

Dr. Holger Erfle

University of Heidelberg
BIOQUANT
BQ 0015

Im Neuenheimer Feld 267, 69120 Heidelberg

Phone: ++49-(0)6221-54 51273

Fax: ++49-(0)6221- 54 51483

Email: holger.erfle@bioquant.uni-heidelberg.de

URL: <http://www.bioquant.uni-heidelberg.de/technology-platforms/viroquant-cellnetworks-rnai-screening-facility.html>



DATE AND PLACE OF BIRTH: August 15, 1960, Ketsch, German citizen

CURRENT POSITION: Head ViroQuant-CellNetworks RNAi-Screening Facility

The RNAi Screening Facility offers a fully automated high-throughput and high-content microscopy-based screening platform. This includes manufacturing human genome-wide siRNA microarrays and multiwell plates, automated time-lapse microscopy of human cells transfected on those arrays or multiwell plates and computerized analysis of the phenotypes by digital image processing. A further decisive point is related to the enhancement of existing technologies in terms of fully automation and, in parallel, the implementation of data management tools using novel standards for monitoring, controlling and storing of the data in a highly efficient way. Furthermore, the group acts as an interface between the underlying biological applications and the successful integration of novel technologies developed by our collaboration partners within VIROQUANT.

SCIENTIFIC VITA

2007 to present	Head ViroQuant CellNetworks RNAi Screening Facility, BioQuant, University of Heidelberg.
2000 -2007	Staff Scientist in "Cell Biology/Cell Biophysics Program" and "MitoCheck Projekt Group" in the laboratories of Dr. Rainer Pepperkok and Dr. Jan Ellenberg, European Molecular Biology Laboratory (EMBL), Heidelberg, Germany
1998-2000	Staff Scientist in "Biochemical Instrumentation Program", in the laboratory of Prof. W. Ansorge, European Molecular Biology Laboratory (EMBL), Heidelberg, Germany
1997-1998	Senior Manager Genomics at LION Bioscience, Heidelberg, Germany
1988-1997	Staff Scientist in "Biochemical Instrumentation Program", in the laboratory of Prof. W. Ansorge, European Molecular Biology Laboratory (EMBL), Heidelberg, Germany

Publications

- 1. A systems biology approach to identify the combination effects of human herpesvirus 8 genes on NF-kappaB activation.**
Konrad A, Wies E, Thurau M, Marquardt G, Naschberger E, Hentschel S, Jochmann R, Schulz TF, Erfle H, Brors B, Lausen B, Neipel F, Stürzl M.
J Virol. 2009 Mar;83(6):2563-74.
- 2. microRNAs for high throughput functional analysis**
Starkuviene V, Sudziuviene U and Erfle H.
European Pharm. Rev., 2008. 3, 10-17.
- 3. Single-cell-based image analysis of high-throughput screens using cell arrays for quantification of viral infection**
Matula P, Kumar A, Wörz I, Erfle H, Bartenschlager R, Eils R and Rohr K.
Cytometry: Part A, 2008 Nov 11; 75A(4), 309-318.
- 4. Workflow for multiplexing siRNA assays by solid phase reverse transfection in multi-well plates**
Erfle H, Neumann B, Rogers P., Bulkescher J., Ellenberg J. and Pepperkok R..
J. Biomol. Screen., 2008, 13 (7), 575-580.
- 5. Measuring secretory membrane traffic: a quantitative fluorescence microscopy approach**
Starkuviene V, Seitz A, Erfle H and Pepperkok R.
Methods Mol. Biol., 2008, 457, 193-201.
- 6. Eml3 is a Nuclear Microtubule-binding protein required for proper Alignment of Chromosomes in Metaphase**
Tegha-Dunghu J., Neumann B, Reber S, Krause R, Erfle H., Walter T., Held M. , Rogers P., Hupfeld K., Ruppert T., Ellenberg J. and Gruss O.J.
J Cell Sci, 2008, 121(Pt 10):1718-26.
- 7. High Throughput Screening of Gene Functions in Mammalian Cells Using Reversely Transfected Cell Arrays: Review And Protocol**

Stürzl M., Konrad A., Sander G., Wies E., Neipel F., Naschberger E., Reipschläger S., Gonin-Laurent N., Horch R.E., Kneser U., Hohenberger W., Erfle H. and Thurau M.

