

References (150 Publications of the PI, cited >10.000 times, H-index ~50)

[chronological order]

1. Joppich M, Olenchuk M, Mayer JM, Emslander Q, Jimenez-Soto LF, Zimmer R. SEQU-INTO: Early detection of impurities, contamination and off-targets (ICOs) in long read/MinION sequencing. *Comput Struct Biotechnol J*. 2020;18:1342-1351. Published 2020 May 23. doi:10.1016/j.csbj.2020.05.014
2. Whisnant AW, Jürges CS, Hennig T, Wyler E, Prusty B, Rutkowski AJ, L'hernault A, Djakovic L, Göbel M, Döring K, Menegatti J, Antrobus R, Matheson NJ, Künzig FWH, Mastrobuoni G, Bielow C, Kempa S, Liang C, Dandekar T, Zimmer R, Landthaler M, Grässer F, Lehner PJ, Friedel CC, Erhard F, Dölken L. Integrative functional genomics decodes herpes simplex virus 1. *Nat Commun*. 2020;11(1):2038. Published 2020 Apr 27. doi:10.1038/s41467-020-15992-5
3. Geistlinger L, Csaba G, Santarelli M, Ramos M, Schiffer L, Turaga N, Law C, Davis S, Carey V, Morgan M, Zimmer R, Waldron L. Toward a gold standard for benchmarking gene set enrichment analysis [published online ahead of print, 2020 Feb 6]. *Brief Bioinform*. 2020;bbz158. doi:10.1093/bib/bbz158
4. Mühlhofer M, Berchtold E, Stratil CG, Csaba G, Kunold E, Bach NC, Sieber SA, Haslbeck M, Zimmer R, Buchner J. The Heat Shock Response in Yeast Maintains Protein Homeostasis by Chaperoning and Replenishing Proteins. *Cell Rep*. 2019;29(13):4593-4607.e8. doi:10.1016/j.celrep.2019.11.109
5. Joppich M, Zimmer R. From command-line bioinformatics to bioGUI. *PeerJ*. 2019;7:e8111. Published 2019 Nov 21. doi:10.7717/peerj.8111
6. Sedlar K, Kolek J, Gruber M, Jureckova K, Branska B, Csaba G, Vasylykivska M, Zimmer R, Patakova P, Provaznik I. A transcriptional response of *Clostridium beijerinckii* NRRL B-598 to a butanol shock. *Biotechnol Biofuels*. 2019;12:243. publ. 2019 Oct 13. doi:10.1186/s13068-019-1584-7
7. da Silva V, Ramos M, Groenen M, Crooijmans R, Johansson A, Regitano L, Coutinho L, Zimmer R, Waldron L, Geistlinger L. CNVRanger: association analysis of CNVs with gene expression and quantitative phenotypes. *Bioinformatics*. 2020;36(3):972-973. doi:10.1093/bioinformatics/btz632
8. Joppich M, Weber C, Zimmer R. Using Context-Sensitive Text Mining to Identify miRNAs in Different Stages of Atherosclerosis. *Thromb Haemost*. 2019;119(8):1247-1264. doi:10.1055/s-0039-1693165
9. Ammar C, Gruber M, Csaba G, Zimmer R. MS-EmpiRe Utilizes Peptide-level Noise Distributions for Ultra-sensitive Detection of Differentially Expressed Proteins. *Mol Cell Proteomics*. 2019;18(9):1880-1892. doi:10.1074/mcp.RA119.001509
10. Berchtold E, Csaba G, Zimmer R. YESdb: integrative analysis of environmental stress in yeast. *Database (Oxford)*. 2019;2019:baz023. doi:10.1093/database/baz023
11. Ammar C, Berchtold E, Csaba G, Schmidt A, Imhof A, Zimmer R. Multi-Reference Spectral Library Yields Almost Complete Coverage of Heterogeneous LC-MS/MS Data Sets. *J Proteome Res*. 2019;18(4):1553-1566. doi:10.1021/acs.jproteome.8b00819
12. Berchtold E, Vetter M, Gündert M, Csaba G, Fathke C, Ulbrich SE, Thomssen C, Zimmer R, Kantelhardt EJ. Comparison of six breast cancer classifiers using qPCR. *Bioinformatics*. 2019;35(18):3412-3420. doi:10.1093/bioinformatics/btz103
13. Haas JG, Weber J, Gonzalez O, Zimmer R, Griffiths SJ. Antiviral activity of the mineralocorticoid receptor NR3C2 against Herpes simplex virus Type 1 (HSV-1) infection. *Sci Rep*. 2018;8(1):15876. Published 2018 Oct 26. doi:10.1038/s41598-018-34241-w
14. Tavakkolkhah P, Zimmer R, Küffner R. Detection of network motifs using three-way ANOVA. *PLoS One*. 2018;13(8):e0201382. Published 2018 Aug 6. doi:10.1371/journal.pone.0201382
15. Natarelli L, Geißler C, Csaba G, Wei Y, Zhu M, di Francesco A, Hartmann P, Zimmer R, Schober A. miR-103 promotes endothelial maladaptation by targeting IncWDR59. *Nat Commun*. 2018;9(1):2645. Published 2018 Jul 6. doi:10.1038/s41467-018-05065-z
16. Wei Y, Corbalán-Campos J, Gurung R, Natarelli L, Zhu M, Exner N, Erhard F, Greulich F, Geißler C, Uhlenhaut NH, Zimmer R, Schober A. Dicer in Macrophages Prevents Atherosclerosis by Promoting Mitochondrial Oxidative Metabolism [published correction appears in *Circulation*.

