EUROPEAN MEDICINES AGENCY
SCIENCE MEDICINES HEALTH

Curriculum Vitae

Personal information

Elisabeth Wischnitzki

Work experience

1. Employer: AGES _ Austrian Agency for Health and Food Safety
    - Start date: 102017
    - End date:
    - Position: Clinical Assessor
    - Activities:
    - Country: Austria
2. Employer: AIT Austrian Istitute of Technology
    - Start date: 122012
    - End date: 102016
    - Position: Research Engineer
    - Activities: De novo transcriptome assembly, comparative transcriptomics and epigenetics, marker development, software development and database design
    - Country: Austria
3. Employer: VIB/Ghent University
    - Start date: 092007
    - End date: 102011
    - Position: PhD Student
    - Activities: Algorithm development, expression and sequence data analysis, statistical evaluation of evolutionary conservation
    - Country: Belgium
4. Employer: Max_Planck_Institute for plant breeding research
    - Start date: 122006
    - End date: 072007
    - Position: Research Assistant
    - Activities: Establishing of software pipeline and data analysis
    - Country: Germany
5. Employer: Helmholtz Institute
    - Start date: 082004
    - End date: 072006
    - Position: Student Assistant
    - Activities: Data Analysis, Software Development
    - Country: Germany

Education and training

1. Subject: Ghent University
    - Start date: 092007
    - End date: 082012
    - Qualification: Phd student in Biotechnology
    - Organisation:
    - Country: Belgium
2. Subject: Ludwig_Maximilians_University and Technical University Munich
    - Start date: 092001
    - End date: 092006
    - Qualification: Diploma in Bioinformatics
    - Organisation:
    - Country: Germany
3. Subject: University Graz
    - Start date: 032017
    - End date: 092017
    - Qualification: Project Management Cerficicate IPMA
    - Organisation: Project Management
    - Country: Austria

Additional information

Publications

Busconi M, Wischnitzki E, Del Corvo M, Colli L, Soffritti G, Stagnati L, Fluch S, Sehr EM, de los Mozos Pascual M, Fernández JA Epigenetic Variability Among Saffron Crocus (Crocus sativus L.) Accessions Characterized by Different Phenotypes Frontiers in Plant Science 12, 349

Hitzenhammer E, Büschl C, Sulyok M, Schuhmacher R, Kluger B, Wischnitzki E, Schmoll M. 2019. YPR2 is a regulator of light modulated carbon and secondary metabolism in Trichoderma reesei. BMC Genomics 20 (1), 211

Madritsch S, Wischnitzki E, Kotrade P, Ashoub A, Burg A, Fluch S, Brüggemann W, Sehr EM. 2019. Elucidating drought stress tolerance in European oaks through cross_species transcriptomics. G3: Genes, Genomes, Genetics 9 (10), 3181_3199

Kotrade P, Sehr EM, Wischnitzki E, Brüggemann W. 2019. Comparative transcriptomics_based selection of suitable reference genes for normalization of RT_qPCR experiments in drought_stressed leaves of three European Quercus species. Tree Genetics & Genomes 15 (3), 38

Hamali B, Pichler S, Wischnitzki E, Schicker K, Burger M, Holy M, Jaentsch K, Molin M, Sehr EM, Kudlacek O, Freissmuth M. 2018. Identification and characterization of the Fasciola hepatica sodium_and chloride_dependent taurine transporter. PLoS neglected tropical diseases 12 (4), e0006428

Trujillo_Moya C, George JP, Fluch S, Geburek T, Grabner M, Karanitsch_Ackerl S, Konrad H, Mayer K, Sehr EM, Wischnitzki E, Schueler S. 2018. Drought Sensitivity of Norway Spruce at the Species' Warmest Fringe: Quantitative and Molecular Analysis Reveals High Genetic Variation Among and Within Provenances. G3: Genes, Genomes, Genetics, g3. 300524.

Ganthaler A., Stöggl W., Mayr S., Kranner I., Schüler S., Wischnitzki E., Sehr EM., Fluch S., Trujillo_ Moya C.. 2017. Association genetics of phenolic needle compounds in Norway spruce with variable susceptibility to needle bladder rust. Plant Mol Biol. 2017 Jun;94(3):229_251.

Busconi M, Colli L, Soffritti G, Del Corvo M, Fluch S, Wischnitzki E, Sehr EM, de los Mozos Pascual M, Fernandez JA. 2017. Epigenetic variability among saffron crocus (Crocus sativus L.) accessions characterized by different phenotypes. JOURNAL OF INTEGRATED OMICS 7 (2), 32_32

Wischnitzki E., Burg K., Berenyi M., Sehr EM. 2016. Selecting hypomethylated genomic regions using MRE_seq. Methods in Molecular Biology (2016), Plant Synthetic Promoters,Springer Nature

Wischnitzki, E., Sehr, E.M., Hansel_Hohl, K., Berenyi, M., Burg, K., and Fluch, S. (2015). How to Isolate a Plant’s Hypomethylome in One Shot. BioMed Res. Int. 2015, 570568.

Hackl E., Pacher_Zavisin M., Sedman L., Arthaber S., Bernkopf U., Brader G., Gorfer M., Mitter B., Mitropoulou A., Schmoll M., Van Hoesel W., Wischnitzky E., Sessitsch A. 2015. Literature search and data collection on RA for human health for microorganisms used as plant protection products. EFSA European Food Safety Authority, external scientific report.

Van Bel M, Proost S., Wischnitzki E., Mohavedi S., Scheerlinck C., Van de Peer Y., Vandepoele K. 2011. Dissecting green plant genomes using the PLAZA 2.5 platform for comparative genomics. Plant Physiology 158, 590_600.

Shu Q.Y., Wischnitzki E., Liu Z.A., Ren H.X., Han X.Y., Hao Q., Gao F.F., Xu S.X., Wang L.S. 2009. Functional annotation of expressed sequence tags as a tool to understand the molecular mechanism controlling flower bud development in tree peony. Physiologia Plantarum 135, 436_449.

Jakoby M.J., Falkenhan D., Mader M.T., Brininstool G., Wischnitzki E., Platz N., Hudson A., Hülskamp, M., Larkin J., Schnittger A. 2008. Transcriptional profiling of mature Arabidopsis trichomes reveals that NOECK encodes the MIXTA_like transcriptional regulator MYB106. Plant Physiology 148, 1583_ 602.

Grunewald W., Karimi M., Wieczorek K., Van de Cappelle E., Wischnitzki E., Grundler F., Inzé D., Beeckman T., Gheysen G. 2008. A role for AtWRKY23 in feeding site establishment of plant_parasitic nematodes. Plant Physiology 148, 358_68

Projects

Memberships

Other Relevant Information