Präsentationen

Tools For Functional Genomics, Standardisation and Production of DNA and Protein Glass Chips

A. Richter, E. Wabek, J. Zimmermann, R. Ventzki, J. Stegemann, H. Erfle, C. Schwager, W. Ansorge

The Second Annual Northwest Microarray Conference, August 15-17, 2001

Tools for functional genomics – standardisation and production of large scale DNA glass chips allowing multiple repeated hybridisations

A. Richter, E. Wabek, V. Benes, J. Zimmermann, R. Ventzki, J. Stegemann, H. Erfle, C. Schwager, W. Ansorge

Chiptechnologien: Vom Genom zum Proteom, 22-23 Januar 2001

5000 bases in a single sequencing reaction on Arakis, towards 1 mega base DNA sequencer with automated loading

J. Stegemann, R. Ventzki, H. Erfle, C. Schwager, K. Faulstich, V. Benes, J. Zimmermann, Y. Li and W. Ansorge

Automation in Mapping and DNA Sequencing Conference, September 1-4, 1999

System for simultaneous sequencing of 240 clones with 5 dyes, 1300 bases readings (up to 5000 bases per sequence reaction) with novel loading technique for vertical and horizontal standard or ultrathin gels.

Stegemann, J., Ventzki, R., Schwager, C., Erfle, H., Benes, V., Voss, H., &Ansorge W.

FASEB J. 1997 11(9)

System for simultaneous sequencing of 240 clones with 5 dyes, 1300 bases readings (up to 5000 bases per sequencing reaction) with novel loading technique for vertical and horizontal, standard or ultrathin gels

Josef Stegemann, Robert Ventzki, Christian Schwager, Holger Erfle, Vladimir Benes, Hartmut Voss and Wilhelm Ansorge

The 1997 Cold Spring Harbor Meeting on Genome Mapping & Sequencing, 14.-18. Mai 1997

Simultaneous loading of 200 sample lanes on vertical and horizontal, standard and ultrathin gels

Holger Erfle, Wilhelm Ansorge, Robert Ventzki, Hartmut Voss, Vladimir Benes, Stefanie Rechmann and Josef Stegemann

AMS ´97, Automation in Mapping and Sequencing conference, 15.-19. März 1997, EMBL Heidelberg

System for simultaneous sequencing of 240 clones with 5 dyes, 1300 bases readings (up to 5000 bases per sequencing reaction) with novel loading technique for vertical and horizontal, standard or ultrathin gels

Josef Stegemann, Robert Ventzki, Christian Schwager, Holger Erfle, Vladimir Benes, Hartmut Voss and Wilhelm Ansorge

AMS ´97, Automation in Mapping and Sequencing conference, 15.-19. März 1997, EMBL Heidelberg

120 Clones throughput Automated DNA Sequencing System and sequencing 500 kB of yeast genome

Wilhelm Ansorge, Josef Stegemann, Robert Ventzki, Jürgen Zimmermann, Christian Schwager, Vladimir Benes, Heiko Drzonek, Holger Erfle, and Hartmut Voss

The 1996 Cold Spring Harbor Meeting on Genome Mapping & Sequencing, 8.-12. Mai 1996

Flexible automated processing systems for large scale DNA sequencing

Zimmermann, J., Schwager, C., Voss, H., Toldo, L., Drzonek, H., Stegemann, J., Erfle, H., Schilke, A. & W. Ansorge

HUGO's Human Genome Meeting Heidelberg 22-24 March, p. 112. 1996

Automated DNA sequencer with a new continuous detection system for simultaneous on-line sequencing of 44 clones

Ansorge, W., Ventzki, R., Grothues, D., Erfle, H., Voie, A.-M. &Stegemann, J.

In "The 1994 CSH Meeting on Genome Mapping & Sequencing Abstract Book", Cold Spring Harbor Laboratory, New York, USA, p. 14