

CURRICULUM VITAE
GERHARD G. THALLINGER

- Present Address** Computational Biotechnology and Bioinformatics Group
Institute of Molecular Biotechnology
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e-mail: Gerhard.Thallinger@tugraz.at
URL: <http://genome.tugraz.at>
- Personal Data** Date of birth: November 9, 1963
Place of birth: Graz, Austria
Nationality: Austria
- Research Activities** Method development and application for the analysis of data from high-throughput technologies with a special focus on next generation sequencing and mass spectrometry. Integrative analysis of multi-omics data sets.
- University Education**
- 04/2007 PhD thesis defense passed *summa cum laude*.
- 07/2002 – 04/2007 PhD student at the Institute for Genomics and Bioinformatics, Graz University of Technology, Austria, with the thesis topic “Data management and analysis for biomolecular arrays”.
- 03/1991 – 04/1993 Project assistant at the Institute of Biomedical Engineering, Graz University of Technology, Austria.
- 03/1988 Final exam for “Dipl.-Ing.” (equivalent to combined MSc and BSc).
- 10/1982 – 03/1988 Studies in “Applied Mathematics” with emphasis on Computer Science at Graz University of Technology. Diploma thesis at the Institute of Physical Chemistry, University of Graz, Austria, with the topic “Analyse stochastischer Zeitreihen”.
- Career History**
- 09/2015 – present Principal Investigator, Institute of Molecular Biotechnology, Graz University of Technology, Austria.
- 01/2014 – 08/2015 Principal Investigator Bioinformatics Group, Institute for Knowledge Discovery, Graz University of Technology, Austria.
- 12/2013 – present Deputy Speaker, BioTechMed OMICS Center Graz, Graz, Austria.
- 05/2010 – 12/2013 Principal Investigator and Head of Bioinformatics at the Institute for Genomics and Bioinformatics, Graz University of Technology, Austria.
- 04/2010 – present Key Researcher, Austrian Centre of Industrial Biotechnology.
- 04/2010 – 12/2014 Head of Core Facility Bioinformatics, Austrian Centre of Industrial Biotechnology.
- 05/2007 – 04/2010 Postdoctoral researcher at the Institute for Genomics and Bioinformatics, Graz University of Technology, Austria. Development of applications for the analysis of data from high-throughput wet-lab technologies with a special focus on mass spectrometry and next generation sequencing.

07/2002 – 04/2007	Research associate at the Institute for Genomics and Bioinformatics, Graz University of Technology, Austria. Management of industrial and basic research projects (e.g., “Bioinformatik Integrations-Netzwerk” of the Austrian Genome Research Programme GEN-AU). Design of applications for data management and analysis in bioinformatics.
05/2000 – 06/2002	Head of application design, Materna Information & Communications, Graz. Design of applications for mobile communication providers.
10/1999 – 04/2000	CIO, Grazer Stadtwerke AG, Graz. IT organization, establishment of a Profit Center structure in the IT department.
08/1994 – 07/1999	Head of software development, Vexcel Imaging GmbH, Graz. Development of imaging solutions for the graphical industry and applications in photogrammetry.
07/1993 – 07/1994	Head of application development, Grips Electronic GmbH, Graz. Development of data collection and security systems for casinos.
03/1991 – 04/1993	Project-assistant at the Institute of Biomedical Engineering, Graz University of Technology, Austria. Project: “Development of an expert system for diagnosis support in a neurosurgical clinic”.
10/1990 – 02/1991	Military service, Belgierkaserne Graz, corpsman training
12/1987 – 02/1991	Head of software development PEEM Förderanlagen GmbH, Graz. Design of logistics applications for wholesalers of pharmaceuticals (from 10/1990 on as a consultant).
08/1983 – 11/1987	Freelance programmer, Grips Electronic GmbH, Graz. Development of data collection and security systems for casinos.