- 2019 Apr 23;139(17):e888]. *Circulation*. 2018;138(18):2007-2020. doi:10.1161/CIRCULATIONAHA.117.031589
17. Erhard F, Halenius A, Zimmermann C, L'Hernault A, Kowalewski DJ, Weekes MP, Stevanovic S, Zimmer R, Dölken L. Improved Ribo-seq enables identification of cryptic translation events. *Nat Methods*. 2018;15(5):363-366. doi:10.1038/nmeth.4631
 18. Geistlinger L, da Silva VH, Cesar ASM, Tizioto PC, Waldron L, Zimmer R, Regitano LCA, Coutinho LL. Widespread modulation of gene expression by copy number variation in skeletal muscle. *Sci Rep*. 2018;8(1):1399. Published 2018 Jan 23. doi:10.1038/s41598-018-19782-4
 19. Glaser LV, Rieger S, Thumann S, Beer S, Kuklik-Roos C, Martin DE, Maier KC, Harth-Hertle ML, Grüning B, Backofen R, Krebs S, Blum H, Zimmer R, Erhard F, Kempkes B. EBF1 binds to EBNA2 and promotes the assembly of EBNA2 chromatin complexes in B cells. *PLoS Pathog*. 2017;13(10):e1006664. Published 2017 Oct 2. doi:10.1371/journal.ppat.1006664
 20. Barann M, Zimmer R, Birzele F. Manananggal - a novel viewer for alternative splicing events. *BMC Bioinformatics*. 2017;18(1):120. Published 2017 Feb 21. doi:10.1186/s12859-017-1548-5
 21. Berchtold E, Csaba G, Zimmer R. RelExplain-integrating data and networks to explain biological processes. *Bioinformatics*. 2017 Feb 6. doi: 10.1093/bioinformatics/btx060. (IF: 7.307)
 22. Geistlinger L, Csaba G, Zimmer R., Bioconductor's EnrichmentBrowser: seamless navigation through combined results of set- & network-based enrichment analysis. *BMC Bioinformatics*. 2016 (IF: 2.435)
 23. Schöppner P, Csaba G, Braun T, Daake M, Richter B, Lange OF, Zacharias M, Zimmer R, Haslbeck M. Regulatory Implications of Non-Trivial Splicing: Isoform 3 of Rab1A Shows Enhanced Basal Activity and Is Not Controlled by Accessory Proteins. *J Mol Biol*. 2016 Apr 24;428(8):1544-57. doi: 10.1016/j.jmb.2016.02.02 (IF: 4.68)
 24. Pesch R, Zimmer R. Cross-species Conservation of context-specific networks. *BMC Syst Biol*. 2016 Aug 17;10(1):76. doi: 10.1186/s12918-016-0304-1. (IF: 2.65)
 25. Berchtold E, Csaba G, Zimmer R., Evaluating Transcription Factor Activity Changes by Scoring Unexplained Target Genes in Expression Data. *PLoS One*. 2016 Oct 10;11(10):e0164513. (IF: 3.534)
 26. Viola JR, Lemnitzer P, Jansen Y, Csaba G, Winter C, Neideck C, Silvestre-Roig C, Dittmar G, Döring Y, Drechsler M, Weber C, Zimmer R, Cenac N, Soehnlein O. Resolving Lipid Mediators Maresin 1 and Resolvin D2 Prevent Atheroprogession in Mice. *Circ Res*. 2016 Oct 14;119(9):1030-1038. Epub 2016 Aug 16.
 27. Florian Erhard, Ralf Zimmer, Count ratio model reveals bias affecting NGS fold changes, *Nucleic Acids Research* 2015 Jul 8. pii: gkv696. (IF: 8.867)
 28. Andrzej J. Rutkowski, Florian Erhard, Anne L'Hernault, Thomas Bonfert, Markus Schilhabel, Colin Crump, Philip Rosenstiel, Stacey Efstathiou, Ralf Zimmer, Caroline C. Friedel, Lars Dölken. Widespread disruption of host transcription termination in HSV-1 infection. *Nature Communications*, vol 6, no. 7126, 2015. (IF: 11.470)
 29. Hüntens S, Kaller M, Drepper F, Oeljeklaus S, Bonfert T, Erhard F, Dueck A, Eichner N, Friedel CC, Meister G, Zimmer R, Warscheid B, Hermeking H., p53-regulated networks of protein, mRNA, miRNA and lncRNA expression revealed by integrated pSILAC and NGS analyses. *Molecular & Cellular Proteomics*. 2015 Jul 16. pii: mcp.M115.050237 (IF: 7.254).
 30. Florian Erhard, Jürgen Haas, Diana Lieber, Georg Malterer, Lukasz Jaskiewicz, Mihaela Zavolan, Lars Dölken, Ralf Zimmer. Widespread context-dependency of microRNA-mediated regulation. *Genome Research*, 2014 Mar 25 2014. (IF: 13,852)
 31. Thomas Bonfert, Gergely Csaba, Ralf Zimmer, Caroline C. Friedel, A context-based approach to identify the most likely mapping for RNA-seq experiments, *BMC Bioinformatics*, 13(Suppl 6), pp. S9, 2012. (IF: 2.435)
 32. Thomas Bonfert, Evelyn Kirner, Gergely Csaba, Ralf Zimmer, Caroline C. Friedel, ContextMap 2: fast and accurate context-based RNA-seq mapping., *BMC bioinformatics*, vol. 16, pp. 122, 2015.
