Bioinformatics

A) Databases

Michael, H., Hogan, J., Kel, A., Kel-Margoulis, O., Schacherer, F., Voss, N. and Wingender, E.
Building a knowledge base for systems pathology
Brief. Bioinform. 9, 518-531 (2008).

Wingender, E.
The TRANSFAC project as an example of framework technology that supports the analysis of genomic regulation
Brief. Bioinform. 9, 326-332 (2008).

Dönitz, J., Goemann, B., Lizé, M., Michael, H., Sasse, N., Wingender, E. and Potapov, A. P.
EndoNet: An information resource about regulatory networks of cell-to-cell communication
Nucleic Acids Res. 36, D689-D694 (2008).

Wingender, E., Crass, T., Hogan, J. D, Kel, A. E., Kel-Margoulis, O. V. and Potapov, A. P.
Integrative content-driven concepts for bioinformatics "beyond the cell"
J. Biosci. 32, 169-180 (2007).

Krull, M., Pistor, S., Voss, N., Kel, A., Reuter, I., Kronenberg, D., Michael, H., Schwarzer, K., Potapov, A., Choi, C., Kel-Margoulis, O. and Wingender, E.
TRANSPATH®: an Information resource for storing and visualizing signaling pathways and their pathological aberrations
Nucleic Acids Res. 34, D546-D551 (2006).

Potapov, A., Liebich, I., Dönitz, J., Schwarzer, K., Sasse, N., Schoeps, T., Crass, T. and Wingender, E.
EndoNet: An information resource about endocrine networks
Nucleic Acids Res. 34, D540-D545 (2006).

Matys, V., Kel-Margoulis, O. V., Fricke, E., Liebich, I., Land, S., Barre-Dirrie, A., Reuter, I., Chekmenev, D., Krull, M., Hornischer, K., Voss, N., Stegmaier, P., Lewicki-Potapov, B., Saxel, H., Kel, A. E. and Wingender, E.
TRANSFAC® and its module TRANSCompel®: transcriptional gene regulation in eukaryotes
Nucleic Acids Res. 34, D108-D110 (2006).

Chen, X., Wu, J.-m., Hornischer, K., Kel, A. and Wingender, E.
TiProD: The Tissue-specific Promoter Database
Nucleic Acids Res. 34, D104-D107 (2006).

Kel-Margoulis, O., Matys, V., Choi, C., Reuter, I., Krull, M., Potapov, A.P., Voss, N., Liebich, I., Kel, A., Wingender, E.
Databases on Gene Regulation
Information Processing and Living Systems, Bajic, V. B. and Wee, T. T. (eds.), Imperial College Press, London, 709-727 (2005).

Kel, A., Kel-Margoulis, O., Borlack J., Tchekmenev, D., Wingender, E.
Databases and tools for in silico analysis of regulation of gene expression
Handbook of Toxicogenomics, Borlak, J. (ed.), Wiley-VCH, Weinheim, 253-290 (2005).

Michael, M., Chen, X., Fricke, E., Haubrock, M., Ricanek, R. and Wingender, E.
Deriving an ontology for human gene expression sources from the CYTOMER® database on human organs and cell types
In Silico Biol. 5, 0007 (2004).

Stegmaier, P., Kel, A. E. and Wingender, E.
Systematic DNA-binding domain classification of transcription factors
Genome Inf. Ser. 15, 276-286 (2004).

Choi, C., Crass, T., Kel, A., Kel-Margoulis, O., Krull, M., Pistor, S., Potapov, A., Voss, N., and Wingender, E.
Consistent re-modeling of signaling pathways and its implementation in the TRANSPATH database
Genome Inf. Ser. 15, 244-254 (2004).

Choi, C., Krull, M., Kel-Magoulis, O., Pistor, S., Potapov, A., Voss, N. and Wingender, E.
TRANSPATH® – a high quality database on signal transduction
Comparative Functional Genomics 5, 163-168 (2004).

Wingender, E.
TRANSFAC®, TRANSPATH® and CYTOMER® as starting points for an ontology of regulatory networks
In Silico Biology <u>4</u>, 0006 (2003).

Matys, V., Fricke, E., Geffers, R., Gößling, E., Haubrock, M., Hehl, R., Hornischer, K., Karas, D., Kel, A. E., Kel-Margoulis, O. V., Kloos, D. U., Land, S., Lewicki-Potapov, B., Michael, H., Münch, R., Reuter, I., Rotert, S., Saxel, H., Scheer, M., Thiele S. and Wingender, E.
TRANSFAC® : transcriptional regulation, from patterns to profiles
Nucleic Acids Res. <u>31</u>, 374-378 (2003).