Research Grants Received (5 most important)

11/2013 – 12/2018	Research Grant from the Ministry of Science and Research (HSRSM call): “OMICS Center Graz” (Co-PI).	€ 208.000,--
07/2013 – 12/2016	Research Grant P26148 from the FWF: “High-Throughput Identification of Lipid Molecular Species in LC-MS/MS Data” (PI).	€ 214.000,--
03/2011 – 02/2014	Research Grant P22737 from the FWF: “Genomic sequencing of two Lake Tanganyika cichlid fish” (Co-PI).	€ 110.000,--
01/2010 – 12/2014	Research Grant 824186 from FFG Comet-K2: “Austrian Centre of Industrial Biotechnology” (as Head of Core Facility Bioinformatics)	€1.070.000,--
05/2008 – 04/2013	Research Grant KBBE-2007-212281 from the European Union 7th FP: “OXYGREEN Effective redesign of oxidative enzymes for green chemistry” (Co-PI).	€ 80.000,--

Service to the Scientific Community (5 most important)

Invited reviewer for Bioinformatics (Oxford), BMC Bioinformatics, BMC Genomics, Briefings in Bioinformatics, Database (Oxford), and Journal of Proteome Research.

Invitations to Present at Academic Conferences

9/08/2015 – 9/12/2015	Genomic sequencing of two members of the eco-morphologically diverse cichlid tribe Tropheini. Cichlid Science 2016, 108 th Ann. Meeting of the German Zoological Society. Graz, Germany.
11/27/2014	Integrative Analysis of <i>Arabidopsis thaliana</i> and <i>Anopheles gambiae</i> OMICS data, Integrative Data Analysis Symposium: Methods and Applications 2014, Graz, Austria
9/21/2012 – 9/24/2012	Genomic sequencing of two members of the eco-morphologically diverse cichlid tribe Tropheini. 105 th Ann. Meeting of the German Zoological Society. Konstanz, Germany.

Student Supervision

4 PostDocs, 5 PhD students (3 completed), 19 Diploma students (16 completed)

Key International Cooperation Partners (past 5 years)

Christopher J. Baker	Dept of Computer Science and Applied Statistics, University of New Brunswick, Saint John, NB, Canada
Aedin C. Culhane	Dept of Biostatistics, Harvard University, Boston, USA
Rhoel R. Dinglasan	Dept of Mol. Microbiology & Immunology, Johns Hopkins University, Baltimore, USA
David R. Graham	Dept of Mol. & Comp. Pathobiology, Johns Hopkins University, Baltimore, USA
Henning Hermjakob	Proteomics Services Team, European Bioinformatics Institute, Hinxton, UK
Ramsay J. McFarlane	North West Cancer Research Institute, Bangor University, Bangor, UK
Richard Sparling	Dept of Microbiology, University of Manitoba, Winnipeg, Manitoba, Canada
Michael Wakelam	Brabraham Institute, Cambridge, UK
Barry R. Zeeberg	Genomics and Bioinformatics Group, National Cancer Institute, NIH, Bethesda, USA

Patent applications

Hartler J, **Thallinger GG**. Analysis of Analytes by Mass Spectrometry with Values in at least 3 Dimensions. EP10171450[WO/2012/013667]. 2010. *European Patent Office*. 30-7-2010.

Hartler J, **Thallinger GG**. Automated structural identification of metabolites by a generic spectra description language utilizing MSn spectra. EP20140185566. 2014. *European Patent Office*. 19-09-2014.

Publications (10 most important)

Ulz P, **Thallinger GG**, Auer M, Graf R, Kashofer K, Jahn SW, Abete L, Pristauz G, Petru E, Geigl JB, Heitzer E, Speicher MR. Inferring expressed genes by whole-genome sequencing of plasma DNA. *Nature Genetics* 2016, in press.

Zeleznik OA, **Thallinger GG**, Platig J, Culhane AC: Topological pathway enrichment analysis of gene expression in high grade serous ovarian cancer reveals tumor-stoma cross-talk. *Research Perspectives CRM Barcelona, Fall 2015*, Trends in Mathematics 2016. Springer-Birkhäuser, Basel, in press.