 33. Bonfert T, Csaba G, Zimmer R, Friedel CC., Mining RNA-seq data for infections and contaminations. *PLoS One*. 2013 Sep 3;8(9):e73071. doi: 10.1371/journal.pone.0073071. (IF: 3.534)
 34. Erhard F, Dölken L, Jaskiewicz L, Zimmer R., PARma: identification of microRNA target sites in AGO-PAR-CLIP data. *Genome Biology* 2013 Jul 29;14(7):R79. (IF: 10,81)

35. Geistlinger L, Csaba G, Dirmeier S, Küffner R, Zimmer R., A comprehensive gene regulatory network for the diauxic shift in *Saccharomyces cerevisiae*. *Nucleic Acids Research* 2013 Oct;41(18):8452-63. (IF: 8.867)
36. Petri T, Altmann S, Geistlinger L, Zimmer R, Küffner R. Addressing false discoveries in network inference, *Bioinformatics*. 2015 Sep 1;31(17):2836-43. doi: 10.1093/bioinformatics/btv215. Epub 2015 Apr 24.
37. Schreiber K, Csaba G, Haslbeck M, Zimmer R. Alternative Splicing in Next Generation Sequencing Data of *Saccharomyces cerevisiae*. *PLoS One*. 2015 Oct 15;10(10):e0140487. doi: 10.1371/journal.pone.0140487.
38. Silva VH, Regitano LC, Geistlinger L, Pértille F, Giachetto PF, Brassaloti RA, Morosini NS, Zimmer R, Coutinho LL. Genome-Wide Detection of CNVs and Their Association with Meat Tenderness in Nelore Cattle. *PLoS One*. 2016 Jun 27;11(6):e0157711. doi: 10.1371/journal.pone.0157711.
39. Beard PM, Griffiths SJ, Gonzalez O, Haga IR, Pechenick Jowers T, Reynolds DK, Wildenhain J, Tekotte H, Auer M, Tyers M, Ghazal P, Zimmer R, Haas J. A loss of function analysis of host factors influencing *Vaccinia* virus replication by RNA interference. *PLoS One*. 2014 Jun 5;9(6):e98431.
40. Robert Pesch, Ralf Zimmer. To be, or not to be: konservierte eukaryotische Regulationsnetzwerke?. *BIOspektrum*, vol 20, no. 5, pp. 514-516, 2014.
41. Markus Gruber, Tim Jeske, Gergely Csaba, Simone Wolf and Ralf Zimmer, An ontology-based project-specific knowledge management system, internal report, LMU, 2014.
42. Simon M Dirmeier, Lars von den Driesch, Johann S Hawe, Eike-Jens Hoffmann, Florian Erhard, Gergely Csaba and Ralf Zimmer, EGOS: an extensible system for querying and analysing big biological data, internal report, LMU, 2014.
43. Maier R, Zimmer R, Küffner R. A Turing test for artificial expression data. *Bioinformatics*. 2013 Oct 15;29(20):2603-9.
44. Harth-Hertle ML, Scholz BA, Erhard F, Glaser LV, Dölken L, Zimmer R, Kempkes B. Inactivation of intergenic enhancers by EBNA3A initiates and maintains polycomb signatures across a chromatin domain encoding CXCL10 and CXCL9. *PLoS Pathog*. 2013 Sep;9(9):e1003638.
45. K. Danowski, JJ Gross, K. Gellrich, T. Petri, HA Van Dorland, RM Bruckmaier, HD Reichenbach, R. Zimmer, HHD Meyer, FJ Schwarz, H. Kliem. Metabolic status and oestrous cycle in dairy cows. *International Journal of Livestock Production*, vol 4, no. 9, pp. 135--147, 11 2013.
46. Erhard F, Dölken L, Jaskiewicz L, Zimmer R. PARma: identification of microRNA target sites in AGO-PAR-CLIP data. *Genome Biol*. 2013 Jul 29;14(7):R79.
47. Kramer R, Wolf S, Petri T, von Soosten D, Dänicke S, Weber EM, Zimmer R, Rehage J, Jahreis G. A commonly used rumen-protected conjugated linoleic acid supplement marginally affects fatty acid distribution of body tissues and gene expression of mammary gland in heifers during early lactation. *Lipids Health Dis*. 2013 Jul 4;12(1):96.
48. Pesch R, Zimmer R. Complementing the Eukaryotic Protein Interactome. *PLoS One*. 2013 Jun 18;8(6):e66635. Print 2013.
49. Lenac Roviš T, Bailer SM, Pothineni VR, Ouwendijk WJ, Šimić H, Babić M, Miklič K, Malić S, Verweij MC, Baiker A, Gonzalez O, von Brunn A, Zimmer R, Früh K, Verjans GM, Jonjić S, Haas J. Comprehensive analysis of varicella-zoster virus proteins using a new monoclonal antibody collection. *J Virol*. 2013 Jun;87(12):6943-54.