Münch, R., Hiller, K., Barg, H., Heldt, D., Linz, S., Wingender, E. and Jahn, D.
PRODORIC: Prokaryotic Database Of Gene Regulation
Nucleic Acids Res. <u>31</u>, 266-269 (2003).

Krull, M., Voss, N., Choi, C., Pistor, S., Potapov, A. and Wingender, E.
TRANSPATH®: an integrated database on signal transduction and a tool for array analysis
Nucleic Acids Res. <u>31</u>, 97-100 (2003).

Liebich, I., Bode, J., Reuter, I. and Wingender, E.
Evaluation of sequence motifs found in scaffold / matrix attached regions (S/MARs)
Nucleic Acids Res. <u>30</u>, 3433-3442 (2002).

Wingender, E.
Modeling regulatory pathways with the use of the TRANSFAC system
Gene Function & Disease <u>3</u>, 3-11 (2002).

Liebich, I., Bode, J., Frisch, M. and Wingender, E.
S/MARt DB: a database on scaffold / matrix attached regions
Nucleic Acids Res. <u>30</u>, 372-374 (2002).

Kel-Margoulis, O. V., Kel, A. E., Reuter, I., Deineko, I. V. and Wingender, E.
TRANSCompel® – a database on composite regulatory elements in eukaryotic genes
Nucleic Acids Res. <u>30</u>, 332-334 (2002).

Schacherer, F., Choi, C., Götze, U., Krull, M., Pistor, S. and Wingender, E.
The TRANSPATH signal transduction database: a knowledge base on signal transduction networks
Bioinformatics <u>17</u>, 1053-1057 (2001).

Hehl, R. and Wingender, E.
Database assisted promoter analysis
Trends in Plant Sciences <u>6</u>, 251-254 (2001).

Wingender, E., Chen, X., Fricke, E., Geffers, R., Hehl, R., Liebich, I., Krull, M., Matys, V., Michael, H., Ohnhäuser, R., Prüss, M., Schacherer, F., Thiele, S. and Urbach, S.
The TRANSFAC system on gene expression regulation
Nucleic Acids Res. <u>29</u>, 281-283 (2001).

Wingender, E.
The TRANSFAC System on Gene Regulation
Trends in Glycoscience and Glycotechnology <u>12</u>, 255-264 (2000).

Wingender, E., Chen, X., Hehl, R., Karas, H., Liebich, I., Matys, V., Meinhardt, T., Prüß, M., Reuter, I. and Schacherer, F.
TRANSFAC: an integrated system for gene expression regulation
Nucleic Acids Res. <u>28</u>, 316-319 (2000).

Kel-Margoulis, O. V., Romashchenko, A. G., Kolchanov, N. A., Wingender, E. and Kel, A. E.
COMPEL: a database on composite regulatory elements providing combinatorial transcriptional regulation
Nucleic Acids Res. <u>28</u>, 311-315 (2000).

Chen, X., Dress, A., Karas, H., Reuter, I. and Wingender, E.
A database framework for mapping expression patterns
Computer Science and Biology. Proceedings of the German Conference on Bioinformatics (GCB '99). R. Giegerich, R. Hofestädt, T. Lengauer, W. Mewes, D. Schomburg, M. Vingron and E. Wingender (eds.). GBF-Braunschweig and University of Bielefeld, pp. 174-178 (1999).

Kolchanov, N. A., Ponomarenko, M. P., Frolov, A. S.,Ananko, E. A., Kolpakov, F. A., Ignatieva, E. V., Podkolodnaya, O. A., Goryachkovskaya, T. N., Stepanenko, I. L., Merkulova, T. I., Babenko, V. V., Ponomarenko, Y. V., Kochetov, A. V., Podkolodny, N. L., Vorobiev, D. V., Lavryushev, S. V., Grigorovich, D. A., Kondrakhin, Y. V., Milanesi, L., Wingender, E., Solovyev, V. and Overton, G. C.
Integrated databases and computer systems for studying eukaryotic gene expression
Bioinformatics <u>15</u>, 669-686 (1999).