Meng C*, Zeleznik OA*, **Thallinger GG**, Kuster B, Gholami AM, Culhane AC: Dimension reduction techniques for the integrative analysis of multi-omics data. *Brief Bioinform* 2016, 17(4):628-41, DOI:10.1093/bib/bbv108.

Näätsaari L, Krainer FW, Schubert M, Glieder A, **Thallinger GG**. Peroxidase gene discovery from the horseradish transcriptome. *BMC Genomics* 2014, 15:227, DOI:10.1186/1471-2164-15-227.

Tomescu OA, Mattanovich D, **Thallinger GG**. Integrative omics analysis. A study based on *Plasmodium falciparum* mRNA and protein data. *BMC Syst Biol* 2014, 8 Suppl 2:S4, DOI:10.1186/1752-0509-8-S2-S4.

Klymiuk I, Högenauer C, Halwachs B, **Thallinger GG**, Fricke WF, Steininger C. A physicians' wish list for the clinical application of intestinal metagenomics. *PLoS Med* 2014, 11(4):e1001627, DOI:10.1371/journal.pmed.1001627.

Fischer C, Koblmüller S, Gully C, Schlötterer C, Sturmbauer C, **Thallinger GG**. Complete Mitochondrial DNA Sequences of the Threadfin Cichlid (*Petrochromis trewavasae*) and the Blunthead Cichlid (*Tropheus moorii*) and Patterns of Mitochondrial Genome Evolution in Cichlid Fishes. *PLoS ONE* 2013, 8(6):e67048, DOI:10.1371/journal.pone.0067048.

Gorkiewicz G*, **Thallinger GG***, Trajanoski S, Lackner S, Stocker G, Hinterleitner T, Gully C, Högenauer C. Alterations in the colonic microbiota in response to osmotic diarrhea. *PLoS ONE* 2013, 8(2):e55817, DOI:10.1371/journal.pone.0055817.

Braun A, Halwachs B, Geier M, Weinhandl K, Guggemos M, Marienhagen J, Ruff AJ, Schwaneberg U, Rabin V, Torres Pazmino DE, **Thallinger GG***, Glieder A. MuteinDB: the mutein database linking substrates, products and enzymatic reactions directly with genetic variants of enzymes. *Database (Oxford)* 2012, 2012:bas028, DOI:10.1093/database/bas028.

Hartler J, Trötz Müller M, Chitraju C, Spener F, Köfeler HC, **Thallinger GG**. Lipid Data Analyzer: Unattended Identification and Quantitation of Lipids in LC-MS Data. *Bioinformatics* 2011, 27(4):572-577, DOI:10.1093/bioinformatics/btq699.

Publications (last 6 years)