50. Kurome M, Geistlinger L, Kessler B, Zakhartchenko V, Klymiuk N, Wuensch A, Richter A, Baehr A, Kraehe K, Burkhardt K, Flisikowski K, Flisikowska T, Merkl C, Landmann M, Durkovic M, Tschukes A, Kraner S, Schindelhauer D, Petri T, Kind A, Nagashima H, Schnieke A, Zimmer R, Wolf E. Factors influencing the efficiency of generating genetically engineered pigs by nuclear transfer: multi-factorial analysis of a large data set. *BMC Biotechnol*. 2013 May 20;13:43.
51. Sorg D, Danowski K, Korenkova V, Rusnakova V, Küffner R, Zimmer R, Meyer HH, Kliem H. Microfluidic high-throughput RT-qPCR measurements of the immune response of primary bovine mammary epithelial cells cultured from milk to mastitis pathogens. *Animal*. 2013 May;7(5):799-805.
52. Erhard F, Dölken L, Zimmer R. RIP-chip enrichment analysis. *Bioinformatics*. 2013 Jan 1;29(1):77-83.
53. Bonfert T, Csaba G, Zimmer R, Friedel CC. Mining RNA-seq data for infections and contaminations. *PLoS One*. 2013 Sep 3;8(9):e73071.

54. Griffiths SJ, Koegl M, Boutell C, Zenner HL, Crump CM, Pica F, Gonzalez O, Friedel CC, Barry G, Martin K, Craigon MH, Chen R, Kaza LN, Fossum E, Fazakerley JK, Efstathiou S, Volpi A, Zimmer R, Ghazal P, Haas J. A systematic analysis of host factors reveals a Med23-interferon- λ regulatory axis against herpes simplex virus type 1 replication. *PLoS Pathog.* 2013;9(8):e1003514.
55. Petri, T, Wolf, S, Zimmer, R. Final report on the DFG project CLA (Conjugated Linoic acids): Bioinformatik, Biostatistik und Systemmodelle CLA supplementierter Milchkühe, LMU, 2013.
56. Windhager L, Bonfert T, Burger K, Ruzsics Z, Krebs S, Kaufmann S, Malterer G, L'Hernault A, Schilhabel M, Schreiber S, Rosenstiel P, Zimmer R, Eick D, Friedel CC, Dölken L. Ultrashort and progressive 4sU-tagging reveals key characteristics of RNA processing at nucleotide resolution. *Genome Res.* 2012 Oct;22(10):2031-42.
57. Marcinowski L, Lidschreiber M, Windhager L, Rieder M, Bosse JB, Rädle B, Bonfert T, Györy I, de Graaf M, Prazeres da Costa O, Rosenstiel P, Friedel CC, Zimmer R, Ruzsics Z, Dölken L. Real-time transcriptional profiling of cellular and viral gene expression during lytic cytomegalovirus infection. *PLoS Pathog.* 2012 Sep;8(9):e1002908.
58. Robert Pesch, Matthias Böck, Ralf Zimmer. ConReg: Analysis and Visualization of Conserved Regulatory Networks in Eukaryotes. Proceedings of the German Conference on Bioinformatics (GCB), Open Access Series in Informatics of the Schloss Dagstuhl, vol 26, pp. 69-81, 2012.
59. Erhard F, Zimmer R. Detecting outlier peptides in quantitative high-throughput mass spectrometry data. *J Proteomics.* 2012 Jun 18;75(11):3230-9.
60. Naeem H, Zimmer R, Tavakkolkhah P, Küffner R. Rigorous assessment of gene set enrichment tests. *Bioinformatics.* 2012 Jun 1;28(11):1480-6.
61. Petri T, Berchtold E, Zimmer R, Friedel CC. Detection and correction of probe-level artefacts on microarrays. *BMC Bioinformatics.* 2012 May 30;13:114.
62. Küffner R, Petri T, Tavakkolkhah P, Windhager L, Zimmer R. Inferring gene regulatory networks by ANOVA. *Bioinformatics.* 2012 May 15;28(10):1376-82.
63. Stögbauer T, Windhager L, Zimmer R, Rädler JO. Experiment and mathematical modeling of gene expression dynamics in a cell-free system. *Integr Biol (Camb).* 2012 May;4(5):494-501.
64. Bonfert T, Csaba G, Zimmer R, Friedel CC. A context-based approach to identify the most likely mapping for RNA-seq experiments. *BMC Bioinformatics.* 2012 Apr 19;13 Suppl 6:S9.
65. Marcinowski L, Tanguy M, Krmpotic A, Rädle B, Lisnić VJ, Tuddenham L, Chane-Woon-Ming B, Ruzsics Z, Erhard F, Benkartek C, Babic M, Zimmer R, Trgovcich J, Koszinowski UH, Jonjic S, Pfeiffer S, Dölken L. Degradation of cellular mir-27 by a novel, highly abundant viral transcript is important for efficient virus replication in vivo. *PLoS Pathog.* 2012 Feb;8(2):e1002510.
66. Petri T, Küffner R, Zimmer R. Experiment specific expression patterns. *J Comput Biol.* 2011 Nov;18(11):1423-35.
67. Gonzalez O, Zimmer R. Contextual analysis of RNAi-based functional screens using interaction networks. *Bioinformatics.* 2011 Oct 1;27(19):2707-13.