Heinemeyer, T., Chen, X., Karas, H., Kel, A. E., Kel, O. V., Liebich, I., Meinhardt, T., Reuter, I., Schacherer, F. and Wingender, E.
Expanding the TRANSFAC database towards an expert system of regulatory molecular mechanisms
Nucleic Acids Res. 27, 318-322 (1999).

Heinemeyer, T., Wingender, E., Reuter, I., Hermjakob, H., Kel, A. E., Kel, O. V., Ignatieva, E. V., Ananko, E. A., Podkolodnaya, O. A., Kolpakov, F. A., Podkolodny, N. L. and Kolchanov, N. A.
Databases on Transcriptional Regulation: TRANSFAC, TRRD, and COMPEL
Nucleic Acids Res. 26, 362-367 (1998).

Karas, H., Kel, A. E., Kel, O. V., Kolchanov, N. A. and Wingender, E.
Integrating knowledge on transcriptional regulation of eukaryotic genes based on information from TRANSFAC, TRRD, and COMPEL databases
Mol. Biol. (Mosk.) 31, 637-646 (1997).
Mol. Biol. Engl. Tr. 31, 531-539 (1997).

Kel, O. V., Kel, A. E., Romashchenko, A. G., Wingender, E. and Kolchanov, N. A.
Composite regulatory elements: classification and description in the COMPEL database
Mol. Biol. (Mosk.) 31, 601-615 (1997).
Mol. Biol. Engl. Tr. 31, 498-512 (1997).

Wingender, E.
Classification scheme of eukaryotic transcription factors
Molekularnaya Biologiya 31, 584-600 (1997).
Mol. Biol. Engl. Tr. 31, 483-497 (1997).

Wingender, E., Kel, A. E., Kel, O. V., Karas, H., Heinemeyer, T., Dietze, P., Knüppel, R., Romaschenko, A. G. and Kolchanov, N. A.
TRANSFAC, TRRD and COMPEL: Towards a federated database system on transcriptional regulation
Nucleic Acids Res. 25, 265-268 (1997).

Wingender, E., Karas, H. and Knüppel, R.
TRANSFAC Database as a Bridge between Sequence Data Libraries and Biological Function
Pacific Symposium on Biocomputing '97 (PSB'97), R. B. Altman, A. K. Dunker, L. Hunter, T. E. Klein (eds.). World Scientific, Singapore - New Jersey - London - Hong Kong 1996, pp. 477-485.

Kel, A., Kel, O., Ischenko, I., Kolchanov, N., Karas, H., Wingender, E. and Sklenar, H.
TRRD and COMPEL databases on transcription linked to TRANSFAC as tools for analysis and recognition of regulatory sequences
Computer Science and Biology. Proceedings of the German Conference on Bioinformatics (GCB'96), R. Hofestädt, T. Lengauer, M. Löffler, D. Schomburg (eds.). University of Leipzig, Leipzig 1996, pp. 113-117.

Wingender, E., Dietze, P., Karas, H. and Knüppel, R.
TRANSFAC: A database on transcription factors and their DNA binding sites
Nucleic Acids Res. 24, 238-241 (1996).

Kel, O. V., Romaschenko, A. G., Kel, A. E., Wingender, E. and Kolchanov, N. A.
A compilation of composite regulatory elements affecting gene transcription in vertebrates
Nucleic Acids Res. 23, 4097-4103 (1995).

Wingender, E., Knüppel, R., Dietze, P., Karas, H., Frech, K., Quandt, K. and Werner, T.
The TRANSFAC database and ConsInd program as tools for describing and understanding regulatory functions of the genome
SAMS 18-19, pp. 823-826; Overseas Publishers Association, Amsterdam 1995

Wingender, E., Knüppel, R., Dietze, P. and Karas, H.
TRANSFAC database as tool for the recognition of regulatory genomic sequences
In: Bioinformatics & Genome Research, H.A. Lim and C.R. Cantor (Eds.), (World Scientific Publishing Co., Inc., New Jersey, 1995), pp. 275-282.

Knüppel, R., Dietze, P., Lehnberg, W., Frech, K. and Wingender, E.
TRANSFAC retrieval program: a network model database of eukaryotic transcription regulating sequences and proteins
J. Comput. Biol. 1, 191-198 (1994)

Wingender, E.
Compilation of transcription regulating proteins
Nucleic Acids Res. 16, 1879-1902 (1988)

B) Regulatory Sequence Analysis

Michael, H., Hogan, J., Kel, A., Kel-Margoulis, O., Schacherer, F., Voss, N. and Wingender, E.
Building a knowledge base for systems pathology
Brief. Bioinform. 9, 518-531 (2008).