- Ulz P, **Thallinger GG**, Auer M, Graf R, Kashofer K, Jahn SW, Abete L, Pristauz G, Petru E, Geigl JB, Heitzer E, Speicher MR. Inferring expressed genes by whole-genome sequencing of plasma DNA. *Nature Genetics* 2016, in press.
- Zeleznik OA, **Thallinger GG**, Platig J, Culhane AC: Topological pathway enrichment analysis of gene expression in high grade serous ovarian cancer reveals tumor-stoma cross-talk. *Research Perspectives CRM Barcelona, Fall 2015*, Trends in Mathematics 2016. Springer-Birkhäuser, Basel, in press.
- Minoska Valli M, Tatto NE, Peymann A, Gruber C, Landes N, Ekker H, **Thallinger GG**, Mattanovich D, Gasser B, Graf AB. Curation of the genome annotation of *Pichia pastoris* (*Komagataella phaffii*) CBS7435 from gene level to protein function. *FEMS Yeast Research* 2016, in press, DOI:10.1093/femsyr/fow051.
- Krause R, Halwachs B, **Thallinger GG**, Klymiuk I, Gorkiewicz G, Hoenigl M, Prattes J, Valentin T, Heidrich K, Buzina W, Salzer HJ, Rabensteiner J, Prüller F, Raggam RB, Meinitzer A, Moissl-Eichinger C, Högenauer C, Quehenberger F, Kashofer K, Zollner-Schwetz I. Characterisation of *Candida* within the Mycobiome/Microbiome of the Lower Respiratory Tract of ICU Patients. *PLoS ONE* 2016;11(5):e0155033, DOI:10.1371/journal.pone.0155033.
- Gomez-Escobar N*, Almobadel N*, Alzahrani O*, Feichtinger J*, Planells-Palop V, Alshehri Z, **Thallinger GG**, Wakeman JA, McFarlane RJ: Translin and Trax differentially regulate telomere-associated transcript homeostasis. *Oncotarget* 2016, 17(23): 33809-33820, DOI:10.18632/oncotarget.9278
- Feichtinger J*, Hernández I*, Fischer C*, Hanscho M, Auer N, Hackl M, Jadhav V, Baumann M, Krempl PM, Schmidl C, Farlik M, Schuster M, Merkel M, Sommer A, Heath S, Rico D, Bock C, **Thallinger GG**, Borth N. Comprehensive genome and epigenome characterization of CHO cells in response to evolutionary pressures and over time. *Biotechnol Bioeng* 2016, in press, DOI:10.1002/bit.25990
- Meng C*, Zeleznik OA*, **Thallinger GG**, Kuster B, Gholami AM, Culhane AC: Dimension reduction techniques for the integrative analysis of multi-omics data. *Brief Bioinform* 2016, 17(4):628-41, DOI:10.1093/bib/bbv108.
- Vogl T, Sturmberger L, Kickenweiz T, Wasmayer R, Schmid C, Hatzl AM, Gerstmann MA, Pitzer J, Wagner M, **Thallinger GG**, Geier M, Glieder A: A Toolbox of Diverse Promoters Related to Methanol Utilization: Functionally Verified Parts for Heterologous Pathway Expression in *Pichia pastoris*. *ACS Synth Biol* 2016, 5(2):172-86, DOI:10.1021/acssynbio.5b00199.
- Eichmann TO, Grumet L, Taschler U, Hartler J, Heier C, Woblistin A, Pajed L, Kollroser M, Rechberger G, **Thallinger GG**, Zechner R, Haemmerle G, Zimmermann R, Lass A. Adipose triglyceride lipase and comparative gene identification-58 are lipid droplet proteins of the hepatic stellate cell-line HSC-T6. *J Lipid Res* 2015, 56(10):1972-1984, DOI:10.1194/jlr.M062372.
- Troppan K, Wenzl K, Pichler M, Pursche B, Schwarzenbacher D, Feichtinger J, **Thallinger GG**, Beham-Schmid C, Neumeister P, Deutsch A. miR-199a and miR-497 Are Associated with Better Overall Survival due to Increased Chemosensitivity in Diffuse Large B-Cell Lymphoma Patients. *Int J Mol Sci* 2015. 16(8):18077-18095, DOI:10.3390/ijms160818077.
- Linke R, **Thallinger GG**, Haarmann T, Eidner J, Schreiter M, Lorenz P, Seiboth B, Kubicek CP. Restoration of female fertility in *Trichoderma reesei* QM6a provides the basis for inbreeding in this industrial cellulase producing fungus. *Biotechnol Biofuels* 2015, 8:155, DOI:10.1186/s13068-015-0311-2.
- Hartler J, Köfeler HC, Trötz Müller M, **Thallinger GG**, Spener F. Assessment of lipidomic species in hepatocyte lipid droplets from stressed mouse models. *Sci Data* 2014, 1:140051, DOI:10.1038/sdata.2014.51.
- Kluger B, Bueschl C, Neumann N, Stückler R, Doppler M, Chassy AW, Waterhouse AL, Rechthaler J, Kamleitner N, **Thallinger GG**, Adam G, Krska R, Schuhmacher R. Untargeted profiling of tracer-derived metabolites using stable isotopic labeling and fast polarity-switching LC-ESI-HRMS. *Anal Chem* 2014, 86(23):11533-11537, DOI:10.1021/ac503290j.
- Mairhofer J, Krempl PM, **Thallinger GG**, Striedner G. Finished Genome Sequence of *Escherichia coli* K-12 Strain HMS174 (ATCC 47011). *Genome Announc* 2014, 2(6):e00975-14, DOI:10.1128/genomeA.00975-14.
- Krempl PM, Mairhofer J, Striedner G, **Thallinger GG**. Finished Genome Sequence of the Laboratory Strain *Escherichia coli* K-12 RV308 (ATCC 31608). *Genome Announc* 2014, 2(6):e00971-14, DOI:10.1128/genomeA.00971-14.