68. Pfeifferle S, Schöpfl J, Kögl M, Friedel CC, Müller MA, Carbajo-Lozoya J, Stellberger T, von Dall'Armi E, Herzog P, Kallies S, Niemeyer D, Ditt V, Kuri T, Züst R, Pumpor K, Hilgenfeld R, Schwarz F, Zimmer R, Steffen I, Weber F, Thiel V, Herrler G, Thiel HJ, Schwegmann-Wessels C, Pöhlmann S, Haas J, Drosten C, von Brunn A. The SARS-coronavirus-host interactome: identification of cyclophilins as target for pan-coronavirus inhibitors. *PLoS Pathog.* 2011 Oct;7(10):e1002331.
69. Geistlinger L, Csaba G, Küffner R, Mulder N, Zimmer R. From sets to graphs: towards a realistic enrichment analysis of transcriptomic systems. *Bioinformatics.* 2011 Jul 1;27(13):i366-73.
70. Florian Erhard, Ralf Zimmer. Detecting outlier peptides in quantitative high-throughput mass spectrometry data. Detecting outlier peptides in quantitative high-throughput mass spectrometry data, September 2011, Weihenstephan, Germany, 2011.
71. Naeem H, Küffner R, Zimmer R. MIRTfnet: analysis of miRNA regulated transcription factors. *PLoS One.* 2011;6(8):e22519.
72. Philipp Angerer. Model Based Data Viewing and Analysis. Bachelor Thesis, LFE Bioinformatik, LMU München, September 2011.
73. Simone Wolf, Pathway extraction for psychiatric diseases via dictionary-based text-mining, Diploma Thesis, LFE Bioinformatik, LMU München March 2011.

74. Fischer W, Windhager L, Rohrer S, Zeiller M, Karnholz A, Hoffmann R, Zimmer R, Haas R. Strain-specific genes of *Helicobacter pylori*: genome evolution driven by a novel type IV secretion system and genomic island transfer. *Nucleic Acids Res.* 2010 Oct;38(18):6089-101.
75. Küffner R, Petri T, Windhager L, Zimmer R. Petri Nets with Fuzzy Logic (PNFL): reverse engineering and parametrization. *PLoS One.* 2010 Sep 20;5(9). pii: e12807.
76. Csaba G, Zimmer R. Vorescore--fold recognition improved by rescoring of protein structure models. *Bioinformatics.* 2010 Sep 15;26(18):i474-81.
77. Erhard F, Zimmer R. Classification of ncRNAs using position and size information in deep sequencing data. *Bioinformatics.* 2010 Sep 15;26(18):i426-32.
78. Gonzalez O, Oberwinkler T, Mansueto L, Pfeiffer F, Mendoza E, Zimmer R, Oesterhelt D. Characterization of growth and metabolism of the haloalkaliphile *Natronomonas pharaonis*. *PLoS Comput Biol.* 2010 Jun 3;6(6):e1000799.
79. Friedel CC, Kaufmann S, Dölken L, Zimmer R. HALO--a Java framework for precise transcript half-life determination. *Bioinformatics.* 2010 May 1;26(9):1264-6.
80. Dölken L, Malterer G, Erhard F, Kothe S, Friedel CC, Suffert G, Marcinowski L, Motsch N, Barth S, Beitzinger M, Lieber D, Bailer SM, Hoffmann R, Ruzsics Z, Kremmer E, Pfeffer S, Zimmer R, Koszinowski UH, Grässer F, Meister G, Haas J. Systematic analysis of viral and cellular microRNA targets in cells latently infected with human gamma-herpesviruses by RISC immunoprecipitation assay. *Cell Host Microbe.* 2010 Apr 22;7(4):324-34.
81. Lukas Windhager, Florian Erhard, Ralf Zimmer. Fuzzy modeling. In: Ina Koch, Wolfgang Reisig, Falk Schreiber (eds.): *Modeling in Systems Biology: The Petri Net Approach*, Springer, 2010.
82. Florian Erhard, Caroline C. Friedel, Ralf Zimmer. FERN - Stochastic Simulation and Evaluation of Reaction Networks. Sangdun Choi (ed.): *Systems Biology for Signaling Networks*, Systems Biology, vol 1, Part 4, pp. 751-775, Springer, 2010.
83. Naeem H, Küffner R, Csaba G, Zimmer R. miRSEL: automated extraction of associations between microRNAs and genes from the biomedical literature. *BMC Bioinformatics.* 2010 Mar 16;11:135.
84. Friedel CC, Dölken L, Ruzsics Z, Koszinowski UH, Zimmer R. Conserved principles of mammalian transcriptional regulation revealed by RNA half-life. *Nucleic Acids Res.* 2009 Sep;37(17):e115.
85. Fossum E, Friedel CC, Rajagopala SV, Titz B, Baiker A, Schmidt T, Kraus T, Stellberger T, Rutenberg C, Suthram S, Bandyopadhyay S, Rose D, von Brunn A, Uhlmann M, Zeretzke C, Dong YA, Boulet H, Koegl M, Bailer SM, Koszinowski U, Ideker T, Uetz P, Zimmer R, Haas J. Evolutionarily conserved herpesviral protein interaction networks. *PLoS Pathog.* 2009 Sep;5(9):e1000570.
86. Friedel CC, Zimmer R. Identifying the topology of protein complexes from affinity purification assays. *Bioinformatics.* 2009 Aug 15;25(16):2140-6.