Kel, A., Voss, N., Valeev, T., Stegmaier, P., Kel-Margoulis, O. and Wingender, E.
ExPlain: finding upstream drug targets in disease gene regulatory networks
SAR QSAR Environ. Res. 19, 481-494 (2008).

Wingender, E.
The TRANSFAC project as an example of framework technology that supports the analysis of genomic regulation
Brief. Bioinform. 9, 326-332 (2008).

Kel, A., Voss, N., Jauregui, R., Kel-Margoulis, O. and Wingender, E.
Beyond microarrays: Find key transcription factors controlling signal transduction pathways
BMC Bioinformatics 7 Suppl. 2, S13 (2006).

Waleev, T. Shtokalo, D., Konovalova, T., Voss, N., Cheremushkin, E., Stegmaier, P., Kel-Margoulis, O., Wingender, E. and Kel, A.
Composite Module Analyst: identification of transcription factor binding site combinations using genetic algorithm
Nucleic Acids Res. 34, W541-W545 (2006).

Kel, A., Konovalova, T., Waleev, T., Cheremushkin, E., Kel-Margoulis, O. and Wingender, E.
Composite Module Analyst: a fitness-based tool for identification of transcription factor binding site combinations
Bioinformatics 22, 1190-1197 (2006).

Sauer, T., Shelest, E. and Wingender, E.
Evaluating phylogenetic footprinting for human-rodent comparisons
Bioinformatics 22, 430-437 (2006).

Krull, M. and Wingender, E.
Eukaryotic regulatory sequences
Encyclopedia of Genetics, Genomics, Proteomics and Bioinformatics; Dunn, M. J., Jorde, L. B., Little, P. F., Subramaniam, S. (eds.), John Wiley & Sons, Ltd., UK, pp. 2895-2899 (2005).

Kel, A., Konovalova, T., Valeev, T., Cheremushkin, E., Kel-Margoulis, O. and Wingender, E.
Composite Module Analyst: A Fitness-Based Tool for Prediction of Transcription Regulation
Lecture Notes in Informatics, Proceedings of the German Conference on Bioinformatics 2005 (GCB 2005). Torda, A., Kurtz, S. and Rarey, M. (eds.). Gesellschaft für Informatik, Bonn, pp. 63-75 (2005).

Kel, A., Kel-Margoulis, O., Borlack J., Tchekmenev, D., Wingender, E.
Databases and tools for in silico analysis of regulation of gene expression
Handbook of Toxicogenomics, Borlak, J. (ed.), Wiley-VCH, Weinheim, 253-290 (2005).

Kel, A., Tikunov, Y., Voss, N., Borlak, J. and Wingender, E.
Application of kernel method to reveal subtypes of TF binding motifs. Causal analysis of gene expression data
Regulatory Genomics: RECOMB 2004 International Workshop, RRG 2004, San Diego, Ca, USA, March 26-27, 2004, Revised Selected Papers. Eleazar Eskin, Chris Workman (eds.), Lecture Notes in Computer Science 3318, 42-51 (2005).

Shelest, E. and Wingender, E.
Construction of predictive promoter models on the example of antibacterial response of human epithelial cells
Theor. Biol. Med. Model. 2, 2 (2005).

Stegmaier, P., Kel, A. E. and Wingender, E.
Systematic DNA-binding domain classification of transcription factors
Genome Inf. Ser. 15, 276-286 (2004).

Kel, A., Voss, N., Konovalova, T., Tchekmenev, D., Wabnitz, P., Kel-Margoulis, O. and Wingender, E.
From Composite Patterns to Pathways – Prediction of Key Regulators of Gene Expression

Lecture Notes in Informatics, Proceedings of the German Conference on Bioinformatics 2004 (GCB 2004). Giegerich, R. and Stoye, J. (eds.). Gesellschaft für Informatik, Bonn, pp. 189-198 (2004).

Kel, A., Tikunov, Y., Voss, N. and Wingender, E.
Recognition of multiple patterns in unaligned sets of sequences: comparison of kernel clustering method with other methods
Bioinformatics 20, 1512-1516 (2004).

Kel, A., Reymann, S., Matys, V., Nettesheim, P., Wingender, E. and Borlak, J.
A novel computational approach for the prediction of networked transcription factors of aryl hydrocarbon-receptor-regulated genes
Mol. Pharmacol. 66, 1557-1572 (2004).