- Bragina A, Oberauner-Wappis L, Zachow C, Halwachs B, **Thallinger GG**, Müller H, Berg G. The Sphagnum microbiome supports bog ecosystem functioning under extreme conditions. *Mol Ecol* 2014, 23(18):4498-4510, DOI:10.1111/mec.12885.
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- Alavi P, Starcher MR, **Thallinger GG**, Zachow C, Müller H, Berg G. Stenotrophomonas comparative genomics reveals genes and functions that differentiate beneficial and pathogenic bacteria. *BMC Genomics* 2014, 15:482, DOI:10.1186/1471-2164-15-482.
- Näätsaari L, Krainer FW, Schubert M, Glieder A, **Thallinger GG**. Peroxidase gene discovery from the horseradish transcriptome. *BMC Genomics* 2014, 15:227, DOI:10.1186/1471-2164-15-227.
- Tomescu OA, Mattanovich D, **Thallinger GG**. Integrative omics analysis. A study based on *Plasmodium falciparum* mRNA and protein data. *BMC Syst Biol* 2014, 8 Suppl 2:S4, DOI:10.1186/1752-0509-8-S2-S4.
- Klymiuk I, Högenauer C, Halwachs B, **Thallinger GG**, Fricke WF, Steininger C. A physicians' wish list for the clinical application of intestinal metagenomics. *PLoS Med* 2014, 11(4):e1001627, DOI:10.1371/journal.pmed.1001627.
- Deutsch AJ, Rinner B, Wenzl K, Pichler M, Troppan K, Steinbauer E, Schwarzenbacher D, Reitter S, Feichtinger J, Tierling S, Prokesch A, Scheideler M, Krogsdam A, **Thallinger GG**, Schaidler H, Beham-Schmid C, Neumeister P. NR4A1-mediated apoptosis suppresses lymphomagenesis and is associated with a favorable cancer-specific survival in patients with aggressive B-cell lymphomas. *Blood* 2014, 123(15):2367-2377, DOI:10.1182/blood-2013-08-518878.
- Vogl T, **Thallinger GG**, Zellnig G, Drew D, Cregg JM, Glieder A, Freigassner M. Towards improved membrane protein production in *Pichia pastoris*: general and specific transcriptional response to membrane protein overexpression. *N Biotechnol* 2014, 31(6):538-552, DOI:10.1016/j.nbt.2014.02.009.
- El-Heliebi A, Kroneis T, Wagner K, Meditz K, Kolb D, Feichtinger J, **Thallinger GG**, Quehenberger F, Liegl-Atzwanger B, Rinner B. Resolving tumor heterogeneity: genes involved in chordoma cell development identified by low-template analysis of morphologically distinct cells. *PLoS ONE* 2014, 9(2):e87663, DOI:10.1371/journal.pone.0087663.
- Kienesberger S, Sprenger H, Wolfgruber S, Halwachs B, **Thallinger GG**, Perez-Perez GI, Blaser MJ, Zechner EL, Gorkiewicz G. Comparative genome analysis of *Campylobacter fetus* subspecies revealed horizontally acquired genetic elements important for virulence and niche specificity. *PLoS ONE* 2014, 9(1):e85491, DOI:10.1371/journal.pone.0085491.
- Bueschl C, Kluger B, Lemmens M, Adam G, Wiesenberger G, Maschietto V, Marocco A, Strauss J, Bodi S, **Thallinger GG**, Krska R, Schuhmacher R. A novel stable isotope labelling assisted workflow for improved untargeted LC-HRMS based metabolomics research. *Metabolomics* 2014, 10(4):754-769, DOI:10.1007/s11306-013-0611-0.
- Fischer C, Koblmüller S, Gully C, Schlötterer C, Sturmbauer C, **Thallinger GG**. Complete mitochondrial DNA sequences of the threadfin cichlid (*Petrochromis trewavasae*) and the blunthead cichlid (*Tropheus moorii*) and patterns of mitochondrial genome evolution in cichlid fishes. *PLoS ONE* 2013, 8(6):e67048
- Chitraju C, Trötz Müller M, Hartler J, Wolinski H, **Thallinger GG**, Haemmerle G, Zechner R, Zimmermann R, Köfeler HC, Spener F. The impact of genetic stress by ATGL deficiency on the lipidome of lipid droplets from murine hepatocytes. *J Lipid Res.* 2013, 54(8):2185-2194
- Gorkiewicz G*, **Thallinger GG***, Trajanoski S, Lackner S, Stocker G, Hinterleitner T, Gully C, Högenauer C. Alterations in the colonic microbiota in response to osmotic diarrhea. *PLoS ONE* 2013, 8(2):e55817

