

## **2008**

Bentink S, Wessendorf S, Schwaenen C, Rosolowski M, Klapper W, Rosenwald A, Ott G, Banham AH, Berger H, Feller AC, Hansmann ML, Hasenclever D, Hummel M, Lenze D, Möller P, Stuerzenhofecker B, Loeffler M, Truemper L, Stein H, Siebert R, Spang R, and the MM (2008).

**[Pathway activation patterns in diffuse large B-cell lymphomas.](#)**

Leukemia, 22(9):1746–1754.

Dierlamm J, Penas EM, Bentink S, Wessendorf S, Berger H, Hummel M, Klapper W, Lenze D, Rosenwald A, Haralambieva E, Ott G, Cogliatti S, Möller P, Schwaenen C, Stein H, Löffler M, Spang R, Trümper L, Siebert R, and Lymphomas" DK (2008).

**[Gain of chromosome region 18q21 including the MALT1 gene is associated with the activated B-cell-like gene expression subtype and increased BCL2 gene dosage and protein expression in diffuse large B-cell lymphoma.](#)**

Haematologica, 93(5):688–696.

Fröhlich H, Beissbarth T, Tresch A, Kostka D, Jacob J, Spang R, and Markowetz F (2008).

**[Analyzing gene perturbation screens with nested effects models in R and bioconductor.](#)**

Bioinformatics, 24(21):2549–2550.

Hirsch B, Hummel M, Bentink S, Fouladi F, Spang R, Zollinger R, Stein H, and Dürkop H (2008).

**[CD30-induced signaling is absent in Hodgkin's cells but present in anaplastic large cell lymphoma cells.](#)**

Am J Pathol, 172(2):510–520.

Jacob J, Jentsch M, Kostka D, Bentink S, and Spang R (2008).

**[Detecting hierarchical structure in molecular characteristics of disease using transitive approximations of directed graphs.](#)**

Bioinformatics, 24(7):995–1001.

Klapper W, Szczepanowski M, Burkhardt B, Berger H, Rosolowski M, Bentink S, Schwaenen C, Wessendorf S, Spang R, Möller P, Hansmann ML, Bernd HW, Ott G, Hummel M, Stein H, Loeffler M, Trümper L, Zimmermann M, Reiter A, Siebert R, and Krebshilfe MM (2008).

**[Molecular profiling of pediatric mature B-cell lymphoma treated in population-based prospective clinical trials.](#)**

Blood, 112(4):1374–1381.

Kostka D, and Spang R (2008).

**[Microarray based diagnosis profits from better documentation of gene expression signatures.](#)**

PLoS Comput Biol, 4(2):e22.

Lottaz C, Kostka D, Markowetz F, and Spang R (2008).

**[Computational diagnostics with gene expression profiles.](#)**

Methods Mol Biol, 453:281–296.

## **2007**

Jaeger J, Koczan D, Thiesen HJ, Ibrahim S, Gross G, Spang R, and Kunz M (2007).  
[Gene expression signatures for tumor progression, tumor subtype, and tumor thickness in laser-microdissected melanoma tissues.](#)

Clin Cancer Res, 13(3):806–815.

Lottaz C, Kostka D, and Spang R (2007).

[Classification of Patients.](#)

In: Genomes to Therapies, ed. by Lengauer, T. Wiley-VCH, vol. 2, chap. Classification of Patient, pp. 957-991.

Lottaz C, Toedling J, and Spang R (2007).

[Annotation-based distance measures for patient subgroup discovery in clinical microarray studies.](#)

Bioinformatics, 23(17):2256–2264.

Markowitz F, and Spang R (2007).

[Inferring cellular networks—a review.](#)

BMC Bioinformatics, 8 Suppl 6:S5.

Markowitz F, Kostka D, Troyanskaya O, and Spang R (2007).

[Nested effects models for high-dimensional phenotyping screens.](#)

Bioinformatics, 23(13):i305–i312.

Roesch A, Becker B, Bentink S, Spang R, Vogl A, Hagen I, Landthaler M, and Vogt T (2007).

[Ataxia telangiectasia-mutated gene is a possible biomarker for discrimination of infiltrative deep penetrating nevi and metastatic vertical growth phase melanoma.](#)

Cancer Epidemiol Biomarkers Prev, 16(11):2486–2490.

Scheid S, and Spang R (2007).

[Compensating for unknown confounders in microarray data analysis using filtered permutations.](#)

J Comput Biol, 14(5):669–681.