Hehl, R., Steffens, N. O. and Wingender, E.
Isolation and analysis of gene regulatory sequences
Handbook of Plant Biotechnology, Christou, P. and Klee, H. (eds.), Wiley and Sons Ltd., 81-102 (2004).

Kel-Margoulis, O. V., Tchekmenev, D., Kel, A. E., Gößling, E., Hornischer, K., Lewicki-Potapov, B. and Wingender, E.
Composition-sensitive analysis of the human genome for regulatory signals
In Silico Biol. 2, 0013 (2003).

Kel, A. E., Gößling, E., Reuter, I., Cheremushkin, E., Kel-Margoulis, O. V. and Wingender, E.
MATCH™: a tool for searching transcription factor binding sites in DNA sequences
Nucleic Acids Res. 31, 3576-3579 (2003).

Shelest, E., Kel, A.. E., Gößling, E. and Wingender, E.
Prediction of potential C/EBP/NF-κB composite elements using the matrix-based search methods
In Silico Biol. 2, 0007 (2003).

Liebich, I., Bode, J., Reuter, I. and Wingender, E.
Evaluation of sequence motifs found in scaffold / matrix attached regions (S/MARs)
Nucleic Acids Res. 30, 3433-3442 (2002).

Kel-Margoulis, O. V., Ivanova, T. G., Wingender, E. and Kel, A. E.
Automatic annotation of genomic regulatory sequences by searching for composite clusters
Pac. Symp. Biocomput. 7, 187-198 (2002).
http://helix-web.stanford.edu/psb02/kel-margoulis.pdf

Kel, A., Kel-Margoulis, O., Ivanova, T. and Wingender, E.
ClusterScan: A tool for automatic annotation of genomic regulatory sequences by searching for composite clusters
Computer Science and Biology. Proceedings of the German Conference on Bioinformatics (GCB 2001). E. Wingender, R. Hofestädt, I. Liebich (eds.). GBF-Braunschweig, pp. 96-101 (2001).

Kel, A. E., Kel-Margoulis, O. V., Farnham, P. J., Wingender, E. and Zhang, M. Q.
Computer-assisted identification of cell cycle-related genes - new targets for E2F transcription factors
J. Mol. Biol. 309, 99-120 (2001).

Hehl, R. and Wingender, E.
Database assisted promoter analysis
Trends in Plant Sciences 6, 251-254 (2001).

Roulet, E., Bucher, P., Schneider, R., Wingender, E., Dusserre, Y., Werner, T. and Mermod, N.
Experimental analysis and computer prediction of CTF/NFI Transcription Factor DNA binding sites
J. Mol. Biol. 297, 833-848 (2000).

Kolchanov, N. A., Ponomarenko, M. P., Frolov, A. S.,Ananko, E. A., Kolpakov, F. A., Ignatieva, E. V., Podkolodnaya, O. A., Goryachkovskaya, T. N., Stepanenko, I. L., Merkulova, T. I., Babenko, V. V., Ponomarenko, Y. V., Kochetov, A. V., Podkolodny, N. L., Vorobiev, D. V., Lavryushev, S. V., Grigorovich, D. A., Kondrakhin, Y. V., Milanesi, L., Wingender, E., Solovyev, V. and Overton, G. C.
Integrated databases and computer systems for studying eukaryotic gene expression
Bioinformatics 15, 669-686 (1999).

Kel, A., Kel-Margoulis, O., Babenko, V. and Wingender, E.
Recognition of NFATp/AP-1 composite elements within genes induced upon the activation of immune cells

J. Mol. Biol. 288, 353-376 (1999).

Sacht, G., Marten, A., Deiters, U., Süssmuth, R., Jung, G., Wingender, E. and Mühlradt, P. F.
Activation of nuclear factor-kappaB in macrophages by mycoplasmal lipopeptides
Eur. J. Immunol. 28, 4207-4212 (1998).

Kolchanov, N. A., Ponomarenko, M. P., Kel, A. E., Kondrakhin, Y. V., Frolov, A. S., Kolpakov, F. A., Goryachkovsky, T. N., Kel, O. V., Ananko, E. A., Ignatieva, E. V., Podkolodnaya, O. A., Babenko, V. N., Stepanenko, I. L., Romashchenko, A. G., Merkulova, T. I., Vorobiev, D. G., Lavryushev, S. V., Ponomarenko, Y. V., Kochetov, A. V., Kolesov, G. B., Solovyev, V. V., Milanesi, L., Podkolodny, N. L., Wingender, E. and Heinemeyer, T.
GeneExpress: a computer system for description, analysis, and recognition of regulatory sequences in eukaryotic genome
Ismb 6, 95-104 (1998).