87. Friedel CC, Krumsiek J, Zimmer R. Bootstrapping the interactome: unsupervised identification of protein complexes in yeast. *J Comput Biol.* 2009 Aug;16(8):971-87.
88. Csaba G, Birzele F, Zimmer R. Systematic comparison of SCOP and CATH: a new gold standard for protein structure analysis. *BMC Struct Biol.* 2009 Apr 17;9:23.
89. Gonzalez O, Gronau S, Pfeiffer F, Mendoza E, Zimmer R, Oesterhelt D. Systems analysis of bioenergetics and growth of the extreme halophile *Halobacterium salinarum*. *PLoS Comput Biol.* 2009 Apr;5(4):e1000332.
90. Fabian Birzele, Gergely Csaba, Florian Erhard, Caroline C. Friedel, R. Küffner, Tobias Petri, Lukas Windhager, Ralf Zimmer. Algorithmische Systembiologie mit Petrinetzen – Von qualitativen zu quantitativen Systemmodellen. *Informatik-Spektrum*, vol 32, no. 4, pp. 310-319, 2009.
91. Moll AG, Lindenmeyer MT, Kretzler M, Nelson PJ, Zimmer R, Cohen CD. Transcript-specific expression profiles derived from sequence-based analysis of standard microarrays. *PLoS One.* 2009;4(3):e4702.
92. Krumsiek J, Friedel CC, Zimmer R. ProCope--protein complex prediction and evaluation. *Bioinformatics.* 2008 Sep 15;24(18):2115-6.
93. Dölken L, Ruzsics Z, Rädle B, Friedel CC, Zimmer R, Mages J, Hoffmann R, Dickinson P, Forster T, Ghazal P, Koszinowski UH. High-resolution gene expression profiling for simultaneous kinetic parameter analysis of RNA synthesis and decay. *RNA.* 2008 Sep;14(9):1959-72.
94. Erhard F, Friedel CC, Zimmer R. FERN - a Java framework for stochastic simulation and evaluation of reaction networks. *BMC Bioinformatics.* 2008 Aug 29;9:356.

95. Csaba G, Birzele F, Zimmer R. Protein structure alignment considering phenotypic plasticity. *Bioinformatics*. 2008 Aug 15;24(16):i98-104.
96. Fundel K, Haag J, Gebhard PM, Zimmer R, Aigner T. Normalization strategies for mRNA expression data in cartilage research. *Osteoarthritis Cartilage*. 2008 Aug;16(8):947-55.
97. Fundel K, Küffner R, Aigner T, Zimmer R. Normalization and gene p-value estimation: issues in microarray data processing. *Bioinform Biol Insights*. 2008 May 28;2:291-305.
98. Gonzalez O, Zimmer R. Assigning functional linkages to proteins using phylogenetic profiles and continuous phenotypes. *Bioinformatics*. 2008 May 15;24(10):1257-63.
99. Schilling T, Küffner R, Klein-Hitpass L, Zimmer R, Jakob F, Schütze N. Microarray analyses of transdifferentiated mesenchymal stem cells. *J Cell Biochem*. 2008 Feb 1;103(2):413-33.
100. Gonzalez O, Gronau S, Falb M, Pfeiffer F, Mendoza E, Zimmer R, Oesterhelt D. Reconstruction, modeling & analysis of *Halobacterium salinarum* R-1 metabolism. *Mol Biosyst*. 2008 Feb;4(2):148-59.
101. Birzele F, Csaba G, Zimmer R. Alternative splicing and protein structure evolution. *Nucleic Acids Res*. 2008 Feb;36(2):550-8.
102. Birzele F, Küffner R, Meier F, Oefinger F, Potthast C, Zimmer R. ProSAS: a database for analyzing alternative splicing in the context of protein structures. *Nucleic Acids Res*. 2008 Jan;36(Database issue):D63-8.
103. Birzele F, Gewehr JE, Zimmer R. AutoPSI: a database for automatic structural classification of protein sequences and structures. *Nucleic Acids Res*. 2008 Jan;36(Database issue):D398-401.
104. Florian Erhard. Petri Net Based System for Spatio-Temporal Simulation of Gene Regulation. Diploma Thesis, LFE Bioinformatik/LMU München, July 2008.
105. Aigner T, Haag J, Zimmer R. Functional genomics, evo-devo and systems biology: a chance to overcome complexity? *Curr Opin Rheumatol*. 2007 Sep;19(5):463-70. Review.
106. Friedel CC, Zimmer R. Influence of degree correlations on network structure and stability in protein-protein interaction networks. *BMC Bioinformatics*. 2007 Aug 9;8:297.
107. von Brunn A, Teepe C, Simpson JC, Pepperkok R, Friedel CC, Zimmer R, Roberts R, Baric R, Haas J. Analysis of intraviral protein-protein interactions of the SARS coronavirus ORFome. *PLoS One*. 2007 May 23;2(5):e459.
108. Gewehr JE, Hintermair V, Zimmer R. AutoSCOP: automated prediction of SCOP classifications using unique pattern-class mappings. *Bioinformatics*. 2007 May 15;23(10):1203-10.
109. Gewehr JE, Szugat M, Zimmer R. BioWeka--extending the Weka framework for bioinformatics. *Bioinformatics*. 2007 Mar 1;23(5):651-3.