- Patz S, Trattng C, Grünbacher G, Ebner B, Gully C, Novak A, Rinner B, Leitinger G, Absenger M, Tomescu OA, **Thallinger GG**, Fasching U, Wissa SM, Archelos-Garcia JJ, Schaefer U. More than cell dust: microparticles isolated from cerebrospinal fluid of brain injured patients are messengers carrying mRNAs, miRNAs and proteins. *J Neurotrauma*. 2013. 30(14):1232-1242
- Müller H, Zachow C, Alavi M, Tilcher R, Krempl PM, **Thallinger GG**, Berg G. Complete Genome Sequence of the Sugar Beet Endophyte *Pseudomonas poae* RE*1-1-14: a Disease-Suppressive Bacterium. *Genome Announcements*. 2013. 1(2):e00020-13
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- Hartler J, Tharakan R, Köfeler HC, Graham DR, **Thallinger GG**. Bioinformatics tools and challenges in structural analysis of lipidomics MS/MS data. *Briefings in Bioinformatics*. 2013. 14(3):375-390.
- Chitraju C, Trötz Müller M, Hartler J, Wolinski H, **Thallinger GG**, Lass A, Zechner R, Zimmermann R, Köfeler HC, Spener F. Lipidomic analysis of lipid droplets from murine hepatocytes reveals distinct signatures for nutritional stress. *Journal of Lipid Research*. 2012. 53(10):2141-52.
- Krempl PM, Mairhofer J, Striedner G, **Thallinger GG**. A Sequence Comparison and Gene Expression Data Integration Add-on for the Pathway Tools Software. *Bioinformatics*. 2012. 28(17):2283-2284.
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- Halwachs B, Gorkiewicz G, **Thallinger GG**. High-Throughput Characterization and Comparison of Microbial Communities. In: *Trajanoski Z (editor) Computational Medicine*. Springer Wien. 2012. 37-58
- Feichtinger J, **Thallinger,GG**, McFarlane RJ, Larcombe L. Microarray Meta-Analysis: From Data to Expression to Biological Relationships. In: *Trajanoski Z (editor) Computational Medicine*. Springer Wien. 2012. 59-78.
- Hartler J, Köfeler HC, Baker CJO, Tharakan R, **Thallinger GG**. Lipidomics, Mass Spectrometry and Bioinformatics. In: *Trajanoski Z (editor) Computational Medicine*. Springer Wien. 2012. 93-109.
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- Hofer E, Laschober GT, Hackl M, **Thallinger GG**, Lepperdinger G, Grillari J, Jansen-Durr P, Trajanoski Z. GiSAO.db: a database for ageing research. *BMC Genomics*. 2011. 12(1):262
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