Reuter, I., Werner, T. and Wingender, E.
Computer-assisted methods for the identification and characterization of polymerase II promoters
Genetic Engineering: principles and methods, Vol. 20; J. K. Setlow (ed.), Plenum Press, New York and London, 25-40 (1998).

Pickert, L., Reuter, I., Klawonn, F. and Wingender, E.
Transcription regulatory region analysis using signal detection and fuzzy clustering
Bioinformatics 14, 244-251 (1998).

Flohé, L., Wingender, E. and Brigelius-Flohé, R.
Regulation of Glutathione Peroxidases
Oxidative stress and signal transduction; H. J. Forman, H. Cadenas (eds.), Chapman & Hall, New York, 415-440 (1997).

Pickert, L., Reuter, I., Klawonn, F. and Wingender, E.
Transcription regulatory regions revealed by signal detection and fuzzy clustering
Proceedings of the German Conference on Bioinformatics GCB '97, Kloster Irsee, Bavaria; H. W. Mewes, D. Frishman (eds.), 99-101 (1997).

Pickert, L., Klawonn, F. and Wingender, E.
Fuzzy Cluster Analysis for Identification of Gene Regulating Regions
Proc. 7th International Fuzzy Systems Association World Congress (IFSA'97) Vol. IV, Academia, Prague, 56-61 (1997).

Kuhlenbäumer, G., Rothenburg, S., Matthes, M., Hollmann, C., Wingender, E., Thiele, H.-G., Koch-Nolte, F. and Haag, F.
Expression of the RT6 mono(ADP-ribosyl)transferases is regulated by two promoter regions
Adv. Exp. Med. Biol. 419, 265-270 (1997).

Ponomarkeno, M. P., Ponomarenko, I. V., Kel, A. E., Kolchanov, N. A., Karas, H., Wingender, E. and Sklenar, H.
Computer analysis of conformational features of the eukaryotic TATA-box DNA promotors
Mol. Biol. (Mosk.) 31, 733-740 (1997).
Mol. Biol. Engl. Tr. 31, 623-630 (1997).

Wingender, E., Karas, H., Dietze, P., Knüppel, R. and Sklenar, H.
Combined approaches for the detection of regulatory DNA-regions
Computer Science and Biology. Proceedings of the German Conference on Bioinformatics (GCB'96), R. Hofestädt, T. Lengauer, M. Löffler, D. Schomburg (eds.). University of Leipzig, Leipzig 1996, pp. 58-63.

Karas, H., Knüppel, R., Schulz, W., Sklenar, H. and Wingender, E.
Combining structural analysis of DNA with search routines for detection of transcription regulatory elements
Comput. Appl. Biosci. 12, 441-446 (1996).

Haag, F. A., Kuhlenbäumer, G., Koch-Nolte, F., Wingender, E. and Thiele, H.-G.
Structure of the gene encoding the rat T cell ecto-ADP-ribosyltransferase RT6
J. Immunol. 157, 2022-2030 (1996).

Quandt, K., Frech, K., Karas, H., Wingender, E. and Werner, T.
MatInd and MatInspector - New fast and sensitive tools for detection of consensus matches in nucleotide sequence data
Nucleic Acids Res. 23, 4878-4884 (1995).

Kel, A. E., Kondrakhin, Y. V., Kolpakov, P. A., Kel, O. V., Romashenko, A. G., Wingender, E., Milanesi, L. and Kolchanov, N. A.
Computer tool FUNSITE for analysis of eukaryotic regulatory genomic sequences

Ismb <u>3</u>, 197-205 (1995).

Wingender, E., Knüppel, R., Dietze, P., Karas, H., Frech, K., Quandt, K. and Werner, T.
The TRANSFAC database and ConsInd program as tools for describing and understanding regulatory functions of the genome
SAMS <u>18-19</u>, pp. 823-826; Overseas Publishers Association, Amsterdam 1995

Wingender, E., Knüppel, R., Dietze, P. and Karas, H.
TRANSFAC database as tool for the recognition of regulatory genomic sequences
In: Bioinformatics & Genome Research, H.A. Lim and C.R. Cantor (Eds.), (World Scientific Publishing Co., Inc., New Jersey, 1995), pp. 275-282.