110. Fundel K, Küffner R, Zimmer R. RelEx--relation extraction using dependency parse trees. *Bioinformatics*. 2007 Feb 1;23(3):365-71.
111. Birzele F, Gewehr JE, Csaba G, Zimmer R. Vorolign--fast structural alignment using Voronoi contacts. *Bioinformatics*. 2007 Jan 15;23(2):e205-11.
112. Schilling T, Küffner R, Klein-Hitpass L, Zimmer R, Jakob F, Schütze N. Microarray analyses and bioinformatic evaluation of the plasticity between human mesenchymal stem cell-derived osteoblasts and adipocytes. *J Stem Cells Regen Med*. 2007 May 16;2(1):152-3.
113. Friedel CC, Zimmer R. Inferring topology from clustering coefficients in protein-protein interaction networks. *BMC Bioinformatics*. 2006 Nov 30;7:519.
114. Aigner T, Fundel K, Saas J, Gebhard PM, Haag J, Weiss T, Zien A, Obermayr F, Zimmer R, Bartnik E. Large-scale gene expression profiling reveals major pathogenetic pathways of cartilage degeneration in osteoarthritis. *Arthritis Rheum*. 2006 Nov;54(11):3533-44.
115. Davis CA, Gerick F, Hintermair V, Friedel CC, Fundel K, Küffner R, Zimmer R. Reliable gene signatures for microarray classification: assessment of stability and performance. *Bioinformatics*. 2006 Oct 1;22(19):2356-63.
116. Saas J, Haag J, Rueger D, Chubinskaya S, Sohler F, Zimmer R, Bartnik E, Aigner T. IL-1beta, but not BMP-7 leads to a dramatic change in the gene expression pattern of human adult articular chondrocytes--portraying the gene expression pattern in two donors. *Cytokine*. 2006 Oct;36(1-2):90-9.
117. Fundel K, Zimmer R. Gene and protein nomenclature in public databases. *BMC Bioinformatics*. 2006 Aug 9;7:372.

118. Friedel CC, Zimmer R. Toward the complete interactome. *Nat Biotechnol.* 2006 Jun;24(6):614-5;
119. Lee DY, Zimmer R, Lee SY, Park S. Colored Petri net modeling and simulation of signal transduction pathways. *Metab Eng.* 2006 Mar;8(2):112-22.
120. Gewehr JE, Zimmer R. SSEP-Domain: protein domain prediction by alignment of secondary structure elements and profiles. *Bioinformatics.* 2006 Jan 15;22(2):181-7.
121. Birzele F, Gewehr JE, Zimmer R. QUASAR--scoring and ranking of sequence-structure alignments. *Bioinformatics.* 2005 Dec 15;21(24):4425-6.
122. Szugat M, Güttler D, Fundel K, Sohler F, Zimmer R. Web servicing the biological office. *Bioinformatics.* 2005 Sep 1;21 Suppl 2:ii268-9.
123. Küffner R, Fundel K, Zimmer R. Expert knowledge without the expert: integrated analysis of gene expression and literature to derive active functional contexts. *Bioinformatics.* 2005 Sep 1;21 Suppl 2:ii259-67.
124. Sohler F, Zimmer R. Identifying active transcription factors and kinases from expression data using pathway queries. *Bioinformatics.* 2005 Sep 1;21 Suppl 2:ii115-22.
125. Aigner T, McKenna L, Zien A, Fan Z, Gebhard PM, Zimmer R. Gene expression profiling of serum- and interleukin-1 beta-stimulated primary human adult articular chondrocytes--a molecular analysis based on chondrocytes isolated from one donor. *Cytokine.* 2005 Aug 7;31(3):227-40.
126. Gebauer M, Saas J, Sohler F, Haag J, Söder S, Pieper M, Bartnik E, Beninga J, Zimmer R, Aigner T. Comparison of the chondrosarcoma cell line SW1353 with primary human adult articular chondrocytes with regard to their gene expression profile and reactivity to IL-1beta. *Osteoarthritis Cartilage.* 2005 Aug;13(8):697-708.
127. Fundel K, Güttler D, Zimmer R, Apostolakis J. A simple approach for protein name identification: prospects and limits. *BMC Bioinformatics.* 2005;6 Suppl 1:S15. Epub 2005 May 24.
128. Hanisch D, Fundel K, Mevissen HT, Zimmer R, Fluck J. ProMiner: rule-based protein and gene entity recognition. *BMC Bioinformatics.* 2005;6 Suppl 1:S14.
129. Aigner T, Bartnik E, Sohler F, Zimmer R. Functional genomics of osteoarthritis: on the way to evaluate disease hypotheses. *Clin Orthop Relat Res.* 2004 Oct;(427 Suppl):S138-43. Review.
130. von Ohsen N, Sommer I, Zimmer R, Lengauer T. Arby: automatic protein structure prediction using profile-profile alignment and confidence measures. *Bioinformatics.* 2004 Sep 22;20(14):2228-35.
131. Sohler F, Hanisch D, Zimmer R. New methods for joint analysis of biological networks and expression data. *Bioinformatics.* 2004 Jul 10;20(10):1517-21.
132. Hanisch D, Sohler F, Zimmer R. TopNet--an application for interactive analysis of expression data and biological networks. *Bioinformatics.* 2004 Jun 12;20(9):1470-1.