CCHTS, 2008, 11 (2), 159-172.

8. Transfected cell microarrays: an efficient tool for high-throughput functional analysis

Starkuviene V., Pepperkok R. and Erfle H.

Expert Rev. Proteomics, 2007, 4(4), 479-489.

9. Reverse transfection on cell arrays for high content screening microscopy

Erfle H, Neumann B., Liebel U., Rogers P., Held M., Walter T., Ellenberg J. and Pepperkok R.

Nature Prot., 2007 VOL.2 NO.2, 392-399.

10. An RNAi screening platform to identify secretion machinery in mammalian cells

Simpson J.C., Cetin C., Joggerst B., Liebel U., Erfle H., Ellenberg J., Pepperkok R.

Journal of Biotechnology, 2007, 129, 352-365.

11. Production of siRNA and cDNA transfected cell arrays on noncoated chambered coverglass for high content screening microscopic in living cells

Erfle H. and Pepperkok R.

Methods in Molecular Biology, 2007, 360, 155 – 162.

12. Knock-down auf dem Zellchip

Erfle H., Starkuviene V. und Eils R.

BIOspektrum, Sonderheft zur Biotechnika, 2007, 36-37.

13. Genome-wide RNAi screening for membrane traffic molecules

Simpson J.C., Cetin C., Erfle H. and Pepperkok R.

Cytometrie Part A, 2007, 71A

14. High-throughput RNAi screening by time-lapse imaging of live human cells.

Neumann, B., Held, M*., Liebel, U*., Erfle, H.*, Rogers, P., Pepperkok, R. & Ellenberg,*

Nature Methods. 2006 May, 3(5), 385-90.

*authors contributed equally to this publication

15. Funktionelle Proteomik mittels Transfektionszellarrays

Erfle H.

Bioforum, 2006, 5, 14-15

16. RNAi-Screening mittels Lebendzellchips und automatischer Fluoreszenzmikroskopie

Holger Erfle, Urban Liebel, Beate Neumann, Rainer Pepperkok und Jan Ellenberg

BIOspektrum · Sonderausgabe · 11. Jahrgang, 2006, 521

17. RNAi auf Lebendzellchips 22.000 Gene einzeln ausschalten

Erfle H., Liebel U., Neumann B., Ellenberg J. and Pepperkok R.

Analytika PRO, 2006, 20-23

18. Arrays of transfected mammalian cells for high content screening microscopy.

Erfle, H. & Pepperkok R.

Methods Enzymol. 2005;404:1-8.

19. High-content screening microscopy identifies novel proteins with a putative role in secretory membrane traffic.

Starkuviene, V., Liebel, U., Simpson, J.C., Erfle, H., Poustka, A., Wiemann, S. & Pepperkok, R.

Genome Res 2004, 14(10A), 1948-56.

20. siRNA cell arrays for high-content screening microscopy.

Erfle, H., Simpson, J.C., Bastiaens, P.I. & Pepperkok, R.

Biotechniques 2004 Sep, 37(3), 454-8, 460, 462.

21. Automatic identification of subcellular phenotypes on human cell arrays.

Conrad, C, Erfle*, H., Warnat, P., Daigle, N., Lorch, T., Ellenberg, J., Pepperkok, R. & Eils, R.*

Genome Res 2004 Jun;14(6):1130-6.

* authors contributed equally to this publication

22. A microscope-based screening platform for large-scale functional protein analysis in intact cells.

Liebel, U., Starkuviene, V., Erfle, H., Simpson, J.C., Poustka, A., Wiemann, S. & Pepperkok, R.

