[Featured Interviews](#)[Author Commentaries](#)[Institutional Interviews](#)[Journal Interviews](#)[Podcasts](#)[Analyses](#)[Featured Analyses](#)[What's Hot In...](#)[Special Topics](#)[Data & Rankings](#)[Sci-Bytes](#)[Fast Breaking Papers](#)[New Hot Papers](#)[Emerging Research Fronts](#)[Fast Moving Fronts](#)[Corporate Research Fronts](#)[Research Front Maps](#)[Current Classics](#)[Top Topics](#)[Rising Stars](#)[New Entrants](#)[Country Profiles](#)[About Science Watch](#)[Methodology](#)[Archives](#)[Contact Us](#)[RSS Feeds](#)

scienceWATCH[®].com

TRACKING TRENDS & PERFORMANCE IN BASIC RESEARCH

[Interviews](#)[Analyses](#)[Data & Rankings](#)

2010 : January 2010 - Fast Moving Fronts : Jay Shendure on Parallel DNA Sequencing Platforms

FAST MOVING FRONTS - 2010

January 2010



Jay Shendure talks with *ScienceWatch.com* and answers a few questions about this month's Fast Moving Front Paper in the field of Molecular Biology & Genetics.

**Article: Multiplex amplification of large sets of human exons**Authors: Porreca, GJ;Zhang, K;Li, JB;Xie, B;Austin, D;Vassallo, SL; LeProust, EM;Peck, BJ;Emig, CJ;Dahl, F;Gao, Y;Church, GM; **Shendure, J**

Journal: NAT METHODS, 4 (11): 931-936 NOV 2007

Addresses: Univ Calif San Diego, Dept Bioengn, La Jolla, CA 92093 USA.

Virginia Commonwealth Univ, Ctr Study Biol Complex, Richmond, VA 23284 USA.

Agilent Technol, Genom Solut Unit, Santa Clara, CA 95051 USA.

(addresses have been truncated.)

SW: Why do you think your paper is highly cited?

New methods for multiplex amplification of complex subsets of the human genome are currently in high demand, as they extend the utility of next-generation DNA sequencing platforms.

SW: Does it describe a new discovery, methodology, or synthesis of knowledge?

The paper describes the synthesis of several methodologies and their extension to a new direction. Specifically, we describe the efficient generation of tens of thousands of molecular inversion probes by a release from programmable microarrays, and then use these molecular inversion probes in a way that has not been utilized before.

Specifically, we demonstrated the capture of approximately 10,000 human exons in a highly multiplex, solution-phase reaction.

SW: Would you summarize the significance of your paper in layman's terms?

New sequencing technologies have dropped the cost of DNA sequence analysis by several orders of magnitude. However, the scales at which these technologies operate are poorly matched to "front end" methods like the polymerase chain reaction (PCR) that enable targeted resequencing. The methods that we describe here are aimed at building a better "front end" for next-generation DNA sequencing platforms.

"The research grew out of our earlier involvement in developing massively parallel DNA sequencing platforms..."

SW: How did you become involved in this research and were any particular problems encountered along the way?

The research grew out of our earlier involvement in developing massively parallel DNA sequencing platforms, as we sought to apply these approaches to human genetics and ran into a new problem (i.e., the lack of technologies for multiplex targeted genome amplification).

SW: Where do you see your research leading in the future?

We are attempting to extend targeted exon capture with molecular inversion probes to the full human exome, i.e., the approximately 1% of the human genome that is protein-coding.

Jay Shendure, M.D., Ph.D.

Principal Investigator

The Shendure Lab

University of Washington

Seattle, WA, USA

Web

KEYWORDS: CODING SEQUENCES; CANCER GENES; GENOME; MUTATION; SNPS.

 PDF

[back to top](#) 

2010 : [January 2010 - Fast Moving Fronts](#) : Jay Shendure on Parallel DNA Sequencing Platforms