## **2006**

Hummel M, Bentink S, Berger H, Klapper W, Wessendorf S, Barth TF, Bernd HW, Cogliatti S, Dierlamm J, Feller A, Hansmann ML, Haralambieva E, Harder L, Hasenclever D, Kühn M, Lenze D, Lichter P, Martin-Subero JI, Möller P, Müller-Hermelink HK, Ott G, Parwaresch R, Pott C, Rosenwald A, Rosolowski M, Schwaenen C, Stürzenhofecker B, Szczepanowski M, Trautmann H, Wacker HH, Spang R, Loeffler M, Trümper L, Stein H, Siebert R, and Krebshilfe MM (2006).

[A biologic definition of Burkitt's lymphoma from transcriptional and genomic profiling.](#)

N Engl J Med, 354(23):2419–2430.

Jaeger J, and Spang R (2006).

[Selecting normalization genes for small diagnostic microarrays.](#)

BMC Bioinformatics, 7:388.

Kirschner-Schwabe R, Lottaz C, Tödling J, Rhein P, Karawajew L, Eckert C, Stackelberg Av, Ungethüm U, Kostka D, Kulozik A, Ludwig WD, Henze G, Spang R, Hagemeyer C, and Seeger K (2006).

[Expression of late cell cycle genes and an increased proliferative capacity characterize very early relapse of childhood acute lymphoblastic leukemia.](#)

Clin Cancer Res, 12(15):4553–4561.

Lottaz C, Yang X, Scheid S, and Spang R (2006).

[OrderedList - a bioconductor package for detecting similarity in ordered gene lists.](#)

Bioinformatics, 22(18):2315–2316.

Toedling J, Rhein P, Ratei R, Karawajew L, and Spang R (2006).

[Automated in-silico detection of cell populations in flow cytometry readouts and its application to leukemia disease monitoring.](#)

BMC Bioinformatics, 7:282.

Yang X, Bentink S, Scheid S, and Spang R (2006).

[Similarities of ordered gene lists.](#)

J Bioinform Comput Biol, 4(3):693–708.

## **2005**

Jaeger J, Weichenhan D, Ivandic B, and Spang R (2005).

[Early diagnostic marker panel determination for microarray based clinical studies.](#)

Stat Appl Genet Mol Biol, 4:Article9.

Kostka D, Lottaz C, and Spang R (2005).

[Traces of molecular disease mechanisms on microarrays.](#)

In: Statistische Methoden in der empirischen Forschung. J. Kauffmann, Schering, Berlin, chap. Traces of molecular disease mechanisms on microarrays, pp. 231–236.

Lottaz C, and Spang R (2005).

[Molecular decomposition of complex clinical phenotypes using biologically structured analysis of microarray data.](#)

Bioinformatics, 21(9):1971–1978.

Lottaz C, and Spang R (2005).

[stam - a Bioconductor compliant R package for structured analysis of microarray data.](#)

BMC Bioinformatics, 6:211.

Markowitz F, Bloch J, and Spang R (2005).

[Non-transcriptional pathway features reconstructed from secondary effects of RNA interference.](#)

Bioinformatics, 21(21):4026–4032.

Scheid S, and Spang R (2005).

[twilight; a Bioconductor package for estimating the local false discovery rate.](#)

Bioinformatics, 21(12):2921–2922.

Yang X, Bentink S, and Spang R (2005).

[Detecting common gene expression patterns in multiple cancer outcome entities.](#)  
Biomed Microdevices, 7(3):247–251.

## **2004**

Kostka D, and Spang R (2004).

[Finding disease specific alterations in the co-expression of genes.](#)  
Bioinformatics, 20 Suppl 1:i194–i199.

Scheid S, and Spang R (2004).

[A stochastic downhill search algorithm for estimating the local false discovery rate.](#)  
IEEE/ACM Trans Comput Biol Bioinform, 1(3):98–108.

## **2003**

Blaxall B, Spang R, Rockman H, and Koch W (2003).

[Differential myocardial gene expression in the development and rescue of murine heart failure.](#)  
Physiol Genomics, 15(2):105–114.

Grzeskowiak R, Witt H, Drungowski M, Thermann R, Hennig S, Perrot A, Osterziel K, Klingbiel D, Scheid S, Spang R, Lehrach H, and Ruiz P (2003).

[Expression profiling of human idiopathic dilated cardiomyopathy.](#)  
Cardiovasc Res, 59(2):400–411.

## **2002**

Müller T, Spang R, and Vingron M (2002).

[Estimating amino acid substitution models: a comparison of Dayhoff's estimator, the resolvent approach and a maximum likelihood method.](#)  
Mol Biol Evol, 19(1):8–13.

Spang R, Rehmsmeier M, and Stoye J (2002).

[A novel approach to remote homology detection: jumping alignments.](#)  
J Comput Biol, 9(5):747–760.

Spang R, Zuzan H, West M, Nevins J, Blanchette C, and Marks J (2002).

[Prediction and uncertainty in the analysis of gene expression profiles.](#)  
In Silico Biol, 2(3):369–381.