133. Crass T, Antes I, Basekow R, Bork P, Buning C, Christensen M, Claussen H, Ebeling C, Ernst P, Gailus-Durner V, Glatting KH, Gohla R, Gössling F, Grote K, Heidtke K, Herrmann A, O'Keeffe S, Kiesslich O, Kolibal S, Korbelt JO, Lengauer T, Liebich I, van der Linden M, Luz H, Meissner K, von Mering C, Mevissen HT, Mewes HW, Michael H, Mokrejs M, Müller T, Pospisil H, Rarey M, Reich JG, Schneider R, Schomburg D, Schulze-Kremer S, Schwarzer K, Sommer I, Springstube S, Suhai S, Thoppae G, Vingron M, Warfsmann J, Werner T, Wetzler D, Wingender E, Zimmer R. The Helmholtz Network for Bioinformatics: an integrative web portal for bioinformatics resources. *Bioinformatics.* 2004 Jan 22;20(2):268-70.
134. Lee DY, Zimmer R, Lee SY, Hanisch D, Park S. Knowledge representation model for systems-level analysis of signal transduction networks. *Genome Inform.* 2004;15(2):234-43.
135. Aigner T, Saas J, Zien A, Zimmer R, Gebhard PM, Knorr T. Analysis of differential gene expression in healthy and osteoarthritic cartilage and isolated chondrocytes by microarray analysis. *Methods Mol Med.* 2004;100:109-28.
136. Aigner T, Zimmer R. The promise and limitations of DNA microarray analysis: comment on the editorial by Firestein and Pisetsky. *Arthritis Rheum.* 2003 Mar;48(3):860;
137. Aigner T, Zien A, Hanisch D, Zimmer R. Gene expression in chondrocytes assessed with use of microarrays. *J Bone Joint Surg Am.* 2003;85-A Suppl 2:117-23.
138. Zien A, Fluck J, Zimmer R, Lengauer T. Microarrays: how many do you need? *J Comput Biol.* 2003;10(3-4):653-67.

139. Hanisch D, Fluck J, Mevissen HT, Zimmer R. Playing biology's name game: identifying protein names in scientific text. *Pac Symp Biocomput.* 2003:403-14.
140. Aigner T, Bartnik E, Zien A, Zimmer R. Functional genomics of osteoarthritis. *Pharmacogenomics.* 2002 Sep;3(5):635-50. Review.
141. Hanisch D, Zien A, Zimmer R, Lengauer T. Co-clustering of biological networks and gene expression data. *Bioinformatics.* 2002;18 Suppl 1:S145-54.
142. Zien, A., T. Aigner, R. Zimmer, and T. Lengauer, Centralization: a new method for the normalization of gene expression data. *Bioinformatics*, 2001. 17 Suppl 1: p. S323-S331
143. von Öhsen, N. and R. Zimmer. Improving profile-profile alignments via log average scoring. in *Algorithms in Bioinformatics (WABI 2001)*. 2001. Aarhus: Springer.
144. Zien, A., R. Zimmer, and T. Lengauer, A simple iterative approach to parameter optimization. *J Comput Biol*, 2000. 7(3-4): p. 483-501.
145. Zien, A., R. Küffner, R. Zimmer, and T. Lengauer, Analysis of gene expression data with pathway scores. *ISMB*, 2000. 8: p. 407-17.
146. Küffner, R., R. Zimmer and T. Lengauer, Pathway analysis in metabolic databases via differential metabolic display (DMD). *Bioinformatics*, 2000, 16(9): 825-836.
147. Thiele, R., R. Zimmer, and T. Lengauer, Protein threading by recursive dynamic programming. *J Mol Biol*, 1999. 290(3): p. 757-79.
148. Zimmer, R., M. Wöhler, and R. Thiele, New scoring schemes for protein fold recognition based on Voronoi contacts. *Bioinformatics*, 1998. 14(3): p. 295-308.
149. Zimmer, R. and T. Lengauer. *Fast and Numerically Stable Parametric Alignment of Biosequences*. RECOMB, ACM Press, 1997.
150. Zimmer, R (1990) *Zur Pragmatik eines operationalisierten λ -Kalküls als Basis für interaktive Reduktionssystem*, Dissertation, Universität Bonn, Oldenbourg (1991), 424pp.

Patents

1. R. Zimmer, F. Birzele, G. Csaba (2008), Verfahren zur Herstellung struktureller und funktioneller Protein Varianten, Deutsches Patentamt, 2.1.2008.
2. Hoffmann, D. and R. Zimmer (2004), Fluorescent Energy for Elucidating the 3D Structure of Biological Macromolecules (FETMA), European patent office 10.08.2001, Patent-No.: PCT/EP 99/01008 (Feb 10, 1999), US 6,713,256 B1 (Mar 30, 2004).
3. Zimmer, R., R. Küffner and A. Zien (2004), Method for Evaluation of Gene Expression and DNA Chip Data using Metabolic/Regulatory Pathways and Statistical Significance Measures with Applications to Drug Target Finding, 2004, Appl-No.: PCT Patent application (12.11.1999), Patent-No.:PCT/EP 00/11171.
4. Zimmer, R. (2001). Frei programmierbares, universelles Parallel-Rechnersystem zur Durchführung von allgemeinen Berechnungen. Europe, GMD - Forschungszentrum Informationstechnik GmbH, Sankt Augustin. PCT Patent application, European patent office 15.04.1998, EP 0 976 060 B1.