Knüppel, R., Dietze, P., Lehnberg, W., Frech, K. and Wingender, E.
TRANSFAC retrieval program: a network model database of eukaryotic transcription regulating sequences and proteins
J. Comput. Biol. <u>1</u>, 191-198 (1994)

Wingender, E.
Recognition of regulatory regions in genomic sequences
J. Biotechnol. <u>35</u>, 273-280 (1994)

Brigelius-Flohé, R., Aumann, K.-D., Blöcker, H., Gross, G., Kiess, M., Klöppel, K.-D., Maiorino, M., Roveri, A., Schuckelt, R., Ursini, F., Wingender, E. and Flohé, L.
Phospholipid hydroperoxide glutathione peroxidase: genomic DNA, cDNA, and deduced amino acid sequence
J. Biol. Chem. <u>269</u>, 7342-7348 (1994)

Möritz, A., Grzeschik, K.-H., Wingender, E. and Fink, E.
Organization and sequence of the gene encoding the human acrosin-trypsin inhibitor (HUSI-II)
Gene <u>123</u>, 277-281 (1993)

Wingender, E., Heinemeyer, T. and Lincoln, D.
Regulatory DNA sequences: predictability of their function
Genome Analysis - From Sequence to Function; BioTechForum- Advances in Molecular Genetics (J. Collins, A.J. Driesel, eds.) <u>4</u>, 95-108 (1991)

C) Network Analysis / Systems Biology

Stegmaier, P., Krull, M., Voss, N., Kel, A. and Wingender, E.
Molecular mechanistic associations of human diseases
BMC Syst. Biol. <u>4</u>, 1024 (2010).

Demir, E., Cary, M. P., Paley, S., Fukuda, K., Lemer, C., Vastrik, I., Wu, G., D'Eustachio, P., Schaefer, C., Luciano, J., Schacherer, F., Martinez-Flores, I., Hu, Z., Jimenez-Jacinto, V., Joshi-Tope, G., Kandasamy, K., Lopez-Fuentes, A. C., Mi, H., Pichler, E., Rodchenkov, I., Splendiani, A., Tkachev, S., Zucker, J., Gopinath, G., Rajasimha, H., Ramakrishnan, R., Shah, I., Syed, M., Anwar, N., Babur, O., Blinov, M., Brauner, E., Corwin, D., Donaldson, S., Gibbons, F., Goldberg, R., Hornbeck, P., Luna, A., Murray-Rust, P., Neumann, E., Reubenacker, O., Samwald, M., van Iersel, M., Wimalaratne, S., Allen, K., Braun, B., Whirl-Carrillo, M., Cheung, K. H., Dahlquist, K., Finney, A., Gillespie, M., Glass, E., Gong, L., Haw, R., Honig, M., Hubaut, O., Kane, D., Krupa, S., Kutmon, M., Leonard, J., Marks, D., Merberg, D., Petri, V., Pico, A., Ravenscroft, D., Ren, L., Shah, N., Sunshine, M., Tang, R., Whaley, R., Letovksy, S., Buetow, K. H., Rzhetsky, A., Schachter, V., Sobral, B. S., Dogrusoz, U., McWeeney, S., Aladjem, M., Birney, E., Collado-Vides, J., Goto, S., Hucka, M., Le Novère, N., Maltsev, N., Pandey, A., Thomas, P., Wingender, E., Karp, P. D., Sander, C. and Bader, G. D.
BioPAX – A Community Standard for Pathway Data Sharing
Nat. Biotechnol. <u>28</u>,935-942 (2010).

Goemann, B., Potapov, A. P., Ante, M. and Wingender, E.
Comparative analysis of topological patterns in different mammalian networks
Genome Inf. Ser. <u>23</u>, 32-45 (2009).

Goemann, B., Wingender, E. and Potapov, A. P.
An approach to evaluate the topological significance of motifs and other patterns in regulatory networks
BMC Syst. Biol. <u>3</u>, 53 (2009).

Michael, H., Hogan, J., Kel, A., Kel-Margoulis, O., Schacherer, F., Voss, N. and Wingender, E.

Building a knowledge base for systems pathology
Brief. Bioinform. 9, 518-531 (2008).

Potapov, A. P., Goemann, B. and Wingender, E.
The pairwise disconnectivity index as a new metric for the topological analysis of regulatory networks
BMC Bioinformatics 9, 227 (2008).