FEBS Lett 2003 Nov 20;554(3):394-8.

23. Sequence and analysis of chromosome 3 of the plant *Arabidopsis thaliana*

Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M., Fartmann B., Valle G., Blöcker H., Perez-Alonso M., Obermaier B., Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P., De Simone V., Choisine N., Artiguenave F., Robert C., Brottier P., Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F., Schafer M., Muller-Auer S., Gabel C., Fuchs M., Benes V., Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S., Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G., Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B., Conrad A., Hornischer K., Kauer G., Lohnert TH., Nordsiek G., Reichelt J., Scharfe M., Schon O., Bargues M., Terol J., Climent J., Navarro P., Collado C., Perez-Perez A., Ottenwalder B., Duchemin D., Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D., de Haan M., Maarse A.C., Alcaraz J.P., Cottet A., Casacuberta E., Monfort A., Argiriou A., Flores M., Liguori R., Vitale D., Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.W., Mayer K.F.

Nature, 2000, 408(6814), 820-2

24. Simultaneous loading of 200 sample lanes for DNA sequencing on vertical and horizontal, standard and ultrathin gels

Erfle, H., Ventzki, R., Voss, H., Rechmann, S., Benes, V., Stegemann, J., Ansorge, W.

Nucleic Acids Res., 1997, 25, 2229-2230

25. Quantitative trait loci for refractoriness of *Anopheles gambiae* to *Plasmodium cynomolgi* B

Zheng, L., Cornel, A.J., Wang, R., Erfle, H., Voss, H., Ansorge, W., Kafatos, F.C., Collins, F.H.

Science, 1997, 276, 425-428

26. Sequencing and analysis of 51kb on the right arm of chromosome XV from *Saccharomyces cerevisiae* reveals 30 open reading frames

Wiemann, S., Rechmann, S., Benes, V., Voss, H., Schwager, C., Vlcek, C., Stegemann, J., Zimmermann, J., Erfle, H., Paces, V., Ansorge, W.

Yeast, 1996, 12, 281-288

27. Efficient low redundancy large scale DNA sequencing at EMBL

Voss, H., Schwager, C., Wiemann, S., Zimmermann, J., Stegemann, J., Erfle, H., Voie, A.M., Drzonek, H., Ansorge, W.

J. Biotechnol., 1995, 41, 121-129

28. Direct sequencing of PCR products using magnetic beads and Fluorescein-15-dATP

Zimmermann, J., Voss, H., Wiemann, S., Erfle, H., Rupp, T., Hewitt, N.A., Schwager, C., Stegemann, J. Ansorge, W.

29. Complete DNA Sequence of yeast XI.

Dujon, B., Alexandraki, D., Andre, B., Ansorge, W., Baladron, V., Ballesta, J.P.G., Banrev, A., Bolle, P.A., Bolotin-Fukuhura, M., Bossier, P., Bou, G., Boyer, J., Bultrago, M.J., Cheret, G., Colleaux, L., Dalgnan-Fornier, B., del Rey, F., Dion, C., Domdey, H., Düsterhoft, A., Düsterhus, S., Entian, K.-D., Erfle, H., Esteban, P.F., Feldmann, H., Fernandes, L., Fobo, G.M., Fritz, C., Fukuhara, H., Gabel, C., Gaillon, L., Carcia-Cantalejo, J.M., Garcia-Ramirez, J.J., Gent, M.E., Ghazvini, M., Goffeau, A., Gonzales, A., Grothues, D., Guerreiro, P., Hegemann, J., Hewitt, N.A., Hilger, F., Hollenberg, C.P., Horaitis, O., Indge, K.J., Jaquire, A., James, C.M., Jauniaux, J.C., Jiminez, A., Keuchel, H., Kirchrath, L., Kleine, K., Kötter, P., Legrain, P., Liebl, S., Louis, E.J., Maria e Silva, A., Marck, C., Monnier, C., Möstl, D., Müller, S., Obermeier, B., Oliver, S.G., Pallier, C., Pascolo, S., Pfeiffer, F., Philippsen, P., Planat, R.J., Pohl, F.M., Pohl, T.M., Pöhlmann, R., Portetelle, D., Purnelle, B., Puzos, V., Ramezani, Rad, M., Rasmussen, S.W., Remacha, M., Revuelta, J.L., Richard, G., Rieger, M., Rodrigues-Pousada, C., Rose, M., Rupp, T., Santos, M.A., Schwager, C., Sensen, C., Skala, J., Soarez, H., Sor, F., Stegemann, J., Tettelin, H., Thierry, M., Tzermia, M., Urrestarazu, L.A., van Dyck, L., van Vliet-Reedijk, J.C., Valens, M., Vandenbol, M., Vilela, C., Vissers, S., von Wettstein, D., Voss, H., Wiemann, S., Xu, G., Zimmermann, J., Haasemann, M., Becker, I., & Mewes, H.W.

