

Journalbeiträge

1. Bhar A, Haubrock M, Mukhopadhyay A, Wingender E (2015) Multiobjective triclustering of time-series transcriptome data reveals key genes of biological processes. BMC BIOINFORMATICS 16: 200, doi: 10.1186/s12859-015-0635-8
2. Dalila N, Brockmüller J, Tzvetkov MV, Schirmer M, Haubrock M, Vormfelde SV (2015) Impact of mineralocorticoid receptor polymorphisms on urinary electrolyte excretion with and without diuretic drugs. PHARMACOGENOMICS 16(2): 115-27, doi: 10.2217/pgs.14.163
3. Koschmann J, Bhar A, Stegmaier P, Kel A, Wingender E (2015) "Upstream Analysis": An integrated promoter-pathway analysis approach to causal interpretation of microarray data. Microarrays 4(2)(2015): 270-286
4. Meckbach C, Tacke R, Hua X, Waack S, Wingender E, Gültas M (2015) PC-TraFF: identification of potentially collaborating transcription factors using pointwise mutual information. BMC BIOINFORMATICS 16: 400, doi: 10.1186/s12859-015-0827-2
5. Schmitt-Engel C, Schultheis D, Schwirz J, Ströhlein N, Troelenberg N, Majumdar U, Dao VA, Grossmann D, Richter T, Tech M, Dönitz J, Gerischer L, Theis M, Schild I, Trauner J, Koniszewski NDB, Küster E, Kittelmann S, Hu Y, Lehmann S, Siemanowski J, Ulrich J, Panfilio KA, Schröder R, Morgenstern B, Stanke M, Buchholz F, Frasch M, Roth S, Wimmer EA, Schoppmeier M, Klingler M, Bucher G (2015) The iBeetle large-scale RNAi screen reveals gene functions for insect development and physiology. NAT COMMUN 6: 7822, doi: 10.1038/ncomms8822
6. Wingender E, Schoeps T, Haubrock M, Dönitz J (2015) TFClass: a classification of human transcription factors and their rodent orthologs. NUCLEIC ACIDS RES 43(Database issue): D97-102, doi: 10.1093/nar/gku1064

Naturwiss. u.a. nichtmed. Diss.

Bhar A, Dr. rer. nat. (2015) Application of a novel triclustering method in analyzing three dimensional transcriptomics data. Dissertation Universität Göttingen.