Zubarev, R. A., Nielsen, M. L., Fung, E. M., Savitski, M. M., Kel-Margoulis, O., Wingender, E. and Kel, A.
Identification of dominant signaling pathways from proteomics expression data
J. Proteom. 71, 89-96 (2008).

Wingender, E., Hogan, J., Schacherer, F., Potapov, A. P. and Kel-Margoulis, O.
Integrating pathway data for systems pathology
In Silico Biol. 7 S1, 03 (2007).

Degenhardt, J., Haubrock, M., Wingender, E. and Crass, T.
DEEP – A Tool for Differential Expression Effector Prediction
Nucleic Acids Res. 35, W619-W624 (2007).

Wingender, E., Crass, T., Hogan, J. D, Kel, A. E., Kel-Margoulis, O. V. and Potapov, A. P.
Integrative content-driven concepts for bioinformatics "beyond the cell"
J. Biosci. 32, 169-180 (2007).

Kel, A., Voss, N., Jauregui, R., Kel-Margoulis, O. and Wingender, E.
Beyond microarrays: Find key transcription factors controlling signal transduction pathways
BMC Bioinformatics 7 Suppl. 2, S13 (2006).

Potapov, A. P., Voss, N., Sasse, N. and Wingender, E.
Topology of mammalian transcription networks
Genome Inf. Ser. 16, 270-278 (2005).

Kel, A., Voss, N., Konovalova, T., Tchekmenev, D., Wabnitz, P., Kel-Margoulis, O. and Wingender, E.
From Composite Patterns to Pathways – Prediction of Key Regulators of Gene Expression
Lecture Notes in Informatics, Proceedings of the German Conference on Bioinformatics 2004 (GCB 2004). Giegerich, R. and Stoye, J. (eds.). Gesellschaft für Informatik, Bonn, pp. 189-198 (2004).

Krull, M., Voss, N., Choi, C., Pistor, S., Potapov, A. and Wingender, E.
TRANSPATH®: an integrated database on signal transduction and a tool for array analysis
Nucleic Acids Res. 31, 97-100 (2003).

Potapov, A. P. and Wingender, E.
Representing the architecture of signal transduction networks in an algebraic form: protein target finding
Ann. N. Y. Acad. Sci. 973, 1-2 (2002).

Wingender, E.
Modeling regulatory pathways with the use of the TRANSFAC system
Gene Function & Disease 3, 3-11 (2002).

Kloos, D.-U., Choi, C. and Wingender, E.
The TGF-β-Smad network: introducing bioinformatic tools.
Trends Genet. 18, 96-103 (2002).

Potapov, A. and Wingender, E.
Modeling the architecture of regulatory networks
Computer Science and Biology. Proceedings of the German Conference on Bioinformatics (GCB 2001). E. Wingender, R. Hofestädt, I. Liebich (eds.). GBF-Braunschweig, pp. 6-10 (2001).

D) Miscellaneous

Crass, T., Antes, I., Basekow, R., Bork, P., Buning, C., Christensen, M., Claußen, H., Ebeling, C., Ernst, P., Gailus-Durner, V., Glatting, K.-H., Gohla, R., Gößling, F., Grote, K., Heidke, K., Herrmann, A., O'Keeffe, S., Kießlich, O., Kolibal, S., Korbel, J. O., Lengauer, T., Liebich, I., van der Linden, M., Luz, H., Meissner, K., von Mering, C., Mevissen, H.-T., Mewes, H.-W.,

Michael, H., Mokrejs, M., Müller, T., Pospisil, H., Rarey, M., Reich, J. G., Schneider, R., Schomburg, D., Schulze-Kremer, S., Schwarzer, K., Sommer, I., Springstubbe, S., Suhai, S., Thoppae, G., Vingron, M., Warfsmann, J., Werner, T., Wetzler, D., Wingender, E. and Zimmer, R.

The Helmholtz Network for Bioinformatics: an integrative web portal for bioinformatics resources

Bioinformatics 19, 268-270 (2004).

Schubert, U., Henklein, P., Boldyreff, B., Wingender, E., Strebel, K. and Porstmann, T.

The human immunodeficiency virus type 1 encoded Vpu protein is phosphorylated by casein kinase-2 (CK-2) at positions Ser52 and Ser56 within a predicted alpha-helix-turn-alpha-helix-motif

J. Mol. Biol. 236, 16-25 (1994)