Nature, 1994, 369, 371-378

30. Separation of up to 1000 bases on a modified A.L.F. DNA sequencer

Grothues, D., Voss, H., Stegemann, J., Wiemann, S., Sensen, C., Zimmermann, J., Schwager, C., Erfle, H., Rupp, T., Ansorge, W.

Nucleic Acids Res., 1993, 21, 6042-6044

31. Sequencing and analysis of 51,6 kilobases on the left arm of chromosome XI from *Saccharomyces cerevisiae* reveals 23 open reading frames including the FAS1 gene

Wiemann, S., Voss, H., Schwager, C., Rupp, T., Stegemann, J., Zimmermann, J., Grothues, D., Sensen, C., Erfle, H., Hewitt, N., Banrevi, A., Ansorge, W.

Yeast, 1993, 9, 1343-1348

32. Direct Sequencing of PCR Products using Magnetic Beads and Fluorescein-12-dUTP

Zimmermann, J., Voss, H., Erfle, H., Rupp, T., Dietrich, T., Hewitt, N.A., Schwager, C., Stegemann, J., Ansorge, W.

Methods in Molecular and Cellular Biology, 1993, 3, 114-115

33. Cycle Sequencing protocol with Fluorescein-12-dCTP

Zimmermann, J., Voss, H., Wiemann, S., Erfle, H., Rupp, T., Hewitt, N.A., Schwager, C., Stegemann, J., Ansorge, W.

Methods in Molecular and Cellular Biology, 1993, 4, 27-28

34. Automated low-redundancy large-scale sequencing by primer walking

Voss, H., Wiemann, S., Grothues, D., Sensen, C., Zimmermann, J., Schwager, C., Stegemann, J., Erfle, H., Rupp, T., Ansorge, W.

Biotechniques, 1993, 15, 714-721

35. Sequencing reactions for A.L.F. (EMBL) automated DNA sequencer. European Molecular Laboratory

Ansorge, W., Zimmermann, J., Erfle, H., Hewitt, N., Rupp, T., Schwager, C., Sproat, B., Stegemann, J., Voss, H.

Methods Mol. Biol., 1993, 23, 317-356

36. High-throughput automated DNA sequencing facility with fluorescent labels at the European Molecular Biology Laboratory

Ansorge, W., Voss, H., Wiemann, S., Schwager, C., Sproat, B., Zimmermann, J., Stegemann, J., Erfle, H., Hewitt, N., Rupp, T.

Electrophoresis, 1992, 13, 616-619

37. Fully Automated Sanger Sequencing Protocol for Double Stranded DNA

Zimmermann, J., Dietrich, T., Voss, H., Erfle, H., Schwager, C., Stegemann, J., Hewitt, N.A., Ansorge, W.

Methods in Molecular and Cellular Biology, 1992, 3, 39-42

38. High-Speed Automated DNA Fragment Analysis for Genome Mapping by Restriction Fingerprinting

Voss, H., Stegemann, J., Schwager, C., Zimmermann, J., Erfle, H., Hewitt, N.A., Rupp, T., Ansorge, W.

Methods in Molecular and Cellular Biology, 1992, 3, 77-82

39. Cycle Sequencing Protocol with Fluorescein-12-dUTP for M13, Plasmid and Cosmid DNA

Zimmermann, J., Voss, H., Wiemann, S., Erfle, H., Rupp, T., Hewitt, N.A., Schwager, C., Stegemann, J., Ansorge, W.

Methods in Molecular and Cellular Biology, 1992, 3, 114-115

40. High speed on-line DNA sequencing on ultrathin slab gels

Stegemann, J., Schwager, C., Erfle, H., Hewitt, N.A., Voss, H., Zimmermann, J., Ansorge, W.

Nucleic Acids Res., 1991, 19, 675-676

41. One label, one tube, Sanger DNA sequencing in one and two lanes on a gel

Ansorge, W., Zimmermann, J., Schwager, C., Stegemann, J., Erfle, H., Voss, H.

Nucleic Acids Res., 1990, 18, 3419-3420

42. Automated DNA sequencing of the human HPRT locus

Edwards, A., Voss, H., Rice, P., Civitello, A., Stegemann, J., Schwager, C., Zimmermann, J., Erfle, H., Caskey, C.T., Ansorge, W.

Genomics, 1990, 6, 593-608

43. Automated fluorescent sequencing of cosmid DNA

Voss, H., Zimmermann, J., Schwager, C., Erfle, H., Stegermann, J., Stucky, K., Ansorge, W.

Nucleic Acids Res., 1990, 18, 1066

44. A simplified protocol for fast plasmid DNA sequencing

Zimmermann, J., Voss, H., Schwager, D., Stegemann, J., Erfle, H., Stucky, K., Kristensen, T., Ansorge, W.

Nucleic Acids Res., 1990, 18, 1067

45. Automated fluorescent sequencing of lambda DNA

Voss, H., Zimmermann, J., Schwager, C., Erfle, H., Stegemann, J., Stucky, K., Ansorge, W.

Nucleic Acids Res., 1990, 18, 5314

46. Automated sequencing of fluorescent label DNA by chemical degradation

Rosenthal, A., Sproat, B., Voss, H., Stegemann, J., Schwager, C., Erfle, H., Zimmermann, J., Coutelle, C., Ansorge, W.

DNA Seq., 1990, 1, 63-71

47. Automated Preparation and Purification of M13 Templates for DNA Sequencing

Zimmermann, J., Voss, H., Kristensen, T., Schwager, C., Stegemann, J., Erfle, H., Ansorge, W.

Methods Mol. and Cell. Biol, 1989, 1, 29-34

48. One-Step Reaction Protocol for Automated DNA Sequencing with T7 DNA Polymerase

Voss, H., Schwager, C., Kristensen, T., Duthie, S., Olsson, A., Erfle, H., Stegemann, J., Zimmermann, J., Ansorge, W.

Methods in Molecular and Cellular Biology, 1989, 1, 155-159

49. Direct genomic fluorescent on-line sequencing and analysis using in vitro amplification of DNA

*Voss, H., Schwager, C., Wirkner, U., Sproat, B., Zimmermann, J., Rosenthal, A., **Erfle, H.**, Stegemann, J., Ansorge, W.*

Nucleic Acids Res., 1989, 17, 2517-2527

50. Automated Sanger DNA sequencing with one label in less than four lanes on gel

*Ansorge, W., Voss, H., Wirkner, U., Schwager, C., Stegemann, J., Pepperkok, R., Zimmermann, J., **Erfle, H.***

J. Biochem. Biophys. Methods, 1989, 20, 47-52